

# Tumor infiltrating neutrophils are enriched in basal-type urothelial bladder cancer

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## Supplementary Figures

**Supplementary Figure 1** shows HR estimate and 95% CI for OS and PFS

**Supplementary Figure 2** shows hierarchical clustering and gene expression heatmaps of the neutrophil gene signature (TCGA dataset)

**Supplementary Figure 3** shows hierarchical clustering and gene expression heatmaps of the neutrophil gene signature (GSE32894 dataset)

**Supplementary Figure 4** shows hierarchical clustering and gene expression heatmaps of the neutrophil gene signature (GSE124305 dataset)

**Supplementary Figure 5** shows hierarchical clustering and gene expression heatmaps of the chemokine gene signature (TCGA dataset)

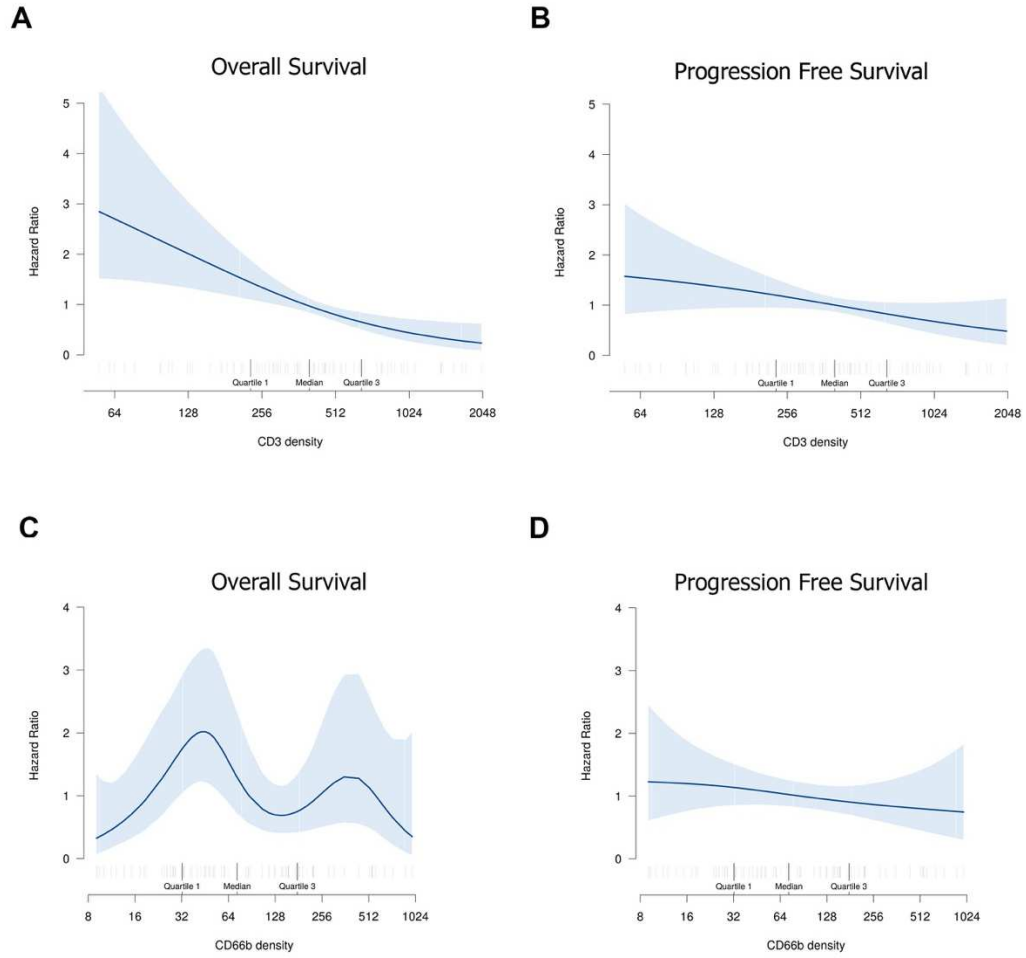
**Supplementary Figure 6** shows hierarchical clustering and gene expression heatmaps of the chemokine gene signature (GSE32894 dataset)

**Supplementary Figure 7** shows hierarchical clustering and gene expression heatmaps of the chemokine gene signature (GSE124305 dataset)

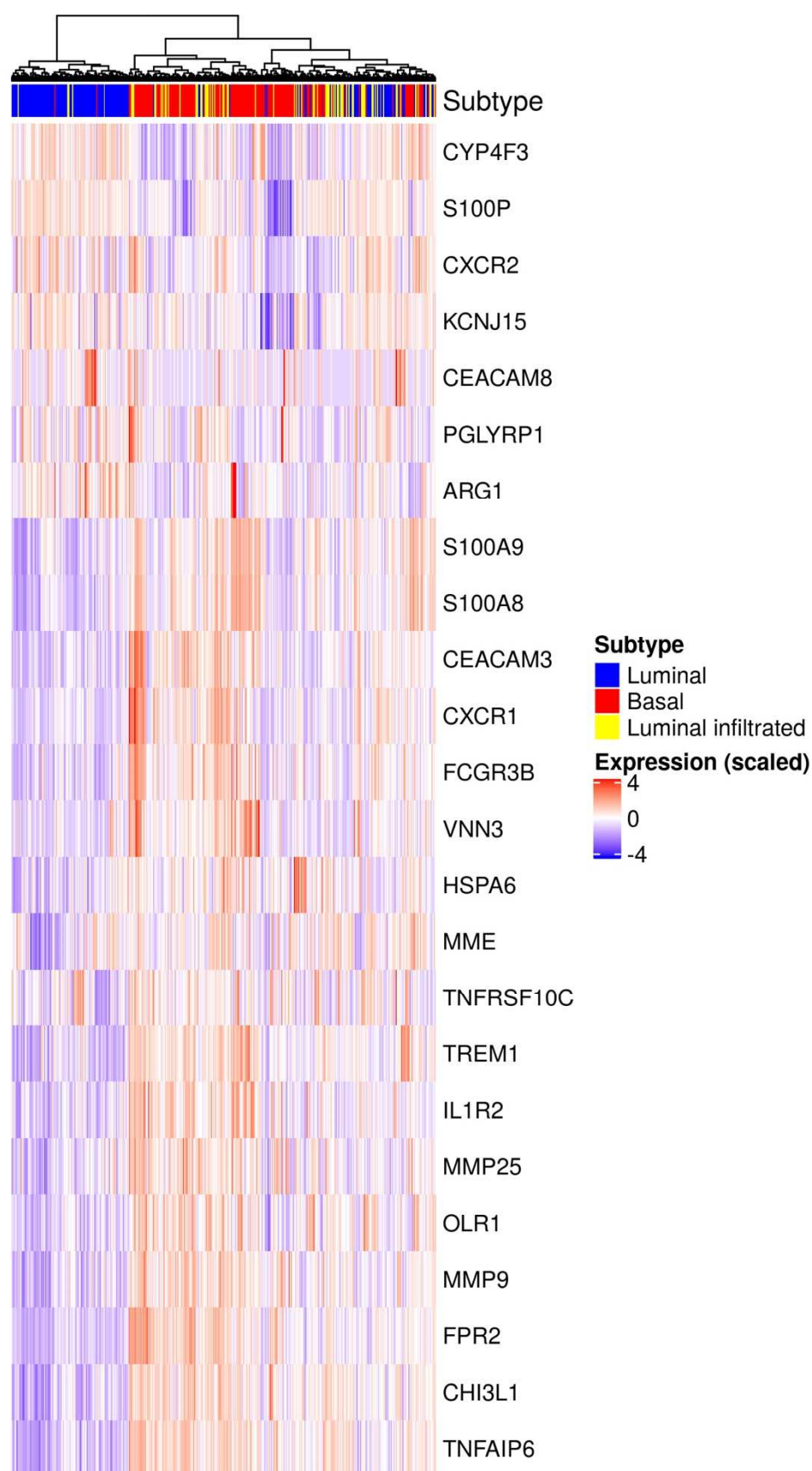
**Supplementary Figure 8** display a Waterfall Plot comparing Basal/Luminal Infiltrated vs Luminal subtype for every Chemokine (TCGA dataset)

**Supplementary Figure 9** display a Waterfall Plot comparing Basal/Infiltrated vs Luminal subtype for every Chemokine (GSE32894 dataset)

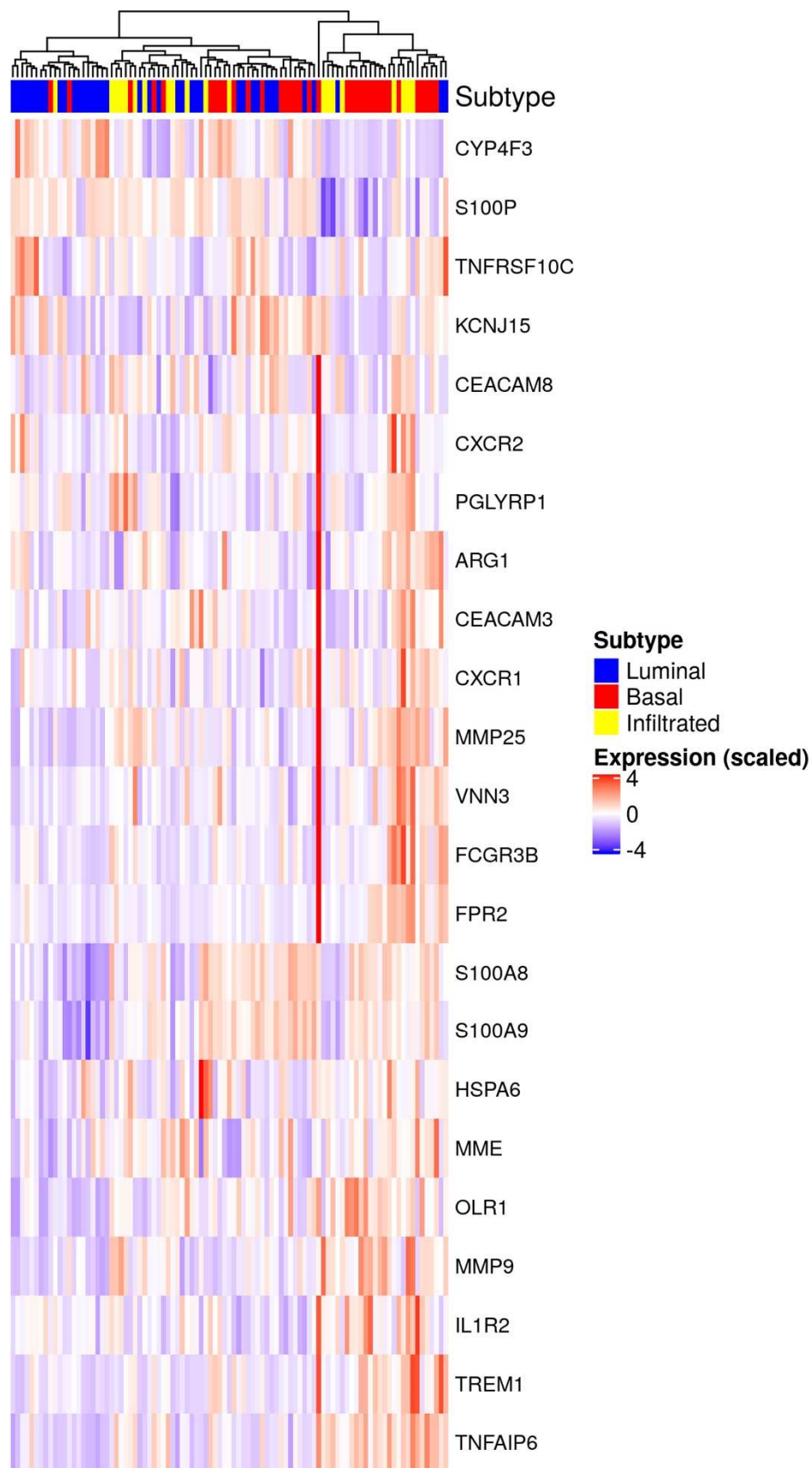
**Supplementary Figure 10** display a Waterfall Plot comparing Basal/Immune vs Luminal subtype for every Chemokine (GSE124305 dataset)



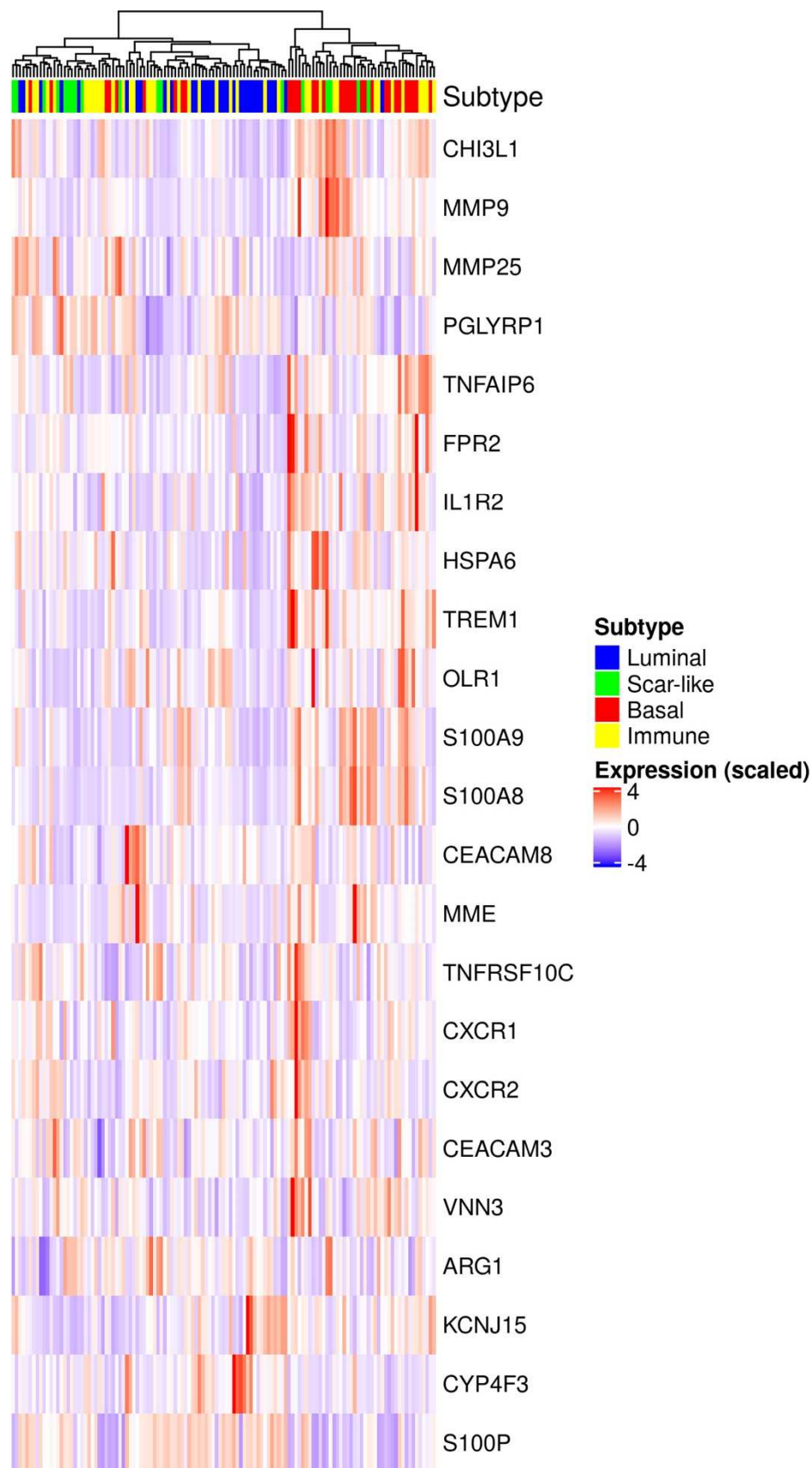
**Supplementary Figure 1.** HR estimate (dark line) and 95% CI (dashed area) for OS and PFS according to CD3<sup>+</sup> T cell density (**A** and **B**) and CD66b<sup>+</sup> TAN density (**B** and **C**), modelled by penalized splines. Reference for HR estimate: mean risk of the whole cohort.



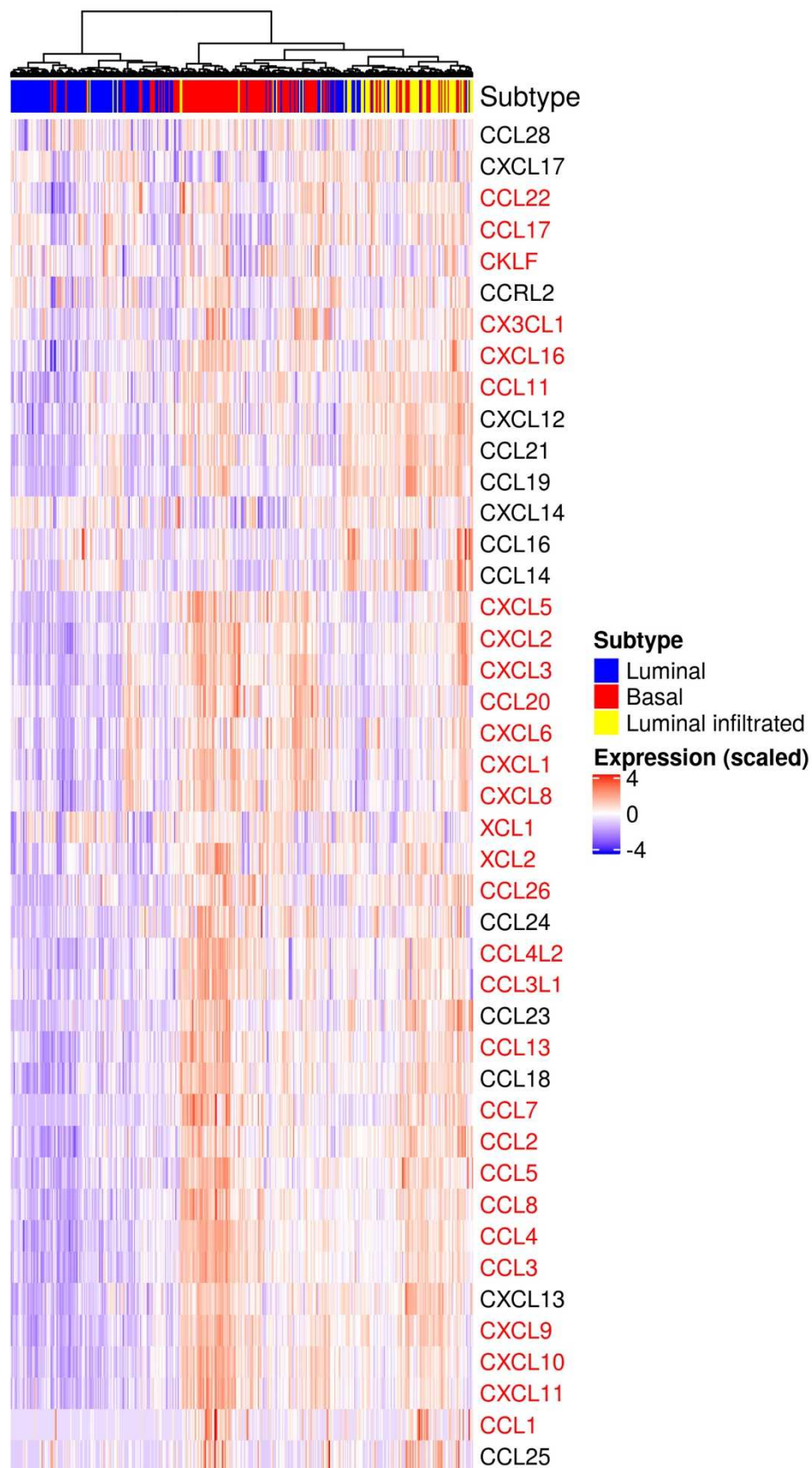
**Supplementary Figure 2.** Hierarchical clustering with gene expression heatmaps for TCGA dataset considering the neutrophil gene signature. Gene-level dendrograms were computed using Euclidean distance while sample-level clustering was based on random forest derived proximity matrix. Both clustering used Ward algorithm. Gene expression values were scaled and mean centered.



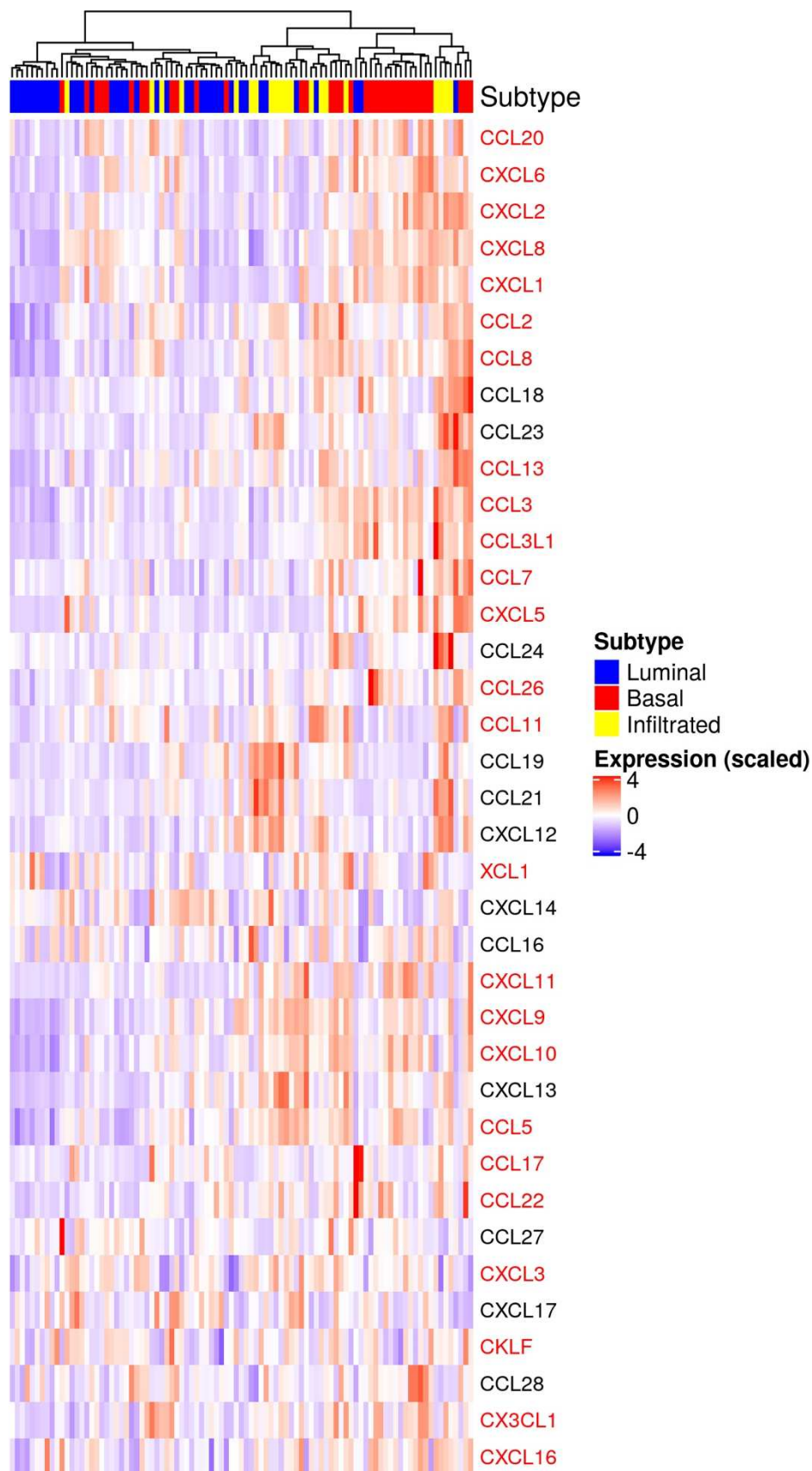
**Supplementary Figure 3.** Hierarchical clustering with gene expression heatmaps for GSE32894 dataset considering the neutrophil gene signature. Gene-level dendrograms were computed using Euclidean distance while sample-level clustering was based on random forest derived proximity matrix. Both clustering used Ward algorithm. Gene expression values were scaled and mean centered.



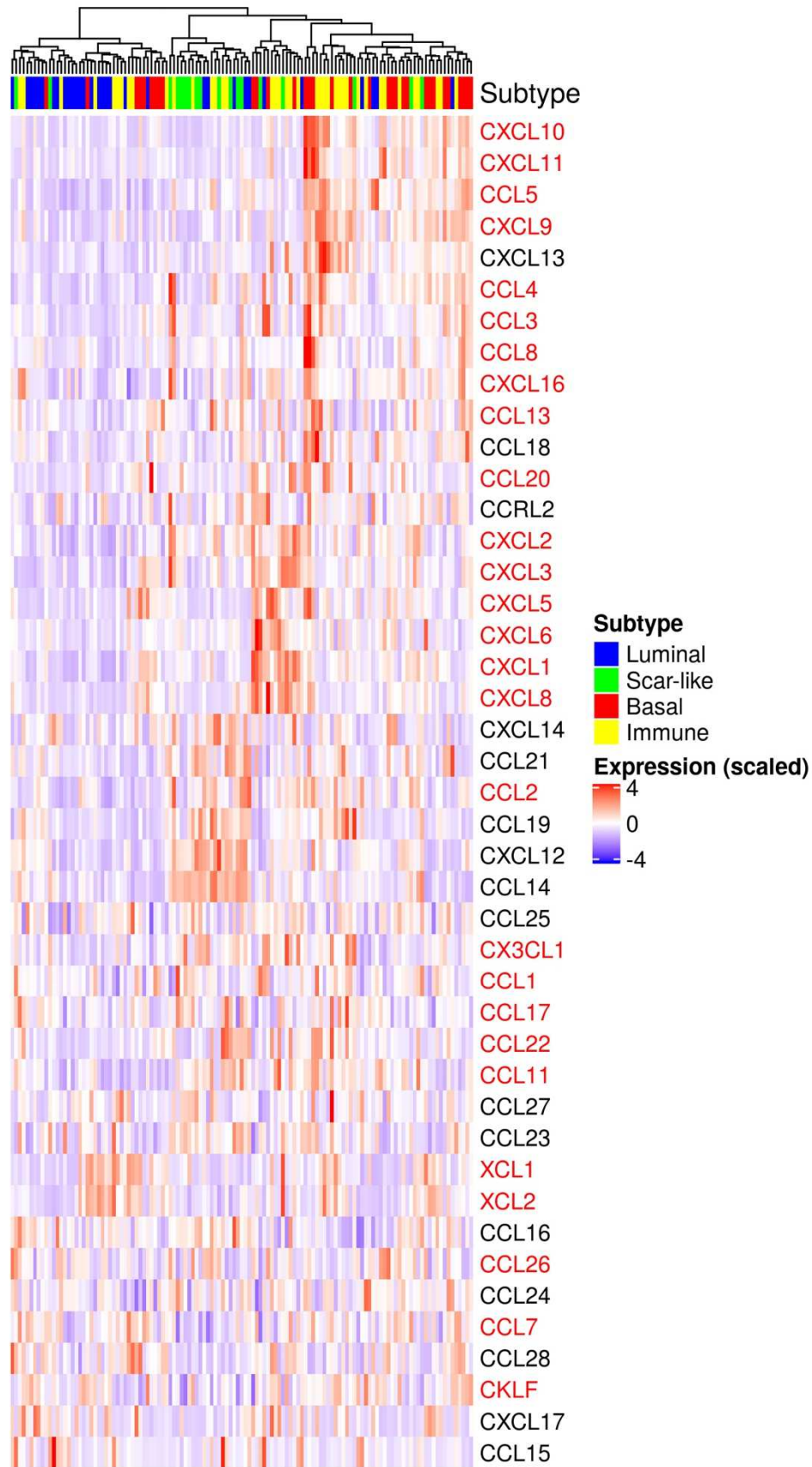
**Supplementary Figure 4.** Hierarchical clustering with gene expression heatmaps for GSE124305 dataset considering the neutrophil gene signature. Gene-level dendrograms were computed using Euclidean distance while sample-level clustering was based on random forest derived proximity matrix. Both clustering used Ward algorithm. Gene expression values were scaled and mean centered.



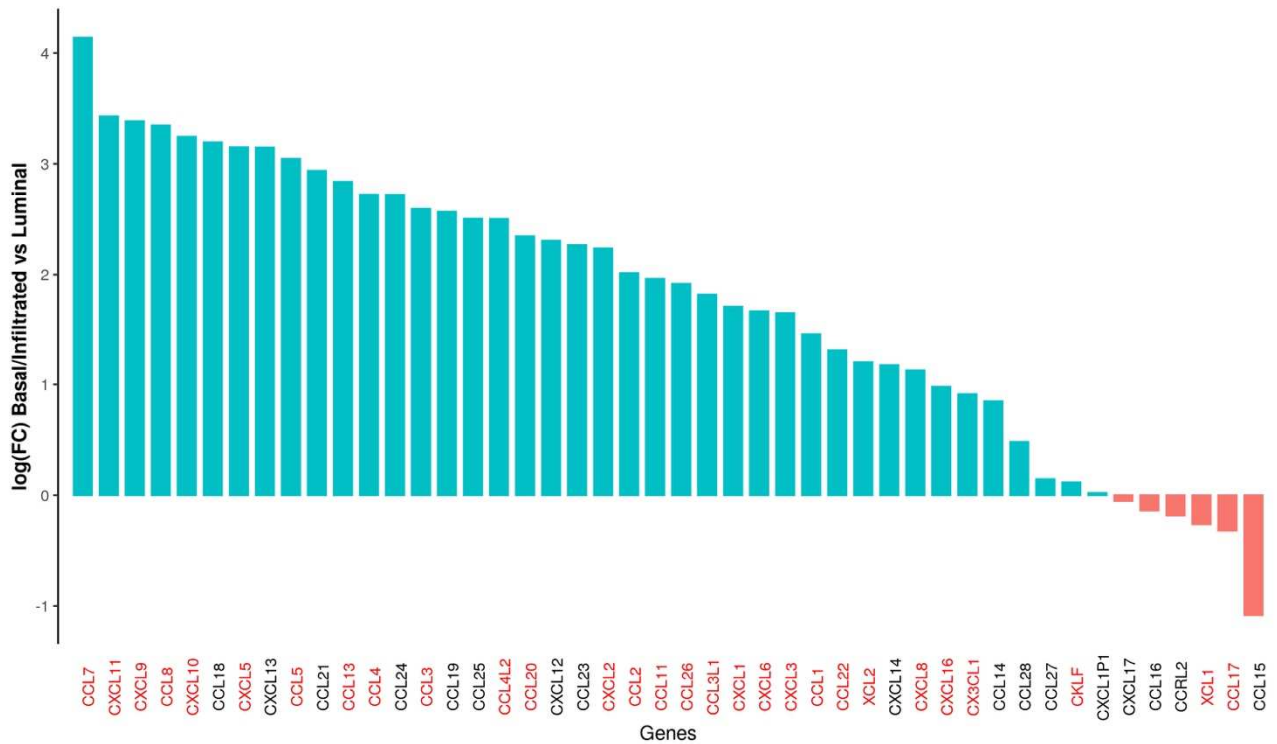
**Supplementary Figure 5.** Hierarchical clustering with gene expression heatmaps for TCGA dataset considering the chemokine gene signature. Both gene-level and sample-level dendrograms were computed using Euclidean distance and Ward algorithm. Gene expression values were scaled and mean centered. Chemokines with pro-inflammatory functions are labeled in red.



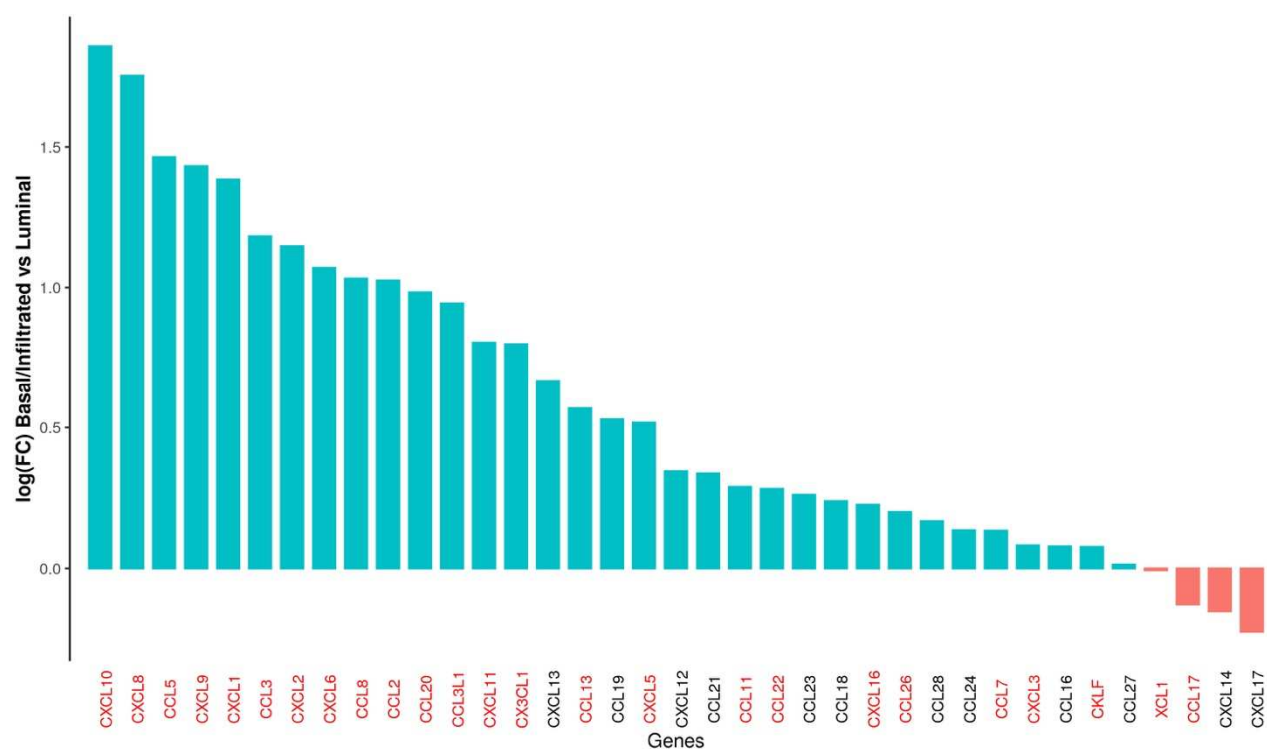
**Supplementary Figure 6.** Hierarchical clustering with gene expression heatmaps for GSE32894 dataset considering the chemokine gene signature. Both gene-level and sample-level dendrograms were computed using Euclidean distance and Ward algorithm. Gene expression values were scaled and mean centered. Chemokines with pro-inflammatory functions are labeled in red.



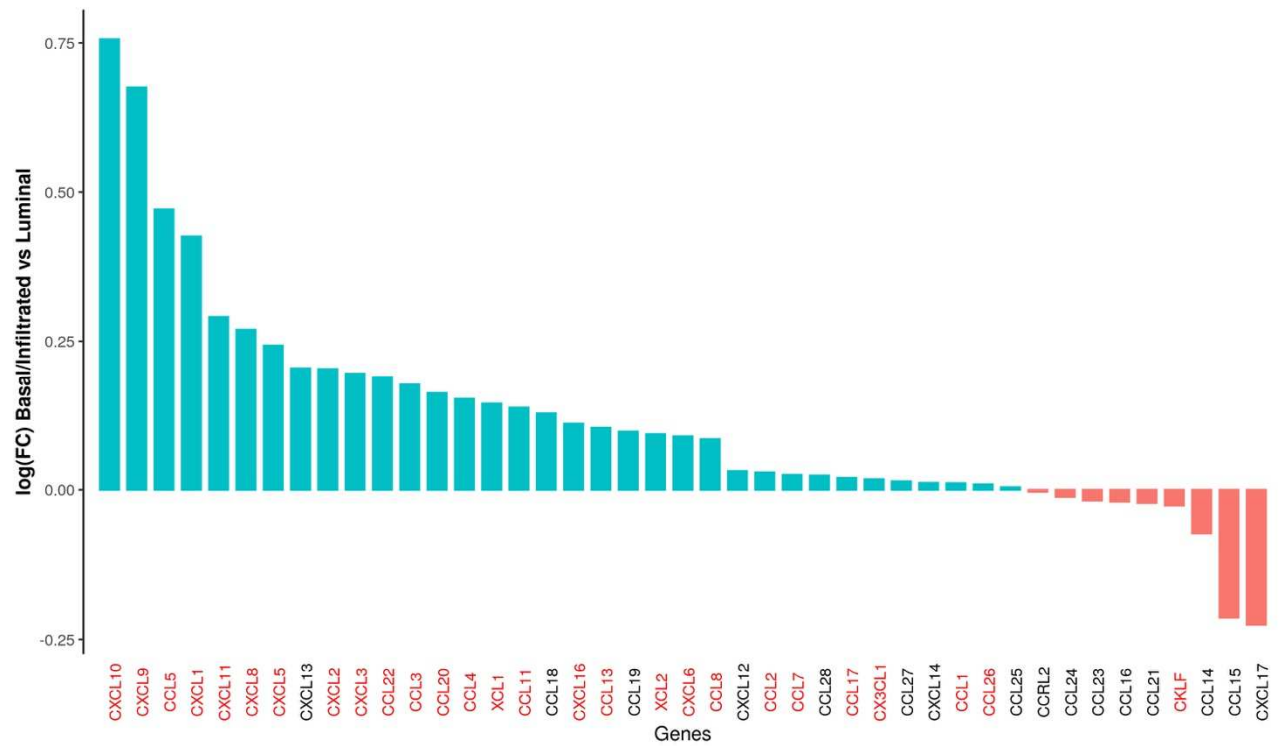
**Supplementary Figure 7.** Hierarchical clustering with gene expression heatmaps for GSE124305 dataset considering the chemokine gene signature. Both gene-level and sample-level dendrograms were computed using Euclidean distance and Ward algorithm. Gene expression values were scaled and mean centered. Chemokines with pro-inflammatory functions are labeled in red.



**Supplementary Figure 8.** Waterfall plots showing Fold Change values (on log<sub>2</sub> scale) comparing Basal/Infiltrated vs Luminal subtype for every Chemokine of the signature in TCGA dataset. Chemokines with pro-inflammatory functions are labeled in red.



**Supplementary Figure 9.** Waterfall plots showing Fold Change values (on log<sub>2</sub> scale) comparing Basal/Infiltrated vs Luminal subtype for every Chemokine of the signature in GSE32894 dataset. Chemokines with pro-inflammatory functions are labeled in red.



**Supplementary Figure 10.** Waterfall plots showing Fold Change values (on log<sub>2</sub> scale) comparing Basal/Infiltrated vs Luminal subtype for every Chemokine of the signature in GSE124305 dataset. Chemokines with pro-inflammatory functions are labeled in red.