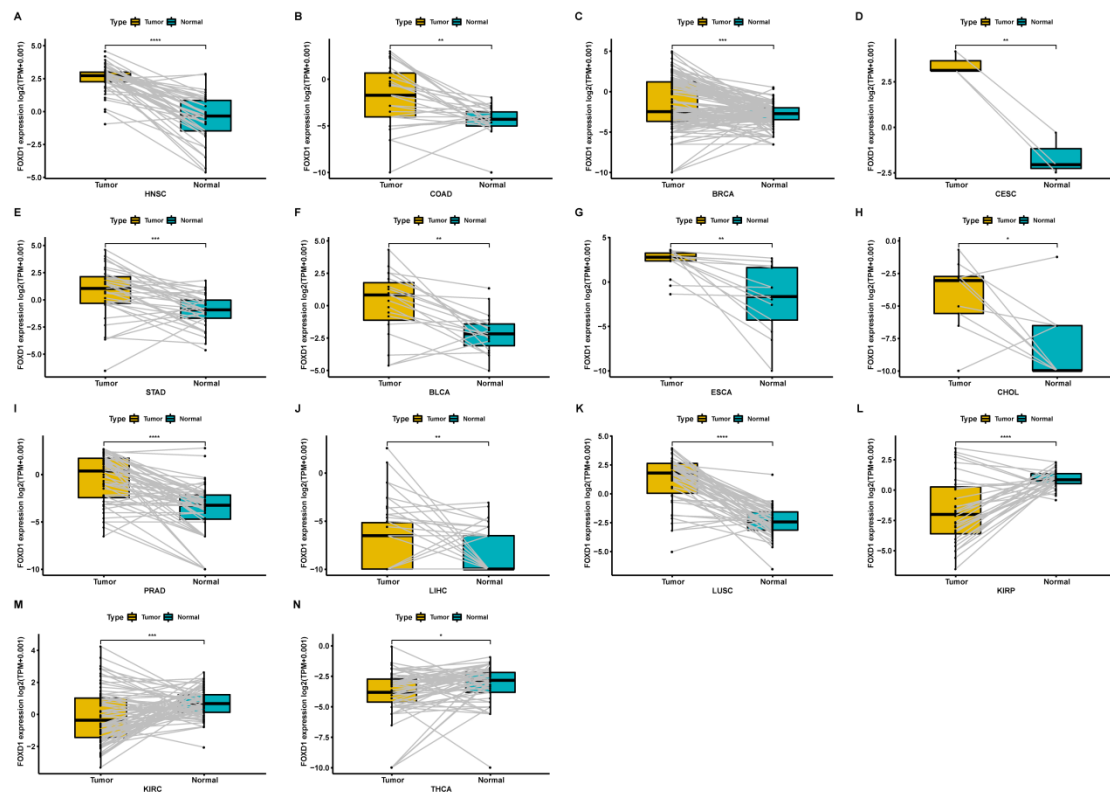
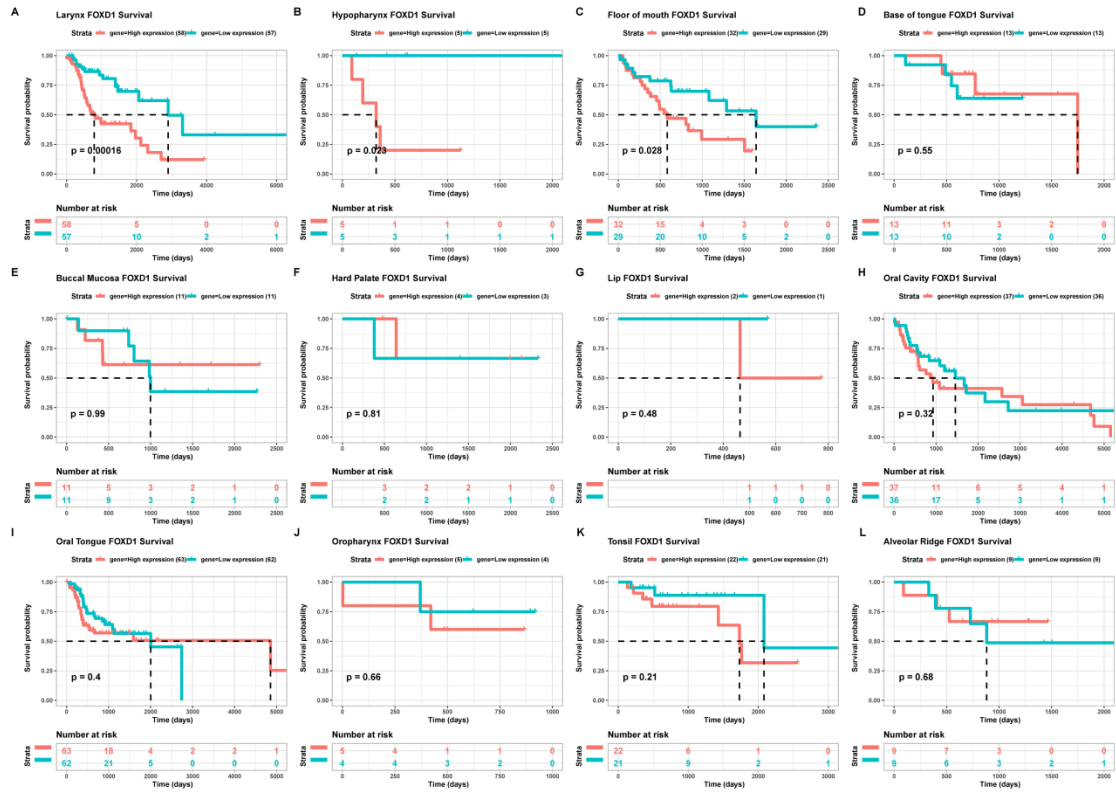


Supplementary figure legends

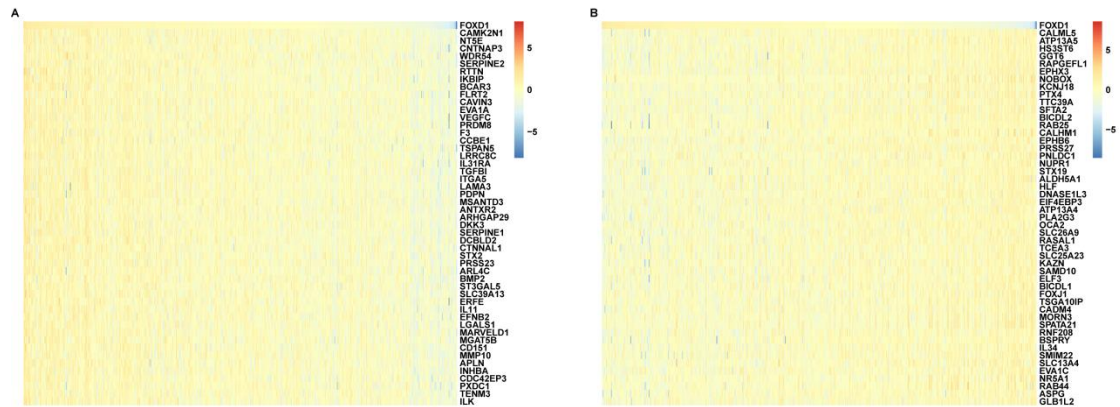


Sup-Figure 1: Pan-cancer FOXD1 expression analysis in paired tumor and normal tissues in TCGA. (A-N), FOXD1 expression in indicated paired tumor and normal tissues in pan-cancer data of TCGA. Gray lines connect paired tissues. Data were shown as mean \pm SD. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001.



Sup-Figure 2: Correlation analysis of FOXD1 in HNSC.

(A-L) Kaplan–Meier analysis of OS in 16 various tumor locations of HNSC, group division was based on the median of FOXD1 expression.



Sup-Figure 3: Correlation analysis of FOXD1 in HNSC.

(A), Top 50 genes most positively associated with FOXD1 were shown in heatmap.

(B), Top 50 genes most negatively associated with FOXD1 were shown in heatmap.