

Supplementary Material

1.1 Supplementary Tables

Table S1. Primer nucleotide sequence of this study.

Gene	Primer nucleotide sequence
GAPDH	Forward: 5'-CTGGGCTACACTGAGCACC-3'
	Reverse: 5'-AAGTGGTCGTTGAGGGCAATG-3'
RIPOR2	Forward: 5'-GAAAATTCCTCCGCTCTCAAGA-3'
	Reverse: 5'-TTCAAGGCCCTGTAGACTTCT-3'
FEN1	Forward: 5'-ATGACATCAAGAGCTACTTTGGC-3'
	Reverse: 5'-GGCGAACAGCAATCAGGAACT-3'
PARP1	Forward: 5'-CGGAGTCTTCGGATAAGCTCT-3'
	Reverse: 5'-TTCCATCAAACATGGGCGAC-3'
PARP2	Forward: 5'-GCCTTGCTGTTAAAGGGCAAA-3'
	Reverse: 5'-TCCTTCACAATACACATGAGCC-3'
POLB	Forward: 5'-TGGAAAAGATTCGGCAGGATG-3'
	Reverse: 5'-CAGATGGACCAATGCCACTAAC-3'
RAD52	Forward: 5'-CCAGAAGGTGTGCTACATTGAG-3'
	Reverse: 5'-ACAGACTCCCACGTAGAACTTG-3'
TIGIT	Forward: 5'-TCTGCATCTATCACACCTACCC-3'
	Reverse: 5'-CCACCACGATGACTGCTGT-3'
CTSS	Forward: 5'-TGTAGATGCGCGTCATCCTTC-3'

Gene	Primer nucleotide sequence
	Reverse: 5'-CCAACCACAAGTACACCATGAT-3'
ICOS	Forward: 5'- CAGGAGAAATCAATGGTTCTGCC-3'
	Reverse: 5'- CCTTTTGTCTTAGTGAGATCGCA-3'

Table S2. The univariate-cox results of differentially expressed genes.

id	HR	HR.95L	HR.95H	pvalue
CLEC3B	0.690849	0.506049	0.943135	0.019881
CD1C	0.802257	0.646196	0.996007	0.04591
BMP6	1.085786	1.030463	1.144079	0.002038
FBN1	1.060564	1.005184	1.118995	0.03164
CCL22	0.85454	0.744968	0.980228	0.024756
PAMR1	0.847191	0.719052	0.998164	0.047488
CYTL1	1.084405	1.021689	1.150972	0.007679
HTRA3	1.006744	1.000122	1.013409	0.045898
PI16	1.036754	1.001712	1.073021	0.039641
RIPOR2	0.453699	0.243171	0.846493	0.013003

Table S3. Enriched KEGG gene sets of different risk groups.

Description	ES	NES	p-value	FDR	group
KEGG_CELL_CYCLE	0.59674	1.92415	0.00201	0.06038	High risk
KEGG_SPLICEOSOME	0.63125	1.91733	0.00606	0.03233	High risk
KEGG_N_GLYCAN_BIOSYNTHESES	0.64276	1.86973	0.00791	0.04056	High risk
KEGG_PROTEIN_EXPORT	0.70734	1.82669	0.00401	0.05685	High risk
KEGG_RNA_DEGRADATION	0.57288	1.81678	0.00389	0.05098	High risk
KEGG_AMINOACYL_TRNA_BIOSYNTHESES	0.64241	1.77450	0.01040	0.06488	High risk
KEGG_TERPENOID_BACKBONE_BIOSYNTHESES	0.71830	1.77232	0.00411	0.05626	High risk
KEGG_MISMATCH_REPAIR	0.66328	1.70069	0.01569	0.09526	High risk
KEGG_PYRUVATE_METABOLISM	0.51599	1.68877	0.01237	0.09301	High risk
KEGG_GLYCOLYSIS_GLUONEOGENESIS	0.50413	1.68764	0.00815	0.08399	High risk
KEGG_RNA_POLYMERASE	0.58910	1.62400	0.02806	0.12781	High risk
KEGG_DNA_REPLICATION	0.64999	1.61066	0.03400	0.13123	High risk
KEGG_HOMOLOGOUS_RECOMBINATION	0.56954	1.57700	0.04038	0.15620	High risk

Description	ES	NES	p-value	FDR	group
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KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.53921	1.55018	0.04225	0.17324	High risk
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	0.48456	1.53295	0.03482	0.17885	High risk
KEGG_PYRIMIDINE_METABOLISM	0.43214	1.53061	0.04356	0.17052	High risk
KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.50213	1.52218	0.07115	0.16836	High risk
KEGG_ONE_CARBON_POOL_BY_FOLATE	0.57612	1.51231	0.05182	0.16867	High risk
KEGG_BASE_EXCISION_REPAIR	0.51368	1.50909	0.06346	0.16299	High risk
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	0.57387	1.50820	0.07143	0.15585	High risk
KEGG_PURINE_METABOLISM	0.37741	1.49544	0.02713	0.16024	High risk
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	0.47879	1.42048	0.08964	0.23451	High risk
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-0.63866	-2.26796	0.00000	0.00000	Low risk
KEGG_CELL_ADHESION_MOLECULES_CAMS	-0.67478	-2.25669	0.00000	0.00000	Low risk
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.68066	-2.23792	0.00000	0.00000	Low risk
KEGG_CHEMOKINE_SIGNALING_PATHWAY	-0.63126	-2.22908	0.00000	0.00000	Low risk
KEGG_HEMATOPOIETIC_CELL_LINEAGE	-0.74466	-2.19673	0.00000	0.00026	Low risk
KEGG_JAK_STAT_SIGNALING_PATHWAY	-0.59643	-2.17246	0.00000	0.00021	Low risk
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	-0.64697	-2.14504	0.00000	0.00049	Low risk
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.65157	-2.12726	0.00000	0.00043	Low risk
KEGG_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	-0.57696	-2.11629	0.00000	0.00062	Low risk
KEGG_LEISHMANIA_INFECTION	-0.70381	-2.10595	0.00000	0.00065	Low risk
KEGG_AUTOIMMUNE_THYROID_DISEASE	-0.78279	-2.09016	0.00000	0.00059	Low risk
KEGG_PRIMARY_IMMUNODEFICIENCY	-0.86387	-2.09002	0.00000	0.00054	Low risk
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	-0.58167	-2.05034	0.00000	0.00121	Low risk
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-0.79264	-2.01267	0.00000	0.00180	Low risk
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.57815	-2.00354	0.00000	0.00196	Low risk
KEGG_VIRAL_MYOCARDITIS	-0.63201	-1.94945	0.00412	0.00380	Low risk

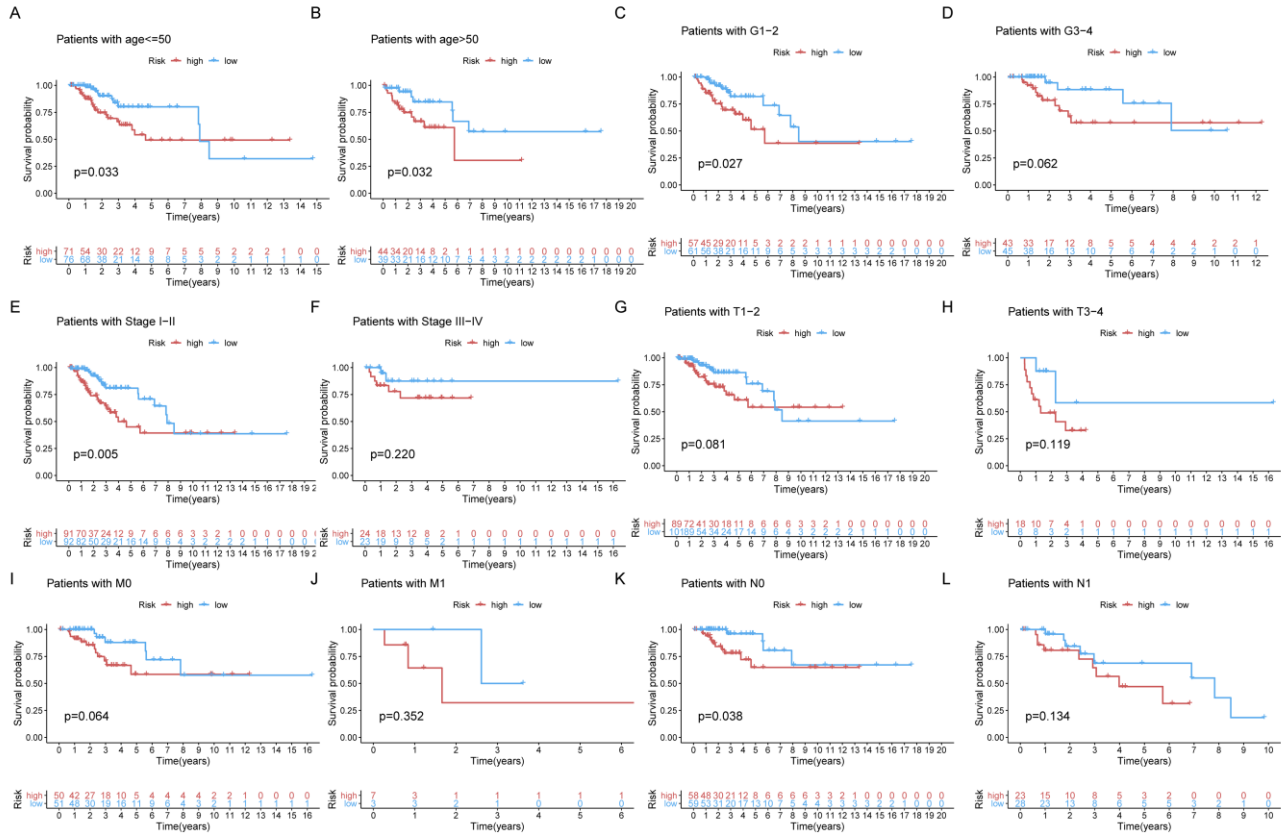
Description	ES	NES	p-value	FDR	group
KEGG_ASTHMA	-0.76574	-1.91912	0.00996	0.00584	Low risk
KEGG_FC_GAMMA_R_MEDIATED _PHAGOCYTOSIS	-0.53958	-1.91324	0.00000	0.00595	Low risk
KEGG_ABC_TRANSPORTERS	-0.58830	-1.91302	0.00204	0.00564	Low risk
KEGG_EPITHELIAL_CELL_SIGNAL ING_IN_HELICOBACTER_PYLORI_ INFECTION	-0.53917	-1.87432	0.00000	0.00888	Low risk
KEGG_DORSO_VENTRAL_AXIS_F ORMATION	-0.61904	-1.84740	0.00202	0.01152	Low risk
KEGG_ALLOGRAFT_REJECTION	-0.81949	-1.84207	0.00609	0.01172	Low risk
KEGG_VEGF_SIGNALING_PATHW AY	-0.48438	-1.83552	0.00000	0.01191	Low risk
KEGG_ACUTE_MYELOID_LEUKE MIA	-0.54467	-1.82763	0.00410	0.01252	Low risk
KEGG_PHOSPHATIDYLINOSITOL_ SIGNALING_SYSTEM	-0.53848	-1.81898	0.00000	0.01345	Low risk
KEGG_COMPLEMENT_AND_COAG ULATION_CASCADES	-0.58616	-1.79560	0.00409	0.01746	Low risk
KEGG_RIG_I_LIKE_RECEPTOR_SI GNALING_PATHWAY	-0.51033	-1.76365	0.00428	0.02433	Low risk

Table S4. Correlation of RIPOR2 with different immune cells via different methods.

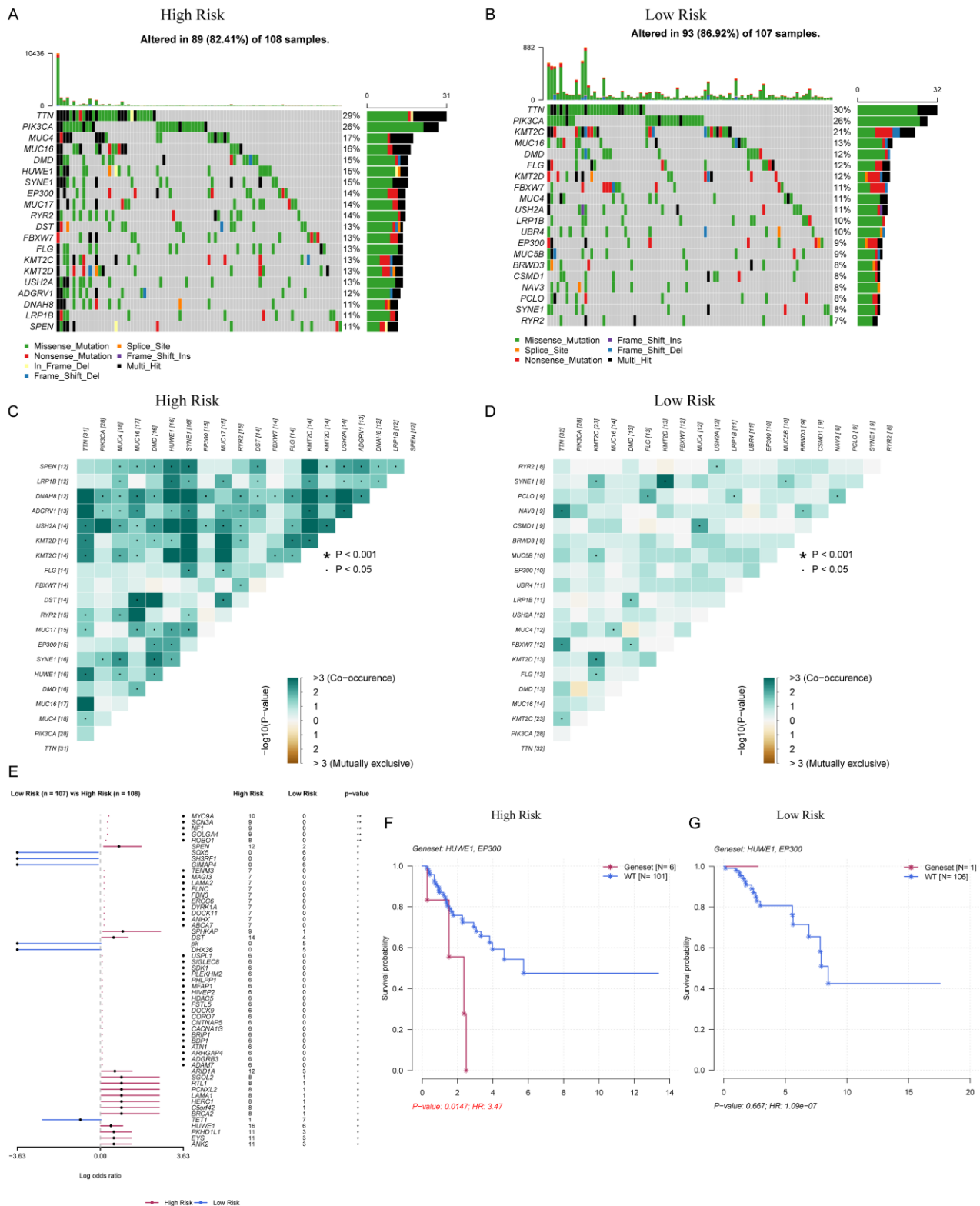
Immune Cells	pvalue
B cell_TIMER	8.07E-16
T cell CD4+_TIMER	1.63E-13
T cell CD8+_TIMER	1.85E-10
Neutrophil_TIMER	1.42E-08
Macrophage_TIMER	0.000506363
Myeloid dendritic cell_TIMER	3.05E-14
B cell_QUANTISEQ	8.29E-11
Macrophage M2_QUANTISEQ	3.52E-09
T cell CD4+ (non-regulatory)_QUANTISEQ	0.007591646
T cell CD8+_QUANTISEQ	5.57E-09
T cell regulatory (Tregs)_QUANTISEQ	1.08E-13
uncharacterized cell_QUANTISEQ	1.88E-12
T cell_MCPCOUNTER	1.07E-13
T cell CD8+_MCPCOUNTER	1.11E-06
cytotoxicity score_MCPCOUNTER	5.39E-08
NK cell_MCPCOUNTER	5.47E-08
B cell_MCPCOUNTER	2.25E-19
Monocyte_MCPCOUNTER	9.63E-08
Macrophage/Monocyte_MCPCOUNTER	9.63E-08
Myeloid dendritic cell_MCPCOUNTER	6.02E-11
Cancer associated fibroblast_MCPCOUNTER	0.0082272

Immune Cells	pvalue
Myeloid dendritic cell activated_XCELL	4.61E-13
B cell_XCELL	2.40E-14
T cell CD4+ naive_XCELL	1.36E-10
T cell CD4+ effector memory_XCELL	0.000196619
T cell CD8+_XCELL	2.27E-13
T cell CD8+ central memory_XCELL	2.36E-14
T cell CD8+ effector memory_XCELL	6.76E-07
Class-switched memory B cell_XCELL	1.51E-07
Myeloid dendritic cell_XCELL	4.11E-12
Endothelial cell_XCELL	0.000364991
Cancer associated fibroblast_XCELL	1.80E-05
Granulocyte-monocyte progenitor_XCELL	0.00400137
Hematopoietic stem cell_XCELL	0.005322691
Macrophage_XCELL	0.000125615
Macrophage M1_XCELL	2.70E-06
Mast cell_XCELL	0.020239227
B cell memory_XCELL	3.29E-10
Monocyte_XCELL	0.000812046
B cell naive_XCELL	7.11E-06
Plasmacytoid dendritic cell_XCELL	7.37E-07
B cell plasma_XCELL	5.70E-06
T cell gamma delta_XCELL	0.000117466
T cell regulatory (Tregs)_XCELL	0.036740797
immune score_XCELL	2.08E-16
stroma score_XCELL	1.41E-05
microenvironment score_XCELL	3.53E-19
B cell_EPIC	2.16E-17
Cancer associated fibroblast_EPIC	0.017421554
T cell CD8+_EPIC	0.002618484
Endothelial cell_EPIC	4.20E-05
Macrophage_EPIC	1.57E-08
NK cell_EPIC	5.58E-05
uncharacterized cell_EPIC	2.61E-07

1.2 Supplementary Figures

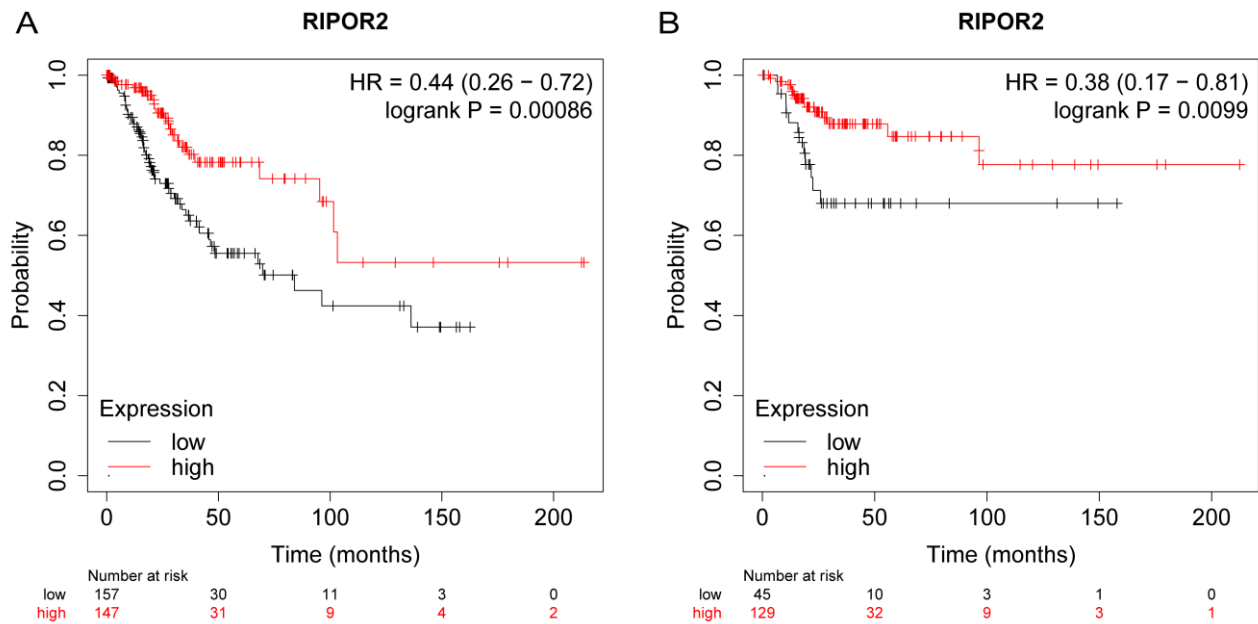


Supplementary Figure 1. Kaplan-Meier curves of overall survival (OS) for cervical cancer patients' clinicopathological characteristics based on risk score. (A, B) Kaplan-Meier curves of OS in age <= 50 and age > 50 CC. (C, D) Kaplan-Meier curves of OS in G1-2 and G3-4. (E, F) Kaplan-Meier curves of OS in Stage I-II and Stage III-IV. (G, H) Kaplan-Meier curves of OS in T1-2 and T3-4. (I, J) Kaplan-Meier curves of OS in M0 and M1. (K, L) Kaplan-Meier curves of OS in N0 and N1.

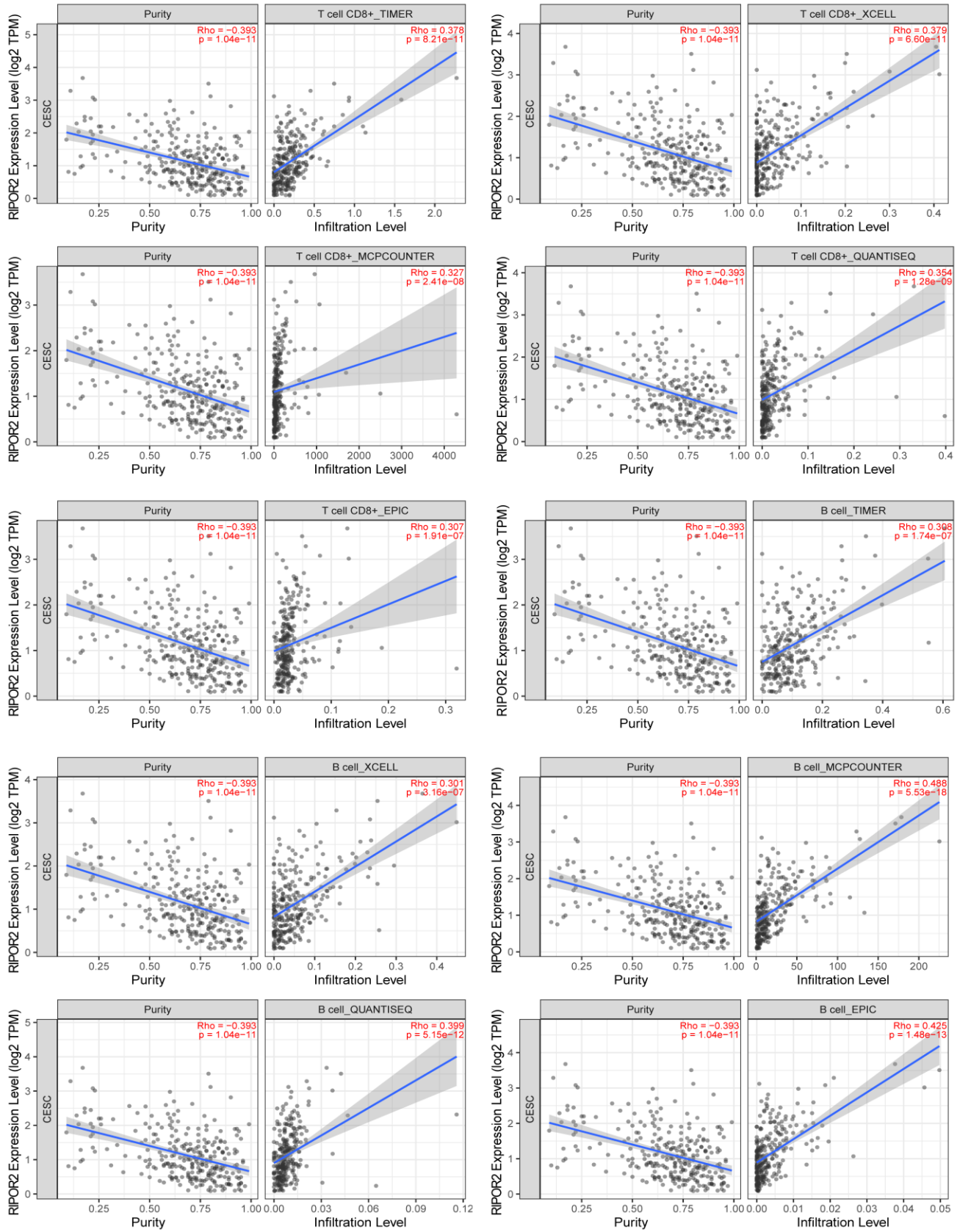


Supplementary Figure 2. Landscape of Somatic Mutation in High-Risk and Low-Risk Cohorts.
(A, B) Waterfall plot shows the mutation distribution of the top 20 most frequently mutated genes. The

central panel shows the types of mutations in each cervical cancer (CC) sample. The upper panel shows the mutation frequency of each CC sample. The bar plots on the left and right side show the frequency and mutation type of genes mutated in the low-risk and high-risk cohort, respectively. The bottom panel is the legend for mutation types. (C, D) The heatmap illustrates the mutually co-occurring and exclusive mutations of the top 20 frequently mutated genes. The color and symbol in each cell represent the statistical significance of the exclusivity or co-occurrence for each pair of genes. (E) Forest plot displays the significantly differentially mutated genes between two cohorts. (F, G) Kaplan-Meier curves show the independent relevance between overall survival time and HUWE1 and EP300 mutation in high-risk and low-risk cohorts.



Supplementary Figure 3. The correlation of APOBEC3A expression with survival time using the Kaplan-Meier plotter. (A) Overall Survival (OS) analysis for CC patients with different RIPOR2 expression by log-rank test, $p = 0.00086$. (B) Relapse free survival (RFS) analysis for CC patients with different RIPOR2 expression by log-rank test, $p = 0.0099$.



Supplementary Figure 4. Correlation of RIPOR2 expression with immune cells via TIMER online database.