

Table S1 The top 20 marker genes of 29 clusters are shown

Cluster0	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9	Cluster10	Cluster11	Cluster12	Cluster13	Cluster14	Cluster15	Cluster16	Cluster17	Cluster18	Cluster19	Cluster20	Cluster21	Cluster22	Cluster23	Cluster24	Cluster25	Cluster26	Cluster27	Cluster28
TRGC2	IL7R	S100A9	CCL3	IL7R	CLIC3	MARCO	MT1G	SPINK1	IGHG3	MGP	TAGLN	ZFP36L2	HLA.DPB1	FXVD2	MS4A1	FCN3	ALDOB	KLRF1	STMN1	CLU	AKR1B10	SLC40A1	MT1G	MT1H	TUBA1B	AIF1	GPR183	MS4A2
CCL5	LTB	G0S2	CCL3L3	TRAC	KLRF1	CD5L	HP	PRAP1	IGHG4	TM4SF1	DCN	HSPB1	HLA.DQB1	KRT8	BANK1	DNASE1L3	GSTA1	CD7	HMGB2	DEFB1	NQO1	LIPA	FGG	CRP	STMN1	LST1	IRF4	SLC18A2
GZMH	CD69	FCN1	MS4A7	IFITM1	CMC1	C1QB	ORM1	APOA1	IGKC	EMP1	IGFBP7	HSPH1	HLA.DQA1	KRT18	LY9	CRHBP	FABP1	IFITM1	TUBA1B	TM4SF4	AKR1C3	CD5L	CD69	SAA1	TUBB	FCER1G	GZMB	CTSG
CD8A	TRAC	LYZ	C1QA	CD3D	AREG	C1QA	SAA1	APOA2	IGHG1	AKAP12	BGN	RGCC	HLA.DPA1	DEFB1	IGHD	FCN2	NNMT	KLRD1	KIAA0101	AKR1C3	KRT8	MARCO	HBB	MT1F	TOP2A	TIMP1	JCHAIN	CPA3
DUSP2	RGCC	IL1B	CXCL8	ISG20	PRF1	C1QC	SAA4	RBP4	IGHG2	SLC9A3R2	ACTA2	CRIP1	HLA.DQA2	ANXA4	CD52	CLEC1B	MT1X	KLRB1	TUBB	VTN	PTGR1	AIF1	DCXR	MT1M	AIF1	FCN1	PLD4	TPSAB1
KLRD1	ZFP36L2	EREG	C1QC	CCL5	SPON2	SLC40A1	APOH	CFB	JCHAIN	GNG11	ADIRF	IL7R	HLA.DRA	TM4SF4	HLA.DQB1	CTSL	MT1E	CST7	HIST1H4C	RARRES2	TM4SF4	C1QB	KLRB1	RARRES2	LYZ	G0S2	ITM2C	HDC
CMC1	KLRB1	SOD2	C1QB	S100A4	KLRD1	LIPA	TTR	AMBP	IGHA2	SDPR	TPM2	HSPA1A	CD74	ELF3	LINC00926	CCL14	ADH4	CMC1	CORO1A	NR0B2	GSTA2	CST3	HBA1	GC	KIAA0101	THBS1	CXCR3	HPGDS
CD3D	SPOCK2	CXCL8	KLF4	CD3G	CD7	MS4A7	APOC3	APOC3	MZB1	SPRY1	CALD1	ANXA1	LYZ	CLDN4	CD74	AKAP12	ADH1B	CTSW	NUSAP1	ANXA4	GTSF1	C1QA	ALOX5AP	APOH	CDKN3	RNF144B	HERPUD1	IL1RL1
CST7	CCR6	BCL2A1	HLA.DRA	CRIP1	CD160	CD163	ORM2	CFHR2	SSR4	RAMP2	COL3A1	LMNA	IDO1	KRT19	FCRLA	OIT3	HPD	GZMA	TOP2A	GC	PAGE2	PDK4	HRG	MT1G	HMGB2	AP1S2	NR4A3	TPSB2
GZMK	CD2	LST1	CXCL2	CD2	KLRB1	MS4A6A	CYP2E1	CFHR1	ITM2C	IFI27	IGFBP3	BIRC3	HLA.DRB1	MMP7	HLA.DQA1	PLPP3	CYP2E1	AREG	PTTG1	LYZ	AFP	MS4A6A	MT1X	ORM1	CD74	CSTA	SEL1L3	LTC4S
ZFP36L2	ANXA1	CSTA	IL1B	CD52	GZMA	CFP	APOA1	VTN	SEC11C	CD9	LUM	DOK2	CST3	CYR61	GPR183	HES1	DCXR	PRF1	GZMA	CA1	SERPINA1	CD163	HBA2	AMBP	HLA.DPB1	IL1B	AREG	AREG
TRBC2	TRAT1	AIF1	HLA.DPA1	GZMK	B3GNT7	VCAM1	RBP4	KNG1	FKBP11	PLPP1	RGS5	LTB	CPVL	SOX4	AC079767.4	STAB1	CYB5A	ISG20	CKS1B	ADH1C	CD63	CCL3	CMC1	TF	HLA.DRA	S100A9	RGS2	CAPG
CTSW	CD3D	CTSS	CTSB	CST7	GZMB	CTSB	APOA2	RARRES2	HERPUD1	HYAL2	CTGF	ITM2A	SNX3	CD24	IGHM	SDPR	ADH1A	CCL5	RRM2	CFH	AMBP	VCAM1	CD7	TTR	CKS1B	CCL20	SOX4	ALOX5AP
AC092580.4	S100A4	SAT1	CST3	TRBC1	KLRC1	CST3	FGA	CLU	PRDX4	SPARCL1	COLEC11	SPOCK2	CSF2RA	SPP1	HERPUD1	IFI27	HRSP12	ALOX5AP	BIRC5	AGT	FGL1	CXCL2	ASS1	HP	CST3	CXCL8	IRF7	RGS13
GZMA	DUSP2	OLR1	CXCL3	GPR171	XCL2	FOLR2	ALB	GC	PIM2	ID1	GPX3	TNFRSF4	RNASE6	KRT7	CD83	CD36	ARG1	CD160	PCNA	TDO2	AKR1C1	BASP1	MT1H	ALB	SNX10	IER3	LDLRAD4	ANXA1
TRGC1	TRBC2	PSAP	LIPA	TRBC2	XCL1	FCGR3A	HPX	F2	CD27	RNASE1	SPARC	NFKB1	GPR183	TNFRSF12A	CCR7	FAM167B	AGXT	GZMB	TYMS	HMGS2	FGG	SDC3	SNHG25	APOC3	CDK1	CXCL2	TSPAN13	C1orf186
XCL2	CLEC2D	C15orf48	SLC40A1	AC092580.4	FGFBP2	FAM26F	FGB	TTR	CD38	CRIP2	C7	CCR7	CLEC9A	NTS	BIRC3	GNG11	GATM	B3GNT7	CENPF	S100A8	CLU	IER3	XCL2	APOA2	MNDA	EREG	IRF8	HPGD
CD8B	CD40LG	S100A8	MS4A6A	GZMH	PTGDS	CPVL	TF	ALB	HSP90B1	SOCS3	RBP1	ANKRD37	HLA.DRB5	TACSTD2	KIAA0226L	LIFR	ADH1C	KLRC1	MKI67	CFHR1	TUBA1B	CYBB	KLRF1	PTTG1	PTTG1	CYBB	TCL1A	VWA5A
TRDC	GPR171	CXCL3	GLUL	CLEC2D	IFNG	VSIG4	MT1H	EPHX1	IGHA1	HES1	SPARCL1	GPR171	CD1E	S100A6	ADAM28	FCGR2B	FBP1	GNLY	TK1	CCL26	AGT	CETP	NNMT	APOA1	HLA.DRB5	S100A8	CLIC3	GATA2
CRTAM	ICOS	CCL20	FGL2	ITM2A	GNLY	CCL3	FGG	ORM1	IGHM	IGFBP7	COL1A1	TRAT1	CD1C	EPCAM	LTB	TSPAN7	ANGPTL3	KLRC2	HBB	S100A9	AKR1C2	ITLN1	AC092580.4	MT2A	HIST1H4C	C15orf48	PTGDS	TSC22D1

**Table S2** The number and proportion of different cluster cells between tumor samples and normal samples

Cluster	Cell type	Tumor_cell_counts	Health_cell_counts	Tumor_cell_Freq	Health_cell_Freq
0	T_cells	904	6227	3.74	22.44
1	T_cells	2580	3736	10.68	13.46
2	Monocyte	2926	1392	12.11	5.02
3	Macrophage	2775	616	11.49	2.22
4	T_cells	1022	2194	4.23	7.91
5	NK_cell	534	2428	2.21	8.75
6	Macrophage	1053	1495	4.36	5.39
7	Hepatocytes	1504	819	6.23	2.95
8	Hepatocytes	1708	163	7.07	0.59
9	B_cell	1315	482	5.44	1.74
10	Endothelial_cells	997	729	4.13	2.63
11	Tissue_stem_cells	1222	350	5.06	1.26
12	T_cells	135	1308	0.56	4.71
13	Monocyte	486	883	2.01	3.18
14	Hepatocytes	1052	294	4.35	1.06
15	B_cell	405	903	1.68	3.25
16	Hepatocytes	153	1072	0.63	3.86
17	Hepatocytes	990	129	4.1	0.46
18	NK_cell	121	952	0.5	3.43
19	T_cells	437	307	1.81	1.11
20	Hepatocytes	673	1	2.79	0
21	Hepatocytes	552	25	2.28	0.09
22	Macrophage	12	521	0.05	1.88
23	T_cells	51	364	0.21	1.31
24	Hepatocytes	279	7	1.15	0.03
25	Monocyte	175	38	0.72	0.14
26	Monocyte	3	177	0.01	0.64
27	Monocyte	34	114	0.14	0.41
28	NK_cell	61	25	0.25	0.09

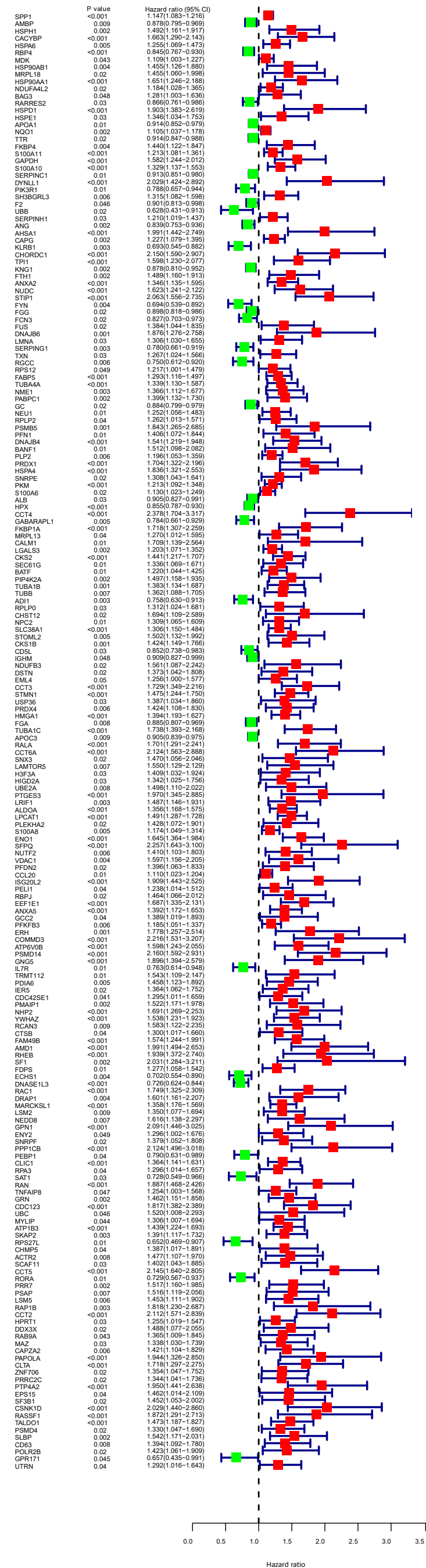
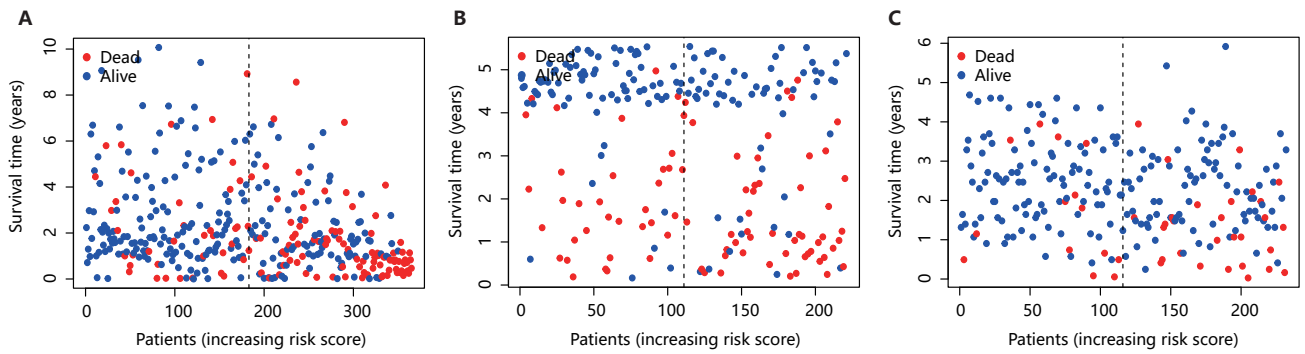


Figure S1 Univariate Cox regression analysis was used to screen the survival-related CD8<sup>+</sup> T cells genes. CI, confidence interval.



**Figure S2** Survival overview of patients in different risk groups in different database. (A) Survival overview of patients in different risk groups in TCGA dataset. (B) Survival overview of patients in different risk groups in GSE14520 dataset. (C) Survival overview of patients in different risk groups in ICGC-LIRI-JP dataset. TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium.