Supplementary Table S1. The cox regression results of *IL32* expression in SKCM and LIHC.

KM plot data using TIMER version 1.0 ($p < 0.05$)

	SKCM						LIHC					
	coef	HR	95% CI _low	95% CI _upper	*P*-value	significant	coef	HR	95% CI _low	95% CI _upper	*P*-value	significant
Purity	−0.218	0.804	0.339	1.907	0.621		0.487	1.627	.660	4.012	0.290	
IL32	−0.252	0.777	0.691	0.874	0.000	***	−0.103	0.903	0.784	1.039	0.155	
Age	0.018	1.018	1.008	1.029	0.000	***	0.011	1.011	0.995	1.027	0.174	
Stage2	0.131	1.140	0.736	1.765	0.558		0.312	1.367	0.811	2.305	0.241	
Stage3	0.528	1.696	1.134	2.538	0.010	*	0.944	2.57	1.623	4.067	0	***
Stage4	1.352	3.866	1.935	7.725	0	***	1.582	4.862	1.441	16.402	0.011	*
Gender	−0.065	0.937	0.686	1.279	0.682		−0.101	0.904	0.574	1.424	0.664	
Race	−1.386	0.250	0.114	0.550	0.001	**	−0.031	0.969	0.608	1.546	0.896	

*$p < 0.01$; **$p < 0.001$; ***$p < 0.0001$.

KM plot data using TIMER version 2.0 ($p < 0.05$, Z< 0)

	SKCM								LIHC							
	coef	HR	Se (coef)	95% CI _low	95% CI _upper	Z-value	*P*-value	significant	coef	HR	Se (coef)	95% CI _low	95% CI _upper	Z-value	*P*-value	significant
Purity	−0.203	0.816	0.442	0.343	1.94	−0.46	0.645		0.52	1.683	0.458	0.686	4.129	1.136	0.256	
IL32	−0.251	0.778	0.06	0.691	0.875	−4.175	0	***	−0.097	0.908	0.071	0.789	1.044	−1.352	0.176	
Age	0.018	1.018	0.005	1.008	1.029	3.393	0.001	**	0.012	1.012	0.008	0.997	1.028	1.523	0.128	
Stage2	0.111	1.117	0.224	0.72	1.734	0.495	0.621		0.319	1.376	0.262	0.823	2.3	1.219	0.223	
Stage3	0.522	1.686	0.206	1.127	2.523	2.54	0.011	*	0.944	2.57	0.234	1.623	4.067	4.028	0	***
Stage4	1.352	3.866	0.353	1.935	7.714	3.824	0	***	1.55	4.71	0.619	1.399	15.862	2.502	0.012	*
Gender	−0.075	0.928	0.159	0.679	1.268	−0.469	0.639		−0.091	0.913	0.029	0.583	1.43	−0.397	0.691	
Race	−1.401	0.246	0.403	0.112	0.542	−3.48	0.001	**	−0.001	0.999	0.236	0.629	1.587	−0.005	0.996	

p < 0.01; **p* < 0.001; ***p* < 0.0001.

Supplementary Table S2. Statistical tests used in Figures and Supplementary data.

Figure	Database	Object	Method	Sample	Statistical test	*p*-value (*p* < 0.05)
Figure 1	GEPIA2	mRNA Expression level	TCGA & GTEx projects	Tumor (*n* = 461) Normal (*n* = 558)	ANOVA Empirical Bayes method	$p = 3.5 \times 10^{-63}$
		Box plot			One-way ANOVA	
Figure 2	GEPIA2	Survival plot (Overall)	TCGA & GTEx projects	High (*n* = 229) Low (*n* = 229)	Log rank test (Mantel-Cox test)	$p = 3.1 \times 10^{-4}$
	TIMER 1.0		TCGA	*n* = 425	Proportional hazards model	$p = 0 \times 10^{+00}$
	TIMER 2.0		TCGA cohorts	*n* = 471	Proportional hazards model	$p = 4.6 \times 10^{-2}$
Figure 3	UALCAN	Promoter methylation	TCGA	Normal (*n* = 2) Primary (*n* = 104) Metastasis (*n* = 368)	Student`s t-test	Nor vs Pri ($p = 4.23 \times 10^{-1}$) Nor vs Met ($p = 5.95 \times 10^{-5}$) Pri vs Met ($p = 9.15 \times 10^{-1}$)
Figure 4	TISIDB	Expression of immune cells	gene set variation analysis (GSVA)	*n* = 472	Empirical bayes estimate	$p = 2.2 \times 10^{-6}$
Figure 5	TIMER Version 1.0	Correlation	TCGA	*n* = 103	Bayesian statistics Gibbs sampling Expectation maximization algorithm	KIR2DL3 ($p = 1.79 \times 10^{-11}$) KIR3DL2 ($p = 2.63 \times 10^{-70}$) KIR2DL4 ($p = 7.41 \times 10^{-82}$) NCR1 ($p = 3.39 \times 10^{-47}$) KNCR3 ($p = 2.09 \times 10^{-119}$)
Figure 6	TIMER Version 2.0	Correlation	CIBERSORT	*n* = 471	Bayesian statistics Gibbs sampling Expectation maximization algorithm	Purity ($p = 7.25 \times 10^{-72}$) Activated NK cells ($p = 1.23 \times 10^{-16}$) Rested NK cells ($p = 3.95 \times 10^{-17}$)
			CIBERSORT-ABS		Bayesian statistics Gibbs sampling Expectation maximization algorithm	Purity ($p = 7.25 \times 10^{-72}$) Activated NK cells ($p = 3.49 \times 10^{-50}$) Rested NK cells ($p = 6.91 \times 10^{-14}$)

|						
Figure 7	TIMER Version 1.0	Correlation	TCGA	$n = 103$	Bayesian statistics Gibbs sampling Expectation maximization algorithm	GZMA ($p = 6.04\times10^{-163}$) GZMB ($p = 0\times10^{+00}$) PRF1 ($p = 1.01\times10^{-146}$)
	cBioportal	Co-expressed gene list	TCGA	-	Clustering statistics	*IL2RG* ($p = 5.15\times10^{-174}$)
Figure 8	UCSC Xena	Correlation	TCGA	$n = 481$		*IL32-IL2RG* ($p = 7.76\times10^{-213}$)
	R2	Correlation	-	$n = 44$	Brute force t-test One way ANOVA	*IL32-IL2RG* ($p = 1.03\times10^{-9}$)
Figure 9	Enricher	GO biological process	-	-	Standard statistical method Fisher's exact test Hypergeometric test	Biological process ($p = 1.49\times10^{-5}$) Molecular Function ($p = 8.19\times10^{-5}$) Cellular component ($p = 3.44\times10^{-8}$)
Supplementary S4	OncoLnc	Cox regression	-	-	Cox proportional Hazards model	$p = 7.90\times10^{-4}$
Supplementary S5	GEPIA2	Survival plot (Disease Free Survival)	TCGA & GTEx projects	High ($n = 229$) Low ($n = 229$)	Log rank test (Mantel-Cox test)	$p = 2.0\times10^{-1}$
Supplementary S7	TIMER Version 2.0	Correlation (BRAF)	TCGA	$n = 465$	Bayesian statistics Gibbs sampling Expectation maximization algorithm	$p = 6.4\times10^{-2}$
Supplementary S8	TIMER Version 1.0	Correlation	TCGA	$n = 103$	Bayesian statistics Gibbs sampling Expectation maximization algorithm	Purity ($p = 7.25\times10^{-72}$) B cell ($p = 3.66\times10^{-11}$) CD8+ T cell ($p = 1.05\times10^{-31}$) CD4+ T cell ($p = 2.05\times10^{-22}$) Macrophage ($p = 1.00\times10^{-10}$) Neutrophill ($p = 1.32\times10^{-32}$) Dendritic cell ($p = 6.01\times10^{-58}$)
Supplementary S13	GEPIA2	Correlation	TCGA & GTEx projects	Tumor ($n = 461$)	Spearman correlation	CXCL9 ($p = 1.7\times10^{-112}$) CXCL10 ($p = 3.0\times10^{-77}$) CXCL11 ($p = 3.0\times10^{-68}$)

Supplementary Table S3. Tumor Abbreviations

Abbreviation	Type of Cancer
ACC	Adrenocortical carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	Cholangio carcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
ESCA	Esophageal carcinoma
GBM	Glioblastoma multiforme
HNSC	Head and Neck squamous cell carcinoma
KICH	Kidney Chromophobe
KIRC	Kidney renal clear cell carcinoma
KIRP	Kidney renal papillary cell carcinoma
LAML	Acute Myeloid Leukemia
LGG	Brain Lower Grade Glioma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung squamous cell carcinoma
MESO	Mesothelioma
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular Germ Cell Tumors
THCA	Thyroid carcinoma

Supplementary Table S4. Cox regression results for *IL32* with TCGA data in various types of cancers by OncoLnc. The data with *p*-value < 0.01 are marked with red.

| Cancer	Cox Coefficient	*p*-Value	FDR Corrected	Rank	Median Expression	Mean Expression
SKCM	−0.224	7.90×10^{-4}	1.20×10^{-2}	1059	630.9	1326.15
SARC	−0.362	1.50×10^{-3}	4.07×10^{-2}	586	1220.88	2354.81
PAAD	0.26	1.90×10^{-2}	1.06×10^{-1}	3030	4441.18	4962.08
LIHC	−0.168	8.30×10^{-2}	2.92×10^{-1}	4498	11949.06	21242.03
UCEC	−0.152	1.50×10^{-1}	9.68×10^{-1}	2492	2084.05	3466.36
BLCA	−0.104	1.70×10^{-1}	4.19×10^{-1}	6528	1100.77	2227.77
BRCA	−0.101	2.30×10^{-1}	6.10×10^{-1}	6186	904.08	1452.49
OV	−0.092	2.40×10^{-1}	7.95×10^{-1}	5005	810.49	1177.3
LUAD	0.085	2.60×10^{-1}	5.04×10^{-1}	8573	2344.86	2989.48
KIRP	−0.161	2.90×10^{-1}	4.76×10^{-1}	9943	10570.44	12843.81
HNSC	−0.073	3.10×10^{-1}	6.43×10^{-1}	7923	2205.22	3464.29
GBM	0.092	3.30×10^{-1}	8.85×10^{-1}	6182	346.67	436.5
KIRC	−0.078	3.40×10^{-1}	4.71×10^{-1}	12002	7784.6	9252.17
CESC	−0.108	3.80×10^{-1}	7.11×10^{-1}	8667	3097.67	4733.14
LUSC	0.062	3.80×10^{-1}	8.17×10^{-1}	7818	1318.88	2071.46
LGG	0.062	5.10×10^{-1}	6.07×10^{-1}	14107	155.38	260.48
READ	−0.114	6.10×10^{-1}	9.77×10^{-1}	10215	5257.51	5898.36
LAML	−0.058	6.40×10^{-1}	8.71×10^{-1}	11143	176.05	295.76
STAD	−0.038	6.40×10^{-1}	8.82×10^{-1}	12202	2537.94	3540.33
COAD	−0.043	6.90×10^{-1}	9.02×10^{-1}	12490	5428.92	6129.97
ESCA	−0.04	7.70×10^{-1}	9.85×10^{-1}	13041	1322.23	1910.35

Supplementary Figure S5. Correlation between *IL32* expression and disease free survival (DFS) of various types of cancers by GEPIA2. (log-rank *p* < 0.05)
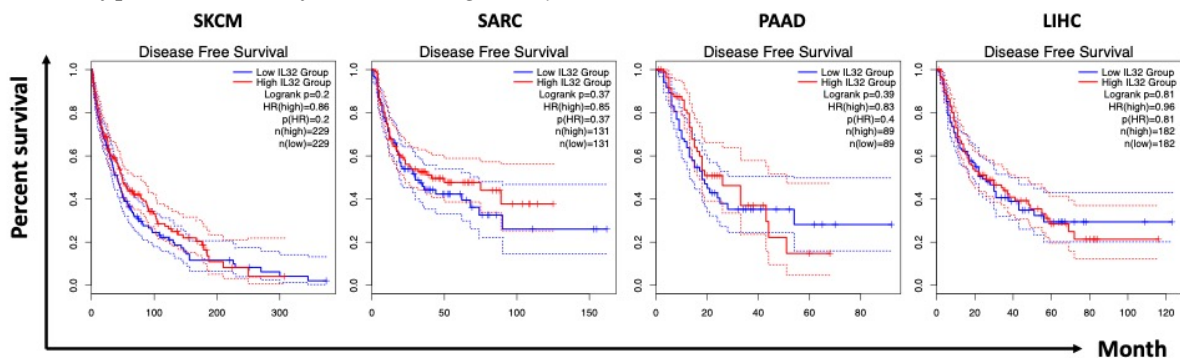
Supplementary Table S6. Fifteen mutations in the *IL32* gene by cBioportal.

| Sample ID	Protein Change	Mutation Type	Copy #	Allele Freq (T)	# Mut in Sample
TCGA-W3-AA1W−06	X10_splice	Splice	Diploid	0.19	586
TCGA-W3-AA1V−06	R70K	Missense	Diploid	0.57	4559
TCGA-W3-AA1V−06	P224L	Missense	Diploid	0.09	4559
TCGA-FW-A3R5−06	S133F	Missense	ShallowDel	0.17	15825
TCGA-FW-A3R5−06	D140N	Missense	ShallowDel	0.29	15825
TCGA-FW-A3R5−06	M155I	Missense	ShallowDel	0.28	15825
TCGA-FS-A1ZZ−06	S34L	Missense	Diploid	0.45	1530
TCGA-ER-A193−06	K234I	Missense	ShallowDel	0.31	1700
TCGA-EE-A2MS−06	K121*	Nonsense	Diploid	0.25	2462
TCGA-EE-A2GO−06	T38I	Missense	ShallowDel	0.28	1909
TCGA-EE-A17X−06	F150S	Missense	Diploid	0.26	680
TCGA-D9-A6EC−06	F3V	Missense	ShallowDel	0.3	3676
TCGA-D3-A51F−06	X10_splice	Splice	Diploid	0.06	103
TCGA-D3-A2JF−06	P53L	Missense	Diploid	0.43	1213
TCGA-D3-A2J8−06	X10_splice	Splice	Diploid	0.1	953

Supplementary Figure S7. Correlation *IL32* expression and BRAF mutation status in SKCM by TIMER v.2.0. ($p < 0.05$)
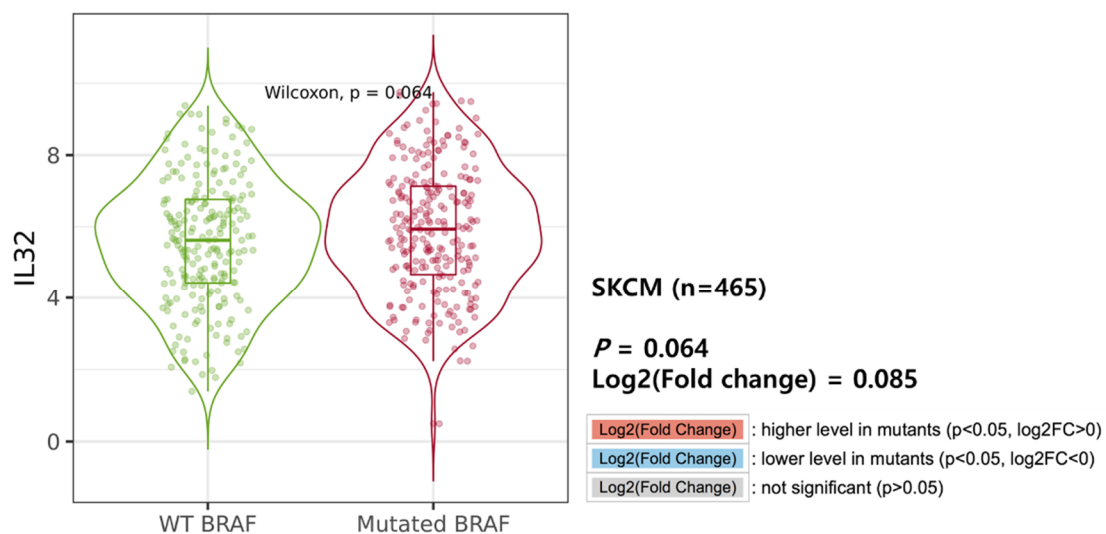
Supplementary Figure S8. Correlation of *IL32* expression with immune cell infiltration level in SKCM and LIHC. (TIMER v.1.0) (*p* < 0.05)
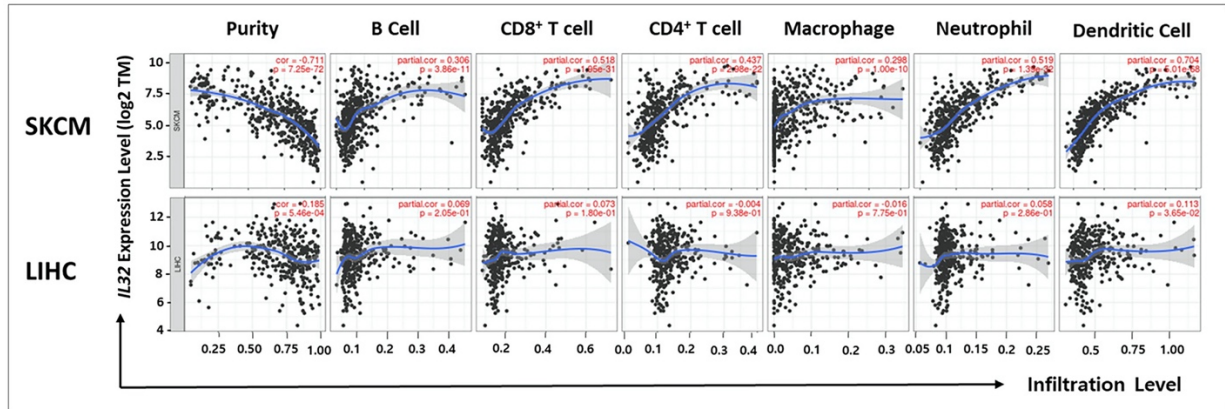
Supplementary Figure S9. Correlations between *IL32* expression and NK cells of various types of cancers by TISIDB. (*p* < 0.05)
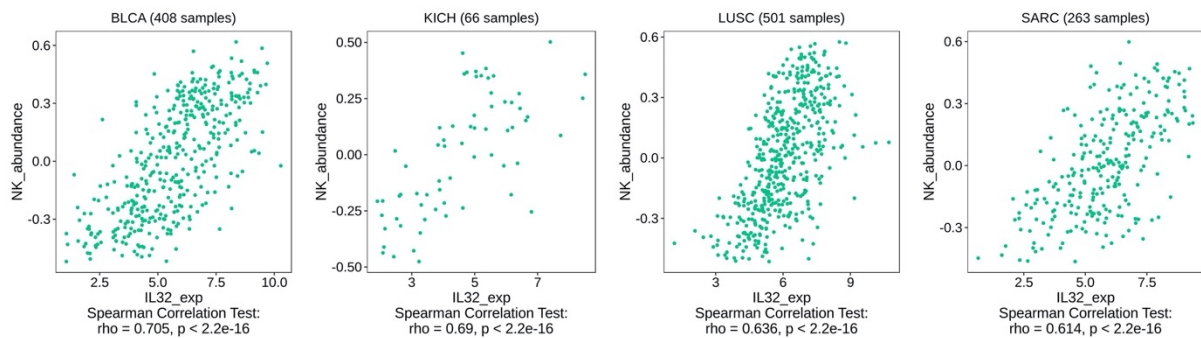
Supplementary Table S10. Correlation analysis between *IL32* and gene markers of immune cells using TIMER (v.1.0).

Description	Gene markers	SKCM				LIHC			
		None		Purity		None		Purity	
		Cor	*P*	Cor	*P*	Cor	*P*	Cor	*P*
	KIR2DL1	0.459	***	0.32	***	−0.048	0.35	−0.066	0.23
	KIR2DL3	0.621	***	0.46	***	−0.014	0.78	−0.051	0.35
	KIR2DL4	0.737	***	0.63	***	0.073	0.16	0.038	0.49
	KIR3DL1	0.618	***	0.49	***	0.006	0.91	−0.028	0.60
Natural killer cell	*KIR3DL2*	0.699	***	0.55	***	0.046	0.38	−0.022	0.68
	KIR3DL3	0.243	***	0.19	***	0.000	1.00	−0.022	0.68
	KIR2DS4	0.513	***	0.40	***	−0.047	0.37	−0.059	0.27
	NCR1	0.599	***	0.487	***	−0.002	0.97	−0.065	0.22
	NCR3	0.827	***	0.712	***	0.218	***	0.137	***

Cell type	Gene	None		Purity		None		Purity	
		Cor	P	Cor	P	Cor	P	Cor	P
CD8+ T cell	CD8A	0.869	0	0.80	***	0.170	***	0.081	0.135
	CD8B	0.882	***	0.81	***	0.138	***	0.044	0.412
Treg	FOXP3	0.809	***	0.68	***	0.057	0.274	0.023	0.664
	CCR8	0.720	***	0.59	***	0.143	***	0.075	0.165
	STAT5B	0.230	***	0.14	***	−0.204	***	−0.177	***
	TGFβ(TGFB1)	0.472	0	0.31	***	0.006	0.901	−0.111	***
TAM	CCL2	0.624	0	0.45	***	0.205	***	0.126	***
	CD68	0.516	0	0.33	***	0.179	***	0.105	***
	IL10	0.610	***	0.43	***	0.117	***	0.012	0.817
T cell(general)	CD3D	0.932	***	0.88	***	0.172	***	0.251	***
	CD3E	0.938	0	0.89	***	0.263	***	0.176	***
	CD2	0.923	0	0.87	***	0.293	***	0.214	***
B cell	CD19	0.683	***	0.56	***	0.112	***	0.040	0.46
	CD79A	0.749	0	0.63	***	0.106	***	−0.003	0.96
Monocyte	CD86	0.806	0	0.68	***	0.210	***	0.122	***
	CD115(CSF1R)	0.738	***	0.60	***	0.241	***	0.145	***
M1 Macrophage	INOS(NOS2)	0.030	0.519	0.03	0.511	−0.003	0.95	−0.012	0.82
	IRF5	0.654	0	0.45	***	0.031	0.55	0.033	0.54
	COX2(PTGS2)	0.014	0.706	−0.11	***	0.123	***	0.032	0.56
M2 Macrophage	CD163	0.586	0	0.42	***	0.082	0.13	0.181	***
	VSIG4	0.607	0	0.47	***	0.233	***	0.156	***
	MS4A4A	0.670	0	0.51	***	0.248	***	0.166	***
Neutrophils	CD66b(CEACAM8)	−0.061	0.184	−0.04	0.461	−0.070	0.18	−0.098	***
	CD11b(ITGAM)	0.652	0	0.53	***	0.342	***	0.284	***
	CCR7	0.821	***	0.69	***	0.188	***	0.092	***
Dendritic cell	HLA-DPB1	0.857	0	0.75	***	0.269	***	0.191	***
	HLA-DQB1	0.792	0	0.66	***	0.246	***	0.168	***
	HLA-DRA	0.847	***	0.74	***	0.287	***	0.215	***
	HLA-DPA1	0.824	0	0.73	***	0.267	***	0.190	***
	BDCA−1(CD1C)	0.616	***	0.42	***	0.105	***	0.032	0.55
	CD11c(ITGAX)	0.636	***	0.43	***	0.234	***	0.163	***

SKCM, skin cutaneous melanoma; LIHC, liver hepatocellular carcinoma; Treg, regulatory T cell; TAM, tumor-associated macrophage; Th, T helper cell; Tfh, follicular helper T cell; Cor, P value of Spearman's correlation; None, correlation without adjustment. Purity and correlation adjusted by purity *P < 0.01; **P < 0.001; ***P < 0.0001.

Supplementary Table S11. Correlation constants and *p*-values in Figure 5 (TIMER v.1.0) ($p < 0.05$)

Gene markers		SKCM		LIHC	
		Cor	***p***	**Cor**	***p***
NK Cell	*KIR2DL3*	0.621	1.79×10^{-51}	−0.014	7.81×10^{-1}
	KIR3DL2	0.699	2.63×10^{-70}	0.046	3.82×10^{-1}
	KIR2DL4	0.737	7.41×10^{-82}	0.073	1.59×10^{-1}
	NCR1	0.599	3.39×10^{-47}	−0.002	9.73×10^{-1}
	NCR3	0.827	2.09×10^{-119}	0.218	2.32×10^{-5}

Supplementary Table S12. Correlation constants and *p*-values in Figure 7 (TIMER v.1.0) ($p < 0.05$)

Gene markers	SKCM		LIHC	
	Cor	***p***	**Cor**	***p***
GZMA	0.891	6.04×10^{-163}	0.271	1.16×10^{-7}
GZMB	0.869	$0E + 00$	0.029	5.8×10^{-1}
PRF1	0.871	1.01×10^{-46}	0.095	6.77×10^{-2}

Supplementary Figure S13. Correlations between *IL32* expression and chemokines (CXCL 9,10,11) in SKCM by GEPIA2. ($p < 0.05$)