**Single-cell transcriptome analysis**

Single-cell RNA-seq data was pre-processed with the scater (1) and normalized by scran (2). Data integration, unsupervised cell clustering, and differential expression analysis were carried out by the Seurat v3.0 (3). Reference-based cell type annotation was generated by SingleR (4).

Cells with more than 3 median absolute deviation were removed as outliers. Cells with less than 800 genes or 1500 UMIs or more than 15% of mitochondria genes were filtered out from the analysis. Altogether, the filtered data contained 27,998 cells and 24,421 genes from 6 samples. Cell-specific biases were normalized with pool-based size factors. The top 3000 highly variable genes were selected using the expression and dispersion (variance/mean) of genes, followed by a canonical correlation analysis (CCA) to identify common sources of variation between the patient and normal datasets. The first 105 CCA results were chosen to generate dimensional t-Distributed Stochastic Neighbor Embedding (tSNE) plots, Uniform Manifold Approximation and Projection (UMAP) plots, and cell clustering by a shared nearest neighbor (SNN) modularity optimization based clustering algorithm.

Cell types were manually identified by marker genes (5), and confirmed by SingleR (Single-cell Recognition) package using 358 mouse RNA-seq (4). Differential expression analysis was performed based on the MAST (Model-based Analysis of Single Cell Transcriptomics) (6).

**Code availability.** The scripts used for analysis and figure generation are available at https://github.com/nyuhuyang/scRNAseq-BladderCancer

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