

Integrative Transcriptome Profiling Reveals Prognostic Marker in Non-Muscle Invasive Bladder Cancer

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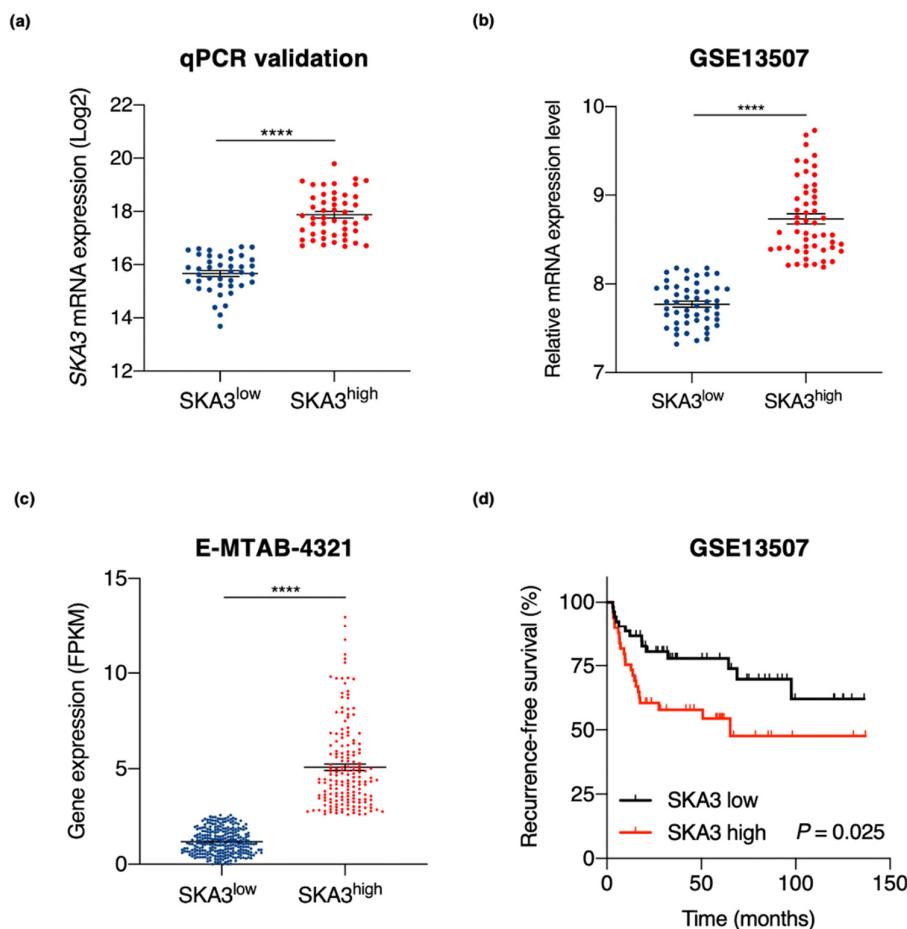


Figure S1. SKA3 predicts poor clinical outcome. (a) SKA3 expression levels of SKA3 high ($n=48$) and SKA3 low ($n=41$) groups in qPCR validation cohort; (b) SKA3 expression levels of SKA3 high ($n=50$) and SKA3 low ($n=53$) groups in GSE13507 cohort; (c) SKA3 expression levels of SKA3 high ($n=225$) and SKA3 low ($n=225$) groups in E-MTAB-4321 cohort; (d) NMIBC Patients were divided into two groups, lower 50th percentile ($n=50$, 14 of them recurred) and upper 50th percentile groups ($n=53$, 22 of them recurred), according to the mRNA expression level of SKA3 in GSE13507 cohort. The recurrence-free survival rate of NMIBC patients was significantly higher in the low SKA3 expression group (log-rank test, $p < 0.05$). NMIBC, non-muscle invasive bladder cancer; RFS, recurrence-free survival. Error bar: mean value with SEM. p values were determined by Welch's t -test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

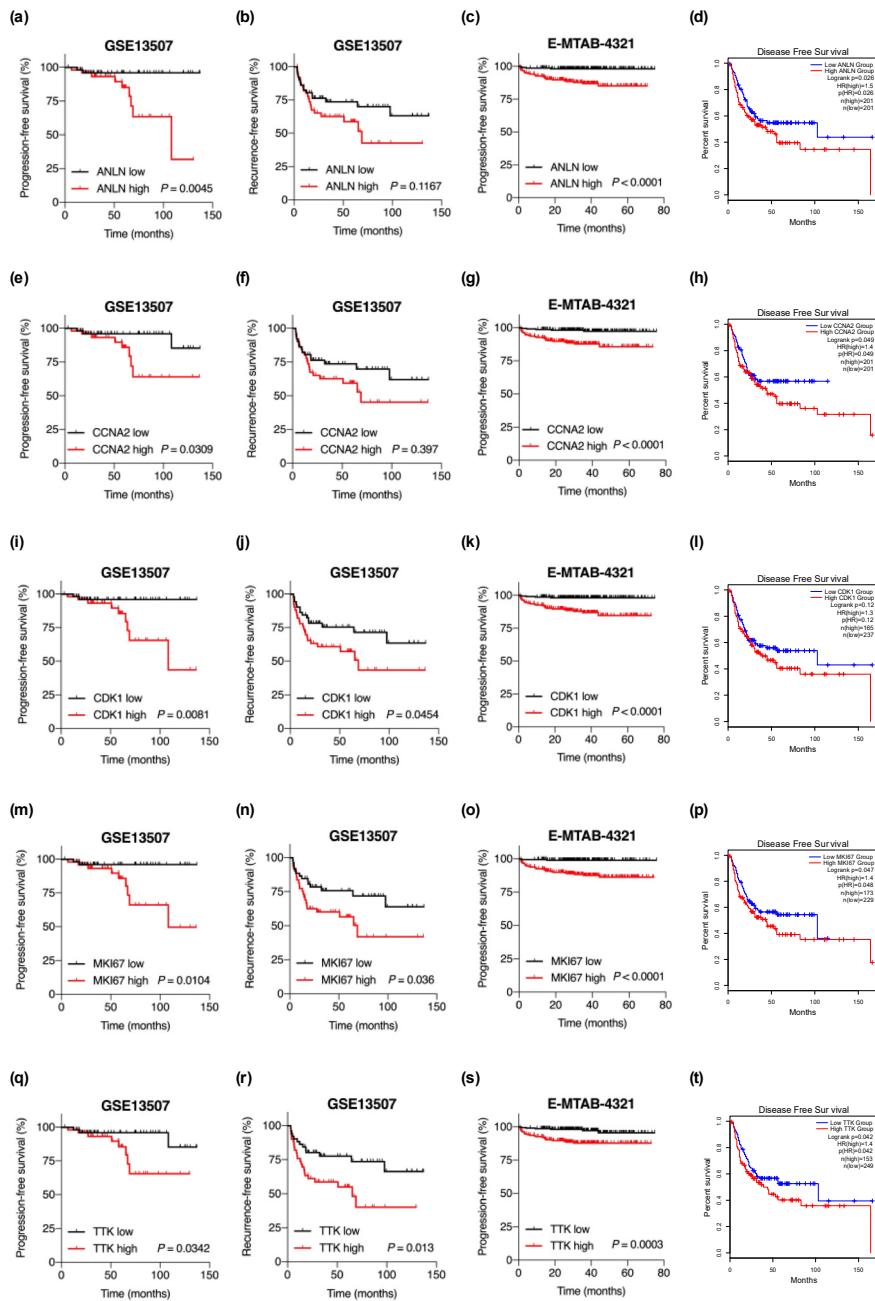


Figure S2. Survival analysis for the expression of candidate genes in patients with bladder cancer. **(a-d)** Kaplan-Meier survival analysis in two groups according to the mRNA expression level of ANLN in multiple cohorts; **(e-h)** Kaplan-Meier survival analysis in two groups according to the mRNA expression level of CCNA2 in multiple cohorts; **(i-l)** Kaplan-Meier survival analysis in two groups according to the mRNA expression level of CDK1 in multiple cohorts; **(m-p)** Kaplan-Meier survival analysis in two groups according to the mRNA expression level of MKI67 in multiple cohorts; **(q-t)** Kaplan-Meier survival analysis in two groups according to the mRNA expression level of TTK in multiple cohorts.

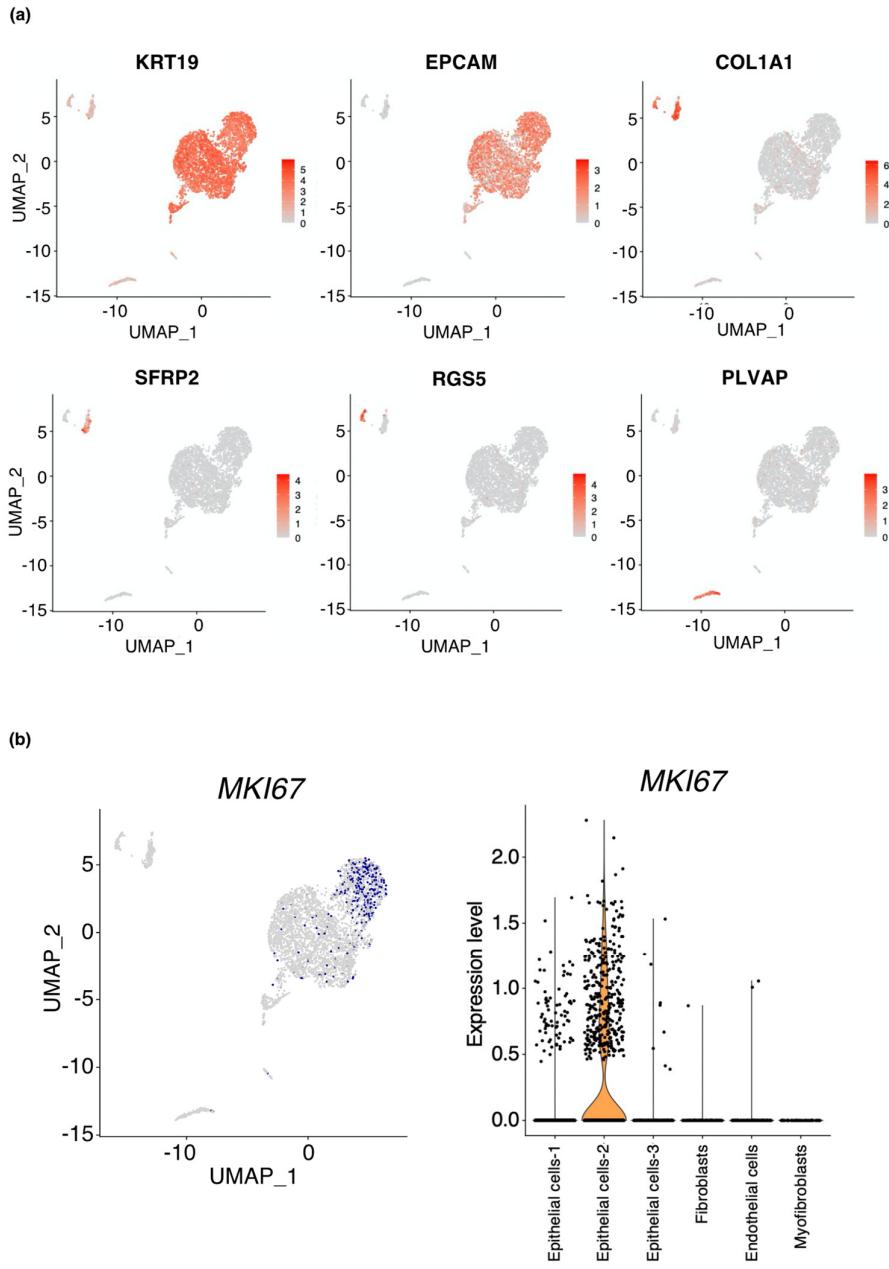


Figure S3. Analysis of public single-cell RNA sequencing data of bladder cancer. (a) Feature plots of the characteristic markers for all cell types and their expression levels analyzed by Seurat; (b) UMAP plot and violin plot displaying the expression of *MKI67* in all cell clusters in bladder cancer patients.

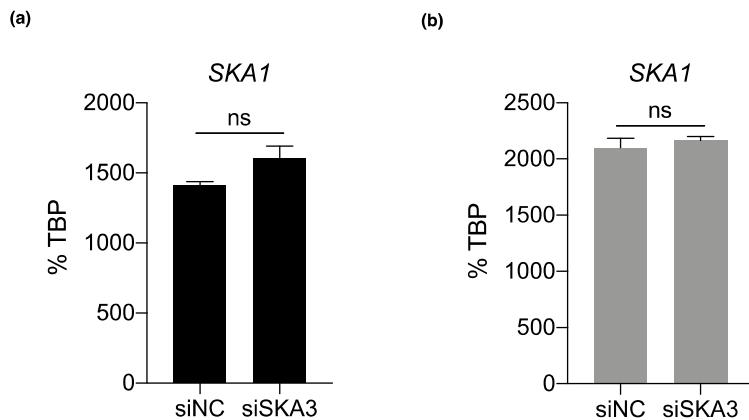


Figure S4. Knockdown of SKA3 in bladder cancer cell lines by siRNA transfection. SKA1 expression levels were analyzed by RT-qPCR in 5637 cell line (a) and T24 cell line (b). Error bar: mean value with SEM. p values were determined by Welch's t -test.