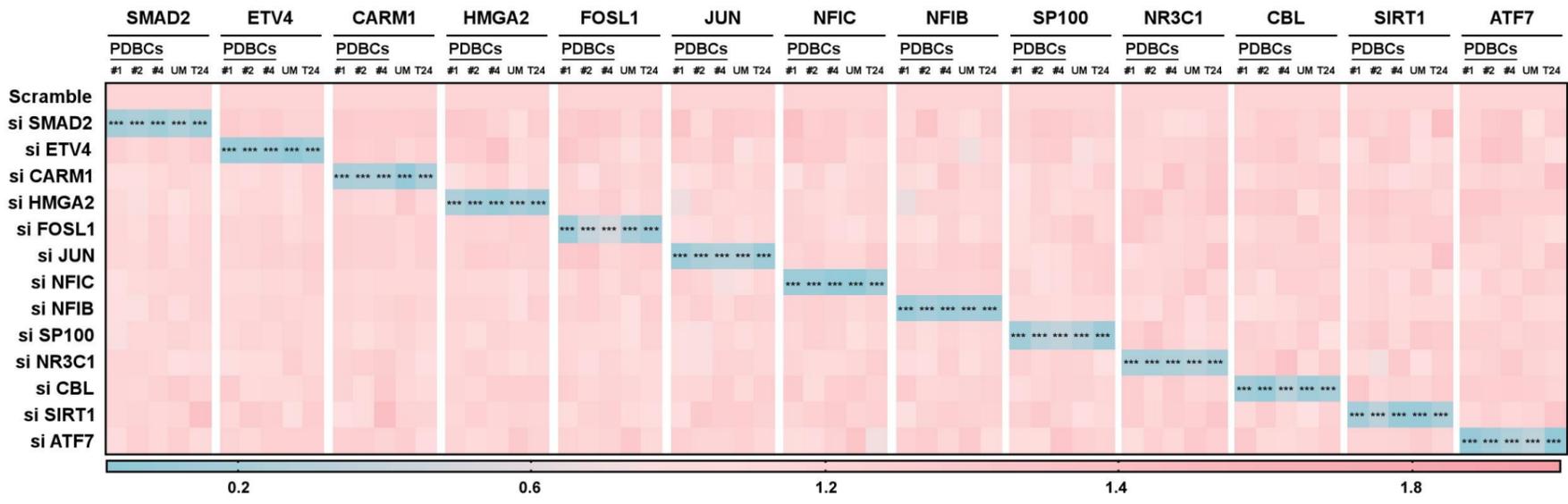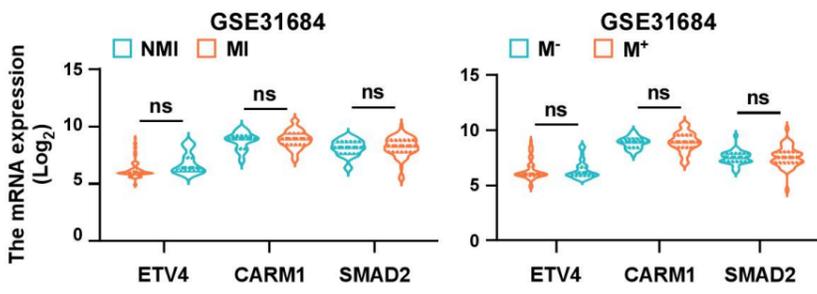**Supplementary Fig. S5. Upregulated TGFβ3 and TβRI was significantly correlated with OS and RFS of bladder cancer patients. (a)** Real-time PCR analysis of the mRNA expression of *RNAPII*, *SMAD2*, *ETV4*, *CARM1*, *PAF1*, *CTR9*, *MRPS27*, *HSF1* and *NF1* in the indicated PDBCs. *GAPDH* served as the loading control. **(b)** The mRNA expression of *SMAD2*, *ETV4*, *CARM1* and *PAF1* in MIBC (n = 78) versus NMIBC (n = 15) tissues, metastatic-bladder cancer (M$^+$/BLCA, n = 47) versus non-metastatic bladder cancer tissues (M$^-$/BLCA, n = 35) based on GSE31684 datasets. **(c)** Elevated expression of *TGFβ3* and *TGFR1* mRNA in MIBC (n = 78) and metastatic-bladder cancer (M$^+$/BLCA, n = 47) compared to NMIBC (n = 15) and non-metastatic bladder cancer tissues (M$^-$/BLCA, n = 35) based on GSE31684 datasets, respectively. **(d-f)** Kaplan–Meier survival analysis of the correlation of *TGFβ3* and *TGFβR1* mRNA level with the overall, and metastasis-free survival in bladder cancer patients according to the datasets TCGA-BLCA, GSE13507 and GSE48075. **(g)** IB analysis of TGFβ3 expression in the bladder cancer cell lines (left) and NMI-PDBC or MI-PDBC cells (right). GAPDH served as the loading control. Each error bar in a, h, i, k and e represents the mean ± SD of three independent experiments. Statistical analysis was performed using unpaired two-tailed t tests for (a-c) and Kaplan-Meier method for (d-f). $*P < 0.05$; $**P < 0.01$; $***P < 0.001$; ns, not significant.
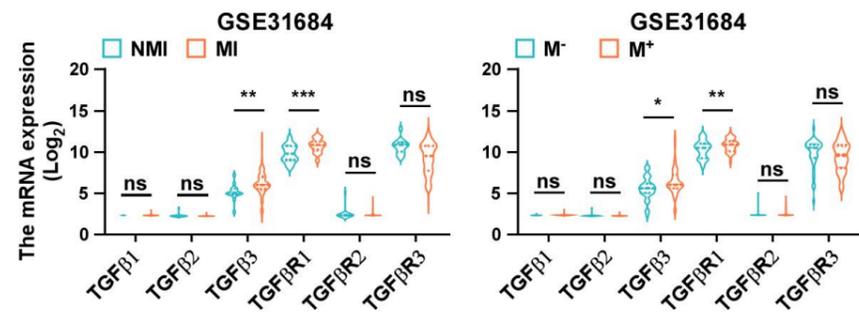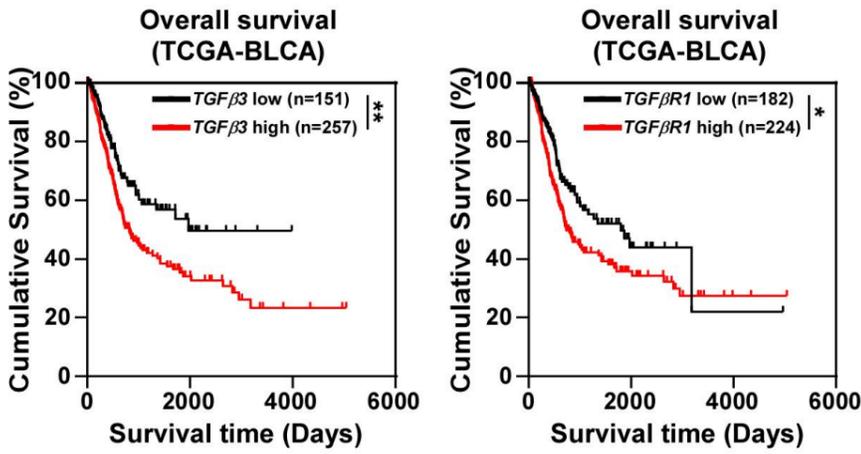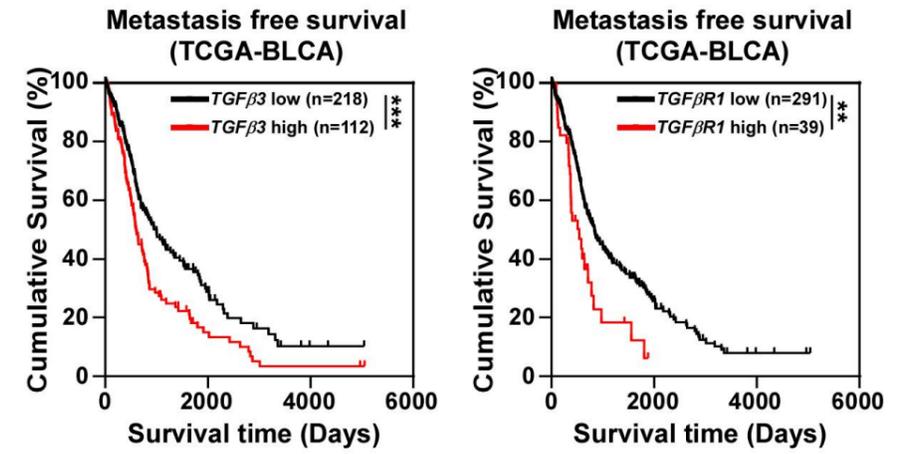
Supplementary Fig. S5

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