Supplementary Figure Legends

Supplementary Figure 1. Integrated single-cell and bulk transcriptomic analyses of gastric cancer. (A) Dot plot showing canonical marker genes used to define major gastric cell populations. (B–C) UMAP plots illustrating the distribution of epithelial cells by sample origin (Normal vs Tumor) and ploidy status (aneuploid, diploid, undefined). (D) Immune landscape comparison between responders and non-responders to ICIs. Upper panels show clinical characteristics (age, sex, BMI, tumor location, clinical T/N stage, TRG). Lower heatmap shows differential immune infiltration estimated by CIBERSORT. (E) Hallmark gene set enrichment analysis of bulk RNA-seq (non-responders vs. responders) showing enrichment of pathways related to protein secretion, MYC targets, G2M checkpoint, and mTORC1 signaling. (F) GO biological process enrichment highlighting RNA processing, mitochondrial RNA metabolism, and cell cycle–related pathways.

Supplementary Figure 2. Validation of SRSF10 expression and its prognostic significance in gastric cancer. (A) IHC images of SRSF10 in different gastric tissue states (normal, intestinal metaplasia, dysplasia/cancer). (B) qPCR validation of SRSF10 expression in paired gastric tumor and adjacent normal tissues. (C) IHC scoring of SRSF10 expression in gastric tumors, illustrating representative cases with low (score 0, 3) and high expression (score 6, 9). (D) Univariate and multivariate Cox regression analyses for disease-free survival (DFS). Scale bars in C are 100 μm.

Supplementary Figure 3. SRSF10 knockdown and overexpression validated in GC cell lines. (A) Western blot analysis of SRSF10 protein expression in various gastric cancer cell lines (HGC-27, KATO-III, AGS, NCI-N87, MKN-45) and a normal gastric epithelial cell line (GES-1). (B) Western blot analysis of FLAG in AGS cells transfected with a control vector or an SRSF10 expression vector (left). Western blot analysis of SRSF10 in AGS cells transfected with shNC, shSRSF10 #1, or shSRSF10 #2(right). (C)

Flow cytometry analysis of cell cycle distribution in AGS cells transfected with shNC or shSRSF10. (D) Flow cytometry analysis of cell cycle distribution in AGS cells transfected with a control vector or an SRSF10 expression vector.

Supplementary Figure 4. HDT induces spasmolytic polypeptide-expressing metaplasia (SPEM). (A) Representative H&E staining of gastric corpus tissues from mice treated with vehicle, 1C8, high-dose tamoxifen (HDT, 72 h), or combination (1C8 + HDT).

Supplementary Figure 5. SRSF10 regulates BCAT2 splicing and correlates with BCAT2 in GC tissues. (A) Gene set enrichment analysis (GSEA) of mTORC1_SIGNALING in gastric cancer cells transfected with shCtrl or shSRSF10. (B) Table of significantly altered alternative splicing (AS) events detected using the junction count-only method. (C) Correlation analyses of SRSF10 IHC scores with p-mTOR (left) and BCAT2 (right) IHC scores in gastric cancer tissues.

Supplementary Figure 6. Combined 1C8 and anti–PD-1 suppress metaplastic cell populations. (A)Immunofluorescence staining images of gastric tissue from mice in different treatment groups (vehicle, 1C8, anti-PD-1 and anti-PD-1+1C8). SOX9 (green), CD44v9 (red), E-Cadherin(white) and DAPI (blue). Scale bars in A,100 μm.