

Supplemental information

Proteogenomic landscape of gastric adenocarcinoma peritoneal metastases

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Proteogenomic Landscape of Gastric Adenocarcinoma Peritoneal Metastases

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Supplementary Figures

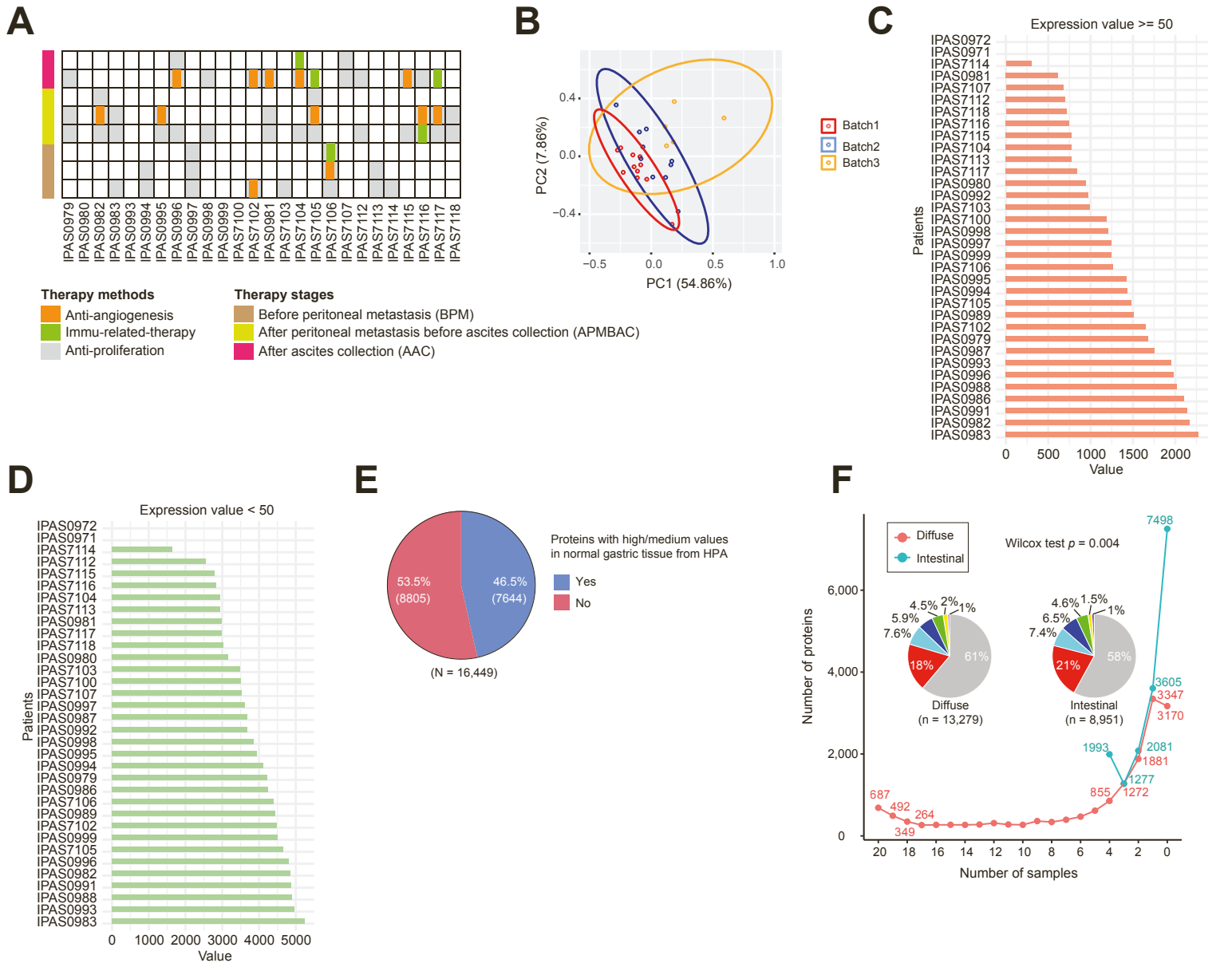


Figure S1. The general features of all proteins from all samples based on the abundance parameter in TCE. A) Heatmap summarizes the treatment information of all samples included in this study. B) PCA (Principal components analysis) plot shows three clusters from all proteins' expression across 26 samples. C) The bar plot shows the distribution of protein abundance across patient for highly expressed proteins. D) The bar plot shows the distribution of protein abundance across patient for lowly expressed proteins. E) Pie plot shows 7,644 of 16,449 TCE proteins with high/medium values in normal gastric tissues from HPA data set. F) Cumulative number of proteins identified as a function of the patient numbers. Proteins family was shown with pipe plots between diffuse and intestinal subtypes. Statistical method: Wilcox test.

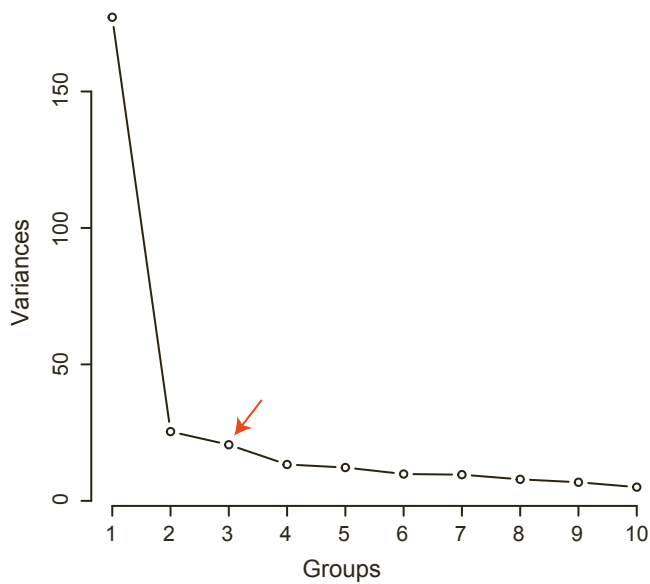
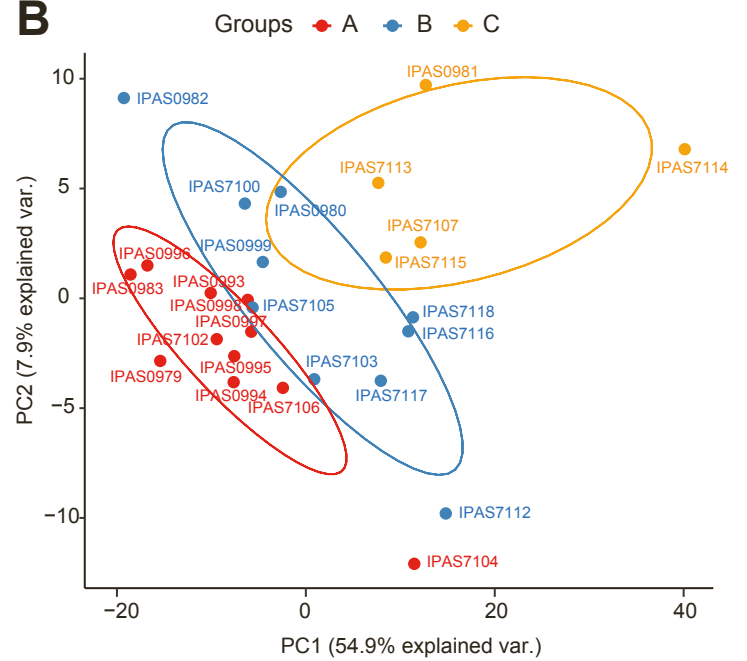
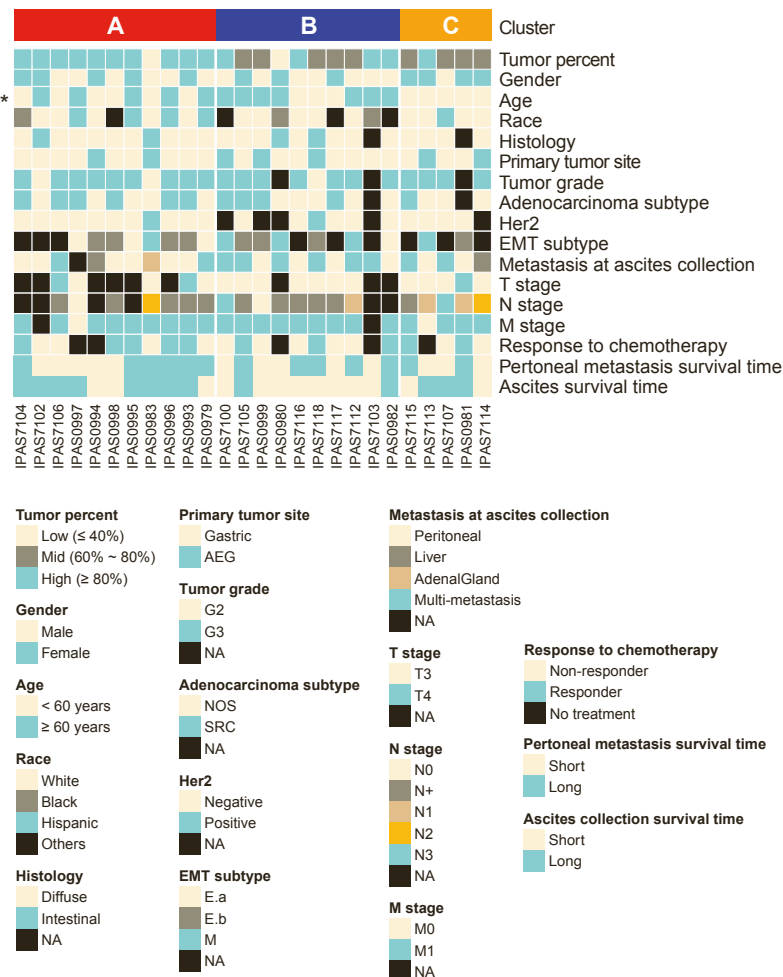
A**B****C**

Figure S2. Molecular subtyping of GACs based on the altered proteomics and their correlations with clinical factors. A) The scree plot is to identify the final clusters with 323 genes from TCE data. B) Three clusters were defined with PCA analysis of 323 genes in TCE platform. C) Clinical factors are shown in the heatmap for samples in three clusters. Fisher exact test, * $p < 0.05$.

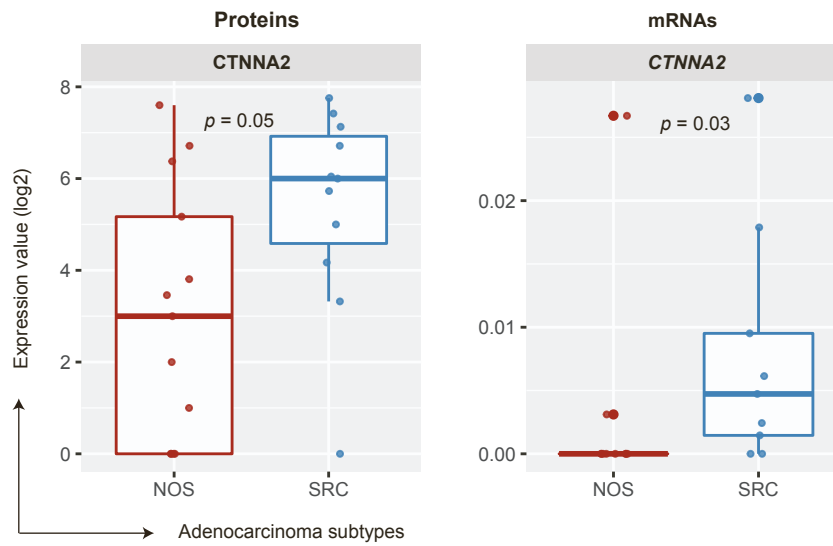


Figure S3. DEGs between adenocarcinoma subtypes. Box plots show the different expression in proteins and mRNAs between NOS and SRC for CTNNA2. Statistical method: Wilcox test.

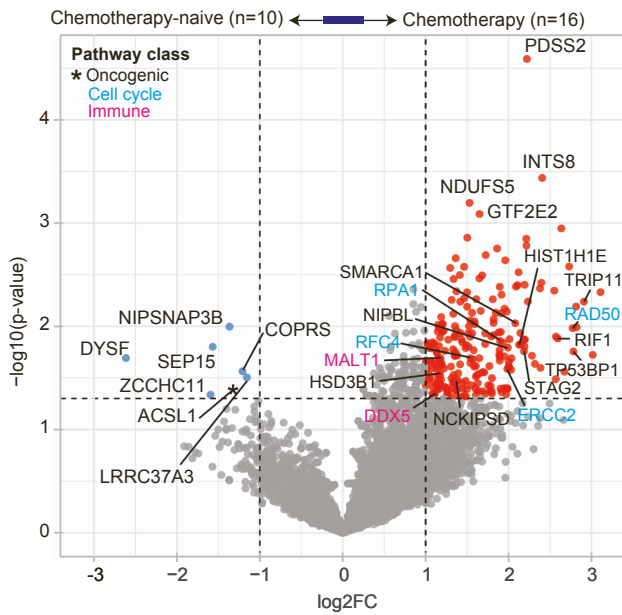
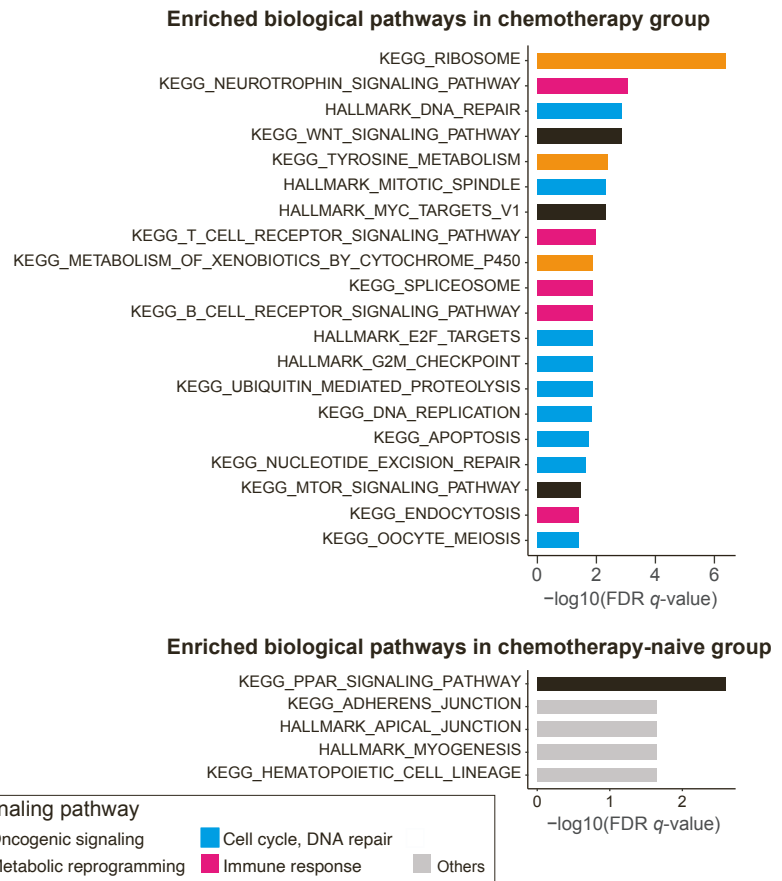
A**B**

Figure S4. Enriched tumor specific proteins and associated biological pathways between the chemotherapy-treated and chemotherapy-naïve subtypes. A) The Volcano plot shows the DEPs between the chemotherapy-treated and chemotherapy-naïve groups with a cutoff of $\log_2(\text{fold change}) > 1$ and $p\text{-value} < 0.05$, different colors indicate the significant genes involving in the oncogenic (black), cell cycle (light blue), and immune response (pink) pathways. B) The Pathway enrichment analysis identified biological pathways enriched in the therapy-specific subtypes. Pathways are colored by their biological functions.