

Figure S1. Single-cell data quality control, cluster characteristics, and cell talk between clusters. (A) Single-cell data quality control. (B) Identification of highly variable genes. (C) Top four marker genes expressed in each cluster. (D) Activation of TNF, BMP, and WNT pathways among cells in the sub-clusters. (E) High RRM2 expression in gastric cancer is associated with increased infiltration of CD8⁺ T cells, CD8⁺ naive T cells, cytotoxic lymphocytes, and cytotoxic cells. RRM2, ribonucleotide reductase regulatory subunit M2.

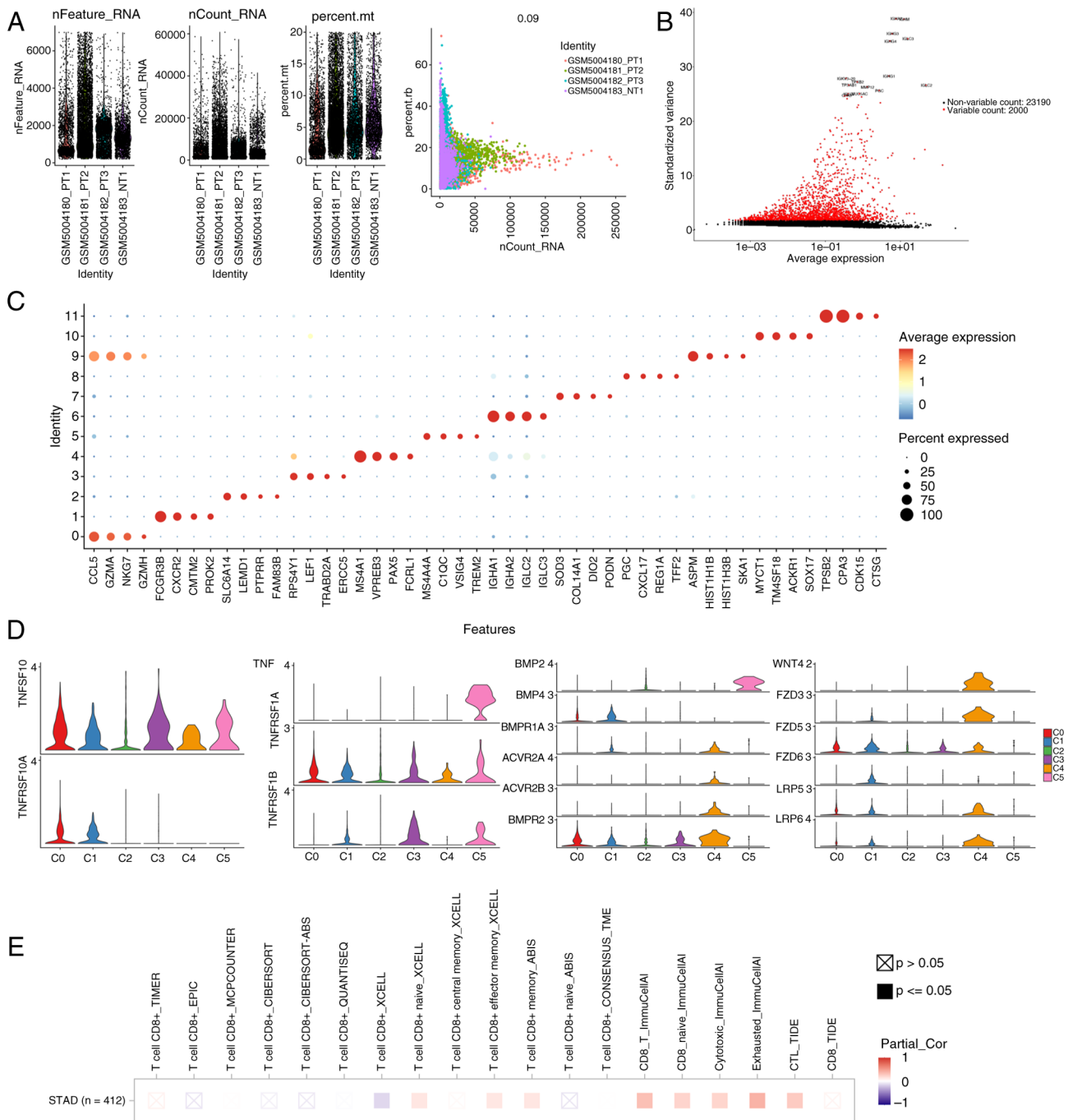


Figure S2. Quality control of GEO and TCGA datasets, and GO/KEGG analyses. (A) Batch effects were removed from the GSE66229 dataset. (B) Differentially expressed genes associated with prognosis in the GSE66229 dataset. (C) Batch effects were removed from the GSE84433 dataset. (D) Differentially expressed genes associated with prognosis in the GSE84433 dataset. (E) Comparison of TIDE immunological scores between patients with high and low RRM2 expression in the GSE66229 and GSE84433 datasets. (F) Differentially expressed genes associated with prognosis in the TCGA dataset. (G and H) GO analysis revealed RRM2-related cellular components, biological processes, and molecular functions in the GEO gastric cancer dataset. (I) KEGG and GO analysis revealed RRM2-related pathways and functions in TCGA gastric cancer dataset. GEO, Gene Expression Omnibus TCGA, The Cancer Genome Atlas; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; RRM2, ribonucleotide reductase regulatory subunit M2; TIDE, Tumor Immune Dysfunction and Exclusion.

