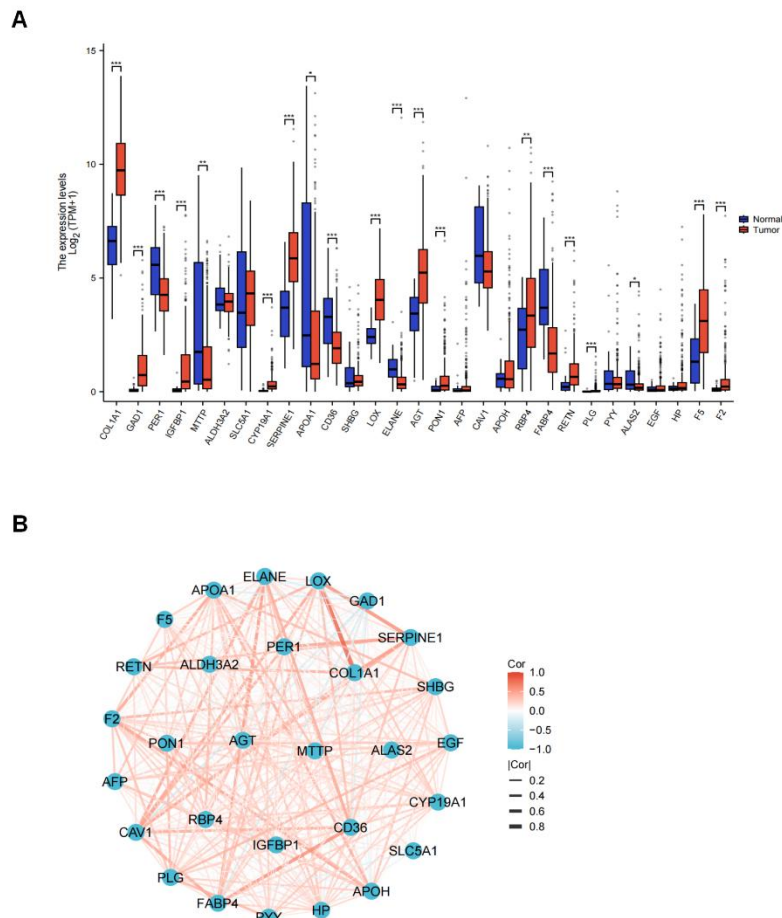
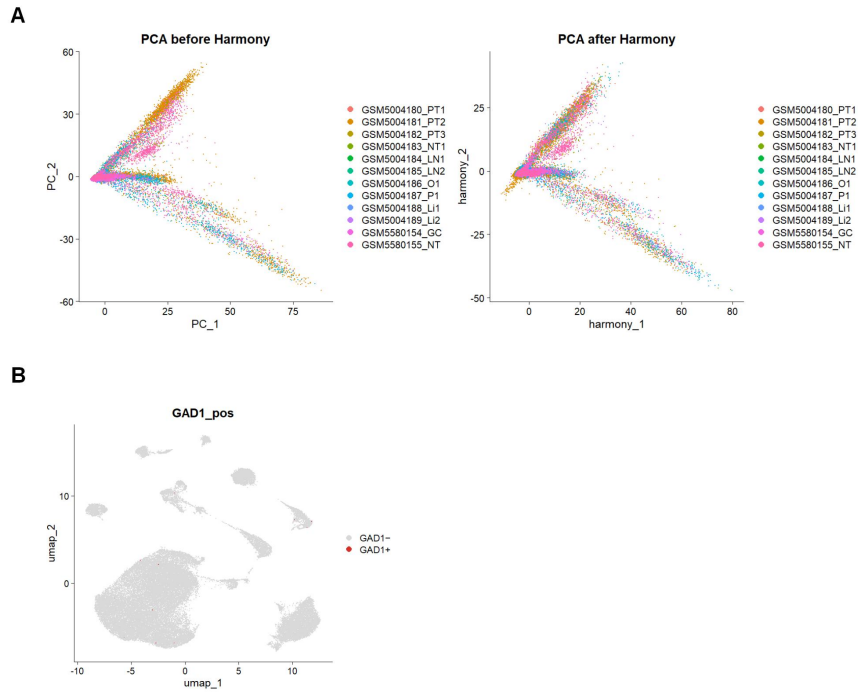




Supplementary Fig. S1 (A) Expression patterns of the 29 genes significantly associated with overall survival (OS) in the TCGA cohort. These genes are shown to be markedly dysregulated in both tumor and normal tissues, indicating their potential involvement in gastric cancer (GC). (B) Interaction network of the 29 OS-related genes, illustrating predominantly positive correlations among them, suggesting coordinated dysregulation in gastric cancer. The high frequency of copy number variations (CNVs) in these genes is also highlighted, with PON1 showing the most significant copy number gain, and RBP4 exhibiting the highest frequency of copy number loss.



Supplementary Fig. S2 (A) UMAP visualization of the cellular distribution within the gastric cancer tumor microenvironment after batch effect correction using the Harmony algorithm, showing multiple distinct cell clusters. (B) Expression pattern of GAD1 at the single-cell level, with low expression detected in a small subset of cells. Cells with detectable GAD1 expression are defined as GAD1⁺ cells for subsequent analyses.