

Table S1 The information on all primary antibodies

Antibody	Source	Location	Diluted concentration
INSM1	BIOSS ANTIBODIES	Beijing, China	1:200
PHF21B	ZSGB-BIO	Beijing, China	1:200
RNF138	CUSABIO	Wuhan, China	1:200
SYTL4	Proteintech	Wuhan, China	1:200
WRNIP1	Origene	Wuxi, China	1:200
ZNF514	ThemroFisher	America	1:200
DAB	ZSGB-BIO	Beijing, China	–

Table S2 Results of univariate analysis: prognostic associated zinc finger protein genes

ID	HR	HR.95L	HR.95H	P value
ZFP42	5.851232004	2.14486836	15.9622458	0.000560081
ZNF514	6.181718867	2.138900632	17.86602312	0.000768123
TRIM60	1.37E+21	332135753.8	5.66E+33	0.001024028
RORC	0.481259662	0.308587987	0.750550481	0.001257486
ZNF556	3.522627647	1.634820304	7.5903789	0.001304872
LHX5	13.40704005	2.667475226	67.38533921	0.001627536
ZKSCAN2	3.799574903	1.612492631	8.953076228	0.002269326
THAP12	0.293803529	0.133555562	0.64632661	0.002326888
TRIP6	2.00312881	1.274256612	3.148914428	0.002611686
RNF4	0.146784268	0.041374211	0.520750029	0.00297928
RNF138	0.336738631	0.163051213	0.695443499	0.003266009
PCM1	0.337567536	0.16308878	0.698710489	0.00343471
ZNF582	0.000637558	4.44E-06	0.091473105	0.003685616
ZNF596	0.019199781	0.001301259	0.283288334	0.003996737
RIMS2	26.02459815	2.727925363	248.2764807	0.004625611
PRR35	1107.504883	8.351131556	146874.3555	0.004937489
WRNIP1	4.608487499	1.572521004	13.50580181	0.005350597
TEX13C	797092057	339.404981	1.87E+15	0.006171348
SCRT1	3669372.118	68.88494714	1.95E+11	0.006484997
ZNF684	0.10658365	0.021082189	0.538846996	0.006772798
ZNF282	6.54090852	1.675157317	25.53997993	0.006886583
TRIM64B	5.12E+22	1335392.43	1.96E+39	0.007276465
BSN	30.56844409	2.509486133	372.3590107	0.007333157
PHF21B	331065564.4	180.9424691	6.06E+14	0.007664176
SYTL4	0.207930888	0.065538333	0.65969414	0.007673292
RBSN	0.086828415	0.013940344	0.540816909	0.008829171
INSM1	2.171368645	1.213777198	3.884437606	0.008979706
ZNF585B	0.191098626	0.055185625	0.661742704	0.009015397
ZNF24	0.275740223	0.104741994	0.725904365	0.009091458

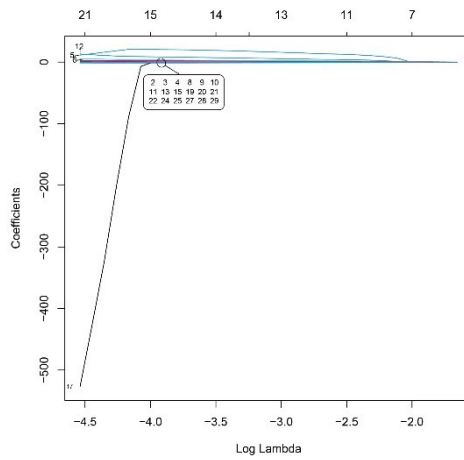


Figure S1 LASSO regression analysis. LASSO, least absolute shrinkage and selection operator.

Table S3 Results of multivariate regression analysis

ID	coef	HR	HR.95L	HR.95H	P value
INSM1	1.739476385	5.694360988	1.187962562	27.29526006	0.029602811
PHF21B	42.53469288	2.97E+18	10691.10623	8.24E+32	0.012186588
RNF138	-1.346164749	0.260236421	0.064221304	1.054525373	0.059349051
SYTL4	-2.553477149	0.077810636	0.002555091	2.369580722	0.142920547
WRNIP1	2.11134543	8.259346187	0.64942849	105.0412793	0.103679732
ZNF514	2.353035417	10.51744615	0.691871564	159.8803582	0.090137616
ZNF585B	-2.816995172	0.059785318	0.004667231	0.765825455	0.030386523

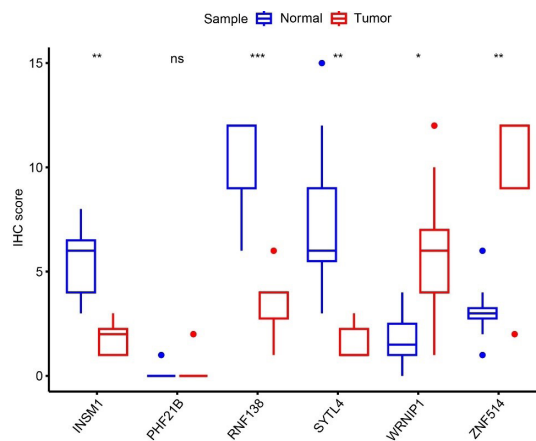


Figure S2 Box plot showed the differential immunohistochemistry (IHC) scores of six prognosis-related zinc finger (ZNF) protein genes between tumor and normal tissues. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$, ns means no significance.

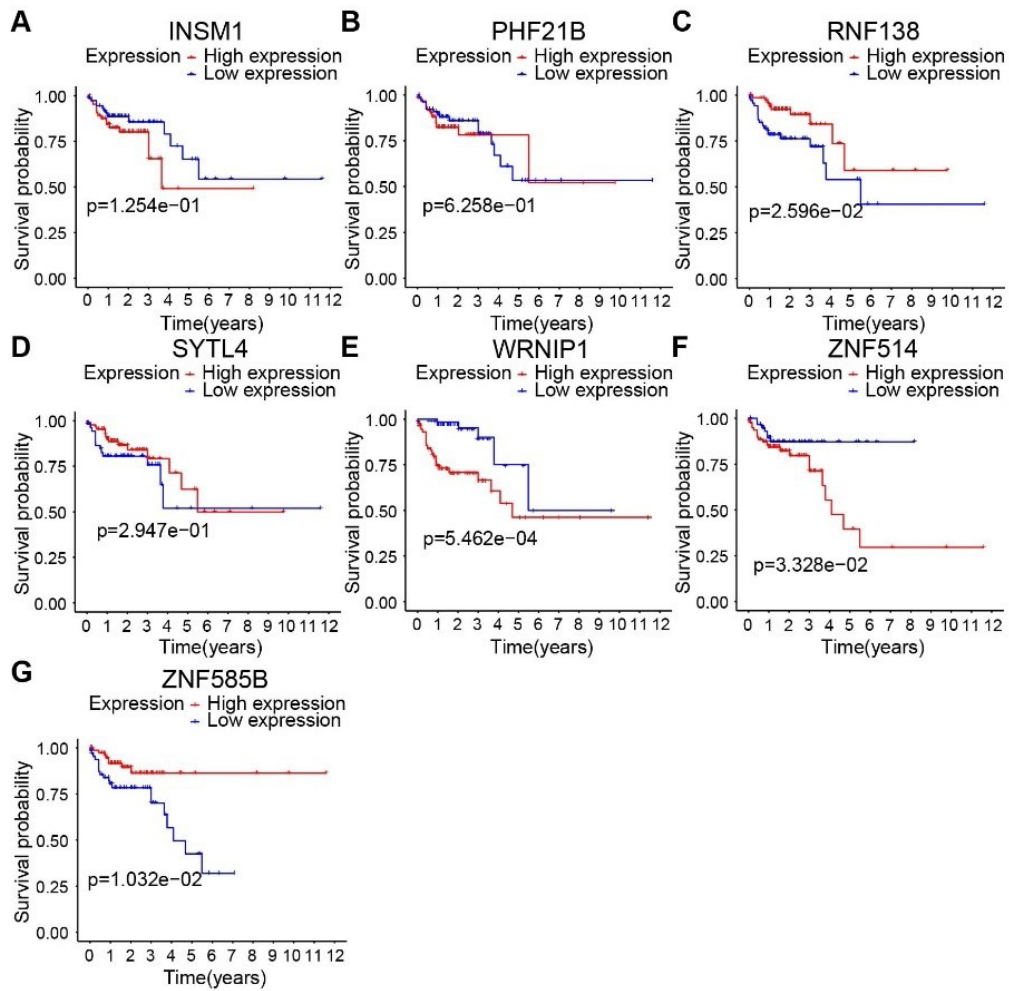


Figure S3 Survival analysis of seven prognostic-related zinc finger (ZNF) protein genes in high and low expression groups of The Cancer Genome Atlas-colon adenocarcinoma (TCGA-COAD) cohort. (A) INSM1, (B) PHF21B, (C) RNF138, (D) SYTL4, (E) WRNIP1, (F) ZNF514, (G) ZNF585B.

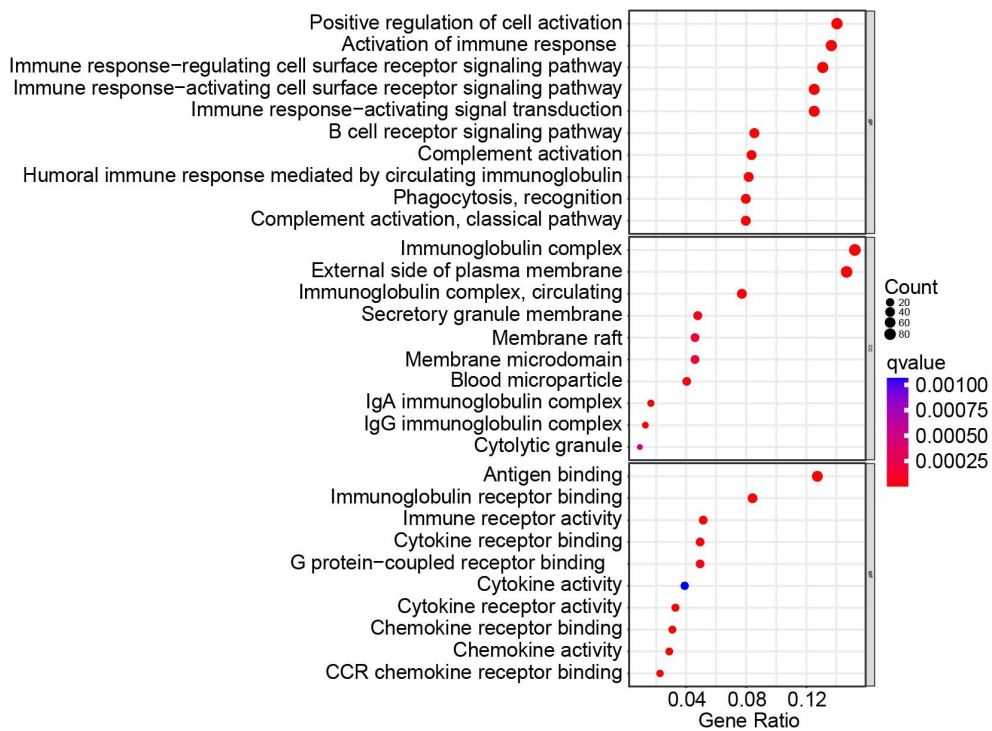


Figure S4 Gene Ontology (GO) enrichment analysis of differentially expressed genes (DEGs).

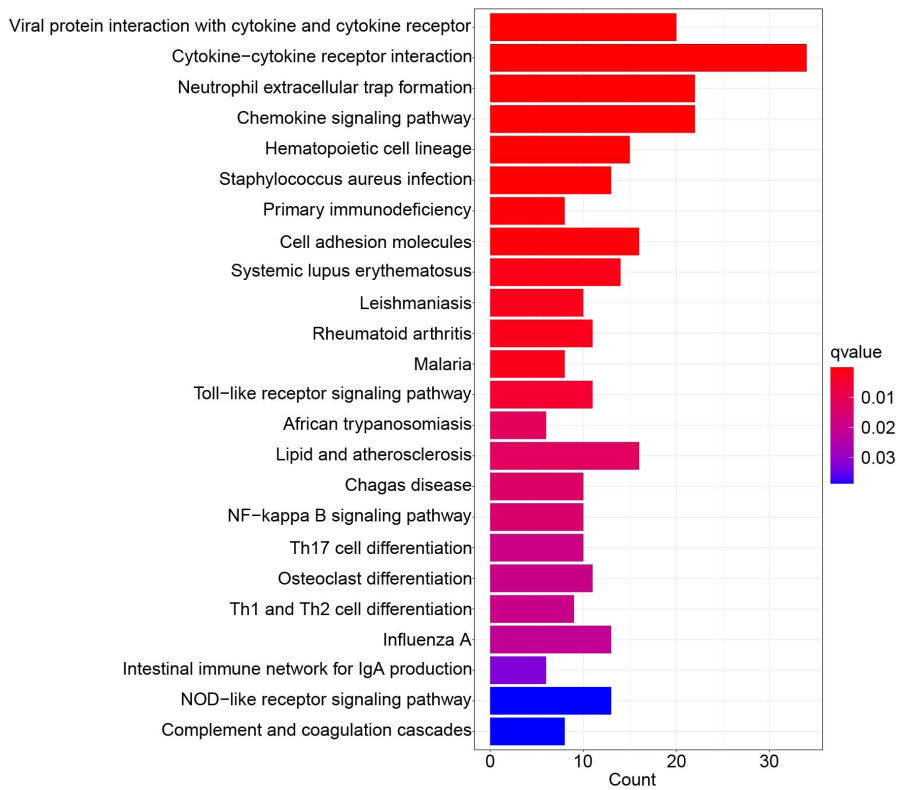


Figure S5 Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of differentially expressed genes (DEGs).

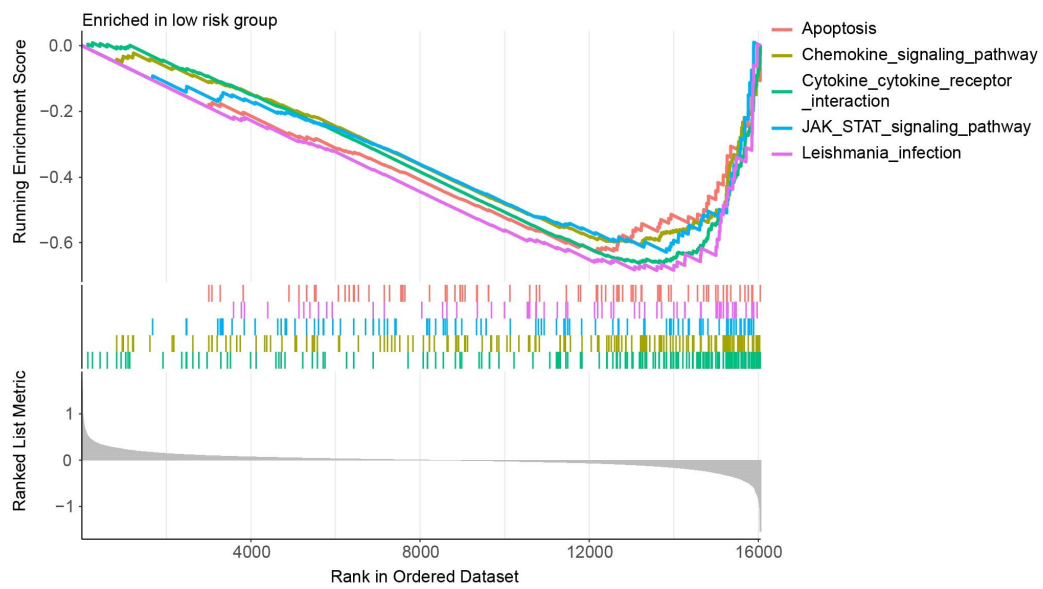


Figure S6 Result of gene set enrichment analyses (GSEA) between high and low-risk groups.