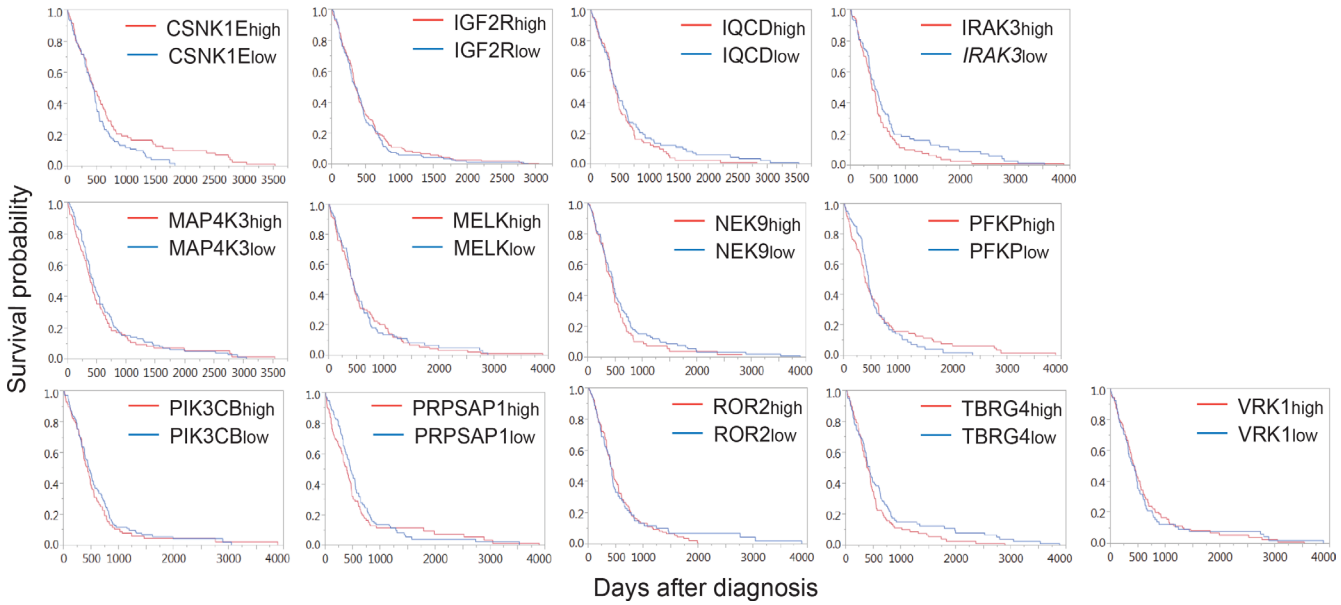
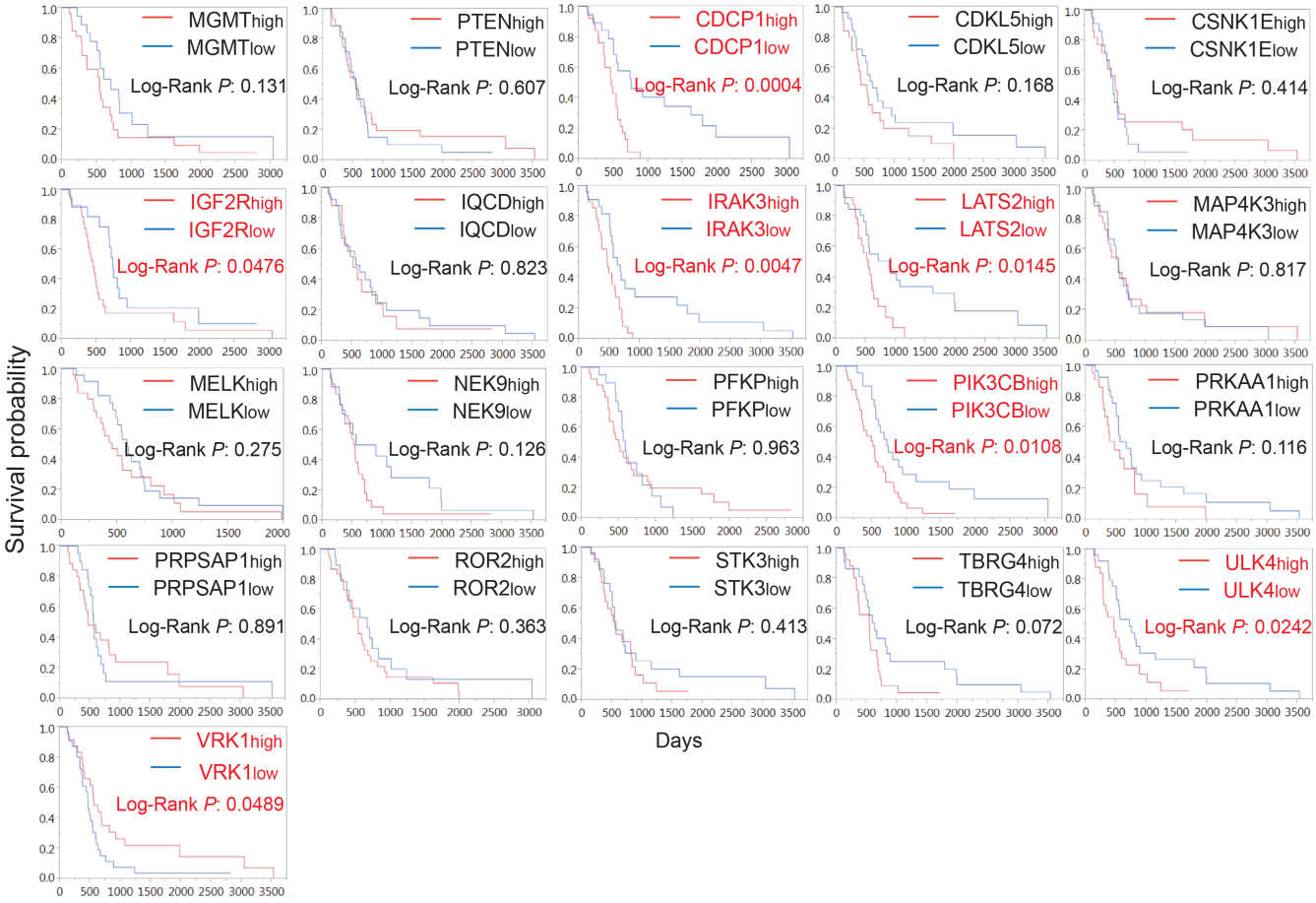
Survival kinase genes present prognostic significance in glioblastoma

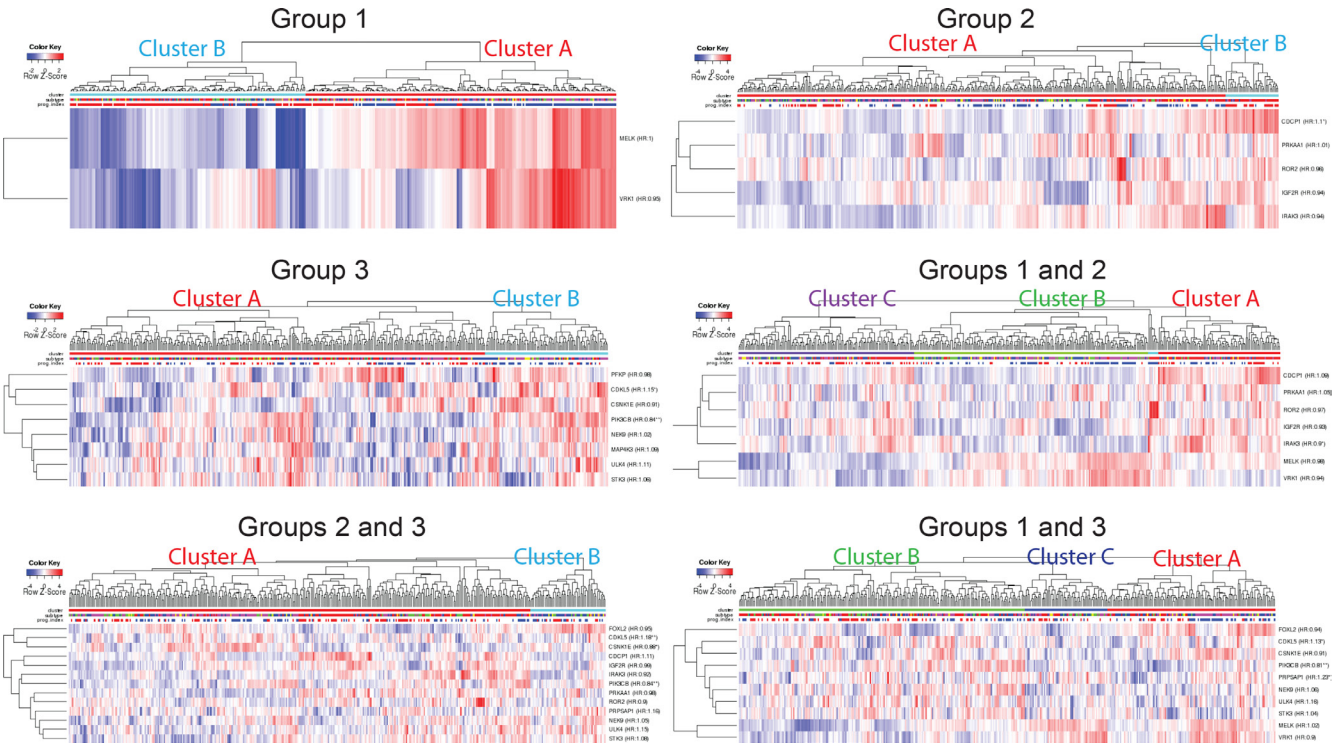
Supplementary Materials



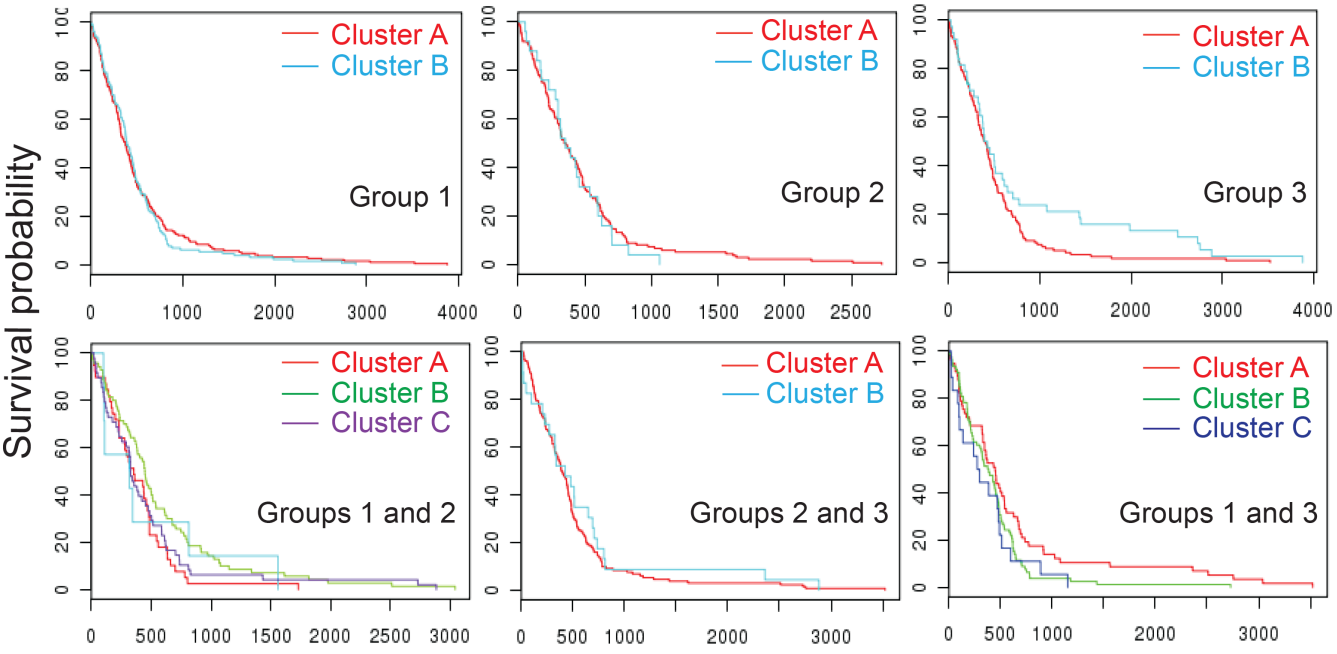
Supplementary Figure S1: Kaplan Meier survival analysis of SKGs with no statistical significance. The survival analysis results of SKGs with no statistical significance were shown.



Supplementary Figure S2: SKGs and the survival of recurrent GBMs. SKGs with a statistical significance in the survival of recurrent GBMs were highlighted in red. MGMT and PTEN were also shown.



Supplementary Figure S3: Clustering of GBM patients based on the gene expression profile of SKGs. GBM datasets from the TCGA database were used. 6 different groups of SKGs were analyzed.



Supplementary Figure S4: Groups of SKGs and GBM survival. GBM datasets from the TCGA database were used for survival analysis. GBM patients were clustered based on the expression profile of SKGs and subject to Kaplan Meier analysis. No statistically significant difference was found.

Supplementary Table S1: SKGs and GBM recurrence

Gene Symbol	Recurrence Rate						
	High level	Nrecur	Ntotal	Low level	Nrecur	Ntotal	*p* (High vs Low)
CDCP1	30.2%	26	86	24.1%	19	79	0.237
CDKL5	31.7%	25	79	32.5%	26	80	0.612
CSNK1E	28.7%	22	78	29.0%	22	76	0.61
IGF2R	33.3%	29	87	21.8%	17	78	0.07
IQCD	21.3%	17	80	31.7%	26	82	0.954
IRAK3	36.4%	28	77	26.8%	22	82	0.131
LATS2	30.1%	25	83	32.9%	26	79	0.709
MAP4K3	30.1%	27	73	28.3%	26	92	0.463
MELK	32.1%	25	78	33.3%	24	72	0.634
NEK9	41.3%	31	75	21.8%	17	78	0.007
PFKP	37.1%	26	70	23.3%	20	86	0.043
PIK3CB	45.8%	33	72	27.1%	23	85	0.011
PRKAA1	25.3%	21	83	33.8%	26	77	0.911
PRPSAP1	37.7%	26	69	25.6%	22	86	0.075
ROR2	34.9%	30	86	30.2%	19	63	0.335
STK3	36.0%	27	75	24.7%	22	89	0.081
TBRG4	31.3%	26	83	28.6%	22	77	0.418
ULK4	32.1%	25	78	30.1%	25	83	0.462
VRK1	30.0%	24	80	41.0%	32	787	0.947
MGMT	32.5%	27	83	27.8%	20	72	0.321
PTEN	35.0%	28	80	31.7%	26	82	0.391

The GBM patients with disease progression information were first divided into two groups based on the expression levels of SKGs (high level vs low level). The GBM recurrence rates were percentages of cases with a recurrent tumor (Nrecur) over the total cases (Ntotal). The statistical difference between the high level group and the low level one was determined using the Fisher's exact test.

Supplementary Table S2: SKGs and cancer prognosis

Gene Symbol	Effect of SKGs on prognosis	Cancer type (Reference*)
CDCP1	High level → poor prognosis.	Ovarian cancer (1); Breast cancer (2); Colorectal cancer (3)
	Low level → poor prognosis.	Esophageal cancer (4)
CDK11B	No reports	
CDKL5	No reports	
CSNK1E	Low level → poor prognosis.	Colerectal cancer (5); Oral cancer (6)
IGF2R	Low level → poor prognosis.	Lung cancer (7); Hepatocellular carcinoma (7); Head and neck cancer (8)
IQCD	No reports	
IRAK3	Low level → poor prognosis.	Hepatocellular carcinooma (9)
LATS2	High level → poor prognosis.	Nasopharyngeal carcinoma (10)
MAP4K3	No reports	
MELK	High level → poor prognosis.	Lung cancer (11); Breast cancer (12, 13); Prostate cancer (14)
NEK9	No reports	
PFKP	No reports	
PIK3CB	High level → poor prognosis.	Rectal carcinoma (15); Colorectal cancer (16); Diffuse large B cell lymphoma (17); Breast cancer (18)
PRKAA1	Low level → poor prognosis.	Colorectal cancer (19); Melanoma (20); Non-Hodgkin lymphoma (21); Ovarian cancer (22)
PRPSAP 1	No reports	
ROR2	High level → poor prognosis.	Cervical cancer (23); Colorectal cancer (24); Breast cancer (25); Gastrointestinal stromal tumor (26); Osteosarcoma (27)
STK3	No reports	
TBRG4	No reports	
ULK4	No reports	
VRK1	High level → poor prognosis.	Breast cancer (28)

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