

Figure S1

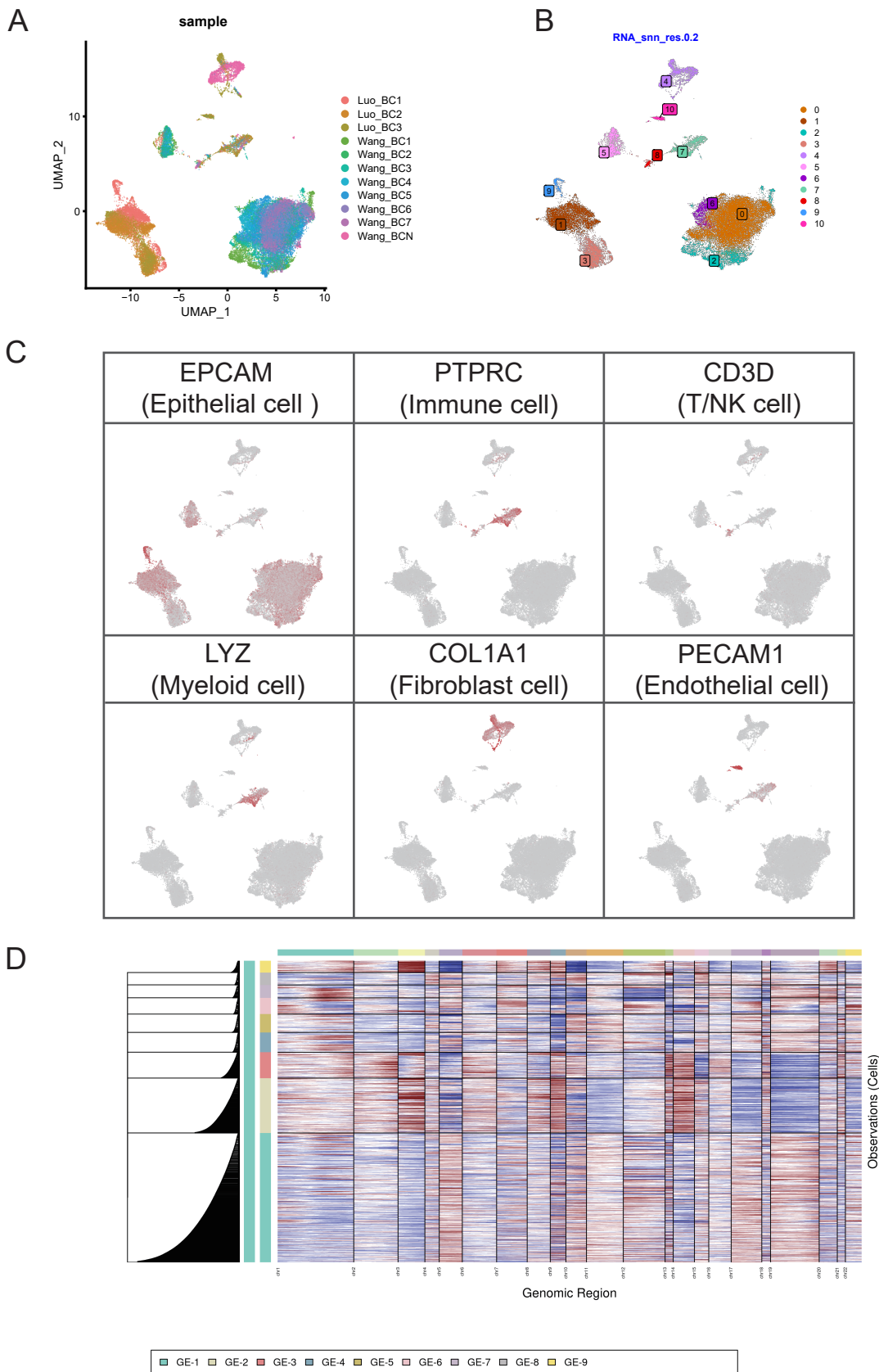


Figure S1. Single-cell clustering and annotation of cell types in bladder cancer samples.

(A) UMAP plot of single-cell RNA sequencing data from 11 bladder cancer samples derived from the GSE190888 and GSE135337 datasets. Each color represents cells from a different sample, highlighting the diversity of cell populations across individual samples. (B) UMAP plot showing the clustering of single cells from bladder cancer samples into 11 distinct clusters (labeled 0~10) based on RNA expression profiles. (C) Expression patterns of marker genes used for cell type annotation. EPCAM is highly expressed in epithelial cells, PTPRC identifies immune cells, CD3D marks T/NK cells, LYZ indicates myeloid cells, COL1A1 highlights fibroblast cells, and PECAM1 is specific for endothelial cells. (D) Heatmap generated by inferCNV displaying inferred copy number variations (CNVs) across epithelial cell subpopulations (GE-1 to GE-9).