Abstract IDDF2019-ABS-0069 Figure 1

especially cancers. However, little is known about their expression and function in gastric cancer (GC).

Methods The hsa_circ_001888 levels in 114 paired GC tissues and adjacent non-tumor tissues, 48 plasma samples from patients with GC and 48 plasma samples from health controls were detected by quantitative reverse transcription-polymerase chain reaction (qRT-PCR). Then, the relationships between hsa_circ_001888 expression and the clinicopathological features of patients with GC were further analyzed. Finally, a receiver operating characteristic (ROC) curve was generated to evaluate the diagnostic value of hsa_circ_001888.

Results Hsa_circ_001888 was first found to be significantly down-regulated in GC tissues ($p < 0.001$, (figure 1A, B)) and plasma samples from patients with GC ($p < 0.001$, (figure 1C)). The higher ΔCt value indicates lower expression. Moreover, we analyzed their association with clinicopathological features of patients with GC. Clinicopathological features showed that hsa_circ_001888 level in GC tissues was correlated with differentiation and in GC plasma linked with CEA and CA199 expression. We did not further find any association between its levels with other clinicopathological features such as age, gender, invasion, lymphatic metastasis. To evaluate the potential diagnostic value, the ROC curve was used. The area under the ROC curve of hsa_circ_001888 in tissues and plasma were up to 0.654 and 0.662, respectively (figure 1D), suggesting good diagnostic value.

Conclusions These results indicated that hsa_circ_001888 was significantly down-regulated in GC and may serve as a novel potential biomarker in the diagnosis of GC.

IDDF2019-ABS-0080

ROSIGLITAZONE ALLEVIATES LPS-INDUCED INFLAMMATION IN RAW264.7 CELLS VIA THE INHIBITION OF NF- κ B IN A PPAR γ -DEPENDENT MANNER

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Background Rosiglitazone is a synthetic peroxisome proliferator-activated receptor γ (PPAR γ) agonist that is widely used to treat type 2 diabetes, recent research has highlighted its anti-inflammatory activity. The aim of this study was to investigate whether rosiglitazone can alleviate the decline in RAW264.7-cells viability due to lipopolysaccharide(LPS) induced inflammation and the underlying mechanism.

Methods RAW264.7 macrophages were stimulated with 100 ng/ml LPS to establish an inflammatory injury model. Cells were treated with LPS and various concentrations of rosiglitazone. Cell viability was assessed by MTT assays. Inflammatory cytokines were detected by ELISA and qRT-PCR. Nitric Oxide (NO) production was accessed using the Griess reagent system. The expression levels of key proteins in the NF- κ B pathway were detected by western blotting.

Results Rosiglitazone alleviated the decline in RAW264.7 cells viability induced by LPS and inhibited inflammatory cytokine expression in a concentration-dependent manner. Rosiglitazone significantly inhibited the upregulation of p65 phosphorylation and the downregulation of I κ B α induced by LPS. The inhibitory effects could be blocked by PPAR γ knockdown.

Conclusions Our findings extend the application of rosiglitazone by demonstrating that it significantly inhibits the LPS induced inflammatory response in RAW264.7 macrophages via PPAR γ activation and NF- κ B suppression.

IDDF2019-ABS-0089 HSA_CIRC_0053063 ACTS AS A SPONGE OF MIR-361-3P IN COLON EPITHELIAL CELLS

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Background The dynamic changes of serum circRNAs, which act as a sponge of microRNA, has a great potential in predicting colonic disease, especially in malignant diseases. However, whether the mechanism of circRNA in regulating colonic epithelial mucosa is still unknown. Here, we explore the sponging effects of hsa_circ_0053063 targeting miR-361-3p in colon epithelial cells.

Methods According to the *ceRNA* analysis, the potential target miRNAs of hsa_circ_0053063 were collected. Dual-luciferase reporter gene assays were performed to confirm the circRNA sponge of miRNAs. Then the potential target gene of miR-361-3p was predicted. Dual-luciferase reporter gene assays and real-time PCR were performed to detect the regulation between ncRNAs and target gene in colon epithelial cells HCoEpiC and NCM460.

Results According to the *ceRNA* analysis, we found that miR-361-3p might be a target of hsa_circ_0053063 (figure 1a). Dual-luciferase reporter gene assays demonstrated that hsa_circ_0053063 bound miR-361-3p directly (figure 1b). Then we predicted that ATG13 was a target gene of miR-361-3p. Dual-luciferase reporter gene assays demonstrated that miR-361-3p bound ATG13 directly. Real-time PCR revealed that miR-361-3p decreased expression of ATG13, however, hsa_circ_0053063 reversed the inhibition of expression of ATG13 by miR-361-3p.

Conclusions Hsa_circ_0053063 released the inhibition of expression of ATG13 by miR-361-3p. hsa_circ_0053063 may

act as a sponge of miR-361-3p targeting ATG13 in colon epithelial cell.

IDDF2019-ABS-0090 CARBOXYLOMICS PROFILES DELINEATE SHORT-CHAIN FATTY ACIDS IN COLORECTAL CANCER DIAGNOSIS AND PROGNOSIS

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Background Colorectal cancer (CRC) is the third most common type of cancer in the world and is a major cause of worldwide cancer morbidity and mortality. Carboxylic acids widely exist in living systems and are the essential components for life, which mainly contain amino acids, TCA cycle intermediates, short-chain fatty acids, long chain fatty acids, bile acids, acylcarnitine, and so on. Carboxylomics study in biological samples is critical for the understanding of physiological processes and the discovery for the onset of relevant diseases.

Methods In the present study, DIAAA derivatization-UHPLC-Q-TOF/MS approach and *carboxylomics* study were employed to discover potential novel biomarkers for carboxylic acids in 58 human CRC and 46 healthy samples.

Results 269 carboxylic acids were determined and confirmed their structures. Among of them, 118 carboxylic acids were first reported in CRC serum. Metabolic pathways were constructed by heat maps, Interactive Pathways Explorer, pathway impact and Volcano plot, etc. (IDDF2019-ABS-0090 Figure 1. Heatmap of 134 carboxylic acids which have difference between healthy and CRC patients in training set (A); Interactive Pathways Explorer analysis (B); Metabolomic pathway of CRC samples in training set (C); Volcano plot of the 269 carboxylic acids profiled (D). Mann-Whitney U tests were used to calculate statistical significance, and p values were corrected using Graphpad prism 5.0. Differentially abundant metabolites of different categories were individually color coded.) Short-chain fatty acids were found to be novel diagnostic and prognostic biomarkers for CRC (IDDF2019-ABS-0090 Figure 2. Relative abundance (A) and ROC curves (B) of representative

Abstract IDDF2019-ABS-0089 Figure 1