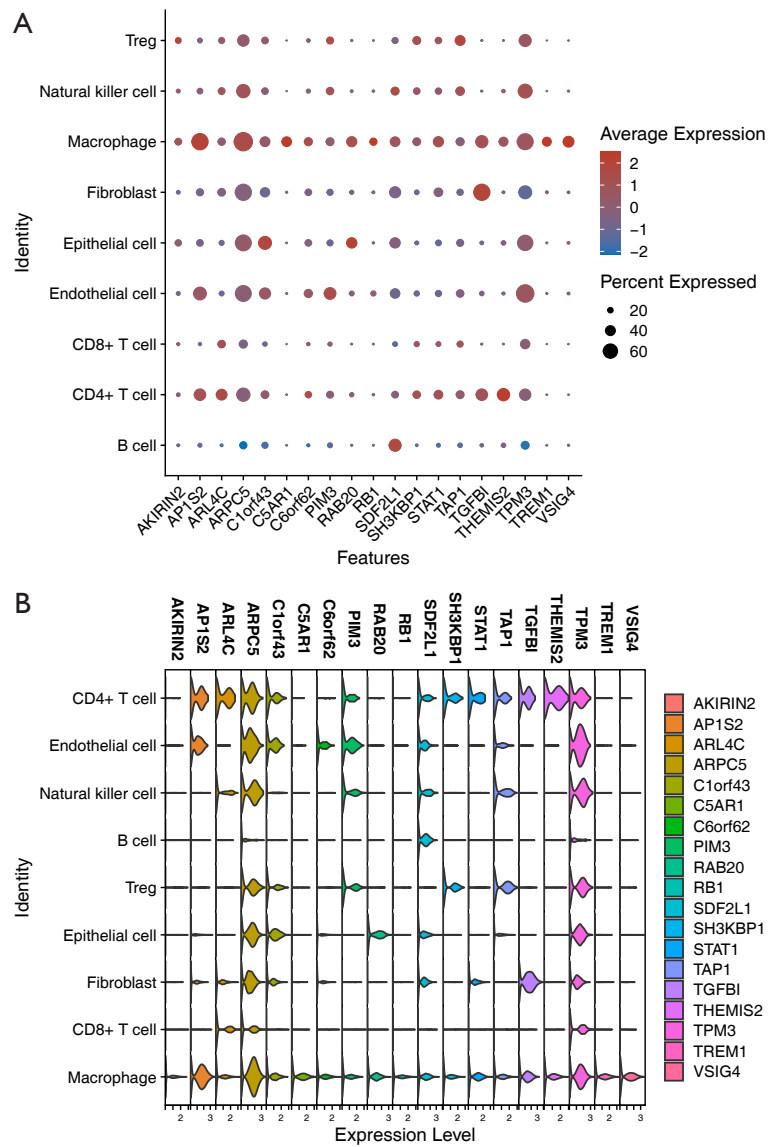
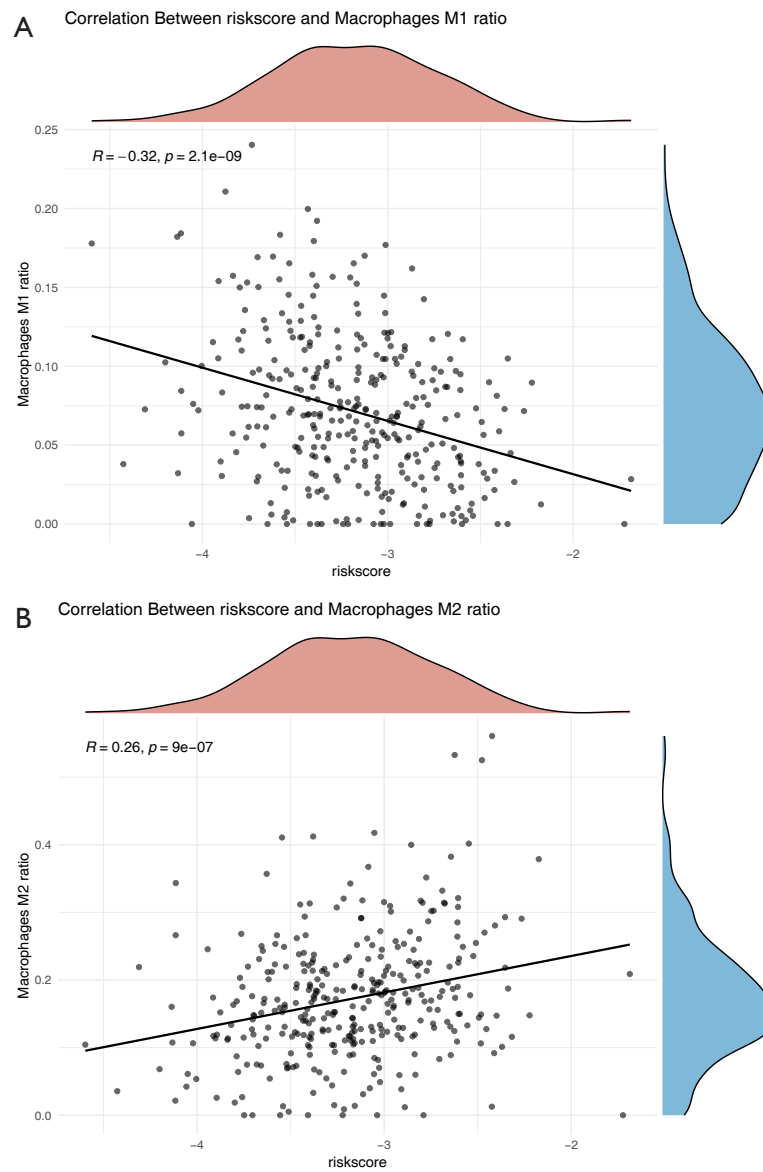


**Figure S1** Enrichment analysis of genes in the prognostic model. (A) GO enrichment analysis results; (B) KEGG enrichment analysis results.



**Figure S2** Expression of prognostic model genes in single-cell data.(A) Bubble plot showing the expression of model genes in single-cell data. (B) Violin plot showing the expression of model genes in single-cell data.



**Figure S3** Correlation analysis between M1 and M2 macrophage infiltration scores and risk scores. (A) Correlation analysis between M1 macrophage infiltration score and risk score; (B) correlation analysis between M2 macrophage infiltration score and risk score.

**Table S1** Univariate Cox regression results for 30 genes significantly associated with prognosis

ID	HR	HR.95L	HR.95H	P value
IL1B	1.14482640883824	1.00047404482033	1.31000650457537	0.0491998219950672
AP1S2	0.776615007659826	0.647772118699493	0.931084949030152	0.00630576369059775
ALOX5AP	1.10562183542531	1.00497595927646	1.21634714908932	0.0392179513193276
VSIG4	1.14571543102862	1.03058123267476	1.27371216094264	0.011821219779812
C5AR1	1.22643218695336	1.05856907683679	1.42091427201882	0.00657033103694225
TREM1	1.29274676978598	1.04432793636628	1.6002580727726	0.0183571292807791
FPR1	1.1592772919261	1.00594241763658	1.33598485958372	0.0411698214504925
RB1	1.25402660901053	1.03904021771938	1.51349554068094	0.018319541849771
ARPC5	0.752990680077272	0.580345714665575	0.976995177107431	0.0327513148076391
THEMIS2	1.13592764200509	1.00221982050419	1.28747364746999	0.0460792027645633
TMSB4X	0.837519917165648	0.706577066414028	0.992729094943674	0.0409444967129268
PFN1	0.728025606732997	0.548526279594292	0.966264158667055	0.0279808749731152
TGFB1	1.17614798302827	1.04517479776305	1.32353371028669	0.00707103274815127
RAB20	1.22686146924827	1.00835638830119	1.49271535559155	0.0410404863148842
FXYD5	1.16687903051108	1.02581743221848	1.32733820763974	0.0188889271371451
STAT1	0.846052096701359	0.731520263396991	0.978515819929247	0.024283745423189
TPM3	0.528925024805686	0.373862663953715	0.74830066984258	0.000320807244875638
VASP	1.34624444839293	1.0360010317665	1.74939412148894	0.0261084375573991
SH3KBP1	0.787768045974173	0.631760790928186	0.982299793164135	0.0341271107743835
C6orf62	0.761908066696259	0.592561394091717	0.97965191098322	0.0339844497153334
IRS2	1.1685938	1.02601175940899	1.33098996792975	0.0189375689495244
AKIRIN2	0.759410221876029	0.591482151626453	0.975014856329957	0.0308964772091201
PIM3	1.25322257728421	1.02589936826369	1.53091704391341	0.027080467317254
GNG5	0.773836790692125	0.618719508848344	0.967843053378597	0.0246830364454578
RUNX1	1.18543753011589	1.01645255895144	1.38251620838743	0.0301638842432387
TAP1	0.891596189627879	0.799428241799823	0.994390395277037	0.0393022750650593
C1orf43	0.714911339752842	0.51667203817107	0.989212084161558	0.0428236401847111
HMGN3	0.800880418526397	0.668875416453674	0.958937089031796	0.0156818904977334
ARL4C	1.14840154532965	1.01008750821093	1.30565530074859	0.0345791871644846
SDF2L1	0.816456640744738	0.686500231157286	0.971014161338942	0.0218768169748333

**Table S2** LASSO-Cox regression coefficients for the optimal 19-feature gene signature

Gene	Coef
AKIRIN2	-0.023054761356063
AP1S2	-0.135979155543539
ARL4C	0.0904625746033956
ARPC5	-0.105626787028937
C1orf43	-0.018044772577372
C5AR1	0.0524285762952519
C6orf62	-0.114409005233997
PIM3	0.0930069745595814
RAB20	0.08339552467693
RB1	0.142549395864149
SDF2L1	-0.147163752471696
SH3KBP1	-0.062520781294064
STAT1	-0.011658552937973
TAP1	-0.137916700741924
TGFBI	0.073894483168057
THEMIS2	0.0225558863100229
TPM3	-0.425023904581366
TREM1	0.0122275216735609
VSIG4	0.0958603281636736