intuitive and interpretable signature, the trend test would disclose the continuous change during the dynamical process. Thus, the linear trend of protein expression during disease development and progression (e.g., across consecutive disease stages) would indicate the important behavior of disease-relevant proteins corresponding to worsening diseases, particularly in the pan-cancer context.

Results

We re-analyzed the TCGA pan-cancer proteomics data on multiple digestive cancer sites, i.e., COAD, COADREAD, LIHC, READ, STAD and STES. The proteins with significant expression trend along cancer stages can be obtained as (figure 1A.) shown. The COAD, COADREAD tend to be similar on protein signatures, and READ, STAD and STES would be grouped together, and LIHC is an outlier due to its more observed progressive protein signatures. Then, by statistics of observation frequency of protein signatures in each cancer (figure 1B), and those of cancer sites for each protein (figure 1C), we found: (i) LIHC indeed have many protein signatures than others; (ii) some protein signatures of LIHC are same in COAD, COADREAD, meanwhile many protein signatures are exclusive for LIHC, i.e., specific protein signatures for liver cancer; (iii) protein signatures would have great differences in their expression trends in different digestive cancer sites, e.g., 4E-BP1 seems to be suppressor-protein except in LIHC (figure 1D), while YB-1 tends to be onco-protein.

Conclusions

Totally, this work revisited the progressive markers of digestive cancers on the proteome and pan-cancer manner, and revealed new insights on understanding dynamic heterogeneity of digestive disease progression by digestive disease signatures.

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UPREGULATION OF THE LONG NON-CODING RNA LINC00460 PROMOTES GASTRIC CANCER PROGRESSION BY EPIGENETICALLY SILENCING P21 VIA EZH2 AND INDICATES POOR OUTCOME

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Background

Multiple studies have revealed that long non-coding RNAs (lncRNAs) extensively participate in human cancer progression. Recently, we found that LINC00460 was an oncogene in promoting colorectal cancer cell proliferation. However, its role in gastric cancer (GC) remains unclear.

Methods

LINC00460 expression was detected in 80 GC and matched non-cancerous tissues by quantitative reverse
transcription PCR. Gain-and loss-of-function experiments were conducted to investigate the biological functions of LINC00460 both in vitro and in vivo. The mechanism of LINC00460 action was explored through bioinformatics, RNA fluorescence in situ hybridization, chromatin immunoprecipitation assay and RNA immunoprecipitation assay.

**Results** LINC00460 was excessively expressed in GC tissues and correlated with advanced stage, larger tumor size and poorer prognosis in GC patients. Forced LINC00460 expression promotes proliferation, whereas loss of LINC00460 function decreased cell proliferation by blocking of cell cycle in GC cells. Mechanistically, LINC00460 could simultaneously interact with EZH2, a core component of polycomb repressive complex 2, and mediates the trimethylation of H3K27 at the promoter region of p21. In addition, rescue experiments determined that LINC00460 oncogenic function is partly dependent on repressing p21.

**Conclusions** Together, our results suggest that LINC00460, as a regulator of proliferation, may serve as a candidate prognostic biomarker and target for the management of GC.

**IDDF2019-ABS-0137** IS MICROSCOPIC COLITIS(MC) RESTRICTED TO COLON? STUDY OF ILEAL CHANGES IN PATIENTS OF MC

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**Background** Chronic diarrhea due to Microscopic colitis (MC) is often overlooked. Restriction of disease to the colon is still unclear, and on drawing analogies from Idiopathic Ulcerative Colitis any proximal disease extension may have bearing on treatment regimes. We evaluated terminal ileum using narrow band imaging (NBI), high definition white light endoscopy (HDWLE) and histopathological findings on biopsy

**Methods** 53 adults with suspected MC were enrolled. All underwent colonoscopy with ileal intubation. Segmental colonic and terminal ileum biopsies were obtained using HDWLE and NBI. Same were analysed by expert gastrointestinal histopathologist

**Results** In 43 patients of confirmed MC, HDWLE of ileum was normal. On NBI, intravillous capillary network was regular and unbranched with semi-circular pattern in 41 (95.4%) of patients of MC and in all controls. It was sparse and irregular in 2 (4.7%) cases. Peyer’s patch vessels were distinct in 5 (9.4%), normal in 38 (88.4%) cases and normal in all controls (p = 0.570). On HDWLE and NBI. Same were observed in 10 (23.2%), 2 (4.6%) and 1 (2.3%) patient respectively

**Conclusions** Ileal NBI findings in MC are hitherto unreported, with up to 12% showing abnormalities. Histologically up to 23% showed abnormalities in ileal biopsies. Ileal pathology may contribute to certain symptoms in MC.

**IDDF2019-ABS-0153** CLINICAL SIGNIFICANCE OF SEPRASE AND CONNEXIN-43 EXPRESSION IN GASTRIC CARCINOMA

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**Background** To investigate the expression of connexin43(Cx43) and Seprase protein in gastric carcinoma and their clinical significance.

**Methods** Immunohistochemical method was used to detect the expression of Seprase and connexin 43 proteins in 45 specimens of gastric carcinoma and 15 specimens of paired adjacent normal gastric tissue. The relationship between their expression and the clinicopathologic characteristics were statistically analyzed.

**Results** 1: The positive rate of Seprase protein in gastric carcinoma was 71.11%(32/45) higher than that in normal tissue 20.00%(5/25) and with statistical significance (χ²=6.67, p=0.01). The positive rate of connexin 43 protein in gastric carcinoma was 68.89%(30/45) lower than that in normal tissue 100%(15/15) and with statistical significance(χ²=12.09, p=0.001). 2: Connexin 43 protein was related to the age and the degree of tissue differentiation of gastric carcinoma (P<0.05), Seprase protein was related to the age and the subtype of gastric carcinoma patients (P<0.05). 3: Overall survival rates of patients with seprase and Connexin 43 expression were detected, Connexin 43 expression was an independent prognosis factor; meanwhile, seprase was correlated with the survival of the patients with gastric carcinoma in our study.

**Conclusions** In gastric carcinoma, Connexin 43 appeared down-expression and seprase appeared up-regulation, That may play important roles in the invasion and metastasis of gastric carcinoma, then provide a new direction for target therapy.

**IDDF2019-ABS-0179** THE ASSOCIATION BETWEEN COMPONENTS OF METABOLIC SYNDROME AND COLORECTAL CANCER RISK IN CHINESE MALES

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**Background** Several researches have reported the metabolic syndrome (MetS) was related to a higher risk of colorectal cancer (CRC). However, it remains unclear to what extent the MetS components individually account for the association between MetS and CRC. To investigate the association of MetS components with the risk of CRC in Chinese males, the study was performed in the Kailuan male cohort, a large prospective cohort study.