

Figure S1 The basic analysis of the samples corresponds to Figure 1. UMAP of expression levels of (A) erythroid genes (pHB) and (B) ribosomal RNA (pRP). Violin plots of RNA expression levels (C) and corrected SCTransform (SCT) expression levels (D) for single-cell data.

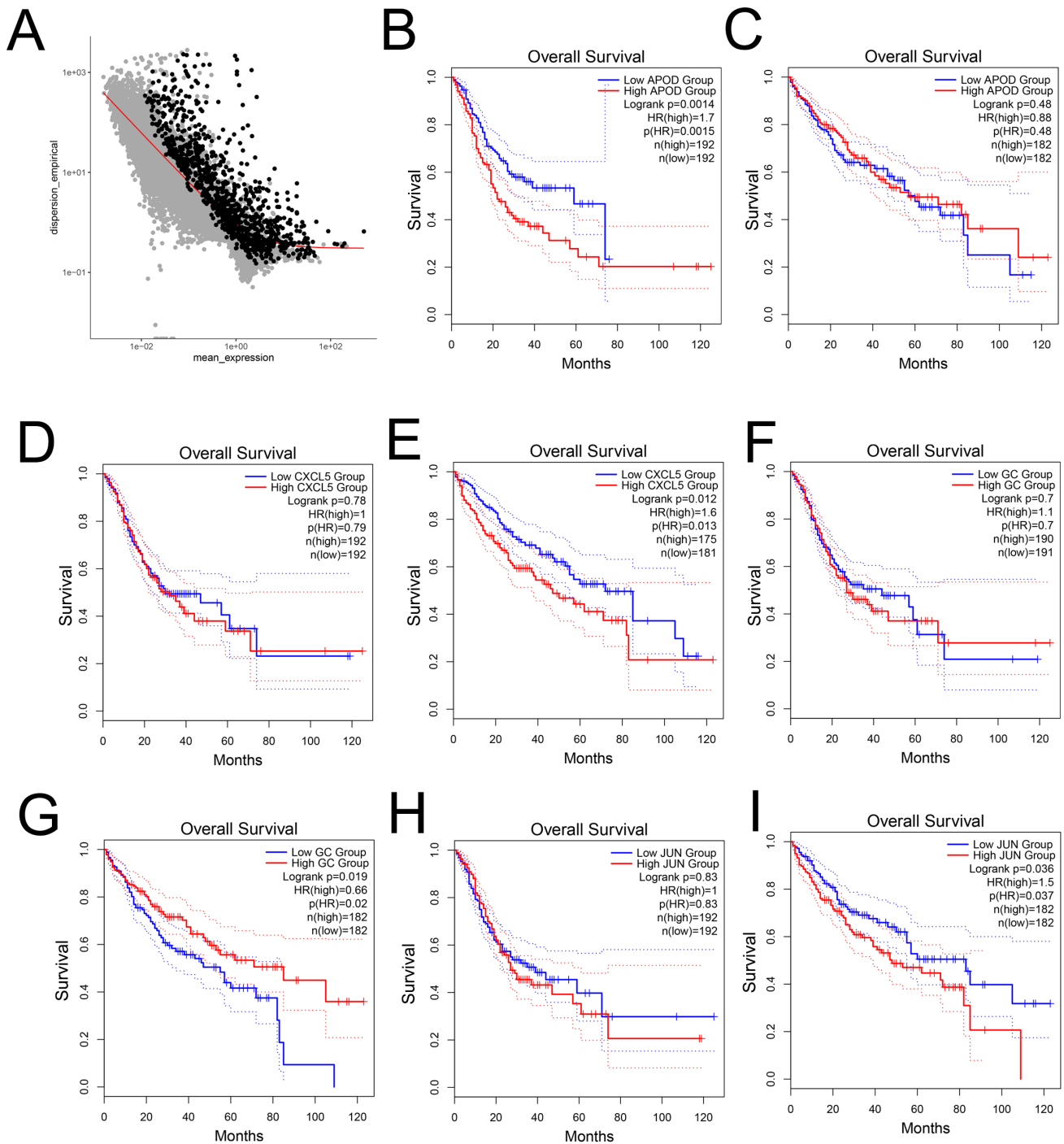


Figure S2 Pseudotime gene screening and survival analysis of genes correspond to Figure 2. (A) Screening the monoclone hypermutated genes construct locus. Gray is background and red line is dispersion trend. Plot of survival curves for gene APOD in STAD ($P=0.0014$, $HR >1$) (B) and LIHC ($P=0.48$, $HR <1$) (C) cohorts. Plot of survival curves for gene CXCL5 in STAD ($P=0.78$, $HR =1$) (D) and LIHC ($P=0.012$, $HR >1$) (E) cohorts. Plot of survival curves for gene GC in STAD ($P=0.7$, $HR >1$) (F) and LIHC ($P=0.019$, $HR <1$) (G) cohorts. Plot of survival curves for gene JUN in STAD ($P=0.83$, $HR=1$) (H) and LIHC ($P=0.036$, $HR >1$) (I) cohorts. STAD, stomach adenocarcinoma; LIHC, liver hepatocellular carcinoma; HR, hazard ratio.

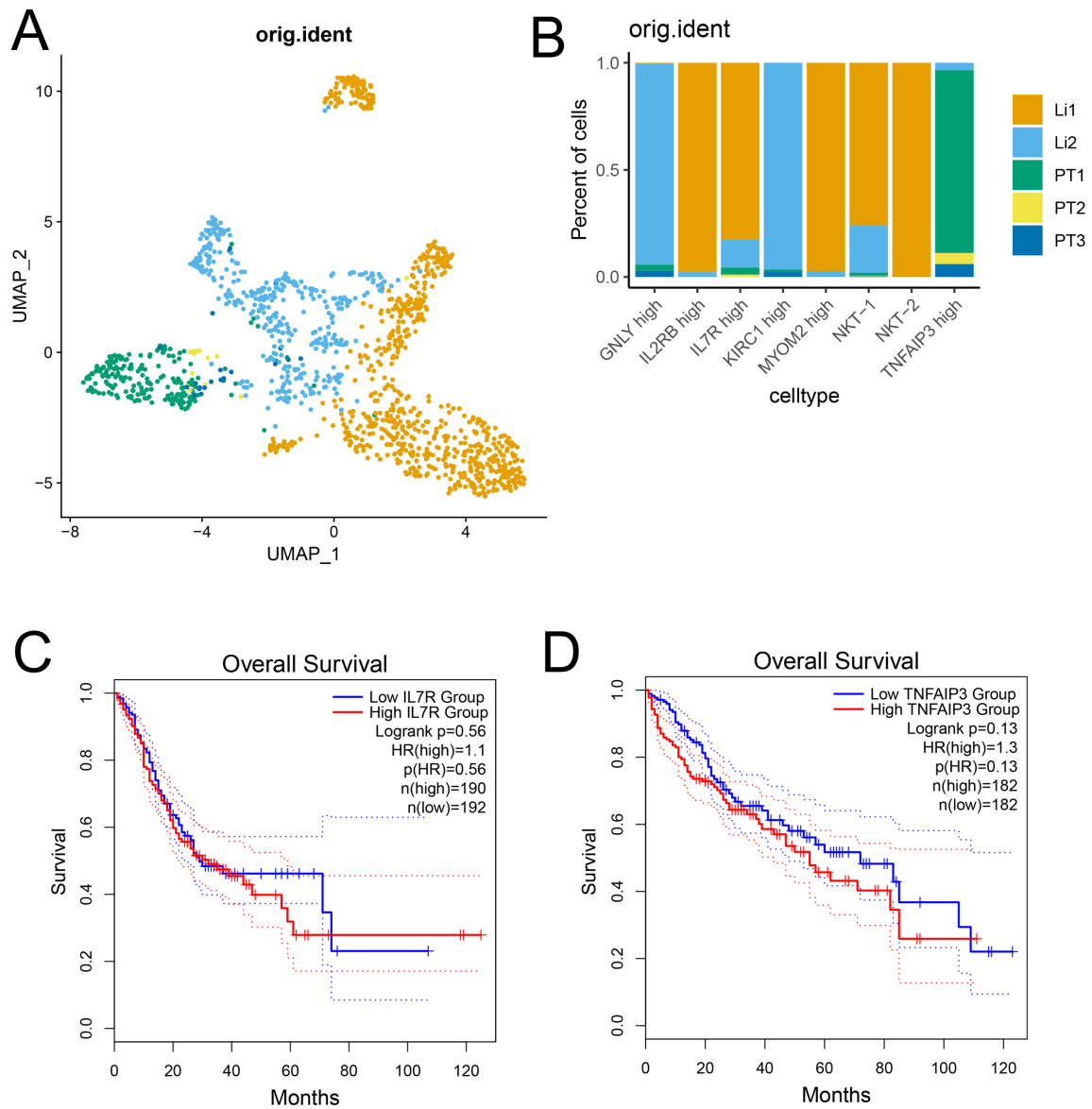


Figure S3 Analysis of NK cell subsets corresponds to Figure 4. (A) UMAP of sample information of NK cells. (B) Percentage of sample sources per cluster. The colors in (A), (B) represent samples. (C) Plot of survival curves for gene IL7R in STAD (P=0.56, HR >1) cohort. (D) Plot of survival curves for gene TNFAIP3 in STAD (P=0.13, HR >1) cohort. NK, natural killer; UMAP, the Uniform Manifold Approximation and Projection; STAD, stomach adenocarcinoma; LIHC, liver hepatocellular carcinoma.

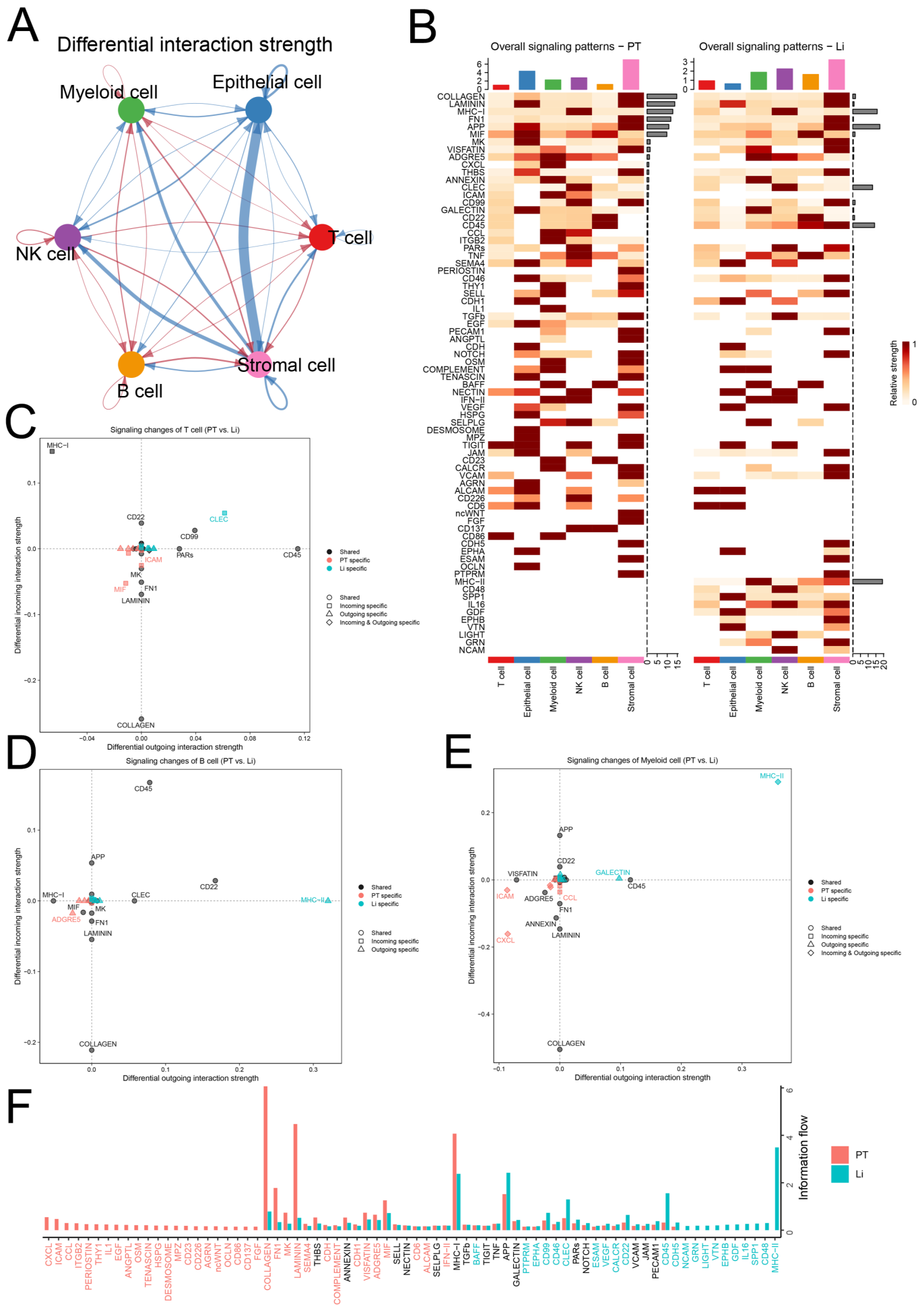


Figure S4 Analysis of cell communication corresponds to Figure 6. (A) Strength of cell communication network. (B) Heatmap of the total signal for each cluster, PT on the left and Li on the right. Red represents signal intensity. (C) T cell, (D) B cell, and (E) myeloid cell are signaling pathway maps with differences between PT and Li. Red and blue represents PT and Li. (F) Information flow statistics for signaling axes. Red represents PT and blue represents Li. PT, primary tumor; Li, liver metastasis.

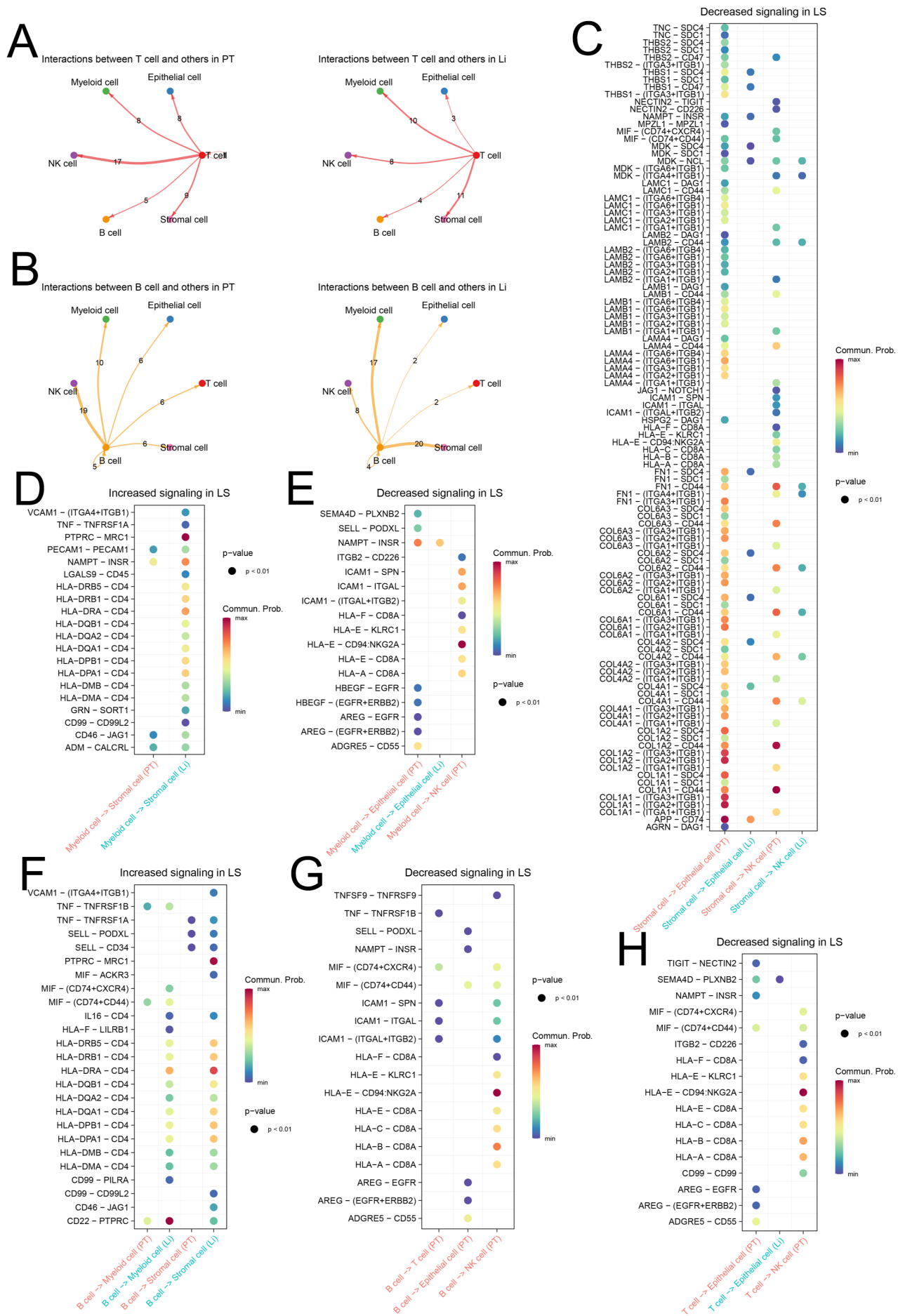


Figure S5 Analysis of signaling axes corresponds to Figure 7. (A) The amount of T cell to other cell interactions, PT on the left and Li on the right. (B) The amount of B cell to other cell interactions, PT on the left and Li on the right. (C) Decreased signal axis of Stromal cells to epithelial cells and NK cells at liver metastasis site (LS). (D) Increased signal axis of Myeloid cells to stromal cells at liver metastasis site (LS). (E) Decreased signal axis of Myeloid cells to Epithelial cells and NK cells at liver metastasis site (LS). (F) Increased signal axis of B cells to Myeloid cells and stromal cells at liver metastasis site (LS). (G) Decreased signal axis of B cells to T cells, Epithelial cells, and NK cells at liver metastasis site (LS). (H) Decreased signal axis of T cells to Epithelial cells and NK cells at liver metastasis site (LS). PT, primary tumor; Li, liver metastasis; NK cell, natural killer cell.