

Supplementary Materials Lu et al

Supplementary Table 1

List of genes targeted and the change in pAKT S473 and T308. The values of pAKT as well as their corresponding z-scores are shown. Genes in green when targeted by siRNA had an average z-score of less than -1.4 and those in red higher than +1.4.

Gene Symbol	values		z-scores		Average Z-score
	Akt_pS473	Akt_pT308	Akt_pS473 z-sc	Akt_pT308 z-sc	
MGC45428	-1.225943988	-1.285730129	-3.33	-2.88	-3.10
KIAA0999	-1.387110933	-1.055730129	-2.74	-3.25	-3.00
TRB2	-1.23649937	-0.905730129	-2.36	-2.90	-2.63
ACVR1C	-0.994913798	-0.975730129	-2.54	-2.33	-2.44
BCKDK	-0.838654253	-1.065730129	-2.77	-1.97	-2.37
GSK3A	-0.87528797	-0.975730129	-2.54	-2.05	-2.30
MARK1	-1.079296476	-0.785730129	-2.05	-2.53	-2.29
FGFR1	-0.901517706	-0.895730129	-2.33	-2.11	-2.22
AKT3	-0.6442204	-1.105730129	-2.86	-1.51	-2.19
FLJ23074	-1.1039163	-0.675730129	-1.74	-2.59	-2.17
PAK6	-0.936200086	-0.805730129	-2.08	-2.20	-2.14
ADMR	-0.227015071	-1.335730129	-3.46	-0.53	-2.00
PRKCN	-0.827506718	-0.745730129	-1.94	-1.94	-1.94
ERK8	-0.65465574	-0.865730129	-2.25	-1.54	-1.89
RIOK1	-0.901970945	-0.615730129	-1.59	-2.12	-1.85
NEK9	-1.129947426	-0.405730129	-1.05	-2.65	-1.85
BRD4	-0.667685428	-0.775730129	-2.02	-1.57	-1.79
FLJ33655	-0.912241484	-0.535730129	-1.39	-2.14	-1.76
HAK	-0.500443649	-0.885730129	-2.31	-1.17	-1.74
STK31	-0.959913825	-0.455730129	-1.19	-2.25	-1.72
MINK	-0.674480562	-0.695730129	-1.81	-1.58	-1.70
SK707	-0.423567419	-0.885730129	-2.29	-0.99	-1.64
MAPK3	-0.434492813	-0.855730129	-2.23	-1.02	-1.62
CAMK2G	-0.913103565	-0.425730129	-1.10	-2.14	-1.62
TTBK2	-0.797880452	-0.495730129	-1.29	-1.87	-1.58
PTK7	-0.519711308	-0.705730129	-1.82	-1.22	-1.52
SMG1	-0.41900903	-0.785730129	-2.04	-0.98	-1.51
MAP3K1	-0.933114822	-0.315730129	-0.81	-2.19	-1.50
INSRR	-0.114699467	-1.045730129	-2.70	-0.27	-1.49
CDK10	-0.806794015	-0.385730129	-1.01	-1.89	-1.45
BMP2K	-0.46011965	-0.675730129	-1.76	-1.08	-1.42
AAK1	-0.269561496	-0.845730129	-2.19	-0.63	-1.41
AKT1	-0.494973278	-0.635730129	-1.66	-1.16	-1.41
HIPK1	-0.754978029	-0.395730129	-1.04	-1.77	-1.40
CDC42BPB	-0.649035566	-0.455730129	-1.19	-1.52	-1.35
ADRB3	-0.534316731	-0.555730129	-1.44	-1.25	-1.35
STK24	-1.091855614	-0.045730129	-0.12	-2.56	-1.34
CAMKK1	-0.866035566	-0.245730129	-0.63	-2.03	-1.33
PHKG1	-0.632581732	-0.455730129	-1.18	-1.48	-1.33
SK723	-0.662031624	-0.425730129	-1.11	-1.55	-1.33
SCYL1	-0.701216303	-0.375730129	-0.97	-1.64	-1.31
HIPK3	-0.538866664	-0.515730129	-1.34	-1.26	-1.30
GPRK5	-0.424102191	-0.605730129	-1.57	-0.99	-1.28
STK16	-0.236929298	-0.765730129	-2.00	-0.56	-1.28
PFTK1	-0.783586517	-0.275730129	-0.70	-1.84	-1.27
ABL2	-0.440814615	-0.575730129	-1.50	-1.03	-1.27
PTK2	-0.523454646	-0.495730129	-1.28	-1.23	-1.26
PAK4	-0.246944265	-0.745730129	-1.93	-0.58	-1.26
MGC16169	-1.084371189	0.014269871	0.04	-2.54	-1.25
PASK	-0.494376729	-0.505730129	-1.30	-1.16	-1.23

FRK	-0.344209417	-0.635730129	-1.65	-0.81	-1.23
FLJ32685	-0.782844498	-0.225730129	-0.58	-1.84	-1.21
ADCK1	-0.575263953	-0.405730129	-1.06	-1.35	-1.21
MARK4	-0.77913654	-0.225730129	-0.57	-1.83	-1.20
ADRA1B	-0.217077264	-0.705730129	-1.84	-0.51	-1.18
STK38L	-0.373049655	-0.565730129	-1.47	-0.88	-1.17
EPHB2	-0.485828863	-0.465730129	-1.20	-1.14	-1.17
TESK1	-0.271212292	-0.645730129	-1.66	-0.64	-1.15
FLJ25006	-0.723403013	-0.225730129	-0.59	-1.70	-1.14
GPRK2L	-0.146058924	-0.725730129	-1.88	-0.34	-1.11
AVPR1A	-0.47128445	-0.425730129	-1.11	-1.11	-1.11
FLJ23119	-0.769760782	-0.145730129	-0.37	-1.81	-1.09
ERBB4	-0.506402031	-0.365730129	-0.94	-1.19	-1.07
ADRA2C	-0.181820414	-0.645730129	-1.67	-0.43	-1.05
MGC8407	-0.553225222	-0.305730129	-0.80	-1.30	-1.05
FLJ10074	-0.292173907	-0.525730129	-1.38	-0.69	-1.03
PXK	-0.044231088	-0.715730129	-1.86	-0.10	-0.98
EPHA1	-0.412204637	-0.375730129	-0.98	-0.97	-0.97
ALS2CR2	-0.466584499	-0.325730129	-0.85	-1.09	-0.97
PIK3R4	-0.525919899	-0.275730129	-0.71	-1.23	-0.97
IKBKB	-0.268795252	-0.495730129	-1.30	-0.63	-0.96
SK650	-0.609792919	-0.185730129	-0.48	-1.43	-0.96
MAPK6	-0.343676291	-0.405730129	-1.06	-0.81	-0.93
SLK	-0.448799839	-0.315730129	-0.81	-1.05	-0.93
CDC2L5	-0.134249585	-0.585730129	-1.52	-0.31	-0.92
ADCK2	-0.026626242	-0.675730129	-1.75	-0.06	-0.90
STK35	-0.14911617	-0.555730129	-1.44	-0.35	-0.90
ZAK	-0.255275427	-0.435730129	-1.14	-0.60	-0.87
KIAA1883	-0.193265865	-0.495730129	-1.28	-0.45	-0.87
MYO3B	-0.462092741	-0.235730129	-0.61	-1.08	-0.85
EIF2AK4	-0.476100926	-0.225730129	-0.57	-1.12	-0.84
EGFR	-0.077585887	-0.575730129	-1.48	-0.18	-0.83
GPRK7	-0.491938504	-0.195730129	-0.51	-1.15	-0.83
ADCK4	-0.508289802	-0.165730129	-0.44	-1.19	-0.82
ADORA2B	-0.282877541	-0.365730129	-0.94	-0.66	-0.80
KSR	-0.37540692	-0.265730129	-0.70	-0.88	-0.79
DKFZP434C1:	-0.561358789	-0.095730129	-0.26	-1.32	-0.79
HSMDPKIN	0.330009147	-0.905730129	-2.35	0.77	-0.79
C8FW	-0.509044478	-0.145730129	-0.37	-1.19	-0.78
SK662	-0.725123637	0.064269871	0.16	-1.70	-0.77
LOC91461	-0.415786067	-0.215730129	-0.55	-0.98	-0.76
MYLK	-0.307627975	-0.305730129	-0.81	-0.72	-0.76
RIPK1	-0.618389496	-0.025730129	-0.07	-1.45	-0.76
GPR116	-0.286932068	-0.315730129	-0.83	-0.67	-0.75
SYK	-0.247208268	-0.305730129	-0.80	-0.58	-0.69
ADRA1A	-0.276200713	-0.275730129	-0.73	-0.65	-0.69
NEK7	-0.21664326	-0.335730129	-0.86	-0.51	-0.68
VRK2	-0.557257262	-0.015730129	-0.05	-1.31	-0.68
CDKL2	-0.416559575	-0.145730129	-0.37	-0.98	-0.67
ALS2CR7	-0.186595548	-0.345730129	-0.90	-0.44	-0.67
CAMK4	0.070358661	-0.575730129	-1.51	0.17	-0.67
SNRK	-0.22877547	-0.305730129	-0.80	-0.54	-0.67

PRKG1	-0.214140792	-0.315730129	-0.82	-0.50	-0.66
MAST205	0.022386775	-0.525730129	-1.37	0.05	-0.66
SRMS	-0.185196569	-0.335730129	-0.87	-0.43	-0.65
NEK1	0.034455882	-0.525730129	-1.36	0.08	-0.64
RNASEL	-0.413181464	-0.115730129	-0.30	-0.97	-0.64
FLJ14813	-0.482102466	-0.055730129	-0.14	-1.13	-0.63
STK36	-0.275217739	-0.235730129	-0.62	-0.65	-0.63
MAP3K12	0.128140053	-0.605730129	-1.57	0.30	-0.63
SGK	-0.25744751	-0.245730129	-0.65	-0.60	-0.63
SK690	-0.396626851	-0.115730129	-0.30	-0.93	-0.62
TTN	-0.690336113	0.154269871	0.39	-1.62	-0.61
SRPK1	-0.157174994	-0.325730129	-0.84	-0.37	-0.60
PRKAA2	-0.150094588	-0.325730129	-0.85	-0.35	-0.60
ABL1	-0.427412323	-0.075730129	-0.20	-1.00	-0.60
IRAK3	-0.296308817	-0.195730129	-0.50	-0.70	-0.60
CAMK1	-0.084595652	-0.385730129	-1.00	-0.20	-0.60
C14orf20	-0.213356134	-0.265730129	-0.69	-0.50	-0.59
CAMK1G	-0.239671472	-0.235730129	-0.62	-0.56	-0.59
ADORA1	-0.185996557	-0.285730129	-0.74	-0.44	-0.59
CDK11	-0.102640708	-0.355730129	-0.93	-0.24	-0.59
LOC340371	-0.551022213	0.044269871	0.12	-1.29	-0.59
NTRK2	-0.248596512	-0.225730129	-0.58	-0.58	-0.58
ERN2	-0.302820438	-0.165730129	-0.44	-0.71	-0.58
AKT2	0.29778808	-0.705730129	-1.84	0.70	-0.57
FER	-0.26829767	-0.195730129	-0.51	-0.63	-0.57
ICK	-0.244190024	-0.215730129	-0.55	-0.57	-0.56
SGKL	0.061183252	-0.485730129	-1.26	0.14	-0.56
TTBK1	-0.306467383	-0.145730129	-0.39	-0.72	-0.55
MAP3K9	-0.753742698	0.254269871	0.67	-1.77	-0.55
KIAA0561	-0.287911046	-0.155730129	-0.41	-0.68	-0.54
PRKCM	0.135391123	-0.535730129	-1.39	0.32	-0.53
BRD2	-0.414466561	-0.035730129	-0.08	-0.97	-0.53
SK643	-0.382619568	-0.045730129	-0.12	-0.90	-0.51
CSF1R	-0.483789732	0.054269871	0.14	-1.13	-0.50
PRKACG	-0.289946514	-0.115730129	-0.31	-0.68	-0.50
STK38	-0.325175044	-0.085730129	-0.22	-0.76	-0.49
TLK2	-0.247295164	-0.155730129	-0.40	-0.58	-0.49
EPHA3	-0.311356298	-0.095730129	-0.24	-0.73	-0.49
EIF2AK3	0.076014064	-0.445730129	-1.15	0.18	-0.49
MARK3	-0.008336789	-0.365730129	-0.95	-0.02	-0.49
PCTK3	0.065914871	-0.435730129	-1.12	0.15	-0.48
MAPK12	0.03103702	-0.395730129	-1.04	0.07	-0.48
FLJ32818	-0.663175589	0.234269871	0.60	-1.56	-0.48
CARK	0.210583872	-0.555730129	-1.44	0.49	-0.47
SK466	-0.192206121	-0.185730129	-0.48	-0.45	-0.47
LYN	0.145199284	-0.485730129	-1.27	0.34	-0.46
MKNK2	-0.200377051	-0.175730129	-0.46	-0.47	-0.46
ACK1	-0.058341488	-0.295730129	-0.76	-0.14	-0.45
PRKWINK2	-0.110191248	-0.245730129	-0.63	-0.26	-0.44
FLJ25965	-0.815027479	0.394269871	1.03	-1.91	-0.44
SK681	-0.196314095	-0.155730129	-0.41	-0.46	-0.44
C20orf64	-0.306789712	-0.055730129	-0.14	-0.72	-0.43

LOC149420	-0.461961153	0.084269871	0.22	-1.08	-0.43
STK29	-0.01325422	-0.305730129	-0.80	-0.03	-0.42
RIOK2	-0.064366698	-0.265730129	-0.68	-0.15	-0.42
MELK	-0.152016334	-0.175730129	-0.46	-0.36	-0.41
PRKWINK4	-0.40467936	0.054269871	0.14	-0.95	-0.41
KIAA1297	-0.517415537	0.154269871	0.40	-1.21	-0.41
ADCK5	-0.551464205	0.184269871	0.49	-1.29	-0.40
IKBKE	-0.134399079	-0.185730129	-0.48	-0.32	-0.40
RPS6KL1	-0.546716268	0.184269871	0.49	-1.28	-0.40
ILK-2	0.255750036	-0.535730129	-1.38	0.60	-0.39
ERBB3	0.188326322	-0.465730129	-1.21	0.44	-0.38
SK558	-0.068488065	-0.225730129	-0.60	-0.16	-0.38
TIE	-0.310609368	-0.015730129	-0.03	-0.73	-0.38
PRKCA	0.420439689	-0.665730129	-1.74	0.99	-0.38
FGR	-0.342222068	0.024269871	0.06	-0.80	-0.37
TXK	-0.628958906	0.284269871	0.75	-1.48	-0.36
FLJ23356	-0.488187797	0.164269871	0.43	-1.15	-0.36
MAPKAPK5	0.582686161	-0.795730129	-2.07	1.37	-0.35
OSR1	-0.361900972	0.064269871	0.16	-0.85	-0.34
SNF1LK	-0.514406697	0.204269871	0.53	-1.21	-0.34
HUNK	0.14632729	-0.385730129	-1.01	0.34	-0.34
AURKB	0.090359923	-0.335730129	-0.88	0.21	-0.33
RIOK3	-0.010719244	-0.245730129	-0.63	-0.03	-0.33
PDGFRA	0.022427035	-0.265730129	-0.69	0.05	-0.32
CLK3	-0.023631899	-0.225730129	-0.58	-0.06	-0.32
ADRBK2	-0.212505693	-0.045730129	-0.13	-0.50	-0.31
PTK6	-0.125385157	-0.125730129	-0.33	-0.29	-0.31
PRKACA	0.149860168	-0.375730129	-0.97	0.35	-0.31
VRK3	-0.049866695	-0.195730129	-0.50	-0.12	-0.31
CSK	-0.01672382	-0.225730129	-0.58	-0.04	-0.31
MGC4796	-0.033735072	-0.195730129	-0.51	-0.08	-0.30
TRIM33	0.082768346	-0.305730129	-0.78	0.19	-0.29
PRKACB	0.083943129	-0.295730129	-0.78	0.20	-0.29
PTK9L	-0.108131021	-0.125730129	-0.32	-0.25	-0.29
PRKCB1	0.017563259	-0.235730129	-0.61	0.04	-0.28
IGF1R	-0.079120762	-0.145730129	-0.38	-0.19	-0.28
EMR2	-0.381136999	0.124269871	0.33	-0.89	-0.28
EPHA7	-0.308663468	0.064269871	0.17	-0.72	-0.28
MARK2	-0.291706623	0.054269871	0.13	-0.68	-0.28
CDK5	-0.392740485	0.144269871	0.39	-0.92	-0.27
PINK1	-0.281068177	0.044269871	0.13	-0.66	-0.27
PRKCI	0.217446598	-0.395730129	-1.04	0.51	-0.26
KIAA0781	-0.237210634	0.014269871	0.04	-0.56	-0.26
STK4	-0.359513585	0.124269871	0.33	-0.84	-0.26
RHOK	-0.319437928	0.094269871	0.23	-0.75	-0.26
ADRB2	-0.183421481	-0.035730129	-0.09	-0.43	-0.26
SAST	-0.546016408	0.304269871	0.78	-1.28	-0.25
TYRO3	0.083463164	-0.265730129	-0.70	0.20	-0.25
TOPK	-0.365472215	0.144269871	0.36	-0.86	-0.25
JAK2	-0.364493425	0.144269871	0.37	-0.85	-0.24
RIPK2	-0.215580573	0.004269871	0.02	-0.51	-0.24
CRK7	0.077084841	-0.255730129	-0.66	0.18	-0.24

PRKG2	0.038959886	-0.215730129	-0.56	0.09	-0.23
MAPK8	0.24597881	-0.405730129	-1.04	0.58	-0.23
MAP3K3	-0.049561945	-0.125730129	-0.33	-0.12	-0.22
GUCY2C	-0.059209961	-0.115730129	-0.30	-0.14	-0.22
FGFR3	-0.14036614	-0.035730129	-0.10	-0.33	-0.21
TEX14	-0.444021724	0.244269871	0.62	-1.04	-0.21
ROCK2	-0.26936712	0.084269871	0.22	-0.63	-0.21
ADRA2B	-0.16113998	-0.015730129	-0.04	-0.38	-0.21
KIAA0551	0.092651589	-0.245730129	-0.63	0.22	-0.21
MGC42105	-0.503146307	0.304269871	0.78	-1.18	-0.20
LIMK2	-0.0948012	-0.065730129	-0.17	-0.22	-0.20
PRKCH	-0.095070631	-0.055730129	-0.16	-0.22	-0.19
LATS2	-0.25349186	0.084269871	0.22	-0.59	-0.19
PDK4	0.223954544	-0.325730129	-0.86	0.53	-0.17
NLK	0.0499039	-0.165730129	-0.44	0.12	-0.16
PRKCD	-0.326833995	0.174269871	0.45	-0.77	-0.16
MAP4K3	0.078048634	-0.185730129	-0.49	0.18	-0.15
ANKK1	-0.364047011	0.214269871	0.56	-0.85	-0.15
PKE	-0.454193567	0.304269871	0.78	-1.07	-0.14
PIM1	0.135489929	-0.235730129	-0.60	0.32	-0.14
PRKWINK3	-0.124335496	0.004269871	0.02	-0.29	-0.14
AGTR2	-0.123581917	0.004269871	0.02	-0.29	-0.13
KIAA1765	-0.422868078	0.274269871	0.72	-0.99	-0.13
CSNK1G1	-0.463840503	0.314269871	0.82	-1.09	-0.13
PIM2	-0.213556163	0.094269871	0.23	-0.50	-0.13
MAP3K7	0.225447661	-0.295730129	-0.76	0.53	-0.12
HIPK2	-0.35703398	0.234269871	0.60	-0.84	-0.12
LYK5	-0.606978377	0.454269871	1.19	-1.42	-0.12
STK22C	-0.498534777	0.374269871	0.96	-1.17	-0.10
STK22B	-0.366285061	0.254269871	0.66	-0.86	-0.10
BCR	0.148171801	-0.205730129	-0.53	0.35	-0.09
RPS6KA6	0.414780624	-0.425730129	-1.12	0.97	-0.07
RIPK3	-0.121946293	0.054269871	0.15	-0.29	-0.07
PSKH1	-0.048146357	-0.005730129	-0.02	-0.11	-0.06
KIAA1361	0.156825665	-0.185730129	-0.48	0.37	-0.06
ULK1	-0.291169284	0.224269871	0.58	-0.68	-0.05
NEK11	-0.333910281	0.264269871	0.69	-0.78	-0.05
MGC22688	-0.072724388	0.034269871	0.08	-0.17	-0.04
IRAK2	0.16378539	-0.165730129	-0.44	0.38	-0.03
STK10	0.071331829	-0.085730129	-0.22	0.17	-0.03
MAK	0.041657637	-0.055730129	-0.14	0.10	-0.02
AURKC/STK1	-0.120527155	0.094269871	0.25	-0.28	-0.02
FLT4	0.299350712	-0.285730129	-0.73	0.70	-0.02
TIF1	-0.053462026	0.044269871	0.10	-0.13	-0.01
PRKCL1	0.237189397	-0.205730129	-0.55	0.56	0.00
KIAA1639	0.132517682	-0.115730129	-0.30	0.31	0.00
TRIO	-0.232006933	0.214269871	0.56	-0.54	0.01
PKMYT1	-0.221492024	0.204269871	0.54	-0.52	0.01
CDK2	0.203610949	-0.175730129	-0.45	0.48	0.01
SSTK	-0.392612586	0.364269871	0.95	-0.92	0.02
ARAF1	-0.43617738	0.404269871	1.06	-1.02	0.02
SRPK2	0.323038333	-0.255730129	-0.67	0.76	0.04

ADORA2A	-0.290420646	0.294269871	0.77	-0.68	0.04
NEK4	-0.084561437	0.114269871	0.29	-0.20	0.05
CASK	0.208862407	-0.145730129	-0.39	0.49	0.05
FGFR4	0.272598263	-0.205730129	-0.53	0.64	0.05
KIAA1079	0.421119302	-0.335730129	-0.87	0.99	0.06
AGTRL1	0.173353047	-0.105730129	-0.28	0.41	0.06
STK33	-0.148377607	0.184269871	0.48	-0.35	0.07
LCK	0.195111934	-0.125730129	-0.33	0.46	0.07
CDC2	0.255189538	-0.175730129	-0.46	0.60	0.07
ROCK1	0.012311679	0.044269871	0.11	0.03	0.07
GRK6	0.005159051	0.044269871	0.13	0.01	0.07
ADORA3	-0.074960807	0.124269871	0.33	-0.18	0.08
KIAA0303	-0.20149164	0.244269871	0.63	-0.47	0.08
MAP3K13	-0.058973429	0.114269871	0.30	-0.14	0.08
DCAMKL1	0.03117734	0.034269871	0.09	0.07	0.08
FZD7	0.005873174	0.054269871	0.15	0.01	0.08
TNK1	0.242821901	-0.145730129	-0.39	0.57	0.09
MST4	-0.357198085	0.404269871	1.06	-0.84	0.11
BMPR1B	0.192267793	-0.085730129	-0.23	0.45	0.11
MET	0.409869711	-0.285730129	-0.74	0.96	0.11
LIMK1	0.275138793	-0.155730129	-0.40	0.65	0.12
MAP3K5	-0.008889653	0.104269871	0.28	-0.02	0.13
MAPK14	0.269374625	-0.145730129	-0.38	0.63	0.13
TESK2	0.049752437	0.064269871	0.15	0.12	0.14
PAK7	-0.157585223	0.244269871	0.64	-0.37	0.14
SGK2	0.199552596	-0.075730129	-0.19	0.47	0.14
MAP4K1	0.188200727	-0.055730129	-0.15	0.44	0.15
ADRB1	-0.175739919	0.274269871	0.71	-0.41	0.15
DYRK3	0.098555437	0.024269871	0.07	0.23	0.15
ROR2	-0.271363132	0.364269871	0.94	-0.64	0.15
MYLK2	-0.625598999	0.684269871	1.77	-1.47	0.15
CDC2L1	0.334222877	-0.185730129	-0.47	0.78	0.16
ADCYAP1R1	0.245146044	-0.095730129	-0.26	0.58	0.16
KIAA1811	-0.135480381	0.254269871	0.65	-0.32	0.17
RPS6KA4	0.162122193	-0.015730129	-0.05	0.38	0.17
MYO3A	0.232373558	-0.075730129	-0.20	0.55	0.17
PDPK1	0.055847994	0.094269871	0.23	0.13	0.18
CSNK2A1	0.303473431	-0.135730129	-0.35	0.71	0.18
CDC42BPA	0.094334546	0.054269871	0.15	0.22	0.18
IRAK4	0.152013978	0.004269871	0.01	0.36	0.18
FLT3	0.395177718	-0.205730129	-0.54	0.93	0.19
CDKL1	0.419260735	-0.225730129	-0.60	0.98	0.19
CNR2	0.036199418	0.124269871	0.33	0.08	0.21
CHEK2	-0.031107258	0.184269871	0.49	-0.07	0.21
PAK1	0.305682831	-0.115730129	-0.30	0.72	0.21
CHEK1	0.121914896	0.054269871	0.13	0.29	0.21
FYN	-0.363520214	0.494269871	1.28	-0.85	0.21
TRIM28	0.057305458	0.114269871	0.29	0.13	0.21
RPS6KA1	-0.311953556	0.444269871	1.16	-0.73	0.22
BMPR1A	0.14614608	0.044269871	0.11	0.34	0.23
GSG2	-0.081031948	0.244269871	0.64	-0.19	0.23
PSKH2	-0.207745001	0.364269871	0.94	-0.49	0.23

SK709	-0.244845301	0.394269871	1.03	-0.57	0.23
YES1	0.131037624	0.064269871	0.16	0.31	0.23
LATS1	0.047851536	0.134269871	0.36	0.11	0.24
MAPKAPK2	0.036051847	0.154269871	0.39	0.08	0.24
DRD5	-0.091255775	0.264269871	0.69	-0.21	0.24
CDKL5	-0.074593695	0.254269871	0.66	-0.17	0.24
MAP4K2	0.099664534	0.104269871	0.27	0.23	0.25
PRKX	-0.098386511	0.284269871	0.74	-0.23	0.26
KIAA1804	0.022766111	0.184269871	0.48	0.05	0.27
ANKRD3	-0.159676059	0.354269871	0.92	-0.37	0.27
TEK	0.152123262	0.074269871	0.19	0.36	0.27
RPS6KA2	-0.071309448	0.284269871	0.74	-0.17	0.28
H11	0.093629208	0.134269871	0.35	0.22	0.29
FES	0.458309556	-0.195730129	-0.50	1.08	0.29
NEK8	-0.069407284	0.284269871	0.74	-0.16	0.29
DKFZp434C14	-0.109170335	0.324269871	0.83	-0.26	0.29
CABC1	0.048262325	0.184269871	0.47	0.11	0.29
TLK1	0.113066959	0.124269871	0.32	0.27	0.29
MGC33182	0.262039883	-0.015730129	-0.03	0.61	0.29
BUB1	0.110221313	0.134269871	0.34	0.26	0.30
STK19	-0.384831676	0.584269871	1.51	-0.90	0.31
BUB1B	0.381411516	-0.085730129	-0.22	0.89	0.33
TYK2	-0.349411495	0.574269871	1.50	-0.82	0.34
PAK2	-0.406584811	0.634269871	1.64	-0.95	0.34
KDR	0.283207734	0.014269871	0.04	0.66	0.35
CSNK1G3	0.133121103	0.154269871	0.39	0.31	0.35
PDK2	0.540734991	-0.215730129	-0.56	1.27	0.35
ARK5	0.560693972	-0.225730129	-0.60	1.32	0.36
FLT1	0.526100341	-0.195730129	-0.51	1.23	0.36
C20orf97	-0.162365703	0.424269871	1.11	-0.38	0.36
ULK2	0.075999086	0.214269871	0.55	0.18	0.37
RPS6KA3	0.41385351	-0.085730129	-0.23	0.97	0.37
KIS	-0.192275407	0.464269871	1.20	-0.45	0.38
TBK1	0.088184537	0.224269871	0.57	0.21	0.39
PHKG2	0.203832822	0.114269871	0.30	0.48	0.39
STK25	0.258826394	0.074269871	0.18	0.61	0.39
GSK3B	0.319374886	0.014269871	0.04	0.75	0.40
FLJ34389	-0.324907455	0.604269871	1.58	-0.76	0.41
NTRK3	0.389854127	-0.035730129	-0.09	0.91	0.41
HSA250839	0.309770874	0.044269871	0.11	0.73	0.42
AATK	0.002684866	0.324269871	0.83	0.01	0.42
CSNK1E	0.401141821	-0.035730129	-0.10	0.94	0.42
TGFBR1	0.214128221	0.134269871	0.35	0.50	0.42
NEK6	0.239373999	0.114269871	0.29	0.56	0.43
MAP3K14	0.241212513	0.114269871	0.29	0.57	0.43
MAP3K4	0.227200133	0.134269871	0.36	0.53	0.45
FASTK	0.595118665	-0.185730129	-0.49	1.40	0.45
MAP3K11	0.196230463	0.184269871	0.49	0.46	0.47
DDR1	0.442117599	-0.035730129	-0.09	1.04	0.48
SRC	0.401396085	0.004269871	0.01	0.94	0.48
BTK	0.140740677	0.244269871	0.63	0.33	0.48
MATK	0.296853952	0.104269871	0.27	0.70	0.48

EPHB6	0.087126533	0.294269871	0.77	0.20	0.49
NTRK1	0.630391311	-0.195730129	-0.50	1.48	0.49
MAPK4	0.384638751	0.034269871	0.09	0.90	0.50
GPR12	0.302565937	0.114269871	0.29	0.71	0.50
TRAD	-0.034840689	0.414269871	1.08	-0.08	0.50
DYRK2	-0.001419976	0.384269871	1.01	0.00	0.50
JAK1	0.433014204	-0.005730129	-0.01	1.02	0.50
EPHA5	0.106576658	0.304269871	0.80	0.25	0.53
PCTK2	0.572612343	-0.105730129	-0.28	1.34	0.53
RPS6KC1	0.462655517	-0.005730129	-0.02	1.09	0.53
PRPF4B	0.10008981	0.324269871	0.83	0.23	0.53
BRD3	0.280162733	0.154269871	0.41	0.66	0.54
CLK2	0.462901291	0.004269871	0.00	1.09	0.54
ADRA2A	0.321409478	0.134269871	0.34	0.75	0.55
VRK1	-0.131239969	0.544269871	1.41	-0.31	0.55
MAPK1	0.507761646	-0.035730129	-0.09	1.19	0.55
FLJ20574	0.344455225	0.114269871	0.29	0.81	0.55
MAP4K5	0.165995998	0.274269871	0.71	0.39	0.55
MAP3K10	0.412141903	0.054269871	0.15	0.97	0.56
PTK9	0.301188339	0.154269871	0.41	0.71	0.56
AGTR1	-0.064791238	0.494269871	1.28	-0.15	0.56
MGC43306	0.17186232	0.284269871	0.73	0.40	0.57
SNARK	-0.221671412	0.634269871	1.66	-0.52	0.57
WEE1	0.078472261	0.374269871	0.96	0.18	0.57
CDK9	0.279062939	0.184269871	0.49	0.65	0.57
TAF1L	0.101028104	0.354269871	0.91	0.24	0.57
CSNK1D	0.148926519	0.304269871	0.80	0.35	0.57
ACVRL1	0.304444498	0.174269871	0.45	0.71	0.58
PRKCE	0.421497875	0.064269871	0.17	0.99	0.58
DKFZp761P10	0.441754282	0.054269871	0.13	1.04	0.58
AMHR2	0.11316997	0.344269871	0.90	0.27	0.58
MAPK7	0.372682684	0.114269871	0.30	0.87	0.59
STK6	0.207133389	0.264269871	0.70	0.49	0.59
BLK	0.149001509	0.324269871	0.84	0.35	0.59
MUSK	0.099549667	0.374269871	0.96	0.23	0.60
EPHB1	0.002055785	0.454269871	1.19	0.00	0.60
CDKL3	0.630768474	-0.105730129	-0.27	1.48	0.61
pknbeta	0.465868087	0.044269871	0.13	1.09	0.61
CCRK	0.187319551	0.304269871	0.78	0.44	0.61
NPR2	0.433591113	0.074269871	0.20	1.02	0.61
CSNK1G2	0.34368152	0.164269871	0.42	0.81	0.61
STK18	0.232069527	0.264269871	0.69	0.54	0.62
GAK	0.151586597	0.344269871	0.89	0.36	0.62
PAK3	0.627970908	-0.085730129	-0.23	1.47	0.62
RYK	0.062982666	0.424269871	1.10	0.15	0.62
RPS6KB2	0.123347823	0.374269871	0.96	0.29	0.62
ACVR1B	0.290657652	0.224269871	0.58	0.68	0.63
EPHA4	0.049388873	0.444269871	1.15	0.12	0.63
LOC91807	0.045809848	0.444269871	1.16	0.11	0.63
MIDORI	-0.053133342	0.534269871	1.40	-0.12	0.64
GUCY2D	0.192360929	0.314269871	0.83	0.45	0.64
CDK7	0.311952832	0.214269871	0.55	0.73	0.64

SNK	0.356658529	0.174269871	0.44	0.84	0.64
CSNK2A2	0.758437327	-0.195730129	-0.50	1.78	0.64
BMX	0.552725255	-0.005730129	-0.01	1.30	0.64
ACVR2	0.415218138	0.124269871	0.31	0.97	0.64
STK22D	-0.037852964	0.524269871	1.37	-0.09	0.64
TGFBR2	0.190642954	0.324269871	0.85	0.45	0.65
CLK1	0.345297682	0.194269871	0.50	0.81	0.65
ACVR2B	0.431344042	0.114269871	0.30	1.01	0.66
TRRAP	0.270305621	0.264269871	0.69	0.63	0.66
MST1R	0.371337369	0.174269871	0.45	0.87	0.66
EPHA2	0.079984054	0.434269871	1.14	0.19	0.66
MAP2K7	0.237744655	0.294269871	0.77	0.56	0.67
MAP3K2	0.438725	0.124269871	0.32	1.03	0.67
ERN1	0.30992079	0.234269871	0.62	0.73	0.67
ROR1	0.411323666	0.154269871	0.39	0.96	0.68
BRDT	0.423996117	0.144269871	0.38	0.99	0.69
MKNK1	0.238334465	0.314269871	0.81	0.56	0.69
NPR1	0.183820468	0.364269871	0.95	0.43	0.69
CAMK2B	0.089143727	0.464269871	1.20	0.21	0.71
STK17B	0.471288291	0.124269871	0.32	1.11	0.71
ADRBK1	0.3582946	0.224269871	0.59	0.84	0.71
TTK	-0.089476347	0.634269871	1.65	-0.21	0.72
SK440	0.202859779	0.374269871	0.97	0.48	0.72
NRBP	0.464476937	0.144269871	0.38	1.09	0.74
AVPR2	0.295940889	0.304269871	0.80	0.69	0.75
PRKCG	0.64695749	-0.005730129	-0.01	1.52	0.75
MAPKAPK3	0.27758899	0.334269871	0.86	0.65	0.76
CHUK	0.371974804	0.244269871	0.65	0.87	0.76
ATM	0.463639493	0.164269871	0.43	1.09	0.76
MAP3K8	-0.102826782	0.674269871	1.76	-0.24	0.76
SK581	0.317788277	0.304269871	0.79	0.75	0.77
MAP3K6	0.303876464	0.324269871	0.84	0.71	0.77
ALK	0.468339625	0.174269871	0.46	1.10	0.78
EEF2K	0.656263273	0.014269871	0.03	1.54	0.79
STK17A	0.203561563	0.434269871	1.12	0.48	0.80
CAMK2D	0.515361945	0.154269871	0.39	1.21	0.80
STK39	0.599913126	0.074269871	0.19	1.41	0.80
TAO1	0.514131049	0.154269871	0.40	1.21	0.80
STK3	0.393182734	0.264269871	0.69	0.92	0.81
ROS1	0.148546083	0.484269871	1.27	0.35	0.81
CDK3	0.578788325	0.104269871	0.27	1.36	0.81
CDC7	0.055733441	0.574269871	1.50	0.13	0.82
MOS	0.409306474	0.254269871	0.67	0.96	0.82
CLK4	0.474036863	0.204269871	0.53	1.11	0.82
PRKD2	0.629088424	0.064269871	0.17	1.48	0.82
AXL	0.511460022	0.174269871	0.44	1.20	0.82
PRKCZ	0.52876548	0.174269871	0.44	1.24	0.84
RET	0.045921929	0.604269871	1.58	0.11	0.84
PRKWINK1	0.134292718	0.534269871	1.38	0.31	0.85
KIAA0472	0.468047804	0.224269871	0.59	1.10	0.85
CDK6	0.416188457	0.274269871	0.72	0.98	0.85
TAF1	0.197972495	0.474269871	1.23	0.46	0.85

EPHA8	0.333558262	0.364269871	0.94	0.78	0.86
FZD1	0.680008871	0.054269871	0.14	1.60	0.87
ADRA1D	0.600026199	0.134269871	0.35	1.41	0.88
PDGFRB	0.658501162	0.084269871	0.21	1.54	0.88
MAPK9	0.226930269	0.474269871	1.23	0.53	0.88
CDK8	0.460342814	0.264269871	0.70	1.08	0.89
CAMK2A	0.33928861	0.394269871	1.02	0.80	0.91
ERBB2	0.337703899	0.394269871	1.04	0.79	0.91
MAP2K1	0.217305235	0.514269871	1.33	0.51	0.92
FGFR2	0.055586714	0.664269871	1.71	0.13	0.92
GNRHR2	0.489573939	0.274269871	0.70	1.15	0.93
MAP2K2	0.276027655	0.474269871	1.23	0.65	0.94
JIK	0.29031968	0.464269871	1.20	0.68	0.94
NEK3	0.603768622	0.184269871	0.47	1.42	0.94
MAP2K5	0.368793444	0.394269871	1.03	0.87	0.95
BMPR2	0.508058351	0.274269871	0.71	1.19	0.95
HCK	0.461879048	0.314269871	0.82	1.08	0.95
EPHB3	0.215126477	0.544269871	1.43	0.50	0.97
CDK4	0.380175264	0.414269871	1.08	0.89	0.99
PRKR	0.585629082	0.234269871	0.61	1.37	0.99
ITK	0.260627888	0.534269871	1.38	0.61	1.00
KIT	0.442837738	0.374269871	0.97	1.04	1.00
NEK2	0.622646297	0.224269871	0.58	1.46	1.02
PRKAA1	0.591480444	0.254269871	0.66	1.39	1.02
EPHB4	0.292099803	0.534269871	1.38	0.69	1.03
STK11	0.386431635	0.444269871	1.16	0.91	1.03
DAPK2	0.429404565	0.414269871	1.07	1.01	1.04
DYRK4	0.523442725	0.344269871	0.90	1.23	1.06
PRKCL2	0.783701321	0.114269871	0.29	1.84	1.06
HRI	0.818750806	0.084269871	0.21	1.92	1.06
DAPK3	0.405051893	0.454269871	1.19	0.95	1.07
AVPR1B	0.481808798	0.404269871	1.05	1.13	1.09
PDK1	0.693749253	0.224269871	0.58	1.63	1.10
ATR	0.408419978	0.484269871	1.26	0.96	1.11
IRAK1	0.487389402	0.414269871	1.09	1.14	1.12
BRAF	0.353925598	0.554269871	1.45	0.83	1.14
RPS6KA5	0.381919587	0.534269871	1.38	0.90	1.14
CAMKK2	0.591524573	0.364269871	0.94	1.39	1.16
CNK	0.542100235	0.414269871	1.07	1.27	1.17
PTK2B	0.393619268	0.554269871	1.44	0.92	1.18
LTK	0.573768996	0.404269871	1.04	1.35	1.19
SK592	0.81893392	0.184269871	0.48	1.92	1.20
DYRK1A	0.457541285	0.514269871	1.33	1.07	1.20
PRKY	0.713079524	0.284269871	0.74	1.67	1.21
FRAP1	0.462979992	0.534269871	1.39	1.09	1.24
MERTK	0.956833751	0.094269871	0.25	2.24	1.25
PDK3	0.78328159	0.254269871	0.67	1.84	1.25
MAPK11	0.452763283	0.564269871	1.47	1.06	1.27
ILK	0.523528172	0.514269871	1.33	1.23	1.28
PRKCQ	0.330706907	0.694269871	1.79	0.78	1.28
ZAP70	0.679353057	0.384269871	1.00	1.59	1.29
DAPK1	0.403015878	0.634269871	1.65	0.95	1.30

INSR	0.554592695	0.504269871	1.32	1.30	1.31
RAGE	0.600501891	0.474269871	1.22	1.41	1.31
DMPK	0.520977376	0.544269871	1.42	1.22	1.32
ACVR1	0.707465512	0.384269871	1.00	1.66	1.33
DYRK1B	0.3220482	0.734269871	1.91	0.76	1.33
MAP2K3	0.328509196	0.734269871	1.90	0.77	1.33
DDR2	0.834768239	0.294269871	0.76	1.96	1.36
JAK3	0.68202996	0.444269871	1.16	1.60	1.38
MAPK10	0.568158358	0.564269871	1.46	1.33	1.40
TEC	0.70091594	0.464269871	1.20	1.64	1.42
MAP2K4	0.813206747	0.374269871	0.96	1.91	1.44
CKLiK	0.553942613	0.624269871	1.63	1.30	1.47
MAP4K4	0.594749956	0.594269871	1.55	1.40	1.47
PCTK1	0.780115923	0.444269871	1.15	1.83	1.49
PACE-1	0.895757988	0.434269871	1.12	2.10	1.61
MAP2K6	0.67465747	0.654269871	1.70	1.58	1.64
STK23	0.663394945	0.664269871	1.74	1.56	1.65
KIAA2002	0.594341012	0.764269871	1.98	1.39	1.68
MAPK13	0.69658671	0.694269871	1.80	1.63	1.72
CSNK1A1	0.641629864	0.814269871	2.12	1.51	1.81
RPS6KB1	0.954762319	0.584269871	1.53	2.24	1.89
RAF1	0.442282219	1.054269871	2.74	1.04	1.89
SK200	0.756774729	0.784269871	2.05	1.78	1.91

Supplementary Table 2

List of antibodies used in the RPPA

Antibody List

Name of the protein	Antibody source	Catalog number
Phospho-AKT (S473)	Cell Signaling Technology	9271
Phospho-AKT (T308)	Cell Signaling Technology	9275
AKT	Cell Signaling Technology	9272
Phospho-GSK3 α/β (S21/9)	Cell Signaling Technology	9331
GSK3	Santa Cruz Biotechnology	sc-7291
Phospho-mTOR (S2448)	Cell Signaling Technology	2971
mTOR	Cell Signaling Technology	2983
Phospho-p70S6K (T389)	Cell Signaling Technology	9205
P70S6K	Epitomics	1494-1
Phospho-S6 (S235/236)	Cell Signaling Technology	2211
Phospho-S6 (S240/244)	Cell Signaling Technology	2215
S6	Cell Signaling Technology	2217
LKB-1	Abcam	Ab 15095
FKHRL1 (FOXO3)	Cell Signaling Technology	9467
PI3K p110 α	Epitomics	1683
Phospho-MEK 1/2 (S217/221)	Cell Signaling Technology	9121
MEK 1/2	Epitomics	1235-1
Phospho-MAPK (T202/Y204)	Cell Signaling Technology	9101
ERK2	Santa Cruz Biotechnology	sc-154
Phospho-p38 (T180/Y182)	Cell Signaling Technology	9211

P38	Cell Signaling Technology	9212
Phospho-JNK (T183/Y185)	Cell Signaling Technology	9251
JNK	Santa Cruz Biotechnology	sc-474
Phospho-c-Jun (S73)	Cell Signaling Technology	9164
c-Jun	Cell Signaling Technology	9165
Phospho-EGFR (Y992)	Cell Signaling Technology	2235
EGFR	Santa Cruz Biotechnology	sc-03
Phospho-Src (Y527)	Cell Signaling Technology	2105
Src	Cell Signaling Technology	2109
Phospho-STAT3 (T727)	Cell Signaling Technology	9134
Phospho-STAT3 (Y705)	Cell Signaling Technology	9131
STAT3	Upstate Cell Signaling Solutions	06-596
P21	Santa Cruz Biotechnology	sc-397
P27	Santa Cruz Biotechnology	sc-528
Phospho-p53 (S15)	Cell Signaling Technology	9284
P53	Cell Signaling Technology	9309
Cyclin B1	Epitomics	1495-1
Cyclin D1	Santa Cruz Biotechnoloty	sc-753
Phospho-PKC α (S657)	Upstate Cell Signaling Solutions	06-822
PKC α	Upstate Cell Signaling Solutions	05-154
E-Cadherin	Cell Signaling Technology	4065
<u>β-Catenin</u>	<u>Cell Signaling Technology</u>	<u>9562</u>

Gene Symbol	Z-score
AKT1	-3.73
AKT2	0.06
AKT3	-2.32
EGFR	-2.91
FRAP1	-4.42
GSK3A	-0.95
GSK3B	0.01
MAP2K1	-2.20
MAPK1	-2.37
MAPK11	2.28
MAPK12	0.51
MAPK13	1.46
MAPK14	-2.98
MAPK8	-0.92
RPS6KB1	-0.83

Supplementary Table 3

List of siRNA gene targets and their corresponding protein levels assayed by RPPA

Supplementary Table 4

Protein names of the 49 siRNA targeted genes that altered pAKT and their known interactions with AKT

Supplementary Table 4

Gene Symbol	Z-score	Name	Function	Relation with AKT
MGC45428	-3.10	doublecortin-like kinase 2	cue and their intracellular signals into changes	Not found
KIAA0999	-3.00	Not known	Not found	Not found
TRB2	-2.63	Tribbles homolog 2	Interacts with MAPK kinases and regulates activation of MAP kinases. Does not display kinase activity. Kiss-Toth E, et al., 2004	TRB2 blocks adipogenesis through the inhibition of Akt activation
ACVR1C	-2.44	activin A receptor, type IC	Serine/threonine protein kinase which forms a receptor complex on ligand binding. The receptor complex consisting of 2 type II and 2 type I transmembrane serine/threonine kinases. Type II receptors phosphorylate and activate type I receptors which autophosphorylate, then bind and activate SMAD transcriptional regulators, SMAD2 and SMAD3. Receptor for activin AB, activin B and NODAL. Plays a role in cell differentiation, growth arrest and apoptosis. Bondestam, et. al, 2001, Xu, et. al, 2004	Activin A activates Akt
BCKDK	-2.37	branched chain ketoacid dehydrogenase kinase	Catalyzes the phosphorylation and inactivation of the branched-chain alpha-ketoacid dehydrogenase complex, the key regulatory enzyme of the valine, leucine and isoleucine catabolic pathways. Key enzyme that regulate the activity state of the BCKD complex. Uniprot database and Chang, et.al, 2002	Not found
GSK3A	-2.30	Glycogen synthase kinase-3 alpha	GSK3 (glycogen synthase kinase-3) participates in the Wnt signaling pathway. It is implicated in the hormonal control of several regulatory proteins including glycogen synthase, and the transcription factors MYB and JUN. GSK3 phosphorylates JUN at sites proximal to its DNA-binding domain, thereby reducing its affinity for DNA. Ali et al. (2001)	Inhibited by AKT when it is phosphorylated by it

MARK1	-2.29	MAP/microtubule affinity-regulating kinase 1	May play a role in cytoskeletal stability. Drewes, et.al, 1997	Not found
FGFR1	-2.22	Fibroblast Growth Factor Receptor 1	FGF receptor with tyrosine kinase activity; binding of ligand (FGF) in association with heparan sulfate proteoglycans induces receptor dimerization, autophosphorylation and signal transduction. Atlas of Genetics and Cytogenetics in Oncology and Haematology	AKT is downstream of FGFR1
AKT3	-2.19	RAC-gamma serine/threonine-protein kinase	IGF-1 leads to the activation of AKT3, which may play a role in regulating cell survival. Capable of phosphorylating several known proteins. Uniprot database and Peng, et.al, 2003	Akt family
FLJ23074	-2.17	SPS1/STE20-related protein kinase YSK4	Not found	Not found
PAK6	-2.14	Serine/threonine-protein kinase PAK6	Interacts tightly with GTP-bound but not GDP-bound CDC42/p21 and RAC1 (By similarity). Interacts with the androgen receptor. Yang, et.al, 2001	Not found
ADMR	-2.00	G-protein coupled receptor 182	Orphan receptor	Not found
PRKCN	-1.94	Putative uncharacterized protein PRKCN (Protein kinase D3, isoform CRA_a)	Calcium-independent, phospholipid-dependent, serine- and threonine-specific kinase. Upon diacylglycerol-activation, phosphorylates a range of cellular proteins. Also serves as the receptor for phorbol esters, a class of tumor promoters. Uniprot database.	Not found
ERK8	-1.89	Mitogen-activated protein kinase 15	In vitro, phosphorylates MBP. Abe, et.al, 2002, Lavarone, et.al, 2006	Not found
RIOK1	-1.85	RIO kinase 1	Not known	Not found

NEK9	-1.85	Serine/threonine-protein kinase Nek9	Pleiotropic regulator of mitotic progression, participating in the control of spindle dynamics and chromosome separation. Phosphorylates different histones, myelin basic protein, beta-casein, and BICD2. Phosphorylates histone H3 on serine and threonine residues and beta-casein on serine residues. Important for G1/S transition and S phase progression. Tan, et.al, 2004	Not found
BRD4	-1.79	bromodomain containing 4	Plays a role in a process governing chromosomal dynamics during mitosis. Uniprot database, Yang, et.al, 2008, Schweiger, et.al, 2006	Not found
FLJ33655	-1.76	EPH receptor A10	Receptor for members of the ephrin-A family. Binds to EFNA3, EFNA4 and EFNA5. Aasheim, et.al, 2005	Not found
HAK	-1.74	alpha-kinase 2	Kinases that recognize phosphorylation sites in which the surrounding peptides have an alpha-helical conformation. Uniprot database.	Not found
STK31	-1.72	serine/threonine kinase 31	This gene is similar to a mouse gene that encodes a putative protein kinase with a tudor domain, and shows testis-specific expression. Genbank.	Not found
MINK	-1.70	potassium voltage-gated channel, Isk-related family, member 1	Ancillary protein that assembles as a beta subunit with a voltage-gated potassium channel complex of pore-forming alpha subunits. Modulates the gating kinetics and enhances stability of the channel complex. Uniprot database, Chen, Goldstein, 2007	Akt stimulates KCNE1
SK707	-1.64	Not found	Not known	Not found

MAPK3	-1.62	mitogen-activated protein kinase 3	Involved in both the initiation and regulation of meiosis, mitosis, and postmitotic functions in differentiated cells by phosphorylating a number of transcription factors such as ELK-1. Phosphorylates EIF4EBP1; required for initiation of translation. Phosphorylates microtubule-associated protein 2 (MAP2). Phosphorylates SPZ1 By similarity. Uniprot database. Phosphorylates heat shock factor protein 4 (HSF4). Hu, et.al, 2006	Not found
CAMK2G	-1.62	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CaM-kinase II (CAMK2) is a prominent kinase in the central nervous system that may function in long-term potentiation and neurotransmitter release. Uniprot database.	Not found
TTBK2	-1.58	tau tubulin kinase 2	TTBK2 is important in the tau cascade and in spinocerebellar degeneration. Houlden, et.al, 2007	Not found
PTK7	-1.52	PTK7 protein tyrosine kinase 7	May function as a cell adhesion molecule that acts as a regulator of planar cell polarity. Seems to lack tyrosine-protein kinase activity. Uniprot database.	Not found
SMG1	-1.51	PI-3-kinase-related kinase SMG-1	This gene encodes a protein involved in nonsense-mediated mRNA decay (NMD) as part of the mRNA surveillance complex. The protein has kinase activity and is thought to function in NMD by phosphorylating the regulator of nonsense transcripts 1 protein. Kashima, et.al, 2006	Not found
MAP3K1	-1.50	Mitogen-activated protein kinase kinase kinase 1	Component of a protein kinase signal transduction cascade. Activates the ERK and JNK kinase pathways by phosphorylation of MAP2K1 and MAP2K4. Activates CHUK and IKBKB, the central protein kinases of the NF-kappa-B pathway. Xia, et.al, 1998	Not found

INSRR	-1.49	insulin receptor-related receptor	This receptor probably binds an insulin related protein and has a tyrosine-protein kinase activity. It phosphorylates the insulin receptor substrates IRS-1 and IRS-2. Hanke, Mann, 2008	INSRR mediates activation of Akt
CDK10	-1.45	Cell division protein kinase 10	This kinase has been shown to play a role in cellular proliferation and its function is limited to cell cycle G2-M phase. Grana, et.al, 1994	Not found
BMP2K	-1.42	BMP2 inducible kinase	May be involved in osteoblast differentiation. This gene is the human homolog of mouse BMP-2-inducible kinase. Bone morphogenic proteins (BMPs) play a key role in skeletal development and patterning. Expression of the mouse gene is increased during BMP-2 induced differentiation and the gene product is a putative serine/threonine protein kinase containing a nuclear localization signal. Therefore, the protein encoded by this human homolog is thought to be a protein kinase with a putative regulatory role in attenuating the program of osteoblast differentiation. Two transcript variants encoding different isoforms have been found for this gene. Genbank.	Not found
AAK1	-1.41	AP2 associated kinase 1	The protein interacts with and phosphorylates a subunit of the AP-2 complex, which promotes binding of AP-2 to sorting signals found in membrane-bound receptors and subsequent receptor endocytosis. Its kinase activity is stimulated by clathrin. Henderson, Conner, 2007	Not found

<p>AKT1</p>	<p>-1.41</p>	<p>v-akt murine thymoma viral oncogene homolog 1</p>	<p>General protein kinase capable of phosphorylating several known proteins. Phosphorylates TBC1D4. Signals downstream of phosphatidylinositol 3-kinase (PI(3)K) to mediate the effects of various growth factors such as platelet-derived growth factor (PDGF), epidermal growth factor (EGF), insulin and insulin-like growth factor I (IGF-I). Plays a role in glucose transport by mediating insulin-induced translocation of the GLUT4 glucose transporter to the cell surface. Mediates the antiapoptotic effects of IGF-I. Mediates insulin-stimulated protein synthesis, partly by playing a role in both insulin-induced phosphorylation of 4E-BP1 and in insulin-induced activation of p70 S6 kinase. Promotes glycogen synthesis by mediating the insulin-induced activation of glycogen synthase. Coffey, et.al, 1991, Walker, et.al, 1998, Kane, et.al, 2002, Fujita, et.al, 2002, Shin, et.al, 2002, Enomoto, et.al, 2005</p>	<p>Akt family</p>
<p>HIPK1</p>	<p>-1.40</p>	<p>homeodomain interacting protein kinase 1</p>	<p>May play a role as a corepressor for homeodomain transcription factors. Phosphorylates DAXX in response to stress, and mediates its translocation from the nucleus to the cytoplasm. May be involved in malignant squamous cell tumor formation. Song, Lee, 2003, Kondo, et.al, 2003</p>	<p>Not found</p>

MAPK10	1.40	JNK3 alpha2 protein kinase	JNK3 alpha 1 is predominantly a neuronal specific MAP kinase that is believed to require, like all MAP kinases, both threonine and tyrosine phosphorylation for maximal enzyme activity. MKK7 is capable of monophosphorylating JNK3 alpha 1 in vitro, whereas both MKK4 and MKK7 were required for bisphosphorylation and maximal enzyme activity	Akt inhibits MLK3/JNK3 signaling by inactivating Rac1: a protective mechanism against ischemic brain injury.
TEC	1.42	tec protein tyrosine kinase	Tec kinases mediate sustained calcium influx via site-specific tyrosine phosphorylation of the phospholipase Cgamma Src homology 2-Src homology 3 linker.	Not found
MAP2K4	1.44	JNK-activating kinase 1, MKK4	MKK4 is a component of a stress and cytokine-induced signal transduction pathway involving MAPK proteins. The MKK4 protein has been implicated in activation of JNK1 and p38 MAPK on phosphorylation by conserved kinase pathways. Acts as metastasis suppressor gene in ovarian cancer.	PI3K/Akt pathway inhibitors can partially block ser-80 phosphorylation of MKK4
CKLiK	1.47	Calcium/calmodulin-dependent protein kinase type 1D	CKLiK kinase activity was dependent on Ca(++) and calmodulin.	Not found
MAP4K4	1.47	HPK/GCK-like kinase (hepatocyte progenitor kinase-like/germinal center kinase-like kinase)	HGK is a member of the human STE20/mitogen-activated protein kinase kinase kinase family of serine/threonine kinases and is the ortholog of mouse NIK (Nck-interacting kinase). HGK to be highly expressed in most tumor cell lines relative to normal tissue.	Not found
PCTK1	1.49	PCTAIRE protein kinase 1	PCTAIRE-1 is a member of a novel subfamily of cdc2/CDC28-related protein kinases.	Not found
PACE-1	1.61	Ezrin- binding protein PACE-1	PACE-1 may play a role in regulating cell adhesion/migration complexes in migrating cells.	Not found

MAP2K6	1.64	MKK6	MKK6, like MKK3, selectively phosphorylates p38	inflammation-activated MKK6-p38 and insulin growth factor 1 (IGF1)-induced PI3K/AKT pathways converge on the chromatin of muscle genes to target distinct components of the muscle transcriptosome.
STK23	1.65	SRPK3	Required for normal muscle development (By similarity)	Not found
KIAA2002	1.68	SGK269	Not known	Not found
MAPK13	1.72	p38delta	Responds to activation by environmental stress and pro-inflammatory cytokines by phosphorylating downstream targets. Plays a role in the regulation of protein translation by phosphorylating and inactivating EEF2K	Not found
CSNK1A1	1.81	casein kinase 1, alpha	Casein kinases are operationally defined by their preferential utilization of acidic proteins such as caseins as substrates. It can phosphorylate a large number of proteins. Participates in Wnt signaling. Phosphorylates CTNNB1 on 'Ser-45'	Casein Kinase I epsilon (CKIepsilon) causes up-regulation of the Akt pathway despite normal protein expression of the pathway inhibitor phosphate and tensin homologue deleted on chromosome ten (PTEN). Conversely, we show that a CKIepsilon/delta-specific inhibitor can inhibit Akt phosphorylation at both Thr308 and Ser473 and drastically reduce phosphorylation of the Akt target Glycogen Synthase Kinase 3beta (GSK3beta).
RPS6KB1	1.89	p70-S6K	Phosphorylates specifically ribosomal protein S6 in response to insulin or several classes of mitogens	Activated by AKT phosphorylation
RAF1	1.89	c-Raf	Involved in the transduction of mitogenic signals from the cell membrane to the nucleus. Part of the Ras-dependent signaling pathway from receptors to the nucleus. Protects cells from apoptosis mediated by STK3	Crosstalk observed between RAS-RAF and PI3K/AKT pathway
SK200	1.91	Not found	Not known	Not found

Supplementary Table 5

Sequences of the siRNA and the corresponding genes that altered pAKT

Gene Name	Seq. 1	Seq. 2	Seq. 3	Seq. 4
AAK1	GACATGCACTGCCTAATTA	GTACAGAACTCTCCCATTC	GATGAAATGTGCCTTGAAA	GAAGGTGGATTTGCTATTG
ACVR1C	GAACAGGGCTCCTTATATG	GCTCAAGTCTTCTGTCATA	GTATATGGCTCCTGAAATG	GAGCTGGCCATCATTATTA
ADMR	GCACACCATTTGCTTCCAA	CCGCTTCACTCACTACTTC	GTAGTCCATTACCTTCTTA	CTACGTGGCCGTCTTTGTG
AKT1	GACAAGGACGGGCACATTA	GGACAAGGACGGGCACATT	GCTACTTCTCCTCAAGAA	GACCGCCTCTGCTTTGTCA
AKT3	GGAGTAAACTGGCAAGATG	GACATTAAATTTCTCGAA	GACCAAAGCCAAACACATT	GAGGAGAGAATGAATTGTA
BCKDK	GAAAGGAGCAAGACGATGA	GCACGTGCATGAGCTATAT	GCAGAGGGCCTACGTGAGA	GTACTCGTCTCTCACCAA
BMP2K	GAACAUAGACCUGAUUAU	GGACUGUGCUGUUAUUA	GGAACUAUGUACUUUGUGA	GAAAUGAUCAACCUUUUUG
BRD4	GAAATGCGCTTTGCCAAGA	GAACCTCCCTGATTACTAT	TAAATGAGCTACCCACAGA	TGAGAAATCTGCCAGTAAT
CAMK2G	GGAAAGATCCCTATGGAAA	GAACCTTCTCAGCTGCCAAA	GCTCGGATATGTCGACTTC	GTACACAACGCTACAGATG
CDK10	GAAGTCTGTTGGGAACCA	GGAAGCAGCCCTACAACAA	GCACGCCCAGTGAGAACAT	GGAAGCAGCCCTACAACAA
CKLIK	TGAAGTGTATCCCTAAGAA	CAAATCACCTGTACTTGGT	CCGAAAATCTCTTGACTA	GAGAAGGACCCGAATAAAA
CSNK1A1	GAATTTGCGATGTACTION	GCTAAAGGCTGCAACAAAG	AGAGTAACATGAAAGGTTT	GCGATGTACTIONAACTATT
ERK8	GTAGTGGACCCTCGCATTG	AGAACGACAGGGACATTTA	GGTCGTGGCCATCAAGAAA	CCTATGGCATTGTGTGGAA
FGFR1	TAAGAAATGTCTCCTTTGA	GAAGACTGCTGGAGTTAAT	GATGGTCCCTTGATGTCA	CTTAAGAAATGTCTCCTTT
FLJ23074	GGCTCAATCTCTAGTATTA	CATGCCAACTGGAATAATA	GGACGGAAATCAGATATCT	ACAGTGACATGCTTAAGTC
FLJ33655	GGACTGCACTGCCAAGTAA	CTGCGAAGGTATCCAGTTG	ACACAGAGGTGCGCGAGAT	GGACCGCCGAGGAAGTTAT
GSK3A	CATCAAAGTGATTGGCAAT	AGTTGACCATCCCTATCCT	CTGATTACACCTCATCCAT	TTCTCATCCCTCCTCACTT
HAK	GCAACAAGCTGAAGATTAT	GAAATTTGCTCTGTAGATA	CAACATACCTGACAATTTT	AGGAAGAGCTCCAGTATTA
HIPK1	GGTCTAATGTCATCAGTTA	GCACAACCACTCAATCTTA	GCAATCATGTTAAGTCTTG	TCAGATGTCTCACTACTAA
INSRR	CCAAATGGCTGGTGAGATT	GGACAGCCCTCATCAAGGA	GAACAAGGCTGAGATCAAC	GAGCAGATCTCGATAATCC
KIAA0999	GCGCCAGGCTTTATCTTAT	GACAGTAAGAGTTCAAGTA	TGACAGCCCTCTGCTCTTG	GCAGCAACCTGAGAAGTGT
KIAA2002	CCAAATCTCTCTTTACATC	GCTAAGAGCACACCTAAGA	TATCAAAGTTCCCATTGTT	GAAAGACCCATCCATAAAG
MAP2K4	GGACAGAAGTGGAATATT	GGATTTGGATGTAGTAATG	GACAGAAGTGGAATATTA	GCGCATCACGACAAGGATA
MAP2K6	CCAAAGAACGGCCTACATA	CGTCAAGCCTTCTAATGTA	GATAAAGGCCAGACAATTC	GCTCATGGATACATCACTA
MAP3K1	GGACAGACCTCCATCAAGA	GCTGAAAGGTCAACAGATA	AGAAGAAGCTTTAGCAATT	GAGCTCAACTCCAGTATTG
MAP4K4	CGAAGACGATTTCAACAAA	TAAGTTACGTGTCTACTAT	CAAAGGGCTCAAAGACTA	GATGAGACCAGAAGCCATA
MAPK10	GGAATAAGGTAATTGAACA	GAAACTATGTGGAGAATCG	GAAAGAACTTATCTACAAG	GAAAGAGAACACACAATTG
MAPK13	TCAAAGGCCTTAAGTACAT	CAACTTCTATGACTTCTAC	GCCGTTTTGATGATTCTTA	GCTCAAAGGCCTTAAGTAC
MAPK3	GACCGGATGTTAACCTTTA	AGACTGACCTGTACAAGTT	GAAACTACCTACAGTCTCT	GGACCTGAATTGTATCATC
MARK1	GGACATCTATTGCCTTTAA	GACCACAGATCGATACGTA	GGAAATTACCGTTTACAAA	GGAACAAATTGGACACATT
MGC45428	GGAGATCTCTTTGATGCAA	GAGTTTGCCCTAAAGATTA	AGAACAATCTCCAGGAAGA	CCAATGCCCTCAGGTATCT
MINK	GAACAGCTATGACATCTAC	GCACTACCGTGTGTGAAA	AACCGTAACTGCATCATGA	GCACAATGACCCAGAAGTG
NEK9	TGATTGAGCTGGAATATTG	GTACTAATGTAATCACTGA	GAAATGCCTTTGAATGGTT	AGAAGGAACTGTACTCTTG

PACE-1	GAACATTGGTGGAAAGTTT	GAGCTGAACTGGGAAGATA	TTAAAGAGCTATACACTGA	CAACAGACCTTGCACTCAA
PAK6	GAAGTGATCTCCAGGTCTT	TCAACGACATCCAGAAGTT	GGACAGCTACGTGAAGATT	GAATGAAGGCTGCCAAGCA
PCTK1	TGACACTACTTCCATATTT	TCACCAAGCTGTTGCAGTT	TAAAGGAGATTGAGCTACA	CAACAAAGACATACTCCAA
PRKCN	GAATGAATCTGGATCAAAG	GAAAGTTCCACACACATTT	GCCAAGGAATGCAGTGTA	GTCAAGGACTGAAATGTGA
PTK7	GAGAGAAGCCCACTATTAA	CGAGAGAAGCCCACTATTA	GGAGGGAGTTGGAGATGTT	GAAGACATGCCGCTATTTG
RAF1	GCACGGAGATGTTGCAGTA	GCAAAGAACATCATCCATA	GACATGAAATCCAACAATA	CAAAGAACATCATCCATAG
RIOK1	GAAATAGCATCTCAAAGGA	GGAAAGGACTTGTTCTGAT	GAATTCAGATTTTCGTCATG	GCAGAGCAATCAAAATTTA
RPS6KB1	GGACATGGCAGGAGTGTTT	GGAAACAAGTGGCATAGAG	GATGAGAAGTGGCCACAAT	CCAGATGACTCAACTCTCA
SK200	GAACATGTATAGTGGCTAA	GGCCAGAGCCTGAGCGTTT	TGAGATGTCTGGAGATCAT	GGCCGTCGCTGGATCAGAT
SK707	GCAGGCGCCTTCTTTAGTG	CCTCAGACCTCTACAGCTT	TATCAGCGTTCGTGCATGA	GGGAGTTGCTGGAGTTGTT
SMG1	GTGAAGATGTTCCCTATGA	GAGGTTAGCTGCGGAAAGA	GGTCAGACATCCACCAGAA	TAACTTGGCTCAGCTGTAT
STK23	TCAAATGGATCATCAAGTC	TGAGGACTCTGGCTTGAGA	GAGGAGAGCTGCGGCACAT	GCAAACGGAAACAGCAGAA
STK31	GCATAAGGCTGACATAATT	TAACTCAGCTGCGCAATAA	GATGAAGGGTGCTTTACTA	GCAAAGAGCTGGAGATAGC
TEC	GAAATTGTCTAGTAAGTGA	CACCTGAAGTGTTTAATTA	GTACAAAGTCGCAATCAA	TGGAGGAGATTCTTATTAA
TRB2	GAAGAGTTGTCGTCTATAA	GAGAGGAGCTGGTGTGCAA	CCAATCACTGAAATTATC	GAAATTATCCTGGGTGAGA
TTBK2	CAAAGAACTTCCTGATCA	CCAGTAAACTCAGCAGATA	GGAGGAAGCAGAACAGATT	CAACACAGATCAGGTCAAT

Supplementary Table 6

List of genes targeted and the corresponding
pMAPK1,2 Z-score

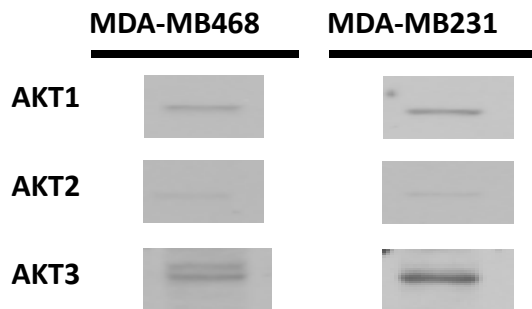
Gene Syml MAPK_pT202

AKT3	1.92	MAP2K1	1.04	NPR2	0.82
GPRK5	1.62	STK17A	1.04	FGFR3	0.82
MAP2K5	1.57	ZAK	1.03	TGFBR2	0.82
NEK3	1.57	PRKWNK4	1.03	MKNK1	0.82
PRKCG	1.50	CAMK1G	1.03	SNK	0.81
ROS1	1.48	RPS6KA5	1.03	CDK3	0.81
MARK3	1.48	ACVRL1	1.03	LYN	0.80
YES1	1.45	DCAMKL1	1.03	DMPK	0.80
NTRK2	1.39	KIAA0781	1.02	ROR2	0.80
MAPK11	1.36	GSK3B	1.01	MYO3A	0.80
PRKCI	1.34	FLJ23119	1.01	HIPK3	0.80
PSKH1	1.32	PCTK2	1.01	ATM	0.80
MAP2K3	1.31	VRK2	1.00	BLK	0.80
PRKACB	1.30	CDK4	1.00	SK723	0.80
CSNK1E	1.29	MAPK7	1.00	FLT4	0.79
KDR	1.28	MST1R	0.99	INSRR	0.79
MAPK10	1.26	JAK1	0.97	ATR	0.79
PDK2	1.26	MGC8407	0.96	PTK9L	0.79
STK25	1.24	HCK	0.96	RIOK2	0.78
PDK4	1.24	MERTK	0.96	MAP4K5	0.77
ULK1	1.23	RYK	0.96	SGKL	0.77
STK36	1.22	MAP4K3	0.95	PRKCCQ	0.77
TRIO	1.22	SRC	0.93	CDK6	0.76
IRAK1	1.21	NTRK1	0.93	C20orf97	0.76
BRD3	1.21	MAP3K13	0.93	RIOK1	0.75
MAP3K10	1.21	BCKDK	0.92	PDGFRB	0.75
MAST205	1.21	MGC33182	0.92	STK38	0.74
CSNK1G1	1.20	RPS6KA3	0.91	ILK	0.74
PDPK1	1.20	CDK10	0.91	ACVR1	0.74
MAPK8	1.18	SMG1	0.91	MAP2K7	0.74
MAP2K6	1.16	RPS6KC1	0.90	PINK1	0.74
PRKR	1.15	MAPK4	0.90	MELK	0.73
FRK	1.14	BUB1B	0.88	STK4	0.73
DYRK2	1.13	PDK1	0.88	NTRK3	0.72
SNARK	1.13	LIMK1	0.87	ERN1	0.72
PTK7	1.12	FGFR1	0.87	AAK1	0.72
TIE	1.12	MAPKAPK	0.87	ABL2	0.71
ABL1	1.12	TESK2	0.86	CCRK	0.71
PRKACA	1.11	DYRK3	0.85	CLK2	0.70
ROCK1	1.11	TBK1	0.85	LIMK2	0.70
PHKG2	1.09	FER	0.85	CSNK2A2	0.70
PRKCL1	1.09	STK33	0.85	BCR	0.70
FRAP1	1.08	PIM1	0.85	DYRK1B	0.70
PRKCB1	1.07	KIT	0.84	INSR	0.69
GPRK2L	1.07	CDC42BPF	0.84	FGFR4	0.68
BTK	1.07	NEK11	0.83	RIPK2	0.68
TRRAP	1.06	GAK	0.83	MAPK9	0.68
NEK2	1.06	MET	0.83	CSNK1D	0.67
PRKCN	1.06	ACVR2	0.83	MATK	0.66
LTK	1.05	SLK	0.83	TRAD	0.66

CAMK2D	0.66	SRPK1	0.51	KIAA1811	0.34
ALK	0.66	DKFZp761	0.51	KIAA1804	0.34
NPR1	0.66	ERBB2	0.51	PRKG2	0.33
PRKWINK3	0.66	BMPR1A	0.51	PCTK1	0.33
PRKX	0.65	SK643	0.49	CSNK1G2	0.33
TEX14	0.65	PAK1	0.49	RPS6KA1	0.33
MAPK14	0.65	SK662	0.49	CSF1R	0.33
SAST	0.65	PXK	0.49	WEE1	0.33
BMPR1B	0.64	STK3	0.49	CHEK1	0.32
MAP3K11	0.64	VRK1	0.48	DAPK3	0.31
PKMYT1	0.64	ADORA2A	0.47	MAP2K4	0.31
MAPK13	0.64	MAP3K3	0.47	SK650	0.31
FYN	0.63	EPHA4	0.46	CABC1	0.31
ZAP70	0.62	IRAK4	0.46	CDC2L1	0.31
TXK	0.62	RHOK	0.46	PACE-1	0.31
GUCY2C	0.62	ACVR1B	0.45	MAP3K2	0.30
TTK	0.61	SSTK	0.45	PRKCE	0.30
FGR	0.61	TRIM28	0.45	CAMKK1	0.30
CDK7	0.60	PRKACG	0.44	PASK	0.30
PRKCM	0.60	MAP4K1	0.44	MGC4796	0.30
PAK3	0.60	ROR1	0.44	FLJ10074	0.29
NRBP	0.59	LATS1	0.44	TESK1	0.28
MAPK1	0.59	STK18	0.43	KIAA0999	0.28
pknbeta	0.58	CSNK2A1	0.43	CDK8	0.28
PRKWINK2	0.58	CDC2	0.43	TOPK	0.26
GRK6	0.58	PRKCZ	0.42	SK709	0.26
BRDT	0.58	SK681	0.42	RNASEL	0.26
BMPR2	0.58	EPHA2	0.41	EPHA8	0.26
EEF2K	0.58	LATS2	0.40	EPHA1	0.26
FASTK	0.58	BRAF	0.40	JAK2	0.25
RPS6KL1	0.57	ACK1	0.40	MST4	0.25
AKT1	0.57	ERBB3	0.39	DYRK1A	0.25
PIM2	0.57	TYK2	0.38	CLK4	0.25
AURKC/ST	0.57	IGF1R	0.37	MAP3K8	0.24
PHKG1	0.56	CSNK1A1	0.37	CNR2	0.23
HUNK	0.56	RIPK3	0.37	IKBKE	0.22
GUCY2D	0.56	EPHB1	0.36	BUB1	0.22
TYRO3	0.55	FLT1	0.36	CHUK	0.21
FLJ23356	0.55	SGK	0.36	PRKCD	0.21
CDK9	0.55	SNF1LK	0.36	FES	0.21
PDK3	0.55	MARK4	0.36	CDK2	0.20
RAF1	0.55	IRAK3	0.35	CDK5	0.20
ARK5	0.55	MAP2K2	0.35	STK39	0.20
SCYL1	0.55	CLK3	0.35	TEK	0.20
STK24	0.54	ICK	0.35	DDR1	0.19
ACVR2B	0.54	MINK	0.35	PRKCA	0.18
STK17B	0.53	MKNK2	0.35	EPHB2	0.18
TRIM33	0.52	HSA25083	0.34	ULK2	0.18
JAK3	0.52	AXL	0.34	RET	0.18
CDK11	0.52	FLJ23074	0.34	TLK2	0.18
C8FW	0.51	STK22D	0.34	EPHB3	0.17

MAP4K2	0.17	HIPK2	-0.08	PTK6	-0.42
CSNK1G3	0.16	FGFR2	-0.08	PTK2B	-0.43
STK31	0.16	MAPKAPK	-0.10	SK200	-0.43
CASK	0.15	ADRBK1	-0.10	DYRK4	-0.45
EPHA7	0.15	H11	-0.10	PRKWINK1	-0.45
STK11	0.14	FZD1	-0.10	DAPK2	-0.48
TRB2	0.14	TAF1	-0.11	MAP3K6	-0.48
PAK2	0.14	ADCK4	-0.11	TAO1	-0.50
PFTK1	0.14	AKT2	-0.11	PRKCL2	-0.51
RPS6KB1	0.13	KIAA0303	-0.12	MAP3K14	-0.53
ERBB4	0.13	CAMK1	-0.13	VRK3	-0.54
SNRK	0.13	CAMK2A	-0.13	RPS6KA4	-0.59
CAMK4	0.13	SRPK2	-0.13	EPHA5	-0.60
STK38L	0.12	ANKRD3	-0.14	PAK6	-0.62
RPS6KA2	0.12	BMX	-0.16	AURKB	-0.65
MARK2	0.12	EIF2AK3	-0.17	CDKL2	-0.67
PRKAA1	0.12	MAP3K5	-0.17	EMR2	-0.68
RAGE	0.10	PAK7	-0.18	CAMK2B	-0.69
PDGFRA	0.10	PTK9	-0.19	MUSK	-0.71
PRKG1	0.09	MAPK12	-0.19	PRPF4B	-0.75
RIOK3	0.09	GSK3A	-0.19	ALS2CR7	-0.76
TGFBR1	0.09	AMHR2	-0.20	RPS6KA6	-0.77
CARK	0.09	CKLiK	-0.20	SGK2	-0.78
MAP3K12	0.08	EPHA3	-0.21	ADRB2	-0.79
MAP4K4	0.08	PTK2	-0.21	LOC34037	-0.79
DDR2	0.08	NEK4	-0.21	MGC45428	-0.81
STK10	0.07	FLT3	-0.22	HRI	-0.81
MAPK6	0.06	BRD2	-0.22	PRKY	-0.82
MAP3K7	0.06	GNRHR2	-0.25	PRKD2	-0.82
GSG2	0.06	GPR116	-0.26	MAPKAPK	-0.85
CDC7	0.05	ROCK2	-0.27	BRD4	-0.87
ADCK1	0.05	FLJ20574	-0.31	MIDORI	-0.87
DAPK1	0.05	RIPK1	-0.31	ERK8	-0.88
TEC	0.04	ARAF1	-0.31	CRK7	-0.88
DRD5	0.00	STK6	-0.31	MAP3K4	-0.90
GPR12	0.00	MARK1	-0.31	STK22C	-1.04
IRAK2	-0.01	OSR1	-0.32	C20orf64	-1.04
CLK1	-0.03	PRKAA2	-0.32	ADRBK2	-1.05
ALS2CR2	-0.03	RPS6KB2	-0.33	MGC22688	-1.06
CDC42BP1	-0.03	BMP2K	-0.34	NEK6	-1.08
TAF1L	-0.04	JIK	-0.36	ADRB3	-1.08
MOS	-0.04	CDC2L5	-0.36	KIAA2002	-1.08
PIK3R4	-0.05	TTN	-0.36	NEK8	-1.11
CAMKK2	-0.06	TLK1	-0.36	KIS	-1.11
CSK	-0.07	CDKL1	-0.36	ADCYAP1I	-1.13
FZD7	-0.07	PRKCH	-0.38	CDKL3	-1.17
CDKL5	-0.07	STK16	-0.38	PKE	-1.20
MYLK	-0.08	EPHB4	-0.39	C14orf20	-1.21
TNK1	-0.08	KIAA1079	-0.39	PCTK3	-1.22
SYK	-0.08	NLK	-0.40	TIF1	-1.25
CNK	-0.08	EPHB6	-0.41	STK29	-1.26

PSKH2	-1.28	HAK	-1.93
PAK4	-1.28	KIAA1639	-1.95
ADRB1	-1.28	SK707	-1.95
FLJ34389	-1.31	GPRK7	-1.96
MGC43306	-1.34	FLJ32685	-1.96
KSR	-1.36	AVPR1B	-1.96
MYO3B	-1.37	KIAA0551	-1.98
TTBK1	-1.38	ADRA1D	-1.99
STK35	-1.39	IKBKB	-2.01
MAP3K1	-1.39	KIAA1765	-2.01
STK22B	-1.42	AGTR1	-2.01
ILK-2	-1.43	ITK	-2.01
ADRA2A	-1.46	ADRA1B	-2.03
NEK7	-1.46	HIPK1	-2.08
MGC16169	-1.49	MYLK2	-2.09
ANKK1	-1.49	SK440	-2.15
CHEK2	-1.50	KIAA1883	-2.16
LOC91461	-1.51	DKFZp434	-2.19
SRMS	-1.53	KIAA1297	-2.20
LOC91807	-1.56	AGTR2	-2.23
SK466	-1.59	FLJ25965	-2.24
KIAA1361	-1.60	LYK5	-2.28
EIF2AK4	-1.65	FLJ33655	-2.31
STK23	-1.66	AATK	-2.32
SK558	-1.66	SK581	-2.35
CAMK2G	-1.67	ADRA2C	-2.39
DKFZP434	-1.67	AVPR2	-2.42
MAPK3	-1.70	AGTRL1	-2.42
ADORA2B	-1.70	NEK1	-2.47
ACVR1C	-1.71	ADMR	-2.88
FLJ25006	-1.72	MAP3K9	-2.89
FLJ32818	-1.73	HSMDPKII	-3.05
ADRA2B	-1.73	SK592	-3.29
NEK9	-1.73	STK19	-3.38
ADCK2	-1.74		
ADCK5	-1.75		
ERN2	-1.75		
KIAA0472	-1.76		
SK690	-1.76		
MAK	-1.76		
ADRA1A	-1.77		
ADORA1	-1.79		
TTBK2	-1.81		
ADORA3	-1.82		
FLJ14813	-1.83		
EGFR	-1.84		
LCK	-1.87		
LOC14942	-1.87		
KIAA0561	-1.88		
MGC42105	-1.92		
AVPR1A	-1.92		



Supplementary Figure 1. Levels of AKT1,2,3 isoforms in MDA-MB488 and MDA-MB231 cells.