

Article title:

Integration of bulk and single-cell transcriptomic sequencing reveals the neutrophil heterogeneity in bladder cancer and establishes a prognostic model

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Fig. S1 Integration of datasets, T/NK cell characterization, myeloid cell quality control, and neutrophil subtypes survival analysis in BLCA

(a) UMAP plot of all cells grouped by tissue type (tumor tissue and urine samples from BLCA patients). (b) Stacked bar plots of the proportional abundance of major cell types in tumor tissue and urine samples. (c) UMAP plot of T/NK cells grouped by subtypes. (d) Dot plot showing the marker genes used to annotate the T and NK cell subtypes. (e) Violin plot showing the number of detected genes (nFeature) per cell across myeloid cell subtypes (f, g, and h) Kaplan-Meier survival curves of Neu_1, Neu_2, and Neu_3 infiltration in the TCGA-BLCA cohort.

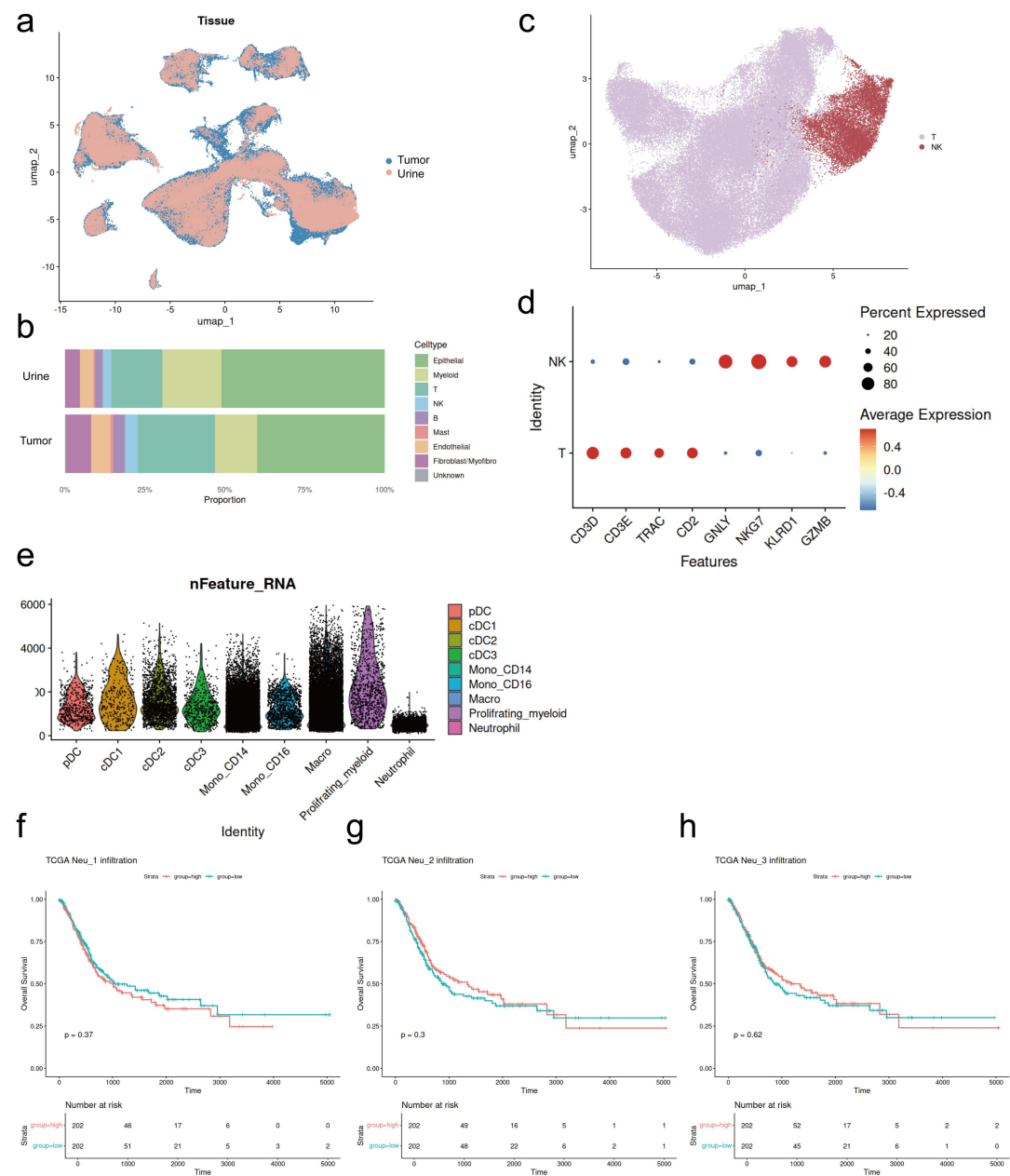


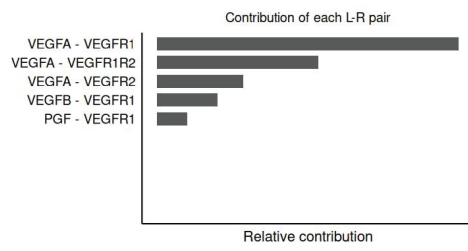
Fig. S2 Supplemental information on cell-cell communication

(a) Circle plots showing the number of outgoing interactions from neutrophil subtypes to other cell types. (b) Bar plot of the relative contributions of individual VEGF ligand-receptor pairs. (c, d, and e) Circle plots of the VEGFA interaction network with its receptor pairs.

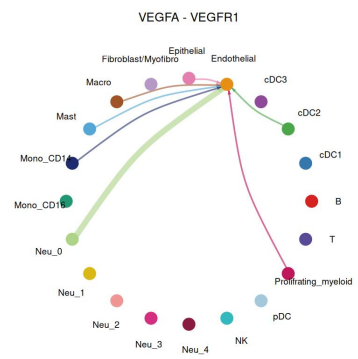
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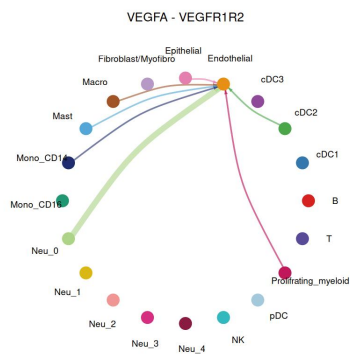
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d



e

