***Additional file***

**Figure S1:** Immune cells associated with patient overall survival risk in TCGA-BLCA and IMvigor210 cohorts based on Cox regression analysis.

**Figure S2:** Expression of antibody-related genes in PCs.

**Figure S3:** PCs were classified into four types based on the median expression of IGHG1 and IGHA1.

**Figure S4:** Branch point analysis based on pseudotime trajectory.

**Figure S5:** Association of IgG1 and IgA1 PCs with different subtypes of bladder cancer.

**Figure S6:** Tumor cell states associated with patient overall survival risk in TCGA-BLCA and IMvigor210 cohorts based on Cox regression analysis.

**Figure S7:** Cell communication analysis for all cell types.

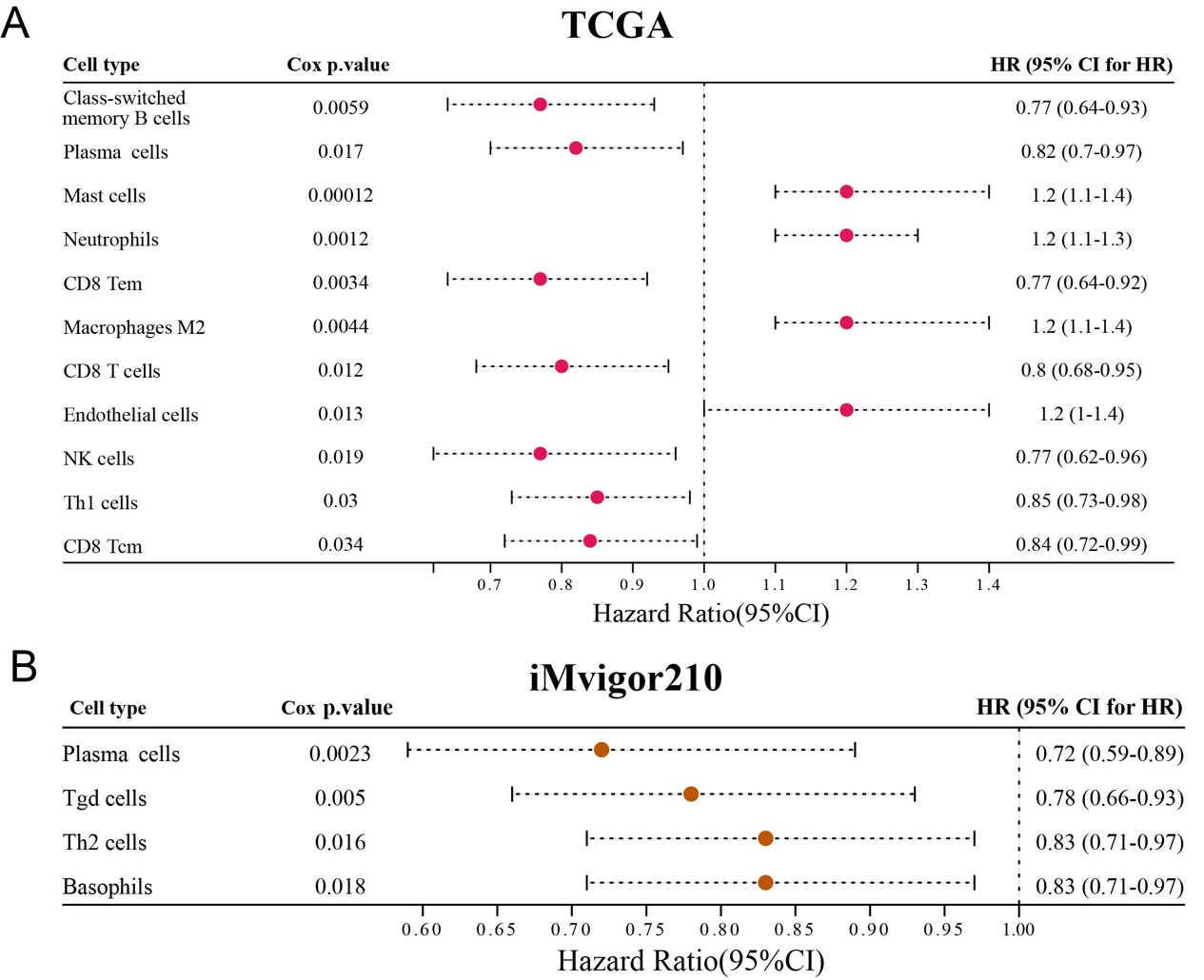
**Figure S8:** Signaling pathways enriched in plasma cell-tumor cell communication.

**Figure S9:** Comparison of PCs and tumor cell crosstalk in low- and high-grade bladder cancer samples

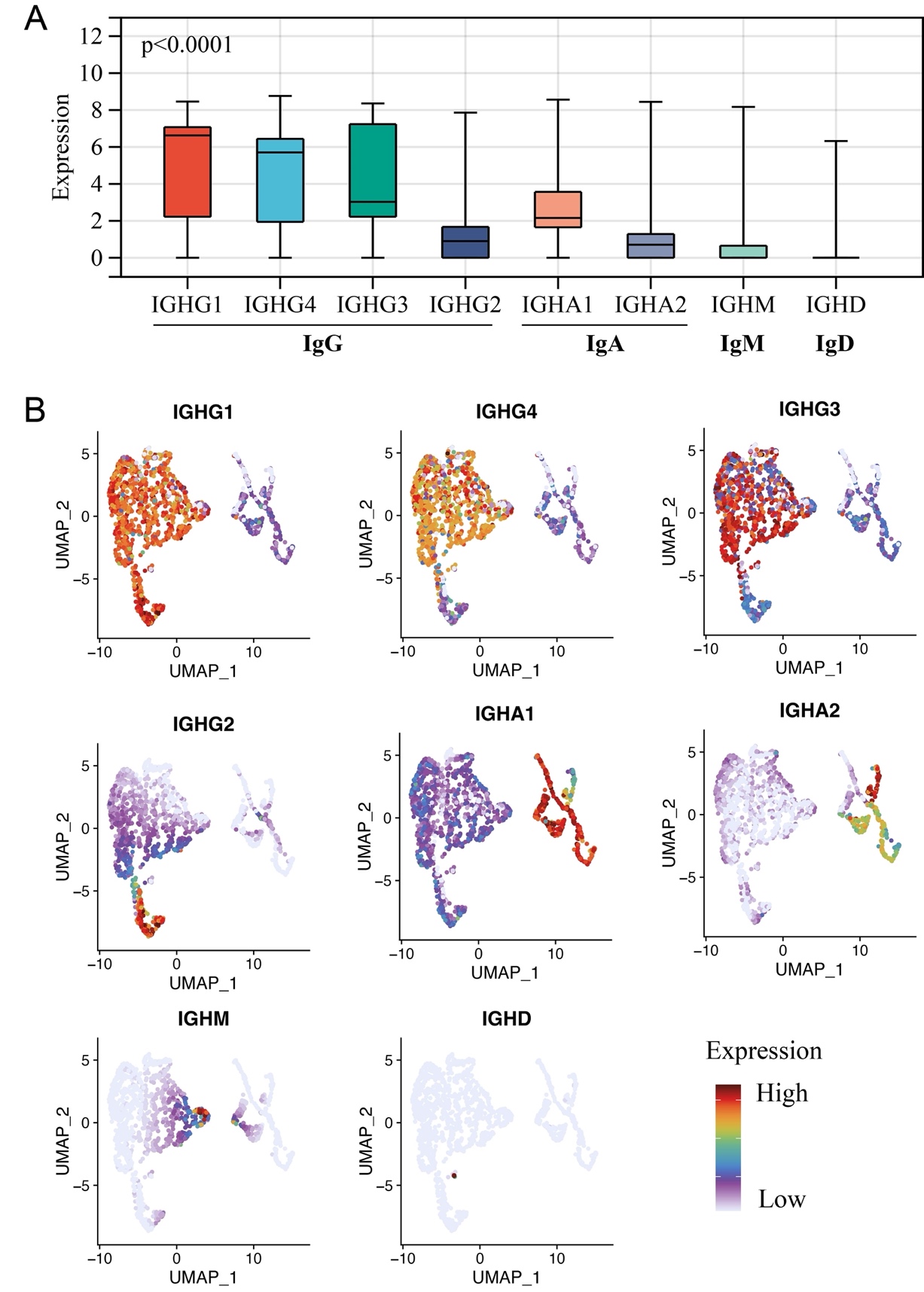
**Figure S10:** Survival analysis for ligand and receptor.

**Figure S11:** Spatial transcriptome cell clustering and expression assessment of selected genes based on sample GSM5224027.

**Figure S12:** Spatial transcriptome cell clustering and expression assessment of selected genes based on validation sample GSM5224029.

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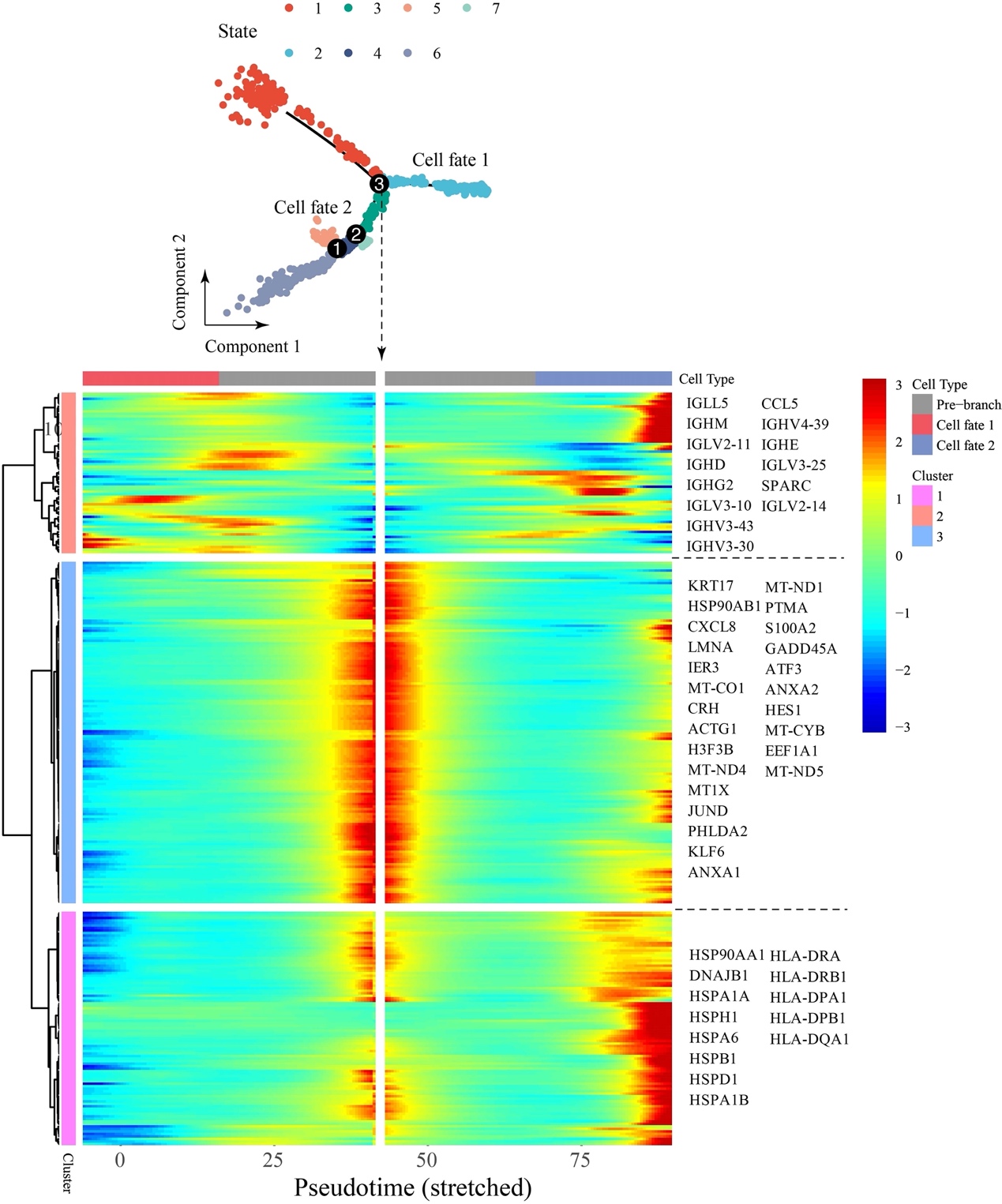
**FIGURE S1|** Immune cells associated with patient overall survival risk in TCGA-BLCA **(A)** and IMvigor210 cohorts **(B)** based on Cox regression analysis.



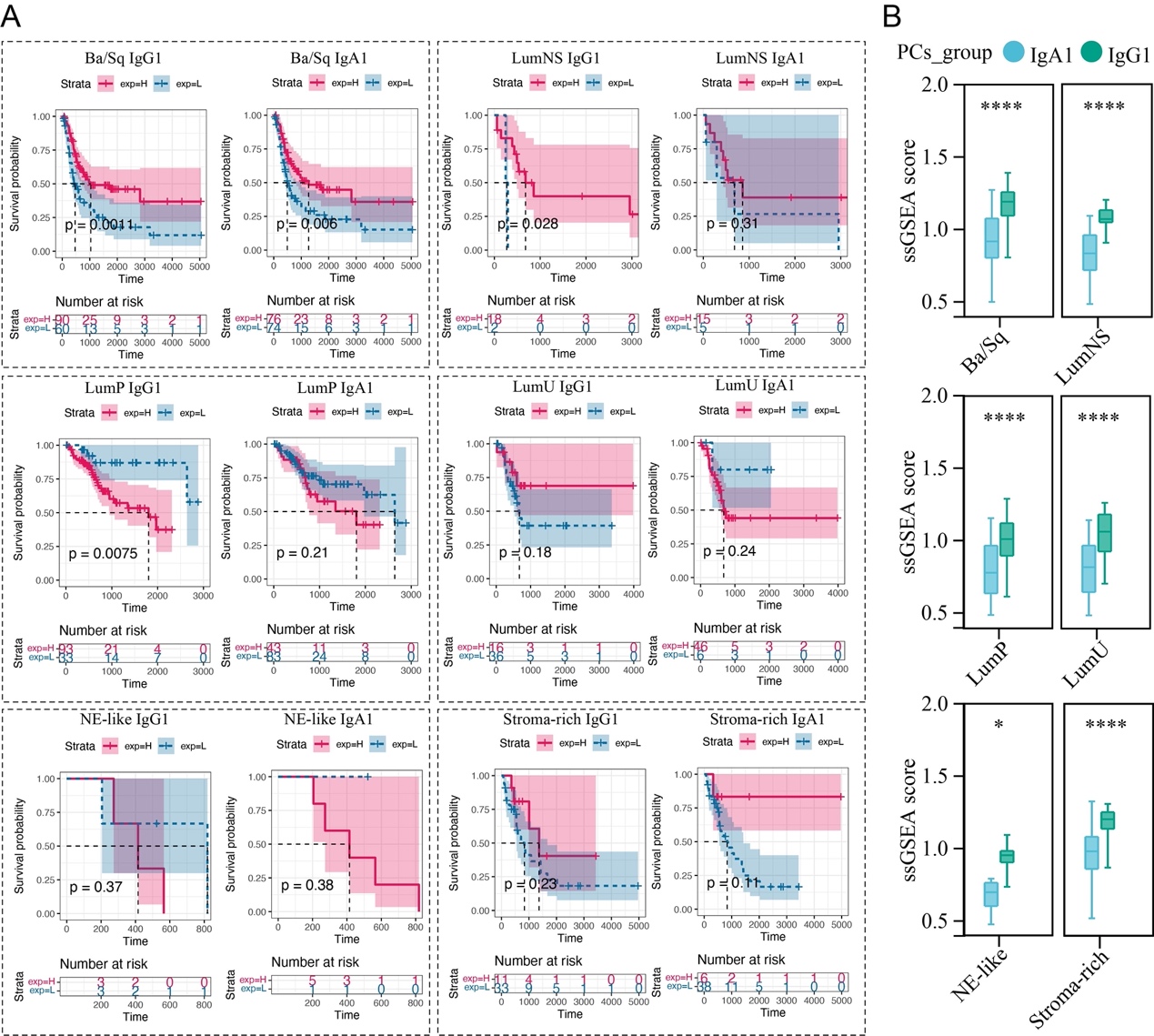
**FIGURE S2|** Expression of antibody-related genes in PCs. **(A)** Box plot shows the expression of IgG-, IgA-, IgM-, and IgD-associated genes in PCs. Kruskal-Wallis test. **(B)** UMAP visualization of antibody-related genes expression showing IgG1 and IgA1 cells are the dominated PCs based on dimension reduction of PCA with selected genes.

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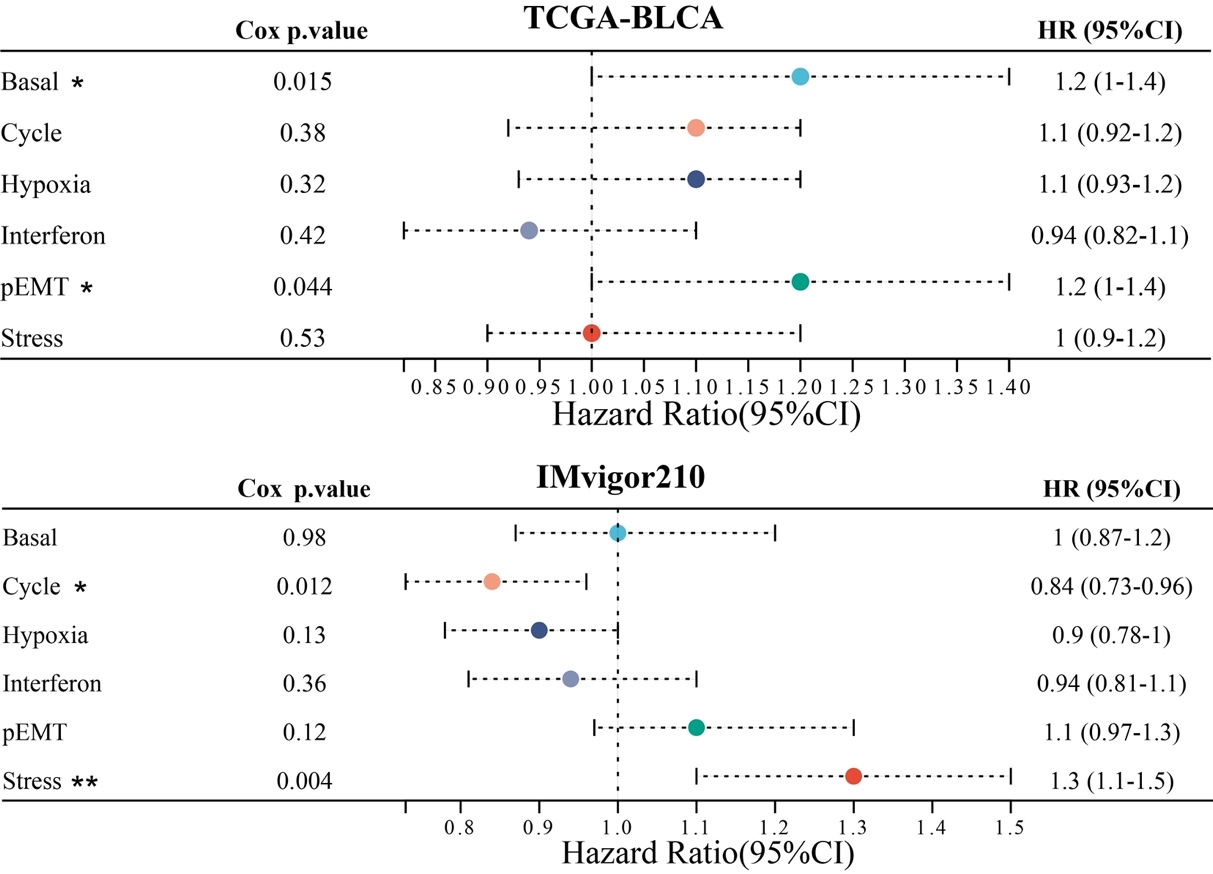
**FIGURE S3|** PCs were classified into four types based on the median expression of *IGHG1* and *IGHA1*.

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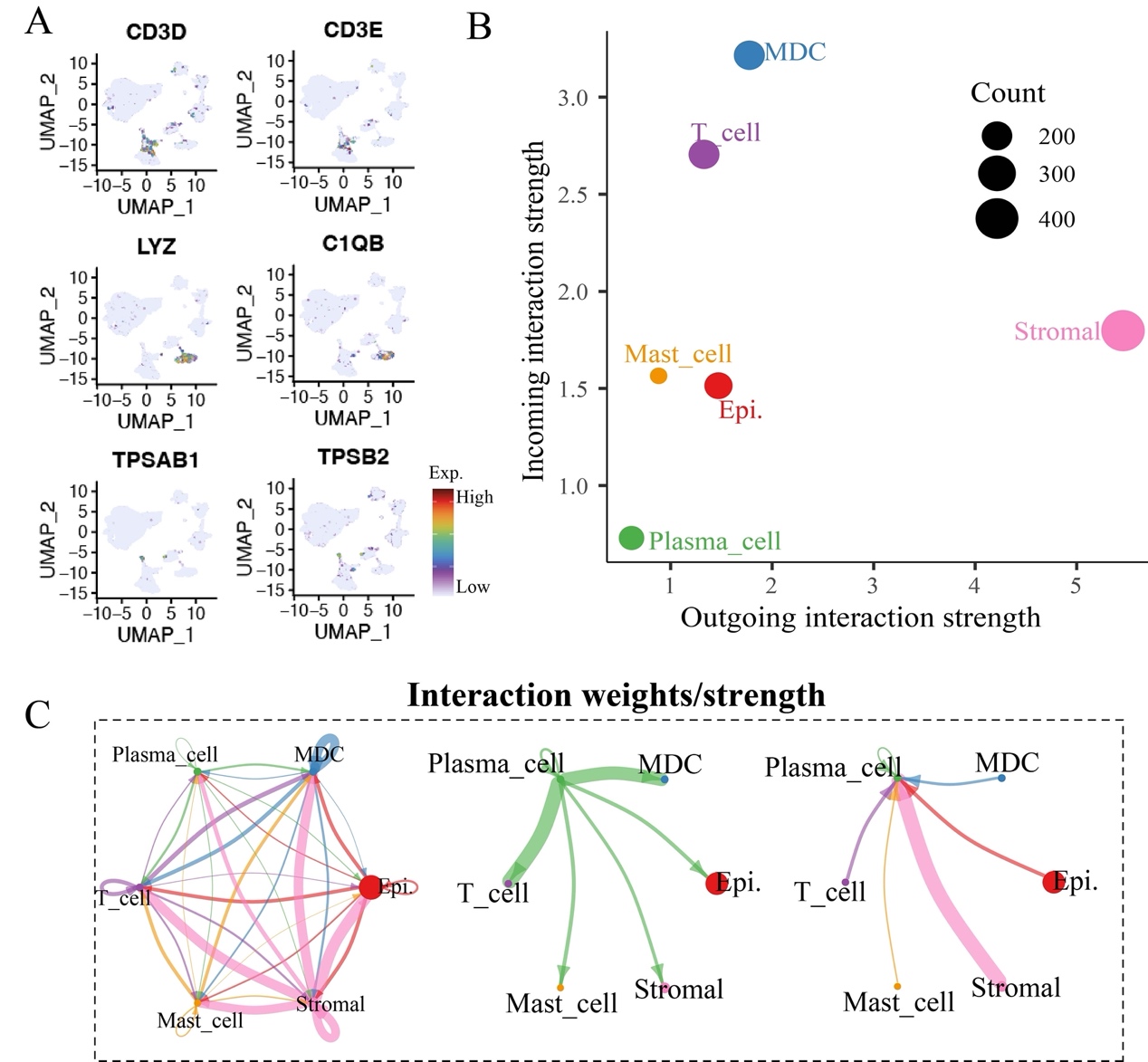
**FIGURE S4|** Branch point analysis based on pseudotime trajectory.

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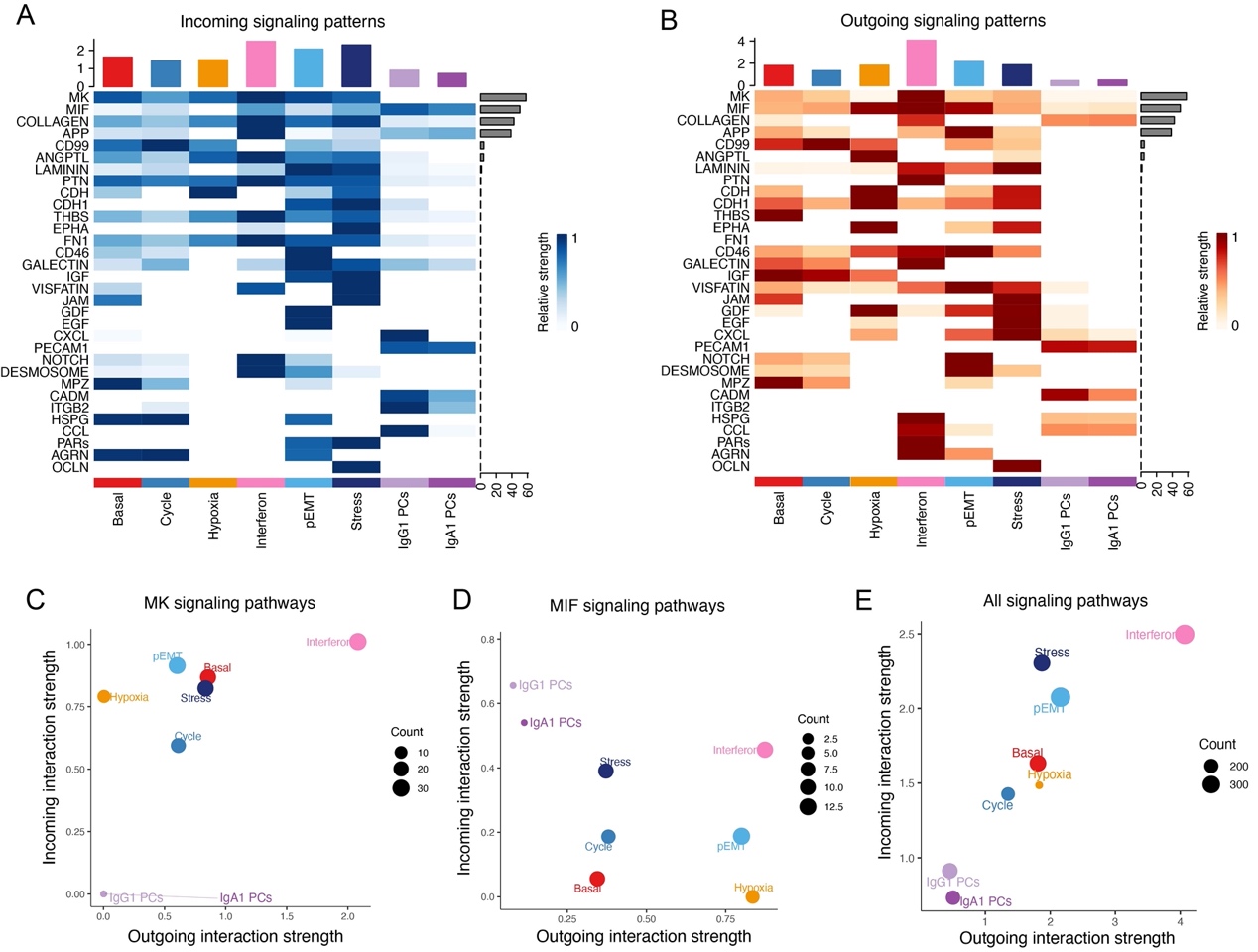
**FIGURE S5|** Association of IgG1 and IgA1 PCs with different subtypes of bladder cancer. **(A)** Heterogeneous survival relevance of IgG1 and IgA1 PCs in patients with different bladder cancer subtypes. **(B)** Abundance of IgG1 and IgA1 PCs in different subtypes of bladder cancer samples inferred by ssGSEA. Wilcoxon test; \*, *P* < 0.05; \*\*, *P* < 0.01; \*\*\*, *P* < 0.001; \*\*\*\*, *P* < 0.0001.

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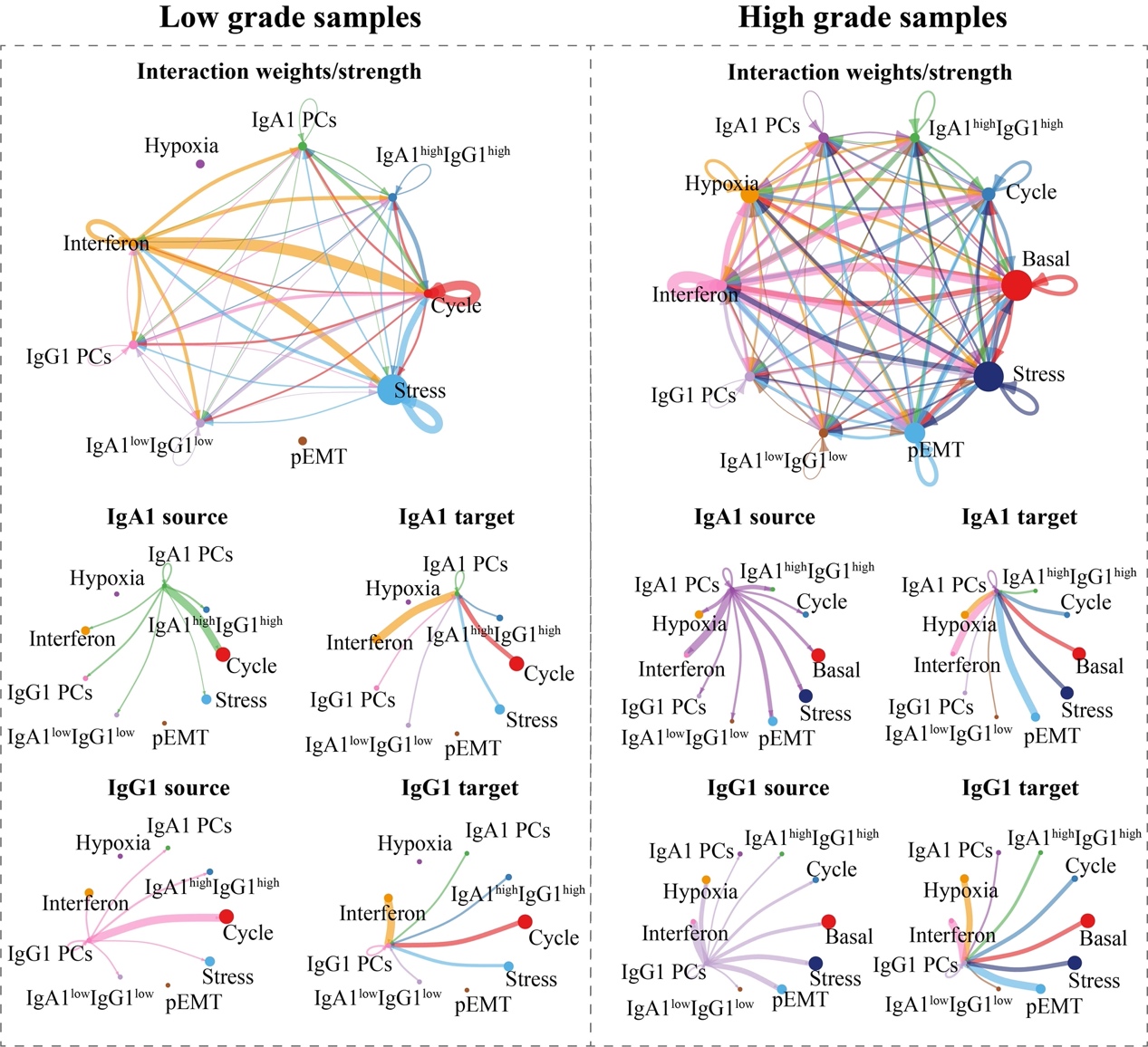
**FIGURE S6|** Tumor cell states associated with patient overall survival risk in TCGA-BLCA **(A)** and IMvigor210 cohorts **(B)** based on Cox regression analysis.

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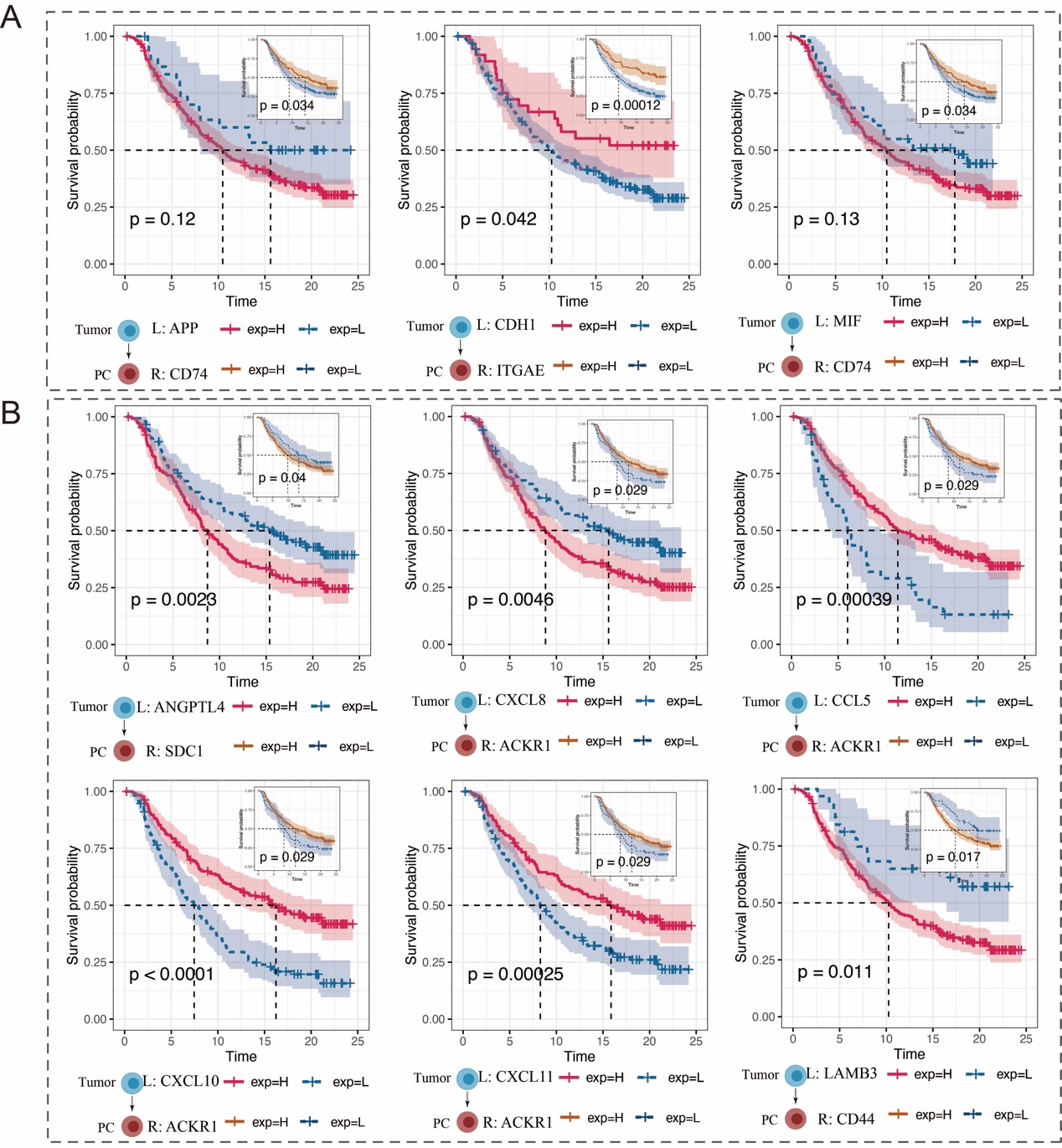
**FIGURE S7|** Cell communication analysis for all cell types. **(A)** The marker genes expression of T cell, myeloid-derived cell (MDC), and mast cell. **(B)** Dot plot shows the incoming and outgoing signal strength in different cell types. **(C)** Crosstalk networks show PCs tend to send signals to T cells and MDCs but receive signals from stromal cells.

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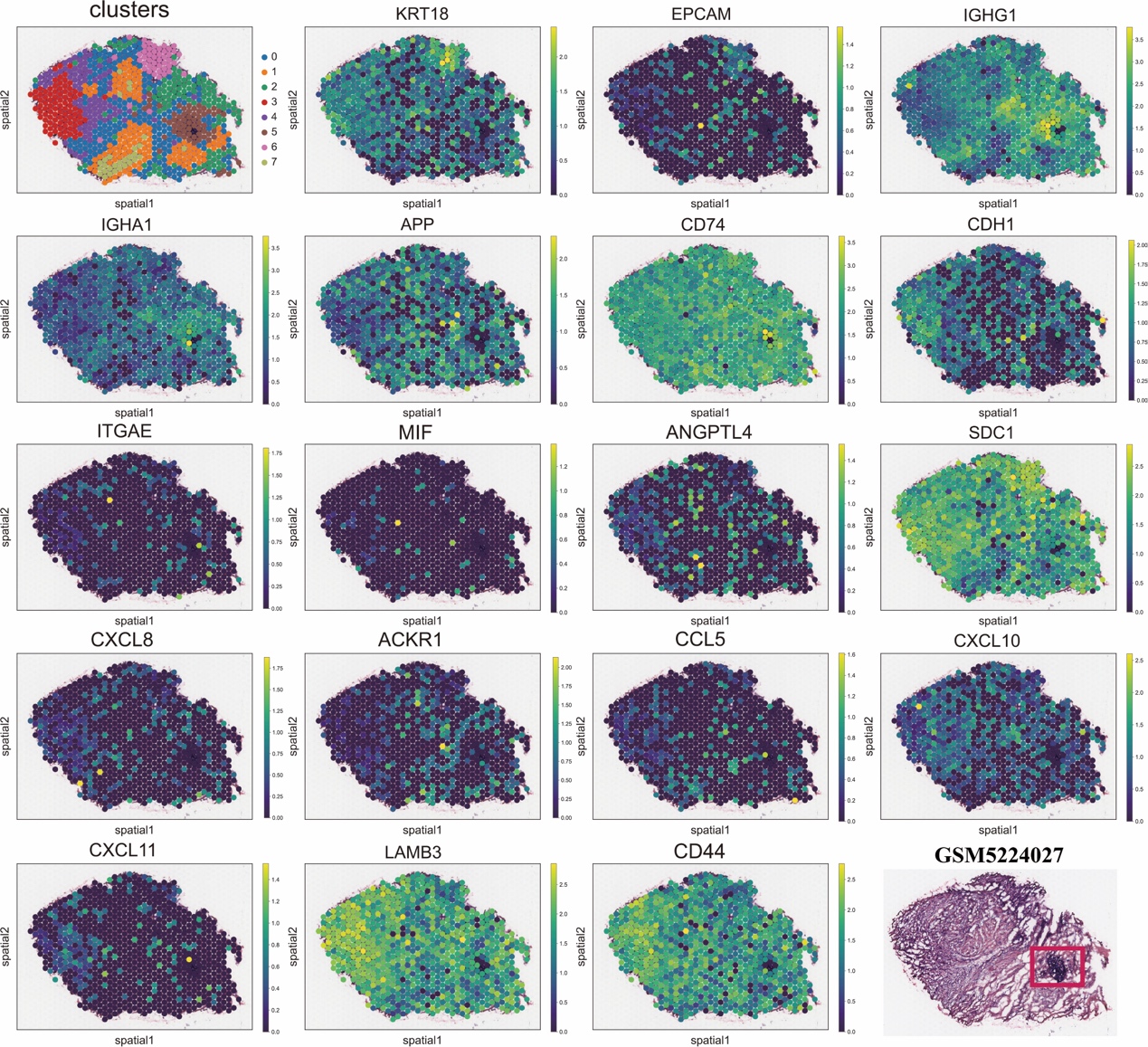
**FIGURE S8|** Signaling pathways enriched in plasma cell-tumor cell communication. **(A&B)** Heat map shows the signaling pathways enriched by each cell type in both incoming and outgoing signaling patterns. **(C-E)** Dot plots show the incoming and outgoing interaction strength of each cell type in MK/MIF signaling and all signaling pathways.



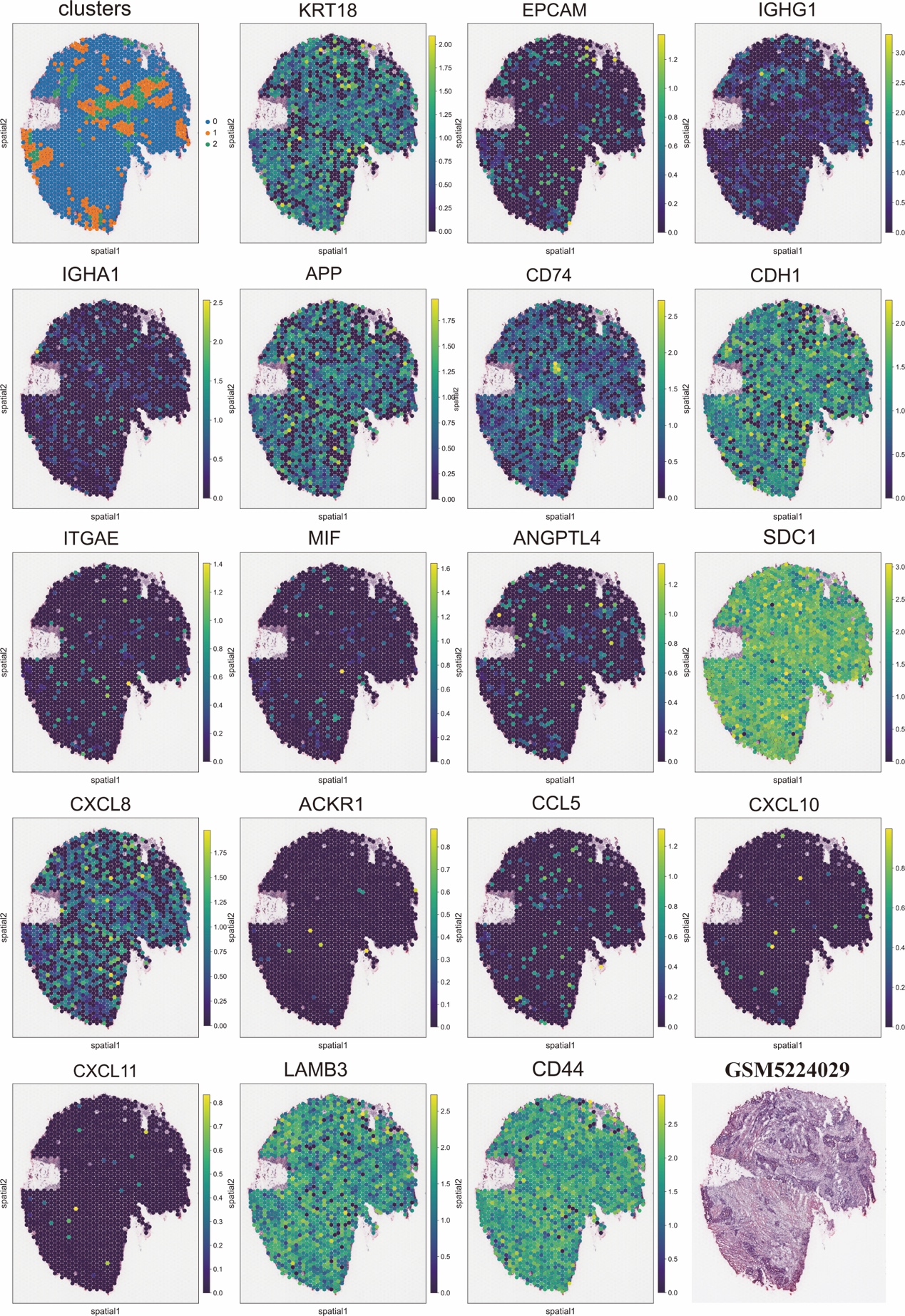
**FIGURE S9|** Comparison of PCs and tumor cell crosstalk in low- and high-grade bladder cancer samples

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**FIGURE S10|** Survival analysis for ligand and receptor. **(A)** Overallsurvival analysis for selected L/R between tumor cells and PCs based on anti-PD-L1 treatment cohort IMvigor210. **(B)** Overallsurvival analysis for selected L/R between tumor cells and IgG1 PCs based on anti-PD-L1 treatment cohort IMvigor210.

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**FIGURE S11|** Spatial transcriptome cell clustering and expression assessment of selected genes based on sample GSM5224027.

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**FIGURE S12|** Spatial transcriptome cell clustering and expression assessment of selected genes based on validation sample GSM5224029.