

Supplementary figures and tables legend

Figure S1: Unsupervised hierarchical clustering analysis of the differentially expressed lncRNAs between prostate cancer and normal tissues.

Figure S2: Enrichment analysis histogram of GO terms for 4-lncRNAs-related PCGs.

Figure S3: KEGG enrichment pathway maps for 4-lncRNAs-related PCGs:(A)Hippo signaling pathway,(B)Focal adhesion and (C)Cell adhesion molecules (CAMs).

Figure S4: KEGG enrichment pathways histogram for 4-lncRNAs-related PCGs.

Table S1: Differentially expressed lncRNAs

Table S2: Univariate Cox regression result

Table S3: Survival risk grouping of all prostate cancer patients. *fuptime: survival time; *fustat: survival state(0: alive, 1: dead); *riskScore: the value of risk score per patient assessed according to our 4-lncRNA model.

Table S4: Enrichment analysis of GO terms for 4-lncRNAs-related PCGs.

Table S5: Enrichment analysis of KEGG pathways for 4-lncRNAs-related PCGs.