

Description of Additional Supplementary Files

Title: Supplementary Data 1

Description: Clinicopathological information of the tissue microarray (TMA) cohort (n = 1,315), including age range, sex, EBV status, tumor location, tumor diameter, Lauren classification, lymphovascular invasion, and T/N/M staging.

Title: Supplementary Data 2

Description: Clinicopathological information of the locally advanced EBV-associated gastric cancer (EBVaGC) cohort (n = 144) receiving neoadjuvant chemotherapy, including age range, sex, EBV status, clinical stage, chemotherapy regimen, tumor regression grade, Lauren subtype, tumor location, lymphovascular invasion, perineural invasion, and the presence of regional tertiary lymphoid structures.

Title: Supplementary Data 3

Description: Tertiary lymphoid structure (TLS) evaluation cohort (n = 191), comprising both EBV-associated (EBVaGC) and EBV-negative (EBVnGC) gastric cancer patients. The dataset includes clinical stage, treatment status, tumor regression grade, and quantification of regional TLS densities and proportions.

Title: Supplementary Data 4

Description: Sample information for the single-cell RNA sequencing (scRNA-seq, n = 21) and spatial transcriptomics (10x Visium CytAssist, n = 11) cohorts (total n = 32), including sample source (primary tumor or paratumor tissue such as gastritis, normal gastric mucosa, non-metastatic lymph node, and ovarian metastasis) and treatment status (treatment-naïve, neoadjuvant chemotherapy, immunotherapy, or chemoimmunotherapy).

Title: Supplementary Data 5

Description: List of malignant gene expression meta-programs (MPs) identified in this study, categorized into functional groups including replication, metabolism, immune response, stress, metastasis, and neuroendocrine-related programs, together with their associated gene sets.

Title: Supplementary Data 6

Description: Top 50 marker genes for each neutrophil subtype identified by single-cell RNA sequencing, used for subtype annotation and functional characterization.

Title: Supplementary Data 7

Description: Probe sequences used for multiplexed fluorescence in situ hybridization (mFISH) targeting the EBV transcripts EBER1 (590 nm), BZLF1 (550 nm), and BLLF1 (647 nm).