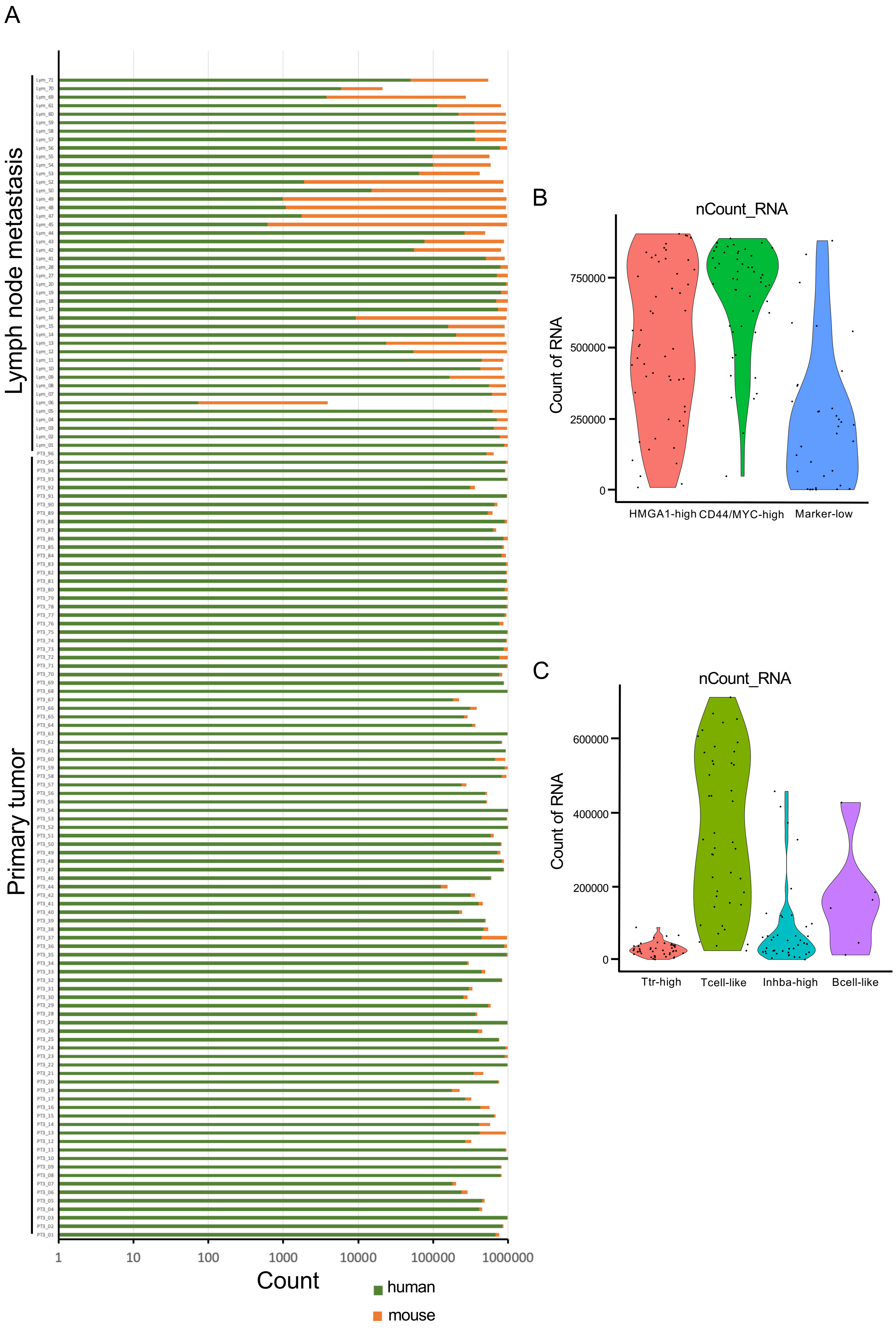


Fig. S1. Read counts and heterogeneity in each spot. (A) Read counts of human and mouse transcripts in each spot. (B) Violin plot of read counts in human cancer clusters. (C) Violin plot of read counts in mouse stromal clusters.

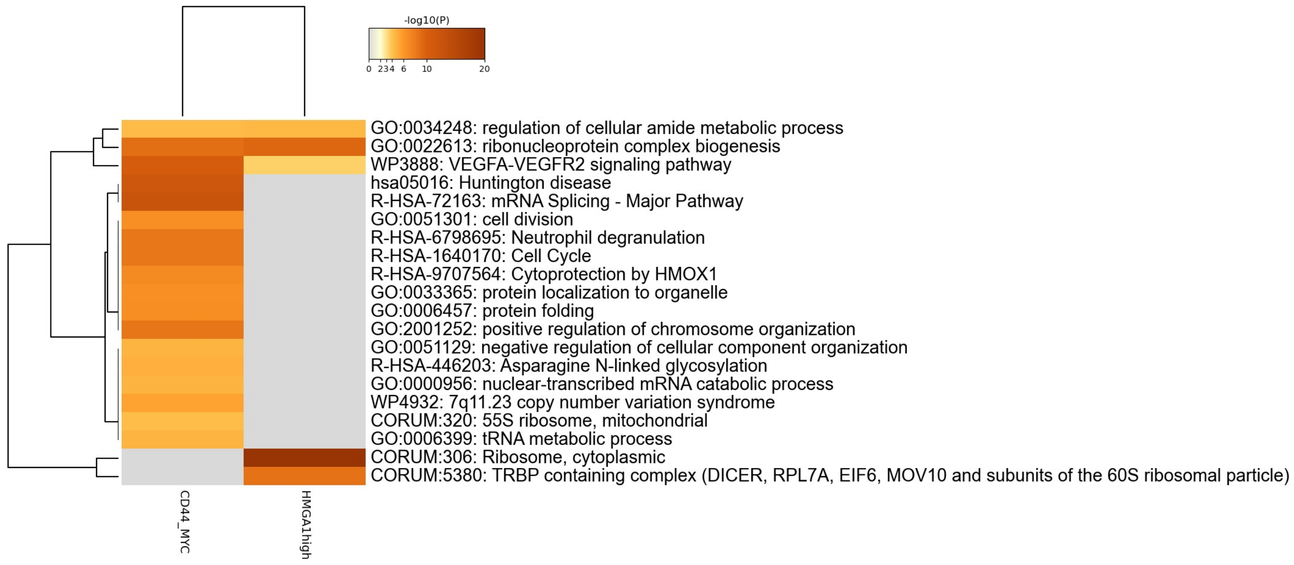


Fig. S2. Enrichment analysis of DEGs in the two CSC-like populations. Heatmap of the results of the enrichment analysis of the differentially expressed genes (DEGs) in the HMGA1-high and CD44/MYC-high clusters using Metascape.

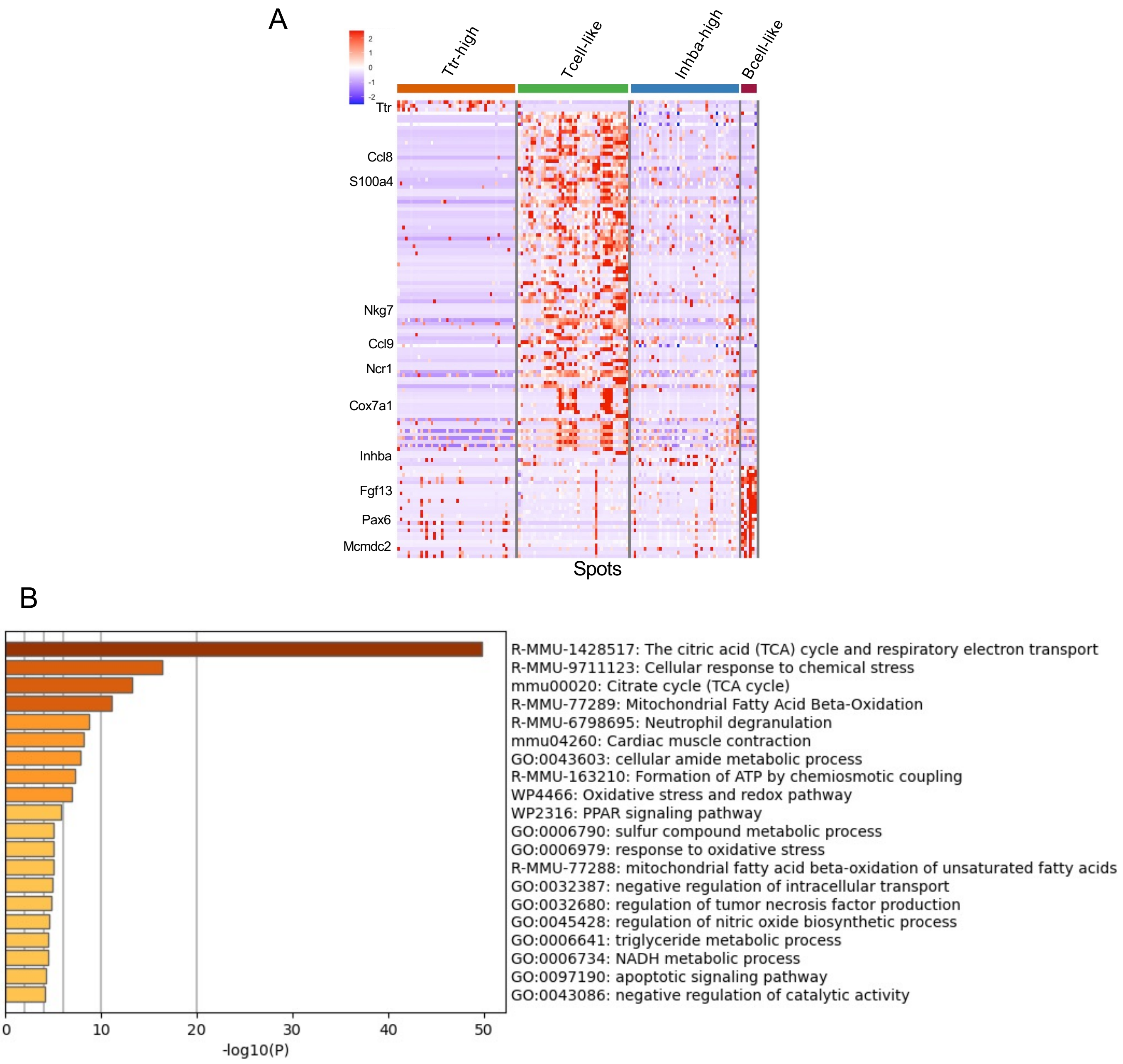


Fig. S3. Stromal cluster DEG analysis and enrichment analysis. (A) Heatmap of the differentially expressed genes (DEGs) (adjusted p value < 0.05 and pct.1 - pct.2 > 0.1) in mouse stromal cells. (B) Heatmap of the results of the enrichment analysis in the Tcell-like cluster.

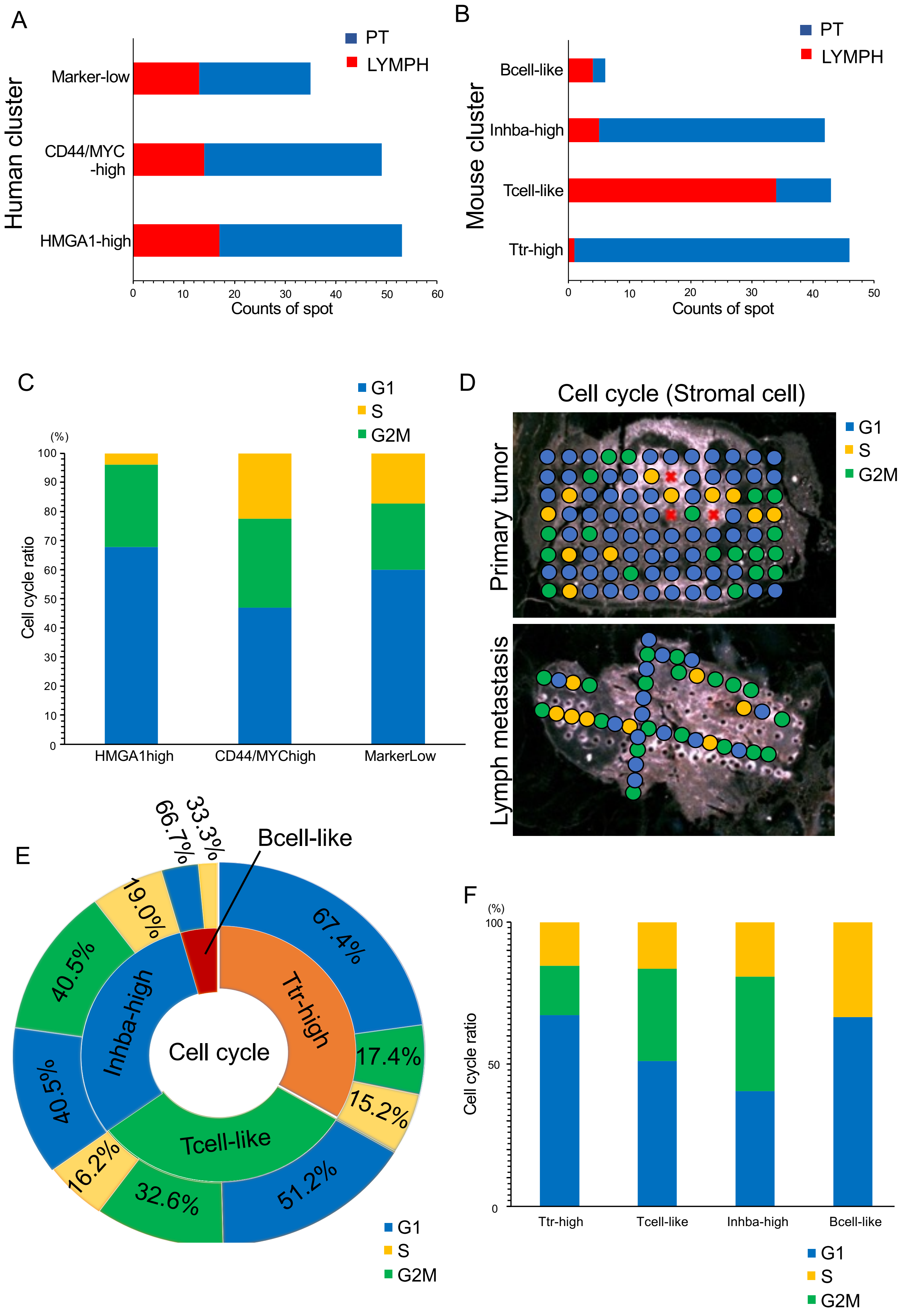


Fig. S4. Spatial analysis of mouse clusters in the primary tumor and lymph node metastasis. (A,B) Bar plots of spot counts in the primary tumor and lymph node metastasis. (A) human and (B) mouse. (C) Cell cycle phase proportions of the human cancer clusters. (D) Cell cycle proportions of the mouse stromal cells in the primary tumor and lymph node metastasis. (E) Sunburst plot of the cell cycle in mouse stromal cell clusters. (F) Cell cycle proportions of the mouse stromal clusters.

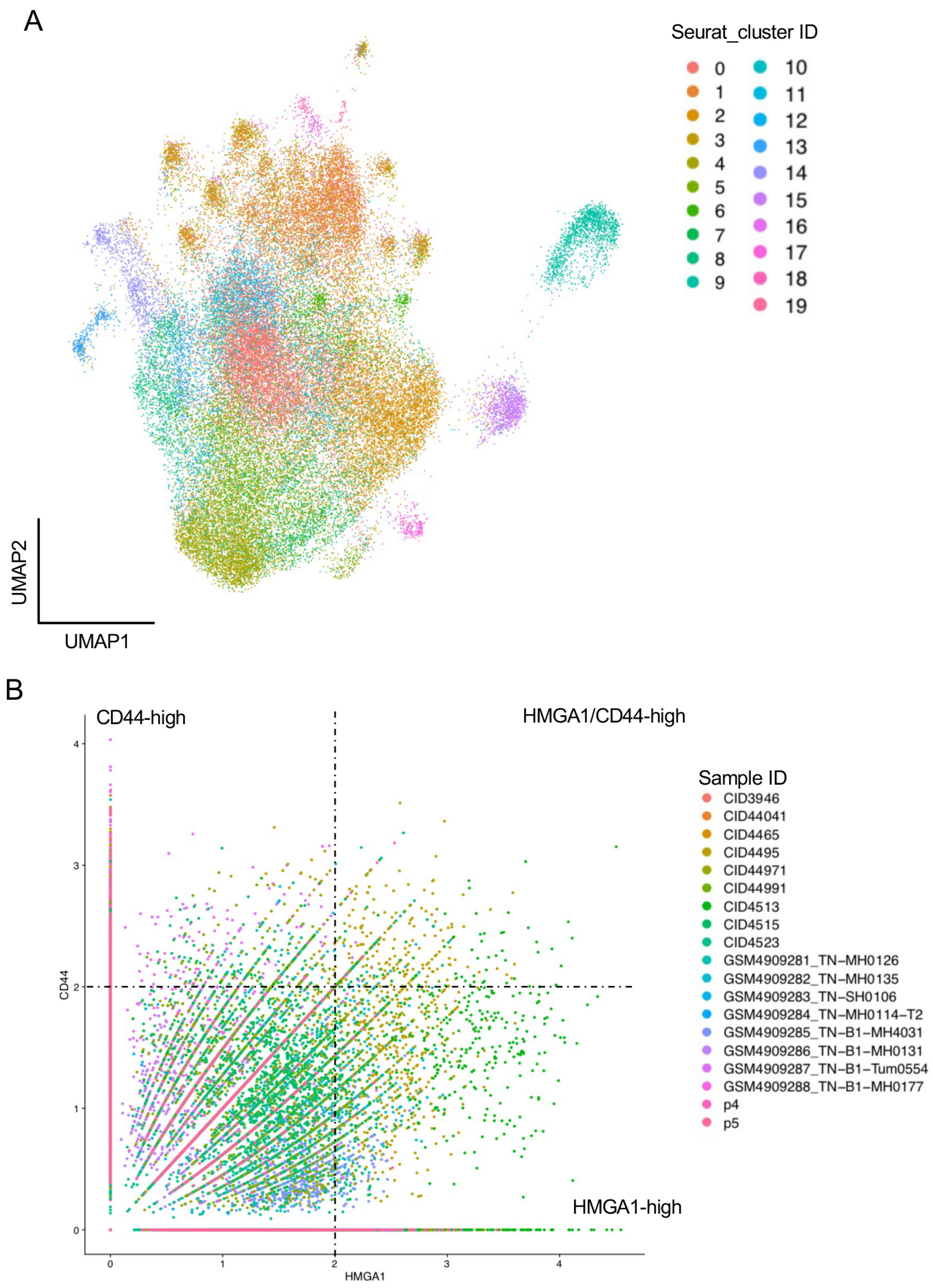
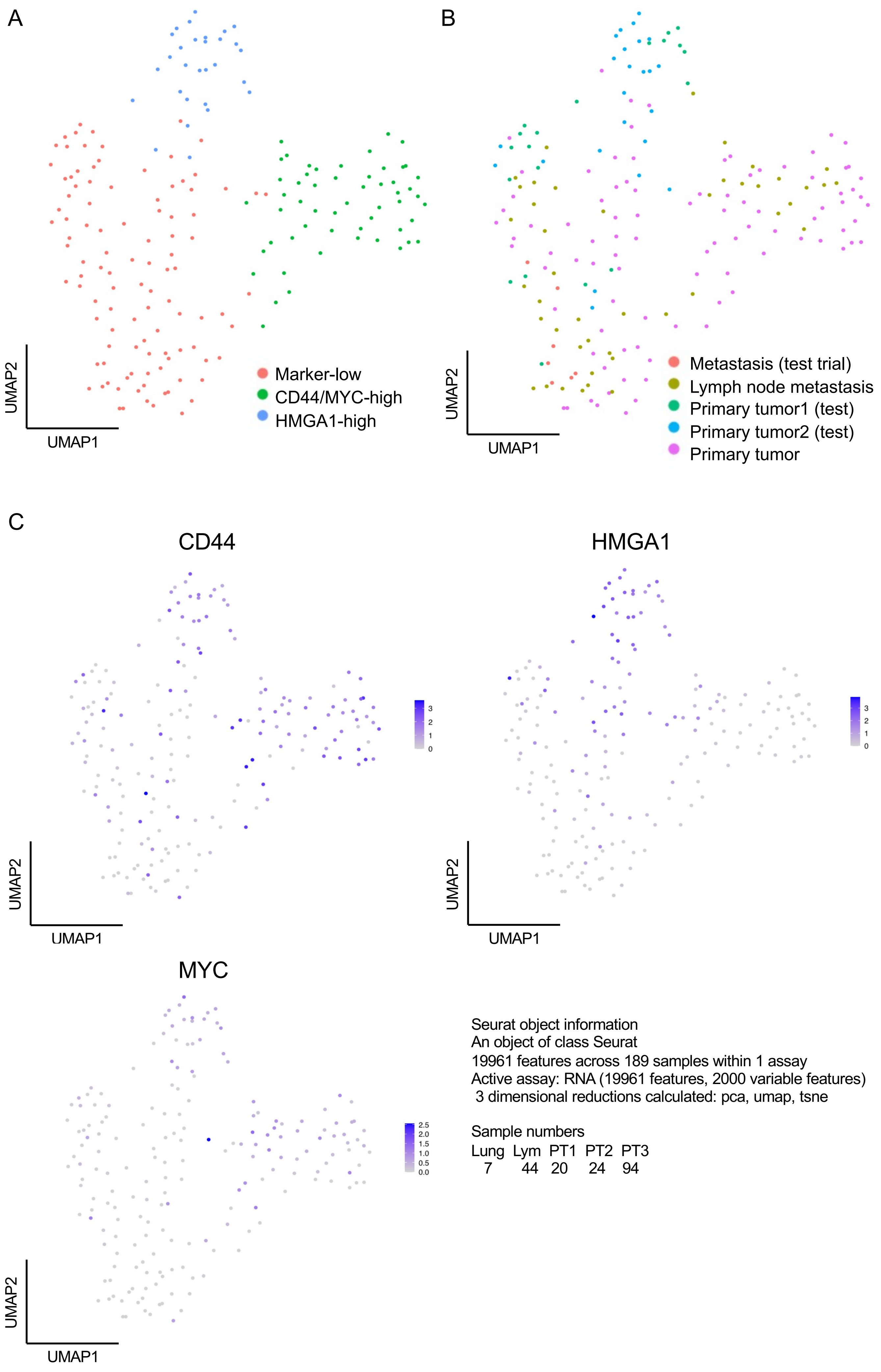


Fig. S5. Reanalysis of integrated scRNA-seq data. (A) UMAP plot of cancer cells with cluster identification by Seurat. (B) Scatter plot of CD44 and HMGA1 expression in the integrated datasets.



```
Seurat object information
An object of class Seurat
19961 features across 189 samples within 1 assay
Active assay: RNA (19961 features, 2000 variable features)
 3 dimensional reductions calculated: pca, umap, tsne

Sample numbers
Lung  Lym  PT1  PT2  PT3
  7    44   20   24   94
```

Fig. S6. Integrated analysis of spatial transcriptomics including other xenografting tumors. (A) UMAP plot of cancer cells with cluster identification by Seurat. (B) UMAP plot cancer cells with xenografting sample identification. (C) Expression analysis of CD44, HMGA1, and MYC in human cancer clusters including pilot samples.

Table S1. Clustering of micro-spots

Click here to download Table S1

Table S2. Marker genes in human cancer cells

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Table S3. Upstream enrichment analysis of cancer cell clusters

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Table S4. GO enrichment analysis of cancer cell clusters

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Table S5. Marker genes in mouse stromal cells

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Table S6. Cell cycle index in clusters

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Table S7. Cell annotation in TNBC patients

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Table S8. DEGs between CSC-like populations in TNBC patients and overlapped genes

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