Supplementary

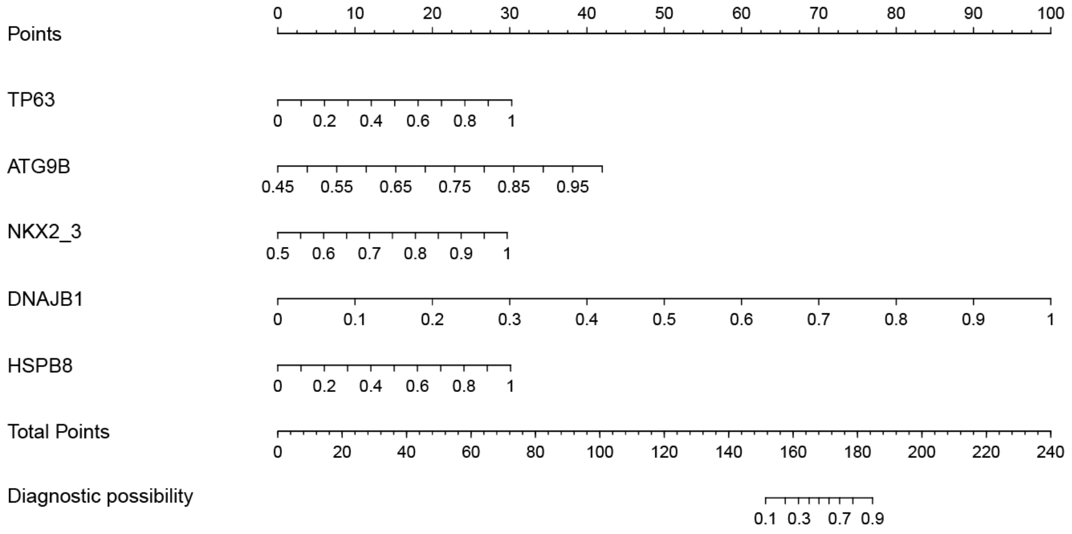

Figure S1 Nomogram of the RI for predicting the risk of PCa consisted of 5 independent diagnostic genes (*ATG9B*, *DNAJB1*, *HSPB8*, *NKX2-3*, *TP63*).

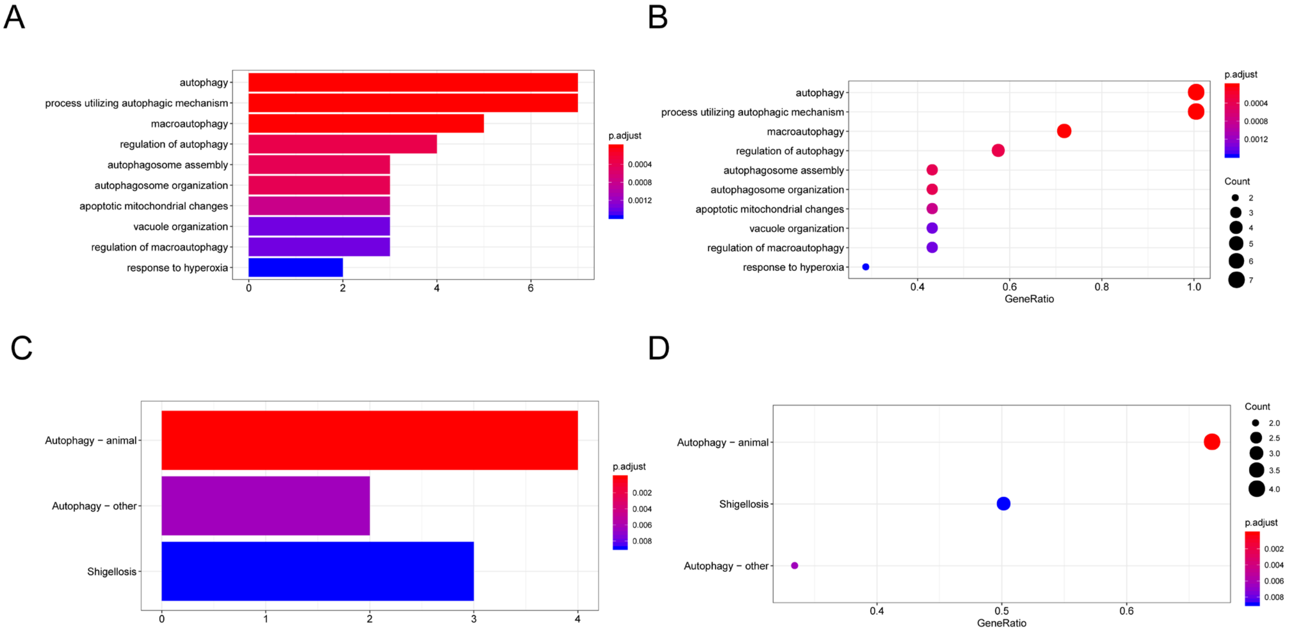

Figure S2 GO and KEGG pathway analysis of survival related ARGs. (A,B) Bar plot and bubble plot of biological process GO terms for survival related ARGs. (C,D) Bar plot and bubble plot of KEGG pathway analysis for survival related ARGs. GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; ARGs, autophagy-related genes.

Table S1 Multicollinearity analysis of DEARGs

Genes	Collinearity statistics	
	Tolerance	VIF
CAMKK2	0.725	1.379
ITPR1	0.675	1.481
TP63	0.121	8.279
HSPB8	0.471	2.123
ATG9B	0.880	1.136
TMEM74	0.598	1.673
NRG1	0.388	2.580
NRG2	0.211	4.748
ITGB4	0.233	4.293
BCL2	0.407	2.455
NKX2_3	0.795	1.258
CDKN2A	0.770	1.299
BIRC5	0.838	1.194
DNAJB1	0.932	1.073
SUPT20HL2	0.683	1.463
FAM215A	0.829	1.206

DEARGs, differentially expressed auto-related genes; VIF, variance inflation factors.

Table S2 Results of Hosmer and Lemeshow test of RI in different datasets

Datasets	c^2 value	P value
TCGA PRAD	1.783	9.87×10^{-1}
GSE32571	4.473	8.12×10^{-1}
GSE46602	0.668	1.00
GSE70768	3.796	8.75×10^{-1}

RI, risk index; TCGA, The Cancer Genome Atlas; PRAD, prostate adenocarcinoma.

Table S3 Multicollinearity analysis of survival related ARGs

Genes	Collinearity statistics	
	Tolerance	VIF
RAB33B	0.473	2.115
ATG16L1	0.385	2.599
NPC1	0.385	2.596
BNIP3	0.723	1.384
ATG3	0.517	1.935
USP10	0.408	2.452
TP53	0.848	1.179

ARGs, auto-related genes; VIF, variance inflation factors.

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