Figure S1. WGCNA analysis in PCa. (A) Sample clustering was applied to exclude outliers; (B) Analysis of the scale-free fit index for various soft-thresholding powers (left) and the mean connectivity for various soft-thresholding powers (right); (C) Heatmap visualizing the correlation between the modules and biochemical recurrence (BCR). PCa: prostate cancer.

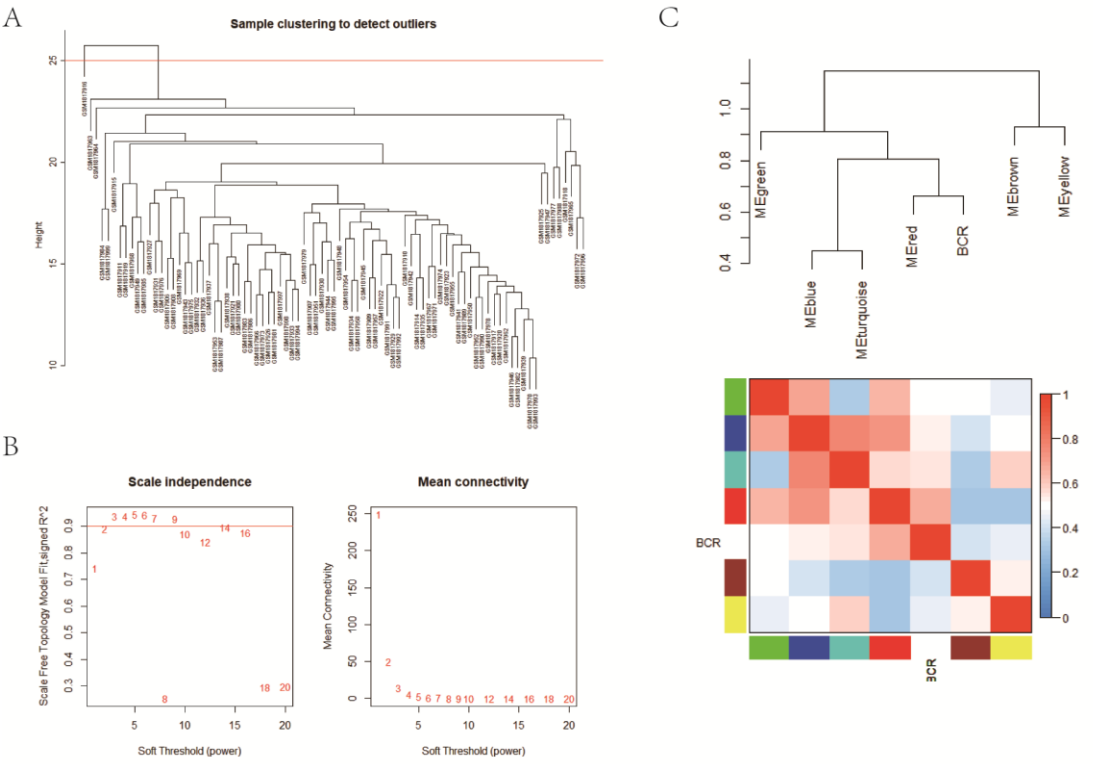

Figure S2. Z-score in BCR patients was significantly higher compared with BCR-free (BCR-F) patients, and had a tendency to increase with the extension of BCR time. BCR: biochemical recurrence.

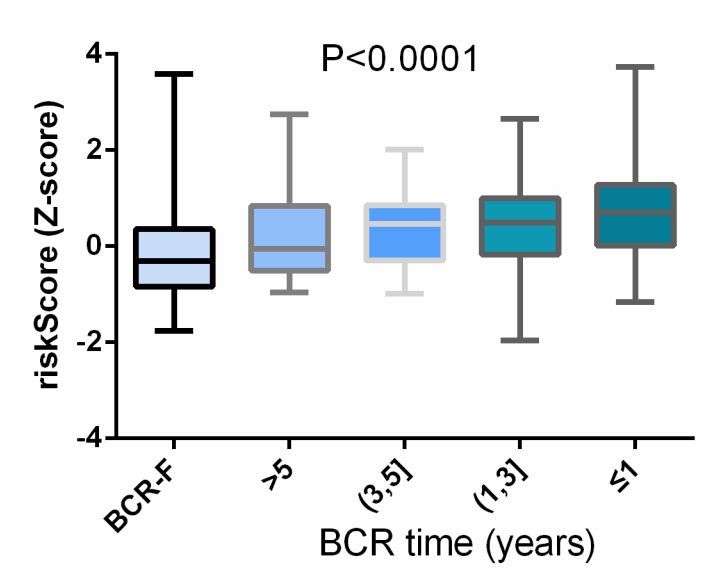

Figure S3. The expression level of IAGs (SSTR1, NFATC3, NRP1, TUBB3, IL1R1, GDF15) in the signature in prostate cancer and normal prostate tissue.

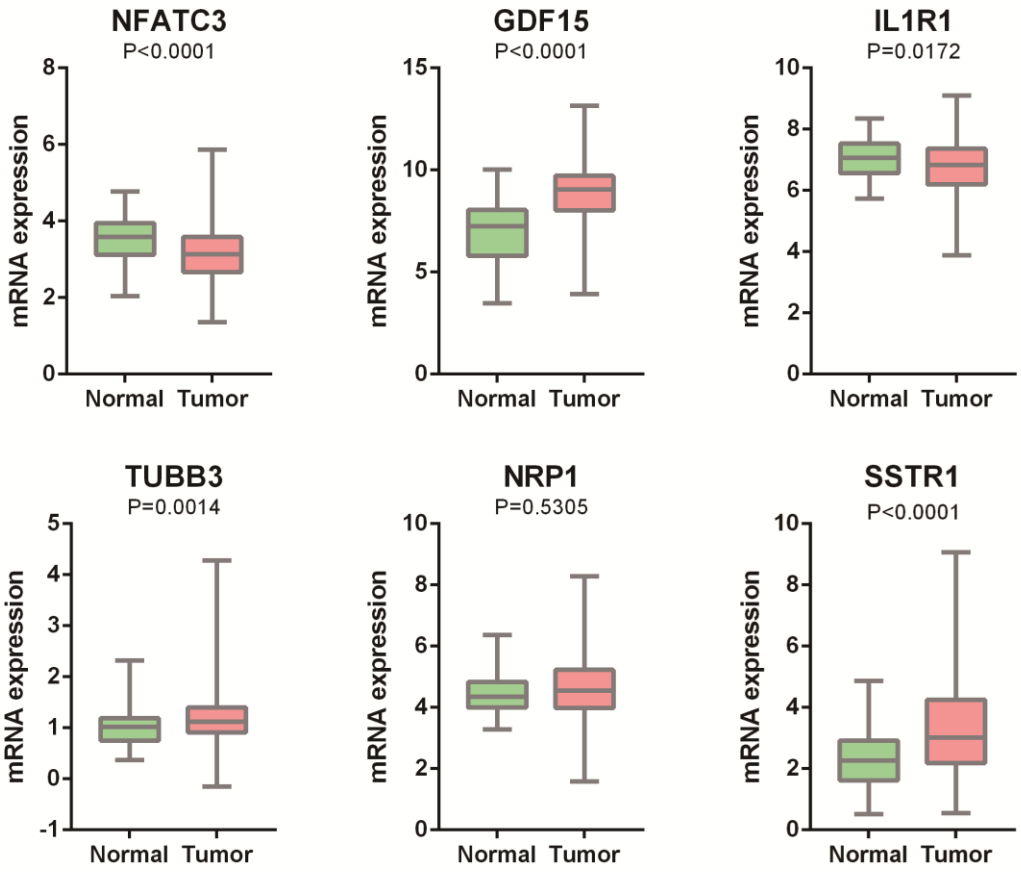

Table S1: Clinicopathological characteristics of prostate cancer patients in the training cohort and validation cohort.

Characteristics	Groups	Training cohort GSE70779	Validation cohort TCGA
		N=92	N=379
Age	≤65	NA	274
	>65	NA	105
	NM	92	0
GS	≤6	20	42
	7	55	191
	≥8	15	146
	NM	2	0
PSA	<10	56	NA
	≥10	34	NA
	NM	2	379
Clinical stage (T)	<T2b	75	180
	≥T2b	14	131
	NM	3	68
Surgical margins	Positive	42	NA
	Negative	50	NA
	NM	0	379

GS: Gleason score; PSA: prostate-specific antigen; NM: not mentioned; NA: not available.