Supplementary Table

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
AAK1		-0.80	-1.21	2.68	-0.46
AATK		-0.70	0.08	-1.05	-0.66
ABL1		-0.70	-1.81	2.39	0.38
ABL2		0.65	-0.50	-0.98	-0.46
ACVR1		0.45	0.03	0.83	-0.30
ACVR1B		-0.57	0.17	-0.74	0.37
ACVR2		-0.54	-0.39	0.00	0.39
ACVR2B		-0.63	1.57	0.42	-0.40
ACVRL1		0.37	2.78	-0.11	-0.55
ADCK1		-1.46	-0.56	0.03	2.62
ADCK2		0.97	-1.06	0.31	0.61
ADCK4		-0.11	-0.55	0.17	1.44
ADCK5		-1.61	-1.08	0.37	0.55
ADK		0.76	1.62	-0.11	0.13
ADRBK1		-0.08	-0.75	-0.29	-1.12
ADRBK2		0.12	1.05	-0.07	1.02
AK1		0.09	-0.94	-0.18	-0.02
AK2		0.24	0.75	0.56	0.36
AK3		-0.62	3.07	0.34	-1.05
AK3L1		-0.65	0.01	-0.57	0.12
AK5		1.02	-1.16	0.39	0.52
AK7		2.22	0.71	-0.32	-0.84
AKAP1		0.41	0.85	0.55	0.50
AKAP10		-0.61	2.06	0.07	1.01
AKAP11		1.18	0.31	-0.27	0.78
AKAP12		-0.41	-0.44	-0.23	0.02
AKAP13		0.28	0.90	-0.02	0.30
AKAP14		-0.44	-0.04	-0.57	0.07
AKAP3		0.22	0.36	1.86	0.87
AKAP4		0.11	0.22	-1.86	-0.66
AKAP5		0.83	0.08	-0.14	1.06
AKAP6		0.31	0.88	-0.42	-1.05
AKAP7		-0.55	-1.67	-0.30	-0.87
AKAP8		0.24	0.42	0.41	0.98
AKAP8L		0.51	-1.73	-0.33	0.21
AKAP9		-0.62	0.32	1.96	0.74
AKIP		0.14	-0.67	-0.22	0.70
AKT1		-1.35	0.06	-1.43	-1.79
AKT2		-1.50	3.18	3.02	4.01
AKT3		0.42	-0.64	-0.81	-0.57

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
ALK		-0.61	-0.08	0.18	-0.33
ALPK1		-0.63	0.72	0.11	-0.97
ALPK2		0.88	-0.43	0.10	0.71
ALS2CR2		-1.80	0.87	-0.46	-0.05
ALS2CR7		0.57	-1.51	-0.78	0.32
ANKK1		1.22	0.00	-2.47	-0.07
APEG1		0.71	-1.49	-0.21	0.29
ARAF		-0.35	0.41	-0.84	0.13
ARHGAP26		0.33	-0.01	1.68	0.73
ARK5		-1.05	0.42	-1.19	-0.31
ASK		3.07	-0.46	-0.53	0.58
ATM		-0.75	1.15	-0.89	0.22
ATR		0.15	-1.01	0.46	0.17
AURKB		0.54	0.05	-1.19	-0.25
AURKC		0.02	-0.19	-0.25	0.77
AXL		0.32	0.24	2.79	0.93
BCKDK		-0.67	0.25	-0.43	0.42
BCR		0.37	0.21	-1.39	0.61
BLK		0.03	-0.37	-0.51	2.98
BMP2K		0.53	-0.16	-0.03	-0.22
BMPR1A		0.68	-0.95	-0.71	-0.77
BMPR1B		-0.97	0.42	3.37	0.16
BMPR2		-0.14	-0.10	-0.53	-0.12
BMX		0.11	-0.85	3.07	0.40
BRAF		-0.78	-0.37	-0.19	1.04
BRSK1		2.25	-0.28	-0.30	-0.35
BTK		-0.09	0.54	1.76	0.70
BUB1		0.41	-1.30	-0.30	0.28
BUB1B		1.41	0.74	0.30	0.12
PDXK	C21orf124	-1.22	-0.85	0.44	-0.11
CALM1		1.12	2.49	-0.53	0.23
CALM2		-0.68	0.15	0.55	-1.38
CALM3		1.25	0.52	-1.27	0.80
CAMK1		-0.20	0.05	0.98	-0.12
CAMK1D		0.28	0.42	0.73	-1.14
CAMK1G		1.86	-1.12	-1.14	-2.29
CAMK2A		-0.61	1.86	-0.79	-0.56
CAMK2B		-0.61	-1.81	0.00	-0.79
CAMK2D		0.09	3.14	-0.77	-0.12
CAMK2G		0.08	1.15	0.55	-0.28
CAMK4		-0.35	0.45	-0.40	0.43

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
CAMK2N1	CaMKIINalpha	0.79	-0.72	-1.09	-0.63
CAMKK1		-0.52	-0.49	0.52	-1.82
CAMKK2		-1.16	-0.88	-0.32	0.39
CARKL		1.23	0.41	0.40	0.55
CASK		0.64	-1.03	-0.82	-0.59
CCRK		-1.09	-1.24	-0.76	1.24
CDC2		0.88	0.66	-2.43	0.26
CDC2L1		-1.20	-1.24	1.28	-1.69
CDC2L5		1.09	0.16	-0.87	0.41
CDC2L6		0.79	0.37	0.93	-1.00
CDC42BPA		0.23	-0.30	0.16	0.66
CDC42BPB		0.81	-0.12	-0.95	-0.85
CDC42BPG		0.16	-0.33	-0.68	0.64
CDC42SE2		-0.70	-0.57	-0.47	-1.84
CDK10		-0.73	0.75	1.43	-1.18
CDK2		0.86	0.28	-1.49	0.82
CDK3		0.25	-0.64	1.09	-1.27
CDK4		0.21	-1.67	0.35	-0.94
CDK5		-1.33	0.84	0.55	-2.27
CDK5R1		-0.32	-1.67	0.41	1.04
CDK5R2		0.12	0.23	0.34	0.72
CDK6		-1.19	0.10	-0.67	1.34
CDK7		-0.04	-0.51	-0.11	-0.41
CDK8		-0.23	2.17	0.77	-0.03
CDK9		0.10	-1.92	0.11	0.27
CDKL1		-0.26	0.02	0.97	-0.50
CDKL2		0.88	0.62	0.13	-0.36
CDKL3		-0.45	-2.42	-0.28	1.23
CDKL4		-0.77	0.24	-0.68	0.55
CDKL5		0.15	0.12	0.94	-1.20
CDKN1A		1.04	0.23	0.30	0.69
CDKN1B		0.54	-1.14	0.37	-1.36
CDKN1C		-0.11	-0.58	1.11	-0.60
CDKN2A		-1.69	0.77	-0.91	0.40
CDKN2B		0.75	0.94	-0.88	0.84
CDKN2C		0.45	0.28	0.29	0.85
CDKN2D		-0.11	1.07	-1.32	0.13
CERK		0.25	-1.32	0.20	0.23
CHEK1		-0.51	-0.55	-0.50	-1.59
CHEK2		-1.57	0.08	0.71	0.36
CHKA		1.01	0.28	-0.82	-0.05

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
CHKB		-0.21	-0.80	-1.25	-0.29
CHUK		-0.47	0.46	-0.50	-1.34
CIB2		-1.32	0.55	-0.26	-0.50
CIB3		-0.86	-0.03	0.07	0.83
CINP		-0.28	-0.31	0.83	-0.18
CIT		0.33	-0.60	0.72	1.25
CKB		-0.64	-0.02	-1.83	0.33
CKM		0.01	0.97	-0.42	1.05
CKMT1		-0.07	-0.24	-0.31	0.76
CKMT2		2.87	0.40	-1.03	-0.31
CKS1B		-0.38	0.16	0.11	-0.94
CKS2		-0.27	-0.25	-0.26	0.53
CLK1		0.01	-0.32	-0.46	0.40
CLK2		-0.37	0.22	0.21	0.37
CLK3		-0.85	-1.52	-0.09	0.12
CLK4		0.67	0.57	3.02	1.24
CNKSR1		0.49	0.52	0.25	1.08
CRK7	CDK12	-1.09	-0.71	0.41	0.03
CSK		0.45	0.91	1.52	0.13
CSNK1A1		0.18	0.09	-0.15	-0.77
CSNK1A1L		0.43	-0.24	0.63	-0.21
CSNK1D		-2.04	-0.18	0.05	-1.28
CSNK1E		-0.08	-0.45	-0.06	-0.55
CSNK1G1		-0.44	0.12	-1.17	-0.31
CSNK1G2		-1.37	-1.12	-0.55	0.84
CSNK1G3		0.58	0.83	0.94	1.43
CSNK2A1		0.86	1.00	-0.92	0.97
CSNK2A2		0.64	0.29	-1.26	-0.81
CSNK2B		-0.28	-0.53	0.44	0.41
DAPK1		0.93	0.11	0.74	0.39
DAPK2		-0.11	2.73	0.79	0.95
DAPK3		0.01	3.59	1.38	-0.69
DCAMKL1		-0.22	0.24	-0.88	-1.13
DCAMKL2		0.19	-1.45	-0.14	-1.49
DCK		-0.19	0.53	1.16	-0.01
DDR1		0.83	0.24	-1.01	0.26
DDR2		-1.14	3.04	1.10	0.68
DGKA		-0.25	0.50	0.71	-0.20
DGKB		-0.11	0.39	0.48	-1.45
DGKD		-1.16	-0.19	-0.36	-0.35
DGKE		0.06	-1.86	0.69	-0.44

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
DGKG		0.30	0.18	0.21	-1.40
DGKH		0.05	0.39	0.19	-1.17
DGKI		2.07	-0.25	0.66	0.95
DGKQ		0.85	-3.16	2.04	-0.16
DGKZ		-0.63	0.24	-1.57	2.41
DGUOK		-0.95	-1.40	-2.01	-3.47
DMPK		-0.97	0.84	0.68	-0.22
DOK1		0.13	-2.00	-0.44	0.05
DTYMK		0.04	-0.27	-0.07	-0.84
DYRK1A		-0.81	-0.60	-1.44	0.05
DYRK1B		-1.30	-1.01	-2.07	-0.65
DYRK2		0.88	0.84	-1.16	3.10
DYRK3		0.67	-0.65	0.65	1.04
DYRK4		0.82	0.58	0.43	0.49
EEF2K		-0.99	-0.37	1.20	-0.66
EGFR		0.36	0.42	-1.27	-0.12
EIF2AK1		0.02	-0.97	0.32	0.24
EIF2AK2		1.67	0.45	-0.10	1.51
EIF2AK3		0.22	-1.56	-0.84	0.51
EIF2AK4		-0.79	-0.30	0.56	0.48
EPHA1		0.04	1.68	-0.65	0.92
EPHA2		0.40	-0.81	-0.40	-0.25
EPHA3		0.71	-0.20	-0.05	0.01
EPHA4		0.80	-1.06	2.28	0.08
EPHA5		-1.41	-3.33	-0.82	4.67
EPHA7		0.91	-1.29	-0.03	-0.39
EPHA8		2.45	0.41	3.02	0.74
EPHB1		3.34	-0.71	-0.57	2.56
EPHB2		0.74	-1.54	0.68	-0.05
EPHB3		-0.79	0.01	0.38	-0.34
EPHB4		0.83	0.56	-1.00	1.28
EPHB6		0.92	-0.74	-0.60	-1.84
EPS8L1		0.07	0.81	-1.06	-0.03
ERBB2		-0.29	-0.43	-2.27	-0.17
ERBB3		-0.93	0.36	-1.81	-1.49
ERBB4		-0.10	0.77	-0.41	-1.88
ERK8		-0.29	-1.00	-0.41	0.80
ERN1		-0.81	0.74	0.10	1.09
ERN2		0.29	-0.95	-0.51	-0.07
ETNK1		0.15	0.56	1.24	-0.37
ETNK2		0.73	0.69	1.91	0.74

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
FASTK		-0.79	-0.01	0.98	-0.46
FER		0.24	-0.57	0.38	-1.08
FES		1.03	-0.99	-0.08	0.13
FGFR1		0.62	0.03	-0.72	-0.15
FGFR2		-0.03	-0.55	-1.17	0.35
FGFR3		0.46	0.37	-0.58	2.78
FGFR4		0.46	-2.09	-0.13	0.27
FGR		2.18	0.31	0.47	0.94
FLJ10986	FGGY	0.13	0.06	0.22	0.59
FLJ13052	NADK	0.37	0.56	0.72	-1.44
FLJ14800	SPRYD3	-1.33	-0.33	-1.31	0.44
FLT1		0.79	-1.46	-0.30	0.49
FLT3		-1.28	-1.65	-0.69	-0.26
FLT3LG		0.98	0.16	-1.18	-0.05
FLT4		0.83	-1.08	0.74	-1.16
FN3K		-0.55	0.53	-0.26	-0.55
FN3KRP		-0.55	-0.09	0.48	1.57
FRK		-0.15	-0.95	0.61	-0.22
FUK		0.39	0.32	-0.14	0.49
FYN		-0.67	0.59	-0.19	-1.22
GAK		-0.34	-0.24	0.14	0.08
GALK1		1.45	-0.16	-1.23	-0.08
GALK2		-1.09	0.68	-0.83	-0.63
GCK		-1.39	-1.23	-2.02	-0.45
GIT1		0.31	0.82	-2.30	0.73
GIT2		2.29	0.16	0.48	-2.58
GK		0.46	-0.93	0.00	0.71
GK2		-0.04	-0.62	0.56	1.00
GKAP1		0.72	-1.29	-1.06	-0.79
GNE		0.07	-0.83	-0.43	0.42
GRK1		-0.51	-0.09	-0.10	-0.52
GRK4		-0.99	-0.27	-0.89	-2.10
GRK5		-1.42	-0.63	-1.01	1.10
GRK6		2.08	0.91	1.10	-0.08
GRK7		-0.33	0.34	0.76	2.64
GSK3A		1.21	-0.67	0.32	0.02
GSK3B		0.11	0.39	0.12	0.47
GUK1		-0.89	3.51	-0.29	-0.19
HCK		-1.50	-0.25	-0.12	-1.40
HGS		1.00	0.34	-0.98	1.00
HIPK1		-1.42	-1.47	-0.13	-0.27

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
HIPK2		-0.47	0.15	-0.97	-1.80
HIPK3		-0.49	-0.74	-0.75	-0.09
HIPK4		-1.12	2.73	0.68	0.29
HK1		-0.38	-2.37	0.51	-1.12
HK2		1.35	0.05	-0.20	0.34
HK3		0.58	0.25	0.47	0.90
HSPB8		-0.18	-0.43	-0.72	-1.06
HUNK		-1.75	0.10	-0.01	-0.81
IBTK		-0.80	-1.71	1.07	-3.38
ICK		0.33	0.60	2.06	2.89
IHPK1		-0.07	0.81	-0.17	0.00
IHPK2		-0.24	0.35	0.44	2.39
IHPK3		-0.78	-0.61	0.20	-2.01
IKBKAP		0.61	0.43	-0.31	0.16
IKBKB		0.48	3.32	0.09	-1.23
IKBKE		-0.08	-0.68	1.23	-1.03
IKBKG		-1.10	-0.74	1.59	-0.62
ILK		0.40	0.89	-0.43	0.29
IRAK1		-0.11	-0.46	-1.52	-1.06
IRAK1BP1		0.93	0.00	0.48	-0.17
IRAK2		3.54	-1.98	0.01	0.98
IRAK3		0.16	-0.87	0.04	0.66
IRAK4		1.11	0.58	-0.04	1.36
ITK		0.46	0.35	0.28	-0.92
ITPK1		-1.88	0.94	0.10	-0.48
ITPKA		-1.12	-0.01	-0.79	-0.01
ITPKB		-0.08	0.72	1.04	0.83
ITPKC		3.86	0.23	1.05	-0.72
JAK1		0.35	-0.54	0.22	-1.36
JAK2		-0.19	-1.36	-0.09	0.18
JAK3		0.62	-0.52	-0.46	-0.13
KDR		2.70	1.29	0.06	0.24
KHK		-0.60	0.44	-1.27	0.04
KIAA1446	BEGAIN	0.55	-0.17	-0.36	0.15
KIAA1804	MLK4	-0.55	0.17	0.59	-0.90
KIDINS220		1.99	2.08	-0.15	0.20
KIT		-0.09	0.45	0.49	0.29
KSR		0.80	-1.35	-0.21	0.87
KSR2		-0.24	-0.18	0.09	-0.05
LATS1		0.67	0.53	-0.38	-0.82
LATS2		-0.72	-0.01	-0.74	1.64

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
LCK		-0.30	-0.60	-0.23	0.43
LIMK1		0.33	-1.13	0.51	-0.31
LIMK2		0.05	-0.21	-0.18	-1.47
LMTK2		-0.20	-0.67	-0.15	-2.17
LMTK3		-0.73	-1.39	-0.98	-1.16
LOC161635	CSNK1A1P1	1.29	0.84	0.22	0.02
LOC283155	WITHDRAWN	-2.12	-1.24	-1.78	1.70
LOC285940	WITHDRAWN	0.99	0.03	-0.41	-1.40
LOC375449	MAST4	-0.17	0.55	1.09	0.18
LOC390777	WITHDRAWN	-0.05	-0.53	-2.50	-0.35
LOC390975	WITHDRAWN	0.53	-0.66	-1.85	-0.36
LOC391295	WITHDRAWN	0.01	0.43	0.14	1.51
LOC391533	INFERRED	-1.06	-0.05	-1.60	0.06
LOC392265	CDK5PS	-0.50	-1.45	-1.80	-0.35
LOC400301	WITHDRAWN	0.16	-0.43	-0.85	3.57
LOC407835	Psuedogene	0.59	-0.79	0.19	0.03
LOC55971	BAIAP2L1	-0.36	-0.96	-0.68	0.09
LOC91807	MYLK3	-1.11	1.03	-0.86	-0.93
LRRK1		-0.63	0.30	0.85	0.73
LRRK2		-0.61	0.21	0.36	0.07
LTK		-2.25	0.82	-0.40	-0.05
LYK5	STRADA	0.58	-0.11	-1.72	-2.31
LYN		0.36	-1.52	0.31	0.75
MADD		0.52	1.05	-0.24	-2.53
MAGI		0.40	-0.04	0.31	-0.87
MAGI1		-0.14	-0.21	-0.41	-1.42
MAK		-0.81	-1.08	0.49	0.58
MAP2K1		-1.21	-1.36	0.58	-0.22
MAP2K1IP1		-0.88	0.27	-1.03	-0.57
MAP2K2		-1.78	0.03	0.92	-0.09
MAP2K3		4.04	-0.19	-1.95	-0.44
MAP2K4		0.47	2.33	0.88	0.80
MAP2K5		-0.13	0.47	0.19	-0.82
MAP2K6		-0.10	-0.96	0.99	0.53
MAP2K7		0.38	-0.06	1.01	0.22
MAP3K1		1.04	-0.06	-0.02	0.82
MAP3K10		0.62	0.00	-1.16	-0.85
MAP3K11		1.10	-0.12	0.62	-1.92
MAP3K12		-0.70	-0.95	0.08	-0.12
MAP3K13		-0.20	0.74	-2.38	-0.22
MAP3K14		-0.16	-0.14	0.01	-0.62

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
MAP3K2		-0.09	-0.34	-0.50	0.83
MAP3K3		-0.21	0.39	-0.28	-1.84
MAP3K4		0.03	-0.56	0.36	0.15
MAP3K5		0.66	-0.23	-0.87	-0.05
MAP3K6		0.14	-0.66	0.87	-0.29
MAP3K7		0.84	0.59	0.30	-0.60
MAP3K7IP1		-1.40	0.11	-0.23	-2.40
MAP3K7IP2		-0.07	0.72	-0.35	0.87
MAP3K8		0.31	0.89	-1.23	0.91
MAP3K9		2.37	-0.60	-0.54	0.16
MAP4K1		-1.31	0.00	-0.13	-0.08
MAP4K2		-1.95	-0.63	-0.04	-0.94
MAP4K3		-0.84	-0.30	-1.38	0.01
MAP4K4		0.56	-0.62	-1.16	0.36
MAP4K5		-0.05	-1.00	0.40	-1.45
MAPK1		1.12	2.11	0.16	-0.70
MAPK10		0.67	0.79	0.49	2.80
MAPK11		-0.88	0.06	0.28	-0.64
MAPK12		-2.38	2.87	0.42	-0.47
MAPK13		-0.95	0.76	1.27	0.49
MAPK14		-0.89	-0.60	0.72	-0.08
MAPK3		1.46	3.56	1.00	1.07
MAPK4		1.47	-1.01	0.11	0.01
MAPK6		0.37	-0.11	0.39	0.67
MAPK7		-1.01	-0.14	-0.14	-0.03
MAPK8		-0.32	2.16	0.55	-1.66
MAPK8IP1		-0.66	-0.98	-0.66	-0.49
MAPK8IP2		1.37	-0.12	-0.69	0.45
MAPK8IP3		0.23	0.31	-0.87	0.31
MAPK9		0.31	-0.06	0.21	0.83
MAPKAP1		-1.18	-0.10	0.03	-0.20
MAPKAPK2		-1.16	0.31	-0.34	0.15
MAPKAPK3		0.75	-0.73	-0.31	-0.15
MAPKAPK5		-0.63	0.36	0.23	1.87
MAPKBP1		0.44	-0.27	1.05	1.28
MARCKS		-0.83	0.59	0.54	0.21
MARK1		-1.20	0.18	-0.21	-0.56
MARK2		0.34	1.53	0.87	1.23
MARK3		-0.20	-0.46	-0.50	-1.27
MARK4		0.63	0.05	-0.07	0.22
MAST2		0.05	-0.71	0.45	-0.57

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
MAST3		0.78	0.33	-2.29	-0.27
MAST4		-1.27	0.12	0.35	0.09
MASTL		-1.27	1.11	0.49	0.23
MATK		0.11	0.99	0.52	0.47
MELK		-0.87	-1.47	-1.02	0.23
MERTK		-0.82	0.82	0.12	0.21
MET		-0.29	0.77	0.51	0.78
MGC40579	GK5	-1.71	0.14	-0.44	0.48
MGC4796	STK40	-0.52	-1.34	0.63	-1.09
MGC75495	NEK5	-0.08	0.23	0.18	-1.12
MINK1		-0.57	-0.14	-0.04	1.01
MKNK1		-0.41	-0.68	0.43	-0.94
MKNK2		1.07	-0.25	-0.76	1.06
MOS		2.91	0.11	0.94	0.97
MST1R		-0.24	-0.06	-0.98	0.14
MST4		0.90	-0.42	-1.09	-0.97
MUSK		-0.12	-0.36	-0.17	-0.39
MVK		-0.27	-1.14	0.61	0.17
MYLK		1.36	-0.22	0.61	-1.35
MYLK2		0.86	-0.29	0.25	-2.45
NAGK		0.47	0.29	0.06	0.45
NEK1		0.45	-1.32	1.05	0.59
NEK11		-1.18	0.89	-0.33	0.62
NEK2		0.05	-0.11	0.57	0.26
NEK3		-0.68	-0.36	1.38	-0.06
NEK4		0.15	-0.32	0.57	-1.23
NEK6		-0.25	0.29	0.51	0.20
NEK7		0.56	-0.64	0.13	-0.01
NEK8		-0.39	-0.92	-0.44	0.05
NEK9		0.48	-1.63	-1.62	-1.89
NJMU		-0.33	0.85	-0.08	0.57
NLK		-0.51	-1.41	-0.74	1.06
NME1		2.27	0.18	0.64	0.11
NME2		-0.30	0.13	-0.10	-1.60
NME3		-0.27	-0.80	0.13	0.62
NME4		0.16	0.77	1.02	-0.25
NME5		-0.76	-0.68	-0.34	0.78
NME6		2.17	4.80	0.44	1.09
NME7		-0.74	0.50	-0.25	1.06
NRBP		0.54	1.30	-0.74	0.58
NRGN		-0.23	-0.03	-0.47	-0.15

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
NRK		-0.99	0.54	-0.52	-0.93
NTRK1		-1.32	0.03	-0.51	-0.94
NTRK2		0.06	0.67	-0.11	-0.26
NTRK3		-0.10	0.07	0.50	-0.92
NUCKS		0.52	0.57	-0.61	0.20
NYD		-0.69	0.26	0.80	-1.22
NYD		-0.62	-0.41	0.10	0.31
OXSR1		0.80	0.36	0.80	0.63
PACSIN1		-0.11	-0.50	1.66	0.41
PACSIN2		2.95	0.38	0.34	-0.83
PACSIN3		3.60	-0.42	0.49	-0.77
PAK1		-0.09	0.41	2.61	0.59
PAK2		-2.29	-1.49	0.07	-1.32
PAK3		0.48	-0.26	-0.73	0.56
PAK4		-0.90	0.18	0.33	-0.46
PAK6		1.40	3.40	-0.60	0.78
PAK7		-0.06	0.74	0.90	-0.05
PANK1		1.10	-0.34	-0.88	2.20
PANK2		-1.31	-0.39	-0.61	0.80
PANK3		0.54	-0.82	0.14	0.15
PANK4		0.70	-0.03	0.58	0.09
PASK		-0.03	0.26	-0.09	3.15
PBK		-0.19	-1.19	0.54	-0.44
PCK1		-0.62	-0.30	-0.48	-0.90
PCTK1	CDK16	0.70	0.67	0.70	1.33
PCTK2	CDK17	0.08	-0.14	0.49	0.88
PCTK3	CDK18	-1.87	-0.73	-0.91	0.66
PDGFRA		0.92	-0.91	-0.06	-0.36
PDGFRB		0.00	-0.35	0.09	-0.99
PDIK1L		0.08	0.12	-1.04	2.29
PDK1		0.09	-0.26	-0.78	0.55
PDK2		0.94	0.54	1.51	0.13
PDK3		0.95	-0.58	1.21	0.36
PDK4		1.56	0.44	0.92	0.42
PDLIM5		-1.18	-0.25	-0.77	0.61
PDPK1		-0.34	0.53	0.80	-0.72
PDXK		-1.04	-0.71	-0.45	-0.45
PFKFB1		-0.50	-0.03	-1.59	-0.68
PFKFB2		-0.54	-0.82	0.56	0.36
PFKFB3		-0.87	-0.44	0.89	-0.46
PFKFB4		0.00	-0.76	1.07	-0.63

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
PFKL		0.13	0.98	-1.52	-1.19
PFKM		-0.37	-1.61	-1.13	-0.03
PFKP		0.52	0.85	0.26	0.04
PFTK1		-0.29	1.76	-1.50	0.55
PGK1		-0.28	-0.49	-0.44	-0.50
PGK2		1.15	1.06	-0.31	0.86
PHKA1		0.49	0.49	-0.21	-1.26
PHKA2		-2.26	0.03	2.86	-0.68
PHKB		-0.86	-0.48	-0.82	-1.00
PHKG1		-0.23	0.41	0.19	0.03
PHKG2		-0.09	0.52	-2.00	-1.09
PI4K2B		-0.14	-1.18	-2.18	-0.63
PI4KII		-1.00	-0.71	0.56	-0.55
PIK3AP1		0.29	-0.87	0.75	-0.05
PIK3C2A		1.24	0.76	0.55	0.77
PIK3C2B		-0.17	-0.02	0.76	-0.24
PIK3C2G		0.94	0.08	-1.00	-0.22
PIK3C3		0.70	0.80	0.86	0.91
PIK3CA		-0.76	-0.99	-0.52	-0.64
PIK3CB		0.41	0.77	0.78	1.71
PIK3CD		-2.48	0.95	1.24	0.15
PIK3CG		-0.26	0.38	-0.36	-0.16
PIK3R1		0.09	4.89	0.48	-0.96
PIK3R2		1.95	0.54	-0.23	1.03
PIK3R3		0.42	-0.29	-1.21	-1.24
PIK3R4		0.02	-0.73	1.34	0.40
PIK3R5		1.28	1.53	1.73	0.03
PIK4CA		1.23	0.12	-0.36	-0.43
PIK4CB		-1.08	-0.72	-1.50	-1.32
PIM1		0.10	0.30	0.17	0.41
PIM2		-1.75	1.36	1.12	0.39
PINK1		-1.01	-1.30	0.06	0.36
PIP5K1A		0.40	0.36	0.25	-1.09
PIP5K1B		-0.27	1.35	0.54	-1.12
PIP5K1C		-1.29	0.96	-0.68	1.80
PIP5K2A		0.05	-0.08	1.63	-0.76
PIP5K2B		2.41	-0.80	-0.53	-0.10
PIP5K2C		0.73	-0.23	-1.24	-1.27
PIP5K3		-0.24	0.04	-0.37	-0.91
PKIA		1.59	-1.07	-0.50	-1.32
PKIB		0.50	1.14	-0.02	1.48

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
PKIG		1.00	0.98	-0.74	-1.36
PKLR		0.71	0.40	0.50	-1.06
PKM2		-0.37	1.25	-1.20	0.36
PKMYT1		1.04	-0.19	1.10	0.63
PKN1		0.13	-1.11	-0.56	-0.35
PKN2		1.21	0.58	-0.64	0.84
PKN3		1.25	0.26	0.08	0.25
PLAU		2.31	-0.59	0.21	0.45
PLK1		-1.74	-0.60	-1.79	0.95
PLK2		2.56	-0.49	-0.39	0.28
PLK3		-0.93	-0.25	1.31	-0.42
PLK4		-1.50	0.38	0.29	1.24
PMVK		1.09	0.81	-0.58	0.21
PNCK		0.17	0.07	-0.42	-0.66
PRKAA1		-0.05	-0.78	0.80	3.12
PRKAA2		-0.97	-0.24	0.68	-0.61
PRKAB1		-0.04	-0.05	0.91	-0.34
PRKAB2		-0.50	-0.10	0.32	0.87
PRKACA		0.16	1.44	-0.77	-0.30
PRKACB		-0.17	0.10	1.03	2.54
PRKACG		-0.43	-0.47	0.76	-0.55
PRKAG1		0.02	3.65	0.34	-0.61
PRKAG2		0.33	-1.55	-1.90	-0.44
PRKAG3		-1.41	-0.87	1.18	1.10
PRKAR1A		0.71	-1.29	0.22	-1.38
PRKAR1B		0.25	0.30	0.72	-0.14
PRKAR2A		-1.36	0.39	-0.83	0.50
PRKAR2B		0.54	-0.62	0.02	-0.11
PRKCA		0.59	1.08	0.36	-0.83
PRKCABP		-1.77	-0.76	0.35	0.65
PRKCB1		0.49	2.01	0.11	-0.47
PRKCBP1		-0.03	0.37	-0.23	-0.33
PRKCD		-0.14	1.09	-1.07	-0.69
PRKCDBP		1.28	0.14	-0.97	0.57
PRKCE		0.30	-0.36	-0.69	0.90
PRKCG		-0.18	-0.12	0.03	-0.66
PRKCH		-0.18	-0.10	1.19	0.47
PRKCI		0.54	0.94	-0.52	1.66
PRKCQ		-1.08	-3.24	0.08	0.15
PRKCZ		0.85	0.19	0.44	-0.10
PRKD1		0.45	-0.02	-0.68	1.61

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
PRKD2		-1.95	1.75	-2.73	-1.17
PRKD3		-0.65	-1.33	-2.13	0.67
PRKDC		0.53	-0.99	1.62	0.31
PRKG1		0.08	-0.76	2.19	-2.19
PRKG2		0.62	-0.01	0.04	-1.78
PRKRA		0.06	0.99	0.14	-0.27
PRKRIR		0.14	0.43	0.84	-0.20
PRKX		0.44	-0.54	-1.04	0.42
PRKY		-0.71	-0.60	-1.01	0.96
PRPF4B		-0.08	-0.51	0.53	0.87
PRPS1L1		0.62	-0.66	-1.19	-0.06
PRSS7		-0.10	0.63	0.31	-0.77
PSKH1		-2.10	0.51	-0.72	0.01
PSKH2		1.77	-0.67	-0.49	0.00
PTK2		-0.58	0.01	0.39	-1.67
PTK2B		0.10	0.42	-1.40	-1.21
PTK6		-1.58	0.40	-1.39	0.14
PTK7		-1.32	0.80	0.93	1.24
PTK9		1.97	0.65	0.36	0.47
PTK9L		-0.66	-2.28	0.25	-1.21
PXK		-0.96	0.20	1.24	-0.07
RAF1		0.02	-1.76	-0.42	1.90
RAGE		0.89	-0.33	-0.46	0.74
RBKS		0.31	2.67	0.30	0.54
RET		-0.70	-1.15	-0.61	-0.12
RFK		2.82	-0.27	0.75	0.25
RIOK1		0.62	-1.26	0.92	-0.47
RIOK2		-0.38	-1.29	0.24	-0.79
RIOK3		0.17	-1.29	-1.59	0.18
RIPK1		-0.53	-0.45	-1.43	-1.36
RIPK2		0.18	-0.42	1.64	-0.64
RIPK3		-0.11	0.44	-0.54	0.35
RIPK4		-0.01	-0.06	0.66	0.67
RIPK5		0.35	0.40	-0.39	0.87
ROCK1		-0.48	0.31	0.19	0.70
ROCK2		0.50	0.09	-0.67	-0.87
ROR1		-0.11	0.17	0.47	0.31
ROR2		-1.16	-1.59	-1.45	0.47
ROS1		1.28	0.40	0.18	0.24
RPS6KA1		-0.10	0.96	1.49	0.81
RPS6KA2		-0.71	1.25	-2.33	-1.03

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
RPS6KA3		-0.03	0.33	-0.74	-0.55
RPS6KA4		2.03	-0.19	-0.47	3.61
RPS6KA5		-0.33	-0.61	-1.56	-0.30
RPS6KA6		-1.85	1.36	-0.59	-2.04
RPS6KB1		1.07	-0.41	0.29	0.50
RPS6KB2		0.20	0.54	0.66	2.65
RPS6KC1		0.23	-0.16	-0.56	0.96
RPS6KL1		-1.03	0.22	-0.42	-0.54
RYK		-0.52	0.40	-0.16	-0.09
SBK1		-0.89	1.68	1.78	0.21
SGK		0.14	0.98	-0.05	2.80
SGK2		2.90	-1.02	0.47	-1.04
SGKL		1.49	-0.18	-0.09	-0.59
SH3KBP1		0.21	0.72	0.18	-0.38
Sharpin		-0.15	1.05	0.70	0.43
SKIP		-0.62	0.65	-0.11	1.43
SKP1A		0.01	-1.75	-0.50	0.57
SKP2		0.02	-1.21	-0.59	0.43
SLK		0.35	-0.95	2.20	-0.31
SMG1		0.11	0.60	0.53	0.41
SNARK		0.18	0.42	-0.13	0.48
SNF1LK		0.55	3.00	-0.84	0.61
SNF1LK2		1.76	0.72	0.69	-0.22
SNRK		0.11	4.14	1.26	3.34
SORCS3		-0.22	0.11	-0.16	-0.53
SPHK1		0.60	-2.36	0.43	-0.30
SPHK2		0.90	-1.10	0.02	0.82
SRC		-1.04	-0.03	0.86	0.64
SRMS		-0.06	0.00	0.19	0.01
SRPK1		-2.14	0.10	-0.75	0.55
SRPK2		0.65	-0.83	-0.55	0.77
SSTK		0.30	-0.06	-0.13	-1.53
STK10		-0.46	-0.88	0.40	-1.60
STK11		-0.01	0.03	1.12	0.05
STK11IP		-1.38	-0.25	-1.27	-1.03
STK16		-0.02	0.71	0.91	0.04
STK17A		0.80	1.43	0.42	-0.43
STK17B		1.22	0.50	1.36	1.11
STK19		-0.12	-0.40	0.02	-0.14
STK22B		-0.74	0.04	-1.46	-0.54
STK22C		-0.52	0.89	1.31	1.53

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
STK22D		-1.79	-0.59	-0.51	-0.56
STK23		1.01	0.74	0.32	-0.25
STK24		0.42	0.49	-1.62	-0.10
STK25		-1.51	-0.82	0.87	-0.64
STK29		-0.74	0.20	1.90	-0.85
STK3		-0.31	-0.20	0.22	-0.96
STK31		0.61	-0.17	0.70	-0.35
STK32A		0.77	1.57	-0.95	-0.08
STK32B		-1.42	-0.07	1.93	-0.10
STK32C		-0.88	-0.34	-0.16	0.34
STK33		-0.65	0.27	-0.69	-0.09
STK35		-1.37	0.63	-0.12	1.62
STK36		0.21	-0.68	-2.02	1.20
STK38		-0.16	0.97	0.77	-0.60
STK38L		0.86	1.09	-2.19	0.85
STK39		0.77	0.30	0.22	-0.44
STK4		0.35	-0.68	0.31	0.66
STK6	AURKA	0.02	0.94	-0.85	0.19
STYK1		2.32	-0.32	-2.74	-0.59
SYK		1.04	1.17	0.04	-0.49
T3JAM		-1.25	-0.98	-1.99	-0.51
TAOK1		1.41	0.35	0.13	-0.81
TAOK2		0.09	0.16	-0.72	-0.52
TAOK2		0.21	0.12	-0.07	-0.57
TAOK3		0.63	-2.31	-0.80	0.86
TBK1		-0.31	0.60	1.24	-0.51
TEC		3.26	-0.14	3.03	0.78
TEK		0.56	0.82	1.65	-0.55
TESK1		-1.93	1.87	0.59	-0.40
TESK2		0.45	-1.06	1.92	-0.19
TGFBR1		-0.06	0.46	-0.83	-0.34
TGFBR2		-0.75	-1.36	0.89	0.54
TIE1		0.05	1.52	0.11	-3.02
TK1		-0.36	0.68	1.26	-0.21
TK2		-0.63	0.68	1.10	-0.14
TLK1		-0.82	-0.42	0.70	0.09
TLK2		-1.30	0.22	-0.20	-1.25
TNIK		-0.51	0.00	0.13	-0.75
TNK1		-0.38	-0.79	-0.56	-0.53
TNK2		-0.97	3.47	-1.54	0.24
TNNI3K		-1.29	0.58	-0.36	0.25

Gene symbol	Alternative gene symbol/current status	siRNA A	siRNA B	siRNA C	siRNA D
TP53RK		2.23	0.97	1.08	-0.32
TPK1		-0.94	-0.84	-0.33	0.12
TRAD		0.76	-0.05	0.88	-0.17
TRIO		1.99	-0.26	0.26	-0.43
TSKS		-1.11	0.14	0.50	1.08
TTBK1		0.10	0.69	0.34	2.30
TTBK2		0.19	0.18	0.93	0.71
TTK		-0.44	0.04	0.34	-1.57
TXK		-0.09	-0.13	0.70	0.35
TYK2		0.52	1.76	-0.70	0.49
TYRO3		0.07	-1.02	0.53	1.22
TYROBP		-0.37	-0.14	-0.14	-0.21
UCK1		-1.54	-0.01	-1.50	-0.20
UCK2		-0.34	0.65	0.89	1.16
UCKL1		-0.64	0.04	1.70	0.32
UGP2		1.46	0.94	-1.52	-0.25
UHMK1		0.79	-0.33	0.45	0.19
ULK1		0.48	-0.47	-0.51	-0.01
ULK2		0.64	0.82	-0.64	1.67
ULK3		-0.20	-0.91	-0.03	-0.03
ULK4		-1.03	-0.49	0.75	0.35
UMP		-0.78	0.38	1.73	1.24
VRK1		0.42	1.24	0.19	0.80
VRK2		0.72	1.87	0.11	0.34
VRK3		-0.80	0.33	-0.15	-0.40
WDSAM1		-0.94	0.31	-0.23	1.10
WEE1		-1.34	-0.47	0.15	-0.96
WNK1		-0.40	-0.48	-0.06	0.60
WNK2		0.60	0.91	-0.05	0.98
WNK3		0.40	0.03	0.63	0.87
WNK4		-1.34	-1.31	-0.47	-0.91
XYLB		0.80	1.03	0.29	0.65
YES1		0.77	0.30	-0.78	0.10
ZAK		0.69	0.47	0.64	0.78
ZAP70		-0.12	2.73	-0.28	-0.34
ZC3HC1		-0.41	-1.40	0.67	-1.23

Supplemental data

Methods:

siRNA based analysis

All siRNAs were arrayed from the Human Druggable Genome siRNA Set Version 2.0 (Qiagen Inc., Germantown, MD). RNAi screens were conducted using synthetic siRNAs corresponding to 691 genes annotated at purchase as associated with kinase activity. See Table S1 for full details of genes targeted including the most recent symbol for those genes for which new nomenclature has been assigned. The majority of the genes within the kinase set encode proteins with defined kinase activity, though a limited number act as kinase co-factors and a few have now been re-annotated as pseudogenes or withdrawn. For each well, 2-pmol siRNA was complexed with 0.06 µl RNAi Max lipid transfection reagent (Invitrogen) in 20 µl DMEM media for 15 minutes at ambient temperature. Seven hundred fifty U87-MG cells in 20 µl DMEM supplemented with 20% FBS were then added to each well. Plates were maintained at ambient temperature for 15 minutes before being placed at 37 °C/5% CO_2. Cell viability was assessed five days post siRNA transfection through quantification of ATP (CellTiter-Glo luminescent Reagent, Promega, Madison, WI). Untransfected cells and wells transfected with negative (All star siNegative, Qiagen) and positive (All star siCell death, Qiagen) control siRNAs were included on every plate. The data for each experimental siRNA was first normalized using the plate median (excluding controls) (**x**) and then z-score transformed using the average (µ)) and standard deviation (σ) for each screen using the following formula: z score = $(x-\mu)/\sigma$. A z-score ≤ -1.6448 was considered significant ($p \leq 0.05$).

Follow up RNAi analysis conducted in 384 well plates was performed as above with all transfections conducted in triplicate. Five hundred U251 cells were used per well of a 384 well

plate. For siRNA transfections conducted in six-well plates, in each well 2-pmol siRNA diluted in 500 µl DMEM was complexed with 4 µl RNAiMax in 500 µl DMEM for 15 min at ambient temperature. $0.1x10^6$ cells in 1000 µl DMEM supplemented with 20% FBS were added and then incubated at 37°C/5% CO_2. Protein for Western blot analysis was harvested 72 hours post siRNA transfection.

Clonogenic assay

Cells were seeded into six-well tissue culture plates and allowed to attach for six hours. GSK461364A or DMSO control was added to the culture media for two hours. For combination treatment, GSK461364A or DMSO control was added to the culture media for two hours followed by treatment with ionizing radiation. Twelve days after seeding, colonies were stained with crystal violet, the number of colonies containing at least 50 cells was determined, and the surviving fractions were calculated. For combination treatment, survival curves were generated after normalizing for the cytotoxicity generated by GSK461364A alone.

Mitotic catastrophe

Cells were grown in 4-well chamber slides, fixed with methanol for 15 minutes at -20°C, washed three times with PBS, blocked with 1% BSA three times for 10 minutes, and stained overnight at 4°C with mouse anti-α-tubulin antibody (Sigma) at 1:1000 dilution. Cells were washed three times with 1% BSA, and were stained with goat anti-mouse-Texas Red antibody (Jackson ImmunoResearch) at 1:200 dilution for 2 hours at room temperature. Cells were washed three times with 1% BSA and slides were mounted in Vectashield mounting medium with DAPI (Vector Labs, Burlingame, California). Images were viewed and captured on a confocal

fluorescent microscope (Zeiss LSM 510, Zeiss Inc., Germany). Images were overlaid in Adobe Photoshop CS (San Jose, CA), and counted in ImageJ (NIH, Bethesda, MD). The mitotic catastrophe was characterized as, "cells with multilobulated giant nuclei and cells with abnormal mitoses." For each treatment condition 100-150 cells were scored, and the average of three separate counts of the same cells was taken.

Histone H2A.X phosphorylation cellular ELISA

We performed cell based ELISA assay for measuring phosphorylation of histone H2A.X according to the manufacturer's protocol (MBL International, Woburn, Massachusetts). Briefly, cells were seeded at 60% confluence in 96 well plates and pretreated with GSA461364A for two hours followed by treatment with radiation. Next, cells were fixed with 95% chilled methanol at room temperature (RT) for 10 min, followed by 1% paraformaldehyde fixation for 5 min at RT. Cells were washed once with wash buffer and fixed for 2 hours at 37^{o}C. Cells were washed once with wash buffer and then incubated with the primary antibody for one hour at RT with shaking at 300 rpm. Wells were washed three times, followed by the secondary antibody for one hour at RT with shaking at 300 rpm. Wells were washed three times, followed by a PBS wash and were incubated with the substrate solution for 20 min in the dark. Reactions were stopped by addition of the stop solution and absorbance was measured at dual wavelengths 450/540 nm.

RNA assays

The expression of *DGUOK*, *PRKD2*, *IBTK* and *RPS6KA6* genes were validated by real-time PCR using Taqman gene expression assays and the ABI PRISM 7500 Sequence Detection System instrument equipped with the SDS version 1.4.0 software (Applied Biosystems, Foster

City, CA). Forward and reverse primers and probes were designed and produced by Applied Biosystems *DGUOK* (Hs00176514_m1), *PRKD2* (Hs00212828_m1), *IBTK* (Hs00539310_m1) and *RPS6KA6* (Hs00179523_m1). PCR was carried out in a 25-µl reaction volume that contained 100 ng of RNA using TaqMan One-Step RT-PCR Master Mix (Applied Biosystems). Each sample was analyzed in duplicate, for 3 different biological sets of RNA and GAPDH RNA was used as an endogenous control (Hs02758991_g1). Negative controls were processed under the same conditions without RNA template. The threshold cycle (C_T) of the endogenous control was used to normalize target gene expression (ΔCt) to correct for experimental variation. The relative change in gene expression ($\Delta\Delta C_T$) was analyzed against the siNegative control.

In vivo tumor growth

All animal studies were conducted in accordance with the principles and procedures outlined in the NIH Guide for the Care and Use of Animals. Four to eight, eight week old, female, athymic NCr *nu/nu*, nude mice (NCI Animal Production Program, Frederick, MD) were used for all *in vivo* studies. Animals were caged in groups of five or fewer and fed animal chow and water *ad libitum*. A single cell suspension ($10x10^6$) of U251 cells was implanted on the lateral aspect of the rear leg. When tumors reached ≈172 mm^3 (*[Length x Width2]/2*), animals were randomized into four groups: untreated controls, or GSK461364A at 25 mg/kg, 50 mg/kg or 100 mg/kg. Mice were given two doses of GSK461364A by gavage, four days apart. To obtain tumor growth curves, perpendicular diameter measurements of each tumor were made twice a week with digital calipers, and volumes were calculated using formula, (*[L x W2]/2*). Tumors were followed until the tumors of the group reached a mean size of 2,000 mm^3. Time taken for control tumors to undergo three doublings was determined. Tumor volumes were interpolated from fit spline

curves for all groups the day control tumors had undergone exactly three doublings. Group means ± standard error is reported.

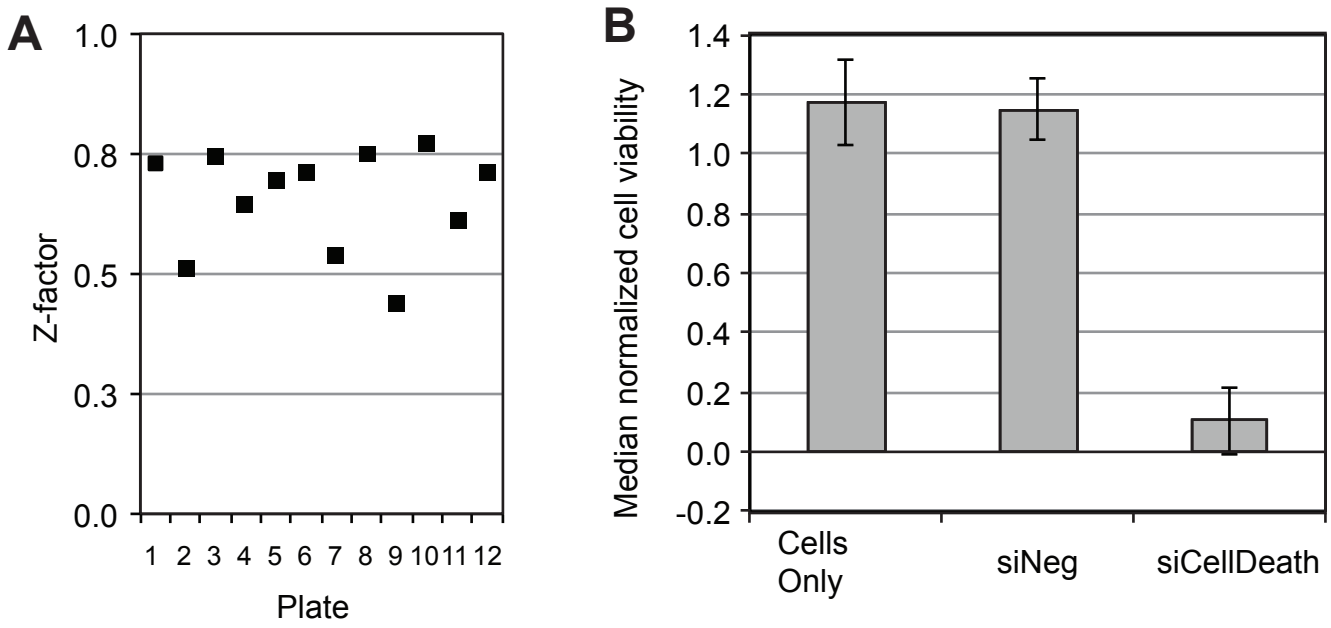
Legends

TABLE S1 A kinome focused siRNA based screen in U87-MG cells

Figure S1 Quality Control data for a kinome focused siRNA based screen in U87-MG cells. (a) Z-factors for each plate calculated using siNeg and siCellDeath controls. (b) Cumulative values for all control wells, cells only (n=383 wells), siNeg (n=191 wells) and siCellDeath (n=130 wells).

Figure S2 Validation of a kinome focused siRNA based screen in U251 cells. The human GBM cell line U251 was transfected with 2 – 6 siRNAs corresponding to *DGUOK*, *PRKD2*, *IBTK* and *RPS6KA6* genes and siNegative, or siCelldeath, (negative and positive control siRNAs) in triplicate. (a) Ninety six hours post siRNA transfection cell viability was assessed. Data is shown as the % viability normalized to siNegative control, each bar represents the mean ±SD of three wells. (b) Seventy two hours post siRNA transfection, expression of each gene assessed using gene specific TaqMan RT-PCR (GAPDH normalized). Data is shown as the median value of six TaqMan RT-PCR reactions.

Supplementary Figure 1



Supplementary Figure 2