**Supplementary figure 1.** Data quality control of TMT-labeled proteomics. (A) Peptide length distribution, mainly in the range 7-25; (B) Mass tolerance distribution of parent ions. The peak type is concentrated near 0, indicating small mass deviation; (C) Number distribution of unique peptide segments. A less steep curve indicates that the protein identification is more reliable; (D) Protein coverage distribution. A higher number of peptides in each protein indicate a higher reliability; (E) Molecular weight distribution of proteins. The molecular weight range indicates the identified protein range. Units: thousand daltons, kDa; (F) Principal component analysis (PCA). The total protein difference between each group and the variation degree between the samples within the group. (G) Premium Coefficient of Variance (CV).

**Supplementary figure 2.** All protein functional annotations from the GO, KEGG, COG and IPR databases. (A) Gene Ontology (GO) annotation including Cellular Component, Molecular Function and Biological Process (top 10 results); (B) Cluster of Orthologous Groups of proteins (COG) for the classification of phylogenetic relationships of coding proteins in complete genomes; (C) Kyoto Encyclopedia of Genes and Genomes (KEGG) for major biochemical metabolic pathways and signal transduction pathways; (D) InterPro (IPR) for domains of proteins with unknown function; (E) Subcellular localization for different organelles or cell regions; (F) Results for total functional annotation of single (one color) or common (overlap) proteins in each database.

**Supplementary figure 3.** Subcellular localization and interaction analysis of differentially abundant proteins between the *cohort 1* subset and *cohort 2* subsets. (A) Subcellular localization of differentially abundant proteins; (B) Interaction analysis of differentially abundant proteins. Node size denotes the number of proteins with interactions. Score>-0.5, red for high level while blue for low level.

**Supplementary figure 4.** The different spatial distributions of TIME represented by tumor cells, typical immune-cell infiltrates and stroma between the *cohort 1* and *cohort 2* subsets. Upward side, 500 × 500μm region, scale bar: 100 μm; Downward side, 100 × 100μm, scale bar: 20μm. *cohort 1*, H. pylori-positive with pCR and high TIL-Ts; *cohort 2*, others; TIME, tumor immune microenvironment; pCR, complete pathological remission; TIL-Ts, tumor-infiltrating T-lymphocytes.