Supplementary

Table S1 Differential expression of apoptotic genes between PTC and normal samples (training set)

Genes	LogFC	AveExpr	t	P value	Adjusted P value	B
TYRO3	1.690135749	9.46546061	12.4871268	8.52E–32	5.81E–30	61.2843423
BCL2	–1.84268259	11.8429722	–12.4556377	1.16E–31	5.81E–30	60.97653478
STING1	1.524876665	12.1599678	11.23768064	1.33E–26	4.45E–25	49.4286768
FNDC4	2.040720612	9.96526266	9.922710637	1.64E–21	4.11E–20	37.82904075
SPATA2	–0.78697983	10.4479538	–9.88133979	2.34E–21	4.68E–20	37.48018157
PRKN	–0.94514178	7.6642456	–9.57512798	3.09E–20	5.15E–19	34.93036028
TNFRSF1A	0.691600988	13.1627647	8.550920891	1.13E–16	1.61E–15	26.83442853
GJB1	–2.24072354	2.19506991	–8.37083153	4.46E–16	5.57E–15	25.48307427
NFKBIA	–0.77115904	12.4968359	–7.55433713	1.69E–13	1.88E–12	19.64351389
CYLD	–0.57574721	12.1416817	–7.0973309	3.80E–12	3.70E–11	16.58874908
PELI1	1.275189294	10.651758	7.087124061	4.07E–12	3.70E–11	16.52233383
CXCL5	2.240649093	3.74737388	6.736975307	3.97E–11	3.05E–10	14.29280825
EZH2	0.812094648	8.04087069	6.643016992	7.20E–11	5.14E–10	13.71087833
HSPA5	–0.8023986	16.0219752	–6.40465734	3.16E–10	1.97E–09	12.26610781
SFTPA1	3.391570328	5.54353353	6.37695813	3.74E–10	2.20E–09	12.10116984
PRKAA2	–0.71215498	9.50541587	–6.30408084	5.82E–10	3.23E–09	11.67017559
FAS	0.849400812	10.6859556	6.218946592	9.70E–10	4.85E–09	11.17215163
DAPK1	–0.91018251	10.2196553	–5.84013247	8.78E–09	3.99E–08	9.028267604
TRPM7	–0.55412718	11.3502302	–5.77697201	1.25E–08	5.22E–08	8.682396889
SLC25A37	0.57472179	11.643642	5.606202165	3.23E–08	1.29E–07	7.764034267
NFE2L2	–0.51595773	13.3081499	–5.56538107	4.03E–08	1.55E–07	7.548156115
TNFAIP3	–0.86347451	10.1415372	–5.54020466	4.62E–08	1.71E–07	7.415718436
IL37	1.201558289	1.43963659	4.683406863	3.53E–06	1.22E–05	3.234899434
MYC	–0.77279052	9.96902752	–4.66701435	3.81E–06	1.27E–05	3.16119041
GNLY	1.179595255	8.60386014	4.643088575	4.27E–06	1.38E–05	3.054037774
TNF	–1.03777142	4.4908648	–4.20033628	3.09E–05	8.84E–05	1.163898276
PPP1R3G	0.656702277	6.948029	4.007806935	6.94E–05	0.00017805	0.397435121
UCHL1	–0.61538584	8.51416657	–3.94896653	8.83E–05	0.00021032	0.169965179
ANGPT2	0.508165695	9.55148704	3.549584969	0.00041773	0.00087027	–1.28941739
NGFR	0.908737302	10.0034983	3.22955365	0.00131132	0.00262265	–2.35136578
FASLG	–0.66455265	4.53539043	–2.80211651	0.00524973	0.00921006	–3.61852502
ZBP1	–0.59614655	5.48668307	–2.1480004	0.03213524	0.0472577	–5.21804045

AveExpr, average expression; FC, fold change.

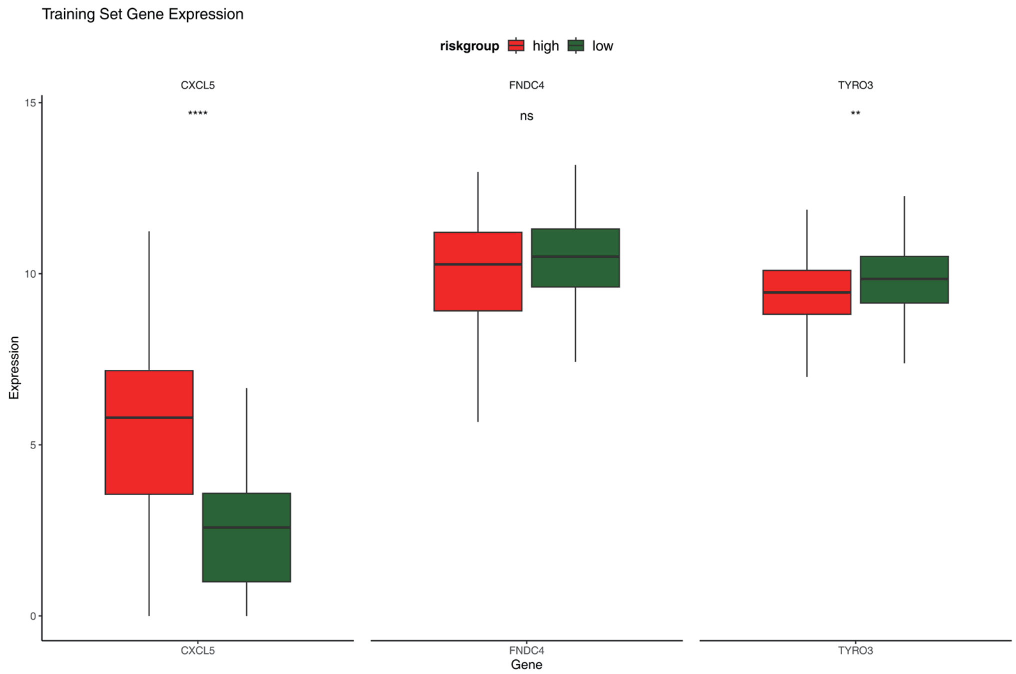

Figure S1 The expression of prognosis-related genes in the high- and low-risk groups. The high-risk group was represented in red, and the low-risk group was represented in green. ns, not significant (P>0.05); **, P<0.01; ****, P<0.0001.

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