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OR-001

An update on the International Society for Laboratory Hematology Guidelines Inventory Initiative: Evidence for Increasing Use by the Global Community

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Objective The International Society for Laboratory Hematology (ISLH) is committed to being a leader in the provision of hematology laboratory education for the international community. In support of this, numerous initiatives have been undertaken to include: webinars, inter-active case studies, e-learning courses and networking and collaboration opportunities. Another resource to support clinical laboratories are laboratory guidelines, with the primary goal being to improve patient care. Numerous international organizations have published laboratory guidelines and consensus recommendations. Laboratory professionals are often challenged to keep abreast of new and/or updated publications. In 2015, ISLH published an inventory of publically listed guidelines that are available to clinical hematology laboratories and laboratory management. To continue to provide the hematology community accessible, relevant and current guideline listing, ISLH built an on-line guideline inventory, posted on the Society website, to encourage international awareness and uptake of guideline recommendations and current, high quality, evidence-based practices across a breadth of hematology laboratory areas with links to free access articles or to the PubMed citation. Another goal of this initiative was to identify gaps in available guidelines that would be of benefit to clinical hematology laboratories. Our goal was to provide an update on the ISLH on-line guideline inventory initiative since 2015.

Methods Various search strategies are used to identify relevant publications to keep the inventory current. Searches are performed at regular intervals in PubMed and include search words such as: hematology; laboratory; guidelines; consensus; coagulation; flow cytometry; hemoglobinopathy. Peer reviewed journal alerts continue to be monitored for relevant publications. Due to the limitation of employed search strategies and to ensure an international pool of guidelines, ISLH members are also encouraged to email our Society with information on new guidelines and best-practice publications from their country or other regions/organizations.

Results The ISLH guideline inventory webpage went live in December 2013 (SPLTrak, Glenview, IL) on the website (www.islh.org). The content is currently organized into eight categories (shown with number of items for that category, posted as of January 2019): Preanalytical (1); Hematopathology (1); Coagulation (10); Hemoglobinopathy and other red cell disorders (3); Cellular analysis, including peripheral blood, bone marrow and body fluid analysis (6); Flow Cytometry (6); Post-analytical (1); and Guidelines not restricted to laboratory testing (8). There are also direct links to guideline papers that are free access through the websites of the International Council for Standardization in Haematology (ICSH) and the British Society for Haematology (BSH). The 36 posted guidelines currently span the publication years 2011 to 2018. Since 2015, when the original inventory was published, there has been increasing numbers of visits to the website guideline page on the ISLH website, with

the following number of visits over the last 3 years: 2016: 2400 visits; 2017: 4500 visits; and 2018: 8000 visits.

Conclusions ISLH continues to provide a web-based listing of guidelines and best practice recommendation documents. The increasing traffic to this content on the ISLH website verifies that this listing represents an important resource that supports the international laboratory hematology community.

OR-002

The role of the LncRNA-FA2H-2-MLKL pathway in atherosclerosis by regulation of autophagy flux and inflammation through mTOR-dependent signaling

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Objective Atherosclerosis is a progressive, chronic inflammation in arterial walls. Long noncoding RNAs (lncRNAs) participate in inflammation, but the exact mechanism in atherosclerosis is unclear.

Methods Our microarray analyses revealed that the levels of lncRNA-FA2H-2 were significantly decreased by oxidized low-density lipoprotein (OX-LDL). Bioinformatics analyses indicated that mixed lineage kinase domain-like protein (MLKL) might be regulated by lncRNA-FA2H-2. In vitro experiments showed that lncRNA-FA2H-2 interacted with the promoter of the MLKL gene, downregulated MLKL expression, and the binding sites between -750 and 471 were necessary for lncRNA-FA2H-2 responsiveness to MLKL.

Results Silencing lncRNA-FA2H-2 and overexpression of MLKL could activate inflammation and inhibited autophagy flux. Both lncRNA-FA2H-2 knockdown and overexpression of MLKL could significantly aggravate inflammatory responses induced by OX-LDL. We found that the 3-methyladenine (3-MA) and Atg7-shRNA enhanced inflammatory responses induced by knockdown of lncRNA-FA2H-2 and overexpression of MLKL. We demonstrated that the effects of MLKL on autophagy might be associated with a mechanistic target of rapamycin (mTOR)-dependent signaling pathways. In vivo experiments with apoE knockout mice fed a western diet demonstrated that LncRNA-FA2H-2 knockdown decreased microtubule- associated expression of microtubule-associated protein 1 light chain 3 II and lysosome-associated membrane protein 1, but increased expression of sequestosome 1 (p62), MLKL, vascular cell adhesion molecule-1, monocyte chemoattractant protein-1, and interleukin-6 in atherosclerotic lesions.

Conclusions Our findings indicated that the lncRNA-FA2H-2-MLKL pathway is essential for regulation of autophagy and inflammation, and suggested that lncRNA-FA2H-2 and MLKL could act as potential therapeutic targets to ameliorate atherosclerosis-related diseases.

OR-003

Colon cancer cell-derived colony stimulating factor 1 involves in the interaction between cancer cells and tumor-infiltrated macrophages

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Objective Colorectal cancer ranks top three of the most commonly diagnosed cancer and cancer-related death worldwide, and the recurrence and mortality of colon cancer remain largely uncontrolled. Immune cells, especially macrophages, are highly represented in the colorectal cancer microenvironment and profoundly associated with the outcome of patients. Colony stimulating factor 1 (CSF1) is a primary chemoattractant and functional regulator for macrophages, and therefore would be a feasible intervention for the macrophage-targeting therapeutics. However, the expression of CSF1 in colon cancer microenvironment and its roles in cancer development is largely unknown.

Methods Immunohistochemistry staining was used to analyze the expression of CSF1 and CD68 (a marker of macrophages) and their association with prognosis and clinicopathological parameters of colon cancer patients. An indirect co-culture system between colon cancer cells and macrophages was formed using transwell chamber. qRT-PCR, ELISA and immunofluorescence were used to analyze the effect of co-cultivation with macrophages on CSF1 expression of colon cancer cells. qRT-PCR, ELISA and Western blotting were used to determine the effects of macrophage-derived IL-8 on CSF1 expression of colon cancer cells and its relevant signaling pathway. Transwell assay and qRT-PCR was performed to analyze the effects of colon cancer-derived CSF1 on recruitment and secretion of macrophages. Finally, A CSF1-overexpressed colon cancer xenograft model was established in nude mice to analyze the effects of cancer-derived CSF1 on development of colon cancer and infiltration of macrophages.

Results The expression of CSF1 was significantly higher in colon cancer tissue compared with peritumoral tissue or normal tissue. Significantly higher numbers of $CD68^+$ cells were observed in both intratumoral and peritumoral stroma compared with normal colon mucosa. High expression of CSF1 and CD68 was associated with TNM stage, and was an independent prognostic factor. The *in vitro* study showed that indirect co-cultivation with THP-1-derived macrophages promoted CSF1 expression in colon cancer cells. In turn, colon cancer cell-derived CSF1 promoted macrophages recruitment to colon cancer and regulated their secretion profile. Macrophages produced high level of IL-8 compared with colon cancer cells. Macrophage-derived IL-8 promoted CSF1 expression and activation of PKC signaling pathway in colon cancer cells. The activation of PKC pathway enhanced CSF1 expression. In the in vivo studies, CSF1 over-expression in colon xenograft tumor promoted macrophages infiltration and partially suppresses tumor growth.

Conclusions Our study analyzed the expression pattern of CSF1 in colon cancer tissue and the roles of over-expressed CSF1 microenvironment in the development of colon cancer. In addition, we demonstrated for the first time that CSF1 played crucial roles in the interactions between colon cancer cells and macrophages, and preliminarily explored the relevant mechanisms. The above results suggested that strategies

targeting CSF1 might synchronously affect two primary components in tumor tissue: cancer cells and tumor-infiltrated macrophages. This study might provide innovative strategies for the treatment of colon cancer.

OR-004

Establishing and validating of an LIS-based auto-verification system for biochemical test results in cancer patients

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Objective To establish and validate an LIS-based auto-verification (AV) system by using large amounts of biochemical test results in cancer patient.

Methods An algorithm of the AV process was designed for pre-analysis, analysis and post-analysis. The limit range check were adjusted 3 times, first by using conservative reference range, and then using 95% confidence interval for each test item from the historical results in 2016, and finally adjusted by 3 technicians and 3 clinicians according to the individual cancer patients. The delta check were first replaced by the same patients' historical extremum and the critical value check and consistency check were also selected for the AV process. AV rules of 51 biochemical test items were tested by using data of 121,123 samples (6,177,273 tests) in 2016 that were manually reviewed through the simulative i-Vertification software of Roche. The improved and optimal AV rules were programed into our LIS and validated by using 140,113 clinical specimens in 2018.

Results The AV passing rate for samples tested in our laboratory increased from 15.57% to the current overall passing rate of 49.70%. The passing rate of each item for rule 3 was between 71.16% and 99.91%. Different cancer groups had different passing rate , while the disease group of liver, gallbladder and pancreas always had the lowest passing rate.

The verified rule 3 showed a passing rate of 58.46% when used on 140,113 clinical specimens in 2018, which is consistent with the testing results. A total of 81,910 reports (58.46%) were verified by AV and MV, while 48,783 reports (34.82%) were not verified and required re-evaluation or dilution. 9,420 reports (6.72%) were not verified by AV but could be verified by MV, while there were no reports that were verified by AV but not by MV. Therefore, the probability of releasing false results is none when the passing rate is increased.

The TAT of 14,505 laboratory samples of March 2018 was compared with the same period last year (March 2017, n = 10,978) by different time period. The TAT decreased with increase in sample size. During the peak detection periods (8 a.m. to 2 p.m.) , the TAT was shortened by more than one hour. The time and labor expended by the laboratory staff were unaffected despite the increasing number of samples, as well as the need for manual validation of some samples. Taken together, the ability to auto-verify even a small percentage of the results can increase productivity and save labor.

Conclusions We have firstly established an LIS-based AV system and implemented it in actual clinical care for cancer patients, although our AV passing rate of the rules still need to be improved compared to the commercially available AV software systems. With the development of information technology, report review will become more and more convenient and personalized.

OR-005

Assessment of the Xpert MTB/RIF Ultra assay on rapid diagnosis of extrapulmonary tuberculosis

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Objective To evaluate the diagnostic performance of Xpert MTB/RIF Ultra for EPTB (Extrapulmonary Tuberculosis) patients on different types of extrapulmonary specimens from different anatomic sites.
Methods Patients with suspected EPTB were prospectively included, extrapulmonary specimens were collected and subjected to culture, Xpert and Xpert Ultra assays in accordance with relevant guidelines.
Results A total of 225 cases were included which contained 200 EPTB cases (43 culture-positive EPTB, 157 culture-negative EPTB which were diagnosed based on pathological results and a satisfied response to anti-TB treatment) and 25 non-EPTB cases. Sensitivities of Xpert Ultra and Xpert for culture-positive cases were 83.7% (95%CI, 68.7-92.7) and 67.4% (95% CI, 51.3-80.5) respectively. Specificities of Xpert Ultra and Xpert were 92.0% (95% CI, 72.5-98.6) and 96.0% (95% CI, 77.7-99.8) respectively. The sensitivities of Xpert Ultra, Xpert and culture for 200 EPTB cases were 52.5% (105/200, 95% CI, 45.4-59.6), 34.0% (68/200, 95% CI, 27.6-41.1) and 21.5% (43/200, 95% CI, 16.2-28.0) respectively. By comparison among different types of specimens, Xpert Ultra can detect 78.9% (56/71) of EPTB on fine-needle aspiration (FNA) tissues which was higher than that on pleural fluid (43.7% (45/103), $p<0.05$.
Conclusions Xpert Ultra assay had a higher sensitivity than those of Xpert and culture on extrapulmonary specimens, which could be a promising approach for rapid EPTB diagnosis.

OR-006

CCNB2, TOP2A, and ASPM are potential prognostic markers for hepatocellular carcinoma, as determined by weighted gene coexpression network analysis

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Objective Hepatocellular carcinoma (HCC) is characterized by increased mortality and poor prognosis. We aimed to identify potential prognostic markers by weighted gene

coexpression network analysis (WGCNA), to assist clinical outcome prediction and improve treatment decisions for HCC patients.

Methods Prognosis-related gene modules were first established by WGCNA. Intersection genes of module genes and differentially expressed genes were obtained by Venn diagrams. The Kaplan-Meier overall survival curves and disease-free survival curves of intersection genes were further validated by Gene Expression Profiling Interactive Analysis (GEPIA). The association between prognostic gene expression and clinicopathological features was analyzed by chi-square tests.

Results *CCNB2*, *TOP2A*, and *ASPM* were identified as both prognosis-related module genes and differentially expressed genes. *TOP2A* (HR: 1.7, $p < 0.001$) and *ASPM* (HR: 1.8, $p < 0.001$) exhibited significant difference between the high- and low-expression groups in the overall survival analysis, while *CCNB2* expression (HR: 1.4, $p = 0.052$) was not statistically significant. However, *CCNB2* (HR: 1.5, $p = 0.006$), *TOP2A* (HR: 1.7, $p < 0.001$), and *ASPM* (HR: 1.6, $p = 0.003$) were all statistically significant in the disease-free survival analysis. All three genes were significantly associated with race and fetoprotein values ($p < 0.05$). *CCNB2* expression was significantly associated with tumor stage ($p = 0.014$). Moreover, a significant association between *ASPM* expression and new tumor events was observed ($p = 0.030$).

Conclusions Overexpression of *CCNB2, TOP2A*, and *ASPM* is associated with poor prognosis, and these genes could serve as prognostic markers and potential therapeutic targets for HCC.

OR-007

Cisplatin or carboplatin? Neutrophil to lymphocyte ratio (NLR) may serve as a useful factor in small cell lung cancer therapy selection

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Objective The present study aimed to investigate the significance of neutrophil to lymphocyte ratio (NLR) in the peripheral blood of patients with small cell lung cancer (SCLC) when selecting a first-line treatment.

Methods A total of 73 patients with SCLC who had complete clinical data and sought treatment at Fujian Medical University Union Hospital between January 2014 and May 2016 were included. Data were retrospectively analyzed, utilizing a receiver operating characteristic curve to determine the NLR cut-off value.

Results Out of the 73 patients, 39 were classified as high-NLR (NLR $\geqslant$3.80) and 34 as low-NLR (NLR <3.80). Compared with the high-NLR group, patients in the low-NLR group had a longer progression free survival (PFS); however, there was no statistically significant difference in overall survival (OS) time. Patients with a high NLR had a significantly longer PFS (P=0.021) and OS time (P=0.042) when treated with a etoposide/cisplatin (EP) therapy regimen, compared with those treated with etoposide/carboplatin (EC). PFS was the longest in the high-NLR patients with limited stage (LS; P=0.002). Among the patients receiving the EC regimen, the PFS of the low-NLR group was significantly longer compared with the high-NLR group (P=0.003).

Patients in the low-NLR group who received thoracic radiotherapy had a longer PFS (P=0.011), when comparing patients in the low-NLR group who did not receive thoracic radiotherapy, and within this group the therapeutic effect of radiation was the greatest in LS patients. Compared with the high-NLR group, the low-NLR group patients who received cranial radiotherapy had a significantly longer PFS (P=0.039).

Conclusions For the initial evaluation of patients with SCLC, pretreatment NLR may be of significance for selecting first-line chemotherapy agents. As the present study was retrospective and investigated a limited number of patients, further research and prospective studies are warranted.

OR-008

Decreased expression of microRNA-31 in HIV infection dampened TCR signaling by lower ERK phosphorylation

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Objective T-cell dysfunction is a hallmark of HIV infection that begins very early in infection. T-cell-receptor (TCR) signaling in response to antigen recognition has a central role in determining T cell function. In HIV infection, TCR signaling was found to be blunted in those with progressive disease compared with long-term nonprogressors and responders. Engagement of the TCR triggers the formation of multi-molecular signalosomes that lead to the generation of second messengers and subsequent activation of multiple distal signaling cascades, such as the NFAT, AP-1 and erk pathways. All these critical TCR signaling pathways have been reported to be post-transcriptional regulated by miRNAs. In our previous study, we identified miR-31 as a biomarker, whose lower expression in rapid progressors associated with faster disease progression. However, the mechanism by which miR-31 regulates immunity of HIV infection is still unclear. On this basis, this study investigated the role of miR-31 in the regulation of TCR signaling pathway in primary T cells.

Methods Samples were collected from HIV negative healthy controls enrolled at The First Hospital of China Medical University with no significant difference in age or gender. PBMCs and 293T cells were transfected using cholesterol-modified CY3 fluorescence labeled miR-31 specific antagonists or antagomir-NC for knocking down. For overexpression, PBMCs and jurkat cells was transfected with 6ug GFP-pMax-miR-31 or GFP-pMax-mock, and 293T cells was transfected with 2nmol miR-31 mimics. The miRNA and mRNA level were detected by real-time PCRs. Flow cytometric analysis was used to detect the CD69 expression and the phosphorylation of ERK1/2.

Results Knockdown of miR-31 inhibited T cell activation. miR-31 reduced erk phosphorylation by targeting DUSP7 to inhibit tcr signaling. Overexpression of miR-31 restored the early activation of T cells in HIV infection.

Conclusions T cell signaling is a prerequisite for T cell proliferation and differentiation, and further exerts cellular immune effects, the damage of which can cause the dysfunction of T cell. Our study found that decreased expression of miRNA-31 in HIV-infected patients targets DUSP7 to reduce ERK phosphorylation to inhibit TCR signaling. Given the importance of miR-31 in HIV disease, our study provides

information for understanding the pathogenesis of HIV and immune intervention strategies.

OR-009

Identification of biomarkers for predicting nasopharyngeal carcinoma carcinogenesis and metastasis by iTRAQ labeling quantitative proteomic analysis

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Objective Isobaric tags for relative and absolute quantitation (iTRAQ) combined with mass spectrometry (MS) provides a powerful tool for screening proteins. In this study, we used this approach to identify novel biomarkers of nasopharyngeal carcinoma (NPC) development and progression and assess their clinical value for predicting NPC carcinogenesis and metastasis.

Methods Proteins differentially expressed between the three cell lines were identified by iTRAQ combined with two-dimensional liquid chromatography tandem MS. The expression of annexin A6, spectrin, and endoplasmic reticulum resident protein (ERP)72 was evaluated in an independent set of paraffin-embedded archival specimens by immunohistochemistry. The clinical utility of these markers for early detection of NPC was evaluated by receiver operating characteristic curve analysis and discriminant analysis.

Results A total of 20 differentially expressed and 191 metastasis associated proteins were eventually screened through established screening principles. Annexin A6, Spectrin and ERP72 achieved a higher sensitivity and specificity in distinguishing normal nasopharyngeal epithelial tissue from NPC, lymph node metastasis from non-metastatic NPC or distant from non-distant metastasis. These three proteins expression level was closely correlated with primary lesion size ,lymph node metastasis, distant metastasis and clinical stage; spectrin expression level was closely correlated with lymph node metastasis, distant metastasis or clinical stage. Finally, in the discriminant analysis, they showed good performance in distinguishing normal patients from NPC patients, non-metastatic from metastatic NPC, and non-distant from distant metastatic NPC, respectively.

Conclusions Their expression can serve as markers for NPC progression and provide a basis for elucidating the molecular mechanisms underlying the malignant transformation of normal human nasopharyngeal epithelia.

OR-010

Study on the type analysis of uropathogenic Escherichia coli(UPEC) in recurrent urinary tract infection(rUTIs)

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Objective To analysis molecular epidemic correlation, differences of antibiotic resistance, biofilm formation in vitro, the carrying rate of different virulence factors and phylogenetic group were compared between UPEC and E. Coli in intestinal tract.

Methods 62 UTI patients were collected from Shanghai No.6 hospital in January 2010 and December 2013,which was diagnosed UTI twice in 6 months or three times in 1 year. 128 isolates of UPEC were obtained in all. According molecular typing, 128 UPEC isolates were defined the relapse group (n=64) and the reinfection group (n=64) .66 isolates of E.coli were obtained in intestinal tract from healthy people between January 2012 and December 2014. These strains were characterized for antibiotic resistance, in vitro biofilm formation, the carrying rate of different virulence factor and phylogenetic group.

Results The relapse group UPEC showed high resistance rates to ciprofloxacin (93.7%) 、ampicillin (89.1%) 、piperacillin (89.1%) 、cefazolin (87.5%) , while low resistance rates to imipenem (0%) 、meropenem (0%) and fosfmycin (6.3%) . The positive rate of Congo red test was 46.88%, while the positive rate of crystal violet test was 1.56%. The most frequent phylogenefic groups were B2 (28.13%) and D (51.56%). The carrying rates of chuA、feoB、iutA、iroN and ireA were 79.69%, 98.43%, 76.56%, 64.06% and 14.06%. The reinfection group UPEC showed high resistance rates to ampicillin (93.8%) 、piperacillin (93.8%) 、cefazolin (82.8%) , while low resistance rates to piperacillin/tazobactam (10.9%) 、imipenem (0%) and meropenem (1.6%) . The positive rate of Congo red test was 35.94%, while the positive rate of crystal violet test was 1.56%. The most frequent phylogenefic groups were B2 (21.88%) and D (54.69%). The carrying rates of chuA、feoB、iutA、iroN and ireA were 71.88%、100%、87.50%、60.94% and 12.50%. E.coli strains in intestinal tract showed high resistance rates to ampicillin (60.6%) 、piperacillin (59.1%) , while low resistance rates to amikacin (0%) 、piperacillin/tazobactam (3%) 、imipenem (1.5%) 、meropenem (0%) 、cefepime (12.1%) and fosfmycin (4.5%) . The positive rate of Congo red test was 25.76%, while the positive rate of crystal violet test was 6.06%. The most frequent phylogenefic groups were B1 (37.88%) and D (30.30%). The carrying rates of chuA、feoB、iutA、iroN and ireA were 46.97%, 100%, 53.03%, 22.72% and 7.58%.

Conclusions Biofilm formation in vitro were not the main factor in different types of UTI. The relapse group UPEC showed high resistance rates to ciprofloxacin、ampicillin、piperacillin、cefazolin, while low resistance rates to imipenem、meropenem and fosfmycin.The reinfection group UPEC showed high resistance rates to ampicillin、piperacillin、cefazolin, while low resistance rates to piperacillin/tazobactam,imipenem and meropenem.The most frequent phylogenefic groups of both the relapse group UPEC and the reinfection group UPEC were B2 and D. The correspondant value in E.coli strains in intestinal tract was B1 and D.The differences virulence factors (chuA、feoB、iutA、iroN and ireA) between the two UPEC groups were

very little. The carrying rate of the virulence factors(chuA、iutA、iroN) in two groups UPEC were almost all higher than E.coli in intestinal tract.

OR-011

The relationship between XDH gene mutation and xanthinuria

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Xanthinuria, which was first reported by Dent and Philiport in 1954, is a rare autosomal recessive inherited metabolic disorder, characterized by low concentration of uric acid in serum and high excretion of xanthine and hypoxanthine in blood and urine. The biochemical mechanism of xanthinuria is the disturbance of purine to uric acid metabolism. According to the enzymes involved, xanthinuria can be classified into 3 types, type Ⅰ (OMIM 278300), type Ⅱ (OMIM 603592) and typeⅢ (OMIM 252150). Type Ⅰ is caused by xanthine dehydrogenase/xanthine oxidase (XDH/XO) deficiency due to mutations in XDH gene, but possess normal activity of aldehyde, while type Ⅱ results from molybdenum cofactor sulfurase (MOCOS) deficiency: combined with XDH/XO and aldehyde oxidase (AOX1) activities caused by mutations in MOCOS and AOX1 gene. The third type of xanthinuria typeⅢ, involves the molybdenum cofactor deficiency related with triple deficiency of sulfite oxidase (SO) as well as XDH/XO and AOX1 activities, due to a defect in the synthesis of molybdopterin, which is a precursor of molybdenum cofactor for all three enzymes. Symptoms of typeⅢ include severe neurological disorder, lens dislocation and dysmorphism, and the outcome is poor.

Type Ⅰ and type Ⅱ are similar in clinical symptoms, but distinct in biochemical manifestation. Type Ⅰ patients can metabolize allopurinol, whereas type Ⅱ patients cannot metabolize due to deficiency of aldehyde activities. Generally, patients with xanthinuria are considered to be asymptomatic. Xanthinuria has large clinical variability and only about half of all patients have urolithiasis. Patients with either type Ⅰ and type Ⅱ sometimes develop xanthine calculi in the urinary tract, acute renal failure and myopathy due to tissue deposition of xanthine.

In this report, three cases from unrelated families with xanthinuria were diagnosed by clinical, biochemical and finally confirmed by molecular genetics. XDH/XO-deficient patients are frequently identified based on measurement of uric acid in blood. Although various diseases or disorders other than xanthinuria may lead to hypouricemia, e.g., renal hypouricemia, which can be caused by decreased re-absorption due to impaired function of urate transporter in the nephrons, is also clinically asymptomatic in most cases. Some drugs like xanthine oxidoreductase inhibitor (e.g., allopurinol, febuxostat), dugs used either as uricosuric agents or to block other aspects of renal tubule excretion (e.g., sulfinpyrazone, probenecid, benzbromarone) may also cause hypouricemia. However, these three cases in the report didn’t have kidney disease and didn’t use any drugs as described above. Ultimately, xanthinuria should be diagnosis by molecular genetics. Four mutations in XDH gene and one mutation in AOX1 were identified, among which, c.3847C>T (p. Arg1283Ter) in XDH gene was documented in 2015, and the rest of mutations are reported firstly. Besides, family analysis was also performed in one of the patients.

Previous case reports showed the patients with xanthinuria were accompanied by rheumatoid arthritis and migratory arthritis. Therefore, the accumulation of xanthine and hypoxanthine might cause the inflammation of muscle of neck, elbow, or other parts of body. In the report, both case 1 and case 3 have the symptoms of muscle soreness in different parts of body. Accumulative evidence is necessary to disclose the complications of xanthinuria.

OR-012

Developing targeted assays for core-fucosylated glycoproteins associated with prostate cancer by Multiple Reaction

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OR-013

Identification of three proteins in synovial fluid as promising biomarkers for diagnosis of periprosthetic jiont infection(PJI)

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Background: Diagnosing periprosthetic joint infection (PJI) requires various laboratory and clinical criteria. The purpose of this study is to explore novel biomarkers that could rapidly diagnose PJI with high accuracy.
Methods: For this retrospective study of prospectively collected samples, 50 synovial fluid aspirates, including 18 from hip and 32 from knee were collected before surgery. Among these included patients, 25 were diagnosed as aseptic loosening (non-PJI) and 25 as PJI (Musculoskeletal Infection Society definition as criteria). Quadrupole-Orbitrap Mass Spectrometer (MS) was performed to compare expression of proteins in PJI patients with those in non-PJI patients. Then we further investigated proteins that were most efficient for diagnosis of PJI with prediction analysis of microarray and random forest model. The altered expression of selected proteins: lactoferrin (LTF), polymorphonuclear leukocyte serine protease 3 (PRTN3) and myeloid nuclear differentiation antigen (MNDA), was verified by ELISA in an extended sample cohort.
Results: 256 proteins were significantly up-regulated (> 3.0-fold) while 14 proteins were down-regulated in synovial fluid of PJI patients, compared with those in synovial fluid of non-PJI patients. Area under curve (AUC) of LTF, PRTN3 and MNDA for PJI diagnosis were 0.9888, 0.9488 and 0.9632, respectively identified by MS. ELISA results verified that LTF, MNDA and PRTN 3 were sensitive and specific for diagnosis of PJI.
Conclusion: The three novel proteins were identified as promising synovial fluid biomarkers for PJI diagnosis in our proteomic study and should be further validated in future clinical trials.

OR-014

Rapid CD4+ T-cell decline is associated with coreceptor switch among men who have sex with men primarily infected with HIV-1 CRF01_AE in Northeast China

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Objective: CRF01_AE is the most prevalent HIV-1 subtype among MSM in China.However, the characteristics and underlying mechanism of the accelerated $CD4^+$ T-cell decline in CRF01_AE-infected MSM remain incompletely understood.

Design: A long-term prospective follow-up study was conducted with 1388 MSM at risk of HIV-1 infection in Northeast China. MSM with primary HIV-1 CRF01_AE infection were identified and followed for 3–6 years to explore the determinants of rapid $CD4^+$ T-cell decline.

Methods: Tropism was determined in primary infection by both single genome amplification-based genotypic prediction using four different algorithms and phenotypic determination using clinical isolates. Serial isolates were used to determine phenotype of coreceptor switch. Human leukocyte antigen genotypes and T-cell activation markers were determined.

Results: Fifty-nine MSM primarily infected with HIV-1 CRF01_AE were discovered and recruited for the follow-up study. CCR5-utilizing (R5) viruses accounted for up to 98% of HIV-1 CRF01_AE infections in Northeast China. Survival analysis indicated 39.5% of the patients underwent coreceptor switch within 3 years after infection. After adjustment for other potential risk factors, linear mixed-effect models demonstrated patients experienced R5 to CXCR4-utilizing/dual-tropic (X4/DM) coreceptor switch within 3 years after infection underwent a faster $CD4^+$ T-cell decline compared to those without coreceptor switch.

Conclusions: Primary HIV-1 CRF01_AE infection among MSM in Northeast China is characterized by R5 viral infection and early R5 to X4/DM coreceptor switch, which is associated with rapid $CD4^+$ T-cell decline. The findings highlight the importance of immediate treatment among the CRF01_AE-infected MSM.

OR-015

Molecular epidemiology and risk factor analysis of Clostridium difficile carried by inflammatory bowel disease patients

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Objective Clostridium difficile infection (CDI) may lead to poor outcomes in patients with inflammatory bowel disease (IBD). And the overlapping clinical presentations of CDI and IBD pose barriers to diagnosis and standardized treatment. Till now, molecular epidemiological researches have been mostly carried on diarrhea patients with CDI, yet have rarely been reported in IBD patients. In our study, we aimed to analyze the current clinical and molecular epidemiology of CDI-IBD in China to provide more evidence on CDI-IBD populations.

Methods Stool samples of the inpatients at Renji Hospital affiated to Shanghai Jiaotong University were collected between July 1st 2014 and June 30th 2017. Both the cell culture cytotoxicity neutralization assay (CCCNA) and toxin A and B enzyme immunoassays(EIA) were used to detect toxigenic strains in all fecal specimens. All the toxigenic *C.difficile* isolates were investigated via multi-locus sequence typing(MLST). And the corresponding demographic data and clinical characteristics of those strains were reviewed simultaneously.

Results A total of 330 toxigenic *C.difficile* were identified from 3600 fecal specimens. After divided into IBD and non-IBD group, the incidence of CDI in IBD patients (12.4%, 143/1153) was significantly higher than that in non-IBD patients (7.6%, 187/2447). MLST analysis illustrated that the predominant genotype in IBD patients was ST54(18.0%), followed by ST2(11.0%) and ST3(10.0%); while in non-IBD patients it was ST81(31.0%), followed by ST2(10.0%) and ST54(9.0%). Clinical characteristics have shown IBD- CDI patients were younger(37 vs. 65, $p<0.001$) and acquired the infection mostly in an outpatient setting compared with non-IBD patients with CDI(2 vs. 7, $p<0.001$). And IBD-CDI patients tended to have lighter systemic inflammatory infections and less complications($p<0.001$).

Conclusions The incidence of CDI in IBD patients was higher than that in non-IBD patients. *C.difficile* ST54 was the predominant genotypes in IBD patients as ST81 in non-IBD patients. In addition, IBD patients were more likely develop community-acquired CD, while the control patients developed nosocomial infections, indicating a changing infection mode in patients with IBD

OR-016

Noninvasive prenatal diagnosis for fetal RhD and achondroplasia

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OR-017

Digital PCR-based EGFR detection in paired plasma and CSF of lung adenocarcinoma patients with central nervous system metastase

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Objective Epidermal growth factor receptor (EGFR) mutation plays an important role in central nervous system (CNS) metastases of lung adenocarcinoma (LAC), and it was also a first-line treatment target for EGFR tyrosine kinase inhibitor (EGFR-TKI). Cerebrospinal fluid (CSF) has the potential to carry tumor DNA in CNS metastases.
Methods EGFR status of ctDNA in paired CSF and plasma from LAC patients with CNS metastases, including 20 brain metastasis (BM) and 15 leptomeningeal metastasis (LM), was detected by droplet digital PCR (ddPCR) assay. The EGFR status-based clinical intervention and outcomes of the 35 patients were also investigated.
Results T790M mutation was detected in the plasma of 55% (11/20) and in the CSF of 14.3% (3/21) LAC patients with EGFR mutations in primary tumors (P=0.006). The sensitivity and specificity of the ddPCR EGFR mutation tests in CSF or plasma samples versus primary tumor samples were 70%, 92% and 52%, 100% respectively. Twelve patients were switched to first generation EGFR-TKI after the detection of sensitive EGFR in their CSF or plasma, whereas 6 patients were switched from first generation EGFR-TKI to osimertinib after detection of T790M mutation.
Conclusions CSF and plasma ddPCR assays could provide minimally invasive and multiple monitoring of EGFR status during CNS metastases from LAC patients. T790M mutation in plasma was a more sensitive index to determine EGFR-TKI resistance when CNS metastases from lung cancer progressed, and CSF significantly increased the diagnostic validity for EGFR status of lung cancer brain metastasis.

OR-018

NIPA1 Deficiency Improves Lipid Metabolism And Attenuates Diabetic Nephropathy In Streptozotocin-treated Mice

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Objective Diabetic nephropathy (DN) is one of the most frequent and serious complications in diabetic patients, leading to induction and progression of end-stage renal failure. The process of diabetic nephropathy is complex, lipid metabolism disorder and abnormal lipoprotein composition are involved in the development of diabetic nephropathy. NIPA1 is a magnesium ion transporter. Some studies have shown that magnesium ions can affect glucose uptake and play an important role in lipid metabolism. However, the influence of NIPA1 on lipid metabolism and the importance of NIPA1 to progress of DN remain unclear. The present study aimed to investigate the contribution of NIPA1 to diabetic renal injury and lipid metabolism in streptozotocin-treated mice.

Methods Type 1 diabetes was induced in male NIPA1 knockout mice (n=5), and WT (n=5) mice (C57BL/6J background) at 10 weeks of age by intraperitoneal streptozotocin injection (125 mg/kg body weight in 10mM citrate, pH 4.5) once a day for 2 consecutive days. Control mice (n=5 per group) received citrate. The animals were divided into the following groups: (1) WT mice, (2) STZ-induced mice, (3) NIPA1-/- mice, (4) STZ induced NIPA1-/- mice. Animals without water restriction were maintained on standard diet and were monitored every 2 weeks for blood glucose. Diabetes was defined as blood glucose levels of 16.7mM. After 21 weeks of streptozotocin injection, mice were anesthetized. Blood glucose levels were measured from tail-vein blood using contour (Bayer). Urinary albumin was measured by ELISA quantitation kit (Bethyl Laboratories, Montgomery, AL), and urine and serum creatinine were determined by enzymatic method. Glycated hemoglobin A1c (HbA1c) was tested by Premier Hb9210 Analyzer. Serum cholesterol, triglyceride, CREA and UREA were determined by autoanalyzer. Liver sections were stained with hematoxylin and eosin (H&E),oil red O to assess lipid accumulation. Kidney sections were stained with H&E and PAS to assess glomerulosclerosis. The mRNA expression of fibronectin and Epcam in mice kidney tissue were determined through RT-PCR. The mRNA expression of Sterol Regulatory Element Binding Proteins 1c (SREBP-1c) in mice liver and kidney tissue were determined through RT-PCR.

Kidney biopsy tissues were obtained from six subjects with type 2 diabetes and biopsy-proven DN and six nondiabetic control subjects. Nondiabetic control renal tissues were obtained from the adjacent tissues of patients with renal carcinoma. The NIPA1 expression in kidney tissue was determined through immunohistochemical staining.

Results In this study, we found increased expression of NIPA1 in the renal tubules of human kidneys with diabetic nephropathy compared with expression of NIPA1 in kidney tissue of control group. After 21 weeks, the diabetic mice lacking NIPA1 had significantly less urine albumin-creatinine ratio and glomerulosclerosis, despite similar degrees of HbA1c, blood glucose levels, CREA and UREA. The fibronectin

expression was decreased and Epcam expression was increased in in NIPA1 knockout diabetic mice. Moreover, diabetic NIPA1-deficient mice had low level of serum cholesterol and triglyceride. The lipid droplets in the liver were also significantly decreased. NIPA1 knockout mice with diabetes exhibited down-regulated mRNA expression levels of SREBP-1c in the liver, which play a key role in lipid biosynthesis.

Conclusions Although diabetic nephropathy has been traditionally considered a complex disease, accumulating evidence indicates the prominent role of lipid metabolism disorders in its development and progression. We investigated the contribution of NIPA1 to nephropathy acceleration in diabetic mice. Our results demonstrate that gene deficiency in NIPA1 protects mice from diabetic renal injury. lacking NIPA1 in diabetic mice improved renal function and attenuated renal fibrosis and improved lipid metabolism. In addition, the NIPA1 expression was increased in kidney tissues of DN patients. Taken together, these data suggest that a NIPA1-mediated pathway may promote lipid metabolism disorders in diabetic nephropathy.

OR-019

MALAT1 is Associated with Poor Response to Oxaliplatin-Based Chemotherapy in Colorectal Cancer Patients and Promotes

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Objective Chemoresistance to oxaliplatin-based therapy has been a key barrier to the efficacy of colorectal cancer (CRC) treatment. One major reason for oxaliplatin chemoresistance in CRC is the acquisition of epithelial-mesenchymal transition (EMT) in cancer cells. The long non-coding RNA MALAT1, is a highly conserved nuclear ncRNA and a key regulator for metastasis development in several cancers. However its role in oxaliplatin-induced metastasis and chemo-resistance is rarely known. In our study, we aim to investigate the prognostic role of MALAT1 in CRC patients receiving oxaliplatin-based therapy, and further explore the potential transcriptional regulation through interaction with EZH2 and miR-218 based on the established HT29 oxaliplatin-resistant cells.

Methods For chemo-response study, 221 serum samples and 48 primary tissues were collected from the patients who received standard Oxaliplatin-based chemotherapy, and 46 serum samples from patients who received standard FOLFOX chemotherapy were collected at Qilu Hospital of Shandong University between 2011 and 2015. RT-qPCR and RT-qPCR-D method previously established by ourselves were used to determine the expression of mRNA expression in primary tissues and serum, respectively. Cell migration and invasion were assessed with Boyden chambers or modified Boyden chambers according to the protocol of the manufacturer. RNA immunoprecipitation (RIP) and Chromatin immunoprecipitation (ChIP) experiments were performed to investigate the potential interaction. Finally, the survival curves of CRC patients were estimated via the Kaplan-Meier method and the difference in survival curves was estimated using log-rank testing.

Results MALAT1 expression level was much higher in patients who did not respond to treatment than those who experienced response to chemotherapy. We then stratified patients into a low (n=37) and a high (n=16) MALAT1 expressing group with an established cut-off value (0.432) by using a ROC curve analysis. In the validation group containing 168 serum samples of CRC patients, proportion of patients not responding to chemotherapy was significantly higher in the high MALAT1 expressing group than in the low group. The diagnostic sensitivity and specificity were 75.0% (72/96) and 61.1% (44/72). Further more, the Kaplan–Meier survival analysis indicated that high MALAT1 expression was associated with shorter OS and DFS in CRC patients.
CRC cell line HT29 that had acquired resistance to oxaliplatin at the clinically relevant concentration of 2 μmol/L (HT29 OxR cells) were built. MALAT1 was significantly increased in HT29 OxR cells and MALAT1 silencing reversed oxaliplatin-induced EMT. Moreover, EZH2 directly interacts with 3' end of MALAT1, which subsequently suppressed the expression of E-cadherin. CRC cells attained increased migration and invasion ability after being treated with oxaliplatin, and this increased migration and invasion ability was partially suppressed by MALAT1 or EZH2 knockdown. Importantly, our results suggest that the interaction between MALAT1 and miRNA-218 has reciprocal effects. The Kaplan-Meier survival analysis showed that patients with low MALAT1 and high miR-218 expression had the longest OS, while the high MALAT1 and low miR-218 group showed the shortest for patients who received standard FOLFOX treatment.
Conclusions In conclusion, the present work has identified that lncRNA MALAT1 was correlated with tumor metastasis and associated with poor response to oxaliplatin-based chemotherapy in CRC patients. MALAT1 mediates oxaliplatin-induced EMT and chemoresistance through EZH2 and interacting with miR-218. Thus, MALAT1 may be a novel functional biomarker and therapeutic target in CRC patients. Suppression of MALAT1 combining with miR-218 over-expression could be a future direction to develop a novel therapeutic strategy to enhance chemosensitivity to FOLFOX chemotherapy regimen.

OR-020

Low paraoxonase 1 arylesterase activity and high von Willebrand factor levels are associated with severe coronary atherosclerosis in patients with non-diabetic stable coronary artery disease

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Objective Chronic stable angina is the most common manifestation of coronary artery disease (CAD). PON1 activity and the release of von Willebrand factor is associated with lesion initiation in atherosclerosis. Diabetes can complicate CAD due to the production of advanced glycation end products. This study was performed to evaluate PON1 activity and VWF levels in post-ACS (acute coronary syndrome) stable CAD (SCAD) patients without diabetes.
Methods We carefully selected 133 SCAD patients without diabetes to exclude abnormal PON1 metabolism and patients experiencing acute stress periods. Forty-seven cases with

normal coronary angiography and 50 healthy individuals served as controls. The SCAD group was then stratified into single-vessel, multiple-vessel lesions, and mild or severe luminal stenosis according to the number and the degree of luminal stenoses. We then measured serum PON1 paraoxonase and arylesterase activity, plasma VWF levels, as well as serum total cholesterol (TC), total triglycerides (TG), high density lipoprotein cholesterol (HDL-C), low density lipoprotein cholesterol (LDL-C), and apolipoprotein A1. PON1 arylesterase activity was detected with an ordinary chemistry system using a novel phenylacetate derivative.

Results Both PON1 paraoxonase and PON1 arylesterase were significantly lower in the SCAD group (versus control), but VWF levels were higher. Decreased PON1 arylesterase activity and increased VWF levels were associated with severe atherosclerosis in SCAD patients. PON1 arylesterase activity and VWF levels could reliably predict the occurrence of severe coronary artery lesions in SCAD patients (AUC for PON1 arylesterase activity: 0.85, AUC for VWF: 0.70, $p < 0.05$). We also observed a slight negative correlation between VWF and PON1 paraoxonase/arylesterase in this study. In addition, we determined that the performance of the novel substrate for PON1 arylesterase activity met the detection requirements.

Conclusions We have successfully established a new methodology for assaying PON1 activity in patients with SCAD. This method could be readily implemented clinically, as it can be used with most general chemistry systems, unlike traditional methods for assaying PON1. Furthermore, we have established that PON1 and VWF are detectable markers that could be used to predict the severity of stenoses, ideally facilitating a SCAD diagnosis before the sudden onset of life-threatening symptoms.

Poster Presentation

PO-001

The role of quality control circles in sustained improvement of qualified rate of sample

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Quality control circle has been gradually introduced to medical institutions in China. QCC activity achieved good application effect in the clinical, and more and more get the attention of the people .To explore the effect of quality control circle approach in improving the qualified rate of sample. The specimen data with unqualified test results in our hospital from February 2017 to June 2017 were collected and statistically analyzed, We used professional tools to solve existing problems of specimen in clinical laboratory following the steps of quality control circle in the pre-analytical phase. A total of 30105 specimens were collected before the improvement of the quality management circle theme activities, of which 297 were unqualified, and the proportion of unqualified cases was 0.98%(297/30105).43125 cases of specimens were collected(including 193 cases of specimens with defect), during the period from July to December 2017, The proportion of unqualified samples was 0.45% (193/43125). We compared the data before and after the implementation, and the difference had statistical significance (p<0.05). The target yield rate and improvement rate of 108.2%, respectively,With the application of quality control circle tools, the defect rate of specimen in clinical laboratory decreases and the quality management ability of quality control circle members to resolve actual clinical problems improves, it is worth to be adapted in clinical laboratories.

PO-002

Genome-wide Evolutionary Characterization of a New HIV-1 CRF01_AE/CRF07_BC Recombination Lineage among Men Who Have Sex with Men in Shenyang, Northeastern China

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Objective HIV is characterized by high frequency of recombination. The recombination between two strains not only introduces a big change in the viral genome to generate a new genotypes but also mediates changes of viral virulence, cell tropism, antiretroviral drug susceptibility, disease progression of host and the performance of diagnostic tests. In recent years, men who have sex with men (MSM) has becoming the most important population for HIV control in China. In recent years, the rapid spreading and co-epidemic of multiple HIV-1 subtype among Chinese MSM population have attracted broad attention. Multiple main epidemic HIV-1 strains, a number of CRF01_AE/B and CRF01_AE/CRF07_BC recombinants had been reported among MSM in different regions of China sporadically. This study aims to explore the genome-wide

evolutionary characterization of a new HIV-1 CRF01_AE/CRF07_BC recombination lineage recombined by the main epidemic strains of MSM populaiton for the first time.

Methods Study subjects. Six treatment naïve CRF01_AE/CRF07_BC infected cases were recruited from newly diagnosed HIV infected MSM in a HIV voluntary counseling and testing clinic of the First Affiliated Hospital, China Medical University.

Phylogenetic analyses and recombination analyses. The sequences of HIV-1 near-full-length genome were got with the single-gene amplification from viral RNAs, sequenced directly and assembled with Sequencher 4.10 and BioEdit 5.0. Maximum Likelihood phylogenetic tree was built using MEGA 5.02 and tested by bootstrap analysis with 500 replicates. Recombination analyses were done with RIP and SimPlot 3.5.1. Sub-region trees were constructed using segments I to XII with maximum-likelihood tree.

Evolutionary Analyses. The most recent common ancestor (tMRCA) were estimated using the Bayesian Markov Chain Monte Carlo (MCMC) inference under the uncorrelated log-normal relaxed molecular clock model with the general time-reversible nucleotide substitution mode. The maximum clade credibility trees were edited using FigTree V1.3.1.

Results Identification of a CRF01_AE/CRF07_BC lineage among MSM in Liaoning province. A unique lineage of six HIV-1 strains is different from any known HIV subtypes, CRFs and URFs (bootscrap=100) in ML tree. Moreover, 5 out of the 6 strains were more phylogenetic linked than another case and formed a subcluster..

Six CRF01_AE/CRF07_BC strains showed similar but inconsistent recombination structures. Six strains were all CRF01_AE/CRF07_BC recombinants. Although there were 4 CRF07_BC segments in CRF01_AE backbone among 4 strains, but only 3 and 2 of CRF07_BC segments in other 2 strains, six strains have some common recombination pattern: First, all of the 6 strains share common breakpoint 1 in pol gene. Second, five out of six strains share common breakpoint 2, 5 and 6 in pol and env gene respectively. Third, four out of six strains share common breakpoint 7 and 8 in nef gene. The main difference was the length of segment IV between breakpoints 3 and 4 in five strains. Another strain had a long CRF07_BC spanning the vif gene to near the end of env gene.

Sub-region tree of CRF01_AE segments support the homology of CRF01_AE backbone of 6 strains, with the CRF01_AE lineage 1 among Chinese MSM as the putative origin (bootscrap≥70). Similarly, sub-region tree of CRF07_BC segments support the homology of CRF07_BC insertions, with the CRF07_BC lineage 3 among Chinese MSM as the putative origin (bootscrap≥70).

The origin time of tMRCA of the new CRF01_AE/ CRF07 _ BC Recombination lineage. The tMRCA of CRF01_AE segments, including segment I, III, V and VII+IX, were 2009.3 [95% HPD: 2007.7-2010.7], 2008.8 (HPD:2006.9-2010.5), 2007.3 (HPD:2004.0-2009.9) and 2008.4(HPD:2006.6-2010.4), respectively. While the tMRCA of CRF07_BC segments, including segment II, IV and VI+VIII were 2009.4 (HPD: 2006.8-2011.5), 2011.9 (HPD: 2008.4 -2013.1), 2008.7(2006.1-2010.9), respectively. Although the tMRCA of different segments were not always consistent, the tMRCA of segment IV seemed later than other segments suggested that segment IV could be the last recombination event on the basis of a progenitor CRF01_AE/CRF07_BC recombinant. High recombination rate of HIV-1 may confound the estimation of evolutionary history in current theoretical and computational settings. Therefore, the discrepancies among the MCC trees may be a result of multiple recombination processes.

Conclusions In conclusion, a CRF01_AE/CRF07_BC HIV-1 recombination lineage among MSM with some new features arouse concern. This is the first report of CRF01_AE/CRF07_BC

HIV-1 recombinants that originated from the strains spreading widely among MSM population in China. The common breakpoints and homologues origin of parental strains likely conserved during viral evolution suggested the existence of a common progenitor. This new recombination lineage was inferred to be originate from multiple recombination steps. This finding call more attention on the monitoring the new trend of HIV recombinants occurrence and the transmission among MSM population.

PO-003

Deafness gene mutations in newborns in Foshan area of South China with bloodspot-based genetic screening tests

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Objective To identify the incidence of congenital hearing loss in newborns by the rate of deafness related genetic mutations in Foshan area of South China.
Methods We enrolled the infants delivered in Foshan Maternity and Children's Healthcare Hospital. The deafness gene mutation was detected by HibriMax method. Our study tested 47538 newborns within 3 days after birth, including 13 sites in four genes: GJB2 (35 del G, 176 del 16, 235 del C, 299 del AT, 155 del TCTG), GJB3 (583 C > T), SLC26A4 (2168 A > G, IVS 7-2 A > G, 1299 C > T) and mtDNA 12S rRNA (1555 A > G, 1494 C > T, 12201 T > C, 7445 A > G). The birth condition of infants was collected, including sex, low or high birth weight, twins and premature delivery.
Results In the whole 47538 newborns, 1415 were identified with a mutation in the four common deafness genes. The total rate of the deafness genes mutation was 2.976%. The carrier rates of GJB2 (35 del G, 176 del 16, 235 del C, 299 del AT, 155 del TCTG), GJB3 (583 C > T), SLC26A4 (2168 A > G, IVS 7-2 A > G, 1299 C > T) and mtDNA 12S rRNA (1555 A > G, 1494 C > T, 12201 T > C, 7445 A > G) mutations were 0.000%, 0.048%, 1.422%, 0.185%, 0.000%, 0.076%, 0.116%, 0.755%, 0.160%, 0.187%, 0.021%, 0.000%, and 0.006%, respectively. Logistic regression analysis showed no statistically significant correlation between mutations and newborns sex, premature delivery, or birth weight.
Conclusions Our study showed that the 235delC GJB2 mutation was the leading deafness related mutation in Foshan area of South China. Deafness gene mutations screening in newborns detected by bloodspot-based genetic screening tests can help the diagnosis of newborn congenital hearing loss.

PO-004

Modified Glasgow Prognostic Score, neutrophil/lymphocyte, platelet/lymphocyt, and C-reactive protein/albumin ratios in different stages of silicosis

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Objective The objective is to evaluate modified Glasgow Prognostic Score (mGPS), C-reactive protein/albumin ratio(CAR), neutrophil/lymphocyte ratio (NLR), and platelet/lymphocyte ratio (PLR) for predicting the prognosis of patients with silicosis.

Methods 148 cases of silicosis patients and 154 cases of Coal Workers' Pneumoconiosis (CWP)patients were collected in Hunan Prevention and Treatment Center for Occupational Diseases (HPTCOD) from January 2018 to December 2018. The values of PLR, CAR, NLR, and mGPS for predicting the prognosis of silicosis were evaluated by ROC, and the relationship between the PLR, NLR, and mGPS of silicosis and CWP patients were analyzed.

Results Silicosis patients exhibited higher serum leukocyte (WBC), neutrophils (N), platelets (PLT),
erythrocyte sedimentation rate (ESR), PLR, CAR, NLR, mGPS, and lower lymphocytes(L) concentrations compared with the control groups ($P<0.05$). The silicosis patients present higher PLR, CAR, NLR, mGPS than CWP patients. However, The CAR levels were of no significant difference between silicosis groups and the control groups ($P >0.05$). The areas under the ROC curves of NLR and PLR were 0.864 (95% CI. 0.805 -0.923, $P = 0.000$) and 0.698 (95% CI. 0.607-0.788, $P = 0.000$).

Conclusions PLR, NLR, and mGPS can be used as indicators of inflammatory state and severity in clinical prognosis of patients with silicosis. NLR is more sensitive to assessing disease activity compared with PLR.

PO-005

Tumor mutation load: a novel independent prognostic factor in stage IIIA-N2 non-small cell lung cancer

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Objective This study aims to investigate the prognostic biomarkers of patients with stage IIIA-N2 NSCLC and to analyze the correlation between tumor mutation load (the frequency and number of tumor mutation) and prognosis.

Methods Clinical data of 35 patients with stage IIIA-N2 NSCLC were collected from Cancer Hospital, Chinese Academy of Medical Sciences. Peripheral blood was taken at different treatment period and the mutations of cfDNA were detected.
Results Multivariate analysis showed that smoking (P=0.0308), mutation number>2 (P=0.0283) and max mutation frequency>0.025 (P=0.0450) were associated with improved progression-free survival (PFS). The OS of well differentiated NSCLC patients was better than that of poor differentiated ones (P=0.0006). The rates of PFS, disease-free survival, locoregional progression-free survival and local progression free survival were significantly higher in the group with mutant number >2 then in the group with mutant number≤2. The mutation number of pre-operation group was significantly higher than that of post-radiochemotherapy group (5 vs. 2.5, P=0.023) and the max mutation frequency change was approximately significant in post-radiochemotherapy group compared with post-operation group (2.6% vs. 1.85%, P=0.067). The max mutation frequency is positively correlated with vascular invasion (21.13% vs. 3.62%, P= 0.04). Furthermore, Met, ALK, APC, PTEN, ERBB4, NF1 and other genes, involving multiple tumor suppressor genes and lung cancer-driven genes, did not mutate in recurrence-free patients when compared with recurrent patients.
Conclusions In conclusion, differentiation, smoking, mutant frequency>0.025 and mutant number>2 are prognostic factors. The frequency and number of gene mutations in cfDNA are expected to be prognostic predictors of NSCLC.

PO-006

Exosomal transfer of stroma-derived long non-coding RNA CCAL promotes chemoresistance in colorectal cancer cells

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Objective Oxaliplatin resistance is a major challenge for advanced colorectal cancer (CRC). Despite the recognition of the crosstalk between carcinoma-associated fibroblasts (CAFs) and cancer cells in tumor microenvironment, how CAFs contribute to drug resistance in neighboring cancer cells is not well characterized.
Methods Cell survival was tested by CCK8. Oxaliplatin resistant SW480/Oxa cells with CCAL stably knocked down were used to establish xenograft models. The indicated protein levels in xenograft tumor tissues were tested by immunohistochemistry assay, and cell apoptosis was analyzed by TUNEL apoptosis assay. RNA-FISH and immunofluorescence assays were performed to assess CCAL levels in tumor stroma and cancer nests. Isolated exosomes were identified by transmission electron microscopy and Western blotting.
Results Long non-coding RNA (lncRNA) CCAL promoted oxaliplatin resistance of CRC cells. tumor stroma expressed higher CCAL compared with cancer nests. Functional studies revealed that CCAL is transferred from CAFs to the cancer cells via exosomes, where it suppresses CRC cell apoptosis, confers chemoresistance and activates β-catenin pathway *in vitro* and *in vivo*.
Conclusions CCAL expressed by CAFs of the colorectal tumor stroma contributes to tumor chemoresistance and CCAL may serve as a potential therapeutic target for oxaliplatin resistance.

PO-007

Comparison of two genotyping methods reveals clusters of Aspergillus fumigatus from chronic pulmonary aspergillosis patients in the UK

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Objective Chronic pulmonary aspergillosis (CPA) patients attending the National Aspergillosis Centre (NAC) in the UK often require long-term antifungal therapy. Resistance to at least one of the triazole antifungal drugs has been found in 28% of clinical isolates of *Aspergillus fumigatus* causing exacerbations, yet their origin is uncertain. The high discriminatory power of genotyping methods (based on tandem repeats) may be helpful for discerning the source of *A. fumigatus* infections and may reflect antifungal resistance patterns.
We compared the performance of two genotyping methods: nSTR*Af* and TRESP to determine: the relationship among isolates from the same patient; and whether genotypes with different resistance patterns could be distinguished.
Methods A total of 31 clinical isolates from 14 CPA patients located in different geographical regions in the UK, and two reference isolates (ATCC46645, AF293) were included and genotyped by nSTR*Af* and TRESP method. The clinical data of these CPA patients and the azole resistance profile of these isolates were collected. The discriminatory power of the two methods was compared and the phylogenetic trees were created using RAxML.
Results A wide distribution of *A. fumigatus* isolates was found across the UK: 23 genotypes according to nSTR*Af* and 18 according to TRESP. The Simpson index of discriminatory power for nSTR*Af* and TRESP was 0.9699 and 0.9398, respectively. In some patients, resistance developed in one genotype over time. In others, the same susceptibility patterns was reflected in different genotypes, suggesting the causal organisms were different. Among azole resistance isolates, two groups were differentiaed consideing their resistance mechanisms: *cyp51A* single point mutations and promoter tandem repeat integrations with or without *cyp51A* modifications.
Conclusions Isolates were not discriminated geographically. The relationship between genotype and susceptibility patterns was variable.

PO-008

Expression Profiling of Peripheral Blood MicroRNAs in Asymptomatic HBsAg Carriers , Chronic Hepatitis B Patients and Heathy controls of Chinese Han Population

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Objective To investigate the differential expression of microRNAs in peripheral blood plasma of patients with chronic hepatitis B, carriers of hepatitis B and healthy persons.

Methods 19 patients in group 1 (chronic hepatitis B patients), 16 in group 2 (carriers of hepatitis B) and 15 in control group (healthy persons) were enrolled in this study. The plasma RNA was extracted and hybridized by gene chip. The candidate genes related to hepatitis B were screened according to the differential expression of microRNAs. The candidate genes were identified by quantitative Real-Time PCR.

Results Microarray hybridization showed an upward or downward trend in the expression profile of microRNAs. Compared with the control group, 16 microRNAs increased (P value was less than 0.05) and 26 decreased (P value was less than 0.05) in the experimental group 1 and the experimental group 2. Quantitative Real-Time polymerase chain reaction (QPCR) showed that the up-regulated candidate genes miRNA-7a-5p, miRNA-7f-5p, miRNA-7i-5p, hsa-mi-16-5p, hsa-mi-29a-3p, hsa-mi-142-3p and hsa-mi-221-3p were all lower than 0.05. MiRNA-518c-5p, miRNA-4750-5p, miRNA-5787, miRNA-7155-3p, miRNA-8069, miRNA-3194-5p and miRNA-518a-5p were all lower than 0.05. There was no significant difference between the experimental group 1 and the experimental group 2.

Conclusions These 14 microRNAs are preliminarily identified as candidate microRNAs in peripheral plasma after hepatitis B virus infection. Through Go, pathway and target gene analysis, candidate genes are involved in regulating PI3K-Akt signal pathway, pathway in cancer, MAPK signal pathway, proteoglycan in cancer, actin cytoskeleton regulation, neurotrophic factor signal pathway, Hippo signal pathway and relaxin signal pathway. The specific mechanism will be further studied.

PO-009

Cluster and factor analysis of elements in serum and urine of diabetic patients with peripheral neuropathy and healthy people

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Objective To investigate imbalance characteristics of magnesium (Mg), calcium (Ca), copper (Cu), zinc (Zn), iron (Fe), chromium (Cr) and selenium (Se) in serum and urine of patients with diabetic peripheral neuropathy (DPN) using cluster analysis and factor analysis.
Methods Fifty patients with DPN were enrolled from the endocrinology department of the First Hospital of Jilin University from January 2010 to October 2011, and fifty healthy subjects were examined in the same period. ICP-MS was used for determination of elements in serum and urine.
Results Serum Mg, Ca, Zn and Cr in DPN patients were significantly lower while they were significantly higher in urine compared to controls'. There were obvious changes of elements correlation under DPN condition. Elements in two groups were clustered into 4 or 5 clusters due to internal association using multivariable analysis. Serum Cr, Se and Fe was clustered. Mg and Ca of DPN group were stronger related in both serum and urine. Factor analysis revealed discrepancies of elements' contribution. Cr, Se, and Fe appeared to be the most crucial factors related to DPN. Serum Zn and Cu contained less information whereas serum Mg included more in DPN. Mg, Ca, Zn and Cu were more influential whereas Cr became less important under disease situation.
Conclusions Contributors of elements in DPN could be determined and specify using multivariate statistical analysis.Future studies and delicate statistical models should be applied to diabetes.

PO-010

The effect of miR-92a-3p on cytokines of inflammation

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Objective To investigate the effect of miR-92a-3p on inflammatory cytokines.
Methods The negative control group was set up with thp-1 cells(NC). Thp-1 cells were treated with 0.1ug/ml and 1ug/ml LPS for 6h and 24h, and the expressions of TNF-a, IL-6 and DcR3 were detected by QPCR,as sepsis group(THP-1+LPS). Thp-1 overexpressing miR-92a-3p was treated with LPS, as sepsis group overexpressing mir-92a-3p(miR-92a-3p+THP-1+LPS). Oligo overexpression of miR-92a-3p was designed,and the restriction site was BsmBI. After annealing, it was recombined into PDS019_pL vector for sequencing verification. 293T cells were transfected with constructed miR-92a-3p overexpressed lentiviral vector and packaged plasmid. Package lentivirus, collect virus venom and

measure titer. Vl1064-pds19_miR-92a-3 infected the target cell thp-1 with MOI=100 and verified the overexpression. Thp-1 cells overexpressing mir-92a-3p were treated with 1ug/ml LPS, as miR-92a-3p+Sepsis group. The expressions of TNF-, IL-6 and DcR3 in each group were detected by qRT-PCR, ELISA and Western-blot.

Results By qRT-PCR, the mRNA expression of TNF-α and IL-6 in Sepsis, miR-92a-3p+Sepsis and NC showed a downward trend($P<0.05$), and DcR3 showed no statistical significance($P>0.05$). By ELISA, the content of TNF-α, IL-6 and DcR3 in Sepsis, miR-92a-3p+Sepsis and NC showed a downward trend($P<0.05$). By Western-blot, the gray level of TNF-α and IL-6 in Sepsis, miR-92a-3p+Sepsis and NC showed a downward trend($P<0.05$), and DcR3 showed no statistical significance($P>0.05$).

Conclusions miR-92a-3p has the function of inhibiting the release of inflammatory cytokines.

PO-011

Effects of DcR3 on the apoptosis of LPS-stimulated human umbilical vein endothelial cells

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Objective To investigate the effects of overexpression or siRNA DcR3 on the apoptosis of lipopolysaccharide (LPS)-stimulated human umbilical vein endothelial cells.

Methods Human umbilical vein endothelial cells were cultured and randomly divided into six treatment groups: normal control group, LPS-induced group, LPS+siRNA DcR3 group, LPS+siRNA control group, LPS+ pEGFP-DcR3 group and LPS+ pEGFP-control group. Western blot assay was performed to detect the expression of DcR3 in each group. The index of apoptosis in each group was determined by flow cytometry and western blot.

Results The expression of DcR3 was significantly increased after transfection with DcR3 plasmid, and decreased after transfection with siRNA DcR3. LPS can induce human umbilical vein endothelial cells apoptosis. The index of apoptosis of HUVEC was increased in LPS-induced group compared to normal control. Interference with the expression of DcR3 can enhanced the apoptosis of HUVEC induced by LPS, and overexpression DcR3 can inhibited the apoptosis of HUVEC induced by LPS.

Conclusions DcR3 can inhibit the apoptosis of endothelial cells induced by LPS, promoting its expression may reduce the blood capillary leakage caused by endothelial cell apoptosis.

PO-012

Establishing a QC strategy for genotyping tests in the molecular laboratory

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NUHS

Objective 1. To develop a quality control (QC) monitoring tool based on the percentage of positive patient results for common genotyping tests including HLA-B*27, HLA-B*1502, and *MTHFR* polymorphisms.
2. To monitor the genotyping results using Levy-Jennings charts by applying Westgard rules to determine when investigation and corrective action need to be taken.
Methods All patient results for the genotyping tests HLA-B*27, HLA-B*1502, and *MTHFR* polymorphisms from November 2017 to August 2018 (10 months) were extracted from the Laboratory Information Systems (LIS). The percentage of positive results (including both heterozygous and homozygous for MTHFR c.677C>T) were calculated out of the total number of tests received for each month and the mean and standard deviation (SD) were calculated. The control limits were set as mean ± 2SD. These results were plotted on a Levy-Jennings chart and control limits were included.
From September to December 2018, patient results for the HLA-B*27, HLA-B*1502, and *MTHFR* polymorphisms genotyping tests were extracted each month at the end of the month and the percentage of positive results calculated and plotted on the Levy-Jennings chart. Westgard rules were used to determine when investigation and corrective action need to be taken.
Results For HLA-B*27, the mean percentage of positive results over the 10 months was 24 ± 16 %. All percentage of positive results over the 4 months of monitoring were within the control limits.
For HLA-B*1502, the mean percentage of positive results over the 10 months was 10 ± 9.9 %. All percentage of positive results over the 4 months of monitoring were within the control limits.
For MTHFR, the mean percentage of heterozygous results over the 10 months was 33 ± 10 % and the mean percentage of homozygous results over the 10 months was 9 ± 4.5 %. All percentage of heterozygous results over the 4 months of monitoring were within the control limits. There were 2 months (September and December) where the percentage of homozygous results was 3% (outside of the -2SD) control limit. This is a Westgard “warning” rule. This may be due to the small number of homozygous results.
Conclusions Adopting QC protocols to monitor system performance for error prevention is feasible in the molecular laboratory for genotyping tests and can be used in our laboratory for continuous monitoring of our genotyping assay systems as an adjunct tool for quality control.

PO-013

Planning Risk-Based Multistage Internal Quality Control Schemes for HbA1c Analyzers

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Objective To help the continuous production HbA1c analyzers maintain quality more economically by planning risk-Based multistage internal quality control (IQC) schemes.
Methods The bias of two HbA1c analyzers which was derived from scheme of trueness verification organized by national center for clinical laboratories and the coefficient of variation which was resulted from routine IQC data were used to calculate sigma metric. Run size, probability of error detection and probability of false rejection of QC schedules for processes of different sigma performance were determined by sigma performance, the maximum number of patient samples to be analyzed in a work day and the desired reporting interval and combined with Sigma-metric run size nomogram and power function graph. Finally, an appropriate IQC scheme was developed.
Results The sigma metrics of Premier Hb 9210 and Sebia Capilarys 2FP analyzers with maximum of 200 patient samples were 4.96σ and 5.35σ respectively. For Premier Hb 9210 and Sebia Capilarys 2FP analyzers, two levels of controls were analyzed once in the startup IQC event ($1_{3s}/2_{2s}/R_{4s}$ with N=2 for Premier Hb 9210 analyzer and 1_{3s} N=2 for Sebia Capilarys 2FP analyzer) and only one level was analyzed once in each subsequent bracketing event (1_{3s} with N=1) every 50 patient samples. For analyzers with 5σ performance and the maximum workload of 1000 patient samples, two levels of controls were analyzed twice in the startup QC event ($1_{3s}/2_{2s}/R_{4s}/4_{1s}$ with N=4) but only once in each subsequent bracketing QC event (1_{3s} with N=2) every 200 patient samples. For analyzers with 5σ performance and the maximum workload of 500 patient samples, the two levels were analyzed only once in the startup QC event ($1_{3s}/2_{2s}/R_{4s}$ with N=2) and only one level was analyzed once in each subsequent bracketing event ($1_{2.5s}$ with N=1) every 125 patient samples.
Conclusions Continuous production HbA1c analyzers can be effectively controlled with multistage IQC designs that employ a startup IQC event followed by periodic bracketing IQC events. Such designs can be optimized to minimize the risk of harm to patients.

PO-014

Effect of Group B Streptococcus screening on pregnancy outcome and neonatals

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Objective To study the effect of Group B *Streptococcus* (GBS) infection during pregnancy on pregnancy outcome and neonatals, and explore the clinical significance of GBS screening.
Methods 800 pregnant women accepting GBS screening in our hospital from January 2016 to June 2017 were selected as the subjects. PCR technique was used to detect the GBS. According to the results of GBS screening and whether willing to receive intervention treatment, the women were divided into three groups: treatment group, non-treatment group and GBS negative group. The pregnancy outcomes and conditions of neonates were compared among the three groups.
Results 136 cases (17%) were positive for GBS. The rates of premature rupture of membranes, premature delivery, intrauterine infection, fetal distress & neonatal pneumonia, asphyxia, septicemia and pathological jaundice in the treatment group were not statistically different from those in GBS negative group (Ps>0.05). However, there were significant differences between treatmet group and non-treatment group in all the indexes expect neonatal meningitis.
Conclusions It is of great significance to conduct screening of GBS during pregnancy. Timely intervention can effectively reduce the incidence rates of bad pregnancy outcome and neonatal infection.

PO-015

Clinical Application of an Improved Mini Flow Cytometry Score in the Differential Diagnosis and Prognosis of Myelodysplastic Symptoms

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Objective In 2012, Della Porte *et al.* proposed a flow cytometric score (FCM-score), which was published for MDS patients. This approach integrated four parameters capable of distinguishing between low-grade MDS and non-clonal cytopenias. The present study applied this method and performed a minor modification to test the clinical practicability of the FCM-score.
Methods A set of antibody combination (CD34/CD19/CD33/CD45) was used to analyze the four parameters. Compared with the published method that used low SSC and CD45 expression to separate progenitor B-cell blasts and myeloblasts, the present minor modified FCM-Score (MFCM-score) used CD19 and CD33 to separate progenitor B-cell

blasts and myeloblasts from myeloid blasts within the CD34+CD45dimm population. In the first stage of the present study, the MFCM-Score were compared with the FCM-score. The study population was analyzed by two kinds of schemes, the specificity and sensitivity were respectively calculated, and the differences were analyzed to evaluate the efficacy of the MFCM-score. The second part of the study analyzed the relationship between the MFCM-score and the Revised International Prognostic Scoring System (IPSS-R) in MDS, as well as the four parameters of the MFCM-Score.

Results There was no significant difference between the MFCM-score and FCM-score in the diagnosis of MDS ($P>0.05$). The MFCM-score had a positive correlation with the IPSS-R prognosis classification of MDS (Spearman $r = 0.848$, $P<0.001$). Every parameter of the MFCM-score had a positive correlation with every grade of IPSS-R in MDS ($P<0.01$).

Conclusions The modified FCM four-parameter score is simple and practical for screening MDS patients, and the FCM-score could be used to evaluate the risk of MDS patients.

PO-016

Low level of plasma ADAMTS-13 activity predicts poor prognosis of ALL patients after bone marrow transplant

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Objective To explore the significance of decreased ADAMTS-13 activity in acute lymphoblastic leukemia (ALL) after bone morrow transplant (BMT).

Methods Thirty-eight ALL patients were included in this research and their ADAMTS-13 activity was measured before BMT, including 21 patients with low ADAMTS13 activity (<481ng/ml) and 17 patients with normal ADAMTS-13 activity (481-785ng/ml). Related medical indicators before BMT and one month after BMT were collected. All the patients were followed and their disease progress was recorded and evaluated. Level changes of the medical indicators and prognosis situations were compared between two groups.

Results Patients with Low ADAMTS13 activity suffered more BMT-related complications than patients with normal ADAMTS13 activity. There was no significant difference for APTT, PT, CRP and D-Dimer between the two groups. Low ADAMTS13 Group underwent higher mortality rate than Normal Group during the one-year follow up after BMT and two-year follow up after the onset of ALL.

Conclusions Low ADAMTS-13 activity predicts poor prognosis of ALL after BMT.

PO-017

Analysis of Prohibitin expression in breast cancer and its clinical significance based on bioinformatics

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Objective To analyze the expression and clinical significance of Prohibitin(PHB) in invasive breast carcinoma(BC) based on highthroughput multi-omics databases through bioinformatics analysis.
Methods By downloading the breast cancer data from TCGA(The Cancer Genome Atlas) and METABRIC databases, we use varieties of bioinformatics tools to compare the expression of PHB in BC tissues and its adjacent tissues, and then analyze the relations of PHB genetic expression change with clinicopathological features and prognosis of the breast cancer patients and perform protein interaction prediction of PHB and functional analysis.
Results PHB are significantly overexpressed in multiple cancer tissues compared with its adjacent tissues, especially in invasive breast carcinoma where the genetic mutation and expression changes of PHB are higher.The expression levels of PHB have good diagnostic efficacy for BC($P<0.01$). The expression levels of PHB are significantly associated with ER status, HER2 status, PAM50 type, tumor purity and so on(all $P<0.05$). Survival analysis showed that the up-regulation of PHB is an independent risk factor for breast cancer ($P<0.01$). HRAS, KSR1, ARAF interacts with PHB, with significantly correlated, and its expression changes can be seen in breast cancer tissues.
Conclusions The expression of PHB is increased in various cancerous tissues including breast cancer, and significantly affects the prognosis of breast cancer patients. PHB may participate in the progress of breast cancer as a cancer-promoting factor, and may become a potential diagnostic marker, prognostic indicator and therapeutic target for breast cancer.

PO-018

Increased progastrin-releasing peptide expression is associated with gastric cancer patients

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Objective To explore the expressions and clinical value of pro-gastrin-releasing peptide (ProGRP) and carbohydrate antigen 72-4(CA72-4) in patients with gastric cancer.
Methods Ninety patients with gastric cancer and fifty healthy subjects were selected from January 2014 to December 2016 in our hospital. Serum levels of ProGRP and CA72-4 were detected by electrochemiluminescence. The relationships between ProGRP and clinicopathological characteristics, postoperative recurrence and CA72-4 were

analyzed. The diagnostic value of ProGRP and CA72-4 in gastric cancer were analyzed by receiver operating characteristic (ROC) curve.

Results The expressions of ProGRP and CA72-4 in patients with gastric cancer were (249.3±28.9) pg/ml and (148.8±33.5) U/ml respectively, which were significantly higher than those of healthy subjects (14.4±7.6) pg/ml and (3.8±1.4) U/ml, and the differences were statistically sigificant (t=56.320, P＜0.001; t=30.504, P＜0.001). The expression of ProGRP in TNM stage Ⅲ-Ⅳ [(269.1±30.9) pg/ml] was obviously higher than that in stage Ⅰ-Ⅱ [(198.5±23.9) pg/ml], with a significant difference (t=11.200, P＜0.001). The expression of ProGRP in patients with lymph node metastasis [(259.9±31.4) pg/ml] was significantly higher than that in patients without lymph node metastasis [(190.3±26.8) pg/ml], with a significant difference (t=9.500, P＜0.001). The expression of ProGRP in patients with postoperative recurrence after one year [(181.3±21.7) pg/ml] was higer than that in patients without postoperative recurrence [(26.1±12.8) pg/ml], with a significant difference (t=31.83, P＜0.001). There was a positive correlation between serum ProGRP and CA72-4 (r=0.792, P=0.012). According to the ROC curve, the cut-off point of ProGRP was 23.6 pg/ml, and the diagnostic sensitivity was 80.0%, the specificity was 70.0%. The cut-off point of CA72-4 was 11.2 U/ml, and the diagnostic sensitivity was 60.0%, the specificity was 89.0%. The sensitivity and specificity diagnostic value of combined detection were 89.7%和 94.8%, better than those of individual detection (x^2=6.028, P=0.009; x^2=4.675, P=0.031).

Conclusions ProGRP and CA72-4 are highly expressed in the serum of gastric cancer patients, with a positive correlation. The combined detection of ProGRP and CA72-4 can improve the diagnostic sensitivity and specificity. ProGRP is significantly correlated with tumor stage, lymph node metastasis and prognosis.

P0-019

The effects of Interleukin-19 on the progression of diabetic nephropathy

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Objective Interleukin-19 (IL-19) is a newly discovered cytokine belonging to the Interleukin-10(IL-10) family. IL-19 have indispensable functions in many inflammatory processes and also can induce the angiogenic potential of endothelial cells. The purpose of present study was to investigate the relation of serum interleukin-19 (IL-19) levels with diabetic nephropathy (DN).

Methods 200 study groups of patients with type 2 diabetes mellitus (T2DM) (109 males and 91 females) were recruited, included normoalbuminuria(n=102), microalbuminuria(n=72) and macroalbuminuria(n=26) . The 50 healthy blood donors were enrolled for the control group. All subjects were assessed for: IL-19, High-sensitivity C-reactive protein (Hs-CRP), Cystatin C , urinary albumin excretion rate (UAE) and glycosylated hemoglobin A1c(HbA1c).

Results The serum IL-19 levels in DN patients were found to be significantly higher compared to controls. IL-19 levels were significantly positively correlated

with Hs-CRP, Cystatin C, UAE and HbA1c(r=0.623, 0.611 ,0.591 and 0.526 respectively, P<0.01). Multivariable logistic regression analysis showed IL-19 levels (P=0.01) were found to be independently associated with patients with DN.

Conclusions IL-19 is significantly positive correlated with UAE and Cystatin C. IL-19 may play an important role that contributes to the progression of diabetic nephropathy.

PO-020

Importance of infection control in Japanese home care and nursing care

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Objective In Japan, about 8 million people will be over the age of 75 in 2025, becoming a super aging society unparalleled in the world。
The Ministry of Health and Welfare of Japan has built a regional comprehensive care system in which residence, medical care, nursing care, prevention, and life support are provided in an integrated manner so that it is possible to continue his / her own life to the end of life even in severe nursing care conditions and in a familiar area.
While medical care is shifting to home more than ever, clinical testing equipment are becoming smaller portable for home use and waiting for that time.
On the other hand, the fact that medical treatment enters at home is not denying the possibility of medical-related infection.
However Infection control performed in Japan is a mainly medical facility of medium size or more, in infection control in the home health care field, most situations are such that no experts exist。
Therefore, this time we will conduct a questionnaire survey to the business establishment that is a key part of the regional comprehensive care system, and clarify the importance of infection control in home care and nursing care in Japan and future tasks.

Methods We conducted a questionnaire survey on infection control in home medical care and nursing care at business establishments with a visiting nursing station.

Results According to the actual situation survey, medical staff and carers were concerned about the lack of knowledge and skills for infection control, and there was anxiety.

Conclusions As for infection control in home care and nursing care, it was suggested that there was a fear that it could be a serious social problem because it could not deal sufficiently.

In the future, it is necessary to educate medical professionals and carers practicing home medical care / nursing care about knowledge on infection control and technical acquisition.

PO-021

Value of fecal TU-M2PK detected with colloidal gold method in diagnosis of colorectal cancer

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Objective To study the value of fecal TU-M2PK detected with colloidal gold method in screening and early diagnosis of colorectal cancer.
Methods Fecal TU-M2PK markers in 39 early colorectal cancer patients,108 persons at high risk of colorectal cancer and 107 colorectal benign controls were detected with M2PK Quick colloidal gold rapid detection reagent produced in Germany ScheBo Company and analyzed.
Results The sensitivity and specificity of fecal TU-M2PK were 64.1% and 85.3% in screening and early diagnosis of colorectal cancer. The serum TU-M2PK level was significantly higher in colorectal cancer patients than in persons at high risk of colorectal cancer and colorectal benign controls, and in persons at high risk of colorectal cancer than in colorectal benign controls($\chi^2=18.113, P<0.001$; $\chi^2=35.031, P<0.001$; $\chi^2=4.245, P<0.05$).
Conclusions It is simple, rapid, accurate to detect the fecal TU-M2PK markers with M2PK Quick colloidal gold rapid detection reagent with a good repeatability, which is easy to be accepted by the patients and can thus be used in screening and early diagnosis of colorectal cancer in a large population.

PO-022

The Clinical value of TCT combined with Immunohistochemistry in the diagnosis of malignant pleural effusion caused by NSCLC

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Objective To examine the cytopathology by the Thin-Cytologic Test (TCT) and test qualitatively the Thyroid Transcription Factor (TTF-1), Cytokeratin 7 (CK7), Cytokeratin 5/6 (CK5/6) and P63 in the pleural effusion by the Immunohistochemistry method, and then evalue the clinical application value of these combined method in diagnose malignant pleural effusion caused by non-small cell lung cancer(NSCLC) and it's classification diagnosis.

Methods Firstly,we have screened out 281 cases of suspected tumor cells and tumor cells by the TCT method from 703 pleural effusion cases.Secondly,137 cases of malignant pleural effusion caused by NSCLC were confirmed by CT, MRI and histopathology, including 88 cases of male and 49 cases of female, aged 30-85 years.Thirdly, we have tested the TTF-1 、 CK7 、 CK5/6 and P63 by the Immunohistochemistry method in the 137 cases pleural effusion caused by confirmed NSCLC to classify the lung adenocarcinoma and squamous cell carcinoma in terms of the histological examination. Finally, We have calculated the area under the curve(AUC) and evalued the clincal diagnostic value of these combined method by analysis for the ROC curve.

Results We found 137 malignant effusion cases caused by NSCLC from 703 pleural effusions cases,including 110 cases of lung adenocarcinoma, 25 cases of lung squamous cell carcinoma and 2 cases of lung adenosquamous carcinoma.The TTF-1 and CK7 were highly expressed in adenocarcinoma with the positive rates 87.18% (68/78) and 94.23% (49/52)respectively; The CK5/6 and P63 were highly expressed in squamous cell carcinoma with the positive rates92.86% (13/14) and 91.67% (11/12) respectively. In the differential diagnosis of squamous cell carcinoma and adenocarcinoma, the sensitivity, specificity and accuracy of CK5/6 in the diagnosis of squamous cell carcinoma were 92.86%, 89.58 % and 90.32% . The sensitivity, specificity and accuracy of p63 in the diagnosis of squamous cell carcinoma were 91.67%, 72.733%and 77.78%.The sensitivity, specificity and accuracy of TTF-1 in the diagnosis of adenocarcinoma were 87.18%,90.63% and 88.18%, respectively. The sensitivity, specificity and accuracy of CK7 in the diagnosis of adenocarcinoma were 94.23%,75.00% and 91.67%,respectively.The AUC of ROC curve for TTF-1 and CK7 in the diagnosis of lung adenocarcinoma were 0.821 and 0.774 respectively; correspondingly, these of the CK5/6 and P63 in the diagnosis of squamous cell carcinoma were 0.805 and 0.755 respectively.

Conclusions The TTF-1, CK7, CK5/6, and P63 are important in guiding the diagnosis of lung adenocarcinoma and squamous cell carcinoma.The examination the cytopathology by Thin-Cytologic Test combined with the Immunohistochemistry method is clinically useful for the pathological diagnosis and classification of malignant effusion caused by NSCLC.

PO-023

Correlation of Matsuda Index with lipid parameters in young Japanese

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Objective To examine the correlation between Matsuda Index on 75g oral glucose tolerance test (75gOGTT) and lipid parameters among healthy young Japanese, and to classify the prolonged glucose elevation group.

Methods Total 595 young healthy Japanese students aged 22-29 years received 75gOGTT. The 75gOGTT was performed with 0-, 30-, 60-, and 120-min sampling to assay plasma glucose (PG0, PG30, PG60, and PG120), insulin levels (IRI0, IRI30, IRI60, and IRI120), HbA1c, high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C) and triglyceride (TG). Body mass index (BMI) was calculated. Informed consent was obtained from all participants. Subjects were divided into 4 groups (I-IV), based upon the time at which their plasma glucose concentration declined below the fasting glucose concentration (30, 60 or 120 min or never). Data were compared among groups. The homeostasis model assessment of insulin resistance (HOMA-IR = PG0 × IRI0/405), β cell function (HOMA-β = IRI0 × 360 / (PG0 - 63)), and Matsuda Index of insulin sensitivity (10,000 / square root of [fasting glucose × fasting insulin] × [mean glucose × mean insulin during 75gOGTT]), were calculated. The insulinogenic index was calculated by dividing the increment in serum insulin by the increment in plasma glucose during the 0-30 min time periods of the OGTT. The Pearson correlation coefficients between Matsuda Index and IRI0 and lipid parameters such as HDL-C, LDL-C, and TG were calculated.

Results Five hundred seventy-five were diagnosed as normal glucose tolerance (NGT). Since one subject was impaired fasting glucose and 19 were impaired glucose tolerance, they were excluded from the subsequent analysis. The mean ± SD of fasting plasma glucose, HbA1c, IRI0, HDL-C, LDL-C, and TG were 90.5 ± 6.7 mg/dL, 5.34 ± 0.21 %, 6.48 ± 3.39 μIU/mL, 63.6 ± 13.7 mg/dL, 98.9 ± 25.8 mg/dL, and 74.0 ± 37.8 mg/dL, respectively. Thirty, 60, and 120 minutes postload plasma glucose values were 131.2 ± 24.9 mg/dL, 113.6 ± 29.1 mg/dL, and 94.8 ± 17.6mg/dL, respectively. Thirty, 60, and 120 minutes postload insulin levels were 57.21 ± 41.53 μIU/mL, 46.37 ± 30.43 μIU/mL, and 35.21 ± 24.22 μIU/mL, respectively. Mean ± SD values of HOMA-IR, HOMA-β, Matsuda Index, and insulinogenic index were 1.51 ± 0.97, 85.9 ± 41.1, 7.74 ± 3.69, and 1.56 ± 3.86, respectively. NGT subjects were divided into 4 groups (I-IV). The population was 28 (4.9%), 120 (20.9%), 143 (24.9%), and 284 (49.4%), respectively. Although differences in PG0 and IRI0 were not observed, significant differences were observed in each group in postload plasma glucose and insulin. Remarkably, plasma glucose and insulin levels were significantly higher in group IV than group I. As for insulin secretion and resistance indices, no significant difference in HOMA-IR, HOMA-β among groups. On the other hand, significant differences were observed in Matsuda Index and insulinogenic index among groups. Matsuda Index was negatively correlated with IRI0, TG, and LDL-C, and positively with HDL-C. We divided their metabolic parameters by IRI0. There was the strongest inverse correlation between Matsuda Index and IRI0/HDL-C. Matsuda Index showed the highest correlation with HDL-C/IRI0 (R^2 = 0.55).

Conclusions Former study suggested that subjects in group III and IV have higher risk for T2DM than group I or II. Unexpectedly, about three fourths of young Japanese showed prolonged plasma glucose elevation on 75gOGTT and that was similar to middle-age Caucasian in former study. Although Matsuda Index is a good indicator for whole-body insulin sensitivity and correlated with the prolongation of plasma glucose elevation, it is stressful because it needs blood sampling at least 4 times. In this manner, Matsuda Index may be substituted by one time sampling and may classify the prolonged glucose elevation group.

PO-024

Correlation of plasma chemerin and visceral adipose tissue-derived serpin in obese people with fasting hyperglycemia and normoglycemia

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Objective This study was designed to examine plasma chemerin and visceral adipose tissue-derived serpin (vaspin) levels and their correlation in obese people with fasting hyperglycemia and normoglycemia.
Methods We performed a cross-sectional study from obese people. A total of 60 volunteers of obese people aged 20 - 69 years were enrolled and divided into obese group with fasting hyperglycemia and normoglycemia. We also recruited 10 non-obese people with normal fasting blood glucose as a control group. Chemerin and vaspin level were measured using ELISA method. Fasting plasma glucose was analysed using hexokinase method. The data were analysed using IBM Statistic SPSS 22.
Results Obese group with fasting hyperglycemia and normoglycemia exhibited higher level of chemerin and vaspin than control group. Mean plasma chemerin levels (ng/mL) were 74.77, 67.46, and 53.52, for obese group with fasting hyperglycemia, obese group with normoglycemia, and control group, respectively. Mean plasma vaspin levels (ng/mL) were 90.66, 91.86, and 60.06 for obese group with fasting hyperglycemia, obese group with normoglycemia, and control group. In Spearman correlation analysis, chemerin was positively associated with vaspin (r=0.457, p=0.001). Chemerin also correlated with fasting plasma glucose (r = 0.251, p = 0.01). There was no significant correlation between vaspin and fasting plasma glucose.
Conclusions It can be concluded that chemerin and vaspin levels increased in obese people with and without fasting hyperglycemia. Chemerin has association with fasting blood glucose than vaspin in obese people.

PO-025

Expression and significance of caspase-1 in patients with systemic lupus erythematosus

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Objective Systemic lupus erythematosus (SLE) is a chronic autoimmune disease involving multiple system, organs, and autoantibodies. Immune dysfunction plays an important role in the formation and development of SLE, especially, the recent found immune regulation mechanism, inflammasome, which has been involved in many immune diseases. The aim of the study was to investigate the expression and clinical significance of

caspase-1, the central enzyme of the inflammasome signaling pathway, in the patients with systemic lupus erythematosus (SLE).

Methods The current study was conducted at the Zhongshan hospital of Sun Yat-sen University laboratory. 74 patients with SLE and 20 healthy control were included in the study. Patients with SLE in accordance with the American College of Rheumatology classification criteria (ACR 2009) for the dignosis of SLE were included in the study, while, patients with liver or kidney disease, infection, cancer, metabolic diseases, and other autoimmune diseases were excluded. SLE disease activity index (SLEDAI) of each patients was determined by clinical and serological data including skin involvement, arthritis, renal involvement, full cell blood count, serum complement levels, anti-dsDNA and other extractable nuclear autoantibodie.ELISA was used to detect the serum levels of caspase-1 in patients and health controls. Correlations between caspase-1 expression and clinical or laboratory parameters were analyzed by SPSS statistical tool.The Mann-Whitney test was used to comparisons between quantitative variables and the Spearman correlation analysis to study the correlation between variables.

Results The study subjects had a mean age of 33.50±11.48 years (SLE) and 36.72±13.43 years (controls).Compared to those in healthy controls, levels of caspase-1 was lower in SLE patients (55.96±30.130 pg/mL vs.74.61±20.384 pg/mL, $p<0.05$); the levels of caspase-1 was inversely correlated with SLEDIA scores ($r=-0.313$, $p=0.006$), globulin ($r=-0.268$, $p=0.024$) and Anti-dsDNA ($r=-0.422$, $p=0.001$), whereas positively correlated with TC ($r=0.326$, $p=0.024$) and C3 ($r=0.352$, $p=0.003$). Further, our study showed that the patients with disease in remission (SLEDAI=0) exhibited higher serum levels of caspase-1 (69.64±30.354 pg/mL vs.50.24±26.63 pg/mL, $p<0.05$) .

Conclusions Our data indicated that the expression of caspase-1was inversely correlated with the disease activity, suggesting it might play a protective role in the pathogenesis of SLE.

PO-026

Development of a preoperative prediction nomogram for lymph node metastasis in colorectal cancer based on a novel serum miRNA signature and CT scans

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Objective Preoperative prediction of lymph node (LN) status is of crucial importance for appropriate treatment planning in patients with colorectal cancer (CRC). In this study, we sought to develop and validate a non-invasive nomogram model to preoperatively predict LN metastasis in CRC.

Methods Development of the nomogram entailed 3 subsequent stages with specific patient sets. In the discovery set (n=20), LN-status-related miRNAs were screened from high-throughput sequencing data of human CRC serum samples. In the training set (n=218), a miRNA panel-clinicopathologic nomogram was developed by logistic regression analysis

for preoperative prediction of LN metastasis. In the validation set (n=198), we validated the above nomogram with respect to its discrimination, calibration and clinical application.

Results Four differently expressed miRNAs (miR-122-5p, miR-146b-5p, miR-186-5p and miR-193a-5p) were identified in the serum samples from CRC patients with and without LN metastasis, which also had regulatory effects on CRC cell migration. The combined miRNA panel could provide higher LN prediction capability compared with computed tomography (CT) scans ($P<0.0001$ in both the training and validation sets). Furthermore, a nomogram integrating the miRNA-based panel and CT-reported LN status was constructed in the training set, which performed well in both the training and validation sets (AUC: 0.913 and 0.883, respectively). Decision curve analysis demonstrated the clinical usefulness of the nomogram.

Conclusions Our nomogram is a reliable prediction model that can be conveniently and efficiently used to improve the accuracy of preoperative prediction of LN metastasis in patients with CRC.

PO-027

Serum and urine β-Trace Protein as potential risk marker for renal disease and metabolic syndrome in type 2 diabetic patients without renal dysfunction

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Objective This study was designed to investigate the association of serum and urine BTP levels with Mets and the early stage of diabetic nephropathy in patients with type 2 diabetes.

Methods A total of 236 patients with type 2 diabetes were evaluated for anthropometric measurements and biochemical studies. The recruit criteria is serum creatinine level <1.2 mg/dl.

Results sBTP and uBTP level tended to increase in parallel with progression of the diabetic nephropathy. sBTP was significantly higher in the Mets group than that in the non-Mets group . Stepwise multiple regression analysis demonstrated that sBTP was independently associated with serum creatinine, UACR .

Conclusions sBTP were significantly associated with Mets. Elevated sBTP and uBTP concentration was a significant predictor for increased UACR independent of conventional risk factors in type 2 diabetic patients. Regular measurements of BTP levels could help stratify patients at high risk for proteinuria and Mets in conjunction with conventional risk factors.

PO-028

Apolipoprotein C1 (APOC1) as a novel diagnostic and prognostic biomarker for gastric cancer

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Objective Gastric cancer (GC) is a common malignant tumor in the worldwide, especially in China. Patients with GC have poor prognosis due to lack of delayed diagnosis and non-specific symptoms in the early stages. Up to now, there is no good biomarker to detect GC at early stage. Apolipoprotein C1 (APOC1), a component of both triglyceride-rich lipoproteins and high-density lipoproteins, is reported to be involved in numerous biological processes. In the study, we investigated if APOC1 was used as a diagnostic and prognostic biomarker for GC.
Methods Serum from 65 GC patients and 40 healthy individuals were collected and detected by ELISA. Expression of APOC1 protein was evaluated in both GC and adjacent issues of GC and normal tissues using tissues array by immunohistochemistry. Expression of APOC1 and clinical characteristic of GC as well as prognosis of patients with GC were analysed respectively.
Results It was firstly found that APOC1 concentration was significantly higher in GC than that in control. Expression of APOC1 protein was also higher in GC than that in adjacent issues of GC and normal tissues using tissues array by immunohistochemistry. Besides, the overall expression of APOC1 is significantly associated with clinical stage (p=0.011), tumor classification (p=0.010), as well as with the lymph node metastasis (p=0.048). Area under the curve of receiver operating characteristic of APOC1 was 0.803. Furthermore, elevated APOC1 concentration in serum was found to be correlated with decreased overall survival (p<0.0001).
Conclusions These results suggest that APOC1 in serum may be used as a potential biomarker to detect GC at early stage and predict prognosis of GC.

PO-029

The chromosomal microarray analysis results of prenatal diagnosis for 449 women with micro malformation examined by ultrasound

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Objective To assess the application value of chromosome microarray analysis (CMA) in prenatal fetal with micro malformation examined by ultrasound.
Methods Four hundred and forty-nine women who pregnancy 24-33 weeks with micro malformation examined by ultrasound from June 2014 to December 2017 were subjected to

amniocytic or cord blood karyotyping and CMA analysis, all participants signed the informed consent.

Results Forth-eight women were found to have a chromasomal aneuploidies fetal, which include 33 cases of trisomy 21, 8 cases of trisomy 18, 1 case of 45, X, 1 case of 47, XXY, 1 case of 47, XXX, 1 case of 46, XY, del (4) (q34.1) , 1 case of 46, XX,dup(9) (p24.3q13) , 1 case of 46, XY, dup (17) (q21.32q22) , 1 case of 47, XX, +9 [21]/46] XX [79] , the detection rate of chromosome number and structure abnormalities in fetus was 10.69%. Fifty-six cases with copy number variations (CNVs) detected by CMA in normal fetal karyotypes of the remaining 401 cases ,which include 21 cases of pathogenic CNVs, 8 cases of likely pathogenic CNVs, 15 cases of uncertain significance CNVs,12 cases of likely benign CNVs, 17 cases of benign CNVs, and the detection rate of pathogenic CNVs was 5.23%.

Conclusions CMA can detect genome-wide CNVs with high resolution compaired with karyotyping. The application of CMA in prenatal diagnosis can improve the detection rate of chromosome microdeletion and microduplication with clinical significance.

P0-030

A comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome

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Objective In order to profile the normal CSF proteome by a TripleTOF 5600 mass spectrometer integrated with high-pH reverse-phase liquid chromatography (hp-RPLC) .

Methods In this study, high-pH reverse-phase liquid chromatography (hp-RPLC) was first integrated with mass spectrometer to profile the normal CSF proteome. A total of 49,836 unique peptides and 3256 non-redundant proteins were identified. Then, 2513 proteins with at least 2 unique peptides were further selected as bona fide CSF proteins. Nearly 30% of the identified CSF proteins have not been previously reported in the normal CSF proteome. More than 30% of the CSF proteins (788 proteins) were related to neurological diseases. This study identified the largest high-precision dataset of the CSF proteome, which offers a baseline reference for CSF biomarker discovery.

Results Knowledge about the normal human cerebrospinal fluid (CSF) proteome serves as a baseline reference for CSF biomarker discovery and provides insight into CSF physiology. In this study, high-pH reverse-phase liquid chromatography (hp-RPLC) was first integrated with a TripleTOF 5600 mass spectrometer to comprehensively profile the normal CSF proteome. A total of 49,836 unique peptides and 3256 non-redundant proteins were identified. To obtain high-confidence results, 2513 proteins with at least 2 unique peptides were further selected as bona fide CSF proteins. Nearly 30% of the identified CSF proteins have not been previously reported in the normal CSF proteome. More than 25% of the CSF proteins were components of CNS cell microenvironments, and network analyses indicated their roles in the pathogenesis of neurological diseases. The top canonical pathway in which the CSF proteins

participated was axon guidance signaling. More than one third of the CSF proteins (788 proteins) were related to neurological diseases, and these proteins constitute potential CSF biomarker candidates. The mapping results can be freely downloaded at http://122.70.220.102:8088/csf/, which can be used to navigate the CSF proteome.
Conclusions This study identified and functionally annotated the largest high-precision dataset of the CSF proteome, which offers a baseline reference for CSF biomarker discovery and reveals insight into CSF physiology.

PO-031

Detection of EGFR Mutations in Circulating Tumor DNA via Raman Spectroscopy

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Objective The epidermal growth factor receptor (EGFR) gene mutations in circulating tumor DNA (ctDNA) have been used to guide the targeted therapy of patients with lung cancer as well as to evaluate the tumor burden and malignant progression. Herein, we try to create a new detection method of EGFR mutations in ctDNA in the peripheral blood without any preprocessing in order to simplify the clinical process and reduce the turnaround time, furthermore, to gain the key information for cancer diagnosis and treatment more timely.
Methods 1. Samples

52 plasma samples of lung cancer patients were collected. The mutations of EGFR gene were identified by Real-time ARMS-PCR after DNA extraction. Except the clinical samples, simulated samples which were made with EGFR wild-type plasma and EGFR mutated plasmid (four different concentrations of 19del, L858R and T790M mutation) were used to establish the detection method.
2. Method

Each sample was taken 5μL onto the slide and detected using a Raman microscope (XploRA PLUS) under the following conditions. 1)Wavelength: 532nm; 2)Collection time: 20s; 3)Collection times: 1 time; 4)Spectral range: 600-1800cm^{-1}; 5)Grating: 1800 gr/mm; 6)50-fold objective lens; 7)100% laser power. All of the results were analyzed by LabSpec 6.
Results 1. Simulated samples

Mixed EGFR wild-type plasma was used to gain the Raman spectrum of plasma as the blank control (Figure 1). On this basis, four different concentrations of simulated EGFR mutated plasma samples were used to confirm the characteristic Raman spectrum of each mutation type (Figure 2). Raman peaks were observed near 1154cm^{-1} and 1518cm^{-1} of all mutated plasma at different concentrations which were similar to the Raman spectrum of mixed wild-type plasma. However, these two peaks were considered as background interference of plasma for the peak height was inversely proportional to the concentration of mutated plasmid. While all three types of EGFR mutated simulated plasma showed obvious Raman peak near 676cm^{-1} only at the concentration of 200ng/μL, such Raman peak was not observed when verified with pure mutated plasmid. To further confirm the difference between the three EGFR

mutation types, we co-analysis three simulated samples at the concentration of 200ng/μL (Figure 3). Although there was no significant difference in L858R and T790M mutation, the Raman spectrum of 19del mutation shows obvious difference when compared with the other two mutations.

Figure 1. Raman spectrum of mixed EGFR wild-type plasma shows two Raman peaks near 1154cm^{-1} and 1518cm^{-1}.

Figure 2. Raman peaks of all mutated plasma at different concentrations were similar to the Raman spectrum of mixed wild-type plasma. Blue curve stands for the concentration of 200ng/μL, green for 50 ng/μL, red for 12.5 ng/μL and purple for 3.125 ng/μL. All three types of EGFR mutated simulated plasma showed obvious Raman peak near 676cm^{-1} only at the concentration of 200ng/μL. (A) 19del mutation; (B) L858R mutation; (C) T790M mutation

Figure 3. The Raman spectrum of 19del mutation shows difference from 750cm^{-1} to 990cm^{-1} when compared with the other two mutations. Blue curve stands for 19del mutation, green for L858R and red for T790M.

2. Clinical samples

Clinical samples were then used to verify the Raman peaks found in simulated samples. Nevertheless, similar Raman spectrum was not observed.

Conclusions In summary, we have tried a new detection method for EGFR mutations in ctDNA via Raman Spectroscopy. The result shows that the current method still needs to be improved for its low specificity and sensitivity. To determine the characteristic Raman spectrum of EGFR mutations, we are going to use sample purification or Surface Enhanced Raman Scattering (SERS) to make the method more specific and sensitive. Hope that Raman Spectroscopy could become a new clinical detection method for ctDNA, furthermore, complement current liquid biopsy approaches for cancer diagnosis and treatment.

PO-032

High levels of antibodies to citrullinated α-enolase peptide-1 (CEP-1) identify erosions and interstitial lung disease (ILD) in a Chinese rheumatoid arthritis cohort

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Objective The presence of autoantibodies against citrullinated peptides (ACPA) represents a hallmark feature of rheumatoid arthritis (RA). The current 'golden standard' for detection of ACPA is the second generation of anti-CCP (anti-CCP2) assay, which utilizes artificial peptides that are thought to be absent in the human joint. Interestingly, serum ACPA fine specificities differ among different ethnic populations, indicating variations in genetic and/or environmental factors may determine different patterns of ACPA fine specificities. In this study, we assessed the clinical relevance of autibodies to peptide 1 of citrullinated a-enolase (anti-

CEP-1), which is a true physiological protein whose levels are significantly increased in the joint in RA, in Chinese patients with RA.

Methods A total of 264 subjects were tested, including 101 RA patients, 38 juvenile idiopathic arthritis (JIA) patients, 46 disease control (DC) and 79 healthy controls (HC). Serum ACPA were determined by anti-CCP2 IgG ELISA (Euro Diagnostica, Malmö, Sweden) according to the manufacturer's instructions. Serum IgG anti-CEP-1 were determined by an anti-CEP-1 ELISA (IgG) kit (Euroimmun, Germany) according to manufacturer's instructions.

Results The presence of anti-CEP-1 in patients with RA, JIA, DCs and HC were 61.4%, 13.2%, 15.2% and 5.1%, respectively. Anti-CCP2 demonstrated the highest positive likelihood ratio of 10.11 in the diagnosis of RA, followed by RF (8.88) and anti-CEP-1 (5.82). Anti-CEP-1 positive RA patients displayed significantly higher DAS28 compared to anti-CEP-1 negative RA patients (p=0.045). Significant associations were identified between anti-CEP-1 and joint erosions at anti-CEP-1 value of >124.78 U/ml (p=0.0026) and between anti-CEP-1 and ILD at anti-CEP-1 value of >185.91 U/ml (p=0.0222).

Conclusions Our findings indicate that anti-CEP-1 may not be able to replace anti-CCP2 for routine diagnosis for RA, but they may be helpful for subtyping of the disease.

PO-033

Decreasing methicillin resistant Staphylococcus aureus (MRSA) infections is attributable to the disappearance of predominant MRSA ST239 clones, Shanghai, 2008–2017

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Objective A consistently decreasing prevalence of MRSA infections in China has been reported, however, the underlying mechanism of molecular processes responsible for this decline in MRSA infections has been poorly understood. Therefore, the present retrospective study aimed at investigating the dynamic changes over the past decadein the molecular characteristics of *S. aureus* infections.

Methods A total of 3695 *S. aureus*isolates was recovered from a comprehensive teaching hospital in Shanghai from 2008 to 2017, subsequently characterized by infection types, resistance profile and subjected to genetic multi-locus sequence typing and *spa* typing.

Results The frequency of respiratory infection decreased over the study period from 76% to 52%, but a concomitant increase from 12% to 27% was observed in the frequency of skin and soft tissue infection (SSTI) cases. The proportion of MRSAremarkably decreased from 83.5% in 2008 to 54.2% in 2017 ($p<0.0001$). The prevalence of two previously predominanthealthcare-associated MRSA (HA-MRSA)clones, ST239-t030 and ST239-t037, significantly decreased (from 20.3% to 1% and 18.4% to 0.5%, 2008-2017, respectively); both of them were replaced by the continually growingST5-t2460 clone (from 0% to 17.3%, 2008-2017). Also of note were the significantly increasing trends in the proportion of well-known epidemic highly virulent community-acquired MRSA

(CA-MRSA) ST59 and ST398 clones (from 1.0% to 5.8% and 1.8% to 10.5%, 2008-2017, respectively).

Conclusions These results demonstrated a significant decrease in the previously dominant HA-MRSA ST239 clones, leading to a marked decrease in the prevalence of MRSA during the past decade, and shed new light on the complex competition of *S. aureus* clones that predominate within the health care environment and the rapidly emerging virulent CA-MRSA clones.

PO-034

Suppression of pro-inflammatory immune response by schistosomiasis infection alleviates experimental cerebral malaria

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Objective Severe neurological complications caused by cerebral malaria (CM) are the leading death cause in children under 5 years old. Inappropriate immune responses are importantly associated with the development of CM. In malaria endemic areas, malaria patients are often accompanied by helminth infections, but the outcome depends on the strains, severity and route of infection. We used *Schistosoma japonicum* and ECM models to explore the role of pro-inflammatory immune responses in co-infection.

Methods The co-infection models was established and monitored the parasitemia and survival time. The frequencies of DC subpopulations, macrophages, Treg and expressing levels of CD86, TLR4 and TLR9 in spleen were analyzed by FACS. The secretion levels of IL-10, TNF-α, IFN-γ and NO in the supernatant were cultured and detected by ELISA and *Griess* method.

Results Co-infection increased the body weight, reduced parasitemia and prolonged survival of mice. The number of splenic DC subsets, macrophages and the expression level of TLR9 were significantly reduced by co-infection. Pro-inflammatory cytokines, such as TNF-α, IFN-γ and NO were significantly decreased, however, the number of Treg and IL-10 level were increased in co-infection group.

Conclusions Infection with *Schistosoma japonicum* can inhibit ECM by inhibiting the pro-inflammatory immune response, which results in prolonging the survival of the host.

PO-035

Hexokinase 2 depletion confers sensitization to metformin and inhibits glycolysis in lung squamous cell carcinoma

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Objective Lung squamous cell carcinomas (SCCs) are highly aggressive tumors, and there is currently no effective targeted therapy owing to the high glycolysis rate and lack of specific mutations.
Methods Molecular analysis of SCC tissues compared with lung adenocarcinoma (ADC) from public databases showed increased HK2 expression only in SCC compared to that in adjacent non-cancer tissues. Biological experiments clarify the role of HK2 in SCC and regulation mechanism.
Results HK2 depletion through RNA interference or lonidamine treatment decreased the glycolysis and proliferation, and also increased the apoptosis of SCC cancer cells. In addition, HK2 ablation or inhibition induced activation of the AMPK signaling pathway, which downregulated mTORC1 activity. Since the oxygen respiration rate was enhanced to compensate for HK2 silencing, metformin treatment showed combinatorial therapeutic value on lung tumor and resulted in greater induction of cancer cell apoptosis.
Conclusions Our study provides a new framework for understanding the basis of HK2 dependency in lung SCC tumors, and provides a therapeutic rationale for combining metformin to suppress oxygen respiration, resulting in sustained energy stress to more effectively inhibit cancer cell growth.

PO-036

Differential expression of miRNAs in breast cancer tissues and the effect of Xihuang Pill on the expression of candidate miRNAs in breast cancer cells in vitro

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Objective To study the differentially expressed miRNAs in breast cancer FFPE tissue and the effect of Xihuang Pill extract on the expression of candidate miRNAs in breast cancer cell line in vitro.
Methods Microarray was used to detect the differentially expressed miRNAs in breast cancer tissues, adjacent tissues and cancer tissues with different molecular types, and the results of unsupervised cluster analysis were processed by cluster software.

Real-time fluorescence quantitative PCR was used to detect the expression of candidate miRNAs in 106 breast cancer tissues, 22 paracancerous tissues and 66 benigh breast lesions. The extract of Xihuang Pill interfered with T-47D cells and MDA-MB-231 cells, then the expression of candidate miRNAs in those cells were detected by real-time fluorescence quantitative PCR.

Results The microarray results showed that the expression of miR-130b was higher in cancer tissues than in adjacent tissues ($p<0.05$). The expression of miR-205 in basal-like cancer tissues with higher malignancy was significantly lower than that in luminal cancer tissues ($p<0.05$). Real-time fluorescence quantitative PCR showed that the expression miR-130b in cancer tissues and adjacent tissues was significantly higher than that in benigh lesion tissues ($p<0.05$), and the expression of miR-205 in cancer tissues was significantly lower than that in benigh lesion tissues ($p<0.05$). Cell experiment in vitro showed that the expression of miR-130b in T-47D cells decreased after the intervention of Xihuang Pill extract ($p<0.05$), while the expression of miR-205 in MDA-MB-231 cells increased after the intervention of Xihuang Pill extract ($p<0.05$).

Conclusions The increase of miR-130b and the decrease of miR-205 are related to the occurrence and development of breast cancer. The increase of miR-130b and the decrease of miR-205 may be one of the anti-tumor ways of Xihuang Pill.

P0-037

Interference analysis for elimination of lipid blood on liver function tests by high speed centrifugal method

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Objective To observe the differences of nine biochemical liver function tests between routine centrifugal and high speed centrifugal method, and investigate whether the high speed centrifugal method can eliminate the interference of lipid blood on biochemical liver function tests.

Methods The lipid blood samples of 50 patients were collected randomly. After routine centrifugal, serum total protein(TP), albumin(ALB), aspartate amino transferase(AST), alanine amino transferase(ALT), alkaline phosphatase(ALP), γ-glutamyl transpoptidase(GGT), total bile acid(TBA), total bilirubin(TBIL), direct bilirubin(DBIL) were measured by the HITACHI 008 automatic biochemical analyzer. Then after high speed centrifugal, clear serum were measured again while the upper lipid were removed. The results were compared between routine centrifugal and high speed centrifugal.

Results There were no statistical difference of most biochemical liver function tests after high speed centrifugal method except TBIL, GGT, ALP.

Conclusions High speed centrifugal method can eliminate the the interference of lipid blood on some biochemical liver function tests.

PO-038

Platelet activation status in the diagnosis and postoperative prognosis of hepatocellular carcinoma

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Objective The venous thromboembolism, which may be caused by increased platelet activation, is a risk factor for tumor prognosis. The aim of this study was to determine the platelet activation status for diagnosis and predicting postoperative prognosis of hepatocellular carcinoma.

Methods We conducted a prospective study of 191 patients diagnosed with HCC at Zhongshan Hospital from April 2016 to July 2016 as well as 99 healthy people. The platelet activation status was assessed by two platelet markers, PAC-1 and CD62p, using flow cytometry. The patients were treated with TACE or resection and monitored for ⩾6 months. The diagnostic value of marker-positive platelets was determined by the receiver operating characteristic curve and the postoperative value were analyzed using the Kaplan-Meier method and COX regression model.

Results All the three groups with high levels of marker-positive platelets were likely to be diagnosed with HCC and the PAC-1+ percentage had the best efficacy. The univariate analysis showed that the levels of PAC-1+ and CD62p+ platelets was risker factors for poor postoperative prognosis after both TACE and resection. Moreover, the multivariate analysis revealed that the level of PAC-1+ platelets was an independent risk factor for poor prognosis.

Conclusions The PAC-1+ percentage of platelets is a new indicator for diagnosis and predicting postoperative prognosis.

PO-039

The clinical significance of alpha-1-acid glycoprotein in children with bronchial pneumonia caused by Mycoplasma pneumoniae infection

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Objective To explore the clinical significance of acute phase reaction protein such as alpha -1-acidic glycoprotein(α1-AGP) in children with bronchopneumonia with *Mycoplasma pneumoniae(MP)* infection.

Methods Inpatients with bronchopneumonia who received treatment in pediatric department in our hospital were enrolled from January to August in 2018 ,58 children had Mycoplasma pneumoniae pneumonia （MPP）and 139 had no MPP (NMPP).Blood samples

were collected to analyze blood routine test, liver function and myocardial enzymes examination and the serum concentration of other laboratory examinations such as α1-AGP, C-reactive protein(CRP) and calcitonin(PCT),which results were compared between the groups. Then multiple logistic regressions analysis were used to select the main related factors of MPP,and the receiver-operating characteristic curves(ROC) and area under the curve[AUC(95 % CI)] comparing were used to evaluate the value of the selected markers used to identify MPP from bronchopneumonia.

Results There were significant differences in levels of white blood cells(WBC), lymphocytes(L), eosinophils(E), PCT and α1-AGP between the two groups(P<0.05). Multiple logistic regressions analysis adjusted for age showed that only WBC, PCT, and α1-AGP were the main related factors for children with MPP . Significant increase was found in serum α1-AGP in children with MPP(P <0.05),which could perhaps be used to identify MPP from common bronchopneumonia and its AUC(95 % *CI*) was 0.688 (0.606-0.769) ,which was higher than that of WBC and PCT(P <0.05). Combination with α1-AGP and PCT and WBC could improve the AUC(95 % *CI*) to 0.768 (0.695-0.841) .

Conclusions There were significant differences in levels of white blood cells(WBC), lymphocytes(L), eosinophils(E), PCT and α1-AGP between the two groups(P<0.05). Multiple logistic regressions analysis adjusted for age showed that only WBC, PCT, and α1-AGP were the main related factors for children with MPP . Significant increase was found in serum α1-AGP in children with MPP(P <0.05),which could perhaps be used to identify MPP from common bronchopneumonia and its AUC(95 % *CI*) was 0.688 (0.606-0.769) ,which was higher than that of WBC and PCT(P <0.05). Combination with α1-AGP and PCT and WBC could improve the AUC(95 % *CI*) to 0.768 (0.695-0.841) .

PO-040

Rapid identification of Acinetobacter baumannii by surface enhanced laser desorption and ionization time of flight mass spectrometry

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Objective To establish protein fingerprinting identification model of Acinetobacter baumannii(A. baumannii) and to lay a foundation for rapid identification of A. baumannii by using surface enhanced laser desorption ionization time of flight mass spectrometry(SELDI-TOF-MS).

Methods A total of 60 A. baumannii strains and 160 control strains were collected, which were divided into training and testing group. SELDI-TOF-MS was used to detect the protein profiling of the bacteria. Data were automatically collected by Ciphergen Proteinchip Software and protein markers of A. baumannii were screened by BioMarker Wizard Software. Classification tree model was developed and validated by BioMarker Patterns Software. The model was blindly tested with twenty A.baumannii and fifty one control bacteria.

Results Seventy two peaks were detected between 3 000 and 30 000Da, among which fifty six ones showed significantly difference between A.baumannii and the control bacteria

(P<0.01). By using BioMarker Patterns Software, proteins(m/z at 1 6737.8 and 5763.61)were chosen to develop a classification tree model. The results exhibited with sensitivity of 85% and specificity of 100%.

Conclusions SELDI-TOF-MS has the potential for rapid identification of A. baumannii.

P0-041

Identification of a serologic biomarker panel based on decision tree algorithms for the diagnosis and differentiation of inflammatory bowel diseases

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Objective Difficulties in diagnosing inflammatory bowel disease (IBD) have motivated the search for new diagnostic tools, including serologic biomarkers. Currently, an increasing amount of experimental data is available on newly discovered biomarkers in IBD, but the role of various antibodies in the current IBD diagnostic algorithm is often questionable due to their limited sensitivity. Therefore, this study aimed to build a diagnostic tool incorporating a panel of serum biomarkers into a computational algorithm to identify patients with IBD and differentiate those with Crohn's disease (CD) from those with ulcerative colitis (UC). We then developed a marker-based calculator to predict the probable diagnosis for individual patients.

Methods We studied sera from 128 CD patients, 82 UC patients, 60 non-IBD controls and 60 healthy controls. Indirect immunofluorescence (IIF) assays were utilized to determine 7 biomarkers previously associated with IBD: atypical perinuclear anti-neutrophil cytoplasmic antibodies [a-ANCA], anti-*Saccharomyces cerevisiae* antibody (ASCA), anti-intestinal goblet cell antibody (GAB), anti-pancreatic exocrine gland antibody (PAB), anti-DNA-bound-lactoferrin antibody (anti-LFS), anti-zymogen granule membrane glycoprotein 2 antibody (anti-GP2), anti-CUB antibody and anti-zona pellucida-like domain protein 1 antibody (anti-CUZD1). The decision tree algorithm was constructed to classify IBD, CD, and UC.

Results The cohort was randomly divided into a training set (70%) and a test set (30%) to produce an ideal model, and the prediction rates were determined and compared for decision tree models of the data developed using C5.0, C&RT, QUEST and CHAID. The C5.0 and CHAID algorithms, which ranked top for the prediction rate in the IBD vs. non-IBD model and the CD vs. UC model, respectively, were utilized for final pattern analysis. The final decision tree model achieved higher classification accuracy than the approach based on conservative marker combinations (sensitivity 75.0% vs. 79.5%, specificity 93.8% vs. 78.3% for differentiating IBD from non-IBD; and sensitivity 84.3% vs. 73.4%, specificity 92.5% vs. 54.9% for differentiating CD from UC, respectively).

Conclusions The decision-tree-based approach used in this study, based on serum biomarkers, has shown to be a valid and useful approach to identifying IBD and differentiating CD from UC.

PO-042

Long Noncoding RNA LINC02418 Regulates MELK Expression by Acting as a ceRNA and may Serve as a Diagnostic Marker for Colorectal Cancer

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Objective Some types of long non-coding RNAs (lncRNAs) are aberrantly expressed in human diseases, including cancers. However, the overall biological roles and clinical significances of most lncRNAs in colorectal cancer (CRC) are not fully understood. We aim to investigate the clinical significance, biological function, and mechanism of lncRNA in CRC.

Methods Firstly, The Cancer Genome Atlas (TCGA) was analyzed to identify the differentially expressed lncRNAs between CRC tissues and noncancerous tissues. Next, we evaluated the effect of LINC02418 on the CRC cells tumorigenesis, and its regulation of absorbing microRNA and indirectly stimulating protein expression by acting as a ceRNA. Further, the diagnostic performance of exosomal LINC02418 was evaluated by the receiver operating characteristic curve (ROC) and the area under curve (AUC).

Results After using publicly available expression profiling data and integrating bioinformatics analyses (Fig.1A), we identified that LINC02418 was highly expressed in CRC tissues, cell lines and peripheral serum (Fig.1B-D). Furthermore, LINC02418 silencing inhibited CRC cell proliferation (Fig.1E) by promoting apoptosis and inducing cell cycle arrest (Fig.1F-H). Mechanistically, LINC02418 acted as a ceRNA to upregulate MELK expression by absorbing miR-1273g-3p (Fig.2A-E), and a positive correlation was also identified for the fold change between the LINC02418 mRNA level and MELK expression (Fig.2F). In addition, exosomal LINC02418 could distinguish patients with CRC from healthy controls (AUC = 0.8997; 95% confidence interval (CI) = 0.8644- 0.9351) (Fig.2G-H).

Conclusions Collectively, we determined that LINC02418 was significantly over-expressed in CRC, and LINC02418－miR-1273g-3p－MELK axis played critical role in MELK tumorigenesis. Additionally, exosomal LINC02418 was a promising novel biomarker that could be used for the clinical diagnosis of CRC.

PO-043

MUS81 intermediates the Progression of Serous Ovarian Cancer Associated with Dysfunctional DNA Repair Systems

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Objective Serous Ovarian Cancer (SOC) is characterized by genomic instability and heterogeneity. Novel insights into SOC are required to reduce mortality rates and drug resistance. MUS81 is a structure-special endonuclease that plays an important role in DNA repair systems and genomic instability of cancer cells. MUS81 was significantly overexpressed in SOC patients in our previous study, which was related to poor clinical outcomes.
Methods To explore the role of MUS81 in genome instability and DNA damage response, RAPD analysis and comet assays were performed to evaluate the DNA damage status of SOC cells. Transcriptional profile analysis and protein interaction screening chip was used to explore the potential pathways MUS81 involved. Inhibition of MUS81 intensified genome instability and reduced homologous recombination (HR) efficiency. Additionally, deficiency of MUS81 could prompt the emergence of DSBs and restrain the formation of RAD51 foci after SOC cells exposure to UV.
Results Further experiments proved that downregulation of MUS81 promoted the sensitivity to camptothecin and HR inhibitors, and the results of transcriptional profile and protein chip revealed that MUS81 was involved in multiple pathways associated with DNA repair, and MUS81 could directly interact with RAD51 and BM28 in SOC cells. Thus, we proposed that MUS81 is involved in SOC cells' DNA damage repair pathway, and has a significant impact on the susceptibility to chemotherapy drug.
Conclusions MUS81 might represent a novel chemotherapy molecular target that is associated with SOC progression and DNA damage repair system.

PO-044

An eleven-miRNA classifier as a novel biomarker for the prediction of recurrence in gastric cancer patients

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Objective The current study aimed to develop a miRNA-recurrence classifier (MRC) that can improve upon the current Tumor Node Metastasis (TNM) staging and identify high-risk gastric cancer (GC) patients.
Methods Using univariate and multivariate Cox regression analysis, a miRNA signature was developed in the training set from TCGA (GC, N=372), which was validated in an independent patient cohort (N=88) of formalin fixed paraffin-embedded (FFPE) tissues by RT-qPCR. A nomogram incorporating both the miRNA signature and clinical-related factors was constructed to predict GC prognosis.

Results An eleven-miRNA signature was developed, which could significantly predict recurrence-free survival RFS in the training set (P<0.0001). An independent clinical cohort validated that MRC-derived high-risk patients succumb to significantly poor RFS in GC (P<0.0001). The AUC of this signature was significantly larger than that of TNM stage in the TCGA (0.733 versus 0.589 at 3 years, P=0.004; 0.802 versus 0.635 at 5 years, P=0.005) and validation cohort (0.835 versus 0.689 at 3 years, P=0.003). The nomogram integrating both MRC and clinical-related variables (T, N, M) did well in the calibration plot and was possessed of favorable discrimination performance (AUC=0.754).
Conclusions The novel eleven-miRNA classifier is superior to currently used clinicopathological features in identifying high-risk GC patients, which can be readily translated into clinical practice with FFPE specimens for specific decision-making applications.

P0-045

Gprc5a depletion enhances the risk of smoking-induced lung tumorigenesis and mortality

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Objective Lung cancer remains the leading cause of cancer incidence and mortality. Although cigarette smoke is regarded as a high risk for lung tumor initiation, the role of the lung tumor suppressor GPRC5A in smoking-induced lung cancer is unclear.
Methods We obtained two lung cancer cohorts from TCGA and GEO database. Bioinformatics analysis showed the difference gene expression. Quantitative real-time PCR and Gprc5a-/- mice uncovered the relationship between cigarette smoke and lung cancer in GPRC5A deletion system in vitro and in vivo.
Results Bioinformatics analysis showed that patients with lung cancer had poor overall survival when GPRC5A was expressed at low levels and in patients who smoked compared to in those with high GPRC5A expression and smoking. Further analysis revealed that cancer-related stemness pathways such as the Hippo signaling pathway were induced in smoking patients with low GPRC5A expression. Additionally, we detected enriched expression of *WNT5A* and *DLX5* in human lung normal epithelial 16HBE cells and human lung cancer H1299 cells *in vitro*. A relationship between cigarette smoke extraction NNK and lung tumor initiation was observed in $Gprc5a^{-/-}$ mice.
Conclusions The lung tumor suppressor gene *GPRC5A* played a protective role in cigarette smoke-induced initiation of lung tumor, providing a target for the prevention of lung cancer development and prognosis monitoring.

PO-046

Identification of SAA and ACTB as potential biomarker of patients with severe HFMD using iTRAQ quantitative proteomics

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Objective Hand, foot and mouth disease(HFMD) is an infectious disease caused by a variety of enterovirus infections, and the most common types of virus infections are the newenterovirus71 (EV71) and coxsackievirus A group 16 (CoxA16). A small fraction of HFMD will cause further severe HFMD. A rapid and accurate diagnosis biomarker of severe HFMD is important for the timely treatment.
Methods . In the study, we conducted a clinical biomarker discovery study using iTRAQ combined with MS. Serum proteome alterations in severe HFMD group(n=32) and health control group(n=32) were analyzed. 47 proteins were upregulated(fold change>1.5) between the severe HFMD group and HC group. The identified proteins were classified into different groups according to the molecular function, biology processes, cellular component. During the up-regulated proteins, serum amyloid A(SAA) and human β-actin (ACTB), were confirmed in the serum of the severe HFMD and HC by ELISA assay.
Results SAA and ACTB levels were significantly higher in the sever HFMD patients(P<0.01), consistent with iTRAQ-LC-MS/MS analysis.
Conclusions
In summary, Our results showed that SAA and human β-actin (ACTB) may be served as a potential biomarker of the clinical diagnosis of severe HFMD.

PO-047

Serum proteinase 3 anti-neutrophil cytoplasmic antibodies (PR3-ANCA) as a marker of disease activity in Chinese patients with ulcerative colitis

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Objective Initial assessment of patients with ulcerative colitis (UC) is challenging and relies on endoscopy and apparent clinical symptoms, monitoring disease activity in UC is of major importance to prevent long-term complications. Our aim was to evaluate the value of serum proteinase 3 antineutrophil cytoplasmic antibodies (PR3-ANCAs) as a biomarker for grading the disease severity of UC.
Methods In total, 85 patients with validated disease activity indices including clinical, endoscopic and histologic indices available were included. In addition to PR3-ANCA, C-reactive protein (CRP), hemoglobin, sedimentation rate (ESR) were measured and compared between patients with active disease and remission. In a 26-

patient subgroup, follow-up samples were also analyzed. The respective performances of the PR3-ANCA with respect to endoscopic disease severity were assessed by computing correlations, sensitivities, specificities, and overall accuracies at adjusted cutoffs and also test operating characteristics compare with other laboratory parameters (CRP, hemoglobin, albumin and ESR).

Results The PR3-ANCA was significantly higher in clinically and endoscopically active UC than in patients with inactive disease and controls, and PR3-ANCA was different (p<0.05) in UC patients with a change in disease activity over time. PR3-ANCA correlated with clinical, endoscopic and histologic scores in UC (r= 0.471, 0.435 and 0.298, respectively; p<0.01). A combination of either PR3-ANCA, ESR, and CRP (sensitivity: 65.91%, specificity: 80.49%, area under curve[AUC]:0.732) using their respective cutoffs to distinguish between endoscopically active and inactive UC appeared similar to that obtained with PR3-ANCA alone (sensitivity: 77.27%, specificity: 75%, AUC: 0.757).

Conclusions The PR3-ANCA is a novel reliable surrogate biomarker with the potential to identify patients with UC with active mucosal inflammation and represents an alternative marker as accurate as endoscopic to predict and monitor the severity of patients with UC.

PO-048

Abnormally expressed long non-coding RNA B3GALT5-AS1 may serve as a biomarker for the diagnostic and prognostic of Gastric Cancer

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Objective Early diagnosis of Gastric cancer (GC) is an important issue to improve the prognosis. More and more long non-coding RNAs (lncRNAs) were reported can be used as biomarkers in several cancers. We aim to explore the expression and correlations with clinical features of lncRNA B3GALT5-AS1, and further analyze its diagnostic and prognostic values in GC.

Methods In this study, we detected serum B3GALT5-AS1 expression in 107 patients with GC, 40 polyp patients and 87 normal controls to investigate the role of serum B3GALT5-AS1 in GC using the quantitative real-time polymerase chain reaction (qRT-PCR) method.

Results The results demonstrated that B3GALT5-AS1 expression level was significantly elevated in GC patients compared with that in normal controls (P<0.001). Serum B3GALT5-AS1 could be used as molecular marker for distinguishing GC patients from healthy people with an area under the curve of 0.816 (95% confidence interval (CI)=0.758-0.874; P=0.03). Further analysis found that high serum B3GALT5-AS1 expression levels correlated with TNM stage (P=0.024), and lymph node metastasis (P=0.023).

Conclusions Serum B3GALT5-AS1 could serve as an ideal combined biomarker for the diagnosis of GC.

PO-049

The pre-treatment platelet count is an independent predictor of tumor progression in patients undergoing Transcatheter Arterial Chemoembolization with hepatitis B virus-related hepatocellular carcinoma

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Objective To explore the prognostic value of the baseline platelet count (PLT) in patients undergoing Transcatheter Arterial Chemoembolization (TACE) with hepatocellular carcinoma (HCC).

Methods We prospectively analyzed 317 hepatitis B virus-related HCC patients undergoing TACE. Time to progression (TTP) was selected to evaluate the clinical significance of PLT level in HCC patients.

Results PLT was the only parameter showing statistical significance of all the clinical characteristics between two distinct tumor response groups. After ruling out cirrhosis as a potential major confounding factor, the conclusion was further established. Higher pre-treatment PLT level, portal vessel invasion and higher stratification of AFP level were independently associated with longer TTP. The prognostic score model combining the three risk factors revealed that higher risk scores might mean shorter TTP.

Conclusions The pre-treatment PLT level is a potentially useful biomarker to predict the prognostic outcomes in HCC patients undergoing TACE and deserved to be further explored in subsequent work.

PO-050

Establishment of quality control strategies for HbA1c by risk management index

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Objective Patient risk management is increasingly valued in medical laboratories. To minimize the risk of patient harm from results, laboratories should establish QC strategies and monitor the performance of assays. Risk management index (RMI) was used

to evaluate different quality control (QC) strategies for glycated hemoglobin (HbA1c) analyzers.

Methods RMI = expected P_H / acceptable P_H, where (P_H is the probability of patient harm). Expected $P_H(SE) = [P_E(0) + E(N_{uf}(SE))/MPBF]*P_{hIu}$. $P_E(0)$ is the probability of unacceptable results by the glycated hemoglobin analyzer in control. $E(N_{uf}$ (SE) is the expected number of final unacceptable reports for the device under systematic error. MPBF is the mean number of tests between two neighboring out-of-control intervals, which is the number of samples measured every day multiplied by the mean number of days between out-of-control intervals. P_{hIu} is the probability of unacceptable test results causing harm to the patients. $P_E(0)$ and $E(N_{uf})$ were calculated using the standard normal cumulative distribution function. The acceptable P_H was obtained from the CLSI EP23-A acceptable risk model and ISO 14971 guideline matrix. A series of QC strategies was designed for laboratory glycated hemoglobin analyzers which test 300 samples every day: The analytical run length was defined as 50, 100, 150, 200, 300, and QC rules 1_{3s} N1, 1_{3s} N2, $1_{2.5s}$ N1, $1_{2.5s}$ N2, 1_{2s} N1, and 1_{2s} N2 were used. The mean number of days between out-of-control intervals was 30 days.

Results $P_E(0) = 6.74*10^{-5}$, MPBF = 300*30 = 9000; $P_{hIu} = 0.50$; acceptable $P_H = 1.00*10^{-4}$. Analytical run lengths were 50, 100, 150, 200, and 300. The $E(_{Nuf})$ of the QC rule 1_{3s} N1 was 0.57, 1.14, 1.71, 2.27, and 3.41, respectively; the expected P_H was $6.53*10^{-5}$, $9.69*10^{-5}$, $1.29*10^{-4}$, $1.60*10^{-4}$, and $2.23*10^{-4}$, respectively; and RMI was 0.65, 0.97, 1.29, 1.60, and 2.23, respectively. For QC rule 1_{3s} N2, the $E(_{Nuf})$ was 0.12, 0.24, 0.37, 0.49, and 0.73, respectively; the expected P_H was $4.05*10^{-5}$, $4.73*10^{-5}$, $5.41*10^{-5}$, $6.08*10^{-5}$, and $7.44*10^{-5}$, respectively; and RMI was 0.41, 0.47, 0.54, 0.61, and 0.74, respectively. For QC rule $1_{2.5s}$ N1, the $E(_{Nuf})$ was 0.23, 0.45 , 0.68, 0.90, and 1.36, respectively; the expected P_H was $4.63*10^{-5}$, $5.88*10^{-5}$, $7.14*10^{-5}$, $8.39*10^{-5}$, and $1.09*10^{-4}$, respectively; and RMI was 0.46, 0.59, 0.71, 0.84, and 1.09, respectively. For QC rule $1_{2.5s}$ N2, the $E(_{Nuf})$ was 0.04, 0.07, 0.11, 0.15, and 0.22, respectively; the expected P_H was $3.58*10^{-5}$, $3.78*10^{-5}$, $3.99*10^{-5}$, $4.20*10^{-5}$, and $4.61*10^{-5}$, respectively; and RMI was 0.36, 0.38, 0.40, 0.42, and 0.46, respectively. For QC rule 1_{2s} N1, the $E(_{Nuf})$ was 0.08, 0.17, 0.25, 0.33, and 0.50, respectively; the expected P_H was $3.83*10^{-5}$, $4.29*10^{-5}$, $4.75*10^{-5}$, $5.22*10^{-5}$, and $6.14*10^{-5}$, respectively; RMI was 0.38, 0.43, 0.48, 0.52, and 0.61, respectively. For QC rule 1_{2s} N2, the $E(_{Nuf})$ was 0.01, 0.02, 0.03, 0.04, and 0.06, respectively; the expected P_H was $3.43*10^{-5}$, $3.48*10^{-5}$, $3.53*10^{-5}$, $3.58*10^{-5}$, and $3.68*10^{-5}$, respectively; and RMI was 0.34, 0.35, 0.35, 0.36, and 0.37, respectively.

Conclusions An RMI $\leqslant$ 1.00 shows that the QC strategy for glycated hemoglobin analyzers can control patient risk to an acceptable range. Our study selected the QC strategy of 1_{3s} N1 and analytical run length of 100 or $1_{2.5s}$ N1 and an analytical run length of 200 to test 300 glycated hemoglobin samples every day.

PO-051

Genetic polymorphisms of long non-coding RNA RP11-37B2.1 associate with susceptibility of tuberculosis and adverse events of anti-tuberculosis drugs in west China

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Objective Little knowledge about the biological functions of *RP11-37B2.1*, a newly defined long non-coding RNA (lncRNA) molecule, is currently available. Previous studies have showed rs160441, located in the *RP11-37B2.1* gene, is significantly associated with tuberculosis (TB) in a Ghanaian and the Gambian populations. We investigated the influence of SNPs within lncRNA *RP11-37B2.1* on the risk of TB and the possible correlation with adverse drug reactions (ADRs) from TB treatment in a Western Chinese population.
Methods Four SNPs within lncRNA *RP11-37B2.1* were genotyped in 554 TB cases and 561 healthy subjects using the improved multiplex ligation detection reaction method, and the patients were followed up monthly to monitor the development of ADRs.
Results No significant association between the SNPs of lncRNA *RP11-37B2.1* and TB susceptibility was observed (all p values > 0.05). Surprisingly, significant association was observed between rs218916 and thrombocytopenia development during anti-TB therapy under the dominant model with the estimated p = 0.003 [odds ratio (OR) = 5.32, 95% CI = 1.54-18.32].
Conclusions Our findings firstly exhibit that rs218916 within lncRNA *RP11-37B2.1* significantly associate with the occurrence of thrombocytopenia and suggest *RP11-37B2.1* genetic variants are potential biosignatures for thrombocytopenia during anti-TB treatment.

PO-052

FASTINS VERSUS NON FASTING STATE FOR EVALUATION OF SERUM LIPID PROFILE

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Objective The serum lipid profile is measured for cardiovascular risk prediction and the test includes six basic parameters: total cholesterol, HDL cholesterol, LDL cholesterol, non-HDL cholesterol, VLDL cholesterol and triglycerides. The measurement of lipid profile has traditionally been recommended to be when the patient is in fasting state. Fasting refers to 12 - 14 hours overnight complete dietary restriction with the exception of water and medication. The European Atherosclerosis Society/European Federation of Clinical Chemistry and Laboratory Medicine (EAS/ EFLM) lauched in 2016 a joint consensus statement proposing recommendations on situations when fasting is not required for a lipid profile. The objective of this study was to

evaluate the standard lipid profile observed in a laboratory routine among patients who performed 12 hours fasting and fasting state less than 12 hours.

Methods The standard lipid profile (total cholesterol, HDL cholesterol, LDL cholesterol, non-HDL cholesterol, VLDL cholesterol and triglycerides) was obtained by calculation using the Martin equation. A total of 46,303 outpatient lipid profile results were analyzed. 40,170 patients (86.7%) reported fasting state for 12 hours and 6,133 patients (13.3%) reported a fasting state less than 12 hours.

Results The observed values of the standard lipid profile (mean ± standard deviation) with and without fasting of 12 hours were, respectively:

Total cholesterol: 186 ± 40 mg/dL and 185±40 mg/dL;

HDL-cholesterol: 55 ± 16 mg/dL and 55 ± 16 mg/dL;

LDL-cholesterol: 109 ± 34 mg/dL and 109 ± 34 mg/dL;

Non-HDL-cholesterol: 131 ± 39 mg/dL and 130 ± 39 mg/dL;

VLDL-cholesterol: 21 ± 9 mg/dL and 21 ± 8 mg/dL;

Triglycerides: 113 ± 77 mg/dL and 112 ± 96 mg/dL.

Conclusions No significant differences were observed between the groups with and without fasting for all parameters evaluated. This finding demonstrates that the sample collection for the standard lipid profile without fasting, previously recommended by the guidelines, can be made more flexible.

P0-053

Expression of low density granulocytes in peripheral blood from patients with gastric cancer and its clinical significance

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Objective A distinct population of neutrophil-like cells termed low-density granulocytes (LDGs) is present in increased numbers in the peripheral blood mononuclear cell (PBMC) fraction of patients with systemic lupus erythematosus (SLE) and other systemic autoimmune diseases and in patients infected with human immunodeficiency virus (HIV) .The functionality and pathogenicity of these LDGs have not been characterized. In this study, we detected the percentage of LDGs in patients with gastric cancer (GC) and analyzed the roles of LDGs in GC development.

Methods 23 GC patients were recruited from Affiliated Hospital of Jining Medical University and 11 healthy volunteers were recruited as control subjects. PBMC fractions were isolated from blood samples using Ficoll-Histopaque by density gradient centrifugation within 24 h after venipuncture. We used flow cytometry to detect low density granulocytes in peripheral blood. We compared expression of LDGs in GC patients with those in healthy controls.

Results The levels of LDGs in GC patients were higher than those in healthy controls. The larger the tumor size, the higher the level of LDGs. There was a reversely correlation between level of LDGs and percentage of $CD4^+$ T cells in total lymphocytes. In addition, the expression of surface marker CD11b, CD15 and CD66b in LDGs was

different from that in normal density granulocytes (NDGs), indicating activated and degranulated features of LDGs.

Conclusions Our findings indicated that a group of activated LDGs were highly accumulated in peripheral blood of GC patients, which were associated with proliferation of tumor and $CD4^+$ T cells.

PO-054

Vitamin D level in rheumatoid arthritis and its correlation with the disease activity

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Objective As well known, Rheumatoid Arthritis (RA) is one of the most prevalent autoimmune diseases. In addition to its well-documented involvement in mineral homeostasis, vitamin D seems to have broad effects on human health that go beyond the skeletal system. Prominent among these so-called nonclassical effects of vitamin D are its immunomodulatory properties. Due to the significance of the relationship between serum vitamin D levels and autoimmune diseases, this exploratory aimed to estimate the relationship between serum vitamin D status and its correlation with the disease activity in patients with newly diagnosed RA.

Methods Quantitative measurement of serum 25-OH vitamin D (25(OH)D) levels used the chemiluminescent immunoassay method ,the disease activity was assessment based on Disease Activity Score of 28 joints -C- reaction protein (DAS28-CRP). In addition, the serum CRP levels, the duration of morning stiffness, and the number of joints with tenderness and swollen were calculated as well. The data were analyzed using the Pearson correlation coefficient.

Results 85 patients(RA group) with newly diagnosed RA (male,11,female 74,mean age 50.35 ± 17.08 years) fulfilling ACR crite-ria for the classification of rheumatoid arthritis ,whereas 85 age and gender matched healthy controls (male,11,female 74,mean age 50.66 ± 16.89 years) were included in this study. Serum vitamin D levels and DAS28-CRP scores were estimated at the first visit. The mean serum vitamin D levels were 24.76 ± 8.33 ng/ml in the RA group and 33.83 ± 7.93 ng/ml in the healthy control group . This difference was statistically significant ($P < 0.05$). Seventy-eight patients (91.76%) belonging to the RA group had serum Vitamin D levels <30 ng/ml, that means, they were Vitamin D deficient, whereas forty participants (47.06%) belonging to the control group had Vitamin D deficiency. In this study, 11 out of 85 of RA patients (12.94%) were in the remission group (DAS28 score <2.6), 23 patients (27.06%) in the low disease activity group (DAS28 score 2.7－3.2), 33 patients (38.82%) in the moderate disease activity group (DAS28 score 3.3－5.1), and 18 patients (21.18%) in the high disease activity group (DAS28 score >5.1). The mean serum Vitamin D levels were 31.06 ± 7.6 ng/ml, 30.18 ± 5.3 ng/ ml, 26.55 ± 5.36 ng/ml, and 16.47 ± 5.86 ng/ml in the remission, low disease activity, moderate disease activity, and high

disease activity groups, respectively ,these differences were statistically significant ($P < 0.05$).

Conclusions It seems that hypovitaminosis D is common in the RA patients and middle-aged healthy women in this study. Vitamin D deficiency is more common in RA patients and may be one of the causes leading to development or worsening of this disease, and association was observed between vitamin D levels and disease activity but further studies on a larger group of patients will be needed to confirm this conclusion.

PO-055

EVALUATION OF THE ANALYTICAL PERFORMANCE OF SERUM FREE LIGHT CHAINS ASSAYS ON TOTAL AUTOMATION

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Objective The free light chain monoclonal immunoglobulin (kappa and lambda free light chains) represent the important tumor markers in serum and urine in the diagnosis and prognosis of patients with monoclonal diseases of plasma cells. The clinical utility of these measures has been demonstrated in: primary amyloidosis, non-secretory myeloma, light chain multiple myeloma, smoldering multiple myeloma, plasmacytoma, light chain deposition disease, monoclonal gammopathy of undetermined significance and macroglobulinemia.

The introduction of a new commercial diagnostic set to quantify the free light chains (FLC) in the fully automated routine of a tertiary public laboratory was the object of the evaluation of its analytical performance. The validation procedures were done to ensure that the new analytical methods are accurate, reproducible, robust in a specific range in the analytes will be analyzed, ensuring compliance with the requirements of good practices in clinical laboratory.

Methods The Cobas 8000 system of the laboratory has two c502 modules, with turbidimetric measurements for the comparison of performance analysis. Were analyzed the performance of Freelite^{R} Human Lambda Free(Ref LK018.CB) and Freelite^{R} Human Kappa Free(Ref LK016.CB) Binding Site Group Limited (Birmingham, UK) both for use on the Roche Cobas^{R} c system following the manufacturer's instructions. The study was done with serum obtained by venipuncture, with a vacuum collection system, after retraction of the clot. The samples were stored at 2-8 ° C for up to 7 days. The standard and control material are provided by the manufacturer. For quality control, two levels (low and high) were checked at each run. The analytical precision was evaluated according to the CLSI protocol EP5-A2. Method comparisons were performed with clinical samples, lower limit of quantification, linearity was evaluated in samples with monoclonal elevations of FLC, carryover evaluation and robustness. The analytical quality specifications for these analytes were also defined. Statistical studies were conducted with EP Evaluator release (Data Innovations, Inc., South Burlington, VT) and Minitab 15.0.

Results Precision

The FLC kappa assay:

Within run coefficient of variation: low: 2.0%; high: 2.2%
Between run coefficient of variation: low: 5.4% ; high: 2.2%
FLC lambda assay:
Within run coefficient of variation: low:1.0%; high: 2.4%
Between run coefficient of variation: low: 1.1% ; high:0.8%

Total error allowed

FLC Kappa: 10% and FLC Lambda: 10%

Comparison between equipments:

There were good levels of agreement between the results obtained in the 2 analyzed modules were 20 samples (FLC Kappa: r = 1.000, R^2: 99.97% and FLC Lambda: r = 0.999 R2 = 99.84%).

The error index between equipments:

FLC Kappa: with samples between 8.2 - 261.3 mg / L was within the total error allowed of 10%.
FLC Lambda: with samples between 1.7- 228.0 mg / L was within the total error allowed of 10%.
Observing that the difference between the two modules had 100% of the samples tested within the allowed error range.

Comparison between reference lab and DLC:

There were good levels of agreement between the results obtained in the 2 labs were 12 samples (FLC Kappa: r = 0.986 R^2: 97.14% and FLC Lambda: r = 0.977 R2 = 95.30%).

The error index between reference lab and DLC:

FLC Kappa: with samples between 0.73- 5.35 mg / L was within the total error allowed of 20%.
FLC Lambda: with samples between 0.67- 5.19 mg / L was within the total error allowed of 20%.
Observing that the difference between the two labs had 100% of the samples tested within the allowed error range.

Analytical Measurements Range:

Range between lower limit quantification and linearity:
Kappa free: 0.8 - 562.0 mg/L
Lambda free:0.7 -748.0 mg/L

Clinical Report Range:

Kappa free: <0.8 mg/L and > 562 mg/L
Lambda free: <0.7 mg/L and > 748 mg/L

Comparison between equipments:

There were good levels of agreement between the results obtained in the 2 modules c502 in the 20 samples analyzed (FLC Kappa: r = 1.000, R^2: 99.97% and FLC Lambda: r = 0.999 R^2 = 99.84%).

Comparison between reference lab and DLC:

There were good levels of agreement between the results obtained in the 2 labs in the 12 samples analyzed (FLC Kappa: r = 0,986 R2: 97.14% and FLC Lambda: r = 0.977 R2 = 95.30%).

Carryover

It was observed that carryover was smaller than the limiting errors (FLC Kappa: 1.70 FLC Lambda: 1.48) for the two analytes.

Robustness

The two systems are robust even with the variation between operators.
Conclusions The analytical systems adapted to the total automation of the lab have been shown to be accurate, with comparable results with the reference laboratory and between the two existing Cobas c502 modules, are robust, have adequate carrying levels, are sensitive, have an adequate analytical range of measurements.

P0-056

Establishment of a reference method for serum Hcy and its application in external quality assessment

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Objective Established a reference measurement procedure for the determination of human serum homocysteine by isotope dilution high performance liquid chromatography-tandem mass spectrometry (ID-LC/MS/MS), and applied to the establishment of sample target values for external quality assessment (EQA) in clinical laboratories
Methods The reference method of Hcy in our laboratory was established according to the method recommended by the Joint Committee for Traceability in Laboratory Medicine (JCTLM). The precision, accuracy, specificity, carryover and matrix effect of the method were evaluated. The reference method was applied to establish Hcy target values for samples of the second EQA in Shanghai of 2018.
Results The method detects 12.5μmol/L and 37.4μmol/L samples in three batches in three days, and the CV between batches is 1.03% and 2.10%, respectively. The measured values of Standard reference material (SRM) 1955 of National Institute of Standards and Technology (NIST) were within the specified uncertainty range. There was no matrix effect and carryover. The second EQA data in 2018 showed that the average value of domestic reagent group was lower than that of reference method, and that of imported reagent group was higher than that of reference method.
Conclusions The ID-LC/MS/MS method which was to determine the homocysteine reference measurement procedure in human serum was successfully established. It is expected to play a role in tracing the quantities of Hcy in clinical laboratories.

PO-057

Comprehensive analysis of a long noncoding RNA-associated competing endogenous RNA network in colorectal cancer

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Objective To explore a lncRNA-associated competing endogenous RNA (ceRNA) network of colorectal cancer based on the cancer genome atlas (TCGA) database, and to further analyze of the ceRNA network and pathogenesis in colorectal cancer (CRC).
Methods Clinical information of CRC patients and expression profiles of mRNA, lncRNA and miRNA were obtained from The Cancer Genome Atlas database. Differentially expressed mRNA, lncRNA and miRNA (referred to as "DEmRNA", "DElncRNA" and "DEmiRNA", respectively) were screened between 454 CRC samples and 80 normal samples. The interaction between DElncRNA and DEmiRNA was predicted by miRcode. DEmiRNA-targeted DEmRNA was searched according to TargetScan, miRTar-Bas and miRDB. The lncRNA-miRNA-mRNA ceRNA network was constructed based on the interaction of DEmiRNA-DElncRNA and DEmiRNA-DEmRNA. Functional enrichment analyzes the biological processes and pathways of DEmRNA involved in CRC development, and the association of key lncRNAs with overall survival and clinical characteristics of CRC patients.
Results A total of 2,239 DEmRNAs, 1612 DElncRNAs and 253 DEmiRNAs were identified as CRC-specific RNAs. 402 DEmiRNA-DElncRNA interactions and 10 DEmiRNA-DEmRNA interactions were identified based on the relevant databases. The lncRNA-miRNA-mRNA ceRNA network was constructed using 29 DEmiRNAs, 7 DEmRNAs and 55 DElncRNAs. Two DElncRNAs, four DEmiRNAs and three DEmRNAs were confirmed to be associated with prognosis in patients with CRC. Three DElncRNAs were found to be associated with clinical features.
Conclusions The cancer-specific lncRNA-associated ceRNA network provide new insights into the molecular mechanisms of CRC. Key RNA transcripts related to the overall survival and clinical features were also found with promising potential as biomarkers for diagnosis, survival prediction, and classification of CRC.

PO-058

Primary mediastinal large B cell lymphomas with aberrations of C-MYC and BCL-2: A case report and literature review

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Objective Primary mediastinal large B-cell lymphomas (PMLBCLs) is an aggressive lymphoma characteristic with distinct clinical, morphologic, and immunophenotypic

features. The rearrangements of *C-MYC, BCL2* and/or *BCL6* which are common in diffuse large B-cell lymphoma (DLBCL) are typically absent in PLMBCLs. Here we report a rare case of PMLBCL with translocation of C-MYC gene and copy number variation (CNV) of BCL2 gene.

Methods Histologic pathology of the mediastinal mass biopsy specimens is standard diagnosis of this case. Fluorescent in situ hybridization (FISH) studys was used to detect the genetic abnormality.

Results Histology showed typical pathomorphological features of PLMBCLs. FISH studies showed rearrangements of *MY C*and copy number variation (CNV) of *BCL2* gene

Conclusions We proved a novel case of PMLBCLs with concurrent rearrangements of *C-MYC* and *BCL2*. It gives evidence that cytogenetic testing is necessary for PMLBCLs to get precise clinical evaluation and appropriate treatment

PO-059

Characterization of MCAM as a novel biomarker for hepatocellular carcinoma

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Objective It is now well established from a variety of researches that Yes-associated protein (YAP) overexpression in hepatocellular carcinoma (HCC) is significantly associated with weak tumor differentiation, which endows YAP with the identification as an independent predictor for HCC-specific disease-free state and overall survival. However, YAP doesn't show up in early diagnosis of HCC because it is primarily in the nucleus and difficult to detect in the sera of patients. Conversely, membrane proteins are promising candidates because they are derived from the tumor lesions and are released easily into the circulation. Melanoma cell adhesion molecule (MCAM) is an integral membrane glycoprotein which promotes tumor growth, angiogenesis and metastasis and is regarded as a promising target for
tumor therapy. Nevertheless, whether and how MCAM boosts tumorigenesis in HCC are largely unknown. Here we report that the membrane protein MCAM was under positive regulation by YAP and was highly elevated in HCC cells.

Methods The expression of cancer-related membrane protein candidates in HCC cells was determined by western blot. MCAM level in HCC, breast and colon cancers was investigated by tissue microarray analysis, western blot and RT-qPCR. pGL4.21 plasmids containing the truncated version of the human MCAM promoter were stably co-transfected with pRL-TK plasmids into HCC cells to test the luciferase activity using a Dual‐luciferase system. Chromatin immunoprecipitation (ChIP)-qPCR was performed using anti-CREB or anti-YAP antibodies to test the combination of CREB or YAP with the promotor of MCAM. ChIP-qPCR was utilized to explore the potential factors that facilitate the recruitment of YAP to the MCAM promoter in HCC cells. Serum MCAM, YAP and alpha-fetoprotein (AFP) from healthy individuals and HCC patients was tested by western blot and ELISA analysis. Spearman's correlation analysis was used to evaluate the correlation between serum MCAM and serum AFP. Cell viability, apoptosis, proliferation was measured by MTT-based assay, caspase3/7 activity and soft-agar

colony formation respectively. Survival of HCC patients with different levels of MCAM expression was analyzed in an 80-month postsurgical follow-up study.

Results MCAM was the best candidate downregulated protein of YAP in HCC cells and the membrane signals of MCAM were stronger in HCC tissues than in normal liver controls. Within the MCAM promoter, we found the presence of a cAMP Response Element (CRE; - 32 to - 25 nt), which is conserved among species and is essential for YAP- and CREB-dependent regulation. Moreover, the interaction between CREB and YAP at the CRE site was dependent on PTPIY - WW domain interactions. However, MCAM expression was low and could not be regulated by YAP in breast and colon cancer cells because of the low levels of the acetyltransferase p300. In HCC cells, high levels of p300 facilitated the binding of YAP to the MCAM promoter, which in turn enhanced histone acetylation and polymerase II recruitment through the dissociation of the deacetylase Sirt1. These results suggest that MCAM is an HCC-specific target of YAP. In clinical serum samples, we found that the serum levels of MCAM were highly elevated in patients with HCC compared with healthy controls and with patients with cirrhosis, hepatitis, colon cancer and breast cancer. MCAM levels were shown to be a slightly better indicator than serum AFP for predicting HCC. We further demonstrated that MCAM is essential for the survival and transformation of HCC.

Conclusions We identified MCAM as a novel YAP target in HCC but not in breast and colon cancer cells, which may make MCAM become a potential tumor marker and therapeutic target for the diagnosis and treatment of HCC.

P0-060

The role of macrophages in cardiac inflammation and fibrosis

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Objective Macrophages are monocytes that originate in circulating blood. Recently, more and more studies have raised new understandings of macrophages, especially the role of macrophages in cardiovascular diseases.

Methods Inflammation is an important cause of heart damage. A variety of inflammation-related factors mediate macrophage infiltration into the damaged heart, representing the initial steps in inflammation during cardiac remodeling.

Results The chemokine CXCL1 and its receptor CXCR2 mediate angiotensin II-induced cardiac mononuclear cell infiltration through CXCL1-CXCR2 signaling, which initiates and aggravates cardiac remodeling. CXCR2 deficiency inhibits the migration and activation of macrophages and attenuates Ang II-induced cardiomyocyte hypertrophy and fibroblast differentiation through various signaling pathways.Studies have found that excessive accumulation of reactive oxygen species (ROS) catalyzed by NADPH oxidase (NOX) is involved in the ischemia-reperfusion (I / R) injury mechanism, and megakaryocyte leukemia 1 (MKL1) acts as an epigenetic link to NOX. Activation of a bridge between ROS production and myocardial ischemia-reperfusion injury, MKL1 levels are specifically elevated in macrophages during ischemia-reperfusion, and macrophage-

specific deletion of MKL1 in mice (MΦcKO) .CD206+ macrophages participate in tissue repair through phagocytosis and fibrosis following myocardial infarction.

Conclusions In conclusion, macrophages participate in the progression of myocardial inflammation and fibrosis through molecular mechanisms such as the chemokine CXCL1 and its receptor CXCR2, β-adrenergic receptors, oxygen species, NADPH oxidase , and the study of these molecular mechanisms provides a new therapeutic target for the treatment of ischemic heart disease.

PO-061

Evaluation of Serum Exosomal LncRNA-Based Biomarker Panel for Diagnosis and Recurrence Prediction of Bladder Cance

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Objective Exosomes are small membrane vesicles of endocytic origin released by many cells. These vesicles can mediate cellular communications in cancer by transmitting active molecules including long non-coding RNAs (lncRNA). However, the relationship between exosomal lncRNAs and the diagnosis and prognosis of bladder cancer (BC) was poorly understood. Our aim was to identify panels of lncRNAs in serum exosomes for the diagnosis and recurrence prediction of BC.

Methods Exosomes were isolated from serum of BC patients and healthy controls and validated by transmission electron microscopy (TEM), nanoparticle tracking analysis (NTA) and Western blotting. We selected 11 lncRNAs (PCAT-1, SPRY4-IT1, MALAT1, UCA1, TUG1, UBC1, GHET1, H19, SNHG16, MEG3 and BC039493) as candidate targets, which were previously reported to be differently expressed in BC tissues. qRT-PCR was performed to analyze the expressions of 11 candidate lncRNAs using a training set (n=200) and a validation set (n=320). Receiver-operating characteristic (ROC) curves were employed to evaluate the diagnostic performance of the identified lncRNAs. Multivariate logistic regression was used to construct an lncRNA panel. Moreover, we determined the correlation between lncRNAs and recurrence-free survival (RFS) of patients with non-muscle-invasive bladder cancer (NMIBC) by Kaplan-Meier analysis. The independent prognostic factors were evaluated by the Cox proportional-hazards regression model.

Results TEM was used to confirm the morphology of exosomes, which should be revealed as spherical vesicles with double layer membrane structure and diameters about 100 nm. Western blotting analysis was used to examine the expressions of exosomal markers at the protein level. CD9 and TSG101 could be detected in the exosome samples but not in the EDS. NTA showed the size distribution of exosomes.

Three lncRNAs (PCAT-1, UBC1 and SNHG16) were significantly up-regulated in serum exosomal samples of BC patients. We compared the expression levels of three lncRNAs between exosome and exosome-depleted supernatant (EDS). The result showed that the expressions of PCAT-1, UBC1 and SNHG16 in exosomes were higher than those in EDS. We investigated the stability of exosomal lncRNAs. The expression levels of lncRNAs in

exosomes remained unchanged upon RNase A treatment. In room-temperature incubation test, the exosome aliquots were maintained at room temperature for 0, 6, 12 and 24 h. No significant changes were found for the expressions of three lncRNAs and GAPDH at different time points.

A three-lncRNA panel (PCAT-1, UBC1 and SNHG16) was finally identified by multivariate logistic regression model. This panel provided high diagnostic accuracy for BC with an the area under the ROC curve (AUC) of 0.857 and 0.826 in the training set and validation set, respectively, which was significantly higher than that of urine cytology. The corresponding AUCs of this panel for patients with Ta, T1 and T2-T4 were 0.760, 0.827 and 0.878, respectively. In addition, we analyzed the association between these three lncRNAs and clinicopathological status in BC patients of validation set. Statistical analysis also represented a moderate correlation between UBC1 expression and lymph node metastasis (p=0.005), and higher PCAT-1 level was correlated with higher tumor grade (p=0.01) . However, no significant associations were found between the three exosomal lncRNAs and age or sex.

The Kaplan-Meier analysis revealed that high UBC1 expression in serum exosomes was significantly correlated with a reduced RFS compared with those with low UBC1 expression in NMIBC patients (n=74) (p=0.01). However, the expression levels of PCAT-1 and SNHG16 had no correlation with RFS. Moreover, univariate and multivariate Cox regression analyses showed that UBC1 expression (p = 0.018) and tumor stage (p = 0.035) were independent prognostic factors for RFS of NMIBC.

Conclusions Liquid biopsy has been reported to be more convenient and have higher sensitivity for cancer diagnosis compared with traditional imaging and biopsy strategies. In the present study, we identified three up-regulated serum exosomal lncRNAs (PCAT-1, UBC1 and SNHG16) in BC and further designed a three-lncRNA panel as a novel diagnostic biomarker for BC based on a multivariate logistic regression model. Moreover, this panel was significantly superior to traditional urine cytology in terms of diagnostic accuracy. In addition, our data proved that these lncRNAs in serum were mainly stored in the exosomes. Among these three lncRNAs, UBC1 and SNHG16 could be used to distinguish MIBC from NMIBC. UBC1 was also identified as an independent prognostic factor for RFS in NMIBC. These results suggested that serum exosomal lncRNAs could be used as an easier and faster noninvasive approach for diagnosis and recurrence prediction of BC. Although we constructed a promising three-lncRNA panel for BC diagnosis, there were some limitations in our study. Further studies, including larger clinical samples, multicenter study and functional analysis, are required to support the importance of these lncRNAs as noninvasive markers in BC.

Taken together, we established a distinctive serum exosomal lncRNA signature that might represent a new complementary marker for BC diagnosis. Moreover, we identified that UBC1 expression was a useful prognostic marker for RFS in BC.

P0-062

The interference of oral low dose biotin on immunoassays

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Objective Streptavidin/biotin-based immunoassays are vulnerable to many different types of interference especially biotin, which can lead to erroneous clinical decisions. To investigate the interference of biotin metabolism, we evaluated the interference of oral low dose biotin in several factors using immunoassays marketed by Roche, Beckman and Mindray.

Methods Healthy subjects were informed to take 10 mg per day within 7 days. Serum samples from healthy subjects at different points were collected. The measurements of thyroid stimulating hormone, 25-hydroxyvitamin D, vitamin B12, folate, Ferrtin, and estradiol in health serum were implemented by chemiluminiscence methods of Beckman coulter, Roche, and Mindray. The measurements of TnI (or TnT), CK-MB, MYO in health serum added cardiac markers positive serum were also implemented by these detection systems.

Results We found significant differences of TSH between the second point and the first points (p value = 0.046), between the second point and the fourth point (p value = 0.034) detected by the Beckman detection system; significant differences of TSH between the second point and the first points (p value < 0.001), between the second point and the third point (p value = 0.006), between the second point and the fourth point (p value < 0.001) detected by the Roche detection system; significant differences of 25-OH VitD between the second point and the first points (p value < 0.001), between the second point and the third point (p value = 0.003), between the second point and the fourth point (p value = 0.001) detected by the Roche detection system; significant difference of TSH between the second point and the first points (p value = 0.017), between the second point and the fourth point (p value = 0.035) detected by the Mindray detection system; significant difference of folate between the second point and the first points (p value = 0.024), between the second point and the fourth point (p value = 0.020) detected by the Mindray detection system. Moreover, the significant differences of 25-OH VitD were found between the first point and the second (p value < 0.001), the first point and the third point (p value = 0.048), the second point and the third point (p value < 0.001), the second point and the fourth point (p value < 0.001) detected by the Mindray detection system. However, no significant differences (p value > 0.05) were found of all cardiac markers in mixed serum samples between different points detected by these three systems, respectively.

Conclusions TSH and 25-OH VitD might be interfered by the oral low dose biotin, with a lower and elevated change, respectively. The interference rejection detected on Beckman coulter and Roche was better than it detected on Mindray. The trend of differences of TnT detected by Roche might exist although the p value was greater than 0.05 in this study. The limitations of this study were small sample sizes and the dilution effect. Serum samples mixed in positive serum might not imitate the metabolism in vivo.

P0-063

Liquid chromatography tandem mass spectrometry method for serum testosterone and application.

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Objective To establish the reference method for the determination of human serum testosterone based on isotope dilution liquid chromatography tandem mass spectrometry (ID-LC/MS/MS), and to use it into assessing the clinical method and assigning target value to sample in Shanghai external quality assessment (EQA) scheme.
Methods Testosterone-2,3,4-13C3 was added as internal standard, serum samples were treated with liquid-liquid extraction,and dried under 40 ℃ with nitrogen flow. Then,the residual were then reconstituted with mobile phase and analyzed by LC/MS/MS. The method was validated according to CLSI:C62A and CLSI:EP15.
Results The LC-MS/MS method was validated over a concentration range of 2-22.5ng/ml. Intra-and inter-run precision was 0.7-3.2% and 2~2.8%, respectively. The biases of analyzing the certified reference material SRM971 (Level male) was 0.2%.Our results in RELA-2017 agreed with others. The linear correlation formula between LC/MS/MS method and testosterone clinical method were $Y_{\text{Beckman Access}} = -0.2916\ X_{\text{LC-MS/MS}} + 1.1421$, r=0.992, its average relative bias was 26.4%.
Conclusions The ID-LC/MS/MS method established for serum testosterone has good precision and accuracy, and may be used as a candidate reference method.

P0-064

microRNA-769 is downregulated in colorectal cancer and inhibits cancer progression by directly targeting cyclin-dependent kinase 1

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Objective MicroRNAs (miRNAs) were reported to be aberrantly expressed in colorectal cancer (CRC). The deregulation of miRNAs is implicated in the formation and progression of CRC, and participates in the regulation of a wide range of biological behaviours. Considering the crucial roles of miRNAs in CRC, miRNAs are thought to have significant promise in the diagnosis and therapy of patients with this malignancy.
Methods CRC tissues and adjacent normal tissues (ANTs) were obtained from 47 patients at Shanghai Eighth People's Hospital. Cells were transfected with miR-769 mimics, siRNA or plasmid, and miR-769 expression was determined by qPCR. MTT assay was performed at each time point to detect cell proliferation. The rate of apoptosis cells was determined using an annexin V-fluorescein isothiocyanate (FITC) apoptosis detection kit. Migration and invasion assays were employed to assess the migratory and invasive abilities of CRC cells.

Results In the present study, miR-769 was frequently lowly expressed in CRC tissues and cell lines. Functional assays showed that resumption of miR-769 expression suppressed CRC cell proliferation, migration, invasion and increased cell apoptosis in vitro. In addition, cyclin-dependent kinase 1 (CDK1) was demonstrated to be direct target of miR-769 in CRC cells. Furthermore, CDK1 was found to be overexpressed in CRC tissue samples and negatively correlated with miR-769 expression. Moreover, inhibition of CDK1 could imitate the tumor suppressor activity of miR-769 in CRC cells. Besides, restoring CDK1 expression was able to partially abolish the tumor-suppressing roles of miR-769 on the malignant behaviors of CRC cells.
Conclusions Collectively, the findings of our current study demonstrated that miR-769 was downregulated in CRC and directly targeted CDK1 to implicate in the regulation of CRC cell proliferation, apoptosis, migration and invasion. Thus, miR-769/CDK1 axis might be effectively therapeutic target for the treatment of patients with CRC.

PO-065

Circulating lymphocyte subsets combined with CRP and WBC improves the ability of diagnosing respiratory infectious diseases in children

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Objective We prospectively evaluated the changes of circulating lymphocyte subsets during respiratory infectious diseases in children, and to explore their characteristics and clinical significance. To evaluate the diagnostic value of $CD4^+$ /$CD8^+$ ratio (T4/T8) in the treatment of respiratory infectious diseases in children.
Methods A total of 121 children with respiratory infectious diseases were selected between January 2018 to October 2018 in Department of pediatrics, the second hospital of Jilin university. The age ranges from 0 to 13 years. According to the type of infection, these patients were divided into Group A(36 cases of upper respiratory tract infection), Group B(33 cases of bronchitis), Group C(14 cases of bronchiolitis)and Group D(38 cases of pneumonia). 19 normal children subjects were selected as control group. The percentage of peripheral blood lymphocyte subsets was detected by flow cytometry, and the changes of WBC and CRP were also monitored. Drawing ROC curves of WBC, CRP and T4/T8 ratio for respiratory infectious diseases in children. The data were analyzed by SPSS 19.0 software.
Results Compared with the control group, there was no significant change in CD3+T lymphocyte. The percentage of CD4+T cells, the T4 /T8 ratio and the percentage of NK cells were all significantly decreased, while the percentage of CD8+T cells was significantly increased in children with respiratory infection ($P < 0.05$ or $P < 0.01$), while there was no significant difference in the proportion of B lymphocyte. In the upper respiratory tract infection, bronchitis, bronchiolitis and pneumonia groups, these changes can be seen in varying degrees, especially in the pneumonia group. The CRP and WBC values of children with respiratory infection increased significantly,

compared with the control group. The CRP, WBC and T4/T8 ratios under the ROC curve were 0.754, 0.759 and 0.696, respectively. When the cut-off value of T4/T8 was 1.47, the sensitivity and specificity were 77.8 and 51.6, respectively. Compared with CRP and WBC, T4/T8 ratio is slightly more sensitive and less specific in the diagnosis of respiratory infectious diseases. When combined with T4/T8, the diagnostic rates of WBC and CRP for respiratory infectious diseases in children, including sensitivity and specificity, were significantly improved.

Conclusions Immune impairment is common in children with respiratory infectious diseases. And the degree of immune dysfunction is probably related to the severity of the disease. Monitoring the changes of lymphocyte subsets is helpful for doctors to know the immune function of children, meanwhile to assess the severity of the disease. T4/T8 ratio has satisfactory sensitivity and specificity for the diagnosis of infectious diseases in children. Combined with CRP and WBC, T4/T8 ratio can be used as a routine indicator to improve the diagnositic value of infectious diseases in children.

PO-066

Hepatotoxicity among MSM PHI patients receiving tenofovir, lamivudine plus efavirenz regimen in China

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Objective This study aimed to investigate the incidence density of liver injury in men who have sex with men (MSM) primary HIV infection (PHI) cohort. Moreover, we assessed the frequency, dynamic characteristics, and risk factors of hepatotoxicity in MSM HIV infected population initiating tenofovir disoproxil fumarate (TDF)/ lamivudine (3TC) plus efavirenz (EFV) regimen.

Methods From June 2009 to August 2017, PHI and chronic HIV infection (CHI) patients were recruited. We compared liver function parameters between the two cohorts after initiating TDF/3TC plus EFV regimen. Multivariate Cox proportional hazards model was constructed to analyze the risk factors of hepatotoxicity development.

Results During the study period, 76 PHI and 253 CHI MSM patients were enrolled. Liver injury occurred in 43.2% (n=142, incidence rate 1.99 cases/100 person-month) of the patients. The liver enzymes elevation (LEE) incidence densities were similar between the PHI and CHI cohort (3.06 cases/100 person-month vs. 1.80 cases/100 person-month, p=0.215), but the LEE developed earlier in the PHI cohort (Log Rank test = 29.48, p< 0.001). The proportion of LEE higher than 10% mostly occurred within 6 months on therapy. In multiple cox regression analysis, the baseline BMI, ALT, GGT and CD4 levels were associated with increased risk of hepatotoxicity development.

Conclusions The drug related hepatotoxicity occurred early in MSM PHI patients after taking TDF/3TC plus EFV regimen. The LEE mostly developed within 6 months after

treatment. It should be given more attention and prophylactic treatments for MSM HIV infected patients with risk factors.

PO-067

Rifampin resistance-associated mutations in the RIF resistance-determining region (RRDR) of the rpoB gene of Mycobacterium tuberculosis clinical isolates in Shanghai, China

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Objective Our objective for this study was to investigate the relationship between specific *rpoB* mutations and the minimum inhibitory concentrations (MICs) of RIF and rifabutin (RFB) against *M. tuberculosis*.

Methods We collected 195 clinical isolates of *M. tuberculosis* including 105 RIF-resistant and 90 RIF-susceptible isolates from Shanghai Pulmonary Hospital in China. The MICs of antituberculosis drugs in 7H10 Middlebrook medium for clinical isolates of *M. tuberculosis* were determined. Strains were screened for *rpoB* mutations by DNA extraction, *rpoB* gene amplification, and DNA sequencing analysis.

Results Twenty different types of mutations were identified in the *rpoB* gene. One hundred isolates (95.24%) were found to have mutations in the RIF resistance-determining region (RRDR) of the *rpoB* gene. Three *rpoB* mutations were identified in 90 RIF-susceptible isolates. Out of 105 isolates, 86 (81.90%) were cross-resistant to both RIF and RFB. The most frequent mutation occurred at codon 531 (65.71%), followed by 526 (8.57%). We also found a novel nine-nucleotide (ATCATGCAT) deletion (between positions 1543 and 1551) in the *rpoB* gene among two strains (1.90%) with resistance to RIF, but susceptibility to RFB. In addition, the mutation frequency at codon 531 was significantly higher in RIF-resistant/RFB-resistant (RIF^R/RFB^R) strains than in RIF^R/RFB^S strains (75.58% versus 21.05%), whereas the mutation frequency at codon 516 was significantly lower in RIF^R/RFB^R strains than in RIF^R/RFB^S strains (1.16% versus 26.32%). The MICs of RIF against 87.62% (92/105) of the *M. tuberculosis* isolates were $\geqslant$ 16 μg/mL.

Conclusions Our data supported previous findings that various *rpoB* mutations are associated with differential levels of resistance to RIF. The specific mutations of the *rpoB* gene in RIF^R/RFB^R isolates differed from those in RIF^R/RFB^S isolates. A novel deletion mutation in the RRDR might be associated with resistance to RIF, but not to RFB. Further clinical studies are required to investigate the efficacy of RFB in the treatment of *M. tuberculosis* infections, which harbor the mutations.

PO-068

A Clinical Investigation and Genome Sequence of the First Reported Human Infection with the Burkholderia thailandensis in China

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Objective With *Burkholderia thailandensis* generally considered avirulent, disease due to *Burkholderia thailandensis* is extremely rare. A 38-year-old man presented to a healthcare facility with fever and productive cough. Laboratory investigations revealed infection with *Burkholderia thailandensis*.
Methods Biochemical testing and 16S rDNA sequencing were performed to identify the infecting species. Survival and histopathological examination were used to determine virulence of the bacterium. The entire genome was also analyzed to reveal the genomic factors.
Results Biochemical testing and 16S rDNA sequencing identified the infecting species as *Burkholderia thailandensis*. The clinical isolated *Burkholderia thailandensis* displays a virulence capacity in mice campared with *Burkholderia thailandensis* E264. The specific virulence factors of VirB/VirD4 type IV secretion system, HSI-I, and WcbR were idenfitied by comparative genomics. In addition, the pan-genome, core genome, and phylogenomic analysis improved understanding of the pathogenic *Burkholderia thailandensis*.
Conclusions We report the first case of *Burkholderia thailandensis* infection in China. The entire genome might help us to understand the mechanisms of *Burkholderia thailandensis* infection and provide some clues for further exploring the evolution of the bacterium.

PO-069

Exploring the correlation between glycosylated hemoglobin and fasting blood glucose based on chemical reaction theory

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Objective To explore the correlation between HbA1c and fasting blood glucose (FPG) by analyzing the HbA1c formation process and its influence factors.

Methods Natural population consist of 14266 cases in Yuxi City,Yunnan Province were collected, aged from 18 to 93 years old, including 8832 males (45.87±13.16) and 5434 females (43.46±12.07), testing their HbA1c, FPG, red blood cell distribution width (RDW) and hemoglobin (Hb) levels. 1) Compare the level differences of HbA1c and FPG between distinct sexual group; 2) analyze the trend of each index along with age changing after age stratification ; 3) divide all the subjects into 5 groups, as FPG＜5.0mmol/L、5.0-5.9 mmol/L、6.0-6.9 mmol/L、7.0-11.0 mmol/L 和≥11.1 mmol/L, calculate the correlation between FPG and HbA1c in each group, then analyze the variation trend of correlation coefficient; 4) divide all the subjects into 4 groups, as HbA1c＜5.7%、5.7-6.4%、6.5-7.4%、≥7.5%, and also calculate the correlation between FPG and HbA1c in each group, then analyze the variation trend of correlation coefficient.

Results 1) This study found that gender differences existed in HbA1c and FPG levels. 2) HbA1c, FPG and RDW varied very sharply with age, while Hb level showed a narrower fluctuation; and the changing trend of these indexes in different gender differed either; 3) The correlation between FPG and HbA1c was lower within the group which FPG below 7.0mmol/L or HbA1c below 6.5%, but with the increasing of their respective levels,the correlation increased , and it turned out similar results in both male and female.

Conclusions The correlation between FPG and HbA1c are influenced by age and FPG level. HbA1c's representativeness of blood glucose vary under different conditions.

P0-070

Serum miR-1301-3p, miR-335-5p, miR-28-5p, and their target B7-H3 may serve as a novel biomarker for colorectal cancer B7-H3 in colorectal cancer

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Objective B7-H3, a member of the B7 family of immune regulatory ligands, plays a critical role in the T cell-mediated immune response, is broadly expressed in several human cancers and contributes to a poor prognosis. Nevertheless, the clinical significance of B7-H3 expression in colorectal cancer remains unclear.

Methods The serum B7-H3, B7-H1, and cancer-associated carbohydrate antigen (CA) and carcinoembryonic antigen (CEA) expression in patients with colorectal cancer, gastrointestinal disease, and healthy control were measured by ELISA. The miRNAs that target B7-H3 were predicted by using the miRTarBase and their expressions in patients with colorectal cancer were measured by Real-time PCR.

Results Results showed that B7-H3, B7-H1, and CA-50 expression were higher in colorectal cancer patients compared with that in healthy controls and the patients with gastrointestinal diseases. B7-H3 expression was correlated with the tumor pathologic stages and metastasis. It was predicted that B7-H3 was a target of miR-1301-3p, miR-335-5p and miR-28-5p, and its expression was negatively related to miR-1301-3p, miR-28-5p and miR-335-5p expression. Serum miR-1301-3p, miR-335-5p, and miR-28-5p expression were also correlated with the tumor pathologic stages and metastasis.

Conclusions Our findings suggest that serum miR-1301-3p, miR-28-5p, miR-335-5p, and B7-H3 expression were correlated with colorectal cancer pathologic stages and metastasis and may therefore serve as a novel biomarker for colorectal cancer diagnosis and treatment.

PO-071

Identification of novel mutations in MYO15A, OTOF, and RDX with hearing loss by next-generation sequencing

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Objective Non-syndromic hearing loss (NSHL) is the most common sensorineural disorder and one of the most common human defects. Autosomal recessive (AR) inheritance accounts for a huge percentage of familial cases. Next-generation sequencing (NGS) is a powerful molecular diagnostic strategy for NSHL. The combination of a microarray gene chip and NGS can better delineate the etiology and genetic cause of deafness in many cases.

Methods One hundred and thirty-one unrelated students with NSHL who attend a special education school in Yunnan Province were recruited. Clinical data and blood samples were collected from these students and their family members. Subsequently, four common deafness-related genes (*GJB2*, *GJB3*, *SLC26A4*, and mtDNA 12S rRNA) were evaluated for mutations using a microarray kit. Furthermore, three Chinese families with AR nonsyndromic hearing loss were enrolled in this study. Two hundred and twenty-seven known human deafness genes were sequenced to identify the responsible genetic mutation of the proband. The mutational status of family members of the probands was validated by Sanger sequencing.

Results Five novel mutations were found in three families using NGS. In family 1, we identified compound heterozygosity at the *MYO15A* gene, including an insertion mutation [his1290-to-ala (H1290A)] and a 3-bp deletion (10251delCTT), resulting in protein length changes and premature protein truncation, respectively. In family 2, two affected siblings from a consanguineous Chinese Dai family with AR deafness-9 (DFNB9; 601071) harbored an arg425-to-pro (A425P) missense mutation in the *OTOF* gene caused by a homozygous 1274C-G transition. In family 3, we identified compound heterozygosity for a 2-bp deletion (129delTA) and a 4-bp deletion (76delGTTT) in the *RDX* gene, predicted to cause premature stop codons that would influence approximately the entire second FERM domain until the N terminus.

Conclusions Five novel mutations were found in three families with NSHL. Our findings extend the mutation spectrum in deafness-related genes and have important implications for genetic counseling.

PO-072

The combined application value of prognostic nutritional index, glasgow prognostic score and systemic inflammatory response in colorectal cancer

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Objective Various biomarkers have been shown to predict prognosis in various types of cancers. The Glasgow prognostic score (GPS) unites serum albumin level and C-reactive protein (CRP).The prognostic nutritional index (PNI) is based on serum albumin level and absolute lymphocyte count. Systemic inflammatory response (SIR) markers includes the neutrophil/lymphocyte ratio (NIR), the platelet/lymphocyte ratio (PIR), and the lymphocyte/monocyte ratio (IMR).The three indicators are the most common in existing studies. However, their assessment ability has not been reported largely in cancer of different stages, and few studies conducted that these biomarkers are combined studies in cancer. The aim of this study was to research the correlation among these indicators in colorectal cancer at different stages

Methods 177 eligible patients were recruit who were diagnosed with colorectal cancer from October 2012 to October 2017. Firstly, we separately calculated PNI, SIR markers and mGPS. Next, the relationship among PNI and mGPS with clinical factors were evaluated during these patients, and also their connections were analyzed.

Results Our results demonstrate that PNI is associated with SIR and GPS in patients with colorectal cancer, and the results show that PNI is negatively proportional to NIR and PLR,but positively proportional to LMR in CRC.

Conclusions We innovatively combined PNI, SIR,GPS with tumor staging, and the results showed that the three indicators were closely related to tumor staging.Therefore, they may serve as a valuable Staging index in patients with colorectal cancer.

PO-073

High Expression of AR Serves As a Novel Biomarker and Drives Cancer Progression in Gastric Cancer

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Objective Androgen receptor (AR) and its variants (AR-Vs) promote tumorigenesis and metastasis in many hormone-related cancers, such as breast, prostate and hepatocellular cancers. However, the expression patterns and underlying molecular mechanisms of AR in gastric cancer (GC) are not fully understood. This study aimed to detect the expression of AR-Vs in GC and explored their role in metastasis of GC.

Methods Here, the AR expression form was identified in GC cell lines and tissues by RT-PCR, qPCR and Western-blot. Finally, the functional roles of AR in GC cell lines and nude mice lung metastasis animal models were used to assess the function of AR in cell migration and invasion.
Results Different from full length of AR, AR-v12 was localized to the nucleus independent of androgen. Up-regulation of AR-v12 in primary GC tissues was significantly associated with metastasis. Our receiver operating characteristic curves analysis showed that high AR expression could distinguish GC patients from normal persons ($p<0.0001$). Kaplan-Meier curves demonstrated that high AR expression predicted poor overall survival ($p<0.0001$). Over expression of AR-v12 promoted migration and invasion independent of androgen. Knockdown of AR-v12 inhibited migration and invasion in vitro, as well as metastasis in vivo.
Conclusions In conclusion, our results suggest that AR splice variant may serve as a promising diagnostic and prognostic molecular marker for patients with GC. Moreover, AR splice variant may represent a novel clinical therapeutic target.

P0-074

Screening models combining maternal characteristics and multiple markers for early prediction of preeclampsia in pregnancy: A nest case-control study

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Objective To examine the association between preeclampsia (PE) and laboratory markers and investigate the performance of biomarkers in screening for PE.
Methods A total of 67 pregnancies that subsequently developed PE at 11-13 weeks, 25 cases at 16-20 weeks, and 73 cases at 24-28 weeks were recruited. The routine laboratory markers were measured according to the procedure recommended by manufacturer. Binary logistic regression analysis was used to determine the models for early prediction of PE.
Results At 11-13 weeks' gestation, there were significantly higher concentrations of platelet, plateletcrit, alanine aminotransferase, aspartate aminotransferase, α-L-fucosidase, 5'-nucleotidase, glutamyl transpeptidase, cholinesterase, and uric acid in patients who later developed PE. At 16-20 weeks' gestation, the levels of inhibin A and platelet were significantly elevated. At 24-28 weeks' gestation, the levels of platelet, plateletcrit, and glucose were significantly elevated. The logistic regression analysis showed that the elevated 5'-nucleotidase level was independently associated with PE at 11-13 weeks' gestation. The combination of inhibin A, diastolic blood pressure and BMI, and the combination of glucose and systolic blood pressure, were predictors of PE at 16-20, and 24-28 weeks' gestation, respectively.
Conclusions Measurement of 5'-nucleotidase, inhibin A, and glucose provides potentially valuable risk assessment of PE in combination with maternal characteristics.

PO-075

Significantly high levels of mast cell activation-related autoantibodies in inflammatory bowel disease

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Objective Mast cells can be activated in various ways and involved in the development of inflammatory bowel diseases (IBD). Our aim was to determine whether mast cell activation-related molecules or published antibody markers could help diagnose IBD, and whether they were associated with particular clinical manifestations in a Chinese cohort.

Methods Serum from 87 IBD patients with either Crohn disease (CD, n=47) or ulcerative colitis (UC, n=40) and healthy controls (HC, n=43) were collected. IgE was measured by rate turbidity turbidimetry; IgG anti-IgE and IgG anti-Fcε RI were assayed by enzyme-linked immunosorbent assay. IgG antibodies to antinuclear antibody (ANA), anti-neutrophil cytoplasmic antibody (ANCA), anti-intestinal goblet cell antibody (GAB), anti-panereatic antibody (PAB), anti-Saccharomyces cerevisiae antibody (ASCA) were determined by indirect immunofluorescence assay. Data were analyzed in relation to the clinical characteristics.

Results Total IgE levels increased in IBD patients compared with HC, but no obvious difference ($P>0.05$). IgG anti-IgE significantly increased only in UC ($P=0.021$). IgG anti-Fcε RI increased both in CD and UC with good performance for diagnosis of IBD (AUC=0.899). Anti-Fcε RI was associated with disease activity and extraintestinal manifestations in CD. The positive rates of ANA in CD and UC were 23.4% and 40%. GAB had similar diagnostic value in CD or UC. Positive ANCA was higher in UC (62.5%), while PAB was highly specific for CD (25.5%). ASCA detection was poor in all groups. Increasing amount of antibodies was associated with higher disease activity [OR: 1.773(1.088, 2.887), $P=0.021$]. Combined detection of all indicators improved the diagnostic sensitivity, up to 87.4%.

Conclusions Except IgE and ASCA, all antibodies, especially IgG anti-Fcε RI may be helpful tools in non-invasive diagnosis of UC or CD. Combination of the autoantibodies may be particularly helpful, as the diagnostic sensitivity is sufficient improved.

PO-076

Differential expression of long noncoding RNAs in Intrahepatic cholestasis of pregnancy

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Objective 长链非编码 RNA（lncRNAs）在 ICP 中的修饰作用最近备受关注；然而，潜在的机制仍然很大程度上未知。在此，我们的目标是分析 ICP 中的 lncRNA 表达谱，并使用生物信息学分析确定 ICP 诊断的有希望的目标。
Methods 通过使用来自 4 名 ICP 的孕妇和 4 名健康孕妇的血清样品进行 lncRNA 的微阵列筛选。通过 Q-PCR 在来自 54 名 ICP 孕妇和 54 名健康对照的血清样品中验证了显着差异表达的 lncRNA。生物信息学分析用于发现这些差异表达的 lncRNA 参与的相关过程。
Results 我们的数据显示，ICP 孕妇血清样本中有 58 个上调的和 85 个下调的 lncRNAs 以及 47 个上调的和 71 个下调的 mRNA（倍数变化> 2.0; P <0.05）。健康的控制。差异表达的 mRNA 和 lncRNA 的 GO 分析突出了甘油酯代谢，破骨细胞分化和肿瘤生长。我们选择验证的三种 LncRNA（ENST00000505175.1，ASO3480 和 ENST00000449605.1）的表达水平在 ICP 患者中与对照相比显着降低。接收器操作特性（ROC）曲线（AUC）下的面积分别为 0.731,0.798 和 0.812。使用多重逻辑回归分析的三种 LncRNA 的组合显示更大的 AUC（0.865），其对于 ICP 的诊断更有效。
Conclusions 我们的研究首先显示了 ICP 孕妇血清中 lncRNAs 的特异性特征。这三种 lncRNA 可作为 ICP 的新型非侵入性生物标志物。

PO-077

NRAGE forms a ternary complex with RNF8–BARD1 to facilitate DNA-damaging chemotherapeutic resistance and cell survival in squamous esophageal Tumorigenesis

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Objective NRAGE, a neurotrophin receptor-interacting melanoma antigen-encoding gene homolog, is significantly increased in the nucleus of radioresistant esophageal tumor cell lines and is highly upregulated to promote cell proliferation in esophageal carcinomas (ECs). Efficient DNA-damage response (DDR) is essential to maintain genomic integrity. In normal organisms, DDR protects cells from tumorigenesis, whereas in tumor cells, DDR enables cells to grow and resist DNA-damaging therapeutic agents. In this study, we aim to study the role and the underlying mechanisms of NRAGE in DDR and to provide possible target for treatment of ECs.
Methods The neutral comet assay and the canonical homologous recombination repair (HR) and non-homologous end joining (NHEJ) reporter system were conducted and the UV-irradiated skin tumor model was established to investigate the direct role of NRAGE in DDR. The sensitivity of NRAGE-deficient EC cells to DNA-damaging therapies both in vitro and in vivo were evaluated by cell sensitivity assays, in vivo esophageal tumor chemotherapy, immunoblotting assays and immunohistochemistry (IHC) assays. The

quantitative real-time PCR (qRT-PCR) and immunoblotting assays were performed to measure the expression of a band of DDR factors in NRAGE knockdown EC cells. GST pull-down assay and immunoprecipitation (IP) were conducted to explore the mechanisms of NRAGE in HR.

Results NRAGE is a positive regulator in homologous recombination (HR) and regulates the chemoresistance of EC cells both in vivo and in vitro. From mechanism, it regulates the stability of RNF8 and BARD1 via the ubiquitin-proteasome pathway and interacts with the RING domains of the two proteins as a chaperon to form a novel ternary complex to participate in DDR. Furthermore, clinical characterization of NRAGE, RNF8, and BARD1 in squamous EC tissues shows that the expression of NRAGE protein is closely related with both RNF8 and BARD1.

Conclusions We conclude that the nuclear localized NRAGE interacts with RNF8 and BARD1 to mediate the resistance of EC cells against DNA-damaging agents and is likely to be a promising target for personalized DNA-damaging therapies in ECs.

PO-078

The Application of Heart Fatty Acid-Binding Protein in Acute Myocardial Infarction

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Objective To discuss the specificity and sensitivity of serum heart fatty acid-binding protein , troponin and myoglobin in patients with acute myocardial infarction, and to compare the diagnostic significance of heart fatty acid-binding protein in early acute myocardial infarction.

Methods The sensitivity and specificity of heart fatty acid-binding protein with the cardiac troponin and myoglobin in patients with acute myocardial infarction were compared by ELISA kit.

Results At the early stage of acute myocardial infarction, heart fatty acid-binding protein appeared earlier than cardiac troponin and myoglobin, and the elevated concentration of heart fatty acid-binding protein was more obvious.

Conclusions Heart fatty acid-binding protein will be a novel Molecular Marker in the diagnosis of Acute Myocardial Infarction.

PO-079

Diagnostic value of PCT, NEUT%, LYMPH%, CRP, PLT, WBC and ESR in bloodstream infection

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Objective :Explore the application value of seven inflammatory factors【Procalcitonin (PCT), white blood cell count (WBC), neutrophil ratio (NEUT%), lymphocyte ratio (LYMPH%), platelet value (PLT), erythrocyte sedimentation rate (ESR), C-reactive protein (CRP)】in bloodstream infection.

Methods Retrospective analysis of patients with positive bloodstream infection in Lianyungang Second People's Hospital from January 2012 to July 2018.According to the results of blood culture, the patients were divided into Gram-positive cocci group, Gram-negative bacillus group and negative control groups.Compare the differences of PCT, WBC, NEUT%, LYMPH%, PLT, ESR, and CRP levels between the three groups and plot the ROC curve,At the same time, compare the inflammation index mentioned above between the three groups.

Results After comparing the levels of inflammation indicators between the Gram-negative bacilli group, the Gram-positive cocci group, and the negative control group: PCT, NEUT% inflammation index was higher in the Gram-negative group than in the Gram-positive and negative control groups, the difference between the Gram-positive group and control group has no significant difference; the CRP inflammation index was higher than the Gram-positive cocci group level in the Gram-negative bacillus group level.The level of Gram-positive cocci was higher than that of the negative control group ($P<0.05$), and the LYMPH% and PLT inflammation indexes were higher in the negative control group than in the Gram-positive cocci group and Gram-negative group ($P<0.05$).There was no significant difference between Gram-negative bacillus group and Gram-positive cocci group ($P>0.05$). There was no significant difference in ESR between the three groups ($P>0.05$).The level of WBC in the Gram-positive cocci group was higher than that in the Gram-negative bacillus group and the negative control level, and the difference between the Gram-negative bacillus group and the negative control group has no significant difference ($P>0.05$).The results of ROC curve analysis of different inflammatory indexes indicated that the diagnostic efficiency of bloodstream infection in Gram-negative bacilli group was PCT, NEUT%, LYMPH%, CRP, PLT, WBC, ESR, from high to low.The diagnostic efficiency of Gram-positive bacteria (G+ bacteria) group from high to low is NEUT%, LYMPH%, PCT, WBC, CRP, PLT, ESR.

Conclusions The diagnostic value of different inflammatory factors in bloodstream infection is different, and the diagnostic value of each inflammatory index of bloodstream infection caused by Gram-negative bacilli is sorted as follows: PCT >NEUT%> LYMPH%> CRP > PLT> WBC;The diagnostic value of each inflammatory index of bloodstream infection caused by Gram-positive cocci is sorted as follows: NEUT%> LYMPH%> WBC > PLT; PCT and CRP are not suitable for the auxiliary diagnosis of bloodstream infection caused by Gram-positive cocci.The auxiliary value of ESR for bloodstream infection caused by Gram-negative bacilli or Gram-positive cocci was not significant.

PO-080

Association of PVL gene with incomplete hemolytic phenotype in clinical SIHP and SCHP strains of S. aureus

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Objective This experiment aimed to evaluate the correlation among the incomplete hemolytic phenotype of *Staphylococcus aureus* (SIHP) and Panton-Valentine Leukocidin gene (*pvl*) in characteristics of antimicrobial resistance.
Methods The antibiotic susceptibility of 211 hospital-acquired *Staphylococcus aureus (S. aureus)* to 20 antibiotics were determined by MicroScan WalkAway 96 (Beckman Coulter, Brea, CA). All strains were cultured in Columbia sheep blood agar plates for 24 hours and then underwent 10 passages for investigation of their hemolytic phenotypes. *S.aureus* produces incompletely β-hemolytic phenotype, termed as SIHP (*S.aureus* strains with incomplete hemolytic phenotype)[1]. The *pvl* are characterized by PCR amplification followed by sequencing. Statistical analyses of the data were performed using SPSS version 16.0 software (SPSS Inc , Chicago, IL).
Results Fifty-two (24.64%) strains were confirmed to keep the incomplete hemolytic phenotype of *S.aureus* (SIHP). Meanwhile, 15(7.11%) of 211 strains were identified to carry *pvl*, and 8 of 15 strains were SIHP. Compared with SCHP (*S.aureus* strains with complete hemolytic phenotype), among the 20 antibiotics, the susceptibility of SIHP to 7 antibiotics (oxacillin, ciprofloxacin, gentamicin, ceftriaxone, cefoxitin, levofloxacin and moxifloxacin) presented statistically significant differences ($P < 0.05$). The resistance rates of *pvl*-positive bacteria to 4 antibiotics (rifampin, ciprofloxacin, levofloxacin and moxifloxacin) were statistically different compared with those of *pvl*-negative strains ($P < 0.05$).
Conclusions Compared with SCHP, *pvl* had a higher frequency than those identified in SIHP. The *pvl*-positive isolates showed less resistance to rifampin, ciprofloxacin, levofloxacin and moxifloxacin. Additionally, SIHP strains had significantly higher susceptibility to oxacillin and cefoxitin in comparison with SCHP, while SCHP strains had significantly higher antibiotic resistance rates to ciprofloxacin, gentamicin, ceftriaxone, levofloxacin and moxifloxacin. The results may provide medical advice for the clinical treatments of *S.aureus.*

PO-081

Genetic Diversity and Epidemiology of Norovirus in Children with acute sporadic gastroenteritis in Shanghai, China, 2012-2017

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Objective Noroviruses (NoVs) are considered the important causes of acute gastroenteritis (AGE) across all age groups especially in children under five years. We investigated the prevalence and molecular epidemiology of norovirus in outpatient children from Children's Hospital of Fudan University in Shanghai, China.

Methods A total of 1433 stool specimens were collected from children under five years of age with acute gastroenteritis between January 2012 and December 2017. All the samples were analysed by conventional reverse transcription-polymerase chain reaction (RT-PCR) for genogroup II targeting the RNA-dependent RNA polymerase and partial capsid genes. Norovirus Genotyping Tool v.2.0 (https://www.rivm.nl/mpf/typingtool/norovirus/) was used for genotyping strains, and phylogenetic analyses were conducted by MEGA 6.0.

Results During 2012 to 2017, NoVs were detected in 15.4% (220/1433) of the samples, with high detection rate in children aged 7-12 months (23.7%, 143/603) and September (27.7%, 33/119). Based on genetic analysis of RdRp, GII.Pe (78.8%%, 145/184) was the most predominated RdRp genotype from 2013-2017 while GII.P4 played a dominant role in 2012 (55.6%, 21/36). The most prevalent NoVs genotype was GII.4 (73.6%, 162/220) during 2012 to 2017 among the capsid genotypes. According to genetic analysis of RdRp and capsid sequences, the strains were clustered into 19 RdRp/capsid genotypes, and 12 of them were discordant RdRp and capsid genotypes including GII.Pe/GII.4-Sydney_2012, GII.P12/GII.3, GII.P7/GII.6, GII.Pe/GII.3, GII.P16/GII.2, GII.Pe/GII.3, GII.Pg/GII.1 and so on.

Conclusions The present study shows high detection rates and genetic diversity of circulating NoVs genotypes in paediatric AGE samples from Shanghai. The findings emphasize the importance of continuous molecular surveillance of NoVs, including typing of both RdRp and capsid genes, for monitoring emerging NoVs strains and supporting on-going vaccine development programs.

PO-082

EVALUATION OF SERUM FREE LIGHT CHAINS RATIO IN PATIENTS WITH HIGH PARAPROTEIN CONCENTRATIONS DETECTED BY CAPILLARY ELECTROPHORESIS

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Objective Monoclonal gammopathies include a wide range of hematological diseases ranging from indolent disorders such as monoclonal gammopathy of undetermined significance (MGUS) to severe diseases such as multiple myeloma (MM) and amyloidosis. Nowadays highly sensitive serum free light chains assays are available for clinical use and they allow quantification of free lambda and kappa chains. Measurement of free kappa and free lambda light chains plays a key role in screening, diagnosis, monitoring, and prognosis for many patients with a monoclonal gammopathy manifestations in addition to serum protein electrophoresis (SPEP) and immunofixation (IFE). An abnormal serum free light chains ratio at baseline is predictive of an increased risk of progression in patients with monoclonal gammopathy of undetermined significance. The majority of patients with intact immunoglobulin multiple myeloma present abnormal serum free light chains ratio. According to the available literature data, about 5% percent of patients may present high concentration of M-component with normal free light chains ratio. We retrospectively studied the frequency of normal and abnormal free light chains ratio in samples with high M-protein concentration detectable by capillary serum electrophoresis in a private laboratory in Latin America.

Methods We studied retrospectively SPEP and free light chains results ordered in conjunction during a 12 month period (January to December 2018). SPEP was analyzed by serum capillary electrophoresis (Sebia, France) and free light chains assay by immunoturbidimetric method (The Biding Site, UK). Abnormal free ligth chains ratio was considered when outside of the reference range (0.26-1.65) and a high level of M-component was considered when serum concentration was higher than 3.0 g/dL. The results were expressed as a frequency percentage and mean±standard deviation.

Results A total of 142,876 SPEP exams were ordered and 3,135 requests had serum free light chains in conjunction. 103 samples had quantifiable M-component on SPEP higher than 3.0 g/dL (4.56±1.26 g/dL). Of these samples, 99 had abnormal free light chains ratio (419.08±646.27 when kappa light chains was involved and 0.05±0.05 when lambda light chais was involved) and 6 had a normal free light chains ratio (1.06±0.45). Among patients with normal free light chains 4 had identifiable IgG Kappa, 1 IgG Lambda and 1 IgM Kappa.

Conclusions Our findings support the literature results regarding the low frequency of normal free light chains ratio in patients with high paraprotein concentrations, which are likely to have a intact immunoglobulin multiple myeloma diagnosis.

PO-083

Plasma D-dimer and CADM1 promoter hypermethylation as a possible metastasis predictor of cervical cancer

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Objective Cervical cancer (CC) is the fourth malignant tumor in women worldwide. The metastasis is still the major reason for the treatment failures of most CC patients. Cell adhesion molecule 1 (CADM1) promoter methylation and plasma D-dimer levels have been reported to be increased in many types of cancers. The purpose of this study was to investigate the value of combinatorial assay of plasma CADM1 promoter hypermethylation and D-dimer as a metastasis marker in CC.
Methods Two hundred and ninety-two patients with newly diagnosed cervical diseases and 70 healthy women were enrolled. A validation set comprised 36 Stage I CC patients and followed for 3 years. Plasma CADM1 promoter methylation and D-dimer levels were detected.
Results The total coincidence rate of CADM1 promoter methylation status was 93.3% between 45 pair-matched tissue and plasma samples. Plasma CADM1 methylation levels in CC patients were higher than other benign disease groups (P=0.000). Plasma CADM1 methylation levels had statistically differences between CC patients with and without lymph node metastasis (P=0.049) or in CC patients with and without distant metastasis (P=0.000). Similarly, plasma D-dimer levels in CC patients were higher than other benign disease groups (P<0.05). D-dimer levels were only statistically different between CC patients with and without distant metastasis (P=0.003). Combined assay of the two parameters for metastasis prediction has high sensitivity (80.4%) and specificity (90.5%).
Conclusions Combinatorial assay of plasma D-dimer and CADM1 methylation is a promising metastasis marker in cervical cancer.

PO-084

A prospective study on association between superoxide dismutase genes polymorphisms and antituberculosis drug-induced liver injury in Western Chinese Han population

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Objective Antituberculosis drug-induced liver injury (ATDILI) is increasing globally, and it is crucial to predicting this risk in the clinical management of antituberculosis therapy. As a major antioxidant, superoxide dismutase (SOD) mainly responsible for providing defense against oxidative stress, which is a factor involved in ATDILI. Present study aimed to investigate the associations between polymorphisms

in SOD genes, including Cu/Zn SOD (SOD1), mitochondrial manganese SOD (Mn SOD, SOD2), and extracellular SOD (SOD3), and the susceptibility to ATDILI in Western Chinese Han population for the first time, and trying to clarify the contradictions between previous studies.

Methods In total, 1060 subjects, all highly suspicious Western Chinese Han TB patients were prospectively enrolled. All clinical data, including demographic and laboratory indicators were obtained through electronic medical record (EMR), and the peak and valley value of indicators such as alanine transaminase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP) and total bilirubin (TBIL) were used to identify the ATDILI. Overall, 746 subjects comprised 118 ATDILI and 628 ATD tolerance were eligible. TagSNPs were selected via Haploview 4.2 software with pairwise tagger method, and seven single nucleotide polymorphisms (SNPs) in three SOD genes (rs4816407, rs1041740, *SOD1*; rs4880, *SOD2*; rs699473, rs2536512, rs2855262, and rs8192290, *SOD3*) were eventually included. The SNP genotyping work was implemented through custom-tailored 2 × 48-Plex SNPscan™ Kit, and tools such as SPSS 24.0 and PLINK 1.90 were employed to analyze the association between genetic variants and susceptibility to ATDILI.

Results In general, no significant differences were found in general characteristics between ATDILI and ATD tolerance patients, showing that both groups were well-matched pertaining to age, gender, body mass index (BMI) and smoking, and both groups mainly comprised middle-age males. Regarding the quantitative baseline parameters of the participants, when compared to ATD tolerance, the TBIL level (P=0.002), ALT level (P<0.001), AST level (P<0.001) and ALP level (P=0.021) of ATDILI group increased significantly, though both groups were in normal ranges. Furthermore, a significant difference was captured in uric acid (URIC) (P<0.001), which was rarely reported. With regard to association analysis, the allele frequency, genetic model and haplotype analysis all showed that genetic variants of SOD genes were no significant association with the susceptibility to ATDILI in Western Chinese Han population after Bonferroni correction, except for a potential association in the *SOD2* rs4880 A>G (G allele, P=0.238, OR=1.53, 95% CI=1.05-2.23; GG genotype, P=0.190, OR=1.53, 95% CI=1.05-2.23).

Conclusions Taken together, our results showed that no significant associations were identified between genetic variants of three *SOD* genes and susceptibility to ATDILI in Western Chinese Han population, in addition to a potential association in SNP rs4880 of *SOD2*, which was showed significant association with DILI in Chinese Taipei and Spanish. Therefore, the promising application of *SOD* SNPs as a genetic marker for ATDILI is challenged, and further study is needed with a larger sample size and in different ethnicities.

PO-085

Characterization of biofilm formation by clinical heterogeneous vancomycin-intermediate methicillin-resistant Staphylococcus aureus exposed to vancomycin

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Objective the precise mechanism of vancomycin involvement in biofilm formation by heterogeneous vancomycin-intermediate Staphylococcus aureus (hVISA), especially by clinical isolates, remains unclarified. The present study aimed to investigate the effect of vancomycin on the major components of biofilm formation by clinical hVISA, and its association with the high frequency of failure in vancomycin treatment failure of hVISA.
Methods A clinical strain of hVISA (05307) and the Mu3 strain (ATCC 700698, used as hVISA reference) were exposed to different concentrations of vancomycin. The broth alone and the bacterial suspension without antibiotics were served as negative and positive controls, respectively. The biofilm biomass of hVISA was measured using the crystal violet (CV) staining and visualized under the Confocal laser scanning microscopy (CLSM). Protein components, polysaccharide intracellular adhesin (PIA) and extracellular DNA (eDNA) in the extracellular matrices (ECM) were quantified directly and indirectly, respectively.
Results One fold minimal inhibitory concentration (MIC) vancomycin enhanced the biofilm formation by hVISA, however no effects of this concentration was noted on the biofilm formation in the two strains when the bacteria were exposed to sub-MICs vancomycin compared with the positive controls. Additionally, no significant increase of PIA and protein components production were observed. Vancomycin-enhanced biofilm formation was remarkably suppressed to a level similar to vancomycin-untreated cells following DNase Ⅰ administration.
Conclusions The 1× MIC vancomycin induced release of eDNAs is an essential factor for vancomycin-enhanced biofilm formation of hVISA, which may help account for the failure of vancomycin treatment in hVISA infections.

PO-086

High incidence and Spread of blaNDM-5-positive E. coli strains in a university hospital in Jiangsu, China

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Objective The emergence and spread of carbapenem-resistant *Enterobacteriaceae* worldwide deserves special concern. Unlike the epidemiological characteristics reported in other studies, we found producing New Delhi metallo-β-lactamase 5 was the

main reason for *Escherichia coli* being resistant to carbapenems.Here, we will study the mechanism of spread of blaNDM-5-positive E. coli strains in a university hospital.
Methods All carbapenem-resistant strains were collected from July 2016 to July 2017 of the First Affiliated Hospital of Nanjing Medical University. The presence of carbapenemase-encoding genes was detected using PCR and gene sequencing. Genetic relatedness of the *bla*$_{NDM-5}$-positive *E. coli* strains was determined with PFGE and MLST. Susceptibility profiles were measured with broth microdilution method and E-test strips. Transferability features of *bla*$_{NDM-5}$ gene were assessed by conjugation experiments, S1-PFGE, southern blotting and PCR-based replicon typing methods. The genetic structures surrounding *bla*$_{NDM-5}$ were acquired by whole genome sequencing and PCR mapping.
Results Among the 28 carbapenem-resistant *E. coli* strains, 18 (64%) were verified as NDM-5 producers. They show high resistance to most antibiotics, but 100% sensitive to colistin and tigecycline. The 18 *bla*$_{NDM-5}$-positive *E. coli* strains belonged to 8 STs, among which the ST167, ST410 and ST101 were thought caused clonal spread in our hospital. The *bla*$_{NDM-5}$ gene of 15 *E. coli* strain were successfully transferred into *E. coli* J53, and they were located on an IncX3 type plasmid, which was highly identical to a previously reported pNDM-MGR 194 plasmid and all harbored an IS*3000*-⊿ISAba125-IS*5*-*bla*$_{NDM-5}$-*ble*MBL-*trpF*-*dsbC*-IS*26* structure.
Conclusions In our study, most of the *bla*$_{NDM-5}$ were carried by transmissible plasmids as well. Further studies were need to investigate the relationship between the plasmids in this study and the prevalence IncX3 plasmids in China. Moreover, the clonal transmission and sporadic emergence of multi-drug resistant bacteria highlight urgent need to implement epidemiological surveillance and stringent infection control measures.

PO-087

Identification a transitional B cell population that promotes CD4 T cell activation in early HIV infection

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Objective Accumulation of transitional B cells were reported in primary HIV infected patients. However little is known about phenotype and function characterization of that B cell subset and their association with HIV disease progression.
Methods While investigating B cell subpopulation in very early HIV-1 infected patients, we identified an accumulated CD27-CD38+B cell subset that associated with HIV disease progression.
Results That B cell subset exhibited transitional B cell phenotypic and functional profile but a high self-turnover rate, which has never been reported by any human transitional B cell subset. In addition, CD27-CD38+B cells were demonstrated a heightened ability to activate CD4+T cells and to enhance HIV replication in comparison with other mature B cell subpopulations.
Conclusions Taken together, accumulation of such unresponsive B cell subpopulation may not only hinder the early production of antiviral antibodies but also contribute to

the immune activation initiated following HIV infection. Our data also emphasized a novel role of B cell dysfunction in HIV pathogenesis.

PO-088

Ursolic acid Reverses Paclitaxel Resistance by targeting miRNA-149-5P/MyD88 in Breast Cancer

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Objective Paclitaxel (PTX) is widely used in the front-line chemotherapy for breast cancer, but resistance limits its use. MyD88 was reported to be associated with PTX sensitivity in breast cancer and we found that Ursolic acid (UA) could regulate the expression of miR-149/MyD88. The objective of this study was to investigate the reversal effect of UA on PTX resistance in breast cancer.

Methods The 231 and 231/PTX cells were infected with lentivirus carrying MyD88 gene, shRNA to MyD88, miR-149 mimics and miR-149 inhibitor respectively. The paclitaxel sensitivity was assessed by CCK-8. Real time PCR and Western blots were used to measure the mRNA and protein expression changes. Flow cytometry was used to measure the cell apoptosis. Luciferase activity assay was used to detect the bind site of miR-149 and MyD88 3'UTR. 231/PTX cells was suspended at a concentration of 3×10^7/mL and injected a 100 μL cell into the flank of female athymic nude mice, and the mice was randomized into 5 groups with PBS, PTX (low), PTX (high),UA and PTX +UA.

Results UA could reverse PTX resistance of breast cancer in vivo and vitro. In 231/PTX cells, the expression of MyD88 was significantly higher and the miR-149 was significantly lower than the 231 cells. After the treatment of UA, the expression of MyD88 was decreased and the miR-149 was increased significantly, also, the apoptosis was increased and the proliferation was inhibited significantly of the 231/PTX cells. Further, overexpression of miR-149-5p and downexpression of MyD88 could increase the sensitivity of 231/PTX cells to PTX, and miR-149-5p could directly regulate the transcriptional activity of MyD88 by targeting MyD88 3'UTR. And Knockdown of MyD88 increased the sensitivity of 231/PTX cells to paclitaxel treatment through the inhibition of activation of NF-κB via PI3K/Akt signal pathway.

Conclusions Our data indicated that UA could reverse PTX resistance by targeting miRNA-149-5P/MyD88 via PI3K/Akt pathway in breast cancer.

PO-089

Tim-3 is an inhibitory receptor on NK cells in HIV-infected individuals but not affects the production of IFN-γ in NFAT pathway

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Objective Tim-3 was initially identified on terminally differentiated $CD4^+$T cells and cytotoxic $CD8^+$T cells and was reported to negatively interfere with cytokine production, tumor proliferation, and HIV and hepatitis C virus (HCV) infection. Although Tim-3 on NK cells has been reported, research results of its expression and function remained controversial. In healthy subjects, Tim-3 was reported to inhibit NK cell-mediated cytotoxicity, however, it was also demonstrated to be inducible after stimulation with various cytokines and function as a receptor to promote IFN-γ production. Furthermore, some researchers have identified that Galectin-9 (Gal-9) was the ligand of Tim-3, while others have shown that the function of Gal-9 was independent of Tim-3. Moreover, controversy exists regarding Tim-3 expression on NK cells after HIV infection. In untreated HIV infected individuals. Jost *et al.* have demonstrated a reduced percentage of Tim-3 on NK cells, while Finney *et al.* have reported an elevated level of Tim-3 on NK cells, especially in $CD56^{bri}$ subset. Because of the discordance in the different research work on function of Tim-3 on NK cells, the relationship between Tim-3 and Gal-9, and the level of Tim-3 on NK cells in HIV-infected individuals, a further investigation is needed to identify the role of Tim-3 and Gal-9 on NK cell function.

Methods 41 subjects were enrolled including 28 chronic HIV-infected subjects and 13 HIV antibody-negative normal controls, and all of patients were selected from the MSM cohort of Red Ribbon clinic in the First Affiliated Hospital of China Medical University. Flow Cytometry Analysis were performed to detect surface expression of CD3, CD4, CD56, CD16, Tim and Gal-9. IFN-γ and CD107a Assays were performed to detect The proportion of IFN-γ and CD107a stimulated with rIL-12 and rIL-15 for 24 hours. Further experiments about blockade of anti-Tim-3 or anti-Gal-9 were performed, and we also detect the of influence of rhGal-9 to Tim-3. Reverse transcription and quantitative real-time PCR were performed to detect the level of mRNA. All data analysis was performed using SPSS 20.0 and GraphPad Prism Version 6.0 software.

Results In this study, the phenotypic analyses demonstrated that Tim-3 expression was downregulated on NK cells in HIV infection, and Gal-9, as the ligand of Tim-3, its surface expression was elevated and associated with the HIV disease progression. Functional assays indicated that Tim-3 mediated suppression of NK cell CD107a degranulation while it had no effect on IFN-γ production, and Gal-9 also influenced NK cell function. Pathway analyses suggested that Tim-3 could only inhibit ERK/MAPK pathway but fail to suppress NFAT pathway, thus insufficiently inhibiting IFN-γ

production in NK cells. Collectively, our findings provide the potential strategy for immune therapy with the characteristics of Tim-3 receptor.

Conclusions In this study, we found that Tim-3 played an inhibitory role on NK cells and was down-regulated on NK cells during HIV infection, however, it failed to affect IFN-γ production in NK cells, the potential mechanism of which was that Tim-3 could not influence the NFAT pathway. Our data also showed that Gal-9, as a ligand of Tim-3, could influence cytotoxic function and its increased expression was linked to advanced HIV disease progression.

PO-090

Dynamic prevalence and evolution of genotyping drug resistance among treatment-failed HIV/AIDS individuals in China

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Objective The emergence of HIV-1 epidemic in China was recognized in Yunnan where always been a hot spot with HIV-1 prevalence, and it also been the first place to implement the National Free Antiviral Treatment in 2004. With extended duration of antiretroviral therapy (ART), appearance of HIV-1 drug-resistant strains dramatically affected the therapeutic effect. We attempt to monitor and clarify dynamic evolution of acquired drug resistance (ADR) after long-term ART in this area.

Methods Plasma samples in different treatment periods isolated from individuals received ART exceed half a year were collected at Yunnan Provincial Hospital of Infectious Disease during January 2014 to December 2016. Genotyping of ADR was conducted using an in-house assay. Viral load, CD4+ T cell counts, and demographic data were obtained from medical records and therapeutic data base

Results A total of 2328 HIV-1 pol sequences were successfully obtained from 2740 collected samples. Factors such as transmission route, CD4+ T cell counts, and ART regimen were significantly correlated with the development of ADR in ART-failed individuals. The total prevalence of ADR was 58.8% (1368/2328) in the ART-failed individuals. The patients were divided into 6 groups according to the treatment duration (6-12, 13-18, 19-24, 25-36, 37-48, 48months exceed), the overall rates of ADR showed a gradual upward trends, with the lowest incidence (51.9%) in 13-18 months and the highest incidence (68.8%) in 48-72 months, respectively, and the ART regimen with NRTIs presented the same tendency. The difference of CD4+, CD8+, CD3+ T cell counts and CD4+/CD8+ ratio between ADR positive and ADR negative group was statistically significant. The mean CD4+ T cell counts were gradually decreased with prolonged treatment from 363 ± 184 cells/μl in 13-18months to 272 ± 93 cells/μl in 48months exceed group. However, the Log_{10} viral load did not change significantly. Along with extension of ART periods, sensitivity of most drugs gradually decreased, and the level of ADR gradually increased, with NRTIs

mutations M184IV, T69ins, K70QER, T215FY, M41L and K219EQ showed an upward trends, but K65R and Y115F showed downward trends, whereas NNRTIs mutations K103N, Y181CIV, P225H, A98G and K238N exhibited uptrend, and V179DLT, V160AIM and F227CL appeared opposite trends.

Conclusions Our work revealed that the proportion of HIV-1 ADR in Yunnan Province increases along with the prolongation of ARTduration, maintained at 72 month without further increasing. Among all the participants underwent ART failure, immune reconstitution in ADR patients is worse than non-resistant patients throughout whole course of treatment. The degree and mutations of ADR also had changes along with ART administered. These findings enhance our understanding of ADR evolution and are valuable for development and implementation of a comprehensive public health approach to HIV-1 ADR prevention and treatment in this region.

PO-091

B-cell CLL/lymphoma 2 (BCL2) genetic polymorphisms are related to anti-tuberculosis drug-induced liver injury susceptibility

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Objective This study aimed to identify the relationship between single-nucleotide polymorphisms (SNPs) of B-cell CLL/lymphoma 2 (BCL2) gene and the susceptibility to anti-TB drug induced liver injury (ATDILI).

Methods Twenty-one selected SNPs were genotyped by custom-by-design 2x48-Plex SNPscanTM kit. The allele and genotypic frequencies between patients with or without ATDILI were compared in 3 different genetic models.

Results A total of 112/727 TB patients were found to have ATDILI. A allele of rs8085707, G allele of rs76986960 and A allele of rs949037 conferred increased risk of ATDIL ($p=0.001$, 0.029 and 0.03, respectively). Bonferroni correction indicated that ATDILI risk was significantly different in additive pattern of rs8085707 ($p_{Bonferroni\ correction}=0.036$).

Conclusions Our study firstly implied the BCL2 polymorphisms were of significant for the susceptibility to ATDILI.

PO-092

Glycated Albumin Regulates Renal Injury-Associated Molecules and Toll-like Receptor Signaling Pathway and the Intervention Effect of Oleanolic Acid

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Objective To investigate the effects of glycated albumin (GA) and oleanolic acid (OA) on the expression of kidney injury molecule-1 (KIM-1), neutrophil gelatinase-associated lipocalin (NGAL) and Toll-like receptor signaling pathway in human proximal tubular epithelial cells (HK-2 cells).
Methods The HK-2 cells were treated with GA, GA and OA for 24h. The mRNA expressions of KIM-1, NGAL, p38 mitogen activated protein kinase (MAPK), interleukin-1 receptor-associated kinase 4 (IRAK4), Toll-like receptor (TLR) 1, TLR2, TLR7 and TLR9 were detected by real-time PCR. The releases of KIM-1 and NGAL in the supernatants were detected by ELISA. The protein productions of p38 MAPK, IRAK4, TLR-1, TLR-2, TLR7 and TLR9 were measured by western blotting.
Results Compared with control group, GA could significantly up-regulate the mRNA and the protein levels released in supernatants of KIM-1 and NGAL ($P < 0.05$), and promoted the expression of p38 MAPK, IRAK4, TLR-1, TLR2 mRNA and protein in HK-2 cells ($P < 0.05$). Adding OA could significantly inhibit theses effects ($P < 0.05$).
Conclusions GA can up-regulate the expression and release of KIM-1 and NGAL, and activate the Toll-like receptor signaling pathway, suggesting that GA could play an important role in regulating renal injury. OA had effective intervention effect on GA.

PO-093

miR-454-3p is an exosomal biomarker and functions as a tumor suppressor in glioma

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Objective Glioma is the most common type of primary malignant brain tumor in adults. Our previous work discovered that plasma miR-454-3p may have some advantages in glioma prognosis, but the clinical significance and the regulatory mechanism of miR-454-3p in glioma have not been systematically investigated, especially regarding the relationship between circulating and tissue miR-454-3p.
Methods The expression level of miR-454-3p in glioma serum and tissues was analysed through quantitative real-time PCR (qRT-PCR). Cell-Counting Kit 8 (CCK-8), wound healing, transwell invasion, apoptosis and immunofluorescence assays were employed to assess the role of miR-454-3p in glioma cancer cells. ATG12 was selected as the target gene of miR-454-3p by bioinformatic analysis. The relationship between

the ATG12 and miR-454-3p was further validated by luciferase reporter assays and western blot analysis.

Results miR-454-3p was significantly downregulated in tumor tissues, while it was remarkably upregulated in exosomes from the same patients with glioma. The area under curve (AUC) of exosomal miR-454-3p for glioma diagnosis was 0.8663. The exosomal miR-454-3p was prominently lower in the post-operative serums than that in the pre-operative serums. High miR-454-3p expression in exosomes or low miR-454-3p expression in tissue was associated with poor prognosis. Restored expression of miR-454-3p suppressed cell proliferation, migration, invasion and autophagy in glioma. ATG12 was validated as a direct target of miR-454-3p. The overexpression of ATG12 could partially reverse the effects induced by miR-454-3p suppression.

Conclusions Our data indicate that miR-454-3p may serve as an exosomal biomarker and may be developed into a novel treatment for glioma.

PO-094

Proteomic Profiling of Placenta from AFLP Patients

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Objective Acute fatty liver of pregnancy (AFLP) is a liver disease unique to pregnancy. Despite the low incidence, AFLP is quick onsets that leads both mother and fetus to dangerous condition and even death. Despite of the relevance to the defect in heredity and fatty acid metabolism, the causes of AFLP are currently not clear. Moreover, some clinical and biochemical manifestations of AFLP are similar to other gestational liver diseases such as preeclampsia and HELLP syndrome. These present a big challenge for early and accurate diagnosis and effective therapy of the disease. This study was conducted to investigate molecular changes in the placenta samples from AFLP patients that may provide insights into subsequent studies on discovery of early diagnostic markers and therapeutic targets of AFLP.

Methods A TMT label-coupled nano LC-MS/MS approach was taken to identify and quantify differential expressed proteins in placenta samples from the subjects with (n=6) and without (n=4) AFLP matched in age and gestation. The bioinformatic tools were further used to analyze the pathophysiological functions of these proteins in terms of the biological processes, cell component, molecular functions, signal pathways and protein interactions they involved in.

Results A total of 4494 species of protein were identified in the amnion, chorion frondosum and decidua basalis of placenta. Amongst of them, 341 proteins (up: 62, down: 279), 210 (up: 73, down: 137) and 203 (up: 118, down: 85) were found to be differentially expressed in the amnion, chorion frondosum and decidua basalis of AFLP placenta, respectively. The results of bioinformatics analysis suggested critical implications of these proteins for transportation of nutrients required for fetal development, lipid metabolism, functions of mitochondrial respiratory chain complexes, oxidative balance, glycometaboloism, and ions homeostasis. Impressively, the proteins functioning in cellular exosomes were significantly altered in the three layers of the placenta, suggesting that placental exosomes play a key role in maternal AFLP.

Conclusions Pathogenesis of AFLP may essentially related to defects in the maternal-fetal substance exchange, metabolic abnormalities, accumulation of toxic substances, mitochondrial dysfunction. It is especially worthy of attention that placental exosomes play an important role in AFLP. This study provides a new angle of view for further research on the discovery of protein markers of AFLP.

PO-095

Accessing the Pre-analytical Effects of Pneumatic Tube System on High-sensitivity Cardiac Troponin T Assay

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Objective The pneumatic tube system (PTS) is widely established in clinical laboratories to accelerate sample transport. However, its impact on high-sensitivity cardiac troponin T (hs-cTnT) assay remains debatable. The aim of this study was to evaluate the pre-analytical effects of PTS on hs-cTnT assay.
Methods The hemolysis distribution of routine PTS specimens were determined by hemolysis index (HI). Gradient hemolysis model at different hs-cTnT levels were prepared and detected. Duplicate samples from 8 healthy volunteers were delivered to the laboratory by manual courier or via PTS and performed for hs-cTnT and HI. In order to investigate the effect of PTS on specimens with insufficient blood volume, another sample with halved blood volume from corresponding volunteers were transported by PTS.
Results The hemolysis ratio in PTS specimens of hs-cTnT was up to 7.26%, among which mild to moderate hemolysis accounted for 80%. Hemolysis was highly negatively correlated with hs-cTnT detection results (R ranged from -0.820 to -0.958, $P \leqslant 0.001$), and we observed obvious bias at mild to moderate hemolysis levels which ranged from -13.85% to -15.75% (all $P<0.05$). The PTS method showed that there was -12.53% of average bias between paired blood samples from healthy volunteers (manual courier: 4.97±1.11ng/L vs. PTS: 4.34±0.96ng/L, $P=0.002$). Besides, specimens with halved blood volume from corresponding volunteers produced greater bias (-15.63%, PTS: 4.18±0.87ng/L, $P=0.003$)
Conclusions We found a statistically significant decrease in hs-cTnT from samples transported by PTS. The mild to moderate hemolysis causing by PTS may lead to pre-analytical errors in hs-cTnT assay, which could be considered in the further study.

P0-096

Investigation of reference intervals for Scr with Jaffe's method in apparently healthy geriatric population

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Objective Measurement of serum creatinine (Scr) is used to diagnose and monitor acute and chronic renal disease, estimate glomerular filtration rate (GFR), or assess the status of renal dialysis patients. In clinical practice, Scr levels are usually measured with Jaffe's method and enzymatic method in clinical laboratories. The Jaffe's method is still more often used in clinical and scientific research in many countries, such as Germany, India, China, Thailand, Iraq, Pakistan and Nigeria etc. Reference intervals （RIs）can help clinicians to evaluate laboratory results, to consider the risk and diagnose of some disease. To our knowledge, reliable RIs for the Jaffe's assayed Scr categorized in small intervals are still lacking in elderly population. Scr levels in elderly are different from those of younger adults, so it is necessary to establish RIs of Scr for the elderly populations with Jaffe's assayed to offer better guidance of medical diagnosis and treatment of diseases for the elderly. To establish the RIs of Scr with Jaffe's assay for apparently healthy elderly of Han ethnicity in Changsha according to the CLSI C28-A3 guideline and WS/T402-2012 of the Health standard of the People's Republic of China.

Methods A total number of 743 healthy elderly Han ethnicity (369 males and 374 females) aged between 61 and 90 years were enrolled in this study. The Scr values were measured by Jaffe's method on ARCHITECT c8000 clinical chemistry analyzer.

Results The Scr values did not conform to a Gaussian distribution, and non-parametric statistical methods were used to calculate RIs. Scr value was significantly increased with age, thus age-dependent RIs were determined. The RIs of Scr in 61-70, 71-80 and 81-90 years old were 69.4-111.3 μmol/L, 74.1-122.1 μmol/L and 75.2-126.9 μmol/L for males, respectively, and 60.7-91.6μmol/L, 62.2-102.54μmol/L and 61.6-107.2μmol/L for females, respectively.

Conclusions We have established scientific and reasonable reference values of Scr by Jaffe's method of the healthy elderly of Han ethnicity in Changsha which can provide a reference for both clinical and laboratory studies.

PO-097

SP70 Targeted Imaging for the Early Detection of Lung Adenocarcinoma

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Objective NJ001 is a monoclonal antibody that can specifically recognize SP70 antigen on lung adenocarcinoma. The goal of this study was to explore its utility in targeted imaging.
Methods Subcutaneous xenograft and orthotopic lung tumor implantation BALB/c mouse models were established. Near-infrared fluorescence CF750-labeled NJ001 was injected into two kinds of tumor mouse model. Mice that received orthotopic lung tumor implantation were also injected with NJ001 conjugated nanomagnetic beads intravenously, and then underwent micro-CT scanning. Meanwhile, other tumor model mice were intravenously injected with normal saline and bare nanomagnetic beads as control.
Results Fluorescence could be monitored in the mice detected by anti-SP70 fluorescence imaging, consistent with tumor burden. Signal intensities detected with SP70 targeted micro-CT scans were greater than those in control mice. More importantly, orthotopic tumor lesions could be found on the fourth week with SP70 targeted imaging, 2 weeks earlier than control.
Conclusions Our results suggest that SP70 is a promising target for molecular imaging, and molecular targeted imaging with NJ001 labeled probe could be applied for early detection of lung adenocarcinoma.

PO-098

Serum complement C3 and α2-macroglobulin are useful biomarkers for inflammatory bowel disease

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Objective Ulcerative colitis (UC) and Crohn's disease are representative inflammatory bowel disease (IBD). Accurate and rapid diagnosis of IBD for subsequent therapeutic planning have been much desired; however, a variety of disease condition of IBD indeed hampered its correct diagnosis so far. Our purpose is to examine whether complement C3 (c-C3) and α_2-macroglobulin (α_2-MG) are new useful biomarkers for IBD, and whether the changes in their serum levels clinically corresponds to the severity of IBD.
Methods Serum samples from out-patients with IBD (n=101) and healthy volunteers (HVs) (n=101) were used. High performance liquid chromatography (HPLC) and sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) were carried out to separate proteins in the samples. Some protein bands in the gel were identified by mass spectrometry (MALDI-TOF). The serum concentrations of the proteins identified were measured by an enzyme-linked immunosorbent assays for each protein. Finally, the

correlations between these proteins and other inflammatory biomarkers were statistically examined.

Results As separated by HPLC, the chromatogram of serum proteins in patients with IBD significantly differed from that of HVs, especially in retention time from 6.3 to 10 min. The serum proteins in patients with IBD and HVs during this retention time were separated by SDS-PAGE, so that eleven protein bands in the gel were identify by mass spectrometry. The two proteins finally identified were c-C3 and α_2-MG with high protein score. Interestingly, the concentrations of two proteins in the serum of patients with IBD apparently differed from that in HVs. The average of c-C3 concentration (177 mg/dL) in the serum of patients with IBD was significantly higher than that (109 mg/dL) of HVs. On the other hand, the average of α_2-MG concentration (102 mg/dL) in the serum of patients with IBD was significantly lower thanthat (149 mg/dL) of HVs. The correlation assay showed that the changes in the serum levels of c-C3 and α_2-MG in patients with IBD hardly correlated with those of other inflammatory markers, such as C-reactive protein (CRP), interleukin 6 (IL-6), IL-1β, and TNF-α (each R-value < 0.2), and that the correlation between disease activity index (DAI) scores and the serum concentration of c-C3 or α_2-MG in patients with IBD was much better (each R-value = 0.581 and 0.457, respectively). These results suggest that c-C3 and α_2-MG may reflect the severity of IBD, particularly UC.

Conclusions The serum c-C3 and α_2-MG are new useful biomarkers for IBD and also good indexes for the severity of IBD.

P0-099

Prevalence and characteristics of genotyping drug-resistance among HIV-1 patients infected URFs strains from 2016 to 2017 in Yunnan province, China

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Objective To investigate the prevalence and characteristics of drug resistance among HIV-1 unique recombinant forms (URFs) infected patients under virologic failure in Yunnan.

Methods The plasma samples were collected from antiretroviral therapy (ART)-failure experienced individuals from 2016-2017 in Yunnan Province. HIV-1 genotyping drug resistance (DR) was implemented using in-house assay. HIV pol gene fragmentswere obtained using reverse transcription nested PCR. , followed amplification product identified by agarose gel electrophoresis . According to the RIP and MEGA 6.0 analyzed on pol region, the HIV URFs strains were screened through analysis defined recombinants.

Results A total 130 URFs pol sequences derived from 1121 samples . The proportion of HIV-1 URFs strains was 11.6% in the ART-failure individuals from 2016-2017 in Yunnan. The total URFs drug-resistant ratio was 56.9%. meanwhile, the percentage of protease inhibitors (PIs), nucleoside reverse transcriptase inhibitors (NRTIs) and non-NRTI (NNRTIs) was 3.8%(5/130), 36.2%(47/130), and 53.8%(70/130),

respectively. Mutations such as M184V/I(35.4%) in NRTIs and K103N/R/S/T(25.4%), V179D/E/T/Y(18.9%), G190A/E/R/S(13.8%) and Y181C(9.2%) in NNRTIs were common appearance among the HIV-1 URFs strains. The ratio of high-level resistance to drugs EFV and NVP was up to be 51.5% and 41.4%, respectively. Factors such as gender, transmission routes and source of the year were significantly correlated with development of HIV-1 URFs drug resistance occurred among ART-failure individuals.
Conclusions The prevalence of HIV-1 URFs drug resistance in Yunnan province likely keeps a relatively hyper-endemic tendency. The emergence of the multiple recombinant forms identified in Yunnan indicates active transmission frequently of HIV-1 subtype/CRFs cross-infection in this region. Therefore, it is necessary to further monitor the molecular epidemiology and drug resistance of HIV-1 in Yunnan.

PO-100

Serum S100A8/A9 is a sensitive biomarker for inflammatory bowel disease: the change in its level represents the clinical severity in the patients

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Objective Ulcerative colitis (UC) and Crohn's disease (CD) are categorized in inflammatory bowel disease (IBD). To date, the clinical significance of human S100A8/A9 (h-S100A8/A9) in the serum of patients with IBD is poorly understood. Our aim is to clarify whether serum h-S100A8/A9 is a sensitive biomarker for IBD, and to verify whether the serum level clinically corresponds to the severity of IBD.
Methods Serum samples from out-patients with IBD (n=101) and healthy volunteers (HVs) (n=101) were used in this study. The concentrations of h-S100A8/A9 and other inflammatory biomarkers, such as tumor necrosis factor-α (TNF-α), interleukin-6 (IL-6), and IL-1β, in the samples were measured using enzyme-linked immunosorbent assays (ELISAs). Based on the results, the correlations between h-S100A8/A9 and the inflammatory biomarkers abovementioned were statistically analyzed to verify clinical significance of h-S100A8/A9 as a sensitive biomarker.
Results The average of serum h-S100A8/A9 concentration in patients with UC (1.08×10^3 μg/L) and CD (1.30×10^3 μg/L) was approximately 20-fold and 25-fold, respectively, higher than that of HVs (0.0528×10^3 μg/L), while that of serum C-reactive protein (CRP) concentration in patients with CD (10.1×10^3 μg/L) was significantly higher than that in patients with UC (1.91×10^3 μg/L) or HVs (1.06×10^3 μg/L). In a viewpoint of the ROC curve, the sensitivity and specificity for h-S100A8/A9 were 0.792 and 0.822, respectively, when the cut-off value was tentatively 0.058×10^3 μg/L. As well as h-S1000A8/A9, the sensitivity and specificity for CRP were 0.734 and 0.743, respectively, when the cut-off value was 1.11×10^3 μg/L. Furthermore, the change in the serum concentration of h-S100A8/A9 slightly correlated with that of TNF-α, IL-6, or IL-1β (each R-value < 0.5). The correlation between the serum concentration of h-S100A8/A9 and the disease activity

index (DAI) score was low as indicated by R-value (0.342); however, this value was significantly higher than those between the DAI score and the concentrations of CRP or the inflammatory cytokines (each R-value < 0.25). These results suggest a possibility that h-S100A8/A9 could reflect the severity of IBD, and that as a sensitive biomarker for IBD the heterodimer may be superior to CRP and other inflammatory biomarkers.

Conclusions h-S100A8/A9 is a useful biomarker for IBD than CRP, and its serum level is also a novel index for the severity of IBD.

PO-101

Detection of simultaneous multi-mutations using base-quenched probe method

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Objective Single nucleotide polymorphisms (SNPs) are the most common form of mutation found in the DNA sequence of the human genome. To identify SNPs, biotechnical fields commonly use oligonucleotide probes that are modified with fluorophores, which target sequence-specific regions of DNA. For instance, the base-quenched probe method detects SNPs by real-time PCR and the use of a 6-carboxyfluorescein (FAM) fluorescently labeled probe that is positioned between a pair of primers. This method has been successfully applied to detect alpha-1 antitrypsin deficiency of Z mutant in patients with pulmonary emphysema and cirrhosis, deafness-associated mitochondrial DNA mutations, and metallothionein 2A genetic polymorphism associated with coronary heart disease, suggesting that the base-quenched probe method is precise, simple, and economic as well as suitable for SNP scanning. At present, the FAM-labeled probe is reported to detect up to two mutations in a single tube, which limits its use for certain clinical and laboratory applications. Additionally, it is currently unclear whether other fluorophores could act as a more suitable fluorophore for detecting SNPs.

Methods Primers and probes were designed based on the base-quenched probe method. Most common commercial fluorescent dyes including FAM, HEX, CY5, CY3, TET, JOE, Texas Red and ROX were applied for labeling probe. Each fluorophore's interference pattern was revealed by PCR together with melting curve analyses for detecting multi-mutations simultaneously according to the different fluorescence channels. Moreover, we used the following two principles as a metric for detecting multi-mutations: (A) If probes are labeled with the same fluorophore, genotyping of different SNP sites is dependent on melting temperatures of each respective probe; (B) If probes are labeled with different fluorophores, the genotyping results can be read from different fluorescent channels. Accuracy of the method was confirmed by direct sequencing.

Results The results demonstrated that FAM, HEX, CY5, CY3, TET, JOE, Texas Red, or ROX could be influenced by bases and could be applied to detect single nucleotide polymorphism. Bases increased the fluorescence of CY5 and CY3 while decreased that of other fluorescent dye. Furthermore, this method was practice applied to detect *apoM rs707921*, *apoM rs707922* and *MCP-1 rs1024611* simultaneously, which demonstrated successfully.

Conclusions Most common commercial fluorescent dyes could be influenced by DNA bases and could be applied for detecting multimutations simultaneously in one PCR amplification, which is useful for the large-scale genotype sample screening. To sum up, simultaneously detecting multimutations by base-quenched probe method simplifies the steps, saves costs and offers a variety of options. Facts have proved that the base-quenched probe method in the field of detection SNP is a breakthrough in technology and worthy of promotion and application.

PO-102

Individualized correction of the interference of hemolysis on glycated albumin determined by the ketamine oxidase method

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Objective The effect of hemolysis on glycated albumin (GA) determined by the ketamine oxidase method was investigated.
Methods *GA and the hemolysis index were detected in nonhemolyzed serum and hemolyzed serum of corresponding patients. An equation was developed to correct the interference of hemolysis on GA using multiple regression analysis.*
Results *The degree of hemolysis was negatively correlated with GA levels (R^2 = 0.9500). A correction equation for GA (corrected GA =2.703 ´ OD of hemolysis + 1.044 ´ measured GA -0.906) can revert GA concentrations of hemolyzed samples to values that were not statistically different from the GA concentration of nonhemolyzed corresponding samples.* The bias of GA concentrations significantly differed between before and after correction (P <0.01).
Conclusions Our results indicate that the level of GA measured through the ketamine oxidase method is negatively affected by hemolysis. The individualized correction of GA results provides increased accuracy in hemolyzed samples.

PO-103

Liquid Biopsy for Non-invasive Assessment of Liver Injury in Hepatitis B Patients

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Objective Hepatitis B is a major public health problem in China. Accurate liver injury assessment is essential for clinical evidence-based treatment. Liver biopsy is considered the gold standard method to stage liver disease, but it is not widely used in resource-limited settings. Therefore, non-invasive liquid biopsy tests are needed.

Here, we quantified cell free DNA combined with other serum biomarker as a liquid biopsy-based method to assess liver injury in hepatitis B patients.

Methods A cohort of 663 subjects including 313 hepatitis B patients and 350 healthy controls were enrolled. The ultrasound-guided liver biopsies followed by histopathological assessments were performed for the 263 chronic hepatitis B patients to determine the degree of liver injury. Cell-free DNA was quantified using a novel duplex real-time polymerase chain reaction assay.

Results Compared with healthy controls, patients with hepatitis B virus (HBV) infection had significantly higher plasma DNA, serum ALT, AST, bilirubin and HBV DNA levels ($P<0.01$). Serum ALT, AST, bilirubin and plasma DNA levels of patients with marked-severe inflammation were significantly higher than those with mild-moderate inflammation ($P<0.01$). There was a statistically significant correlation between hepatocyte inflammation severity and serum bilirubin ($R^2=0.673$, $P<0.01$) or plasma DNA ($R^2=0.597$, $P<0.01$) levels. AUCs *of serum ALT, bilirubin, plasma DNA, and their combination to distinguish between patients with mild-moderate and marked-severe inflammation was 0.8059, 0.7910, 0.7921 and 0.9564, respectively.*

Conclusions The combination of plasma DNA, serum ALT and bilirubin could be a candidate liquid biopsy for non-invasive assessment of liver injury in hepatitis B patients.

PO-104

Identification of Reference Genes in Human Tumors for Tumor Educated Platelets (TEPs) Study Based on RNA-Seq Data

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Objective The previous studies have shown that Tumor Educated Platelets (TEPs) RNA may complement currently used biosources and biomolecules employed for liquid biopsy diagnosis. RT-PCR is a regular method to measure gene expression levels to stage the patients and evaluate their prognosis. As there are little research on reference mRNA in platelets, especially in cancer, our study is to find the proper internal controls for RT-PCR in platelet study.

Methods Firstly, based on dataset GSE68086, we found 285 genes with relatively equal expression in 4 kinds of high incidence cancer (non-small cell lung cancer (NSCLC), colorectal cancer (CC), breast cancer (BC) and liver cancer (LC)) and healthy control (HC). 95 genes left after screening with the criteria of mean>1 and coefficient of variation (cv) <1. Secondly, we gained 73 common reference genes from previous reported studies. Thirdly, we obtained 7 candidate reference genes (ACTB, B2M, GAPDH,

GNAS, OAZ1, PTMA and YWHAZ) after intersected the 95 genes and 73 genes. At last, we extracted total RNA from 1.5 ml blood in 30 unselected persons, including 6 NSCLC, 6 CC, 6 LC, 6 BC, and 6 HC, and performed RT-PCR with equal quantity of RNA to measure the expression levels of the candidate reference genes.

Results All of 7 candidate reference genes performed well in 5 tested groups with a cv<0.1. Both B2M and GAPDH were the most stably expressed with a cv<0.05, but the expression of B2M was much higher than GAPDH in platelets.

Conclusions We have found 7 platelets mRNA with relatively same expression levels among several solid tumors and healthy people, which can be used as reference genes for mRNA measuring of platelets. Among them, B2M may be the best reference control gene.

PO-105

Correlation between cancer cell stemness and glucose metabolism characteristics in hepatocellular carcinoma

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Objective Hepatocellular carcinoma (HCC) is the third most common malignant tumor worldwide. Cancer stem cells (CSC) are considered to be the seeds of tumor recurrence, while Warburg effect refers to the aerobic glycolysis characteristic of tumor cells. Our objective is to investigate the relationship between tumor cell stemness and cell glucose metabolism characteristics.

Methods Flow cytometry was used to sort the tumor cells with high expression of stem-cell markers in liver tumor cell lines Huh-7 and MHCC97H for serum-free suspension culture, and to observe its morphological changes. The expression of stem cell markers and glycolysis enzymes, the glucose uptake capacity and lactic acid production ability of the two cells were compared.

Results Cancer stem cells can become spheroid in a serum-free suspension culture system. Compared with non-stem tumor cells, the expression of key glycolysis enzymes and stem-cell markers in spheroid cells was significantly increased ($P<0.05$). The ability to produce lactic acid is also significantly enhanced ($P<0.05$), and the stemness of tumor cells have some relationship with the activation of their glycolysis.

Conclusions Serum-free suspension culture can be used to enrich cancer stem cells. Compared with non-stem tumor cells, the glucose metabolism is much more transformed in tumor stem cells. There is a relationship between the stemness of tumor cells and the activation of glycolytic pathway.

PO-106

Detecting circulating tumor cells in liver cancer patients by qRT-PCR and CellSearch

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Objective To compare the positive rates and harmonization of CellSearch system and qRT-PCR platform in the detection of circulating tumor cells and analyze the clinical significance comprehensively.
Methods The whole blood samples of 32 hepatocellular carcinoma (HCC) patients were collected, of which circulating tumor cells (CTCs) were detected for the result of cell numbers and mRNA expression of biomarkers via CellSearch system and qRT-PCR platform. Single- and multi-marker patterns were both employed to label and detect CTC. The positive rates of each experiment was calculated respectively. The positive rates and harmonization of the three analyses were compared and analyzed subsequently.
Results There existed a significant correlation between CellSearch system and single-marker qRT-PCR platform in CTC detection. The coincidence rate was 24/32 [75.0%, positive rate 46.9% (single-marker qRT-PCR) vs. 28.1% (CellSearch), P=0.002]. Multi-marker qRT-PCR platform was able to enhance the positive rate (65.6%). What's more, there still existed significant correlations between all three analyses, and the coincidence rate was respectively 18/32 [56.3%, 65.6% (multi-marker qRT-PCR) vs. 28.1% (CellSearch), P=0.034] and 26/32 [81.3%, 65.6% (multi-marker qRT-PCR) vs. 46.9% (single-marker qRT-PCR), P=0.000]. Multi-marker qRT-PCR platform offered an intuitive view of the heterogeneity of HCC.
Conclusions Multi-stem-cell marker labeled tumor cell detection plays an optimistic role in lifting positive rates of CTC. Compared with CellSearch system, qRT-PCR platform can link the heterogeneity of HCC and clinical practice, offer personalized shifts in marker selection according to various detection purposes, and further satisfy a wider variety of detection demands.

PO-107

Application of 5S Management Mode in Emergency Laboratory of Hospital

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Objective In order to discuss the applied of 5S management mode in the emergency loboratory of hospital.
Methods The 5S practice was carried out in the emergency loboratory of Shanghai Chest Hospital, and the difference was evaluated before and after 5S practice by comparing the number of items in the work area, the number of walking steps and kilometers per year, and the 5S score.

Results After the 5S practice in the emergency loboratory, a significant reduction in the number of items in the work area and the number of walking steps and kilometers per year, the 5S score improved.
Conclusions After the 5S management mode is carried out in the emergency loboratory of hospital, the work environment is improved effectively, the work flow is optimized, the staff initiative is stimulated and the quality and efficiency are improved.

PO-108

Allergen detection analysis of 398 children from Sichuan Province

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Objective To investigate the effects of children in Sichuan province allergens distribution, and provide the basis for clinical diagnosis and treatment.
Methods Using the allergen specific IgE antibody detection kit, 14 allergen serological tests were performed on 389 children in this area, and the differences in different genders and ages were analyzed.
Results Of the 389 subjects tested, the total positive rate was 48.7%. The top five allergens were house dust mite/dust mite (71 cases,17.8%), cat dander/dog dander (26 cases,6.5%), milk (14 cases,3.5%), beef/mutton (14 cases,3.5%), cypress/elm/sycamore-tree/willow/poplar (12 cases,3.0%). There was no significant difference in age or sex.
Conclusions
The main allergens of children in this area are house dust mite/dust mite, cat fur dander/dog fur dander and other respiratory allergens. The types of allergens in children of different ages are not completely the same. The detection of serum allergen IgE antibody is helpful to understand the allergic state of children and assist in the diagnosis of allergic diseases.

PO-109

Study on the methodology evaluation and clinical significance of small dense low-density lipoprotein cholesterol

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Objective To verify the detection performance of small dense low-density lipoprotein cholesterol, and to analyze the changes of serum sdLDL-C in the enrolled patients and the severity of coronary heart disease and its correlation with traditional risk factors.

Methods 1. Methodological performance verification, assessment of direct clearance method detection sdLDL-C kit precision, accuracy, linear range, clinical reportable range and reference interval.
2. A case-control study was conducted to analyze serum sdLDL-C levels in patients with CHD and their relationship with classic lipid profile. From January to May of 2018, 188 cases of CHD hospitalized in the Department of Cardiology of Shanghai Chest Hospital were selected, including 134 males and 54 females. Including 47 patients with acute coronary syndrome, 34 males and 13 females; 141 patients with chronic myocardial ischemic syndrome, 100 males and 41 females. The healthy control group selected 94 healthy examinees in Shanghai Chest Hospital from January to May 2018, including 50 males and 44 females.
3. using Beckman's automatic biochemical analyzer detection of sdLDL-C and classic lipid indicators low-density lipoprotein cholesterol (LDL-C), high-density lipoprotein cholesterol (HDL-C), triglycerides (TG), total cholesterol (TCH), apolipoprotein B (ApoB), apolipoprotein AI (ApoA I), apolipoprotein E (ApoE), lipoprotein a (Lpa), troponin I (cTnI), homocysteine (Hcy) level.
4. Statistical analysis using SPSS statistical software linear regression equation analysis, rank correlation coefficient (Spearman correlation), rank sum test, median and quartile, binary logistic regression analysis and ROC curve analysis.
Results 1. The intra- and inter-assay CVs of the two levels of sdLDL-C in the direct scavenging method were 3.6%, 2.1%, 3.9%, 2.5%, respectively; 0.39%, linear regression equation Y=0.9534x+0.0363, r2=0.996; linear range verified 0.15-2.60 mmol/L, linear regression equation Y=0.9961x+0.011, r2=0.9999; validated clinical reportable range It is 0.15-83.2 mmol/L; the validated reference interval is 0.25-1.17 mmol/L.
2. The level of sdLDL-C was positively correlated with LDL-C, TG, TCH, Apo B, and Apo E (correlation coefficients r were 0.748, 0.436, 0.677, 0.795, 0.404, $P<0.01$); and HDL-C, Apo AI There was no correlation between Lp(a), cTnI, and Hcy (r was -0.095, -0.029, 0.027, -0.048, 0.028, $P>0.05$, respectively).
3. The levels of sdLDL-C, TG, Lp(a), cTnI, and Hcy in the CHD group were significantly higher than those in the healthy control group ($P<0.05$,), and the levels of HDL-C and Apo AI in the CHD group were significantly higher than those in the healthy control group. The levels of LDL-C, TCH, Apo B and Apo E in CHD group were not significantly different from those in healthy controls ($P>0.05$).
4. sdLDL-C, LDL-C, TCH and Apo B in ACS group were significantly higher than those in chronic myocardial ischemia ($P<0.05$), while TG levels were significantly lower than those in chronic myocardial ischemia ($P<0.05$), but HDL- C, Apo AI, Apo E, Lp(a), cTnI, Hcy had no significant difference between the two groups ($P>0.05$). sdLDL-C, TG, Lp(a), cTnI in ACS group were significantly higher than those in healthy control group ($P<0.05$), while HDL-C and Apo AI levels were significantly lower than those in healthy control group ($P<0.05$), but LDL-C There was no significant difference between TCH, Apo B, Apo E, and Hcy groups ($P>0.05$). The levels of TG, cTnI, and Hcy in chronic myocardial ischemic syndrome were significantly higher than those in healthy controls ($P<0.05$), while the levels of LDL-C, TCH, HDL-C, Apo B, and Apo AI were significantly lower than those in healthy controls ($P<0.05$).), but there was no significant difference between sdLDL-C, Apo E, and Lp(a) groups ($P>0.05$).

5. In addition to Hcy, four indicators of sdLDL-C, TG, Lp(a), and cTnI have diagnostic significance for CHD ($P<0.05$), and combined detection of indicators greatly improves the diagnostic efficiency.
Conclusions The performance of sdLDL-C kit was met by the direct clearance method. The sdLDL-C was associated with some classic lipid parameters and had certain significance in the detection of CHD. It was a valuable risk factor and predictor.

PO-110

High Expression of Long Noncoding RNA PCNA-AS1 Promotes Non-small-cell Lung Cancer Cell Proliferation and Oncogenic Activity via Upregulating CCND1

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Objective Accumulating evidences showed that aberrantly expressed long noncoding RNAs (lncRNAs) have critical roles in many cancers.
Methods In this study, we aimed to investigate the expression, clinical significance, biological role, and functional mechanism of PCNA-AS1 in NSCLC.
Results Our results showed that PCNA-AS1 was upregulated in NSCLC tissues and cell lines, and correlated with TNM stages. Functional experiments showed that overexpression of PCNA-AS1 promoted NSCLC cell proliferation and cell cycle progression. Depletion of PCNA-AS1 inhibited NSCLC cell proliferation and cell cycle progression, and also inhibited NSCLC tumor growth *in vivo*. Mechanistically, we found that PCNA-AS1 upregulated CCND1 expression. The expression of PCNA-AS1 was positively correlated with that of CCND1 in NSCLC tissues. Moreover, depletion of CCND1 abrogated the oncogenic roles of PCNA-AS1 in NSCLC. In conclusion, highly expressed PCNA-AS1 promotes NSCLC cell proliferation and oncogenetic activity via upregulating CCND1.
Conclusions Our results imply that PCNA-AS1 may serve as a therapeutic target for NSCLC.

PO-111

MiR-203a-3p inhibits proliferation and metastasis of hepatocellular carcinoma by reducing autocrine of TGF-beta 1

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Objective Hepatocelluar carcinoma (HCC) is one of the leading causes of cancer-related deaths worldwide. Although deregulation of microRNAs has been frequently described in HCC, the precise molecular mechanisms by which microRNAs modulate the process of

tumorogenesis and the behavior of cancer cells were poorly understood.This article aims to explore the molecular mechanism by which miR-203a-3p acts on HCC to inhibit its proliferation and metastasis.

Methods The paired specimens of clinical liver cancer tissues were collected, and the expression of miR-203a-3p in clinical liver cancer tissues was detected by Real-time PCR, and the correlation of clinical features was analyzed.Construction of miR-203a-3p overexpressing lentiviral vector and infection of HepG2 cell line to detect the effect of miR-203a-3p overexpression on proliferation, apoptosis, colony formation and migration of HepG2 cells.Expression of the intracellular signaling pathway is detected by an expression profiling chip, Real-time PCR, Western blot and ELISA experiments were used to verify the expression of key factors in signaling pathways. The expression of E-Cadherin, N-Cadherin and vimentin, the main factors of epithelial-mesenchymal transition (EMT), was detected by TGF-β1 stimulation of miR-203a-3p overexpressing HepG2 cells.MTT detects the proliferative capacity of the cells, and the scratch test detects the invasive ability of the cells.

Results The results showed lower expression level of miR-203a-3p in HCC than in adjacent cancer tissues ($p<0.001$), The expression level of miR-203a-3p in HCC patients with TNM stage III was significantly lower than those in stages I and II ($p<0.001$). The constructed miR-203a-3p overexpressing lentiviral virus titer was above $1x10^{8}$TU/ml, After transfection of miR-203a-3p lentiviral particles, the expression of miR-203a-3p was significantly increased ($p<0.001$). Overexpression of miR-203a-3p significantly reduced cell proliferation ($p<0.001$), clone formation ($p<0.001$) and invasive ability ($p<0.001$), and promoted apoptosis ($p<0.001$). The expression microarray showed that the difference of TGFB1, TIMP1, TGFBR1 and SMAD2 gene expressions was related to TGF-β1 signaling pathway when miR-203a-3p was overexpressed in HepG2 cells, The expression of the TGFB1 and TIMP1 gene was decreased ($p<0.05$), expression was decreased ($p < 0.05$), TGFBR1 and SMAD2 gene was increased ($p < 0.05$), ELISA results showed that the expression of cell culture supernatant TGFB1 protein was significantly decreased ($p<0.05$),Western blotting confirmed that the expression of TGFB1 in HepG2 cells with overexpression of miR-203a-3p was significantly decreased ($p < 0.05$).After treatment of miR-203a-3p overexpressing HepG2 cells with TGF-β1 (10 ng / ml) for 48 hours, the expression of N-Cadherin and vimentin was decreased ($p <0.05$). Although the expression of E-Cadherin was always higher than that of the control HepG2 cells ($p < 0.05$), it was lower than that of miR-203a-3p overexpressed 0 h of HepG2 cells ($p < 0.05$).The results of real-time PCR were consistent with those of Western blotting. MTT assay showed that the proliferation of HPG2 cells overexpressing miR-203a-3p was significantly decreased ($p<0.05$). The scratch assay showed that TGF-β1 was overexpressed by miR-203a-3p. There was no significant change in the invasion ability of HPG2 cells ($p>0.05$).

Conclusions Our results indicated that miR-203a-3p as a tumor suppressor and played a crucial role in HCC, which inhibited proliferation and metastasis of HCC by reducing the expression of TGF-β1 in HCC cells, affect the autocrine of TGF-β1, thereby blocking the formation of HCC EMT.

PO-112

Evaluation of performance of gram staining for various clinical microbiological specimens using RAL-STAINER automatic staining instrument

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Objective To evaluate the performance of gram staining for various clinical microbiological specimens using RAL-STAINER automatic staining instrument.
Methods Specimens were collected and performed gram staining respectively by manual operation and by instrument. The staining results of automatic staining instrument, the consistency with manual operation, cross contamination and working performance were evaluated.
Results The smears by RAL-STAINER show clear background with no impurity substances. The bacteria and cells show a bright color and a vivid structure. The qualification rate of staining is 100%. The consistency rate of automatic staining and manual staining is 100%. No cross contamination occurs when batch staining. RAL-STAINER automatic staining instrument has advantages such as easy operation, high flux, stable staining results and good biological safety.
Conclusions RAL-STAINER automatic staining instrument performs well in gram staining for clinical microbial specimens.

PO-113

The dose-response relationship between Gamma-glutamyl transferase and risk of Diabetes Mellitus using publicly available data: a longitudinal study in japan

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Objective *The purpose of this study was to examine the association between baseline serum gamma-glutamyl transferase (GGT) and incident diabetes and to explore their dose-response relationship in a cohort of Japanese adults.*
Methods Data were drawn from the NAGALA (**NA**fld in the **G**ifu **A**rea, **L**ongitudinal **A**nalysis) study between 2004 to 2015, including hierarchical information on participants ⩾18 years of age without diabetes, preexisting diabetes, heavy alcohol drinking or other liver diseases (eg, hepatitis B/C). The final analytic sample included 15 464 participants, 373 of who were diagnosed as diabetes mellitus with a maximum 13-year follow-up. The risk of incident diabetes according to baseline serum GGT was estimated

using multivariable Cox proportional hazards models and a two-piecewise linear regression model was developed to find out the threshold effect.

Results *Being in the highest quintile versus the lowest quintile of GGT levels was associated with an almost twofold increased risk of incident diabetes mellitus (Hazard ratio 1.83 (95% CI 1.06, 3.15)), independent of age, gender, smoking status, alcohol intake, BMI, SBP, triglycerides, fatty liver, ALT, AST, fasting plasma glucose. A nonlinear dose-response relationship was observed and the risk of developing diabetes mellitus increased when serum GGT level was less than 24 IU/L (HR 1.04 (1.02, 1.07), P=0.0017). Besides, the association was more significant in non-smoking participants than ex- or current-smokers (P for interaction=0.0378).*

Conclusions Serum GGT level was significant predictors of subsequent risk of diabetes mellitus when serum GGT level was less than 24 IU/L.

PO-114

The specimen matrix stability differences for ProGRP highlight the importance of understanding the preanalytical conditions affecting small cell lung cancer

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Objective We investigated the stability of ProGRP in serum specimens with understanding the preanalytical conditions affecting small cell lung cancerWe investigated the stability of ProGRP in serum specimens with understanding the preanalytical conditions affecting small cell lung cancer

Methods Peripheral blood were obtained from 20 patients with small cell lung cancer, which were placed under different preanalytical conditions. The serum levels of ProGRP were measured with a commercially available electrochemiluminiscent assay (Elecsys;Roche Diagnostics, Germany)

Results The variation in change by individual specimens increased as storage time increased either at room temperature or 2-8℃,which have already undergone some degradation of ProGRP, the levels of ProGRP difference were statistically significant (P<0.05). The difference weren't statistically significant (P>0.05) among the values of the different preanalytical. The average ProGRP level in freshly drawn serum was within 20%(7% -30%) of the baseline level for up to 24h after storage at 2-8℃ and for up to 2-3h after storage at room temperature. The average ProGRP level in freshly drawn serum was within 50%(32% -62%) of the baseline level for up to 7 days after storage at 2-8℃ and for up to 24h after storage at room temperature

Conclusions The different serum samples preanalytical had an impact on ProGRP level.The use of low temperature may improve the clinical reliability of this marker by minimizing preanalytical changes in ProGRP concentrations

PO-116

Survey and Consensus of “Critical Value” in Chongqing

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Objective To investigate the formulation, implementation, quality control and effect evaluation of clinical laboratory critical value in Chongqing and to constitute a consensus based on actual problems, literatures and expert opinions.
Methods Questionnaires were send to all levels of hospitals in Chongqing. All laboratories filled in the information online through the WeChat Network platform. The data were analyzed by statistical software.
Results 108 laboratories submitted information, mainly from level II general hospitals. All laboratories had a critical value reporting system, and 96% of these laboratories had critical value items. 62% of critical value items and scope sources were developed jointly by the laboratory and the clinic; 11% of them were learned from other hospitals and 8% of them were developed within the laboratory. Only 37% of laboratories had personalized critical values for different departments. Except for blood gas, 61% of laboratories set blood calcium, potassium, blood glucose, white blood cell count, platelet count, prothrombin time, and activated partial thromboplastin time as critical items. 73% of the laboratories had a reporting time limit of 30 minutes, but 7.4% of the laboratories had no requirement for the reporting time limit of the critical value.
Conclusions The critical value system in Chongqing still has great problems in the establishment of the critical value items and boundary. In accordance with their own conditions and the clinician's advice, all laboratories need to develop a suitable critical value management system by using this consensus.

PO-117

LC-MS/MS based quantitative proteomics analysis of different stages of non-small cell lung cancer

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Objective cancer is a major public health problem worldwide and the second leading cause of death in China. In 2012-2016, lung cancer mortality in poor areas was 40% higher than in developed ourntries. Howerver, early diagnosis and treatment of lung cancer remains a huge challenge. Therefore, basic and clinical medical research for lung cancer patients, especially the discovery of biomarkers, is crucial for the diagnosis and treatment of diseases.

Methods Baded on this, we used iTRAQ8-plex labeling technology combined with liquid chromatography-tandem mass spectrometry to nanlyze the serum and urine of patients with different stages of non-samll cell lung cancer and healthy individuals.
Results 441 proteins were identified in the serum, and a total of 1161 proteins were identified in the urine. Among them, the levels of Elongation factor 1-alpah 2, Proteasome subunit alpha type and Spermatogenesis-associated protein were significantly increased in the serum of lung cancer at all times, transmembrane protein 143, Cadherin 5, Fibronectin 1, Collectin-1.The amount of expression is significantly decreased in the serum of patients with metastasis; In urine sample, prostate-sapecific antigen and prostatic acid phosphatase decreased significantly in stage III and IV lung cancer, while neutrophil defensin 1 increased significantly.
Conclusions There differential proteins may be protential diagnositic markers for lung cancer, and could be combined with the relative content of serum and urine to distinguish the progerssion of lung cancer in order to achieve accurate staging and early diagosis of lung cancer.

PO-118

Two new inflammatory markers associated with Disease Activity Score-28 in patients with rheumatoid arthritis: albumin to fibrinogen ratio and C-reactive protein to albumin ratio

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Objective The albumin to fibrinogen ratio (AFR) and C-reactive protein to albumin ratio (CAR) have emerged as useful biomarkers to predict systemic inflammation. The aim here is to investigate the relation between AFR/CAR and Disease Activity Score of 28 joints (DAS-28) in rheumatoid arthritis (RA).
Methods This retrospective study included 160 patients with RA and 159 healthy controls. We divided the RA patients into two groups according to the DAS 28-ESR score. Group 1 included 40 patients with a score of lower than 2.6 (patients in remission) and Group 2 included 120 patients with a score of 2.6 or higher (patients with active disease). The correlations between AFR, CAR and the disease activity were analyzed.
Results For RA patients, the AFR was lower than those in the control group ($P < 0.001$). Patients in group 2 had higher CAR than those in group 1 ($P < 0.001$). The AFR was lower in group 2 than that in group 1. A positively correlation was observed between DAS 28-ESR score and CAR ($r = 0.645$, $P < 0.001$), while the correlation between DAS 28-ESR and AFR ($r = -0.836$, $P < 0.001$) was negative. AFR was related with decreased risk of RA disease activity (EXP (B) = 0.33, 95% CI (0.21-0.53), $P < 0.001$).
Conclusions AFR and CAR are two novel inflammatory markers for monitoring disease activity in patients with RA.

PO-119

Comparison of in vitro susceptibility of carbapenem-resistant Enterobacteriaceae bacteria to polymyxins B by E-test and microbroth dilution

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Objective To detect the in vitro antimicrobial activity of polymyxin B against carbapenem-resistant Enterobacteriaceae isolated in our hospital in 2018, and provide laboratory basis for clinical application of polymyxin B; To evaluate the in vitro susceptibility test results of polymyxin to carbapenem-resistant Enterobacteriaceae by different sensitivity test methods, and provide reference for the in vitro drug sensitivity method of polymyxin in clinical microbiology laboratory.
Methods 230 non-repetitive carbapenem-resistant Enterobacteriaceae isolated from patients in clinical departments from January 2018 to December 2018 were collected. In order to analyze the differences between the two drug sensitivity test methods, E-test method and microbroth dilution were used to detect their sensitivity to polymyxin b in vitro and the break point judgment was made according to the European union drug sensitivity test standard (EUCAST).
Results The sensitivity and resistance of 230 CRE E-test were 96.52% and 3.48% respectively, and microbroth dilution were 95.65% and 4.35% respectively. The consistency rate of the two methods was 95.65%, the consistency rate of classification was 99.13%, and the significant error (VME) was 0.86%.
Conclusions The microbroth dilution method is more sensitive than E-test for CRE strains, and the E-test method has large errors. It is recommended that the strain with E-test detect resistance be further confirmed by microbroth dilution

PO-120

Enhanced Resistance to Radiation and Chemotherapeutics in Human Colorectal Cancer Cells by AKAP12 Over-expression

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Objective Combining with latest new research, we hope that this study can make new contributions to understand the role of AKAP12 in cancer, and provide a new solution to the current situation of resistance to radiotherapy and chemotherapy.
Methods Lentivirus transfection assay was conducted to change the expression levels of AKAP12 in colorectal cancer cell lines. Cell viability assay, flow cytometric analysis and western-blotting were carried out to make further study.

Results The expression of AKAP12 changed the colorectal cancer cells viability exposed to chemotherapeutic agents 5-FU and L-OHP. AKAP12 can change the expression levels of apoptosis related proteins in CRC cells after exposing to 5-FU. The expression of AKAP12 changed the viability of colorectal cancer cells exposed to radiation. AKAP12 could change the expression levels of apoptosis related proteins in CRC cells after being exposed to radiation.
Conclusions AKAP12 can improve the survival rate of colorectal cancer cells under the condition of chemotherapeutic drugs, but also can increase the survival rate of colorectal cancer cells after radiation.

PO-121

Association of serum lipids with autoantibodies and inflammatory markers in rheumatoid arthritis patients

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Objective The study aims to study the relationship between serum lipids and autoantibodies and inflammatory markers in rheumatoid arthritis (RA) patients to explore the effect of serum lipids on the diagnosis and judgment of disease activity in RA patients.
Methods Serum lipids including TCHO, TG, HDLC and LDLC and anti-CCP, RF, CRP, ESR of RA patients from May 2013 to August 2017 were retrospectively analyzed in the First Affiliated Hospital of Fujian Medical University. Correlation statistical analysis was performed using Graphpad Prism 7 and IBM SPSS 22.0 analysis software.
Results With the dilution factor increased, the levels of serum lipids and anti-CCP, CRP and RF showed the same downward trend, indicating that the detection methods of the above indicators were reasonable and would not be affected by hyperlipidemia. CRP and ESR levels were negatively correlated with HDLC level in male and female RA patients. However, the concentration of anti-CCP and RF were closely related to TG. In all the RA patients and female RA patients, the RF level was negatively correlated with the TG concentration. Moreover, with the TG concentration increased, the proportion of patients with high concentrations of anti-CCP levels decreased. In addition, in male RA patients, anti-CCP and ESR concentration increased with the increase of LDLC.
Conclusions The levels of HDLC, TG and LDLC were associated with the concentration of anti-CCP, RF, CRP and ESR in RA patients. Therefore, clinical diagnosis of RA and determination of disease activity should consider the impact of the concentration of serum lipids in order to make a reasonable judgment on the diagnosis of the disease.

PO-122

Association of serum miR-186 with the prognosis of acute coronary syndrome patients after percutaneous coronary intervention

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Objective Kinetic signatures and physiologic states of circulating miR-186 in acute coronary syndrome (ACS) patients undergoing percutaneous coronary intervention (PCI) and their association with ACS prognosis have not been investigated.
Methods 60 ACS patients and 62 healthy controls were enrolled. Serum miR-186 levels in ACS patients (on admission and at different time points within one week after PCI) and controls were detected by quantitative reverse-transcription PCR. The predominant form of serum miR-186 was analyzed by comparing its absolute concentration in isolated exosomes and exosome-depleted supernatant. An average of one-year follow-up for ACS patients was performed and the incidence of major adverse cardiovascular events (MACE) was calculated.
Results Serum miR-186 levels were significantly increased in ACS patients on admission compared with controls, but their high levels were gradually decreased within one week after PCI and returned to near control levels within 1~2 days after PCI. Serum miR-186 was mainly existed as exosome-free form rather than membrane-bound exosomes. Within one-year follow-up, ACS patients with higher miR-186 levels on admission exhibited a higher incidence of MACE. Cox regression analyses validated the potential values of serum miR-186 for prognostic evaluation in ACS patients after PCI.
Conclusions Serum miR-186 may act as a promising biomarker for monitoring and assessing prognosis of ACS patients after PCI.

PO-123

The diagnostic value of pre-operative inflammatory markers in patients with glioma: a multicenter cohort study

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Objective Glioma is the most common form of brain tumor with high lethality. This study aimed to elucidate the efficiency of pre-operative inflammatory markers

including neutrophil lymphocyte ratio (NLR), derived neutrophil lymphocyte ratio (dNLR), platelet lymphocyte ratio (PLR), lymphocyte monocyte ratio (LMR), prognostic nutritional index (PNI) and their paired combinations as tools for the preoperative diagnosis of glioma with a particular interest on its most aggressive form, glioblastoma (GBM).

Methods A total of 750 patients with glioma (grade I, n=81; grade II, n=208; grade III, n=169; grade IV (GBM), n=292), 44 patients with acoustic neuroma, 271 patients with meningioma, 102 patients with non-lesional epilepsy and 682 healthy participants were enrolled in this retrospective study. The levels of NLR, dNLR, PLR, LMR and PNI were compared in patients suffering from glioma, acoustic neuroma, meningioma, non-lesional epilepsy and healthy controls by non-parametric tests. The correlations between NLR, dNLR, PLR, LMR, PNI and tumor grade were analyzed. The receiver operating characteristic (ROC) curve analysis was performed to evaluate the diagnostic significance of NLR, dNLR, PLR, LMR, PNI and their paired combinations for glioma, particularly for GBM.

Results Compared with healthy participants, patients with acoustic neuroma, meningioma, or non-lesional epilepsy, patients with glioma had higher levels of pre-operative NLR and dNLR as well as lower levels of LMR and PNI while PLR was higher in glioma patients than healthy controls and patients with non-lesional epilepsy Subgroup analysis revealed a positive correlation between NLR, dNLR, PLR and tumor grade whereas a negative correlation between LMR, PNI and tumor grade in glioma. For glioma diagnosis, the area under curve (AUC) obtained from ROC curve was 0.722 (0.697-0.747) for NLR, 0.696 (0.670-0.722) for dNLR, 0.576 (0.549-0.604) for PLR, 0.760 (0.738-0.783) for LMR, 0.672 (0.646-0.698) for PNI. The best performance was obtained by combination of NLR plus LMR and dNLR plus LMR, with AUC of 0.777 and 0.778 respectively. Additionally, NLR (AUC:0.860 ; 95%CI: 0.832-0.887), dNLR(AUC: 0.840 ; 95%CI: 0.810-0.869), PLR(AUC: 0.678 ; 95%CI: 0.641-0.715), LMR(AUC: 0.837 ; 95%CI: 0.811-0.863) and PNI(AUC: 0.740 ; 95%CI: 0.706-0.773) had significantly predictive value for predicting GBM when compared with healthy controls, patients with acoustic neuroma, meningioma, or non-lesional epilepsy. When compared to glioma patients with grade I, II or III, the AUC was 0.811(95%CI: 0.778-0.844) for NLR, 0.797(95%CI: 0.763-0.832) for dNLR, 0.662(95%CI: 0.622-0.702) for PLR, 0.743(95%CI: 0.707-0.779) for LMR, 0.661(95%CI: 0.622-0.701) for PNI. For paired combinations, NLR plus LMR demonstrated the highest accuracy.

Conclusions NLR-LMR combination demonstrates a noninvasive biomarker with relatively high sensitivity and specificity for glioma diagnosis, differential diagnosis of glioma from acoustic neuroma and meningioma, GBM diagnosis and differential diagnosis of GBM from low-grade glioma.

PO-124

Low Fibrinogen level may be a risk factor of poor prognosis of HELLP syndrome

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Objective Liver inflammation and haemostatic abnormality are obvious in HELLP syndrome, therefore, haemostatic system monitoring may be helpful with estimating severity and prognosis of HELLP syndrome. This literature means to search for a valuable predicted marker by exploring the relation between haemostatic system and prognosis of HELLP syndrome.

Methods Screening 127 patients who were diagnosed as HELLP syndrome and terminated pregnancy in Peking University Third Hospital from August 2010 to August 2018 were. Collecting demographic characters of maternals and fetus、postpartum complications、days of hospital stay、prothrombin time(PT)、activated partial thromboplastin time(APTT)、Fibrinogen(Fg) and D-Dimer(D-D) of parturient.

Results There wasn't statistical difference between maternals with and without postpartum hemorrhage of HELLP syndrome in parturient PT [9.6 (9.0, 11.5) vs 9.4 (8.9, 9.7), P=0.243], APTT [30.2 (29.1, 38.3) vs 29.8 (27.7, 31.8), P=0.151], D-D [0.80 (0.52, 4.52) vs 0.91 (0.55, 2.48), P=0.923] There was a obvious difference in parturient Fg(2.94±1.48 vs 3.61±1.00, P=0.022) between maternals with and without postpartum hemorrhage; The receiver operating characteristic curve(ROC) showed that the AUC of fibrinogen level when estimating postpartum hemorrhage is 0.688(95%CI:0.600~ 0.767), critical value is 3.04g/L, negative predictive value is 0.944; There was a negative correlation between parturient Fg and days of hospital stay of HELLP syndrome maternals(r= -0.182, P=0.040). There wasn't statistical difference between viable(n=93) and dead(n=34) fetus who were given birth to by maternals of HELLP syndrome in parturient PT, APTT, Fg and D-D of the maternals. The same relation also existed between viable fetus with(n=23) and without(n=70) fetal distress (P>0.05).

Conclusions The low parturient Fg level may be a risk factor of poor prognosis of HELLP syndrome maternals. By intervening the Fg to a stable level may reduce the incidence rate of HELLP syndrome.

PO-125

Ursolic acid protects against proliferation and inflammatory response in LPS-treated mice gastric tumor model and human gastric carcinoma cells by inhibiting NLRP3 inflammasome activation

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Objective Inflammation is considered one of the hallmarks of cancer development and progression. Ursolic acid (UA) showed strong effects on anti-inflammatory and antioxidant. However, the anti-cancer effects of ursolic acid is still need further study. So, this study aimed to investigate the role of ursolic acid in lipopolysaccharide (LPS)-treated mice gastric tumor model and human gastric carcinoma cells lines (BGC-823 cells) and to confirme whether ursolic acid can protect against proliferation and inflammatory response induced by LPS by inhibiting NLRP3 inflammasome activation via NF-κB pathway.

Methods Mice were subcutaneously injected with BGC-823 cells to induce gastric tumor model. The mice were randomly divided into four groups and each group treated with PBS, UA, LPS and LPS + UA respectively. BGC-823 cells were pretreated with ursolic acid before exposure to LPS. Cell viability were measured by CCK8 kits. NLRP3 inflammasome, Pro-IL-1β, IL-1β, NF-κB expression were examined by western blot. Production of IL-1β were measured by ELISA kit. mRNA levels of inflammatory cytokines were detected by quantitative real-time RT-PCR.

Results Ursolic acid attenuated significant LPS-treated proliferation in vitro and in vivo, reduced the expression of NLRP3 inflammasome and suppressed the release of pro-inflammatory cytokines. In addition, ursolic acid inhibited the LPS-induced activation of NF-κB. Furthermore, NLRP3 inflammasome activation was regulated by the NF-κB pathway.

Conclusions Our results demonstrated that ursolic acid could suppress proliferation and inflammatory response in LPS-induced mice gastric tumor model and human BGC-823 cell by inhibiting NLRP3 inflammasome activation via NF-κB pathway. Thus ursolic acid might be beneficial for the treatment of gastric cancer.

PO-126

Development of a multi-epitope peptide vaccine of OMP2b against brucellosis by bioinformatics

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Objective Brucella poses a serious threat to human health, there is an urgent need for high-quality vaccines of Brucella to effectively reduce the incidence of Brucellosis. OMP2b is a essential components of Brucella outer membrane antigen, and expressed in various species of Brucella, We analysis OMP2b protein of brucella, predicted the dominant epitopes of possible T and B cells and validated the effects of these epitopes as vaccines.
Methods we used the bioinformatics software ProtParam, SOMPA, SWISS-MODEL, Rasmol, BepiPred, SYFPEITHI and IEDB to analyze the structure of OMP2b and predict the dominant epitopes of T cells and B cells; Identification of immunoreactivity of T-B combined epitopes by IFN- γ ELISPOT assay, ELISA assay was used to detecte the specific antibodies against the T-B combined epitope peptide of OMP2b in the serum of Brucellosis patients.
Results we predicted three Th cell epitopes, seven CTL epitopes, eight B cell epitopes, and one T-B combined epitope of OMP2b protein. The IFN-γ ELISPOT assay showed that the T-B combined epitope peptides of OMP2b activated Th cell immune responses. ELISA analysis detected the specific antibodies against the T-B combined epitope peptide of OMP2b in the serum of Brucellosis patients.
Conclusions our study not only demonstrated that the T-B combined epitopes and CTL epitopes we verifed of OMP2b have strong immunogenicity, but also provides a novel bioinformatics approach for the prediction T-B combined epitopes and CTL epitopes, which may lay a theoretical foundation for the development of vaccine against Brucella.

PO-127

Thromboinflammatory Response Presents in Preeclampsia

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Objective Preeclampsia (PE), which is a leading cause of maternal and perinatal mortality, is characterized by new-onset hypertension and proteinuria at ≥20 weeks of gestation. Treatment with aspirin to inhibit platelets activation is the only way, with clinical trial evidences support, to prevent it. However, it is often limitedly administrated while pregnancy for the bleeding tendency. It is urgent to define the abnormality of hemostasis balance to find more effective and safe measures to prevent the occurrence of PE.
Methods We enrolled 6 pregnant women with PE, 6 healthy pregnant women, and 5 healthy non-pregnant women. Their plasma was analyzed by a chip focusing on detecting

coagulation and inflammatory biomarkers. Moreover, their circulating microparticles from platelets (PMPs), endothelial cells (EMPs) and leukocytes (LMPs) were confirmed by transmission electron microscopy and were analysed by flow cytofluorimetric.

Results Chip analysis showed that protein abundance related to hypercoagulation and inflammatory response presented significant difference among pregnant women with PE, healthy pregnant women, and healthy non-pregnant women. Differential protein mainly involved in inflammation mediated by cytokines and chemokines, coagulation cascades and plasminogen activation pathways. The levels of PMPs in the healthy pregnant group were significantly higher than those in the non-pregnant group (45.04 vs 17.41, $P = 0.007$). In addition, EMPs and LMPs were significantly higher in the PE group than in the healthy pregnant group (14.62 vs 11.48 and 8.94 vs 5.03, $P = 0.015$ and $P < 0.001$, respectively).

Conclusions Preeclampsia PE is characterized by thromboinflammatory response. Determining the circulating microparticles level may reflect the endothelial dysfunction and inflammation involved in PE pathogenesis.

PO-128

MICA alleles are associated with colorectal cancer especially for MSI and KRAS mutation subtypes

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Objective The human major histocompatibility complex class I chain-related gene A (MICA) regulates tumor immunesurveillance and eliminates the tumor cells through activation of its receptor, NKG2D. As a highly polymorphic gene, its genetic association with colorectal cancer (CRC) has not been explored. In this study, we will analyze MICA polymorphism in CRC to find the potential immune-therapeutic target of CRC.

Methods We examined MICA alleles in 104 CRC patients and 536 healthy controls for genetic association studies, and analyzed sequence data for potential somatic mutation of MICA gene at coding exon 2-5 in 89 CRC tumor tissues by comparing to their paracancerous tissues. Specific MICA single nuclear polymorphisms and alleles were analyzed for association with CRC susceptibility, clinical outcomes and selected CRC-associated microsatellite instability, -driver gene mutation, -immune checkpoint PD-L1 and -diagnosis biomarker CA19-9, CEA and CYFRA21-1.

Results Our study found that no somatic mutation of MICA gene occurred in CRC tumor tissues compared to the paracancerous tissues. The results of disease association showed that MICA *009:01 or *049 allele was protective to CRC ($p=0.0049$, $OR=0.35$). In addition, different clinical presentations also were associated with specific MICA alleles. In particular, MICA *045 allele was dramatically increased in the ulcerated CRC ($p=0.0028$); MICA *027 was associated with the later stage (III/IV stage) of UICC (Union for International Cancer Control),($p=0.044$); MICA *012:01 allele was significantly increased in the CRC patients carrying KRAS codon 12 mutation ($p=0.027$, $OR=3.33$), and together with MICA *A4, dramatically increased in the CRC patients with

MSI (microsatellite instability) (p=0.0026/OR=7.59 and p=0.011/OR=4.93, respectively); *A5.1 of MICA gene was decreased in medium or low differention state of CRC (p=0.019). **Conclusions** MICA alleles are important genetic factors for CRC, especially for MSI and KRAS mutation subtypes of CRC.

PO-129

The efficiency evaluation and endocytosis exploration of cationic liposome delivery systems optimized by different condensed agents

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Objective DNA condensed agents can improve the transfection efficiency of the cationic liposome delivery system. However, various condensed agents have distinct transfection efficiency and cellular cytotoxicity. The object of this study was to screen the optimal agents with the high transfection efficiency and low cytotoxicity from four polymer compressive materials, polyethylenimine (PEI), chitosan, poly-L-lysine (PLL), and spermidine.
Methods DNA was pre-compressed with these four agents and then combined to cationic liposomes. Subsequently, the entrapment and transfection efficiency of the obtained complexes were investigated. Finally, the particle sizes, cytotoxicity, and endocytosis fashion of these copolymers (Lipo-PEI, Lipo-chitosan, Lipo-PLL, and Lipo-spermidine) were examined.
Results It was found that these four copolymers had significantly lower cytotoxicity and higher transfection efficiency (51.0%, 41.9%, 22.4%, and 57.6%, respectively) than those in the control groups. The transfection efficiency of Lipo-PEI and Lipo-spermidine copolymers were better than the other two copolymers. In 293T cells, nystatin significantly inhibited the transfection efficiency of Lipo-PEI-DNA and Lipo-spermidine-DNA (46.33% and 32.68%, respectively), which suggest that the endocytosis pathway of Lipo-spermidine and Lipo-PEI copolymers was probably caveolin-dependent.
Conclusions Our study indicated that these dual-degradable copolymers especially liposome-spermidine copolymer could be used as the potential biocompatible gene delivery carriers.

PO-130

hsa_circ_0006459 and hsa_circ_0015962 affect prognosis of Dengue fever

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Objective To investigate the role of circRNA and its possible mechanisms in dengue fever (DF).
Methods Four patients with a preliminary diagnosis of dengue fever (DF), peripheral whole blood sample in anticoagulant was collected before treatment (pretreatment group) and after effective treatment (posttreatment group), and white blood cells (WBCs) were separated and used to screen differentially expressed circRNAs with microarray analysis. The relative expression level of circRNAs was determined using reverse-transcription polymerase chain reaction (RT-PCR). TargetScan v7.1 and miRDB v5 bioinformatics software were used to predict circRNA-binding miRNAs; dual luciferase reporters were constructed to detect binding between circRNA and miRNA.
Results Microarray screening revealed 263 differentially expressed circRNAs in peripheral leukocytes pretreatment versus posttreatment; 107 of these were upregulated and 156 were downregulated. RT-PCR confirmed that hsa_circ_0015962 was significantly upregulated and hsa_circ_0006459 significantly downregulated ($P < 0.05$). Moreover, hsa_circ_0015962 binds to miR-4683, and hsa_circ_0006459 binds to miR-133b.Downregulation of hsa_circ_0006459 and upregulation of hsa_circ_0015962 affect the treatment response of DF and are potential biomarkers in DF patients.
Conclusions The molecular mechanism involves hsa_circ_0006459-mediated targeted negative regulation of miR-133b and hsa_circ_0015962-mediated targeted negative regulation of miR-4683.

PO-131

O25b-ST131 and O16-ST131 subclone is one of the main causes of urinary tract infection Escherichia coli isolates from women in Changsha, China

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Objective The aim of this study was to investigate the prevalence and molecular characteristics of ST131 among unselected UTI *E. coli* isolates from women in central China.

Methods Between January 2014 and December 2015, a total of 216 non-repetitive E. coli isolates were recovered from urine samples from women with UTI in Changsha, China. All the isolates were analyzed for phylogenetic groups, susceptibility profiling and virulence genotypes. ST131 clonal groups were identified using PCR and characterized by O serotyping, CTX-M genotypes, *fimH*, *gyrA*, and *parC* alleles, fluoroquinolone resistance genes and PFGE patterns.

Results Overall, 41 (19.0%) of 216 *E. coli* were identified to be ST131 strains, among which 27 were O25b-ST131 strains and 14 was O16-ST131 strains. ST131 isolates had higher resistance rates to ampicillin (95.1% vs. 82.9%), ciprofloxacin (70.7% vs. 53.7%), ceftriaxone (78.0% vs. 58.9%) and ampicillin/sulbactam (87.8% vs. 66.9%) than non-ST131 isolates ($p < 0.05$). ST131 accounted for 23.9% of ESBL-producing isolates and 23.6% of the FQ-R isolates, but only 11.0% of non-ESBL-producing isolates and 12.9% of the FQ-S isolates. ST131 isolates possessed more virulence traits than non-ST131 isolates. ESBL-producing *E. coli* ST131 prevalence was 78.0% (32/41). 93.8% (30/32) of the isolates were detected to harbor blaCTX-M genes. Of the 30 isolates, 15 (50.0%) produced CTX-M-14, 6 (20.0%) CTX-M-55, 4 (13.3%) CTX-M-15, 4 (13.3%) CTX-M-27, 1 (3.3%) CTX-M-24. Ciprofloxacin resistance was found to be significantly higher in O25b-ST131 isolates than O16-ST131 isolates (96.3% vs. 21.4%). O25b subgroups accounted for 75% and 89.7% of ST131 isolates within ESBL and the FQ-R groups, but only 33.3% and 8.3% of those within non-ESBL-producing and the FQ-S groups. The majority of O25b-ST131 isolates belonged to *fimH*30 (25/27, 92.6%), followed by *fimH*41 (n=1) and *fimH*27 (n=1). O25b-*H*30 and O25b-*H*41 isolates were resistant to ciprofloxacin, and possessed a set of 4 conserved QRDR amino acid substitutions (GyrA S83L, D87N and ParC S80I, E84V). While, all of the O16-ST131 isolates were found to belong to *fimH*41, and of which, two of the ciprofloxacin-resistant strains harbored 3 mutations (GyrA S83L, D87N and ParC S80I). Three PFGE clusters, consisting of 38 (92.3%, 38/41) isolates, with more than 70% similarity were identified.

Conclusions Despite the lower ciprofloxacin resistance of the O16-ST131 isolates, these isolates did not exhibit significant differences in MDR, resistance score or virulence genotype compared with classic O25b-ST131 isolates. The implementation of effective antimicrobial stewardship and infection control interventions in China is urgently required to reduce the possibility of transmission by this pandemic clone.

PO-132

Performance of serum biomarkers in ARDS diagnosis and mortality prediction

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Objective The objective of current study is to explore the change in serum of Angiopoietin 2(Ang-2), Krebs von den lungen 6(KL-6), Surfactant protein D (SP-D), Von Willebrand factor(vWF), and Interleukin-8(IL-8) and evaluate their powers to detect the occurrence and to predict the mortality of ARDS.

Methods In this prospective study, 49 ARDS patients and 50 non-ARDS were enrolled in two Intensive Care Units (ICUs). Blood samples collected from participants at admission to ICU(T_1) and the time-point when diagnosed for ARDS(T_2) were tested for 5 serum biomarkers by enzyme-linked immunosorbent assay. Receiver operating characteristic curve(ROC) was used to evaluate the performance of biomarkers in ARDS diagnosis and mortality prediction.

Results The levels of all 5 serum biomarkers elevated in ARDS compared with non-ARDS ($P<0.05$). At T_2 time-point the serum concentrations of 5 biomarkers in ARDS patients were significantly higher than T_1 time-point. The death patients (n=17) in ARDS group had higher levels of Ang-2, KL-6, SP-D, and IL-8 than survivals (n=32) ($P<0.05$), unlike vWF($P>0.05$). With respect to the diagnosis of ARDS, at T_1 time-point the largest areas under the receiver operating characteristic curve (AUCs) for single biomarker and combination were 0.816[95% confidence interval (CI): 0.730, 0.902] (KL-6) and 0.869(95% CI: 0.795, 0.942) (KL-6+Ang-2), respectively. The best predictive AUCs of 28-day mortality for single biomarker and combination at T_2 time-point were 0.764(95% CI: 0.627, 0.901)(IL-8) and 0.829(95%CI: 0.715, 0.943)(IL-8+KL-6), respectively.

Conclusions The 5 serum biomarkers are associated with the occurrence, development, and poor prognosis of ARDS in ICU. It is possible that serum KL-6 and Ang-2 should be as diognostic indicators for ARDS and IL-8 and KL-6 as predictive markers for poor prognosis in ARDS.

PO-133

AKAP12 endogenous transcripts suppress the proliferation, migration and invasion of colorectal cancer cells by directly targeting oncomiR-183-5p

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Objective Restoring lost function to suppressor gene products has captured the interest of the research community in the field of gene therapy. *AKAP12*, also known as *Gravin/AKAP250*, is a tumor suppressor gene, and its deregulation may be responsible for cancer progression. The aim of this study was to investigate whether *AKAP12* mRNA has an anti-cancer function by regulating onco-miRNA expression in colorectal cancer (CRC) cells.

Methods miRNAs targeting *AKAP12* were predicted by bioinformatics analysis and further confirmed by dual-luciferase reporter assays and RT-qPCR. miRNA-183-5p expression in CRC cells after up- or down-regulating endogenous *AKAP12* mRNA were measured by quantitative RT-qPCR. Overexpression and Interference experiments were conducted to investigate the biological functions of miR-183-5p both *in vitro* and *in vivo*. The expression of miR-183-5p was detected in early-stage CRC tumors tissues by miRseq. miR-183-5p co-expression analysis was implemented using the Spearman correlation coefficient.

Results miR-183-5p was predicted as a microRNA targeting *AKAP12* by bioinformatics analysis. Luciferase assays revealed that *AKAP12* directly targeted miR-183-5p. The miRseq data showed that miR-183-5p was also dysregulated at the early stage of tumor development and upregulated in late sub-stage II CRC patients ($P<0.01$). Mechanistic analysis both *in vitro* and *in vivo* demonstrated that anti-miR-183-5p depressed cell proliferation, migration, and invasion in CRC cells while miR-183-5p overexpression resulted in opposite effects.
Conclusions Our findings suggested that oncomiR-183-5p promoted the proliferation, migration, and invasion of CRC cells. *AKAP12* miRNA-binding elements (MREs) suppressed miRNA-183-5p activities. Any change in expression of *AKAP12* thus affected miRNA-183-5p. This may be another anti-tumor mechanism in addition to protein-mediation that regulates tumor suppressor genes.

PO-134

Glutathione in combination with trehalose has supplementary beneficial effects on cryopreserved red deer (cervus elaphus) sperm

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Objective In this study, we evaluated the effects of glutathione in combination with trehalose addition to semen extenders on the quality parameters of frozen-thawed red deer (cervus elaphus) spermatozoa.
Methods The semen samples collected from six mature red deer once a week were diluted with Tris-egg yolk-based extenders. The diluted semen samples were supplemented with glutathione (8 mmol L) and or trehalose (5%, w/v), cryopreserved, thawed and then subjected to sperm quality parameter evaluation.
Results Both glutathione and trehalose addition to the extender significantly improved progressive motility, acrosome integrity, membrane integrity, superoxide dismutase and glutathione peroxidase activity and decreased percentage abnormality and sperm malondialdehyde level compared with the control group ($P<.05$). Moreover, glutathione in combination with trehalose addition to semen extenders had higher efficiency compared with the glutathione or trehalose addition alone ($P<.05$).
Conclusions Therefore, glutathione in combination with trehalose could be a promising cryoprotectant for red deer sperm.

PO-135

Unusual cause of pancytopenia: bone marrow smear showing Histoplasma capsulatum

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Objective In this paper,we wan to introduce an unusual cause of pancytopenia.
Methods On admission, she had new-onset pancytopenia with a white blood cell count of 2.16×10^9/l (normal range, 3.5-9.5$\times10^9$/l), hemoglobin7.9 g/dl (normal range, 11.5-15g/dl), and a platelet count of 81×10^9/l (normal range, 101-320$\times10^9$/l). Initial peripheral blood smear showed left shift with toxic granulation. Biochemical studies showed markedly elevated ferritin (14740 mg/l), decreased fibrinogen (148 mg/dl) and total protein (58.2 g/l). Computed tomography showed bilateral pulmonary micronodular infiltrates and splenomegaly. Bone marrow aspirate (Wright-Giemsa stain) showed numerous histiocytes with intracellular and extracellular fungal organisms morphologically consistent with histoplasmosis. These organisms stained bright pink on periodic acid-Schiff stain.
Results The patient was promptly started on amphotericin B and responded rapidly to the treatment. Finally, BM and bronchoalveolar lavage cultures confirmed *Histoplasma capsulatum.*
Conclusions BM examination, in conjunction with clinical and laboratory findings, is crucial for timely intervention. A diligent BM search for fungal microorganisms is also warranted because BM can sometimes be the only location to obtain the diagnosis.Timely diagnosis of disseminated histoplasmosis requires a high index of clinical suspicion owing to the high mortality associated with it. Bone marrow studies may aid in the diagnosis and should be considered in the appropriate clinical scenario.

PO-136

Clinical and molecular characterization of three novel ARHGEF9 mutations in patients with developmental delay and epilepsy

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Objective To study the clinical and molecular characterization of three patients with developmental delay and epilepsy.
Methods Targeted panel sequencing of genes known to cause inherited disorders were used for detecting the causative variants. Variants detected were further confirmed by Sanger sequencing. Reverse transcription - polymerase chain reaction was used to analyze the splicing patterns in the patient's leukocytes. The *ARHGEF9* wild type and mutant (I294T and p.R357I) expression vectors were constructed. Transient transfection

was performed in HEK293T cells. Western blot analysis was performed to evaluate the effects of the missense variants on the expression of the *ARHGEF9*. Immunofluorescence assay was utilized to analyze the collybistin (CB) mediated gephyrin clustering.
Results Two novel missense variants (p.I294T and p.R357I) and one novel splicing variant (c.381+3A>G) in *ARHGEF9* were identified in the three patients respectively. *In vitro* studies confirm the two missense variants disrupt the CB-mediated accumulation of gephyrin in submembrane microclusters, while transcription experiment of the splicing variant revealed the presence of aberrant transcripts leading to truncated protein product.
Conclusions Three novel ARHGEF9 mutations were identified in patients with developmental delay and epilepsy.Our cases and functional studies enriched the phenotypic and genotypic spectrum of *ARHGEF9*.

PO-137

Changes of urine NAG activity index and CysC index in patients with hemorrhagic fever with renal syndrome (HFRS)

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Objective To investigate the relationship between urine NAG activity index, CysC index and proximal renal tubular injury and functional changes in patients with different stages and types of hemorrhagic fever with renal syndrome (HFRS).
Methods NAG activity, CysC concentration and creatinine concentration in urine samples of 21 patients at different stages were measured. NAG activity index and CysC index were calculated and compared with those parameters of 30 healthy people.
Results The urine NAG activity index and CysC index except the restoration stages were significantly different from those of the control group ($p<0.05$). And were the clinical stages and clinical types as well($p<0.05$).
Conclusions Urine NAG activity index and CysC index are closely related to proximal renal tubular injury in patients with HFRS, and detection can provide changes in resorption function for clinical treatment

PO-138

Epidemiological Analysis of Common Non-bacterial Pathogens of Acute Respiratory Tract Infection in 18252 Children

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Objective To analyze the detection condition of nine common pathogens in 18252 children with acute respiratory tract infection (ARI) in Tianjin, so as to provide basis for early prevention and clinical diagnosis and treatment.
Methods Indirect immunofluorescence was used to detect Legionella pneumophila (LP), Mycoplasma pneumoniae (MP), Q fever rickettsia(COX), Chlamydia pneumoniae (CP), Adenovirus (ADV), Respiratory syncytial virus (RSV), Influenza A virus (INFA), Influenza B virus (INFB) and Parainfluenza virus (PIV) in 18252 children with acute respiratory infection admitted to Tianjin Children's Hospital from March 2017 to February 2018. Statistical analysis was then performed by SPSS 19.0.
Results The overall positive rate was 27.64% and there was no difference between the detection rates of two genders. According to the detection rate from high to low, MP (22.47%) was the dominant pathogen, following were INFB (2.56%), PIV (2.31%), RSV (0.72%), LP (0.71%), ADV (0.64%), CPN (0.27%), COX (0.15%) and INFA (0.03%). Among the 5046 positive cases, the single infection rate was 92.03%, and the mixed infection rate was 7.97%. The detection rates of MP were more than 20% in spring, summer and winter. INFB showed the highest detection rate in March, followed by February, April and January. Epidemic peak of PIV occurred in late spring and early summer. The detection rates of MP, INFB and PIV in preschool children were the highest, followed by the >6-year-old age group and the 1-3-year-old age group; detection rates of the <1-year-old age group were the lowest.
Conclusions The main non-bacterial pathogens of ARI in Tianjin were MP, followed by INFB and PIV. The prevalence months and seasons of different pathogens were different, but the detection rates were all highest in the 4-6-year-old age group, which suggested that extra attention should be paid to prevent and treat ARI in preschool children.

PO-139

LncRNA NORAD as a potential biomarker in colorectal cancer and associates with malignant behavior

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Objective To elucidate the potential function and clinical significance of long noncoding RNA-activated by DNA damage (NORAD) in colorectal cancer (CRC).

Methods We detected the expression levels of NORAD in sixty pairs of tumorous and adjacent nontumorous tissues derived from CRC patients by quantitative real-time polymerase chain reaction. The serum levels of NORAD expression were also measured in an independent cohort of CRC patients as well as patients with benign diseases and healthy controls. Comparative analyses were performed to investigate the relationships between NORAD levels in tissues and clinicopathological features of CRC. Receiver operating characteristic (ROC) curve analysis was used to assess the diagnostic value of NORAD in patients with CRC. Furthermore, the potential functions of NORAD in the development of CRC were explored *in vitro*, using the HCT116 and SW1116 CRC cell lines.
Results NORAD expression was significantly up-regulated in the tumorous tissues of CRC patients compared to the adjacent nontumorous tissues. Higher NORAD expression was associated with advanced CRC. Moreover, serum levels supported that NORAD could distinguish CRC patients from healthy controls and patients with benign diseases, indicating a potential diagnostic role in CRC. The ROC curve analysis showed a diagnostic efficacy with area under the curve of 0.800 (95% confidence interval: 0.737-0.853). Mechanistic investigations indicated that NORAD silencing reduced CRC cell proliferation, migration and invasion.
Conclusions NORAD may serve as a novel predictor in CRC and may be a potential target for future therapy.

PO-140

Non-neutralizing epitopes induce robust hepatitis C virus (HCV)-specific antibody-dependent CD56+ natural killer cell responses in chronic HCV-infected patients

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Objective Natural killer (NK) cell-mediated antibody-dependent cellular cytotoxicity (NK-ADCC) is of considerable interest in viral infection. However, little is known about NK-ADCC responses in chronic hepatitis C virus (HCV) infection.
Methods In this study, impaired non-specific antibody-dependent $CD56^+$ NK cell responses were observed in chronic HCV infection, as shown by decreased degranulation (extracellular CD107a expression) and interferon (IFN)-γ production in response to antibody-bound P815 cells.
Results A peptide pool composed of epitopes recognized by anti-HCV-E1/E2 antibodies could induce pronounced HCV-specific antibody-dependent NK cell responses in sera from approximately half the chronic HCV carriers. Additionally, HCV-specific epitopes with the capacity to induce robust NK-ADCC activity were identified. Five linear NK-ADCC epitopes (aa211-aa217, aa384-aa391, aa464-aa475, aa544-aa551 and aa648-aa659 of the HCV envelope) were identified and do not overlap with putative linear neutralizing epitopes.
Conclusions This study revealed the dysfunctional characteristics of antibody-dependent $CD56^+$ NK cell responses in chronic HCV carriers. The key non-neutralizing

NK-ADCC epitopes identified in this study may act as new targets for immunological intervention.

PO-141

Characteristics of HPV genotypes in Baoshan District of Shanghai

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Objective To investigate the HPV infection rate among women in Baoshan district of Shanghai and its relationship with age and the distribution of each subtype, so as to provide the theoretical basis for the prevention and treatment of cervical cancer in this region.

Methods Cervical exfoliated samples from a total of 7709 female population were collected and detected by flow fluorescence hybridization. Total 27 HPV genotypes were found and the association between HPV infection rate and age coupling with the distribution characteristics of HPV subtypes were analyzed.

Results In 7709 cases, 1237 cases were HPV positive, the infection rate was 16.05%. Among them, 833 cases were high-risk type with the infection rate of 10.81%. The first five constituent ratio of high-risk types included HPV 52 (12.00%), HPV 16 (10.35%), HPV 53 (9.14%), HPV 58 (7.86%) and HPV 39 (6.27%). 254 cases were low-risk type with the infection rate of 3.29%. The first five constituent ratio of low-risk types included HPV 61 (5.18%), HPV 43 (4.02%), HPV 55 (3.78%), HPV 81 (3.47%) and HPV 6 (2.92%). There were 958 cases of single genotype HPV infection, accounting for 77.44% and the infection rate was 12.43%.There were 198 cases of double genotype HPV infection, accounting for 16.01%, and the infection rate was 2.57%. Multigenotypic HPV infection was found in 81 cases, accounting for 6.55% and the infection rate was 1.05%. The peak age of HPV infection was 41-50 years old, followed by 31-40 years old, then 21-30 and 51-60 years old, the corresponding infection rate was 38.64%, 28.05%, 17.38% and 9.86%, respectively. The infection rate of people over 61 and under 21 years old was relatively low. There were significant differences in HPV infection rates among these age groups (p <0.001) .The most frequently infected HPV subtype in the 31-40 age group was HPV16, HPV52, HPV53, HPV58 and HPV39 successively. However, it was HPV52, HPV16, HPV53, HPV58 and HPV39 successively in other age groups.

Conclusions HPV was mainly infected by single genotype HPV, and the most frequently infected high-risk genotypes were HPV52, 16, 53, 58 and 39 respectively. The peak of HPV infected age group was between 41 and 50 years. HPV genotype and age should be taken into account in screening, prevention and development of vaccines for cervical cancer.

PO-142

Assessment of biological variation for 23 laboratory routine tests from healthy adults for 5 consecutive years

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Objective To assess biological variation of 23 routine laboratory tests from 100 healthy subjects for 5 consecutive years.

Methods One hundred healthy study participants were enrolled from a tertiary hospital and fasting blood samples were collected once a year for 5 consecutive years and analyzed for 23 routine laboratory tests, including white blood cell counting (WBC), red blood cell counting (RBC), hemoglobin (HGB), Hematocrit (HCT), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), platelet count (PLT), total bilirubin (TBIL), total protein (TP), albumin(ALB), Alanine aminotransferase (ALT), aspartate aminotransferase (AST), glutathione transdermal enzyme (GGT), alkaline phosphatase (ALP), uric acid (URIC), urea (UREA), creatinine (CREA), glucose (GLU), triglyceride (TG), total cholesterol (CH), high density lipoprotein cholesterol (HDL) and Low density lipoprotein cholesterol (LDL), using a Hematology analyzer or biochemical analyzer. The data were subject to within-subject biological variation (CV_I) and between-subjects biological variation (CV_G) analysis.

Results We found that CV_I varied from 1.26% to 26.42%. Of these CV_I, those of TBIL, ALT, GGT and TG were displayed above 20% while those of RBC, HGB, HCT, MCV, MCH, MCHC, TP and ALB were less than 5%. For CV_G, there were more significantly different among these parameters. The estimates of CV_G were obtained from 2.49% for MCHC to 52.98% for GGT. Of 23 parametres, CV_G of TBIL (30.25%), ALT (37.72%), TG (39.70%) and GGT (52.98%) were above 30%, whereas those of MCHC, MCV and MCH were less than 5%, 2.49%, 3.71% and 3.73%, respectively. Most CV_I and CV_G estimates appear to be higher than those previously published in the online 2014 Westgard updated database. However, a few CV_I and CV_G estimates were superior to those online, such as CV_I for RBC, MCH and PLT and CV_G for MCV, MCH, PLT, ALT, ALP, CH, HDL and LDL.

Conclusions Most biological variation estimates in this study were similar with the online database in Westgard website except a few of parametres. And our study made up for the lack of long-term biological variation in the database.

PO-143

Correlation of plasma folic acid, vitamin B12 and homocysteine levels with cerebral infarction and vascular dementia------Supported by science and technology program of gansu province, project No. : 18JR3RA081

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Objective vascular dementia (Va D) is caused by all sorts of cerebrovascular disease, accompanied by persistent cognitive impairment and a kind of intelligent obstacle syndrome, Va D not only increases the risk of death in patients with occurrence, and reduce the patient's quality of life, increase health economic efforts, to family and society bring heavy burden, so in recent years the Va D become scholars research hot spot.The purpose of this study was to analyze and explore the related levels of Va D and plasma Hcy plasma homocysteine, folic acid and vitamin B12, so as to clarify the etiology and related influencing factors of Va D and provide a basis for the prevention and treatment of Va D.

Methods the object of study of 30 patients with vitamin D and 25 cases of cerebral infarction patients with dementia, enzyme circulation method was applied on the Toshiba 120 r automatic biochemical analyzer determination of Hcy concentration, application of mindray Ci2000 chemiluminescence analyzer test vitamin B12 and folic acid level, using a simple scale mental state examination (MMSE) in 30 patients with vitamin D for assessment of the severity of dementia.

Results 1. Plasma Hcy level in the Va group was significantly higher than that in the non-dementia cerebral infarction group ($P<0.001$), folic acid level was significantly lower than that in the non-dementia cerebral infarction group ($P<0.001$), and vitamin B12 level was significantly lower than that in the non-dementia cerebral infarction group ($P<0.05$).

2. Compared with the mild dementia group, the plasma Hcy level in the two groups of moderate and severe dementia patients with Va D was significantly increased ($P<0.05$).Plasma Hcy level in patients with severe dementia was also significantly higher than that in patients with moderate dementia ($P<0.05$).The correlation analysis showed that the plasma Hcy level of patients in the Va D group was negatively correlated with the MMSE score ($r = -0.458$, $P<0.05$).

Conclusions elevated plasma Hcy level is one of the risk factors for Va D.The level of Hcy is negatively correlated with folic acid and vitamin B12. The decrease of folic acid and vitamin B12 may be an important factor leading to the increase of plasma Hcy.The increase of plasma Hcy level is one of the factors affecting the severity of Va - D dementia.

PO-144

Correlation of serum uric acid and homocysteine levels with vascular dementia----Supported by science and technology program of gansu province, project No. : 18JR3RA081

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Objective vascular dementia (VaD) is a type of dementia with high incidence in China.The incidence of vascular dementia is second only to Alzheimer's disease (AD).The basic disease of VaD is mostly cerebrovascular disease. When the lesion affects the higher functional areas related to cognitive function, it may lead to cognitive impairment and gradually or rapidly develop dementia.Therefore, it is extremely urgent to fully understand and prevent the occurrence of vascular dementia (VaD).Whether the level of serum uric acid is correlated with the occurrence and development of vascular dementia remains to be determined. This paper aims to explore whether the level of serum uric acid and homocysteine are risk factors for vascular dementia.

Methods selected inpatients or outpatients in the department of neurological rehabilitation of gansu rehabilitation center hospital from January 2017 to December 2018.Into the standard set: sexs, age 55 years of age or older, no obvious kidney disease, heart disease, liver disease, ruled out after central nervous system infection secondary to dementia, there is no chronic alcoholism, no other organic brain lesions, head trauma, did not suffer from mental illness (e.g., mania and depression, etc.), recent not taking a cholesterol-lowering drugs and vitamins such as influence of lipid metabolism of patients.Diagnostic criteria for vascular dementia VaD: according to the diagnostic criteria for probable vascular dementia formulated by the Swiss international association for neurological research and the national institute of neurological diseases and stroke (NINDS/AIREN CCDVD) in 1993, clinical history, neurological examination and brain CT scan are diagnosed by specialists.A total of 32 patients with VaD were selected as the case group, and the degree of dementia was assessed by the simple intelligent state scale (MMSE).The control group included 30 healthy subjects with non-dementia at the same age.Both uric acid and homocysteine were detected, and the changes in the above indicators in the two groups were observed. SPSS 13.0 statistical software was used for data processing, and the difference was statistically significant when $P< 0.05$.

Results compared with the control group, serum uric acid level was significantly decreased in the vascular dementia group, and the difference was statistically significant ($P<0.05$); serum homocysteine level was significantly increased in the vascular dementia group, and the difference was statistically significant ($P<0.05$).The serum uric acid level of patients with mild vascular dementia was higher than that of patients with moderate vascular dementia, and the serum uric acid level of patients with moderate vascular dementia was higher than that of patients with severe vascular dementia, and the difference was statistically significant ($P<0.05$).The higher the MMSE score, the higher the serum uric acid level, and the lower the degree of vascular

dementia.The lower the MMSE score, the lower the serum uric acid level, and the higher the severity of vascular dementia (P<0.05).

Conclusions compared with the control group, the serum uric acid level of vascular dementia patients was significantly decreased, while the homocysteine level was increased, and the decrease of homocysteine level was directly proportional to the degree of dementia of vascular dementia patients.This indicates that the level of serum uric acid is inversely proportional to the severity of dementia, that is, the lower the level of serum uric acid, the more severe the dementia of vascular dementia patients; on the contrary, the higher the level of serum uric acid (not exceeding the normal value), the cognitive function of vascular dementia patients will be improved.The detection and intervention of uric acid level may help to understand the severity of vascular dementia and guide the prevention, diagnosis and treatment.

PO-145

The risk factors analysis of bacterial encephalitis in infants with severe hand-foot-mouth disease based on Logistic- regression

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Objective To investigate the risk factors of bacterial encephalitis in children with severe hand-foot-mouth disease, and to provide basis for the prevention of hand-foot-mouth disease complicated with bacterial encephalitis.

Methods Retrospective analysis was performed to select the children diagnosed with severe hand-foot-mouth disease between February 2010 and January 2018. Among them, 56 cases were diagnosed as bacterial encephalitis by routine examination and culture of cerebrospinal fluid as a research group. 114 children with severe hand-foot-mouth who had no bacterial encephalitis at the same time 、matched for age and sex were selected as controls. The Logistic regression methods was used to analyze the differences between the two groups.

Results Based on the analysis,the rate of severe HFMD combined bacterial encephalitis in children was 12%. The gender, age, WBC count, fever, blood glucose levels, creatine kinase isoenzyme CK-MB levels，long time to onset were not insignificance between those groups(P>0.05). mental disparity, vomit,high PCT levels, positive bacterial cultures in the respiratory system, enterovirus EV71 ratio and abnormal nerve reflex were significant difference between groups by single factor analysis(P<0.05). After the analyzed by the conditional Logisitic analysis.which was fitting by the Logistic multivariate model. the independent risk factors for severe HFMD with bacterial encephalitis were increased PCT levels (OR=4.265, 95% CI 1.514-7.362), positive respiratory bacterial culture (OR=2.535, 95% CI 1.029-4.568), and abnormal nerve reflex (OR=2.592, 95% CI 1.358-6.453).

Conclusions This study indicated that high PCT levels, positive bacterial cultures in the respiratory system and abnormal nerve reflex were independent risk factors of

Severe HFMD combined with bacterial encephalitis. When these risk factors appear, it is necessary to prevent the occurrence of bacterial encephalitis.

PO-146

Development and Verification of a Discriminate Algorithm for Diagnosing Post-neurosurgical Bacterial Meningitis - a multi-center observational study

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Objective To evaluate the diagnostic accuracy of cerebrospinal fluid (CSF)-based routine clinical examinations for post-neurosurgical bacterial meningitis (PNBM) in multi-center post-neurosurgical patients.

Methods The diagnostic accuracies of routine examinations to distinguish between PNBM and post-neurosurgical aseptic meningitis (PNAM) were evaluated with the values of the area under the curve (AUC) of the receiver operating characteristic (AUC_{-ROC}) by retrospectively analyzing the post-neurosurgical patients in four centers.

Results An algorithm was constructed with liner discriminant analysis as a classic method to maximize the capacity for differentiating the two classes by integrating the measurements of five variables above. The AUC_{-ROC} value of this algorithm was 0.907 (95% CI 0.737-0.782), which was significantly higher than those of individual routine blood/CSF examinations. The predicted value from 70 PNBM patients was greater than the Cut-off value, and the diagnostic accuracy rate was 75.3%. The results from 181 patients with PNAM showed that 172 patients could be correctly identified with the specificity as 95.3%, while the overall discriminant correctness rate of the algorithm was 88.6%.

Conclusions Routine biomarkers, such as CSF/blood glucose ratio (C/B-Glu), CSF lactate (C-Lac), CSF glucose concentration (C-Glu), CSF leukocyte count (C-Leu), and blood glucose concentration (B-Glu), can be used as an auxiliary diagnosis of PNBM. By means of the multi-center retrospective research, we can effectively improve the PNBM diagnosis efficacy with combination of the five biomarkers mentioned above.

PO-147

LncRNA HOTAIR Contributes to 5-fluorouracil Resistance through Suppressing MiR-218 and Activating NF-κB/TS Signaling in Colorectal Cancer

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Objective In clinical situations, acquired drug resistance and enhanced metastasis frequently follow chemotherapeutic regimens, leading to treatment failure in tumor patients. Despite the extensive research on chemoresistance, the detailed mechanism underlying this phenomenon remains unclear. Long non-coding RNA HOTAIR has been considered as a pro-oncogene in multiple cancers. However, the precise functional mechanism of HOTAIR in chemoresistance is not well known. To further explore the possible mechanisms and promote chemosensitivity of CRC treatment, we evaluated the prognostic effect of HOTAIR in patients received 5-FU-based treatment and investigated the underlying regulatory mechanism of HOTAIR in 5FU resistance.

Methods The small interfering RNAs (siRNAs) that specifically target human HOTAIR, EZH2, and VOPP1 mRNA were designated. The coding sequence of VOPP1 was amplified, cloned into PCDNA3.1 vector. The lentivirus vector containing HOTAIR short-hairpin RNA (Lv-ShHOTAIR) was amplified and cloned. Human CRC cells lines were transfected with small interfering RNAs or overexpressing precursor followed by assays to investigate the influence of HOTAIR and VOPP1 on cell proliferation, cell-cylce phase and pathways involved in molecular mechanisms of chemoresistance to 5-FU. RNA immunoprecipitation (RIP) and Chromatin immunoprecipitation (ChIP) experiments were performed to investigate the potential interaction. Western blot and immunofluorescence analysis were performed to detect the protein expression of NF-κB/TS signaling pathway. Primary tumor specimens and adjacent non-tumor sites were used to determine the HOTAIR expression distribution and explore the potential prognostic value of HOTAIR on the chemoresponse to 5-FU-based treatment in CRC patients.

Results HOTAIR negatively regulated miR-218 expression in CRC cells. RIP and ChIP assay showed that HOTAIR interacted with EZH2, and this interaction subsequently silenced miR-218-2. Both HOTAIR and miR-218 suppressed cell proliferation, and HOTAIR knockdown dramatically inhibited cell viability and induced G1-phase arrest by promoting miR-218 expression. Luciferase activity assay showed that VOPP1 was a functional target of miR-218. More importantly, the main downstream targets signaling of NF-κB, including the pathway involved in cell survival (p65-NF-κB, pAkt, pERK), cell cycle (E2F-1) and 5FU-targeted protein (thymidylate synthase, TS), were inactivated by HOTAIR through the suppression of miR-218 expression. Additionally, HOTAIR knockdown partially reversed 5FU resistance through promoting miR-218 and inactivating NF-κB signaling. Furthermore, HOTAIR restrained 5FU-induced cytotoxicity on CRC cells through promotion of TS expression.

Clinical exploration of HOTAIR indicated that the HOTAIR expression level was much higher in CRC tissues from patients who did not respond to 5FU treatment than those from patients who experienced response to chemotherapy. ROC curve analysis was

performed, and these patients were stratified into a low (n=56) and a high (n=96) HOTAIR expression group with an established cut-off value (4.01). The area under the curve (AUC) and diagnostic sensitivity and specificity reached 0.716, 81.58%, and 55.26% with the established cut-off value, respectively. Furthermore, the proportion of patients not responding to chemotherapy was significantly higher in the high HOTAIR expression group than in the low expression group. Kaplan-Meier survival analysis indicated that high HOTAIR expression was associated with poor overall survival (OS) and recurrence-free survival (RFS) in CRC patients, and Cox regression univariate/multivariate analysis showed that HOTAIR expression level maintained its significance as independent prognostic factors for OS of CRC patients receiving 5FU treatment.

Conclusions Our integrated approach demonstrated for the first time that HOTAIR contributes to CRC tumorigenesis and 5FU resistance through downregulation of miR-218 and activation of NF-κB signaling. This lncRNA directly recruits EZH2 and suppresses miR-218 by binding to its promoter, which provides a mechanistic foundation for the aberrant VOPP1 activation in CRC. This pro-resistant role of HOTAIR was further validated in an independent set of CRC patients who received standard 5FU treatment. Thus, HOTAIR may be a novel prognostic biomarker and therapeutic target in CRC patients. Suppression of HOTAIR could be a future direction for enhancing chemosensitivity to 5FU-based chemotherapy regimens.

PO-148

MicroRNA-218 is a prognostic indicator in colorectal cancer and enhances 5-fluorouracil-induced cytotoxicity through suppressing BIRC5

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Objective One major reason for the failure of advanced colorectal cancer (CRC) treatment is the resistance to fluoropyrimidine(FU)-based chemotherapy. The enhanced ability of tumor cells to undergo anti-apoptosis process is the main contributor to drug resistance. Various reports showed that ectopic expression and function of miRNAs play key roles to mediate apoptosis by primarily down-regulating protein expression at the post-transcriptional level. To further explore the possible mechanisms and promote chemosensitivity of CRC treatment, we evaluated the prognostic effect of miR-218 in patients received 5-FU-based treatment and investigated the pro-apoptotic role of miR-218.

Methods Primary tumor specimens and adjacent non-tumor sites were used to determine the miR-218 expression distribution and explore the potential prognostic value of miR-218 on the chemoresponse to 5-FU-based treatment in CRC patients. Human CRC cells (HCT116 and HT29) were transfected with precursor miR-218 or negative control followed by assays to investigate the influence of miR-218 on cell apoptosis, cell proliferation and pathways involved in molecular mechanisms of chemoresistance to 5-FU.

Results The expression of miR-218 was significantly decreased in tumour tissues compared with paired normal tissues. Moreover, the CRC tissues in 68.3% (43 of 63) of cases had at least two-fold lower expression of miR-218. In addition, miR-218 expression level was much lower in patients who did not respond to 5FU treatment than those who experienced response to chemotherapy. ROC curve analysis was performed to establish the optimal cut-off value of miR-218 (6×10^{-3}) for distinguishing the responding and non-responding patients. Under these stratification criteria, patients were stratified into high (n = 34) and low (n = 29) miR-218 expression groups. The proportion of patients that responded to chemotherapy was significantly higher in the high miR-218 expression group than in the low miR-218 expression group. Kaplan-Meier survival analysis was performed to further investigate the effect of miR-218 on 5-FU treatment for CRC. The results indicated that high miR-218 expression was associated with long overall survival and progressive-free survival rate.
Up-expression of miR-218 promoted apoptosis, inhibited cell proliferation in CRC cells. The anti-apoptotic gene-BIRC5, was identified as a direct target of miR-218 and the intrinsic apoptotic pathway triggered by miR-218 was through the silence of BIRC5. Gain and loss function assay indicated that miR-218 enhanced 5-FU-induced cytotoxcity and it has a strong synergistic effect with 5-FU on CRC cell growth. More importantly, western blotting showed that miR-218 silenced the 5-FU targeted enzyme, thymidylate synthase (TS).
Conclusions In this study, we demonstrated that high miR-218 predicted positive response to 5-FU-based treatments in CRC patients and discovered a novel mechanism mediated by miR-218 to promote apoptosis and to function synergically with 5-FU to promote chemosensitivity by suppressing TS in CRC. These suggests a unique potential of miR-218 as a tumor suppressor and a novel candidate for developing miR-218-based therapeutic strategies in CRC.

PO-149

Topographic distribution influences the prognostic impact of CD68 and CD204 positive macrophages in NSCLC

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Objective The purpose of this study was to clarify the correlation between TAMs location and the clinicopathological features of non-small-cell lung cancer(NSCLC), as well as explore the prognostic impact of TAMs in NSCLC.
Methods CD68 and CD204 positive macrophages were detected in tumor cell nest, tumor stroma and alveolar air space in 297 patients with NSCLC using immunochemistry staining. The clinicopathological and genetic factors surveyed were the disease-free survival, age, gender, smoking status, histological type, disease stage, histological grade, pleural invasion, lymph node metastasis, EGFR gene mutations, ALK rearrangements and miR-451 expressions.

Results The number of $CD68^+$ macrophages was significantly more than $CD204^+$ macrophages in each location, and they were strongly correlated($P<0.0001$ each). Factors such as male gender, being a smoker, advanced disease stage and histological grade, positive pleural invasion and node status and wild-type EGFR gene were significantly correlated with a higher expression of $CD68^+/CD204^+$ TAMs in tumor stroma($P<0.05$ each). While the age of patients, ALK rearrangement status or miR-451 expression levels in NSCLC was not correlated with $CD68^+/CD204^+$ TAMs($P>0.05$ each). In tumor cell nest, a higher number of $CD68^+/CD204^+$ TAMs significantly correlated with smokers and EGFR gene mutations($P<0.05$, respectively). Moreover, both of univariate and multivariate analyses revealed that a high number of $CD68^+/CD204^+$ TAMs in tumor stroma, but not in tumor cell nest or alveolar air space, was a significant prognostic factor for disease-free survival time of NSCLC($P<0.05$, respectively). In adenocarcinoma, a lower number of $CD68^+/CD204^+$ TAMs in tumor stroma and higher expression of $CD68^+/CD204^+$ TAMs in tumor cell nest were found than that in non-adenocarcinomas($P<0.05$, respectively). Furthermore, the survival analysis showed that a higher $CD204^+$ TAMs in tumor stroma was an independent predictor of a poor prognosis for adenocarcinoma.

Conclusions This clinicopathological study clarified the relationship between prognosis and TAMs location in NSCLC, and confirmed the worse prognostic value of higher $CD68^+/CD204^+$ stromal TAMs in NSCLC.

PO-150

C/EBPβ participates in the regulation of high expression of novel bladder cancer-specific gene UCA1 in bladder cancer

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Objective Urothelial Carcinoma Antigen 1 gene (UCA1) has been validated to be a cell- and tissue-specific lncRNA over-expressed in bladder cancer, It has been regarded as a novel tumor marker and is associated with the tumorigenesis and invasion of bladder cancer. However, the mechanism of its transcriptional regulation remains unclear. Our study aims to identify the functional region of UCA1 promoter and key transcription factor contributing to its high expression in bladder cancer.

Methods A series of different length of UCA1 promoter was constructed into luciferase report gene vector. A functional region in the promoter was then identified by 5'deletion analysis. Silico analysis, site directed mutagenesis and RNAi were used to assess and locate important transcriptional factors. A further ChIP and EMSA analysis were performed to confirm the combination of the transcriptional factors and their binding sites.

Results A region of 180bp in the UCA1 gene promoter upstream -1513bp~-1333bp was restricted to be closely associated with the high expression of UCA1 and ModelInspector predicted ten potential binding sites for the loss of transcriptional activity from the deletion constructs. Site-directed mutagenesis (SDM) and RNAi showed

that the expression of UCA1 had a significant decrease in 5637 cells in which the transcription factor of C/EBPβ was down regulated. ChIP and EMSA results confirmed that C/EBP combined to key element of UCA1 promoter.
Conclusions C/EBPβ was involved in transcriptional regulation of UCA1 and highly contributed to its high expression in bladder cancer.

PO-151

Clinical Laboratory Investigation of a Patient with Extreme High D-dimer

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Objective The case report describes an unusual example of an old woman with extreme high D-dimer value.
Methods A 82-year-old woman, admitted to the ward with a diagnosis of chronic heart failure, was noted to have a markedly elevated D-dimer value beyond the qualified scope(>100 mg/L) using Innovance D-dimer for Sysmex CS-5100 System™ without clinical symptoms, radiographic evidence of thromboembolic disease or parallel FDP values. To verify analytical interference was involved, a series of approaches including diluting sample, reanalyzing with alternative methodology and treating sample with specific heterophilic antibodies blocking reagent were performed.
Results A marked discrepancy of D-dimer values was shown in the samples after treated in the upper last two approaches (4.49, 9.42, 9.06, and 12.58 mg/L respectively), which highly confirmed for the presence of heterophilic antibodies in the sample. Meanwhile, DNA-load (3.4E04 copies/mL) and positive serum antibodies testing against Epstein-Barr virus (EBV) helped to diagnose this patient with infection of EBV, which might be contribute to case of such interference on D-dimer testing using Innovance D-dimer.
Conclusions In conclusion, heterophilic antibodies should be considered while elevated D-dimer value do not in conformity with clinical evidence, and virus infection should be taken into account when heterophilic antibody interference exists.

PO-152

The clinical significance of Mda-7/IL-24 and C-myb expression in tumor tissues of patients with diffuse large B cell lymphoma

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Objective The aim of the present study was to investigate the association between the expression of Mda-7/IL-24 and C-myb, and their prognostic significance for DLBCL patients.
Methods The tumor tissues were collected from 72 cases of DLBCL patients and detected with reverse transcription-quantitative polymerase chain reaction, western blotting and immunohistochemistry assays.
Results The results showed that, the expression of Mda-7/IL-24 mRNA and protein was lower while the expression of C-myb was higher in DLBCL tissues, compared with the specimens of normal lymph node tissues. Furthermore, C-myb expression was negatively correlated with Mda-7/IL-24 expression at mRNA and protein levels in DLBCL tissues. The expression of Mda-7/IL-24 and C-myb in DLBCL tissues was associated with some clinicopathological parameters such as clinical stage, infiltration in bone marrow, Ki67 expression level in the tumor tissues and overall survival rates.
Conclusions These results indicated that low expression of Mda-7/IL-24, along with high expression of C-myb, are predictor for poor prognosis of DLBCL patients, suggesting that Mda-7/IL-24 and C-myb may be potential targets for clinical treatment of DLBCL.

PO-153

The preliminary study on the diagnostic value of serum exosome microRNAs in the diagnosis of the ovarian cancer

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Objective Purpose: The traditional serum tumor marker are known to play important roles in the diagnosis of tumor.The aims of our study were to evaluate the serum exosome microRNAs as a potential markers in patients diagnosed with ovarian cancer.
Methods Method: Total exosome isolation reagent(MINUTE) was used to isolate serum exosome,then the exosomes were then ready for RNA extraction or exosome identification.The exosome was identified by transmission electron microscope and western-blot.The patients were divided into screening group and verification group. the four miRNAs have been well-documented to have significantly different expression levels in blood of ovarian cancer patients.The four miRNAs were miR-101-3P、miR-320a、miR-3184 和 miR-1246.The screening group included 10 patients with ovarian cancer(OC),10 with benign ovarian tumor(BOT) and 10 with healthy participants(HPs).

Results Then we found miR-1246 and miR-320a were stably expressed in the serum exosome,whereas there was low expression of miR-3184and miR-101-3P,.There was no significant difference in the expression levels of miR-320a between OC,BOT and HP .The validation group including 35 patients with advanced ovarian cancer,15 with early ovarian cancer ,20 with BOT and 20 with HPs.The mean levels of miR-1246 were significantly higher in OC patients than in HPs and BOT patients.
ROC curve analyses were performed to evaluate the diagnostic value of miR-1246 for OC.At the cutoff values of 13.526 for miR-1246,OC diagnostic sensitivities and specificities were 75.3% and 89.5% for miR-1246.The serum exosome miR-1246 was significantly elevated in the group of advanced stage and metastatic OC patients.
Conclusions Conclusion: Over the pastfew years,people's lifestyle has changed dramatically.Ovarian cancer is one of the commonest cause of gynaecological cancer-associated death.Early detection of OC remains a challenge for clinical doctors. More than 70% of patients with OC who were diagnosed with advanced stage disease(International Federation of Gynecology and Obstetrics[FIGO]stage IIIandIV) could not be cured by surgical resection and chemotherapy. Most women with advanced disease will develop many episodes of recurrent disease with progressively shorter disease-free intervals, although this treatment can be curativefor most patients with early stage disease. Thus, it is still necessary to search for better diagnostic biomarkers that accurately represent biological characteristicof OV,can be used to screen for early-stage OV.microRNAs are approximately 22-nucleotide noncoding RNAs, are highly conserved among a wide range of species, and are generally involved in posttranscriptional gene regulation. miRNAs negatively regulate genes expression by binding to the 3'-untranslated region (URT)of target mRNAs. Since miRNAs do not require perfectly complementary target sites ,onemiRNA could regulate hundreds of mRNAs and multiple miRNAs might regulate one mRNA.miRNAs are predicted to regulate approximately 60% of all human genes and are involved in processes such as development, differentiation, metabolism, proliferation, cell cycle, and the immune system.Exosome are enclosed in a lipid bilayer and are released from many types of cells, such as malignant cells, macrophages, endothelial cell and dendritic cell. Exosome derived from malignant tumors promote tumor proliferation, metastasis and angiogenesis by transferring their genetic information ,such as mRNAs and microRNAs, to surrounding cells or distant organs. In summary, we found the serum exosome microRNA could be potential biomarkers in the patients diagnosed with ovarian cancer.

PO-154

High Glucose Stimulates Tumorigenesis in Hepatocellular Carcinoma Cells Through AGER-Dependent O-GlcNAcylation of c-Jun

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Objective Epidemiologic studies suggest that hepatocellular carcinoma (HCC) has a strong relationship with diabetes. However, the underlying molecular mechanisms stillremain unclear.
Methods Cell viability, colony formation and caspase3/7 activity were assessed using MTT, soft agar and caspase 3/7 Glo assays, respectively. O-GlcNAcylated c-Jun was measured using co-immunoprecipitation (co-IP) combined with Western Blotting (WB). Immunofluorescence (IF), WB and Immunohistochemistry (IHC) were used to investigate the activity of c-Jun after glucose treatment. Luciferase reporter assay, chromatin immunoprecipitation (ChIP) and quantitative RT-PCR (qPCR) were used to investigate the mechanism how c-Jun interacted with the promoter of the target genes.
Results Here, we demonstrated that high glucose (HG), one of the main characteristics of diabetes, was capable of accelerating tumorigenesis in HCC cells. Advanced glycosylation end product-specific receptor (AGER) was identified as a stimulator during this process. Mechanistically, AGER activated a hexosamine biosynthetic pathway, leading to enhanced O-GlcNAcylation of target proteins. Notably, AGER was capable of increasing activity and stability of proto-oncoprotein c-Jun via O-GlcNAcylation of this protein at Ser73. Interestingly, c-Jun can conversely enhance AGER transcription. Thereby, a positive autoregulatory feedback loop that stimulates diabetic HCC was established. Finally, we found that AG490, an inhibitor of Janus kinase, has the ability to impair AGER expression and its functionsin HCC cells.
Conclusions In conclusion, AGER and its functions to stimulate O-GlcNAcylation are important during liver
tumorigenesis, when high blood glucose levels are inadequately controlled.

PO-155

Detection of serum ActivinA in patients with rheumatoid arthritis and its clinical significance

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Objective Objective to investigate the level of serum activin A (ActivinA, ACTA), rheumatoid factor (rheumatoid factor, RF), C reactive protein (C-reactive protein) and anti cyclic citrullinated peptide antibody in patients with rheumatoid arthritis

(Rheumatoid arthritis, RA). The role and clinical significance of the development of birth.

Methods Methods the serum levels of ACTA, CCP, RF and CRP in 65 patients with RA and 30 healthy controls were detected by enzyme linked immunosorbent assay (ELISA) and immuno turbidimetry, and the correlation between ACTA and RF, CRP and anti -CCP indexes was analyzed.

Results Results the serum levels of ACTA, CCP, RF and CRP in the RA group were significantly higher than those in the control group ($P<0.01$), and ACTA was positively correlated with RF, CRP and CCP ($r=0.4821$, $P<0.05$.

Conclusions Conclusion ACTA plays an important role in the development of RA disease. The combined detection of ACTA and RF, CRP and CCP is of great significance for the analysis, treatment and prognosis of RA disease.

PO-156

Reference intervals for serum progastrin-releasing peptide in healthy Chinese adults with electrochemiluminescence immunoassay

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Objective Reliable reference intervals for serum progastrin-releasing peptide (ProGRP) in healthy Chinese adults with electrochemiluminescence immunoassay (ECLIA) are still lacking in the Chinese population.The study aims to establish reference intervals for ProGRP with ECLIA in apparently healthy Chinese adults.

Methods A total of 384 apparently healthy individuals from six representative geographical regions in China were enrolled: 200 males and 184 females with a mean age of 43.4 ± 12.2 years, and an age range from 21 to 85 years. Serum ProGRP levels were analyzed on Cobas e601 automatic immunoassay analyzer with ECLIA. Reference intervals for serum ProGRP with ECLIA were determined following CLSI C28-A3 guidelines using a nonparametric method.

Results In an apparently healthy Chinese population, the reference intervals for serum ProGRP with ECLIA were $\leqslant$53.92 ng/L for adults aged 21-70 years and $\leqslant$75.69 ng/L for adults aged >70 years, respectively.

Conclusions The reference values for serum ProGRP with ECLIA in an apparently healthy Chinese population were established according to the CLSI C28-A3 document, providing a reference for the clinical work.

PO-157

Changes of serum homocysteine levels during pregnancy and the establishment of reference intervals in pregnant Chinese women

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Objective Reference intervals (RIs) of clinical laboratory indexes are important basis for interpretation of corresponding test results. While elevated homocysteine (HCY) level is a risk factor of some severe gestational diseases, HCY RIs for pregnant women have not been reported so far. The current use of HCY RIs established for general population in pregnant women may challenge clinicians' judgment. This study aims to investigate the changes of serum HCY levels during pregnancy and establish the RIs of serum HCY in healthy pregnant Chinese women to provide valuable data to clinicians and enable the provision of more appropriate therapy.

Methods 354 healthy pregnant Chinese women were randomly selected and divided into three groups according to gestational age: 114 in first trimester (1-13 week), 120 in second trimester (14-27 week) and 120 in third trimester (≥28 week). 120 healthy non-pregnant Chinese women were randomly selected as the non-pregnant control group. Serum HCY levels were determined on automatic biochemical analyzer with enzymatic cycling method. The RIs of serum HCY for healthy pregnant women were established using a nonparametric method.

Results the RIs of serum HCY for healthy pregnant women is 5.79-11.86 μmol/L in first and second trimester (combined) and 6.13-16.75 μmol/L in third trimester. Besides, the RIs of serum HCY for healthy non-pregnant women is 8.25-22.92 μmol/L.

Conclusions Rigorously according to CLSI C28-A3 guidelines, the authoritative document of RIs establishment, the RIs of serum HCY for healthy pregnant Chinese women were established, which will provide a valuable reference for clinical work and laboratory researches.

PO-158

Establishing reference intervals for ALT, AST, UR, Cr, and UA in apparently healthy Chinese adolescents

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Objective The current child-specific reference intervals (RIs) are inadequate or even unavailable for many analyses in China. Many of the RIs used in Chinese laboratories were derived from Chinese adult standards or from foreign studies. The aim of this study was to establish specific RIs for alanine aminotransferase (ALT), aspartate aminotransferase (AST), urea (UR), creatinine (Cr) and uric acid (UA) for apparently healthy Chinese adolescents.

Methods Overall, 1682 apparently healthy adolescents were enrolled. Serum ALT, AST, UR, Cr and UA were measured by an ARCHITECT C-8000 automated chemistry analyzer. The 2.5th and 97.5th percentile RIs were determined using non-parametric methods.
Results The established reference intervals for ALT, AST, UR, CR and UA were 7.5 - 42.8 U/L, 12.8 - 40.2 U/L, 3.12 - 6.38 mmol/L, 42.7 - 91.2 μmol/L, and 180.2 - 409.6 μmol/L in boys and 6.5 - 32.8 U/L, 10.4 - 32.5 U/L, 3.05 - 6.47 mmol/L, 40.2 - 88.8 μmol/L and 176.5 - 394.0 μmol/L in girls, respectively. The median and upper and lower limits for the RIs of ALT, AST, Cr and UA were higher in boys than they were in girls ($P < 0.05$).
Conclusions RIs based on adult criteria are not applicable to adolescents. It was necessary to establish specific, accurate and suitable RIs for Chinese adolescents. We have established reference intervals of ALT, AST, UR, Cr and UA that are defined specifically for Chinese adolescents and are appropriate for universal use among Chinese laboratories.

PO-159

Statistical Analysis of Blood Transfusion in 685 Cases of Cardiac Surgery.

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Objective To analyze the form of blood transfusion and the difference of donor blood transfusion volume in patients undergoing elective cardiac surgery, so as to provide some reference information for clinical work in the future.
Methods We collected the clinical blood transfusion data of a total of 685 cases of clear clinical diagnosis in patients undergoing cardiac surgery in our hospital from January 1, 2014 to March 31,2018, and analyzed the distribution of gender, age, blood type, disease type. The form of blood transfusion and the transfusion volume of allogeneic blood components were studied in retrospective statistical analysis.
Results Of 685 cases of patients undergoing cardiac surgery with intraoperative blood transfusion,601 cases with suspension red blood cells(RBC) transfusion ,171 cases only with RBC transfusion.The blood consumption of congenital heart disease patients was lower than that of other patients with simple allogeneic blood transfusion. There was a significant difference between congenital heart disease patients and other patients with simple allogeneic blood transfusion. Autotransfusion is used in 490 patients patients ,430 of them received combined transfusion(both allogeneic and autologous transfusion),another 60 patients only received autologous transfusion.Because of their younger age, congenital heart disease patients consume relatively less blood per capita;aortic dissection patients are in dangerous condition and consume more blood per capita.There was significant difference in age between patients with combined transfusion and those with RBC transfusion only or without RBC transfusion, but no significant difference in age between patients with combined transfusion and those with autologous transfusion only. For rheumatic heart valvular disease, autologous blood transfusion significantly saves the amount of RBC transfusion. For congenital heart disease patients who use less blood, autologous blood transfusion does not significantly reduce the amount of RBC transfusion.

Conclusions Most of cardiac surgery need extracorporeal circulation, with long operation time and more bleeding amount, so the use of blood is more. We should do well in the preoperative blood preparation work, and actively carry out blood conservation measures such as autologous blood transfusion.

PO-160

Decreased siglec-9 expression on Natural Killer cell subset associated with persistent HBV replication

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Objective Siglec-9 is a MHC-independent inhibitory receptor selectively expressed on $CD56^{dim}$ NK cells. Its role in infection diseases has not been investigated yet. Here we studied the association of NK Siglec-9 with chronic hepatitis B (CHB) infection.
Methods Flow cytometry evaluated the expression of Siglec-9 and other receptors on peripheral NK cells. Immunofluorescence staining was used to detect Siglec-9 ligands on liver biopsy tissues and cultured hepatocyte cell lines. Siglec-9 blocking assay was carried out and cytokine synthesis and CD107a degranulation was detected by flow cytometry.
Results Compared to healthy donors, CHB patients had decreased $Siglec\text{-}9^{+}$ NK cells, which reversely correlated with serum HBeAg and HBV DNA titer. Siglec-9 expression on NK cells from patients achieving SVR (sustained virological response) recovered to the level of normal donors. Neutralization of Siglec-9 restored cytokine synthesis and degranulation of NK cells from CHB patients. Immunofluorescence staining showed increased expression of Siglec-9 ligands in liver biopsy tissues from CHB patients and in hepatocyte cell lines infected with HBV or stimulated with inflammatory cytokines (IL-6 or TGF-β).
Conclusions These findings identify Siglec-9 as a negative regulator for NK cells contributing to HBV persistence and the intervention of Siglec-9 signaling might be of potentially translational significance.

PO-161

Evaluation for Analytical and Iron Deficiency Anemia Diagnosis Performance of Three Soluble Transferrin Receptor Measurement Systems: a Retrospective Study

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Objective To investigate the application value of soluble transferrin receptor (sTfR) kits based on three different methods for the diagnosis of iron deficiency anemia (IDA).

Methods The sTfR concentrations in two groups of patient specimens with high-level and low-level sTfR concentrations and in quality control materials were measured four times a day for five consecutive days to evaluate the precision of the three methods. We selected patients with IDA, anemia of chronic disease (ACD), or chronic diseases with iron deficiency anemia (CIDA) and apparently healthy subjects. sTfR kits based on three different methods were used to measure the serum sTfR concentrations in all subjects. The cut-off points for an IDA diagnosis using these three assays and their corresponding clinical sensitivities and specificities were calculated by receiver operating characteristic (ROC) analysis

Results For the diagnosis of IDA, the cut-off points of sTfR measured by the chemiluminescent, immunoturbidimetric, and immunonephelometric assays were 2.5, 55.0, and 2.5 mg/L, respectively. The corresponding sensitivities were 80.7%, 83.8%, and 73.2%, the specificities were 84.2%, 83.1%, and 91.5%, and area under the curve were 0.65, 0.67, and 0.65, respectively. The sTfR concentrations measured by the different methods were significantly higher in the IDA and CIDA groups than in the other two groups ($P<0.05$).

Conclusions The sTfR kits based on the three different measurement methods presented promising analytical performances and met the clinical requirements for sensitivity and specificity, but the different measurement methods had markedly different cut-off points for an IDA diagnosis.

PO-162

Clinical application of ALA test in rapid identification of Haemophilus

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Objective To evaluate the concordance of Aminolevulinic Acid test(ALA) and biochemical method in the identification of *Haemophilus*, and evaluate the value of clinical application with the results of β-lactamase.

Methods Information of cases with lower respiratory tract infection were collected and their specimens were cultured to screen for *Haemophilus influenzae*. The suspicious colonies were identified by VITEK2 compact and the ALA test was done at the same time and the concordance was evaluated. Chromogenic nitrocefin method was used to check the β-lactamase and the antibiotic minimal inhibitory concentration (MIC) were detected by ATB HAEMO strips. Antibiotics sensitive data were statistical analyzed by SPSS17.0

Results 3503 cases and their samples were collected and 329 strains of *Haemophilus.spp* were isolated at the rate of 9.4%(329/3503),most of them came from children under the age of 10(80.2%,264/329).The strains were identified by the two methods, 314 strains of *Haemophilus influenzae* and 11 strains of non-*Haemophilus influenzae* had consistent results, the concordance rate was
98.8 %(325/329). 54.5 %(171/314) of the *Haemophilus influenzae* produced β-lactamase but 22.4%(32/143) of the β-lactamase negative strains were BLNAR(Beta-Lactamase Negative Ampicillin Resistant. The antibiotics susceptibility difference between β-

lactamase positive and negative strains had no statistical significance except Ampicillin and Cefotaxime but that between the normal β-lactamase negative strains and BLNAR were very significant.

Conclusions *Haemophilus* are mainly isolated from children.ALA test has good concordance with traditional biochemical identification, it can be used as an effective complement to routine identification methods. Rapid report with β-lactamase result can be provided for clinical .It is worthy of promotion in basic medical institutions.

PO-163

Analytical Evaluation of a Latex-enhanced Immunoturbidimetric Assay for Measurement of Neutrophil Gelatinase-associated Lipocalin

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Objective Serum creatinine is not an sensitive or early biomarker of renal function after kidney transplantation. Neutrophil gelatinase-associated lipocalin (NGAL) can early detect acute kidney injury, and it is suggested to be an ideal biomarker to assessing renal function for patients. The aim of this study was to evaluate the analytical characterization a latex-enhanced immunoturbidimetric assay for measurement of NGAL.

Methods 124 healthy volunteers (65 males and 59 females) for routine physical examinations who met the inclusion criteria of reference interval study were recruited in this study, and they were divided into 5 age groups: 20y-29y, 30y-39y, 40y-49y, 50y-59y and ≥ 60y. Serum NGAL levels of these healthy volunteers were determined on AU5800 system (Beckman Coulter). We evaluated precision, linearity of the assay and determined reference intervals.

Results The percentage coefficients of variation (CV) of repeatability and within-laboratory precision were 7.52% and 8.35% at a mean concentration of 77.20 ng/mL, and 2.40% and 3.59% at a mean concentration of 1165.00 ng/mL. Linear range of the method is 52-5284 ng/mL. There was no significant different between males and females or among 5 age groups (20y-29y, 30y-39y, 40y-49y, 50y-59y and ≥ 60y) in NGAL values. The reference intervals were 52.05 ng/mL - 160.90 ng/mL.

Conclusions This study provided supports that the assay is a reliable and robust test for measuring serum NGAL.

PO-164

Similar clinical phenotypes but different mutations in 2 cases of Dent disease and 1 case of Fanconi syndrome: a case report

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Objective Dent disease is a rare X-linked recessive renal tubular disorder that affects patients in childhood or early adult life, caused by mutations in CLCN5 (Dent disease 1) or OCRL (Dent disease 2) genes, respectively. It presents mainly with low-molecular-weight proteinuria, hypercalciuria, nephrocalcinosis and progressive renal failure.

Methods The clinical and laboratory data of 3 boys with Dent disease were analyzed retrospectively. Genetic testing of these cases was carried out. Genomic DNA was extracted from the peripheral blood of the patients. The expected segregation of putative mutations was confirmed in families, whenever possible, and their absence was confirmed in SNPs databases of common benign variants.

Results All of 3 cases were boys. Proteinuria was presented as the first impression in Case 1. The first impression of Case 2 and 3 was Fanconi syndrome. All 3 boys presented with low-molecular weight proteinuria (LMWP) and hypercalciuria, including 1 case with hematuria and kidney stones (Case 3). Mutation of the CLCN5 gene transmitted from his mother was revealed in Case 1 which was diagnosed as Dent disease 1. Case 2 carried the heterozygous mutation in exon 3-4 in the OCRL gene NM_000276.3, and this boy was diagnosed as Dent disease 2. Genetic analysis of Case 3 showed a p.R63W mutation in the HNF4A gene (c.187C>Tchr20-43034835*1p.R63W) that is responsible for Fanconi syndrome.

Conclusions Urine protein electrophoresis should be performed for patients with proteinuria. Dent disease should be taken into consideration when the patients with Fanconi syndrome have hypercalciuria. Genetic analyses are needed for a definite clinical diagnosis.

PO-165

Analysis on predictive value of neutrophil to lymphocyte ratio in influenza A virus and influenza B virus infection

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Objective To investigate the predictive value of neutrophil to lymphocyte ratio(NLR) in influenza A virus and influenza B virus infection

Methods 14828 patients were suspected influenza virus infection,including 3425 patients were influenza A,326 patients were influenza B,7 patients were positve both influenza A and influenza B virus simultaneously,150 individuals healthy control were selected in the first affiliated hospital of xi'an jiaotong university from Jan 2018 to Feb 2019,comparing the WBC, NC, LC, NLR, CRP and PLT in the three groups, analyzing the difference,and calculating the AUC of WBC, NC, LC, NLR in influenza A and influenza B virus infections.

Results Among the 14828 samples, 23.10% was positive for influenza A virus,2.2% was positive for influenza B virus. WBC,NC, NLR were higher in Flu A and Flu B than healthy controls,LC was lower than that of healthy controls, the difference of NC, LC ,NLR were statistically significant($p < 0.05$) , there was no statistically significant difference of WBC in Flu B and healthy controls($p > 0.05$),CRP was higher in Flu A than Flu B, there was no statistically significant difference of PLT in Flu A , Flu B and healthy controls($p > 0.05$). WBC, NC, LC, NLR, CRP, PLT were significantly different between groups A and B, and between groups A and C ($p < 0.05$),WBC, NC, LC and NLR of group B and group C showed no statistically significance difference($p > 0.05$), The AUC value of NLR,LC for predicting Flu A was 0.76,0.75.The cutoff value of NLR is 3.12(SEN57.13%,SEP95.33%), the cutoff value of LC is 1.22(SEN53.33%,SEP94.00%). The AUC value of NLR,LC for predicting Flu B was 0.68,0.72.The cutoff value of NLR is 3.12(SEN47.24%,SEP 95.33%), the cutoff value of LC is 1.34 (SEN54.60%,SEP87.33%)

Conclusions NLR was expected to apply as a new biomarker for independently predicting the influenza virus infections.The increasion of NLR plays a significant role in predicting the influenza virus though can not reflect the immune balance and inflammatory status,it provide a guide of prognostic management of influenza virus infections.

PO-166

Rapid Diagnosis of Hepatocellular Carcinoma Using Fuc-Hp

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Objective Fucosylated glycans play a critical role in cell biology processes during the occurrence and development of tumor, such as cell signal transduction, cellular differentiation, ligand-receptor interactions and metastasis formation. In our previous study, we detected and confirmed that various types of fucosylated structure on haptoglobin (Fuc-Hp) were increased significantly in serum from hepatocellular carcinoma (HCC) patients by lectin blot, high performance liquid chromatography, as well as mass spectrometer.

Methods In this study, we aimed to develop a convenient and sensitive AAL@Magbeads-based Hp ELISA assay to rapid detect Fuc-Hp in 270 serum samples from HCC patients and

normal controls, which based on the differential binding of Hp to AAL@Magbeads. The system contained two steps, AAL@Magbeads capture and polyclonal antibody detection.
Results Fuc-Hp levels was significant increased in HCC compared to healthy controls. Additional, Fuc-Hp exhibited an area under the ROC curve (AUC) of 0.818 with sensitivity of 72.59% and specificity of 79.26% as well as accuracy of 75.93% in distinguishing HCC patients from healthy controls. For 40 AFP-negative HCC (AFP$^-$HCC) cases and 135 normal volunteers, AUC of Fuc-Hp was 0.892 with sensitivity of 80%, specificity of 81.48% and accuracy of 81.14%.
Conclusions The results of present study demonstrated that AAL@Magbeads-based Hp ELISA assay could efficiently determine Fuc-Hp, which may serve as a promising glycobiomarker in the diagnosis of HCC, including AFP$^-$HCC patients.

PO-167

Cyr61 decreases Cytarabine chemosensitivity in acute lymphoblastic leukemia cells via NF-κB pathway activation

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Objective To investigate the role of Cyr61 in regulating ALL cell chemosensitivity to Cytosine arabinoside (Ara-C)
Methods Cyr61 levels in plasma and bone marrow (BM) from ALL patients were determined by enzyme-linked immunosorbent assay. The expression of Cyr61 in Jurkat (T ALL cell lines), Nalm-6 (B ALL cell lines), and bone marrow mononuclear cells from ALL patients were measured by real-time PCR and western blotting. Cell apoptosis was analyzed using an Annexin V-FITC and PI Double-Staining Kit. Activation of signal transduction pathways was determined by western blotting. Bcl-2 expression was analyzed by real-time PCR and western blotting.
Results Cyr61 was increased in plasma, bone marrow (BM), and bone marrow mononuclear cells from ALL patients as compared with samples from normal controls. Furthermore, we observed that increased Cyr61 effectively decreased Ara-C-induced apoptosis of ALL cells, and its function was blocked by the use of the anti-Cyr61 monoclonal antibody 093G9. Furthermore, Cyr61 increased the level of Bcl-2 in Ara-C-treated ALL cells. Mechanistically, it was shown that Cyr61 affected ALL cell resistance to Ara-C partially via the NF-κB pathway.
Conclusions Cyr61 is a secreted ECM protein, which is not only important for cell proliferation, survival, and migration, but also drug resistance in various tumors. It was recently reported that the level of Cyr61 is increased in BM supernatants from patients with ALL, and this change could promote ALL cell survival. Previous studies showed that BM stromal cells are the major source of Cyr61. Our current study showed that Cyr61 was overexpressed not only in the BMMNCs from patients with ALL, but also two ALL cell lines. It is speculated that, in addition to stromal cells, ALL cells could also be one of the sources generating Cyr61 in the bone marrow in an autocrine manner.

Although multi-agent chemotherapy regimens are highly effective for patients with ALL, some responding patients eventually became refractory to initial therapy. Resistance to chemotherapeutic agents is a significant clinical problem for the successful treatment of leukemia. More studies have shown that the BM microenvironment contributes to leukemia cell resistance to chemotherapeutic agents. However, no study has yet explored the role of Cyr61 in ALL drug resistance, to the best of our knowledge. In the present study, the results showed that Cyr61 was highly expressed in BMMNCs from patients with ALL, and elevated Cyr61 levels conferred ALL cells with resistance to Ara-C-induced apoptosis, partially via the activation of the NF-κB pathway. The present study indicates, for the first time, that Cyr61 may act as a chemoprotective factor for ALL cells, and that targeting Cyr61 directly or its relevant effectors' pathways might improve the clinical responses of patients undergoing treatment for ALL.

PO-168

A Novel double Heterzygous Mutations HBB c.(-78A>G/-81A>C) : Clinical Diagnosis And Gene Analysis

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Objective To identity a novel double heterzygous mutations of β-thalassemia by direct DNA sequencing and polymerase chain reaction (PCR)reverse dot-blot hybridization in a Chinese famliy.

Methods Blood routine examination was finished by Sysmex XN-20 antomatic Hematology Analyzer (Sysmex Corporation, Kobe, Japan); Quantification of Hbs was performed on the capillarys electrophoresis divice (Sebia, Lisses, France).Then the thalassemia genetypes were screened by reverse dot blot(RDB).The mutation of the double heterzygous mutations were identified by the direct DNA sequencing.

Results Hematological indexs of this family show that they all suffered microcytic hypochromic anemia.And from the results of direct DNA sequencing of this family,the children were both double Heterzygous Mutations at TATA box -28/-31 (HBB: c. -78A>G/-81A>C) on the β-Globin Gene.The father carried single mutation at TATA box -28(HBB: c .-78A>G),while the mother was the TATA box -31(HBB: c.-81A>C).

Conclusions A Novel double Heterzygous Mutations at TATA box -28/-31 (HBB: c. -78A>G/-81A>C) on the β-Globin Gene was identified in China.This will enrich the β-thalassemia gene mutation spectrum in Chinese population.

PO-169

Association of serum total cholesterol with pegylated interferon-α treatment in HBeAg-positive chronic hepatitis B patients

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Objective Recent studies suggest that serum lipids are associated with pegylated interferon-alpha (PegIFNα) treatment response in chronic hepatitis C patients. However, the role of serum lipids in influencing the outcome of HBV treatment is not well understood. This study aims to investigate the association of serum lipids with the response to interferon-alpha treatment for chronic hepatitis B (CHB) patients.
Methods We dynamically measured 11 clinical serum lipid parameters of 119 HBeAg-positive CHB patients, including 53 patients who achieved sustained response (SR) and 66 patients who achieved nonresponse (NR) induced by PegIFNα treatment for 48 weeks.
Results The dynamic analysis showed that the baseline serum total cholesterol (TCHO) level was higher in the NR group than that in the SR group (P = 0.004). Moreover, the correlation analysis demonstrated a significant positive correlation between TCHO and HBsAg at baseline (P = 0.009). In addition, CHB patients with the high baseline TCHO levels exhibited higher HBV DNA, HBsAg, HBeAg and HBeAb levels during early treatment periods (weeks 0, 4, 12 and 24) than those with the low TCHO levels. Furthermore, the logistic regression analysis identified that baseline serum TCHO was a risk factor of NR achievement (OR = 4.94, P = 0.047).
Conclusions Our results indicated that serum TCHO was associated with PegIFNα therapeutic response in HBeAg-positive CHB patients which suggested that serum TCHO could be useful as an auxiliary clinical factor to predict poor efficacy of PegIFNα therapy.

PO-170

Real-time PCR for quantitative detection of mitochondrial DNA from peripheral blood mononuclear cell in patients with HBV-related hepatocellular carcinoma

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Objective The alteration of mitochondrial DNA (mtDNA) content could affect the expression of genes which causes many tumor diseases. However, the association between mtDNA content in peripheral blood mononuclear cell (PBMC) and hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) remains undetermined. First of all, establishing a reliable assay to detect mtDNA content is of great clinical significance.

Methods The method of real-time quantitative polymerase chain reaction (RT-qPCR) with SYBR Green I was established to evaluate mtDNA content in PBMC of healthy controls (n=23) and non-surgical HBV-related HCC cases (n=46). Receiver operating characteristic (ROC) curve analysis was carried out to assess the clinical significance of mtDNA content for diagnosing HCC.
Results Linear range of the assay was between 1×10^{10} copies/μl and 1×10^{3} copies/μl. Sensitivity was 800 copies/μl. Besides, HCC cases had a significantly lower mtDNA content than healthy controls (378.55[58.20－784.85] vs 715.48[292.00－1280.00]; P<0.001). When 489.90 copies/μl was set as the cut-off point, the sensitivity and specificity of mtDNA content to diagnose HCC were 82.6% and 71.7%, respectively.
Conclusions A simple, cost-effective, highly sensitive and specific method to detect mtDNA content is established. This method can be applied to clinical laboratory for detecting mtDNA content. Moreover, our study provides the first epidemiological evidence that mtDNA content in PBMC is significantly associated with HCC. MtDNA content in PBMC could serve as a novel clinical diagnostic indicator for HCC which may need more researches to validate.

PO-171

Genetic analysis of four pedigrees with hereditary coagulation factor XI (FXI) deficiency and one novel mutation identification

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Objective we analyzed the phenotype and genotype in four pedigrees with hereditary coagulation factor XI (FXI) deficiency from Chaozhou area in the southern Chian, and further investigate the molecular mechanisms of FXI deficiency.
Methods The prothrombin time (PT), activated partial thromboplastin time (APTT), FXI activity (FXI:C) and FXI antigen (FXI:Ag) were tested for phenotypic diagnosis in the proband and families. All the exons and exon-intron boundaries of FXI gene of proband were analyzed by PCR and direct sequencing. The family members were tested for the mutant site of proband.
Results A markedly prolonged APTT and FXI:C, FXI:Ag decreased significantly in all the proband. Five mutations were detected, including three nonsense, c.841C>T(p.Gln263X, c.1107C>A(p.Tyr351X) and c.1033A>T(p.Lys327X) respectively, one frameshift mutation c.1325 delT (p.Leu424 CysfsX8).
Conclusions c.1033A > T (p. Lys 327X) was firstly reported worldwide which lead to a premature stop codon at amino acid position 327, it may be have an influence on protein characteristics and cause the corresponding disease.

PO-172

Assessing clinical evaluation of the FilmArray BCID panel for the rapid detection of pathogens from bloodstream infections

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Objective Traditional method as the gold standard, by comparing with the conventional culture -based methods, to analyze the sensitivity and specificity and consistency of the FilmArray BCID panel ,at same time,to evaluate whether FilmArray BCID panel can provide a faster and more accurate diagnosis of bloodstream infections in the clinic.
Methods Collecting 170 positive blood culture bottles from hospital and tested them by laboratory traditional culture method and FilmArray BCID detection system. Comparing the detection results and turn-around time.
Results Collecting 170 positive blood culture bottles from hospital and tested them by laboratory traditional culture method and FilmArray BCID detection system. Comparing the detection results and turn-around time.
Conclusions The FilmArray BCID panel has high sensitivity and specificity for detection of gram-negative bacteria and gram-positive bacteria. Compared with conventional culture -based methods, it is more sensitive for polymicrobial culture blood cultures. Ti can reduce the whole blood culture turnover time of the laboratory and has high clinical value for the diagnosis of bloodstream infection.

PO-173

Development and Evaluation of a Real-Time RT-PCR Assay for Detection of a Novel Avian Influenza A (H5N6) Virus

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Objective As of Aug 25, 2017, 17 incidences of human infection and 6 deaths due to the novel H5N6 virus have been reported in China. Genetic analysis of the viral genome revealed that this reassortant virus is highly pathogenic to poultry, and the virus has a risk of transmission to humans. Accordingly, the development of a rapid, sensitive, and specific molecular diagnostic assay is critical for public health.
Methods In this study, a real-time reverse transcription-PCR (RT-PCR) assay was developed to specifically detect the novel H5N6 virus, with primer pairs targeting the hemagglutinin and neuraminidase gene sequences of this virus. RNA was extracted from throat swab specimens from patients with influenza-like illness (ILIs), and environmental samples were collected from live poultry markets (LPMs) for H5N6 virus detection by real-time RT-PCR.
Results The method was demonstrated to enable specific detection of the avian H5N6 virus, with no cross-reactivity with seasonal influenza viruses (H1N1, H1N1 pdm09,

H3N2 or B), H5N1, H7N9, H9N2 viruses, and other human respiratory viruses. The detection limit of the assay was 1.0×10^1 copies per reaction for N6 and 1.0×10^2 copies per reaction for H5 assays, using ten-fold serially diluted in-vitro transcribed viral RNA.

Conclusions Therefore, the established real-time RT-PCR assay provided a rapid, sensitive, specific, and reliable method for the detection of the avian H5N6 virus in clinical and environmental samples, with potential utility in clinical diagnostics and influenza surveillance.

PO-174

Study on characteristics of peritoneal macrophages in mouse acute myeloid leukemia model

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Objective Macrophages (Mϕ) provide immune function for almost all the organs and tissues in the body. In different tissue microenvironment educated macrophages were called tissue-specific macrophages. Moreover, tissue-specific macrophages show heterogeneity in different organs and tissues, and even in the same tissue this heterogeneity exists. The same tissue macrophages are also heterogeneous in different pathologic microenvironments. The phenotype of educated resident macrophages varies greatly, depending on the microenvironment. So far, there have been few reports about the heterogeneity of peritoneal macrophages but no studies about characteristics of peritoneal resident macrophages in leukemia. Therefore, in the present study, characteristics of peritoneal macrophages in mouse acute myeloid leukemia were explored

Methods we explored characteristics of peritoneal macrophages in mouse acute myeloid leukemia model and compared with Mϕ in LPS-induced acute inflammation. In this section, normal mice models, MLL-AF9 induced acute myeloid leukemia mice models and LPS-induced inflammation mice models were established. Three kinds of LPM in these three models were obtained by cell sorting, which were referred to as normal LPM, AML-associated LPM (AML-LPM) and LPS-induced inflammatory LPM (LPS-LPM), respectively. The dynamics, phenotypes, gene expressions and functions of these three LPM were assessed.

Results The dynamics of AML-LPM was similar as that of LPS-LPM, significantly different from that of normal LPM. Both the proportion and absolute number of LPS-LPM in $F4/80^+$ cells decreased following an increase. The reduction of LPS-LPM in the early phase may be associated with inflammatory macrophage disappearance reaction (MDR). Gene expression profiles of LPM in these three microenvironments (normal, inflammatory and leukemia) were comparatively analyzed with RNA sequencing (RNA-Seq). Results showed that the AML-LPM exhibited a similar expression profile as LPS-LPM. Compared to normal LPM, found that AML-LPM and LPS-LPM were clustered by Hierarchical clustering analysis, and there were 669 up-regulated genes and 295 down-regulated genes commonly shared by AML-LPM and LPS-LPM; expressions of only 23 genes showed an opposite alteration. However, GO-analysis and KEGG pathway analysis revealed that these two

cells were significantly different. The differentially expressed genes in AML-LPM and LPS-LPM were enriched at binding in molecular function, but there were many significant differences in cell signal pathway. At the same time, RNA-Seq was used to compare the expression of AML-LPM and LPS-LPM. AML-LPM and LPS-LPM were significantly different in binding and presentation of antigens and killing-related functions, which was possibly caused by microenvironment differences. RT-PCR analysis verified the results of RNA-Seq. By comparison of gene iNOS and intracellular NO content associated with macrophage killing, there were significantly different among the three LPM, with LPS-LPM having highest levels of iNOS expression and intracellular nitrogen activity. The killing function of macrophages which were educated in inflammation microenvironment was significantly improved. The phagocytosis of these three LPM was different as well. The FITC-GFP microspheres phagocytized in AML-LPM were mainly FITC-GFP^{medium}, while microspheres in LPS-LPM and normal LPM are primarily FITC-GFP^{low} and FITC-GFP^{high}.

Conclusions The results revealed that the leukemia microenvironment was closely related with inflammation, suggesting that leukemia might have characteristics of chronic inflammation. Additionally, we demonstrated that leukemia and inflammatory microenvironment which educated macrophages had the same point and different points, which could provide theoretical basis for studying the development of leukemia and macrophage-associated cell therapy from the perspective of inflammatory response.

PO-175

Dysregulation of host cellular genes targeted by HPV integration contributes to HPV related cervical carcinogenesis

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Objective Integration of HPV viral DNA into the human genome has been postulated as an important etiological event during cervical carcinogenesis. Several recent reports suggested a possible role for such integration targeted cellular genes (ITGs) in cervical carcinogenesis.

Methods HPV integration sites were came from NCBI Pubmed database. GO and KEGG pathway were used for analyse enriched terms of ITGs. Real-time PCR were used for detecting expression of genes. Cell cycle were detected by Flow cytometry.

Results A comprehensive analysis of HPV integration events was undertaken using data collected from 14 publications with 499 integration loci on human chromosomes included. It revealed that HPV DNA preferred to integrate into intragenic regions and gene-dense regions of human chromosomes. Intriguingly, the host cellular genes nearby the integration sites were found to be more transcriptionally active compared with control. Furthermore, analysis of the integration sites in the human genome revealed that there were several integration hotspots although all chromosomes were represented. The ITGs

identified were found to be enriched in tumor-related terms and pathways using gene ontology (GO) and KEGG analysis. In line with this, 3 of 6 ITGs tested were found aberrantly expressed in cervical cancer tissues. Among them, *MPPED2* was demonstrated for the first time could induce HeLa cell and SiHa cell G1/S transition block and cell proliferation retardation. Moreover, 'knocking out' the integrated HPV fragment in HeLa cell line decreased expression of *MYC* located ~500kb downstream of the integration site, which provided the first experimental evidence supporting the hypothesis that integrated HPV fragment influence *MYC* expression via long distance chromatin interaction.

Conclusions Overall the results of this comprehensive analysis implicated that dysregulation of ITGs caused by viral integration as possibly having an etiological involvement in cervical carcinogenesis.

PO-176

Distribution features and functions of γδT cells infiltrated in ovarian cancer microenvironment

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Objective The role of γδT cells, an innate-like lymphocyte with unrestrained MHC, in various malignancies has been vigorously addressed recently. However, there is limited research regarding γδT cells in ovarian cancer (OC) patients.

Methods Here, we investigated the distribution patterns of γδT cells and main subsets in peripheral blood, and tumor tissues among OC patients, benign ovarian tumor (BOT) patients, age-matched healthy controls (HC) by flow cytometry, as well as the expression levels of IFN-γ and IL-17A secreted from γδT cells. Moreover, immunohistochemical staining was utilized to detect the numbers of γδT cells and main subsets in different types of ovarian tumor tissues. Additionally, we also investigated the chemotaxis effects, along with cytotoxicity activity and proliferative assay of γδT cells in vitro.

Results We found that the percentages of γδT cells and Vδ1 T cells were significantly higher in OC tissues than BOT tissues and normal (N) ovarian tissues, while have no obviously differences in peripheral blood. Meanwhile, higher numbers of γδT cells and Vδ1 T cells were described in OC tissues by immunohistochemistry, which were positively related to advanced clinicopathological features of OC patients. Further, the levels of IFN-γ secreted by γδT cells were relatively lower, while IL-17A was in a high level both in peripheral blood and tissues of OC patients. Chemotaxis assay revealed that supernatants derived from OC tissues, possessed stronger capacity of attracting and recruiting γδT cells. However, γδT cells sorted from OC tissues showed the weakened cytotoxic activity against ovarian cancer cells, and γδT cells cocultured with OC tissues supernatants could effectively inhibit the proliferative activity of Naïve $CD4^+$ T cells.

Conclusions These data suggested that γδT cells might be key players in OC progression and have the potential for treatment or prognosis prediction.

PO-177

Predictive factors of recurrence after radiofrequency catheter ablation in patients with non-valvular atrial fibrillation

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Objective To explore the predictive factors of recurrence in patients with non-valvular atrial fibrillation after catheter radiofrequency ablation.
Methods From January 2015 to June 2017, 251 patients with non-valvular atrial fibrillation who underwent catheter radiofrequency ablation of atrial fibrillation in our hospital were selected. All the selected patients met the 2014 AHA/ACC/HRS guidelines. Preoperative data (sex, age, history of atrial fibrillation, basic complications, clinical biochemical indicators, etc.) were collected. Outpatient follow-up (chief complaint, electrocardiogram, 24-hour ambulatory electrocardiogram, etc.) was conducted 3 months, 6 months and 12 months after operation. 251 patients with atrial fibrillation were divided into recurrence group (n=82) and non-recurrence group (n=169) according to clinical symptoms and electrocardiogram results. SPSS19.0 statistical software was used for data analysis.
Results During the 12-month follow-up period, 82 patients had atrial fibrillation recurrence, 169 patients maintained sinus rhythm, the recurrence rate was 32.6%. Univariate analysis shows that the proportion of persistent atrial fibrillation (41% VS 21%, $P < 0.05$), Early recurrence rate (47% VS 27%, $P < 0.05$), prevalence of hypertension (65% VS 39%, $P < 0.05$), and the hs-CRP level in recurrence group was significantly higher than that in non-recurrence group 3-6 months after catheter radiofrequency ablation ($P < 0.05$).
Conclusions The results of this study suggest that the recurrence rate of atrial fibrillation after radiofrequency ablation of non-valvular atrial fibrillation is about 32.6%. The comparison between the recurrence group and the non-recurrence group showed that there were significant differences in the type of atrial fibrillation, early recurrence, hypertension, and hs-CRP levels between the two groups, which could predict the recurrence of atrial fibrillation after catheter radiofrequency ablation.

PO-178

Modified Glasgow Prognostic Score,Neutrophil/lymphocyte, platelet/lymphocyte and C-reactive protein/albumin ratios in different stages of Coal Workers' Pneumoconiosis

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Objective To evaluate modified glasgow prognostic score(mGPS), C-reactive protein/albumin ratio(CAR),neutrophil/lymphocyte ratio (NLR) and platelet/lymphocyte ratio (PLR) for predicting the prognosis of patients with Coal Workers' Pneumoconiosis(CWP).
Methods 154 cases CWP and 148 cases of silicosis patients were collected in Hunan Prevention and Treatment Center for Occupational Diseases (HPTCOD) from January 2018 to December 2018. The value of PLR,CAR,NLR and mGPS for prediting the prognosis of CWP were evaluated by ROC and the relationship between the PLR, NLR and mGPS of CWP patients were analyzed;
Results CWP patients exhibited higher serum leukocyte(WBC),neutrophils(N),platelets(PLT),erythrocyte sedimentation rate (ESR), PLR,CAR,NLR ,mGPS and lower lymphocytes(L) concentrations compared with the control groups P<0.05). The silicosis patients present higher PLR, CAR, NLR, mGPS than CWP patients(P<0.05).The areas under the ROC curves of NLR and PLR were 0.864 (95% CI. 0.805 -0.923) (P = 0.000) and 0.698 (95% CI. 0.607-0.788) (P = 0.000).
Conclusions PLR,NLR and mGPS can be used as indicators of inflammatory state and severity in clinical prognosis of patients with CWP. NLR is more sensitive to assessing disease activity compared with PLR.

PO-179

Platelets promote invasion and induce epithelial to mesenchymal transition in ovarian cancer cells by TGF-β signaling pathway

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Objective Ovarian cancer is the leading cause of death among all gynecological malignancies. The high mortality is partly due to metastasis. Studies have shown that platelets play an important role in cancer metastasis by promoting epithelial-mesenchymal transition (EMT). EMT is mainly induced by the transforming growth factor-beta (TGF-β). Platelets could secret TGF-β, and promote EMT in murine colon and breast cancer cells through the TGF-β pathway. However, it is unclear whether the

TGF-β pathway is activated by platelets in human ovarian cancer cells. Therefore, we want to test whether platelets initiated EMT and invasion in ovarian cancer cells via the TGF-β signaling pathway and to examine whether TGF-β type I receptor (TβR I) inhibitor A83-01 could abolish the pro-metastatic effects of platelets on ovarian cancer cells.

Methods Blood samples were collected in 69 patients with ovarian cancer, 16 patients with benign ovarian tumor and 64 healthy donors. Clinico-pathological data of the patients were collected from their electronic medical files. Serum TGF-β levels were measured by commercial ELISA kit. SK-OV-3 and OVCAR-3 ovarian cancer cells were treated with platelets, and EMT was assessed by measuring the levels of EMT-related markers by quantitative real-time PCR (qPCR) and Western blotting. Transwell assays were used to analyze the invasive capacity of the cells. The activation of TGF-β/Smad pathway was examined using ELISA and Western blotting. TβR I inhibitor A83-01 was used to confirm the role of TGF-β/Smad pathway in platelet-induced EMT and invasion of ovarian cancer cells *in vitro* and *in vivo*.

Results (1) Ovarian cancer patients with platelet counts of more than 350×10^9/L had a higher incidence of metastasis to the omentumand mesentery. Analysis of the mesenchymal markers and transcription factors involved in EMT revealed that snail family transcriptional repressor-1 (*SNAI1*), vimentin (*VIM*), neural cadherin (*N-cadherin*), fibronectin-1 (*FN1*) and matrix metalloproteinase-2 (*MMP2*) were significantly up-regulated in platelet-treated cell lines, while the epithelial marker epithelial cadherin *(E-cadherin)* was significantly down-regulated in SK-OV-3 cells co-cultured with platelets. Western blot analysis revealed reduced E-cadherin, and increased N-cadherin and MMP-2 protein levels in platelet-treated SK-OV-3 and OVCAR-3 cells. Co-culture with platelets markedly increased the invasive properties of SK-OV-3 and OVCAR-3 cells by 3.1-fold and 3.7-fold respectively.

(2) Significantly higher TGF-β levels were seen in patients with increased platelet counts compared to those with normal platelet counts. Active TGF-β levels in the ovarian cancer cells and platelets co-culture conditioned medium was markedly increased compared to the medium from tumor cell cultures alone. SK-OV-3 and OVCAR-3 cells treated with platelets also showed increased phosphorylation of the TGF-β signaling effector Smad2 compared to the untreated cells, indicating that the platelets activated the TGF-β/Smad pathway in ovarian cancer cells.

(3) Upon addition of the TβR I inhibitor A83-01 to the platelets-treated cells, the EMT-like alterations were inhibited at the mRNA level. A83-01 treatment also restored the expression of E-cadherin and repressed that of N-cadherin and MMP2- in both cell lines at the protein level. Concordantly, exposure of the platelets-treated SK-OV-3 and OVCAR-3 cells to A83-01 resulted in a 2.6- and 2.3-fold reduction respectively in their invasive abilities compared to those incubated with platelets alone. A83-01 could also reverse the EMT-like alterations and inhibited platelet-induced invasion *in* vivo.

Conclusions Higher platelet counts were significantly associated with a higher incidence of intraperitoneal dissemination and may lead to elevated TGF-β levels in ovarian cancer patients. Platelets induced EMT and promoted invasive ability of ovarian cancer cells by activating the TGF-β pathway, and the TβR I inhibitor A83-01 inhibited the platelet-related EMT and invasiveness. These findings suggest that TβR I inhibition may be an effective anti-metastatic therapy in ovarian cancer.

PO-180

Serum Long Noncoding RNAs Act as Potential Novel Diagnosis and Prognosis Biomarkers in Non-small Cell Lung Cancer

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Objective Lung cancer is the first leading cause of cancer deaths worldwide. Non-small cell lung cancer (NSCLC) is the most common type of lung cancer. Increasing evidence shows that long non-coding RNAs (lncRNAs) are capable of modulating tumor initiation, proliferation and metastasis. In the present study, we aimed to evaluate whether circulating lncRNAs could be used as biomarkers for diagnosis and prognosis of NSCLC.
Methods Expression profiles of 14 lncRNAs selected from other studies were validated in 20 pairs of tissues by quantitative real-time PCR (qRT-PCR), and the dysregulated lncRNAs thus identified were further validated in serum samples from two independent cohorts along with three tumor makers(CEA, CYFRA21-1 and SCCA). Receiver-operating characteristic (ROC) analysis was utilized to estimate the diagnostic efficiency of the candidate lncRNAs and tumor markers. Importantly, we observed an association between lncRNA expression and overall survival (OS) rate of NSCLC.
Results SOX2OT and ANRIL were shown to be obviously upregulated in NSCLC samples. A panel composed of two lncRNAs (SOX2OT, ANRIL) and three traditional tumor markers (CEA, CYFRA21-1, SCC) was built in training set. The AUC of this panel was superior to any biomarker alone. This result appeared in validation set yet. Intriguingly, the low expression of SOX2OT and ANRIL correlated with high survival rate. SOX2OT could be the independent prediction factor.
Conclusions our study demonstrated that the newly developed diagnostic panel consisting of SOX2OT, ANRIL, CEA, CYFRA21-1 and SCCA could be valuable in NSCLC diagnosis. LncRNAs SOX2OT and ANRIL might be ideal biomarkers for NSCLC prognosis.

PO-181

Influence of Common interference factors and different Pretreatment methods on High risk HPV Detection Reagent of Shengxiang

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Objective To study the influence of common interference factors and different pretreatment methods on the detection ability of high risk human papillomavirus (HPV) kit of Hunan Shengxiang Biotechnology Co., Ltd
Methods The effect of chlamydia trachomatis and hemoglobin on HPV16/18 detection was analyzed by adding different concentrations of chlamydia trachomatis nucleic acid and

hemoglobin into the samples. Four different methods were used to pretreat the HPV16/18 samples with blood and the degree of hemoglobin removal and the effect on the results were analyzed.

Results High concentration trachoma Chlamydia nucleic acid (1.0E8 IU/mL) and high concentration hemoglobin (3g/L) had no effect on the HPV16/18 detection ability of the kit. Two of the four different pretreatment methods for HPV16/18 samples with blood could not significantly remove hemoglobin from the samples (observed by naked eyes), but had no effect on the HPV16/18 detection. The other two methods could significantly remove hemoglobin from the samples (observed by naked eyes), but significantly delayed the threshold cycle (CT) ($P < 0.05$).

Conclusions The kit achieves the anti-interference ability to chlamydia trachomatis and hemoglobin as stated in its instructions for the detection of HPV16/18. For the samples with blood, the kit can reach a satisfied result without special hemoglobin removal, which shows that the reagent has a certain anti-interference ability to hemoglobin.

PO-182

A diagnostic model combined with multiple laboratory indexes for ovarian cancer based on integrated machine learning

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Objective To construct a diagnostic model based on machine learning algorithm consisting of characteristic reduction and artificial neural network classification, so as to develop the auxiliary diagnostic value of routine hematological parameters for ovarian cancer.

Methods We selected 185 patients with ovarian cancer as the case group, and integrated 3 control groups as a single whole control group, which was comprised of 138 patients with other malignant gynecological tumors and 339 patients with benign gynecological diseases, as well as 92 healthy volunteers. A total of 28 tested indexes consisting of 6 categories, such as tumor markers, blood cell analysis and sex hormones, were obtained through the electronic medical record mining system. We adopted the analysis of principal components to extract the characteristics, and then established the diagnosis model using the low-dimensional feature set as input layer variable of the neural network accompanied by optimization of genetic algorithm aiming to improve the training speed and classification accuracy.

Results The top three principal components with the largest eigenvalue were selected to represent the information of the initial 28 indicators. The study population was divided into two groups by stratified random sampling, one thirds (62 ovarian cancer samples and 191 control samples) of which were defined as the training group and two third (123 ovarian cancer samples and 378 control samples) as the test group. The model was used to make a blind prediction for the test group using the above training group. The area under the ROC curve of the diagnosis model based on machine learning

was 0.948. The sensitivity and specificity were 91.9% and 86.9%, respectively. The diagnostic efficiency of the model was significantly superior to that of the traditional CA125 detection. Further validation indicated the model had high accuracy in discriminating different clinical stages of ovarian cancer from the whole control group. The diagnose performance of the model was independent of any subgroups of the 3 controls.

Conclusions In methodology, the mainstream of the neural network diagnosis model is improved for the use of principal component analysis and genetic algorithm to solve the two problems of feature dimensionality of training parameter optimization, improving the learning ability and the classification accuracy of the model. In design, the existing data resources for secondary development, many conventional mining test indicators achieve highly collaborative after fusion diagnosis purposes; in addition, 3 control subgroups were set up to enhance the discrimination ability of the model for related diseases. In summary, this machine learning can substantially improve the diagnostic efficiency of ovarian cancer through data consolidation of existing routine laboratory indexes, which provides a novel approach to intelligent auxiliary diagnosis for ovarian cancer.

PO-183

Clinical significance of serum interleukin 33 changes in different types of obese individuals

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Objective IL-33 is a newly identified cytokine of the interleukin-1 (IL-1) family, which is broadly expressed in various tissues and play a significant role as an 'alarmin' of some deseases. There were conflicting reports regarding the exact effect since the pathophysiological importance of IL-33 is highly dependent on cellular and temporal expression. Recently, several studies have showed IL-33 involved in metabolic homeostasis and participated in the process of obesity and its related metabolic complications in animal models, however, there were few reports on serum IL-33 levels in different types of obese individuals.Our aim was to determine the level of serum IL-33 in various types of obese subjects, and to investigate possible associations with clinical and metabolic parameters.

Methods Eighty-eight subjects were divided into metabolically healthy obesity (MHO), metabolic obesity (MO), metabolic obese normal weight (MONW) and healthy subjects (CON) based on BMI and metabolism indexes. Serum level of IL-33 was measured using ELISA kits. Spearman's rho test was used to determine the correlations with metabolic syndrome risk factors (eg. BMI, SBP, DBP, TG, CHOL, HDL, LDL, GLU).

Results Serum IL-33 levels in MO group and MONW group were significantly higher than those in CON group respectively (P=0.019; P=0.013). Among the three obese groups, the IL-33 levels in those people with metabolic disorder (MO group and MONW group) were also significantly higher than those in MHO group (P=0.010; P=0.007). No gender differences were found in both healthy subjects and obese subjects. IL-33 levels were positively associated with GLU levels only in MO group (r=0.448, P=0.047). However,

IL-33 levels were respectively positively associated with TG (r=0.431, P=0.001), LDL (r=0.239, P=0.035) and GLU(r=0.502, P=0.000) and were negatively associated with HDL(r=-0.487, P=0.000) in all types of obese subjects (MHO+MO+MONW). There was no significant correlation between IL-33 and BMI.

Conclusions IL-33 levels were different in various obesity types and significantly increased in obese individuals with metabolic abnormalities but not metabolically healthy obesity. Our data suggest that IL-33 is associated with lipid profiles and glucose levels in obese subjects and can serve as a novel marker to predict those who may be at increased risk of developing metabolic syndrome.

PO-184

The clinical observation on the treatment of IgA nephropathy by Invigorating and the spleen of nourishing the kidney and activating blood circulation Curative of effect observation

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Objective To study the effect of the clinical symptom score, hematuria, urinary protein, 24hutp and other indexes of IgA nephropathy by reinforcing the spleen and kidney and promoting blood circulation, and to prove its effect on IgA nephropathy, which can be used to guide clinical treatment.

Methods according to the inclusion criteria and exclusion criteria, 60 patients with uric acid nephropathy were selected. The patients were divided into 30 groups, 30 cases in the experimental group and cases in the experimental group. Ordinary group were treated with prednisone tablets, 24hutp is equal to or more than 1G., the dose is 0.6-1mg/kg/d, is more than or equal to 24hutp 3.5G, dosage of 1mg / kg / D, Po, the morning meal service, after 8 weeks of rules reduction. And experimental group on the basis of the above-mentioned western medicine in the treatment of giving oral supplementation of spleen and tonifying the kidney and promoting blood circulation, two groups of observation time for 1 year, the follow-up for 6 months, through the collection and analysis of each patient indicators in the before treatment, the clinical symptom scores and hematuria, proteinuria, 24hutp etc., and the SPSS22.0 statistical software for analysis and observation of supplement spleen Yishenhuoxue decoction treatment.

Results through the treatment of two groups were compared before and after clinical symptom score and blood in the urine, urinary protein, 24hutp index decreased, with statistical significance ($P < 0.05$). Studies have confirmed that complement spleen Yishenhuoxue decoction combined with western medicine in treatment of this disease is better than pure western medicine treatment.

Conclusions reinforcing the kidney and promoting blood circulation can significantly improve the clinical symptoms of IgA nephropathy and significantly reduce hematuria, urinary protein, 24hutp index, it is worth to clinical large sample experimental study.

PO-185

Study on the cytotoxic effect of CIK activated by DC-SW480 fusion tumor vaccine on SW480 in vitro

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Objective DC and CIK were isolated and cultured from peripheral blood to prepare fusion cells of DC and colon cancer SW480, observed fusionEffect of cell-stimulated CIK on colon cancer SW480 cells in vitro.

Methods 1. Peripheral blood mononuclear cells (PBMCs) are isolated from the blood of healthy adults. Cytokines are then used to induce dendritic cells (DCs) and cytokine-induced killer cells (CIKs), and the surface is subjected to flow cytometry. Identification of molecular markers.

2. DCs were fused with colon cancer SW480 with polyethylene glycol (PEG), purified DC-SW480 fusion cells were selected and screened with HAT/HA selection medium, and the morphology of DC-SW480 fusion cells was observed.

3. Effect of fused cell-stimulated CIK against colon cancer SW480 cells in vitro

1) DC-SW480 fusion tumor and CIK cell co-culture group

2) DC and SW480 mixed cells (DC: SW480=1:5) and CIK cell co-cultivation group

3) DC and CIK cell co-cultivation group,

4) Simple CIK cell control group,

After 72 hours of co-culture, the levels of IFN-γ, TNF-α, and IL-2 in the cell culture supernatant of each group were measured by ELISA, and then the SW480 cells were killed by using the co-cultured cells as effector cells, and the CCK-8 was measured. Kill rate.

Results 1.The dendrites of DC cultured cells were obviously matured. The results of flow cytometry showed that CD80 was 75.23%, CD83 was 61.25%, and HLA-DR was 89.69%.

2. The proportion of $CD3^+CD56^+$ cells in CIK cells was 25.21% on day 7 of CIK cell culture, and the percentage of $CD3^+CD56^+$ cells on day 14 was 57.33%, indicating that CIK cells were mature.

3. DC-SW480 fusion tumor cell fusion but the respective cell nuclei are not fused, and the pure DC-SW480 fusion cells can be obtained after suspension in HAT/HA selection medium.

4.The amount of cytokines IFN-γ, TNF-α and IL-2 secreted by DC-SW480 fusion cells stimulated by CIK cells were （24.40±0.01）ng/ml、(195.24±14.30）ng/ml、(594.73±7.73pg/ml）and DC, respectively. Compared with SW480 mixed cells group, DC cell coculture group, and CIK group alone, $P<0.05$, the difference was statistically significant.

5. The killing rate of colon cancer SW480 cells by DC-SW480 fusion cell group was (65.99±2.42)% and that of DC and colon cancer SW480 cell mixed group (48.27±7.56)%, and the kill rate of DC cell group （43.48±2.42）%, the killing rate（24.01±4.90）% of the CIK group alone was $P<0.05$, and the difference was statistically significant.

Conclusions 1. DC-SW480 fusion tumor vaccine can enhance the secretion of cytokines IFN-γ, TNF-α and IL-2 levels in CIK cells.

2. DC-SW480 fusion tumor vaccine can significantly enhance the ability of CIK to kill colon cancer SW480 cells.

PO-186

Diagnostic value of SCCA, Cyfra21-1 and GDF15 in oral squamous cell carcinoma

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Objective To detect the diagnostic value of SCCA, Cyfra21-1, and GDF15 in oral squamous cell carcinoma (OSCC).
Methods Two hundred oral squamous cell carcinoma patients and two hundred healthy control serum samples were collected. The value of SCCA and Cyfra21-1 were detected by automatic chemiluminescence immunoassay analyzer. GDF15 was examined *via* enzyme-linked immunosorbent assay.
Results The diagnostic values of three candidate biomarkes were summary as follows: SCCA (AUC: 0.5411; cut-off: 0.624 ng/ml), Cyfra21-1 (AUC: 0.8356; cut-off: 2.123 ng/ml), and GDF15 (AUC: 0.7094; cut-off: 106.8 pg/ml).
Conclusions Our data indicate that comparing with SCCA and GDF15, Cyfra21-1 is a potential diagnostic biomarker of oral squamous cell carcinoma.

PO-187

The clinical significance of exosomal long non-coding RNA HOTTIP in gastric cancer and the value of HOTTIP in drug resistance of gastric cancer cells

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Objective Gastric cancer (GC) is a huge burden worldwide with high morbidity and high mortality, especially in Eastern Asia and drug resistance is the major obstruction for gastric cancer chemotherapy. Long noncoding RNA HOTTIP (HOXA transcript at the distal tip) has gained growing attention among cancer-related lncRNAs, it plays important roles in the generation, progression, chemical resistance and so on of human cancers. Our study aims at estimating the potential novel diagnostic and prognostic values of exosomal HOTTIP for GC and further exploring the role of lncRNA HOTTIP in cisplatin based resistance in gastric cancer.
Methods Firstly, Serum exosomal HOTTIP from 246 subjects (126 GC patients and 120 healthy people) were detected by reverse transcriptionreal-time quantitative polymerase chain reaction (RT-qPCR) and serum CEA, CA 19-9 and CA 72-4 were measured by electrochemiluminescence method on Cobas E601. Receiver operating characteristic curve (ROC) was built to estimate the diagnostic values of exosomal HOTTIP, CEA, CA 19-9 and CA 72-4. The Kaplan-Meier analysis was used to analyse the relationship between exosomal HOTTIP, CEA, CA 19-9 and CA 72-4 expression levels and overall survival (OS) of GC. Cox proportional hazards models were performed to identify independent prognostic factors for GC. Then, expression levels of lncRNA HOTTIP from

212 tissues (106 GC tissues and 106 para-carcinoma tissue) and GC cells (SGC7901 and SGC7901/DDP) were detected by RT-qPCR. Plasmid vector of HOTTIP and HOTTIP-specific siRNA were transfected into GC cells to regulate gene expression. CCK-8 analysis was used to measure the chemosensitivity of cells to cisplatin. Tunel apoptosis analysis was peformed to estimate the celluar apoptosis ability. Western blot analysis was used to evaluate the protein expression.

Results 3.1 Exosomal HOTTIP was directly released by GC cells. And RT-qPCR results showed that the expression levels of exosomal HOTTIP in serum were typically higher in GC than in normal control ($P < 0.001$) and its expression levels were significantly correlated with tumor invasion depth ($P = 0.0298$) and TNM stage ($P < 0.001$). We also proved the stability of exosomal HOTTIP by treated serum samples with prolonged exposure to room temperature or mutiple freeze-thaw cycles.

3.2 The area under the curve (AUC) for exosomal HOTTIP was 0.827 ($P < 0.001$), which was significantly higher than the AUCs for CEA, CA 19-9, CA 72-4 with 0.653, 0.685 and 0.639, respectively ($P < 0.001$), indicating that exosomal HOTTIP was superior to them in GC diagnosis.

3.3 The Kaplan–Meier analysis showed a correlation between increased exosomal HOTTIP levels and poor overall survival (OS) ($P < 0.001$) and there was no significant relationship between CEA, CA 19-9, CA 72-4 and OS ($P > 0.05$). The online (www.kmplot.com) survival analysis results, basing on the detection data from GC tissues, supported our conclusion.

3.4 Univariate and multivariate COX analysis revealed exosomal HOTTIP overexpression was an independent prognostic factor in GC patients (HR = 2.037, 95% CI = 1.085-3.823, $P = 0.027$).

3.5 The expression levels of lncRNA HOTTIP were upregulated in chemo-relapsed GC patients and cisplatin based resistanced cell, SGC7901/DDP ($P<0.001$).

3.6 Upregulated the expression levels of lncRNA HOTTIP might promote SGC7901 cells chemoresistance and decreased cells apoptosis. Downregulated the expression levels of lncRNA HOTTIP could inhibite SGC7901/DDP cells chemoresistance and increase cells apoptosis.

3.7 Downregulated lncRNA HOTTIP could inhibite GC cell chemoresistance via promoting autophagy.

3.8 LncRNA HOTTIP could regulate the apoptosis, autophagy and chemoresistance ability of GC cells by miR-216a/Bcl2/Beclin1 axis.

Conclusions Exosomal long noncoding RNA HOTTIP may be a potential biomarker for GC in diagnosis and prognosis. Overexpression of lncRNA HOTTIP could relate to the cisplatin resistance in gastric cancer patients and lncRNA HOTTIP might increase cisplatin resistance of gastric cancer cells via miR216a/BCL-2/Beclin1/autophagy pathways.

PO-188

he effects of LAIR-1 on the Proliferation, Apoptosis and migration of the Hepatoma Cell Line HepG2

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Objective To investigate the effects of the expression of leukocyte-associated immunoglobulin-like receptor-1 (LAIR-1) on the proliferation, apoptosis and migration of the hepatoma cell line HepG2, and to explore the role of LAIR-1 in the hamatocarcinoma.
Methods (1)LAIR-1 gene was introduced into HepG2 cells by LAIR-1 lentiviral vector (LV-LAIR-1), to establish cell line with high and stable expression of LAIR-1 (LAIR-1^{+} HepG2). (2)The expression and localization of LAIR-1 on HepG2 cells were measured by RT-PCR, Western Blot, FCM and confocal microscopy (LCSM). The influence of LAIR-1 on the proliferation, apoptosis and migration of HepG2 cells was detected by CCK-8 kit, FITC Annexin V apoptosis detection kit and transwell assay respectively. Simultaneously, cell proliferation and migration were also detected by RTCA method.
Results (1) The expression of LAIR-1 at both mRNA and protein levels significantly increased in HepG2 cells after stable gene transfection with LV-LAIR-1. (2)Functional experiment results showed that compared with control, high expression of LAIR-1 could distinctly inhibit the proliferation (P<0.05) and migration (P<0.05) of HepG2 cells, but had no obvious effect on cell apoptosis (P>0.05).
Conclusions High expression of LAIR-1 could affect the proliferation, apoptosis, and migration of HCC cell, and indicate that LAIR-1 may play a crucial role in hepatocarcinoma cells.

PO-189

Expression signatures of exosomal long non-coding RNAs in urine serve as novel non-invasive biomarkers for diagnosis and recurrence prediction of bladder cancer

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Objective Expression signatures of exosomal long non-coding RNAs (lncRNAs) have been proposed as potential non-invasive biomarkers for the diagnosis and prognosis of malignant tumors. However, only few urinary exosome (UE)-derived lncRNAs are characterized as potential biomarkers in bladder cancer (BC) patients. We aimed to develop a UE-derived lncRNA panel for diagnosis and recurrence prediction of BC.
Methods Exosomes were extracted from urine of BC patients and healthy controls and confirmed using transmission electron microscopy (TEM), Western blotting analysis, nanoparticle tracking analysis (NTA) and flow cytometry. Then, quantitative real-time polymerase chain reaction (qRT-PCR) was performed to screen and evaluate the

expressions of eight candidate lncRNAs in a training set (208 urine samples) and a validation set (160 urine samples). Multivariate logistic regression model was used to establish the selected lncRNA panel. Receiver-operating characteristic (ROC) curves were employed to evaluate the performance of the panel. In addition, the correlation between lncRNAs and recurrence-free survival (RFS) of non-muscle-invasive BC (NMIBC) patients was evaluated to explore prognostic value.

Results Three UE-derived lncRNAs (MALAT1, PCAT-1 and SPRY4-IT1) were identified to be significantly up-regulated in BC, and a three-lncRNA panel based on this result was established for BC diagnosis. The performance of such three-lncRNA panel was verified with an area under the ROC curve (AUC) of 0.854 and 0.813 in the training set and validation set, respectively, which was significantly higher than that of urine cytology (0.619). In addition, Kaplan-Meier analysis suggested that the up-regulation of PCAT-1 and MALAT1 was associated with poor RFS of NMIBC ($p<0.001$ and $p=0.002$, respectively), and multivariate Cox proportional hazards regression analysis revealed that PCAT-1 ($p=0.018$) and the tumor stage ($p=0.036$) were independent prognostic factors for the RFS of NMIBC ($p=0.018$).

Conclusions Our findings indicated that UE-derived lncRNAs possessed considerable clinical value in the diagnosis and prognosis of BC.

PO-190

Histamine induces microglia activation and the release of inflammatory mediators in rat brain

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Objective Histamine is a major peripheral inflammatory mediator and a neurotransmitter in the central nervous system. We have reported that histamine induces microglia activation and releases proinflammatory factors in primary cultured microglia. Whether histamine has similar effects *in vivo* is unknown. In the present study, we aimed to investigate the role of histamine and its receptors in the release of inflammatory mediators and activation of microglia in rat brain.

Methods We site-directed injected histamine, histamine receptor agonists or histamine receptor antagonists in the rat lateral ventricle using stereotaxic techniques. Immunofluorescence images were acquired with a confocal microscope to assess the expression of histamine receptors in microglia. Microglia activation was assessed by Iba1 immunohistochemistry. The levels of tumour necrosis factor-alpha (TNF-α), interleukin-1beta (IL-1β) and interleukin-10 (IL-10) were measured with commercial enzyme-linked immunosorbent assay (ELISA) kits.

Results We found that all four types of histamine receptors were expressed in rat brain microglia. Histamine was able to induce microglia activation and subsequent production of the inflammatory factors TNF-α, IL-1β and IL-10, and these effects were partially abolished by H_1R and H_4R antagonists. However, H_2R and H_3R antagonists significantly increased production of TNF-α and IL-1β, and decreased IL-10 levels. The H_1R or H_4R agonists stimulated the production of TNF-α and IL-1β, while the H_2R or H_3R agonists increased IL-10 release.

Conclusions Our results demonstrate that histamine induces microglia activation and the release of both proinflammatory and anti-inflammatory factors in rat brain, thus contributing to the development of inflammation in the brain.

PO-191

Analysis of the distribution and antimicrobial resistance of Enterobacteriaceae in a tertiary general hospital

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Objective To retrospectively analyze the distribution and resistance changes of Enterobacteriaceae bacteria from 2014 to 2017, and provide evidence for clinical rational drug use.
Methods The clinical isolates were identified and tested by automated instrumentation using K-B method. The CLSI M100-S24 standard was used to judge drug susceptibility results and WHONET 5.6 software for data analysis.
Results A total of 5987 strains of Enterobacteriaceae were detected, the first being Escherichia coli accounted for 51.7%, followed by Klebsiella pneumoniae accounting for 28.5%, the third being Enterobacter cloacae accounted for 5.8%; the urinary system was Enterobacteriaceae The most common infection sites of bacteria accounted for 44.9%, followed by the respiratory system, accounting for 29.0%; Enterobacteriaceae had higher resistance to cephalosporins and lower resistance to carbapenems. The isolation rates of ESBLs-producing Escherichia coli, Klebsiella pneumoniae and Proteus mirabilis were 54.3%, 39.3% and 42.5%, respectively. The segregation rate of ESBLs-producing Escherichia coli and Proteus mirabilis showed a downward trend year by year, while CRE The overall separation rate is increasing year by year.
Conclusions The Enterobacteriaceae bacteria isolated in our hospital showed different degrees of drug resistance, and the monitoring of bacterial resistance should be strengthened, and the antibiotics should be rationally used according to the results of drug sensitivity experiments.

PO-192

Diagnostic value of Galactomannan in Serum and Bronchoalveolar Lavage Fluid for Invasive Pulmonary Aspergillosis in Nonneutropenic Patients

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Objective To evaluate the diagnostic performance of GM detection in serum and BALF for IPA in nonneutropenic patients.
Methods A total of 291 patients in the Second XiangYa Hospital between January 2016 and October 2018 were included in the final analysis. According to the 2016 Infectious Diseases Society of America (IDSA), the European Organization for Research and Treatment of Cancer/Invasive Fungal Infection Group (EORTC/IFICG), and the American Mycosis Research Group (MSG) guidelines, all cases were divided into an IPA group (24 cases) and a non-IPA group (267cases).Their serum and BALF concentrations of GM were detected by enzyme-linked immunosorbent assay (ELISA). Receiver operating characteristic (ROC) curves were drawn to compare the diagnostic efficiency of BALF and serum GM. And, the optimal cut-off value for BALF GM assay was determined by calculating the Youden index. We analyzed its sensitivity, specificity, positive predictive value, and negative predictive value.
Results According to the ROC curves of BALF and serum GM, the areas under the curve are 0.961 and 0.699, respectively. When the BALF GM value of 0.87 is the best threshold, the sensitivity was 91.7%, the specificity was 92.5%, the positive predictive value was 52.1%, and the negative predictive value was 99.2%.
Conclusions BALF GM detection is a more sensitive diagnostic tool than serum GM. Our retrospective study suggests that the optimal cut-off value of GM detection in BALF is 0.87.

PO-193

Effectiveness of bronchoalveolar lavage in the treatment of pulmonary abscess

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Objective Evaluating the effectiveness of bronchoalveolar lavage in the treatment of pulmonary abscess.
Methods Select 86 hospitalized pulmonary abscess patients including 43 treated only by drugs and 43 treated by the combination of drugs as well as bronchoalveolar lavage. Retrospectively analyze the indexes of recovery time, improvement of chest CT scan, changes of leukocyte counting, procalcitonin as well as blood gas, and improvement of pulmonary function.

Results After 6 weeks of treatment, the changes of chest CT scan, and FEV1,FVC as well as PaO2 values of the two groups were improved compared to pretreatment, and the improvement in combination therapy group was significantly more obvious than that in drug treatment group (all P < 0. 05). The hospital stay, and the duration of abnormal body temperature, leukocyte counting as well as procalcitonin are significantly shorter in combination therapy group than those in drug treatment group (all P < 0. 05). Acute respiratory failure occurred in 1 patient and the blood pressure decreased in 3 patients in the combination therapy group, while no obvious complications were found in the drug treatment group.
Conclusions The combination of bronchoalveolar lavage and drugs in the treatment of acute pulmonary abscess is remarkably effective, and worthy of widely clinical application.

PO-194

Peripheral blood circulating microRNA-4636/-143/-200c for early detection of cervical cancer

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Objective 宫颈癌是世界上女性死亡的第三大原因。在先前关于 SEC3 基因与宫颈癌之间相关性的研究中，microRNA-143 / -4636 / -200c 通过微阵列在宫颈癌 Hela 细胞和 SEC3 过表达组中显示出显着差异。同样，它们在宫颈癌组织和正常组织之间存在显着差异。侵袭性和创伤性活检是目前确定宫颈癌严重程度的唯一可靠方法。因此，需要用于宫颈癌的非侵入性诊断标志物。
Methods 本研究收集了 70 例宫颈癌和 20 例健康对照。通过定量逆转录聚合酶链反应（qRT-PCR）评估三种微小 RNA。Spss25.0 软件用于评估血清 miRNA 水平与病理分期，分化，肿瘤总体积和侵袭深度的相关性。
Results 与健康对照相比，miR-143 / -4636 对宫颈癌具有特异性（p = 0.013 /。宫颈癌验证 miRNA 的分类性能[受试者工作特征曲线下面积（AUC）= 0.896]优于鳞状细胞癌抗原（SCC-Ag）（AUC = 0.727）。血清 miR-4636 / -143 / -200c 水平较低，分化程度较差（p <0.05）。血清 miR-4636 / -143 / FIGOⅠ期患者-200c 明显低于 CIN（p <0.05），miRNA-4636 / -143 在腺癌中的表达水平高于鳞癌（p <0.01）.miR-4636 水平与肿瘤总体积和浸润深度相关（p <0.0001）。
Conclusions 循环 microRNA-4636 / -143 / -200c 显示出比常规血清标志物更好的诊断潜力，以鉴定宫颈癌患者。

PO-195

Stenotrophomonas-maltophilia inhibits host cellular immunity by activating PD-1/PD-L1 signaling pathway to induce T cell death

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Objective Smalotrophomonas maltophilia is common in nosocomial infections, and its research is mainly focused on its extensive drug resistance. However, few studies have revealed the effect of S. maltophilia on cellular immunity in the host's immune system. In an accidental clinical work we found that S. maltophilia directly stimulates T lymphocytes to secrete IFN-γ. In this study, we explored the effects of S. maltophilia on T lymphocytes.
Methods S. maltophilia was co-cultured with lymphocytes to detect secretion of cytokines and expression of cell surface molecules of T cells. Light microscopy and electron microscopy were used to observe the cell morphology and subcellular structure of S. maltophilia co-cultured with lymphocytes. Flow cytometry and Western Blot were used to detect the expression of PD-1 / PD-L1 in cells.
Results T cells stimulated by S.maltophilia secreted a large amount of IL-2, IFN-γ and TNF-α, and the expression of cell surface molecules, CD4 and CD8, were degraded, accompanied by activation of PD-1/PD-L1 pathway and a massive death of T cells. Electron microscopy showed that cells showed significant apoptotic morphology.
Conclusions These indicates that T cells are activated first after being stimulated by S. maltophilia, and then accelerated to induce death without immunologic cascade. This paper demonstrates for the first time the inhibitory effect of S.maltophilia on cellular immunity, and thereafter the immunosuppressive effect induced by infection by S. maltophilia should be considered.

PO-196

Analysis of molecular pathogenesis of 3 Glanzmann's thrombasthenia pedigree

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Objective To explore the molecular pathogenesis of 3 Glanzmann's thrombasthenia pedigree by using bioinformatics software and provide evidence for in vitro experiments.
Methods The genetic analysis of 3 pedigree confirming diagnosed with Glanzmann's thrombasthenia was carried out. Clustalx-2.1-win software was used to analyze the conservatism the conservatism of mutant sites in homologous sequences. Bioinformatics software such as PolyPhen-2, PROVEAN, SIFT and Mutationtaster was used to analyze the

harmfulness of mutant sites. SPDBV software constructed the molecular structure model of mutant protein and analyzeed the influence of mutant sites on protein structure.
Results The "new mutations" found in 3 Glanzmann's thrombasthenia pedigree were ITGA2B:c.814G>C (p.Val272Leu), ITGA2B:c.432G>A (p.Trp144Ter) and ACTN1:c.2458A>G (p.Ile820Val). All three mutations were highly conserved among homologous species. Mutationtaster software showed that 3 new mutations were likely to cause disease. PolyPhen-2 and PROVEAN software showed ITGA2B p.Val272Leu and ACTN1 p.Ile820Val were benign and SIFT software showed that ITGA2B p.Val272Leu were harmful, while ACTN1 p.Ile820Val is benign. The result of SPDBV software showed that the Val272 of ITGA2B was transformed to Leu, leading to all the original hydrogen bond connections disappeared. The Trp144 of ITGA2B is transformed to Ter, resulting in forming the truncated proteins with only 113 amino acid residues. All these mutations caused changes in the molecular structure of GPIIb, resulting in a decrease in GPIIb/IIIa expression. When the Ile820 of ACTN1 is transformed to Val and only the hydrogen bond of Ile820 and Asp822 is retained, the rest of the hydrogen bond disappear caused the change of ACTN1 molecular structure and affected the function of protein.
Conclusions The mutations of ITGA2B:c.814G>C (p.VAL272LEU), ITGA2B:c.432G>A (p.Trp144Ter) and ACTN1:c.2458A>G (p.Ile820Val) are pathogenic.

PO-197

Effects of CYP2C9 and VKORC1 Genetic Polymorphisms on Maintenance Dosage of Warfarin

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Objective To investigate CYP2C9 and VKORC1 gene polymorphisms in Chinese population and the effects on maintenance dosage of Warfarin, in order to explore the causes of Warfarin individual difference.
Methods PCR-Fluorescent probe methods was applied to detect CYP2C9* 3 and VKORC1-1639A>G gene polymorphisms in 458 patients from Peking University People's Hospital between August and October 2017, and recorded the 130 included patients information, the individual Warfarin dosage requirements and INR values. The statistical data of dosages of Warfarin in patients with different genotypes were compared with the reference table recommended by FDA. Predicted Warfarin dose calculated by 2 published pharmacogenomics based Warfarin algorithms were compared for accuracy with actual maintenance doses.
Results Among the 458 patient, the CYP2C9*1/*1(AA) genotype frequency was 90.8%, while the CYP2C9*1/*3(AC) genotype frequency was 8.5%, and the CYP2C9*3/*3(CC) genotype frequency was 0.7%. The VKORC1-1639GG genotype frequency was 0.9%, the VKORC1-1639GA genotype frequency was 14.2%, and the VKORC1-1639AA genotype frequency was 84.9% (389/458).CYP2C9 genotyping in 130 included patients (INR 2.0～3.0) showed that the variant CYP2C9*1/*3 and CYP2C9*3/*3 required lower daily maintain doses [(2.92±1.29) mg] than wild-type CYP2C9*1/*1 patients did [(3.91±1.63) mg], with statistically significant difference (P=0.018). And variant VKORC1-AA required lower daily maintain doses [(3.68±1.64) mg] than variant VKORC1-GA patients did [(4.54±1.29) mg], with

statistically significant difference (P=0.001). According to grouping comparison of mutations of the two genes, the results showed that patients with CYP2C9 mutation and VKORC1 homozygous mutation required the least dose of Warfarin, while patients with no mutation of CYP2C9 and no mutation or only heterozygous mutation of VKORC1 required the most Warfarin dose. The difference between the four groups was statistically significant (P=0.012), among which the difference between the AA&*1*1 group and the AG&*1*1 group was statistically significant (P=0.016), and the difference between the AG&*1*1 group and the AA&* 1*3 groups was statistically significant (P=0.001). The difference between the other groups was not statistically significant. The dosing trend of Warfarin in patients with different genotypes was consistent with the recommended dosing trend of the FDA reference table, but the specific dose was slightly different. In this test, the prediction error of genotype-based Warfarin dosing algorithms is large and the percentage of ideal predicted dose is low. The dosages of Warfarin in patients with different genotypes were basically consistent with the reference table recommended by FDA. Among the 2 published algorithms, IWPC model had the smallest absolute difference between predicted and actual Warfarin doses of 0.326mg and highest prediction accuracy of 35.2% which was assessed by the percentage of the predicted dose within 20% of actual doses. Miao's model had the biggest absolute difference of 1.672 mg and the lowest prediction accuracy of 11.8%, and the predicted dose for 16 patients (17 in total) was lower than the actual dose, Warfarin doses were underestimated in 94.1% of patients. So the Miao2007's model tends to underestimate actual Warfarin dose.

Conclusions CYP2C9 and VKORC1 polymorphisms had clinical significance in guiding the individualized Warfarin dosage in Chinese patients, which is partly the factor causing Warfarin individual difference.

PO-198

MTB-evidence negative pulmonary tuberculosis prediction model: development and validation of nomogram and the value of lnRNA -- n344917

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Objective LncRNA--n344917 has been found significantly down-regulated in MTB-evidence negative pulmonary(nPTB) patients(FC=2.5, P <0.05). This article aimed to build a nPTB diagnosis model and evaluate the diagnostic potential of n344917.

Methods We prospectively recruited 486 suspected PTB patients admitted to west China hospital from January 2008 to May 2017 and collected corresponding electronic medical record information (demographic informatics, laboratory examination and imaging data). The expression of n344917 was detected by qRT-PCR. Three types of prediction models with nomogram graph form --n344917 univariate model, electronic health record(EHR) model and the combined model of both n344917 and EHR (combined model), were built by using multivariable logistic regression.

Results The expression of n344917 in patients with nPTB decreased significantly. The predictors in the EHR model included age, low fever, computed tomography (CT) calcification, CT bronchus sign, interferon-γ release assay (TB-IGRA). It showed excellent ability of discrimination (AUC=0.867, sensitivity=0.873, specificity=0.721), calibration accuracy and clinical effectiveness in the training set. And it was internally verified (area under the curve (AUC)=0.834, sensitivity=0.821, specificity=0.740) in the testing set. According to the calculation results of NRI (net reclassification improvement) and IDI (integrated discrimination improvement), the diagnostic efficiency of the model has no obvious improvement compared with the EHR model after the inclusion of n344917.

Conclusions The EHR model improved the diagnostic performance effectively for nPTB patients, however, there was no significant finding when adding n344917 into this model, which requires further study.

PO-199

Quantification of oleic acid in serum by LC-MS/MS and its application in Classification of nonalcoholic fatty liver disease

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Objective To establish a method for the determination of oleic acid (OA) in serum by an isotope-labelled internal standard-based liquid chromatography-tandem mass spectrometry (LC-MS/MS), and to investigate the role of OA in classification of nonalcoholic fatty liver disease(NAFLD).

Methods The isotope-labelled internal standard was OA-[13C5] and the ion pairs of OA and OA-[13C5] were 281.3/281.3 and 286.3/286.3, respectively. The mobile phase A was ultrapure water and the mobile phase B was methanol: acetonitrile (1:1, v/v), and the gradient elution system was carried out in a ZORBAX SB-Aq C18 reversed phase column with a flow rate of 0.3 mL/min. The developed method was then validated in accordance with the CLSI guidelines (EP15-A3) in terms of specificity, linearity, LLOD, precision, stability and carrying pollution rate. 180 patients with NAFLD diagnosed by B scan and clinical manifestations, and 100 healthy subjects were as well as detected by LC-MS/MS. The classification of NAFLD is evaluated by B scan results. One-way analysis of variance was used for comparison between groups.

Results The method for the determination of OA in serum by LC-MS/MS was in a good specificity and linearity in the range of 10~1000 μmol/L, and the linear regression was y = 0.00737x+0.00673, correlation coefficient r = 0.9994, and the limit of quantitation (LLOQ) was 10 μmol/L. The within-run and total coefficients of variation (CV) was not more than 0.88% and 1.41% respectively. The concentration of OA in serum ($\bar{x} \pm s$) in the control group (200.53±67.45, μmol/L) was significantly lower than

that in the NAFLD group (337.81±141.84, μmol/L); and the concentration of OA in serum was significantly positive correlated with the classification of NAFLD.
Conclusions The method for the determination of OA in serum using LC-MS/MS was a scientific and efficient method, which was beneficial to the dynamic monitoring of changes of OA in NAFLD patients.

PO-200

Berberine inhibits the MexXY OprM efflux pump to reverse imipenem resistance in a clinical carbapenem resistant Pseudomonas aeruginosa isolate in a planktonic state

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Objective Explore the biological effect of berberine combine with imipenem to kill multidrug-resistant Pseudomonas aeruginosa and further study the internal mechanism.
Methods The minimum inhibitory concentrations (MICs) of berberine and imipenem were assessed using the broth microdilution method. Checkerboard assay was used to evaluate the synergistic effect of berberine and imipenem, and the best ratio of bacteriostatic concentration was determined. Reverse-transcription quantitative polymerase chain reaction (RT-qPCR) was detected the gene expression of MexZ, MexX, MexY and OprM
Results Screening revealed that the minimum inhibitory concentrations (MICs) of BEB and IMP were 512 and 256 μg/ml, respectively. The combination of BEB (1/4 MIC) and IMP (1/8 MIC) exhibited a synergistic effect with a fractional inhibitory concentration index of 0.375. The syner-gism of BEB and IMP was also demonstrated in a time kill test and by scanning electron microscopic observation. Treatment with BEB at ¼ MIC in combination with IMP at 1/16, 1/8, 1/4 and ½ MIC revealed a concentration dependent promoting effect of IMP on the intracellular accumulation of BEB and inhibition of bacterial adhesion. Further analysis of gene expression revealed that BEB (1/4 MIC) combined with IMP (1/8 MIC) decreased MexZ, MexX, MexY and outer membrane protein (Opr)M by 38, 35, 46 and 49% in PA012.
Conclusions These results suggested that IMP had synergistic effects with BEB against the clinical isolate PA012 via inhibition of the MexXY OprM efflux pump.

PO-201

Application of biological variation and six sigma models to evaluate analytical quality of six HbA1c analyzers and design quality control strategy

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Objective To apply biological variation and six Sigma models to evaluate analysis performance of 6 HbA_{1c} analyzers and design the new quality control strategy.
Methods We collected data of imprecision and inaccuracy from routine internal quality control(Jun 2017 to Dec 2017) and proficiency test of NGSP respectively. The Coefficient of Variance(CV)% and Bias% were plotted in the biological variation and six sigma models. The new quality control strategy was designed by the sigma value and OPSpecs. The quality improvement was guided by the QGI.
Results The analytical performance of 6 HbA_{1c} analyzers in our laboratory were good in the routine model, However, 50%(3/6) and 67%(4/6)of the HbA_{1c} analyzers reached the acceptable level in the biological variation and six Sigma model, respectively. We also design personalized control strategy and promote quality improvement by combining the sigma value, OPSpecs and QGI.
Conclusions Biological variation model and six sigma model could visually display the performance of 6 HbA_{1c} analyzers and personalized control strategy could be designed based on the sigma value, OPSpecs and QGI.

PO-202

Anti-domain 1 of beta2-glycoprotein I aids risk stratification in lupus anticoagulant positive patients

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Objective Lupus anticoagulant (LA) is considered as a risk factor for thromboembolism (TE) and adverse pregnancy outcomes (APOs). However, quite a few patients diagnosed with LA positivity do not suffer these adverse events. Further testing of anticardiolipin (aCL), anti-beta2-glycoprotein I (anti-β2GPI) or anti-domain 1 of β2GPI (anti-D1) may help to assess the occurrence risk of TE and APOs. Therefore we aimed to study how to stratify LA positive patients.
Methods In our study, adult patients who had tested LA positivity twice or more occasions at least 12 weeks apart were consecutively enrolled from January 2015 to December 2016. Serum aCL and anti-β2GPI (IgG, IgM and IgA), and anti-D1 IgG were simultaneously measured by chemiluminescence immunoassay. Besides, they were followed up for the occurrence of TE or APOs.

Results A total of 167 LA positive patients who met the inclusion criteria were consecutively enrolled. The outcomes showed 21 patients experienced TE, 89 patients suffered APOs (5 patients had both TE and APOs) and 62 patients were LA carriers. Comparing with LA carriers, the Diluted Russell's viper venom time ratio (dRVVT-R) and Silica Clotting Time ratio (SCT-R) were significantly increased in patients with the history of TE ($p<0.001$ and $p<0.05$, respectively) and APOs ($p<0.001$ and $p<0.05$, respectively), especially with the patients who had both TE and APOs ($p<0.001$ and $p<0.001$, respectively).
By analyzing antiphospholipid antibodies (aPL) panel, we found that anti-D1 had a good consistency with triple positivity (LA+, aCL+, anti-β2GPI+) (kappa=0.742) in LA positive patients. Compared with LA carriers, the titers of anti-D1 were significantly high in patients with TE and APOs ($p<0.001$ and $p<0.001$, respectively). And elevated anti-D1 was related to a stronger risk for TE [odds ratio (OR) =29.87, 95% confidence interval (CI), 8.05-110.74] and APOs (OR=8.73, 95%CI, 3.41-22.31) in comparison with aCL, anti-β2GP1 or triple positivity. Area under curve (AUC) showed that diagnostic power of anti-D1 for TE and APOs were 0.856 (95%CI, 0.743-0.970) and 0.682 (95%CI, 0.599-0.765), respectively. And the optimal cut-off value of anti-D1 to help predict TE and APOs were 24.6 CU (sensitivity and specificity were 81% and 90.3%) and 32.4 CU (sensitivity and specificity were 57.2% and 91.9%), respectively.
Moreover, 114 patients (68.3%) were followed up for an average of 36.5 months. During follow-up, none of patients suffered TE events, while we observed that 37 patients were pregnant. Among them, there were 15 patients suffering APOs events. And their pregnancy outcomes were 1 early miscarriages, 7 fetal deaths, 7 preterm due to placenta insufficiency. The levels of anti-D1 were significantly increased compared with the non-APOs patients. 37 pregnant LA positive patients were divided into two groups High value group (n=16) and Low value group (n=21) based on the anti-D1 cut-off value (32.4 CU). The Kaplan-Meier survival analysis showed that high anti-D1 titers had a significant higher cumulative incidence of APOs compared with the Low value group ($p=0.009$) and the hazard ratio (HR) was 4.66 (95%CI, 1.46-14.87).
Conclusions Anti-D1, based on a good consistency with triple positivity in LA positive patients, has a stronger association with TE or APOs and in some degree could predict the pregnancy outcomes. Therefore anti-D1 may aid risk stratification in LA positive patients.

PO-203

Diagnostic significance of serum cystatin C in patients with lung cancer

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Objective To investigate the expression of serum cystatin C (CysC) and its clinical significance in patients with lung cancer. Patients (n=161) with lung cancer were first diagnosed at the 901th Hospital of the Joint Logistics Support Force of the Chinese People's Liberation Army.

Methods We included 74 healthy individuals and 66 patients with benign diseases as controls. CysC levels in serum were detected using an automatic biochemical analyzer, serum creatinine(Cr) and urea nitrogen(Urea) levels were measured, and the estimated glomerular filtration rate (eGFR) was calculated.
Results Serum CysC levels in patients with lung cancer were significantly higher compared with those of healthy subjects and those with benign disease. There was no significance in serum CysC levels in patients with lung cancer before and after anticancer treatment.
Conclusions The serum CysC levels of patients with lung cancer are significantly associated with tumors and facilitate the development of better strategies for the early diagnosis and treatment of lung cancer.

PO-204

Study on the diagnostic value of ACAN, a protein regulated by Hippo/YAP signaling pathway

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Objective Hippo/YAP signaling pathway is a highly conserved signaling pathway that controls organ size by controlling cell proliferation and apoptosis.YAP can be combined with a variety of transcription factors such as TEAD, CREB and TFCP2 to promote the transcription of downstream genes such as CTGF and BICC1 and play a role in promoting liver cancer.In liver cancer, the transgenic mice with high liver specific YAP expression quickly developed liver injury symptoms and eventually developed liver cancer.YAP regulated membrane protein is highly expressed in liver cancer and can be released into the blood. This study aims to explore whether YAP regulated membrane protein can be used as a tumor marker for early and accurate diagnosis of liver cancer.
Methods All specimens were collected from Shanghai ruijin hospital from May 2015 to December 2016.The cell lines were purchased from the cell bank of the Chinese academy of sciences.After RNA extraction, cDNA was obtained by reverse transcription and analyzed by quantitative PCR.Elisa assay kit was purchased from Shanghai yingxin experimental equipment co., LTD.Statistical methods include t test, Bonferroni multiple comparative analysis, Spearman rank correlation test, area under ROC curve, etc.$P<0.05$ was considered statistically significant.
Results The mRNA expression of ACAN increased significantly after overexpression of YAP, while the expression level of ACAN decreased significantly after knockdown of YAP.Several common yap-binding transcription factors, CREB, TEAD, TFCP2 and RUNX2, were overexpressed in hepatocellular carcinoma cell lines 7402 and 7721. We found that only CREB overexpression promoted the mRNA expression of ACAN, while TEAD, TFCP2 and RUNX2 had no significant effect on ACAN expression.The creb-binding motif exists in the promoter sequence -610 ~ -599nt of ACAN, which is directly regulated by YAP and CREB.Compared with the normal population, we found that the expression level of ACAN in the serum of patients with liver cancer was significantly increased, and the expression level of ACAN was not increased in the serum of patients with liver benign

diseases such as hepatitis b and c, as well as patients with gastric cancer, colorectal cancer, breast cancer and lung cancer.The expression of ACAN was positively correlated with AFP, ALT and AST.The area under the ROC curve of ACAN was 0.978, the optimal diagnostic threshold was 66ng/ml, the detection sensitivity was 96.4%, and the specificity was 98.2%. The diagnostic efficiency was better than AFP to some extent.
Conclusions Aggrecan (ACAN), a sugar complex composed of negatively charged glycosaminoglycans covalently connected to core proteins, is mainly secreted and produced by chondrocytes. ACAN plays an important role in intercellular information transmission, maintenance of cell phenotype, mediation of interactions with other matrices, and maintenance of overall tissue function.In this study, we found that the expression level of ACAN in the serum of patients with liver cancer was significantly increased, and ACAN had the potential to become a new serum marker of liver cancer, which provided the possibility for early treatment and precision medicine of patients with liver cancer.

PO-205

Neuropilin 1 (NRP1) is a novel tumor marker in hepatocellular carcinoma

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Objective TEA domain transcription factor (TEAD) has an oncogenic role in hepatocellular carcinoma (HCC). However, whether a membrane protein can serve not only as a tumor marker that reflects TEAD function but also as a therapeutic target that stimulates tumorigenesis in HCC remains unknown.
Methods Tissue NRP1 was measured using immunohistochemistry. Cell viability, colony formation and caspase3/7 activity were assessed using MTT, soft agar and caspase 3/7 Glo assays, respectively. Serum NRP1 was examined using ELISA and Western blotting.
Results NRP1 expression was up-regulated by TEAD. We also identified a TEAD-binding motif in the NRP1 promoters, which was essential for the TEAD-NRP1 interaction. NRP1 was up-regulated in HCC tissues and cell lines, and knockdown of NRP1 inhibited the transformative phenotypes of HCC cells. Notably, the concentrations of serum NRP1 in the HCC patients were higher than those of hepatitis B, hepatitis C, cirrhosis, breast cancer, colon cancer, gastric cancer and lung cancer patients. Moreover, serum NRP1 was significantly associated with AFP, γ-GT, Alb, bile acid, ALT, AST, ALP and pre-Alb. The area under the receiver operating characteristic curve (AUC-ROC) for serum NRP1 was 0.971, presenting better diagnostic performance compared to AFP.
Conclusions NRP1 is a novel tumor marker in HCC.

PO-206

Using risk management to plan quality control of serum free light chains in the total automation

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Objective A condition that produces out-of-control results increases the likelihood that the laboratory generates erroneous test reports. Laboratory tests support about 70% of medical decisions. The TAT and the accuracy of results are critical to the diagnostic reliability and treatment effectiveness. Reliable analytical results of serum free light chains monoclonal immunoglobulin (SFLC kappa or SFLC lambda) are important in patient care because of the critical decisions that that are taken from its.

If patients' erroneous results are released, they may induce the physician to error, with the potential to cause harm and therefore pose a hazard to the patient. Especially for SFLC kappa and SFLC lambda that are used in the diagnosis and prognosis of patients with monoclonal diseases of plasma cells.

The statistical control of the laboratory process has its impact on this sequence of events, which begins with the occurrence of inadequate QC results, followed by wrong results of the patient and damage to health care with diagnostic inefficiency, incorrect treatments or ineffective, even causing injury to the patient with monoclonal gammopathy, macroglobulinemia or primary amyloidosis.

Laboratory quality control (QC) planning establishes the current state, defines the objectives and goals by analyzing the current situation and its influences, outlining a plan of action, monitoring mechanisms; applying necessary adjustments and continuity of the cycle. Planning QC correctly increases the chances of achieving the primary goal of the clinical laboratory: ensuring accurate and reliable examination results in a timely manner, because the oncological patient requires agility and effectiveness in the decisions about the treatment. New risk management practices for the development of Quality Control Plans (QCP) should be integrated with existing error management practices to provide an effective system for analytical quality management.

This work presents the Failure Mode and Effects Analysis (FMEA) tool, in a public tertiary clinical laboratory, to evaluate risks and contribute to the QC planning of new assays for serum free light chains (SFLC) using total automation.

Methods The failure mode and effects analysis (FMEA) was chosen as the risk analysis tool to QC in SFLC and a 3-factor model was used to identify the probability of failure occurrence, degree of effect severity, and detection mechanisms. A different scale was used for each factor: failure occurrence (from 1 to 5), effect severity (from 1 to 4), probability of failure detection (from 1 to 4). The risk priority score (RPS) limit was forty (40) points, from which preventive actions would be taken to prevent risk, minimize it or extinguish it, and dissemination of information to increase safety. This tool was applied in two stages: at the beginning of the project and after the implementation of the proposed measures inside of QCP.

Results The application of Plan- Do- Study- Act (PDSA) cycle in association with process description and study of each stage and their interactions were done. The

essence of risk management is risk assessment, which depends on the identification of possible causes of errors throughout the laboratory examination cycle and the risk estimation by probability of occurrence, severity of damage and error detection capability of the QC, evaluating the acceptability of risks. The preventive actions helped to prepare the QCP for SFLC kappa and lambda.

Failure Mode / RPS pre / RPS end

Lack of inspection of the biological material in the lab: 48 -12
Method validation: 60-24
Production control Internal QC: 60 - 18
Production control Proficiency Test: 48 - 18
Interferers pre analytical: 48 - 24
Equipments: 60 - 16
Comparison between analytical systems: 60- 12
Analytical specification: 48 - 18
Validation between batches of reagents:45 -3
Water: 45 - 3
Environmental conditions: 40 - 12

Conclusions FMEA was used as a proactive tool allowing a thorough assessment of vulnerability and preventing the occurrence of adverse events. The occurrence should be controlled by validation of the of the method. Detection should be optimized by designing QC statistical procedures according to the quality required for the intended use of the test, the accuracy and bias observed for a measurement procedure. The damage must be reduced by the detection of possible errors with medical repercussions, followed by preventive actions. This approach places the focus of quality control directly on the patient, mitigating the patient's risks. For this reason, the laboratory should design and implement a QCP to bring these risks to an acceptable level.

The content of the QCP to serum free light chains assays corresponds to the result of the preventive actions undertaken: production, biological material, method used to analyte, equipment used, equivalence between analytical systems, kit, calibration, PT, IQC, method validation, total error, validation between batches, supervision, water, environmental conditions.

In the end, we observed a paradigm shift and the consolidation of a failure prevention culture.

PO-207

SP70 Targeted Tumor Cell Enrichment and Analysis in Body Fluids

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Objective Currently the diagnosis of malignancy in body fluid, including the detection of circulating tumor cells (CTC) in blood, suffer low sensitivity due to the lack of specific tumor cell enrichment method. In the previous study, we produced a monoclonal antibody designated NJ001, which targets tumor specific antigen SP70. The

aim of this study is to assess the value of NJ001 coated immuno-magnetic beads capturing technique in distinguishing benign and malignant body fluid samples.
Methods In the present study, two hundreds and sixty-one body fluid specimens were obtained and analyzed from Department of Laboratory Medicine, the First Affiliated Hospital of Nanjing Medical University (NMU) and Department of Pathology and Laboratory Medicine, University of California, Los Angeles (UCLA), between March and July 2017. Tumor cells were enriched by the NJ001 monoclonal antibody coated magnetic beads. SP70 positive cells were detected by microscopic examination after Papanicolaou staining. CTCs from thirteen patients were sequenced by Next Generation Sequencing (NGS).
Results Comparing with routinecytologytechnique,cytology withSP70 targeted immuno-magnetic beads increased the sensitivity and accuracy.The accuracy of cytology with SP70 and routine cytologywere 82.4%, and 55.6%,respectively. In a follow-up study, 68of 76patients, who werepreviously diagnosed benign disease withnegative cytologyresult but positive in our new technology with SP70,were confirmed malignant by MRI, needle biopsy and NGS.
Conclusions Our results showedthat SP70 could be a novel biomarker for identifying and distinguishing benign and malignant body fluid samples and enrich tumor cells for subsequent molecular analysis.

PO-208

Diagnostic performance of PIVKA-II and interleukin-18 in patients with hepatocellular carcinoma

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Objective 本研究旨在评估维生素 K 缺乏或拮抗剂-II 和白细胞介素（IL）-18 诱导的肝细胞癌患者的诊断性能。
Methods 在该研究中，收集了总共 322 个血清样品，包括 132 个肝细胞癌患者，50 个非肝细胞癌患者和 140 个健康志愿者。通过 ARCHITECT 平台上的化学发光微粒免疫测定法测量由维生素 K 缺失或拮抗剂-II 水平诱导的蛋白质，进行夹心 ELISA 以测量白细胞介素（IL）-18 的血浆浓度。对每种生物标志物进行接受操作特征曲线分析。组合。
Results 结果显示，维生素 K 缺乏或拮抗剂-II 联合诱导的白细胞介素（IL）-18 和蛋白质在整个患者中与维生素 K 缺乏或单独使用拮抗剂-II 诱导的蛋白质相比，曲线下面积更大（0.905）肝细胞癌早期患者（0.803 vs 0.75）和乙型肝炎病毒相关肝细胞癌患者（0.851 vs 0.788）与 ARCHITECT 平台相比，维生素 K 缺乏或拮抗剂-II 诱导的蛋白质在曲线下面积更大白细胞介素（IL）-18 用于诊断乙型肝炎病毒相关肝细胞癌患者（0.901 vs 0.768）。
Conclusions We conclude that Combining interleukin (IL)-18 and protein induced by vitamin K absence or antagonist-II may improve the diagnostic value for early detection of hepatocellular carcinoma. Protein induced by vitamin K absence or antagonist-II performs better than interleukin (IL)-18 in diagnosis of hepatitis B virus - related hepatocellular carcinoma patients.

PO-209

Value of thromboelastography, mean platelet volume/platelet count ratio and fibrinogen in diagnosis of recurrent spontaneous abortion

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Objective To explore TEG parameters, MPV/PLT ratio and FIB values in patients with recurrent spontaneous abortion in non-pregnant condition, and to evaluate their diagnostic value in the disease.

Methods 206 patients with RSA history were selected as the study group from February 2018 to January 2019 in the reproductive clinic of the Second Hospital of Jilin University. The criteria were as follows: all patients were not pregnant at the time of consultation, more than three months before the last abortion, and were excluded from anatomy, endocrine, immune function, reproductive tract infection and chromosomal abnormalities by relevant examinations. 68 healthy women who underwent prenatal examination during the same period were selected as the control group. They had no adverse pregnancy history in the past and had at least one normal pregnancy, and now they are in the infertile state. There was no significant difference in age and body mass between the two groups ($P > 0.05$). All subjects had no history of diabetes mellitus, thyroid disease, autoimmune diseases, and no contraceptives, anticoagulants or fibrinolytic drugs were used within 2 months before consultation. All other examinations were normal. The coagulation reaction time (R), coagulation time (K), coagulation angle (a), maximum amplitude (MA), mean platelet volume (MPV), platelet count (PLT) and fibrinogen (FIB) in the two groups were measured, and the diagnostic value of the related indicators for recurrent abortion was evaluated.

Results The K value of TEG parameters in RSA group was lower than that in control group, the α angle and MA value were higher than those in control group, and the MPV/PLT ratio and FIB value in RSA group were higher than those in control group, with statistical differences ($P < 0.05$). There was no significant difference in R value between the two groups in TEG ($P > 0.05$). Compared with the normal control group, the MA, MPV/PLT and FIB values in the recurrent spontaneous abortion group were significantly increased, and the differences were statistically significant ($P < 0.01$). The ROC curves of the patients with recurrent abortion were plotted with three indicators. The MA value, MPV/PLT ratio and FIB value under the ROC curve were 0.680, 0.692 and 0.677 respectively. When the cut-off value of MA was 64.15mm, the sensitivity and specificity were 69.5 and 63.5 respectively; when the cut-off value of MPV/PLT was 0.038, the sensitivity and specificity were 57.1 and 58.8 respectively; when the cut-off value of FIB was 3.16 g/L, the sensitivity and specificity were 67.9, 64.3 respectively.

Conclusions The results of this study show that K, alpha angle, MA, MPV/PLT ratio and FIB value of RSA patients have changed in non-pregnant state, suggesting that PTS exists in some patients with history of habitual abortion before pregnancy. The results show that MA, MPV/PLT and FIB values under the ROC curves were 0.680, 0.692 and 0.677, respectively, indicating that they have certain diagnostic value for

recurrent abortion. Compared with the MPV/PLT ratio and FIB value, the sensitivity of MA value in the diagnosis of recurrent spontaneous abortion was slightly higher. Based on the above results, the detection of MA, MPV/PLT ratio and FIB value has good diagnostic value for recurrent spontaneous abortion. Patients with history of recurrent abortion should be detected as soon as possible, which is of great significance to the etiology and early treatment.

PO-210

Relationship between the polymorphism of MIRU-VNTR loci in Mycobacterium tuberculosis and its diverse protein composition

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Objective To study the relationship between the difference in the copy numbers of repetitive units at mycobacterial interspersed repetitive unit-variable-number tandem repeat (MRU-VNTR) loci and the protein composition of *Mycobacterium tuberculosis* (MTB).
Methods The MTB complex (MTBC) was subjected to genotyping using MIRU-VNTR typing method. The principal component analysis (PCA) was performed for bacterial proteins of MTBC using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). Also, the relationship between the difference in the copy numbers of repetitive units at MIRU-VNTR loci (polymorphism of MIRU-VNTR allele) and PCA clustering was analyzed.
Results A total of 157 strains of MTB were collected. There were polymorphic differences in the 24 MIRU-VNTR loci, including 7 with high, 7 with moderate, and 10 with low polymorphism. The distribution of the copy number levels of the repetitive units at the polymorphic loci, including Mtub39, QUB26, and QUB4156, was statistically significant in PCA clustering ($P < 0.001$, $P=0.035$, $P=0.017$), suggesting that the polymorphism of the copy numbers of these loci was correlated with the bacterial protein composition in MTB.
Conclusions The difference in the copy numbers of repetitive units at the polymorphic alleles, including Mtub39, QUB26, and QUB4156, in MTB was attributed to the differential fingerprints of the bacterial proteins.

PO-211

Interferents of Automated Reticulocyte Analysis Integrated with Relevant Clinical Cases

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Objective Reticulocyte count (RET) has been used for many years to estimate the erythropoietic activity of the bone marrow. Fully automated methods not only provide enhanced precision and accuracy, but also enable reliable measurements of mRNA content and cellular indices. However, problems still exist, such as interference. The aim of the present study was to investigate the interferents of Sysmex XN 9000 reticulocyte analysis and ensure the accuracy of the results.
Methods We collected a total of 510 specimens from normal control patients and patients with various diseases including anemias, leukemias, infectious diseases, immune diseases, kidney disease, etc. Correlation of the agreement for reticulocytes between the new methylene blue (NMB) visual microscopy method and automated reticulocyte counting was evaluated by paired sample method according to the CLSI-ICSH document H44-A2-Methods for Reticulocyte Count. Blood smear microscopic examination was carried out on the disturbed samples, and the interferents were analyzed with the medical history, flagging algorithms, the warning information and the microscopic examination.
Results A total of 44 (8.6%) cases exhibited interference. The main interferents of spuriously high reticulocyte count were caused by parasites, such as malaria, as well as suspicious autofluorescence due to drugs, while the main interferents of spuriously low reticulocyte count were caused by RBC fragments.
Conclusions Detection of potential interferences may be accomplished through alarm information and flagging algorithms incorporated into the instrument, and by examination of a blood film to ensure absence of relevant interferences.

PO-212

Simultaneous Mutations of COL4A5 and LAMB2 Genes Responsible for Alport Syndrome and Focal Segmental Glomerulosclerosis in a Chinese Woman

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Objective Alport syndrome is clinically, pathologically, and genetically heterogeneous kidney disease. Whereas the mechanism lead to this heterogeneity is still not fully known. The aim of this study is to identify the cause of clinical heterogeneity in a three-generation Chinese family with inherited kidney disease.

Methods The variations of the proband were detected by targeted capture associated with next-generation sequencing. The pathogenicity of variations was confirmed via bioinformatics analyses and pedigree verification.
Results The proband carried a heterozygous nonsense mutation p.R1569* in *COL4A5* gene and a compound heterozygous mutation *LAMB2* p.G699R and p.V600M, which responsible for Alport syndrome (AS) and focal segmental glomerulosclerosis (FSGS) respectively. Her daughter who inherited the *COL4A5* p. R1569* and *LAMB2* p.G699R heterozygous mutations was diagnosed with Alport syndrome without FSGS under light microscope.
Conclusions All these suggested that except for *COL4A5* p. R1569* mutation, *LAMB2* compound heterozygous mutations might serve as pathogenic factors leading to this heterogeneity in proband. The heterogeneity of partial patients might be caused by the existence of other gene mutation, which resulted in two different monogenetic disorders in a pedigree. Additionally, next generation sequence (NGS) played a crucial role in diagnosis of this extremely rare case caused by *COL4A5* and *LAMB2* gene mutations simultaneously, which will support clinical practices, including precise diagnosis, normalized treatment, and clarifying the pathogenesis of inherited nephropathy.

PO-213

Evaluation of spleen cytology counts and their classification by Sysmex XN-350

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Objective To shorten the TAT time and ensure the quality of the test,we analyze the difference between Sysmex XN-350 and the manual method in the counting and cell classification of pleural effusion specimens.
Methods Collection of pleural effusion specimens of hospitalized patients from July toOctober of 2018 in the First Affiliated Hospital of Xi'an Medical College. Using Sysmex XN-350 blood analyzer to count and classify samples and then using a modified bovine abalone to counting white cells ,after that,the specimens were smear centrifugation and stained for microscopic examination.After the results are summarized, statistical methods were used for analysis.
Results For the samples with white blood cell count greater than 100×106/L, the results were not statistically significant (P>0.05), while the white blood cell counts were less than or equal to 100×106/L. The difference was statistically significant (P<0.05).Both the Instrument method and Manual method were similar in the classification of neutrophils、eosinophils、basophilsand lymphocytes , while monocytes was quite different-the instrument method was higher than the manual method.
Conclusions Under certain conditions (white blood cells ≥100 × 106 / L), Sysmex XN-350 analyzer can be used for white blood cell count of cerebrospinal fluid, in contrast (white blood cells ≤ 100 × 106 / L) specimens should be manually re-examined .

PO-214

Relationship between estimated glomerular filtration rate and serum biomarkers of cardiovascular disease

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Objective Chronic kidney disease (CKD) is associated with an increased cardiovascular disease (CVD) mortality risk. The purpose of this study was to investigate the relationship between alterations in estimated glomerular filtration rate (eGFR) and serum biomarkers of CVD.

Methods We examined the cross-sectional associations of eGFR and high sensitive cardiac troponin I (hs-cTnI), creatine kinase (CK), CK-MB, lactate dehydrogenase (LDH) and brain natriuretic peptide (BNP) in 812 individuals without overt CVD.

Results There were significant differences of hs-cTnI, CK, CK-MB, LDH and BNP among eGFR < 60, 60 - 90 and ≥ 90 ml/min/1.73 m^2. There was a strong and significant negative correlation between eGFR and hs-cTnI, CK-MB, LDH, BNP whereas there was no significant correlation between eGFR and CK when eGFR was taken into consideration as a continuous variable. eGFR was associated with these biomarkers of CVD. For example, eGFR < 60 ml/min/1.73 m^2 (vs ≥ 90 ml/min/1.73 m^2) was significantly associated with a [ratio (95% CI, *P* value)] 11.22 (5.58-22.54, $P < 0.001$), 3.05 (1.83-5.09, $P < 0.001$), and 7.84 (4.93-12.45, $P < 0.001$) times higher hs-cTnI, LDH and BNP, respectively. After adjustment for potential confounders, eGFR was associated with a 2.83 (1.08-7.41, $P = 0.035$) times higher of elevated hs-cTnI.

Conclusions Reduced eGFR is associated with elevated hs-cTnI, LDH and BNP among individuals without clinically evident CVD.

PO-215

AID recruits the RNA exosome to degrade HIV-1 nascent transcripts through interaction with the Tat-P-TEFb-TAR RNP complex

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Objective Acquired immunodeficiency syndrome (AIDS) is caused by infection with human immunodeficiency virus (HIV). Although significant advances have been made in HIV research, a cure has not been found for more than 30 million people infected with HIV. The HIV is incurable mainly because the HIV provirus is integrated into the host's genomic DNA and does not actively replicate and no antiviral drugs or technology can target an integrated virus. Activation-induced cytidine deaminase (AID), a member of the APOBEC family that induces antibody diversification, has been shown to inhibit the replication of hepatitis B virus, Kaposi's sarcoma-associated herpesvirus, and retro-

transposons. However, whether AID can inhibit human immune deficiency virus 1 (HIV-1) replication remains unclear. Here, we report that AID impairs the synthesis of HIV-1 components by interacting with the complex of Tat. This interaction recruits the RNA exosome to degrade the nascent HIV-1 transcript. AID also targets the HIV-1-integrated genome the Tat-P-TEFb-TAR complex. Thus, we propose a novel function for AID as an adaptor protein that represses viral transcription. Our findings provide insights into developing anti-HIV therapeutics and understanding how host cells restrict integrated virus replication.

Methods In the study, pAID/ P19, the AID mutant, and pNL4.3-Luciferase/pSeap were co-transfected in both 293T cell line and primary cells, then Luciferase and SEAP assay were conducted and found that AID and P19 could significantly inhibit HIV-1 replication. Further, we used Co-IP to verified that AID bound with Rrp40, an essential component of RNA exosome exonuclease. Additionally, we used ChIP and Co-IP experiments classified that AID bound to integrated HIV-1 genome by Tat.

Results Our study revealed that AID could suppress HIV-1 replication but not depend on cytosine deaminase activity. Further, AID binds integrated HIV-1 genome by Tat and recruit RNA exosome to degrade HIV-1 RNA to inhibiting HIV-1 transcription. Besides, we found P19, the AID mutant, also have antiviral activity but without cytosine deaminase activity, which may be a new therapeutic strategy to cure AIDS.

Conclusions AID functions as an adaptor between RNA exosomes and HIV-1 transcripts through viral Tat. RNA exosome-mediated cleavage is likely responsible for the anti-HIV-1 activity of AID. Thus, the anti-HIV activity of AID may not involve either HMGA1 or TRBP. Taken together, the antiviral activity of AID may be widespread, and future studies are required to determine whether endogenous AID is induced to physiologically suppress HIV-1replication in host cells.

PO-216

INCREASED PERCENTAGE OF CD8+ T CELL SENESCENCE ASSOCIATED WITH HIGH LEVEL OF INFLAMMATORY CYTOKINES IN SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS

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Objective To assess the correlation between T lymphocytes senescence markers such as end stage differentiated T cells ($CD4^+CD57^+$ and $CD8^+CD57^+$) and memory T cells ($CD4^+CD45RO^+$ and $CD8^+CD45RO^+$) with IFNγ and IL-2 serum levels in female SLE patients.

Methods This study was conducted in 61 female SLE patients, aged 16-56 years, recruited from Internal Medicine Outpatient Clinic, Dr. Saiful Anwar Hospital, Malang. 10 -15 cc of peripheral blood were collected from every subjects and PBMCs were isolated. Percentage of $CD4^+CD57^+$ and $CD8^+CD57^+$; $CD4^+CD45RO^+$ and $CD8^+CD45RO^+$ T lymphocytes were assayed using flow-cytometry. IFN-γ and IL-2 serum levels were measured using ELISA. Unpaired T test and Pearson correlation test were used to analyze the collected data ($p \leqslant 0.05$ considered as significance value).

Results Our study showed that there were positive significant correlation between percentage of $CD8^+CD45RO^+$ T cells with IFN-γ and IL-2 cytokines level ($r = 0.527$, $p = 0.021$; $r = 0.382$, $p = 0.047$) ; $CD8^+CD57^+$ T cells percentage with IFN-γ and IL-2 cytokines level ($r = 0.427$, $p = 0.03$; $r = 0.401$, $p=0.010$). However, there were no significant correlation between $CD4^+$ T cells senesence with these cytokines.
Conclusions Increased memory and end stage differentiated $CD8^+$ T cells associated with high level of IFN-γ and IL-2 cytokines found in SLE patients. We suggest that inflammatory process in SLE induce $CD8^+$ T cells senescence.

PO-217

Cancer-associated VTE exclusion diagnosis by D-dimer

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Objective Venous thromboembolism (VTE) is a common disease throughout the world, mainly consists of two parts: pulmonary embolism (PE, 40%) and deep venous thrombosis (DVT, 60%). It is reported that at least 12% of all deaths was caused by PE in Europe, and half of all PEs were confirmed by autopsy. At the same time, VTE is a serious important complication of cancer patients with high incidence(4%-20%). Evidence-based medicine study found that, compared with other patients, cancer patients had 4.1 times the risk of suffering VTE, which also results in the huge health-care costs and considerable acute or long-term morbidity. Early and accurate diagnosis of VTE is of significance for reducing the mortality and disability rate. D-dimer and FDP, both widely-used biomarkers of thrombosis are significantly increased in VTE. D-dimer assays usually have a high diagnostic sensitivity and a low specificity as an exclusion diagnostic indicator. It has been reported that the false positive rate with D-dimer is about 3 times higher in canner versus non-canner patients. Confirmation of a VTE exclusion diagnosis cutoff level in cancer patients should prove useful for diagnostic purposes. This is what we attempted to establish in this study.
Methods The plasma concentration of D-dimer and FDP were detected in canner patients who visited the Second Hospital of Jilin University from January to October 2018, and the diagnosis of thrombosis was verified by using imaging techniques. The patient population was made up of 80 cases of lung cancer, 45 hepatocellular carcinomas, 82 cervical cancers, 33 colon cancers, 60 ovarian cancers, 4 prostate cancers, 30 breast cancers, 21 esophageal cancers, 25 gastric cancers, 69 rectal cancers and 34 endometrial cancer patients. Another 1224 healthy volunteers were selected as control group. D-dimer and FDP concentration were measured with a fully automatic coagulation analyzer (CP3000, Sekisui medical, Japan) using Nanopia D-dimer (Sekisui medical, Japan) and Nanopia P-FDP reagents (Sekisui medical, Japan).
Results The D-dimer was 0.6±0.12μg/mL, in healthy volunteers compared to 2.09±4.36μg/mL, 2.05±3.78μg/mL, 2.19±2.78μg /mL and 3.46±0.74μg /mL for lung cancer, ovarian cancer, and gastric cancer patients, respectively. Other cancer patients also showed higher levels than healthy volunteers, but no statistically significant difference was observed. Provisionally setting the 99th percentile limit

as the cut-off for D-dimer, yields the following cut-offs: lung cancer 2.31μg/ml, colon cancer 3.26μg/ml, ovarian cancer 7.40μg/ml and gastric cancer 6.29μg/ml. The FDP was 1.7±0.4μg/ml in healthy volunteers, and the value of all types of cancer patients examined this time were higher than those of healthy volunteers.

Conclusions The diagnostic value of D-dimer for VTE is still significant, although a low specificity. In this study, we found that D-dimer level of lung, ovary, colon, and gastric cancer patients show a statistically higher than in healthy volunteers when using the 99th percentile limit as a cut-off, and indicated this may be a suitable provisional value. Due to the single detecting system and reagent, the result of this study is still limited. As such we will conduct a multicenter study in which diagnostic utility will be verified based on sensitivity and specificity of the provisional cut-off value using ROC analysis and including cancer patients with and without VTE.

PO-218

A blood management method based on exponential smoothing model

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Objective To strengthen the management of blood transfusion in clinical departments, to implement the individual blood supply audit system, to provide reference for the rational booking of blood volume and to promote the rational allocation of resources in blood stations.

Methods The monthly blood consumption data from January 2015 to July 2018 in our hospital were collected, and the exponential smoothing model of time series analysis was established by using SPSS22.0 statistical software. The blood consumption data from January 2015 to December 2017 were used to predict the future blood consumption of clinical departments. The data from January to July 2018 were used to verify the model. Type.

Results The analysis covers four high blood volume departments in our hospital, including tumor hematology department, hepatobiliary surgery department, cardiac surgery department and central monitoring room. Among them, the model fitting better in tumor hematology department and hepatobiliary surgery department is simple seasonal, the stable R-squares are 0.760, 0.870, and the standardized BIC is 4.292 and 3.889, respectively. The good model is Holt-Winters multiplication, the stationary R-square is 0.765, the standardized BIC is 4.886; the better model fitting in the central monitoring room is Holt-Winters additivity, the stationary R-square is 0.844, the standardized BIC is 5.432; the error between the predicted value and the actual value of the exponential smoothing model is in a controllable range, and dynamic.

Conclusions The blood management method based on exponential smoothing model can be applied to short-term prediction and dynamic analysis of blood use in various departments of our hospital. It is helpful to strengthen the blood transfusion management and relieve the tension of clinical blood use.

PO-219

The Per-1 short isoform inhibits de novo HIV-1 transcription in resting CD4+ T-cells

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Objective Understanding of the restriction of HIV-1 transcription in resting CD4+ T-cells is critical to eliminate viral latent reservoir . Though many mechanisms for HIV-1 latency involve transcription have been proposed, there are still unknown mechanisms to explore. This study aims to explore the mechanisms for the suppression of de novo HIV-1 transcription in resting $CD4^+$ T-cells.
Methods In this study, Per-1-001 and Per-1-002 expression plasmids were deliveried into 293T cells with or without Tat to identify which isoform restricts HIV-1 replication and whether Tat can influence the inhibitory effect. Silencing of Per-1 in post-activated resting $CD4^+$ T-cells and monocyte-derived macrophages(MDMs) to evaluate the antiviral properties of Per-1. Additionally, we analyzed the relationship between Per-1 expression and viral load as well as the number of $CD4^+$ T-cells and investigated the potential anti-HIV-1 roles in vivo through silencing of Per-1 in total $CD4^+$ T-cells from untreated HIV-1-infected individuals.
Results We identify the short isoform Per-1-002 restricts HIV-1 replication and Tat ameliorates the inhibitory effect. Silencing of Per-1 in post-activated resting CD4+ T-cells and MDMs alleviates HIV-1 restriction and is associated with a significant accumulation of viral RNA. The Per-1 transcript levels were inversely correlated with viral loads and positively correlated with the number of CD4+ T-cells in rapid progressors(RPs) but not in long-term nonprogressors (LTNPs).
Conclusions These data suggest that Per-1 is a novel negative regulator of HIV-1 transcription in resting $CD4^+$ T-cells. This restrictive activity of Per-1 to HIV-1 replication may induce HIV-1 latency in resting CD4+ T-cells.

PO-220

Establishment and Application of performance verification scheme of urine formed component analyzer according to ISO 15189

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Objective To establish a comprehensive and feasible performance verification solution for urine formed component analyzer according to ISO 15189 and related industry standards.

Methods Some tests of iQ200 urine microscopy system including detection limit, precision, recognition rate, stability, biological reference interval, and reportable range were detected in this scenario depending on ISO 15189 and existing industry standards.
Results The detection limits, precision, recognition rate, stability, biological reference interval, and reportable range were all in line with the evaluation criteria according to our plan.
Conclusions Under the corresponding stipulations of ISO 15189, the above solution can be used for performance verification of iQ200 urine microscopy system.

PO-221

NDRG1 is a promising biomarker for diagnosing and predicting poor outcome in bladder cancer

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Objective Bladder cancer is the most common tumor of the urinary system connected with high recurrence and mortality if not treated accurately. Although cystoscopy and pathological assay are the key tools, there remains a great need for effective markers to help diagnosing and predicting prognosis.
Methods NDRG1 expression in tissues and urine from bladder cancer patients and healthy controls were examined by RT-PCR, Western blot assay, ELISA methods and immunohistochemistry respectively. ROC analysis was used for defining its cut-off value, sensitivity and specificity. Additionally, four online datasets of bladder cancer were also harvested for further confirmation.
Results NDRG1 expression was significantly upregulated in both tissues and urine of bladder cancer patients. The protein levels in urine could distinguish bladder cancer patients from healthy controls with an AUC (area under the curve) of 0.909 (95% confidence interval = 0.829 - 0.989). Its protein expression in tissue correlated with tumor stage (p=0.025), lymph node metastasis (p=0.034) and overall survival (p=0.016). The patients with high NDRG1 expression had a worse outcome than those with low NDRG1 expression. Notably, in non-muscle invasive bladder carcinoma, high NDRG1 expression was associated with a higher risk of progression to muscle invasive bladder carcinoma (p=0.026).
Conclusions Our study identified NDRG1 could serve as a promising diagnostic and prognostic biomarker for bladder cancer patients.

PO-222

Epidemiology analysis of the Acinetobacter by the Phage Open Reading Frame Typing (POT) method in Gunma, Japan

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Objective It is necessary to develop a rapid, simple and easy method for analyzing *Acinetobacter baumannii* strains for suspected nosocomial infections in clinical settings. To evaluate the usefulness of the POT method, we performed epidemiological analysis of *Acinetobacter* genus in Gunma, Japan using by the POT method.

A. baumannii is glucose-non-fermentative, Gram-negative bacillus that is one of the causative organisms of hospital infection. In particular, *A. baumannii* epidemic clones, the called international clones Ⅰand Ⅱ, usually show multidrug resistance, and only limited antimicrobials are efficacious for treating infections caused by them. An outbreak by multidrug resistant *Acinetobacter* (MDRA) is reported in Japan in 2008.

It is necessary to determine the presence or absence of blaoxa-51 that *A. baumannii* contains on its chromosome, and to analyze 16srRNA for accurate identification of the strain. Therefore it is difficult to identify *A. baumannii* in the routine examination. Furthermore, the IC (international clones) uses the multilocus sequence typing (MLST) method, but much time, complicated operation are necessary. This problem is settled by using the phage open reading frame (ORF) typing (POT) method reported by Suzuki et al. POT is a rapid, PCR-based method.

The POT method detects the possession different ORF which is in a state every strain in multiplex PCR. We determine a genotype by a possession pattern. PCR is a principle and is testable if there are a thermal cycler and agarose gel electrophoresis.

The POT method which is a rapid, simple and easy technic, enables us to identify several kinds of bacteria including *A. baumannii*, and to examine epidemical analysis between the different strains.

Methods We collected 91 *Acinetobacter* genus bacteria between January 2014 and March 2015 at 12 hospitals in Gunma Prefecture.

Ninety-one *Acinetobacter* strains were analyzed by the POT and PFGE method, and evaluated by drug sensitivity testing.

We analyzed it about the detection of identification of *A. baumanni* and the IC by the POT method.

We analyzed presence of MDRA in the drug sensitivity test. The criteria used M100-S22.

The POT method was performed using a commercially available Cica Geneus ™ Acineto POT KIT (Kanto Chemical) according to the manufacturer's instructions. The several ORFs specific to the certain strains of *Acinetobacter* spp. were detected using multiplex PCR. The distribution patterns of the ORFs were calculated from three categories of the POT codes. The first category of the POT code indicates the species identification, such as <1000 for *A. baumannii*, 1000－1999 for *Acinetobacter pittii*, 2000－2999 for *Acinetobacter nosocomialis*, 3000－3999 for *Acinetobacter* spp. close to *A. nosocomialis* and 4000 and more for the other *Acinetobacter* spp. Furthermore, the first category of

the POT code denotes the types of international clones, for example, no. 69 for international clone I and no. 122 for international clone II. If the identified species are *A. baumannii* and also if they are obtained from an outbreak, all three categories of POT code will be the same.

Results Identification of 91 *Acinetobacter* genus bacteria collected in Gunma, Japan, by the POT method: *A. baumannii* 50/91, *A. pittii* 21/91, *A. nosocomialis* 7/91.

Identification of the IC among 50 *A. baumannii* strains by the POT method: Eight ICII were found out of 50, whereas the IC Ⅰ was not found.

POT type: Eight 8-13-0 strains, five 8-12-0 strains, four 122-58-53 strains, three 8-13-9 strains, two 44-40-32 strains, two 122-58-55 strains, two 28-8-8 strains, and two 0-12-0 strains were found. 22 strains were singularity type.

Drug sensitivity testing: The IPM (Imipenem) resistant strain was not found. However, 87.5% of strains which became IC II by the POT method were resistant to Ceftazidime and Aminoglycoside, Fluoroquinolone.

Conclusions Identification of clinically significant *A. baumannii* was possible with the POT, and it was found to be a rapid, simple and easy testing compared with the PFGE. It was also useful for the identification of ICII of which drug resistance was observed.

The preparation of the reagents are easy, and specific equipment are not necessary for POT. Therefore, POT can be used in many clinical laboratories, and is a very useful tool to analyze strains for suspected nosocomial infections in clinical settings.

PO-223

circHIPK3 as a prognostic marker and mediator of chemoresistance in colorectal cancer via autophagy through the miR-637/Stat3/Bcl-2/Beclin-1 axis

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Objective Resistance to oxaliplatin-based chemotherapy is a major cause of recurrence in colorectal cancer (CRC) patients. There is increasing evidence that circHIPK3 is involved in the development and progression of tumors. However, little is known about the potential role of circHIPK3 in CRC chemotherapy and its molecular mechanisms in the chemoresistance also remain unclear.

Methods Quantitative real-time PCR was used to detect circHIPK3 expression in tissues of CRC patients received oxaliplatin-based chemotherapy. The chemoresistance effects of circHIPK3 were assecced by cell viability, apoptosis and autophagy assays. The relationships among circHIPK3, miR-637, and Stat3 were confirmed by biotinylated RNA pull-down, luciferase reporter and western blot assays.

Results In intial study, increased circHIPK3 expression was observed in CRC chemoresistance patients. Overexpression of circHIPK3 promoted cell viability and inhibited cell apoptosis under oxaliplatin treatment. And, silencing of circHIPK3 sensitized HCT116oxR to oxaliplatin by promoting autophagy. Meanwhile, autophagy inhibition also attenuated proliferative and anti-apoptosis effects of circHIPK3.

Mechanistically, circHIPK3 sponged miR-637 to promot Stat3 expression, thereby activing the downstream Bcl-2/Beclin-1 signaling pathway. Clinical cohort study showed circHIPK3 was upregulated in recurrence CRC tissues and correlated with tumor size, regional lymph nodes metastasis, distant metastasis, and survival.
Conclusions Our findings demonstrate that circHIPK3 functions as a chemoresistance gene in CRC cells by targeting the miR-637/Stat3/Bcl-2/Beclin-1 axis and may provide a prognostic predictor in CRC patients.

PO-224

Genome-wide DNA methylation analysis by MethylRad and the transcriptome profiles reveals the potential cancer-related lncRNAs in colon cancer

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Objective Colon cancer (CC) is characterized by global aberrant DNA methylation that may affect gene expression and genomic stability. Although previous studies have identified methylation changes associated with a limited set of genes, profiles of lncRNA gene methylation of CC still has not been elucidated clearly. In the present study, we try to figure out colon-cancer related lnRNAs that regulated by abberant methylation by co-analyzing the lncRNA gene methylation profile by MehtylRAD and lncRNA expression data from TCGA database.
Methods The genome-wide DNA methylation profile of CC was constructed using MethylRAD technology which can discriminates between CG and non-CG methylation sites. The differential methylated sites (DMSs) and differentially methylated lncRNA genes (DMGs) were identified by EdgeR using R software. Meanwhile, the RNA expression data of colon adenocarcinoma were downloaded and analyzed from TCGA database. Then the intersection analysis was performed between lncRNA gene methylation level and lncRNA expression level. The hypermethylated and downregualted lncRNAs, hypomethylated and upregulated lncRNAs were indetified as colon cancer related lncRNAs. The coexpressed protein-coding genes of cancer-related lncRNA were subjected to subjected to Gene Ontology (GO) and KEGG pathway enrichment analysis.
Results We constructed DNA methylation profiles using MethylRAD technology which can discriminate between CG and non-CG methylation sites. Totally 132,999 CCGG/8,487 CCWGG sites were identified as differential methylated sites (DMSs) which were mainly located on the intron and intergenic elements. Also 1359 CCGG/1052 CCWGG deferentially methylated genes (DMGs) were screened respectively. Our results demonstrated that lncRNAs genes occurred frequently in DMGs including 510 (37.5%) lncRNAs genes in CCGG DMGs and 466 (44.3%) lncRNAs genes in CCWGG DMGs. As a result, we totally got 963 differentially methylated lncRNA genes including 387 hypermethylated and 576 hypomethylated genes. The RNA sequencing data of 480 patients with colon adenocarcinoma and 41 controls were downloaded from TCGA. We totally got 1328 differentially expressed lncRNAs including 1311 upregulated and 16 downregulated lncRNAs. Finally, we figured out 15 lncRNAs might be colon cancer-related lncRNAs.

ZNF667-AS1 and MAFA-AS1 were downregulated and might be silenced by hypermethylation. And 13 lncRNAs (AC008781.2, HULC, AC100839.1, CRAT37, LINC01198, LINC01482, SMAD1-AS2, TH2LCRR, DISC1-IT1, ABCC5-AS1, NFIA-AS1, AC007431.1, AC012494.1) were hypomethylated and upregulated in colon cacner.

Conclusions We fiugred out 15 colon cancer related lncRNAs that might regulated by aberrant methylation. This study might provide novel potential biomarkers, therapy targets and new insight of molecular mechanism in tumorigenesis and development of CC.

PO-225

Bioinformatics analysis of common DEGs in coronary artery disease and myocardial infarction

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Objective This paper aimed to screen out the common differentially expressed genes (DEGs) of coronary artery disease (CAD) and myocardial infarction (MI), and through the online pathway analysis and protein-protein interaction (PPI) network analysis of the common DEGs to explore the underlying molecular mechanisms of CAD and MI.

Methods The gene expression profile of GSE71226 and GSE19339 were downloaded from the Gene Expression Omnibus (GEO) database, and the DEGs between normal people and patients were screened using “limma” package in R language. Genome Ontology (GO) term enrichment analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis on the common DEGs using the DAVID database, and PPI network were constructed by the STRING database and visualized with Cytoscape software.

Results A total of 506 common DEGs were screened from GSE71226 and GSE19339, of which 59 were up-regulated and 447 were down-regulated. The GO analysis indicated that up-regulated DEGs were mainly enriched in ‘leukocyte migration’ and ‘angiogenesis’; the common down-regulated genes were significantly enriched in ‘regulation of transcription, DNA-templated’, ‘transcription, DNA-templated’ and ‘mRNA splicing, via spliceosome’. The KEGG analysis identified that the up-regulated DEGs were mainly enriched in ‘ECM-receptor interaction’, ‘Protein digestion and absorption’, ‘Tuberculosis’, ‘Focal adhesion’ and ‘PI3K-Akt signaling pathways’; the down-regulated DEGs were primarily enriched in the ‘mRNA surveillance signaling pathway’. From the PPI network, the top hub genes mainly including C-X-C motif chemokine ligand 12 (CXCL12), nestin (NES), splicing factor 1 (SF1), LUC7 like 3 pre-mRNA splicing factor (LUC7L3), serine and arginine rich splicing factor 11 (SRSF11).

Conclusions The present study can provide new ideas for understanding of molecular mechanisms of CAD and MI. Furthermore, CXCL12, NES, SF1, LUC7L3, SRSF11 may as newbiomarkers for the diagnosis and treatment of the two diseases.

PO-226

Effect of urea nitrogen on HbA1c detected by HPLC

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Objective HbA1c can reflect the average blood glucose level of patients at 6-8 weeks, which is a good indicator to evaluate the blood glucose control of diabetes mellitus (DM). In 2011, HbA1c was listed as a diagnostic index of diabetes by WHO. At present,HPLC are used to detect HbA1c by most laboratories , but this detection method is susceptible. This paper mainly studied the effect of urea nitrogen on HbA1c detected by HPLC.

Methods Thirty-six patients in our hospital from November 2018 to December 2018 were selected for the study, except for the pregnant women, heavy drinking, taking anti-inflammatory drugs and vitamins C and E, infectious diseases, blood system diseases (such as iron deficiency anemia, hemolytic anemia, etc.), and elevated urea nitrogen caused by any diseases. 2 ml of Blood was collected from 36 by patients using EDTA-K2 anticoagulant tubes. Appropriate blood of every patient was divided into observation group and control group. In the observation group, 5ul blood was placed in pure water, reversed and mixed for 10 minutes, and then configured into a solution with a final concentration of 35mmol/L of urea nitrogen.In the control group, 5ul blood was placed in pure water. Observation group and control group were put in the 37 ℃ water bath. HbA1c was detected by HPLC at 0, 2, 4, 6, 8, 10, 12 and 24 hours and determined whether the changes were statistically significant by SPSS 23.0.

Results 1. In observation group, HbA1c increased significantly at 8, 10, 12 and 24 hours compared with 0 hours ($P<0.05$).

2.In control group, HbA1c decreased significantly at 4, 6, 8, 10, 12 and 24 hours compared with 0 hours ($P<0.05$).

3. HbA1c of observation group at 4, 6, 8, 10, 12 and 24 hours increased significantly compared with control group ($P<0.05$).

Conclusions The effect of urea nitrogen on the determination of HbA1c by high performance liquid chromatography in simulated high urea nitrogen environment was studied. 37 ℃ water bath was used to simulate body temperature in order to accelerate biochemical reaction. In the observation group, HbA1c increased significantly after 8 hours, which was related to the formation of CarHb by non-enzymatic reaction of urea nitrogen, its metabolites and hemoglobin. Because the isoelectric points of CarHb and HbA1c are similar, the peak value of HbA1c may overlap with CarHb in HPLC analysis, resulting in the false increase of HbA1c in patients. The decrease of HbA1c in the control group after 4 h was related to the natural degradation of hemoglobin in 37 ℃ water bath. In conclusion, when patients use high performance liquid chromatography to detect HbA1c, clinicians should consider the effects of urea nitrogen.

PO-227

The morphological difference of fungal colonies among several potato dextrose agars

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Objective During the last decade, new technologies have provided a great progress on bacterial identification in clinical laboratories. However, the revolution of fungal identification remains on-going, and thus currently morphological approach is still highly inevitable to identify fungi in a daily routine, which requires specialized experience in clinical mycology. Together with the fact that we barely experience molds isolation, while routinely isolate a numbers of bacteria, complicates the whole identification procedure and the accuracy management of the laboratory. Therefore, we aimed to analyze the impact of the difference among several potato dextrose agars on fungal identification to make clear the one of the causes of the complication and ultimately to improve the quality of the clinical laboratories. Potato dextrose agar is a general purpose basal medium, which is one of the media commonly used. Although the most widely used media is Sabouraud dextrose agar, the proportion of potato dextrose agar has been gradually getting higher in Japan.
Furthermore, we are currently evaluating the utility of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) for the identification of filamentous fungi which are cultured on those potato dextrose agars.
Methods Strains and cultures; Genetically identified 20 strains of 20 species, *Alternaria alternata*, *Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus lentulus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus terreus*, *Cunninghamella bertholletiae*, *Exophiala dermatitidis*, *Exophiala jeanselmei*, *Fonsecaea pedrosoi*, *Fusarium solani*, *Microsporum canis*, *Microsporum gypseum*, *Paecilomyces lilacinus*, *Pseudallescheria boydii*, *Scopulariopsis brevicaulis*, *Sporothrix schenckii*, *Trichophyton mentagrophytes* and *Trichophyton rubrum*, were cultured on potato dextrose agars from Becton, Dickinson and Company (BD), Eiken Chemical Co., Ltd. (EIKEN), Kanto Chemical Co.,Inc. (KANTO), Kyokuto Pharmaceutical Industrial Co., Ltd. (KYOKUTO), Kohjin Bio Co., Ltd. (KOHJIN), Nikken Bio Medical Laboratory (NIKKEN), Nissui Pharmaceutical Co., Ltd.(NISSUI) at 30 °C for 3-30 days.
MALDI-TOF MS assay; Those strains are subjected to MALDI-TOF MS assay. Samples are prepared using direct transfer method, on-plate formic acid preparation and off-plate protein extraction. MALDI-TOF MS spectra are obtained using the MALDI Biotyper (Bruker).
Results Surprisingly, some of the strains showed a discriminative colonies on some agars compared with on the others even the components of the all agars are almost the same. In particular, colonies of *Exophiala dermatitidis*, *Exophiala jeanselmei*, *Fonsecaea pedrosoi and Sporothrix schenkii* dramatically differ from each other on all 7 agars, while *Aspergillus* spp. showed comparatively similar colonies on all agars. Colonies tends to grow slowly on the KYOKUTO and NIKKEN agars and wrinkle on the NIKKEN agar. *Microsporum gypseum* showed a typical colony on the EIKEN agar and the

Kohjin, by contrast, atypical on the KYOKUTO agar, which could cause a trouble. *Pseudallescheria boydii* didn't show the typical pale-brown color on the KYOKUTO agar. As mentioned above, morphological characteristics are keystone of fungal identification at the moment. Because of the lack in fungal identification experience, we might have to refer to a text for the pictures sometimes. But here, we must mention the possibility that the reference colonies can look a lot different from the ones on your own agar, as a strain showed various colonies depending on what agar is used in this research. Even if we could find the type of the agar used in the reference, we hardly find the manufacture of the agar. So that means, we better to assess the own agar with several reference fungal strains to check their morphological characteristics.

The morphological difference might result from the difference in the protein expression, which means the MALDI-TOF MS spectra could vary depending on the agar. Thus, we also evaluate the impact of the various potato dextrose agars on the MS spectra. Surprisingly, some strains show various identification scores depending on the agar used as expected. Here, we must emphasize the impact of growth conditions on MS spectra.

Conclusions In conclusion, the present study has firstly demonstrated that the morphological characteristics of the fungal colonies on various potato dextrose agars are incredibly diverse, which could lead to a failure on the routine identification of fungi in clinical laboratories. In addition, our studies are the first to demonstrate that the slight difference of agars affect the MS identification scores. The most important thing is to learn more about the feature of your own agar.

PO-228

Characterization of Mir-92a as a New Biomarker and Therapeutic Target for Hepatoblastoma

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Objective Hepatoblastoma (HB) is a common type of primary malignant hepatic tumor usually seen in children during the first 3 years of life. Annual incidence rate of HB is extremely low with 1.5 per million of population. The pediatric cancer has received considerable critical attention because of its dreadful prognosis owing to the ambiguous incipient symptoms and the high frequency of metastasis and recurrence. Various researches have shown that aberrant expression of miRNAs, plays a pivotal role in multifarious cancers. However, the role of miRNAs in HB is not clearly understood.

Methods Cell survival rate and apoptosis were examined by CCK-8 assay and Annexin V-FITC assay. Migration and invasion was detected by Transwell assay. qRT-PCR and Western blotting were used to measure the expression level of a gene at mRNA and protein level. The downstream target of miR-92a in HB cells were detected Dual Luciferase assay and RNA pull down assay.

Results In this study, we first analyzed the expression patterns of miR-92a in HB tissues and matched non-tumor liver tissues using qRT-PCR and in situ hybridization. Results demonstrated its expression level was significantly up-regulated in HB tissues. Additionally, we found that miR-92a could influence the proliferation, migration, invasion and apoptosis of HB through directly regulate its target gene PTEN. Furthermore, we found elevated expression of miR-92a is associated with poor prognosis in HB patients.
Conclusions These results provide adequate evidence that miR-92a plays a critical role in HB and may act as a potential diagnostic marker and therapeutic target in HB.

PO-229

Six-Year Seroprevalence of HBV, HCV, Syphilis and HIV in a large medical center in Nanjing, China

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Objective Hepatitis B (HBV) & C (HCV), Syphilis (TP) and human immunodeficiency virus (HIV) are the common and important causes of blood borne infection worldwide. This study is aimed to investigate the seroprevalence of HBV, HCV, TP and HIVin a large medical center in China.
Methods A retrospective analysis was performed on the patients who were screened for hepatitis B & C, Syphilis and HIV from January 2010 to December 2016.
Results The prevalence of newly diagnosed HBV, HCV, TP and HIV was 8.36%, 1.12%, 2.01% and 0.055% in 2010, and it changed to 6.45%, 0.76%, 2.06% and 0.041% in 2016 respectively. Males constitute 83.59% (275/329) of this newly diagnosed HIV population. 44.36% (122/275) of them were MSM(man who have sex with man).
Conclusions These results show declining prevalence of HIV, HBV, and HCV over time from 2010 to 2016, and the change in the mode of transmission of HIV infection mainly from blood and blood products to sexual transmission.

PO-230

The applicate prospect of AI in clinical laboratory

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Objective To explore the prospects of the practical applications of various test methods in clinical laboratory with AI.
Methods PubMed and CNKI journal database were used to search for related documents of 01/2018-12/2018 with the words "artificial intelligence and medicine" as keywords. A total of 1616 English documents and 204 Chinese documents were retrieved. Inclusion criteria: 1) artificial intelligence and medical laboratory; 2) artificial

intelligence and clinical laboratory. According to the included criteria, 36 papers were finally analyzed.

Results AI is a promising strategic technology that is developing at a rapid pace, and it is highly driven by a new round of industrial change. The latest AI has many fields, high intelligence ,and full autonomy. With the update and upgrade of AI, its application in clinical medicine is also very promising. The current clinical laboratory has the following aspects for the applications of AI: 1) Intelligent identification of cells. Computer numerical analysis, including hematuria and other body fluids, has been in existence for decades. Today, digital analysis equipment and digital analysis systems can save 90% of medical staff time, after manual review and can issue reports. 2) Intelligent analysis of chromosomes. The AI software automatically segments 46 chromosomes to identify abnormalities such as number, distortion, and translocation. Reports can be issued after manual review and analysis. 3) Verify data mining. The AI big data is used to analyze the test data, and the connection and development rules of various pathological markers are found, which provides high-value reference information for medical personnel to research and explore the mechanism of disease and diagnosis and treatment. There is no doubt that AI is inextricably linked to the future development of clinical tests. For the existing functions, it is necessary to continue to improve its recognition and identification capabilities in the future and improve the learning ability of the machine. At the same time, it can increase the networking function, create a national and even the world's testing medical platform, and interpret and update difficult cases online, thus achieving remote diagnosis and treatment. In addition, there are great development prospects in many aspects such as accurate interpretation, auxiliary diagnosis, audit error and equipment combination.

Conclusions With the continuous development of AI, the method of clinical laboratory is also constantly updated, but the clinical laboratory in China is not rich enough for AI application, and there are many aspects that can be integrated with AI to obtain higher efficiency and accuracy. The AI test database based on the test of big data will play an important role in disease diagnosis, tumor screening, auxiliary diagnosis, and test analysis. In the Internet era, the inspectors should not only learn how to use AI to simplify their work, but more importantly, they can take advantage of the human brain while using AI, play a greater role in decision-making and diagnosis, and improve the efficiency of inspection work. Make the inspection discipline and AI continue to develop and progress.

PO-231

Evaluation of serum exosomal lncRNAs as potential diagnostic and prognostic biomarkers for esophageal squamous cell carcinoma

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Objective Long non-coding RNAs (lncRNA) in exosomes have been recognised as promising stable biomarkers in cancers. The aim of this study was to identify serum-derived exosomes lncRNA signatures for diagnosis and prognosis of esophageal squamous cell carcinoma (ESCC).

Methods Based on previous studies, 24 ESCC-related lncRNAs were chosen and detected in 34 ESCC vs. adjacent tissues using quantitative real-time PCR. Exosomes from serum of ESCC and healthy subjects were isolated and identified. In the training set, exosomal lncRNA profiles from 202 ESCC patients and 202 healthy subjects was performed and established new models for ESCC detection. In the validation set, the diagnostic accuracy of candidate lncRNAs was further validated with an 222 additional individuals (111 ESCC patients and 111 healthy controls) using receiver operating characteristic curve.

Results There were 20 differentially expressed lncRNAs in ESCC compared to adjacent tissues. A 4-lncRNA signature (UCA1, POU3F3, ESCCAL-1 and PEG10) in serum exosomes for diagnosis of ESCC was finally developed by logistic regression model. The diagnostic accuracy of four-lncRNA panel was evaluated with AUC value of 0.844 and 0.853 for training and validation stage, respectively. The corresponding AUCs for patients with TNM stage I-II and III were 0.820 and 0.935, significantly higher than squamous cell carcinoma antigen ($P<0.001$), which were 0.652 and 0.642, respectively. Kaplan–Meier analysis indicated that patients with high levels of UCA1 and POU3F3 had significantly lower survival rate ($P<0.001$). In addition, POU3F3 was independently associated with ESCC prognosis ($P=0.004$).

Conclusions This findings demonstated that a exosomal 4-lncRNA panel in serum was identified as novel and reliable molecular biomarker for ESCC diagnosis and POU3F3 was an independent factor for ESCC prognosis. This discovery of the novel lncRNA biomarkers in circulating exosomes could open up new avenues for investigating the ESCC progression.

PO-232

Genetic Characterization and Recombinant History of a Novel HIV-1 Circulating Recombinant Form (CRF101_01B) Identified in Yunnan, China

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Objective A novel HIV-1 circulating recombinant form (CRF101_01B) was identified and named.

Methods The study was approved by the Yunnan Provincial Hospital of Infectious Diseases Ethics Committee, AIDS Care Center (Approval No. YNACC [2015]-12). All participants supplied written informed consent for specimen collection and subsequent analyses.The near full-length genome (NFLG) amplification and sequencing were performed as previously described (Grossmann et al., 2015). In brief, RNA was isolated from 200 μl plasma using the Virus RNA Mini Kit (Tiangen) according to the procedure described in the manual. Then the near full-length HIV-1 genome was amplified separately using reverse transcription (RT)-nested polymerase chain reaction according to the method described in previous reports (Grossmann et al., 2015). The generated products were analyzed by agarose gel electrophoresis, and the positive PCR samples were purified using the PCR Product Gel Extraction Kit (Tiangen) and were then sequenced by Invitrogen Co (Guangzhou, China).Phylogenetic trees were constructed based on the obtained datasets with the maximum-likelihood method using MEGA v.6.0.6 and the general time reversible + gamma distribution + invariant sites (GTR + τ + I) model. Bootstrap values were calculated based on 1000 replications of the alignment. The reference sequences relevant to HIV-1 epidemics in Asia were downloaded from the Los Alamos National Laboratory HIV sequence database. Recombination breakpoints were determined using SimPlot 3.5.1 software to perform bootscanning, and informative-site analyses. Based on the information generated from Simplot, the structure of the new HIV-1 recombinant forms (01AE/B) were elucidated using the Recombinant HIV-1 Drawing Tool.

Results The high frequency of multiple HIV-1 recombinant events among the B, C and CRF01_AE were constantly occurring in Yunnan China. Here, we characterized a novel HIV-1 circulating recombinant form (CRF) consisting of CRF01_AE and subtype B (CRF101_01B) from three epidemiologically unlinked individuals. Phylogenetic analysis based on near full length genome (NFLG) sequences revealed that CRF101_01B formed a distinct monophyletic cluster supported by a high bootstrap value of 100%, distantly related to all known HIV-1 CRFs. CRF101_01B had a CRF01_AE backbone with two B segments inserted, respectively, in the gag and pol region. Further, subregion tree analysis showed that CRF01_AE backbone and subtype B segment inserted originated from a Thailand lineage. In addition, our study found that CRF101_01B originated around the year 1996-1998.

Conclusions This findings described a novel HIV-1 CRF, and highlighted the importance of continual monitoring of genetic diversity and complexity of HIV-1 strains in Yunnan, China.

PO-233

Exosome-transmitted miR-128-3p increase chemosensitivity of oxaliplatin-resistant colorectal cancer

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Objective Oxaliplatin resistance is a major challenge for treatment of advanced colorectal cancer (CRC). Both acquisition of epithelial-mesenchymal transition (EMT) and suppressed drug accumulation in cancer cells contributes to development of oxaliplatin resistance. Aberrant expression of small noncoding RNA, miR-128-3p, has been shown to be a key regulator in tumorigenesis and cancer development. However, its roles in the progression of CRC and oxaliplatin-resistance are unknown.
Methods Oxaliplatin resistant CRC and normal intestinal FHC cells were transfected with a miR-128-3p expression lentivirus. After transfection, FHC-derived exosomes were isolated and co-cultured with CRC cells. miR-128-3p expression in resistant CRC cells, FHC cells, and exosomes was quantified by quantitative real-time PCR (RT-qPCR). The mRNA and protein levels of miR-128-3p target genes in resistant CRC cells were quantified by RT-qPCR and western blot, respectively. The effects of miR-128-3p on CRC cell viability, apoptosis, EMT, motility and drug efflux were evaluated by CCK8, flow cytometry, Transwell and wound healing assays, and atomic absorption spectrophotometry. Xenograft models were used to determine whether miR-128-3p loaded exosomes can re-sensitize CRC cells to oxaliplatin in vivo.
Results In our established stable oxaliplatin-resistant CRC cell lines, in vitro and vivo studies revealed miR-128-3p suppressed EMT and increased intracellular oxaliplatin accumulation. Importantly, our results indicated that lower miR-128-3p expression was associated with poor oxaliplatin response in advanced human CRC patients. Moreover, data showed that miR-128-3p-transfected FHC cells effectively packaged miR-128-3p into secreted exosomes and mediated miR-128-3p delivery to oxaliplatin-resistant cells, improving oxaliplatin response in CRC cells both in vitro and in vivo. Lastly, miR-128-3p overexpression up-regulated E-cadherin levels and inhibited oxaliplatin-induced EMT by suppressing Bmi1 expression in resistant cells. It also decreased oxaliplatin efflux through suppressed expression of the drug transporter MRP5.
Conclusions We demonstrate that miR-128-3p delivery via exosomes represents a novel strategy enhancing chemosensitivity in CRC through negative regulation of Bmi1 and MRP5. Moreover, miR-128-3p may be a promising diagnostic and prognostic marker for oxaliplatin-based chemotherapy.

PO-234

A Biomarker LncRNA MAFTRR for Identifying High-Risk Patients with Ulcerative Colitis-Associated Colorectal Cancer

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Objective Long noncoding RNA (lncRNA) play important roles in tumorigenesis and progression, as a field defect in some instances, and may be an early event in colitis associated carcinogenesis (CAC). We aimed to determine whether specific lncRNA signature patterns could be used to identify patients with ulcerative colitis (UC) who are at increased risk for colorectal neoplasia.

Methods We use TCGA and GEO database to analyze the data and obtain top 10 aberrant lncRNA (5 up-regulated and 5 down-regulated) which play important roles in UC and CRC progression. Then we obtained 573 colorectal tissue specimens collected from patients with UC (354 without neoplasia, 81 with dysplasia, and 138 with CAC), from 3 independent cohorts for three phase experiment in The First Affiliated Hospital of Traditional Chinese Medicine University, Qilu Hospital and Second hospital of Shandong University between 2008 and 2018. We quantified these lncRNAs by RT-qPCR analysis. We analyzed clinical data to determine whether lncRNA patterns were associated with age, location, or segment of the colorectum. Cohort 2 and 3 were used to perform studies to training or validation the association between specific lncRNA in non-tumor rectal mucosa from patients with UC at risk of CAC.

Results Based on GEO and TCGA analysis, we selected top 10 aberrant CAC-related lncRNA as potential diagnostic candidates. Then expression profiles of 10 lncRNA selected were validated in 58 UC (30 without neoplasia, 10 with dysplasia, and 18 with CAC) of tissues by quantitative real-time PCR, only lncRNA MAFTRR thus identified were further validated in tissue samples from two independent cohorts. Among patients with UC without neoplasia, rectal tissues had significantly higher levels of MAFTERR than in proximal mucosa; expression levels of MAFTRR were associated with severity of inflammation and duration of UC in rectal mucosa. MAFTRR was significantly higher in samples from patients with dysplasia or CAC compared with samples from patients without neoplasia. Receiver operating characteristic analysis revealed that methylation levels of MAFTRR in rectal mucosa accurately differentiated patients with CAC from those without. MAFTRR in rectal mucosa was an independent risk factor for CAC. MAFTRR could discriminate UC patients with or without dysplasia or CAC in the training cohort (area under the curve, 0.79) and the validation cohort (area under the curve, 0.82).

Conclusions In training and validation cohorts, we found MAFTRR was high expressed in rectal mucosal samples from patients with UC with dysplasia or CAC compared with patients without neoplasms. MAFTRR also associated with severity of inflammation and might be used to identify patients with UC at greatest risk for developing CAC. Our findings provide evidence for a field defect in rectal mucosa from patients with CAC.

PO-235

Increased expression of the long noncoding RNA CRNDE-h indicates a poor prognosis in colorectal cancer, and is positively correlated with IRX5 mRNA expression

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Objective The long noncoding RNA (lncRNA) colorectal neoplasia differentially expressed - h (CRNDE-h) plays important roles in the early stages of human development and cancer progression. We investigated the expression and clinical significance of lncRNA CRNDE-h in colorectal cancer (CRC).

Methods The expression level of lncRNA CRNDE-h was analyzed in 142 CRC tissues and 142 paired adjacent nontumorous tissues, along with 21 inflammatory bowel diseases, 69 hyperplastic polyp, and 73 colorectal adenoma samples, using quantitative real-time polymerase chain reaction. The association between lncRNA CRNDE-h, and Iroquois homeobox protein 5 (IRX5) mRNA was examined in the same 142 CRC tissues.

Results We found that lncRNA CRNDE-h level was elevated in the CRC and adenoma groups compared with the other groups (all at P,0.001). In CRC, upregulation of lncRNA CRNDE-h was significantly correlated with large tumor size, positive regional lymph node metastasis, and distant metastasis (all at P,0.05). Area under the curve for lncRNA CRNDE-h showed diagnostic capability for distinguishing CRC from other groups. Patients with CRC with high lncRNA CRNDE-h expression level had poorer overall survival than those with low lncRNA CRNDE-h expression (log-rank test, P,0.001). Further, multivariable Cox regression analysis suggested that increased expression of lncRNA CRNDE-h was an independent prognostic indicator for CRC (hazard ratio [HR]=2.173; 95% confidence interval [CI], 1.282–3.684, P=0.004). Furthermore, lncRNA CRNDE-h expression was positively correlated with IRX5 mRNA in CRC tissues.

Conclusions Our data offers convincing evidence for the first time that lncRNA CRNDE-h is associated with adverse clinical characteristics and poor prognosis, which suggests that it might play an important role in CRC development and progression and might have clinical potential as a useful prognostic predictor.

PO-236

Exosomal long noncoding RNA CRNDE-h as a novel serum-based biomarker for diagnosis and prognosis of colorectal cancer

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Objective Cancer-secreted long non-coding RNAs (lncRNAs) are emerging mediators of cancer-host cross talk. The aim of our study was to illustrate the clinical significance of the lncRNA CRNDE-h in exosomes purified from the serum of patients with colorectal cancer (CRC).

Methods The study was divided into four parts: (1) The exosome isolated methods and lncRNA detected methods which accurately and reproducibly measure CRC-related exosomal CRNDE-h in serum were optimized in preliminary pilot stage; (2) The stability of exosomal CRNDE-h was evaluated systematically; (3) The origin of exosomal CRNDE-h was explorated in vitro and in vivo; (4) The diagnostic and prognostic value of exosomal CRNDE-h for CRC were validated in 468 patients.

Results In pilot study, our results indicated that exosomal CRNDE-h was detectable and stable in serum of CRC patients, and derived from tumor cells. Then, the increased expression of exosomal CRNDE-h was successfully validated in 148 CRC patients when compared with colorectal benign disease patients and healthy donors. Exosomal CRNDE-h level significantly correlated with CRC regional lymph node metastasis ($P = 0.019$) and distant metastasis ($P = 0.003$). Moreover, at the cut-off value of 0.020 exosomal CRNDE-h level of serum, the area under ROC curve distinguishing CRC from colorectal benign disease patients and healthy donors was 0.892, with 70.3% sensitivity and 94.4% specificity, which was superior to carcinoembryogenic antigen. In addition, high exosomal CRNDE-h level has a lower overall survival rates than that for low groups (34.6% vs. 68.2%, $P < 0.001$).

Conclusions In conclusion, detection of lncRNA CRNDE-h in exosome shed a light on utilizing exosomal CRNDE-h as a noninvasive serum-based tumor marker for diagnosis and prognosis of CRC.

PO-237

Analysis of Protein Biomarkers in Serum of Patients with Schizophrenia

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Objective Schizophrenia is one of the most severe mental disorders characterized by fundamental disturbances in thought, affect, emotion, and perception. Rapid diagnosis and treatment have been shown to positively impact the progression and outcome of schizophrenia. The aim of this study was to explore a high-throughput analysis of the serum protein profiles from individuals with schizophrenia and healthy controls, and to screen for potential biomarkers as a "signature" coupled with an artificial neural network (ANN) to predict schizophrenia.

Methods Sera were separated from the fasting blood specimens from 66 patients with schizophrenia and 62 control individuals. Protein fingerprints were detected using the ProteinChip technology. Data were comparatively analyzed to select protein biomarkers that were used to construct a predictive model based on an ANN. The model was repeatedly trained and blindly tested to validate the predictive efficacy for schizophrenia.

Results Overall, a total of 428 signal clusters were detected. Among them, 56 proteins were differentially expressed ($P<0.05$) between the two groups. Among them, five protein markers (mass-to-charge ratio at 2820, 3219, 3317, 4284, and 4347) were chosen to develop an ANN predictive model. The established model was blindly tested. Among the 32 schizophrenia subjects, thirty were correctly predicted and two were misjudged, and from the 36 control subjects, 33 were correctly predicted and three were misjudged. The model yielded a sensitivity of 91.7% and a specificity of 93.8%.

Conclusions No established laboratory tests, electrophysiological paradigms, or neuro-imaging studies are yet available to explicitly diagnose schizophrenia. The diagnostic or discriminating process based on clinical symptoms always takes several weeks, months, and even years. Thus, there is often a delay in therapeutic opportunity until the correct diagnosis is established. It is urgent to establish a novel method for diagnosing schizophrenia as early as possible to avoid a serious outcome. Our preliminary study showed the potential of proteomic method for predicting schizophrenia. The established model based on the protein markers and ANN technology could be a promising method to predict and differentiate schizophrenia and deserves further study. The screened biomarkers might also be important indicators of schizophrenia risk and may give substantial insight into the pathogenesis of this devastating disorder.

PO-238

Emergence and Potential Spread of Multidrug-Resistant Sequence Type 307 Klebsiella pneumoniae Clinical Bloodstream Isolates Co-producing OXA-48 and NDM-1 in Shanghai, China

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Objective Our study assessed antimicrobial susceptibility and phylogenetic relationships of *Klebsiella pneumoniae* bloodstream isolates in Shanghai, in order to facilitate managements of these infections and highlight some unknowns for future prevention.

Methods Fifty-three carbapenem-resistant *K. pneumoniae* bloodstream isolates were obtained in a general hospital in Shanghai. Antimicrobial susceptibility tests, MLST and eBURST were constructed. The plasmids harboring bla_{OXA-48} were analyzed through conjugation experiments, S1-nuclease pulsed-field gel electrophoresis (S1-PFGE), and hybridization with specific probes. Whole genomes of bla_{OXA-48}-producing isolates were sequenced by MiSeq (Illumina).

Results Of 53 isolates, 24 (60.0%) harbored carbapenemase-encoding genes, including bla_{KPC-2}, bla_{KPC-3}, bla_{OXA-48}, and/or bla_{NDM-1}. Of these 24 isolates, 3 harbored bla_{OXA-48} and bla_{NDM-1}, belonging to sequence type 307 (ST307); 1 harbored bla_{OXA-48} and bla_{KPC-2}, belonging to ST11. S1-PFGE showed that 4 OXA-48-producing *K. pneumoniae* all harbored 3 or more plasmids. Southern hybridization analysis revealed bla_{OXA-48} located on a 60-kb IncL/M conjugative plasmid (Figure1). The genetic context of bla_{OXA-48} (IS*1999*-*LysR*- bla_{OXA-48}-IS*1*-IS*1999*) displayed overall nucleotide identity (99%) to pRJ119-OXA48.

Conclusions This paper indicated potential spread of multidrug-resistant ST307 *K. pneumoniae* isolates co-producing OXA-48 and NDM-1 in Shanghai, which highlightedc increased surveillance of OXA-48 is urgently needed in China.

PO-239

Study on the Difference of Serum detection technology of mycoplasma pneumoniae pneumonia (MPP) based on Raman spectroscopy in children

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Objective To explore a new method of serum diagnosis based on Raman spectroscopy by using Raman spectroscopy of blood serum to discriminate patients with Mycoplasma pneumoniae pneumonia (MPP) from normal children.
Methods The Raman signals of 100 normal children and 100 patients with mycoplasma pneumonia were measured and analyzed.
Results Peaks at wave numbers 444.71,490.47,998.89,1028.07,1152.93,1200.27, 1245.68,1267.48,1333.92,1444.98,1515.33,1653.34 cm^{-1} could be consistently observed in all the two groups,and the intensity of peaks different in each group.In comparison with control group,the intensities at 1653.34 cm^{-1} were weakened (t=2.137,P<0.05) , the intensities at 1152.93,1515.33 cm^{-1} were enhanced of the patients' serum (t=2.027 , P<0.05 ; t=2.028 , P<0.05) .
Conclusions This preliminary study demonstrates that serum Raman spectroscopy can be used as a complementary method in the early diagnosis of mycoplasma pneumonia.

PO-240

Advance of Biomarkers Detection Assays Based on Catalytic Hairpin Assembly

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Objective Nucleic acids are considered as perfect programmable materials for nanostructures with various sizes and shapes, not merely genetic iniformation carriers. Catalytic hairpin assembly (CHA) is an enzyme-free, high-efficiency and isothermal amplification method. For this reason, CHA has been applied for developing various biosensors.
Methods Hundreds of literatures regarding CHA based biomarkers' detection assays have been referred in this review. We first describe the reaction mechanism, development, kinetics characterization of CHA and anslysis techniques of CHA products. Furthermore, we summarize the representive biosening application of CHA. Finally, challenges and outlook about CHA development are considered.
Results CHA, first proposed in 2008, is performed with two partially complementary DNA hairpins and one single-strand oligonucleotide under isothermal condition in three steps, and realizes cascade signal amplification in a short time. For more perfect performance, diverse CHA systems have been presented including simplified and typical CHA circuit, mismatCHA, cross-CHA, self-replicating CHA, two-layer CHA, dual CHA, branched CHA and genetically encoded RNA CHA. The versatile CHA is able to be adapted for multiple different analytical formats such as fluorescent, electrochemical, colomeric, surface plasmon resonance and electrophoretic. Studies also indicate that CHA can be easily and rationally integrated with other isothermal amplification reactions in various conditions (different temperatures, buffers and enzymes) to improve the sensitivity and specificity of assays. Though the entity of CHA is nucleic acid strand displacement, the detection targets are not confined to nucleic acids. Many other biomarkers including metal ions, proteins, enzymes and even cancer cells have been measured based on CHA.

Conclusions In the past decade, tremendous achievements have been obtained about CHA from origin to development. CHA circuits with unique properties have provide diversiform biosensors with promising performance and extreme convenience. In order to further extend the application suitable for pratice, more efforts need to be made, suach as more interesting CHA system, mor pecific and stable recognization elements, coupling with absolute quantification technologies (such as droplet microfluidics) .

PO-241

Zymosan promotes Candida albicans adhesion, proliferation and IL-1β production of oral squamous cell carcinoma

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Objective Oral squamous cell carcinoma (OSCC) is the most common type of head and neck squamous cell carcinoma (HNSCC), and the interaction between *Candida albicans* and oral cancer remains unclear.
Methods Cell proliferation assay was performed with CCK-8 to evaluate the effect of zymosan on OSCC cell lines, and potential mechanism was explored by quantitative real-time PCR, immunofluorescence assay and western blot. Cell adhesion assay was conducted to determine the adhesion of *Candida albicans* to OSCC cells, and related gene expression and protein was detected. Also, the proinflammatory cytokines including IL-6, IL-8, TNF-α and IL-1β were detected by ELISA.
Results In current study, fungi cell wall zymosan promotes proliferation of OSCC cell lines including WSU-HN4, WSU-HN6 and CAL-27 by MTT and CCK-8 assay via TLR2/MyD88 pathway. By cell adhesion assay, number of *Candida albicans* per oil field was significantly increased in ZYM-treated OSCC cells compared to controls. When treated with zymosan, OSCC cells secreted significantly more pro-inflammatory cytokine IL-1β, which could enhance inflammation in oral cancer microenvironment.
Conclusions Fungi cell wall zymosan promotes proliferation, *Candida albicans* adhesion and IL-1β production of oral squamous cell carcinoma.

PO-242

Clinical application of HMAM and CXCL16 and CA153 in the diagnosis of breast cancer.[1. Funded by Health Commission of Sichuan Province(Project No 120112); 2. Funded by Science and Technology Department of Sichuan Province (Project No.5345)]

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Objective To discuss clinical application of HMAM gene expression and HCY and CA153 and CXCL16 in the diagnosis and therapy of breast cancer.
Methods HMAM in 50 health women, 78patients with benign breast disease and 117 patients with malign breast disease and 86 patients with other malignant tumors were detected by FQ-PCR. HCY was detected by enzyme method. CXCL16 was detected by ELISA. CA153 was detected by chemical luminous method. The relationships between four index and the clinic opathological characteristics of breast cancer patients including patients' age, tumor size, histological grade, TNM stage and lymph node metastasis status and before and after surgery were analyzed.
Results HMAM and HCY and CA153 and CXCL16 in breast cancer group were higher than those in normal controls and benign breast disease group. HMAM and CA153 in breast cancer group were higher than those in other malignant tumors group. There were no significant difference in HCY and CXCL16 between breast cancer group and other malignant tumors group. In breast cancer group, with the increase of clinical stages, and HMAM and CA153 and HCY and CXCL16 in the stage of III+IV were higher than I+II. HMAM and CA153 and CXCL16 decreased after operation, while HCY had no difference. The specificity of HMAM was highest. The sensitivity of CXCL16 was highest. Four index showed a statistical difference among invasive breast cancer patients with different tumor sizes, TNM stages and with or without lymph node metastasis , but no significant difference was observed between different age groups and between the patients with different histological grades The sensitivity and negative predictive value were improved by the combined of CA153 and HCY and CXCL16. The specificity and positive predictive value were improved by the combined of four index.
Conclusions HMAM and CA153 play a role to predict the prognosis of breast cancer. HMAM and CA153 and CXCL16 can follow-up the curative effect of breast cancer after operation, the joint detection of HMAM、CA153、HCY and CXCL16 is helpful to improve the early diagnosis of breast cancer.

PO-243

Diagnostic efficacy evaluation of IL-1RI, IL-1 β and CDK2 in peripheral blood and synovial fluid with RA

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Objective To explore the diagnostic efficacy of interleukin 1 receptor typeI(IL-1RI), interleukin 1β(IL-1 β) and cyclin dependent kinase 2(CDK2) in peripheral blood and synovial fluid with rheumatoid Arthritis (RA).

Methods There were selected 94 cases with RA patients in rheumatology outpatient and inpatient department, 40 cases with systemic lupus erythematosus (SLE) patients in outpatient department, 20 cases with acute upper respiratory tract infection(AURTI) patients in emergency department, 20 healthy persons. All subjects were eligible for inclusion criteria. All subjects were drew vein blood 3 ml besides 1 ml knee joint fluid from 24 patients with active RA patients. The level of IL-1RI, IL-1β and CDK2 were detected in serum and synovial by quantitation ELISA, then the three items were evaluated diagnostic efficacy.

Results There were all significant differences among experimental groups on either IL-1RI, IL-1β or CDK2 by square variance analysis(P<0.001), respectively. On IL-1RI, there were significant differences between RA patients group and RA patients joint synovial fluid group or SLE patients group or acute upper respiratory tract infection group and control group (P<0.001), respectively. On CDK2, there were significant differences between RA active phage and RA relieve phage, between RA patients group and RA patients joint synovial fluid group or SLE patients group or acute upper respiratory tract infection group or control group (P<0.001) , respectively. On IL-1β, there were significant differences between RA active phage and RA relieve phage, between RA patients group and RA patients joint Synovial fluid group or healthy people group (P<0.001), respectively. Compared RA patients active phage with RA relieve phage, area under curve of ROC in CDK2 was largest, followed IL-1β andIL-1RI. Compared RA patients group with SLE patients group, area under curve of ROC in CDK2 was largest, followed IL-1RI. Compared RA patients group with acute upper respiratory tract infection patients group, area under curve of ROC in IL-1RI was largest, followed CDK2. Compared RA patients group with control group, area under curve of ROC in CDK2 was largest, followed IL-1RI.

Conclusions IL-1RI had low diagnostic efficiency next to CDK2, but it could efficiently differentiate RA and acute upper respiratory infection (AURI). CDK2 had higher diagnostic efficiency, which could efficiently differentiate active phase and relieve phase of RA, and differentiate RA and SLE, but had low diagnostic efficacy next to IL-1RI, in differentiating RA and AURI. CDK2 plus IL-1RI plus IL-1β paralleling joint diagnosis may increase diagnostic value of RA. CDK2 plus IL-1RI plus IL-1β tandem joint diagnosis may increase early diagnostic value of RA.

PO-244

Application of alanine aminotransferase reference method without pyridoxal 5-phosphate

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Objective To investigate the accuracy and comparability of alanine aminotransferase measurement results on human serum samples and commercial materials before and after calibration with a common human serum calibrator assigned by the reference method without pyridoxal 5-phosphate.
Methods Five frozen human-pooled serum samples were assigned values by the reference method without pyridoxal 5-phosphate for ALT in four candidate reference laboratories, which were used to evaluate the results of ALT catalytic activity from ten testing systems in Guangzhou. One of the serum samples was used as the common calibrator. The results of serum samples and commercial materials from difference systems before and after calibration were analyzed for bias and intersystem variation.
Results After calibration, the variance of the systems for the results of serum samples decreased from between 11.09% and 8.60% to between 6.78% and 2.30%, and the bias decreased dramatically from between -12.52% and -8.44% to between -3.36% and -0.08%.Slope of the regression line of ALT results of serum samples between reference systems and routine systems after calibration were closer to value 1 and intercept closer to 0 than those obtained before calibration.
Conclusions Accuracy and comparability of ALT measurement can be improved by using a common human serum calibrator. But commercial materials may not be commutable for human serum in ALT measurements.

PO-245

Candidate reference measurement procedure for determination of urea in serum by liquid chromatography-tandem mass spectrometry

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Objective Urea is an important indicator of liver and kidney disease, and very frequently determined in clinical chemistry.
Methods The reference measurement procedures (RMPs) for serum urea recognized by the Joint Committee for Traceability in Laboratory Medicine are spectrophotometry, and isotope dilution (ID)-mass spectrometry (MS) coupled with gas chromatography. This study investigated a candidate RMP (cRMP) for detecting serum urea directly via ID-liquid chromatography (LC)-MS/MS, without derivatization, which simplifies pre-processing samples. The cRMP was developed and evaluated relative to the recognized RMP, inter- and intra-laboratories.

Results The intra-precisions were 1.35%, 1.98% and 1.47% at 4.95, 24.74 and 31.36 mmol/L, respectively; inter-precision was 2.10%, 2.60% and 2.10%. The relative bias for the measurement of standard human serum (SRM 909c) was -0.49%. The relative biases were 0.41% and 0.02% for IFCC-RELA (International Federation of Clinical Chemistry and Laboratory Medicine-External Quality Assessment Scheme [EQAS] for reference laboratories) 2015A and 2015B. The linearity response between 2.4 mmol/L and 53.7 mmol/L was R^2 = 0.9989. No carryover, ion suppression, or interference was detected. Correlation was acceptable with the reference spectrophotometry (R^2 = 0.9985, $P < 0.0001$).

Conclusions Between our laboratory and other reference laboratories, the absolute deviation range for IFCC-RELA 2016A and 2016B was from -0.63 to 1.52 mmol/L. This well-characterized cRMP for urea can provide a base of accuracy for the traceability of clinical systems.

PO-246

The differential analysis and functional verification of miRNAs expression profile in breast cancer

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Objective Breast cancer is one of malignant tumor which causes serious damage to the women's health. MiRNA is a fascinating kind of biomolecule due to their vital functions in gene regulation and potential value as biomarkers for serious diseases including cancers. Genome-wide miRNA expression may be useful for predicting risk and/or for the early detection of breast cancer.

Methods 10 cases diagnosed breast cancer patients and 10 cases of normal controls were selected. By high-throughput miRNA sequencing from 10 pairs breast cancer tissues, adjacent normal tissues, serum and serum from normal persons, and using Target Scan and Clip-seq database, we selected miRNAs specifically expressed in breast cancer. Then we used real-time fluorescence quantitative PCR test the level of miRNA expression from serum of large samples. We picked the miRNA with statistical difference. For the miRNA function, we designed and synthesised the miRNAs inhibitors, and transfected to breast cancer cells MDA-MB-435, MDA-MB-468 to detected cell vitality by CCK8.

Results After the analysing of miRNA high-throughput sequencing from breast cancer pathology organization, adjacent tissues, serum and serum from normal persons, we picked out 28 cases difference expression of miRNAs in 986 cases.More than 2 times different expression and less than 30 CT value of RT-PCR as the standard, we selected 4 miRNAs: miR-374a-5p, miR-223-3p, miR-423-5p and miR-320a. To RT-PCR results showed the stable and different expression of miRNA in 113 cases of breast cancer patients from 104 cases of healthy control group. The miRNA expression of miR-374a-5p, miR-223-3p, miR-423-5p and miR-320a in the breast cancer group was up-regulated with diffenence respectively($P < 0.05$). Besides, the expression of miRNA had significant correlation with clinical pathological characteristics. MiR-374a-5P had higher expression in lymph node metastasis group (P = 0.001); MiR-223-3P expressed

differently between the different molecular classification (P = 0.040), the higher expression of miR-223-3P associated with ER negative estrogen receptor status (P = 0.035); The expression of miR-423-5p, miR-320a are positive correlation with clinical stages(P = 0.001,0.014) and Ki-67 (P = 0.001,0.015). Functionally, we designed and synthesised the miRNAs inhibitors, and transfected to breast cancer cells MDA-MB-435, MDA-MB-468 to detected cell vitality by CCK8. We found that miR-223-3p inhibitor could inhibit miR-223-3p in MDA-MB-468, result in the inhibition of MDA-MB-468 energy. At the same time, miR-423-5p could inhibit in MDA-MB-468 and MDA-MB-435, suggesting that miR-223-3p, miR-423-5p could be inhibitors of tumor suppressor genes and regulate activity of breast cancer cells.

Conclusions With help of the new generation of high throughput sequencing method of breast cancer, we have picked out specific differentially expressed miRNAs, including miR-374a-5p, miR-223-3p, miR-423-5p, miR-320a. The expression of the miRNAs were stable in serum and tissue. Meanwhile, The miR-223-3p inhibitor and miR-423-5p inhibitor can effectively inhibit breast cancer cell activity, which lay a foundation for subsequent function study. So we hypothesized they can be used as potential biomarkers of breast cancer for early diagnosis, prognosis and therapy target.

PO-247

Derivatization-free candidate reference measurement procedure for determining the concentration of 17β-estradiol in serum by isotope dilution liquid chromatography-tandem mass spectrometry

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Objective 17β-Estradiol (E_2) is routinely analyzed in clinical laboratories for the assessment of female reproductive function and plays expanding roles in other fields. Herein, a highly accurate candidate reference measurement procedure (RMP) for the determination of E_2 in human serum was developed with the technique of isotope dilution liquid chromatography-tandem mass spectrometry (ID-LC-MS/MS).

Methods

The serum samples require no derivatization and are extracted by liquid-liquid extraction. Bracketing calibrators was used for quantification. The accuracy of the method was confirmed by certified reference materials (CRMs) for E_2: BCR-576, BCR-577, and BCR-578. In addition, the method was further validated by split-sample comparison to established RMPs. The highly accurate method was used to measure E_2 in serum samples from 60 patients for the evaluation of three immunoassays that are commonly used in clinical laboratories in China, i.e., Siemens IMMULITE 1000 (Siemens), ARCHITECT $i2000_{SR}$ (Abbott), and Cobas 6000 (Roche).

Results The lowest limit of detection (LLoD) and the lowest limit of quantification (LLoQ) for the method were estimated to be 2 pg/mL (7 pM) and 5 pg/mL (18 pM), respectively. The intra- and inter-assay imprecisions were ≤ 2.91% at 15.24, 141.50, and 483.13 pg/mL, respectively; the analytical recoveries were 98.73–100.77%; and the

linear response was 12 – 3,783 pg/mL (44 – 13,889 pM). The method demonstrated high agreement with CRMs and established RMPs. Bland-Altman plots of the E2 results revealed concentration-dependent immunoassay biases.

Conclusions The newly developed ID-LC-MS/MS method is precise, facile, and reliable. It does not require lengthy derivatization and can provide an accurate concentration to which routine methods for E2 determination can be compared.

PO-248

Measurement of HbA1c and HbA2 by Capillarys 2 Flex Piercing HbA1cprogram for simultaneous management of diabetes and screening for thalassemia

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Objective Hemoglobin A_{1c} (HbA_{1c}) is an important index for diabetesmanagement.Thalassemia, one of the most common genetic abnormalities, could interferesome assays for HbA_{1c}measurement.Therefore, it is useful to be able to screen for thalassemia while measuring HbA_{1c}.Here, we used Capillarys 2 Flex Piercing(Capillarys 2FP)HbA_{1c} programto simultaneously measure HbA_{1c} and screen thalassemia.

Methods A cohort of 498 normal controls and 168 thalassemias wereanalyzed by Capillarys 2FP HbA_{1c} program (Sebia, France). For method comparison, 98 thalassaemias were quantified byPremier Hb9210 (Trinity Biotech, Ireland).For verification, eight thalassemias were confirmed by the International Federation of Clinical Chemistry and Laboratory Medicine (IFCC) reference method.

Results Among 98 thalassaemias, Capillarys 2FP did not provide a HbA_{1c} result in 3 samples with HbHdue to the overlapping of HbBart's with HbA_{1c} fraction;for the remaining 95 thalassaemias, Bland-Altman plot showed 0.00±0.35% absolute bias between two systems, and a significant positive bias above 7% was observed only in two HbH samples. For verification, the HbA_{1c}values obtained by Capillarys 2FP were consistent with the IFCC targets (relative bias < ±6%) in all of the 8 samples tested by both methods. For screening samples with α-thalassaemia silent/trait or β-thalassemia trait,the optimal HbA_2 cut-off values were ≤2.2% and >2.8%, respectively.

Conclusions Our results demonstrated the Capillarys 2FP HbA_{1c} program could report an accurate HbA_{1c} value in thalassemia, andHbA_2 valueand abnormal bands (HbH and/or HbBart's, elevated HbA_2 and/orHbF)could provide valuable information for itsscreening.

PO-249

Comparison of human serum 17β-estradiol quantification using the ID-LC-MS/MS assay with the chemiluminescent immunoassays

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Objective 17β-Estradiol is routinely analyzed in clinical laboratories of the assessment of female reproductive function and has expanding roles in other fields.However, due to low concentration levels aswell as the presence of the metabolites or structural analogues which having molecular masses close to 17β-Estradiol that can cross react with the immunoassay,measurements of 17β-Estradiol in human serum are complicated.

Methods [2,3,4-$^{13}C_3$]17β-estradiol was used as an internal standard. Theestradiol and its internal standard were extracted fromserum matrix using liquid-liquid extractionprior to reversed-phase LC-MS/MS and require no derivatization.The analysis was carried out withelectrospray ionization in the negative ion mode monitoringthe m/z 271→145 m/z as the quantifier, 271→183 m/z as the qualifier, and 274→148 m/z for [2,3,4-$^{13}C_3$]17β-estradiol. Bracketing calibrators was used for quantification. The accuracy of the measurement was evaluated bya comparison of results of this reference method onlyophilized human serum reference materials for estradiol[2015 IFCC external quality assessment scheme for Reference Laboratories in Laboratory Medicine] with the certified values determined by six reference laboratory from different countriesand by a recovery study for the added E2.Weevaluated intra-assay and inter-assay imprecision.The method procedure was validated against the JCTLM-certified reference method and used in measuring 17β-estradiol of 60 patient serum samples for evaluating 3 immunoassays, that are commonly used in China, i.e.,Siemens IMMULITE 1000(Siemens), ARCHITECT i2000$_{SR}$(Abbott), and Cobas 6000(Roche).

Results The LC-MS/MS method was validated andshowed limit of detection 5pg/mL; limit of quantification 10pg/mL; linearity of response to 14.82 ng/mL; The intra-assay precisionCVs (n = 15) were3.69%, 1.92%, and 1.84%; and the inter-assay precision CVs (9 runs/day, over 5 days) were4.21%, 2.54%, and 2.74%, respectively.And analyticalrecoveries werefrom 98.73to 100.77%. The linear regressionequationshowed r^2=0.9395 (Siemens IMMULITE 1000 = 0.9429LC-MS/MS+28.1300, 95% CI for the slope 0.8800 to 1.0060, 95% CI for the intercept: -1.8790 to 58.1400pg/mL, $S_{y.x}$=88.64, P < 0.0001). r^2=0.9797 (Cobas 6000 = 1.0390LC-MS/MS+16.5300, 95% CI for the slope 1.0000 to 1.0790, 95% CI for the intercept:-2.2490 to 35.3000pg/mL, $S_{y.x}$=55.46, P < 0.0001). r^2=0.9962 (ARCHITECT i2000$_{SR}$ = 1.0630LC-MS/MS-12.9200, 95% CI for the slope 1.0460 to 1.0810, 95% CI for the intercept:-21.1700 to-4.6740pg/mL, $S_{y.x}$=24.36, P < 0.0001). Bland-Altman plots were achieved by MedCalcand showed: By Siemens IMMULITE 1000, there are 16.7% of samples showed exceed ±30% biases from the mean of difference (2.4%). And there are only 5.0% and 6.7% of samples showed exceed ±30% biases in Cobas 6000 and ARCHITECT i2000$_{SR}$ systems.

Conclusions We report a direct comparison of the ID-LC-MS/MS assay with the chemiluminescent immunoassays for human serum 17β-estradiol. Linear regression

revealed good overall correlation with the LC-MS/MS and chemiluminescent immunoassays, and Bland-Altman plots showed that the differences were concentration dependent.

PO-250

Serological diagnosis of syphilis: a comparison of six diagnostic assays

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Objective This study was to compare the diagnostic efficacy of fluorescence assay (FTA-ABS), electrochemiluminescence (Roche ECL), chemiluminescence (SIEMENS CLIA), treponema pallidum particle agglutination (TPPA), turbidimetric immunoassay (Turbidity) and toluidine red unheated assay (TRUST) for diagnosis of syphilis.

Methods Patients with syphilis and suspected infected with syphilis were enrolled in Guangdong Provincial Hospital of Chinese Medicine. The above six assays were used to detect the concentration of syphilis. FTA-ABS assay was regarded as the gold standard. Sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), kappa values, and receiver operating characteristic (ROC) curve of other diagnostic assays were calculated. The combined diagnostic efficacy of the two assays was also evaluated. The auto antibodies were tested when the patients with positive in TRUST and negative in other treponemal antibody assays.

Results A total of 253 patients with syphilis (163) or suspected infected with syphilis (90) were enrolled. The ROC curve areas of Roche, Turbidity, SIEMENS, TPPA and TRUST assays were 0.991, 0.978, 0.960, 0.952, and 0.806, respectively ($P < 0.05$). The area of TRUST assay was significantly different with other four assays. Positive predictive value and negative predictive value of Roche, Turbidity and SIEMENS were greater than 0.9. Kappa coefficients of Roche ECL, Turbidity and TPPA were greater than 0.9. Kappa coefficient of TRUST was equal to 0.577. For Roche ECL, Turbidity SIEMENS CLIA and TPPA, PPV and NPV were greater than 0.9. PPV and NPV of TRUST were equal to 66.7% and 89.9%. The combined diagnostic efficacy of the following two assays (Roche ECL + TPPA, SIEMENS CLIA + TPPA, Turbidity + TPPA, TPPA + TRUST, Roche ECL + TRUST, SIEMENS CLIA + TRUST, and Turbidity + TRUST) also had good ROC curve areas (> 0.95). There were 11 patients who were positive in TRUST and negative in other treponemal antibody assays. Among them, the auto antibodies were positive in 8 patients.

Conclusions Roche, SIEMENS, TPPA and Turbidity were recommended to replace FTA-ABS for diagnosis of syphilis. TRUST assay should be combined with Roche, SIEMENS, TPPA and Turbidity to diagnose syphilis. Meanwhile, auto antibodies may interfere with the results of TRUST assay.

PO-251

Development of a Candidate Reference Measurement Procedure for the Determination of Glycocholic acid in Human Serum Using Isotope-Dilution Liquid Chromatography-Tandem Mass Spectrometry

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Objective Glycocholic acid (GCA) is an important identified biomarker for hepatobiliary diseases. The results obtained from clinical routine methods varied significantly. There are no reports about the established reference measurement procedure (RMP) for GCA measurement. Thus, a critically evaluated RMP to which routine methods could be traceable is highly desirable.

Methods GCA measurement in serum samples using isotope dilution coupled with liquid chromatography-tandem mass spectrometry (ID-LC-MS/MS) method was firstly developed. Serum samples spiked with GCA-d4 were extracted with protein precipitation. GCA and GCA-d4 negative ions were detected using the specific transitions m/z 464.4→74.0 and 468.4→74.0, respectively. Performance of the candidate RMP was fully validated. Forty-three serum samples were applied for method comparison.

Results Excellent linearity coefficients (R^2=1.000) were obtained in wide concentration range of 0.039-40 μg/mL. The lowest limit of detection (LLoD) and lowest limit of quantification (LLoQ) was 0.01 ng/mL and 0.05 ng/mL, respectively. The intraassay, interassay, and total CVs were below 1.39%, 2.01%, and 2.14% for three levels samples. Good Recoveries (98.0-100.9%) were achieved at five spiked levels. No interference, matrix effect, carryover, and stability problems were observed. The relative expanded uncertainty was ≤ 2.70%. Poor agreement was displayed among the results obtained by routine method and LC-MS/MS method.

Conclusions A sensitive and accurate candidate RMP for GCA measurement using ID-LC-MS/MS method was firstly developed. The well characterized method displayed high reproducibility, good accuracy, definitive uncertainty, and could be used as a candidate RMP to provide serum value assignments for calibration and verification for method performance.

P0-252

Analysis of true positive rate of Roche Cobas e602 in detection of specific antibodies against Treponema pallidum and its optimum threshold

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Objective Roche Cobas e602 automatic chemiluminescence microparticle immunoassay for the detection of positive results of Treponema pallidum specific antibodies were retrospectively analyzed and explore the true positive rate of the results and optimum threshold which can help reduce the false positive rate of CMIA assay for detection of specific antibody results of treponema pallidum and ensure the accuracy of the results and provide reliable evidence for clinical diagnosis.

Methods 18908 inpatients and outpatients in .Guangdong Provincial Hospital of Chinese Medicine from July 1, 2016 to June 30, 2017 were tested for Treponema pallidum specific antibody by Chemiluminescence Microparticle Immuno assay (CMIA).The positive samples were confirmed by treponema pallidum particle assay(TPPA).Using the statistical methods and ROC curve to analyze the true positive rate and optimum threshold (the true positive predictive value ⩾ 95%) .

Results There were 411 positive specimens screened from Roche Cobas e602 in 18908 specimens and the positive rate was 2.17%.In addition, the random test of TPPA was performed on 301 specimens of all 411 positive specimens. The results showed that the true positive specimens were 252 cases and the true positive rate was 83.72%.When S/CO ⩾ 33, the true positive rate is 100%.The ROC curve analysis showed that the optimum threshold was 19.085.

Conclusions The true positive rate of Roche Cobas e602 detection for Treponema pallidum specific antibody was 83.72%. When S/CO ⩾ 33, the true positive rate is 100%.The optimum threshold was 19.085.Therefore,when the positive result was less than 19.085,we have to do the TPPA experiment and combined with clinical judgment.[1] This study can help reduce the false positive rate of CMIA assay for detection of specific antibody results of treponema pallidum and ensure the accuracy of the results and provide reliable evidence for clinical diagnosis.

PO-253

The effects of deletion of lasI/rhlI and Azithromycin on the expression of virulence gene in Pseudomonas Aeruginosa

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Objective To investigate the effect of lasI/rhlI gene deletion and azithromycin on the expression of virulence gene of *Pseudomonas aeruginosa.*
Methods PA strains of wild type and lasI/rhlI gene deletion (PA-ΔlasI, PA-ΔRhlI, PA-ΔlasIrhlI) were cultured for 6 hours, and the four strains were treated with 2 μg/mL azithromycin for 6 hours. The effects of lasI/rhlI gene deletion and azithromycin on the QS system and the expression of virulence genes in *Pseudomonas aeruginosa* were observed by fluorescence quantitative PCR.
Results After deletion of lasI gene, the expression of lasA, aprX, rhlA, rhlB, phnA and phnB were all down-regulated ($P<0.05$, $P<0.01$), while the expression of those genes did not change significantly after the deletion of the rhlI gene. After treatment with azithromycin, the expression of lasI gene was significantly decreased ($P<0.01$), while the expression level of virulence gene downstream of lasI was significantly higher ($P<0.01$, $P<0.001$), and the expression level of QS system inhibitor qscR was also increased ($P<0.001$).
Conclusions The deletion of lasI gene may significantly inhibit the expression of virulence genes of QS system in *Pseudomonas aeruginosa*, and azithromycin may promote the expression of virulence genes by inhibiting qscR.

PO-254

Transcriptome Analysis Reveals Distinct Gene Expression Profles Between Breast cancer and Mastitis

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Objective Breast cancer has become one of the malignant tumors that seriously threaten the health of women. However, the pathogenesis of Breast cancer remains unclear. Here, we performed next-generation RNA sequencing and a comprehensive bioinformatics analyses to characterize the transcriptome profles, including long noncoding RNAs (lncRNAs) and mRNAs, in patients with Breast cancer, Mastitis and control group. A total of 260 lncRNAs and 110 mRNA transcripts were differentially expressed between Breast cancer and control group; .A total of 1013 lncRNAs and 357 mRNAs were differentially expressed between Mastitis and control group; .A total of 563 lncRNAs and 274 mRNAs were differentially expressed between Breast cancer and Mastitis. We showed Breast cancer and Mastitis display distinct transcriptome profles. We identifed

crucial pathways, including the MHC protein complex and Drug metabolism - cytochrome P450, connected to the pathogenetic mechanism of the two breast diseases.

Methods The selected cases of breast cancer, mastitis are from March 2017 to June 2017 in Guangdong Provincial Hospital of Chinese patients admitted to the treatment, are female. Breast cancer cases were pathologically diagnosed as untreated early breast cancer patients; mastitis cases were pathologically diagnosed as breast inflammation in patients with no other cancers; normal peripheral blood collected by the Guangdong Provincial Hospital of Traditional Chinese Medicine during the same period, To determine its clinical ultrasound breast ultrasound photography without breast disease, are women. Peripheral blood samples were collected for exosome RNA extraction and sent to Guangzhou Ruibo Biotechnology Co., Ltd. for next-generation RNA sequencing analysis.

Results In the Breast cancer group, 260 lncRNA transcripts (170 up-regulated and 90 down-regulated) and 110 mRNA transcripts (79 up-regulated and 31 down-regulated) were differentially expressed compared to the control group (Fig. 1A and Supplementary Table S1). In Mastitis, 1013 lncRNA transcripts (547 up-regulated and 466 down-regulated) and 357 mRNA transcripts (135 up-regulated and 222 down-regulated) were differentially expressed compared to the control group (Fig. 1B and Supplementary Table S2). And in the Breast cancer group, 563 lncRNA transcripts (356 up-regulated and 207 down-regulated) and 274 mRNA transcripts (233 up-regulated and 41 down-regulated) were differentially expressed compared to the Mastitis group (Fig. 1C and Supplementary Table S3). In unsupervised hierarchical clustering analysis, heat maps were generated using the differentially expressed lncRNAs and mRNAs respectively and they clearly self-segregated into Breast cancer, Mastitis and control clusters

Conclusions There are several advantages of using RNA-Seq over microarrays: (1) the ability to identify novel transcripts, not confined to annotated transcripts in databases; (2) sensitive detection and reliable quantification of coding and noncoding transcripts, which is particularly important because of the low expression level of lncRNAs. However, our study has limitations. For example, the sample size was relatively small. Nevertheless, we provided indirect experimental evidence to imply the functional link between lncRNA and its predicted target gene. Therefore, we will confirm our RNA-Seq data in larger cohorts of well-controlled subjects and illustrate the functional role of lncRNAs with direct evidence in subsequent research.

In conclusion, differences in the pathophysiology of Breast cancer and Mastitis demonstrate the significance and necessity of developing specific biomarkers and personalized therapeutic strategies. The high consistency between predicted functions of dysregulated lncRNAs and functions of dysregulated mRNAs indicates lncRNAs play a critical role in regulating the expression of protein-coding genes in Breast cancer and Mastitis. This study lays a solid foundation for subsequent functional studies of mRNAs and lncRNAs as diagnostic and therapeutic targets in Breast cancer and Mastitis by providing a candidate reservoir.

PO-255

The Function Of VitD And MBCI In Estimating the function of beta-cell in patients with type 2 diabetes

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Objective To study the correlation between the combination of MBCI and vitamin D and the function of beta-cell in patients with type 2 diabetes.
Methods 21 subjects with normal glucose tolerance and 31 patients with type 2 diabetes are involved in this study. Collecting the results of OGTT, insulin test, vitamin D, Hb_{A1c} and calculating Homa-β, MBCI, $\Delta I_{60}/\Delta G_{60}$, Homa-IR. Parameter means and Linear regression analysis were used to analyze the correla- tion between the combination of vitamin D and different beta-cell functional indexes and the changes of blood glucose levels.
Results (1)Vitamin D was significantly correlated with PG_{60} and PG_{120}($r=-0.373$, $r=-0.408$, all $P<0.05$), but not significantly correlated with Hb_{A1c} ($r=-0.369$, $P>0.05$). (2) Homa-β, MBCI, $\Delta I_{60}/\Delta G_{60}$, Homa-IR were not significantly correlated with vitamin D(all $P>0.05$). (3)R^2 of general linear regression are 0.290, 0.174, 0.506 respectively when the PG_{2h} as the dependent variable and vitamin D+HBCI, vitamin D+MBCI, vitamin D+$\Delta I_{60}/\Delta G_{60}$ as the independent variables. R^2 of general linear regression are 0.576, 0.789, 0.675 respectively when the PG_{2h} as the dependent variable and Homa-IR+HBCI, Homa-IR+MBCI, Homa-IR+$\Delta I_{60}/\Delta G_{60}$ as the independent variables.R^2 of general linear regression are 0.607, 0.783, 0.707 respectively when the PG_{2h} as the dependent variable and Homa-IR+HBCI+vitamin D, Homa-IR+MBCI+vitamin D, Homa-IR+$\Delta I_{60}/\Delta G_{60}$+ vitamin D as the independent variables.
Conclusions (1) Vitamin D was significantly correlated with PG_{60} and PG_{120};(2) beta-cell functional indexes, Homa-IR were not significantly correlated with vitamin D;(3) Only a small part of the changes of glucose levels can be explained by the combination of vitamin D and MBCI. (4)When estimating the function of beta-cell in patients with type 2 diabetes, MBCI is more reliable than other indexes, which can explain more changes of glucose levels.

PO-256

Association between HLA-DQB1 alleles and susceptibility to coronary artery disease in southern Han Chinese

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Objective Human leukocyte antigens (HLA) play very important roles in inflammation which is involved with coronary artery disease (CAD). This study aimed to investigate whether polymorphisms in HLA-DQβ1 is associated with susceptibility to CAD, and deepen understanding of the pathogenesis of CAD from a novel insight.

Methods 336 eligible CAD patients and 278 eligible controls from Southern Han Chinese were included in the case-control study, the case group and controls are age and gender matched. The polymorphisms in the exon2 of HLA-DQB1 were investigated by genotyping with sequencing-based typing (SBT) in an age and gender matched CAD and normal control group. A significant difference in the frequency distribution of HLA-DQB1 alleles or genotypes between groups or subgroups was evaluated by chi-square test with Yates' continuity correction (P_{c1}) and Bonferroni correction (P_{c2}). The influence of confounding factors such as smoking, hypertension, diabetes, hyperlipidaemia, and the level of plasma glucose, triglyceride and high density lipoprotein cholesterol (HDL-C) on the results was tested by logistic regression analysis.

Results Compared to the controls, the allele frequency of DQB1*03:01:01G and DQB1*05:03:01G was significantly decreased in CAD group (21.28% Vs 30.40%, P_{c1} = 0.0003, P_{c2} = 0.009, OR = 0.619; and 4.91% Vs 8.81%, P_{c1} = 0.009, P_{c2} = 0.205, OR = 0.534, respectively). The genotypes (DQB1*03:01:01G/DQB1*03:01:01G and DQB1*03:01:01G/DQB1*05:03:01G) were also remarkably decreased in CAD group than in the controls (2.68% Vs 9.35%, P_{c1} = 0.0007, P_{c2} = 0.031, OR = 0.267; and 1.79% Vs 7.19%, P_{c1} = 0.0019, P_{c2} = 0.07, OR = 0.534, respectively). A notably higher frequency of DQB1*04:01:01G (5.21% Vs 2.70%, P_{c1} = 0.0384, OR = 1.982) and the genotype DQB1*03:01:01G/DQB1*05:01:01G (5.36% Vs 1.08%, P_{c1} = 0.0074, OR = 5.189) was observed in the CAD patients than in the controls. Further analysis in subgroups showed that DQB1*03:01:01G was expressed at a significantly lower frequency in both female and male CAD patients than in the corresponding controls (22.52% Vs 31.86%, P_{c1} = 0.0346, OR = 0.622; 20.67% Vs 29.39%, P_{c1} = 0.0065, OR = 0.627, respectively), yet DQB1*04:01:01G was overtly higher only in male CAD patients than in male controls (5.33% Vs 1.21%, P_{c1} = 0.0042, P_{c2} = 0.0484, OR = 4.592). CAD patients with diabetes showed a negative association with DQB1*03:01:01G ($P < 0.01$) and DQB1*05:03:01 ($P < 0.05$), and a positive association with DQB1*04:01:01G and DQB1*03:03:02G. The frequency of DQB1*03:01:01G and DQB1*05:03:01G was decreased sequentially in the 3 subgroups (controls without diabetes, CAD without diabetes and CAD with diabetes). However, only DQB1*03:01:01G and DQB1*05:03:01G showed a significant association with CAD by logistic analysis, it was showed that DQB1*03:01:01G and DQB1*05:03:01G could independently predict a decrease in risk of CAD. The carriers of DQB1*03:01:01G (OR = 0.457, $P < 0.001$) and DQB1*05:03:01G (OR = 0.39, P = 0.005) may have an about 54.3% and 61% less chance of developing CAD, respectively

Conclusions It was reported for the first time that HLA-DQB1*03:01:01G and HLA-DQB1*05:03:01G play protective roles against CAD, which may be promising genetic factors to predict the risk of CAD. However, the roles of HLA-DQB1*04:01:01G and other alleles in CAD need be further investigated.

PO-257

Collaborative Studyingof ID-LC/MS/MS Methods for uE3

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Objective To promote the standardization for serum unconjugated estriol(uE3), the collaborative studyingprogram was carried out in reference laboratories by using isotope dilution liquid chromatography tandem mass spectrometry (ID-LC/MS/MS) candidate reference measurement procedure (cRMP), as well as to validate the performance (accuracy and precision) of this cRMP and application in reference laboratories.

Methods Theprotocolforcollaborative studyingprogram was proposed according to ISO/WD 15725-1 and GB/T 6379, two stages of the program, preliminary test and formal experiment were scheduled, and a total of 9 reference laboratories have been participated in this study. Five serum pooled samples for uE3 was collected and distributed to the 9 reference laboratories after evaluation of their homogeneity. All samples were required to measure 5 times each day in 3 continuous days. Grubbs and Cochran tests were used to distinguish and remove the outliers by evaluating the bias and precision for the result of each reference laboratory. Target value was calculated and suggestion was provide for the removed laboratories.

Results (1) Homogeneity for samples: the F values of all samples were less than the critical value of $F_{0.05}$（9, 20）, it indicated thatthatthe uE3 in test samples were homogeneous.(2) Preliminary test: one outlier was removed by Grubbs test and two outliers were removed by Cochran test. Thetarget values were calculated after removing the outliers, which were 2017E301: 22.08±0.24nmol/Land 2017E302:33.46±1.67nmol/L. The results of two laboratories were outside the allowable range. (3)Formal experiment: no outlier was detected by Grubbs test and three outliers were removed by Cochran test.Thetarget values after removing the outliers were2017E303: 10.36±0.35nmol/L, 2017E304:15.47±0.26nmol/L and 2017E305: 46.97±1.19nmol/L. The precision for the three samples among the laboratories was 1.14%～2.21%，0.79%～1.93% and 0.60%～2.09%，respectively.And the bias was -6.18%～4.83%，-2.26%～2.39% and -4.19%～4.07%.

Conclusions The cRMP for uE3 was quickly reproduced in reference laboratories and the good characters of precision （＜3.0%) and bias （＜7.5%) were achieved in the most laboratories through the collaborative studyingprogram. The performance for the cRMP and the ability for running this reference method by reference laboratorieswere further validated. This experiment was verified and perfected after the preliminary and formal test.The cRMP for uE3 was promoted in reference laboratories, which built up the platform for the joint value of main calibrators for manufacturers and reference materials. This collaborative studyingprogram promotes the standardization of uE3.

PO-258

Identification and classification of Non-tuberculosis Mycobacterium by Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry

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Objective Reference standard of The *RPOB* (rifampin resistance gene) gene recommended by CLSI-MM18A (Interpretive Criteria for Identification of Bacteria and Fungi by DNA Target Sequencing) was used to evaluation of MALDI-TOF MS techniques for the identification and classification of non tuberculous *Mycobacterium.*
Methods Fifth clinical starins were collected from 2012 to 2016 with different parts, combined with the analysis of *RPOB* gene sequence and the homology; MALDI-TOF MS technology was used to identify the strains and cluster analysis。To evaluate the consistency of two methods for NTM identification and typing.
Results The *RPOB* gene showed a good ability to identify the 55 strains (similarity>99.0%) and the ability to differentiate between species (subspecies of the complex); The French BioMerieux MALDI-TOF MS identified of 55 strains to the level of genus was 89.1% and the species was 78.2%; Meanwhile cluster analysis of protein fingerprint by SARAMS Premium software also showed good typing ability.
Conclusions MALDI-TOF MS technology can be used to identify and classify non tuberculous *Mycobacterium* effectively, Detection shortly, easy operation and combined with *RPOB* gene has a very good complementarity in the laboratory.

PO-259

Description of Vitamin D Serum in Patient and Healthy Population at Saiful Anwar General Hospital Malang

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Objective In South East Asia, there is huge prevalence of vitamin D deficiency, although South East Asia is in tropic area. Similarly in Saiful Anwar General Hospital Malang population, there is high prevalence of vitamin D deficiency; therefore we need to make a study about prevalence of vitamin D serum level in healthy population. Vitamin D has many functions in body regulation including adaptive immunity so that vitamin D deficiency can lead to autoimmunity. Vitamin D deficiency also can increase risk of cardiovascular disease also increased mortality. The aim of this study is find out the prevalence of vitamin D serum level in patient and in healthy population in Saiful Anwar General Hospital.
Methods Hospital population data was collected from retrospective study from Laboratory Information System (LIS) data since September 2014 until April 2018 in Saiful Anwar General Hospital, Malang. Health population data was collected from

general check up patient that had normal value of CBC and urine analysis tests. Vitamin D was checked with ELISA method.

Results The prevalence of vitamin D deficiency in patient and healthy population are 38.32% and 20.83% respectively; the prevalence on vitamin D insufficiency in patient and healthy population are 31.87% and 43.06% respectively; the prevalence on normal level of vitamin D in patient and healthy population are 29.81% and 36.11% respectively. The mean of vitamin D serum level in patient group is 17.00 ng/mL whilw in healthy population is 18.94 ng/mL. Mann-Whitney test in two groups shows that there is significant different of vitamin D serum level between those groups.

Conclusions The prevalence of vitamin D deficiency in patient group is higher than in healthy population; while the prevalence of vitamin D insufficiency in healthy population is higher than in patient group; and the prevalence of normal level of vitamin D deficiency in patient group is higher than in healthy population. Although there is significant different statistically between vitamin D serum level in both goups, but clinically mean of vitamin D level from both groups are insufficient. Discovering that, routinely check vitamin D serum level is needed.

PO-260

Study on the expression of sperm protamines in the male infertility patients in Chengdu area [Funded by Health Commission of Sichuan Province(Project No 16PJ471)]

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Objective To detect the express of PRM1 and PRM2 in sperm of the male infertility patients in Chengdu area by fluorescence quantitative polymerase chain reaction. To investigate the correlation between mRNA transcription level of protamines(PRM1 and PRM2) and the male infertility patients.

Methods Taking GAPDH as internal control, mRNA levels of the sperm protamine (PRM1 and PRM2) in 30 healthy men, 83 oligozoospermia and 61 teratospermia patients were detected by FQ-PCR .

Results The express of PRM1 and PRM2 in oligospermia group was significantly lower than normal control group and teratozoospermia group($P<0.05$). There was no difference in the express of PRM1 and PRM2 between teratozoospermia group and normal control group($P>0.05$). The sensitivity and negative predictive value were improved by combined detection of PRM1 and PRM2 to the diagnosis of oligozoospermia.

Conclusions The sensitivity and negative predictive value were improved by combined detection of PRM1 and PRM2 to the diagnosis of oligozoospermia. It also can be effective in diagnosis of oligozoospermia though the advantages of simple operation, low price and easy sample source. There were low expression of PRM1 and PRM2 in oligozoospermia in Chengdu, suggesting a close relationship with spermatogenesis, which is helpful for clinical detection, diagnosis and individualized treatment of male infertility patients, as well as large-scale epidemiology survey.

PO-261

Identification of cell marker in palindromic rheumatism using mass cytometry

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Objective Palindromic rheumatism (PR) is a recurrent inflammatory disease. Unlike rheumatoid arthritis (RA), PR patients frequently have extra-capsular inflammations and without progression to joint erosion after a 5-year follow-up. The pathogenesis of pure PR remains unclear. This study aimed to identify cell markers for accurate diagnosis and prognosis of PR.
Methods We set up a mass cytometry panel consisting of 22 antibodies for the detection of different lymphoid and myeloid immune cell subsets. Blood were collected from healthy controls and pure PR patients at attack and at inactive disease stages. Peripheral blood mononuclear cells (PBMCs) were isolated from participants and underwent mass cytometry analysis.
Results Using the auto-annotation function of SPADE 3.0, cell populations detected by mass cytometry were being classified to CD3+, CD3-, CD16+, CD19+, CD33+, CD4+, CD57+, and CD11b+ groups. In the lymphoid subsets, we found that PR patients had higher percentages of CD4+CD69+CD25- cells, as compared with controls. In the myeloid subsets, PR patients showed higher percentages of CD33+CD16-CD11b+ cells. Further gating using the Cytobank software revealed that PR patients had increased percentages of CD11b+CD11c+ double-positive cells.
Conclusions We have established a mass cytometry panel for detecting potential cell markers for immune monitoring in a complex unknown immune disease. We are currently investigating the role of CD11b+CD11c+ cells in PR pathogenesis.

PO-262

Stress Assessment by Automatically Determined Salivary Cortisol in Long Distance Runners

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Objective Production of physical and mental stress due to excessive workload, called overtraining syndrome, is a serious problem among many athletes of various sports. It is important to monitor exercise intensity to prevent athlete's excessive stress with

appropriate biomarkers. Cortisol plays a crucial role in metabolism and immune function. Cortisol is regulated in hypothalamus-pituitary-adrenal (HPA) axis and secreted based on circadian rhythm. Physical exercise activates the HPA axis and increases the secretion of cortisol in adrenal cortex. Several studies have investigated the serum and salivary cortisol concentrations to evaluate the stress with various types and intensities of exercise. Although serum specimens are often used in clinical and research situations, venipuncture to obtain blood for measuring serum cortisol requires the medical professional staff and increases cortisol secretion due to stress. , saliva can be collected easily and noninvasively without medical professionals. Salivary cortisol detected by electrochemiluminescence immunoassay (ECLIA), which is a simple method for automatic measuring, may have more advantages for stress assessment in non-clinical situations, such as exercise training. Salivary cortisol has advantages for exercise stress assessment because even nonprofessionals can collect saliva easily and noninvasively without stress, however, this method has not been applied in non-clinical situations, such as exercise training. Moreover, tThere has not been definite criteria for appropriate time in a day to assess the stress by cortisol measurement. Establishment of this criteria may prevent the overstress overtraining syndrome in various sports athletes. In the present study, we evaluated the accuracy and usefulness of salivary cortisol concentrations determined by ECLIA automatically in comparison with salivary cortisol determined by a conventional method of enzyme-linked immunosorbent assay (ELISA) ELISA and serum cortisol. Furthermore, we also investigated the appropriate usage of the salivary cortisol measurement to assess the stress response by different intensities and types of exercise within the circadian rhythm in the Japanese women long distance runners.

Methods We enrolled a total of 54 young Japanese healthy subjects (men male 17; women female 37) for correlation analyses to evaluate the accuracy of salivary cortisol concentrations detected by ECLIA method. Saliva samples were collected from all subjects, and blood samples were also collected from 27 subjects (men 17; women 10) of them within 0900-1000h. We enrolled twelve Japanese women female runners who participated in the all-japan women's long long-distance relay race for analyses of stress response by exercise within the circadian rhythm. We collected salivary samples for two consecutive days on conditions with different intensities and typescontinuing habitual usual exercise with different intensities and types in early morning and afternoon. Salivary and serum cortisol concentrations were analyzed by ECLIA using Elecsys Cortisol Ⅱ on Modular Analytics E170 system (Roche Diagnostics K.K, Japan). Salivary cortisol concentration was also analyzed by cortisol EIA kit, Expanded Range, High Sensitivity, Salivary (Salimetrics LLC, USA) as salivary cortisol by ELISA. Change rate of salivary cortisol concentrations from before to after exercise were calculated salivary cortisol concentration at after exercise / salivary cortisol concentration at before exercise (%), and were compared between the two time points in same days or between other time points in two days.

Results The salivary cortisol concentration by ECLIA has a strong positive correlation with the salivary cortisol concentration by ELISA in healthy subjects ($\rho = 0.924$, $p < 0.001$). While sSalivary cortisol concentration determined by each method was positively correlated with the serum cortisol concentration determined by ECLIA and ELISA (salivary cortisol by ECLIA and serum cortisol; $\rho = 0.591$, $p = 0.001$, salivary cortisol by ELISA and serum cortisol; $\rho = 0.554$, $p = 0.003$). In women long- distance runners, change rates of salivary cortisol concentrations from before to after

exercise in the early morning showed a significantly lower than that in the afternoon, because of the influence of circadian rhythm. However, there were significant differences among in the change rates of salivary cortisol concentrations in the early morning between two days by exercise with different intensities in early morning between two days.

Conclusions In conclusion, the salivary cortisol automatically determined by ECLIA were positively correlated with salivary cortisol by ELISA and serum cortisol by ECLIA, suggesting that this method is usefulhas advantages to determine salivary cortisol in various situation because of its simplicity and accuracy. It is difficult to evaluate the difference in stress response of salivary cortisol due to exercises during a day because of the effects of circadian rhythm, especially early morning. In contrast, it may be possible to compare stress response assessed by salivary cortisol due to different exercise intensities between days at the same time, even within the circadian rhythm and to prevent the overstress overtraining syndrome in various sports athletes.

PO-263

An analysis of 116 anti-GBM antibody-positive patients: Is this antibody a potential marker for predicting CKD 4-5?

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Objective To assess the risk of advanced end stage renal failure (CKD 4-5) in anti-GBM antibody-positive patients and analyze their clinical features and laboratory characteristics.

Methods Consecutive anti-GBM antibody-positive patients (n = 116) were collected in a large cohort over five years at the hospital and retrospectively analyzed. In addition, the further clinical and laboratory characteristics of the anti-GBM antibody-positive patients were identified, indicating the relative risk of CKD 4-5.

Results Forty-eight (41.4%) anti-GBM antibody-positive patients presented with CKD 4-5. Rapidly progressive glomerulonephritis (RPGN) (37.5%) and chronic renal insufficiency (CRI) (35.4%) were more frequently diagnosed in anti-GBM antibody-positive patients with CKD 4-5. Logistic regression modelling revealed that anti-GBM antibody-positive patients presenting with anemia, oliguria/anuria and a history of smoking have a greater probability of predicting CKD 4-5 and are considered high-risk patients when compared to anti-GBM antibody-positive patients with none of the mentioned clinical criteria.

Conclusions Overall, an increased risk of CKD 4-5 was found in the cohort of anti-GBM antibody-positive patients taking part in this study. Regular screening tests, including clinical and laboratory values, are justified in anti-GBM antibody-positive patients who exhibit the mentioned clinical criteria.

PO-264

FBXW7/mTOR axis as novel biomarkers for diagnosis and metastasis prediction of colorectal cancer

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Objective F-box and WD repeat domain containing 7 (FBXW7) encodes a substrate adaptor for an SCF E3 ubiquitin ligase complex and lies at the nexus of many pathways which control cell growth, cell differentiation, and tumorigenesis by negatively regulating the abundance of different oncoproteins. Increased cell migration and invasion lead to cancer metastasis and are crucial to cancer prognosis. In this study, we explore whether FBXW7 plays any role in metastatic process.
Methods Wound healing assay, transwell assay and matrigel assay were used to detect the migration and invasion of colorectal cancer cells. Spheroid formation assay was used to detect the capability of self-renewal of colorectal cancer cells. Rapamycin was used to inhibit the mTOR signaling.
Results Depletion of FBXW7 induces epithelial-mesenchymal transition (EMT) in human colorectal cancer cells along with the increase in cell migration and invasion. Moreover, FBXW7 deficiency promotes the generation of colorectal cancer stem-like cells in tumor-sphere culture. mTOR inhibition by rapamycin suppresses FBXW7 loss-driven EMT, invasion and stemness, suggesting accumulation of mTOR in *FBXW7*-depleted cells play a role in induction of stem-like properties.
Conclusions EMT and stem cell-like properties are essential for tumor cells to disseminate from adjacent tissues and seed new tumors in distant sites. Our results demonstrated that FBXW7 regulated these two essential characteristics of metastatic disease through mTOR signaling pathway.

PO-265

A Case Report of Smear of a Patient with Posttraumatic Endophthalmitis and Literature Review for Microbiologic Diagnosis

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Objective To improve the cognition of the smear of retinal pigment layer in endophthalmitis.
Methods One case of the smear of retinal pigment layer of a patient with endophthalmitis was reported and relevant literature were reviewed.

Results We report on a 50-year-old male presenting with endophthalmitis caused by trauma. During operation, the specimen of retinal pigment layer sampled by the ophthalmologist were sent for microbiological analysis. The smear showed Gram-positive cocci and pigment granules, but did not have bacterial growth in the culture. Beside the case description, we searched through published cases for laboratory diagnosis and treatment of endophthalmitis in recent years. Acute onset, severe symptoms and poor prognosis are clinical features of posttraumatic endophthalmitis. Endophthalmitis is a clinical diagnosis supported by microbiological analysis, which is the most valuable and reliable method, mainly including smear and culture. Molecular diagnostic techniques are available mainly in research laboratories. When ocular trauma involves the retina, ciliary body, choroid and other tissues,caution must be exercised to avoid mistaking pigment granules for Gram-positive cocci.

Conclusions Endophthalmitis is a medical emergency, and prompt diagnosis and treatment are essential for saving vision. To improve the cognition of smear of retinal pigment layer is helpful for early diagnosis of traumatic endophthalmitis.

PO-266

Urinary dipstick protein/creatinine ratio increases the sensibility of proteinuria screening in chronic kidney disease patients

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Objective Based on the evaluations of ACR and 24hP results, this study evaluated whether dipstick protein-to-creatinine ratio increases the sensitivity of proteinuria screening in chronic kidney patients than dipstick protein alone.

Methods 252 chronic kidney disease (CKD) patients and 90 non-kidney disease patients were investigated. All the patients underwent spot urinary dipstick PCR and quantitative ACR tests. 24-hour protein of all the CKD patients were assessed. Correlations of semi-quantitative dipstick PCR with quantitative ACR and 24hP were measured. With 30mg/g and 300mg/g as the ACR cut-off values of microalbuminuria and macroalbuminuria, receiver operating characteristic (ROC) curve was calculated to determine the cut-off values of dipstick PCR in screening microproteinuria and macroproteinuria.

Results The results of semi-quantitative creatinine correlated well with the quantitative results (r=0.808, P≤0.001). Correlations of dipstick PCR with ACR and 24hP were 0.904 (P≤0.001, n=342), 0.861 (P≤0.001, n=252), respectively. ROC curve showed dipstick PCR cut-off values of micro- and macro-albuminuria were 58.35mg/g (sensitivity 0.903, AUC 0.944), 341.50mg/g (sensitivity 0.974, AUC 0.983).

Conclusions As a screening testing method, semi-quantitative PCR increases the sensitivity of proteinuria screening compared with dipstick protein alone. We suggest 58.35mg/g and 341.50mg/g as the cut-off values of micro- and macro- proteinuria and further large cohort studies should be performed to conform the cut-off values.

PO-267

Study the Effect of Pretreatment with Pure Water Boiling on Analyzing HER2/neu Gene Amplification by Fluorescence In Situ Hybridization

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Objective To study the effect of two pretreatment methods of the boiling pure water and the NaSCN solution with high-temperature on detecting the expression of HER2/neu in breast cancer patients by FISH analysis.
Methods Invasive breast cancer tissue specimens were collected from ten breast cancer patients. The individual specimen was duplicated and pretreated with either boiling pure water (Group1) or the NaSCN solution with high-temperature at 80℃(Group 2) parallel followed by the same FISH analyzing procedure to detect HER2/neu gene amplification. The staining results was reviewed under fluorescence microscope.
Results The intensity of FISH signals of nucleus background with red(HER-2/neu) and green(CEP17 control) signals were observed clearly under the fluorescence microscope. The similar results derived from two different pretreatment methods were met the experimental requirements for FISH analysis. However, the pretreatment with boiling pure water method was simple and easy to operate in compared with NaSCN solution with high-temperature pretreatment.
Conclusions the tissue specimens can be pretreated with boiling pure water method instead of NaSCN solution with high-temperature in detecting HER2/neu gene amplification in breast cancer tissue by FISH analysis.

PO-268

Decoding Gene Polymorphism of Female MTHFR and MTRR in the Region of Anhui Province, China

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Objective To investigate the gene polymorphism of folic acid metabolism-related enzymes and to explore its distribution in the female population in the region of Anhui province, China.
Methods Blood samples with EDTA anticoagulation were collected from 134 female , and 62% of which are childbearing age (20-45 years old) . The genotypes of 5,10-methylene tetrahydrofolate reductase (MTHFR) C667T and A1298C , methionine synthase reductase (MTRR) A66G were analyzed by Folic acid Catabolism ability Kit (fluorescence).
Results Among the 134 samples, the rate of MTHFR C677 wild type homozygote(CC), heterozygous mutants(CT) and homozygous mutants(TT) were accounted for 25.37%, 47.01%, and 27.61%, respectively. And the frequency of the overall mutant T allelic was 51.12%.

For MTHFR A1298C polymorphism, the frequencies were 64.93% for wild type AA , 32.84% for heterozygous AC and 2.24% for homozygous CC with 18.66% of the overall mutant C allelic. For MTRR A66G polymorphism, the frequencies were 54.48% for wild type AA, 39.55% for heterozygous AG and 5.97% for homozygous GG with 25.75% of the overall mutant G allelic. The results also showed that both the MTHFR A1298C and MTRR A66G homozygous mutant occurred in the group of childbearing age women. In compared both the average gene polymorphism and the overall mutant frequency of MTHFR C677T, A1298C and MTRR A66G in the female population in the region of Anhui province with in other regions of China (Jiangsu, Shanxi, Henan, Shandong, Hubei), there was no significant difference (gene polymorphism 2=1.653, P ＞0.05; the mutant frequency 2=0.659, P ＞0.05).

Conclusions The polymorphism of folic acid metabolism-related genes MTHFR and MTRR in the region of Anhui Province China is similar to other regions of China. The MTHFR A1298C and MTRR A66G homozygous mutants in women of childbearing age are higher than of other age female groups in Anhui Province.

P0-269

Analysis of high-risk human papillomavirus test results in 5654 female cervical exfoliated cells

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Objective To understand the infection status and genotype distribution of high-risk human papillomavirus (HPV) in cervical exfoliated cells of women in this region, and to provide reference for the development of clinical control measures.

Methods A retrospective analysis of 5654 patients who were admitted to hospital from July 2017 to December 2018 with high-risk HPV, using high-temperature amplification-fluorescence method for high-risk HPV detection, statistical HPV infection rate, genotype distribution characteristics, Age trends, etc.

Results Among the 5654 patients, 810 were high-risk HPV positive, the infection rate was 14.33%, HPV13 infection was 634, HPV16 infection was 138, and HPV18 infection was 38; the infection rates were 11.22%, 2.44%, 0.67% ; The infection rate in the age group ≤20 years and ≥60 years was the largest, However, the infection rate in the age group 30 to 39 years was the lowest.

Conclusions High-risk HPV infection rate is high in this area. HPV high-risk subtype infection is mainly distributed in the age group ≤20years and ≥60years. Early monitoring of high-risk HPV infection in the age group ≤20years and ≥60years should be emphasized.

PO-270

Microbiological Spectrum of community-acquired Brain Abscess in a tertiary-care hospital in Central South China: a 5-year retrospective study

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Objective To retrospectively analysis microbiological spectrum of community-acquired Brain Abscess in a tertiary-care hospital in Central South China.
Methods Clinical isolates were identified by Matrix assisted laser dissociation ionization time mass spectrometry and automatic microbial identification system.Antibiotic susceptibility test was performed using the Kirby-Bauer disc diffusion method for Maximum antibacterial zone diameter or Broth microdilution method for Minimal inhibitory concentrations (MICs) according to the Clinical and Laboratory Standards Institute 2014 guidelines.
Results Eighty-three patients (63 males and 20 females) with community-acquired brain abscesses resulting from bacteria infection were identified over a period of 5 years.More than two-thirds patients were presented as single brain abscesses. The organisms most frequently involved were Streptococcus viride, including Streptococcus constellatus , intermadius , anginosus , pyogenes and parasanguis,which were were associated with Congenital heart disease(CHD),Diabetes mellitus(DM) and Chronic otitis media/sinusitis underlying diseases.other bacteria including Nocardia,Mycobacteia tuberculosis and Cryptococcus neoformans,which were associated with pneumonia and Autoimmune diseases(AID)underlying diseases.one or more infection lesions were found in pulmonary or intra-abdominal or urinary tractin in 53 patients,and otogenic infection were found in 20 patients. Headache was the most common clinical manifestations,account for 69.88 percent.Fever,nausea or hemiplegia appeared in 20 percent of patients,other clinical manifestations such as disturbance of consciousness,Seizure,Speech disturbance or Stiff neck appeared in about 10 percent of patients with Community-acquired brain abscesses.Although CT or MRI images were rapid means of diagnosing brain abscess, 22.89 percent of the 83 patients were highly suspected of being brain tumors.In total,eleven patients died,representing an overall mortality rate of 13.25 percent.
Conclusions Although CT or MRI images were rapid means of diagnosing brain abscess, characteristic indicators of imaging diagnosis of brain abscesses need to be found and improved.In light of the high mortality rate,early diagnosis and treatment is essential to maximize the chances of survival.once community-acquired brain abscesses are diagnosed for CHD,DM and Chronic otitis media/sinusitis patients,a diagnosis of Streptococcus viride infection should be considered.

PO-271

A Study on Reference Intervals Transference by Linear Regression Method

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Objective Reference intervals (RIs) transference can expand the applicability of established RIs. However, the studies on the transference methodology were few, and RIs validation based on small sample cannot adequately assess the transferred risk under complex situations. This study aimed to analyse the transferability under different conditions.

Methods We established the RIs of Roche and Beckman systems for 27 analytes based on 681 enrolled healthy individuals. The Roche RIs were converted into the Beckman by linear regression method (least square method). With the RIs established by Beckman results as a standard, we assessed the accuracy, precision and trueness of transferred results under various conditions.

Results 29.6% and 48.1% of analytes were consistent between the two systems for the lower and upper reference limits, respectively, and the concordance rates were up to 70.4% and 92.6% after transference when test number was 500. The trueness remained stable under different test numbers and data distribution ranges. CV of transferred results decreased gradually with increasing test number under the same distribution range, and CV is similar among different distribution range group with the same test number. For most analytes except for some electrolyte tests, we could obtain accurate results when $r > 0.800$ and test number was sufficient regardless of the regression equation types.

Conclusions Transferability of RIs is affected by many factors, such as correlation, test number, regression equation type, and quality requirement. It is very important for reducing the risk of transference to select the right method with reasonable conditions.

PO-272

Circulating tumor cells (CTCs) and SALL4 expression in CTCs for distinguishing patients with gestational trophoblastic disease

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Objective Gestational trophoblastic disease (GTD) is a group of tumors arising from the placenta with varying tendencies for invasion and metastases. With the development of effective chemotherapy, recognition of prognostic factors, and use of sensitive

assays for human chorionic gonadotropin (hCG), gestational trophoblastic neoplasia (GTN) has become one of the curable human malignancies. However, for most patients with non-molar pregnancy especially postpartum choriocarcinoma, delays in diagnosis can lead to unfavorable outcomes due to widespread metastatic disease. Also, evaluation the malignancy potential of complete hydatidiform mole (HM) after suction is not only time wasting but also confused by residual pregnancy. Therefore, the exploration of new biomarkers for distinguishing GTN from other hCG-elevated circumstances is still of the utmost importance. In this study, we investigate the epithelial-mesenchymal composition and SALL4 mRNA expression in individual CTCs from GTD patients using Canpatrol™ system, which rely on a filter-based enrichment followed by identification with a cocktail of epithelial and mesenchymal markers to characterize subgroups of CTCs, to find out the correlations of CTCs subgroups and SALL4 expression with patients' clinical features.

Methods GTD patients visiting Peking Union Medical College Hospital from October 2016 to May 2018 were recruited. Normal intrauterine pregnant volunteers (first trimester) were included as controls. The Canpatrol™ CTC enrichment technique was used to isolate and identify the EMT phenotype-based subsets of CTCs. Briefly, nucleated cells were isolated using an 8 μm filtration system after erythrocytes were lysed. Then, RNA in situ hybridization (ISH) was applied to identity and classify CTCs using a cocktail of probes which target on four epithelial transcripts [cytokeratins (CK) 8, 18, 19, and epithelial cell adhesion molecule (EpCAM)], two mesenchymal transcripts (Twist1 and Vimentin), and a leukocyte transcript (CD45). Finally, the cells were stained with 4, 6-diamidino-2-phenylindole (DAPI) (Sigma, USA) for 5 min and analyzed with an automated imaging fluorescence microscope (Zeiss, Germany). Leukocytes were characterized as CD45+ cells. CD45- cells were defined as CTCs and classified into three phenotypes according to the expression of epithelial and mesenchymal markers (Figure 1): (1) epithelial marker positive cells (E-CTCs); (2) epithelial and mesenchymal marker co-positive cells (E/M-CTCs); (3) mesenchymal marker positive cells (M-CTCs). SALL4 expression in each CTC was also determined by using optimized four-color RNA-ISH approach.

Results A total of 12 HM, 29 GTN (12 IHM, 13 CCA, 3 PSTT and 1 ETT) patients and 22 healthy pregnant volunteers within the 1st trimesterwere enrolled in this study. For the GTN patients, a median count of 11 CTCs was detected (range: 1 to 49). Subsequent classification of CTCs into three phenotypes shows the average number of E-CTCs, E/M-CTCs and M-CTCs was 1 (range: 0 to 6), 8 (range: 0 to 37), and 1 (range: 0 to 15), respectively. Upon stratification by age, FIGO stage, pretreatment serum β-hCG level and prognostic scores, the distribution of each CTC phenotype was assessed. As results, pretreatment serum β-hCG level was significantly correlated with the number of total CTCs ($r=0.473$ and $P=0.009$) and E/M-CTCs ($r=0.375$ and $P=0.033$). Besides, significant correlation ($r=0.362$ and $P=0.038$) between prognostic score and M-CTC number was also revealed.

Kruskal-Wallis test indicated significant differences in total CTC, E/M-CTC and M-CTCs number among NIUP, HM and GTN ($P<0.01$) except for E-CTC. To further validate the clinical utility of CTC detection in distinguishing GTD from NIUP patients, ROC curve analysis was conducted and area under the ROC was 0.826 with 95% CI 0.728 to 0.925. According to the Youden index, the most optimal cut-off point was set at 8.5 cells/4 ml (sensitivity 53.66%, specificity 100%). The sensitivity of CTCs in the diagnosis of HM and GTN was 41.7% (5/12) and 58.6% (17/29), respectively.

SALL4 RNA-ISH of single CTC was performed using SALL4 mRNA probes mixed with EMT marker probes for every CTC detected in 20 of 22 positive cases, including 5 HMs and 15 GTNs. SALL4 expression level was analyzed and then CTC was categorized according to the number of purple signal dot, namely CTC0~2, CTC3~5, CTC>=6 (Figure1). As shown in Table1, CTC0~2 was detectable in all 20 positive cases, while CTC3~5 or CTC>=6 was only detected in GTN cases with detection rate as high as 66.67% (10/15), no CTC3~5 or CTC>=6 was detected in HM cases. For different types of GTN, the detection rate of CTC3~5 or CTC>=6 was 50%, 100% and 66.67%, respectively in IHM (4/8), CCA (4/4) and PSTT (2/3).

Conclusions The findings suggest that identification of CTCs could serve as potential adjuncts for early diagnosis. Evaluating SALL4 expression in CTCs has perspective in distinguishing malignant GTN from benign GTD patients. The specific detection of SALL4 high expressing CTC in GTN also casts new evidence supporting that SALL4 might play a role in trophoblast carcinogenesis.

PO-273

Establishment of a novel rule for bandemia estimation using hematology analyzer

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Objective Bandemia is often associated with severe infectious diseases. Currently, unlike white count, platelet count, and red blood cell count, which are analyzed automatically by most hematology analyzers, bandemia is often identified under manual microscope examination. This study aimed to use the signals from hematology analyzer to establish a rule for automated bandemia estimation.

Methods Specimens of light microscope-confirmed bandemia (>6%) cases and non-bandemia cases (band<1%) were collected, and signals were retrieved from the hematology analyzers DxH 800(Beckman Coulter, USA). Heatmap analysis was used to find out the differential patterns.

Results There were 256 signals collected per WBC gate. We found that as compared with non-bandemia cases, bandemia cases had higher signal levels over signal C25~C30 (mean value 19.5 vs. 79.4, p=0.02); and a trend of lower signal intensities over C135~C145 (mean value 75.9 vs. 42.1, p=0.08). The ratio of C135/C25 signal was higher in bandemia cases (4.81 vs. 1.05, p=0.01). ROC analysis showed that the C135/C25 ratio at a cutoff of > 1.217 had an AUC of 0.94 for predicting bandemia.

Conclusions In our preliminary study, we have established a score using hematology analyzer WBC channel signal C135/C25 ratio as a potential rule for automated bandemia estimation. We are currently increasing our sample size to further validate our data.

PO-274

iTRAQ-based quantitative proteome analysis of carbapenem-resistant Klebsiella pneumoniae

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Objective The aim of this study was to understand the differential protein expression between carbapenem-resistant and susceptible strains, and to explore the role of iTRAQ in the selection of susceptible drugs for carbapenem-resistant Klebsiella pneumoniae.The proteome of carbapenem-resistant Klebsiella pneumoniae was detected by isobaric tags for relative and absolute quantification (iTRAQ) combined with LC-MS/MS.
Methods Three carbapenem-resistant Klebsiella pneumoniae and two carbapenem-sensitive strains were isolated from the Affiliated Hospital of Putian University in 2017and one standard strain were made into protein samples respectively .The quality of samples including protein concentration, SDS-PAGE test and parallelism between samples were preliminarily judged.ITRAQ labeling and LC-MS/MS were performed to identify the total number of proteins and quantitative determination of proteins. Gene ontology functional and pathway enrichment anlalysis were performed for all the proteins with significant differences.
Results A total of 317 proteins were identified in this project. Among them, 2920 proteins had quantitative results. The number of proteins with significant difference was screened according to up_regulate (> 1.5) or down_regulate (< 0.67), P_value (< 0.05). 538 proteins with significant difference were found in the quantitative results. There were significant differences in GO functional classification and functional concentration. Proteins related to drug resistance of Klebsiella pneumoniae, such as beta-lactamase activity, penicillin-binding protein, aminoglycoside-modified inactivating enzyme, metalloproteinase, etc. were obtained. Pathway enrichment analysis of beta-lactam-related proteins was carried out. *KPC* and *SHV* genes related to beta-lactamase activity were identified.
Conclusions The proteome of carbapenem-resistant Klebsiella pneumoniae was different from that of susceptible strains, and there were positive proteins related to bacterial resistance, which provided a basis for the detection of drug susceptibility of Klebsiella pneumoniae by iTRAQ combined with LC-MS/MS.

PO-275

miR-10b-5p, miR-589-3p, miR-651-3p, miR-335-3p, miR-373-3p, miR-372-3p and miR-205-3p affect the expression of TIAM1, a metastasis-related protein, in the gastric cancer cell line BGC823

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Objective T cell lymphoma invasion and metastasis 1 (TIAM1) plays an essential role in the metastasis of tumors, including gastric cancer (GC). microRNAs, which are small noncoding RNAs, are thought to participate in the process of tumor metastasis. This study aimed to explore potential TIAM1-related molecular mechanisms about microRNAs in GC metastasis.

Methods In the present study, we used seven online databases to predict microRNAs that target the TIAM1 gene. The relationship between microRNAs and TIAM1 expression was validated by qRT-PCR. A direct target effect was investigated by the dual-luciferase assay with two types of luciferase reporter gene plasmids (pGL3-TIAM1-3' UTR and psi-TIAM1-3' UTR) in two different cell lines (BGC823 and 293T). The relative expression of the eleven predicted microRNAs in GC was explored by mining The Cancer Genome Atlas (TCGA) database.

Results Several microRNAs were bioinformatically predicted to target the TIAM1-3'-untranslated region (3' UTR) and were included for further experimental validation. According to the qRT-PCR results, several microRNAs (miR-10b-5p, miR-589-3p, miR-651-3p, miR-335-3p, miR-373-3p, miR-372-3p and miR-205-3p) affect TIAM1 expression. Among these microRNAs, only miR-10b-5p directly regulated TIAM1 expression by binding to the 3' UTR of TIAM1.

Conclusions miR-10b-5p, miR-589-3p, miR-651-3p, miR-335-3p, miR-373-3p, miR-372-3p and miR-205-3p affect TIAM1expression in the GC cell line BGC823. miR-10b-5p negatively regulates TIAM1 through direct interaction. Our results could contribute to further mechanistic studies of GC metastasis. Moreover, these negative results showed the limitations of bioinformatics forecasting and may help avoid repetitive labor.

PO-276

Genome sequence analysis of 112 Helicobacter pylori isolates identifies the population structure and molecular genetic characteristics

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Objective To explore their population genetics characteristics, identify candidate genes associated with disease severity and investigate the population structure of 112 Shanghai *H. pylori* isolates and provide an insight into the genetic diversity that exists among *H. pylori* isolates from diverse clinical and geographic origins.
Methods we sequenced the genomes of 112 clinical *H. pylori* isolates isolated from patients in Shanghai with different gastric diseases, including chronic superficial gastritis, chronic atrophic gastritis, peptic ulcer and gastric cancer. Then the Gene prediction and annotation, MLST and Population Structure analysis, Core genome analysis were made by corresponding methods and softwares. All statistical analyses were performed using Stata/SE 14.0 for Mac
Results We found the draft genome sequence of 112 Shanghai *H. pylori* isolates showed their chromosome sizes ranging from 1.52 to 1.69 Mb. The genomes also revealed a low average G+C content of 38.7% which is characteristic of *H. pylori* and between 1511 and 1624 genes were identified per genome. The positive rates of virulence genes *cagP*, *cagH*, *cagY* ,*cag5*, *babA/hopS*, *fliQ*, *futA*, *futB*, *gluE* and *ureB* were linked to different disease backgrounds. CRISPRs were detected in 80.8% (21/26) GU group isolates, 48.5% (32/66) CAG group isolates and 42.1% (8/19) CSG group isolates and there was statistical significance of the different positive rates. A total of 88 STs were detected from the 112 *H. pylori* isolates
Conclusions Several meaningful signifcant differences, including virulence genes and CRISPRs were found among different isolates from four disease background, while if they could be used as biomarkers indicating severity the isolate might cause need further studies.

PO-277

The Clinical Significance of Detection Thyroid Hormone Levels in Nephropathy Patients with Type 2 Diabetes

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Objective To investigate the association of **thyroid hormone** and diabetic nephropathy (DN) in euthyroid patients with type 2 diabetes.
Methods ***Methods*** Analyzed the status of 224 type 2 diabetes retrospectively in this study. The following parameters were recorded: age and old, diabetes duration,

estimated glomerular filtration rate(eGFR), free triiodothyronine (FT3), free thyroxine(FT4), thyroid-stimulating hormone levels(TSH), 24 hours urinary protein. Patients with 24 hours urinary protein of ≥30mg/24h were defined as those suffering from DN.

Results ***Results*** Of the 224 patients that 77(52.4%) suffered from DN. The patients with DN yielded significantly lower FT3 levels than those without DN ($P < 0.01$), While there is no significant difference between FT4 and TSH ($p=0.31$ 和 $P=0.53$). Linear regression analysis showed that FT3 levels were found to correlate positively with eGFR ($R^2=0.038$, $P<0.01$). When eGFR<60, the FT3 levels decreased significantly, and the prevalence of DN increased significantly ($P<0.01$).

Conclusions ***Conclusion*** The level of serum FT3 may be related to the severity of DN with euthyroid patients in type 2 diabetes.

PO-278

Mean Platelet Volume: A Biomarker In Discriminating Adult Onset Still's Disease And Sepsis

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Objective Mean Platelet Volume , as a proportion of routine complete blood count tests, has been studied as a simple biomarker for inflammatory disease. The aim of our study was to investigate whether MPV could be a useful tool to distinguish Adult onset Still's disease(AOSD) from sepsis

Methods We retrospectively reviewed 55 patients with AOSD and 46 sepsis patients diagnosed at the First Affiliated Hospital of Nanjing Medical University between January, 2015 to December 2018. Laboratory data including Complete blood counts, ferritin and C-reactive protein (CRP) level, and the neutrophil-to-lymphocyte ratio (NLR), Platelet-to-Lymphocyte(PLR) were collected and analyzed.

Results There were no signifcant differences in white blood cell counts, neutrophil counts and CRP between two groups. However, we found that AOSD patients showed higher ferritin, lymphocyte and Platelet counts, but lower MPV than sepsis patients (all P<0.01). In receiver operating characteristic (ROC) curve analysis of MPV for distinguish of sepsis, the area under the curve (AUC) was 0.772 (95% CI=0.674 - 0.852) with a cutoff value of 11.1fl. The cutoff value showed the sensitivity (56.10%) and specificity (88.89%), Meanwhile, the area under the receiver operating characteristic curve (AUC) of MPV was slightly lower than that of ferritin, but the difference was not significant.

Conclusions We suggest that MPV may be a useful tool to make a distinction between AOSD and sepsis, as a supplementary biomarker to ferritin.

PO-279

New serum biomarker identification and and analysis by Mass Spectrometry in cervical precancerous lesion and acute cervicitis in South China

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Objective By selecting the potential plasma and metabolic biomarkers which can indicate the precancerous lesions of cervical cancer, cervical cancer and cervicitis through LC-MS technology, the article analyzes its potential mechanism and function.
Methods Plasma samples are selected from healthy Chinese southerners (Control), Low grade squamous intraepithelial lesion (LSIL), High grade squamous intraepithelial lesion (HSIL), Cervical cancer (CC) and post-treatment patients. All polypeptide types and sequences are detected by LC-MS/MS and the results are normalized by using Pareto-scaling. The potential metabolic biomarkers are screened out by applying MetaboAnalyst 4.0 software and XCMS software and subjected to variance analysis and enrichment analysis. The significance and pathomechanism of the potential biomarkers are further studied through metabolic pathway analysis and functional enrichment analysis.
Results According to the results, it is found that compared to healthy people, 9 differential expressive metabolites are screened, among which 4 of them shows up-regulation and 5 of them shows down-regulation; 7 differential expressive metabolites are screened out in LSIL group, among which 5 of them shows up-regulation and 2 of them shows down-regulation; 12 differential expressive metabolites are screened out in CC group, among which 9 of them shows up-regulation and 3 of them shows down-regulation; 8 differential expressive metabolites are screened out in IF group, among which 5 of them shows up-regulation and 3 of them shows down-regulation. In functional enrichment analysis, it is found that the differential metabolism is related to the the addiment and coagulation cascade. Among all potential biomarkers, 2-Amino-3-methyl-1-butanol, L-Carnitine, Asn Asn Gln Arg, Ala Cys Ser Trp, Soladulcidine, Ala Ile Gln Arg, 2-Amino-3-methyl-1-butanol, L-Carnitine, Asn Asn Gln Arg, Ala Cys Ser Trp, Soladulcidine, Ala Ile Gln Arg can serve as the predictors of precancerous lesions of uterine cervix and cervical cancer in different stages. Among all biomarkers, 6alpha-Fluoro-11beta,17-dihydroxypregn-4-ene-3,20-dione have higher expression in CC and HSIL group and lower expression in the Treatment group.
Conclusions the accuracy and specificity of the diagnosis can be enhanced by applying the molecular markers to evaluate the progression of the disease, which has certain prospective in clinical application.

PO-280

Using FOCUS-PDCA to improve the management level of hazardous chemicals

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Objective To standardize the management of hazardous chemicals by scientific management methods, improve the accuracy of registration of hazardous chemicals in and out of warehouse, as well as ensure the safety and accurate use of hazardous chemicals in clinical work.
Methods According to the FOCUS-PDCA procedure, the problems existing in hazardous chemicals storage and registration were analyzed, the improvement measures were formulated, the management system was improved, hazardous chemicals files were established, and the management of hazardous chemicals in and out of the warehouse was standardized and improved continuously.
Results Through the application of FOCUS-PDCA, the registration accuracy of hazardous chemicals was increased from 12.5% to 78.9%; It improves the staff's understanding and familiarity of hazardous chemicals, so as to ensure using them in clinical laboratory safely, timely and accurately.
Conclusions FOCUS-PDCA has a good effect on standardizing the entry, classification, and storage of hazardous chemicals, and plays an important role in achieving continuous improvement of medical quality and safety, which is worth promoting.

PO-281

Elevated expression of kin17 in cervical cancer and its association with cancer cell proliferation and invasion

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Objective Cervical cancer is one of the most common cancers in females worldwide. Emerging evidence suggests that kin17 is a tumor-promoting protein in some types of solid tumors. However, whether kin17 contributes to cervical cancer carcinogenesis remains unknown.Thus,the roles and mechanisms of kin17 in cervical cancer were investigated in the study.
Methods Kin17 expression in clinical samples from Guangdong Women and Children's Hospital and Health Institute was detected by immunohistochemical staining. A series of functional experiments including MTT assay, BrdU assay, colony formation, transwell assay, flow cytometry of apoptosis and cell cycle were performed to explore the roles of kin17 in cervical cancer cells HeLa.
Results In this study, we showed for the first time that the expression of kin17 was significantly increased in clinical cervical cancer samples, and associated with tumor differentiation, lymph node metastasis and ki-67 expression in a clinicopathologic

characteristics review. Furthermore, silence of kin17 in HeLa cells inhibited cell proliferation, clone formation, cell cycle progression, migration and invasion, and also promoted cell apoptosis.

Conclusions Our findings demonstrate that Kin17 is closely related to the cell proliferation and invasion of cervical cancer, and could be a novel diagnostic and therapeutic target for cervical cancer management. The underlying mechanisms should be elucidated in future research.

PO-282

VALUE OF INTERPHASE FLUORESCENCE IN SITU HYBRIDIZATION IN DECECTION OF MULTIPLE MYELOMA

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Objective To investigate the value of interphase fluorescence in situ hybridization(I-FISH) in prognosis of multiple myeloma (MM).

Methods In combination with conventional cytogenetics(CG) and Interphase fluorescence in situ hybridization(I-FISH) were used to detect 20 cases of multiple myeloma (MM) suggested by clinical manifestation , cytomorphology and cytochemistry.

Results In the 20 cases of multiple myeloma (MM) studied , conventional cytogenetics detected 14 numerical and 60 structural chromosome abnormalities;30 derivative and 15 marker chromosomes were characterized precisely by interphase fluorescence in situ hybridization(I-FISH) .

Conclusions Interphase fluorescence in situ hybridization(I-FISH) is helpful for multiple myeloma (MM) diagnosis . Conventional cytogenetics(CG) in combination with interphase fluorescence in situ hybridization(I-FISH) may characterize the complex chromosomal abnormalities more precisely.

PO-283

STUDY ON MECHANISM OF IMMUNE RESPONSE INDUCED BY STREPTOCOCCUS PNEUMONIAE HYDROGEN PEROXIDE-MEDIATED MITOCHONDRIAL DYSFUNCTION

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Objective To investigate whether *Streptococcus. pneumoniae* hydrogen peroxide induces mitochondrial dysfunction and oxidative damage of mtDNA in alveolar epithelial cells, and whether this aberrant mtDNA was leakaged into cytoplasm to induce host immune response.

Methods Part one: *In vitro*, HE staining and immunohistochemistry were used to detect the expression of PINK-1 （PTEN induced putative kinase 1）in lung tissue and the decrease of Pgc1-a （Peroxisome proliferator-activated receptor gamma coactivator-1 alpha）to verify whether *S. pn* H_2O_2 could cause mitochondrial damage in lung tissue of mice. *In vivo*, mitochondrial membrane potential was determined to verify whether *S. pn* H_2O_2 causes mitochondrial damage in alveolar epithelial cells, electron microscope was used to observe the changes of mitochondrial ultrastructure ; Immunofluorescence tested the co-localization of oxidative DNA with mitochondria by counting the 8-OHdG-positive cells. Meanwhile, the changes of mitochondrial DNA content in alveolarepithelial cells and the expression level of mtDNA leakaged into the cytoplasm were detected by PCR.

Part two: ELISA and PCR tested the expression of type I interferons in alveolar epithelial cells. At the same time, constructing mtDNA-deficient alveolar epithelial cells, we explored whether mtDNA plays a key role in *S. pn* H_2O_2-mediated type I interferon cascade; furthermore, we used STING-deficient MEF cells to verify whether STING participates in this process.

Results Result 1. *S. pn* H_2O_2 could cause the lung tissue damage in mice, indicated by PINK1 accumulation and decreased expression of Pgc1-a. It can cause decreased mitochondrial membrane potential and mitochondrial morphological changes in alveolar epithelial cells, including mitochondrial swelling, shrinkage, and the shape of mitochondrial crista changed.

Result 2. *S. pn* H_2O_2 can cause oxidative damage of mtDNA in alveolar epithelial cells and decrease of mitochondrial DNA content, accompanied with mtDNA leakage into the cytoplasm.

Result 3. *S. pn* H_2O_2 can mediate the IFN cascade of alveolar epithelial cells, which is initiated by mtDNA leakage caused by *S. pn* H_2O_2 in alveolar epithelial cells , and STING signaling pathway plays a key role in this process.

Conclusions This study confirmed that H_2O_2 secreted by *S. pn* induced mitochondrial damage in alveolar epithelial cells, and oxidative damage of mitochondrial DNA and then leakaged into the cytoplasm, this aberrant mtDNA thereby activated the STING signaling pathway and induced type I IFN cascade. This study firstly elucidated the molecular mechanism by which *S. pn* H_2O_2 induces type I IFN expression, and also demonstrated that mtDNA plays an important role in mediating host immune responses. Therefore, this study will help us to further understand the interaction mechanism between bacteria and host, and also provide new ideas and theoretical basis for treatment of pneumococcal disease.

PO-284

Clinical application of combined detection of saliva acid and hydroxyproline in gastrointestinal diseases

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Objective To investigate the characteristics of serum SA、Hyp in gastrointestinal patients and the effect of chemotherapy treatment on its level, evaluate the clinical application of SA、Hyp for gastrointestinal diseases, providing reference for clinical application of SA、Hyp in gastrointestinal diseases.
Methods Serum SA and Hyp levels were analyzed in 251 patients with gastrointestinal malignant tumors (rectal cancer, gastric cancer, colon cancer) and 138 patients with benign lesions (stones, intestinal polyps, incomplete intestinal obstruction). 60 patients with malignant tumors received chemotherapy were followed up and the changes of SA and Hyp before and after chemotherapy were dynamically monitored
Results There was no significant difference in serum SA and Hyp levels between patients with malignant tumors and patients with benign lesions ($p > 0.05$); there was no significant difference between patients with malignant tumors except those with colon cancer ($p < 0.01$) and those with rectal cancer ($p > 0.05$); there was significant difference between patients with benign lesions ($p < 0.01$); and between patients with stones, patients with intestinal obstruction and patients with intestinal polyps ($p < 0.05$). Compared with SA and Hyp before and after three courses of chemotherapy, SA and Hyp in patients with malignant tumors decreased significantly ($p < 0.01$), with an average decrease of 17.133U/ml. There was no significant difference in the levels of SA and Hyp between different courses of chemotherapy ($p > 0.05$).
Conclusions Serum SA and Hyp can be used as correlative indicators of gastrointestinal malignant tumors, and can dynamically monitor the level of chemotherapy for malignant tumors

PO-285

Sperm protein 17: an immunotherapeutic and diagnostic target for cancers

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Objective To review the Sp17 as an immunotherapeutic and diagnostic target for malignancies.
Methods Papers on Sp17 expression、function and immunotherapy have been reviewed.
Results Sperm protein 17 (Sp17) is a small molecular protein with 151 amino acids. It is a conserved protein with high homology among different species. Sp17 is an antigenic protein highly expressed in spermatozoa and testis, very limited expression

in other normal tissues. Although the function of Sp17 is not completely elucidated, it is speculated that it might have a role in fertilization, cell migration and other biological functions. Sp17 protein is demonstrated immunogenic and has T cell and B cell epitopes. Moreover, Sp17 has an aberrant expression in tumours with different origins such as ovarian cancer, multiple myeloma, non small cell lung cancer, supporting Sp17 protein as a tumour associated antigen (TAA) target in immunotherapy. In various malignancies, Sp17 has been shown to be an immunotherapeutic target. Sp17 and anti-Sp17 antibodies have been investigated as diagnostic markers for several cancer types.

Conclusions Sp17 is a suitable target for immunotherapy and might serve as a biomarker for cancer diagnosis

PO-286

Weighted Gene Co-Expression Network Analysis Identifies Specific Module and Hub Genes Related to Grade and Survival of Glioma

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Objective Gliomas account for the majority of fatal primary brain tumors, and there is much room for development in the underlying pathogenesis, the multistep progression of glioma and how to improve survival.

Methods In our study, we downloaded microarray datasets (GSE43378 and GSE7696) from the Gene Expression Omnibus (GEO) database. Then, we used weighted gene co-expression network analysis (WGCNA) to screen potential biomarkers or therapeutic targets and employed functional enrichment analysis to explore the underlying mechanism involved in the tumor progression.

Results Through these robust method, we identified yellow module which was positively correlated with WHO grade (correlation coefficient = 0.4, p = 5e-06) but negatively correlated with overall survival (correlation coefficient = -0.36, p = 5e-05). Then, the hub genes were screened by cytoHubba and tested in Oncomine and Gene Expression Profiling Interactive Analysis (GEPIA) databases. Finally, a total of 13 real hub genes that were positively correlated with glioma grade and had significant prognostic value were identified.

Conclusions In summary, these hub genes associated with multistep progression and prognosis of glioma provide a novel and adequate candidate reservoir for further studies in glioma management.

PO-287

Identification of an independent long non-coding RNA signature for predicting clinical survival in Glioblastoma multiforme

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Objective Glioblastoma multiforme (GBM) is an often-fatal brain malignancy characterized by poor prognosis, high recurrence rate and lacking effective therapies. We aimed at constructing an independent long non-coding RNA (LncRNA)-signature to separate patients into different risk groups for personalized clinical management.
Methods The LncRNA gene expression profile of GBM was re-annotated from the Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) databases. A four-LncRNA signature was established in TCGA and further validated in GSE13041.
Results Our LncRNA-signature could significantly subdivide GBM patients into high-risk and low-risk groups not only in the training TCGA dataset (log-rank test P = 0.00054) but also in an independent validation dataset GSE13041 (log-rank test P = 0.00016). In addition, we applied multivariate Cox analysis and stratification analysis demonstrated that this LncRNA-signature was an robust prognostic factor, which was independent of age, gender, especially status of IDH, EGFR and G_CIMP. Moreover, weighted gene co-expression network analysis (WGCNA) and relevant Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis revealed that the signature-related pathway was mostly involved in neurotransmission related signaling pathway.
Conclusions Our findings provided an extensive understanding and a more accurate prognostic predictor of GBM. And consequently, this signature may contribute to help clinical personalized decision making of GBM. Further experimental verifications are still needed.

PO-288

COMPARISON BETWEEN SERUM PROCALCITONIN MEASUREMENT USING FLUORESCENT IMMUNOASSAY (FIA) METHOD AND ELECTROCHEMILUMINESCENCE IMMUNOASSAY (ECLIA) METHOD IN SEPSIS DETECTION

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Objective Sepsis is a critical patient condition with multiple organ dysfunction, caused by a dysregulated host response to infection. It is estimated to affect more than 30 million people worldwide every year, potentially leading to 6 million deaths. Early identification and initiation of antibiotic therapy could improve outcome

dramatically. Procalcitonin is currently widely used as a newer indicator in detecting sepsis, but it requires relatively large cost, big analyzer, with a large sample capacity. Analyzer with small size and throughput, monotest and more economical costs is already considerable for clinicians and laboratories along with technological development, especially in national health coverage era, including health care facilities in remote area. The aim of the study is to compare procalcitonin values between both methods for detecting sepsis.

Methods We conducted an observational study with cross sectional design among serum patients diagnosed with sepsis in Saiful Anwar General Hospital, Malang. Procalcitonin was measured paralleled with FIA method (FREND™ PCT) and ECLIA method (Cobas e411 Roche). Each result was compared between two methods and correlated with SOFA or PELOD-2 score. Statistical analysis was performed using the Spearman's correlation coefficient.

Results From July 2018 to December 2018, we identified and analyzed 99 patients diagnosed with sepsis, ranges from 2 days to 85 years old of age with total of 69 adults and 30 children. There was no significant difference of procalcitonin measures between two methods with Wilcoxon test ($p > 0.05$). Strong correlation was also found between both methods ($r = 0.941$, $p < 0.0001$). There was no significant difference between two methods for detecting sepsis in adult patient. However, there were 40% discrepancies between procalcitonin value and PELOD-2 score from both methods among pediatric patients, this maybe caused of incomplete and limited data of PELOD-2 score.

Conclusions Serum procalcitonin measurement using FIA method (FREN™ PCT) can be used for detecting sepsis, since it has good correlation and there's no significant difference with the ECLIA method (Cobas e411 Roche), particularly in adult patient. Pediatric patients need special attention and further research recommendation.

PO-289

Ultrastructural change of mixed junction in desmosomal gene mutation ARVC pateints comparing to other gene mutation patients: an electron microscopy investigation on transplanted heart samples

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Objective Arrhythmogenic right ventricular cardiomyopathy (ARVC) is an inherited cardiomyopathy caused mostly by desmosomal gene mutations, but part of ARVC carrying extradesmosomal gene mutations or non-gene mutations. The ultrastructural character of ARVC is intercalated disc remodeling, however, the difference among different genotypic patients remains unknown.

Methods In this study, there were fifteen patients divided into three groups: four patients with desmosomal genes mutation (desmosomal gene mutation group, DGM), five patients with extradesmosomal genes mutation (extradesmosomal gene mutation group, EDGM) and the rest six patients with non-gene mutation (non-gene mutation group, NGM). The characters of intercalated disc of both ventricles was analyzed to compare the ultrastructural changes among different genotypic patients. Besides, lipid droplets were observed.

Results Of the fifteen participants included in the analysis, ten (66.7%) were male; mean (SD) age was 35.1 (11.1) years. Of right ventricular ultrastructural performances: the desmosome percent length of intercalated disc of right ventricle was higher in DGM (22.66±2.09% vs. 17.62±1.02%, p=0.035; 22.66±2.09% vs. 15.25±4.52%, p=0.003) and the results were similar in both EDGM and NGM; the mixed junctions percent length of intercalated disc and mixed junction mean gap was higher in DGM than NGM (32.97±8.14% vs. 25.29±4.37%, p=0.037; 0.50±0.013μm vs. 0.037±0.007μm, p=0.026; respectively); besides, the desmosome gap was similar in different genotypic groups (0.07±0.03μm vs. 0.05±0.01μm vs. 0.06±0.02μm, p=0.517). In left ventricular ultrastructural performances: the mixed junction mean length was longer in EDGM than NGM (0.54±0.07μm vs. 0.41±0.09μm, p=0.027); and the mixed junction mean gap was wider in DGM than NGM (0.058±0.006μm vs. 0.039±0.008μm, p=0.006). As to lipid droplet existence or not, none of the DGM patients (0%) was with existence of lipid droplet; 4 of the EDGM patients (80%) and 6 of the NGM patient (100%) were with existence of lipid droplet and lipid droplet distributed around the mitochondria or/and between myocardial fibers. The distribution of lipid droplet was significantly different among the three groups (p=0.001).

Conclusions Different genotypic ARVC patients were characteristic with different ultrastructural findings: the mixed junction was the major difference between DGM and other. Besides, the lipid droplet was absent in DGM patients but present in EDGM and NGM patients suggesting that the pathogenesis of different genotypic patients may be not same.

PO-290

AIM2, DHX36, and BAX are critical for the diagnosis and treatment of tuberculosis

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Objective Tuberculosis (TB) is usually caused by *Mycobacterium tuberculosis*, which has the highest mortality among infectious diseases. This study is designed to identify the key genes affecting the diagnosis and treatment of TB.

Methods GSE54992, which included 39 peripheral blood mononuclear cell (PBMC) samples, was extracted from Gene Expression Omnibus database. After the samples were classified into type and time groups by limma package, the differentially expressed genes (DEGs) were analyzed using Analysis of Variance. Using pheatmap package, hierarchical cluster analysis was performed for the DEGs. Followed by the key modules

correlated with TB were selected using WGCNA package. Finally, functional and pathway enrichment analyses was carried out using clusterProfiler package.

Results There separately were 3731 and 3952 DEGs in type group and time group. Among these DEGs, 17 common DEGs in type group and 8 common DEGs (including *AIM2*) in time group were identified. The DEGs in subclusters 3, 6, 7, and 8 were chose for further analyses. Based on WGCNA analysis, blue and green modules in type group and pink module in time group were selected as key modules. From the key modules, 9 (including *BAX*) hub genes in type group and 6 (including *DHX36*) hub genes in time group were screened. Through pathway enrichment analysis, the TNF signaling pathway was enriched for the green module.

Conclusions *IM2*, *DHX36*, and *BAX* might be key genes acting in the mechanisms of TB. Besides, the TNF signaling pathway might also be critical for the diagnosis and therapy of the disease.

PO-291

Apolipoprotein M serum levels correlate with Henoch-Schonlein purpura and and ISKDC grading score

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Objective Henoch-Schonlein (HSP) is the most frequent vessel vasculitides in children and the prognosis is related to the children's age and degree of renal involvement. The aim of this study was to investigate serum apoM levels in patients with HSP patients and to evaluate the association between apoM and disease severity.

Methods A total of 109 HSP patients and 76 age- and sex-matched healthy controls were included. The age and gender of the study participants were matched. ApoM levels were measured by an enzyme-linked immunosorbent assay. Additionally, the serum levels of lipids, apolipoproteins, kidney biochemical profiles, immunoglobulins (IgA, IgG, IgM and IgE) and the complements were assessed using an automatic biochemical analyzer.

Results apoM was increased significantly in HSP patients compared to healthy controls. apoM, meanwhile, was lower in patients with nephritis than in those without nephritis. The apoM was higher in class I and II HSPN patients than in class III and IV. In addition, the apoM serum level <24.81mg/L was an independent predictive factor for HSPN and can be independently associated with the presence of nephritis in HSP patients. Meanwhile, the serum apoM concentration negatively correlated with ISKDC grading score in the HSPN patients.

Conclusions Serum apoM was elevated in HSP patients and decreased gradually with ISKDC grading score. ApoM(OR=0.32, 95 % CI =0.12-0.85, p=0.023) was identified as protective factors for nephritis in all HSP patients.

PO-292

Association of HLA-A, -B, -C, -DPA1, -DPB1, -DQA1, -DQB1, and -DRB1 with end-stage renal disease in Malang, Indonesia

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Objective The aim of this study was to investigate the distribution and the contribution of HLA in the ESRD patients in Malang.
Methods This report is a retrospective study. We examined HLA class I and II alleles to find out distribution of HLA-A, -B, -C, -DPA1, -DPB1, -DQA1, -DQB1, -DRB1 in renal transplant recipients and to ascertain their role in susceptibility to ESRD in 41 ESRD patients considered renal transplantation and 41 healthy controls in Malang. HLA typing was assayed with Luminex LabScan 100, allele frequencies were obtained by direct counting and statistical analysis was estimated using SPSS v. 23 software.
Results A total of 9 HLA-A, 16 HLA-B, 10 HLA-C, 12 HLA-DRB1, 6 HLA-DQA1, 5 HLA-DQB1, 3 HLA-DPA1, and 14 HLA-DPB1 alleles were identified at the four digit level in the renal transplant recipients. High frequency alleles were HLA-A*24 (25%) for HLA-A, -B*15 (42%) for HLA-B, -C*08 (33%) for HLA-C, -DRB1*12 (51%) for HLA-DRB1, -DQA1*06 (44%) for HLA-DQA1, -DQB1*03 (54%) for HLA-DQB1, -DPA1*02 (45%) for HLA-DPA1, and -DPB1*04 (29%) for HLA-DPB1. Only HLA-A*24 was associated with ESRD (p=0.025).
Conclusions The result showed considerable heterogeneity in both HLA class I and class II antigens. The most frequent alleles observed in ESRD patients in Malang were HLA-B*15 in the HLA class I and HLA-DQB1*03 in HLA class II.

PO-293

Comparison of two molecular assays for detection of Mycobacterium tuberculosis Complex in extra-pulmonary samples

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Objective Molecular assays can improve diagnosis of extra-pulmonary infection of *Mycobacterium tuberculosis* complex (MTBC) in terms of accuracy and analytical turnaround time. Roche COBAS TagMan 48 and Cepheid GeneXpert were two commonly used molecular assays for assisting in diagnosis of pulmonary MTBC infection. This study compared these two systems for detection of MTBC in extra-pulmonary specimens.
Methods A hundred and thirty-eight extra-pulmonary specimens submitted for both MTBC DNA detection and MTBC culture were recruited at random. Types of specimens included cerebral spinal fluid (47), tissues (32), abscess (21), pleural fluid (17), urine (7), pericardial fluid (4), ascites (4), synovial fluid (3) and others (3). For those

specimens collected from contaminated sites, concentrated sediments after digestion and decontamination were obtained on receipt. Aliquots of clinical samples or sediments were subsequently tested for MTBC DNA within 24 hours after receipt or appropriately kept frozen until analysis. All aliquots were analyzed by GeneXpert and TagMan for MTBC DNA using Xpert MTB/RIF and COBAS MTB reagents, respectively. These two qualitative assays were based on real-time polymerase chain reaction. The GeneXpert could estimate by grading amount of DNA. Results were compared against mycobacterial culture which was regarded as the gold standard in this study. Sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) of both assays were evaluated.

Results Forty samples (29%) were MTBC culture-positive. Concordance rates between MTBC culture and molecular assays were 92.8% for GeneXpert and 89.1% for TagMan, respectively. Sensitivity, specificity, PPV and NPV for GeneXpert were 92.5% (37/40), 92.9% (91/98), 84.1% (37/44) and 96.8% (91/94), whereas they were 80% (32/40), 92.9% (91/98), 82.1% (32/39) and 91.9% (91/99) for TagMan. Among eight culture-positive and TagMan-negative specimens, five were GeneXpert-positive with low or very low DNA amounts.

Conclusions GeneXpert had a better analytical performance for detection of MTBC DNA in extra-pulmonary specimens than TagMan in terms of sensitivity, PPV and NPV. Both assays were promising in assisting diagnosis of extra-pulmonary infection of MTBC.

PO-294

Serum D-dimer as a diagnostic index of PJI and retrospective analysis of etiology in patients with PJI

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Objective To investigate the diagnostic value of serum D-dimer in patients with periprosthetic joint infection (PJI). Moreover, to provide evidence for PJI by investigating distribution of pathogenic bacteria and drug resistant situation among patients with PJI.

Methods A retrospective study of the medical records of all patients undergoing arthroplasty from the Second Xiangya Hospital of Central South University from 2014 to 2018, 40 patients with periprosthetic joint infection , 37 patients with aseptic loosening and 59 patients with extra-articular infection were selected. The results of serum D-dimer, C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR), as well as the bacterial types and antimicrobial susceptibility test results from tissue or joint fluid samples around the prosthetic joint of the patients were collected, and the relevant data were analyzed.

Results The serum D-dimer, CRP and ESR level were significantly higher in the patients with PJI. The mean D-dimer level was 2.0795 μg/mL in PJI group compared with 0.6854 μg/mL in aseptic loosening group ($p = 0.000$) and 0.4556 μg/mL in extra-articular infection group ($p = 0.000$). The serum D-dimer test demonstrated better sensitivity (87.50%) , and better specificity (89.19%) , for diagnosing PJI. The serum CRP and ESR had a sensitivity of 80.00% and 82.50% and a specificity of 78.38% and 64.86%,

respectively. The sensitivity and specificity of ESR and CRP combined was 75.00% and 83.78%, respectively. 29 strains of pathogens around the prosthesis after joint replacement were detected, including 22 strains of Gram-positive bacteria, 3 strains of Gram-negative bacteria, and 4 strains of fungi. The staphylococcus was the major pathogen showing high resistance to Cefoxitin and ampicillin.

Conclusions Patients with PJI have high levels of serum D-dimer, which is a promising marker for the diagnosis of PJI. The Gram-positive bacteria are major pathogen in PJI after prosthetic joint replacement, and Staphylococcus aureus is the most common organism. Clinical efficacy is significantly improved by reasonable choice of antibiotics and effective medicine education.

P0-295

Tubulin alpha-1B - a potential biomarker for lung cancer diagnosis and prognosis

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Objective Because lung cancer is the leading cause of cancer deaths worldwide, it is important to develop clinically useful biomarkers for the disease. The aim of this investigation was to assess the potential application of tubulin alpha-1b (TUBA1B) as a biomarker for diagnosis and monitoring the outcome of lung cancer.

Methods Immunohistochemistry (IHC) analysis in a tissue microarray containing 90 lung cancer cases and adjacent nontumor tissue was performed to examine the expression of TUBA1B. Serum was collected from healthy donors and patients with lung cancer before and during therapy, and in the follow-up period. TUBA1B levels were quantified in serum by an enzyme-linked immunosorbent assay.

Results The IHC analysis showed that the expression levels of TUBA1B protein were significantly higher in lung cancer than matched non-cancerous tissues. TUBA1B expression in lung cancer was statistically correlated with T category ($p = 0.003$). Patients with higher TUBA1B expression had shorter overall survival than patients with lower TUBA1B expression ($p < 0.0001$). Moreover, the multivariate analysis suggested TUBA1B was an independent predictor of overall survival ($p = 0.030$). TUBA1B levels in serum were significantly higher in lung cancer patients compared to healthy human volunteers ($p < 0.0001$), achieving a 0.97 AUC value for the receiver-operating characteristic curves. TUBA1B levels in serum dropped significantly after therapy.

Conclusions The results of our study demonstrate that TUBA1B might serve as potential diagnostic and prognostic biomarker in patients with lung cancer.

PO-296

Serum Lp-PLA2, CEA, CA125, NSE and CYFRA21-1 in patients with lung cancer Level change and its clinical significance

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Objective To study the value of lipoprotein associated phospholipase A2 (Lp-PLA2) in the diagnosis of lung cancer.
Methods 82 cases were randomly selected as normal reference group, 82 cases of lung cancer were treated as lung cancer group, compared two groups of subjects of LP-PLA2, CEA, CA125, NSE, CYFRA21-1 levels and diagnostic sensitivity, specificity. ROC curve analysis indicators Diagnostic value.
Results 82 cases were randomly selected as normal reference group, 82 cases of lung cancer were treated as lung cancer group, compared two groups of subjects of LP-PLA2, CEA, CA125, NSE, CYFRA21-1 levels and diagnostic sensitivity, specificity. ROC curve analysis indicators Diagnostic value.
Conclusions Both Lp-PLA2, CEA, CA125, NSE and CYRFA21-1 levels were elevated in lung cancer patients; Lp-PLA2 combined with 4 tumor markers can improve the diagnostic sensitivity and specificity of patients with lung cancer, and effectively improve the value of diagnosis and treatment.

PO-297

Correlation between Single Nucleotide Polymorphisms in beta-catenin/WNT signaling pathway genes with Cervical carcinoma in Chinese Han Patients

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Objective Cervical cancer is a multifactorial gynecologic tumor in women worldwide.Its occurrence and development are related to genetic and epigenetic changes in genes encoding proteins that are vital components of various signaling pathways such as WNT signaling pathway.In this study,we investigated the correlation between genetic variants in WNT key genes with predisposition to cervical cancers.
Methods We peformed a case-control study(147 cases vs. 158 controls) in Chinese Han populations to identify cervical carcinoma risk variants by genotyping 7 SNPs (rs11564475,rs1798802,rs3864004,rs4135385, rs2293303,rs454886 and rs3755557) located in 3 genes related to WNT canonical signaling(CTNNB1,APC and GSK3).The chi-square test was used to evaluate the genetic association with the cervical cancer suspectibility.Stratified anylsis was performed based on age of on-set of cervical cancer.

Results In the case-control study,genotypic analysis of individual locus revealed significant difference between cases and controls in 3 SNPs(rs1798802,rs2293303 and rs3864004)located in Dominant model of rs1798802 and recessive model of rs3864004 were associated with cervical cancer risk(p=0.042 and p=0.018).The rs3864004 A allele gene and rs2293303 T allele gene had a hazardous influence on cervical cancer(p=0.031 and p=0.040).Besides,the frequency of CTNNB1 rs4135385 A allele were significant higher in cervical cancer patients whose age were above 46(p=0.026).Evaluation of WNT pathway SNPs for CTNNB1 rs11564475,APC rs454886 and GSK3 3755557 did not show any association in the overall study nor in the stratified anylsis.
Conclusions Altogether,our study demonstrated that CTNNB1 rs1798802,rs2293303 and rs3864004 increase susceptibility to cervical cancer.In addition,CTNNB1 rs4135385 were significantly associated with old aged cervical cancer patients.Confirmation of our finding in large samples of multi-regional and multi-ethnic researches can provide accurate evidence for the use of SNPs in beta-catenin/WNT pathwy genes as screening biomarkers for early-detection of cervical cancer.

PO-298

Determination of high-sensitivity cardiac troponin T upper reference limits under the improved selection criteria in a Chinese population

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Objective It is important to establish 99th percentile upper reference limit (URL) of high-sensitivity cardiac troponin (hs-cTn), which is widely acknowledged in the universal definitions of myocardial injury and different types of MI. However there is no common consensus on how to define the reference population. This study aimed to establish 99th percentiles URLs of hs-cTnT under both currently recognized selection criteria and improved selection criteria for further judging whether two 99th percentiles URLs of hs-cTnT established different.
Methods From January to July in 2014, applying the stratified cluster sampling protocol, this study took apparently healthy subjects through questionnaire in Shenyang China as the screening objects. We first followed currently recognized selection criteria using surrogate biomarker for diabetes, myocardial dysfunction, renal dysfunction and maging modality . Then we followed improved selection criteria to exclude hypertension, overweight and obesity and dyslipidemia. 99th percentiles URLs of hs-cTnT were established under different selection criteria.
Results We recruited 1850 apparently healthy subjects through questionnaire. Under the currently recognized selection criteria a total of 1646 individuals were enrolled. Under the improved selection criteria a total of 929 individuals were enrolled. No matter under each criteria, median values of hs-cTnT male were higher than that of female in every age group. If the currently recognized criteria was applied, 99th percentile URLs (90% Confidence Interval) of hs-cTnT male and female were 19(17-20) ng/L and 16(15-19) ng/L respectively. If the improved selection criteria was applied,

99th percentile URLs (90% Confidence Interval) of hs-cTnT male and female were 15(12-17) ng/L and 14(11-16) ng/L respectively.

Conclusions Compared with currently recognized selection criteria, improved selection criteria through questionnaire survey, physical examination and laboratory screening to further exclude hypertension, overweight and obesity and dyslipidemia can avoid overestimation of the 99th percentile URL of hs-cTnT.

PO-299

Study on the characteristics of protective T cell responses in HLA-B*13 positive CRF01_AE subtype HIV-1 infected MSM in China

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Objective The human leukocyte antigen-I (HLA-I)-restricted T cell response plays a critical role in controlling HIV-1 replication. Many current vaccine strategies focus on identifying immunogens which can induce T cell responses against HIV. Our previous study found several B*13 restricted T cell responses which were associated with slow disease progression in B' clade HIV-1 infected HLA-A*30-B*13-C*06 positive patients. And we also found that the variation rates were relatively lower in B*13 restricted several optimal epitopes in HIV-infected men who have sex with men (MSM). Therefore, characterizing the protective T cell responses in B*13 positive CRF01_AE clade-infected patients is helpful for the vaccine design of this population.

Methods Twelve HIV-1 primary infected cases were recruited form Liaoning MSM prospective cohort. T cell responses to B*13 restricted six optimal epitopes (Gag-HQSLSPRTL (HL9), Gag-VQNAQGQMV(VV9), Gag-GQMREPRGSDI(GI11), Gag-RQANFLGRL(RL9), Pol-GQDQWTYQI(GI9), Pol-RQYDQILIEI(RI9)) at 3 month and 1 year were detected with IFN-g ELISPOT assays. The viral quasispecies sequences from the synchronous plasma were detected by next generation sequencing (NGS). Cross reactivity to variant epitopes were also analyzed.

Results T-cell responses to 6 optimal epitopes were analyzed in six patients at 3 month and in twelve patients at 1 year after infection. Results showed that Pol-GI9, Gag-GI11 and Gag-VV9 were immunodominant epitopes in B*13 positive CRF01_AE clade-infected patients according to the frequencies and magnitudes of T cell responses. The variations within the three dominant epitopes were analyzed by NGS. The mean reads of the sequences containing Pol-GI9, Gag-GI11 and Gag-VV9 epitopes were 16321, 18469 and 3710, respectively. Among the twelve patients, 8.33% (1/12) of the patients showed a D490G variation in the Pol-GI9 epitope, and D490G abrogated T cell recognition in patient 320019 and 325029. 25.00% (3/12) of the patients showed an M228I variation in the Gag-GI11 epitope. Patients 320019 and 325020 had a slightly diminished responses to the M228I variant. 58.33% (7/12) of the patients showed multiple variations in Gag-VV9 epitope and patients 320088, 320019 and 325029 had a different degree of diminished IFN-g responses to the M142W/V143T, V143T, A139T and V143A variants. In addition, we also found that Gag-GI11 specific T cell response was positively

correlated with $CD4^+$T cell counts at 1 year (R=0.537, P=0.072); Pol-GI9 specific T cell response was positively correlated with viral loads at 3 months (R=0.786, P=0.064). The $CD4^+$T cell count was significantly higher in patients with Gag-VV9 epitope specific T cell responses than those without Gag-VV9 epitope specific T cell responses (246.50±83.5 vs. 555.75±48.54, P=0.026), which might be related to the rapid disease progression.

Conclusions Pol-GI9, Gag-GI11 and Gag-VV9 were the immunodominant epitopes in B*13 positive CRF01_AE clade-infected patients. The variation rate of amino acids in Gag-GI11 epitope was relatively lower and Gag-GI11 epitope specific T cell responses was associated with slow disease progression. Therefore, Gag-GI11 epitope was preferred for the T cell-based vaccines, while Pol-GI9 and Gag-VV9 might not be suitable for the immunogen for the target population.

PO-300

The Clinical Application in Diagnosis Influenza A and Influenza B Virus by Colloidal Gold Method

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Objective To evaluate the clinical application value of Influenza Diagnosis Kit (Colloidal Gold, Wondfo®) for detecting influenza A and influenza B virus antigen.

Methods Pharyngeal swab samples were collected from 95 cases of outpatients and 226 cases of inpatients who were suspected of influenza at The Xiangya Second Hospital of Central South University from January 2019 to February 2019. Influenza A and influenza B virus were detected by Colloidal Gold (Wondfo®) method and real time-polymerase chain reaction(RT-PCR) was used to verify the diagnosis.

Results The positive detection rate of Colloidal Gold (Wondfo®) method was 19.6% (63/321). Compared with RT-PCR method, its sensitivity and specificity for influenza A and influenza B virus were 31.5%, 94.9% and 20.0%, 95.9% respectively. Meanwhile, the positive predictive value and negative predictive value were 79.6% and 68.8% for influenza A virus, and 7.1% and 98.7% for influenza B virus.

Conclusions Colloidal Gold (Wondfo®) Influenza Diagnosis Kit was prone to misdiagnosis of influenza A and B virus due to low sensitivity and high specificity. So patients who were suspected of influenza, whether influenza virus positive or negative detected by Colloidal Gold (Wondfo®) method, need RT-PCR to confirmed.

PO-301

The histological and biochemical evaluation of transforming growth factor-ß activation and its clinical significance in patients with chronic liver disease

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Objective Transforming growth factor-ß (TGF-ß) is a key driver for liver fibrogenesis. TGF-ß must be activated in order to function. Plasma kallikrein (PLK) is a TGF-ß activator that cleaves the latency-associated protein (LAP) between arginine^{58} and lysine^{59} residues and releases active TGF-ß from the latent TGF-ß-LAP complex. Thus, the generation of two LAP degradation products, ending at arginine^{58} (R^{58}/LAP-DPs) and beginning from lysine^{59} (L^{59}/LAP-DPs), reflects PLK-dependent TGF-ß activation. However, the significance and details of TGF-ß activation in patients with chronic liver disease remain uncertain. The aim of this study was to examine the PLK-dependent TGF-ß activation in patients by detecting R^{58} and L^{59}/LAP-DPs and clarify its role in liver fibrogenesis.

Methods This study included a total of 234 patients, who had received treatment or follow-up care for chronic liver disease at Jikei University Hospital between 2007 and 2015. Liver biopsy specimens were used for immunostaining to detect R^{58}/LAP-DPs, while plasma samples were subjected to an enzyme-linked immunosorbent assay to measure the L^{59}/LAP-DP concentration. Informed consent was obtained from all patients in accordance with the Declaration of Helsinki. This study protocol was approved by the Ethics Committee of the Jikei University School of Medicine for Biomedical Research.

Results R^{58}/LAP-DP was robustly expressed in and around the sinusoidal cells before the development of the fibrous regions. The R^{58}/LAP-DP expression at fibrosis stage 1 was higher than at any other stages, and the relationship between the plasma L^{59}/LAP-DP level and the stage of fibrosis also showed a similar trend. The abundance of plasma L^{59}/LAP-DP showed no correlation with the levels of direct serum biomarkers of liver fibrosis; however, its changes during interferon-based therapy for chronic hepatitis C were significantly associated with virological responses.

Conclusions Our results suggest that PLK-dependent TGF-ß activation occurs in the early stages of fibrosis and that its unique surrogate markers, R^{58} and L^{59}/LAP-DPs, are useful for monitoring the clinical course of chronic liver disease.

PO-302

Utility of PAX1 methylation in triage of high-risk human papillomavirus-positive women

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Objective HPV-testing has been shown to provide a superior detection of women at risk of cervical precancer. However, as it is a long time process from High-risk HPV(hrHPV) infection to cancer and most hrHPV can be clear, additional triage testing of HPV-positive women is necessary to identify those with cervical precancer. DNA methylation is a promising biomarker in cervical cancer. We evaluated the clinical performance of potential methylated genes as a triage assay for hrHPV-positive women.
Methods A retrospective hospital-based case-control study in cervical cancer project was performed, with 342 hrHPV-positive cervical scrapings enrolled. The samples were randomly classified into a training set (n = 153) and testing set (n = 189). All sample were tested for hrHPV using a SeqHPV assay, then multiple gene methylation status analysis was conducted by next-generation sequencing based on the residual cervical genomic DNA. The methylation ratio was calculated by BSMAP. The receiver operating characteristic (ROC) curves were used to predict and validate the positive cutoff value.
Results In the training set, six genes (CADM1, MAL, EPB41L3, FAM19A4, PAX1, SOX1) were performed to plot ROC curves, and among them, PAX1 showed the highest area under the curve (AUC) of 0.872 for distinguish between CIN2(+) and CIN1/normal, corresponding to a sensitivity of 0.775(95% CI:0.734-0.813) and specificity of 0.855(95% CI: 0.775-0.894). In the testing set, PAX1 yielded an AUC of 0.871, under which, the sensitivity was 0.729 and specificity of 0.894, revealing good clinical performance in triage of hrHPV-positive women for detecting CIN2 or worse.
Conclusions PAX1 methylation has a prospect to be a potential biomarker for triage in detecting CIN2+ in hrHPV-positive women.

PO-303

OptrA mediating low-level linezolid resistance in Enterococcus faecalis

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Objective To investigate the resistant mechanisms of low-level linezolid-resistant *Enterococcus faecalis*, this will lay the foundation for the prevention and treatment of drug resistant enterococci and the development of novel antibacterial drugs, the improvement of scientific management level, and preventing the generation and spread of bacterial resistance.

Methods PCR amplification, DNA sequencing and sequence alignment method were used to detect 23S rRNA, rplC and rplD gene mutations, as well as cfr gene and optrA gene carried by *E. faecalis*.

Results The cfr gene and optrA gene were detected in 100 strains of E. faecalis isolates, the results showed that no optrA gene were detected in all strains of MIC 1-2 mg/L, but detected in all strains of MIC 4-8 mg/L. No cfr gene was found in all strains. 30 strains of linezolid sensitive and resistant E. faecalis were selected and the 23S rRNA, rplC, rplD gene mutations were detected, the results showed that in MIC 1 mg/L of E. faecalis (8 strains), there were C208T, A282G two kinds of mutation were found in 23S rRNA of 2 strains, in which 1 strain was found T1505C mutation simultaneously. In MIC 2 mg/L of E. faecalis, C208T, A282G, C2163T three kinds of mutation were found, in which 6 strains appeared A282G mutation and 1 strain occured C2163T mutation. In MIC 4-8 mg/L of E. faecalis (12 strains), G353A mutation was increased and appeared in 5 strains, in which 1 strain of MIC 4 mg/L also occured C2059T mutation. In MIC 8 mg/L E. faecalis, EF494 strain occured known resistance mutation in the A2062C locus. In all 30 strains of E. faecalis, there were 2 strains showed rplC gene mutations,11 strains showed rplD gene mutations, but all of them were synonymous mutations, which did not cause the change of amino acids of L3 and L4 proteins. In addition, we found that 2 strains of linezolid resistant E. faecalis simultaneously occured 23S rRNA V gene mutation and optrA gene.

Conclusions The low-level linezolid-resistant mechanism of *Enterococcus faecalis* in this region is mainly related to point mutation in the V region of 23S rRNA and optrA gene. It is worth noting, we find that 2 strains of linezolid resistant E. faecalis are simultaneously detected 23S rRNA V gene mutations and optrA gene, suggesting that the development of linezolid resistance may be in the direction of multiple mechanisms, and the clinical treatment of infections caused by linezolid resistant bacteria will be challenged.

PO-304

Clinical application value of hepatitis B virus basal core promoter1762/1764 and pre-core 1896 gene mutation combined with GGT/ALT in hepatitis B related hepatocellular carcinoma

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Objective To study the application value of *hepatitis B virus* basal core promoter(BCP) 1762/1764 and pre-core(PreC) 1896 mutation with GGT/ALT ratio in hepatitis B virus related hepatocellular carcinoma (HBV-HCC).

Methods 159 cases of hepatitis B related diseases with HBV-DNA level more than 1000 IU/ml were collected: 63 cases of chronic hepatitis B (CHB), 50 cases of liver cirrhosis (LC), and 46 cases of HB-HCC. At the same time, the biochemical results of GGT and ALT were collected. Then their viral BCP1762/764 and pre-core 1896 mutation was determined by ARMS-PCR.

Results The serum GGT level and GGT/ALT ratio in HBV-HCC group were higher than those in LC group and CHB group, and the difference was statistically significant ($P<0.05$). The mutation rates of HBV gene BCP 1762/1764 in HBV-HCC group, LC group and CHB group were 91.30%, 84.00% and 22.22%, respectively. The mutation rates was significant difference between HBV-HCC and CHB ($P<0.05$), while the mutation rates of HCC and LC group were no significant ($P>0.05$). The mutation rates of HBV gene pre-C 1896 were 84.78%, 64.00%, 39.68% respectively. The pre-C 1896 mutation rate of HCC was markedly different with that of CHB and LC ($P<0.001$; $P<0.05$, respectively). The GGT/ALT mean had significant difference between HBV BCP1762/1764 mutant and non-mutant ($P < 0.05$), and there was significant difference between pre-C 1896 mutant and non-mutant ($P < 0.05$). ROC curve analysis showed that sensitivity was 66.7% and specificity was 83.9% when BCP172/1764 mutated; sensitivity was 64.1% and specificity was 86.0% when pre-C 1896 mutated; sensitivity was 63.9% and specificity was 92% when BCP region and precore region mutated simultaneously.

Conclusions The HBV BCP 1762/1764 mutation, pre-core 1896 mutation and GGT/ALT ratio are all positively related to the state of HBV related diseases, and the combined analysis of those had a certain early diagnostic value for HBV-HCC.

P0-305

Value of procalcitonin in neonatal infection within 24 hours after birth: a retrospective cohort study

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Objective Neonatal infections, especially neonatal pneumonia, are clinically common and have a high mortality rate. Early diagnosis and the duration of appropriate antibiotic treatment are critical. The value of PCT, CRP, and WBC in the diagnosis of early neonatal pneumonia is not clear.PCT is an indication of infection and may be valuable.

Methods This is a retrospective cohort of 269 neonates within 24 hours after birth, analyzing the value of procalcitonin, C-reactive protein, and white blood cells in neonatal infections, especially neonatal pneumonia, and antibiotic therapy.

Results The median of PCT, CRP, and WBC in the severely infected group, neonatal pneumonia group, neonatal infection group, and non-infectious disease group were (1.76, 1.20-4.29; 5.25, 0.74-15.60; 15.8, 8.8-20.9), (0.20, 0.12-0.68; 0.53, 0.30-2.56; 13.8, 9.7-19.6), (0.22, 0.15-0.57; 3.64, 0.52-6.92; 10.4, 10.9-19.9) and (0.15, 0.10-0.27; 0.39, 0.30-0.93; 10.6, 8.9-13.8), respectively.The differences of PCT and CRP between the groups were statistically significant ($P<0.05$). It can be seen that the PCT and CRP concentrations are at a higher level than any non-infectious disease, regardless of the type of neonatal infection. Then the WBC did not perform well in this respect, which also shows that the WBC is not a good indicator of whether or not to identify infection.

There was no difference between the pneumonia group and the non-pneumonia neonatal infection group, $P>0.05$; there were significant differences between the other groups, both $P<0.05$. There was no difference between the pneumonia group and the non

infectious diseases group, $P>0.05$; there was no difference between the neonatal severe infection group and the non-pneumonia neonatal infection group, $P>0.05$; there were significant differences between the other groups, both $P<0.05$. There was no difference between the pneumonia group, the neonatal severe infection group and the non-pneumonia neonatal infection group, $P>0.05$; there were significant differences between the non-pneumonia neonatal infection group and one of the other groups, both $P<0.05$.

Our study showed that in the neonatal pneumonia group, 20 neonates were newly diagnosed with non-neonatal pneumonia and eventually diagnosed with neonatal pneumonia (group i), 14 neonates were newly diagnosed with neonatal pneumonia and eventually diagnosed with other neonatal infections. (Group ii). We compared the clinical data of these two groups of neonates. The median of PCT, CRP and WBC for group i and group ii were (0.343, 0.138-0.490; 0.340, 0.300-0.800; 14.1, 12.3-22.9) VS (0.155, 0.103-0.200; 0.350, 0.300-0.485; 9.0, 7.7-10.4). Compared with 20 neonates who were misdiagnosed as neonatal pneumonia, 14 neonates with missed neonatal pneumonia had higher PCT and WBC levels, $P<0.05$. However, CRP did not perform well in this regard. We analyzed all newly diagnosed neonatal pneumonia data in an attempt to reduce the rate of misdiagnosis of neonatal pneumonia. In all cases of neonatal pneumonia, we performed ROC curve analysis for PCT, CRP and WBC. WBC has a largest area under curve.

There was significant difference between group i and group ii, $P<0.001$. There was no difference between group i and group ii, $P>0.05$. There was significant difference between group i and group ii, $P<0.001$. In ROC curves, PCT had an area under the curve (AUC) of 0.64 (95% CI, 0.49-0.0.79); CRP had an AUC of 0.61 (95% CI, 0.49-0.74); WBC had an AUC of 0.78 (95% CI, 0.67-0.88). The optimal cutoff of PCT, CRP and WBC for the diagnosis of pneumonia were 0.10 ng/mL, 0.5 mg/L and 12.7 cells/L, respectively.

（**i**:First diagnosed as non-neonatal pneumonia and finally diagnosed as neonatal pneumonia，n=20; **ii**: First diagnosed as neonatal pneumonia and finally diagnosed as non-neonatal pneumonia.）

CRP-led decision-making led to a significant reduction in the duration of antibiotic treatment. The median of antibiotic treatment difference in effect between the PCT group and the untested PCT group was -0.9 d (4.0 d, 95% CI 3.7-4.8 in the neonatal pneumonia with PCT results group vs 4.9d, 95% CI 4.5-5.6 in The standard group; $P<0.001$). Pediatricians decided to discontinue antibiotics mainly for the following reasons: clinical manifestations, CRP results, combined clinical manifestations and CRP results, combined with clinical manifestations and culture results, combined with clinical manifestations and culture results, combined with clinical manifestations, culture outcomes, and CRP results and other reasons. Multiple regression analysis showed that the duration of antibiotic treatment depends on the risk category, gestational age (term or late preterm birth) and birth weight. Of all neonates, 4 of the 146 infected neonates were hospitalized for re-infection. At the same time, no deaths were found in our study.

Conclusions PCT helps identify neonate infections and grades infections, and assists pediatricians in deciding when to stop antibiotic treatment; PCT and WBC help improve the accuracy of neonatal pneumonia diagnosis.

P0-306

Circulating miRNA Expression Profile and Bioinformatics Analysis in Patients with Occult Hepatitis B Virus Infection

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Objective Emerging evidences suggest that miRNAs play important roles in the occurrence and development of hepatitis B virus (HBV) infectious disease. However, miRNAs in occult hepatitis B infection (OBI), a special stage of HBV infection, remain largely unknown. Herein, we conducted this study to identify differentially expressed miRNAs and then to explore the potential roles of these miRNAs in OBI.

Methods Plasma miRNA expression profiles of 3 OBI patients and 3 healthy controls were determined with high through-put miRNA sequencing technology. Altered expression of miRNAs was further confirmed with reverse transcription-quantitative polymerase chain reaction (qRT-PCR). Finally, bioinformatics analysis was performed to investigate the involved pathways and target genes for these differentially expressed miRNAs.

Results Totally, 32 differentially expressed miRNAs were identified between OBI and healthy controls by deep sequencing (Fold change ≥1.5, P <0.1 and CPM≥1), including 16 down-regulated miRNAs (hsa-miR-7706,-511-5p,-1299,-3913-5p,-99b-3p,-503-5p,-296-3p,-501-3p,-3158-3p,-3615,-15b-5p,-451a,-486-5p,-25-3p,-106b-3p,-92a-3p)and 16 up-regulated miRNAs (hsa-miR-187-3p, -219a-5p,-491-5p,-514a-3p,-221-5p,-132-5p,-203a-3p,-3168,-206,-218-5p,-1224-5p,-1-3p,-9-5p,-30a-5p,-30c-5p,let-7f-2-3p). Differential expression of hsa-miR-486-5p, -25-3p and -92a-3p and -1-3p was further validated by qRT-PCR analysis, which was consistent with miRNA sequencing analysis.Bioinformatics analyses indicated that the differentially expressed miRNAs were primarily involved in various biological processes related to gene expression and transcription, cell development and metabolism, protein modification and kinase activity regulation, as well as multiple signaling pathways such as PI3K/Akt signaling pathway.

Conclusions This study provided a global view of miRNA expression in plasma from OBI patients. These abnormally expressed miRNAs might play important roles in the development of OBI, which provided intriguing insights into the molecular mechanism of OBI.

PO-307

Latest status of bacterial species and anti-microbial susceptibility cultured from blood specimens in a Japanese University Hospital.

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Objective Septic shock is one of the most serious conditions for hospitalized patients. Treating sepsis, identification of bacterial species and information of antimicrobial susceptibility is very important, but blood culture requires several days to get the result. Because sepsis patients require administration of antimicrobial agents as quick as possible, it is quite common to start “empiric therapy” before identification of bacterial species. In order to resolve this problem, statistical analyses of local factors such as bacterial species and antimicrobial susceptibility identified inside the hospital are provided as “antibiograms”.

Our facility is a university hospital, located in the suburbs of Tokyo metropolitan area, having 23 departments, 689 beds with 1300 out patients per day. The aim of this study is to introduce our antibiograms to compare to those of other nations’ teaching hospitals.

Methods All the blood culture specimens tested in the year 2014 to 2018 were enrolled (N=18,182). The specimens were analyzed using Becton and Dickinson’s Bactec™ FM system. When the same bacterial species with same susceptibility were cultured from an identical patient within the same year, they were considered as one strain. We investigated positive ratio of bacterial detection, their species, and antimicrobial susceptibilities. Multi-drug resistant bacteria such as methicillin resistant *staphylococcus aureus* (MRSA), extended-spectrum beta-lactamase (ESBL) producing and carbapenem-resistant enterobacteriaceae (CRE) producing bacteria were also identified. This study was performed under the authorization of the local ethical committee.

Results In total, 1,311 patients showed positive with blood culture. Among them, 1,915 bacterial strains were identified. The most common strain was methicillin sensitive *staphylococcus aureus* (MSSA, N=161), which occupied 8.4% of total bacteria identified. Other species were; MRSA (N=83, 4.3%), *E.coli* (N=289, 15.1%), *Klebsiella spp.* (N=170, 8.9%), other enterobacteriaceae (N=113, 5.9%), and *Psudomonas spp.* (N=40, 2.0%).
Among 588 strains of enterobacteriaceae, ESBL was identified in 56 strains (9.5%), CRE was identified for 10 strains (1.7%). The ratio of ESBL among enterobacteriaceae had been increasing gradually. Ratio of susceptible strains of *K.pneumoniae* (N=32) was 93% with ampicillin, 100% with meropenem, levofloxacin and vancomycin. *E.coli* (N=289) showed susceptible against cefmetazole (99%) and levofloxacin (90%).

Conclusions Recently, antimicrobial stewardship is considered to be an important issue in order to prevent hazard by multi-drug resistant bacteria. In order to prevent outbreaks, our hospital has an infection control team and an antimicrobial stewardship team. Authorized infection control doctors, nurses, pharmacists and medical technologists play important part every day. Those information on bacterial strains

and antimicrobial susceptibility have been provided to medical staffs by using electrical medical record. Although ratio of ESBL has not decreased, there has been no outbreak of ESBL or CRE. We hope to exchange the data to foreign hospitals because number of patients from overseas is increasing these days.
Bacterial species and antimicrobial susceptibility were analyzed using blood culture obtained from our university hospital in recent five years. The most common strain was MSSA. ESBL and CRE showed 9.5% and 1.7% of enterobacteriaceae.

PO-308

Evaluation of New Haematology Parameters in End Stage Chronic Kidney Disease

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Objective The purpose of this study was to evaluate some parameters of advanced red blood cell that getting from automated hematology analyzer in diagnosed iron deficiency anemia in end-stage renal disease with hemodialysis.
Methods This cross-sectional study was recruited minimum 100 patients with chronic kidney disease (CKD) undergoing hemodialysis therapy in Cipto Mangunkusumo Hospital, Jakarta, Indonesia, through voluntary participation. This study was approved by the Ethics Committee of Faculty of Medicine Universitas Indonesia – Cipto Mangunkusumo Hospital (No.0087/UN2.F1/ETIK/2018). All patients were fully informed about the study and gave their consent. Demographic characteristics and clinical data were recorded using a questionnaire and patient's medical records. Automated Hematology Analyzer Sysmex XN-3000 (Sysmex, Kobe, Japan) was used to examine hematology parameters such as hemoglobin concentration, percentage erythrocyte microcytic (%Micro-R), percentage erythrocyte hypochromic (%Hypo-He), and reticulocyte hemoglobin (Ret-He). Biochemical analytes like serum ferritin and transferrin saturation levels were also examined to diagnose iron deficiency anemia. The iron deficiency was classified into absolute and functional iron deficiency. Absolute iron deficiency was confirmed when feritin serum < 200 ng/mL and transferrin saturation less than 20%. Functional iron deficiency was defined when feritin serum ≥ 200 ng/mL and transferrin saturation less than 20%. The data were analyzed using SPSS 20.0. Accuracy and precision test for each parameter were measured in mean, standard deviation (SD), *coefficient of variant* (CV), and deviation (d). Kolmogorov Smirnov (KS) was use for normality test. Measurements normally distributed ($P>0,05$) are reported as mean $\pm$ SD, and non-normally distributed ($P<0,05$) as median and minimal-maximal value. The difference between the mean of two variables was calculated by upaired T-Test if normal distributed and Mann-Whitney rank test if not. The statistical analysis to compare differences between groups with $P<0.05$ was considered as statistically significant. Analyses of the correlation of each parameter were performed using Pearson or Spearman correlation coefficients. $P<0.05$ was considered significant.

Results This study was recruited 127 CKD patients undergoing hemodialysis, with almost the same number between men and women, 18 until 79 years old of age. The most common cause of CKD was hypertension then followed by diabetes mellitus. The duration of hemodialysis was varied from 0.5 years to 30 years. Almost all patients were suffered anemia and got ESA therapy, but only 12 % of patients were got iron therapy. Fourteen patients who received erythropoietin and iron therapy within the last three months showed a median for %Hypo-he within range normal value but %Micro-R higher than normal. Inversely, the patients who received only iron therapy had a %Hypo-He value greater than normal. The value of %Hypo-He and% Micro-R were obtained higher in absolute iron deficiency compared to functional iron deficiency and without iron deficiency, although it was no difference statistically. Conversely the Ret-He value was obtained lower in absolute iron deficiency compared to functional iron deficiency and without iron deficiency. Functional iron deficiency and without iron deficiency showed almost the same value in% Mikro-R,% Hypo-He, and Ret-He. There was an inversely correlation and significant between %Micro-R with transferrin saturation ($r = -0.248$, $P=0.005$) and between %Hypo-He with transferrin saturation ($r = -0.250$, $P=0.005$). Ret-He parameter with transferrin saturation also showed significant and moderate correlation ($r = 0.343$, $P < 0.001$). Beside transferrin saturation, RDW was measure as the marker of iron depletion where %Hypo-he has a moderately significant positive correlation with RDW ($r=0.672$, $P<0.001$).

Conclusions Both% Micro-R,% Hypo-He, and Ret-He could not distinguish between functional iron-deficiency anemia and no iron deficiency. However,% Micro-R and% Hypo-He can be used to detect absolute iron deficiency anemia.

PO-309

PLASMA FREE FATTY ACID AND RANDOM URINARY PROTEIN RATIO AS A PREDICTOR AND PROGNOSTIC INDEX FOR PRE-ECLAMPSIA IN IFE,NIGERIA.

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Objective Background Mother and child health is one of the cardinal goal in MDGs. Pregnancy induce hypertension has been one of the factor limiting the goal in developing countries. Gynaecologists are still oscillating on a specific marker for predicting occurrence or its pathogenesis.

Methods Twenty hypertensive pregnant women and twenty normotensive pregnant women attending anti-natal clinic and admitted to labour and post-natal ward of teaching hospital were involved in this study. Plasma free fatty acid (FFA) and random urinary protein(RUP) levels were analysed. Their blood pressure before and after delivery were measured at the clinic and ward.

Results The mean FFA in hypertensive pregnant women and normal in various stages are ;second trimester 2.7 ± 0.2 and 2.3 ± 0.3mmol/l, $P<0.02$;third trimester 2.7 ± 0.4

and 2.4±0.5mmol/l, P<0.05;24 hours before delivery 3.0± 0.4 and 2.5± 0.4mmol/l, P<0.01;72 hours after delivery 2.5±0.5 and 1.3±0.4mmol/l, P<0.001.RUP excretion in hypertensive pregnant women increases from 1.2±0.6g/l at second trimester to 4.5g/l ±1.1 twenty four hours before delivery and return to 0.25±0.3g/l three days after delivery. Normotensive pregnant women have average of 0.23±0.3g/L 24 hours before delivery and 0.20±0.2g/l three days after delivery. FFA correlate positively with diastolic blood pressure(DBP) r<0.027, mean arterial pressure(MAP) r<0. 046.RUP positively correlate with systolic (SBP)r<0.026 and DBP r <0.009, MAP r<0.017.However,FFA ratio with RUP correlate positively with all vascular status index considered; SBP r<0.01,DBP r<0.003, (MAP) r<0.005 and urinary protein r<0.002.

Conclusions Increase in FFA and RUP ratio may be a good early predictor and diagnostic index in resource limited and standard laboratory where the patients lack fund. Increase in FFA may likely involved in the pathogenesis of pregnancy induce hypertension due to its positive correlation with mean arterial pressure.

PO-310

A study on the effect of hepatitis C virus infection on maintenance hemodialysis patients

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Objective To investigate the effect of hepatitis C virus (HCV) infection on liver and kidney function, blood cell analysis and immune system in maintenance hemodialysis (MHD) patients.

Methods It is a matched case-control study. Twenty-eight patients on MHD with HCV infection (Hemo+HCV Group) were matched 1:1 with patients on MHD without HCV (Hemo Group) by gender, age, dialysis duration, kidney transplantation, immunosuppressant use, complications and primary pathogenesis. In addition, 21 Healthy controls (Control Group) were enrolled at the Medical Checkup Centre with age and gender matched at the group level. The liver and kidney function, blood cell analysis and immune index (CD3+, CD4+, CD8+,treg, IL-10) were compared among the three groups.

Results ALT and AST increased significantly in Hemo+HCV group compared with Hemo group (ALT: 26.64±18.64 vs. 10.14±7.14, P<0.05, AST: 20.00±8.99 vs. 11.75±5.45, P<0.05), but none of ALT and AST reached the high reference limits. No significant differences were found in Hb(100.96±16.41 vs. 108.46±19.27), PLT(138.93±60.73 vs. 147.11±53.35), NEU(3.77±2.09 vs. 4.15±1.46) and LY(0.95±0.35 vs. 1.15±1.24) between Hemo+HCV group and Hemo group, while all of the indexes appeared a decreasing trend among the two groups. The proportion of CD3+ cells (76.90±13.68, 74.03±12.49, vs. 63.43±8.42, P_{1vs3}<0.05, P_{2vs3}<0.05) and CD4+T cells (46.55±10.42, 42.59±*10.70, vs. 34.51*±9.11, P_{1vs3}<0.05, P_{2vs3}<0.05) were higher in Hemo+HCV group and Hemo group compared with the control group, while no differences were found between the Hemo+HCV group and Hemo group, although Hemo+HCV group appeared to have the higher CD3+ and CD4+ T cells.

Treg of Hemo+HCV group were significantly higher than that of the Control group (2.96±2.50 vs. 1.73±1.24, P<0.05). IL-10 of Hemo+HCV group were significantly higher than that of Hemo and control group (77.74±65.52 vs. 34.19±15.15, 30.64±13.03, P_{1vs2}<0.05, P_{1vs3}<0.05).

Conclusions

①Serum ALT and AST of patients with MHD might not be a good index to judge liver function. The bone marrow hematopoiesis could be inhibited to a certain extent in patients with HCV infected under MHD . ② CD4+T cell might play an important role on immune response of MHD patients, and the elevation of Treg and IL-10 level in MHD with HCV infection patients might lead to abnormal regulation of immune response, which is not conducive to the removal of HCV virus.

PO-311

Absolute quantification of cholesteryl esters using LC-MS/MS uncovers novel diagnostic potential of urinary sediment

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Objective Urine has been utilized as a source of biomarkers in renal disease. However, urinary lipids have not attracted much attention so far. Here we studied urinary cholesteryl ester (CE) and its relevance in renal disease.

Methods Quantitative analysis of CE molecular species in serum, urinary supernatant, and urinary sediment from patients with renal disease and non-renal disease was carried out using liquid chromatography-tandem mass spectrometry (LC-MS/MS) and deuterated CEs as internal standards.

Results Validation study showed good precision and accuracy of LC-MS/MS. Many CE species were detected in the urinary sediment and supernatant in the renal disease group, whereas only a few CE species were detected in the other group. In the renal disease group, the sum of the concentrations of all CE species showed a significant correlation between the sediment and the supernatant from urinary samples ($r = 0.876$, $p < 0.001$); however, the composition of CEs was significantly different between them. Further, the composition of CEs of the supernatant was similar to that of the serum.

Conclusions Our LC-MS/MS analysis uncovered a distinct CE profile in urinary sediment from patients with renal disease, suggesting a possible contribution of CEs in urothelial cells to the development of renal disease.

PO-312

The Relationship Between Insulin Secretion and Thyroid Function Tests

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Objective Insulin resistance is defined as a glucose homeostasis disorder involving reduced insulin sensitivity of muscle, adipose tissue, liver, and other body tissues, despite the normal or increased insulin concentration. Insulin resistance may be asymptomatic or may accompany conditions such as glucose intolerance, type 2 diabetes, and metabolic syndrome. The prevalence of thyroid disease in diabetic patients is significantly higher than in the general population. This indicates a possible interaction between thyroid function and insulin sensitivity. Therefore, we aimed to investigate the relationship between insulin resistance, pancreatic β cell function, and thyroid function tests.

Methods In this study; insulin, glucose, TSH, free T3 and free T4 levels in the same samples of 1340 adult patients without thyroid disease which were admitted to the laboratory between 08:00-12:00 hours in 2018 and 2019 were examined retrospectively. The ratio of fT3 to fT4, HOMA-IR and HOMA-β values were calculated. The correlation between HOMA-IR, HOMA-β values , and thyroid function tests and differences between hormone levels of patients with (HOMA-IR> 2.5 - Group I) and without (HOMA-IR < 2.5 - Group II) insulin resistance according to the HOMA-IR values were examined. All data were analyzed by SPSS 21.

Results There was a positive correlation between HOMA-IR and TSH, negative with fT4. Also, a weak positive correlation between HOMA-β and fT3, weak negative correlation with fT4 were observed (r = 0.185, r = -0.117, respectively). In Group I, fT3 levels were found to be significantly higher and fT4 levels were lower (p = 0.030, p = 0.012, respectively), although TSH levels were higher in this group no statistically significant difference was found between the groups. The fT3 / fT4 ratio was found to be significantly higher in Group I (p <0.001) and correlated weakly positively with HOMA-IR and HOMA-β values (r = 0.114, r = 0.228, respectively).

Conclusions In our study, the relationship between insulin levels and thyroid function tests were shown. While fT3 values are increased in both insulin resistance and pancreatic β cell dysfunction, the decrease in fT4 levels may indicate that peripheral fT3 synthesis from fT4 changed. In addition, the severity of pathology in both cases correlates with thyroid dysfunction. As a result, new clinical studies are needed to determine the relationship between insulin resistance, pancreatic β cell function, and thyroid function tests.

PO-313

Novel Rapid Identification and Quantification Method of Bacteria in a Septic Blood Sample Can Produce an Effective Biomarker for Monitoring Patient Care

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Objective Severe systemic infections, such as sepsis, are the primary cause of morbidity and mortality in hospitalized patients. Current biomarkers in sepsis do not always reflect the severity of sepsis at a particular point in time. Acquiring the earliest possible identification of pathogenic microorganisms is critical for selecting the appropriate antimicrobial therapy and obtaining a favorable outcome in infected patients. Here we developed a novel rapid identification and quantification method of unknown pathogenic bacteria in a clinical sample, and estimated the usability of blood bacterial concentration as a novel biomarker in sepsis.

Methods We have already reported the development of a rapid diagnostic method, called the Tm mapping method, which requires neither microbial cultures nor DNA sequencing to identify the causative pathogenic bacteria. This method is based on real-time PCR with seven primer sets, and the algorithm generates a unique “finger-print” of the bacterial species from the data of the melting temperature (Tm) of each PCR amplicon. This “finger-print” is compared with those of more than 150 bacterial species in the database. The software and database is accessible by Internet, and the output is the list of the bacterial species in the order of the matching score, called Difference Value. As a result, we can get an identification result of pathogenic bacteria around four hours after whole blood collection. In this research, we tried to improve the Tm mapping method to not only identify but also quantify bacteria in a sample.

Results We identified and quantified pathogenic bacteria in 34 septic blood samples, and the blood bacterial concentrations were correlated with the severity of sepsis (qSOFA, septic shock, Pitt Bacteremia Score). We subsequently examined the time-dependent changes (pretreatment, and 24 to 72 hours after antibiotic treatments) of blood bacterial concentration, and found that the time-dependent changes of blood bacterial concentration were dramatically decreased compared with the change of Body temperature (BT), White blood cells (WBC), C-reactive protein (CRP), Procalcitonin (PCT), Presepsin (P-SEP) and Interleukin-6 (IL-6).

Conclusions We developed a novel rapid identification and quantification method of unknown pathogenic bacteria in a whole blood sample, and found that the blood bacterial concentration would be useful as a novel biomarker not only to estimate the severity of sepsis but to monitor the therapeutic effect.

PO-314

Progress of new molecular biology techniques combined with metabolomics in vaginal microecology detection

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Objective Vaginal microecology plays a significant role in the balance of vaginal microenvironment, it has the potential to prevent female reproductive tract infections. The functions and applications of vaginal flora are complicated. Traditional evaluation of microecological did not fully reflect the implications of microecology. Nowadays, molecular biology and metabolomics have become two main technologies for microbial research. This article reviewed the published literature pertaining to the new molecular biology techniques combined with metabolomics in vaginal microecology detection.

Methods We reviewed the corresponding literature of China Journals Net during 2010-2018,
to understand the new discoveries in the application of molecular biology techniques in microbiology combined with metabolomics for microecological evaluation. Sequencing is one of the most used molecular biology techniques in microecology, used to screen out the differences in the structure and abundance of the vaginal flora, it can even predict the functional differences. Nevertheless, the metabolomics is a direct reflection of the interaction between the flora and the host. The two methods complement each other and are indispensable. In this paper we not only compared different sequencing technologies in microecological evaluation to summarize the advantages and limitations of different sequencing technologies but also explored the value of microbiology combined with metabolomics in the precise medicine of female genital tract infections.

Results Routine evaluation methods for vaginal microecology include biochemical evaluation, microbiological evaluation, immunological evaluation, and molecular biological evaluation. These tests above are designed to detect bacterium like lactobacilli and local biochemical immune indicators. With the development of sequencing technology, we can have a deeper understanding of the composition of the vaginal microecology. To detect vaginal flora, extracting, amplifying and sequencing of bacterial 16s rRNA and then conducting cluster analysis, alpha diversity analysis, and beta diversity analysis of sequencing results are one of the most commonly used methods. The first generation of sequencing technology with low throughput is time-consuming, the emergence of the second-generation sequencing technology makes up for the shortcomings. However, the reads of the second generation of sequencing technology are short and the splicing of the genome is difficult which the third generation of sequencing technology can compensate. The third-generation sequencing technology is not yet widely available. It is a kind of single molecule sequencing with high error rate, but its mistakes are random. In addition, metagenomic sequencing, based on the first-generation shotgun sequencing, detects the entire DNA fragment to obtain a complete flora genome for more accurate classification. However, 16s rRNA sequencing cannot distinguish the transcriptional activity of the bacterial genome, nor can it tell the live and dead bacteria apart. Metabolomics which complements the information

obtained by sequencing has the ability to indicate the interactions between the host, the environment, and the vaginal microbiota. The purpose of metabolomics is to extract relative biological metabolic markers by detecting the overall and dynamic changes in metabolite levels. On this basis, we would find the relevant metabolic pathways affected and establish the mechanism of metabolic regulation. Common research methods in metabolomics include liquid chromatography-mass spectrometry, gas-mass spectrometry, and nuclear magnetic resonance. With the development of sequencing technology, the diagnostic accuracy of vaginal flora is getting higher and higher. The combination of microbiology and metabolomics can not only obtain information about vaginal bacterial composition, gene abundance, and function but also understand the changes of metabolites in organisms.

Conclusions In recent years, with the continuous development of microbiology, more and more researchers have begun to combine microbiology and metabolomics to explain scientific issues, thereby contributing to a better understanding of the process of disease and metabolic pathways. Many exciting results was obtained based on the advanced technologies, helping to discover the biomarkers of diseases for further application in clinical diagnosis. However, the application of microbiology and metabolomics in the analysis of female vaginal microecology is still in its infancy. The development is helpful for the accurate diagnosis and treatment of female genital tract infections and the discovery of marker metabolites for early warning of female genital tract malignant tumors.

PO-315

Anti-Domain 1 of beta2-glycoprotein I Aids Risk Stratification in Lupus Anticoagulant Positive Patients

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Objective Lupus anticoagulant (LA) is considered as a risk factor for thromboembolism (TE) and adverse pregnancy outcomes (APOs). However, quite a few patients diagnosed with LA positivity do not suffer these adverse events. Further testing of anticardiolipin (aCL), anti-beta2-glycoprotein I (anti-β2GPI) or anti-domain 1 of β2GPI (anti-D1) may help to assess the risk of occurrence of TE and APOs. Therefore we aimed to study how to stratify LA positive patients.

Methods In our study, a total of 167 LA positive patients were consecutively enrolled from January 2015 to December 2016. Meanwhile, serum aCL and anti-β2GPI (IgG, IgM and IgA), and anti-D1 IgG were simutaneously measured by chemiluminescence immunoassay. Among them, 114 patients (68.3%) were followed up for an average of 35.6 months for the occurrence of TE or APOs.

Results The outcomes showed 21 patients experienced TE, 89 patients with APOs (5 patients had both TE and APOs) and 62 patients were LA carriers who did not suffer these adverse events. By analyzing antiphospholipid antibodies (aPL) panel, we found that anti-D1 had a good consistency with triple positivity (LA+, aCL+, anti-β2GPI+) (kappa=0.742) in LA positive patients. Compared with LA carriers, the titers of anti-

D1 were significantly high in patients with TE and APOs ($p<0.001$ and $p<0.001$, respectively). And elevated anti-D1 was related to a stronger risk for TE [odds ratio (OR) =29.87, 95% confidence interval (CI), 8.05-110.74] and APOs (OR=8.73, 95%CI, 3.41-22.31) compared with aCL, anti-β2GP1 or triple positivity. Area under curve (AUC) showed that diagnostic power of anti-D1 for TE and APOs were 0.856 (95%CI, 0.743-0.970) and 0.682 (95%CI, 0.599-0.765), respectively. During follow-up, none of the patients had TE events while 27 patients were pregnancy. Among them, there were 10 patients suffering APOs. Survival analysis found high anti-D1 titers had a higher cumulative incidence of APOs compared with the low anti-D1 value group (p=0.035) [hazard ratio (HR) =4.89, 95%CI, 1.41-16.98].

Conclusions Anti-D1, based on a good consistency with triple positivity in LA positive patients, has a stronger association with TE or APOs and in some degree could predict the pregnancy outcomes. Therefore anti-D1 may aid risk stratification in LA positive patients.

PO-316

Analysis of the changes of glycocholic acid(CG) levels in HBV-DNA positive patients

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Objective To explore the changes of serum CG, ALT, and AST levels in HBV-DNA positive patients, and to compare the advantages of CG over routine liver function tests.

Methods 289 HBsAg positive samples were collected in Lianyungang TCM Hospital Affiliated to Nanjing University of Chinese Medicine from May 1, 2018 to September 30, 2018. According to the results of PCR, they were divided into 142 HBV-DNA positive (HBV-DNA content > 1.0E+2 IU/ML) groups and 147 HBV-DNA negative (HBV-DNA content < 1.0E+2 IU/ML) groups. 150 healthy people were selected as the control groups.The concentration of serum CG was determined by homogeneous enzyme immunoassay , and the concentration of ALT and AST were measured by enzymic method.

Results The levels of CG, ALT and AST in HBV-DNA positive groups were significantly higher than those in the control groups ($P < 0.05$). The level of CG in HBV-DNA negative groups was higher than that in the control group ($P < 0.05$), and the levels of ALT and AST were not statistically significant ($P > 0.05$).

Conclusions China is a high incidence area of HBV infection. HBV-DNA is the most direct indicator of HBV replication in vivo. Hepatocytes of HBV-DNA positive patients have different degrees of inflammation and injury in the process of viral replication. ALT and AST can better reflect the pathological state of hepatocytes. However, most of them are chronic asymptomatic. Although HBV-DNA is negative in these infections, it may be due to the lower viral content than the detection limit or the replication of viruses is in hepatocytes. In fact, the ultrastructure of hepatocytes has been changed. This study showed that there was no significant difference in ALT and AST levels between the experimental groups and the control groups. However, the level of CG was higher than those of the control groups, suggesting that CG can sensitively reflect

the changes of hepatocyte damage in the early stage. Therefore, for HBV infected patients, the detection of the concentration of CG while measuring the routine liver function tests can reflect the damage degrees of hepatocytes more early and sensitively, and is of great importance.

PO-317

Database-related Identification Variation of Elizabethkingia by the Matrix-Assisted Laser Desorption/ Ionization Time of Flight Mass Spectrometry

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Objective Automated microbial identification systems (AMIS) can improve identification of microbial pathogens isolated from clinical specimens. The AMIS which provides analytical efficacy in terms of analytical turnaround time and accuracy relies primarily on precise validation of AMIS database of microbes. Such database is updated after a new version has been approved for clinical use. Although the changes of such updated database are mentioned by manufacturers, the influence on previous isolates is less addressed or evaluated by laboratories. We herein presented identification variation of *Elizabethkingia* using the matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) based on different versions of database.

Methods A total of 209 isolates of *E. meningoseptica* acquired from blood culture and other clinical specimens was identified by a MALDI-TOF MS (VITEK MS, bioMérieux) using a database (V3.0) from March 2017 to March 2019. Among them, two and 16 isolates of them had been respectively identified as *E. anopheles* respectively by the whole genome sequencing (WGS) and the extended 16S ribosomal RNA (rRNA) gene sequencing (1.5 kb) in previous investigations. All isolates were kept frozen appropriately in a microbial bank and were inoculated onto blood agar plates before investigation. After inoculation, optimal amounts of pure isolates were obtained after incubation and prepared for identification by the MALDI-TOF MS (VITEK MS) installed with an updated version of database (V3.2). The between-version agreement of microbial identification by the VITEK MS for 209 isolates and between-method agreement for 18 isolates were evaluated.

Results After evaluation by the MALDI-TOF MS (V3.2), 202 (96.7%), 5 (2.4%) and 2 (0.9%) isolates were revealed as *E. anopheles*, *E. miricola* and *E. meningoseptica*, respectively. The between-version agreement of microbial identification by the MALDI-TOF was only 1.1%. For 18 isolates of *E. anopheles* identified previously by molecular testing, the MALDI-TOF MS (V3.2) displayed 100% agreement with either WGS or 16S rRNA gene sequencing.

Conclusions *E. meningoseptica* has been recognized as an important nosocomial pathogen. Our investigation revealed that 99.1% of previous isolates of *E. meningoseptica* were identified as either *E. anopheles* or *E. miricola* by the MALDI-TOF using an updated database which added the latter two species in addition to *E. meningoseptica*.

Laboratories were recommended to interpret cautiously and verify previous identification as needed when a new version of AMIS database containing newly added species.

PO-318

PADI4 promotes the polarization of M1 and hypoxia is associated with M2 macrophage activation in rheumatoid arthritis

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Objective The joint cavity in patients suffered from rheumatoid arthritis (RA) has characteristic hypoxic environment. The present study aimed to investigate the effect of the role of PADI4 and hypoxia in the polarization of macrophages.
Methods The distribution of M1- and M2-type macrophage in synovial tissues from RA and osteoarthritis (OA) patients was examined by immunohistochemical and double immunofluorescence analysis. THP-1 were induced into macrophages by PMA, cells were cultured under normoxic (21% oxygen) or hypoxic (3% oxygen) concentrations. M1 and M2 specific surface molecular markers CCR7 and CD206 were detected by Immunofluorescence and quantitative real-time PCR, Transfection of AdPADI4 and PADI4 inhibitor was conducted to manipulate the expression of PADI4.Protein expression was detected by Western blot.
Results M1 and M2 were both more abundant in RA synovial tissues than that of OA, the mean M1/M2 ratio was 1.633 ± 0.1443. Immunofluorescence assay showed that hypoxia led to the increase of CCR7(M1) and CD206(M2) positive cells. Quantitative RT-PCR showed gene expression of M2 markers in macrophages were significantly increased under 3% O2 condition. PADI4 overexpression induced macrophages polarize to M1, and M1 could transferred to M2 after using PADI4 inhibitor under normoxia.
Conclusions PADI4 may take part in the M1 macrophages activation and can be a target to improve the pro-inflammatory microenvironment, while hypoxia may regulate the M2 macrophages polarization through other pathway and the function of M2 in RA need to be reassessed.

PO-319

The diagnostic assessment of IP-10 compared to IFN- γ in differentiate the LTBI and ATBI by meta-analysis

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Objective We conducted a systematic review and meta-analysis to evaluate the diagnostic potential of interferon γ-induced protein 10 kDa (IP-10) as bimarkers for the diagnosis of latent tuberculosis.
Methods Related studies were identified through searches of PubMed, Embase, Web of Science up to August.31, 2018. We used standard methods recommended for meta-analyses of diagnostic test evaluations. The analysis was based on a summary receiver operating characteristic (SROC) curve. Meta-regression analysis was used to assess the effects of some confounding factors on the results of the meta-analysis. The potential presence of publication bias was tested using the Deeks' funnel plots.
Results The pooled estimates of IP-10 for LTBI diagnosis were as follows: sensitivity, 0.77 [95 % confidence interval (CI), 0.72 to 0.81]; specificity, 0.73 (95 % CI, 0.68 to 0.78); We found that the SROC curve is positioned near the upper left corner of the curve and the area under the curve (AUC) was 0.86.The overall sensitivity and specificity estimates of IFN- γ for LTBI diagnosis were 0.67(95% CI,0.61-0.73) and 0.75(95% CI,0.68-0.80).The AUC of IFN- γ was 0.8031.
Conclusions The IP-10 was a potential biomarker to distinguish the LTBI and ATBI.

PO-320

Molecular Prognostic value of circulating Epstein-Barr viral DNA in nasopharyngeal carcinoma: a meta-analysis of 27,235 cases in endemic area

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Objective This meta-analysis evaluated the value of Epstein-Barr viral (EBV) DNA as a predict factor in nasopharyngeal carcinoma (NPC) patients with different cut-off values and different time points.
Methods A systematic search was performed in PubMed, the Cochrane Library and Embase online databases. Eligible studies with complete baseline information and extractable hazard ratios (HRs), 95% confidence intervals (CIs) and other details were included. All pooled statistics were treated in RevMan 5.3 with inverse variance methods and results were showed in tables, forest plots or funnel plots directly. Between-study heterogeneities were fully analyzed by subgroup analyses, meta-regression and sensitivity analyses.
Results Forty studies involving 27,235 subjects were included eventually. Higher EBV DNA levels

in pre-treatment, mid-treatment and post-treatment groups were all associated with at least 2.5-fold higher risk of death than that of low levels (HRs and 95% CIs were 2.47 [2.10, 2.89], 2.67 [1.50, 4.75] and 5.25 [3.58, 7.71] respectively, p <0.05), so as the risk of other progressions, regardless of cut-off values and time points. The heterogeneities among studies could be explained reasonably.

Conclusions Higher pre-treatment, mid-treatment and post-treatment EBV DNA levels were all significantly correlated with poor outcomes of NPC after treatments. There still needed to be further investigations in EBV DNA levels, combined with TNM stages, as guidelines for clinical diagnosis and treatment.

PO-321

Study on clinical application of VISION-C automatic ESR analyzer

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Objective In this study, we evaluated the main performance of VISION-C Automatic ESR analyzer instrument, discussed its clinical application value for clinical laboratory selection.

Methods 1 Repeatability evaluation: 12 samples of EDTA anticoagulated whole blood samples, including ESR normal, median, high-value specimens of 4 cases, respectively, with VISION-C automatic ESR analyzer test instrument repeated detection 21 times, remove the first The results were analyzed and their coefficient of variation (CV) was analyzed.

2 Batch precision evaluation: the use of the United States Bole Corporation to provide the normal value and high value of the two levels of quality control, continuous testing for 20 days, the initial assessment of VISION-C automatic ESR analyzer inter-assay precision.

3 Stability evaluation: random selection of 32 cases of EDTA anticoagulant, the use of VISION-C automatic ESR analyzer test instrument to detect the detection period: the specimen collection, room temperature within 30 minutes, room temperature for 2 hours, 4 hours, 8 hours, 12 hours, 24 hours, and 4-8 ℃for 24 hours. The results obtained were compared with the results of 30 minutes to evaluate the stability of the VISION-C automatic blood test.

4 Sensitivity and specificity evaluation: 1038 patients were randomly selected samples, with VISION-C automatic ESR analyzer to measure its ESR value to the manufacturer to provide the reference range (male 0 ~ 15mm / h, women 0 ~ 20mm / h) to determine Negative number and Positive number, the Westergren method as a reference method to calculate the sensitivity and specificity of VISION-C automatic ESR analyzer.

5 Correlation analysis: randomly selected from June 2016 to December 2016 in China-Japan Union Hospital of Jilin University outpatient and hospitalized patients in 1038 cases, the collection of 1038 cases of blood samples with Westergren method and VISION-C automatic ESR analyzer test Perform laboratory ESR value detection. The data were analyzed by the Wilcoxon sign test, and the linear regression was used to analyze the correlation analysis.

Results 1 Repeatability evaluation:The CV value of the VISION-C automatic ESR analyzer test was from 2.61% to7.51%.
2 Batch precision evaluation: the CV value of the normal value and high value of quality control, were 11.63% and 6.20%, respectively.
3 The stability of the samples of EDTA anticoagulant :The results showed that there was no significant difference in ESR values at room temperature for 2 hours, 4 hours, 6 hours, 12 hours and 30 minutes (P> 0.05), and 24 hours at room temperature and 24 hours after 4~8℃. (P <0.05).
4 The sensitivity and specificity of ESR: in 1038 patients showed that the sensitivity and specificity of VISION-C automatic ESR analyzer test were 84.8% and the specificity was 90.20%.
5. Correlation analysis: 1038 patients, VISION and Westergren method to measure ESR correlation analysis showed that the two methods showed a significant linear positive correlation (r = 0.886, P <0.05).
Conclusions 1. In this study, VISION-C automatic ESR analyzer measurement ESR value has good repeatability, stability, sensitivity and specificity.
2. The VISION method has a good correlation with the ESR results of the Westegren method.
3. VISION-C automatic ESR analyzer test to shorten the time of ESR, blood samples can be shared with a specimen of whole blood cell count to reduce blood collection, and in a closed environment to detect, to avoid the potential biological hazards.

PO-322

Establishment and validation of sex- and age-specific serum electrolyte reference intervals in healthy Han Children

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Objective For lack of feasible interval values from population differences and potential analytical discrepancies caused by diversed condition of clinical laboratory, it is essential to ascertain potassium (K), sodium (Na), chlorine (Cl), calcium (Ca) and phosphorus (P) ions reference intervals within Chinese children to fill the gap.
Methods Healthy children (n=1391, 2~14 years old) were recruited from communities and schools in Changchun to establish sex- and age-specific serum electrolyte reference intervals of Han children in Changchun, China. Levels of K, Na, Cl, Ca and P ions were measured in serum samples using Hitachi 7600-210 automatic biochemical analyzer. Reference intervals were established according to the Clinical and Laboratory Standards Institute C28-A3c guidelines. Data from five representative hospitals located across Changchun was used to validated the pediatric serum electrolyte reference intervals.
Results There were sex-specific differences in serum Na, Cl, Ca, and P reference intervals in children aged 13~14 years. Serum Na, Cl, and Ca reference intervals

showed a stable trend within the early age groups but began to fluctuate in later age groups. Each serum electrolyte had ⩽ 3 age-specific reference intervals. Results of five hospitals revealed the intervals were valid, suggesting they were applicable across Changchun.

Conclusions This study established and validated serum electrolyte reference intervals for children aged 2~14 years that can be applied across Changchun, which was quite specific against the other reference values applied now world widely or domestically.

PO-323

Comparison of Chromium and Iron Distribution in Serum and Urine among Healthy people, Pre-diabetes and Diabetes Patients

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Objective Effect of chromium (Cr) and iron (Fe) on prevalence of diabetes has received great attention.

Methods This study investigated serum and urinary Cr and Fe levels among patients with impaired fasting glucose (IFG), impaired glucose tolerance (IGT), type 1 diabetes (T1D), type 2 diabetes (T2D) in Northeast Chinese population. From January 2010 to October 2011, patients with IFG (n=12), IGT (n=15), T1D (n=25), T2D(n=137) and healthy controls (n=50) were enrolled in the First Hospital of Jilin University. Trace elements were detected using inductively coupled plasma spectrometer.

Results Serum Cr levels decreased in T2D without complications, diabetic retinopathy (DR), diabetic peripheral neuropathy (DPN), and diabetic nephropathy (DN) (P<0.05). Urinary Cr level in T1D were the highest of all, which significantly exceeded those of T2D groups with and without complications. No significant differences of serum Fe levels were found among all groups. Urinary Fe level of T1D was significantly increased (P<0.05). The correlation between serum Cr and serum Fe in T2D was obviously positive (P<0.05). One month of simvastatin therapy exerted no effects on serum or urinary Cr and Fe levels.

Conclusions These results suggest the potential role of Cr and Fe in diabetes should be received attention.

PO-324

Graphene Quantum Dots Regulates the Radiosensitivity in Colorectal Cancer Cells

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Objective Colorectal cancer (CRC) is a common gastrointestinal malignant tumor with high rate of postoperative recurrence. And the risk of metastasis of CRC is still one of the main reasons for the failure of CRC treatments. Radiation therapy is a commonly methods of CRC treatments, which occupies an irreplaceable important position in surgery and chemotherapy and other treatments. In this study, we detected the enhancement of radiosensitization of Graphene Quantum Dots(GQDs) which have great biocompatibility and rich oxygen groups on CRC cells. Meanwhile, we investigated the mechanism of the increased radiosensitivity of GQDs. Our study would provide reliable experimental basis for GQDs as a radiotherapy sensitization agent in potential clinical applications.

Methods The GQDs were prepared with graphene oxide(GO) and the safe concentration of GQDs were determined by CCK8 assay. In addition, laser confocal microscope and transmission electron microscopy are carried out to measure the sub-cellular localization of GQDs. CCK8 assay and colony formation assay were performed to compare the cell viability and clonal formation post-irradiation between the control and treated group. The cell apoptosis rate and the cell cycle arrest of each treatment group was detected by Flow cytometry. The cell damage was observed by transmission electron microscopy. The production of ROS and mitochondrial ROS in each treatment group was measured by DCFH-DA and MITOSOX Red Indicator, respectively. The expression of γH2AX which reflect the degree of DNA double-strand breaks was detected by western blot after different treatments.

Results CCK8 assay showed that the 50μg/mL concentration of GQDs were safe to SW620 and HCT116 cells. Transmission electron microscopy and laser confocal microscope revealed the distribution of GQDs in the cells. In addition, our study indicated that GQDs could decrease the cell viability, increase the degree of cell damage and cell apoptosis of SW620 and HCT116 cells after irradiation. after co-exposure of ionizing radiation and GQDs. Meanwhile, GQDs could synergize with irradiation to enhance intracellular ROS generation, including the ROS levels in mitochondria increase the degree of DNA double-strand breaks and G2/M phase cell cycle arrest occurred in SW620 and HCT116 cells.

Conclusions Our study demonstrated that GQDs have good radiosensitizing effects at cell levels in vitro, which can improve the killing effects of irradiation on tumor cells, and ultimately achieve the purpose of treatment of cancer. Our study showed that GQDs present great potentials in tumor therapy as a new type of radiosensitizing agent.

PO-325

The explore of Gene expression profile through RNA Sequencing in Ajuba overexpressed T47D cells

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Objective To explore the effects of Ajuba on the transcriptome of breast cancer cell line T47D.
Methods Establish the T47D cell lines for stable expression of Ajuba (T47D-Ajuba). RNA-seq analysis was performed by taking samples of total RNA extracted from T47D-vector and T47D-Ajuba and millions of short reads were created. After read mapping, transcriptome reconstruction, normalization and expression quantification, a list of differentially expressed genes (DE) were identified. Then gene ontology comparison (GO) and KEGG pathway enrichment analysis were carried as well as RT-qPCR validation of several DEs.
Results A total of 568 DEs were identified, including 239 significant up-regulated genes and 329 down-regulated genes. In GO analysis, 3,23 and 8 up-regulated genes ,respectively, were annotated to Molecular function (MF), biological process (BP) and Cellular component (CC). While 21,35 and 9 down-regulated genes ,respectively, were annotated to MF, BP and CC. In KEGG analysis, six relevant pathways were significantly enriched, two within up-regulated genes and four within down-regulated genes.
Conclusions Overexpression of Ajuba has remarkable effects on a series of biological function and multiple signal pathways, it might play a key role in the tumorigenesis and development of breast cancer.

PO-326

Analysis of related factors and pathogen characteristics in patients with maintenance hemodialysis complicated with bloodstream infection

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Objective To analysis of related factors and pathogen characteristics of bloodstream infection in maintenance hemodialysis patients in our hospital.
Methods Retrospective analysis of 58 patients with maintenance hemodialysis complicated with bloodstream infection in the Xinjiang Production and Construction Corps Hospital from January 2016 to October 2018 (bloodstream infection group); Collection of data from 40 patients who underwent maintenance hemodialysis in our hospital but did not have bloodstream infection (uninfected group). The differences and correlations between the two groups were compared, and the distribution of pathogens and drug susceptibility results of bloodstream infection in the bloodstream infection group were statistically analyzed.
Results There were no significant differences in age, sex ratio,SCr,BUN and HB levels ($P>0.05$). WBC,CRP and SF in bloodstream infection group were significantly higher than those in uninfected group($P<0.05$).The level of ALB in blood stream infection group was significantly lower than that in uninfection group($P<0.05$); The bloodstream infection group with diabetes was higher than the uninfection group. Multivariate logistic regression analysis showed that ALB and diabetes mellitus were independent risk factors for bloodstream infection in hemodialysis patients. A total of 64 pathogenic

bacteria were isolated from 58 hemodialysis patients with bloodstream infection, of which 39 were Gram-positive bacteria, accounting for 60.94%.They are mainly Staphylococcus epidermidis and Staphylococcus aureus, and have high resistance rates to penicillin, erythromycin,clindamycin and oxacillin; 20 strains of Gram-negative bacteria accounted for 31.25%, mainly consisting of Enterobacter cloacae and Klebsiella pneumoniae, Klebsiella pneumoniae has high resistance rate to cephalosporins(except for the fourth generation cephalosporins),aminoglycosides and penicillins;5 strains of fungi(7.81%) were sensitive to fluorouracil, fluconazole, voriconazole,itraconazole and amphotericin B.

Conclusions The related factors of bloodstream infection and the characteristics of pathogenic bacteria in maintenance hemodialysis patients have certain characteristics. Clinicians should give close monitoring to strengthen the rational use of antibiotics.

PO-327

The effect of macroenzyme complex on liver function examination

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Objective to explore the influence factors of the examination of glutamic-oxaloacetic transaminase via a case of asymptomatic glutamic-oxaloacetic transaminase abnormally increased in clinical practice.

Methods in the clinical practice, it was found that glutamic-oxaloacetic transaminase increased abnormally reaching 900U/L while the alanine aminotransferase, lactate dehydrogenase and myocardial enzyme were normal during the physical examination of the patients.The doctor diagnosed fatty liver according to the results of liver function examination, and suggested that the patient be hospitalized for conservative treatment with liver-protecting drugs.After a week of treatment, the patient's liver function was reviewed, and the glutamic-oxaloacetic transaminase decreased slightly, so the effect of the tratement was not obvious.The patient asked for leave to go on a business trip . A few days later, the patient returned to the hospital and took out the liver function report sheet presented by another hospital. The result showed that glutamic-oxaloacetic transaminase was normal, so the patient doubted the accuracy of the result of the first liver function examination sheet.Then the laboratory staff found out the patient's blood sample to repeat the previous test in different machines.

Results It was found that the result of the glutamic-oxaloacetic transaminase in the VITORS5600 was almost the same as the previous result, but the result of the glutamic-oxaloacetic transaminase in beckman coulter 5800 biochemical automatic analyzer was normal.After repeatedly reading the AST detection instructions and consulting relevant literature, the staff found that in a few cases, AST could form giant enzyme complex with immunoglobulin, resulting in continuous increase of serum enzyme activity.The detection of the giant enzyme complex requires the presence of pyridoxal phosphate, which happens to be present in the reagent of the first hospital, but not in the reagent behind, so the presence of the giant enzyme complex was not

detected in the next hospital .In view of this conjecture, an abnormal AST zone was found between mAST and sAST by electrophoresis of the patient's serum, which was isolated and purified with a molecular weight of 250KDa and composed of Ig and AST.
Conclusions the abnormal increase of AST in patients was due to the presence of giant enzyme complex, which affected the detection results.The VITORS5600 reagent in the emergency laboratory contains pyridoxal phosphate, which can detect the presence of giant enzyme complex, so the detection result is on the high side.The detection reagent of beckman coulter 5800 in the back and another hospital did not contain pyridoxal phosphate, so there was no detection of the giant enzyme complex, and the result was relatively low.

PO-328

Application of PAX1 gene methylation detection in cervical cancer screening

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Objective To detect the methylation modification of the promoter region of paired box family gene 1 (PAX1) in cervical cancer patients, thus to explore the clinical application value of PAX1 gene methylation detection in cervical cancer screening.
Methods From June 2017 to November 2018, 546 cervical exfoliated cell specimens were collected in the Second Hospital of Shandong University. Of which, 198 cases were cervical intraepithelial neoplasia grade 3 (CIN3) and cervical cancer, 348 cases were CIN2, CIN1 and healthy individuals based on cervical pathology. The level of PAX1 gene methylation in specimens were detected using the PAX1 gene methylation test kit. Receiver operating characteristic curve (ROC) analysis was used to evaluate the capability of PAX1 gene methylation for distinguishing CIN3 and cervical cancer from CIN2, CIN1 and healthy individuals.
Results The level of PAX1 gene methylation in CIN3 and cervical cancer was significantly increased compare with CIN2, CIN1 and healthy individuals. The sensitivity and specificity of PAX1 gene methylation for detecting CIN3+ were 75.3% (95% CI: 68.6%-82.0%) and 90.9% (95%CI: 86.3%-93.5%) respectively.
Conclusions These findings support the utility of PAX1 methylation as an auxiliary biomarker in cervical cancer screening. It can be combined with cytology to improve the diagnosis rate.

PO-329

Analysis of laboratory biochemical indexes in maintenance hemodialysis patients

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Objective To determine the Laboratory biochemical indexes in maintenance hemodialysis(MHD) patients, the status of renal function, liver function, bone metabolism marker, iron metabolism marker and myocardial marker were analyzed to provide laboratory evidence for monitoring the progress of patients.
Methods A total of 93 MHD patients (53males) received renal dialysis treatment in blood purification center of Xinjiang production and Construction Corps Hospital from October to December 2017. The concentrations of 21 biochemical indexes were measured, and the data were analyzed statistically by non-parametric test and Pearson correlation analysis.
Results Parathyroid hormone was higher in 90.9% of patients than 65pg/mL. Significant correlation ($p<0.001$) was observed between PTH and ALP (Pearson coefficient $r=0.482$), between PTH and P ($r=0.357$). Calcium concentrations were decreased in 54% of patients and positive correlation($p<0.05$) between Ca and serum bicarbonate($r=0.254$). Significant correlation ($p<0.001$) was observed between urea and creatinine ($r=0.512$). There was no significant increase in ALT and AST concentrations. Elevated cardiac troponin concentration(hs-TNI) in 24% of patients.74% of the patients had varying degrees of anemia, of which 28% had low iron status(serum iron <11μmol/L), while 64% had elevated levels of ferritin. Albumin and TIBC levels showed a significant number of patients with malnutrition.
Conclusions Chronic complications such as Secondary hyperparathyroidism, anemia, malnutrition, myocardial injury were found in MHD patients, and laboratory indicators are important for evaluating the overall status of MHD patients.

PO-330

Significance and application of serum phospholipase A2 receptor antibody detection in idiopathic membranous nephropathy

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Objective To investigate the diagnostic value of serum phospholipase A2 receptor (PLA2R) antibody in adult idiopathic membranous nephropathy (IMN) and the monitoring of disease activity.
Methods A retrospective analysis of 387 PLA2R specimens from the Second Hospital of Shandong University from April 2018 to January 2019 was conducted. Among them, 79

patients with IMN diagnosed by renal biopsy were diagnosed by renal biopsy. 112 patients with non-idiopathic membranous nephropathy (NIMN) were in the control group. The levels of PLA2R antibody in serum of each group were detected by enzyme-linked immunosorbent assay (ELISA), and renal function related indicators were detected. The sensitivity and specificity of anti-PLA2R antibody in the diagnosis of idiopathic membranous nephropathy were calculated by using pathological tissue test results as the gold standard. At the same time, the analysis and comparison of renal function indexes of each group were carried out. The sensitivity and specificity of serum PLA2R were detected by ELISA. In addition, the PLA2R antibody concentration of IMN patients was correlated with 24 hours urine protein, serum creatinine, serum albumin and other clinical indicators to explore the clinical value of serum PLA2R detection. According to the results of PLA2R, patients were divided into PLA2R positive group and PLA2R negative group. The above clinical indexes were compared between the two groups to analyze the clinically relevant indicators of PLA2R positive and negative patients with idiopathic membranous nephropathy.

Results (1) Among the 79 confirmed IMN patients, serum PLA2R antibody was positive in 62 cases and negative in 17 cases, the positive rate was 78.5%. In 112 control group, PLA2R antibody positive patients only had 5 positive, and the remaining PLA2R were negative, with specificity reaching 95.5. %.

(2) Serum PLA2R antibody was positively correlated with 24-hour urine protein, $P<0.005$, and correlation coefficient $r^2 = 0.514$. The correlation between the two was relatively close.

(3) After treatment, PLA2R levels gradually decreased to normal and the disease was relieved.

Conclusions Serum PLA2R antibody has high diagnostic specificity in IMN and can be used as a diagnostic index of IMN. The increase of PLA2R antibody concentration has a strong correlation with the diagnosis of IMN. Dynamic monitoring of serum PLA2R antibody and 24-hour urine protein can reflect the condition. Change and evaluate clinical outcomes.

PO-331

The value of red blood cell distribution width and monocyte to lymphocyte ratio in ankylosing spondylitis

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Objective To evaluate the diagnosis value of red cell distribution width(RDW) and monocyte to lymphocyte ratio(MLR) in the ankylosing spondylitis(AS).

Methods A total of 131 AS patients who initially diagnose in the First Hospital of Jilin University and 135 healthy subjects were included in this study. The fasting blood samples were collected for the detection of blood routine and IgG, IgA, IgM, C3, C4, RF, hs-CRP.The monocyte/lymphocyte ratio was calculated according to the blood routine results.Correlations of RDW and MLR with the clinical indexes of AS were evaluated.

Results RDW and MLR were significantly higher than healthy controls (P<0.05). There were significant differences between RDW and MLR in the positive and negative patients defined by inflammation-related indicators hs-CRP and ESR (P<0.05).There was a statistically significant difference in MLR between patients with abnormal Ig (IgG, IgA, IgM) and normal patients (P<0.05).RDW was positively correlated with ESR and hs-CRP. The correlation coefficients were 0.277 and 0.225, respectively. MLR was positively correlated with ESR, hs-CRP, IgG, IgA, and C3, and the correlation coefficients were 0.358, 0.399, 0.214, 0.183, and 0.241, respectively.
Conclusions Both RDW and MLR values may prove to be potential indices for AS diagnosis and disease observation, which are expected to serve as a new biomarker for independently predicting the AS inflammation severity.

PO-332

The anti-tumor effect of Compound Kushen Injection combined with oxaliplatin on colon cancer stem cells

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Objective to observe the possible synergistic effect of the Traditional Chinese Medicine and chemotherapeutic drugs, the Compound Kushen Injection (CKI) alone、oxaliplatin (OXA) alone and combined effects for cell proliferation and apoptosis on human colon cancer stem cells (CSCs).
Methods CCK8 was used to estimate the inhibition of proliferation on CSCs, flow cytometry was applied to analyze the apoptosis and the distribution of cell cycle.
Results CKI and OXA could markedly inhibit the cell proliferation, and the effect depended on exposure dose (p<0.05); The combined effect of CKI and OXA was additive or synergistic, which had statistical significance comparing with the single drug (p<0.05). Annexin V-FIFC/PI showed that CKI (2.08mg/mL), OXA (1μg/mL), as well as the two combined, could induce the apoptosis of CSCs. The apoptosis index were 16.53%, 16.58% and 21.28% respectively (p<0.05), which were obvious that the combined group was significantly excelled the single work. Flow cytometry showed that the proportion of cells increased at G0/G1 phase, while it decreased at S phase, indicating that drugs blocked cells at G0/G1 phase. The effect of pair work was clearly superior to the sigle drug (p<0.05).
Conclusions Both CKI and OXA could inhibit the proliferation, induce the apoptosis of CSCs, and block the cell cycle at G0/G1 phase. These results suggested that the effect of the two drugs CKI and OXA combined may be synergistic for the treatment of colon cancer stem cells.

PO-333

Correlation analysis of hepatitis B virus viral load and cellular immune function

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Objective To investigate the changes of T lymphocyte subsets, B cells and NK cells and its clinical significance in peripheral blood of patients with hepatitis B. And to explore the relationship between the content of HBV deoxynucleotides (HBV-DNA) and the T lymphocyte subsets, B cells and NK cells in HBV infected persons with the development of the disease.
Methods The flow cytometry was used to detect the T lymphocyte subsets, B cells and NK cells of 17 cases of chronic hepatitis B (CHB), 17 cases of hepatitis B cirrhosis (LC), 10 cases of liver cancer (PHC) and 19 cases of healthy control group. And real-time fluorescence quantitative polymerase chain reaction (RT-PCR) technique was used to detect the serum level of HBV-DNA in the above 63 cases.
Results Compared with the control group, the percentage of $CD3^+$, $CD4^+$ and $CD4^+/CD8^+$ was significant decreased in CHB and LC patients ($P<0.05$). The ratio of CD3+ had declined significantly in PHC group ($P<0.05$), but not in $CD8^+$. There was no changes of NK cells and B cells in CHB, LC and PHC group.
Conclusions The disorder of cellular immune function in hepatitis B patients was not only related to the course of disease, but also related to the content of HBV-DNA.

PO-334

Difference expression and clinical significance of Rab27A in colon cancer

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Objective o study the expression of Rab27A in colon cancer tissue, and to investigate the clinical significance of Rab27A proteins expression, and to determine whether Rab27A expression is emerging as a prognostic biomarker for survival in colorectal cancer patients.
Methods Detected expression of Rab27A in 90 paired primary colon cancer samples and adjacent normal tissues by immunohistochemical method, and analysed relationship between Rab27A expression and pathological features in colon cancer. Survival rate was examined by Kaplan-Meier method and Log-rank test.
Results The positive rate of Rab27A staining in primary colon cancer (35.6%, 32/90) was significantly lower than that in the matched adjacent tissue (96.7%, 87/90, $p<0.001$). Analysis of clinicopathological characteristics of 90 colon cancer specimens, however, revealed a significant positive correlation between Rab27A expression and TNM stage (III) ($p<0.01$). On the other hand, no significant differences were observed

regarding gender, age, and tumor size. Rab27A positive cases showed an obviously shortened median survival time (35.5 month [mo]) in comparision with the Rab27A negative cases (Log rank =5.269, p = 0.0217) . The overall 5-year survival rate for the Rab27A negative patients (37.9%) was higher than that of the Rab27A positive group (21.9%).

Conclusions Rab27A abnormal expression is associated with development and progression of colon cancer, and Rab27A may act as a prognostic indicator for colon cancer patient survival.

PO-335

New design of probe and central-homo primer pairs to improve TaqMan PCR accuracy for HBV detection

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Objective The qPCR assay using TaqMan probe was widely used in the detection of different nucleic acids. However, this technology has several drawbacks, including false negative results caused by primer-dimer (PD) and false positive issues due to primer-probe aggregations. The object of our assay is weak the false negative results and the false positive results in real time PCR (qPCR).

Methods We designed a modified TaqMan-Molecuar Beacon probe by adding an antisense base and a new type of primer pair named central-homo primer pairs bearing 5-10 bases homologous sequence on the 3' end. Using the HBV qPCR assay as a proof of concept. Firstly, primer-probe aggregation experiments (Ordinary probe HBVP1, HBVP2 HBVP3 and the new designed probe HBVP4) was processed. Secondly, the amount of primer dimer (PD) was compared between the central-homo primer pairs and ordinary primer pair in SYBR Green qPCR. Furthermore, we designed a new system with the improved probe and primer pair, and evaluated it and validated this customized duplex qPCR system using 208 clinical samples collected from patients in clinic and compared it with the traditional system with X^2 test.

Results Different from other probes, the modified probe HBVP4 containing an antisense base did not produce any detectable signal in repeating primer-probe aggregation experiments. Application of the central-homo primer pair led to significantly delayed Ct values by 5-10 cycles compared with conventional primer design. The linear coefficient, R^2, of the standard curve of the duplex PCR was 0.997. The detection sensitivity of HBV plasmids and clinical samples was 100IU/mL, cut-off level of the Ct value was 37 and, CV of the duplex system was less than 5 percent. The P value was less than 0.01.

Conclusions The new design significantly improved the accuracy of the TaqMan qPCR assay for HBV detection. And the use of the central-homo primer pair and the non-competitive internal control could solve the false negative problem caused by PD formation. The accuracy of the new system was higher than that of the conventional qPCR method.

PO-336

Hypoxia increases adipogenesis at the exprense of osteogenesis of RA-FLS

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Objective Fibroblast-like synoviocytes (FLS) have been recognized to play a major role throughout the course of rheumatoid arthritis (RA), especially in bone erosion and bone loss. However, the regulation on bone formation of RA-FLS in RA was little to know. This study aimed to investigate the performance of RA-FLS on multipotential differentiation under the anoxia condition.

Methods RA-FLS were isolated and cultured form the synovium of RA patients. Flowcytometry was used to identify the expression of CD90, CD105 and CD73 both on RA-FLS and osteoarthritis related RLS (OA-FLS). OA-FLS were referred as control. RA-FLS and OA-FLS were cultured and induced with osteo-induced medium for 21 days under 21% O_2 and 3%O_2 condition, respectively.All the induced cells were stained with Alizarin Red to evaluate the osteogenicpotential. Hypoxic effect on adipogenesis of RA-FLS and OA-FLS were assessed with oil red O staining after adipogenic differentiation for 21 days. Bioinformatical analysis was performed to figure out the key pathways and different express genes from gene expression omnibus (GEO) database. Osteogenesis- and adipogenesis-specific markers were detected with westernblot.

Results RA-FLSs and OA-FLSs were uniformly positive for CD73, CD90, CD105 and negative for CD45. Both of RA-FLS and OA-FLS showed messenchyal stem cell (MSC)-like phenotype. The percentages of these markers were not influenced by hypoxia. The Alizarin Red and Oil Red O staining RA-FLS and OA-FLS displayed the ability of osteogenic and adipogenic differentiation. The Alizarin Red staining of RA-FLS was weaker under anoxia condition than normoxia condition while the Oil Red O staining was stronger. GSE21959 was downloaded from GEO database. GSEA analysis revealed VEGF pathway was the most important pathway and protein-protein interaction network proved that VEGF as hub gene which owned highest degree. After 48h hypoxic treatment, the expression of adipogenetic-specific makers (leptin) increased in RA-FLS, which in line with bioinformatical result above.

Conclusions RA-FLS showed similar characteristics of MSC. Hypoxia did not change the phenotype of RA-FLS, but destroyed the balance of osteogensis and adipogenesis. RA-FLS preferred to differentiate to adipocytes instead of osteocytes. VEGF pathway may respond to this imbalance.

PO-337

Factors associated with the progression and viral replication of patients with the hepatitis B virus

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Objective So far, Hepatitis B virus (HBV) infection remains a severe problem in China. However, the damage to the liver function caused by chronic HBV infection varied in different populations, especially among individuals due to physical differences.This research aimed to identify the factors that influence the disease progression and prognosis of HBV infection.

Methods Total 478 HBV infected patients were enrolled and all of the biomarkers of liver function, HBV DNA levels and hepatic fibrosis index values were analyzed.

Results Firstly, the results demonstrated that there was a significant difference in hepatitis B e antigen (HBeAg) expression between male and female patients (x^2=4.061, P=0.044). Secondly, when comparing either HBeAg-negative or positive male and female patients, male patients exhibited greater differences in HBV DNA levels. Although the hepatic fibrosis values and a few of the abnormal ratios of liver function parameters were significantly different between male and female patients, there was a trend in the differences observed in the HBeAg-negative and positive groups. When considering age, the present study confirmed that HBV DNA levels decreased with advanced age, and the values of the majority of biomarkers exhibited an evident decreasing trend with increasing age. In addition, it was demonstrated that all seropositive HBeAg patients had higher levels of hepatic fibrosis indexes and higher abnormal ratios of hepatic fibrosis values in their serum when compared with seronegative HBeAg patients, especially serum IV collagen. The present results revealed that HBV DNA replication was closely associated with liver function; however, it was notable that in HBeAg negative patients, the association between DNA levels and liver functions was only observed in those aged <61, as it was not observed in the senior patients (≥61 years). Furthermore, this result was not observed in HBeAg positive patients.

Conclusions In conclusion, the present study revealed the importance of host factors (such as sex and age) and viral factors (including HBeAg expression pattern and HBV DNA levels) in the treatment, prognosis and progression of HBV infection. All of the results provide a foundation for clinical management strategies for HBV infection, particularly in individual schemes.

PO-338

Serum-based miRNAs as promising biomarkers for screening gastric cancer and predicting lymph node metastasis

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The first hospital of Jinlin Univesity

Objective We investigated whether serum microRNAs(miRNAs) could be a potential circulating biomarker for detecting gastic cancer(GC) and associated with lymph node metastasis(LNM).
Methods In this study,157 GC patients and 102 healthy controls were recruited.Serum miRNAs expression levels were detected using quantitative reverse transcription polymerase chain reaction(qRT-PCR).CEA and CA19-9 were measured by electrochemiluminescence assay.Computed Tomography(CT) was also performed.
Results Our datas showed that five serum miRNAs(miR-17-5p,miR-93-5p,miR-143-3p,miR-182-5p and miR-183-5p) were higher in GC patients than in healthy controls(HCs)(P<0.05).ROC analyses showed that the area under the reciver operating characteristic curve(AUC) for five serum miRNAs were 0.891 for distinguishing GC from HCs,Higher than CA19-9 and CEA.The combimation of two serum miRNAs(miR-10b-5p,miR-143-3p) and CT increased the AUC of prediction for LNM from 0.605 to 0.808.
Conclusions These results indicate five serum miRNAs have stong potential as a novel noninvasive biomarker in GC detection.High serum levels of two serum miRNAs in GC may indicate LNM and a unfavorable prognosis.

PO-339

Prognostic significance of interleukin 17 in cancer: A Systematic Review with a meta-analysis.

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Objective The prognostic value of Interleukin 17 (IL-17) in cancer patients is currently under debate and remains inconclusive. We performed a systematic review and meta-analysis to evaluate the role of IL-17 as a prognostic marker in cancer.
Methods Hazard ratios (HRs) and corresponding 95% confidence intervals (CIs) were combined to measure the effective value of IL-17 expression on prognosis. Nineteen eligible studies enrolling 2390 patients were identified.
Results We found expression of IL-17 was not significantly correlated with overall survival (OS) in cancer (HR=1.29, 95% Cl: 0.94-1.76; P=0.12). Furthermore, compared to the data from our analysis that high expression of IL-17 predicted poor OS in both non-small cell lung carcinoma (NSCLC) (HR=2.30; 95% CI: 1.45-3.64; P<0.001; I^2=0%) and hepatocellular carcinoma (HCC) (HR=2.02; 95% CI: 1.44-2.83; P<0.001; I^2=0%), high expression of IL-17 was associated with favorable OS in esophageal squamous cell carcinoma (ESCC) (HR=0.63; 95% CI: 0.51-0.79; P<0.001; I^2=0%).

Conclusions This meta-analysis showed that IL-17 has the potential to become a novel prognostic marker in HCC, NSCLC and ESCC. It could potentially help to monitor patients' prognosis and assess therapeutic efficacy in clinical treatment.

PO-340

Clinical relevance of lnc-AC145676.2.1-6 and lnc-TGS1-1and their variants in western Chinese tuberculosis patients

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Objective Tuberculosis (TB) remains a global public health problem, and improvements in timely and effective diagnosis are urgently needed. Long non-coding RNAs (lncRNAs) are novel transcripts that may play important roles in many diseases, including tuberculosis diseases. Our study aimed to explore the potential of lnc-AC145676.2.1-6 and lnc-TGS1-1and their variants as biomarkers in TB diseases.
Methods Lnc-AC145676.2.1-6 and lnc-TGS1-1 were selected from lncRNA microarrays, which showed a downward trend in healthy controls, latent TB infection individuals and TB patients. The expression level of lncRNAs were analyzed by using qRT-PCR in 940 peripheral blood samples, from 467 active tuberculosis patients (TB) and 473 healthy controls (HC). And the SNP genotyping work was performed using a custom-by-design 2x48-Plex SNPscanTM Kit. Then, logistic regression analyses were conducted to evaluate the associations of lncRNA expression with clinical information of TB patients, including labratory results and common adverse drug reactions.
Results Lnc-AC145676.2.1-6 and lnc-TGS1-1 expression were both obviously down-regulated in TB patients [TB *vs* HC: 0.77 (0.31-1.27) *vs* 1.39 (0.35-3.16), $P < 0.001$; 0.23 (0.08-0.58) *vs* 1.17 (0.36-2.66), $P < 0.001$, respectively]. And lower expression level of lnc-TGS1-1 was associated with the presence of thrombocytopenia in TB patients after anti-tuberculosis treatment[Presence *vs* Absence: 0.06 (0.04-0.32) *vs* 0.25 (0.08-0.59), $P = 0.033$]. However, no significance association were found between lnc-AC145676.2.1-6 rs111352767, lnc-TGS1-1 rs4737420 and the predisposition to TB diseases (all $P > 0.05$). Interestingly, the homozygous CC genotype of rs4737420 was correlated with the decreased risk for the arise of leukopenia compared with those with T allele (TT/CT genotype) under the dominant model (OR = 0.20, 95% CI = 0.04-0.93, $P = 0.023$).
Conclusions Lnc-AC145676.2.1-6 and lnc-TGS1-1 could serve as potential diagnostic biomarkers for tuberculosis diagnosis. Lnc-TGS1-1 and its varient rs4737420 may be the indicators of predicting anti-TB drug adverse reactions. Larger validation studies with different populations are warranted to confirm these findings.

PO-341

Regulatory effect of FK506 on the expression of activated Caspase-8 in T cells of liver allo-recipients

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Objective Observing the expression of T cells activated Caspase-8 and surface CD69 as well as the apoptosis of T cells in the peripheral blood of liver allo-recipients, discuss the impact of FK506 on the signal mediated by Caspase-8.
Methods Flow cytometry combined fluorescent labeled monoclonal antibody technique was used to determine the expression of activated Caspase-8 and surface CD69. The apoptosis of T cells was determined through dual staining of Annexin V/7-ADD.
Results The expression of activated Caspase-8 in $CD3^+$T cells and $CD4^+$T cells from disease control decreased obviously compared with health control ($P<0.05$). Through eight-week treatment after liver transplantation, the expression of activated Caspase-8 in T cells and T cell subsets was obviously higher than that in disease control ($P<0.05$), and was also higher than that in health control, but no significant difference was found ($P>0.05$). The expression of CD69 on T cells and T cell subsets in each group had no significant difference ($P>0.05$). After liver transplantation, the percentages of apoptosis for $CD4^+$T cells and $CD8^+$T cells were obviously higher than that in health control and disease control ($P<0.05$). The ratio of the apoptosis for $CD4^+$T cells and $CD8^+$T cells in treatment group was also significantly higher than that in health control and disease control ($P<0.05$).
Conclusions FK506 could induce the increase of lymphocyte apoptosis, thus control the number of effector lymphocyte, prevent the allo-rejection and induce transplant tolerance.

PO-342

The efficacy evaluation of combined detection of PGI、PGR and G-17 and its evaluation for diagnosis of chronic gastritis and gastric cancer□

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Objective To detect expression of pepsinogens (PGI and PGII), gastrin-17(G-17) in the patients with gastric cancer or precancerous lesion, and to evaluate the efficiency of combined diagnosis index of PGR(PGI/PGII) in these patients.
Methods The levels of PGs, G-17 were deteced in 50 healthy volumeers, 96 patients with atrophic gastritis, 54 patients with gastric cancer by enzyme-linked immunosorbent assay (ELISA). And the ROC curve were used to evaluate its efficacy in diagnosis of gastric carcer.

Results The 54 cases of gastric cancer group, compared with healthy by the analysis of ROC curve, area under PGI curve is 0.788, the optimal value of PGI<37.00 ng/ml, its sensitivity and specificity were 0.882 and the area under the 0.769.PGR curve was 0.788, the optimum value of PGR<2.7, the sensitivity and specificity was 0.882 and the area under the 0.692.PGR curve was 0.765, the optimum value of G17>26.8, its sensitivity And specificity were 0.706 and 0.89.
Conclusions The combined detection of PGs and G-17 was helpful for diagnosis of gasric cancer, and it was a useful supplement to traditional tumor markers. Thus, a new diagnostic model was established for a better diagnostic value of gastric cancer.

PO-343

SP70 as a potential biomarker for the diagnosis and dynamic monitoring of breast cancer

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Objective A new type of protein SP70, can be highly expressed in serum of non-small cell lung cancer patients was verified. The aim of this study was to evaluate SP70 as a new biomarker in diagnosis and dynamic monitoring in breast cancer via serological expression.
Methods Sixty-nine Paraffin-embedded specimens and 228 peripheral blood samples were obtained from breast cancer patients. Serum samples from 100 healthy individuals and 187 benign breast diseases patients served as controls. Expression of SP70 in tissues was evaluated by immunohistochemistry. The serum concentration of SP70 was measured by enzyme-linked immunosorbent assay (ELISA). Carcinoembryonic antigen (CEA), carbohydrate antigen 125(CA125), and carbohydrate antigen 153cytokeratin(CA15-3) were detected prior to diagnosis in breast cancer for comparison. Furthermore, we explored the monitoring values of serum SP70 in 39 breast cancer patients by analyzing the preoperative and postoperative serum SP70 levels of the same patients.
Results The positive expression of SP70 in breast cancer tissues was highly correlated with tumor stages and lymphatic metastasis (P<0.05, respectively). Simultaneously excessive expression of serum SP70 also obviously manifested in breast cancer patients compared with heathy controls and benign group(P<0.05, respectively). The higher concentration of serum SP70 also positively associated with advanced tumor stages and lymph node metastasis in breast cancer patients(P<0.05 and P<0.05). Furthermore, CEA showed closely linked to tumor stages, while CA15-3 was correlated with tumor sizes. However, CA125 performed no obviously interplay with tumor stages and tumor sizes in breast cancer patients. Additionally, the serum levels of SP70 in postoperative patients were lower than those in preoperative patients (P < 0.001).
Conclusions Our study firstly demonstrated that excessively expression of SP70 in breast cancer tissues and serum level, which could acted as a valuable biomarker for discriminating breast cancer patients from healthy individuals and benign diease.

Moreover, the expression of SP70 in cancer tissues and serum were positively correlated with lymphatic metastasis in breast cancer patients. Therefore, SP70 may serve as a potential diagnostic and dynamic monitoring biomarker in breast cancer.

PO-344

Relationship between serum CA19-9 and CEA levels and prognosis of pancreatic cancer

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Objective To explore the relationship between preoperative serum CA19-9 and CEA levels and prognosis of pancreatic cancer (PC).
Methods The clinicopathological data of 300 patients with pancreatic adenocarcinoma who were treated in our center between January 2012 and December 2015 were retrospectively analyzed. The relationships between serum CA19-9 and CEA levels and survival were analyzed using Kaplan-Meier method, log-rank test, and Cox regression analysis. The cut-off values for serum CA19-9 and CEA levels were 39 U/mL and 4.7 ng/mL, respectively.
Results Among these 300 patients, the mean age was 65 years, and median survival was 15.2 months. The positive rate of CA19-9 and CEA was 72.1% and 38.4%, respectively. Patients with increased CA19-9 or CEA level suffered a poorer prognosis than those with normal CA19-9 or CEA level (CA19-9: P=0.012; CEA: P=0.032). Cox logistic analysis revealed that lymphatic metastasis, CA19-9 >39 U/mL, and CEA >4.7 ng/mL were independent prognostic factors in patients with pancreatic carcinoma.
Conclusions Preoperative serum CA19-9 and CEA level are closely related with survival time in PC patients and therefore may be used for evaluating the prognosis for PC.

PO-345

Correlation Analysis High-risk Human Papillomavirus (HPV) Types and Cervical Infection in Shanghai, China

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Objective To observe the distribution of high-risk Human Papilloma Virus (HPV) subtypes in Pudong New Area, Shanghai, China, and to analyze the correlation between high-risk HPV subtypes and ThinPrep Cytology test (TCT) results and cervical pathological biopsy results.
Methods The clinical data of 7 360 cases of high-risk HPV DNA typing and TCT screening for cervical diseases were retrospectively analyzed. 421 of them underwent cervical

pathological biopsy. The distribution of high-risk HPV DNA subtypes and their correlation with TCT and cervical pathological biopsy were analyzed.

Results A total of 1 255 cases of HPV infection with high risk subtypes were screened out in 7 360 female patients. The infection rate was 17.05%. The top five HPV infection subtypes (including single infection and multiple infections) were HPV 16、52、58、18 and 56, of which 316 cases were HPV 16, accounting for 25.18% of the total infected population. 183 cases were infected, accounting for 14.58% of the total infected population; 174 cases were infected with HPV 58, accounting for 13.86% of the total infected population; 138 cases were infected with HPV 18, accounting for 10.99% of the total infected population; 111 cases were infected with HPV 56, accounting for 8.84% of the total infected population; 308 cases were infected with multiple HPV subtypes, accounting for 24.54% of the total infected population. Among multiple infections, the proportion of double infections was the highest, accounting for 72.40% of multiple infections. HPV 52、58 and 16 were the most common types of double infections. Logistic regression analysis showed that patients infected with HPV 16、18、33、56、58 and 68 may have a greater risk of TCT cytological abnormality; the greater the OR value of HPV 16、18、52、56、58 and 68 may be the high risk factor for the occurrence and aggravation of high-grade pathological changes. Compared with the staining group, there was no significant difference in low-grade squamous intraepithelial lesion (LSIL) and above lesions in the multiple infection group ($P > 0.05$); there was no significant difference in cervical squamous intraepithelial lesion in the multiple infection group ($P>0.05$).

Conclusions High-risk HPV DNA infection is closely related to cervical cytological abnormalities, cervical precancerous lesions and cervical cancer. Compared with single HPV DNA infection, multiple HPV subtypes infection does not increase the possibility of cytological abnormalities and cervical squamous intraepithelial lesions.

PO-346

A case of acute myelomonocytic leukemia misdiagnosed as upper respiratory tract infection

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Objective To investigate the clinical features of acute myelomonocytic leukemia, less misdiagnosis and mistreatment.

Methods A case of acute myelomonocytic leukemia(AML-M4) misdiagnosed as upper respiratory tract infection was selected to analysis clinical manifestation, a complete blood count , blood smear, biochemistry, coagulation, bone marrow aspiration, flow cytometry, gene testing.

Results Blood smear of this patient showed a rise of WBC and the blast cells (32%) occured . The further examination discovered that the ratio of blast cell was beyond 52.5%in bone marrow smear, the flow cytometry detected the CD34, CD13, CD33 have the

positive expressions, and gene testing shows FLT3-ITD and NPM1mutations . After antimicrobial therapy ,supportive treatment and combination chemotherapy , the acute myelomonocytic leukemia entered remission.

Conclusions Accurate diagnosis of AML is an important basis for clinical treatment and prognosis evaluation.

PO-347

The Genetic and Antigenic polymorphisms of VP4 and VP7 Proteins in Group A Human Rotavirus Outbreak in Yunnan Province, China

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Objective Group A rotavirus (RV) accounts for most of the severe dehydrating diarrhea and is associated with the high morbidity and mortality in children worldwide. A rotavirus outbreak of 874 outpatient cases occurred in Yunnan province in southwestern China. This study aims to investigate the prevalence of RV and explore the gene polymorphisms and antigenic variability of RV VP4/VP7 proteins in this outbreak.

Methods The VP7/VP4 genes rotavirus positive samples were amplified, followed by DNA sequencing and genotyping. Phylogenetic trees were constructed by the maximum likelihood methods of MEGA6.0 software, followed by molecular characterization and secondary structure diversity analysis.

Results G9P[8] was the predominant combination type in outbreak in Yunnan province. A total of 16 single nucleotide changes were observed in VP4 sequences, with 5 nonsynonymous mutations. Meanwhile, 27 mutations were observed in VP7 coding sequences, with 7 nonsynonymous mutations. Phylogenetic analysis showed that the epidemic RV strains in this outbreak are most similar to the epidemic strain in Zhejiang (2013) and Jiangsu (2012) province, which indicated an internal recycling epidemic trend of RV in China.

Conclusions This study may help us to understand the intrinsic geographical relatedness of the viruses and further contribute to research on their infectivity and pathogenicity, as well as to vaccine development.

PO-348

LncRNA TUG1 sponges mir-1299 to promote cell proliferation and migration in ovarian cancer by up-regulating Notch3

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Objective Ovarian cancer is one of the most aggressive gynecological cancers burdened by the highest mortality rate. Notch3 have been consistently reported as an oncogene in the malignant progression and drug-resistance of ovarian cancer (OC), while little is known about its regulatory molecules. In this study, we aimed to elucidate the role of non-coding RNAs that regulate Notch3 in OC.
Methods Bioinformatics analysis, GEO datasets and luciferase reporter assay were used to screen and verify the potential targets. A series of in vivio and in vitro assays were performed to confirm the effect of mir-1299 and TUG1 on Notch3-mediated malignancy in OC.
Results We identified mir-1299 as a negative regulator of Notch3 in OC. The expression of miR-1299 was down-regulated in OC, and was significantly correlated with tumor differentiation, nodal metastasis and chemotherapy response. Overexpression of mir-1299 in OC cells substantially reduced cell proliferation, invasion and migration, and blocked the cells in the G0/G1 phase. In vivo studies showed that miR-1299 overexpression suppressed tumor growth with reduced Notch3 expression. LncRNA TUG1 was identified as a competing endogenous RNA (ceRNA) of miR-1299. It was up-regulated in OC and played an oncogenic role by suppressing the expression of mir-1299 to upregulate Notch3. Knock-down of TUG1 in OC cells suppressed cell proliferation, invasion and migration.
Conclusions Downregulation of mir-1299 plays an important role in the malignant progression of ovarian cancer. Mir-1299 was a potent suppressor of Notch3. LncRNA TUG1 functions as a ceRNA to regulate Notch3 expression via sponging miR-1299 in ovarian cancer.

PO-349

The study of serum biomarkers and the establishment of diagnostic models for HBV-related HCC

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Objective By measuringthe levels of expression of alpha-fetoprotein (AFP), des-γ-carboxy-prothrombin (DCP) and Golgi protein 73(GP73) in the serum of HBV-related liver cancer patients, the diagnostic value of single and combined detection of the above

indicators in HBV-related liver cancer shall be discussed, and the mathematical model of differential diagnosis by the Support Vector Machine (SVM) shall be established to provide reference for the diagnosis of HBV-related liver cancer.

Methods A total of 181 patients and healthy persons from March 2016 to January 2018 from Beijing Tongren Hospital affiliated to Capital Medical University have been selected. These lection includes 27 cases of hepatitis B related liver cancer, 31 cases of non-hepatitis B related liver cancer, 22 cases of hepatitis B cirrhosis, 27 cases of chronic hepatitis B, and 74 healthy persons in the same period. The levels of serum DCP, AFP and GP73 in each group were measured.

Results The expression level of serum DCP, AFP and GP73 in HBV-related liver cancer group was significantly higher than that in the hepatitis B cirrhosis group, chronic hepatitis B group and normal control group. Also, the difference was statistically significant (P<0.05).In contrast, the differences of the three indexes between the hepatitis B cirrhosis group, the chronic hepatitis B group and the normal control group were not statistically significant (P>0.05).When AUC_{DCP} = 0.848, 95% CI (0.741-0.955), the optimum critical value was 6.705ng/ml, sensitivity, specificity, positive predictive value and negative predictive value were 77.8%, 97.3%, 91.3%, 92.3%, AUC_{GP73} = 0.984, 95% CI (0.965-1.0), the optimum critical value was 84.31ng/ml, sensitivity, specificity, positive predictive value and negative predictive value were 77.8%, 97.3%, 91.3%, 92.3%, respectively. 92.6%, 95.9%, 89.3%, 97.3%, AUC_{AFP} = 0.827, 95% CI (0.728-0.927), the best critical value is 1.497 ng/ml, the sensitivity, specificity, positive predictive value and negative predictive value are 66.7%, 89.2%, 69.2%, 88%, respectively. Logistic regression analysis was used to obtain the combined predictive factors, and ROC curves were drawn for the combined diagnosis of the three indicators. The results showed that $AUC_{DCP+GP73+AFP}$=0.997, 95% CI (0.4930-1.0), sensitivity, specificity, positive predictive value and negative predictive value were 100%, 98.6%, 96.4% and 100%, respectively. Combined diagnosis of three indexes is better than single diagnosis, P<0.001. Through ROC curve, the area under curve (AUC) of serum DCP, GP73 and AFP, it was found that the AUC of HBV-related hepatocellular carcinoma was between 0.7 and 0.9, and that of HBV-related hepatocellular carcinoma and cirrhosis was less than 0.7. Using SVM mathematical diagnosis model, the specificity and sensitivity of diagnosing HBVHCC and HC reached 100%, while the specificity and sensitivity of diagnosing HBVHCC and LC reached 90.91% and 96.3%, respectively.

Conclusions Serum DCP, AFP and GP73 can be used independently as a useful reference for diagnosing HBV-related liver cancer patients. Combined detection of the three indicators can improve the sensitivity of HBV-related liver cancer diagnostic test. The SVM model can be used to diagnose and identify liver diseases at different stages.

PO-350

Changes of early damage indexs of renal function in patients with viral hepatitis and cirrhosis

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Objective To understand the renal function injury of patients with viral hepatitis and cirrhosis, and to screen the effective indicators that can early indicate the renal function injury.
Methods 61 patients with viral hepatitis and 63 patients with cirrhosis from the First Affiliated Hospital of Zhejiang University School of Medicine were enrolled as the viral hepatitis group and the cirrhosis group, and their blood and urine samples were collected. In addition, urine specimens of 60 healthy subjects were collected as the control group, and indicators such as Creatinine, Urea Nitrogen, Urine Protein(UP), β2-microglobulin(β_2-MG), Microalbumin(mAlb), Immunoglobulin G(IgG) and Retinol-Binding Protein(RBP) were detected in urine specimens of each group. Serum liver biochemical parameters were also detected in patients with viral hepatitis and cirrhosis. Statistical analysis was performed on the changes of early renal function markers in the viral hepatitis group, cirrhosis group and healthy control group, and the indicators sensitive to early renal damage were screened.
Results The levels of UP, Uβ_2-MG, URBP, UIgG and UmAlb in early renal function injury indicators of the viral hepatitis group and the cirrhosis group were all higher than those of the control group, with significant differences ($P<0.01$). The serum TP and Alb levels in the cirrhosis group were lower than those in the viral hepatitis group, and UP/Cr and CYC levels were higher than those in the viral hepatitis group, with statistically significant differences ($P<0.05$), among which serum CYC, TP, Alb and UREA were significantly different ($P<0.01$). There was no significant difference in other indexes of early renal function injury ($P>0.05$).
Conclusions Changes in urine levels of β_2-MG, mAlb, IgG, and RBP may suggest early renal injury in patients with cirrhosis and viral hepatitis, and timely guide clinical diagnosis and treatment.

PO-351

Comparison of gene mutation spectrum of thalassemia in different part of China and Southeast Asia

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Objective Compare gene spectrum of α and β-thalassemia in northern and southern China in our group, and compared our data with the largest meta-analysis in southern China, and data from Southeast Asian countries. The results may help to understand the similarities and differences of people from different area and different ethnic groups.

Methods During 2012 to 2017, suspected thalassemia people were detected for common α and β-thalassemia mutations by gap-PCR and reverse dot blot (RDB) analysis in Peking Union Medical College hospital (PUMCH). 1059 people who carried thalassemia genes were analyzed retrospectively. We picked mutated individuals with northern identity card numbers and conducted telephone follow-up survey in order to collect their ancestral information. Besides, we used 'thalassemia', 'mutation', and Southeast Asian countries as keywords to search potential related studies in PubMed and EMbase.
Results All carriers included in our study resided in northern China. Among them, 17.3% were native northerners and 82.7% were immigrants from southern China. Although significant difference was found between our data and data from the meta-analysis literature of southern China in both α and β-thalassemia, we also found some similarities between them. Similar gene mutation spectrum were found between Malaysia Chinese and Guangdong people, while other ethnic people in Southeast Asia had totally different gene spectrum from that of Chinese people.
Conclusions Chinese People originated from north may have lower percentage of α-thalassemia mutations. Chinese people in different area had similar gene mutation profile and Chinese people had significantly different gene spectrum from other ethnic people in Southeast Asia.

PO-352

Gene spectrum analysis of thalassemia carriers residing in the northern China

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Objective To analyze gene spectrum of sporadic cases that found in northern China.
Methods Positive patients or carriers were analyzed from suspected thalassemia carriers who resided in north China and were referred to Peking Union Medical College Hospital for diagnosis from 2012 to 2017. Gap-PCR and reverse dot blot analysis were applied for mutation detections. Basic clinical data and ancestral information of these patients were collected by telephone follow-up survey.
Results Most of our people with positive thalassemia gene findings had no or mild symptoms. People of north origin had higher percentage of β-thalassemia gene mutations compared with those of south origin (72.8% vs 62.4%, χ^2=9.92, P =0.001). Analysis of the individual gene distribution of the south and north did not show significant difference either in α- thalassemia (P=0.221) or β-thalassemia (P=0.979). No significant difference in the frequency of α mutation was found in different altitude levels. But in β thalassemia, the frequency of the 6 most common mutations were significantly different in provinces with altitude below 500 meters, about 500-1000 meters, and above 1000 meters (χ^2 test, $P < 0.05$).
Conclusions Most of people with positive thalassemia gene findings who reside in the north China are thalassemia carriers. People with north lineage may have higher frequency of β mutation than those of south origin, but they had similar spectrum of α and β mutations. People lived at different level of altitudes may have different spectrum of β mutation

PO-353

Long non-coding RNA CCAT1 promotes colorectal cancer progression by regulating miR-181a-5p expression from exosomes

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Objective Our study aimed at elucidating the function and mechanisms of long non-coding RNA CCAT1 via regulating miR-181a-5p expression from exosomes in the colorectal cancer (CRC).
Methods The Cancer Genome Atlas (TCGA) makes available lncRNA expression level data on cases and controls in matched 38 colorectal patients. We detected 10 lncRNAs that were upregulated and 10 that were downregulated specifically from exsomes in CRC. 50 cases of CRC tissues were collected to analyze the correlation between expression of CCAT1 and clinical pathology. The quantification of CCAT1 and miR-181a-5p was done using qRT-PCR and western blot. The target relationship between CCAT1 and miR-181a-5p was verified using dual-luciferase reporter gene assay. Cell viability was determined using MTT assay, colony formation assay and EdU assay. Cell aggression was determined using Transwell and wound healing assays. Flow cytometry analysis was used to demonstrate cell apoptosis. Further xenograft model experiments displayed the oncogenicity of CCAT1.
Results The expression of lncRNA CCAT1 was significantly upregulated in CRC tissues. The CCAT1 expression was positively associated with American Joint Committee on Cancer stage ($P < 0.05$). CCAT1 could promote the cell proliferation, growth and mobility by targeting miR-181a-5p from exsomes. The silence of CCAT1 could increase the cell apoptosis. Knocking down the expression level of CCAT1 could inhibit tumor growth in vivo.
Conclusions CCAT1 could promote CRC cell proliferation, invasion, migration and suppress cell apoptosis by regulating miR-181a-5p expression from exsomes.

PO-354

Effects of RHEB gene silencing on cell proliferation, differentiation and apoptosis in colorectal cancer via the mTOR signaling pathway

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Objective We explored whether RHEB gene silencing affects cell proliferation, differentiation and apoptosis by targeting the mTOR signaling pathway in cells harvested from colorectal cancer (CRC) patients.

Methods Eighty-three adjacent normal tissues and cancerous tissues were selected. HE staining was used to observe the pathological changes of adjacent normal tissues and cancerous tissues. Immunohistochemistry was employed to detect the positive expression rate of RHEB and Ki-67 in cancerous tissues. Cells were assigned into the blank, negative control (NC), RHEB-siRNA, RAPA and RHEB-siRNA + RAPA groups. The mRNA and protein expressions of RHEB, 4EBP1, p70S6K, PCNA, bax and bcl-2 were determined by RT-qPCR and Western blotting. CCK8, cell cloning and flow cytometry were conducted to measure the proliferation, cell cycle and apoptotic rate of CRC cells.
Results Compared with their adjacent tissues, cancerous tissues were associated with a higher expression of RHEB, Ki-67, p-mTOR, p-p70S6K, p-4EBP1, mTOR, p70S6K, 4EBP1, bcl-2 and PCNA, but a lower expression of bax. Compared with the blank and NC groups, the RHEB-siRNA group showed a decreased expression of RHEB, Ki-67, p-mTOR, p-p70S6K and p-4EBP1, mTOR, p70S6K, 4EBP1, bcl-2 and PCNA, as well as a decreased activity of cell proliferation and differentiation, although the expression of bax was higher in the RHEB-siRNA group. Similar trends were also observed in the RHEB-siRNA + RAPA group.
Conclusions Our study demonstrated that RHEB gene silencing might repress cell proliferation and differentiation while accelerating apoptosis *via* inactivating the mTOR signaling pathway.

PO-355

Reference intervals for serum bilirubin, urea, and uric acid in healthy Chinese geriatric population

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Objective The study aims to establish the reference intervals (RIs) for total bilirubin (TBIL), direct bilirubin (DBIL), urea (UR), and uric acid (UA) in healthy Chinese geriatric population.
Methods Eight hundred and twenty cases from six representative geographical regions in China (including male 413 cases and female 407 cases) of apparently healthy individuals aged 60-96 years were recruited. Serum TBIL, DBIL, UR, and UA were analyzed by automatic biochemical analyzer and RIs were determined following CLSI C28-A3 guidelines using a non-parametric method.
Results In apparently healthy Chinese geriatric population of China, the RIs of TBIL, DBIL, UR, and UA were 6.6~21.8 μmol/L, 1.9~8.0 μmol/L, 3.60~9.51 mmol/L, 179.2~460.9 μmol/L in males and 6.1~20.0 μmol/L, 1.8~7.1 μmol/L, 3.35~8.89 mmol/L, 130.2~443.4 μmol/L in females, respectively.
Conclusions The RIs of TBIL, DBIL, UR, and UA were established within apparently healthy geriatric Chinese population according to CLSIC28-A3 document, providing a reference for the clinical.

PO-356

Paeoniflorin Ameliorates EAE via Inhibition of the Function of Dendritic Cells and Th17 Cell Differentiation

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Objective Paeoniflorin (PF), extracted from the root of Paeonia lactiflora, is widely used as an anti-inflammatory remedy in Chinese medicine. The aim of this study was to investigate the effects and underlying mechanism of PF on experimental autoimmune encephalomyelitis (EAE), an animal model for multiple sclerosis (MS).

Methods The efficacy of PF was determined by observing clinical symptoms daily and histopathological examination. The infiltration of inflammatory cells in CNS and spleen derived from EAE mice and the expression of co-stimulatory molecules in $CD11c^+$ DCs and bone marrow DC (BMDCs) were determined by FACS. qRT-PCR was used to investigate the mRNA expression of Th cell differentiation-specific transcription factors and the mRNA levels of cytokines in $CD11c^+$ DC. The production of inflammatory cytokines in spleen derived from EAE mice and BMDCs was measured by ELISA. The activation of IKK/NF-κB and MAPKs signaling pathway was detected by western blot. Moreover, the effect of PF-treated DC on Th17 cell differentiation was measured by co-culture of naïve $CD4^+$ T cells with PF-treated DCs under Th17-polarizing conditions.

Results After administered with PF, the onset and clinical symptoms of EAE mice were significantly ameliorated, and the number of Th17 cells infiltrated in CNS and spleen was also dramatically decreased. Instead of inhibiting the differentiation of Th17 cells directly, PF influenced Th17 cells via suppressing the expression of co-stimulatory molecules and the production of IL-6 in $CD11c^+$ DCs and BMDCs, which may be attributable to the inhibition of IKK/NF-κB and JNK signaling pathway. When naïve $CD4^+$T cells were co-cultured with PF-treated DCs under Th17-polarizing conditions, the percentage of Th17 cells was decreased, as well as STAT3 phosphorylation and the mRNA levels of IL-17, RORα, and RORγt.

Conclusions In our present study, PF decreased IL-6 production and down-regulated co-stimulatory molecules expression in DCs via impairing the IKK/NF-κB and JNK signal activation, thus the inflammatory response induced by Th17 cells was significantly decreased. Our findings support the potential therapeutic effect of PF for MS/EAE.

PO-357

The effects of high-salt intake on the intestinal microbiota composition in wistar rats

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Objective High-salt diet has been considered to be implicated in the pathogenesis of some chronic diseases. And emerging data reveal a relationship between the chronic diseases and intestinal microbiota. However, it remains elusive how high-salt intake affects the composition of intestinal microbiota. The current study aims to investigate the possibility that high salt intake can cause changes in the gut microbiota composition in an animal model of wistar rats.

Methods we administered four-week-old male wistar rats with high-salt water (10% NaCl) intragastrically three times per week for four weeks, and collected the fecal pellets two weeks after the last administration. Fecal microbiota was then characterized by 16S rRNA gene sequencing targeting V4 region. For microbial diversity, the operational taxonomic units (OTUs) underwent taxonomic analyses with the Bayesian classifier. Principle component analyses (PCA) were then employed to visualize the data and species classification tree statistics. Linear discriminant analysis (LDA) of the effect size was used to detect the differences in bacteria species between two groups.

Results The results indicated that no significant difference in alpha diversity of fecal microbial in two groups was observed, whereas principal component analysis (PCA) illustrated a structural segregation between two groups. At phylum level, the most abundant was Bacteroidetes in high-salt group (58.4%) and Firmicutes in control group (48.0%). Further analysis using LEfSe according to the criteria of LDA≥4 showed that the microbial alteration in rats administered by high-salt featured by the significant decrease of *Lactobacillus* and *Prevotella NK3B31*, and *Alloprevotella* and *Prevotella 9* were increased. However, no significantly difference were observed in body weight, the morphological changes, and blood pressure in two groups.

Conclusions As a pilot investigation to characterize the alteration of microbiota composition in high-salt intake rats, our study provide a foundation to improve our understanding of the role of microbiota in the pathogenesis of high-salt-associated diseases.

PO-358

Hypoxia-induced miR-191-C/EBPβ signaling regulates cell proliferation and apoptosis of fibroblast-like synoviocytes from patients with rheumatoid arthritis

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Objective Hypoxia plays an important role in the proliferation of rheumatoid arthritis fibroblast-like synoviocytes (RA-FLS), leading to pathology of RA. This study was conducted to evaluate hypoxia-induced-microRNAs (hypoxamiR) in RA-FLS and its role in the function of RA-FLS.
Methods RA-FLS were cultured under normoxic (21% O_2) or hypoxic (3% O_2) condition, followed by a microRNA (miRNA) array analysis. The upregulation of miR-191 by hypoxia was confirmed in RA-FLS and FLS from osteoarthritis (OA) patients by quantitative real-time polymerase chain reaction (RT-PCR). Transfection of miR-191 mimic and inhibitor was used to investigate the function of miR-191 in RA-FLS. The functional targets of miR-191 were predicted by bioinfomatics, and then validated by reporter gene assay.
Results A subset of miRNAs was identified to be induced by hypoxia including miR-191. The upregulation of miR-191 was found to be specific in hypoxic RA-FLS, compared to hypoxic OA-FLS. We observed that miR-191 in RA-FLS increased cellular proliferation via promoting G1/S transition of the cell cycle and suppressed cell apoptosis induced by cell starvation. Bioinformatical analysis and experimental assays identified CCAAT/enhancer binding protein β (C/EBPβ) as a target gene of miR-191 in RA-FLS. Enforced expression of C/EBPβ rescued the cellular phenotypes induced by miR-191. In addition, an inverse correlation between the C/EBPβ level and hypoxia stimulation was found in RA-FLS, and overexpression of C/EBPβ could partly rescue the hypoxia-induced cell proliferation.
Conclusions We demonstrated the miR-191-C/EBPβ signaling pathway mediating the hypoxia-induced cell proliferation in RA.

PO-359

The role of long non-coding RNA in ototoxicity induced by cisplatin

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Objective Ototoxicity is the most common side effect in clinical chemotherapy of tumor, which seriously affects the application and effectiveness of chemotherapy drugs. Due to the unclear pathogenesis of ototoxicity, molecular markers which can monitor its occurrence and development are currently lacking in clinical practice. As an emerging and important regulatory molecule, long non-coding RNA (lncRNA) has been proved to

play an important role in the occurrence and development of a variety of diseases. This study will focus on the lncRNA that are differentially expressed and function in the process of ototoxicity caused by the chemotherapy drug cisplatin, and futhermore explore the possibility of using them as detection markers for the occurrence of clinical ototoxicity.

Methods 40 c57 mice were randomly divided into control group and experimental group, 20 mice/group. Mice in the control group and experimental group were intraperitoneally injected with PBS or cisplatin for 7 consecutive days. Cochlea tissues of the two groups of mice were isolated and total RNA was extracted, and then high-throughput sequencing was performed. The different expression of lncRNA between the two groups was analyzed and screened, and the lncRNA CORL was determined as the target molecule in this study. Then, the mouse hair cell precursor cell line HEI-OC1 was used, and the total RNA was extracted after the cells were treated with 20μM cisplatin for different times. The expression of lncRNA CORL was detected by q-PCR after reverse transcription into cDNA. SiRNA was designed for lncRNA CORL, and the one with the best interference effect was selected for cell transfection. NC siRNA was transfected into cells of the control group, and cisplatin was added for 48h after transfection. MTT and TUNEL were used to detect cell viability and apoptosis levels. Finally, the changes of caspase-3 in each group were detected by immunofluorescence staining.

Results (1) High-throughput sequencing showed that there were a large number of lncRNA molecules with different expressions between the control group and the experimental group. According to the correlation analysis of differentially expressed lncRNA and mRNA, a coding non-coding gene co-expression (CNC) network was constructed to screen and finally obtained 5 candidate lncRNA molecules. Through further in vitro verification, it was found that lncRNA CORL was significantly associated with the occurrence of ototoxicity. (2) q-PCR showed that cisplatin treatment increased the expression of lncRNA CORL in a time-dependent manner. Compared with the control group at 0h, the expression of lncRNA CORL increased gradually after 12h of cisplatin treatment and reached the maximum value at 48h. (3) Specific siRNA were designed for lncRNA CORL, and the transfection efficiency of siRNA was over 90% by exploring the transfection conditions. (4) After the transfection of the siRNA into cells, the lncRNA CORL expression was interfered by siRNA. Then MTT detection showed that cisplatin-induced ototoxicity was significantly weakened, with statistically significant differences ($p<0.05$). TUNEL assay also revealed that the number of tunel-positive apoptotic cells was significantly reduced after the expression of lncRNA CORL was disturbed, indicating that the cisplatin-induced apoptosis was significantly inhibited. (5) Immunofluorescence of cleved-caspase3 revealed that the activation of caspase3 in HEI-OC1 cells was significantly inhibited after siRNA interference, which further proved that interference of lncRNA CORL could effectively reduce cisplatin-induced ototoxicity.

Conclusions lncRNA CORL is involved in cisplatin-induced ototoxicity and plays an important role, which may be achieved by weakening the caspase-3 dependent mitochondrial apoptosis pathway. Further studies on lncRNA CORL in peripheral blood and other media will help reveal the possibility of lncRNA CORL as a marker for ototoxicity detection.

PO-360

Tegafur deteriorates established cardiovascular atherosclerosis in colon cancer: A case report

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Objective Cardiac toxic effect of tegafur (S-1) is extremely rare, and there has been no report on this issue so far.

Methods We herein report a typical case of single S-1 administration after radical operation for colon cancer. The patient had no background or medical history of acute coronary syndrome (ACS), and only aortic and coronary atherosclerosis was revealed by computed tomography (CT) before surgery. He complained of sternum pain during the fifth cycle of S-1 treatment.

Results Electrocardiogram (ECG) and serum cardiac marker cardiac troponin T (cTnT) strongly suggested ACS, which was possibly caused by S-1 cardiotoxicity.

Conclusions Monitoring protocols based on ECG, CT, and cTnT should be performed in real time to evaluate cardiac function during S-1 administration.

PO-361

Mechanism study of targeting IL-7R on the treatment of rheumatoid arthritis

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Objective Rheumatoid arthritis (RA) is an organ-specific autoimmune disease mainly involving joints. It manifestates intra-articular synovial inflammation and effusion, cell proliferation, granuloma formation, cartilage and bone damage, eventually leads to joint stiffness and loss of daily living. Autoimmune reaction are the central link in the pathogenesis of RA. Moreover, infection, endocrine, genetic and environmental factors increase the susceptibility to disease.

Methods This paper discussed the immunoregulatory mechanism of treatment of RA by blocking IL-7/IL-7R signal pathway. We analyzed the correlation of IL-7Ra gene rs6897932 polymorphism and disease susceptibility of RA population from Chinese Han by DNA sequencing, detected cytokine contents of IL-7, IFN-g, IL-17, TNF-a, IL-6, IL-1β, IL-21, IL-23 and MMP-13 in the blood of RA patients to analyse the correlation of content of IL-7 with other cytokines such as IFN-g, TNF-a and IL-1b. In addition, we used FACS method to study the distribution of IL-7Ra in the T cell subsets of the healthy controls and RA patients, and study the effect of IL-7 to the proliferation and differentiation of naive $CD4^+$ T cells. In vivo experiments, the CIA mouse model was

established by immunization of mice with collagenⅡ (CⅡ). The treatment group and the control group were given IL-7Ra antibody and its isotype antibody respectively after secondary immunization. We tested the concentration of cytokines in the culture supernatant of splenocytes and the pattern of T cell subsets distribution of two groups to clarify the mechanism of blocking IL-7/IL-7R pathway by IL-7R antibody to CIA.

Results The results show that there is no statistical significance of the relevance between IL-7Ra gene rs6897932 SNP and disease susceptibility in Han Chinese RA patients. C may be the dangerous gene in RA. The concentration of inflammatory cytokins in plasma from RA patients which IL-7Ra rs6897932 SNP is CC is significantly higher than those corresponding is TT or TC. The level of IL-7 and other inflammatory cytokines in plasma of RA patients are higher, compared with the healthy controls. According to our analysis, the content of IL-7 has a significant positive correlation with IFN-g, TNF-a and IL-1b, and IL-7 can promote the secretion of IFN-g and TNF-a. The results also show that IL-7Ra mostly expresses on the $CD4^+$T cells of PBMC from healthy controls and RA patients. The expression level of IL-7Ra in RA is significantly higher than that in healthy controls. In addition, IL-7 can promote the proliferation of naïve $CD4^+$ T cells and Th1 cell differentiation. In vivo experiments show that IL-7Ra antibody treatment can relieve the clinical symptoms of CIA. It not only can reduce the infiltration of inflammatory cells in joints and destruction of cartilage, but also inhibit the proliferation of CⅡ specific $CD4^+$ T cells. The mechanism of IL-7R antibody to alleviate CIA and reach immunomodulatory effects is reducing the number of Th1 and Th17 subsets, the secretion of inflammatory cytokins and decreasing expression of corresponding transcription factors.

Conclusions The results suggest that IL-7Ra gene rs6897932 SNP and concent of cytokines in RA plasma have obvious relevance. IL-7 can aggravate RA by promoting proliferation of naïve $CD4^+$ T cells through IL-7R, and promoting secretion of inflammatory cytokines. IL-7Ra antibody treatment can significantly improve the clinical symptoms of CIA mice, and reduce the infiltration of inflammatory cells and the destruction of cartilages. Our results indicate that IL-7Ra antibody has the potential development value for clinical treatment of RA.

PO-362

Value of New Plasma Coagulation and Fibrinolysis Biomarker in Patients with Cancer

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Objective To investigate the usefulness of the new plasma coagulation and fibrinolysis biomarkers－TM (Thrombomodulin), TAT (Thrombin -antithrombin complex), PIC (Plasmin alpha 2-plasmin inhibitor complex) and tPAI•C (Tissue plasminogen activator-plasminogen activator inhibitor-1 complex) for monitoring cancer patients with metastasis.

Methods A total of 138 cancer patients who didn’t take any anticoagulant drugs were enrolled, of which 88 patients had metastases. TM, TAT, PIC and tPAI•C were detected

by high sensitivity chemiluminescence immunoassay in all of these cancer patients. Meanwhile, 20 healthy volunteers were recruited for the verification of the reference interval of TM, TAT, tPAI•C and PIC. The correlation between the new plasma biomarkers and traditional biomarkers (APTT, PT, TT, FIB, FDP and D-dimer) were analyzed. Then, the new plasma coagulation and fibrinolysis biomarkers in cancer patients with metastasis and these without metastasis were compared. The receiver operator characteristic (ROC) curve was used to evaluate the performance of TAT, PIC, D-dimer and their combination in detection of cancer patients with metastasis.

Results the data of healthy volunteers were all within the reference range recommended by the TM, TAT, tPAI•C and PIC reagent specification. TAT and PIC in high level of D-dimer group were both significantly higher than these in normal level of D-dimer group ($P<0.01$, respectively). Meanwhile, both TAT and PIC were significantly positively correlated with D-dimer and FDP ($P<0.01$, respectively). TAT and PIC in cancer patients with metastasis were significantly higher than those without metastasis ($P<0.01$, respectively). ROC showed that AUC of PIC was 0.797 [0.721, 0.874]. When the cutoff value of PIC was 0.9945 μg/ml, the sensitivity 83.00% and specificity 68.00%. The AUC of TAT was 0.754 [0.670, 0.837]. When the cutoff value of TAT was 4.45 ng/ml, the sensitivity 65.90% and specificity76.00%. The AUC of D-dimer was 0.783 [0.697, 0.869]. When the cutoff value of D-D was 1.52 mg/L FEU, the sensitivity 86.40% and specificity 62.00%. The sensitivity of combination assay (either D-dimer elevation or PIC elevation) were 92.05%. Parallel test of the three markers (TAT, PIC and D-dimer) improved the sensitivity and NPV to 94.32% and 83.87%, respectively.

Conclusions Combining TAT, PIC with D-dimer could be useful surveillance biomarkers for cancer patients with metastasis.

PO-363

An abnormal elevation of serum CA72-4 due to taking King Ratsnake in health care individual

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Objective Serum CA72-4 has been widely used as tumor marker in clinical treatment. It has been reported that some food, drug or health promotion products such as ganoderma lucidum spore powder and colchicine can cause abnormal elevation of serum CA72-4 in different patients.

Methods In this case, a patient with abnormal elevation of serum CA72-4 level owing to having King Ratsnake was found in our laboratory.

Results However, it is observed that the CA72-4 level was not elevated in the drug contained the snake ingredients and in respiratory disease patients who drunk the drug made from snake.

Conclusions It is speculated that having King Ratsnake meat may affect the detection results of serum CA72-4 from this report, which also suggests that clinicians could think of the case reported in our case when they have similar problems.

PO-364

Small RNA sequencing reveals changes of exosomal miRNAs in pediatric acute lymphoblastic leukemia

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Objective Exosomal microRNAs (miRNAs) have attracted major interest as a biomarker to diagnosis the tumor process. However, little is known about the roles of exosomal miRNAs in pediatric acute lymphoblastic leukemia (ALL). The study herein aimed to identify exosomal miRNAs involved in ALL and their relative functions.
Methods Serum exosomal miRNA expression pattern in pediatric ALL patients and healthy donors was comprehensively analyzed by RNA-seq. Differently expressed miRNAs were verified by quantitative reverse transcription PCR (qRT-PCR). The effect of miRNAs on cell cycle was measured via flow cytometric.
Results 363 and 463 miRNAs were identified in the normal and ALL exosomes, respectively. Moreover, exosomal miR-370-3p, miR-493-3p, miR-432-5p and miR-409-3p were significantly downregulated in the ALL compared to those in healthy control. These downregulated miRNAs were mainly involved in function of cell cycle, immune, cell proliferation and adhesion, and pathways of MAPK, Wnt, and mTOR signaling. Expressed results of qRT-PCR were consistent with the sequencing data. Furthermore, miR-493-3p promoted Jurkat cell cycle arrest at G2/M.
Conclusions Our data revealed several potential exosomal miRNA biomarkers and associated function and pathway, collectively, will advance our understanding of exosomes biology in ALL and facilitate the development of exosomes-based diagnostics and therapeutics in ALL.

PO-365

Clinical value of serum isoform [-2] proprostate-specific antigen and its derivatives in predicting aggressive prostate cancer

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Objective To explore the clinical value of serum isoform [2] proprostate-specific antigen (p2PSA) and its derivatives % p2PSA and Prostate Health Index (PHI) in predicting aggressive prostate Cancer (PCa).
Methods The pre-operation serum and basic clinical data of 322 patients with PCa (including 143 patients diagnosed PCa by transrectal ultrasound-guided prostate biopsy and 179 patients undergoing radical prostatectomy) in Peking University first hospital were collected from August 2015 to May 2018. The prostate pathologic result was considered as the gold standard to evaluate Gleason score of the patients with PCa. Serum total PSA (tPSA), free PSA (fPSA) and f/tPSA and the p2PSA level of all these

patients were measured on DxI800 analyzers (Beckman Coulter), and then % p2PSA and PHI were calculated. The Receiver operator curves (ROC) were used to assess the ability of p2PSA, %p2PSA and PHI to predict aggressive PCa (pathologic Gleason score≥ 7) compared with those traditional markers tPSA, fPSA and f/tPSA.

Results Among these patients, the p2PSA, %p2PSA and PHI median levels were significantly higher in patients with pathologic Gleason score≥7 than those with Gleason score<7 (all p values<0.05). The proportion of patients with aggressive PCa increased with the PHI value. Among those patients diagnosed PCa by transrectal ultrasound-guided prostate biopsy, the area under curve (AUC) of p2PSA, %p2PSA and PHI (AUC=0.710, 0.744 and 0.798 respectively) in predicting Gleason score≥7 were higher than those of the traditional indicators tPSA, fPSA and f/tPSA (AUC=0.625, 0.507 and 0.697 respectively). Among those patients undergoing radical prostatectomy, p2PSA, %p2PSA and PHI also had higher predictive value. The AUC of p2PSA, %p2PSA and PHI were 0.751, 0.808 and 0.801 while the AUC for tPSA , fPSA and f/tPSA were 0.729, 0.655 and 0.665, respectively.

Conclusions Compared with currently available markers tPSA, fPSA and f/tPSA, p2PSA especially its derivatives %p2PSA and PHI had much higher predictive value for aggressive PCa, which may help clinicians to evaluate the therapeutic regime and make more appropriate management plan for patients.

PO-366

Contribution of Hepatitis B Virus in Primary intrahepatic cholangiocarcinoma in China: Experience from Chinese National Cancer Center

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Objective The relationship between HBV infection and Primary intrahepatic cholangiocarcinoma is still controversial. We aimed to understand the impact of HBV infection on ICC by retrospective analysis.

Methods A total of more than 14,000 patients with liver cancer who were treated at National Cancer Center/Cancer Hospital, Chinese Academy of Medical Sciences (NCC/CH-CICAMS) during January 1, 2000 and December 31, 2015 were enrolled. In some ICC cases, immunohistochemical expression of HBsAg and HBcAb were explored in cancer tissues and adjacent liver tissues.

Results Totally 339 histologically confirmed ICC patients in 16 years. Among the 339 ICC patients, single HBV infection, indicated by serum HBsAg(-)/(+)&anti-HBc(+), was found in 83 cases (24.48%), of them 139 (41.00%) was serum HBsAg(-)&anti-HBc(+), and 112 ICC patients (33.04%) were serum HBsAg(-)/anti-HBc(-)/HCV(-), and 6 patients did not detect infectious indicators. HBsAg and anti-HBc immunohistochemical staining were performed in cancer tissues and adjacent liver tissues in 32 ICC patients, 13 patients with serum HBsAg(+), and 17 with serum HBsAg(-)/anti-HBc (+).

In adjacent liver tissues, in 13 serum HBsAg(+) ICC patients, 8 with single HBsAg(+) Immunohistochemical expression results, 1 patient with HBsAg(+)/anti-HBc(+), and the remaining 4 weres HBsAg(-)/anti-HBc(-); In 17 serum HBsAg(-)/anti-HBc(+) ICC patients, only 1 had liver tissue HBsAg(+)/anti-HBc(+), and the remaining 16 liver tissues were HBsAg(-)/anti -HBc(-). In biliary cancer tissues, HBsAg(-)/anti-HBc(-) Immunohistochemical express were found in all 13 serum HBsAg(+) ICC patients, and only one case of biliary tissue was HBsAg(+)/anti-HBc(-) in 17 serum HBsAg(-)/anti-HBc(+) ICC patients.

Conclusions Immunohistochemistry results showed that ICC patients have association with HBV infection to a certain degree. However, compared with HCC patients with HBsAg infection rate close to 80%, the association of HBV and ICC patients needs further confirmation.

PO-367

Evaluation of platelet indices as diagnostic biomarkers for colorectal cancer

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Objective This study aimed to evaluate the role of platelet indices as potential biomarkers for the diagnosis of colorectal cancer (CRC), and to assess the association between platelet indices and CRC clinicopathological characteristics.

Methods The study included 783 subjects with CRC, 462 subjects with colorectal adenomas (CA), and 462 control subjects from June 2015 to October 2017. All participants' clinicopathological characteristics were collected and analyzed. PC, MPV, PDW and PCT were measured routinely with Beckman Coulter LH 780 hematology analyzer (Beckman Coulter, Brea, CA, USA) according to the manufacturer's instructions. The serum levels of CEA and CA19-9 were determined by a Cobas 6000 Analyzer (Roche Diagnostics, Mannheim, Germany).

Results we found that PC, MPV and PCT levels in CRC patients were significantly higher than those in CA patients and healthy participants (p <0.001); however, PDW level in CRC patients was significantly higher than that in healthy participants while lower than that in CA patients. Receiver-operating characteristic (ROC) analysis indicated that combined detection of PCT and CEA appears to be a more effective marker to distinguish CRC patients from CA patients, with 72% sensitivity and 80% specificity. Among CRC patients, PC and PCT levels were associated with TNM stages and tumor size; MPV and PCT levels were associated with vascular invasion.

Conclusions Our findings suggest that altered PC, MPV and PCT levels might serve as potential biomarkers for the diagnosis and prognosis of CRC.

PO-368

A comparative study of Carba NP test in detection of different medium separation of carabapenemase-producing strains

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Objective To investigate the sensitivity and specificity of Carba NP test in detection of different medium separation of carbapenemase-producing strains, and to provide reference for clinical laboratory tests.
Methods 221 strains from clinical separation were served as object, this collection of strains included 58 Klebsiella pneumonia, 47 Escherichia coli, 58 Acinetobacter baumannii and 58 Pseudomonas aeruginosa, all strains were grown for 24h on the 6 kinds of medium, Carba NP test was conduct to be detect carbapenemase production.
Results The sensitivity of the Carba NP test was 93.58%、86.24%、82.57%、87.16%、77.98% of the strains recovered from blood agar, China Blue agar, MacConkey agar, MH agar and Nutrient agar, respectively. The sensitivity of the Carba NP test was 91.74% of the strains recovered from Nutrient agar supplemented with $ZnSO_4$.
Conclusions Accuracy and rapid of the Carba NP test when carbapenemase-producing strains were recovered on blood agar, the Carba NP test was not suitable to identify carbapenemase producers grown on China Blue agar, MacConkey agar, MH agar and Nutrient agar.

PO-369

Expression of miR-1269a in esophageal carcinoma and its effect on biological function of esophageal cancer cells and its mechanism

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Objective Accumulating evidence has indicated that miR-1269a exerts tumor promoter roles in several types of cancer. However, the expression pattern and roles of miR-1269a in esophageal cancer progression remain unknown. This study aimed to reveal the role of miR-1269a in esophageal cancercell proliferation and its potential mechanisms.
Methods 1 The expression levels of miR-1269a , SOX7 and SOX6 in esophageal carcinoma tissues were detected by Realtime PCR.
2 MTS , transwell mirgration and matrigel invasion chamber assays were used to detect the cell proliferetion, migration and invasion abilities of esophageal cancer cells with miR-1269a high-expression or low-expression , respectively.
3 The sequence of predicted miR-1269a binding site and the wild-type (Wt-SOX7) or mutant (Mut-SOX7) putative target site in the 3′-UTR of SOX7 mRNA sequence.

4 The expression level of SOX7 in esophageal carcinoma tissues were detected by immunohistochemical.
5 The expression levels of Wnt/β-catenin related proteins of esophageal cancer cells were detected by Western blot.
6 Method of application of nude mouse transplantation tumor were performed to detect proliferation of esophageal cancer cells with miR-1269a high-expression in vivo.
Results 1 Realtime PCR demonstrated that the expression levels of miR-1269a in esophageal carcinoma tissues were higher than those in normal esophageal epithelial tissues and adjacent normal esophageal tissues.The immunohistochemical assay showed that the expression levels of SOX7 in esophageal carcinoma tissues were lower .
2 The high expression of miR-1269a promoted cancer cell proliferation,invasion and migration,compared with the control group.
3 Dual luciferase reporter assays in HEK293T cells revealed that miR-1296a over-expression significantly attenuated activity with the wild-type SOX7 luciferase reporter but failed to reduce mutant SOX7 luciferase activity.
4 Western blot demonstrated that the expression level of β-catenin, cyclin D1 and c-Myc protein were higher and phosphorylation of β-catenin with were lower with miR-1269a over-expression. The expression level of β-catenin, cyclin D1 and c-Myc protein were lower and phosphorylation of β-catenin with were lower with miR-1269a low-expression. Western blot demonstrated that the expression level of β-catenin, cyclin D1 and c-Myc protein were lower and phosphorylation of β-catenin with were higher miR-1269a over-expression associated with SOX7 over-expression than miR-1269a over-expression.
5. The experimental results shower that the nude mouse transplantation tumor suppressed product and weight significantly after increasing miR- 1269a , compared with control.
Conclusions Expression level of miR-1269a in esophageal carcinoma tissues is significantiy increased. miR-1269a could promote the proliferetion of esophageal cancer cells in vitro and in vivo. miR-1269a could promote the migration and invasion abilities of esophageal cancer cells in vitro. miR-1269a stimulates the Wnt/β-catenin pathway by targeting SOX7.

PO-370

Relationship between serum sulfatides and platelet aggregation function in rabbits during high-fat diet

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Objective Atherosclerosis is one of the most widespread conditions that seriously threaten human health and survival in today's society. Hyperlipidemia is a major risk factor for AS. Therefore, attention should be paid to the study and prevention of hyperlipidemia and AS. Studies have shown that platelets play an important role in the pathogenesis of AS. The activation and aggregation of platelets promote the development of AS, which is closely related to the occurrence of cardiovascular events in the future. Sulfatides, as a kind of glycosphingolipid,

are present in serum as lipoproteins. Studies have shown that sulfatides have a dual effect of anti-coagulation and promotion of coagulation activity, they are found accumulated in the plaque of atherosclerosis. In view of this, the aim of this study is to explore the changes of sulfatides and platelet aggregation function as well as the relationship and the possible role between them in the process of atherogenesis induced by hyperlipidemia, so as to seek a new way to monitor or interfere with the process of atherosclerotic cardiovascular disease.

Methods Ten healthy male New Zealand rabbits were randomly divided into two groups with each group containing 5 rabbits. Control group was offered continued normal diet, while model group a high-fat diet containing 0.5% cholesterol and 5% lard. The food intake was limited to 150g/d for each rabbit. The body weight, serum lipids and sulfatides levels as well as platelet aggregation function were measured at the end of the first, second, third and fourth month after treatment and before treatment in both groups. Four months later, the carotid artery was measured by ultrasound and then the animals were sacrificed. The rabbit aorta was collected and pathological slices were made and stained. The results were observed under a microscope.

Results The hyperlipidemia and atherosclerosis model were established successfully. Model group had greatly increased serum total cholesterol(TC), low-density lipoprotein cholesterol(LDL-C) and high-density lipoprotein cholesterol(HDL-C) compared with control group. Hematoxylin and eosin (HE) staining showed that the aortic intima was significantly thickened in the model group, filled with foam cells, and the vessel lumen was significantly narrowed. The frozen section of aorta with oil red O staining also showed marked accumulation of adipose tissue inside the arterial wall in model group. Ultrasound imaging showed that the wall of the carotid artery was rough in the model group, hyperechoic plaques were presented and the blood flow is filling detect. Platelet aggregation rates in model group showed the trend of first increasing and then decreasing with the extension of feeding time. Platelet aggregation rates were significantly higher than those before modeled. The level of serum sulfatides continued to increase with the prolongation of time in model group. There was a significantly negative correlation between the level of serum sulfatides and platelet aggregation function in model group. There was a significantly positive correlation between the levels of serum sulfatides and LDL-C in model group.

Conclusions In the process of gradual development of hyperlipidemia into atherosclerosis, the change of serum sulfatides may reflect the process of atherosclerosis to a certain extent and sulfatides may be expected to a novel predictive factor for future cardiovascular events. In the course of this process, the high reactivity of platelets significantly decreased, suggesting that gradual increase of the level of sulfatides may inhibit the platelet aggregation function to some extent.

PO-371

The value of combined detection of anti cycliccitrullinated peptide antibody and rheumatoid factor in early diagnosis of rheumatoid arthritis

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Laboratory

Objective To investigate the clinical value of anti cycliccitrullinated peptide (CCP) antibody and rheumatoid factor (RF) in the diagnosis of rheumatoid arthritis (RA).
Methods 117 patients with rheumatoid arthritis (RA) were selected as the control group, and the other patients with autoimmune diseases (n = 86) and normal healthy subjects were selected as control group (n = 120). The anti - CCP and rheumatoid factor were detected by immune turbidimetry.
Results RA group of anti CCP and RF positive rates were higher than those of autoimmune group and healthy control group (P < 0.05). The immune group of anti CCP antibodies and the positive rate of RF was higher than that of the control group (P < 0.05). The positive rate of combined detection of two in the RA group was significantly higher than the other two groups (P < 0.05), anti CCP antibody sensitivity was 78.4%, specificity was 95.6%, the sensitivity of RA was 82.1%, the specificity was 82.5%; the two combined detection, the sensitivity was 78.6%, specificity was 97.6%.
Conclusions RF combined with anti -CCP antibody is helpful to improve the positive rate of RA detection, and has important clinical significance for early diagnosis of RA.

PO-372

Relationship between serum Homocysteine, Cystatin C levels and blood pressure types in elderly patients with essential hypertension

LiNa Wang
Cardiology

Objective To study the correlation of Homocysteine,serum Cystain C and blood pressure type in aged patient with essential hypertension.
Methods 381 aged patients with essential hypertension were collected from geriatrics department. According to the results of ambulatory blood pressure monitoring, the patients were divided into three groups: dipper group (n = 113) ,non-dipper group (n = 172) ,reverse dipper group (n=96). All biochemical items were examined, body mass index was calculated, and the results of ambulatory blood pressure monitoring and biochemical tests were analyzed.

Results The levels of Hcy were significantly different among the three groups (P=0.000), reverse dipper group (31.14 ± 14.73 μmol / L), dipper group (21.91 ± 9.52 μmol / L), non-dipper group (24.17 ± 10.46 μmol / L). The levels of serum Cystatin C were reverse dipper group (1.19 ± 0.31 mg / L), dipper group (0.90 ± 0.25 mg / L) and non-dipper group (1.12 ± 0.27 mg / L). There was statistical significance (P =0.028).To compared with the dipper group, Hcy (OR1.520 , 95%CI 1.297-1.834,P=0.005) and Cys-C (OR1.852, 95%CI 1.139-2.702,P=0.010) were influence factors of reverse-dipping hypertension. In addition, the decline rate of night SBP and DBP was negatively correlated with the level of Hcy (r= -0.277、-0.215, P=0.001、0.009), the Cys-C level was negatively correlated with the decline rate of night SBP and DBP (r= -0.249、-0.189, P=0.002、0.012).

Conclusions The levels of Hcyand Cys-C were higher in elderly patients with reverse-dipping hypertension than those with dipping hypertension.The detection of Hcy and Cys-C levels has predictive value for the risk of hypertension in the elderly.

PO-373

Establishment of maternal high microbial load - offspring asthma model

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Objective

In recent years, the incidence of asthma and other allergic diseases has increased significantly, and has become one of the major diseases affecting human health. Currently, 22% ~ 25% of the global population (about 200 million in China) suffer from allergic diseases, among which children account for the largest number. Although genetic susceptibility is one of the reasons for the increase in asthma, given the rapid increase in its incidence, environmental changes clearly play a role. Many studies have found that environmental microbial load plays a key role in asthma prevention. Although the prophylactic and protective effects of microbial rich environments in early life on childhood asthma have been widely confirmed in cohort studies and are expected to be a feasible method to reduce the incidence of asthma, in-depth studies on the molecular immune mechanism and safety in animal experiments are still lacking. Therefore, the establishment of a safe and stable animal model is the key to the research.

Methods Model establishment method 11 weeks SPF Balb/c mice were divided into 6 groups: control group, Bifidobacterium Tablets group, Bacterial Lysates (BL) high concentration group, BL medium concentration group, BL low concentration group and high fibre diet group, assessed by the preliminary experiment index of mice weight, serum levels of cytokines and spleen Tregs cells number, choose a BL high concentration group and the control group as a follow-up experiment model is established in this paper. The two groups of female mice began to be intragastric10 days before mating until delivery. Weaning on the 21st day after delivery. The offspring of all BL mice were sensitized and attacked with ovalbumin (OVA) (n = 6).

The offspring of the control group were divided into two groups: OVA sensitization and aggression (n =6), PBS sensitization and stimulation (n =6). Intraperitoneal injection of 20 μg OVA and 0.4mg aluminum hydroxide dissolved in 0.2ml PBS at 25, 32 and 39 days after birth sensitized each mouse (asthma group). The offspring were atomized with 1% OVA (level II) for 30 minutes per day on 46-53 days after birth (asthma group). The control group was replaced with PBS instead of OVA. Blood, lung, and bronchoalveolar lavage (BALF) were obtained 24 hours after the last attack. Hematoxylin and eosin (H&E) staining, cell count and cell classification in BALF were detected. Th1 and Th2 related genes and cytokines in plasma and BALF were detected byRTt-PCR and ELISA.

Results 1. There was no difference in maternal body weight, birth rate and death rate, and growth curve of offspring between the BL high concentration group and control group, while Tregs count of spleen cells was significantly higher than that of the control group.

2. Mother high microbial load reduce offspring's characteristics of asthma: the mother control –offspring asthma model group show the airways mucosal thickening of basement membrane, mucous membrane of inflammatory cell infiltration, goblet cells increased, the cell count in the BALF increased and eosinophil percentage increase, OVA in BALF and plasma specific IgE concentration increased. When the mother took the bacterial lysate orally, the above characteristics of asthma were significantly reduced, and the inflammation score was reduced.

3. The imbalance of Th1 /Th2 cell axis in the offspring of the mother mouse under high microbial load was reduced: IL-4, and IL-5 in plasma and BALF were decreased, and the concentration of Th1 cytokinesIFN-γ cytokines was increased.

Conclusions A safe, stable and easy to popularize "mate-offspring asthma model with high microbial load" was established. The protective mechanism of asthma in offspring of maternal mice under high microbial load was related to the reduction of imbalance of Th1 /Th2 cell axis.

PO-374

Analysis on the Distribution of APOE Gene Polymorphism by gene chip technology and its relationship with Serum APOE and Lp (a) level

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Objective To analysis the distribution of APOE gene polymorphism in patients with cardiovascular and cerebrovascular diseases in our hospital, and investigate the relationship between APOE genotype and serum APOE, Lp (a) level

Methods Research the patients (n=3256) with cardiovascular and cerebrovascular diseases with APOE genotype which detected in our outpatient department and inpatient department from December 2017 to December 2018, collected and statistical analyzed these personal information, APOE genotype test results and serum APOE, Lp (a) test results. analysis of the distribution characteristics of different APOE genotype, and

its relationship with Serum APOE and Lp（a） level. chi-square test was used to analyze of different APOE genotype Variance analysis was used to analyze ApoE and Lp（a） levels in the persons with different genotype

Results There were a total 3256 objects be analyzed .2143 male patients, with the age range (60.7±12.5). 1113 female patients (34.2%), with the age range (63.4±11.8) . APOE genotype distribution were ε2/2 (0.74%), ε2/3 (11.64%), ε2/4 (1.47%), ε3/3 (69.53%), ε3/4 (15.73%), ε4/4 (0.89%).Genotype ε2/ε2、ε2/ε3、ε2/ε4、ε3/ε3、ε3/ε4 和 ε4/ε4 distribution in male and female patients were 0.51%、11.58%、1.25%、69.72%、16.06%、0.88% and 1.19%、11.75%、1.93%、69.15%、15.06%、0.92%. There was no significant difference in APOE gene distribution between different genders (P＞0.05). The serum APOE level in descending order were ε2/2（88.51）＞ε2/3（42.98）＞ε2/4（41.72）＞ε3/3（32.34）＞ε3/4（29.75）＞ε4/4（27.81），The serum Lp（a） level increasing order were ε2/2（164.13）＜ε2/3（176.84）＜ε2/4（194.31）＜ε3/3（206.31）＜ε3/4（215.84）＜ε4/4（218.96）the difference is significant（P＜0．05）

Conclusions There was no significant difference in APOE gene distribution between different genders .There are significant correlated between APOE genotype and serum APOE.lp(a) level.

PO-375

Overexpression of AcrAB-TolC efflux pump and transcriptional activator gene ramA in third-generation cephalosporin resistant Enterobacter cloacae

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Purpose The rising level of antimicrobial resistance in E. cloacae has become a serious problem worldwide.
Among several antimicrobial resistance mechanisms, overexpression of multidrug efflux pumps and their
regulators have emerged as important mechanism in many pathogenic bacteria. However, the roles of
multidrug efflux pumps and regulators in E. Cloacae has not been studied much yet. In this study, we
investigated the relationship between multidrug efflux pump systems and antimicrobial resistance in
Multidrug resistant (MDR) E. cloacae clinically isolated from a korean tertiary hospital.

Method From January 2017 to December 2018, we collected non-duplicated 69 MDR E. cloacae from a university hospital in Korea. We extracted RNA from all isolates, and made complementary DNA. To measure expression level of multidrug efflux pump and their regulator genes, including acrA, acrB, ampC, ompD, ompF, oqx B, cusA, ramA, eefB, robA,

soxS, we performed real-time PCR using rpoB as a reference gene. We compared the results of genetic test with those of antibiotic susceptibility test.
Result MDR E. cloacae showed resistance to average 4.6 antibiotic reagents. Among antibiotic reagents,
Cefotaxime, Aztreonam, and Ceftazidime were observed with the highest frequency, 99%, 94%, and 84%,
respectively. Relative expression levels of acrB, ompD, ompF and ramA genes in MDR isolates were more
10-fold than those in standard E. cloacae strain. Especially, we found significant association between the
increased expression of ramA and Ceftazidime, acrB and Ceftazidime. Also, ramA showed close relation to piperacillin/tazobactam resistance with Odds ratio 8.4.
Conclusion We demonstrated that clinically isolated MDR E. cloacae are mainly resistant to third-generation
cephalosporins and monobactam. We also found relative overexpression of multidrug efflux pump acrB gene and their regulator ramA gene in Ceftazidime resistant starains. In conclusion, increasing expression level of transcription activator RamA and multidrug efflux pump AcrAB play major role in MDR E. cloacae.

PO-376

Implementation of rapid liquid chromatography-tandem mass spectrometry assays to determine plasma atorvastatin and rosuvastatin concentrations

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Purpose The aim of this study was to implement and validate the analytical performance of rapid liquid chromatography-tandem mass spectrometry (LC-MS/MS) assays to determine plasma atorvastatin (AT) and rosuvastatin (RST) concentrations for the pharmacokinetic study in Korean population.

Method We developed two LC-MS/MS methods based on the analysis of 10 ㎕ of buffered human plasma with atorvastatin-d5 (1 μg/mL in 50% acetonitrile) and with rosuvastatin-d6 (5 ng/mL in 50% methanol) as internal standards (IS). Sample preparation of the both assays were based on liquid-liquid extraction with tert-butyl methyl ether (MTBE), and followed by drying, reconstitution, and followed by LC-MS/MS analysis in electrospray ionization positive mode. Mass spectrometry was performed in multiple reaction monitoring mode. Linearity, lower limit of quantitation, accuracy, imprecision, sample stability, carry over, and matrix effect were evaluated for the performance validation of the method.
Result The separation of all compounds was achieved in less than 5 min. The LC-MS/MS method for atorvastatin (AT) and rosuvastatin (RST) showed a good linearity (R2=0.9999)

from 0.5 to 20.0 ng/mL and from 0.75 to 15.0 ng/mL, respectively. The lower limit of quantitation (LLOQ) were 0.050 ng/mL for all the analytes. Intra- and inter-run mean percent accuracy were within 94.7 - 103.1 % and percent imprecision was ≤6%. Stability studies after preparation revealed that all the analytes were stable on 4 ℃ auto-sampler (at 30 and 75 h for AT, and at 24 and 48 h for RST), and also stable at each end of three times freeze and thaw cycles. Carry-over was found to be less than 0.04 % for all the analytes. Ion suppression or enhancement were not observed in blank and 6 patient samples.

Conclusion. The implemented LC-MS/MS assays to determine atorvastatin and rosuvastatin concentrations in human plasma showed a good accuracy, precision, sensitivity and linearity. The LC-MS/MS assays could be used in various clinical pharmacokinetic studies for atorvastatin and rosuvastatin.

PO-377

Evaluation of Analytical Performance of the IgG subclass 4 assay using the Optilite

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Purpose: The Increased concentration of immunoglobulin G subclass 4 (IgG4) is one of important markers for the diagnosis of autoimmune pancreatitis and other IgG4-related diseases including sclerosing cholangitis, Mikulicz disease, and so on. The aim of our study was to evaluate the analytical performance of the IgG4 assay using Optilite® (The Binding Site Ltd., Birmingham, UK), a turbidimetric immunoassay analyzer.

Methods: According to the Clinical Laboratory Standards Institute (CLSI) guidelines, its precision, linearity, and comparison to SPAPLUSTM (The Binding Site Ltd.). Carryover was assessed by two different specimens. Statistical analyses were performed. Statistical analyses were performed Excel 2016 (Microsoft Co., Redmond, WA, USA).

Results: The coefficients of variation for within-run and within laboratory precision were less than 6.5% at two levels (27.2 and 162.3 mg/dL). In the range of 6.0-263.8 mg/dL, the coefficient of determination (R2) was 0.998. The relationship between the expected value and the measured value was described by the following linear regression equation (y = 0.9716x - 0.7644). Carryover between high level (204.7 mg/dL) and low level (8.5 mg/dL) was -0.15%. In the range of 5.1-314.0 mg/dL, the results of Optilite® were good agreement with those of SPAPLUSTM. The coefficient of determination (R2) was 0.9838.

Conclusions: The IgG4 assay on the Optilite® showed excellent precision, linearity, and good correlation with SPAPLUSTM. Therefore, its analytical performance is satisfactory for diagnosis various IgG4-related diseases.

PO-378

Evaluation of Exdia TRF Plus in vitro diagnostic medical devices for βhCG

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Purpose: Human chorionic gonadotropin (hCG) is a glycoprotein hormone secreted by the placenta developed after fertilization. It is composed of alpha and beta regions. In healthy non-pregnant healthy individuals, the value is below 5 mIU/ mL. However, during normal periods of pregnancy, βhCG in the serum becomes approximately 50 mIU/ mL after implantation, with increasing levels during pregnancy and lower levels during the remaining reproductive period. During pregnancy, if a non-ideally low or sudden decrease is seen, it can be extrauterine pregnancy or sudden spontaneous abortion. The recently launched Exdia βhCG is based on the Europium fluorescence-based immunoassay to detect βhCG in human blood. In this study, the performance and efficacy of Exdia TRF Plus in vitro diagnostic medical devices for βhCG (Exdia βhCG) were evaluated by comparing the measured values of Exdia TRF Plus with those of Abbott Architect i2000 (Abbott Laboratories, Chicago, United States).

Method: For method comparison, according to the CLSI guidelines EP9A, serum samples requested for serum βhCG were collected and stored until analysis. Analysis between two instruments were measured dupilicate within 2 hours. Diagnostic sensitivity, specificity, positive and negative predictive value were also calculated. MedCalc version 15.0 (MedCalc Software, Ostend, Belgium) was used for statistical analysis.

Results: A total of 121 samples were analyzed. The slope, intercept and correlation coefficient were 1.009 (CI, -0.968~ 1.040), 0.516 (CI: -0.311 ~ 1/334) and 0.978 (95% CI, 0.969 ~ 0.985), respectively. According the Bland-Altman analysis, most of the results were within 95% CI of limits of agreement. Analytical sensitivity, specificity, positive predictive value and negative predictive value were 98.7% (95% CI: 96.1 ~ 99.7%), 91.3% (95% CI: 79.2 ~ 97.6%), 83.0% (95% CI: 77.9 ~ 87.2%, and 98.2% (95% CI: 95.6 ~ 99.3%), respectively.

Conclusion: Exdia βhCG showed excellent correlation with Abbot Architect i2000 and general performance was excellent in clinical use. In addition, it is capable of processing small amounts of specimen immediately. Therefore, Exdia βhCG could be very useful for the diagnosis, treatment, and monitoring.

PO-379

Current status of perioperative transfusion in orthopedic surgery in a local hospital of South Korea

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Purpose: Patient blood management has been recognized as an essential approach for the optimization of patient care when transfusion is in need. Orthopedic surgery such as total hip replacement often requires perioperative blood transfusion due to extensive blood loss during surgery. Numerous efforts has been made to reduce perioperative blood transfusion since it is often associated with an increased risk of perioperative morbidity such as lung injury, renal failure, hemolysis, and transfusion reaction, and besides mortality.

Method: This retrospective observational study assessed the data obtained from 114 patients between January 2017 and December 2018 at the Kyungpook National University Hospital. The Data were retrospectively collected from the medical records, and the following parameters were reviewed: age, gender, preoperative hemoglobin, postoperative hemoglobin, length of hospital stay, and amount of transfused red blood cells in the perioperative period.

Result: The cohort was divided to two groups; those with preoperative hemoglobin over 11.5 and those with preoperative hemoglobin below 11.5. The former group included 89 patients and the latter group included 25 patients.

The mean preoperative hemoglobin for the former group was 13.1 g/dL and the mean preoperative hemoglobin for the latter group was 10.4 g/dL. The mean amount of transfused red blood cells was 1.4 pint for those with preoperative hemoglobin below 11.5 and 0.0 pint for those with preoperative hemoglobin over 11.5.

Conclusion:

Patients with preoperative anemia can benefit from patient blood management approach such as usage of epoietin alpha, iron supplementation, and preoperative autologous donation of blood.

Our data suggest that screening patients with anemia and correcting the anemia before orthopedic surgery can help avoid unnecessary perioperative transfusion and resource utilization related to transfusion.

PO-380

Real-world performance of HIV-1/2 Ab immunochromatographic assay as an additive test for the positive HIV screen tests

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Purpose: HIV antibody immunoassays have a high sensitivity, but frequent false positive tests are also a limiting factor in medical judgement. New test algorithms suggested HIV Ag/Ab assay followed by HIV-1/2 differentiation immunoassay alternative to Western blot (WB). We tried to find out whether additional immunochromatographic assay (ICA) is clinically helpful in a medical setting using 4th generation HIV-1/2 Ag/Ab assays with WB confirmation.
Method: All samples submitted for HIV Ab screening were tested using HIV-1/2 Ag/Ab electrochemiluminescence immunoassay (ECLIA); Elecsys HIV combi PT (Roche Diagnostic). From Jan, 2011 to Dec, 2018, 426 sera were positive on ECLIA. All of them were re-tested with an ICA kit; SD Bioline HIV1/2 3.0 ICA (Alere Inc.) and then requested WB confirmation according to the national policy.
Result: Sixty-six ECLIA positive samples (66/401, 16.4%) showed positive results on ICA and 97.0% (64/66) of them confirmed positive on WB. Two samples (2/66, 3.0%) were false positive on ICA comparing final WB results. ICA showed negative results in 83.5% (335/401) of ELCIA positive samples and 98.5% of them (330/335) were negative on WB. Five specimens (1.5%) from patients with symptoms compatible to acute HIV syndrome were falsely negative on ICA with positive p24 antigen and indeterminate WB results at their initial specimens.
Conclusion: ICA followed by 4th generation HIV immunoassay was helpful for earlier medical decision for frequent false positive screening. But, ICA might be falsely negative in patients suspicious of acute HIV syndrome necessitating more sensitive p24 Ag or nucleic acid tests.

Published Only

PU-001

Circular RNA circ_0002138 is down-regulated and suppresses cell proliferation in colorectal cancer

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Objective Circular RNAs (circRNAs) have been recently identified as widespread and diverse endogenous noncoding RNAs that may harbor vital functions in humans. However, the role of circRNAs in the process of tumorigenesis and development of colorectal cancer (CRC) remains hitherto vague. The goal of the present study is to explore the role of circ_0002138 in progression of CRC and its diagnostic values.
Methods The quantitative real-time polymerase chain reaction (qRT-PCR) was used to investigate the expression level of circ_0002138 in 35 paired CRC tissues. Fisher's exact test was further conducted to analyze the relationship between circ_0002138 expression level and clinicopathological factors of CRC patients. A receiver operating characteristic (ROC) curve was applied to evaluate the diagnostic value of circ_0002138. Functional involvement of circ_0002138 in proliferation of the two CRC cells were evaluated in vitro.

Results The results showed circ_0002138 was stably down-regulated in CRC tissues compared to paired adjacent normal tissues ($P < 0.001$). Circ_0002138 expression was significantly correlated with age. The area under the ROC curve was 0.7249. Additionally, functional analysis demonstrated that circ_0002138 significantly inhibited CRC cell proliferation *in vitro*.
Conclusions Overall, our data suggest that circ_0002138 may become a novel potential biomarker for diagnosis and treatment target of CRC.

PU-002

International Society for Laboratory Hematology initiatives to support continuing education and promote best practices worldwide through educational workshops and web-based educational resources

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Objective The International Society for Laboratory Hematology (ISLH) is an international society that is dedicated to supporting the laboratory hematology community worldwide and has laboratory professional members from 73 countries. The

field has benefited from the continuous development of newer technologies and methodologies in the field of hematology laboratory, and this has made it important for ISLH to support education and ongoing learning initiatives to support best laboratory practices and quality improvement. In 2015, ISLH initiated a program of educational workshop and web-based educational resources that cover the spectrum of laboratory hematology fields to better meet the needs of laboratory hematology professionals, including trainees, and foster the uptake of learning from the educational workshop at the ISLH annual scientific meeting. ISLH also developed an International mentorship program, an international networking and collaboration program, and began offering its latest webinar and e-learning materials to the worldwide community "free-of-charge" to further support global education and practice updates.

Methods Since 2015, ISLH has continued to offer a full day, pre-meeting educational workshop before its annual meeting, with 8-10 world renowned experts covering a wide variety of important subjects in laboratory hematology. ISLH also launched a program of web-based educational resources to laboratory professionals, which include a new webinar on a monthly basis, live and archived (on the website), e-courses by experts in various disciplines, and interactive educational e-cases in hematology selected from laboratory professionals worldwide. To evaluate this program, we assessed the educational contributions and accomplishments of the workshops and web-based educational resources for the period between 2015 and 2018, including how many individuals have accessed these materials around the globe.

Results The ISLH annual pre-meeting educational workshops aim to provide up-to-date knowledge and technical advancements on broad topics and guidelines, and support and promote best practices in laboratory hematology professionals including trainees in both developing and developed countries. The four pre-meeting educational workshops (with restricted enrollment) brought an average 128 attendees per each workshop. The webinar series that followed, with unrestricted, free-registration, covered the laboratory perspectives for assessment and diagnosis of benign and malignant hematologic disorders, blood cell and bone marrow morphology, coagulation/thrombotic disorders, platelet disorders, hemoglobinopathies, flow cytometry, molecular genetic testing, evidence-based practice, standards, quality and guidelines relevant to hematology laboratories. A total 24 live webinars have been presented by worldwide hematology experts. Each has included a live session, with opportunities to take questions and provide answers at the end of webinar, and additional questions and answers posted with the webinar on the website. The total number of visits to view ISLH webinars has grown continuously, reaching 43,064 visits by November, 2018. Each live webinar has averaged 215 participants (range 104-432), and the archived webinars have had an average of 400 participants (range 129-1,824) by November, 2018. A survey of webinar's participants, conducted in February and March, 2018, yielded interesting results. Participants of live webinars have had approximately 2.6-fold more non-ISLH members than ISLH members, and were from 25 countries. Web-based e-courses, which have provided basic and advanced courses for various subjects, each requiring about 1-2 hours for completion, have continued to be developed to offer new topics. Each e-course has average 563 participants (range 152-873) by November, 2018. E-courses offered to date have covered topics such as basic bone marrow pathology-related courses, and more advanced topics related to acute myeloid leukemia, lymphoma involvement of the bone marrow, coagulation factor inhibitor assays and

hemoglobinopathy investigations. Interactive, web-based, e-cases (16 cases by November 2018) have been developed by hematology professionals and trainees worldwide to cover educational topics and very rare interesting cases, typically covering both clinical and laboratory findings, morphological/histological findings with digital microscope slides, interactive questions and answers, diagnosis with discussion of the case and differential diagnosis, and references. Each e-case has averaged 260 visits (range 114-598) by November, 2018. International mentorship program has connected selected several hematology laboratory professionals from developing countries and hematology experts worldwide every year, developed and progressed training projects depending on proposal of mentees, and attend to present the project in annual ISLH meeting. The mentorship program resource information on the ISLH website has been popular, with 5,960 visits by November, 2018.

Conclusions ISLH has successfully extended its educational outreach with the launch of educational workshops, web-based webinar series, e-courses and interactive e-cases as well as an international mentorship program to provide a high quality of continuing education in both developing and developed countries worldwide. The ISLH web-based educational resources, including those provided with "free" access, have been very appreciated by hematology laboratory community, with continuing growth in the number of participants from both developed and developing countries around the world.

PU-003

NF-κB involved in the Decoy receptor 3 up-regulation in bacterial infection

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Objective To observe if LPS, LTA and zymosan can induce DcR3 expression in HUVEC and to study the related mechanism.

Methods The human umbilical vein endothelial cell (HUVEC) line was cultured in vitro. The expression of TLR2 and TLR4 on the surface of HUVEC was observed by flow cytometry. Under the stimulation with LPS, LTA and zymosan, the levels of DcR3 in supernatant were quantitated by ELSIA. Real time PCR and western blot were used to detect the DcR3 expression at mRNA and protein levels respectively. The expression of DcR3 in the supernatant and cells was detected by ELISA, real-time PCR and western blot in cells treated or untreated with P38 inhibitors and NF-κB inhibitors, respectively.

Results Both TLR2 and TLR4 expressed on the surface of HUVEC. The DcR3 level in the culture supernatant increased remarkably at 24h under the conditions of stimulating with LPS, LTA or zymosan at middle and higher doses ($P<0.05$), especially under the conditions of stimulating at a higher doses ($P<0.05$). The DcR3 level in the culture supernatant showed a little change at 12h stimulation, then increased remarkly at 24h after stimulation at a higher doses. The expression of DcR3 at mRNA and protein levels increased sharply with the increase in the concerntration and the prolonged stimulation time. The DcR3 level in cells and supernatants was inhibited by NF-kB inhibitors, but on effect was observed in P38 inhibitors.

Conclusions LPS, LTA and zymosan upregulated DcR3 expression of HUVEC line partly through NF-kB signal transduction pathway.

PU-004

Distribution of carbapenemases and efflux pump in carbapenems-resistance Acinetobacter baumannii

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Objective To study mechanism of carbopenems resistancein in Acinetobacter baumannii.
Methods 100 isolates of carbapenems-resistance in *Acinetobacter baumannii*(CRAB) were collected from clinical specimens. Agar dilution was conducted to determine the minimum inhibitory concentrations (MICs) to 15 kinds of antibiotic. Genes of carbapenemases and efflux pumps were amplified by PCR. The expression difference of pump genes was also analyzed by real-time PCR between CRAB and carbapenems- sensitive *Acinetobacter baumannii* (CSAB).
Results Most antibiotics, including aminoglycosides, fluoroquinolones and cephalosporins showed high MIC values in CRAB. While, all isolates were sensitive to polymyxin B. Among CRAB, 54, 32 and 16 isolates were positive for SHV-12, PER-1 and TEM-1, respectively. 86 isolates were positive for OXA-23. 55,4 and 33 isolates carried adeB, adeE and adeJ genes. The expression level of adeB in CRAB was ten times higher than that in CSAB.
Conclusions The resistance of Acinetobacter baumannii in our hospital is serious. Carbapenemases and efflux pumps play an important role in the carbopenems resistance. Moreover, isolates with single adeE gene were detected for the first time in *Acinetobacter baumannii*.

PU-005

The diagnostic value of anti-cmDNA combined with ANA and anti-dsDNA in systemic lupus erythematosus

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Objective This study was aimed to compare the diagnostic value of anti-cmDNA, ANA, and anti-dsDNA separately and assembly, and further evaluated the significance of combined detection of these markers in SLE.
Methods The current study was constructed at Department of Laboratory medicine, Zhongshan Hospital of Sun Yat-sen University. 101 patients with SLE, 94 patients with other rheumatic diseases and 78 healthy volunteers were recruited from September 2017 to December 2017. ANA was detected by indirect immunofluorescence assay. Anti-cmDNA and anti-dsDNA were both detected by enzyme linked immunosorbent assay(ELISA). Statistical analyses including receiver operating curves (ROCs) and chi-square($\chi 2$)test were applied in the study.
Results The positive percentage of anti-cmDNA was higher in the SLE group, with the percentage of 68%. While, the positive percentages of the other rheumatic disease

group and the healthy control group were 19% and 0%, respectively (P <0.05). When evaluating the diagnostic values of three mentioned antibodies separately, anti-cmDNA had the highest accuracy (82%), Youden's index(YI 0.58), and area under ROC curve(AUC 0.79) . While using combined makers, anti-dsDNA /anti-cmDNA, ANA+(anti-dsDNA/anti-cmDNA), anti-dsDNA/(ANA+anti-cmDNA), anti-cmDNA /(ANA+anti-dsDNA) and (ANA+anti-cmDNA)/(anti-dsDNA+anti-cmDNA)/(ANA+anti-dsDNA)all have the highest accuracy(84%), YI(0.65) and AUC(0.83).

Conclusions Anti-cmDNA was the vital marker for the diagnosis of SLE with higher accuracy compared with ANA and anti-dsDNA . Further, the combined detection of the three mentioned antibodies was crucial in the early diagnosis of SLE, resulting in improving both the disease prognosis and the patient's quality of life.

PU-006

Expression and significance of ILK, CD44v6 and EGFR in bladder cancer

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Objective To investigate the expression of ILK, CD44v6 and EGFR in bladder cancer and their roles in the occurrence and development of bladder cancer.

Methods The expression of ILK, CD44v6 and EGFR in 112 cases of bladder cancer and 35 cases of adjacent normal tissues were detected by S-P immunohistochemical method. The clinical significance of single and combined detection of ILK, CD44v6 and EGFR was studied.

Results The positive expression of ILK was 62.5% (70/112) in 112 cases of bladder cancer and 11.4% (4/35) in 35 cases of adjacent normal tissues. The expression rate of ILK in bladder cancer was significantly higher than that in adjacent normal tissues, and the expression of ILK was moderately positive in low-grade bladder cancer and strongly positive in high-grade bladder cancer (P < 0.05). The positive expression of CD44v6 was 26.8% (30/112) in 112 cases of bladder cancer and 77.1% (27/35) in 35 cases of adjacent normal tissues. The expression of CD44v6 was the strongest in normal bladder tissues, and the expression rate of CD44v6 decreased with the increase of malignancy of bladder tumors (P< 0.05). The positive expression of EGFR was 67.9% (76/112) in 112 cases of bladder cancer and 22.9% (8/35) in 35 cases of adjacent normal tissues. The expression of EGFR was moderately positive in low-grade bladder cancer and strongly positive in high-grade bladder cancer (P < 0.05). Compared with ILK, CD44v6, ILK, EGFR, ILK, CD44v6 and EGFR, the positive rate of combined ILK, CD44v6 and EGFR in bladder cancer patients was significantly higher (P < 0.05).

Conclusions ILK protein is overexpressed in bladder cancer, which is correlated with pathological grade, suggesting that ILK is involved in the occurrence and metastasis of bladder cancer and is closely related to its malignant degree. The expression of CD44v6 was negatively correlated with pathological grade. The lower the pathological grade of tumors, the stronger the expression of CD44v6. CD44v6 was strongly positive in basal cell layer of normal bladder mucosa, moderately positive in low grade bladder cancer and moderately positive in high grade bladder cancer. The positive expression

rate of EGFR increased with the pathological grade of bladder cancer. EGFR is closely related to the depth of invasion and differentiation of tumors. Overexpression of EGFR is related to the occurrence and development of tumors, and it is an effective reference index for the pathological stage of tumors. The positive rate of triple test in patients with bladder cancer increased significantly, which is helpful for clinical diagnosis.

PU-007

A serum piRNA signature as promising non-invasive diagnostic and prognostic biomarkers for colorectal cancer

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Objective Piwi-interacting RNAs (piRNAs) are a novel class of small non-coding RNAs, which are not easily degraded but detectable in human body fluids. Recent studies have shown that aberrant piRNA expression is a signature feature across multiple tumor types. However, the expressions of piRNAs in serum of tumor patients and their potential clinical values remain largely unclear.
Methods High-throughput sequencing was performed to investigate the serum piRNA profiles, followed by evaluations in serum samples of 220 colorectal cancer (CRC) patients and 220 healthy controls using reverse transcription quantitative real-time PCR (RT-qPCR). Biomarker panels including piRNA-based Panel I and carcinoembryonic antigen (CEA)-based Panel II, were developed by logistic regression model, and their diagnostic potentials were compared. Fagan's nomogram was plotted to promote clinical application.
Results We identified five differently expressed serum piRNAs (piR-001311, piR-004153, piR-017723, piR-017724 and piR-020365), which, when combined in the piRNA-based Panel I, outperformed the CEA-based Panel II ($P < 0.001$) and could detect CRC with an area under the receiver operating characteristic curve of 0.867. In addition, Kaplan-Meier analysis showed that patients with low serum piR-017724 level had worse overall survival (OS) and progression-free survival (PFS). In multivariate Cox regression analysis, serum piR-017724 was an independent prognostic factor for OS and PFS ($P < 0.05$).
Conclusions Our findings suggest serum piRNA expression signatures have potential for use as biomarkers for CRC detection and to predict prognosis at the time of diagnosis.

PU-008

CD83+CCR7+ NK cells induced by interleukin 18 promote experimental autoimmune uveitis

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Objective Uveitis, an inflammatory disease involving the uvea, retina, retinal vessels and/or vitreous body, can result in visual impairment and blindness. A disorder of the immune system represents an essential pathogenesis for autoimmunity uveitis. In specific, the large number of lymphocytes, including mature dendritic cells (DCs), T cells and natural killer (NK) cells infiltrating the eye may be a critical factor which drives this disorder of the immune system to result in tissue damage. Natural killer (NK) cells have been reported to play a pathological role in autoimmune uveitis. However, the underlying mechanisms of NK cells in uveitis remain unclear.

Methods Experimental autoimmune uveitis (EAU) mice were established by immunizing human interphotoreceptor retinoid-binding protein peptide (IRBP)1-20 and pertussis toxin (PTX) intraperitoneally. To analyze the role of $CD83^+CCR7^+$NK cells in EAU, $CD83^+CCR7^+$NK or $CD83^-CCR7^-$NK cells were isolated from the inflamed spleen on days 12-16 post-immunization by flow sorting instrument. These cells were then adoptively transferred into EAU mice that had been immunized 4 days prior. The cells from eyes, lymph nodes and spleens were analyzed by flow cytometry The severity of retinal tissue damage was assessed by H&E staining. DCs were isolated from spleens or ocular cells from EAU mice using a CD11c+isolation kit. For anti-IL-18R treatment, NK cells were isolated from the eyes of EAU mice and were pretreated with anti-IL-18R for 24h, and then were added to the DCs, T cells or combination of DCs and T cells

Results We found $CD83^+CCR7^+$ NK cells were increased within the eyes in the EAU mice. Both clinical and histopathological scores of eyes from mice receiving $CD83^+CCR7^+$ NK cell-transfers were greater higher than those of mice without cells transfer or those receiving $CD83^-CCR7^-$ NK cell-transfers. The number of lymphocyte subsets generated, including $CD4^+$IFN-γ^+ T cells, $CD4^+$IL-17^+ T cells, $CD4^+$GM-SCF^+ T cells, $CD11c^+$ MHC-II^+ DCs and $CD3^-$NK1.1^+ cells within the eyes of mice receiving $CD83^+CCR7^+$ NK cell-transfers were greater than that in mice without a $CD83^+CCR7^+$ NK cell transfer or those with a $CD83^-CCR7^-$ NK cell-transfer. Furthermore, we found $CD83^+CCR7^+$ NK cells promote maturation of DCs when $CD83^+CCR7^+$ NK cells co-cultured with immature DCs in vitro. Since it has been found that $CD83^+CCR7^+$NK cells could secrete IFN-γ to influence the statues of DCs, we used anti-IFN-γR antibody to block IFN-γR on DCs, then we found the expression levels of CD80, CD86 and CD54 in above DC were lower than non-blockage when co-cultured with $CD83^+CCR7^+$NK cells. As IL-18 has been reported to be an important factor involved in inducing subsets of $CD83^+CCR7^+$ NK cells, we examined IL-18 in this EAU model. IL-18, as well as IFN-γ, were significantly increased both in the aqueous humor of inflamed eyes and serum of EAU mice. When IL-18 Binding Protein (IL-18 BP) was injected into EAU mice to neutralize IL-18, the symptoms of EAU and percent of $CD83^+CCR7^+$NK cells within the eyes were decreased. Furthermore, we found Anti-IL-18R antibody treatment relieved EAU symptoms and decreasd NK cell infiltration within inflamed eyes.

Conclusions Our current data provide further evidence that the increasing CD3-NK.1.1+CD83+CCR7+cells in EAU play a pathological role in the development of EAU by promoting the activation of DCs and T cells. IL-18 is a cytokine that belongs to the IL-1 super-family and is an inflammatory factor in many diseases. However, the mechanisms of IL-18 as related to uveitis remain unknown. In our study, we now provide evidence indicating that IL-18 is a pathogenic factor in EAU and provide a description for some possible mechanisms of IL-18 in uveitis. IL-18 can induce NK cell activation to secrete IFN-γ and increase expression levels of CCR7, CD83, NKG2D and CD69 on NK cells. Thus, IL-18 has the capacity to promote NK cell activity and migration to inflammatory sites, where it may then function as a critical factor in EAU through induction of $CD83^{+}CCR7^{+}$ NK cells. IL-18 is mainly produced by macrophages, neutrophils and DCs. In our experiments, we found that macrophages, neutrophils and DCs were all increased in EAU and secreted IL-18. But macrophages and neutrophils were not primary increasing cells in inflamed eyes of EAU. DCs as an important pathogenic factor for EAU, might participate in producing IL-18 to promote pathogenic $CD83^{+}CCR7^{+}$NK cell activation in the eyes of EAU. And then, these NK cells migrate into lymph nodes to promote DC maturation and T-cell activation. Thus, IL-18 might play a key role in inducing the cycle of DC maturation and NK activation. An axis may exist between DC-NK interactions to regulate Th1 responses in this EAU model. Furthermore, anti-IL-18R antibody might serve as a possible therapeutic candidate for the treatment of autoimmune uveitis.

PU-009

Effect of Xihuang pill aqueous extract on MDA-MB-231 breast cancer cells

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Objective To study the effect of Xihuang pill aqueous extract on MDA-MB-231 breast cancer cells' function.
Methods The semi-inhibitory concentration (IC50) of Xihuang pill aqueous extract and cell viability were detected by CCK-8 assay. Cell apoptosis was detected by flow cytometry, cell migration was detected by Transwell assay, and cell proliferation was detected by clone formation assay. SPSS 16 software was used for statistical analysis. The difference was statistically significant with $p<0.05$.
Results The IC50 value of Xihuang Pill aqueous extract for 72 hours was 15.08mg/mL, and the cell viability decreased significantly ($p < 0.01$), the early apoptosis and late apoptosis increased significantly ($p<0.01$), and the cell migration and proliferation ability decreased significantly ($p<0.01$) after the treatment of Xihuang Pill aqueous extract for 72 hours, compared with untreated group.
Conclusions This study confirms that Xihuang pill has the ability of promoting cell apoptosis, inhibiting cell proliferation, migration and cell viability.

PU-010

Polymorphisms of gene cassette promoters of class 1 integron in clinical Proteus isolates

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Objective To describe the polymorphisms of gene cassette promoters of class 1 integron in clinical *Proteus* isolates and their relationship with antibiotic resistance.

Methods Polymorphisms of the gene cassette promoter in 153 strains of *Proteus* were analyzed by PCR and nucleotide sequencing. Variable regions of atypical class 1 integrons were detected by inverse PCR and nucleotide sequencing. Enterobacterial repetitive intergenic consensus (ERIC)-PCR was used to analyze the phylogenetic relations of class 1 integron-positive clinical *Proteus* isolates. Representative beta-lactamase genes(BLAs), including bla_{TEM}, bla_{SHV}, $bla_{CTX-M-1}$, $bla_{CTX-M-2}$, $bla_{CTX-M-8}$, $bla_{CTX-M-9}$, $bla_{CTX-M-25}$ and bla_{OXA-1}, and plasmid-mediated quinolone resistance (PMQR) genes including *qnrA, qnrB, qnrC, qnrD, qnrS, oqxA, oqxB, qepA* and *aac(6')-Ib* were also screened by using PCR and sequence analysis.

Results Fifteen different gene cassette arrays and 20 different gene cassettes were detected in integron-positive strains. Of them, *aadB-aadA2* (37/96) was the most popular gene cassette array. Two of these gene cassette arrays (*estX-psp-aadA2-cmlA1, estX-psp-aadA2-cmlA1-aadA1a-qacI-tnpA-sul3*) have not previously been reported. Three different Pc-P2 variants (PcS, PcW_{TGN-10}, PcH1) were detected among the 96 *Proteus* strains, with PcH1 being the most common (49/96). Strains carrying promoters PcS or PcW_{TGN-10} were more resistant to sulfamethoxazole, gentamicin and tobramycin than those carrying PcH1. Further, among 153 isolates, representative BLA genes were detected in 70 isolates (bla_{TEM-1}, 54; bla_{OXA-1}, 40; $bla_{CTX-M-3}$, 12; $bla_{CTX-M-14}$, 12; $bla_{CTX-M-65}$, 5; $bla_{CTX-M-15}$, 2) and representative PMQR genes were detected in 87 isolates (*qnrA*, 6; *qnrB*, 3; *qnrC*, 5; *qnrD*, 46; *qnrS*, 5; *oqxA*, 7; *aac(6')-Ib*, 13; *aac(6')-Ib-cr*, 32).

Conclusions To the best of our knowledge, this study provides the first evidence for polymorphisms of the class 1 integron variable promoter in clinical *Proteus* isolates which generally contain relatively strong promoters. Moreover, resistance genotypes showed a higher coincidence rate with the drug-resistant phenotype in strong-promoter-containing strains, resulting in an ability to confer strong resistance to antibiotics among host bacteria and a relatively weak ability to capture gene cassettes, and strains with relatively "weak" integron promoters can "afford" a heavier "extra-integron antibiotic resistance gene load". Furthermore, Gene cassettes *estX*, *psp* and gene cassette arrays *estX-psp-aadA2-cmlA1, estX-psp-aadA2-cmlA1-aadA1a-qacI-tnpA-sul3* have been confirmed for the first time in clinical *Proteus* isolates. BLAs and PMQR has been investigated, bla_{TEM-1} and bla_{OXA-30} were the most common, *qnrD* and *aac (6')-Ib-cr* were dominant also.

PU-011

Impact of subinhibitory concentrations of antibiotics on leucocidin ED gene transcription in Staphylococcus aureus strain Newman

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Objective The study aimed to assess the subinhibitory concentrations (sub-MICs) of commonly used antibiotics stimulation on the transcription of leucocidin ED gene (*lukED*) and *agr* regulatory RNA molecule RNAIII in *S. aureus* Newman strain *in vivo* and *in vitro*.

Methods *S. aureus* Newman was grown *in vitro* with sub-MICs (1/8, 1/4 and 1/2 MIC) of 11 antibiotics commonly used in clinic, and *lukE* and *RNAIII* mRNA levels were detected by relative quantitative RT-PCR (qRT-PCR). A mouse abscess model was produced to examine both genes expression *in vivo* following 6 representative drugs challenge.

Results For 3 h of treatment *in vitro*, vancomycin significantly improved *lukED* transcription from 1/8 MIC to 1/2 MIC, ranging from 2.54 to 2.77 folds the growth control level ($p=0.002$ at 1/8 MIC, $p=0.004$ at 1/4 MIC, $p=0.006$ at 1/2 MIC). Trimethoprim-sulfamethoxazole induced *lukED* mRNA production at 1/8 MIC (2.07 times, $p=0.026$) and 1/2 MIC (2.12 folds, $p=0.031$). Tigecycline only at 1/4 MIC enhanced the *lukED* transcription level 1.89-fold ($p=0.019$) higher than the no antibiotic control level. On the contrary, cefazolin dramatically reduced the expression of lukED (0.65 times, $p=0.037$) at 1/4 MIC. The remaining drugs, gentamicin, ciprofloxacin, erythromycin, clindamycin, linezolid, rifampicin and daptomycin, did not modify the expression of *lukED* at any of the sub-MICs tested.

After 5 h of exposure, 11 antibiotics all affected the *lukED* mRNA transcription. The treatment of vancomycin, trimethoprim-sulfamethoxazole, clindamycin, gentamicin or daptomycin significantly increased *lukED* expression levels compared to the no drug control at all sub-MICs studied. Ciprofloxacin had important effect on *lukED* transcript levels with remarkably increase at 1/8 MIC and 1/4 MIC, ranging from 1.46 ($p=0.034$) to 4.09-fold ($p<0.001$). The transcription levels of *lukED* were remarkably reduced by 3.92-fold ($p=0.003$), 5.10-fold ($p=0.001$), 15.38-fold ($p<0.001$), when exposed to 1/8 MIC, 1/4 MIC and 1/2 MIC of cefazolin. Newman strain showed reduced *lukED* expression in the presence of 1/4 MIC and 1/2 MIC of erythromycin (1.47-fold, $p=0.019$; 2.16-fold, $p=0.002$) and rifampicin (1.88-fold, $p=0.006$; 2.10-fold, $p=0.007$). The addition of 1/8 MIC (1.91-fold, $p=0.015$) and 1/4 MIC (2-fold, $p=0.020$) of linezolid and 1/4 MIC (2.71-fold, $p<0.001$) of tigecycline led to reduced levels of *lukED* transcript.

The expression of *RNAIII* had the same trend with *lukED* in some groups *in vitro*. When exposed to vancomycin, trimethoprim-sulfamethoxazole, clindamycin and rifampicin for 3

h and 5 h, the variation of *RNAIII* expression levels all had a consistent trend with that of *lukED* mRNA at all sub-MICs examined.
In murine model, clindamycin, daptomycin and linezolid had no effect on *lukED* mRNA transcription. However, the expression of *lukED* was strikingly inhibited by tigecycline (10.10 folds, $p<0.001$), and elevated by vancomycin (2.03 folds, $p=0.009$) and cefazolin (2.57 folds, $p=0.006$). For *RNAIII* gene, the transcription levels were remarkedly reduced by tigecycline by 5.37-fold ($p=0.004$), and increased by vancomycin and cefazolin to 5.58-fold ($p<0.001$) and 2.05-fold ($p=0.002$), respectively. Therefore, the *RNAIII* gene expression level had a great consistency with the *lukED* gene expression *in vivo*.
Conclusions Variations in *lukED* expression stimulated by exposure to subinhibitory antibiotics should be concerned, and these changes caused by some agents may be associated with regulator *agr* (RNAIII) activity.

PU-012

CD73 promotes hepatocellular carcinoma progression and metastasis via activating PI3K/AKT signaling by inducing Rap1-mediated membrane localization of P110β and predicts poor prognosis

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Objective Hepatocellular carcinoma (HCC) is one of the most prevalent malignancies worldwide because of rapid progression and high incidence of metastasis or recurrence. Accumulating evidences show that CD73-expressing tumor cell is implicated in development of several types of cancer. However, role of CD73 in HCC cell has not been systematically investigated and its underlying mechanism remains elusive.
Methods CD73 expression in HCC cell was determined by RT-PCR, western blot and immunohistochemistry staining. Clinical significance of CD73 was evaluated by Cox regression analysis. Cell counting kit-8 and colony formation assays were used for proliferation evaluation. Transwell assays were used for motility evaluations. Co-immunoprecipitation, cytosolic and plasma membrane fractionation separation, and ELISA were applied for evaluating membrane localization of P110β and its catalytic activity. NOD/SCID/γc(null) (NOG) mice model was used to investigate the in vivo functions of CD73.
Results In present study, we demonstrate that CD73 was crucial for epithelial-mesenchymal-transition (EMT), progression and metastasis in HCC. CD73 expression is increased in HCC cells and correlated with aggressive clinicopathological characteristics. Clinically, CD73 is identified as an independent poor prognostic indicator for both time-to-recurrence and overall survival. CD73 knockdown

dramatically inhibits HCC cells proliferation, migration, invasion, and EMT in vitro, and hinders tumor growth and metastasis in vivo. Opposite results could be observed when CD73 is overexpressed. Mechanistically, adenosine produced by CD73 binds to adenosine A2A receptor (A2AR) and activates Rap1, which recruits P110β to the plasma membrane and triggers PIP3 production, thereby promoting AKT phosphorylation in HCC cells. Notably, combination of anti-CD73 and -A2AR achieves synergistic depression effects on HCC growth and metastasis than single agent alone.

Conclusions CD73 promotes progression and metastasis through activating PI3K/AKT signaling, indicating a novel prognostic biomarker for HCC. Our data demonstrate the importance of CD73 in HCC in addition to its immuosuppressive functions and revealed that co-targeting CD73 and A2AR strategy may be a promising novel therapeutic strategy for future HCC management.

PU-013

The oncogenic miR-491-5p/miR-875-5p-NOTCH3-PHLDB2 axis in gastric tumorigenesis

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Objective Gastric cancer remains one of the leading cancer-related deaths in Asian countries. A better understanding of the oncogenic signaling in GC would facilitate the development of precision therapeutics for cancer treatment. Aberrant Notch activation has been implicated in multiple malignancies and the identification of NOTCH receptors and related pathways is critical for targeted therapy. We aim to delineate the most prominent dysregulated NOTCH receptor and comprehensively reveal its deregulation in gastric cancer (GC).

Methods The clinical relevance of NOTCH1-4 in GC were analyzed using published datasets. The mRNA and protein expression of NOTCH3 was examined by qRT-PCR and Western blot. The biological role of NOTCH3 was demonstrated by a series of functional assays through siRNA-mediated knockdown. The regulation of NOTCH3 by potential miRNAs was validated by qRT-PCR, Western blot and dual luciferase activity assays. The downstream effectors of NOTCH3 were revealed by expression profiling.

Results NOTCH3 was uniformly upregulated and correlated with poor survival in multiple GC datasets. NOTCH3 knockdown suppressed cell proliferation, reduced colony formation, and inhibited cell invasion. NOTCH3 depletion also induced apoptosis, which was validated by gene set enrichment analysis. NOTCH3 was confirmed to be a direct target of tumor suppressor miRNAs, miR-491-5p and miR-875-5p. PHLDB2 was confirmed to be the functional downstream effector of NOTCH3. PHLDB2 expression demonstrated positive correlation with NOTCH3, but was negatively correlated with miR-491-5p. GC cells treated with siNOTCH3, siPHLDB2, miR-491-5p, miR-875-5p, were more sensitive to Cisplatin and 5-FU.

Conclusions The activation of NOTCH3 is partly due to the silence of tumor suppressor miRNAs, miR-491-5p and miR-875-5p. NOTCH3 exerts its oncogenic role through PHLDB2 in gastric carcinogenesis. The miR-491-5p/miR-875-5p-NOTCH3-PHLDB2 cascade is associated

with patients' survival and may serve as a therapeutic target. Our findings highlighted the miR-491-5p/miR-875-5p-NOTCH3-PHLDB2 axis in gastric carcinogenesis and provided insights into the underlying molecular mechanisms, implying its clinical significance in GC prognosis and therapy.

PU-014

MUS81 Inhibition Increases the Sensitivity to Therapy Effect in Epithelial Ovarian Cancer via Regulating CyclinB Pathway

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Objective MUS81 is a key endonuclease involved in homologous recombination (HR) repair after DNA double-strand damage. Structure-specific endonuclease (SSE) plays a crucial role in DNA replication, repair and transcription, which is also important for maintaining the secondary structure of DNA, therefore, their activity must be precisely controlled to ensure genome stability.
Methods We described previously that MUS81 was significantly correlated with CyclinB by protein microarray. CyclinB is a cell-cycle regulatory protein involving in the activation of DNA damage repair checkpoints, which induced G2/M phase arrest, promoted apoptosis, and participated in the regulation of chemotherapeutic drug sensitivity through inducing nuclear degradation, as shown by immunofluorescence assays.
Results In this study, MUS81 down-regulated cells were constructed using Lentivirus-mediated RNAi. Our results demonstrated that the inhibition of MUS81 expression activated CHK1 and CyclinB signaling pathways and sensitized ovarian cancer to X-ray and Olaparib both *in vitro* and *in vivo*.
Conclusions MUS81 may be a potential therapeutic target for epithelial ovarian cancer (EOC).

PU-015

The role of SIRT4-induced oxidative stress on regulating the growth of renal clear cell carcinoma

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Objective Clear cell renal cell carcinoma is a common type of malignant kidney tumors, approximately accounting for 60%～85% in renal carcinoma. ccRCC is not sensitive to chemotherapy or radiotherapy, these therapies usually have great side-effect.Thus, it is very necessary to develop an effective therapeutic method.
Methods Sirt4 is located in mitochondria and represses the metabolism of glutamine into tricarboxylic acid cycle. Our date uncover that Sirt4 act as a tumor suppressor

gene in ccRCC ,the expression levels of Sirt4 is significantly decreased in carcinoma compared with para-carcinoma tissues .Overexpression of Sirt4 in ACNH and Caki-2 cell lines resulted in intracellular ROS levels increasing ,promoting apoptosis and increasing p53 expression. However, whether Sirt4 play role in promoting apoptosis by increasing ROS in a p53 -dependent manner remains unclear.

Results We found that Sirt4 and p53 both have AP-1 binding sites through the database.Therefore, we hypothesize that Sirt4 exerts a synergistic effect by interacting with normal p53 via AP-1.To research the molecular and mechanism, we established SIRT4 over-expressing or p53 knock-out ccRCC cell lines(ACNH , Caki-2), further investigated their effects on proliferation, migration, formation and apoptosis. To investigate Sirt4 role on carcinoma growth inhibition in vivo, we inject AAV to Clear cell renal cell carcinoma model mice .

Conclusions This project will provide a novel view in the mechanism of ccRCC apoptosis regulated by Sirt4.

PU-016

Increased Expression of the Long Noncoding RNA LINC02163 Promotes Glycometabolism in Colorectal Cancer by Interaction with Glyceraldehyde-phosphate Dehydrogenase

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Objective Increasing evidence shows that altered activities of long noncoding RNAs (lncRNAs) have been associated with tumorigenesis. We investigated the clinical significance, biological function, and mechanism of LINC02163 in colorectal cancer (CRC).

Methods First, the combined The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) database revealed the alterations of LINC02163 in CRC tissues. Next, the effect of LINC02163 on the CRC cell proliferation, apoptosis and migration were evaluated by real time cell analysis, flow cytometer and cell invasion assays after LINC02163 knock-down or knock-out via small interfering RNAs or CRISPR/Cas9 vectors and overexpression by transfected plasmids. By virtue of soft-agar colony forming assay and nude mouse tumorigenesis test, the tumorigenesis abilities of LINC02163 in vitro and vivo were respectively identified. Their interactions with other genes were determined by RNA pull-down and RNA immunoprecipitation (RIP) assays. Given expression signatures of exosomal lncRNAs have been proposed as potential non-invasive biomarkers for cancer detection, the diagnostic value of exosomal LINC02163 was evaluated.

ResultsbAfter using publicly available expression profiling data and integrating bioinformatics analyses(Fig.1A-B), we screened and identified LINC02163 significantly increased in CRC tissues and cell lines (Fig.1C-D). Importantly, we also demonstrated that knockdown of LINC02163 suppressed cell proliferation (Fig.1E), invasion (Fig.1F) and migration (Fig.1G) in vitro and inhibited tumorigenesis in vivo (Fig.1F). Mechanistically, RNA pull-down and RIP assays (Fig.1H-K) showed that RNA binding

proteins including glyceraldehyde-phosphate dehydrogenase (GAPDH), suggesting LINC02163 may produce cancerization via regulating glucose metabolism. Further, the diagnostic performance of exosomal LINC02163 (Fig.2A-D) was evaluated. The area under the receiver operating characteristic (AUC-ROC) for exosomal LINC02163 was 0.866 with a sensitivity of 97.5% and a specificity of 97.2% (Fig.2E).

Conclusions Collectively, we determined that LINC02163 may play important roles in CRC oncogenesis via regulating tumor glycometabolism and might be developed as a diagnostic biomarker of CRC in patients. Targeting LINC02163 may provide new strategies in CRC diagnosis and therapy.

PU-017

Sphere-forming culture enriches liver cancer stem cells and reveals Stearoyl-CoA Desaturase 1 as a potential therapeutic target

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Objective The role of sphere-forming culture in enriching subpopulations with stem-cell properties in hepatocellular carcinoma (HCC) is unclear. The present study investigates its value in enriching cancer stem cells (CSCs) subpopulations and the mechanism by which HCC CSCs are maintained.

Methods HCC cell lines and fresh primary tumor cells were cultured in serum-free and ultra-low attachment conditions to allow formation of HCC spheres. In vitro and in vivo experiments were performed to evaluate CSC characteristics. Expression levels of CSC-related genes were assessed by qRT-PCR and the correlation between sphere formation and clinical characteristics was investigated. Finally, gene expression profiling was performed to explore the molecular mechanism underlying HCC CSC maintenance.

Results We found that both cell lines and primary tumor cells formed spheres. HCC spheres possessed the capacity for self-renewal, proliferation, drug resistance, and contained different subpopulations of CSCs. Of interest, 500 sphere-forming Huh7 cells or 200 primary tumor cells could generate tumors in immunodeficient animals. Sphere formation correlated with size, multiple tumors, satellite lesions, and advanced stage. Further investigation identified that the PPARa-SCD1 axis plays an important role in maintenance of the CSC properties of HCC sphere cells by promoting nuclear accumulation of β-Catenin. Inhibition of SCD1 interfered with sphere formation, down-regulated expression of CSC-related markers, and reduced β-Catenin nuclear accumulation.

Conclusions Sphere-forming culture can effectively enrich subpopulations with stem-cell properties, which are maintained through activation of the PPARa-SCD1 axis.

Therefore, we suggest that targeting the SCD1-related CSC machinery might provide a novel insight into HCC treatment.

PU-018

Platelets in acute coronary syndrome patients with high platelet reactivity after dual antiplatelet therapy exhibit upregulation of miR-204-5p

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Objective Acute coronary syndrome (ACS) patients treated with dual antiplatelet therapy (DAPT) show individual differences in platelet reactivity (PR). Here, we aimed to find differences in platelet microRNA (miRNA) expression profiles of high PR and low PR patients to serve as potential biomarkers.
Methods ADP-induced platelet aggregation (PAG) was used to determine PR. High-throughput sequencing technology was used to profile differentially expressed platelet miRNAs in high PR (PAG ＞ 50%) and low PR (PAG ≤ 50%) patients. We used real-time quantitative reverse transcription-polymerase chain reaction (RT-qPCR) to validate the sequencing results. Finally, we statistically evaluated the diagnostic value of the miRNAs and explored their molecular function using bioinformatic analysis.
Results The results showed that miR-204-5p was confirmed to be significantly upregulated in the high PR group. The area under the ROC curve (AUC) of miR-204-5p was 0.667 and its expression significantly correlated with the Gensini score. Stepwise binary logistic regression analysis suggested that miR-204-5p expression level was an independent predictor of PR. Furthermore, bioinformatic analysis showed that miR-204-5p may be associated with platelet synapse formation and platelet vesicle release.
Conclusions Our data indicate that platelet miR-204-5p may serve as a novel biomarker of PR to guide treatment with antiplatelet drugs.

PU-019

Surveillance of antibiotic resistance in the bacterial strains isolated from hospitals in Baotou , Inner Mongolia during 2017

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Objective To investigate the resistance profile of clinical bacterial isolates to commonly used antimicrobial agents in baotou,Inner Mongolia during 2017.

Methods Antimicrobial susceptibility testing was carried out for the clinical isolates collected from 11 hospital taking part in the China Antimicrobial Resistance Surveillance System(CARSS) in Baotou, Inner Mongolia from January 1 to December 31, 2017 according to a unified protocol using Kirby-Bauer(K-B) method or automated systems.Results were analyzed according to CLSI 2017 breakpoints.Statistical was analyzed using software WHONET 5.6.

Results A total of 7922 non-repetitive clinical isolates were collected from the above hospitals, of which Gram-positive cocci and Gram-negative bacilli accounted for 26.3% and 73.7%,respectively.The prevalence of methicillin-resistance strains was 15.6% in MRSA and 75.7% in MRCNS,respectively.The resistance rates of methicillin-resistant strains (MRSA and MRCNS) to most commonly used antimicrobial agents were significantly higher than those of methicillin-sensitive strains (MSSA and MSCNS).No staphylococcal strains were found resistant to linezolid, vancomycin and teicoplanin.The resistance rate of Enterococcus faecium to most of the antimicrobial agents tested was significantly higher than that of Enterococcus faecalis.The resistance rates of non-meningitis S.pneumoniae isolated from children and adult to erythromycin, tetracycline and clindamycin were higher.The prevalence of ESBLs-producing strains was 49.8% in E. coli, 17.2% in Klebsiella spp. and 35.9% in Proteus mirabilis.ESBLs-producing Enterobacteriaceae strains were more resistant than non-ESBL-producing strains in term of antibiotic resistance rate.The resistance rate of Escherichia coli to quinolone antibiotics was above 60.0%. The prevalence of CRE was 1.1%. The CRE strain had the lowest resistance to amikacin, which was 34.4% .The resistance rates of Pseudomonas aeruginosa to imipenem and meropenem were 16.1% and 14.4%, respectively.The resistance rates of Acinetobacter to imipenem and meropenem were 26.3% and 21.4%, respectively.

Conclusions The antibiotic resistance situation in our city is also very serious.The problem of bacterial drug resistance poses a serious threat to clinical anti-infective treatment. It should be comprehensively understood in time and use the surveillance results of bacterial resistance in this area to carry out prevention and control of hospital management, and must strengthen antibacterial Rational use of the drug.

PU-020

Application of cholyglycine in common hepatic diseases

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Objective To investigate the significiance of cholyglycine(CG) and combined detection of total bile acids and leucine aminopeptidase(LAP) in hepatic diseases.

Methods Serum samples obtained from 49 healthy individuals an 161 patients in Xiangya Hospital of Central South University from October 2016 to March 2017 with asymptomatic hepatitis B virus(HBV) infected , hepatitis, biliary obstruction, hepatocirrhosis and primary liver cancer were examined for CG and LAP by corresponding kits. The data were analyzed statistically with the indices of hepatic functions and coagulate functions.

Results The expression of CG were elevated in the 4 liver disease groups and differed statistically from the normal group or the asymptomatic HBV group; CG expression was significantly associated with LAP, total bilirubin(TB), total bile acid(TBA), alkaline phosphatase(ALP), fibrinogen(Fib) and thrombin time(TT); LAP and TBA were introduced into regression equation Y=-0.835+0.157X1+0.312X2 (X1: LAP, X2: TBA, R2=0.685) as final variables in multivariate linear regression analysing the influencing factors of CG; ROC curve analysis showed that CG had the strongest ability to diagnose liver diseases in combination with LAP.
Conclusions Expression of CG plays a momentous role in diagnosis of liver diseases especially combined detection of LAP .

PU-021

O-GlcNAcylation of YY1 stimulates tumorigenesis in colorectal cancer cells by targeting SLC22A15 and AANAT

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Objective Emerging studies have revealed that O-GlcNAcylation plays pivotal roles in the tumorigenesis of colorectal cancers. However, the underlying mechanism still remains largely unknown.
Methods YY1 was overexpressed and knocked out using the lentivirus in HCT116 cells and LoVo cells. The expressions of the proteins were detected by WB and IHC. The bioinformatics analysis was performed in the Omics bean system.
Results Here, we demonstrated that YY1 was O-GlcNAcylated by OGT and O-GlcNAcylation of YY1 could increase the protein expression by enhancing its stability. O-GlcNAcylation facilitated transformative phenotypes of CRC cell in a YY1-dependent manner. Also, O-GlcNAcylation stimulates YY1-dependent transcriptional activity. Besides, we also identified the oncoproteins, SLC22A15 and AANAT, which were regulated by YY1 directly, are responsible for the YY1 stimulated tumorigenesis. Furthermore, we identified the main putative O-GlcNAc site of YY1 at Thr236, and mutating of this site decreased the pro-tumorigenic capacities of YY1.
Conclusions We concluded that O-GlcNAcylation of YY1 stimulates tumorigenesis in CRC cells by targeting SLC22A15 and AANAT, suggesting that YY1 O-GlcNAcylation might be a potential effective therapeutic target for treating CRC.

PU-022

DosR antigen Rv1737c induces activation of macrophages dependent on TLR2 pathway

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Objective Latent *Mycobacterium tuberculosis* infection (LTBI) is the main reservoir of Mtb and retards the attempts of eradication by the host immune system. The dormancy survival regulator (DosR) is held as essential for *Mtb* persistence. Rv1737c is predominantly expressed by the *Mtb* in latent phase. However, whether latent *Mtb* exploits its Rv1737c in involving in the immune evasion is still largely unknown.

Methods rRv1737c was cloned and C57 mice were used for vaccination. The mice was treated intraperitoneally with recombined protein and, intraperitoneal lavage was performed in 24h with 10ml PBS containing 5% BSA. The cells were analysed by Flow Cytometry. In addition, PMA-differentiatedTHP-1cells were treated with various concentrations of rRv1737cwith or without TLR2 blocking to detect the role of TLR 2 in rRv1737c activated macrophage.

Results We have characterized the role of Rv1737c in influencing the recruitment, activation and function of macrophages, which paly a cardinal role in innate and adaptive immunity. For the first time, we have revealed a novel mechanism of Rv1737c in inducing tolerogenic phenotype of macrophage by modulating the expression of (Indoleamine 2,3-dioxygenase 1) IDO1. Meanwhile, we found that rRv1737c-activated macrophages can induce T cells to upregulate IL-4, IL-10, and Foxp3 expression in vitro. Furthermore, Rv1737c interacted with macrophages through TLR2. It augmented NF-κB phosphorylation and co-stimulatory moleculeexpression.

Conclusions This study provides a crucial insight into a strategy adopted by *Mtb* to survive in the host by inducing tolerogenic macrophage expansion.

PU-023

Reduced eIF3d Accelerates HIV Disease Progression by Attenuating CD8+ T cell Function

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Objective In HIV infection, 10–15% individuals show a rapid decline of CD4+ T cells and become rapid progressors (RPs). Understanding the factors affecting rapid disease progression in early HIV infection (EHI) can aid the commencement of treatment. Recent studies show that eIF3s, the classic scaffold protein during the translation initiation process, can directly promote or inhibit the translation of mRNA, therefore participating in the regulation of cell function. However, whether eIF3s are involved in the diverse prognosis of HIV infection has not been addressed to our knowledge.

Methods The expressions of eIF3s in primary cells from early or chronic HIV infected patients were detected by real-time PCR. Complete transcriptomes were sequenced with RNA sequencing (RNA-Seq) in eIF3d inhibited Jurkat T cell to study the potential mechanisms of eIF3d in the regulation of CD8+ T cell function. To study the effect of eIF3d on CD8+ T cell function, eIF3d expression was inhibited alone or combined with the knocking-down of SOCS-7 in CD8+ T cells by introducing the according siRNA to isolated CD8+ T cells. The proliferation, IFN-r secretion and apoptosis of CD8+ T cells were detected by flow cytometry. The effect of eIF3d in the replication of HIV was studied by infected the eIF3d knocking-down Jurkat cells or PBMCs with pNL4-3 pseudotyped virus.

Results We ensured that only the eIF3d in RPs was remarkable decreased compared with chronic progressors (CPs) at approximately 100 days of infection. The expression of eIF3d significant correlated with disease progression in EHI. *In vitro* studies showed that reduced eIF3d expression lead to decreased proliferation, IFN-γ secretion and the increased apoptosis of CD8+ T cells. Inhibited expression of eIF3d caused the enhanced expression of SOCS-7 and inhibiting SOCS-7 expression by siRNA rescued the attenuated CD8+ T cell function caused by eIF3d. Finally, when eIF3d was inhibited in Jurkat cells and peripheral blood mononuclear cell (PBMC), the replication of pNL4-3-VSV-G virus was increased.

Conclusions The current data highlighted the importance of eIF3d in HIV infection by inhibiting CD8+ T cell function and promoting viral replication. Our study provides potential targets for improved immune intervention.

PU-024

Interferon-γ Release Assays for Tuberculous Meningitis Diagnosis: A meta-analysis

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Objective Systematically evaluate the diagnostic performance of cerebrospinal fluid (CSF) and peripheral blood (PB) IGRAs in tuberculous meningitis.

Methods Relevant studies were systematically searched in both foreign and Chinese databases up to March 2018. Studies in which TBM diagnosis was based on microbiological or clinical criteria were included. The quality of the included studies was assessed through the Quality Assessment of Diagnostic Accuracy Studies-2 (QUADAS-2) tool. Main outcome measures, including sensitivity, specificity, positive likelihood ratio (PLR), negative likelihood ratio (NLR) and diagnostic odds ratio (DOR), were pooled statistically using random effects models. The potential heterogeneity was explored by threshold effect analysis, subgroup analyses and meta-regression. Funnel plots and the Egger's test were used to test the potential publication bias. Statistical analyses were performed using Stata and Meta-DiSc software.

Results 26 out of 656 publications were eligible for meta-analysis, including 1892 participants in total. The pooled estimates of PB IGRAs for TBM diagnosis are as follows: sensitivity, 0.81 (95% CI, 0.78–0.84); specificity, 0.76 (95% CI, 0.73–

0.78); PLR, 4.23 (95% CI: 2.95-6.07); NLR, 0.24 (95% CI: 0.19-0.32) and DOR,21.06(11.91-37.24); The corresponding estimates for CSF IGRAs were obtained: sensitivity, 0.81 (95% CI, 0.76-0.85); specificity, 0.89 (95% CI, 0.86-0.92); PLR, 7.87 (95% CI: 4.98-12.46); NLR, 0.19 (95% CI: 0.13-0.29); and DOR,47.74(25.02-91.12). **Conclusions** The diagnostic performance of IGRAs is suboptimal. In terms of cost, turn-around time and accessibility, it is unsuitable to use these assays as biomarkers for TBM diagnosis.

PU-025

Effects of silencing ZEB1 gene on epithelial to mesenchymal transition in glioma U87 cells

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Objective Glioma is the most common primary malignant tumor in the central nervous system (CNS). An important biological characteristic of gliomais highly invasive growth, but the mechanism of this invasive growth has not been fully clarified.The tumor cells undergoing epithelial to mesenchymal transition (EMT) have high migration and invasiveness, which are important reasons for invasion, metastasis and recurrence of tumors.We and other researchers have shown that glioma cells can undergo EMT-like process, which may play a key role in the invasive growth of glioma.The zinc finger E-box binding homeobox (ZEB) is one of the important transcription factors inducing EMT , including ZEB1 and ZEB2. It has been proved that ZEB1 can induce EMT in some cancer cells and promote metastasis. However, the effect of ZEB1 on EMT in glioma cells has not been fully studied.The purpose of the present study was to investigate the effects of silencing ZEB1 gene on expression of mesenchymal markers, cell migration and invasion in glioma U87 cells, and to clarify the effects of ZEB1 on EMT in glioma cells.
Methods The glioma U87cells cultured in DMED medium. The constructed ZEB1 shRNA interfering plasmid (shZEB1#1 and shZEB1#2) and control plasmid were transfected into glioma U87 cells using TransLipid HL Transfection Reagent and the interfering effects were detectedby Western blotting method. The glioma U87 cells were divided into control group (the glioma U87 cells transfected with control plasmid), EMT group (the glioma U87 cells transfected with control plasmid were induced EMT by TGF-β1) and ZEB1 silence group(the gliomaU87cells transfected with ZEB1 shRNAs plasmid were induced EMT by TGF-β1). The protein expression levels of mesenchymal markers (N-cadherin,Vimentin), and matrix metalloproteinase-9 (MMP-9) in glioma U87 cells were measured by Western blotting method. The scratch-healing assay and Transwell invasive assay were performed to examine the migration and invasion rates of glioma cells.
Results Western blotting results showed that expression levels of ZEB1 in glioma U87 cells transfected with shZEB1#1 and shZEB1#2 were significantly lower than those transfected with control plasmid, and the inhibitory effect of shZEB1#2 on ZEB1 expression was more obvious, indicating that ZEB1 was stably transfected into U87 cells. Compared with control group, the expression levels of mesenchymal markers N-

cadherin(0.97±0.13*vs.*1.37±0.14, P<0.05), Vimentin (0.98±0.16*vs.*1.51±0.10, P<0.01) and MMP-9 (0.97±0.07*vs.*1.24±0.09,P<0.05) in EMT group was significantly increased. Compared with EMT group, the expression levels of the N-cadherin (1.37±0.14*vs.*0.83±0.14, P<0.01), Vimentin (1.51±0.10*vs.*1.25±0.08, P<0.05) and MMP-9 (1.24±0.09*vs.*0.73±0.10,P<0.01) in ZEB1 silencing group markedly reduced. The cell migration rate in EMT group (69%±7%) was obviously elevated compared with control group (51%±5%,P<0.01), and the migration rate of the glioma U87 cells in ZEB1 silence group (38%±4%) was significantly lower than that in EMT group(P<0.01). Compared with EMT group(42%±5%),the invasion rate of the glioma U87 cells inEMT group was significantly increased (69%±6%, P<0.01),whilethe cell invasion rate of ZEB1 silencing group (34%±4%) was apparentlylower than that of EMT group (P<0.01).

Conclusions Silencing ZEB1 gene expression inhibits EMT in glioma U87 cells and reduces cell migration and invasion abilities, suggesting ZEB1as an importanttherapeutic target of invasive glioma.

PU-026

Age is an independent factor positively and negatively associated with blood lipid levels in particular age ranges, a large-scale cross sectional study

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Objective Lifetime trends in total cholesterol (TC), triglycerides (TG), high-density lipoprotein cholesterol (HDL-C) and low-density lipoprotein cholesterol (LDL-C) with age remain unclear.

Methods A cross-sectional study with data from 103,461 and 74,706 men and women, respectively, was conducted to explore lifetime trends in the abovementioned lipid parameters with age; turning points of age were established using age stratification and were validated by fitted multivariate linear logic regression modeling.

Results Age was an independent factor extensively associated with lipid levels in both sexes, when adjusted for serum glucose, BMI, lifestyle, drinking and smoking. Age was positively associated with TC, logarithm transformed TG (LnTG) and LDL-C levels in men ⩽ 40, ⩽ 40 and ⩽ 60 years old (yo); and in women ⩽ 60, ⩽ 70 and ⩽ 60 yo, respectively. Conversely, age was negatively associated with TC, LnTG and LDL-C levels in men ⩾ 61 ⩾ 41 and ⩾ 61 yo; and in women ⩾ 61 and ⩾ 71 and ⩾ 61 yo, respectively. TC, TG and LDL-C levels of women were initially lower than those in men

and then surpassed those of men in the age groups of 51-55, 61-65 and 51-55 yo. The trends in HDL-C levels with age are relatively irregular, while women's HDL-C levels are higher than men's throughout all age groups.

Conclusions Age-related trends in lipid levels and sex difference should be fully considered in the definition of dyslipidemia and in associations with atherosclerotic cardiovascular disease.

PU-027

Small interfering RNA target for long non-coding RNA PCGEM1 increases sensitivity of LNCaP cells to baicalein

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Objective To investigate the inhibitory effect and mechanism of long non-coding RNA PCGEM1 siRNA combined with baicalein on prostate cancer LNCaP cells.

Methods The effect of baicalein or lentiviral vector (LV3-shRNA-PCGEM1) alone and the combination of the two on the proliferation of LNCap cells was detected with WST-8. The capability of cell colony formation was detected by a colony formation experiment. The effect on cell cycle was detected by flow cytometry. The relative expression of PCGEM1 was detected by RT-PCR. The formation of autophagosomes was observed by immunocytochemistry and the levels of protein were detected by western blotting.

Results LNCaP cells transfected with small hair RNA lentiviral vector targeting PCGEM1 were constructed and their expression in LNCaP cells was silenced. The stable cell line of LNCaP cells infected with LV3-shRNA-PCGEM1 was successfully constructed. LV3-shRNA-PCGEM1 was also able to increase the baicalein-induced inhibitory effects on LNCaP cells. The increased susceptibility multiples was 2.3. LV3-shRNA-PCGEM1 combined with baicalein inhibited the formation, increased G2 and S phase cells, inhibited the expression of PCGEM1, and induced autophagy of LNCaP cells.

Conclusions LV3-shRNA-PCGEM1 may improve the sensitivity of LNCaP cells to baicalein, and the molecular mechanism may be associated with the decrease of PCGEM1 expression and the induction of autophagy, providing an experimental basis for the combined treatment of Chinese traditional and Western medicine on prostate cancer in a clinical setting.

PU-028

Increased expression of antisense lncRNA SPINT1-AS1 predicts a poor prognosis in colorectal cancer and is negatively correlated with its sense transcript

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Objective Colorectal cancer (CRC) is a leading cause of cancer-associated mortality worldwide. Natural antisense transcripts (NATs) are pervasively expressed in human genome and have been confirmed to contribute to cancer progression. In our study, we aimed to investigate the expression and clinical pertinence of serine peptidase inhibitor, Kunitz type 1 antisense RNA1 (SPINT1-AS1) in CRC.
Methods The expression levels of SPINT1-AS1 and the corresponding sense transcript SPINT1 mRNA were analyzed in 150 pairs of CRC tissues and adjacent normal (AN) tissues, along with 45 pairs of preoperative and postoperative serum exosomes samples using stand-specific RT-qPCR.
Results Compared with AN tissues, expression level of SPINT1-AS1 was increased ($P<0.001$, 3.771) in CRC tissues. SPINT1-AS1 yielded an area under the receiver operating characteristic (ROC) curve (AUC) value of 0.865 (95% confidence interval [95%CI], 0.821-0.902) for discriminating CRC tissues from AN tissues. SPINT1 mRNA expression was decreased ($P<0.001$) in CRC tissues, and a statistical inverse expression level ($r=-0.701$, $P<0.001$) was confirmed. Dual luciferase reporter assay showed decreased SPINT1 mRNA 5' UTR luciferase activity in SPINT1-AS1 overexpression cells. These phenomena may indicate a regulatory role of SPINT1-AS1 to SPINT1 mRNA. Moreover, high SPINT1-AS1 expression correlated with regional lymph node metastasis ($P<0.001$), distant metastasis ($P<0.001$) and shorter recurrence-free survival (RFS) time ($P<0.001$), and Cox regression analysis indicated that SPINT1-AS1 was an independent prognostic factor for RFS. Meanwhile, significant reduction of SPINT1-AS1 expression level ($P=0.001$) was observed in CRC serum exosomes after surgical resection.
Conclusions SPINT1-AS1 is up-regulated in CRC and plays an essential role in CRC progression and prognosis. Thereby, SPINT1-AS1 may sever as a candidate prognostic biomarker and molecular therapy target for CRC.

PU-029

Exosome-mediated transfer of antisense lncRNA SPINT1-AS1 promotes oncogenesis and development in colorectal cancer

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Objective The contribution of natural antisense transcripts (NATs) to tumorigenesis and cancer progression is an area of intense investigation. Previously, we demonstrated that highly expressed SPINT1-AS1 in colorectal cancer (CRC) was linked to poor clinical outcome. In this study, we investigated the regulatory role of SPINT1-AS1 on CRC cell phenotypes and determined the expression pattern of exosomal SPINT1-AS1.

Methods Loss- and gain-of-function assays based on lentivirus transfection were used to evaluate the regulation ability of SPINT1-AS1 and SPINT1 mRNA on CRC cell phenotypes. Exosomes were purified by differential ultracentrifugation and identified by transmission electron microscopy, nanoparticle tracking and western blot assay. Strand-specific RT-qPCR was used to detected SPINT1-AS1 expression in a cohort of serum exosome samples including 100 normal colonoscopy, 93 hyperplastic polyp, 104 inflammatory bowel disease (IBD), 113 adenoma and 240 CRC.

Results SPINT1-AS1 overexpression significantly promoted CRC cell proliferation and cytoprotective autophagy while inhibited cell apoptosis in vitro. SPINT1-AS1 overexpression also drove CRC cell tumorigenesis in vivo. Consistently, knockdown of SPINT1-AS1 almost completely abolishes CRC tumorigenesis manifested as decreased cell proliferation and autophagy activity, as well as increased cell apoptosis rate. Interestingly, overexpression of SPINT1 mRNA led to the same phenotypes as knockdown of SPINT1-AS1 in CRC cell. In addition, SPINT1-AS1 could spread among CRC cells by means of exosome-mediated intercellular communication. Furthermore, high expression of serum exosomal SPINT1-AS1 was observed in CRC which could distinguish between CRC from normal colonoscopy and benign colorectal diseases. Patients with high expression of serum exosomal SPINT1-AS1 had adverse clinical manifestation and shorter Relapse-free survival (RFS).

Conclusions SPINT1-AS1 plays a carcinogenic role in CRC which suggests that SPINT1-AS1 is a potential therapeutic target for CRC. Serum exosomal SPINT1-AS1 has potential to act as a noninvasive diagnostic marker and prognostic indicator for CRC.

PU-030

Clinical analysis of lymphocyte subsets in peripheral bloodof patients with autoimmune diseases

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Objective We detect the expression of lymphocyte subsets in peripheral blood of patients with autoimmune diseases (AID), to explore the changes of lymphocyte subsets in peripheral blood of patients with AID, and to analyze the correlation between these changes and complement C3, C4 and ESR.

Methods Flow cytometry was used to analyze the expression of lymphocyte subsets in peripheral blood of 72 AID patients and 35 normal healthy individuals, and the levels of C3, C4 and ESR in peripheral blood of AID patients. The lymphocyte subsets in peripheral blood of AID patients were detected. Change and analyze the correlation between the parameter CD4+/CD8+ ratio and the ratio of double negative cells (CD3+CD4-CD8-, DNT) to C3, C4 and ESR, respectively. Statistics were analyzed using SPSS 16.0 statistical software. The measurement data of the normal distribution was expressed by x±s, and the difference analysis was performed by group t test. The data of the skewed distribution were expressed as median, and the difference analysis was performed by Mann-Whitney U test. Correlation analysis was performed using Spearman correlation test, and the significance test was P value <0.05.

Results The CD3+ lymphocyte ratio (%) in the AID group was significantly lower than that in the healthy control group (Control), the difference was statistically significant (P<0.05), and the AID group CD3+CD4+, CD4+/CD8+, CD56+ and DNT accounted for lymphocyte ratio (%).) were significantly lower than the Control group, the $CD3^{+}CD8^{+}$ lymphocyte ratio (%) was higher than that of the Control group, the difference was statistically significant (P<0.05), and the AID group CD3-CD19+ lymphocyte ratio (%) was slightly lower than the Control group. Group, but the difference was not statistically significant (P>0.05). Systemic lupus erythematosus (SLE), ANCA-associated vasculitis (AAV), and Sjogren's syndrome (SS) group CD3+, CD3+CD4+, DNT lymphocyte ratio (%), CD4+/CD8+ ratio, complement C3 and C4 The water level was significantly higher than that of the Control group, and the difference was statistically significant (P<0.05). The CD3+CD8+ lymphocyte ratio (%) and ESR in the SLE group, AAV group and SS group were higher than that in the Control group. The difference was statistically significant. Significance (P<0.05), there was no significant difference in peripheral blood T lymphocyte subsets and complement C3, C4 and ESR between SLE group, AAV group and SS group (P>0.05). The ratio of CD4+/CD8+and DNT to lymphocyte ratio (%) was the most significant difference between the disease group and the control group (P<0.01). The ratio of CD4+/CD8+ in peripheral blood of AAV group, SLE group and SS group was significantly different from serum C3. Positive correlation (r=0.832, P<0.01; r=0.599, P<0.01; r=0.749, P<0.01); and C4(r=0.212, P=0.34; r=0.199, P=0.43; r=0.149 , P = 0.51) and ESR (r = -0.132, P = 0.65; r = -0.109, P = 0.61; r = -0.129, P = 0.45) have no significant correlation. Peripheral blood DNT% in AAV group, SLE group and SS group were respectively associated with C3 (r=0.123, P=0.46; r=0.231, P=0.31; r=0.132, P=0.122), C4(r=0.134, P=0.088 ; r=0.599, P<0.01;

r=0.142, P=0.211) and ESR (r=-0.217, P=0.345; r=-0.148, P=0.264; r=-0.117, P=0.153) Sex.

Conclusions There were multiple imbalances in lymphocyte subsets in AID patients, and there was a significant correlation between peripheral blood CD4+/CD8+ and complement C3 in AAV, SLE, and SS groups. Analysis of the expression of lymphocyte subsets of this type of disease, especially CD4+/CD8+ ratio, has important clinical significance for the assessment of the severity of AID patients and the establishment of individual immunotherapy regimens and prognosis.

PU-031

Mis-judgement of a patient with Diffuse Large B-cell Lymphoma and the influence of uncapped-statue time on APTT mixing study

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Objective The results of APTT mixing study provide information about clotting factor deficiency or the presence of inhibitors. The aim of this study is to investigate the influence of uncapped-statue time on the interpretations of APTT mixing study.

Methods A patient with Diffuse Large B-cell Lymphoma (DLBCL), who was triple-positive of antiphospholipid antibodies, was reported because of the misdiagnosis of the presence of factor VIII inhibitor indicated by the APTT mixing study. Further detection of plasma pH values, factor V activities and factor VIII activities was conducted according to various uncapped-statue times.

Results

Plasma pH values gradually increased with the longation of uncapped-statue time from 30min to 120min. While factor V and factor VIII activities changed in the opposite trend. As a consequence, the patient was mis-judged with factor VIII inhibitor when the uncapped-statue time were 60min and 120min, because the extended APTT values were more than 3 seconds in Incubated Mix. Moreover, we chose 3 other patients with positive lupus anticoagulant (LA) to verify above phenomena. Drifts of pH and factor V and factor VIII activities were as same as the reported case. However, mis-judgement only occurred in one patient with the uncapped-statue time of 120min. Further, we analyzed that the discrepancy might be related to different disease types, triple-positive of antiphospholipid antibodies and different LA ratios.

Conclusions Uncapped-statue may, to some extent, impact the interpretation of APTT mixing study.

PU-032

The analysis of associativity hand-foot-and-mouth disease and leukocyte differential count

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Objective To explore the characteristics of blood routine and its value in predicting the disease of children with hand-foot-mouth disease (HFMD) in this area.
Methods The basic information and the routine blood test results of children with hand-foot-mouth disease diagnosis were collected from April 2015 to July 2015. The routine blood test mainly included white blood cells, neutrophils, lymphocytes and mononuclear cells. The results were compared positive EV71, CVA16 with the normal group. ROC curve was used to evaluate the positive predictive value of each index for EV71, CVA16.
Results he results of a total of 7409 children with hand-foot-mouth disease were collected. The virus detection rate was higher in males than in females, with the highest detection rate in infants (1-3 years old) and the second highest in preschool (4-6 years old). WBC, neutrophil, lymphocyte and monocyte in patients with positive EV71 and CVA16, were all higher than those in the normal group (P values were 0.031, 0.00, 0.038 and 0.00, respectively), and the monocyte value in the CVA16 group was higher than that in the EV71 group (P =0.00). The difference was statistically significant. The area under the curve of lymphocytes in EV71 and CVA16 was 0.865 (0.832-0.897) and 0.865 (0.840-0.889), respectively, and the area under the curve of monocytes was 0.617 and 0.672, respectively.
Conclusions Leukocyte, neutrophil, lymphocyte and monocyte have certain diagnostic value for CVA16 and EV71 infection. Monocytes have certain predictive value between CVA16 and EV71.

PU-033

Effects of storage time on leukocyte volume, conductivity and scatter parameters

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Objective It has been demonstrated that leukocyte volume, conductivity and scatter (VCS) parameters have diagnostic utility in hematological and non-hematological abnormalities conditions. But the pre-analytical factors, such as storage time, affecting the reliability of VCS parameters have not been explored.
Methods The complete blood count (CBC) with differential tests(including the leukocyte VCS parameters) were performed at 1 (as soon as possible), 15, 30, 60 and 120 minutes aftersampling blood. The VCS parameters were measured using the Coulter LH750 hematology analyzer.

Results Prolongedstorage time significantly increased MNV and MEV, MNS and MES, but not other parameters.
Conclusions Storage time should be considered when VCS parameters are used in clinical practice.

PU-034

High Prevalence of Scabies in Mambaul Maarif Islamic Boarding School (MMIBS) Denanyar Jombang Indonesia during 2013

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Objective Scabies is a zoonotic disease caused by mites *Sarcoptes scabiei* through prolonged skin contact. This disease is still a major problem in dense population areas in developing countries, for example Islamic boarding schools. Islamic boarding schools are religious education institutions in Indonesia with students living together in dormitories. MMIBS has been established since 1917 and has contributed a lot to Islamic education in Indonesia. Scabies infection can affect the quality of life of the students. This study was conducted to determine the prevalence of scabies in MMIBS during 2013.
Methods The study was conducted during January 2014. Data were obtained from the number of visits and patients diagnosed with scabies in the MMIBS medical center during January to December 2013. The diagnosis of scabies was based on the presence of 2 out of 4 cardinal signs by examining physicians, including nocturnal pruritus, occurring in a population group, skin lesions are tunneled, and mites are found in skin scrapings. The prevalence of scabies in MMIBS in 2013 was calculated by dividing the number of patients diagnosed with scabies with a total of students who lived in the dormitory.
Results MMIBS had 9 dormitories with 547 male students and 11 dormitories with 723 female students. The total of 12 boarding institutions had 1,270 students. The number of visits in the MMIBS medical center during January to December 2013 was 3,883 patients. The highest visit was 592 patients in March 2013. The number of patients diagnosed with scabies in the MMIBS medical center during January to December 2013 was 258 patients. The highest number of patients diagnosed with scabies was 36 patients in March 2013. The MMIBS prevalence of scabies in 2013 was 20.3%. This figure was higher than the data from the Indonesian Ministry of Health which stated that the national prevalence of scabies in 2008 was 5.60-12.95%.
Conclusions Prevalence of Scabies in MMIBS Denanyar Jombang Indonesia during 2013 is high, with the result of 20.3%.

PU-035

The Effect of Different Timing Parameters on the Blood ALT Determination Result in Donors

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Objective To evaluate the effect of timing point parameters on the donored blood ALT resuluts, which stored in different circumstances.
Methods The whole blood samples and the corresponding plasma samples are stored under the circumstance of 4° C, 20° C, 30° C respectively.And the detecting process are carried out for all samples on automatic biochemical analyzer at 0h, 4h, 8h, 24h. Different timing parameters are set up on analyzer to calculate the corresponding ALT results.
Results Plasma ALT results are unaffected by stored temperature, time interval, timing parameters. Under the circumstance of original timing parameters, the blood ALT results display gradually incremental trend in accordance with the increased temperature and prolonged time interval, respectively. While under the circumstance of delayed timing parameter modes, the effects are attenuated.
Conclusions The ALT results are likely affected by stored temperature and time interval in donor's' blood samples, but not in plasma samples. The problem can be attenuated by the means of adjusting timing parameters.

PU-036

IL-10 dampens the Th1 and Tc development in BCG vaccination

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Objective BCG, the only registered vaccine against *Mycobacterial Tuberculosis* (TB) infection, has been questioned for its protective efficacy for decades. Although lots of efforts were made in the improvement of BCG antigenicity, few studies were devoted to understand host factors in the variability of the BCG protection. Our current findings provide a new strategy for better vaccine development, as well a plausible mechanism to explain the heterogeneous outcomes after BCG vaccination in different populations.
Methods By using IL-10KO mice and pulmonary tuberculosis infection model, we have addressed the role of IL-10 in the BCG vaccination efficacy. In vivo BCG immunization in IL-10KO mice promotes IFN γ production, which was consistent with the protective effects after BCG challenge. The mild lung pathologic changes after BCG vaccination/challenge supported that IL-10 deficiency resulted in higher protective response. In clinical practice, it was reported an increased susceptibility toward the development of progressive tuberculosis in humans with increased IL-10 levels .Our

study explored the molecular mechanisms of the notorious role of IL-10 in the BCG vaccination.

Results The data showed that IL-10 deficient Dendritic Cells (DCs) could boom the immune responses through upregulation of surface co-stimulatory molecule expression, and play an immune orchestra role through activating $CD4^+$T cell. IL-10 deficient mice had higher IFN γ, TNF α and IL-6 production after BCG vaccination, which was consistent with the higher proportion of IFN γ^+CD3^+, IFN γ^+CD4^+ and IFN γ^+CD8^+ T cells in spleen. Especially, the BCG vaccinated IL-10KO mice showed less inflammation after TB challenge compared to WT mice, which was supported by the promoted Th1and Tc, as well as the suppressed Treg responses in IL-10 deficiency.

Conclusions In a conclusion, we demonstrated the inverse relationship between Th1/Tc responses with IL-10 production. IL-10 deficiency restored the type 1 immune response through DC activation, which provided better protection against TB challenge. Hence, our study offers the first experimental evidence that, contrary to the modulation of BCG, host immunity plays a critical role in the BCG protective efficacy against TB.

PU-037

MicroRNA-638 Regulates Lung Adenocarcinoma Cell Proliferation and Invasion by Targeting p21-activated Kinase 2

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Objective The dysregulation of micro (mi)RNAs exhibiting oncogenic or tumor suppressor activities may be involved in the modulation of cancer cell behaviors including proliferation, invasiveness, and apoptosis.

Methods MiRNA array and gene expression array were performed to acquire miRNA and gene expression profile of SPC-A1 cells after treatment with mAb NJ001. Quantitative real-time-PCR was carried out to validate the results of microarray approach. Transient transfection of miRNA mimics into lung adenocarcinoma cells was used to analyze the effect of miRNA on tumor cell proliferation, invasion, and apoptosis. After that, TargetscanPictar was used to forecast the targets of the significantly changed miRNA. Luciferase report gene assay and interference technology were applied to elucidate the molecular mechanisms of miRNA in the target gene regulation. Finally, we detect the expression level of miR-638 and PAK2 in tumor tissues and corresponding normal tissues of 69 lung cancar patients to revel their relationship to lung cancer clinical pathological features.

Results The expression of miR-638 was dynamically increased in monoclonal antibody NJ001 treated lung adenocarcinoma cells. A reduction of miR-638 inversely correlated with PAK2 up-regulation in human lung cancer tissues. miR-638 positively regulated apoptosis, but negatively regulated the proliferation and invasion of SPC-A1 through targeting PAK2 by directly binding to its 3′ untranslated region. Silencing of PAK2 inhibitd proliferation and invasion of SPC-A1 similar to miR-638 overexpression.

Conclusions These findings indicate that miR-638 is a putative tumor suppressor miRNA, and provides a basic rationale for its use in the treatment of lung adenocarcinoma.

PU-038

The monocytes VCS parameters: potential hematological indicators for distinguish between active tuberculosis and latent tuberculosis patient

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Objective It is important to distinguish those with active Mycobacterium tuberculosis infection (ATB) from latent tuberculosis infection (LTBI) for monitoring and treating the disease. Monocytes play an important role and may undergo morphological changes against active TB infection. The aim of this study is to investigate the clinical usefulness of the monocyte morphometric parameters and monocyte chemoattractant protein-1 (MCP-1) to distinguish active tuberculosis (ATB) from latent tuberculosis infection (LTBI) and healthy controls (HC).
Methods Peripheral blood was collected from 97 ATB patients, 113 LTBI patients and 101 healthy controls. The monocyte morphometric parameters were obtained using UniCel coulter DxH800 system. MCP-1 level was determined by enzyme-linked immunosorbent assay method. Cut-off values were established based on receiver operator characteristic (ROC) curve analysis.
Results Mean monocyte volume with its standard deviation, mean monocyte conductivity and MCP-1 were significantly increased in ATB compared with LTBI and HC. ROC curve analyses showed that simultaneous measurements of mean monocyte volume with its standard deviation, mean monocyte conductivity and MCP-1 achieved a good sensitivity and specificity (93.8%,93.1%), which may be clinically useful.
Conclusions The findings using monocyte morphometric parameters and MCP-1 to distinguish ATB from LTBI with high sensitivity and specificity may be potential parameter for clinical.

PU-039

Diagnosis of mycoplasma pneumoniae by loop-mediated isothermal amplification: systematic review and meta-analysis

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Objective A novel method, termed loop-mediated isothermal amplification (LAMP), was developed by Notomi et al. (2000). Individually published results have been reported that this technology has been successfully applied to the detection of a variety of pathogens. However, the overall diagnostic accuracy of LAMP for Mycoplasma pneumoniae (MP) remains unclear. A meta-analysis was therefore performed to review the accuracy of LAMP for Mycoplasma pneumoniae.

Methods Cochrane Library and PubMed were systematically searched and checked for studies using LAMP for detecting mycoplasma pneumoniae. We used PCR as a reference standard to evaluate the quality of the studies eligible for inclusion in the meta-analysis. Then, the data from the studies were extracted by two independent assessors. Meta-DiSc 1.4 software was utilized to test the heterogeneity of sensitivity (SEN), specificity (SP), positive likelihood ratio (PLR), negative likelihood ratio (NLR), and diagnosis odds ratio (DOR). The pooled analysis results were plotted, and the summary receiver operating characteristic (SROC) curve was plotted by calculating the area under the curve (AUC). Generated pooled summary estimates (95% CIs) were calculated for the overall accuracy, and a bivariate meta-regression model was used for the meta-analysis.

Results Seven studies with nine fourfold tables were included in this meta-analysis. The pooled SEN and SPE for diagnosing Mycoplasma pneumoniae were 0.90 (95% CI: 0.87－0.93) and 0.98 (95% CI: 0.96－0.99), respectively. The PLR was 31.25 (95% CI: 14.83－65.87), NLR 0.10 (95% CI: 0.05－0.22), DOR 399.32 (95% CI: 172.01－927.00), and AUC 0.9892

Conclusions In conclusion, compared with PCR, LAMP is a valuable alternative method for Mycoplasma pneumoniae diagnosis in clinic with high sensitivity and specificity. However, more evidence is required to confirm that LAMP can fully replace other methods in the clinical diagnosis of MP.

PU-040

Targeting Neddylation Pathway with MLN4924 (Pevonedistat) Induces Apoptosis in Renal Cell Carcinoma

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Objective Renal cell carcinoma (RCC) is one of the most common genitourinary malignancies with 102,000 mortalities per year worldwide. Therefore, identifying new anti-RCC molecular targets and understanding the pivotal molecular events are crucial for the development of novel therapeutic strategies for the treatment of RCC. Neddylation is a type of posttranslational modification that adds the ubiquitin-like molecule neural precursor cell expressed, developmentally downregulated 8 (NEDD8) to substrate proteins, and thus regulates a variety of biological processes. Neddylation pathway was recently reported to be overactivated and contributed to the progression of several malignant human solid tumors, which implied that it might serve as an effective anticancer target. Preclinical studies have reported that targeting neddylation pathway was a promising anticancer strategy since by the efficacy of the Nedd8-activating enzyme (NAE) inhibitor MLN4924. In this study, we firstly reported that NAE inhibitor MLN4924 specially inhibited the neddylation pathway in RCC cells, following induced intrinsic apoptosis, suggesting that neddylation pathway as a promising therapeutic target against RCC.

Methods ① **Cell culture:** Human RCC cell lines 786-0 and Caki-1 cells were DMEM containing 10% fetal bovine serum and 1% penicillin-streptomycin solution at 37℃ with 5% CO_2. ② **ATPlite cell viability assay:** Cells were seeded in 96-well plates with 3,000 cells per well in triplicate, cultured for 24 hours, and treated with DMSO or MLN4924 at various concentrations for 72 hours. Cell viability was determined by using the ATPlite kit. ③ **Cell clonogenic assay:** Cells were seeded into 6-well plates in triplicate for 16 hours, then the fresh medium in the absence (DMSO) or presence of MLN4924 (0.1, 0.33, 1.0μM), followed by incubating at 37℃ for 8 days. The colonies on the plates were fixed with 4% paraformaldehyde and stained with crystal violet. ④ **Transwell migration assay:** The chemotactic motility of the RCC cells was assayed using transwell chambers. Cells were allowed to migrate for 24 hours. Stationary cells on the top surface of the membrane were scraped with a cotton swab, and the cells that migrated were fixed with paraformaldehyde, then the cells were stained with 1% crystal violet. The cells that passed through the polycarbonate membrane of the transwell were counted. ⑤ **AnnexinV and PI staining and FACS analysis:** Cells treated with DMSO or MLN4924 (0.3 mM) were collected and stained with FITC and PI using an Annexin V-FITC Apoptosis Detection Kit.

Results ① **MLN4924 inhibits protein neddylation:** We found that global protein neddylation and cullin neddylation were dose-dependently MLN4924. ② **MLN4924 inhibits malignant phenotypes of RCC cells:** Furthermore, we evaluated the effect of MLN4924 on the malignant phenotypes of RCC cells in vitro. MLN4924 remarkably induced cell apoptosis, and IC50 values for renal cancer cell lines 786-0 and caki-1 were 45.83nM and 75.37nM, respectively. In addition, clonogenic survival and transwell cell migration were also significantly inhibited in a dose-dependent manner. ③ **Neddylation inhibition by MLN4924 triggers G_2 cell-cycle arrest:** We observed that cell populations

in G_2-M phase were significantly increased in both 786-0 and caki-1 cell lines in a dose-dependent manner. Furthermore, MLN4942 induced the accumulation of G_2-M phase transition inhibitor Wee1, as well as cell cycle inhibitors P21 and P27, while the downregulation of M phase marker p-histone H3, indicating that MLN4924-treated cells were arrested at the G_2 phase. **④ MLN4924 induces apoptosis in RCC cells:** MLN4942 significantly induced apoptosis in 786-0 and caki-1 cell lines in a dose-dependently manner. Consistently, MLN4924-treated RCC cells exhibited higher levels of cleaved PARP and cleaved caspase3, two classical marks of apoptotic induction.

Conclusions Here we reported that MLN4924 specifically inhibited protein neddylation pathway, leading to statistically significantly suppress the proliferation, survival and migration of RCC cells by inducing G_2 cell-cycle arrest, followed by apoptosis in a MLN4924 dose-dependent manner. Our findings obtained from this study highlighted neddylation pathway as an attractive therapeutic target in RCC.

PU-041

Discussion on clinical influencing factors of Multidrug Resistant Acinetobacter baumannii

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Objective To analyze clinical factors, distribution characteristics and change trend of Acinetobacter baumannii (AB) and Multidrug Resistant Acinetobacter baumannii (MDR-AB) isolated in Shanghai Chest Hospital, to provide theoretical basis for hospital controlling MDR-AB infection.

Methods 499 strains of AB isolated in our hospital from January 2015 to December 2017 were identified by VITEK MS microbial mass spectrometry identification system. The drug sensitivity test in vitro was carried out by VITEK-2 COMPACT, and the related clinical data were analyzed.

Results The detection rate of AB increased year by year (x^2=7.168, P<0.05), while the detection rate of MDR-AB decreased year by year (x^2=35.086, P<0.01). The detection rate of AB and MDR-AB in male patients was higher than that of female (P>0.05). The rates of AB and MDR-AB all reached the highest in patients aged 60-69 years old and there was a yearly upward trend of MDR-AB detection rate in patients aged 70-79, and difference was statistically significant(x^2=6.775, P<0.05). The specimens detected by AB and MDR-AB were mainly sputum specimens, most of which were from ICU, followed by thoracic surgery department.

Conclusions With the increase of the AB detection rate in the hospital, the monitoring of MDR-AB should be strengthened, disinfection and isolation should be done well to control the development of multi-drug resistant strains.

PU-042

De novo truncating variant in WHSC1 leading to mild Wolf-Hirschhorn syndrome phenotype

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Objective Wolf-Hirschhorn syndrome (WHS) is a characterized by distinctive craniofacial features including "Greek warrior helmet" appearance, prenatal and postnatal growth deficiency, developmental delay, and hypotonia. The WHS critical region (WHSCR) has been narrowed down and WHSC1 falls within this 200kb region. Mutations in WHSC1 has been rarely reported in patients.
Methods Whole exome sequencing was used to identify pathogenic genetic vairants in patient. Interpretation and biological analysis was carried out using Inguenity Vairants Analyzer and TGex softwar. Detail phenotypic information was collected and analyzed.
Results The patient has similar but mild clinical features comparing with typical 4p16.3 deletion related WHS. An insertion variant c.4029_4030insAA leading to frameshift muation (p.Glu1344Lysfs*49) was detected and thought to have high probability as a candidate mutation.
Conclusions This case report further supported the pathogenesis of de novo truncating variants in WHSC1 in syndromic intellectual disability and developmental delay and these variants lead to a mild form of WHS.

PU-043

The performance of pleural fluid T-SPOT.TB assay for diagnosing tuberculous pleurisy in China

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Objective The performance of T-SPOT.TB (T-SPOT) assay in diagnosing pleural tuberculosis (plTB) is inconsistent. In this study, we compared the performance of peripheral blood (PB) and pleural fluid (PF) T-SPOT assay in diagnosing plTB.
Methods Between July 2017 and March 2018, 218 and 210 suspected plTB patients were prospectively enrolled from Wuhan (training) and Guangzhou (validation) cohort, respectively. PB T-SPOT, PF T-SPOT, and other conventional tests were simultaneously performed.
Results Our data showed the performance of PB T-SPOT in diagnosing plTB was limited, especially with low sensitivity. However, the results of early secreted antigenic target 6 (ESAT-6) and culture filtrate protein 10 (CFP-10) in PF T-SPOT were significantly increased compared with those in PB T-SPOT in plTB patients. If using 76 as the cutoff value of MAX (the larger of ESAT-6 and CFP-10) in Wuhan cohort, the sensitivity and specificity of PF T-SPOT to diagnose plTB were 89.76% and 96.70%,

respectively. The diagnostic accuracy of PF T-SPOT was better than other routine tests such as pathogen detection methods and biochemical markers. The diagnostic accuracy of PF T-SPOT in Guangzhou cohort was similar to that in Wuhan cohort, with a sensitivity and specificity of 91.07% and 94.90%, respectively. Furthermore, $CD4^+$ T cells were more activated in PF compared with PB, and the frequency of *mycobacterium tuberculosis*-specific $CD4^+$ T cells in PF was significantly higher than that in PB in plTB patients.

Conclusions In conclusion, the performance of PF T-SPOT is obviously better than PB T-SPOT or other laboratory tests, which suggests that PF T-SPOT assay has been of great value in the diagnosis of pleural tuberculosis.

PU-044

Low serum amylase increases risk of stroke: A cross-sectional study

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Objective Reduced serum amylase is commonly observed in metabolic syndrome, diabetes mellitus, and nonalcoholic fatty liver disease. High blood glucose is considered an independent risk factor for stroke . In this study, we aimed to examine the correlation between serum amylase and acute ischemic stroke (AIS). We evaluated the levels of serum amylase in patients with AIS relative to healthy individuals.

Methods Fasting venous blood samples were collected from patients with AIS (n = 198; 69.2% men) and healthy individuals (n = 112; 67% men). Various biochemical parameters were determined and the groups were compared by Student's t-test, Spearman's correlation analysis, and multivariate logistic regression analysis.

Results AIS patients had significantly lower serum amylase levels compared with the healthy controls ($P < 0.01$), and also significantly lower high-density lipoprotein cholesterol, hemoglobin and percentage of lymphocytes. Levels of the following were significantly higher in the AIS patients compared with the control group: systolic and diastolic blood pressure; white blood cell count; fibrinogen; D-dimer, fasting blood glucose, total cholesterol, total triglyceride, lipoprotein(a), glycated hemoglobin, and high sensitivity C-reactive protein. The multivariate logistic regression analysis revealed that serum amylase was an independent factor that could predict AIS (OR: 1.768, 95% CI: 1.108-2.930, P = 0.027). Serum amylase is significantly and negatively correlated with glycated hemoglobin and fasting blood glucose, and significantly and positively with high-density lipoprotein.

Conclusions Serum amylase may be a viable marker to identify patients who are at higher risk of AIS.

PU-045

Transmembrane protein 106C promotes the development of hepatocellular carcinoma

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Objective Protein coding genes have been shown to have essential roles in cancer biology and are dysregulated in many tumors. Transmembrane protein 106C (TMEM106C), previously shown to be differently expressed in human and porcine. The aim of this study is to determine expression levels of TMEM106C in hepatocellular carcinoma (HCC).

Methods We used quantitative real-time polymerase chain reaction (qRT-PCR) assays to analyze TMEM106C expression. The effect of TMEM106C on proliferation was detected by Cell Counting Kit-8 and colony formation assays. The effect of TMEM106C on cell cycle distribution and apoptosis was detected by flow cytometry. We also used transwell assays to test the migration and invasion of TMEM106C.

Results TMEM106C is significantly elevated in HCC tissues and cell lines from public databases and our specimens. Survival analysis revealed that high TMEM106C expression is a good predictor of poor prognosis of HCC patients. TMEM106C overexpression promotes cell growth, migration and invasion, and inhibits cell apoptosis. While, TMEM106C knockdown impedes cell proliferation and metastasis and accelerates cell apoptosis.

Conclusions

TMEM106C is up-regulated in hepatocellular carcinoma, and may serve as a potential therapeutic target for hepatocellular carcinoma in the future.

PU-046

AKAP12 promotes cancer stem cell-like phenotypes and activates STAT3 in colorectal cancer

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Objective A-Kinase Anchor Protein 12 (AKAP12) is a scaffolding protein considered to act as a potential suppressor in colorectal cancer, but its role in CSCs remains unclearly. The current study aimed to investigate the role of AKAP12 in CCSCs and to explore the mechanisms involved which may provide a new therapeutic approach for patients with colorectal cancer.

Methods AKAP12 gene and protein expression was monitored by quantitative polymerase chain reaction (qPCR), reverse transcription (RT)-PCR and Western blotting in colon cancer cell lines HCT116 and LoVo. The effect of AKAP12 on cancer stem-like characteristics was determined using gene overexpressing and silencing approach. The

role of AKAP12 in various pathways involved in cancer cell stemness was investigated in in vitro and in vivo.
Results Enhanced expression of AKAP12 was firstly observed in stem-like cell spheres in both HCT116 and Lovo cell lines accompanied by elevated level of typical stemness-related markers, eg Sox-2, Nanog, CD133 et al. More, exogenous expression of AKAP12 significantly increased colony number, sphere formation and expression of stem cell markers in vitro and in vivo, whereas depletion expression of AKAP12 negatively regulated those cell malignant phenotypes accordingly. Mechanically, AKAP12 expression levels also affected the expression of stemness markers associated with STAT3, potentially via regulating the expression of protein kinase C.
Conclusions These data suggest that AKAP12 may be an effective therapeutic target for the elimination of CCSCs.

PU-047

The long non-coding RNA PTTG3P promotes cell growth and metastasis via up-regulating PTTG1 and activating PI3K/AKT signaling in hepatocellular carcinoma

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Objective To investigate the clinicopathologic significance and potential role of long non-coding RNA (lncRNAs) PTTG3P in hepatocellular carcinoma (HCC).
Methods We compared the expression profiles of lncRNAs in 3 HCC tumor tissues and adjacent non-tumor tissues by microarrays. In situ hybridization (ISH) and quantitative real-time polymerase chain reaction (qRT-PCR) were applied to assess the level of PTTG3P and prognostic values of PTTG3P were assayed in two HCC cohorts (n=46 and 90). Artificial modulation of PTTG3P (down- and over-expression) was performed to explore the role of PTTG3P in tumor growth and metastasis *in vitro* and *in vivo*. Involvement of PI3K/AKT signaling and its downstream signals were validated by qRT-PCR and western blot.
Results We found that PTTG3P was frequently up-regulated in HCC and its level was positively correlated with tumor size, TNM stage and poor survival of patients with HCC. Enforced expression of PTTG3P significantly promoted cell proliferation, migration, and invasion *in vitro*, as well as tumorigenesis and metastasis *in vivo*. Conversely, PTTG3P knockdown had opposite effects. Mechanistically, over-expression of PTTG3P activated PI3K/AKT signaling and its downstream signals including cell cycle progression, cell apoptosis and epithelial-mesenchymal transition (EMT)-associated genes.
Conclusions Our findings suggest that PTTG3P, a valuable marker of HCC prognosis, promotes tumor growth and metastasis via activation of PI3K/AKT signaling in HCC and might represent a potential target for gene-based therapy.

PU-048

Application strategies of serum HBV DNA detection in HBV infection patients: a retrospective study of 5611 specimens

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Objective The detection of HBV DNA plays a critical role in determining the level of viral replication in HBV infected patients. However, how to select appropriate HBV DNA detection method, low-sensitivity (ls) and hypersensitivity (hs), remains unclear.
Methods HBsAg, HBeAg, ALT, AST and hs HBV DNA titers in serum of 5611 cases with suspected HBV infection were reviewed. Besides, the dynamic changes of HBV DNA and HBsAg in 85 chronic hepatitis B (CHB) patients receiving PegIFNα or entecavir (ETV) were observed.
Results The positive rate of HBV DNA was 32.8%, of which low viral load (20~500 IU/ml) accounted for 51.8%. In the 5611 cases, when the HBsAg<1000 IU/ml, the proportion of low viral load was 76.3%. Moreover, in patients receiving antiviral treatment, when HBsAg<2000 IU/ml (PegIFNα) or HBsAg<3500 IU/ml (ETV), the proportion of patients with low viral load was 79.5% or 78.0%, respectively. We developed a strategy of serum HBV DNA detection in HBV infection patients. When HBsAg was negative, HBV DNA detection should be unnecessary. When HBsAg was 0.05~1000 IU/ml, hs HBV DNA should be detected in patients with abnormal level of ALT, AST or HBeAg. While HBsAg was ≥1000 IU/ml, ls HBV DNA was recommended. Moreover, the cut-off value of HBsAg increased during antiviral therapy of CHB patients.
Conclusions Hypersensitivity HBV DNA is of great value in HBV infected patients with low viral load. HBV DNA detection methods should be selected reasonably according to the levels of HBsAg, HBeAg, ALT and AST.

PU-049

Blocking of YY1 Reduce Neutrophil Infiltration by Inhibiting IL-8 Production via PI3K-Akt-mTOR Signaling Pathway in Rheumatoid Arthritis

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Objective Our previous study has revealed that YY1 played an important part in promoting IL-6 production in rheumatoid arthritis (RA). However, whether YY1 has any role in regulation of IL-8 in RA remains unclear.
Methods YY1 and IL-8 expression in RA patients were analyzed by real-time PCR. Ingenuity pathway analysis (IPA) was used to analyzed signaling pathway involved in YY1-induced IL-8 production. The expression of YY1 and proteins involved in pathway

were detected by western blot and ELISA. Migration of neutrophils was done by chemotaxis assay.

Results In this study, we found high expression of IL-8 was positively associated with YY1 expression in RA. Blocking YY1 expression by YY1-shRNA lentivirus reduced IL-8 production. Mechanistically, we showed YY1 activated IL-8 production via PI3K/Akt/mTOR signaling pathway. Further, using a co-culture system consisting of peripheral blood mononuclear cell (PBMC) and neutrophils, we found that migration of neutrophils would be inhibited by YY1 RNA interference. Finally, using the collagen-induced arthritis animal model, we showed that treatment with the YY1-shRNA lentivirus led to reduction of IL-8 levels and attenuation of inflammation and neutrophils infiltration *in vivo*.

Conclusions Our results reveal a role of YY1 involved in neutrophils infiltration in RA via a PI3K/Akt/mTOR/IL-8 signaling pathway. YY1 may be a new therapeutic target for treatment of RA.

PU-050

MAb NJ001 inhibits lung adenocarcinoma invasiveness by directly regulating TIMP-3 promoter activity via FOXP1 binding sites

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Objective *Previously, we developed a monoclonal antibody (mAb) NJ001 that binds to the antigen SP70 in human non-small cell lung cancer (NSCLC) cells and showed it could inhibit lung adenocarcinoma (AD) growth. Here, we investigated the effect and mechanisms of NJ001 in lung AD metastasis.*

Methods Human lung AD cells (SPC-A1 and A549) were treated with different concentrations of mAb NJ001, and the effects of NJ001 on cell migration and invasive activity were investigated using wound-healing assays and Matrigel assays, respectively. The molecular mechanism of this inhibition was explored by microarrays, qRT-PCR, western blot, luciferase assays and electrophoretic mobility shift assays (EMSA).

Results MAb NJ001 markedly suppressed lung AD cell migration; and the invasiveness of SPC-A1 and A549 cells treated with mAb NJ001 was diminished by 65%. Tissue inhibitor of metalloproteinase-3 (TIMP-3) was highly expressed in SPC-A1 cells treated with mAb NJ001, whereas knockdown of TIMP-3 by shRNA significantly increased SPC-A1 and A549 invasiveness. MAb NJ001 affects lung AD by inhibiting TIMP-3 through direct transcriptional regulation of FOXP1 binding sites in the TIMP-3 promoter region, as shown in luciferase assays and EMSA.

Conclusions MAb NJ001 inhibits invasiveness and metastasis in lung AD through the FOXP1 binding sites in the TIMP-3 promoter region. It may have clinical applications in preventing and treating metastatic lung AD.

PU-051

CircHMGCS1 Promotes Hepatoblastoma Cell Proliferation by Regulating the IGF Signaling Pathway and Glutaminolysis

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Objective Circular RNAs (circRNAs), a novel class of endogenous RNAs, have been recently shown to participate in cellular development and several pathophysiological processes. The identification of dysregulated circRNAs and their function in cancer have attracted considerable attention. Nevertheless, the expression profile and role of circRNAs in human hepatoblastoma (HB) remain to be studied. In this report, we analyzed the expression prolife of circRNAs in HB tissues and identified circHMGCS1 (3-hydroxy-3-methylglutaryl-CoA synthase 1; hsa_circ_0072391) as a remarkably upregulated circRNA.

Methods The expression prolife of circRNAs in HB tissues were investigated through circRNA sequencing analyses. ISH and qRT-PCR assays were performed to measure the expression level of circHMGCS1. The effect of knocking down circHMGCS1 in HB cells in vitro and in vivo were evaluated by colony formation assay, flow cytometry, xenograft tumors assay and untargeted metabolomics assay. MRE analysis and dual luciferase assay were performed to explore the underlying molecular mechanisms.

Results HB patients with high circHMGCS1 expression have shorted overall survival. Knockdown of circHMGCS1 inhibits HB cells proliferation and induces apoptosis. CircHMGCS1 regulates IGF2 and IGF1R expression via sponging miR-503-5p, and affects the downstream PI3K-Akt signaling pathway to regulate HB cell proliferation and glutaminolysis.

Conclusions The circHMGCS1/miR-503-5p/IGF-PI3K-Akt axis regulates the proliferation, apoptosis and glutaminolysis of HB cells, implying that circHMGCS1 is a promising therapeutic target and prognostic marker for HB patients.

PU-052

The Occurrence of Low Level Viremia and Its Impacts on Virologic Failure during First-line Antiretroviral Therapy in China

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Objective Low-level viremia (LLV) can be detected in HIV infected people during the course of antiretroviral treatment (ART), and its effect on virologic failure remains controversial. The purpose of this study is to analyze the occurrence of low level viremia and its impact on virologic failure under the first line ART therapy in China.

Methods A total of 2156 patients with HIV infection who received first-line ART treatment for at least one year between 2000 and 2018 were collected from the First Affiliated Hospital of China Medical University. The data of viral load (VL) every 3-6 months from these patients were retrospectively analyzed. According to the level of low level viremia, all HIV infected patients were divided into four groups: N group, L group, M group and H group, with viral load of less than 20 copies/ml, 20-200 copies/ml, 200-400 copies/ml and more than 400 copies/ml, respectively. In this study, logistic regression test and chi-square test were used to analyze the risk of virologic failure at different among patients with different levels and duration of LLV.

Results The impacts on virology failure were different among groups with different LLV level . First, the virology failure rates were in descending order in group H (9.31%), group M (5.92%), and group L (1.28%). Second, the risk of virologic failure in both group H (OR 4.81, 95%CI 2.57-8.99) and group M (OR 2.95, 95%CI 1.27-6.88) was increased significantly compared with group N ($p < 0.05$), but that was not the case in group L (OR 0.61, 95%CI 0.29-1.28, $p=0.20$). Third, in cases of group H and M (LLV levels greater than 200 copies/ml) , both the baseline CD4 lymphocyte counts less than 300 cells/ul (OR 3.60, 95CI 1.73-7.52, $p < 0.01$) and the baseline viral load greater than 10^6 copies/ml (OR 2.54, 95CI 1.43-4.50, $p < 0.01$) increased the risk of virologic failure further. In term of the duration of LLV, we found that high level of LLV even detected at a single time increased the risk of virologic failure (OR 2.57, 95%CI 1.15-5.82, $p<0.01$). Medium level of low level viremia that last longer than 6 months increased the risk of virologic failure (OR 5.86, 95%CI 1.62-21.13, $p<0.05$). However, Low level of LLV rarely failed in virology even lasting for longer than 12 months ($p=0.69$).

Conclusions The level and duration of low level viremia were both associated with the risk of virologic failure under the first-line ART regimen in China. Higher the level and longer duration of LLV increased the risk of virologic failure. To control plasma viral load to less than 200 copies /ml during ART is critical to ensure successful ART.

PU-053

Molecular mechanism of hereditary protein S deficiency causing recurrent venous thrombosis

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Objective A 18-year-old proband had a history of venous thrombosis of the lower extremities seven years ago and came to our hospital again for pulmonary embolism last year. The aim of our study was to investigate the molecular pathogenesis leading to recurrent venous thrombosis in this patient.

Methods Thrombophilia screening tests were performed in both the proband and his family members, including the activities of protein C (PC:A), protein S (PS:A) and antithrombin (AT:A), lupus anticoagulant (LA), anticardiolipin antibody (ACA), anti-β2 glycoprotein 1 (anti-β2GP1), total homocysteine (Hcy), as well as he total protein S antigen and free protein S antigen. The genetic analysis of *PROS1* gene were

performed by direct sequencing, and corresponding mutation sites in the family members were confirmed by reverse sequencing to confirm the presence of the mutation. 50 healthy subjects were selected as normal controls to exclude gene polymorphisms. Thrombin generation assay (TGT) was used to assess PS inhibition of thrombin generation in the plasma of proband's parents. Recombinant Protein S expression experiments was also performed. The RNA level of expressed PS was measured by real-time PCR, and the protein level was qualified by western blot and quantified by ELISA. The cellular distribution of the expressed protein S was analyzed with confocal microscopy.

Results The activity level of protein S in proband was significantly reduced to only 1.8%, while that in his parents decreased slightly, with 57% and 20.6% respectively. The total antigen level of PS was 13.5% in the proband, and 63.3% and 66.5% in his patients, which is consistent with the decrease level of their free protein S antigens, with 3.5% in the probands, and 53.4% and 37.6% in his parents, respectively. Direct sequencing results showed that the proband had compound heterozygous mutations in PROS1 gene. The first one is a heterozygous frameshift mutation (g. 99835-36 delCA insG) in the exon 13 of PROS1, resulting in early termination of protein coding (p.S517Sfs40X), which was inherited from his mother and was an unreported novel mutation; The second one is a heterozygous missense mutation in exon 14 of PROS1 (g.101936C>T, p.R561W), which may be associated with deep vein thrombosis as reported by the PROS1 database and was inherited from his father. Since the proband was treated with warfarin after diagnosis, we evaluated the inhibition of thrombin generation using his parents plasma. The experimental data showed that the inhibition rate of thrombin generation induced by protein S was only 15 ± 0.13% in proband's mother, which was significantly lower than that in normal control (42.8 ± 0.21%), while the inhibition rate of thrombin generation in the proband's father (40.6±0.3%) was slightly lower than that in normal control. In recombinant protein S expression study, we found that no significant difference was identified at mRNA level in these two mutations, compared to that in normal control. However, significant reduced level of PS was found in cell supernatant transfect with mutant plasmid, which was consistent with the significant elevated level of PS found in the certain cell cytoplasm. In addition , truncated PS protein was also found in cell cytoplasm transfect by PROS1 99835-36 delCA insG mutant plasmid, according to the western blot result. Mutant PS protein were further proved to be retained in cell cytoplasm analyzed by confocal microscopy.

Conclusions PROS1 p.R561W and PROS1 p.S517Sfs40X compound heterozygous mutations lead to hereditary type I PS deficiency in the current study. PROS1 p.S517Sfs40X mutation lead to truncated PS protein production. Both mutations affect the PS secretion from cell cytoplasm to plasma. The decrease activity and antigen level of protein S in the circulation affect the anticoagulant effect of PS, which ultimately lead to the recurrence of deep vein thrombosis in the proband.

PU-054

Analysis of early diagnostic value between galactomannan (GM) test in serum and bronchoalevolar lavage fluid in patients with invasive pulmonary aspergillosis

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Objective To analysis galactomannan (GM) test in serum and bronchoalevolar lavage fluid (BALF) in patients with invasive pulmonary aspergillosis (IPA) and its clinical value for early diagnosis.
Methods 25 cases of confirmed and clinically diagnosed IPA patients and 75 cases of non-pulmonary aspergillosis patients were enrolled in the study as patient group and control group, respectively. By using the GM test kits to carry out GM test in BALF and serum samples according to the instructions of the kit. The difference of I value were compared between two different samples. Different diagnostic thresholds and the value of detecting GM in two types of samples for early diagnosis of IPA were determined by ROC curve analysis.
Results There was significant difference of I value for GM test between serum and BALF both in patient and control groups (all＜0.05). When the I value for serum GM set at 0.5, the sensitivity was 40% and the specificity was 96%; when the I value of BALF GM set at 0.8, the sensitivity was 92% and the specificity was 65.3%. There is a high false positive in BALF GM . According to the ROC curve ,the area under the curve(AUC) of serum GM and BALF GM was 0.791 and 0.837, respectively.
Conclusions GM testing in serum and BALF samples has different value for early diagnosis of IPA. The GM test in serum has higher specificity, while the GM test in BALF has higher sensitivity. In clinical application, its should be combined with each other to better play the diagnosis of GM test.

PU-055

Three Groups of Full-length Real-time PCR assays for Rapidly Detecting Fifteen Carbapenem Resistance Genes of Molecular class A and B

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Objective Carbapenems possess the broadest spectrum of activity and greatest potency against Gram-positive and Gram-negative bacteria and therefore are widely regarded by clinicians as "last-line agents" or "antibiotics of last resort". Unfortunately, the recent emergence of carbapenemase-producing Gram-negative bacteria are of high concern because they are often associated to the occurrence of multidrug-resistant isolates for which very few (if any) antibiotic options remain available. Because of

the diversity and the risk of wide spreading of carbapenemases, reliable methods for their identification are especially important in clinical laboratories, where they can help to choose the optimal methods for treatment of patients and provide epidemiological control over the spreading of this type of resistance. Here, we are aimed to develop a rapid, labor saving method for the detection of 15 types of carbapenem resistance genes of molecular class A and B in clinical isolates.

Methods Three groups of full-length real-time PCR assays were developed for detecting 15 types of carbapenemase genes (molecular classes A and B) and 16S rDNA in clinical isolates. A total of 15 pairs of primers for carbapenemase genes and one pair of 16S rDNA primer were designed and divided into three groups according to the difference of Tm values of the amplicons. The sensitivity and specificity of the full-length real-time PCR assays were measured using purified recombinant plasmids containing the targeted complete carbapenemase genes. The application of the full-length real-time PCR assays was evaluated with 65 strains of clinical carbapenem-resistant isolates.

Results Based on the difference of Tm values of the amplicons, three groups of full-length real-time PCR assays were developed. The first group was for the amplification of blaIMP-2-like, blaDIM, blaSPM, blaGES and blaVIM-1-like, the second set targeted blaSIM, blaNMC, blaKHM, blaBIC and blaKPC, and the third group was for blaSME, blaGIM, blaSFC, blaVIM-2-like, blaNDM and 16S rDNA. Under optimized conditions, these assays achieved a limit-of-detection as low as 100 copies of each targeted genes. The presented method was applied to analyze the distribution of carbapenemases genes in 65 clinical carbapenem-resistant isolates, and their results were consistent with that of the conventional PCR assay.

Conclusions The three groups of full-length real-time PCR assays were suggested to be a rapid, cost-effective method with high sensitivity and specificity for detecting 15 types of carbapenemase genes (molecular classes A and B) and 16S rDNA in clinical isolates.

PU-056

Primary plasma cell leukaemia with “Spindle-shaped” morphology

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Objective Plasma cell myeloma presents highly diverse morphologies, which include mimicking variant hairy cell leukaemia (vHCL) morphology (Hazarika B *et al*, 2018), histiocyte-like morphology, large vacuoles, azurophilic granules(Shi M *et al*, 2016), as well as variant crystalline and Auer rod-like inclusions within cytoplasm (Mary T *et al*, 2017). The rare morphology of plasma cells is often misleading. Herein we report a strange case of plasma cell leukaemia with “Spindle-shaped” morphology which has not yet been reported .

Methods Magnetic resonance imaging showed no obvious abnormality. The complete blood count showed hemoglobin 71g/L, RBC 2.32×10^{12}/L, leukocytes 34.96×10^{9}/L, neutrophils 8.041×10^{9}/L and platelets 32×10^{9}/L. Peripheral blood smears revealed medium-to-

large atypical lymphoid cells (32%) with spindle morphology. Biochemical investigations showed creatinine 221.9μmol/L, uric acid(UA) 1098 μmol/L, LDH 2989 U/L, normal serum calcium 2.25 mmol/L. Coagulation tests results: PT 14.5s, INR 1.39, APTT 43s, fibrinogen 0.81g/L, D-Dimer 3.49 mg/l fibrinogen equivalent units (normal range <0.55); fibrin degradation products (FDPs) 15.2 μg/ml (normal range <5.0). Humoral immunity: IgG 6.32 g/L(7.0-16.0), IgA 0.34g/L(0.7-4.0), IgM 0.196g/L(0.4-2.8), complement C3c 0.866g/L(0.9-1.8), C4 0.746g/L(0.1-0.4), κ light chains 0.76g/l(1.7-3.7), λ light chains 1.33g/l(0.9-2.1), κ/λ 0.57. Immunofixation electrophoresis showed a trace amount of IgG-λ M protein. On flow cytometry, the side scatter/CD45 gated cell cluster lacked expression of CD19, CD20, CD10, or CD117 but expressed CD38, CD138 and CD56 (partly expressed) and λ light-chain restriction (bottom). The results of karyotyping analysis showed super complex karyotypes of multiple chromosomal aberrations (including number 1,3,4,7,8,9,10,13,14,15,1718,19,22 chromosomes). Carbohydrate antigen125 (CA125) >1000U/mL (normal range <35), ferritin 291.45 ng/mL (normal range <204), Cytokeratin19 (CYFRA21-1) 6.92ng/mL (normal range <2.08). Screening for 43 leukaemia-related fusion genes showed negative expression. A bone marrow aspiration revealed plasma cell clones accounted for 86.5% of total nucleated cells, most of which showed “Spindle-shaped” morphology (top).

Results Based on the clinical, biochemical, and radiologic parameters, and combined with the morphology and flow cytometry findings, a diagnosis of primary plasma cell leukaemia (PCL) was made.

Conclusions The present case highlights the importance of recognizing rare plasma cell variants, as well as the continuing value of morphological evaluation. The clinical significance or the cause of this morphologic change is not well characterized in current literature.

PU-057

Large malformed nuclear and flamboyant plasma cells in a patient of refractory multiple myeloma

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Objective Plasma cell neoplasms with large size, malformed nuclear and flamboyant morphology have not been described. The present case highlights the importance of recognizing rare plasma cell variants, as well as the continuing value of morphological evaluation.

Methods A 76-year-old man presented with a four-year history of bone pain, fatigue and weight loss. He had been diagnosed with multiple myeloma (MM) four years prior. He had since received numerous lines of treatment, including several immunomodulatory agents (Melphalan, thalidomide, lenalidomide, pomalidomide) and proteasome inhibitors (bortezomib, carfilzomib). Bone mineral density (BMD) scans and CT scans revealed thoracic fractures.The complete blood count showed hemoglobin 77g/L, RBC 2.36×10^{12}/L, leukocytes 4.32×10^{9}/L and platelets 219×10^{9}/L. Humoral immunity showed IgG 4.33 g/L(7.0-16.0), IgA 42.8g/L(0.7-4.0), IgM 0.186g/L(0.4-2.8),

κ light chains 14.6g/l(1.7-3.7), λ light chains 0.5g/l(0.9-2.1), κ/λ 29.2. On flow cytometry, the side scatter/CD45 gated cell cluster lacked expression of CD19, CD20, CD10, or CD117 but expressed CD38, CD138 and CD56 (partly expressed) and κ light-chain restriction. Serum protein electrophoresis and immunofixation electrophoresis revealed M-component immunoglobulin A (IgA)-κ paraprotein. Fluorescence in situ hybridization (FISH) displayed IGH(14q32) rearrangement, 1q21 site amplification. Bone marrow smear showed accumulation of mature and immature plasma cells up to 36.5%. These plasma cells are large in size and vary widely in morphology, most of which showed malformed nuclear and flamboyant morphology.

Results Based on the above results, the patient was eventually diagnosed with immunoglobulin A κ type, stage III group A multiple myeloma (MM).

Conclusions Plasma cell myeloma presents highly diverse morphologies, especially in refractory MM (Sarid N *et al*, 2016). The rare morphology of plasma cells is often misleading. Meanwhile, plasma cell neoplasms with large size, malformed nuclear and flamboyant morphology have not been described. The present case highlights the importance of recognizing rare plasma cell variants, as well as the continuing value of morphological evaluation.

PU-058

NLRP3 promotes tumor growth and metastasis in human oral squamous cell carcinoma

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Objective Oral squamous cell carcinoma (OSCC) is a well-known malignancy that accounts for more than 90% of all oral cancers. Inflammasomes are thought to have critical roles in cancer-related inflammation. This study was designed to investigate the expression and the role of the NLR family pyrin domain containing protein 3 (NLRP3) in OSCC.

Methods The mRNA and protein levels of NLRP3 in OSCC cell lines and the normal human immortalized oral epithelial cells (HIOEC) were determined by Real-time PCR and western blot analysis. The expression of NLRP3 and IL-1β in the paraffin-embedded OSCC tissues was evaluated by immunohistochemistry(IHC). The proliferation of OSCC cells was detected by MTT [3-(4,5-dimethylthiazol- 2-yl)-2,5-diphenyl tetrazolium bromide] assay and cell colony formation assay after reducing NLRP3 expression. The impact of NLRP3 knockdown on migration and invasion of OSCC cells was measured by transwell assay, epithelial phenotype marker E-cadherin and mesenchymal phenotype marker Vimentin, N-cadherin were examined by western blot. A xenograft mouse model was applied to investigate the influence of NLRP3 silence on tumor growth *in vivo*.

Results Significant higher expression of NLRP3 was observed in the OSCC cells. Obvious expression of NLRP3 and IL-1β was found in the paraffin-embedded OSCC tissues, and the NLRP3 expression levels were correlated with the tumor size, lymphonode metastatic status and IL-1β expression. Downregulating NLRP3 expression markedly inhibited the OSCC cell proliferation, migration and invasion. Further investigation about

EMT(Epithelial-to-mesenchymal transition)-related proteins indicated that the expression levels of E-cadherin and vimentin in OSCC cells were increased, while N-cadherin expression was decreased after NLRP3 knockdown. Downregulating NLRP3 expression in OSCC cells significantly reduced the tumor growth *in vivo*.
Conclusions Our data suggested that the increased expression of NLRP3 in OSCC was associated with tumor growth and metastasis, NLRP3 could be considered as a potential target for OSCC therapy.

PU-059

Study of Virulence factors and their correlation of Candida albicans isolated from oral cavity

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Objective To detect the expression of virulence factors of oral *Candida albicans in vitro*, including secretion of hydrolytic enzymes, biofilm formation and mycelium phase production
Methods The activities of secreted aspartylproteinase (SAP), phospholipase (PL) and lipase (Lip) of *Candida albicans* strains were detected by bovine serum albumin agar, egg yolk agar and tributyrate agar, respectively. The formation of biofilm was determined by crystal violet staining assay, and the expression of hyphal wall protein 1 gene (HWP1) was detected by real-time PCR. And antifungal susceptibility testing was performed by ATB FUNGUS 3 assay. Pearson correlation analysis and T tests were performed for statistical analyses.
Results Eighty percent of strains produced a high level of SAP. And 98% of strains displayed a high level of PL. While 78% of strains produced a medium level of Lip, none displayed a high level of Lip. All strains were able to form biofilm, and the ability of biofilm formation of 30 strains (60%) was strong. There was an association between the secretion of SAP and PL ($P<0.05$). No relationship was found between the other virulence factors, while there was no significant difference in the level of virulence factors in vitro and of HWP1 between drug-resistant strains and drug-sensitive strains.
Conclusions Most of strains displayed a high level of SAP, PL and a medium level of Lip, and produced biofilm strongly. And there was an association between the secretion of SAP and PL. The virulence of oral Candida albicans was independent of drug-resistance.

PU-060

Amelioration of type 1 diabetes induced by rSjFBPA derived from Schistosoma japonicum in murine model

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Objective Infections with helminth parasites or administration with their antigens could prevent or attenuate autoimmune diseases.
Methods Here we show that recombinant *Schisotosoma japonicum* Fructose-1,6-bisphosphate aldolase (rSjFBPA) alleviated type 1 diabetes mellitus (T1DM) accelerated by cyclophosphamide (CY) in nonobese diabetic (NOD) mice. The rSjFBPA, administered to the mice at a dose of 50μg once a week for 4 weeks via intraperitoneal injection, significantly reduced the diabetes incidence and ameliorated the severity of T1DM.
Results Disease attenuation was associated with suppression of IFN-γproduction of autoreactive T cells and with a switch to the production of Th2. Following rSjFBPA injection, regulatory T cells (Tregs) were remarkably increased, characterized by increased expression of IL-10 and TGF-β1
Conclusions Our study suggests that the helminth-derived proteins may evolve strategies to limit pathology by elevating the Th2 response and up-regulating Tregs towards the inflammatory tissue-damage proccess in T1DM.

PU-061

Changing trend in antimicrobial resistance of clinical gram-negative bacilli, 2013-2017: a retrospective study from a tertiary hospital in Shanghai

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Objective The aim of this study was to investigate the distribution and antimicrobial susceptibility of gam-negative bacilli isolated from patients in a tertiary hospital, Shanghai.
Methods From 2013 to 2017, all gram-negative bacilli strains were secretively collected and antimicrobial susceptibility testing was determined by using the Kirby-Bauer method.
Results A total of 3799 non-duplicate gram-negative bacilli strains were collected and E.coli were mostly isolated with a proportion of 50.7% (1925/3799), followed by P.aeruginosa (16.1%). A majority of organisms were isolated from sputum specimen (41.57%) and urine (34.95%). The average rates of extended-spectrum β-lactamase production among E.coli and K.pneumoniae were 63.3% and 52.5%. The carbapenem (imipenem and meropenem) resistance rates in E.coli were still less than 5%, while these among K.pneumoniae isolates increased from 3.4 to 17.9%. The resistance rate of P.aeruginosa strains to all antimicrobial agents ranged from 15% to 45% with a marked

resistance increase level in carbapenem. All A.baumannii isolates showed high resistance rates to most antimicrobial agents with a high rate of extensively drug resistance, but still susceptible to minocycline and tigecycline. At present, no resistance to tigecycline was detected among these gam-negative bacilli isolates.
Conclusions E.coli isolates were mostly common gram-negative bacilli in this study. All strains showed different resistance rates to antimicrobial agents and attention should be paid to the carbenem-resistance gram-negative bacilli and extensively drug resistance strains.

PU-062

Changes of adiponectin and adiponectin receptor 1 in diabetic rats of different courses during myocardial ischemic preconditioning

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Objective To investigate the different effects of adiponectin (APN) and adiponectin receptor 1 (Ad-R1) on myocardial ischemia-reperfusion (IR) injury and ischemic preconditioning (IPC) in different course of diabetic rats in vitro.
Methods The rat models of type 1 diabetes mellitus (T1DM) and type 2 diabetes mellitus (T2DM) were successfully established using streptozotocin and high-fat diet plus streptozotocin, respectively. These rats were divided into 2 groups: 4 weeks and 8 weeks. The model of isolated cardiac perfusion was established by Langendorff method. Each group was further divided into control (Con) group, IR group and IPC group. The activity of lactate dehydrogenase (LDH) and creatine kinase (CK) in coronary effluent was detected. The serum and myocardial levels of APN were determined by ELISA. The expression of Ad-R1 in the myocardial tissues was detected by Western blot. The area of myocardial infarction was detected, and the ultrastructure of ventricular papillary muscle was observed by transmission electron microscopy.
Results Compared with the corresponding IR group, the activity of LDH and CK in the IPC group at 4 weeks was significantly decreased ($P<0.01$), and the area of myocardial infarction was significantly reduced. However, no significant difference of each index in DM groups at 8 weeks was observed. Serum APN level was decreased in diabetic rats, especially in T2DM rats ($P<0.05$). The levels of APN and Ad-R1 in myocardium of normal rats had no difference among Con, IR and IPC groups. The level of APN in myocardium of T1DM rats had no difference in all subgroups, while the expression of Ad-R1 in myocardial tissue of IR group was significantly increased as compared with Con group ($P<0.01$) and IPC group ($P<0.01$) both at 4 and 8 weeks. In T2DM rats, the levels of APN in myocardium both at 4 and 8 weeks were decreased in IR group compared with Con group ($P<0.05$). The level of APN in IR group at 4 weeks was significantly decreased compared with IPC group, but had no significant difference at 8 weeks. The expression of Ad-R1 in myocardial tissue of IR group was significantly increased compared with Con group ($P<0.05$) both at 4 and 8 weeks. The level of Ad-R1 in IR

group at 4 weeks was significantly increased compared with IPC group (P＜0. 05), but had no significant difference at 8 weeks.

Conclusions The protective effect of IPC exists in diabetic rats at 4 weeks, whereas it disappears at 8 weeks. APN and Ad-R1 in myocardium were probably involved in the protective effect of IPC on T2DM rats.

PU-063

The effect of acupoint selection on the expression of ghrelin and ghrelin in the gastric fundus of diabetic gastroparesis rats---Supported by science and technology program of gansu province, project No. : 18JR3RA081

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Objective
To investigate the effect of different acupoints on GHSR and ghrelin expression in diabetic rats with gastroparesis (DGP)

Methods Fifty male Sprague-Dawley(SPF SD) rats were randomly divided into a blank control group, a model group, a ZNA group, a ZZN group, and a ZNA group (10 rats in each group).Except the blank group, the other 40 rats were established DGP model.After the model was successfully constructed, acupuncture treatment was performed once a day for 4 weeks.Serum and gastric fundus tissues were collected and real-time polymerase chain reaction (rt-pcr) was used to detect the expressions of ghrelin and GHSR mRNA in gastric fundus tissues.

Results Compared with the control group, dietary intake, GHSR mRNA expression and GHSR mRNA expression were significantly increased in the gastric fundus tissue model group, while intestinal propulsion rate, serum GHSR content and gastric fundus gray value were significantly decreased ($p< 0.05$).Compared with the model group, the intestinal propulsion rate, GHSR mRNA, serum ghrelin content and gastric fundus gray scale were significantly increased ($p< 0.05$).Dietary intake was significantly increased in the ZN group and ZNA group ($p<0.05$), and the expressions of ghrelin and GHSR mRNA in gastric fundus tissues were significantly increased ($p<0.05$), while serum ghrelin expression was significantly increased ($p<0.05$), and the content of ZN group was significantly decreased ($p<0.05$).

Conclusions These results suggest that acupuncture can improve gastrointestinal motility in patients with DGP, which is related to the content of GHSR and GHSR.It was suggested that local acupoint compatibility was superior to distal acupoint compatibility, and the selected part of acupoints was the key factor affecting compatibility effect and curative effect of acupoints.

PU-064

PLEK2 mediates metastasis and vascular invasion via ubiquitin-dependent degradation of SHIP2 in Non-small cell lung cancer

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Objective Metastasis is the leading cause of death for non-small cell lung cancer (NSCLC) patients. However, how lung cancer cells invade blood vessels during metastasis remains unclear. Here, based on bioinformatics analyses of GEO datasets, we found that PLEK2 might regulate NSCLC migration and vascular invasion. As little is known about the function of PLEK2 in NSCLC, we aimed to clarify this.

Methods We determined the prognostic value of PLEK2 in NSCLC tissue specimens. Expression analysis and wound healing, migration, and invasion assays were performed after modulating PLEK2 expression in vitro. A mouse xenograft model was used to assess its function in vivo. Human lung microvascular endothelial cells (HMVEC-Ls) were used to determine the effect of this protein on vascular invasion via endothelial-to-mesenchymal transition (EndoMT). Co-immunoprecipitation and His-tag pull-down assays were performed to identify PLEK2 functional interactors.

Results PLEK2 was significantly upregulated in TGFβ1-treated NSCLC cells through ELK1 transcriptional activation, highly expressed in NSCLC tissues, and negatively correlated with NSCLC overall survival. Meanwhile, PLEK2 overexpression significantly promoted NSCLC epithelial-to-mesenchymal transition (EMT) and migration, HMVEC-L EndoMT, and destruction of vascular endothelial barriers. PLEK2 knockdown inhibited TGFβ1-induced EMT and EndoMT. Furthermore, PLEK2 directly interacted with SHIP2 and targeted it for ubiquitination and degradation in NSCLC cells. Next, we confirmed that SHIP2 overexpression inhibits NSCLC EMT, migration, and invasion and showed that PLEK2 overexpression can activate SHIP2-associated TGF-β/PI3K/Akt signaling.

Conclusions Our results suggest that PLEK2 could be a novel prognostic marker and potential therapeutic target for NSCLC metastasis and vascular invasion.

PU-065

The PAX6-ZEB2 axis promotes metastasis and cisplatin resistance in non-small cell lung cancer through PI3K/AKT signaling

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Objective Paired-box 6 (PAX6) is an important transcription factor required for the function of human neuroectodermal epithelial tissues. Previous studies have suggested that it is also expressed in several types of tumors and has an oncogenic role. However, very little is known about its role in non-small cell lung cancer (NSCLC).

Methods Immunohistochemistry was used to detect PAX6 expression in human NSCLC tissue arrays (HLug-Ade050CD-01) and determine the relationship between PAX6 expression and clinical outcome in a microarray dataset with clinical follow-up information (HLugA180Su05). The effects of PAX6 on cell migration, invasion, epithelial-to-mesenchymal transition (EMT), and stem cell transformation were explored. Cisplatin resistance was assessed *in vivo* and *in vitro*. The Human Tumor Metastasis RT^2 Profiler PCR Array was used to analyze the molecular mechanism of PAX6 in NSCLC metastasis. GEO data was downloaded for survival and correlation analyses. Signaling pathway was assessed by western blotting.

Results PAX6 expression levels were upregulated in human lung cancer tissues and correlated with poor clinical outcomes. Overexpression of PAX6 significantly promoted NSCLC EMT and metastasis, whereas knockdown of PAX6 inhibited these processes. PAX6 was found to commonly correlate with EMT-mediated stem cell transformation, thereby inducing cisplatin resistance. Using the RT^2 Profiler PCR Array, we found that *WNT5A*, *EGFR*, *ZEB2* were differentially regulated in response to PAX6 modulation. PAX6 directly bound to the promoter region of *ZEB2*. ZEB2 was upregulated upon PAX6 overexpression and downregulated upon PAX6 knockdown, whereas E-cadherin expression showed opposite patterns. Moreover, p-PI3K and p-AKT were significantly enhanced by PAX6, which was reversed by the addition of the PI3K-AKT inhibitor, LY294002. These data suggest that PAX6 can mediate E-cadherin downregulation through PI3K/AKT signaling pathway by directly binding the promoter region of *ZEB2* in NSCLC cells.

Conclusions The PAX6-ZEB2 axis promotes metastasis by mediating E-cadherin downregulation via the PI3K/AKT signaling pathway, thereby mediating cell migration, stem cell transformation, and cisplatin resistance, ultimately affecting survival in NSCLC patients.

PU-066

ERBB3 novel compound heterozygous variant impairs PI3K/AKT and ERK signaling pathways in a patient with Silver-Russell like syndrome

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Objective Gain-of-function mutations in the *Erb-B2 receptor tyrosine kinase 3* (*ERBB3*) gene contribute to the occurrence and development of a variety of human carcinomas through activation of phosphatidylinositol 3-kinase/AKT and extracellular signal-regulated kinase (ERK) signaling. Homozygous germline variants of the *ERBB3* gene were recently identified whose loss of function may cause autosomal recessive congenital contractural syndrome. Our aim is to identify the disease-causing gene in an individual with several features of Silver-Russell syndrome as well as atypical features including bilateral nystagmus and amblyopia, immunodeficiency, anemia, and liver damage.

Methods Clinical-exome sequencing was performed to identify disease-causing gene in a 24-month-old Chinese female patient. The pathogenicity of the identified variants was evaluated using in silico tools and in vitro functional studies.

Results DNA sequencing revealed the compound heterozygous mutation c.1253T>C (p.I418T) and c.3182dupA (p.N1061Kfs*16) in the *ERBB3* gene. Although the p.I418T variant was predicted to be harmful, functional studies showed that it resulted in normal expression of ERBB3, which was capable of interacting with ERBB2. However, the mutation impaired ERBB3 phosphorylation, consequently blocking ERBB2 phosphorylation and AKT and ERK activation. The c.3182dupA variant generated a novel truncated protein that also lacked the capacity to activate downstream signaling pathways.

Conclusions A novel compound heterozygous variant of the *ERBB3* gene associated with a complex phenotype was identified. Germline loss of function of the ERBB3 protein contributed to the phenotype of the patient.

PU-067

Circulating tumor cells and SALL4 expression in CTCs for distinguishing patients with gestational trophoblastic disease

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Objective Gestational trophoblastic disease (GTD) is a group of tumors arising from the placenta with varying tendencies for invasion and metastases. With the development of effective chemotherapy, recognition of prognostic factors, and sensitive assays for human chorionic gonadotropin (hCG), GTN has become one of the curable human malignancies. However, for most patients with non-molar pregnancy, especially postpartum choriocarcinoma, delays in diagnosis can lead to unfavorable outcomes due to widespread metastasis. Also, evaluation the malignancy potential of HM after suction is not only time wasting but often confounded by residual pregnancy. Therefore, exploring new biomarkers that can discriminate GTN from other hCG-elevated circumstances is of utmost importance. In this study, we applied Canpatrol™ CTC enrichment technique, which relies on an ISET (isolation by size of epithelial tumor cells) system, and set of probes for detecting epithelial and mesenchymal markers in conjunction with SALL4 probes to characterize subsets of CTCs in GTD patients.

Methods GTD patients visiting Peking Union Medical College Hospital and Cancer Hospital, Chinese Academy of Medical Sciences, from October 2016 to May 2018 were recruited in this study. Normal intrauterine pregnant volunteers (NIUP, first trimester) were included as controls. The CanPatrol™ CTC detecting technique (SurExam, Guangzhou, China) was used to isolate and classify CTCs in peripheral blood as previously described. Briefly, erythrocytes were lysed and nucleated cells were isolated using an 8μm filtration system. RNA in situ hybridization (ISH) was performed to identity and classify CTCs using a cocktail of probes for four epithelial biomarkers [cytokeratins (CK) 8, 18, 19, and epithelial cell adhesion molecule (EpCAM)], two mesenchymal biomarkers (Twist1 and Vimentin), and a leukocyte marker (CD45). Finally, cells were stained with 4, 6-diamidino-2-phenylindole (DAPI) (Sigma, USA) for 5 min and analyzed with under automated imaging fluorescence microscope (Zeiss, Germany). Leukocytes were characterized as CD45+ cells. Based on the expression of epithelial and mesenchymal markers, CD45- CTCs were further classified into three phenotypes as: (1) E-CTC -cells positive for epithelial markers; (2) E/M-CTCs -cells co-expressing epithelial and mesenchymal markers; (3) M-CTCs- cells positive for mesenchymal markers. SALL4 expression in each CTC was also determined by using optimized four-color RNA-ISH approach.

Results A total of 41 patients, including 12 HM, 12 IHM, 13 CCA, 3 PSTT and 1 ETT, were enrolled from 2016-2018. 22 age matched volunteers in their 1st trimester of pregnancy, confirmed as normal intrauterine pregnancy (NIUP) by obstetricians, were enrolled as controls. For the GTN patients, CTCs were detected in all the 29 patients, which included 12 IHM, 13 CCA, 3 PSTT and 1 ETT, with a median of 11 (range: 1 to 49). The average number of E-CTCs, E/M-CTCs and M-CTCs was 1 (range: 0 to 6), 8 (range: 0

to 37), and 1 (range: 0 to 15), respectively. The distribution of each CTC phenotype was assessed after stratification of patients by age, FIGO stage, serum β-hCG level and prognostic scores. The results of Spearman's rank correlation analysis indicated a strong correlation between serum β-hCG level and the number of total CTCs (r=0.473 and P=0.009) as well as E/M-CTCs (r=0.375 and P=0.033). Besides, significant correlation between prognostic score and M-CTC number was also revealed(r=0.362 and P=0.038).

Kruskal-Wallis test indicated significant differences in total number of CTC, E/M-CTC and M-CTCs among the NIUP, HM and GTN groups (P<0.01). ROC analysis was conducted to further validate the clinical utility of CTC in distinguishing GTD from NIUP, and area under the ROC was 0.826 with 95% CI 0.728 to 0.925. According to the Youden index, the most optimal cut-off point was set at 8.5 cells/4 ml (sensitivity 53.66%, specificity 100%). The sensitivity of CTCs in the diagnosis of HM and GTN was 41.7% (5/12) and 58.6% (17/29), respectively.

SALL4 transcript and EMT markers were detected in 20/22 cases, including 5 HMs and 15 GTNs. Depending on SALL4 expression (number of purple signal dot), CTCs were classified as: $CTC^{SALL4=0\sim2}$, $CTC^{SALL4=3\sim5}$, $CTC^{SALL4>=6}$. As shown in table 4, $CTC^{SALL4=0\sim2}$ was detectable in all 20 positive cases, while $CTC^{SALL4=3\sim5}$ or $CTC^{SALL4>=6}$ was only detected in GTN cases with detection rate as high as 66.67% (10/15), no $CTC^{SALL4=3\sim5}$ or $CTC^{SALL4>=6}$ was detected in HM cases. For different type of GTN, the detection rate of $CTC^{SALL4=3\sim5}$ or $CTC^{SALL4>=6}$ was 50%, 100% and 66.67%, respectively in IHM (4/8), CCA (4/4) and PSTT (2/3).

Conclusions In conclusion, our findings provide evidence for the first time on the potential application of CTC phenotypes and SALL4 expression in GTD. Confirmation by large-scale trials would shed more light on the carcinogenic role of SALL4 in trophoblasts.

PU-068

The Relationship between Sulfatides and Cardiovascular Diseases

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Objective The sulfatide is an ester of sulfuric acid with galactosamide at the C3 position of the galactosyl residue.

Methods Sulfatide is extensively distributed in human organs and serum. It plays an unique role in multiple systems with the development of the detection means and related researches on sulfatide.

Results Sulfatide has been found to be involved in the mechanism of human cardiovascular diseases such as atherosclerosis in recent studies. Regulating the level of sulfatide may be a novel method for improving even preventing from cardiovascular disease.

Conclusions Here we mainly elaborated the pthological mechanism of sulfatide in cardiovascular disease, with a review to further understanding the relevance of sulfatide and cardiovascular disease, seeking for new therpy target for the disease.

PU-069

TFCP2 Is Required for YAP-Dependent Transcription to Stimulate Liver Malignancy

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Objective Although YAP-dependent transcription is closely associated with liver tumorigenesis, the mechanism by which YAP maintains its function is poorly understood.
Methods Cell viability, colony formation and caspase3/7 activity were assessed using MTT, soft agar and caspase 3/7 Glo assays, respectively. Transcription factors binding with TFCP2 and YAP were measured using co-immunoprecipitation (co-IP) combined with Western Blotting (WB). Immunofluorescence (IF), WB and Immunohistochemistry (IHC) were used to investigate the activity of YAP after indicated treatment. Luciferase reporter assay, chromatin immunoprecipitation (ChIP) and quantitative RT-PCR (qPCR) were used to investigate the mechanism how TFCP2 and YAP interacted with the promoter of the target genes.
Results Here, we show that TFCP2 is required for YAP-dependent transcription and liver malignancy. Mechanistically, YAP function is stimulated by TFCP2 via a WW-PSY interaction. TFCP2 also maintains YAP stability by inhibiting bTrCP. Notably, genomic co-occupancy of YAP and TFCP2 is revealed. TFCP2 acts as a transcription co-factor that stimulates YAP transcription by facilitating YAP binding with YAP binding motif (YBF)-containing transcription factors. Interestingly, TFCP2 also stimulated the YAP-TEAD interaction and TEAD target gene expression. Finally, several genes co-regulated by YAP and TFCP2 that contribute to YAP-dependent tumorigenesis are identified and verified.
Conclusions We establish a model showing that TFCP2 acts as a YAP co-factor to maintain YAP-dependent transcription in liver cancer cells, suggesting that simultaneous targeting of both YAP and TFCP2 may be an effective therapeutic approach.

PU-070

Unique mutation of ERG11 of Candida auris in Shenyang, China

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Objective The multidrug-resistant yeast *Candida auris* was first reported in 2009 in Japan and has since been independently, almost simultaneously, emerging in many places worldwide. In 2018, we have reported fifteen cases of fluconazole-resistant *Candida auris* in Shenyang, China. As recently described in this journal, different mutations in *ERG11* of *C. auris* were associated with azole resistance in each geographic clade.

The aim of this study was to better understand evolutionary patterns of C. auris from China at the molecular level by investigating the mutations in *ERG11*.

Methods We sequenced the genome of RICU4 (the first bloodstream *C. auris* isolate found in China) using Illumina next-generation sequencing technology. Furthermore, we also sequenced the Erg11 amino acid mutation region of the 22 C. auris isolates discovered in China following RICU4 using Sanger sequencing for the verification purpose.

Results Whole-genome sequence of RICU4 fell within the South African *C. auris* clade, but formed a single subclade. Sequence analysis of *ERG11* revealed the mutation of F126L, a hot-spot amino acid substitution which was proved to significantly increase the fluconazole resistance in *C. auris*. By the BLAST comparison, I74L, a unique substitution of Erg11 amino acid, was identified within these isolates. This new substitution of Erg11 amino acid has not yet been reported in homologous sequence of *Candida albicans*.

Conclusions By comparing the Erg11 amino acid sequences of the C. auris isolates representing distinct geographic regions, China and South Africa (PIS55918) exhibit almost identical Erg11 sequence with the same F126L substitution as the South Africa clade except for the newly discovered I74L substitution. Geographically, Shenyang is in the Northeast of China, which is more adjacent to Asian countries than to South Africa, but the RICU4 isolate is genetically closer to the South Africa clade than to those Asian clades. This may suggest that the South Africa strains have higher transmission power or that Chinese people have a higher susceptibility to the South Africa strain. In addition, the role of I74L in the fluconazole resistance of *C. auris* remains unclear and needs a close study. A more comprehensive study on the *C. auris* isolates from China was required to further discover the fluconazole resistance mechanisms and the potential evolutionary trajectories of the *C.auris* clones.

PU-071

Association between mitochondrial DNA content and baseline serum levels of HBsAg in chronic hepatitis B infection

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Objective Recent studies have demonstrated a potential link between mitochondrial DNA (mtDNA) content and cirrhosis or hepatocellular carcinoma (HCC). However, there are few studies evaluating mtDNA content as a noninvasive marker of chronic hepatitis B infection (CHB).

Methods We conducted a case-control study to determine mtDNA content in peripheral blood leukocyte (PBL) samples from 76 CHB cases naïve to antivirus therapy and 96 healthy controls, and then evaluated the association between mtDNA content and baseline serum concentration of HBV markers.

Results CHB cases had significantly higher mtDNA content than healthy controls (1052.85 vs 618.98, $P < 0.001$). Pearson's correlation analysis revealed that mtDNA content was negatively correlated with the baseline levels of hepatitis B surface

antigen (HBsAg) (r=-0.291, *P*=0.011) in CHB patients. In a trend analysis, a statistically significant association was detected between lower mtDNA content and increasing levels of HBsAg (*P*=0.015).

Conclusions

Our study provides the first epidemiological evidence that mtDNA content of CHB cases naïve to antivirus therapy is significantly higher than healthy controls and the levels of mtDNA content is negatively associated with HBsAg. mtDNA content may serve as a potential noninvasive biomarker of CHB which may need more researches to validate.

PU-072

LPS enable murine "CD4+ T cell help"-independent CD8+ T cell responses in the liver

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Objective Chronic hepatitis B virus (HBV) infection is difficult to overcome because of exhaustion of cytotoxic CD8+T cells. The hepatic microenvironment is known to constrain rather than to support development of anti-viral immunity. Recently, it has been reported that signaling via Toll-like receptors (TLR) induced intrahepatic myeloid-cell aggregates for T cell population expansion (iMATEs) without causing immunopathology. The iMATEs arise during acute viral infection but are absent during chronic viral infection. In the current study, we investigated the impact of TLR4 ligand lipopolysaccharide (LPS) on iMATEs formation and virus-specific CD8+ T cell response by using the HBV hydrodynamic injection (HI) mouse model.

Methods 6-8 weeks old male C57BL/6 mice were hydrodynamically injected with HBV replicating plasmid pSM2. One day after the HBV plasmid injection, HBV-replicated mice were peritoneal injected with TLR4 ligand LPS and CD4 antibody, either separately or in combination.

Results We found that injection of LPS resulted in an accelerated virus clearance in HBV HI mouse model, which is mediated by a fast intrahepatic CD8+ T cell expansion and activation independent of CD4+ T cell help. The frequencies and the absolute numbers of HBV-specific CD8+ T cells were higher in the livers of LPS-treated mice than that of control. Further histochemistry analysis showed that LPS induced intrahepatic lymphocyte infiltrates resembling intrahepatic myeloid cell aggregates of T cell expansion, which were also observed in CD4-depleted mice, but were almost absent in HBV-replicated wild-type controls. Moreover, we also found that Treg depletion enhanced the formation of iMATEs and HBV-specific CD8+ T cell responses.

Conclusions The data suggest that LPS has the potential to induce the iMATEs formation. And thereby iMATEs enhance HBV-specific CD8+ T cells immunity which was independent of CD4+ T cell help but was restricted by regulatory control of CD25+CD4+ Treg cells. iMATEs are believed to be dynamic structures that overcome liver tolerant environment limiting CD8+ T cell responses during chronic HBV infection and may be used in new therapeutic vaccination strategies.

PU-073

A case report of craniofrontonasal syndrome in China

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Objective Craniofrontonasal syndrome (CFNS) is a rare craniofacial dysplasia disease with X-linked dominant inheritance. The patients present brachycephaly, frontal bossing, coronal craniosynostosis, a bifid nasal tip, hypertelorism, sprengel deformity, syndactyly, wiry hair and so on. Its expressivity is different between females and males, and heterozygous females are usually more severe than hemizygous males. The causative gene *EFNB1* is at Xq13, consisting of 5 exons, and the protein ephrin B1 encoded by this gene is a type I membrane protein. This syndrome has been rarely reported in China at present. Here we reported a study on clinical phenotype and gene mutation of a case of CFNS in China, hoping to improve the clinician's understanding of the disease.
Methods The genomic DNA of the patient, her parents and brother was extracted from venous blood. We analyzed and confirmed the causative gene by utilizing targeted next generation sequencing and Sanger sequencing.
Results The patient was a 1-month-old female infant, and she showed brachycephaly, low forehead, low set ears, widening of palpebral fissure, abnormal palms, shortened the fourth phalanx of right foot and asymmetry face and thorax. The result of chromosome examination was normal. We detected a heterozygous nonsense mutation (c.196C>T, p.Arg66*) in *EFNB1* gene, while her parents and brother were wild type, indicating a de novo mutation. What's more, this mutation has been reported to be pathogenic in foreign literatures.
Conclusions According to the clinical phenotype and sequencing results of *EFNB1* gene, the patient was diagnosed as craniofrontonasal syndrome. Our work broadened the mutation spectrum of the *EFNB1* gene and extended the genotype-phenotype relationship in the study of EFNB1.

PU-074

Patients with respiratory tract infection of respiratory syncytial virus detection rate and The analysis of clinical features

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Objective Patients with respiratory tract infection in respiratory syncytial virus detection and analysis of clinical features.
Methods 745 cases of patients' sputum with respiratory tract infection in Sichuan Mianyang 404 hospital Between April 2016 to January 2017, using immunofluorescence method to detect respiratory syncytial virus.

Results (1) 301 cases of Respiratory syncytial virus were positive, the total detection rate 40.403% .(2) espiratory syncytial virus infection of specimens mainly comes from the spring and winter.(3) Most of patients with respiratory syncytial virus infection for infants and young children under the age of 3, clinical diagnosis of bronchial pneumonia and acute bronchitis.

Conclusions espiratory syncytial virus in winter and spring season has the highest detection rate, and with more infants and young children under the age of 3 bronchial pneumonia and acute bronchitis.

PU-075

Pro-coagulant circulating microparticles carry proteins and participate in the pathogenesis of preeclampsia

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Objective In this study, we aimed to detect the level of total circulating microparticles (MPs) in pregnant women with preeclampsia (PE) and analyze the proteome in MPs to explore the role of MPs in the pathogenesis and progression of PE.

Methods From December 2016 to June 2018, we consecutively enrolled 98 pregnant women with PE, 54 healthy pregnant women, and 51 healthy non-pregnant women, whose MP levels were detected by flow cytometry and compared. Protein products extracted from subjects MPs were analyzed by high performance liquid chromatography mass spectrometry.

Results The level of total MPs in the healthy pregnant group was significantly higher than those in the non-pregnant group [159.87 (113.25, 218.18)/μl vs 94.10 (53.35, 140.23)/μl, P = 0.004], but was not significantly different from those of the PE group. By proteomic profiling, 30 differential proteins were obtained between healthy pregnant women and healthy non-pregnant women, which were closely related to biological processes such as complement and coagulation cascades, angiogenesis and so on; 14 differential proteins were found between PE patients and healthy pregnant women, which were closely related to biological processes such as coagulation cascades, complement and inflammatory reactions, angiogenesis and so forth.

Conclusions The level of circulating MPs may reflect the hypercoagulability of preeclampsia. In addition, circulating MPs may be involved in the pathogenesis of PE by their carrying proteins through various pathways, and have potential value in the intervention of PE.

PU-076

Donor polymorphisms of Rap1A rs494453 associated with the risk of hepatocellular carcinoma recurrence following liver transplantation in a Han Chinese population.

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Objective Hepatocellular carcinoma (HCC) recurrence after liver transplantation(LT) severely restricts the long-term survival of patients. Rap1A has been considered to be involved in hepatocarcinogenesis and metastasis. Additionally, there is a study demonstrating the significant association between Rap1A gene rs494453 polymorphism and HCC, but no study investigated the association of the Rap1A rs494453 polymorphism with the risk of HCC recurrence following LT.
The purpose of this study was to assess the potential association between the Rap1A gene rs494453 polymorphism of donors and recipients and hepatocellular carcinoma recurrence after LT.
Methods Seventy-four patients with HCC undergoing LT from July 2005 to June 2015 were identified for this analysis. We genotyped a single-nucleotide polymorphism (rs494453) in both donors and recipients and evaluated the association between the polymorphism and risk of tumor recurrence.
Results The donor Rap1A rs494453 polymorphism was found to be significantly associated with HCC recurrence following LT. In multivariate logistic regression analysis, Milan criteria, microvascular invasion and donor Rap1A rs494453 genotype were confirmed to be independent risk factors for HCC recurrence. Kaplan-Meier survival curves showed that patients carrying donors homozygous GG/AG had a significantly lower recurrence-free survival and overall survival than AA patients. Cox proportional hazards modeling indicated that TNM stage or Milan criteria, microvascular invasion, and donor Rap1A rs494453 genotype were independent factors for the clinical outcomes of LT patients.
Conclusions Donor Rap1A rs494453 polymorphism is associated with an increased risk of HCC recurrence following LT and has a potential clinical value for the prediction of HCC recurrence after LT.

PU-077

p62/SQSTM1 Overexpression Enhances Proliferation and Metastasis Via Promotion of ERK Signaling and EMT Progression in Nasopharyngeal Carcinoma

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Objective Increasing evidence has shown that p62 plays an important role in tumorigenesis. However, relatively little is known about the association between p62 and tumor invasion and metastasis; in addition, its role in NPC (nasopharyngeal carcinoma, NPC) has not been investigated.
Methods In this study, we analyzed NPC paraffin tissues and cell lines. p62 was down-regulated with shRNA and up-regulated through plasmid transfection. Subsequently, cell viability, colony formation, migration, invasion and autophagy assays were performed . The expression of p62 was also assessed in patient tumor samples by immunohistochemistry and anti-p62 autoantibodies in sera were detected by ELISA. These data were correlated with clinicopathological parameters.
Results We confirmed that p62 was significantly up-regulated in NPC tissues. Furthermore, high expression of p62 was observed in NPC cell lines, and especially in the highly metastatic 5-8F line. In vitro, down-regulation of p62 inhibited proliferation, clone forming ability, autophagy, migration, and invasion in 5-8F cells, whereas p62 overexpression resulted in the opposite effects in 6-10B cells. Moreover, we confirmed that p62 promotes NPC cell proliferation, migration, and invasion by activating ERK. Clinical analysis indicated that high p62 expression correlates with lymph node and distant metastasis ($P < 0.05$). Serum anti-p62 autoantibodies were increased in NPC patients and levels were associated with metastasis.
Conclusions Taken together, our findings provide evidence that p62 is closely related to the tumorigenesis and metastasis in NPC and might be a promising therapeutic target for this disease. Furthermore, serum anti-p62 autoantibodies represent a potential diagnostic marker for NPC.

PU-078

Analysis of the correlation between PCT and commonly used clinical infectious indicators

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Objective To explore the correlation between PCT and common clinical infectious indicators: white blood cell count (WBC), neutrophil percentage (NEU%), lymphocyte percentage (LYM%) and C-reactive protein (CRP), in order to further analyze the value

of PCT in the diagnosis of clinical infectious diseases, and to provide experimental basis for clinical diagnosis, treatment and prognosis judgement.
Methods Data of patients including PCT, white blood cell count, lymphocyte percentage, neutrophil percentage and C-reactive protein, were collected from the Laboratory Department of Affiliated Hospital of Shaanxi University of Traditional Chinese Medicine from January to March 2017. The correlation between them was analyzed by SPSS 20.0 software.
Results The values of WBC, NEU (%), LYM (%) and CRP in abnormal PCT group were higher than those in normal PCT group.
Conclusions PCT is positively correlated with WBC, NEU (%) and CRP, and negatively correlated with LYM (%). Therefore, PCT is closely correlated with commonly used infection indicators, which is of great significance in the diagnosis of clinical infectious diseases.

PU-079

Drug resistant mechanism and homology analysis of carbapenem-resistant Enterobacteriaceae isolated from different sites of same patient in intensive care units

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Objective To investigate the drug resistant mechanism and homology of carbapenem-resistant *Enterobacteriaceae* (CRE)isolated from different sites of one patient in the intensive care unit(ICU).
Methods The active screening of CRE in fecal or anus swabs was carried out for the patients who were hospitalized the ICU of a grade-A tertiary hosipital in Yunnan from January 1, 2017 to December 30,2018. If CRE was colonized in fecal or anus swabs ,some specimens for example, urine, sputum, drainage fluid, wound tissue, etc from other parts of the patient during the same period were collected to screen CRE. The collected CRE were identified and tested for drug sensitivity and phenotypic validation, and the clinical data and laboratory results were analyzed. Carbapenems resistance genes were detected by Polymerase chain reaction(PCR)and sequenced.The homology of CRE isolated from different sites of one patient was analyzed by Randomly amplified polymorphism DNA(RAPD) technique.
Results There were 1518 hospitalized patients to the ICU during the study period,and 1502 patients involved in screening, The rate of active screening of CRE was 98.95%（1502/1518）, the rectum colonization rate of active screening of CRE was 4.73%（71/1502）, The rate of CRE was detected only in rectum was 25.35%（18/71）,The rate of CRE was detected in two parts was 11.27%（8/71）, The rate of CRE was detected in three parts was 49.30%（35/71）, The rate of CRE was detected in four parts was14.08%（10/71）, Carbapenem-resistant *Klebsiella pneumoniae*(CRKP) strains were dominant among the pathogens,accounting for 87.32%（62/71）, All the CRE screened from two or more parts were CRKP.The results of drug sensitivity and phenotypic validation of CRE

isolated from different sites of one patient were same.The positive rate of carbapenems resistance genes KPC-2,NDM-1,VIM-2 and IMP respectively were 69.83%、17.32%、8.38% and 6.70%, the gene OXA-48was not detected.The type of carbapenems resistance genes of was same (92.45%). 161 strains of CRE isolated from two or more sites of one patient were classified into seven different clones by the RAPD technique,and the clone D was epidemic strain. CRE isolated from different sites of 94.34% patients were from same clone.

Conclusions Carring KPC-2 gene is the main cause leading to the drug resistance of CRE isolated from patient, and the CRE isolated from different sites of one patient have higher relatedness. It is necessary to active screening CRE and Strengthen prevention and control measure in clinic, the therapy method for the patient of CRE colonization and infection by early detection, early intervention, early treatment.

PU-080

Prenatal diagnosis of Down screening in the second trimester

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Objective With the development of society and the change of people's ideas, the state's emphasis on the quality of the next generation of the population has also increased significantly compared with the previous years.At the same time, in view of the recent relaxation of the two-child policy, women of appropriate age are marrying late and having childbearing later.It is foreseeable that older mothers will become more and more common.In order to further promote sustainable development, the importance and importance of improving the quality of population should be paid more attention to.In turn, prenatal screening and prenatal diagnosis are all the more important. Among them, Down's is the first child to be found and most frequently born, and at present there is no effective cure for the children born. Families have to pay a heavy economic price and bear tremendous mental pressure, and the country has to pay a lot of manpower and material resources.As a result, people should be more careful to prevent the birth of congenital children in advance of the tragedy in maternal and fetal situations.

Methods The application of time-resolved fluorescence immunoassay in 2491 cases of the second trimester (14-20(+6day)week) women serum markers of alpha-fetoprotein and free chorionic gonadotropin β subunit two indicators double labeling kit, screening results are associated with the use of risk computer software, such as LifeCycle for Prenatal Screening, to calculate Down's syndrome risk.Ds cutting risk value is 1:250, when more than 1:250 for Ds high-risk pregnant women, the analysis of the karyotype of fetal blood or amniotic fluid cells after 20 weeks of gestation can effectively track the real-time situation of fetus and pregnant women.

Results In 2491 pregnant women after prenatal screening, 213 high-risk pregnant women were screened out, the positive rate was 8.6% (213/2491), of which Ds accounted for 172 cases, the positive rate was 6.9% (172/2491),Among them, there were 172 cases of Ds positive pregnant women, and the positive rate was 6.9% (172/2491) Prenatal

diagnosis of umbilical cord blood sampling was performed in 73 patients, accounting for 42.4% (73/172) of high-risk pregnant women screened for Ds, 8 cases of fetal chromosomal abnormalities were found, the abnormal detection rate was 11% (8/73), There were 5 Down's syndrome, 2 trisomy 18- syndrome, and 1 balanced translocation. The risk value of adverse pregnancy outcomes in the Down's screening high-risk group and the low-risk group was 6.1% (13/213) and 2.5% (56/2278), respectively, with a significant difference (P <0.05).

Conclusions Prenatal screening during the second trimester of pregnancy can effectively predict whether the intrauterine fetus is abnormal and whether or not it will lead to an adverse pregnancy outcome, and as age increases, the incidence of Down's syndrome will increase accordingly, combining prenatal diagnosis can reduce the birth of a congenital defect to some extent.

PU-081

Analysis of tuberculosis drug resistance in Xi'an in 2017

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Xi'an Chest Hospital

Objective The occurrence and prevalence of multidrug-resistant tuberculosis (MDR-TB) is one of the main reasons for the rebound of tuberculosis since the mid-to-late 1980s. Prevention and control of resistant (poly) drug tuberculosis has become the main task of current tuberculosis control, and understanding the basic data and epidemiological characteristics of tuberculosis drug resistance is an important basis for the development of prevention and control of drug-resistant tuberculosis. Epidemiological surveys showed that drug-resistant tuberculosis epidemics are particularly serious in areas with poor economic and health conditions and medical conditions, and there are significant regional differences in the epidemiological characteristics of tuberculosis and drug-resistant tuberculosis. Therefore, it is important to understand the relevant data and epidemiological characteristics of tuberculosis resistant (multiple) drugs in this city to promote the control of tuberculosis.

Methods Body fluid samples from patients from Xi'an Chest Hospital from January 2017 to December 2017 was collected, Mycobacterial liquid culture was performed, Mycobacterial species identification was detected by PCR-fluorescence probe method and DNA microarray method. MGIT 960 liquid susceptibility method was used to mesure the anti-tuberculous mycobacterial first-line susceptibility (streptomycin, isoniazid, rifampicin, ethambutol), solid ratio method was used for Mycobacterium tuberculosis Second-line susceptibility testing (prothioanisone, capreomycin, moxifloxacin, rifabutin, amikacin, sodium p-aminosalicylate, levofloxacin).

Results A total of 27867 specimens were collected, and 5941 cases were positive for mycobacterial culture. Among them, 2718 were positive in Xi'an area, 41 cases were non-tuberculous mycobacteria and 2677 cases were Mycobacterium tuberculosis. A total of 2677 samples of Mycobacterium tuberculosis were tested for anti-tuberculosis drug susceptibility. The results showed that a total of 619 specimens were drug resistant, and the total drug resistance rate was 23.12%, including 369 multidrug-resistant cases,

and the multi-drug resistance rate was 13.78%. The resistance rates of 11 anti-tuberculosis drugs were as follows: streptomycin (697/2677, 26.03%) > isoniazid (670/2677, 25.03%) > rifampicin (429/2677, 16.03) %) > Levofloxacin (297/2677, 11.10%) > rifabutin (295/2677, 11.02%) > ethambutol (268/2677, 10.01%) > Moxifloxacin (261/2677, 9.75%) > Sodium p-aminosalicylate (134/2677, 5.01%) > Amikacin (83/2677, 3.10%) > Capreomycin (81/2677, 3.03%) > Propionamide (27/2677, 1.01%).

Conclusions The basic data of tuberculosis drug resistance and the resistance rate of common anti-tuberculosis drugs in Xi'an City were obtained through this study. The results of this study have certain reference value for the diagnosis and treatment of tuberculosis and drug-resistant tuberculosis in the region and the use of drugs by clinicians.

PU-082

A case report of Salmonella in the intracranial and intestinal tract

Rui Cui,Feng Xie,Wei Lei,Lihong Li
China-Japan Union Hospital of Jilin University

Objective Salmonella is an important zoonotic disease, also a common pathogenic microorganism that causes bacterial foodborne origin worldwide

Methods Now report a case of patient with intracranial and intestinal infections of Salmonella in Dublin

Results The intracranial pus secretion was cultured as Salmonella, and the culture results were the same as those of the pus culture. The serotype was identified as Salmonella dublin. The results of drug susceptibility test showed that it was sensitive to ceftriaxone and compound sulfamethoxazole, and it was resistant to levofloxacin and ampicillin.

Conclusions Salmonella infection in Dublin should be paid attention to, and strive for early detection and early treatment to minimize the suffering of patients.

PU-083

Methodological evaluation of CK-MB by latex immunoturbidimetry

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Objective To evaluate the performance of latex immunoturbidimetric as a method for quantifying CK-MB mass, which provides a reference to select suitable detection methods.

Methods The linear range, detection limit, reference interval, precision and recovery rate were evaluated. And then according to the test results of CK-MB and CK activity, samples were divided into inverted group (n=40), control group (n=28) and normal group (n=40). CK-MB mass were determined by latex immunoturbidimetric assay and chemiluminescence assay for statistical analysis.

Results The linearity from 2.24 ng/mL to 173.04 ng/mL (Y=0.992X+1.421, R^2=1.000), and the lower limit of detection was 0.69 ng/mL, the biological limit of detection was 1.30 ng/mL. Male and female reference intervals were <3.28 ng/mL and <2.66 ng/mL, respectively. The average recovery rate was 99.75%. The within-run coefficient of variation (CV) and between-day CV were 2.33%-8.48% and 2.20%-5.37%, respectively. It had a good consistency with the chemiluminescence method (Y=1.81X+6.16, R^2=0.958). There was no statistical difference in the activity of CK-MB between inverted group with control group, but CK-MB mass of the inverted group was lower than that of the control group.

Conclusions The latex immunoturbidimetry is able to specifically determine CK-MB mass with its high accuracy and precision. It can accurately reflect the true level of CK-MB in vivo and meet the requirements of clinical laboratories.

PU-084

Inhibiting miR-21 by ursolic acid ameliorates podocytes dedifferentiation induced by high glucose by restoring defective autophagy

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Objective Diabetic nephropathy is the leading cause of end stage renal disease. In the previous studies, we reported that ursolic acid (UA), a pentacyclic triterpenoid presented in various plants, ameliorated podocytes dedifferentiation caused by high glucose. However, little addresses the mechanism. The present study aimed to investigate the mechanism by which UA ameliorates podocytes dedifferentiation in diabetic nephropathy.

Methods The protective effects of ursolic acid on kidney were investigated in db/db mice, a model of type 2 diabetes. Conditionally immortalized murine podocytes were treated with high glucose and the effects of UA were determined to investigate the potential molecular mechanisms in vitro.

Results Therapeutic role of UA was evaluated using 0.3% UA-supplemented diet for 10 weeks. The results from both morphologic and histological detections indicated that UA significantly attenuated kidney injury of db/db mice. Besides, UA reversed the expression of miR-21 and PTEN, revealing a therapeutic potential of UA for diabetic nephropathy by targeting miR-21. Inhibition of miR-21 in podocytes further promoted the effect of UA on cell protection and autophagy restoration, however, which was partially abolished by overexpression of miR-21. Furthermore, UA up-regulated the expression of PTEN, inhibited Akt/mTOR pathway activation and restored autophagy, effects that were prevented by miR-21 overexpression and enlarged by miR-21 inhibition.

Conclusions The present study indicates that UA protects against diabetic nephropathy by targeting miR-21.

PU-085

Evaluation of time series model in blood transfusion quality management

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Objective To strengthen the blood management of different transfusion nature in the Department of transfusion and improve the early warning mechanism of blood stock, so as to provide scientific reference for the Department of transfusion to make clinical blood plan scientifically, so as to realize the fine management of blood stock and improve the management level of blood transfusion.
Methods According to the quantity of blood transfusion from May 5, 2017 to August 5, 2018, the number of emergency cases and hospitalizations in our hospital were analyzed. By using SPSS22.0 statistical software, the autoregressive integral moving average model (ARIMA) for time series analysis was established. On the basis of controlling the minimum inventory, the blood for rescue was strictly guaranteed, the perioperative blood was basically guaranteed, and the blood for treatment was satisfied as far as possible. The optimal parameters of ARIMA are determined in principle, and the ARIMA model is used to predict the amount of blood used in our hospital for 10 weeks from August 13, 2018 to October 15, 2018.
Results The best model for predicting the amount of blood used in our hospital was ARIMA (1,2,1) (1,2,0), the stable R-square was 0.795, the mean square error (RMSE) was 10.144, the BIC was 5.177, the Ljung-Box Q test P = 0.331, the minimum warning stock was 1 unit (U); the best model for predicting the amount of blood used in our hospital was ARIMA (2,1,0) (1,1,1), the stable R-square. The best model for predicting perioperative blood consumption in our hospital was ARIMA (2,1,1) (2,1,2), the stable R was 0.675, RMSE was 15.224, BIC was 6.185, Ljung-Box Q was P = 0.495, and the lowest warning stock was 22U. The minimum stock required for blood demand is 15U. The actual values of the models are all within the 95% confidence interval of fitting values and predicted values, and the dynamic changes are consistent.
Conclusions The application of quality control method based on ARIMA model in the prediction of blood consumption with different transfusion properties is beneficial to the rational booking of blood, optimizing the allocation of blood resources and perfecting the early warning mechanism of blood inventory. Safety, so as to enhance the management level of blood transfusion.

PU-086

Fishing and Synthesizing a Specific Peptides Targeting Sox2 Protein for Esophageal Squamous Cell Carcinoma Therapy

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Objective esopahgeal squamous cell carcinoma(ESCC) is the predominant type of esophageal cancer, and approximately 90% of esophageal cancer is ESCC in China. Moreover, aberrant *SOX2* expression was detected in ESCC, and multiple processes and clinical outcome was closely correlated with Sox2 protein. In this study, we aim to screen and synthesize peptide that could inhibit the activities of Sox2 protein for ESCC therapy. We tested the effect of optimal candidate of these peptides, P42 and peptide 42, in esophageal squamous cancer cells and xerograft model.

Methods We tested the expression pattern of Sox2 protein in ESCC clinical sample and cell lines, and performed Kaplan-Meier analysis for its clinical survival relevance. We established a peptide library with scaffold structure, and then performed an unbiased drug screening based on bimolecular fluorescence complementation (BiFc) and immunoprecipitation, then we obtained several peptide candidates from the library. KYSE450, TE-1 and EPC2 stable cell lines was established after infection with lentivirus, which could drive the overexpression of Sox2 protein. These stable cell lines were analyzed for proliferation, migration, invasion, apoptosis, tumor growth and metastasis in xerograft mice. Moreover, the roles of two synthetic peptides including control peptide and peptide 42, which both are composed of penetrating peptide (YGRKKRRQRRR) and fuorescent molecule TAMRA, were further validated *in vitro* and *in vivo*, potential mechanism was explored using proteomics and bioinformatic analyses.

Results Several Peptides including P42 were fished from the peptide libaray, and P42 overexpression or incubation with synthetic peptide 42 not only inhibited multiple processes including cell proliferation, colony formation, migration, invasion. Intriguingly, the synthetic peptide 42 significantly inhibited the tumor growth in xerograft model after multiple drug injections. Moreover, we found that 133 protein was up-regulated and 99 protein was down-regulated in P42-overexpression cell line when comparing with control, which may be responsible for their inhibitive effect in ESCC.

Conclusions Besides the inhibitive roles in cancer progress caused by ectopic expression of P42 peptide *in vitro*, we also found that it also play inhibitive roles *in vivo*, including the capability of tumor formation and metastasis. Moreover, we also mimic the amino acid sequence of control and P42 peptide to chemically synthesize them and validate their roles *in vitro* and *in vivo*. Intriguingly, similar to the effect caused by ectopic expression of P42, two synthetic peptides including control peptide

and peptide 42 can also lead to anti-cancer effect *in vitro* and *in vivo*. After injection of control peptide and peptide 42 in the tumor-bearing mouse, we found that more keratin pearls and intercellular bridges in the section of tumor injected with peptide 42, it may promote the differentiation of tumor to achieve better therapeutic effect. In addition, we also tested the specificity of binding between peptide 42 and Sox2 protein, SOX2 knockout in KYSE450 cells could relieve the inhibitive effect caused by peptide 42. Furthermore, no adverse effect on cell proliferation and apoptosis after adding peptide 42 in the medium of normal epithelium cells and progenitor cells, suggesting that Sox2 may have different DNA binding sites and protein partners in cancer cells and normal cells. All these results suggest that a small specific peptide targeting Sox2 protein has therapeutic potential for ESCC. Taken together, our work set up a high throughput method for peptide drug screen, thereby obtaining the peptide P42 which against Sox2 protein to reduce proliferation, migration and invasion of ESCC cancer cells, and slow the growth of tumors in xerograft model and metastasis in zebrafish, and prptide P42 could be served as a candidate drug for ESCC therapy.

PU-087

Levels of inflammatory markers in patients with polycystic ovary syndrome

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Objective To measure the levels of inflammatory markers in obese and non-obese patients with polycystic ovary syndrome (PCOS) by using 2 separate groups with matching body mass index (BMI).
Methods A total of 80 women of reproductive age with (n=40) and without (n=40) PCOS were included in this study. Based on their BMI, patients with PCOS and controls were divided into 2 groups as obese (n=20) and non-obese (n=20) groups respectively. Interleukin-6 (IL-6), C-reactive protein (CRP), neutrophil-to-lymphocyte ratio (NLR) and vitamin B12 were assessed.
Results No significant difference was found between patients with PCOS and control subjects in IL-6 and CRP levels. However, NLR levels were significantly higher (p 0.045) and vitamin B12 levels were significantly lower (p 0.033) in patients with PCOS compared to control subjects. No statistically significant difference was found between obese and non-obese patients with PCOS and control subjects in IL-6 and NLR levels. However, CRP levels were significantly higher in obese patients with PCOS compared to obese control subjects (p 0.016).
Conclusions It can be concluded that inflammatory activity is increased in patients with PCOS, which can lead to an increased risk for atherosclerosis, and this increase is not caused by obesity but rather by the polycystic ovary syndrome itself.

PU-088

Identification of key regulatory factors of coronary artery disease using bioinformatics analysis of microarray data

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Objective The objective of present study was to investigate the key genes and microRNAs(miRNA/miRs) associated with coronary artery disease (CAD) progression through the analytical work in GEO.

Methods The gene expression profile GSE28829 dataset and the miRNA expression profile GSE28858 dataset were downloaded from the Gene Expression Omnibus (GEO) database. The differentially expressed genes (DEGs) in GSE28829, and the differentially expressed miRNAs (DEMs) in GSE28858 were screened using the GEO2R online analytical tool. The target genes of DEMs were identified using the miRWalk (version 3.0 now) web-based tool and 2 miRNA-gene regulatory networks were constructed using Cytoscape software. Common miRNA-target DEGs were selected for Kyoto Encyclopedia of Genes and Genomes pathway analysis and Gene Ontology enrichment analysis.

Results In the present study, 2599 DEGs and 196 DEMs were screened. A total of 1340 target genes were identified from the DEMs, and 223 of these target genes and established DEGs were identified to overlap. The enriched functions and pathways of overlapped genes include “RNA splicing”, “regulation of G1/S transition of mitotic cell cycle”, “positive regulation of SMAD protein import into nucleus”, and “positive regulation of I-kappaB kinase/NF-kappaB signaling”, “PI3K-Akt signaling pathway”, “Cell cycle”, “Pathways in cancer” and “Jak-STAT signaling pathway”. We subsequently constructed a protein-protein interaction network consisting of 120 genes and 205 interactions. In addition, 3 genes in the network were identified as hub genes in CAD, e.g. VAMP2, MKI67 and TWIST1. Additionally, we also constructed miRNA-gene regulatory network to describe the interaction between DEM and target molecules, including upregulated miR-646, miR-615-3p, downregulated miR-571 and their target genes.

Conclusions HMGA1, IFNAR2, SCD, BIRC5 and ABL1, might be as new biomarkers for the prognosis and treatment of CAD. Our exploration though the analysis of the database might contribute to reveal molecular mechanism underlying CAD.

PU-089

Laboratory analysis of 1 case of especially hyperglycemia

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Objective Fasting blood glucose (FBG) is the most commonly used and most important index in the diagnosis of glucose metabolism disorder. The reference range of glucose oxidase method is 3.9-6.1mmol/L. FBG of hyperglycemia is higher than 7mmol/L. Urine sugar can be positive when FBG exceeds 9mmol/L (renal sugar threshold). The most common disease with pathological increase in FBG is diabetes mellitus, and the most dangerous complication of diabetes is diabetic ketoacidosis and hyperosmolar nonketotic diabetic coma, diabetic ketoacidosis patients most of the blood glucose was 16.7-33.3 mmol / L, occasionally up to 55 mmol / L; Hyperosmotic nonketotic diabetic coma patients were mostly with blood glucose of 33.3-66.6 mmol / L, and those with blood glucose over 70 mmol/L were rare.

Methods Su xx, female, 26 years old, was admitted to the emergency department of our hospital on November 20, 2018 due to poor appetite, palpitation for 1 month, nausea and vomiting for 3 days, and aggravation with unconsciousness for 3 hours.The patient was in poor general condition, with vague consciousness and restlessness. Physical examination showed no obvious abnormality.Oliguria is present. Arterial blood gas analysis showed:PH7.21 , PCO2 6mmHg , HCO3-10.4mmol/L , BE-17.5mmol/L.Glucose: 93mmol/L.The patient was admitted to hospital immediately. After admission, the glucose was measured as 98.3mmol/L again, HbA1c15.3%, blood ketone body 5 mmol/L , ALT 56U/L, AST 43U/L, TG 10.15mmol/L, BUN 18.5mmol/L, CR 312 umol/L, K 2.85 mmol/L, WBC 10×10^9/L, NE 91.2%, urine routine: occult blood 3+、protein 3+、glucose 3+. Urine routine examination was performed again the next day for urinary ketone body 2+, and no obvious abnormalities were found in the remaining items.

Results Combined with the patient's medical history, physical examination and auxiliary examinations, the diagnosis was considered to be shock, multi-organ dysfunction syndrome, type 1 diabetes, diabetic ketoacidosis, decompensated metabolic acidosis with respiratory alkalosis, renal failure, hyperlipidemia and hypokalemi. Her condition was significantly improved after massive fluid rehydration, ketohypoglycemic therapy, CRRT, anti-infection therapy, organ protection therapy, and the treatment of electrolyte and acid-base imbalance correction in our hospital, and all the test indicators were basically returned to normal.

Conclusions Patients with type 1 diabetes tend to have spontaneous DKA. The blood glucose of this patient was above 93mmol/L on admission, indicating that the blood glucose of diabetic patients had been increasingly high, which should be paid attention to. The patient had a negative urinary ketone body on admission and a positive reexamination the next day. The reasons may be as follows:1. When renal function is obviously impaired in diabetic ketoacidosis, the urinary ketone body decreases or even disappears； 2. The ketone bodies includes hydroxybutyric acid, acetoaceticacid and acetone in the blood. The qualitative reagent only reacts with acetoaceticacid, weakly with acetone, but not with β- hydroxybutyric acid. The main

component determined by the blood ketone body is β-hydroxybutyric acid, so the two methods can compensate each other.

PU-090

SIRT6 induces cell autophagy and plays an oncogenic role in esophageal cancer cells

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Objective Sirtuin 6, a member of sirtuin family, is generally regarded as a tumor suppressor as it participates in suppressing hypoxia-inducible factor 1α and MYC transcription activity by deacetylating H3K9 (histone H3 lysine 9) and H3K56 (histone H3 lysine) at promoters of target genes, leading to the aerobic glycolysis inhibition and cell growth suppression. However, its expression has recently been reported to be highly elevated in a series of tumors, including prostate cancer, breast cancer, and non-small cell lung cancer, indicating that sirtuin 6 plays dual roles in tumorigenicity in a cell/tumor type-specific manner. To our knowledge, the biological roles of sirtuin 6 in esophageal cancer cells have still been underestimated.
Methods Quantitative real-time PCR（qPCR） and immunohistochemistry were used to investigate the expression level of SIRT6 in esophageal carcinoma tissues; Cell proliferation ability were evaluated by CCK8 and colony formation assay and apoptosis detected by flow cytometry; confocal microscope assay detection of autophagy flow assays to monitor autophagy levels; SIRT6 interacting proteins were detected by co-immunoprecipitation assay; Total RNA was extracted after overexpression of SIRT6 in esophageal cancer cell 109 cells and differentially expressed genes were then subjected to Gene Ontology (GO) analysis (molecular function) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis.
Results In the study, using the quantitative polymerase chain reaction assay (qPCR) and immunohistochemical (IHC) assays, we found that SIRT6 was highly upregulated at both messenger RNA (mRNA) and protein levels. The following biological tests, colony formation assays, demonstrated that SIRT6 greatly promoted cell proliferation, further confirmed by the elevated expression of BCL2, a key anti-apoptotic oncogene, in SIRT6-overexpressed EC cells. Furthermore, results from autophagy-related assays, including the western blotting assays of autophagy biomarker,[24] LC3II/I, the autophagy flux assays, and immunoprecipitation (IP) assays, showed that SIRT6, specifically interacting with ULK1, positively participated in autophagy regulation by inhibiting mTOR activities and enhancing its downstream ULK1 activities.
Conclusions Above all, our studies first uncover the oncogenic roles of SIRT6 in EC cells and provide evidence to support the potential capabilities of SIRT6 as a target candidate in treating EC patients as well as other SIRT6-overexpressed tumors.

PU-091

RAD51 regulates autophagy to promote cell growth in esophageal squamous carcinoma cells

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Objective In the study, we aimed to investigate the functions and mechanisms of homologous recombination repair factor RAD51 in regulating the expression of protein kinase CHK1 in esophageal squamous tumorigenesis and to provide a better molecular target for precise diagnosis and treatment of esophageal squamous tumor patients.
Methods Real-time PCR and immunohistochemistry assays were firstly used to detect the expression of RAD51 in esophageal squamous tumor tissues; then, to study the biological roles of RAD51 in esophageal carcinogenesis (EC), cells transfected with siRNAs against RAD51 were subjected to colony formation assays and MTT assays in vitro; Moreover, EC cells infected with shRNA against RAD51 (shRAD51) or nonspecific sequence (shCon.) were subcutaneously injected into the nude mice to further confirm the roles of RAD51 in EC cell growth in vivo. Afterwards, EC cells overexpressed with different domains of RAD51were put into western blotting assays to test the expression of CHK1. Besides, immunoprecipitation assays were also employed to explore the exact interaction domains of CHK1 on the RAD51 protein. Using the autophagy flux analysis and western blotting assays, we analyzed the role of RAD51 in autophagy.
Results We find that RAD51 is highly upregulated in esophageal squamous tumor tissues and its DMC1 domain significantly promotes cell growth of EC cells through CHK1. In the presence of 3-methyladenine (3MA), an autophagy inhibitor, we find that the reduction of CHK1 and the inhibition of cell growth in RAD51 deficient EC109 cells are strikingly restored. Subsequently, the autophagy related experimental data reveal that RAD51 negatively participates in autophagy. Moreover, results from *in vitro* clonogenic survival assays show that autophagy inhibitors 3MA and hydroxychloroquine (HCQ) significantly inhibits the survival of cells. Contrarily, RAD51 interruption enables EC cells to survive from these inhibitors treatments.
Conclusions Our studies firstly highlight a direct role of RAD51 in autophagy process and characterize its functional domain in cell growth regulation. Moreover, our data firstly shed insights into the possible application of autophagy inhibitors in treating RAD51 overexpressed EC patients.

PU-092

Autophagy induced by human metapneumovirus infection in 16HBE

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Objective Human metapneumovirus (hMPV) was discovered as an important viral pathogen causing acute lower respiratory tract infection in children by Dutch scholars in 2001, second only to respiratory syncytial virus (RSV). Autophagy is a process of phagocytizing autologous cytoplasmic proteins or organelles which plays an important role in cell growth and viral infection . Since hMPV discovered, research has focused on epidemiological investigations. The process of hMPV-infected-cell is not fully understood. The first step in infection is the entry of nucleic acid material into the cell and replication. Our previous study found that hMPV enters cells through lipid rafts, but the response after entry was unclear. In this study, we explore whether intracellular mechanisms caused by hMPV infection are associated with autophagy.

Methods The expression of autophagy-related genes ATG5, ATG7, Beclin1 was detected by QPCR and western blot; the autophagy-marker LC3 was labeled and its distribution were observed by indirect immunofluorescence staining; GFP-RFP-LC3 plasmid transfection was used to observe the dynamic observation of autophagy after hMPV infection. QPCR and western blot were used to discover the pathway of autophagy primarily; specific pathway inhibitors SP600125, PD98059 and siRNA to further verify the pathway after hMPV infection. Autophagy specific inhibitor 3-MA and inducer Rapamycin, siRNA, pathway-specific inhibitors were used to detect the relationship between autophagy and hMPV replication. The existence of autophagy and specific pathways were tested and verified in animal experiments.

Results hMPV infection activates autophagy in 16HBE through JNK and MEK/ERK pathway; we verify the accuracy of the pathway by SP600125, PD98059 and siRNA-JNK, MEK; induction of autophagy by rapamycin reduce the viral replication, inhibition of autophagy by 3MA, siRNA, pathway inhibitor have the opposite result; hMPV-induced autophagy also occurs in mice through JNK, MEK/ERK pathway.

Conclusions We first demonstrate that hMPV infection can induce autophagy in 16HBE and this process are regulated by JNK, MEK/ERK pathway, and autophagy can reduce hMPV replication. This study provides theoretical and experimental basis for anti-hMPV drug research.

PU-093

The mechanism of CCN1 inducing local inflammation via upregulating IL-36 expression in psoriasis

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Objective Psoriasis is a common chronic auto-inflammatory disease characterized by hyperplasia of the epidermis and inflammatory infiltration. The pathogenesis of Psoriasis is not completely clear. Our previous study found that the extre-cellular matrix protein CCN1 (a new inflammatory factor) was highly expressed in the dermal epidermis of psoriatic patients and mouse models. In addition, the skin inflammation of mice was significantly reduced under the blockade of anti-CCN1 monoclonal antibody. But how CCN1 regulating the local inflammation in psoriasis remained unclear.Psoriasis is a common chronic auto-inflammatory disease characterized by hyperplasia of the epidermis and inflammatory infiltration. The pathogenesis of Psoriasis is not completely clear. Our previous study found that the extre-cellular matrix protein CCN1 (a new inflammatory factor) was highly expressed in the dermal epidermis of psoriatic patients and mouse models. In addition, the skin inflammation of mice was significantly reduced under the blockade of anti-CCN1 monoclonal antibody. But how CCN1 regulating the local inflammation in psoriasis remained unclear.

Methods We firstly established a time-point mouse model of Psoriasis to confirm the exact phase of CCN1 during the pathogenic process. Upon confirmation of the upstream phase of CCN1 expression, we compared CCN1 and other known major factors in psoriasis. Then we specified a possible regulatory relationship between CCN1 and IL-36. In vivo, we utilized mAb of CCN1 and $CCN1^{flox/flox}$ CK14-cre cKO mice to confirm the regulatory function further. In vitro, human primary keratinocytes culture system was established, and we stimulated the primary KC with human recombinant extra CCN1. ELISA, RNAseq, WB, luciferase reporting gene, CHIP are used for the signaling pathway downstream of CCN1 regulating IL-36. And we also confirmed the result in the human patient samples about the relationship between CCN1 and IL-36 inducing the local inflammation.

Results CCN1 is highly expressed in lesional epidermal skin in psoriatic patient. Blockade of CCN1 by mAb significantly relieved the symptoms of psoriasis model and IL-36 expression was also reduced efficiently. In vitro study have proved that CCN1 induced IL-36 expression in a time and dose dependent manner. After knock down of CCN1 in KC , we observed an evidenced reduction of IL-36 expression. Then we found that CCN1 indeed promote downstream IL-36 expression from upstream. Further, we found that CCN1 can promote transcription factors: NF-κB and ERK binding to IL-36α and IL-36γ promoter by interact with integrin receptor α6β1 on keratinocyte to mediate local inflammatory infiltration in an autocrine manner, respectively.

Conclusions According to the previous study on CCN1 and inflammation, we found that CCN1, secreted from tissue cells but lymphocytes can enlarge the local inflammation and tissue cell proliferation significantly. The high expressed CCN1 in local epidermal skin in psoriasis reminded us that CCN1 could play an important role in local inflammation in psoriasis, which is a typical auto-inflammatory disease. Then we found a upstream upregulation of CCN1 and there is no doubt that CCN1 functions as a

upstream factor to regulating downstream factors. We proved that CCN1 can remarkably upregulate IL-36, an inflammatory factor belongs to IL-1 family, to trigger the downstream inflammation. Our study demonstrated that extracellular matrix proteins play an important role in the local inflammatory of psoriasis. Also, we provide new evidence of CCN1 to become a new therapy target for psoriasis.

PU-094

The study on the value of AMH in patients with cervical cancer

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Objective to investigate the level of AMH in serum of cervical cancer patients and research on the value of anti-mullerian hormone in cervical cancer diagnosis.
Methods Serum samples of 65 cervical cancer patients were collected and a control group (normal human AMH level) was established. The AMH levels in serum were detected by isotopic labeling.
Results The difference in AMH levels between patients with cervical cancer and normal people was statistically significant ($P<0.05$). The AMH levels of serum samples of cervical cancer patients was significantly lower than that of normal control group.
Conclusions AMH is valuable for the diagnosis of cervical carcinoma , but we need to do some further experiments to testify it.

PU-095

Tryptophan metabolite 3-HAA induces hepatocarcinoma apoptosis through up-regulation of DUSP6

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Objective Tryptophan metabolism remarkably increases in tumor, and promotes tumorigenesis and immune evasion. 3-hydroxyanthranilic acid (3-HAA), a intermediate metabolites of the kynurenine pathway, decreased in a variety of pathological conditions. However, little is known about the metabolic status of 3-HAA in tumor. The aim of this study was to investigate the metabolic changes of 3-HAA and its effects on hepatocarcinoma(HCC).
Methods GC-MS was applied to detect the content of 3-HAA and other tryptophan metabolites. The effect of 3-HAA on HCC were investigated by cytometry, CCK8 assay, clone-formation assay, apoptosis detection and was further validated in Xenograft model. The mechanism was revealed by RNA-sequencing and gene ontology analysis.
Results In this study, we found that kynureninase (KYNU), kynurenine-3-monooxygenase (KMO) decreased and kynurenine aminotransferse (KATs) and 3-Hydroxyanthranilate-3,4-

dioxygenase (3HAO) increased in HCC, resulting in the cellular content of 3-HAA, a tryptophan metabolite, was selectively reduced in HCC cells. Unlike its upstream and downstream metabolic intermediates, 3-HAA significantly inhibited the growth of HCC cells by inducing apoptosis *in vitro* and *in vivo*. Moreover, RNA-sequencing and gene ontology analysis revealed that 3-HAA induced apoptosis by up-regulating the expression of dual-specificity phosphatase 6 (DUSP6), latter down-regulated the expression of Bcl-2 and Bcl-xl and up-regulated the expression of Bad. Unlike kynurenine, 3-HAA did not activate AHR. The stable isotope labeling with amino acids (SILAC) results showed that 3-HAA treatment increased nuclear accumulation of transcription factor YY1, thus activating DUSP6 transcription.
Conclusions This findings suggested that 3-HAA induced HCC cell apoptosis by promoting the YY1-regulated DUSP6 expression, with a hope of improving the efficacy of HCC therapy.

PU-096

A LncRNA Signature Associated with Metastasis of T1 Colorectal Cancers to Lymph Nodes

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Objective Most T1 colorectal cancers treated by radical surgery can now be cured by endoscopic submucosal dissection. Although 70%-80% of T1 colorectal cancers are classified as high risk, <16% of these patients actually have lymph node metastases. Biomarkers are needed to identify patients with T1 cancers with the highest risk of metastasis, to prevent unnecessary radical surgery.
Methods (1) Discovery and validation of dysregulated lncRNA in tissue and serum; (2) Verification of expression of the selected lncRNA in serum; (3) Validation of the constructed lncRNA panel.
Results Expression profiles of top 10 lncRNA selected from The Cancer Genome Atlas (TCGA) were validated in 20 pairs of tissues by quantitative real-time PCR, and the dysregulated lncRNA thus identified were further validated in serum samples identified 3 lncRNAs (LINC01234, LINC08375, and MALAT1) with significant changes in expression in T1 and T2 colorectal cancers with vs without lymph node metastases. Levels of the 3 lncRNAs identified patients with lymph node invasion by T1 or T2 cancers with an area under the receiver operating characteristic curve (AUC) value of 0.79. We validated these findings in 2 independent cohorts of patients with T1 cancers, using findings from histology as the reference. The 3-lncRNA signature identified T1 cancers with lymph node invasion in cohort 2 with an AUC value of 0.85, and in cohort 3 with an AUC value of 0.78. When we analyzed biopsy samples from untreated patients, the 3-lncRNA signature identified cancers with lymph node metastases with an AUC value of 0.71.
Conclusions The 3-lncRNA therefore identifies high-risk T1 colorectal cancers with a greater degree of accuracy than currently used pathologic features.

PU-097

Relationship between metabolic abnormalities and kidney stones and their components

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Objective To analyze the metabolic products of blood and urine in patients with kidney stones and analyze the relationship between kidney stones and types of stones and metabolites.
Methods The kidney stone patients who were admitted to a hospital in zhejiang university from 2013 to 2017 were tested for stone composition, urine routine, blood routine and blood biochemistry. According to the main components of stone, the study group was divided into healthy group, calcium oxalate stone group, apatite calculus group and other stone groups. Statistical analysis of the relationship between calculus and its composition and hematuria metabolites has been done.
Results Of the 134 kidney stones specimens, calcium oxalate was the most common, accounting for 96 cases (71%), uric acid in 11 cases (8%), apatite in 18 cases (14%), and mixed stones in 9 cases (7%). The ratio of male to female patients with kidney stones was 1.83:1, 29 patients (21%) were under the age of 40, 97 (71%) were 41-70 years old, and 8 (6%) were older than 70 years old. Gender, triglyceride, serum sodium, serum creatinine, and serum uric acid were independent risk factors for the formation of kidney stones. High-density lipoprotein-C, serum potassium, and total calcium were protective factors. Urine specific gravity, total calcium, and serum uric acid were independent risk factors for the calcium oxalate stone group, and serum potassium was a protective factor. Serum creatinine and serum uric acid were independent risk factors for the apatite stone group, and serum potassium was a protective factor. Blood sodium, serum creatinine, and serum uric acid were independent risk factors for other stones.
Conclusions Blood calcium and blood uric acid are related to kidney stones and are risk factors for calcium oxalate stones

PU-098

Development and validation of a personalized social media platform-based HIV incidence risk assessment tool for men who have sex with men in China

Ke Yun
CMU

Objective Personalized risk assessments can help medical providers determine targeted populations for counseling and risk reduction interventions. The objective of this study was to develop a social media platform-based HIV risk prediction tool for men

who have sex with men (MSM) in China based on an independent MSM cohort in order to allow medical providers determine target populations for counseling and risk reduction treatments.

Methods A prospective cohort of MSM from Shenyang, China followed from 2009 to 2016 was used to develop and validate the prediction model. The eligible MSM were randomly assigned into the training and validation dataset and Cox proportional hazards regression modeling was conducted using predictors for HIV seroconversion selected by the training dataset. Discrimination and calibration were performed, and the related nomogram and social media platform based-HIV risk assessment tool were constructed.

Results The characteristics of the sample between the training dataset and the validation dataset were similar. The risk prediction model identified the following predictors for HIV seroconversion: the main venue used to find male sexual partners; had condomless receptive/ insertive anal intercourse in the past 3 months (P3M); and used rush poppers in the P3M. The bootstrap C-index was 0.75 in the training dataset, and 0.60 in the validation dataset. Nomogram and WeChat-based HIV incidence risk assessment tools for MSM were developed.

Conclusions We developed and validated an HIV infection risk prediction model, and constructed a nomogram and a social media platform-based HIV risk assessment tool. The social media platform-based tool can be distributed easily, improve awareness of personal HIV infection risk, and stratify the MSM population based on HIV risk.

PU-099

Performance Evaluation of Mindray BS-800 Automatic Biochemistry System

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Objective To evaluate the analytic performance of Mindray BS-800 Automatic Biochemistry System, designed and manufactured by Shenzhen Mindray Bio-medical Electronics Co., Ltd.

Methods According to the Clinical and Laboratory Standards Institute (CLSI)'s guidelines files (EP5-A2, EP6-A2, EP7-A2 and EP9-A2) and other relative experimental plans, it was evaluated the analytic performance of BS-800 Automatic Biochemistry System, including precision, linearity, clinical reportable range, interference, method comparison, by testing 23 clinical routine items (including ALT, AST, UA, TG, and so on). Comparison with the manufacturer's claims or other performance criteria was performed.

Results For all items, the within-run CV of the results for all items was between 0.32% and 2.56%, and the total CV for all items was between 0.78% and 4.08%. The data showed that the system had good linearity, good correlation between sample concentration and the expected value, and the clinical reportable range was wide. Most items had good anti-interference effects, and the experimental results were consistent with the manufacturer's claims. In the method comparison experiment with Roche modular PPI analyzer, the data showed that the compared 23 items on BS-800 had high correlation, the square of the correlation coefficient (R^2) was greater than 0.975.

The expected bias meeted the requirements of 1/2 acceptable total error defined in the CLIA'88.

Conclusions On BS-800 Automatic Biochemistry System, the main analytic performance for the analyzed routine items was consistent with the acceptable quality standards. The feature is simple operation, high speed, accuracy, and high performance, and it deserves to be popularized and applied in middle-scale and large-scale clinical laboratories.

PU-100

Evaluation of homogeneity in Proficiency Test samples for International Reference Laboratory

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Objective Evaluate the homogeneity of the proficiency test samples to verify whether it meets the requirements of the comparison for the International Reference Laboratory.

Methods According to the Guidance on Evaluating the Homogeneity and Stability of Samples Used for Proficiency Testing (CNAS-GL03), 14 biochemical indexes including ALT, AST, ALP, GGT, CK, LDH, TP, T-Bil, Urea, Cr, UA, Glu, TG and TC in the past three years (from 2014 to 2016) were tested by the Roche detection system Modular P800 Biochemical analyzer. The mean ( ), standard deviation (SD) and coefficient of variation (CV) of the samples were calculated. And we used One-way analysis of variance (ANOVA) and the guideline of $S_S \leqslant 0.3\sigma$ to evaluate the between-bottle differences.

Results The results showed that the CVs of AST in RELA 2014A and B were higher than 2.0%. Additionally, the CVs of CK were over 2% in all tests except for RELA 2016B.The results of ANOVA for RELA samples demonstrated that the F values of CK were over the critical values 4.39, which was statistically significant ($P < 0.05$); the F values of the ALT and T-Bil in 2015B and the Cr in 2014A were also over 4.39($P < 0.05$) respectively. Whereas, the F values of other measurements were less than the critical value of F, indicating there was no statistical significance ($P > 0.05$). The CK measurement data $S_S > 0.3\sigma$ in all the samples by the guideline of $S_S \leqslant 0.3\sigma$, suggested that there was a between-bottle difference in the CK, and others were $S_S \leqslant 0.3\sigma$, showing no between-bottle difference in those items.

Conclusions There were significant differences between the bottles of the CK item in the past three years, and the homogeneity of other items in the samples can all meet the requirements of Proficiency Testing for the international reference laboratory.

PU-101

A case report of Salmonella in the intracranial and intestinal tract simultaneously

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Objective Salmonella is an important zoonotic disease, also a common pathogenic microorganism that causes bacterial foodborne origin worldwide.
Methods Now report a case of patient with intracranial and intestinal infections of Salmonella in Dublin.
Results The intracranial pus secretion was cultured as Salmonella, and the culture results were the same as those of the pus culture. The serotype was identified as Salmonella dublin. The results of drug susceptibility test showed that it was sensitive to ceftriaxone and compound sulfamethoxazole, and it was resistant to levofloxacin and ampicillin.
Conclusions Salmonella infection in Dublin should be paid attention to, and strive for early detection and early treatment to minimize the suffering of patients.

PU-102

Association of biofilm formation with antibiotic resistance and efflux pumps in Acinetobacter banumannii

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Objective Biofilm formation and its drug resistance is a focus of research. The expression of active effluBiofilm formation and its drug resistance is a focus of research. The expression of active efflux pumps is an important mechanism of antibiotics resistance in *Acinetobacter banumannii*. This study aims to investigate the association of biofilm formation with antibiotic resistance and efflux pumps in *A. banumannii*.
Methods A total of 92 *A. baumannii* clinical isolates were collected and identified by multiplex PCR. Biofilm formation was detected by crystal violet staining. The antibiotic susceptibility of *A. baumannii* was tested by VITEK 2 COMPACT®. Genotypes were determined by enterobacterial repetitive intergenic consensus sequence type 2-based PCR (ERIC-2 PCR). The effect of phenylalanine-arginine beta- naphthylamide (PAβN), an efflux pump inhibitor, on *A. baumannii* biofilm formation and dispersion was tested and the gene expression of efflux pumps was determined.
Results In the 92 identified strains, 42 were not biofilm producers and 50 were biofilm producers, including weakly positive (n=15), positive (n=17) and strongly positive with biofilm formation ability (n=18). Compared with non-biofilm producers, resistant rate of biofilm producers decreased with biofilm formation capacity from weak to strong. However, when the biofilm was strongly positive, the drug resistance

rate rebounded. There were 7 clonal groups in 92 strains of *A. baumannii* and no dominant clones were shared among the studied isolates. Despite no difference was observed in the expression of *adeB*, *adeJ*, *adeG*, *abeM* and *amvA* among different biofilm formation ability groups, PAβN could inhibit *A. baumannii* biofilm formation and enhance dispersion significantly.

Conclusions These results indicated there was some association between biofilm formation and antibiotic resistance in *A. baumannii*. Biofilm formation caused by clinical *A. baumannii* isolates was inhibited by PAβN, independent of drug efflux pump mechanism.

PU-103

The comparison of three different human tissue derived mesenchymal stem cells on the regulation of macrophages polarization

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Objective Immunoregulation of mesenchymal stem cells (MSCs) is an important mechanism for its therapeutic effect. However, MSCs have a wide range of tissue sources, and its tissue microenvironment has an important impact on its biological characteristics. Therefore, MSC from different tissue sources may have different immune regulation ability. In this study, we compared the regulation on macrophage polarization by MSCs derived from human adipose tissue (ADSCs), umbilical cord (UCMSCs) and endometrium (EMSCs).

Methods Mouse macrophages were cocultured with three MSCs in Transwell for 24 hours, respectively, then stimulated by LPS for 4 hours, and then for another 24 hours' coculture. Flow cytometry was used to detect the proportion of M1 and M2 cells. The expression levels of M1 and M2 related genes in co-cultured macrophages were detected by q-PCR. The concentration of NO in cell supernatant was measured by spectrophotometer.

Results After co-culture and LPS stimulation, we examined the cell shape changes and found that macrophages all showed obvious change and became an elongation shape. In addition, the proportion of M1 type of inflammation-promoting macro- phages decreased significantly, while the proportion of M2 type of inflammation- suppressing macrophages increased gradually. The proportion of M1 type after co- cultured with ADSCs was significantly lower than that of UCMSC and EMSC groups, while the proportion of M2 type was higher. The expression of M1-related genes TNF-alpha and IL-1beta in ADSCs co-culture group was significantly lower than that in control group, and the expression of M2-related genes CD36 and Arg-1 was significantly higher than that in ADSCs co-culture group, while the change trend of macrophage gene expression in UCMSCs and EMSCs co-culture group was not uniform. The concentration of NO secreted by M1 type cells in the supernatant of macrophages co-cultured with ADSCs was significantly lower than that of other experimental groups. There was no difference in NO concentration between UCMSCs and EMSCs group and control group.

Conclusions Cell shape changes have been proved to be associated with many cells functional states. The cell shape changes in macrophages are demonstrated to be associated with its polarization state conversion. This most intuitive and perceptible change is a convenient way to initially detect the inflammatory regulatory status changes of macrophages. In this study, after non-contact co-culture with three different MSCs, we found that macrophages all showed obvious change and became an elongation shape, which is previously proved that M2 polarization correlates with an increased degree of cell elongation. Therefore, we speculated that three MSCs all have a regulatory effect and promote M2 polarization in macrophages. In addition, TNF-α release is the standard response of LPS-stimulated macrophages. In our research, ADSCs, UCMSCs and EMSCs all uniformly decreased M1-related IL-1β and increased M2-related Arg-1, but the expression of CD36 and TNF-α was variously regulated in UCMSCs and EMSCs, respectively. In other words, only ADSCs consistently reduced M1 related IL-1β and TNF-α expression, and increased the expression of M2 related Arg-1 and CD36. UCMSCs downregulated the CD36 expression, and EMSCs increased the expression of TNF-α. Totally, not all MSCs brought uniform changes on the M1/M2 related factors. This trend is also proved by Yin et al., who demonstrate that coculture with BMSCs result in the increased M2- related Arg1 and IL-10 and the decreased levels of M1-related cytokine TNF-α and iNOS in RAW264.7 macrophages, but M2-related TGF-β is decreased while M1- related IL-1β is increased. This inconsistency may be explained as follows: macrophages polarization is a continuous process, and M1 and M2 phenotypes are only two extreme examples. At any intermediate stage of polarizing to M1/M2 phenotype, there may be a certain special cytokines and proteins secretion. However, we used RAW264.7 as the source of macrophages here. Although it could eliminate the instability and immaturity of mouse derived macrophages in vivo and avoid possible influences from other cells mixed with in-vivo isolated macrophages, RAW264.7 may not reflect the real in vivo situation as they have been previously modified. The different results of similar studies it caused still need further study. Totally, our results demonstrate different tissues derived MSCs show different regulations on macrophages. This may provide additional evidence for the influence of tissue origins on stem cell properties, and is helpful for MSCs origin selection to treat inflammatory disorders.

PU-104

Fibrinogen and D-dimer during pregnancy

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Objective During pregnancy, fibrinogen and d-dimer are gradually elevated while hyper-coagulation state generally formed as gestational week increases. However, in some disease status, change of fibrinogen and D-dimer throughout pregnancy don't follow traditional pattern. Pregnant related complications lead to abnormal change of fibrinogen and D-dimer. This article aimed to figure out the characteristic changes of fibrinogen and D-dimer during normal pregnancy, pregnancy with preexisting disorders

and pregnancy with complications and provide clinical doctors with assistance when predicting pregnancy outcomes.

Methods We evaluated fibrinogen and d-dimer throughout pregnancy in women who delivered at Peking University Third Hospital between Dec 2015 and Dec 2018. The Subjects were divided into three groups: uncomplicated women, women with preexisting disorders (hypothyroidism, antiphospholipid syndrome, thrombocytopenia, lupus erythematosus, nephritis, nephropathy, connective tissue disease), women with pregnant related complications (HELLP syndrome, hypertension before or during pregnancy, diabetes before or during pregnancy, preeclampsia, placental abruption, placenta previa, placenta accreta) and were categorized according to four stages(first trimester, second trimester, third trimester, delivery). All the measured results were compared between and within groups. Non-pregnant women serve as control groups and were selected from patients without hemostatic change.

Results Among the 17124 deliveries that occurred during the study period, 14257 women had sufficient data and were included for our analysis. Of these women, 7629 had uncomplicated pregnancies, 5967 had pregnancy-related complications, and 661 had preexisting disorders. The data of both fibrinogen and D-dimer were skew distribution, so median was used for analysis. Among the women who had pregnant related complications, the median of D-dimer was 0.55, which was higher than the median D-dimer of both the uncomplicated women (0.46) and those who had preexisting disorders (0.48). As for fibrinogen, both the pregnant women with related complications and with preexisting disorders show no clear distinction compared with uncomplicated women. Yet, women with some pregnant related complications and preexisting disorders such as placenta previa, placenta increta, thrombocytopenia, lupus erythematosus, connective tissue disease reach a lower fibrinogen level throughout pregnancy. On the contrary, kidney diseases such as nephritis, nephropathy and hypothyroidism indicated higher fibrinogen level during pregnancy. Preexisting disorders did not show clear influence on D-dimer during pregnancy. Some pregnant related complications such as eclampsia, placental increta, placental previa and placental abruption were closely related to higher D-dimer level.

Conclusions Fibrinogen and D-dimer exhibit different kinetics features during normal pregnancy, pregnancy with preexisting disorders and pregnancy with complications, which render it possibility to predict pregnancy outcomes and raise precaution in advance.

PU-105

Study on the relationship between intestinal flora imbalance and disease susceptibility in patients with Henoch-Schönlein purpura nephritis (HSPN)

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Objective Henoch-Schönlein purpura nephritis (HSPN) is one of the common secondary glomerular diseases in childhood. About 20-30% of children with HSPN can progress to

chronic kidney disease within 20 years. It constitutes one of the main causes of chronic renal failure in children. Its pathogenesis involves abnormal intestinal barrier function, mucosal immune imbalance, and activation of systemic immune response. The intestinal flora is the leading factor in the maturation and response of the intestinal mucosal immune system. Therefore, this study explored whether intestinal flora disorder is involved in the pathogenesis of HSPN by analyzing the fecal flora of HSPN children, HSPN mouse model, and the proportion of lymphocytes in HSPN mouse model.

Methods The feces of newly diagnosed patients admitted to our center from 2018.1 to 2018.12 were collected (strictly according to inclusion/exclusion criteria). Among them, 15 cases of HSPN, 12 cases of HSP, and 27 healthy relatives of each level were used as controls. Eight-week-old Balb/c female mice were randomly divided into model group and control group. The HSPN model was established by continuous intragastric administration of ginger, medlar and pepper (0.35 g/kg/d) followed by OVA immunization. The bacterial composition of each sample was analyzed by 16S rRNA V4 variable region PCR amplification and deep sequencing (Illumina® HiSeq platform). Automatic biochemical analyzer detects urine protein, serum creatinine, and blood urea nitrogen. Renal lesions were assessed by routine pathological staining of renal tissue (HE, PAS, etc.). Flow cytometry detects lymphocytes.

Results (1) The abundance of intestinal flora decreased in children with HSPN compared with healthy group ($P<0.05$); (2) Compared with healthy group, Bacteroides and actinomycetes in feces of HSPN children The number of Clostridium and soft-wall bacteria was significantly decreased ($P<0.05$), while the Proteus and Mycobacterium gates increased ($P<0.05$). (3) The children of HSPN and HSP were formed in the intestinal flora. The differences were mainly reflected in the thick-walled bacteria, Bacteroides (Pyphilis) and Fusobacterium; (4) proteinuria +~++ in the HSPN model, and urinary red blood cells increased; (5) the renal lesions in the mouse model were Mesangial hyperplasia; (6) The intestinal flora of the model mouse was significantly imbalanced, the Lactobacillus was significantly reduced, and the genus of the genus Trichophyton was increased; (7) The spleen volume and weight of the mouse model were increased; the blood lymphocyte count was significantly reduced; The proportion of lymphocytes changes.

Conclusions There is an imbalance of intestinal flora in children with HSPN and HSPN models, which is marked by a significant decrease in resident symbiotic bacteria and an increase in other dominant bacteria. At the same time, we found that there is a significant lymphoid immune disorder in the HSPN mouse model, and its role in the pathogenesis of HSPN will be revealed in subsequent studies.

PU-106

Type I Interferon Induced by NTHi-DNA Modulates Inflammatory Cytokine Profile to Promote Susceptibility to Nontypeable Haemophilus influenzae

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Objective To investigate the role of NTHi-DNA-induced IFN-I in host against NTHi infection and its regulatory mechanism.
Methods 1. PEMs (Primary peritoneal macrophage) were pre-treated with NTHi-DNA and IFN-β , respectively, and then infected with NTHi, the effect of NTHi-DNA-induced IFN-I on host cell against NTHi infection was studied;Further use IFNAR-/-PEMs to verify the role of IFN-I signaling in macrophage against NTHi infection;Based on the establishment of a simulated COPD mouse model, NTHi-DNA and exogenous IFN-β were instilled in the airway, and mice was infected intranasally with NTHi. The body weight and survival rate of the mice were monitored;The role of IFN-I signaling in mice defense against NTHi infection was confirmed using IFNAR-/- mice.
2. q-PCR and ELISA were used to detect the production of inflammatory factors IL-1β, IL-6, IL-12, CXCL10 and IL-10 in NTHi-infected PEMs after pretreatment with NTHi-DNA and IFN-β, respectively, in the lungs of simulated COPD mice and IFNAR-/- mice.The expression of profiles was further confirmed by IFNAR-/-PEMs.
3. The expression levels of P38 MAPK and NLRP3 in NTHi-infected PEMs pretreated with NTHi-DNA and IFN-β were detected by q-PCR and Western blot to determine the effect of NTHi-DNA-induced IFN-I on inflammatory factors;The role of the P38 signaling molecule in NTHi-DNA-induced IFN-I-mediated inflammatory factor expression was further confirmed using a P38 MAPK inhibitor.
Results 1. NTHi-DNA-induced IFN-I attenuates phagocytosis and killing of NTHi. NTHi-DNA-induced IFN-I aggravates pulmonary inflammatory response and is harmful to host defense during NTHi infection in vivo. The inflammatory response and body weight loss in IFNAR-/- mice were significantly lower than in WT mice.
2. NTHi-DNA-Induced IFN-I promotes pacrophage inflammatory cytokines profile response to NTHi. Inflammatory cytokines production is impaired in response to NTHi in the absence of type I IFN signaling in vitro.
3. NTHi-DNA-induced IFN-I activates the activation of P38 MAPK and NLRP3 signaling molecules to facilitate regulation of PEMs inflammatory cytokine profiles.
Conclusions This work demonstrates that NTHi-DNA-induced IFN-I is not conducive to host resistance to NTHi infection in vitro and in vivo. NTHi-DNA-induced IFN-I-activated p38 MAPK and NLRP3 signaling molecules serve as key regulators of inflammatory cytokine expression. This study found that NTHi-DNA-induced IFN-I plays a detrimental role in NTHi infection, which will provide us with new targets and new therapeutic strategies for the prevention and treatment of NTHi infection.

PU-107

Development of A Simple Sample Preparation Method for Direct Microbial Identification and Susceptibility Testing from Positive Blood Cultures

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Objective Rapid identification and determination of theantibiotic susceptibility profiles of the infectious agents in patients with bloodstream infections are critical for the following effective targeted antibiotic treatment choices. Few efforts have been done to develop combined methods for directly identification and antibiotic susceptibility test of bacteria in positive blood cultures. In this study, we aimed to develop an easier and cheaper combined method to directly identify and determine the antibiotic susceptibility profiles of the infectious agents in patients with bloodstream infections.

Methods We constructed a lysis-centrifugation-wash procedure to prepare bacterial pellet from positive blood culture. The bacterial pellet can be used directly for the identification by MALDI-TOF MS and antibiotic susceptibility testing by Vitek AST systems. Comparison between conventional laboratory culture-dependent bacteriological procedures and our developed protocol was then carried out to evaluate the method.

Results Using a gentle iron buffer solution, we successfully developed a simple lysis-centrifugation-wash procedure to prepare bacterial pellets from positive blood cultures. No more than 15 min are taken for the developed sample preparation process, which are faster than the convectional laboratory biological procedures as well as most of other reported protocols. Meanwhile, the prepared bacterial pellet can be use not only for MS identification, but also for antibiotic susceptibility test. Moreover, the protocol of our method is quite easy to carry out for the clinical laboratory technicians as described in the materials and methods. The correct rate of direct MALDI-TOF MS identification was 96.49% for gram-negative bacteria and 97.22% for gram-positive bacteria. For direct VITEK II antimicrobial susceptibility testing, category agreement of antimicrobials tested was 96.89% for gram-negative bacteria with 2.63% minor error, 0.24% major error, and 0.24% very major error of antimicrobials. Category agreement of antimicrobials tested was 92.81% for gram-positive bacteria with 4.51% minor error, 1.22% major error, and 1.46% very major error of antimicrobials. The results indicated that our direct antibiotic susceptibility analysis method worked well compared to the conventional culture dependent laboratory method. Overall, our study demonstrated a fast, easy and accuracy method for direct identification and antibiotic susceptibility testing of the bacteria in positive blood cultures.

Conclusions In summary, we demonstrated an easy, fast and accurate combine method for direct identification and AST analysis of bacteria in positive blood cultures. The rapid, actuary identification and AST results will better dictate the diagnostic measures taken of patients with bacteremia, which willsignificantly reduce mortality, morbidity and hospital costs.

PU-108

Characteristic and Complete Genome Sequencing of A Novel Member of Infective Endocarditis Causative Bacteria: Bergeyella cardium QL-PH

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Objective Recently,worldwide, three case of *Bergeyella cardium sp.* were reported to be isolated from patients with infective endocarditis. The strains were recognized as a new species belonging to of the genus Bergeyella. The increasing cases of *Bergeyella cardium*in patients with infective endocarditissuggested their important pathogenesis roles. However, studies regarding themicrobiological characteristics and genetic feathers of this species are very rare. In this study, we reported the isolation, identification and characteristic ofanother *Bergeyella cardium*from blood cultures of patient with infective endocarditis. Then, whole genome sequencing was carried out and the possible original of this newly identified speices was investigated.

Methods Morphological, physiological and biochemical characteristics of the newly isolated strain was performed. E-test method was ultimately selected for AST analysis. The whole genome of the newly isolated strain *Bergeyella cardium QL-PH*was sequenced using Novogenwith MPS (massively parallel sequencing) Illumina technology. Genomic assembly and annotation were carried out at Novogen Bioinformatics Technology Co., Ltd.

Results We reported another isolation and identification of a *Bergeyella spp*from blood cultures of patient with infective endocarditis. Both NCBI Blastn analysis andphylogenetic analysis results indicated the new isolation belonged to the novel specie of *Bergeyella cardium*. Detailed phenotypic analysis demonstrated that the strain is a fastidious gram-stain-negative, aerobic, non-motile, oxidase-positive, catalase-negative, rod-shaped bacterium.PDM Epsilometer test indicated that the minimum inhibitory concentration values for most tested antibiotic were low, with the exception of fluoroquinolones. The whole genome sequenceof the isolate consists of a circular chromosome with a total length of 2,036,902 bp. Four antibiotics related genes and eighty-six pathogenesis related genes were predicted from the genome sequences. To our knowledge, this is the first complete genome sequence of *Bergeyella*.

Conclusions Our data, together with other studies, clearly document that *Bergeyella cardium*strains is an important newly identified human pathogen. The phylogenetic, phenotypic results and whole genome sequencing extensively expand the knowledge of the newly identified *Bergeyella spp* related to human infective endocarditis. Our results will provide clues for the clinicaldiagnosis and treatment of this pathogen.

PU-109

Construction and protein expression of prokaryotic expression plasmid of a novel metallo-β-lactamase gene blaIMP-38 and its hydrolysis activity

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Objective Constructing the prokaryotic expression plasmid of a novel metallo-β-lactamase gene *bla*$_{IMP-38}$ to obtain the solvable IMP-38 recombinant protein and detect its hydrolysis activity of carbapenem antibiotics.

Methods The novel metallo-β-lactamase gene *bla*$_{IMP-38}$ was cloned through PCR using the genome of *bla*$_{IMP38}$-producing Klebsiella pneumonia as a template. Then the prokaryotic expression plasmid pet-28a(+)-IMP-38 and pcold TF-IMP-38 was constructed and their accuracy was verified. The solubility of the proteins expressed by Escherichia Coli competence BL21 (DE3) with pet-28a(+)-IMP-38and pcold TF-IMP-38 was explored. The expression condition of solvable IMP-38 recombinant protein was optimized, the recombinant protein was purified and concentrated. The expression of proteins in the prokaryotic cells were approved by SDS-PAGE and western blotting method. The protein hydrolysis experiment was employed to detect the hydrolysis activity of IMP-38 recombinant protein against carbape-nem antibiotics including meropenem, imipenem and ertapenem, at the same time, the relative prevention rates of EDTA for these drugs were detected.

Results The prokaryotic expression plasmid pet-28a(+)-IMP-38 and pcold TF-IMP-38 were successfully constructed and verified. The recombinant protein produced by BL21(DE3) with the pet-28a(+)-IMP-38 formed inclusion body while produced by BL21 (DE3) with the pcold TF-IMP-38 showed solublility. The expression of the protein reached highest at 15 ℃ after being induced for 24h when the concentration of IPTG was 1mM. The results of protein hydrolysis experiment showed that the hydrolysis rates of the IMP-38 recombinant protein against meropenem, imipenem and ertapenem were 73.98%、65.04% and 87.24%. The relative prevention rates of EDTA for these drugs were 87.41%、85.17%和87.24%.

Conclusions We constructed the prokaryotic expression plasmid pet-28a(+)-MP-38 and pcold TF-IMP-38 successfully and obtained the soluble and novel carbapenem enzyme IMP-38 which showed strong hydrolysis activity against meropenem, imipenem and ertapenem.and the EDTA exhibited significant inhibitory action against it's protease activity.

PU-110

Correlation between blood lipids and blood pressure and osteoporosis in postmenopausal women with type 2 diabetes

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Objective The relationship between blood lipids, blood pressure and osteoporosis in postmenopausal women with type 2 diabetes was discussed.
Methods 80 patients with postmenopausal women with type 2 diabetes mellitus and osteoporosis admitted to our hospital from January 2017 to December 2017 were enrolled in the T2DM and OP groups. 80 postmenopausal women with type 2 diabetes were enrolled in the same period. Osteoporosis patients were T2DM non-OP group, and 80 postmenopausal women with abnormal glucose metabolism were selected as the control group. Blood glucose, blood lipids and blood pressure were measured in all three groups. The data differences between the groups were analyzed and compared, and the influencing factors of osteoporosis were analyzed.
Results Blood glucose, total cholesterol, low-density lipoprotein cholesterol, and systolic blood pressure were higher in the T2DM and OP groups than in the T2DM non-OP group. The data were significantly different from the control group ($P<0.05$). The age and total of the OP group were statistically significant ($P<0.05$). Cholesterol, low-density lipoprotein cholesterol, high systolic blood pressure, body mass index, double femur bone density, and lumbar spine 1-4 bone density were lower, which was significantly different from non-OP group, which was statistically significant ($P<0.05$). From the results of this study, age, total cholesterol, low-density lipoprotein cholesterol, and systolic blood pressure are risk factors for OP.
Conclusions Postmenopausal type 2 diabetes patients have more risk factors for osteoporosis, and are associated with age, total cholesterol, low-density lipoprotein cholesterol, and systolic blood pressure.

PU-111

(1-3)-□-D-GLUCAN (BDG) IN DIAGNOSING INVASIVE FUNGAL DISEASE (IFD) IN IMMUNOCOMPROMISED PATIENT

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Objective The aim of this study was to evaluate the use of the BDG assay in order to exclude or confirm suspected IFDs and their correlations with hematological parameters.
Methods An analytical cross-sectional study was performed using sera from 65 patients for the detection of BDG. 39 patient with proven IFD and 26 patient with probable/possible IFD using The European Organization for Research and Treatment of Cancer/Invasive Fungal Infections Cooperative Group and the Mycoses Study Group

(EORTC/MSG) revised criteria. BDG was performed by ELISA method. Leukocyte, neutrophil, lymphocyte, and monocyte counts were measured with Sysmex XN-1000. CD4 levels were analyzed using BD FACSPresto. Sensitivity, specificity, PPV and NPV were calculated using ROC curve analysis and 2x2 contingency table. Correlations were tested using Spearman's correlation coefficient.

Results BDG with cut off level of 169 pg/mL (AUC=0.839) had sensitivity, specificity, NPV and PPV of 92,3%, 64%, 84% and 80% respectively for IFD diagnosis. There were significant correlations between BDG and leukocyte, neutrophil count, lymphocyte count, monocyte count, CD4 (r = 0.312, 0.296, -0.399, 0.304, and -0.327 respectively).

Conclusions BDG can be considered for the diagnosis of IFD as indicated in the diagnostic test. Hematological parameters show a good correlation with BDG immunocompromised patient.

PU-112

Performance Evaluation of STRATUS CS200 for Cardiac Markers

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Objective The STRATUS CS200 (Siemens Healthcare Diagnostics Inc., USA) has recently been developed as an on-site diagnostic instrument for assaying several kinds of cardiac markers within a short duration. The purpose of this study was to analyse the clinical usefulness of the STRATUS CS200 by evaluating its precision and linearity and comparing it with another conventional device.

Methods The precision, linearity, comparison, limit of quantification, and turnaround time (TAT) were evaluated for troponin I, creatine kinase-MB (CK-MB),N-terminal pro-brain natriuretic peptide (NT-proBNP), and myoglobin assays according to guidelines provided by the Clinical and Laboratory Standards Institute.

Results The total coefficients of variation of the four items were between 1.90% and 4.25%. All markers showed a linearity that was ⩾0.99, and the values were within the manufacturer's range. All items showed a close correlation with E170 (Roche Diagnostics, Germany). The limits of quantification for troponin I, CK-MB, myoglobin, and NT-proBNP were 0.03 ng/mL, 0.3 ng/mL, 1 ng/mL, and 15 pg/mL, respectively. The TAT was 14 minutes.

Conclusions The performance of the STRATUS CS200 for assaying cardiac markers was highly satisfactory in terms of the precision, linearity, limit of quantification, and TAT, and it showed a good correlation with the comparative method.

PU-113

Antimicrobial susceptibility testing of Enterobacteriaceae: determination of disk content and Kirby-Bauer breakpoint for ceftazidime/avibactam

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Objective Detection of ceftazidime/avibactam (CAZ/AVI) antibacterial activity is absolutely vital with the rapid growth of carbapenem resistant *Enterobacteriaceae* (CRE). But now, there is no available automated antimicrobial susceptibility testing card for CAZ/AVI, so Kirby-Bauer has become an economical and practical method for detecting CAZ/AVI antibacterial activity against *Enterobacteriaceae*.

Methods In this study, antimicrobial susceptibility testing of CAZ/AVI against 386 Enterobacteriaceaes (from Chongqing and Chengdu. 188 klebsiella pneumoniae , 122 Escherichia coli, 76 Enterobacter cloacae) isolated from clinical patients was performed by broth microdilution and Kirby-Bauer, extended spectrum β lactamases and carbapenemases were confirmed using the guideline of Clinical & Laboratory Standards Institute (CLSI, M100, 28th Edition, 2018). T-test was employed to assess the statistical significance of differences intra-group comparisons using GraphPad Prism 5 software (GraphPad Software, Inc., La Jolla, CA, USA). Differences were considered statistically significant at $p < 0.01$.

Results Of the 386 strains, 54 extended spectrum β lactamases negative (ESBL(-)), 104 extended spectrum β lactamases positive (ESBL(+)), 228 CRE. 287 isolates were susceptible to CAZ/AVI and 99 isolates were resistant to CAZ/AVI. At the same time, to obtain optimal content avibactam (AVI) disk containing ceftazidime (30μg), zone diameters of four kinds of ceftazidime(30μg) disk containing different AVI content (0μg, 10μg, 25μg, 50μg) were tested by Kirby-Bauer method. The microdilution broth method interpretation was used as the standard to estimate susceptible or resistance and then coherence analysis was carried out between Kirby-Bauer and broth microdilution. The result shows the zone diameter of 30μg/50μg disk, susceptible isolates: 20.5mm-31.5mm, resistance isolates: 8.25mm-21mm. The zone diameter of 30μg/25μg disk, susceptible isolates: 19.7mm-31.3mm, resistance isolates: 6.5mm-19.2mm. The zone diameter of 30μg/10μg disk , susceptible isolates: 19.5mm-31mm, resistance isolates: 6.5mm-11mm. The zone diameter of ceftazidime(30μg), susceptible isolates: 6.5mm-27.5mm, resistance isolates 6.5mm.

Conclusions Our results show that 30μg/50μg, 30μg/25μg, 30μg/10μg CAZ/AVI disk have significant statistical differences to determinate CAZ/AVI antibacterial activity, but for 30μg/50μg disk, there has a cross section between susceptible isolates (minimum 20.5mm) and resistance isolates (maximum 21.5mm). For 30μg/25μgdisk, it is hard to distinguish the difference between susceptible isolates (minimum 20.5mm) and resistance isolates (maximum 21.5mm), so 30μg/10μg CAZ/AVI disk is more conducive to determinate antibacterial activity.

PU-114

Changes of intestinal flora in patients with systemic lupus erythematosus in northeast China

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Objective The human gut harbors diverse microbes that play a fundamental role in the well-being of their hosts. Microbes can cause autoimmunity, trigger autoimmunity in genetically susceptible individuals or prevent autoimmunity. There were reports about intestinal flora changes in Systemic Lupus Erythematosus (SLE) patients, but no data were available in northeast China. In this study, we investigated the intestinal flora changes of SLE patients in Heilongjiang province located in northeast China.

Methods Feces from 16 SLE patients and 14 healthy volunteers were employed to extract bacterial DNA, amplify 16s RNA of bacteria, and analyze the biological information by sequencing. The statistical analysis used the SPSS version of 17.

Results We found that there were 1 phylums, 4 families and 9 genera in the intestinal flora of SLE patients. And the nine differences genera can be used to distinguish SLE patients from normal people.

Conclusions It is well known that the intestinal flora is closely related to the living habits and diet of the population. The intestinal flora of SLE patients varies greatly due to their different regions of life.In this study, we found that the intestinal flora of patients with SLE in Heilongjiang Province, northenesat China, was different from that the
SLE patients of foreign countries and southern China reported previously.The differences between the results of this study and others is possibly due in part to the unique geographical location and diatery habits. Whatever, this study is of great significance to improve the study of intestinal flora of SLE patients.Therefore, the increase of Proteobacteria and the decrease of Ruminococcaceae in SLE patients might indicate that these two microbes play an important role in the occurrence and development of SLE disease, but the specific mechanism needs to be further studied.
In addition to the above comparison of microflora in different populations, we also draw the following conclusions through functional prediction analysis. First, compare to healthy control, some proteins were significantly increased in SLE patients, such as fimbrial protein, chaperone, outer membrane usher protein and siderophore group nonribosomal peptides. The increase of these proteins may be
related to hypercoagulability , kidney injury , drug resistance and control
of some pathogenic microorganisms in SLE patients. Secondly, the
oxidation-related enzymes (such as monooxygenase, dehydrogenase and xenobiotics by cytochrome P450) and transferases (such as glutathione stransferase and PTS) were significantly increased in SLE patients. The increase of these enzymes may be related to oxidative stress , signal pathway protein phosphorylation and drug metabolism in patients with SLE. Thirdly, the huntington's disease and ALS are also associated with SLE. We found an increase of Proteobacteria and a decrease of Ruminococcaceae in SLE patients in different regions. In addition, we found that some proteins, enzymes, and diseases were significantly associated with SLE.

PU-115

Improved microRNA extraction using an alternative binding enhancer solution

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Objective MicroRNA (miRNA) analysis has various clinical applications, including diagnosis of diseases such as cancer, determination of patients' responses to treatment, and prognosis. Recently, miRNA analysis by liquid biopsy and next-generation sequencing has been demonstrated. We performed miRNA analysis using a variety of clinical samples but, in some cases, the analysis was unsuccessfully. For example, we could not obtain the required Cp value from the reverse transcription quantitative real-time PCR (RT-qPCR) analysis. The quality and quantity of the miRNA samples affected the downstream miRNA analysis, indicating high quality samples are crucial for obtaining reliable data. We found that polyethylene glycol (PEG) with molecular weights 1540 and 2000 enhanced the miRNA extraction with only a small volume needed to be added to a conventional extraction kit. However, PEG1540 and PEG2000 have high viscosity, which makes them difficult to measure using a pipette, and a high melting point, which means they must be heated and dissolved before use. We remediated these issues by mixing PEG1540 with tetraethylene glycol dimethyl ether (TDE), which is easy to handle, and compared the performance when the mixture replaced the binding enhancer supplied as part of a commercial extraction kit.

Methods We determined the best mix ratio for PEG1540 and TDE, with PEG1540 used above 60° C, by measuring the viscosity of several mix ratios. Each ratio was measured five times. We determined the target viscosity of the mix ratio to be 20 mPa・s because the mixture can then be dispensed with high precision. The viscosity was measured using a VISCO-895 viscosity meter (ATAGO).

We tested the binding enhancement solutions using a synthetic miR-21 product and formalin-fixed paraffin-embedded (FFPE) tissue samples obtained from patients with colon cancer (n=10). Tissue samples were serially sectioned (5-μm thick) and placed onto glass slides. Tissue was scraped from each glass slide with a scalpel. For all the samples, we used a HighPure miRNA Isolation Kit (Roche) according to the manufacturer's instructions for the one-column protocol with 100 μL elution buffer. We used 100－500 μL of the PEG1540:TDE mix solutions as the binding enhancer solutions instead of the Binding Enhancer (Roche) solution supplied in the HighPure miRNA Isolation Kit. We extracted miRNA from five samples for each mix ratio. MiR-21 analysis was performed by stem-loop RT-qPCR using a Universal ProbeLibrary probe (Roche). The extracted miRNA was transcribed into cDNA by a miRNA-specific reverse transcription (RT) reaction using a designed miRNA-specific stem-loop RT primer and a Transcriptor First Strand cDNA Synthesis Kit (Roche). We obtained the miR-21 Cp values by qPCR using a hydrolysis probe and a LightCycler 96 instrument with LightCycler 1.1 software (Roche).

Results As expected, the viscosity of the PEG1540:TDE solutions decreased when the TDE content was increased. At a ratio of 1:1, the viscosity was 21.8 ± 0.3 (mean ± SD) mPa・s, the targeted optimum ratio. The Cp values obtained using the synthetic miR-21

oligonucleotide with 100 - 500 μL of the 1:1 PEG1540:TDE solution were: 100 μL, 18.25 ± 0.13; 200 μL, 12.79 ± 0.20; 300 μL, 12.07 ± 0.14; 400 μL, 11.94 ± 0.28; and 500 μL, 11.98 ± 0.22. The corresponding Cp value obtained using the HighPure miRNA Isolation Kit was 14.60 ± 0.36 (mean ± SD), indicating the substitution of 200 μL of the mixed solution as the binding enhancer improved the quality of the miRNA extraction. We also performed the miRNA extraction from the FFPE tissue samples. The obtained Cp values were 19.87 ± 0.82 for 200 μL of the 1:1 PEG1540:TDE solution and 22.94 ± 1.15 for the HighPure miRNA Isolation Kit, indicating the FFPE samples showed a similar trend as the synthetic miR-21 product.

Conclusions We found that PEG1540 and TDE, which are relatively readily available and easy to use, in a mix ratio of 1:1 can replace the binding enhancer solution in a commercial extraction kit and improve miRNA extraction efficacy. This method will be useful when sufficient miRNA yields are difficult to obtain for whatever reason. Our results show it is possible to improve the effectiveness of miRNA extraction methods by using an alternative binding enhancer.

PU-116

THE EFFECT OF EXPOSURE TO Toxoplasma gondii PROFILIN ON LEPTIN LEVEL IN Rattus Norvegicus WISTAR STRAIN RATS GIVEN NORMAL DIET AND HYPERCALORIC DIET

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Objective Obesity is an abnormal accumulation of body fat and has multiple etiologies including an infection. Based on previous study, there is a possible association between *Toxoplasma gondii* (*T. gondii*) infection and obesity. *T. gondii* is classified as zoonotic disease and has a profilin-like protein recognized by toll-like receptor (TLR-11) and stimulates pro-inflammatory cytokines which leads to inflammation of the host cell and possibly associated with leptin level research is done to know the effect of exposure to *Toxoplasma gondii* profilin on leptin levels in *Rattus Norvegicus* Wistar Strain rats given normal diet and hypercaloric diet

Methods This research was done at Pharmacologyand ParasitologyLaboratory of Medical Faculty Brawijaya University for rats maintenance, interventions and leptin level measurement. For the positive control groups, the tested concentrations of *T. gondii* profilin was 15 μg/ml, 30 μg/ml, and 45 μg/ml on two group of rats, consuming normal diet and hypercaloric diet. The leptin level measured by using ELISA methods.

Results The result was analyzed using one way ANOVA and shows a significant differences between *Toxoplasma gondii* profilin and leptin level ($p=0.001<\alpha$), ($alpha=0.05$). The Pearson correlation shows that there is a positive direction and a strong enough correlation between *T. gondii* profilin and leptin level in Wistar rats given normal diet ($R=0.557$), with no significant effect ($p=0.087>\alpha$); whereas a negative direction and a strong correlation between *T. gondii* profilin and leptin level

in Wistar rats given hypercaloric diet (R=-0.616), with a significant effect (p=0.014<α).

Conclusions This research shows that the exposure to*Toxoplasma gondii*profilin increasethe leptinlevel in rats given normal diet but decrease in rats given hypercaloric diet.

PU-117

Optimization of Enterococcal Infection Drug Delivery Strategy by Monte Carlo Simulation

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Objective To investigate the local infection situation, antibiotic resistance and linezolid MIC distribution of enterococci in 2009-2016, and evaluate the probability of PK/PD target value of linezolid therapy in critical patients with different enterococci infection using PK/PD model and Monte Carlo stimulation, which lay a theoretical foundation for the optimization of linezolid treatment.

Methods WHONET5.6 software was used to analyze antibiotic susceptibility of linezolid. Oracle Crystal Ball software was used to evaluate the probability of AUC24/MIC in critical patients by Monte Carlo simulation.

Results The MIC of linezolid of local enterococci was mainly distributed at 2 mg/L (>66%), in which the distribution of E. faecium, E. faecalis and E. casseliflavus was >85%, the distribution of *E. hirae* and *E. durans* was >90%. Through the PK/PD analysis and Monte Carlo simulation, we found that the treatment of linezolid conventional scheme (600 mg q12 h) in critical patients with MIC 1 mg/L, AUC24/MIC=80-120 can get PTA 100%. However, when the MIC was 2 mg/L, with the increase of AUC24/MIC, PTA was decreased rapidly, AUC24/MIC=80, PTA 99.91%, AUC24/MIC=100, PTA 82.49%, AUC24/MIC=120, PTA 19.14%. When the MIC was increased to 4 mg/L, the PTA was almost 0.

Conclusions Medication project should be adjusted, according to the evaluation results obtained from PK/PD model and Monte Carlo simulation, to improve the success probability of antibacterial drugs in clinical treatment.

PU-118

The role of Circulating microRNAs in breast cancer: potential biomarkers and therapeutic targets

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Objective Breast cancer is a highly heterogeneous disease and multiple cancer subtypes have been discovered. It is crucial to ensure early diagnosis and having proper treatment of breast cancer patients. Accumulating evidence indicates that

microRNAs(miRNAs) play important roles in the breast cancer, including the initiation, proliferation, differentiation and metastasis of the tumor. In particular, the circulating miRNAs have been suggested as diagnostic and prognostic biomarkers which have been identified dysregulated in breast cancer. Therefore, some therapies use specific miRNA as target. We aimed to discuss the potential applications of circulating miRNAs for breast cancer diagnosis prognosis and treatment.

Methods Using “circulating miRNAs and breast cancer” as key words to trace related literatures from January 2009 to January 2019 in the database system of PubMed and CNKI. The literatures inclusion criteria were as follows : 1) the role of circulating miRNAs in breast cancer, 2) the circulating miRNAs in diagnosis of breast cancer, 3) the circulating miRNAs in prognosis of breast cancer , 3) the applications of microRNAs in breast cancer treatment.

Results Firstly, circulating miRNAs have good stability and the samples are easy to access in blood circulation and body fluid. There are various highly sensitive qualitative and quantitative methods to detect miRNAs, such as Quantitative real-time PCR, microarray and Next-generation sequencing. Based on this, A great deal of dysregulated circulating miRNAs have been identified to associated with different breast tumor subtypes and disease states, which suggests these miRNAs as potential diagnosis tool. What’s more, multiple circulating miRNAs or circulating miRNAs combined with other conventional diagnosis methods have shown improved sensitivity and specificity of diagnosis. Secondly, circulating miRNAs are novel, noninvasive prognosis biomarkers for monitoring breast cancer patient’s survival and disease progression. Some specific circulating miRNAs have been demonstrated to be associated with stage, grade and histological subtype of breast cancer patients. Therefore, the miRNA has the potential to provide and improve treatment choice by monitoring the tumor metastasis, recurrence and treatment response. In addition, it is proved that the using of specific miRNA as therapeutic target can enhance anti-tumor effect with other conventional therapy by inhibiting the growth and promoting the apoptosis of the tumor cells. Therapies that target specific miRNA also increase sensitivity of breast cancer cells to chemotherapy and radiotherapy.

Conclusions Here we summarize the current findings concerning the critical role of miRNAs in the regulation of breast cancer. We also discuss the current challenge and possibility of using miRNAs as potential diagnosis and therapeutic biomarkers for breast cancer.

PU-119

Association between Blood Lead Levels and Socio-demographic Factors among Outpatient Children in Ningbo, China

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Objective Lead exposure is a well-known health concern, affecting children worldwide. We aim to assess children's blood lead levels (BLLs), and the association of risk factors with elevated BLL in children since the phase-out of leaded gasoline.
Methods We enrolled 8,085 outpatient children to assess their blood lead levels, and the associations with social-demographic factors. Social-demographic information was obtained by using questionnaires. Multivariable linear and logistic regression models were performed to explore the associations between social-demographic factors and elevated BLLs.
Results The geometric mean BLL was 15.96μg/L. The prevalence rates of elevated BLLs(≧100μg/L and≧50μg/L) were 2.0% and 10.9%, respectively. BLLs in boys were higher than that in girls(P<0.001). Girls had a lower risk of BLLs above 50μg/L than boys (OR=0.83, 95%CI: 0.71-0.96). Father's occupation as a skilled laborer or professional worker and living in the suburbs significantly contributed to the elevated BLLs(≧50μg/L), with the ORs of 1.39(1.06-1.81), 1.33(1.01-1.75) and 1.24(1.02-1.50), respectively.
Conclusions Our results suggested that children who lived in suburbs and whose fathers were skilled laborers and professional workers were more likely to have BLLs above 50μg/L.

PU-120

Application of Xpert-Mtb/RIF in the detection of Mycobacterium tuberculosis in non-sputum

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Objective To explore the application of Xpert-Mtb/Rif in detection of Mycobacterium tuberculosis, in non-sputum specimens of tuberculosis patients.
Methods From Jan. to Dec., 2018, non-sputum specimens (including plerual effusion, ascites, lung lavage fluid, pericardial effusion, urine, feces, pus, tissue, secretion, gastric juice) from 247 tuberculosis patients were collected, and respectively subjected to Fluorescence coating technology, MGIT BD 960 culture, Xpert-Mtb/Rif, proportional drug sensitivity test.

Results In non-sputum specimens of tuberculosis patients, the positive rates of three methods were 11.3%, 55.9% and 70% respectively. Proportional drug sensitivity test were carried out on samples with positive culture. The drug resistance rates of Rifampicin and isoniszid were 23.9% and 31.2 %, respectively. Rifampicin resistance rate, detected by Xpert-Mtb/Rif, was 25.4%. Rif. Resistance often occurs with Iso. Resistance, the comparison showed that 66% of the Rif.resistant specimens detected by Xpert showed Iso. Resistance by solid culture-based drug sensitivity test. Drug resistance was not detected in 3 specimens by Xpert, but detected by proportional method. Confirm that the bacteria contained in the specimens are NTM.
Conclusions Xpert-Mtb/Rif can quickly and accurately detect Mycobacterium tuberculosis and Rif resistance, in non-sputum samples (results within 2 hours), and has high authenticity and reliability. The specificity and sensitivity are high, especially for the samples with low content of Mycobacterium tuberculosis, the detection rate is higher than other detection methods. Xpert has a higher detection rate than MGIT BD960 culture, in non-sputum specimens of tuberculosis patients. Xpert has great value for rapid screening of multidrug-resistant tuberculosis (MDR-TB). When Rif. Resistance was detected by Expert, whether Iso. Resistance need to be considered. It's beneficial to the detection of bacteria-negative tuberculosis and reduces missed and wrong diagnosis. When the culture is positive and Xpert is negative, NTM can be considered.

PU-121

The meta-analysis for ideal cytokines to distinguish the latent and active TB infection

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Objective One third whole-world population is infected with Mycobacterium tuberculosis (*Mtb*), but 90% of them are asymptotic latent infection. There is lack of ideal strategy to distinguish active tuberculosis (TB) and latent tuberculosis infection (LTBI). Some scientist had focused on a set of cytokines as biomarkers besides interferon- gamma (IFN-γ) to distinguish active TB and LTBI, but with considerable variance of results. This meta-analysis aimed to evaluate the overall discriminative ability of potential immune molecules to distinguish active TB and LTBI.
Methods PubMed, the Cochrane Library, and Web of Science databases were searched to identify studies assessing diagnostic roles of cytokines for distinguishing active TB and LTBI published up to August 2018. The quality of enrolled studies was assessed using Quality Assessment of Diagnostic Accuracy Studies-2 (QUADAS-2). The pooled diagnostic sensitivity and specificity of each cytokine was calculated by using Meta-DiSc software. Area under the summary receiver operating characteristic curve (AUC) was used to summarize the overall diagnostic performance of each biomarker.
Results Fourteen studies with 982 subjects met the inclusion criteria, including 526 active TB and 456 LTBI patients. Pooled sensitivity, specificity and AUC for discriminating between active TB and LTBI were analyzed for IL-2 (0.87, 0.61 and 0.9093), IP-10 (0.77, 0.73 and 0.8609), IL-5 (0.64, 0.75 and 0.8533), IL-13 (0.75,

0.71 and 0.8491), IFN-γ (0.67, 0.75 and 0.8031), IL-10 (0.68, 0.74 and 0.7957) and TNF-α (0.67, 0.64 and 0.7783). The heterogeneous subgroup analysis showed that cytokine detection assays, TB incidence, and stimulator with *Mtb* antigens are main influence factors for their diagnostic performance.

Conclusions The meta-analysis showed serum cytokine production could assist the distinction between active TB and LTBI, IL-2 with the highest overall accuracy. No single biomarker is likely to show sufficiently diagnostic performance due to limited sensitivity and specificity. Further prospective studies are needed to identify the optimal combination of biomarkers to enhanced diagnostic capacity in clinical practice.

PU-122

Clinical value of plasma miR-544a and miR-3151 in the diagnosis and treatment of lung cancer

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Objective To detect the expression levels of miR-544a and miR-3151 in plasma, and to explore its clinical value in the diagnosis and treatment of lung cancer

Methods 100 healthy subjects, 160 lung cancer patients (100 patients without any anti-tumor therapy, 60 patients with lung cancer undergoing surgery or chemotherapy), and 100 benign lungs were detected by real-time quantitative PCR (RT-qPCR). T-test was used to compare the expression levels of miR-544a and miR-3151 in plasma of different groups. The diagnostic efficacy of miR-544a, miR-3151 and various tumor markers for lung cancer was analyzed by ROC curve

Results Compared with the normal group, the expression of miR-544a and miR-3151 in the lung cancer group was significantly higher than that in the normal group, and it was statistically significant. Compared with the benign nodules group, the expression of miR-544a in lung cancer group was significantly increased, but the expression level of miR-3151 was lower than that of nodules. The expression levels of miR-544a and miR-3151 in lung cancer patients one week after surgery and one week after chemotherapy were significantly higher than those in untreated lung cancer patients, but the *P* values were all greater than 0.05. The area under the ROC curve (AUC) for miR-544a diagnosis of lung cancer was 0.908, the sensitivity was 73%, and the specificity was 94%. The AUC of miR-3151 is 0.755, with a sensitivity of 66% and a specificity of 73%. The AUC of miR-544a combined with miR-3151 for the diagnosis of lung cancer was 0.845 with a sensitivity of 81% and a specificity of 77%.

Conclusions miR-544a is highly expressed in lung cancer and has a good diagnostic power for diagnosis of lung cancer, suggesting that miR-544a may become a novel marker for the diagnosis of lung cancer. miR-3151 is highly expressed in benign pulmonary nodules and plays a role in the differential diagnosis of benign pulmonary nodules. The expression levels of miR-544a and miR-3151 were significantly increased after treatment of lung cancer, which may have certain effects on the treatment of lung cancer

PU-123

Ursolic acid targets KLF4 and competitively blocks the formation of TEADs-YAP1 complex to inhibit gastric cancer growth

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Objective The present study was to evaluate the antitumor effect of ursolic acid and to investigate the mechanisms of it through interacting with Hippo pathways.We found ursolic acid activated KLF4 dose-dependently which obviously suppressed the proliferation of BCG-823 cells. We also found ursolic acid inhibited tumor growth in an orthotopic tumor transplantation model.

Methods We measured the mRNA levels of a typical oncogene CTGF and its downstream genes Cyclin D2,P21,p27 and GII2 by RT-qPCR both in vivo and in vitro. We found with the activation of KLF4, CTGF was decreased and its downstream genes were correspondingly regulated. Flow cytometry further helped to demonstrate that inhibition of CTGF arrested tumor cells in G2/M which blocked the proliferation progress. Confocal laser scanning results finally showed KLF4 combines with YAP1 and blocked the formation of TEADs-YAP1 complex to interrupt the expression of CTGF and the downstream oncogenic process.

Results In conclusion, ursolic acid inhibited gastric cancer growth both in vivo and in vitro. It activated KLF4 which may competitively bind with YAP1 against TEADs and block the oncogenic HIPPO pathways.

Conclusions In conclusion, although multiple signaling pathways have been demonstrated to be involved in anti-cancer effect, our results presented here are particularly novel because the data revealed, for the first time, that KLF4 as a tumor suppressor, which interacted with YAP1 and negatively inhibited oncogenic gene CTGF and downstream PI3/Akt pathways. Moreover, we also found a natural compand-ursolic acid can block the oncogenic pathway of gastric cancer through activating KLF4 both in vivo and in vitro.

PU-124

Probiotics Lactobacillus reuteri abrogates immune checkpoint blockade-associated intestinal inflammation by preserving group 3 innate lymphoid cells

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Objective Numerous studies have confirmed, ICB-associated colitis is quite frequent and severe in immune checkpoint blockade immunotherapy and is routinely treated with immunosuppressive therapy, which has significant side effects diminishing the antitumor response. Simultaneously, the exact mechanism of ICB associated colitis needs to be still explored. At the same time, studies have shown that the gut microbiome is closely related to the body's immune function. Therefore, this study attempts to analyze the changes of microbiome in the body of patients with colitis, and the effect of the microbiome on the intestinal inflammation, which will provide new ideas for mitigating intestinal inflammation.

Methods 1.We combined ICB (anti－CTLA4 and anti-PD1) treatment with a standard colitis model giving mice more severe colitis to imitate the clinical observations of patients who received plus ipilimumab (anti-CTLA4) and nivolumab (anti-PD1).Observing the mouse weight loss index, serum inflammatory cytokine levels KC, IL-6, TNF-α, IFN-γ, IL-12, colon pathology score and analysis mouse feces flora by 16s RNA metagenomic sequencing. 2.By depletion of Lactobacillus by vancomycin to verify that mouse enteritis is associated with altered intestinal flora.3.Through the daily administration of Lactobacillus reuteri in mice with enteritis,and the various inflammatory indexes were observed to determine the effect of probiotic Lactobacillus reuteri on the symptoms of intestinal inflammation in mice.4.Flow cytometry analysis of mouse colonic T lymphocyte lineage, neutrophil cell line, and changes in innate lymphoid cells (ILCs) to explore the mechanism of Lactobacillus reuteri alleviating immune enteritis in mice.

Results 1.We found that composition of gut microbiota impacted the immunopathology of ICB associated colitis. Principal component analysis of gut microbiome showed an obvious less abundance of Lactobacillus in severe ICB associated colitis.2. Depletion of Lactobacillus by vancomycin augments the immunopathology of ICB which verifing that mouse colitis is associated with altered intestinal flora.3. Furthermore, we found that the toxicity of ICB can be totally eliminated via administration of a widely available probiotic Lactobacillus reuteri. 4.Mechanically, the protective effect of L. reuteri was associated with the decreased distribution of group 3 innate lymphocytes (ILC3s).

Conclusions Our study highlights the immunomodulatory mechanism of gut microbiota and suggests that manipulating gut microbiota by administrating L. reuteri to mitigate the autoimmunity caused by ICB allowing immune checkpoint blockade to achieve the desired immune response without an apparent immunopathology.

PU-125

C allele of Fork I decrease the risk of cardiovascular diseases in obese children and adolescents in West China

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Objective The most of obesity could lead to dyslipidemia and increase the risk of cardiovascular diseases (CVDs). Obesity closely correlates with vitamin D and vitamin D receptor (VDR). The objective of this study is to reveal the effects of obesity, serum vitamin D leveland VDR *Fok I* genotype on serum lipid profile of children and adolescents in west China. And reveal the relationship among them in risk of cardiovascular diseases in Chinese children and adolescents.

Methods 452 children and adolescents were recruited from West China Second University Hospital to participate in this cross-section study. All the participants were divided into two groups -- obese group and non-obese group according to the body mass index (BMI). Serum vitamin D level, serum lipid level and VDR *Fok I* gene polymorphism were detected in the laboratory. Based on the level of serum vitamin D, all subjects were divided into three group, vitamin D normal group, vitamin D insufficiency group and vitamin D deficiency group. All children and adolescents were classified into TT genotype and C allele carriers on the basis of the different expression of VDR *Fok I* gene. The impact of obesity, vitamin D level and VDR *Fok I* genotype on lipid level was investigated by analysis of the experiment data. All data were analyzed by independent-samples T test and One-way ANOVA, and adjusted for age by covariance test.

Results 1. The concentrations of serum vitamin D in the obese group was lower than that in the non-obese group. The levels of serum TC, TG, HDL, LDL, $ApoA_1$, Apo-B, LDL/HDL, TG/HDL in the obese group were higher than those in the non-obese group (P=0.000, P=0.003, P=0.000, P=0.000, P=0.000, P=0.000 P=0.000, P=0.000). 2. There was no difference in genotype distribution and allele frequency of VDR *Fok I* site between Obese and non-obese group. 3. In all children and adolescents, there was no difference in serum vitamin D level and lipid profile between C allele carriers and TT genotype in non-obese group.However, in obese group, the C allele carriers had much lower concentrations of TC, TG, Apo-B, TC/TG, LDL/HDL, TG/HDL than TT genotype (P=0.000, P=0.017, P=0.000, P=0.009, P=0.033, P=0.020). 4. The concentration of HDL-C and Apo-A1 in the vitamin D deficiency group was significantly higher compared with the insufficiency and normal group (P=0.007, P=0.001; P=0.013, P=0.002). Moreover, the vitamin D insufficiency and deficiency group had higher concentration of TC and LDL-C compared with vitamin D normal group (P=0.025, P=0.012; P=0.044, P=0.032). 5. In non-obese group, C allele carriers had higher TC, HDL, Apo-A_1 in vitamin D deficiency group compared with TT genotype (P=0.039, P=0.025, P=0.009). In obese group, C allele carriers had lower concentrations of TC, TG, Apo-B, TC/HDL, LDL/HDL and TG/HDL in vitamin D deficiency group than TT genotype (P=0.009, P=0.011, P=0.001, P=0.000, P=0.007, P=0.008).

Conclusions The level of lipid is influenced by mutation of VDR *Fok I* gene, the level of vitamin D and obesity in children and adolescents in West China. The effect of C allele genotype that decreased the risk of CVDs could be reinforced when the subjects

had low concentration vitamin D. The molecular mechanism of VDR genotype effect on lipid level requires a further research.

PU-126

Rapid identification of an infection case of the central nervous system caused by Prevotella bivia with Clin-TOFII mass spectrometry system

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Objective Prevotella bivia belongs to obligate anaerobic bacterium, which is mainly parasitic in the oral cavity, gastrointestinal tract and female reproductive tract. When the patient has low immune function or trauma, it can cause gums, female reproductive tract, abdominal cavity or pelvic cavity infections. The bacteria often cause mixed infection of adjacent organs or nearby tissues of normal colonization sites, and cases of central nervous system infection have rarely been reported at home and abroad.

Methods The patient, male, 16 years old, underwent a resection of the sacrococcygeal abscess about a week ago, and followed by high fever and headache. Later, due to high fever, headache, vomiting and neck stiffness was admitted to hospital. After admission, Blood routine, C-reactive protein, cerebrospinal fluid routine, cerebrospinal fluid biochemistry and other tests were performed. The cerebrospinal fluid was collected and injected into anaerobic and aerobic blood culture bottles for bacterial identification. Clin-TOFII mass spectrometry system was used to identify pathogens.

Results Blood tests: WBC 13.19×10^{9}/L, N 89.70%, CRP: 39.16 mg/L; cerebrospinal fluid routine: WBC 3820×10^{6}/L, percentage of polynuclear cells 95%; cerebrospinal fluid biochemistry: Cl 114.9 mmol/L, M-TP 4796.68 Mg/L, Glu 0.01 mmol/L. After 20 hours of culture, the anaerobic blood culture bottle was positive, and the Columbia blood plate medium was used for inoculation. After 24 hours of anaerobic culture, small, smooth, moist and gray colonies grew. Microscopically, a gram stain revealed gram-negative small bacilli. The pathogen was identified as Prevotella bivia by Clin-TOFII mass spectrometry system. According to the identification results, the application of antibacterial drugs was adjusted, and the central nervous system infection was quickly controlled.

Conclusions In this case, the pathogen was isolated from cerebrospinal fluid of the patient, and it was highly suspected that the pathogen was retrogradely infected due to the resection of the sacrococcygeal abscess. The traditional microbial identification methods are time-consuming, especially for the isolation and identification of anaerobic bacteria and the drug sensitivity test due to the lack of uniform standards and specifications. The Clin-TOFII mass spectrometry system has outstanding advantages in microbial identification, shortens the identification time, provides guarantee for accurate, rapid and stable identification results, and provides strong support and scientific basis for clinical diagnosis.

PU-127

Human papillomavirus infection in Twelfth Division of the Crops

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Objective To investigate human papilloma virus(HPV) infection and subtype distribution in Twelfth Division of the Crops, and to provide a reference for the control and prevention of cervical cancer.
Methods A total of 6189 female cervical secretion samples from Twelfth Division of the Crops were collected from December 2018 to January 2019. HPV genotyping was performed, and the subtype distribution in different ages was analyzed.
Results There were 861 positive samples, including 648 cases of single infection and 213 cases of multiple infection, and the infection rate was 13.9%. The infection rates were 14.1% in <40-year-old group, 12.7% in 40-44-year-old group, 13.4% in 45-49-year-old group, 13.1% in 50-54-year-old group, 15.8% in 55-59-year-old group and 17.1% in >60-year-old group ($P<0.05$). The top 7 subtypes were type 52(23.8%), 16(16.8%), 53(12.0%), 58(11.1%), 51(10.5%), 68(10.0%), and 39(9.9%).
Conclusions HPV infection rate in >60-year-old group is the highest in Twelfth Division of the Crops. The proportion of women infected with HPV 52 and 16 is higher. HPV screening for high-risk population is helpful for the prevention and treatment of cervical cancer.

PU-128

Rab27B Promotes the Stemness of Colon Cancer Cells via Up-regulation the secretion of VEGF and TGF-β

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Objective Recent evidences have unveiled critical roles of cancer stem cells (CSCs) in tumorigenicity, but how maintain CSC initiation remains obscure. The small GTPases Rab27B regulates autocrine and paracrine cytokines by monitoring exocytosis of extracellular vesicles, and is reported to promote certain tumor progression. Here , We want to explore the molecular mechanism of Rab27B to regulate
stemness and proliferation on CSCs.
Methods Flow cytometry was used to estimate the stem cell proportion and the distribution of cell cycle; ELISA was employed to analyze the VEGF and TGF-β secretion level of CSCs ; human colon cancer cell line subcutaneous xenograft models in nude mice was established to assessed tumor growth and angiogenesis.
Results We observe that overexpression of Rab27B increased sphere formation efficiency (SFE) by increasing the proportion of $CD44^{+}$ and $PKH26^{high}$ cells in HT29 cell lines, and accelerating the growth of colosphere with higher percentage of cells at S phase.

Mechanism study revealed that the supernatant derived from HT29 sphere after Rab27B overexpression was able to expand sphere numbers with elevated secretion of VEGF and TGF-β. In tumor implanting nude mice model, tumor initiation rates and tumor sizes were enhanced by Rab27B with obvious angiogenesis. As a contrast, knocking down Rab27B impaired the above effects.

Conclusions Altogether, our findings reveal that Rab27B could promote the Stemness of Colon Cancer stem Cells via Up-regulation the secretion of VEGF and TGF-β.

PU-129

The impact of sharing primer, the quantity of the internal control gene and the primer dimer on reaction system in duplex PCR

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Objective o find out the relationship of interference among templates with different primer pairs, the internal control gene and the primer dimer in duplex PCR.

Methods e designed and synthesized plasmids with partial same sequence and different types of primers , include central-homo primer pair, ordinary primer pair and complementary primer pair. Then we compared the amplify efficiencies of different kinds of primer pairs. Besides, we adjusted the amount of IC plasmid and IC primer to find out the key factor that influencing the sensitivity of the target template.

Results The concentration ratios for two plasmids appeared interference for sharing universal primer pair, sharing one forward primer and sharing no primer were 50:1, 200:1 and 500:1, respectively. And the amplify efficiency of the ordinary primer pair was higher than that of the universal primer pair for the plasmid. Sensitivity of the duplex qPCR unchanged when we increased the amount of PDs, but it declined rapidly when the quantity of the IC was increased.

Conclusions IC who is the major factor influencing the sensitivity of the duplex qPCR and it would be better to use one universal primer for IC and target template to achieve minimum interference and it would be better to use one universal primer for IC and target template to achieve minimum interference.

PU-130

Perturbation of Glutamatergic Transmission and Ephrin Receptor Signaling in the Hypothalamus of Inflammation-associated Depression by Proteomics Integrated with Metabolomics

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Objective Hypothalamic dysfunction is a key pathological factor in inflammation-associated depression. In this study, we attempt to gain further insights into the mechanisms of depression during inflammatory disequilibrium using a combination of metabolomic and proteomic profiling of mice hypothalamus.

Methods (1) In present study, isobaric tags for relative and absolute quantitation (iTRAQ) combined with mass spectrometry and gas chromatography-mass spectrometry (GC-MS) were employed to detect the proteomes and metabolomes in the hypothalamus of the lipopolysaccharide (LPS)-induced depressive-like mouse, respectively.

(2) Ingenuity Pathway Analysis (IPA) software was performed to search for biological functions, canonical pathways, and molecular interaction networks of differential metabolites and proteins

(3) qRT-PCR and WB were applied to validate the expression of key genes and proteins in Ephrin receptor signaling, and glutamatergic pathway in the hypothalamus.

Results 187 proteins were differentially expressed against the control group. The multi-omics integrated analysis contributes to explore yet unknown molecular mechanisms. Our previous result showed that 27 metabolites were differentially expressed by GC-MS. Following integrated analysis of double-omics data by IPA software, relevant pathways and molecular interaction networks were established. The results indicated that several key molecules might be associated with the neuroinflammation stress, including glutamatergic transmission-related proteins and metabolites, and Ephrin receptor signaling-related proteins. The expression of mRNA level of Glul, Gad1 & 2, GluN1, GluN2A, Ephrin-B1 and EPHB2, as well as changes in protein level of EPHB2, Glul, and GluN2A, indicated that LPS perturbed glutamatergic transmission and Ephrin receptor signaling in the hypothalamus. Changes in these regulatory and structural proteins provide insight into the molecular mechanisms underlying the abnormal synaptic functional plasticity. Interestingly, the expression levels of the hypothalamic PSD-95, p-Akt and BDNF, potentially involved in regulation of synaptic plasticity, was significant alteration in the LPS-induced depressed group.

Conclusions This result suggested that a possible EPHB2-GluN2A-AKT cascade affected synaptic plasticity in the hypothalamus of LPS mice and might be an underlying pathogenesis in inflammation-associated depression. Therefore, hypothalamic EPHB2 and GluN2A might be potential antidepressant targets. To sum up, our findings potentially unraveled the differences of molecular mechanisms between LPS depressed mice and controls, and then provided the basis for additional discovery and validation research for determining biomarkers to diagnose depression earlier, and identifying new therapeutic targets.

PU-131

The association between the migration inhibitory factor -173G/C polymorphism and cancer risk: A meta-analysis.

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Objective Previous studies have suggested that macrophage migration inhibitory factor (MIF) -173G/C polymorphism may be associated with cancer risk. However, previous research has demonstrated conflicting results. Therefore, we followed the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines and the meta-analysis on genetic association studies checklist, and performed a meta-analysis to investigate the association between MIF -173G/C polymorphisms and the risk of cancer.

Methods Odds ratios (ORs) and corresponding 95% confidence intervals (CIs) were combined to measure the association between MIF promoter polymorphisms and cancer risk. The pooled ORs were performed for the dominant model, recessive model, allelic model, homozygote comparison, and heterozygote comparison. The publication bias was examined by Begg's funnel plots and Egger's test. A total of ten studies enrolling 2,203 cases and 2,805 controls met the inclusion criteria.

Results MIF (-173G/C) polymorphism was significantly associated with increased cancer risk under the dominant model (OR=1.32, 95%, CI=1.00-1.74, P=0.01) and the heterozygote comparison (OR=1.38, CI=1.01-1.87, P=0.04). In subgroup analysis, MIF polymorphism and prostate were related to increased risk of prostate and non-solid cancer.

Conclusions In conclusion, MIF polymorphism was significantly associated with cancer risk in heterozygote comparison. The MIF -173G/C polymorphism may be associated with increased cancer risk.

PU-132

HDAC7 Ubiquitination by the E3 Ligase CBX4 Is Involved in Contextual Fear Conditioning Memory Formation

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Objective Histone acetylation, an epigenetic modification, plays an important role in long-term memory formation. Recently, histone deacetylase (HDAC) inhibitors were demonstrated to promote memory formation, which raises the intriguing possibility that they may be used to rescue memory deficits. However, additional research is necessary to clarify the roles of individual HDACs in memory.

Methods In this study, we demonstrated that HDAC7, within the dorsal hippocampus of C57BL6J mice, had a late and persistent decrease after contextual fear conditioning (CFC) training (4 –24 h), which was involved in long-term CFC memory formation. We

also showed that HDAC7 decreased via ubiquitin-dependent degradation. CBX4 was one of the HDAC7 E3 ligases involved in this process. Nur77, as one of the target genes of HDAC7, increased 6 –24 h after CFC training and, accordingly, modulated the formation of CFC memory.

Results Finally, HDAC7 was involved in the formation of other hippocampal-dependent memories, including the Morris water maze and object location test. The current findings facilitate an understanding of the molecular and cellular mechanisms of HDAC7 in the regulation of hippocampal-dependent memory.

Conclusions The current findings demonstrated the effects of histone deacetylase 7 (HDAC7) on hippocampal-dependent memories. Moreover, we determined the mechanism of decreased HDAC7 in contextual fear conditioning (CFC) through ubiquitin- ependent protein degradation. We also verified that CBX4 was one of the HDAC7 E3 ligases. Finally, we demonstrated that Nur77, as one of the important targets for HDAC7, was involved in CFC memory formation. All of these proteins, including HDAC7, CBX4, and Nur77, could be potential therapeutic targets for preventing memory deficits in aging and neurological diseases.

PU-133

miR-124-3p inhibits proliferation, migration and invasion by adjusting ITGB3 in gastric cancer cells

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Objective The aim of the present study was to investigate the underlying molecular mechanism by which miR-124- 3p suppresses gastric cancer cell in the proliferation, migration and invasion by adjusting ITGB3.

Methods RT-PCR and western blot are used to detect the expression of miR-124-3p, ITGB3 and their proteins intergrin β3 in three kinds of human gastric cancer cells MKN45, AGS, MGC-803 and normal human gastric epithelial cells GES-1, and further to identify the proliferation, migration and invasive capabilities of those cells. Select two kinds of GC cells with relatively high and low invasion and migration ability and divided into the blank control group, pEGFP-ITGB3 group, pEGFP-NC group, ITGB3 siRNA group, and control siRNA group. The wound healing, CCK-8 assay, transwell migration, and invasion assay was performed to test the effect of ITGB3 in cell proliferation, migration and invasion. Similarly, set the blank control group, miR-124-3p mimics group, miR-NC group, miR-124-3p inhibitor group and inhibitor-NC group, use the same method to detect the effect of mir-124 -3p in cell function, and RT-PCR and western blot are used to detect the expression of mir-124-3p, ITGB3 and intergrin β3.

Results The trend of ITGB3 expression level of four kinds of cell lines is MGC803 > AGS > MKN-45 > GES-1 and the trend of miR-124-3p expression level of cell lines is the opposite (p all < 0.05). CCK-8 assay, wound healing and transwell invasion and migration experiments showed that the cell lines with low expression of miR-124-3p and high expression of ITGB3 gene as well as protein have high proliferation and invasion ability, vice versa. In GC cell lines MGC-803 and MKN45, the results of ITGB3

interference and overexpression experiment have shown that compared with control siRNA group, GC cell proliferation, invasion and metastasis ability has been restricted in ITGB3 siRNA group ($p < 0.05$). Compared with pEGFP-NC group, GC cell proliferation, invasion and metastasis ability are all higher in pEGFP-ITGB3 group. MiR-124-3p interference and over-express test results have all shown that ITGB3 and integrin β3 expression level decreased ($p < 0.05$) and GC cell proliferation, invasion and metastasis ability has been restricted in miR-124-3p mimics group compared with the miR-NC group ($p < 0.05$). In addition, the ITGB3 and integrin β3 expression levels as well as GC cell proliferation, invasion and metastasis ability increased in miR-124-3p inhibitor group compared with inhibitor-NC group.

Conclusions We confirmed that the change of miR-124-3p expression level can regulate ITGB3 expression levels, thus affect the expression of integrin β3 and GC cell proliferation, invasion, migration ability. These data indicated that miR-124-3p might be a novel anti-tumor factor of GC and may provide a new strategy for diagnose of GC.

PU-134

Effects of TNF-α antibody on apoptosis in the hypothalamus after subarachnoid hemorrhage

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Objective Subarachnoid hemorrhage (SAH) can induce apoptosis in many brain regions such as cortex and hippocampus. However, few studies have focused on apoptosis in the hypothalamus after SAH. Although some anti-apoptotic strategies have been developed in SAH, the related molecular mechanism is still not fully addressed. Therefore, the purpose of this study is to evaluate whether SAH could induce apoptosis in the hypothalamus and find the potential molecular mechanism of therapeutic regimen on the apoptosis.

Methods Rats were performed with SAH. Anti-tumor necrosis factor-alpha (TNF-α) antibody or U0126 was microinjected into the left lateral cerebral ventricle 30 min before SAH. In addition, phorbol-12-myristate-13-acetate (PMA) was injected intraperitoneally immediately after anti-TNF-α antibody microinjection. Then, real-time PCR, western blot and immunohistochemistry were used to detect expression of caspase-3, bax, bcl-2, phosphorylated Erk (p-Erk) and Erk. Anxiety-like behavior was identified by using open field.

Results We found temporally increased caspase-3, bax and bcl-2 after SAH in the hypothalamus, suggesting the induction of apoptosis in this brain region. Interestingly, we found that anti-TNF-α antibody microinjection could selectively block the elevated bax, suggesting the potential role of anti-TNF-α antibody in inhibiting SAH-induced apoptosis in the hypothalamus. Moreover, we found that Erk activation was necessary for apoptosis after SAH, and microinfusion of anti-TNF-α antibody could inhibit apoptosis by suppressing the increase of p-Erk in the hypothalamus. Finally, we found that anti-TNF-α antibody infusion could improve the anxiety-like behavior.

Conclusions These results demonstrate that anti-TNF-α antibody attenuate the apoptosis in the hypothalamus by inhibiting activation of Erk, which plays an important role in the treatment of SAH.

PU-135

Conditioned Taste Aversion Memory Extinction Temporally Induces BDNF Secretion and Synthesis in the Insular Cortex

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Objective Brain-derived neurotrophic factor (BDNF) and its receptor, tropomyosin-related kinase receptor B (TrkB), play important roles in different memory process, including memory extinction. It has been shown that BDNF secretion and synthesis temporally regulate different memory phases through activation of TrkB receptors. However, whether memory extinction could induce BDNF release and synthesis on the basis of its location has not been fully understood. In this study, we aim to investigate activity-dependent BDNF secretion and synthesis in the insular cortex (IC) in conditioned taste aversion (CTA) memory extinction.
Methods Rats were performed with CTA memory extinction. BDNF antibody or the same volume of vehicle was microinjected into the IC immediately after the extinction test. After the second extinction test, real-time PCR and *in situ* hybridization were used to detect gene expression of BDNF. BDNF protein levels were identified by enzyme-linked immunosorbent assay. In addition, the phosphorelated TrkB levels normalized to total TrkB were examined by immunoprecipitation and immunoblotting.
Results We found that blocking BDNF signaling in the IC could disrupt CTA extinction, which suggest that BDNF signaling in the IC is necessary for CTA extinction. In addition, temporal changes in both BDNF gene expression and protein of IC were found during CTA extinction. Moreover, we found that TrkB phosphorylation increased at the time point before the enhanced BDNF expression, which suggest that CTA extinction induce rapid activity-dependent BDNF secretion in the IC.
Conclusions These data suggest that CTA memory extinction temporally induced BDNF release and synthesis through activation of TrkB receptors in the IC.

PU-136

Long noncoding RNA PVT1 facilitates colorectal cancer cell proliferation and invasion by IRS1 downregulation through sponging miR-214-3p

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Objective Long non-coding RNAs (lncRNAs) involved in the occurrence and tumorigenesis of different malignant cancers, therefore, they can be also used as potential biomarkers for diagnosis and treatment of cancers. This study is designed to investigate the regulatory role of lncRNA plasmacytoma variant translocation 1 (PVT1) in colorectal cancer (CRC) to reveal molecular pathogenesis mechanism of CRC.
Methods Microarray expression profiles were used to screen differentially expressed genes and lncRNAs associated with CRC. Subcellular localization of PVT1 was examined using fluorescence in situ hybridization. The interaction between PVT1 and microRNA-214-3p (miR-214-3p) as well as between insulin receptor substrate 1 (IRS1) and miR-214-3p were predicted using RNA22 website, and then verified by dual luciferase reporter gene assay, RNA pull-down and RIP assays.The expression pattern of PVT1, miR-214-3p, IRS1, PI3K and Akt was characterized in response to PVT1 silencing or miR-214-3p up-regulation. Meanwhile, their regulatory effects on cell proliferation, invasion and apoptosis were also detected in CRC cells.
Results The expression of IRS1 and PVT1 were robustly induced in CRC. LncRNA PVT1, located in the cytoplasm, was identified as a competitive endogenous RNA (ceRNA) against miR-214-3p, while IRS1 was found to be a downstream target gene of miR-214-3p. With increased level of miR-214-3p and decreased level of PVT1 in CRC cells, PI3K and Akt expression was reduced, and as a consequence, the cell apoptosis was stimulated and cell proliferation and invasion was suppressed.
Conclusions LncRNA PVT1 competitively binds to miR-214-3p to upregulate the expression of IRS1 through PI3K/Akt signaling pathway activation, thus accelerating CRC progression, suggesting that PVT1 might be a potential target of therapeutic strategies for CRC.

PU-137

Mesenchymal Stem Cell-Derived Exosomal Long non-coding RNA LINC01093 Alleviates Hepatic Fibrosis in Alcoholic Hepatitis via Suppressing Nuclear Factor-κB Signaling Pathway by Negatively Targeting ICAM-1.

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Objective Alcoholic hepatitis (AH) can result in profound impairment of liver function with high morbidity and mortality rate, and mesenchymal stem cells (MSC) is considered as a hopeful option for AH therapy. Increasing evidence demonstrated that long non-coding RNA (lncRNA) expression was involved in AH development, and we have identified lncRNA LINC01093 derived from MSC exosomes is closely associated with AH. Thus, we aim to explore the effect and mechanism of MSC-derived exosomal LINC01093 in regulating AH development.

Methods The lncRNA and differentially expressed mRNA were obtained from GEO database and our previous microarray results, and the AH model had already successfully established. The MSC-derived exosomes were collected using ExoCap™ Exosome Isolation and Enrichment Kits. The expression of ICAM-1, caspase3, TGF-β1, Bax, B-cell leukemia/lymphoma 2 (Bcl-2) and NF-κB p65 in tissues and in cells was detected by quantitative polymerase chain reaction (qPCR) and Western blot. The expression of tumor necrosis factor-α (TNF-α), hyaluronic acid (HA), laminin (LN), procollagen III (PC III) was determined by ELISA. Lastly, the effect of LINC01093 on NF-kB p65 nuclear translocation was observed by immunofluorescence.

Results AH mice had decreased LINC01093 and Bcl-2 expression and up-regulated expression of ICAM-1, caspase3, TGF-β1, NF-κB p65 and bax as well as severe inflammatory reaction. ICAM-1 was targeted by LINC01093 negatively. Moreover, after transplanting umbilical cord mesenchymal stem cells (UCMSC), overexpressed expression of LINC01093, decreased expression of ICAM-1, caspase3, TGF-β1, NF-κB p65 and bax was found accompanied with promoted cell apoptosis and alleviated hepatic fibrosis.

Conclusions Taken together, overexpression of LINC01093 derived from UCMSC could alleviate hepatic fibrosis, promote apoptosis of hepatocytes in AH via suppressing NF-κB signaling pathway by down-regulating ICAM-1, which provides a novel therapeutic target for the treatment of AH.

PU-138

Investigation on reference intervals of blood cells parameters for apparently healthy population in Changsha area

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Objective To establish the reference intervals (RIs) of venous blood cell parameters among the healthy population in Changsha area.
Methods 18 parameters of venous blood cells of 3176 healthy people with18-85yearsoldwere detected by Beckman Coulter LH750 Hematology Analyzer, which included white blood cell (WBC), neutrophil (NEU), leukomonocyte (LC), neutrophils percentage(NEU%), lymphocyte percentage(LYM%), monocyte (MONO), eosinophil (EO), basophil (BASO), red blood cell(RBC), platelet (PLT), hemoglobin (HGB), hematocrit (HCT), mean corpuscular volume(MCV), mean corpuscular hemoglobin(MCH), mean corpuscular hemoglobin concentration (MCHC), red cell distribution width (RDW),etc according to C28-A3 and WS/T406-2012 document standards and requirements.
Results The reference intervals of blood cell parameters in Changsha area of healthy people aged 18-85 years have differences among different age groups; RBC, HGB and HCT have differences in gender, no gender differences in the rest of the parameter. HGB, HCT, MCV, MCHC, LYM, MONO, MONO%, EO, EO% are different in the Siemens ADVIA2120 and Beckman Coulter LH750, the remaining parameters have no difference between two instruments. Some parameters are different with WS/T405-2012.
Conclusions In this study, the reference intervals of 18 venous blood cell parameters among the healthy people in Changsha area have been established. It can provide a reference for both clinical and laboratory studies.

PU-139

Serotype distribution and antimicrobial resistance of invasive Streptococcus pneumoniae isolates in children prior to vaccination, in China.

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Objective The invasive *Streptococcus pneumoniae* was the most important pathogen in children worldwide especially in developing countries, which caused the invasive pneumococcal diseases (IPD) such as bacteremia, meningitis and severe pneumonia with high morbidity and mortality. The World Health Organization reported that the invasive pneumococcus killed more than a million children under the age of 5 years each year in developing countries. China was one of the five Asian countries with the highest mortality from IPD in children. The polyvalent pneumococcal conjugate vaccines (PCV)

based on serotypes formulation have been used for protecting children from IPD in developed countries since 2000. In China, PCV7 became available at the end of the year 2008 with limited uptake in several good-paying families and few children use PCV13. Serotype prevalence data are rare for invasive *Streptococcus pneumoniae* in Chinese children, and vaccine coverage of different serotypes formulation is uncertain. Few data is available concerning the antimicrobial resistance of invasive *Streptococcus pneumoniae* for the current pre-vaccination period in Chinese children. The aim of this study was to determine the serotype distribution, antimicrobial resistance and the potential coverage rates of polyvalent vaccine in invasive *S.pneumoniae* isolated from Chinese children prior to vaccination. This work could be an aid to guide appropriate antimicrobial therapies and the use of different vaccines in children, suggesting the development of a new generation of conjugate vaccines.

Methods A total of 79 non-duplicate strains of invasive *S.pneumoniae* collected from January 2009 through December 2016 were included in this study. The study population was pediatric patients with no PCV vaccination in Mainland China. *Streptococcus pneumoniae* isolates were identified with the VITEK 2 microbial analysis system. The antimicrobial susceptibility was performed using the VITEK 2 *S. pneumoniae* susceptibility card (AST-GP68), supplemented E-test for penicillin and clindamycin. The interpretation of the results complied with the accordance to the Clinical and Laboratory Standards Institute. *S. pneumoniae* ATCC 49619 was used as the control strain for the susceptibility test. Pneumococcal isolates were serotyped by multiplex PCR and capsule-Quellung reaction with a set of antisera from the Statens Serum Institute (Copenhagen, Denmark). Those determined as serotype 6A/B or as non-typeable by the multiplex PCR method were characterized by Quellung reaction.

Results Out of 79 invasive pneumococcal isolates, 72 strains (91.1%) were successfully typed with 16 serotypes by multiplex PCR and capsule-quellung reaction. Serotype 3 (26.6%), 19F (15.2%), 14 (10.1%), 23F (6.3%) were the most prevalent serotypes, followed by 6B, 6D/3 (5.1%, respectively), 19A, 6A/3 and 6C (3.8%, respectively). Another seven serotypes were detected in fewer than three strains, which included serotype 6D (2),5 (2), 19A/3 (1), 13(1), 15B/C(1), 20 (1), 34(1). The coverage rates of PCV7, PCV10, and PCV13 serotypes were 36.7%, 39.2% and 74.7%, respectively. The vaccine serotypes 19F, 14, 23F, 6B, 5, 3, 19A, and 6A were identified. Additionally, 16.5% of the non-vaccine Serotypes 6C, 6D, 13, 15B/C, 20, and 34 were observed. In northern Chinese children, serotype 19F was the most common, whereas in southern Chinese children serotype 3 was the most predominant. For 10.1% of the IPD isolates, dual-serotype was observed, and one or both serotypes (3/6D, 3/6A and 3/19A) were covered by PCV13. Serotype 3 was observed within all dual-serotype IPD isolates. Among invasive strains, penicillin resistance rates were significantly higher in meningitis isolates (93.3%) than in non-meningitis (1.6%) isolates ($P<0.05$). Which was also observed for cephalosporins such as ceftriaxone (40% vs 23.4%, respectively) or cefotaxime (46.7% vs 20.3%, respectively). The invasive S. pneumoniae isolates showed highly resistant to macrolides, clindamycin, tetracycline, and trimethoprim/sulfamethoxazole. All strains were susceptible to vancomycin, Linezolid, telithromycin, levofloxacin or moxifloxacin. The most prevalent serotype 3 presented higher resistance to β-lactams than the other serotypes ($P<0.05$).

Conclusions PCV vaccination could provide an effective way for protecting children from IPD. In 2000, PCV7 was firstly introduced to the national immunization program for childhood vaccination in the United States. In China, PCV7 was introducted in

October, 2008, substituted by PCV13 in the end of 2016. However, these vaccines are not included in the national immunization program for childhood vaccination. This study provided important data on serotype distribution and antimicrobial resistance of invasive *S. pneumoniae* in Chinese children during pre-vaccination period. Serotype 3 and 19F were the most prevalent serotypes in children. The potential coverage of PCV13 is higher than PCV7 and PCV10 because of the predominance of serotype 3. Penicillin remains highly active for IPD in children except meningitis. The high resistance rate to macrolides and clindamycin is alarming. Rational use of antimicrobial is crucial to prevent the selection of multidrug-resistant pneumococci. The data showed that PCV13 conjugate vaccine could cover up to three-quarters of the circulating IPD isolates in Chinese children. The inclusion of a PCV13 in the immunization program for childhood vaccination could be useful for reducing the burden of IPD in China.

PU-140

Galangin inhibits growth of human head and neck squamous carcinoma cells in vitro and in vivo

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Objective To investigate the effects of galangin on human head and neck squamous cell carcinoma (HNSCC)*in vitro*and *in vivo*.
Methods The cell viability of HNSCCcells treated with or without galangin was measured by the MTT assay. The clonogenic ability of HNSCC cells after galangin treatment was determined by colony formation assay. Cell cycle progression and apoptosis were assessed by flow cytometry, and the activation of related signaling pathways was examined by immunoblotting. The in vivo anti-tumor effect of galangin was examined using a xenograft mouse model. Immunohistochemistry and TUNEL staining were used to determine the expression of cyclin D1 and the presence of apoptotic cells in tumors from mice treated with or without galangin.
Results Galangin inhibited proliferation in the HNSCC cell lines WSU-HN4, WSU-HN6 and WSU-HN6 in a time- and dose-dependent manner, and significantly reduced the colony formation of HNSCC cells in vitro. Galangin induced an apparent cell cycle arrest at the G0/G1 phase, which was accompanied by reduced AKT phosphorylation and mammalian target of rapamycin (mTOR) and S6 kinase (S6K) activation. Decreased expression of cyclin D1, cyclin-dependent kinase (CDK) 4, CDK6 and phosphorylation of retinoblastoma protein (Rb) were observed in galangin-treated HNSCC cells. In addition, galangin induced apoptosis of HNSCC cells, down-regulating anti-apoptotic protein Bcl-2 and Bcl-xL while up-regulating pro-apoptotic protein Bax and cleaved-caspase3. Immunohistochemical analysis further showed a dose dependent reduction in cyclin D1-positive cancer cells and an increase in TUNEL-positive cancer cells in galangin-administrated mouse tumor sections.
Conclusions Our data demonstrate for the first time that galangin has a novel pharmacological function of anti-HNSCC. Galangin effectively inhibited cell proliferation, induced cell cycle arrest and apoptosis of HNSCC cells. Treatment with

galangin resulted in suppression of HNSCC growth in vivo. It is expected that galangin may serve as a new anti-tumor herbal medicine in HNSCC treatment.

PU-141

The regulation of lnc NOS2P3-miR-939-5p axis in the regulation of chronic heart failure and its early diagnostic value

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Objective To investigate the long non-coding RNA lnc-NOS2P3-miR-939-5p axis regulated inflammation induced apoptosis of HUVEC and H9C2 cells according to the targets iNOS and TNFα by influencing the synthesis of NO. Which was the critical pathogenesis of chronic heart failure(CHF).

Methods The effects of miR-939-5p on apoptosis and cardiac function of myocardium and endothelial cells were detected by in vitro and in vivo. cDNA microarray and software to screen the target gene and verify it. Intracellular detection of lncRNA-NOS2P3 sequence-specific regulation of miR-939-5p expression; confirmed the influnce of NOS2P3 on myocardial and endothelial cell apoptosis and the target genes; The expression of miR-939-5p was validated and evaluated as the clinical value of early warning markers of CHF.

Results MiR-939-5p could inhibit the apoptosis of cytokines IL-1β and IFNγ in human vascular endothelial cells (HUVEC). INOS was predicted to be the target gene of miR-939-5p by cDNA microarray and western blot detection of iNOS expression can be regulated by miR-939-5p. LncRNA chip and predictive software (DIANA-LNCBASE) showed that lncRNA NOS2P3 might act as a ceRNA to regulate the expression of miR-939-5p. Quantitative analysis of serum miR-939-5p expression in CHF patients by q-PCR showed that the expression of miR-939-5p was significantly up-regulated in different NYHA grades, and the level of I-II was significantly higher than that of patients with grade III-IV.

Conclusions Our results suggest that lncRNA NOS2P3 can mediate NO synthesis by miR-939-5p to regulate the synthesis of NO and regulate the apoptosis of myocardial and endothelial cells, and then regulate chronic heart failure, which may be used as lncRNA-miRNA network in early warning of CHF.

PU-142

Retrospective analysis of clinical and laboratory characteristics of 34 Brucella patients

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Objective To analyze 34 cases of brucellosis from January 2015 to December 2017 in the First Affiliated Hospital of Nanjing Medical University. Clinical infection and laboratory detection characteristics of these patients were discussed.
Methods The clinical manifestations of 34 cases of brucellosis were analyzed retrospectively. The imaging data of B-ultrasonography, laboratory test indexes and positive alarm time of blood culture were collected. Epidemiological data such as sex, age, occupation, living area, location and distribution of lesions were collected.
Results 18 of the 34 patients with a clear history of contact were associated with sheep contact; The main clinical manifestations were fever (100.0%), joint pain (38.2%), hyperhidrosis (32.4%), hepatosplenomegaly (29.4%), lymphadenopathy (14.7%) and fatigue (11.8%); 12 cases (35.3%) had abnormal leukocytes, 25 cases (73.5%) had abnormal liver function, 24 cases (70.6%) had elevated erythrocyte sedimentation rate, 30 cases (88.25%) had elevated CRP, 30 cases (88.2%) had elevated PCT ; The positive alarm time of blood culture was 101.5 hours (quartile time was 98h-109h), and the positive alarm time of bone marrow culture was 85.5 hours (quartile time was 74.5 hours), which is shorter than that of blood positive alarm ($P<0.05$).
Conclusions For suspected cases of *Brucella* infection, clinicians and microbiologists should pay attention to the patient's epidemic contact history, strengthen communication, combine the patient's clinical manifestations, imaging examination, the patient's laboratory test indicators and blood culture positive alarm time, make early diagnosis and prompt treatment.

PU-143

Analysis of drug resistance of Acinetobacter baumannii to commonly used clinical antibiotics in a hospital from 2013 to 2018

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Objective To understand the trend of drug resistance of *Acinetobacter baumannii* isolated in our hospital from 2013 to 2018.
Methods 2808 *Acinetobacter baumannii* strains isolated from clinic were tested by disk diffusion method or automated instrument method according to the unified scheme. The drug sensitivity results were interpreted according to CLSI 2013-2107 standard. Data were analyzed by WHONET 5.6 software.

Results From 2013, the resistance rates of *Acinetobacter baumannii* to Cephalosporins, Quinolones and Aminoglycosides were over 60%, while the resistance rates to Cefoperazone-sulbactam and Minocycline were 26.6% and 22.7%, respectively. However, with the increase of years, the drug resistance rate of most drugs has reached more than 80%.

Conclusions The resistance rate of *Acinetobacter baumannii* to Carbapenems is obviously increasing, the resistance rate to Cefoperazone-sulbactam and Minocycline is also increasing year by year, the ratio of multi-drug-resistant bacteria and extensively drug-resistant bacteria is also significantly increasing, the situation of drug resistance is severe, and the rational use of antibiotics is urgent.

PU-144

Disseminated Talaromyces marneffei and Mycobacterium abscessus in a 16-year-old Chinese teenage without HIV infection

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Objective *Talaromyces (Penicillium) marneffei* and is an important pathogenic thermally dimorphic fungus causing systemic mycosis in Southeast Asia especially in HIV-infected individuals. However, there are increasing numbers of reports on T. marneffei infections in the immunocompromised adults and children. *Mycobacterium abscessus* is ubiquitous in the environment, found in water and soil. The incidence of *Mycobacterium abscessus* infections appears to be increasing in most areas of the world especially in those people treated with surgery. In this case, we report on disseminated *Talaromyces (Penicillium) marneffei* and *Mycobacterium abscessus* infection in a 16-year-old Chinese teenage, human immunodeficiency virus noninfected, with CD4(+) T-cell reduction.

Methods The 16-year-old Chinese teenage, from Guangxi Zhuang Autonomous Region, southern of China, with no prior history of immunosuppression was suffering from recurrent fever for 5 years, with multiple abscesses and bilateral lymphadenopathy for more than 3 years. The patient was initially diagnosed as “hematopoietic system disease, connective tissue diseases, polyarthritis, infectious osteomyelitis” at a local hospital based on the histopathology finding of bone marrow and abscess biopsy, which showed chronic suppurative inflammation with inflammatory granulation tissue hyperplasia. On admission, the patient's vital signs were evaluated and laboratory inspection were performed.

Results The patient's vital signs were within normal ranges. However, the infectious markers including white blood cells, C-reactive protein, Procalcitonin, ESR and Fungal D-glucan were increased obviously. A third-generation human immunodeficiency virus (HIV) antibody assay was nonreactive. Computer tomography of the bones revealed 1. Left scapula, left rib, bilateral humeral head, left humerus, 12th thoracic vertebrae, multiple joints of the extremities, upper middle humerus, lower left tibia, right foot tibia Shadow, considered multiple bone invasion of Penicillium marneffei, in which the 12th thoracic vertebrae showed obvious compression fractures; 2. Cardiac enlargement,

pericardial effusion; bilateral lymph nodes in the axillary fossa, partially enlarged. The biopsied skin tissue culture revealed fungal organism growth consistent with *Talaromyces* (*Penicillium*) *marneffei and Mycobacterium abscessus*.

Conclusions The patient was successfully treated with antimicrobial therapy. we highlight that it is important for clinicians to recognize difficult rare pathogens infection in individuals with no prior history of immunosuppression.

PU-145

Down-regulation of ZIP2 and ZIP8 expression in peripheral blood mononuclear cells from hepatitis B patients and hepatitis C patients

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Objective ZIP2 and ZIP8 belong to the ZIP family of metal-ion transporters. It can transport zinc. ZIP8 is closely related with inflammation and immunity. ZIP8 caused T cells to exhibit enhanced activation. Our lab found that ZIP2 was over-expressed in leukocytes of asthmatic infants and pulmonary tuberculosis patients with lower serum zinc level. The persistence of virus that resulted from the low antiviral immune response had been thought to contribute to the pathogenesis of Hepatitis B virus (HBV)-induced diseases. So we wondered whether ZIP2 and ZIP8 were changed in the patients with chronic hepatitis B patients (CHB) and chronic hepatitis C patients (CHC).

Methods We examined the mRNA and protein expression levels of ZIP2 and ZIP8 zinc transporters in peripheral blood mononuclear cells (PBMCs) from patients with CHB (n=40), CHC (n=23) and healthy controls (n=39). The diagnosis of these CHB and CHC patients were made according to the riteria established in the National Viral Hepatitis Conference of China.PBMCs was isolated by density gradient centrifugation.The total RNA of PBMCs was extracted by Trizol total RNA purified kit from the leukocytes. The cDNA was synthesized from 2 ug of total RNA using the RevertAidTM First Strand cDNA Synthesis Kit , following the manufacturer's introduction.Both ZIP2 and ZIP8 mRNA levels as well as protein expression levels were evaluated by quantitative real-time PCR and Western blot analysis. and HBV-DNA copy numbers and HCV-RNA copy numbers were evaluated by quantitative real-time PCR.

Results Both ZIP2 and ZIP8 mRNA levels as well as protein expression levels were significantly decreased in CHB and CHC patients compared with healthy controls. We analyzed the correlation between ZIP2 level and HBV DNA copies/ml, between ZIP2 level and HCV RNA copies/ml, between ZIP8 level and HBV DNA copies/ml, between ZIP8 and level and HCV RNA copies/ml, the results showed that there were no correlations with them. On the one hand, It may be that the cases samples which we collected were not big enough, so we can not directly say that there were no correlation with them in the ZIP2 or ZIP8 expression levels and the pathology grade of CHB and CHC. This result may also need to increase the sample size in order to prove once again. On the other hand,

decreased levels of ZIP2 and ZIP8 expression might be related to virus infection but has nothing to do with the HBV DNA copies and HCV RNA copies.
Conclusions The results indicated that decreased expression of ZIP2 and ZIP8 genes are closely associated with immunity of CHB and CHC patients and suggest a role for ZIP2 and ZIP8 genes in the initial control infection and mediate the resistance and immunity of CHB and CHC patients through the promotion and maintenance immune response of adaptive T cell.

PU-146

Distribution and drug resistance of Enterobacteriaceae in 2016

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Objective To evaluate the clinical distribution and drug resistance of *Enterobacteriaceae* in our hospital; and to explore the application value of modified carbapenem inactivation method with different incubation time in the detection of carbapenemase-producing *Enterobacteriaceae* and analyze the clinical feasibility of the "0.5+9h incubation mode".
Methods A total of 1179 strains of *Enterobacteriaceae* were recruited as the study objects, then the strains were identified by using VITEK-2 compact automatic microorganism analyzer, the drug susceptibility testing was performed ,the data were analyzed with the use of WHONET 5.6 software ,and the carbapenemase was detected by modified carbapenem inactivation method with different incubation time.
Results Escherichia coli and Klebsiella pneumoniae were the main pathogenic bacteria among the Enterobacteriaceae in our hospital in 2016, and according for 55% and 32%, respectively. The highest detection rate of Enterobacteriaceae was ICU , according for 19% , followed by nephrology department , according for 16%. The drug resistance rates of Escherichia coli isolated from ICU to imipenem and meropenem were 17.6%、16.4%, respectively. Klebsiella pneumoniae isolated from ICU has a high resistance rate to common antibiotics, and the resistance rate to imipenem and meropenem were 58.8%, 56.8%, respectively. The drug resistance rate of Escherichia coli isolated from nephrology department to imipenem and meropenem were all 0% , and the Klebsiella pneumoniae has the lowest resistance rate to meropenem was 5.0%. Totally 152 cases of carbapenem-resistant Enterobacteriaceae were isolated in our hospital in 2016, and the majority of CRE was Klebsiella pneumoniae, according for 84%. There is no difference between the results of the modified carbapenem inactivation method with "0.5+9h incubation mode " and traditional incubation time detecting the CRE .The modified carbapenem inactivation method with "0.5+9h incubation mode" can also detect KPC and NDM carbapenemase effectively.
Conclusions The detection rates of different species *Enterobacteriaceae* were vary in different departments and the drug resistance were diverse. It is necessary for the hospital to comprehensively analyze the antimicrobial treatment and use antibiotics reasonably. The modified carbapenem inactivation method with "0.5+9h incubation mode" can be detected within 1 working day for carbapenemase, as a primary report

of nosocomial infection monitoring, and improve the hospital infection control efficiency.

PU-147

Analysis and detection of drug resistance of non-fermenting bacteria during 2011-2016

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clinical laboratory

Objective To investigate the distribution and drug resistance of non-fermenting bacteria in the various departments of the hospital, and to evaluate the method for detection of the carbapenemase by the non-fermenting strains , so as to provide scientific basis and methods for the control of nosocomial infection.

Methods The results of non-fermenting bacteria were analysed by using WHONET 5.6 software in order to know the composition,distribution,drug resistance rate ,during 2011-2016.Then the Carbapenem Inactivation Method(CIM),Carba NP test(CNP),rapid Carba NP Test(RCNP) were performed for the resisitant strains to carbapenem in non-fermenting bacteria to detect whether they were carbapennemase producers.

Results A total of 4526 strains of non-fermenting bacteria were isolated, among which Pseudomonas aeruginosa ,Acinetobacter baumannii respectively accounted for 48%(2194/4526), 44%(1989/4526);Distribution of non-fermenting bacteria in the ICU was the highest, followed by thoracic surgery, respectively 36%(1617/4526), 16%(688/4526); Pseudomonas aeruginosa and Acinetobacter baumannii of ICU to imipenem, meropenem resistance rate of >50%, In thoracic surgery,Pseudomonas aeruginosa and Acinetobacter baumannii resistance rates are lower than that of ICU; Pseudomonas aeruginosa to the carbapenems resistance rate was gradually decreased, while the Acinetobacter baumannii was not significant change,during 2011-2016. The sensitivity and specificity of CIM、CNP、RCNP were high, and the consistency of that was good.

Conclusions The main strains of non- fermenting bacteria in the hospital are Pseudomonas aeruginosa and Acinetobacter baumannii , and that resistances are serious. Screening of carbapenem resistant strains by RCNP can improve the monitoring efficiency and control the spread of resistance genes.

PU-148

The clinical value of rapid Carba NP Test for detection of Carbapenemase producers

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Objective To explore the practicability and evaluate the clinical value of the rapid Carba NP Test for detection of carbapennemase producers in Gram-negative bacteria.
Methods A total of 264 strains of Gram-negative rods were detected by Rapid Carba NP(RCNP) Test and compared with Modified Hodge test(MHT) ,Carbapenem Inactivation Method(CIM) and Carba NP test(CNP).
Results The sensitivity and specificity of the Modified Hodge test was 85.4% (123/144) ,87.5% (105/120) and the value of Kappa was 0.726;the sensitivity and specificity of the Carbapenem Inactivation Method was 96.5% (139/144) ,97.5% (117/120) and the value of Kappa was 0.939 ;the sensitivity and specificity of the Carba NP was 93.8% (135/144) ,97.55% (117/120) and the value of Kappa was 0.909; the sensitivity and specificity of the Rapid Carba NP test was 90.3% (130/144) ,99.2% (119/120) and the value of Kappa was 0.886.
Conclusions The rapid Carba NP test is more faster and cheaper than the Carba NP test ,by using rub instead of incubation. It can detect the carbapenemaese producers within 15min and may may contribute to improve nosocomial infection control.

PU-149

Evaluation of different discs in carbapenem inactivation method

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Objective To evaluate the effects of carbapenem inactivation method in detecting carbapenemase- producing strains, and to explore the value of imipenem, meropenem and ertapenem discs using in carbapenem inactivation method.
Methods s A total of 264 strains isolated from clinical were screened by three methods including modified Hodge test, Carba NP test and carbapenem inactivation method, the sensitivity and specificity were compared; imipenem, meropenem and ertapenem discs were used in carbapenem inactivation method, and the differences in between were analyzed.
Results The sensitivity, specificity and Kappa value of modified Hodge test were 75.00% (108/144) , 85.00% (102/120) and 0.593; Carba NP test 91.67% (132/144) ,97.50% (117/120) and 0.886; carbapenem inactivation method 94.44% (136/144) , 97.50% (117/120) and 0.916. The positive rates of three methods and PCR were compared separately using McNemar c^2 test, the c^2 values were 92.06,204.72 and 218.29,separately.The P value of carbapenem inactivation method was 0.227,greater than

0.05, showing no difference between carbapenem inactivation method and PCR. The areas under the ROC curve for imipenem, meropenem and ertapenem discs were 0.927(95%CI:0.890-0.964), 0.948(95%CI:0.915-0.980), 0.948(95%CI:0.915-0.980).
Conclusions Compared with modified Hodge test and Carba NP test, carbapenem inactivation method has high sensitivity, specificity and strong consistency detecting carbapenemase-producing strains. The use of meropenem or ertapenem in carbapenem inactivation method brings a high accuracy, while may cause false positive results, imipenem should be avoided in this method.

PU-150

Study on the correlation between PDW, PLT and TCM syndromes of iron deficiency anemia

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Objective The purpose of this paper is to detect patients with iron-deficiency anemia with peripheral blood RDW(red blood cell volume distribution width)、PLT (platelet count), analysis of its relationship with iron deficiency anemia treatment based on syndrome differentiation of traditional Chinese medicine.
Methods The principle of randomization was used to screen 50 cases of iron-deficiency anemia, the spleen and stomach weak type 25 cases, 25 cases of liver and kidney Yin deficiency type. Thirty healthy patients were selected as normal control group. Using The XE - 2100 automatic blood cell analyzer to detect peripheral blood RDW、PLT.
Results iron deficiency anemia syndrome type belongs to the spleen and stomach weak crowd peripheral blood results respectively : RDW 、 PLT (21.25±3.50) 、 (279.32±142.03)×10^9/L; the liver and kidney Yin deficiency type of peripheral blood results respectively: RDW、PLT: (19.04±3.82),(170.72±107.57)×10^9/L.normal control group peripheral blood results respectively : RDW 、 PLT : (13.16±0.54) 、 (200.17±52.90)×10^9/L; The differences in peripheral blood RDW were statistically significant(P ＜ 0.05). PLT results the difference between the two types is statistically significant(P＜0.05).
Conclusions There is a correlation between RDW, PLT and iron deficiency anemia syndrome type belong the spleen and stomach weak type and liver and kidney Yin deficiency type.

PU-151

Xi 'an 168 preschoolers lymphocyte subsets for the establishment of the reference range

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Objective Establish preschoolers lymphocyte subsets reference range.
Methods Collected 168 preschool children (2.2 -6.5) venous blood specimens, with four-color flow cytometry to detect $CD3^+$,$CD3^+CD4^+$,$CD3^+CD8^+$, $CD3^-CD19^+$, $CD3^-CD16^+CD56^+$lymphocyte count absolutely, percentage and $CD4^+$/ $CD8^+$ratio.
Results $CD3^+$,$CD3^+CD4^+$,$CD3^+CD8^+$, $CD3^-CD19^+$, $CD3^-CD16^+CD56^+$ lymphocyte count absolutely, percentage are respectively (62.02-72.32) %, (2051-3783) cells/uL; (32.07-42.80) %, (1076-2190) cells/uL (17.24-26.74) %, (609-1297) cells/uL; (15.12-24.12) %, (646-1366) cells/uL; (6.56-15.10) %, (276-842) cells/uL ; And $CD4^+$/ $CD8^+$ ratio (1.25-2.34); Lymphocyte subsets between different gender differences in relative count and absolute count, according to the results of $CD3^+CD4^+$helper T cells, $CD3^-CD16^+CD56^+$NK cells and $CD4^+$/ $CD8^+$ratio between different genders of preschool children was statistically difference ($P < 0.05$);
$CD3^+$,$CD3^+CD8^+$, $CD3^-CD19^+$, between different genders of preschool children with no statistical difference ($P > 0.05$). Preschool children compared with adult lymphocyte subsets reference, adult lymph subgroup reference range has the remarkable difference compared with the preschool children.
Different in preschool-age children lymphocyte subsets reference range compared with the results, B ($CD3^-CD19^+$) and NK cells ($CD3^-CD16^+CD56^+$) cells result is low, difference is bigger, the result was statistically significant, there was no statistically significant difference other project results.
Conclusions In this study successfully established the preschoolers (2.2-6.5) lymphocyte subgroup normal reference range, for the region's pediatrician provides valuable scientific basis.

PU-152

The risk factors analysis of bacterial encephalitis in infants with severe hand-foot-mouth disease The risk factors analysis of bacterial encephalitis in infants with severe hand-foot-mouth disease based on Logistic-regression

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Objective Objective To investigate the risk factors of bacterial encephalitis in children with severe hand-foot-mouth disease, and to provide basis for the prevention of hand-foot-mouth disease complicated with bacterial encephalitis.

Methods s Retrospective analysis was performed to select the children diagnosed with severe hand-foot-mouth disease between February 2010 and January 2018. Among them, 56 cases were diagnosed as bacterial encephalitis by routine examination and culture of cerebrospinal fluid as a research group. 114 children with severe hand-foot-mouth who had no bacterial encephalitis at the same time 、matched for age and sex were selected as controls. The Logistic regression methods was used to analyze the differences between the two groups.

Results Based on the analysis,the rate of severe HFMD combined bacterial encephalitis in children was 12%. The gender, age, WBC count, fever, blood glucose levels, creatine kinase isoenzyme CK-MB levels , long time to onset were not insignificance between those groups(P>0.05). mental disparity, vomit,high PCT levels, positive bacterial cultures in the respiratory system, enterovirus EV71 ratio and abnormal nerve reflex were significant difference between groups by single factor analysis(P<0.05). After the analyzed by the conditional Logisitic analysis.which was fitting by the Logistic multivariate model. the independent risk factors for severe HFMD with bacterial encephalitis were increased PCT levels (OR=4.265, 95% CI 1.514-7.362), positive respiratory bacterial culture (OR=2.535, 95% CI 1.029-4.568), and abnormal nerve reflex (OR=2.592, 95% CI 1.358-6.453).

Conclusions This study indicated that high PCT levels, positive bacterial cultures in the respiratory system and abnormal nerve reflex were independent risk factors of Severe HFMD combined with bacterial encephalitis. When these risk factors appear, it is necessary to prevent the occurrence of bacterial encephalitis.