Figure S1. Correlation between MAPK12 expression and survival prognosis for various types of cancer based on data obtained from TCGA. The correlation between MAPK12 mRNA expression and (A) overall survival, and (B) disease-free survival in different types of cancer using Cox regression survival analysis on TCGA datasets. MAPK12, P38 mitogen-activated protein kinase 12; TCGA, The Cancer Genome Atlas; CI, confidence interval.

A

Cancer code	P-value	Hazard ratio (95% CI)
TCGA-PCPG(N=170)	0.02	0.43(0.22,0.83)
TCGA-GBMLGG(N=619)	1.30E-13	0.53(0.45,0.63)
TCGA-LGG(N=474)	7.10E-05	0.58(0.45,0.76)
TCGA-PAAD(N=172)	0.05	0.85(0.72,1.00)
TCGA-KIPAN(N=855)	1.50E-03	1.13(1.05,1.22)
TCGA-LAML(N=209)	0.02	1.13(1.02,1.26)
TCGA-HNSC(N=509)	0.01	1.15(1.03,1.29)
TCGA-LIHC(N=341)	7.90E-03	1.16(1.04,1.29)
TCGA-LUAD(N=490)	0.02	1.16(1.03,1.31)
TCGA-BLCA(N=398)	2.10E-03	1.17(1.06,1.29)
TARGET-LAML(N=142)	0.05	1.19(1.00,1.42)
TCGA-COADREAD(N=368)	0.02	1.20(1.03,1.40)
TCGA-COAD(N=278)	0.03	1.21(1.02,1.44)
TCGA-ACC(N=77)	3.30E-03	1.27(1.08,1.49)
TCGA-MESO(N=84)	9.90E-04	1.99(1.32,2.98)
TCGA-THCA(N=501)	0.02	2.05(1.14,3.70)
TCGA-UVM(N=74)	7.60E-05	2.22(1.47,3.36)

−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0 1.5 2.0
Log2 (Hazard ratio (95%CI))

B

Cancer code	P-value	Hazard ratio (95% CI)
TCGA-GBMLGG(N=598)	5.20E-13	0.52(0.44,0.62)
TCGA-LGG(N=466)	5.80E-05	0.56(0.42,0.74)
TCGA-KIPAN(N=840)	0.04	1.10(1.00,1.22)
TCGA-STES(N=524)	0.05	1.13(1.00,1.27)
TCGA-HNSC(N=485)	0.01	1.21(1.04,1.40)
TCGA-BRCA(N=1025)	0.02	1.24(1.03,1.49)
TCGA-KIRP(N=272)	0.05	1.24(1.00,1.55)
TCGA-BLCA(N=385)	2.70E-04	1.25(1.11,1.41)
TCGA-ACC(N=75)	5.20E-03	1.27(1.07,1.50)
TCGA-COAD(N=263)	0.02	1.31(1.04,1.67)
TCGA-COADREAD(N=347)	0.01	1.32(1.06,1.64)
TCGA-UVM(N=74)	2.50E-05	2.56(1.60,4.09)
TCGA-MESO(N=64)	7.50E-05	3.38(1.88,6.08)
TCGA-THCA(N=495)	2.70E-03	3.49(1.52,8.01)

−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0 1.5 2.0 2.5 3.0
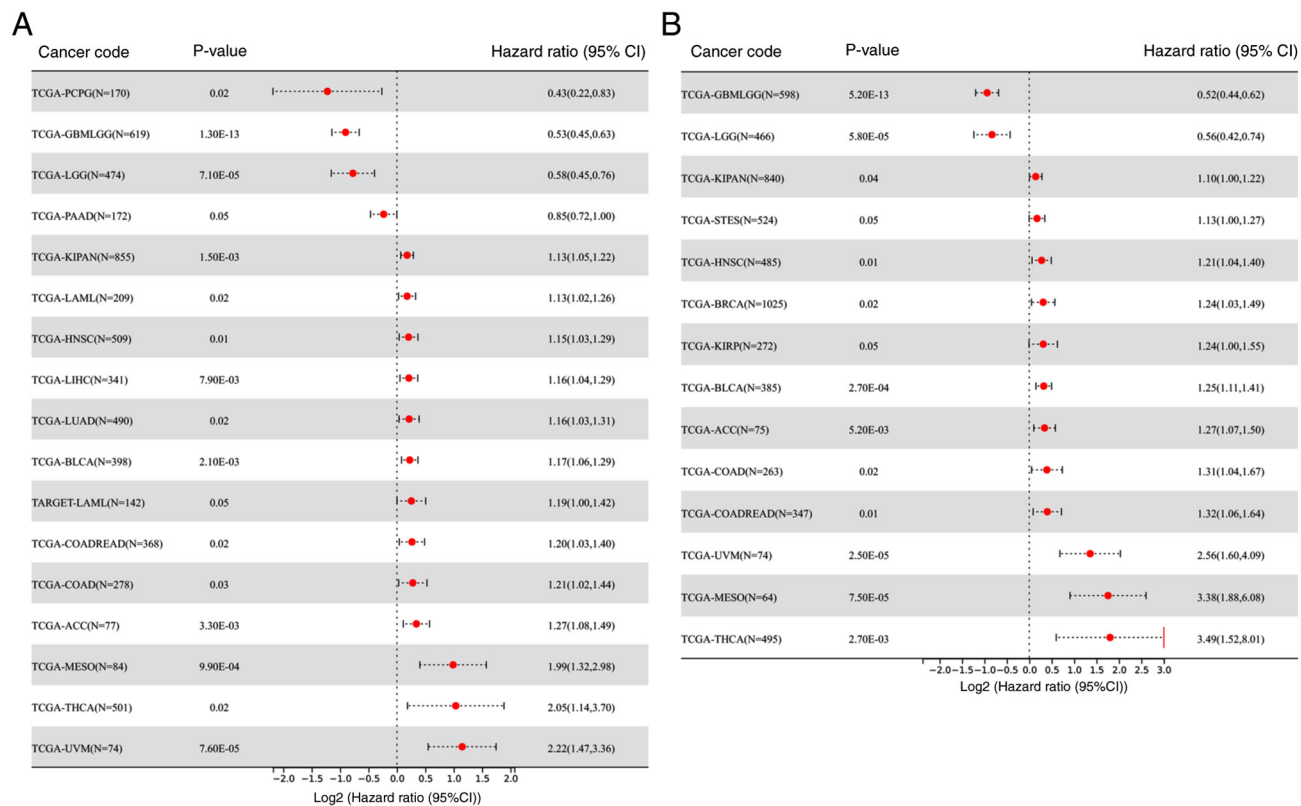Log2 (Hazard ratio (95%CI))

Figure S2. Experimental verification of MAPK12 overexpression in THCA cell lines. (A) The mRNA and protein expression levels of MAPK12 following MAPK12 overexpression in the TPC-1 cell line. (B) Cytotoxicity assays were used to measure cell viability and proliferation following MAPK12 overexpression in HTH-83 cells. (C) EdU assays were used to measure cell viability and proliferation following MAPK12 overexpression in TPC-1 cells. $^{**}P<0.01$, $^{****}P<0.0001$. MAPK12, P38 mitogen-activated protein kinase 12; THCA, thyroid carcinoma.
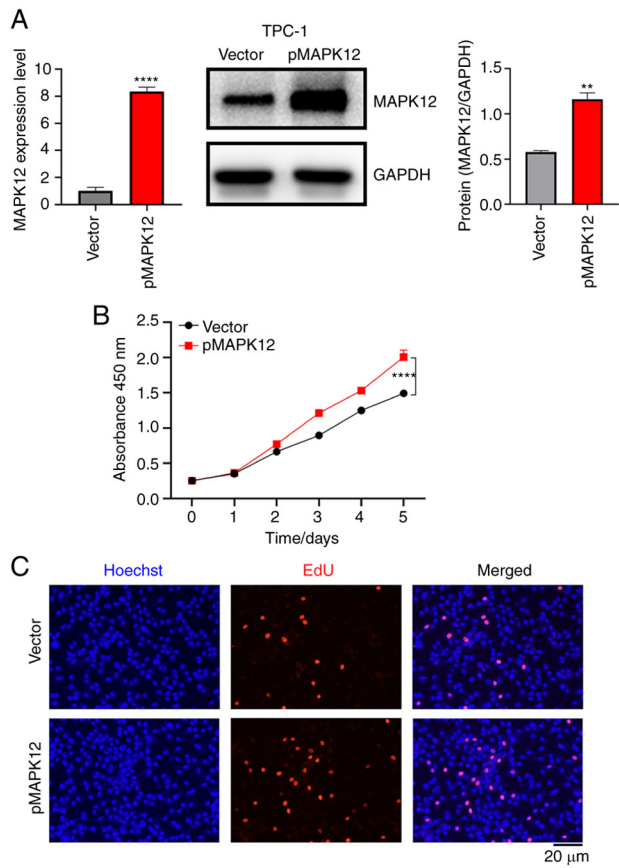
Figure S3. The correlation between MAPK12 mRNA expression and tumor immune-related cells in THCA. Correlation between MAPK12 mRNA expression and immune cell types in THCA calculated using the ImmuCellAI algorithm on the data obtained from TCGA. *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001. MAPK12, P38 mitogen-activated protein kinase 12; THCA, thyroid carcinoma; pMAPK12, pcDNA3.1-MAPK12; ICA, Immune Cell Abundance Identifier (ImmuCellAI).