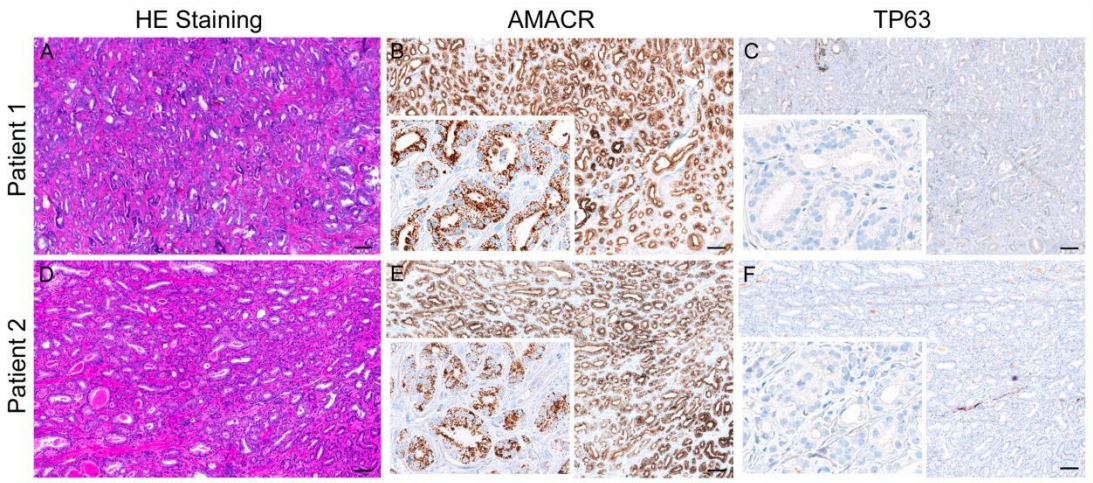
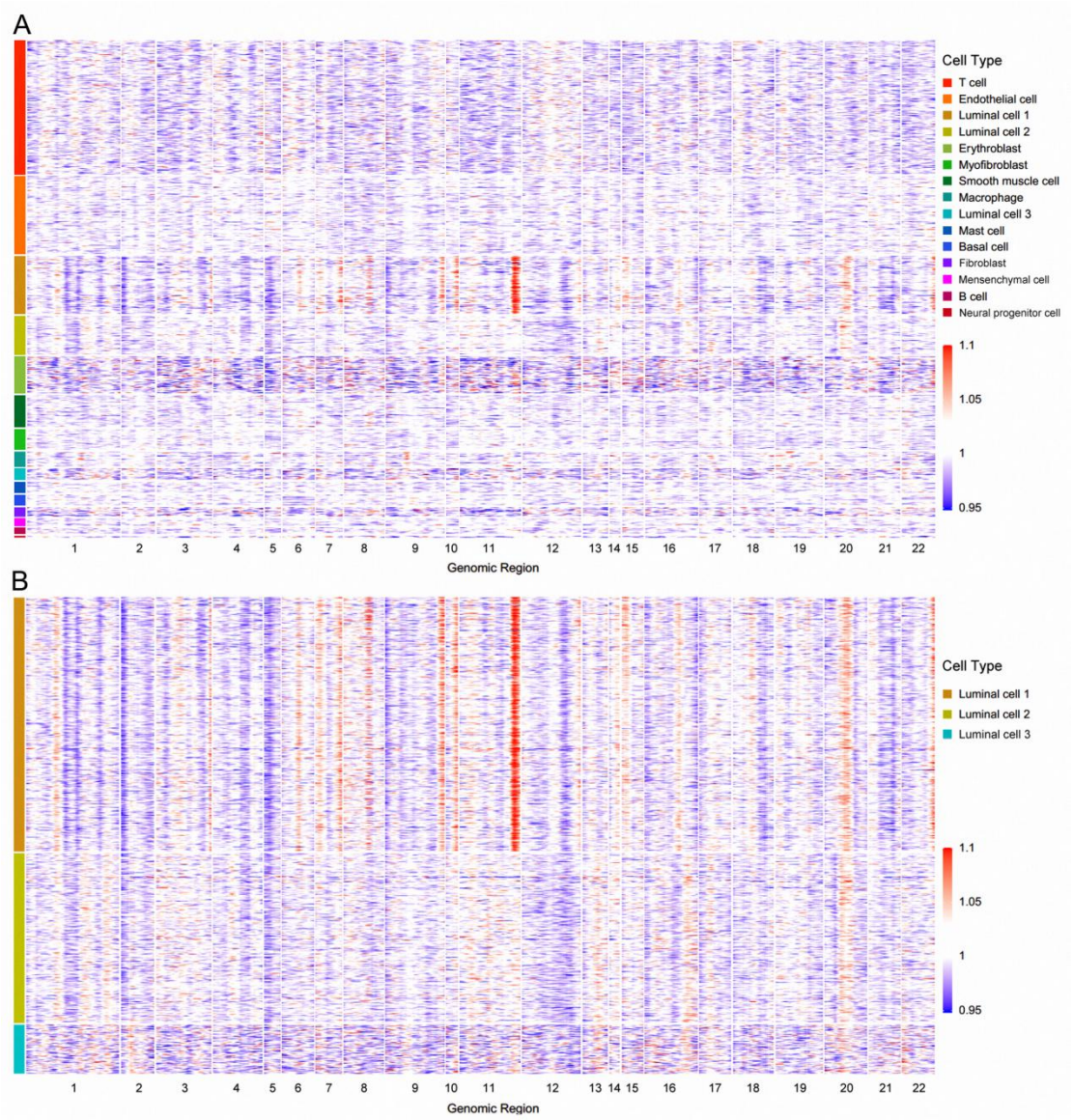
Supplementary Fig. 1



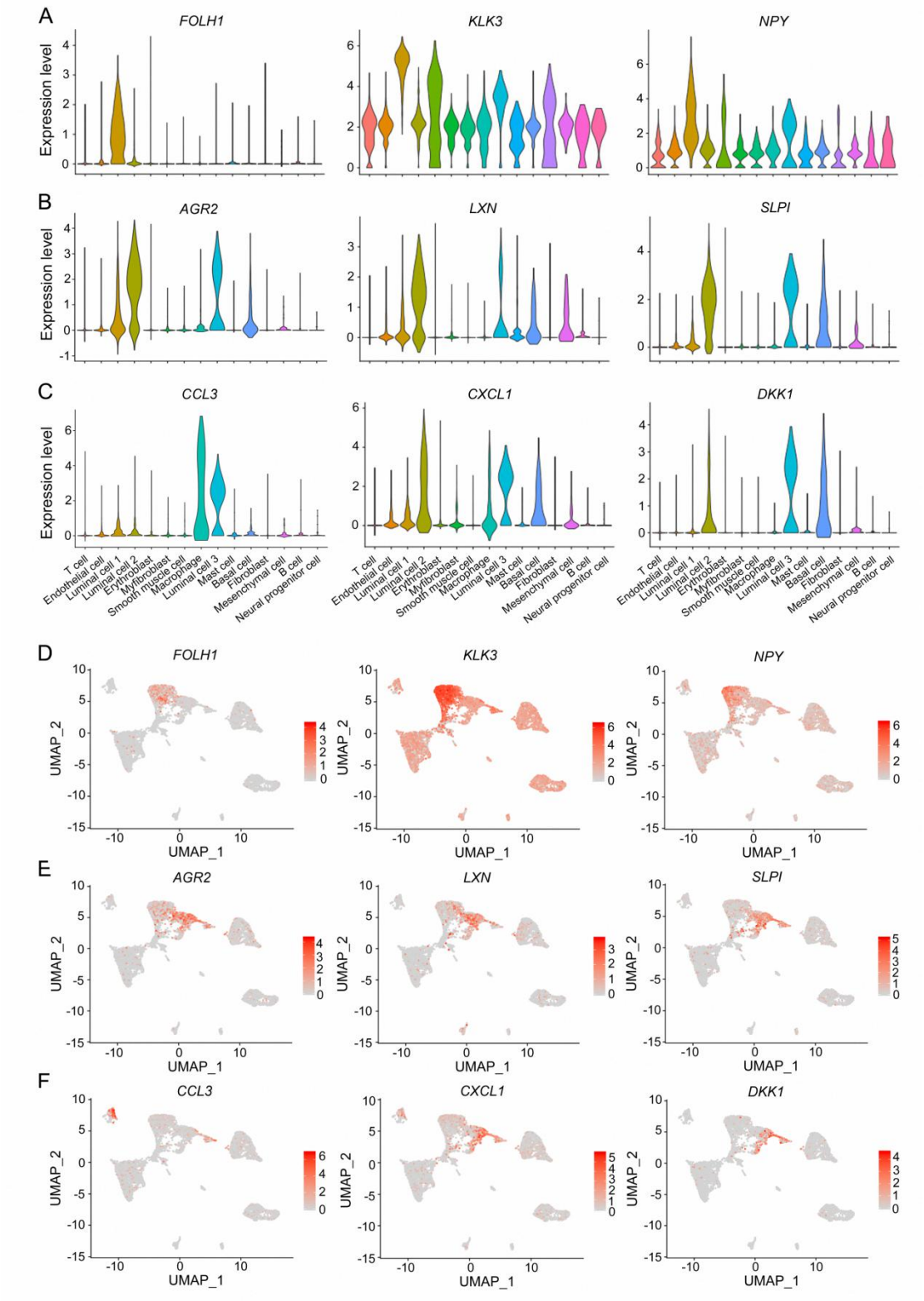
PCa pathology grading diagnosis by histology observation and the expression of AMACR and TP63. A, D HE staining of PCa tissues. **B, E** Immunostaining of AMACR on PCa tissues. **C, F** Immunostaining of TP63 on PCa tissues. Bar = 50 μm.

Supplementary Fig. 2



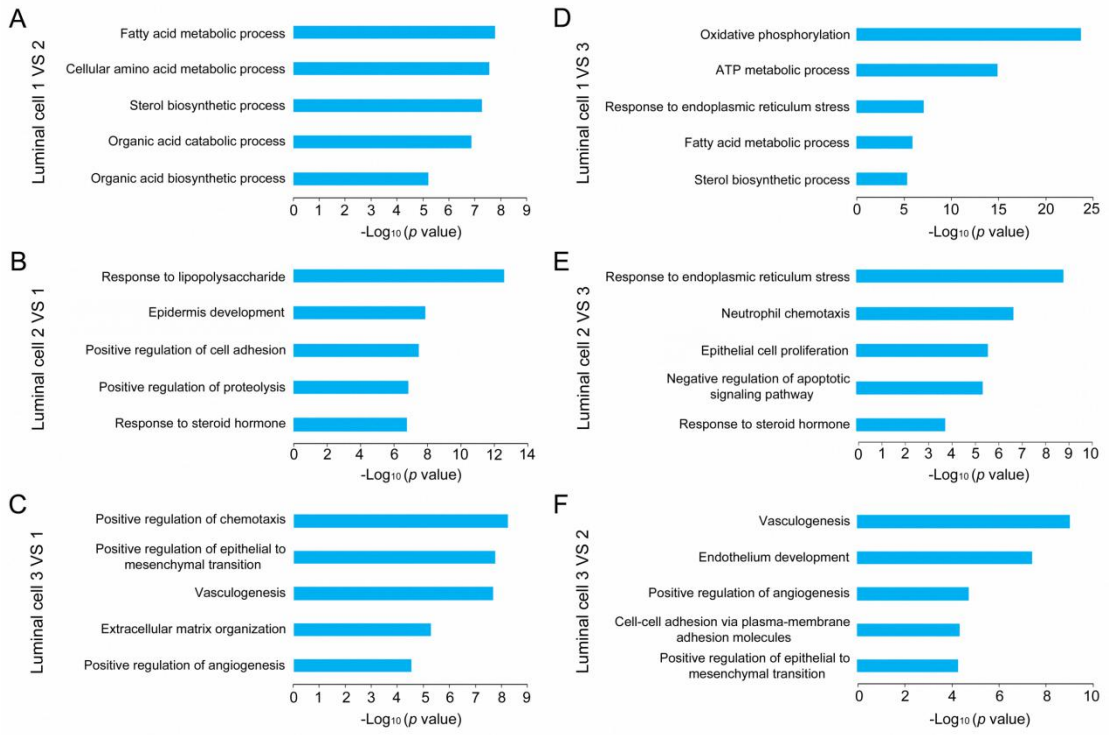
CNV analysis of different type of cells in PCa tissues. A All clusters in PCa tissues; **B** Three types of luminal clusters in PCa tissues.

Supplementary Fig. 3



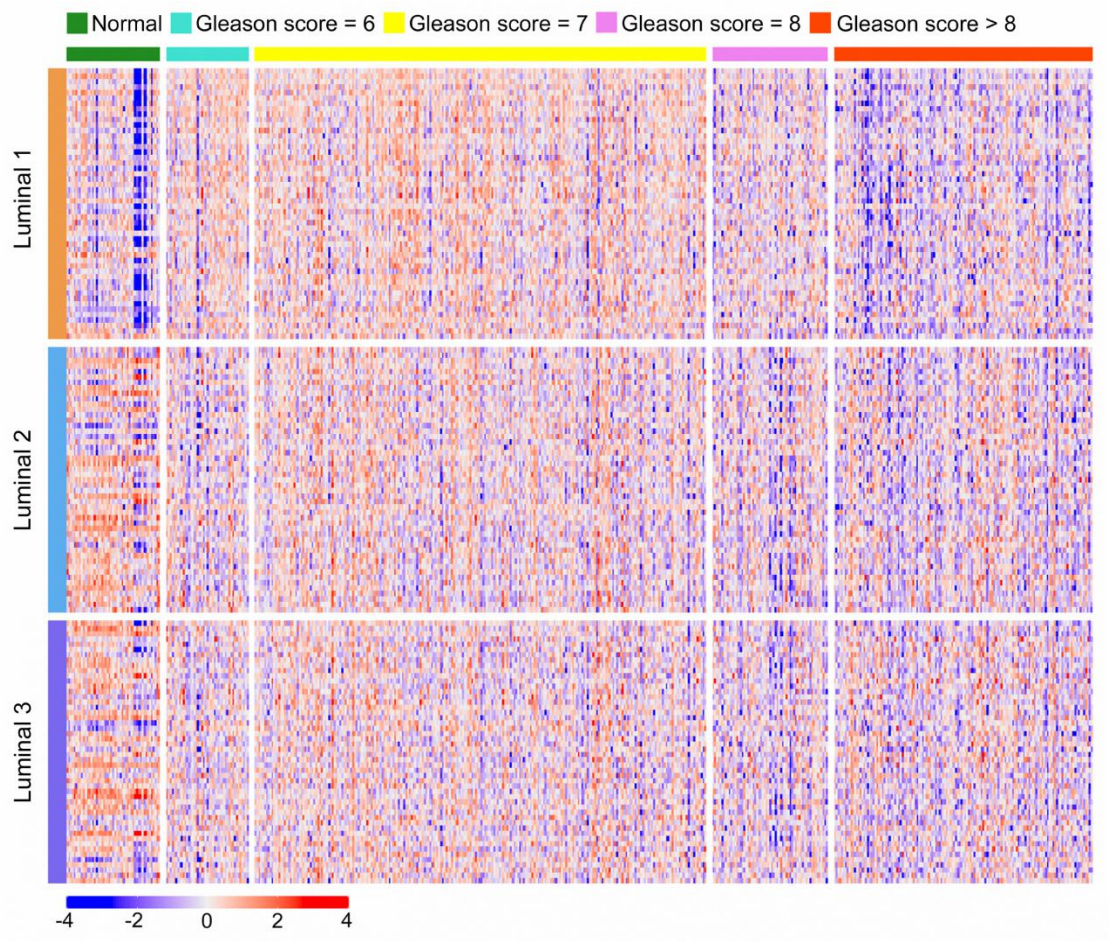
Highly expressed genes distributed in PCa. A-C Violin plots displaying the expression of highly expressed genes in each luminal cluster across the cell types identified in PCa (from luminal 1 to luminal 3, respectively); **D-F** Expression levels of highly expressed genes in each luminal cluster plotted onto the UMAP (from luminal 1 to luminal 3, respectively), color key from gray to red indicates relative expression levels from low to high.

Supplementary Fig. 4



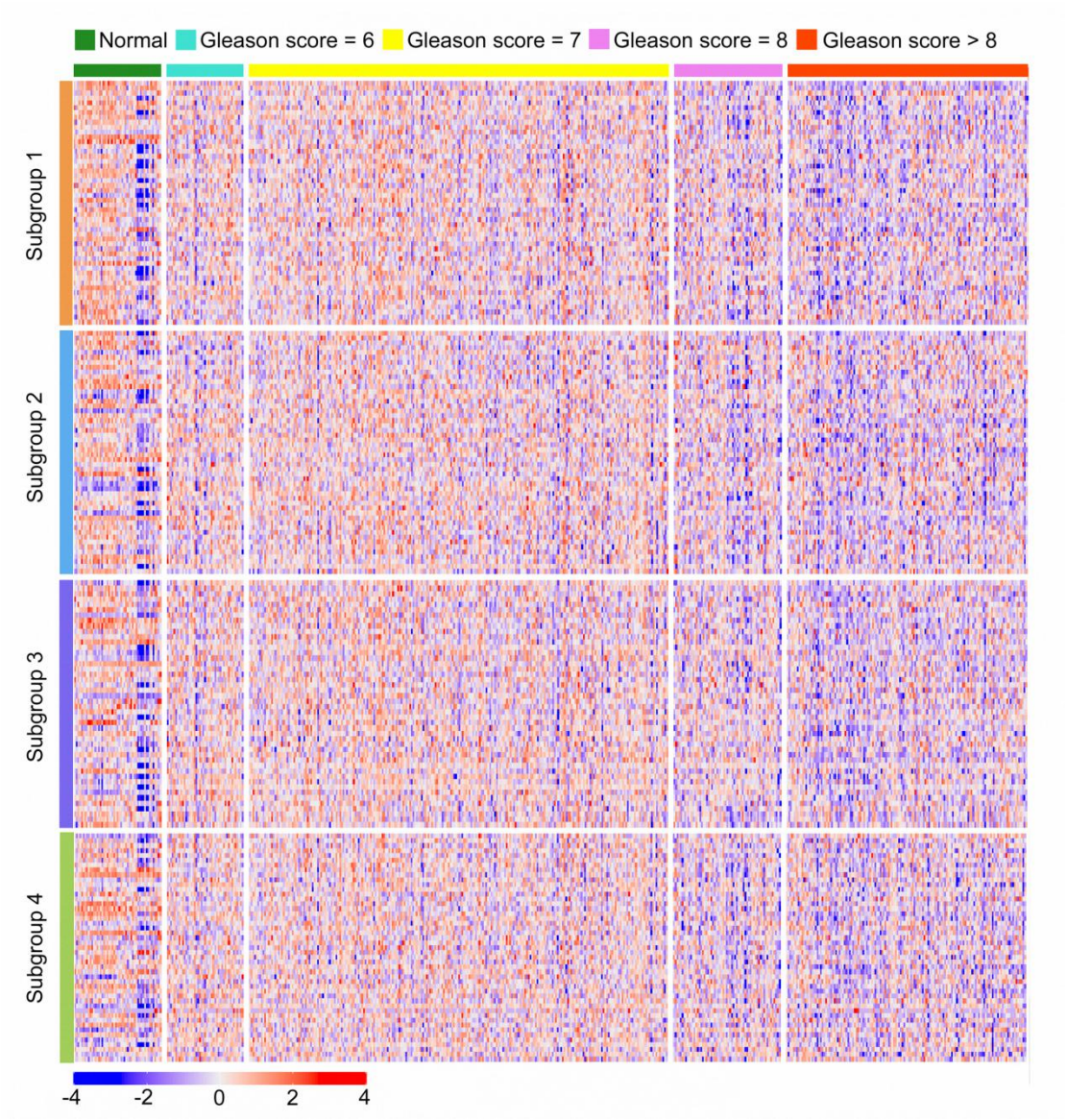
GO enrichment of differentially expressed genes (DEGs) of each luminal cluster analyzed by pairwise comparison. A, B The enriched GO terms for DEGs between type 1 and type 2 luminal cells; **C, D** The enriched GO terms for DEGs between type 1 and type 3 luminal cells; **E, F** The enriched GO terms for DEGs between type 2 and type 3 luminal cells.

Supplementary Fig. 5



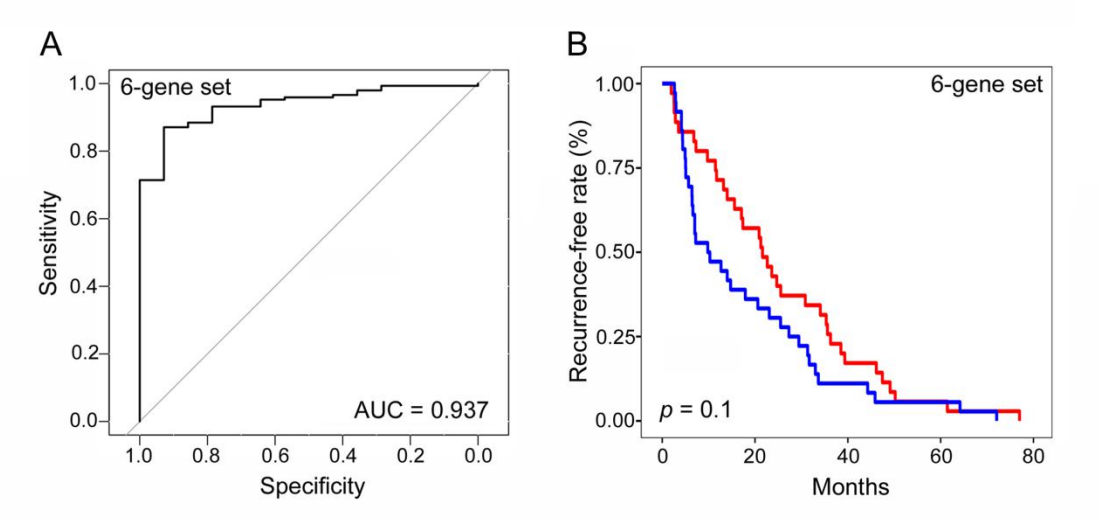
Clustering heatmap demonstrating the correlation between PCa status and the marker gene expression of each luminal cluster using TCGA data.

Supplementary Fig. 6



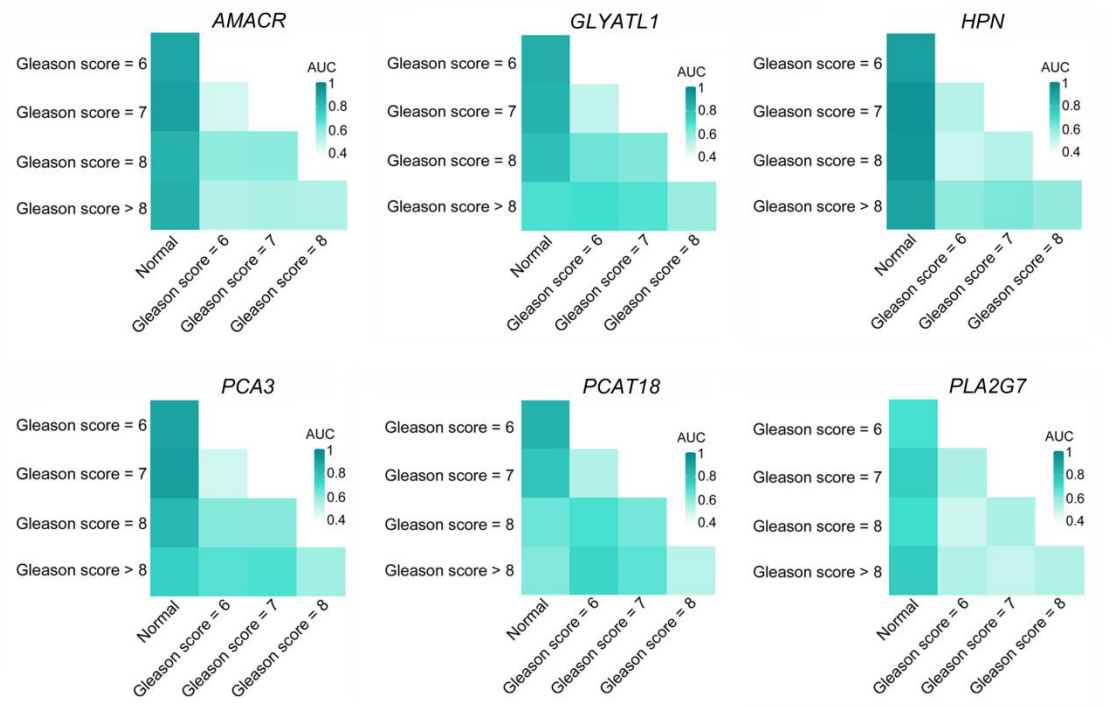
Clustering heatmap demonstrating the correlation between PCa status and the marker gene expression of subgroup 1-4 using TCGA data.

Supplementary Fig. 7



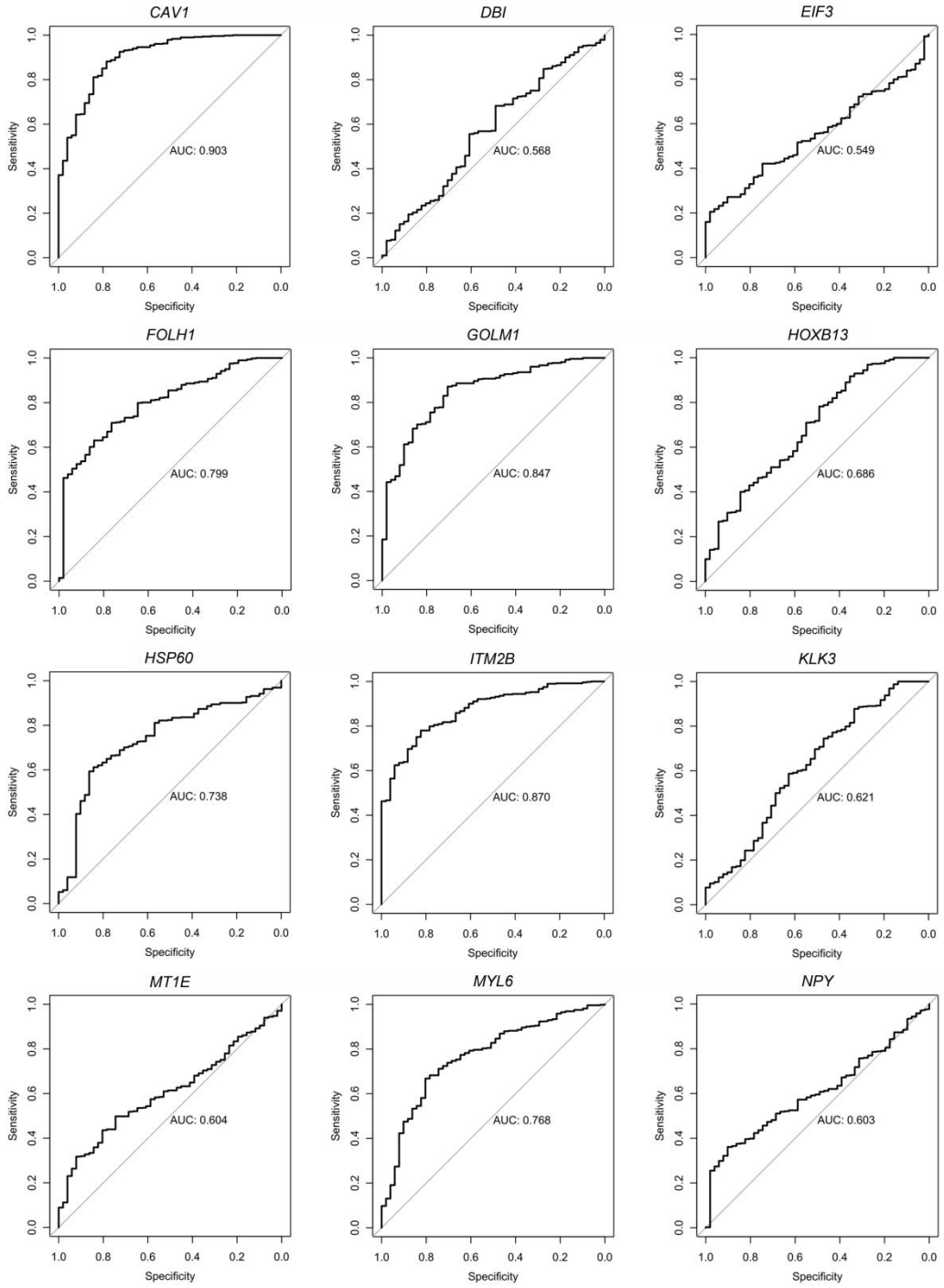
Clinical correlations of 6-gene set from subgroup 5 marker genes were analyzed with their expression patterns in PCa patients from TCGA. A ROC analysis for 6-gene set from subgroup 5 marker genes in distinguishing normal prostate from cancerous prostate; **B** Kaplan-Meier analysis predicting recurrence-free rate of PCa patients based on the expression changes of 6-gene set from subgroup 5 marker genes.

Supplementary Fig. 8



Heatmap showing different distinguishing abilities of subgroup 5 marker genes in patients with various pathology gradings.

Supplementary Fig. 9



ROC analysis of reported candidate marker genes for PCa diagnosis.