Supplementary Table S2. Statistical tests used in Figures data.

Figure	Database	Object	Method	Sample		Statistical test	p-value (p<0.05)
Figure 1	GEPIA2	mRNA Expression level, Box plot	TCGA & GTEx projects	SKCM	T(n=461) N(n=558)	ANOVA Empirical Bayes method One-way ANOVA	$p=2.94\times10^{-111}$ (Log2FC=-1.521)
				LUAD	T(n=483) N(n=347)	ANOVA Empirical Bayes method One-way ANOVA	$p=1.66\times10^{-117}$ (Log2FC=-2.379)
	GENT2	Gene expression	Microarray datasets	SKCM	T(n=547) N(n=263)	Two-sample T-test	p<0.0001 (Log2FC= -1.136)
				LUAD	T(n=2362) N(n=508)		p<0.0001 (Log2FC= -0.767)
Figure 2	GEPIA2	Survival plot (Overall)	TCGA & GTEx projects	SKCM	High(n=223) Low(n=221)	Log rank test (Mantel-Cox test)	$p=1.8\times10^{-6}$
				LUAD	High(n=239) Low(n=238)		$p=1.4\times10^{-3}$
	Prognoscan	Survival plot (OS, RFS)	Microarray datasets	SKCM	High(n=11) Low(n=27)	Minimum P-value approach	$p=4.23\times10^{-2}$
				LUAD	High(n=117) Low(n=21)		$p=3.41\times10^{-2}$
Figure 4	TISIDB	Expression of immune cells	gene set variation analysis (GSVA)	SKCM	n=472	Empirical bayes estimate	Activated B cell ($p<2.2\times10^{-16}$) Activated CD8+ T cell ($p<2.2\times10^{-16}$) Effector memory CD8+ T cell ($p<2.2\times10^{-16}$) NK cell ($p<2.2\times10^{-16}$)
				LUAD	n=517		Activated B cell ($p<2.2\times10^{-16}$) Activated CD8+ T cell ($p<1.84\times10^{-11}$) Effector memory CD8+ T cell ($p<2.15\times10^{-16}$) NK cell ($p<1.61\times10^{-11}$)

Figure	Platform	Method	Tools	Dataset	Algorithm	Cell	p-value
Figure 5	TIMER Version 2.0	Correlation	EPIC QUANTISEQ MCP_COUNTER CIBERSORT_ABS	SKCM (n=471) LUAD (n=515)	Bayesian statistics Gibbs sampling Expectation maximization algorithm	B cell (SKCM)	$(p=5.83\times10^{-32})$ $(p=1.30\times10^{-34})$ $(p=2.56\times10^{-36})$ $(p=2.53\times10^{-12})$
						B cell (LUAD)	$(p=2.32\times10^{-35})$ $(p=4.44\times10^{-32})$ $(p=2.08\times10^{-40})$ $(p=1.01\times10^{-20})$
			MCP_COUNTER CIBERSORT-ABS QUANTISEQ XCELL		Bayesian statistics Gibbs sampling Expectation maximization algorithm	CD+8 T cell (SKCM)	$(p=7.25\times10^{-72})$ $(p=3.49\times10^{-50})$ $(p=6.91\times10^{-14})$ $(p=6.91\times10^{-14})$
						CD+8 T cell (LUAD)	$(p=2.73\times10^{-10})$ $(p=3.49\times10^{-50})$ $(p=6.91\times10^{-14})$ $(p=6.91\times10^{-14})$
			MCP_COUNTER Activated CIBERSORT-ABS Resting CIBERSORT Resting CIBERSORT-ABS		Bayesian statistics Gibbs sampling Expectation maximization algorithm	NK cell (SKCM)	$(p=2.40\times10^{-22})$ $(p=9.09\times10^{-13})$ $(p=2.50\times10^{-5})$ $(p=4.45\times10^{-4})$
						NK cell (LUAD)	$(p=1.47\times10^{-10})$ $(p=8.399\times10^{-7})$ $(p=2.16\times10^{-1})$ $(p=2.68\times10^{-1})$
Figure 6	UCSC Xena	Profiling of co-expressed genes with PKHD1L1	TCGA	SKCM(n=481)			$p=2.53\times10^{-81}$
				LUAD(n=706)			$p=3.228\times10^{-35}$
	R2 platform		TCGA	SKCM(n=80)			$p=1.45\times10^{-4}$
				LUAD(n=410)			$p=5.97\times10^{-64}$