Article

Supplemental Materials: Multi-Omics Data Analysis of Gene Expressions and Alterations, Cancer-Associated Fibroblast and Immune Infiltrations, Reveals the Onco-Immune Prognostic Relevance of STAT3/CDK2/4/6 in Human Malignancies
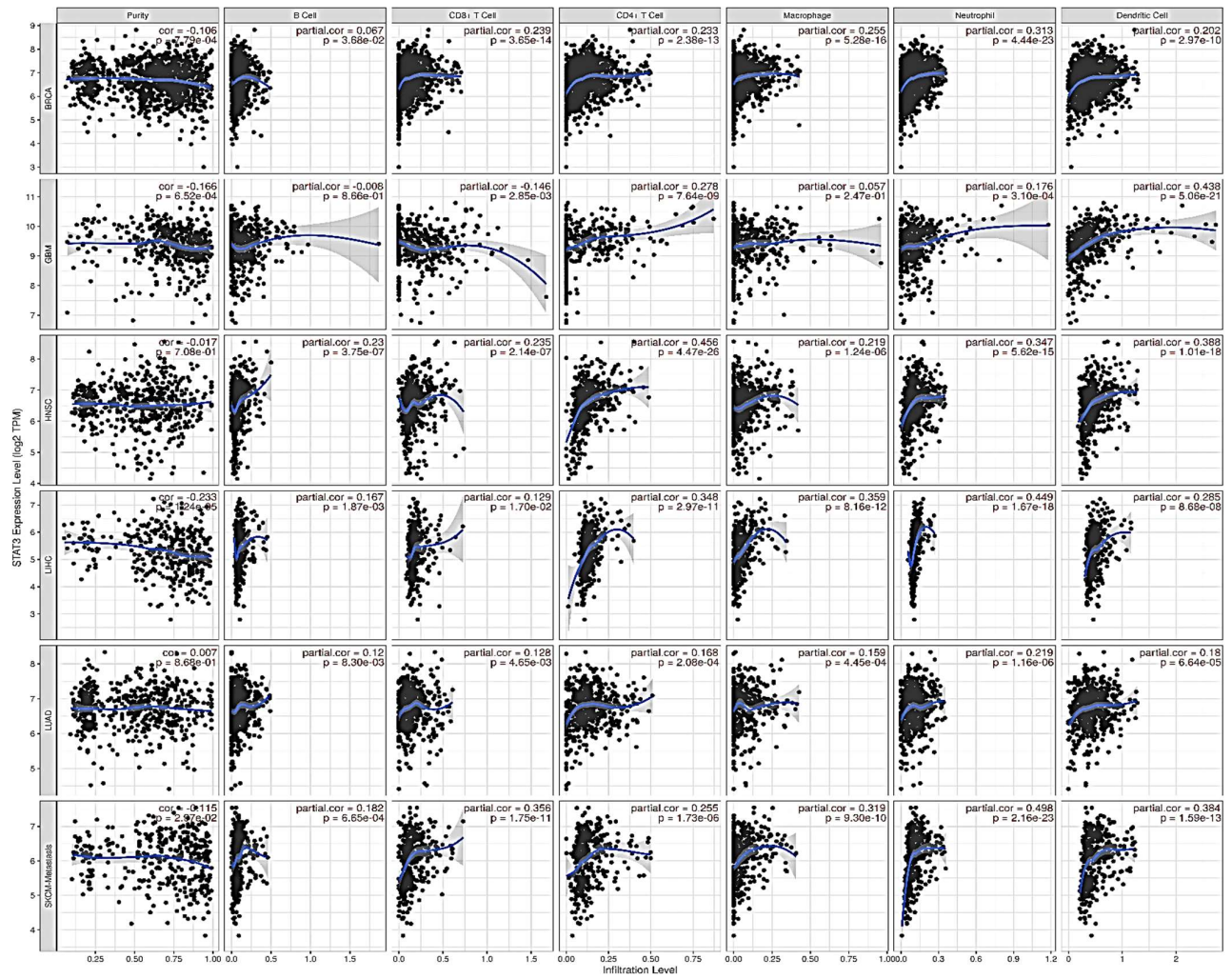
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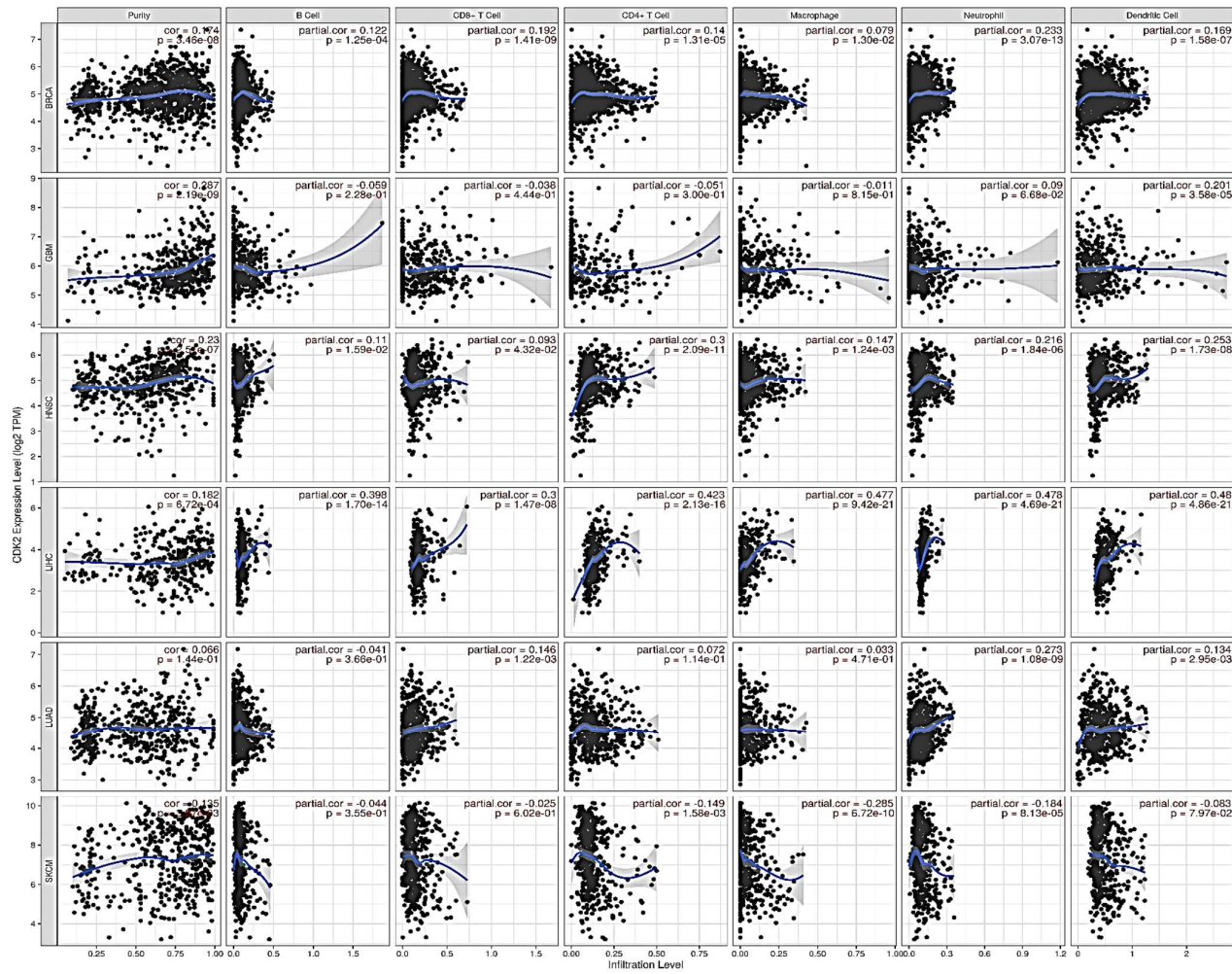
Table S1. Proteins directly interacting with CDK2/4/6.

CDK2		CDK4		CDK6	
Interactive Proteins	Interactive Scores	Interactive Proteins	Interactive Scores	Interactive Proteins	Interactive Scores
PLK1	0.603	PLK1	0.507	MCM6	0.453
ESPL1	0.707	MCM6	0.543	PLK1	0.455
CDKN2C	0.744	ORC2	0.551	ORC2	0.524
MAD2L1	0.775	ESPL1	0.598	MCM4	0.527
CDK4	0.926	MCM4	0.602	CDT1	0.556
ORC5	0.936	MAD2L1	0.619	MAD2L1	0.597
ORC3	0.937	MCM5	0.672	MCM7	0.598
ORC6	0.954	MCM7	0.693	ESPL1	0.609
MCM6	0.969	CDT1	0.746	MCM5	0.612
CDK6	0.974	ORC3	0.884	MCM2	0.928
MCM7	0.979	MCM2	0.884	CKS1B	0.963
E2F1	0.985	CKS1B	0.972	E2F1	0.973
MCM5	0.988	CDK6	0.975	RB1	0.989
ORC2	0.991	E2F1	0.977	CDKN1B	0.995
CDT1	0.993	CDKN1B	0.997	CDKN2C	0.999
MCM2	0.994	CDKN2C	0.997		
MCM4	0.995	RB1	0.999		
CDKN1B	0.999				
CKS1B	0.999				
RB1	0.999				

Table S2. Proteins directly interacting with STAT3.

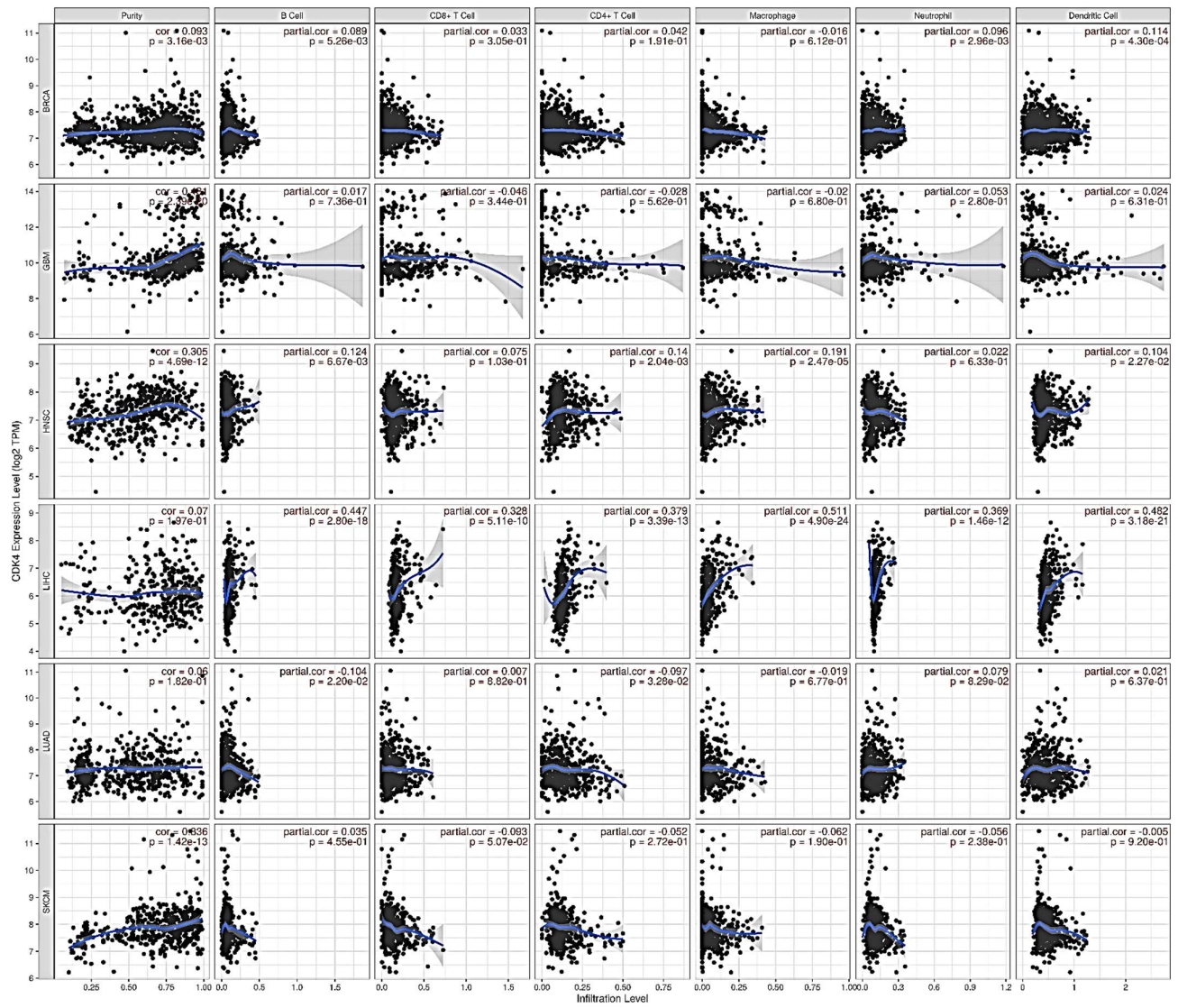| Query Protein	Interactive Proteins	Interactive score
STAT3	AKT1	0.994
STAT3	EGFR	0.998
STAT3	IL10	0.995
STAT3	IL6	0.997
STAT3	JAK1	0.997
STAT3	JAK2	0.998
STAT3	JAK3	0.994
STAT3	SOCS3	0.995
STAT3	SRC	0.995
STAT3	EGF	0.984
STAT3	GSK3B	0.684
STAT3	KDR	0.789
STAT3	MTOR	0.989
STAT3	NOS3	0.695
STAT3	SRC	0.995
STAT3	STAT5B	0.961
STAT3	STAT5A	0.976
STAT3	VEGFA	0.994

Figure S1. Scatterplots showing the correlation of STAT3 expression with immune infiltration level in diverse cancer types. SKCE; Skin cutaneous melanoma, LUAD; Lung adenocarcinoma; LIHC; Liver hepatocellular carcinoma; HNSC; Head and neck cancer, GBM; glioblastoma, BRCA; Breast invasive carcinoma.
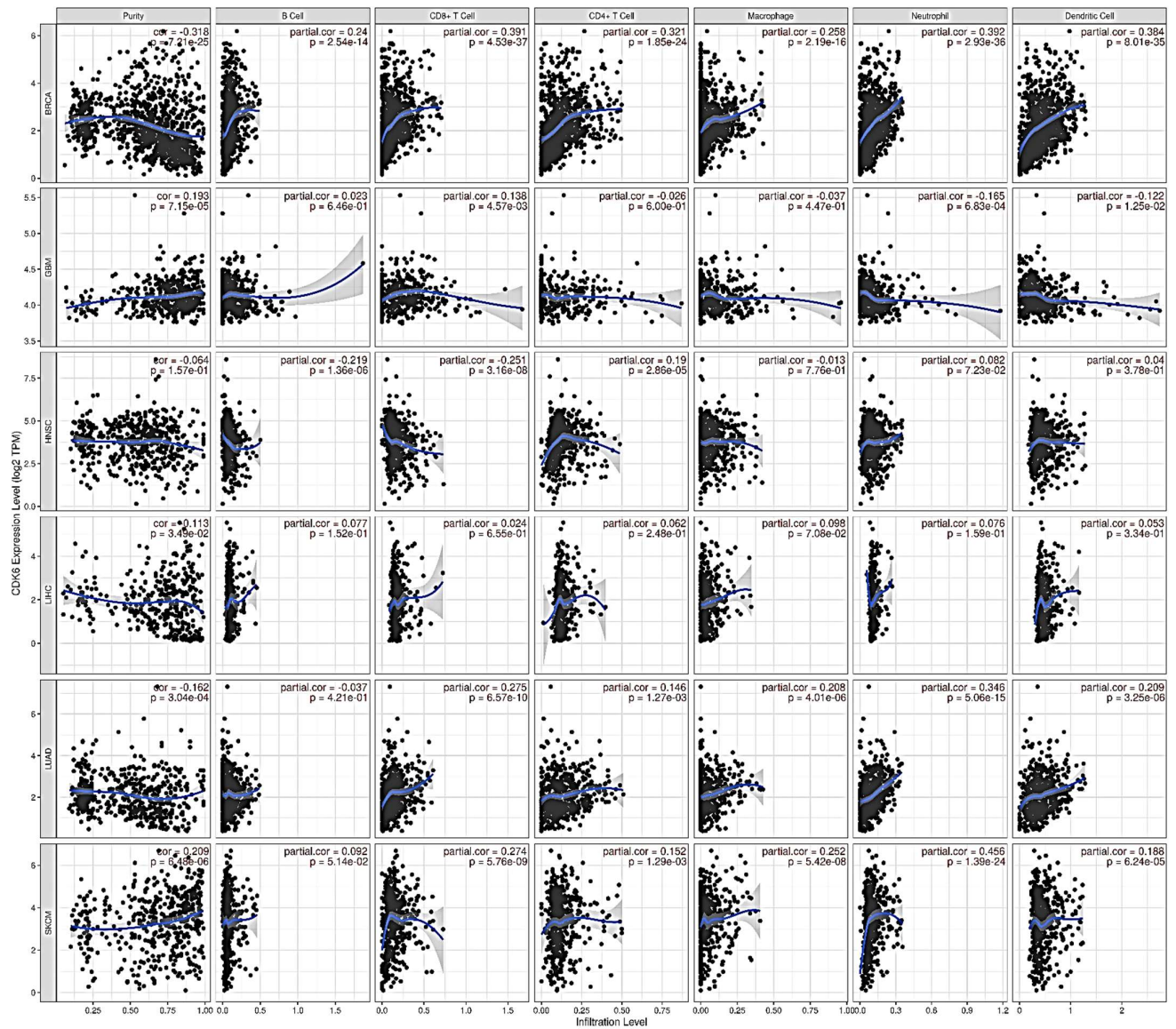
Figure S2. Scatterplots showing the correlation of CDK2 expression with immune infiltration level in diverse cancer types. SKCE; Skin cutaneous melanoma, LUAD; Lung adenocarcinoma; LIHC; Liver hepatocellular carcinoma; HNSC; Head and neck cancer, GBM; glioblastoma, BRCA; Breast invasive carcinoma.

Figure S3. Scatterplots showing the correlation of CDK4 expression with immune infiltration level in diverse cancer types. SKCE; Skin cutaneous melanoma, LUAD; Lung adenocarcinoma; LIHC; Liver hepatocellular carcinoma; HNSC; Head and neck cancer, GBM; glioblastoma, BRCA; Breast invasive carcinoma.
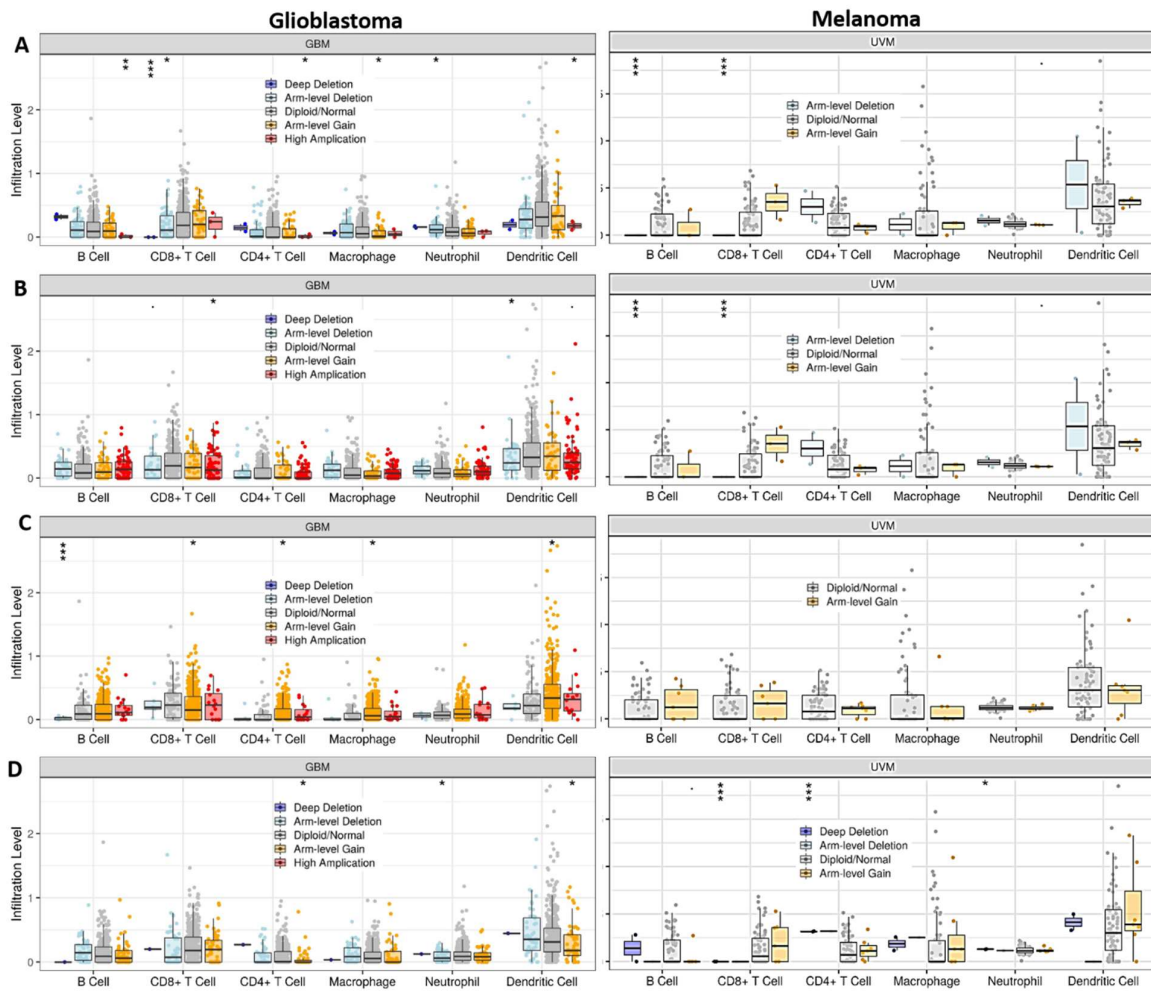
Figure S4. Scatterplots showing the correlation of CDK6 expression with immune infiltration level in diverse cancer types. SKCE; Skin cutaneous melanoma, LUAD; Lung adenocarcinoma; LIHC; Liver hepatocellular carcinoma; HNSC; Head and neck cancer, GBM; glioblastoma, BRCA; Breast invasive carcinoma.

Figure S5. Box plots showing tumor immune infiltration levels in GBM patients with different somatic copy number alterations for CDK2/CDK4/CDK6/STAT3. The infiltration abundance in every SCNA category was compared to the diploid/normal. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

	Cohort	Cancer	Subtype	CTL Cor	T Dysfunction	Risk	Risk.adj	Count
CDK2	TCGA	Lymphoma	DLBC	-0.168👁	0.09👁	2.219👁	2.031	41
	TCGA	Leukemia	AML	0.025👁	0.816👁	2.141👁	2.205	156
	TCGA	Breast	Her2	-0.073👁	1.001👁	2.005👁	1.988	54

	Cohort	Cancer	Subtype	CTL Cor	T Dysfunction	Risk	Risk.adj	Count
CDK4	TCGA	Brain	Glioma	0.11👁	-1.171👁	6.346👁	5.956	510
	TCGA	Lymphoma	DLBC	-0.168👁	0.097👁	2.223👁	2.035	41
	TCGA	Breast	Her2	0.09👁	0.87👁	2.13👁	2.133	54

	Cohort	Cancer	Subtype	CTL Cor	T Dysfunction	Risk	Risk.adj	Count
CDK6	TCGA	Breast	LumB	-0.102👁	2.374👁	-2.771👁	-2.926	120
	TCGA	Brain	Glioma	0.083👁	-0.601👁	2.562👁	2.054	510

	Cohort	Cancer	Subtype	CTL Cor	T Dysfunction	Risk	Risk.adj	Count
STAT3	TCGA	Stomach		-0.063👁	-0.272👁	2.776👁	2.78	376
	TCGA	Lymphoma	DLBC	-0.285👁	-2.317👁	2.082👁	1.822	41
	TCGA	Endometrial		0.067👁	-0.426👁	-2.485👁	-2.45	533
	TCGA	Brain	Glioma	-0.05👁	4.402👁	-2.254👁	-1.913	510

Figure S6. Graphical data representation of association between CNA of STAT3/CDK2/4/6 and dysfunctional T-cell phenotypes and prognostic relevance in multiple cancers.