

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1	SK-ES-1_b	RD-ES_a	RD-ES_b	siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1	SK-ES-1_b	RD-ES_a	RD-ES_b
AAK1_A	-3.57793	-3.70131	-0.86070	-1.26705	-1.78212	-2.04450	-1.13517	-1.18900	BCR_A	0.84158	0.65491	0.48929	0.52974	0.63977	0.41767	0.33063	0.47678
AAK1_B	-2.53570	-2.56092	-2.51738	-2.53301	-1.05795	-1.51890	-1.38335	-1.19250	BCR_B	-0.88590	-1.21825	-2.70686	-2.51125	-2.06226	-1.97257	-1.55115	-1.95029
AATK_A	-1.82525	-2.35760	-2.10342	-1.79362	-2.40628	-2.00224	-1.48119	-1.28424	BMP2K_A	-1.47722	-1.56570	-0.53665	-1.30938	-0.01008	-0.07186	-0.57807	-0.61357
AATK_B	-1.24760	-0.85182	-1.01418	-1.48963	-0.83995	-0.76646	-0.85811	-0.99575	BMP2K_B	0.43498	0.43592	0.79100	0.80733	0.10550	0.14900	0.33211	0.29502
ABL1_A	-0.59753	-0.53651	-1.17624	-1.16445	-0.78968	-0.72872	-0.74993	-0.73592	BMPR1A_A	0.24923	0.19894	0.56890	0.52936	0.63531	0.55655	-0.06603	-0.03450
ABL1_B	0.42315	0.44335	0.28484	0.18298	0.55935	0.35204	0.48155	0.62453	BMPR1A_B	0.28235	0.35524	0.61099	0.45015	0.07175	0.03653	0.44437	0.70674
ABL2_A	0.25927	0.50105	0.66281	0.50948	0.75476	0.73566	0.85109	1.01599	BMPR1B_A	-2.07755	-2.59724	-2.16132	-2.23492	-2.84276	-2.67156	-1.77486	-3.26595
ABL2_B	0.46519	0.50809	-0.77732	-0.75461	-0.09597	-0.08360	-0.22341	-0.03929	BMPR1B_B	0.68031	0.66087	-0.14176	0.00173	0.61994	0.57775	0.37727	0.28907
ACVR1_A	-0.07307	0.06132	-0.02471	0.09591	-0.61256	-0.39944	0.25308	0.29027	BMPR2_A	-0.65573	-0.82814	-0.31979	-0.27553	0.03857	0.03580	0.36424	0.30328
ACVR1_B	1.08334	0.95918	0.83835	0.92801	1.09825	1.14678	0.85586	0.92557	BMPR2_B	0.07185	0.01066	-0.36381	-0.36586	0.05072	0.08558	0.04285	-0.21058
ACVR1B_A	0.82281	0.73840	0.66913	0.65464	0.70158	0.44700	0.11817	0.07582	BMX_A	-0.21028	-0.16704	0.05563	0.48258	0.85310	0.84336	0.01473	-0.05985
ACVR1B_B	-1.30689	-1.05350	-0.40044	-0.55523	-2.24403	-2.01909	-2.19268	-2.44467	BMX_B	-0.11950	0.11574	-0.06280	0.02973	-0.63324	-0.97996	-0.24183	-0.09596
ACVR2_A	-0.96294	-0.77186	0.91625	0.99439	1.13271	0.74820	0.23159	0.48037	BUB1_A	-1.62875	-1.40636	-0.50678	-0.81677	-1.69565	-1.90820	-0.86095	-1.11832
ACVR2_B	0.16533	0.03584	-0.10817	-0.08006	-0.56519	-0.70591	-0.92374	-1.20643	BUB1_B	0.80821	0.95511	0.94369	0.10491	0.97942	0.86861	0.41246	0.33975
ACVRL1_A	0.41181	0.18252	0.35296	0.38474	1.00036	1.03342	0.48561	0.43419	BUB1B_A	0.01443	0.08261	-1.64588	-1.48978	-1.16798	-1.31251	-0.39393	-0.25470
ACVRL1_B	0.39587	0.18129	0.69852	0.78071	0.28511	0.24672	0.68934	0.60497	BUB1B_B	0.35612	0.23355	-0.19659	-0.12173	0.40787	0.50594	0.29533	0.48198
ADCK1_A	-1.32594	-1.33663	-0.23952	-0.30631	0.12989	0.06292	-0.11662	-0.13470	CALM1_A	-0.05533	-0.11442	-0.11872	-0.18176	-0.59118	-0.77316	0.44426	0.52307
ADCK1_B	-0.23158	-0.19864	0.47492	0.49530	0.61463	0.45415	0.32808	0.36922	CALM1_B	0.17583	0.03154	-0.02729	-2.87300	-0.89878	-0.94721	-0.31734	-0.04410
ADCK2_A	-0.60262	0.04031	-0.83988	-0.62611	-0.16029	-0.40796	-0.69115	-1.00326	CALM2_A	0.10199	1.07577	0.70420	0.88978	0.92995	0.91944	1.03064	0.97314
ADCK2_B	0.20009	0.14276	-0.39196	-0.67587	-0.35249	-0.36904	-0.44391	-0.28206	CALM2_B	0.07276	-0.28571	0.06823	0.34184	0.24945	0.40827	0.71344	0.76680
ADCK4_A	0.89595	0.57753	0.34255	0.28980	0.45213	0.23727	0.61207	0.62003	CALM3_A	0.84093	0.98020	0.86117	0.95846	1.04558	0.85808	0.65970	0.62371
ADCK4_B	0.86921	0.65333	0.47602	0.52550	1.14348	0.92331	1.12789	0.97273	CALM3_B	0.58331	0.48339	0.13119	0.11551	-0.13484	-0.44239	0.57177	0.76668
ADCK5_A	-1.28659	-1.02699	-2.72804	-2.64591	-2.78863	-2.65063	-2.32457	-2.33917	CAMK1_A	0.91100	0.94993	0.66503	0.62442	1.04190	0.66008	0.34532	0.53033
ADCK5_B	-2.87021	-2.91298	-2.37477	-2.40546	-1.44501	-0.50052	-0.70418		CAMK1_B	0.80379	0.74751	0.05571	0.30174	0.22609	0.09033	-0.05043	0.07929
ADK_A	0.82316	0.88541	1.21010	0.89923	0.68045	0.59228	0.69769	0.83160	CAMK1D_A	-0.52633	-0.50895	-1.15592	-0.97108	-1.23021	-1.20962	-1.32559	-1.27170
ADK_B	0.91739	0.93831	1.34116	1.11017	1.24396	1.26028	0.80654	0.96648	CAMK1D_B	0.24854	0.05059	0.58120	0.51166	0.51598	0.25456	0.15491	0.26543
ADRBK1_A	0.03650	0.16851	0.30584	0.24522	0.94052	1.00602	1.21088	1.30936	CAMK1G_A	0.26971	0.09211	-0.12416	-0.20660	-0.29840	-0.46952	-0.63126	-0.52351
ADRBK1_B	-2.61052	-1.56570	-0.12690	-0.17340	-0.17857	-0.09071	0.22994	0.34067	CAMK1G_B	-0.55408	-1.66851	-0.71835	-0.51837	0.25182	-1.05329	-0.91467	-0.18285
ADRBK2_A	-0.14686	0.05396	-0.83027	-0.71863	-1.78676	-1.52249	-0.90951	-0.68082	CAMK2D_A	0.43603	0.79739	0.02848	-0.03081	0.00480	0.06267	0.53893	0.58763
ADRBK2_B	0.41014	0.37963	-0.78243	-0.44772	-0.11772	-0.05939	0.27159	0.27607	CAMK2D_B	1.25568	1.08256	1.18189	1.18727	0.88339	0.95620	0.62333	0.52535
AK1_A	-0.12547	-0.94101	0.17593	0.17262	-1.84614	-1.81259	-1.93640	-2.29435	CAMK2G_A	0.96479	1.16043	0.90391	0.95399	0.88033	0.81971	0.55766	0.57810
AK1_B	1.17208	1.49391	0.75523	0.73701	0.86635	0.91952	0.76641	0.49709	CAMK2G_B	-0.87858	-0.84244	-0.24450	-0.20313	-0.10663	-0.16798	0.22880	0.14602
AK2_A	-0.73642	-0.62517	0.28866	0.24782	0.84612	0.94450	0.73711	0.65307	CAMK4_A	1.08053	0.92814	0.91476	0.95822	1.07643	1.01338	0.81172	0.93615
AK2_B	0.50085	0.58142	1.00167	1.03146	1.12276	1.39133	0.89512	0.88158	CAMK4_B	0.08852	0.09260	-0.17846	0.10774	0.48978	0.52044	0.48536	0.57650
AK3_A	0.81715	0.79865	0.27314	0.30520	0.03047	0.28222	0.72022	0.70562	CaMKIIalpha_A	1.17645	1.28256	0.99828	1.00810	0.50267	0.61775	1.02906	1.15596
AK3_B	-0.40236	-0.57439	0.06601	-0.13750	0.96773	1.06605	0.33198	0.41695	CaMKIIalpha_B	-1.76796	-1.79466	-1.14401	-1.03508	-1.40087	-1.63318	-0.84253	-1.03032
AK3L1_A	-2.12468	-1.89613	-0.11386	0.12679	-1.84289	-1.93195	-0.07545	-0.22172	CAMKK1_A	0.78985	0.88102	0.90072	0.77598	0.91228	0.65600	0.65627	0.70760
AK3L1_B	0.60934	0.07792	-0.03680	0.23236	-0.64582	-0.45165	0.38334	0.43316	CAMKK1_B	-1.32620	-1.25180	-0.11716	0.01237	-1.97405	-2.09350	-1.15948	-1.20101
AK5_A	0.87141	1.12321	0.96696	0.89277	0.99986	0.79036	0.77900	0.57867	CAMKK2_A	-1.23670	-0.97733	0.44559	0.43308	0.49281	0.62735	0.54024	0.60024
AK5_B	1.00341	1.20739	1.09439	1.02432	1.31243	1.32306	1.24784	0.99536	CAMKK2_B	-0.14680	-0.59490	-0.78962	-0.80434	0.43237	0.46055	0.21111	0.33556
AK7_A	0.47404	0.57103	0.52257	0.12891	0.23519	0.33827	-0.18272	-0.23846	CARL_A	0.99219	1.10382	1.02362	1.11122	1.22283	1.18352	1.23755	1.23516
AK7_B	1.10314	1.31405	1.33651	0.95842	1.26475	1.31827	1.06268	1.12457	CARL_B	0.89930	0.88420	0.74433	0.64163	0.79443	1.01560	0.69040	0.58041
AKAP1_A	0.40806	0.64521	0.12250	-0.00662	-0.11226	-0.10898	-0.01133	-0.16872	CASK_A	-0.17007	-0.35754	-0.42704	-0.36659	-0.48747	-0.33743	-0.93744	-0.99679
AKAP1_B	0.72674	0.77212	1.20769	1.10363	-0.04282	-0.14896	0.20400	0.21674	CASK_B	-2.21099	-2.11394	0.06049	0.05773	-0.59750	-0.38381	-0.10448	-0.24671
AKAP11_A	0.06216	-0.72498	0.29356	-0.04815	0.59934	0.90367	0.88530	0.77071	CDC2_A	1.10397	1.18122	0.68457	0.46882	-0.00542	0.10342	0.03552	0.11121
AKAP11_B	0.27704	0.45968	0.02056	0.03419	0.42685	0.10908	0.31439	0.28099	CDC2_B	0.92740	0.95743	0.55751	0.43003	0.56088	0.20497	0.74912	1.08017
AKAP12_A	-0.82416	-1.28195	-0.79054	-0.71404	-1.11221	-1.20409	0.11251	-0.30593	CDC2L1_A	-1.82711	-2.46436	-2.70763	-3.00406	-0.79609	-0.73703	-0.57090	-0.74933
AKAP12_B	0.10715	0.04485	-0.06305	-0.57781	-0.11920	-0.09851	0.52325	0.40034	CDC2L1_B	-0.02277	-0.11452	-1.66395	-1.94609	0.26824	0.36282	0.19431	0.36355
AKAP13_A	0.72339	0.93091	0.84484	0.871136	1.10170	1.10187	0.93903	0.81644	CDC2L5_A	0.65606	0.97776	0.38268	0.18072	0.43901	0.58897	0.47695	0.67051
AKAP13_B	1.21464	1.47827	1.09789	1.13237	1.23857	1.31360	1.22471	0.92010	CDC2L5_B	1.02241	1.11306	1.08164	0.99763	0.76481	0.87199	0.71515	0.78646
AKAP28_A	0.08385	0.13803	0.94271	1.13037	0.46545	0.41004	0.44189	0.50422	CDC42BPB_A	-1.32175	-0.57815	-0.14826	-0.97418	-2.28020	-2.38903	-2.74269	-2.58485
AKAP28_B	0.90295	0.90338	0.74680	0.77537	0.78377	0.59771	0.99538	0.88191	CDC42BPB_B	-0.51945	-0.84698	-0.68125	-0.66816	-2.48504	-2.52828	-2.27284	-2.35281
AKAP3_A	-1.21487	-1.34523	0.47024	0.61590	1.11764	1.07084	0.55068	0.66705	CDC42BPB_B	0.80615	0.77880	1.05932	1.07937	0.61012	0.59491	0.80172	0.66080
AKAP3_B	-3.31230	-3.17921	-0.50174	-4.87012	-3.30082	-3.20863	-4.55575	-4.35065	CDC42BPB_B	-0.10285	-0.23195	0.11569	0.13904	-0.59907	-0.63015	0.17805	0.03509
AKAP4_A	1.23791	1.21390	0.89528	0.79836	1.28357	1.10495	1.08833	1.03053	CDK11_A	0.25487	0.32236	0.28975	-0.26824	-0.63608	-0.59113	0.36589	0.41755
AKAP4_B	0.79930	0.52034	0.84625	0.52660	2.23363	0.25921	0.49443	0.44247	CDK11_B	0.24463	0.14404	1.07985	0.88197	0.68933	0.77163	0.20031	0.25676
AKAP5_A	1.55426	1.39471	1.06987	1.06428	1.15205												

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells (cont)

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b	siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b
CHUK_A	0.58995	0.60391	1.00877	0.98957	0.44754	0.46447	0.36984	0.43933	EPHA5_A	1.43894	1.44875	1.07435	1.02547	1.35879	1.31360	1.11349	1.08100
CHUK_B	-0.28106	-0.21417	-0.37099	-0.16488	-0.68970	-0.71110	-0.16210	-0.01684	EPHA5_B	-2.28126	-1.21116	-2.31362	-2.14188	-2.31159	-2.14994	-3.22560	-3.49696
CIB3_A	-0.36447	-0.45235	-0.97874	-0.51707	-1.02264	-1.14141	0.00986	0.31067	EPHA7_A	1.24755	1.37679	1.11852	1.15066	1.32505	1.41713	1.12362	1.09598
CIB3_B	-0.55682	-0.67837	-0.77351	-0.58775	-1.77348	-1.66951	-1.34671	-1.39389	EPHA7_B	0.94526	0.98316	0.77738	0.91793	0.89344	0.64874	0.91230	0.74030
CINP_A	0.90527	0.81266	0.66692	0.76975	0.45488	0.54405	0.23194	0.08827	EPHA8_A	1.38681	1.44554	1.12347	1.06819	1.32685	1.37923	1.25445	1.28458
CINP_B	0.19686	0.21075	0.56150	0.59173	0.63975	0.57493	-0.00055	-0.09094	EPHA8_B	0.68784	-0.40954	0.60768	0.49817	-0.12765	0.01798	0.36414	0.35480
CIT_A	0.59067	0.54822	0.11611	-0.11265	0.58382	0.53112	0.00849	-0.00094	EPHB1_A	1.33821	1.29212	1.10715	1.15737	1.36495	1.40308	1.28816	1.34774
CIT_B	-0.20423	-0.24548	-0.34320	-0.92070	-0.04198	-0.26329	-0.53318	-0.47626	EPHB1_B	-0.13623	-0.18545	-0.77748	-0.60090	-1.56961	-1.50130	-2.66530	-2.09297
CKB_A	-0.31373	0.10219	-1.30952	-0.19477	-1.04210	2.29442	-0.26127	-0.50153	EPHB2_A	0.75271	0.66582	1.14263	0.89882	1.15402	1.15839	1.32977	1.29615
CKB_B	-0.25954	-0.10565	-1.08076	-1.19420	-0.87463	-0.90227	-0.41907	-0.62217	EPHB2_B	0.90151	0.76311	0.67572	0.69495	1.08496	1.00256	0.80887	0.56498
CKM_A	1.13333	1.35327	0.97956	0.83720	1.02227	1.18237	0.50046	0.64924	EPHB3_A	-1.13086	-1.14513	-0.60915	-0.76651	-1.05638	-0.99961	-2.13480	-1.97151
CKM_B	-0.16698	0.02783	-0.56665	-0.79482	0.32326	0.47419	0.23547	0.36317	EPHB3_B	0.59495	0.56678	0.12351	0.13949	0.69089	0.81378	0.23648	0.37932
CKMT1_A	0.82340	0.64372	0.68787	0.69363	0.25104	0.21355	0.33456	0.35198	EPHB4_A	1.45840	1.39996	1.16016	1.07011	1.35409	1.51318	1.24654	1.13846
CKMT1_B	-2.28632	-2.12004	-1.02168	-1.06468	-1.08576	-1.05260	-1.09095	-1.13788	EPHB4_B	0.38023	0.23007	0.53005	0.44505	0.41180	0.57349	0.47101	0.59500
CKS1B_A	-1.77718	-1.45157	0.17966	0.54033	0.11832	-0.02487	0.24423	0.40455	EPHB6_A	-0.53037	-0.69214	-0.12806	-0.04936	-0.24565	-0.31842	-0.56386	-0.46798
CKS1B_B	0.79268	0.73821	0.95398	1.10999	1.03504	0.79808	1.32291	1.37721	EPHB6_B	-0.70259	-0.53447	-0.31915	-0.30652	-0.24246	-0.11464	-0.05282	0.10692
CKS2_A	0.21622	0.00909	-0.07352	-0.07679	-0.19026	-0.45286	0.43457	0.38980	ERBB2_A	-0.70616	-0.90047	-0.89926	-1.05641	-0.86995	-0.89454	-0.66639	-0.62728
CKS2_B	1.10225	1.15103	1.04439	0.96195	0.87740	0.92147	0.94997	0.88232	ERBB2_B	-0.26092	-0.33146	-0.45066	-0.40472	-0.25355	0.10475	0.07894	0.15065
CLK2_A	-0.57256	-0.33697	-0.05559	0.17038	0.82376	0.67755	-0.46397	-0.39381	ERBB3_A	-0.48792	-0.45877	0.35580	0.41391	-0.63341	-0.45604	-0.18098	-0.34991
CLK2_B	-0.26636	-0.35157	-0.89552	-0.84663	-2.27173	-2.05660	-2.37500		ERBB3_B	-1.33132	-1.24757	-0.87430	-0.80727	-1.79906	-1.68074	0.05025	0.03004
CLK3_A	-1.09781	-1.10677	-0.80842	-0.71014	0.05720	-0.25028	-0.39945		ERBB4_A	0.09999	0.16363	-0.39786	-0.40297	-0.76238	-0.51312	-0.23658	-0.21800
CLK3_B	-0.46925	-0.50661	-0.22582	-0.16446	0.41384	0.46163	0.50867		ERBB4_B	0.47018	0.52923	0.58626	0.57781	-0.25665	-0.08379	0.31250	0.33372
CNKS1R1_A	-0.20723	0.12582	-0.06043	-0.25597	0.65664	0.69562	-0.24027	-0.24705	ERK8_A	-0.91632	-0.90418	-0.27074	-0.13810	0.88064	0.84288	0.89689	0.92506
CNKS1R1_B	0.35099	0.69207	0.75251	0.81623	0.70064	0.48799	0.19545	0.19972	ERK8_B	-0.30348	-0.33829	-0.95139	-1.02138	-0.21119	-0.24898	-0.41471	-0.55097
CRK7_A	-0.77884	-0.91025	-0.06364	-0.38106	-0.35131	-0.43497	-0.03156	0.17137	ERN1_A	1.00030	0.99183	0.47272	0.60218	1.16906	1.13703	0.65968	0.55242
CRK7_B	0.43920	0.48464	0.09681	0.14295	0.39139	0.28629	0.15050	0.20117	ERN1_B	0.39922	0.29836	0.74102	0.87696	0.56532	0.32364	-6.88824	0.10073
CSK_A	0.12846	0.11147	0.03363	0.05173	0.63961	0.48582	-0.34075	-0.39309	FASTK_A	-0.06733	-0.21421	-0.45959	-0.55410	-0.34024	-0.31587	0.28043	0.12137
CSK_B	0.39673	0.52657	0.22757	0.46007	0.33933	0.44235	-0.19869	-0.41889	FASTK_B	0.41344	0.31187	-0.43137	-0.42044	0.11158	0.19222	0.34385	0.23691
CNKN1A1_A	0.09180	-0.02337	0.41443	0.73809	-0.04212	-0.14296	0.19092	0.26286	FER_A	-0.13907	-0.20896	-0.65824	-0.89750	-0.90761	-0.76562	0.38465	0.20796
CNKN1A1_B	-1.99465	-1.82756	0.66763	0.93804	0.49253	0.50243	-0.02118	-0.12279	FER_B	-0.36203	-0.35869	-0.98495	-0.97862	-0.72639	-0.70130	0.11757	0.05465
CNKN1A1L_A	-0.43609	-0.35531	0.36267	0.47551	0.13707	0.40808	0.61446	0.54154	FES_A	-0.74628	-1.04280	-1.36193	-1.30785	-0.94244	-0.95781	-0.26980	-0.11129
CNKN1A1L_B	-0.67482	-0.84244	-1.11615	-0.88216	-0.54054	-0.58532	0.08230	-0.30974	FES_B	0.50701	0.52137	-0.34540	-0.29561	0.46504	0.60507	-0.35926	-0.15167
CNKN1D_A	-0.96343	-0.64389	-0.67149	-0.41142	-0.91333	-0.94603	-1.10914	-1.08974	FGFR1_A	1.08682	0.90254	0.42746	0.37648	0.43701	0.35586	0.59406	0.72451
CNKN1D_B	-0.40109	-0.25840	0.59846	0.83333	0.07978	0.05379	-0.29390	-0.56356	FGFR1_B	0.47853	0.63896	0.56043	0.64204	0.81217	0.79618	0.54614	0.47382
CNKN1E_A	0.76325	0.67632	0.95968	1.08304	0.63650	0.64600	0.45770	0.43878	FGFR2_A	0.96551	0.98994	0.70695	0.69083	0.91880	0.97898	0.98809	0.93078
CNKN1E_B	-0.00771	-0.26141	0.47027	0.64284	0.05612	0.13252	-0.80867	-0.97276	FGFR2_B	-0.29953	-0.13703	-0.80731	-0.69776	-0.80287	-0.75280	-1.31750	-1.32786
CNKN1G1_A	0.17652	0.17893	0.47249	0.73983	0.06038	0.05553	0.31404	0.27270	FGFR3_A	0.98868	0.97070	0.74432	0.87509	0.73068	0.88388	0.39747	0.33376
CNKN1G1_B	0.88091	0.65849	1.10033	1.15780	0.89104	1.01662	0.33980	0.41934	FGFR3_B	0.61855	0.45409	0.09683	0.21750	0.68302	0.65679	0.58416	0.77666
CNKN1G2_A	0.41963	0.18388	0.20612	0.17477	-0.19428	-1.00683	-0.54984	-0.24446	FGFR4_A	-1.02761	-0.98091	-0.98611	-0.76700	-0.61131	-0.43808	0.04777	-0.12858
CNKN1G2_B	-0.65850	-0.60594	-0.18883	-0.26313	-0.93153	-0.97489	0.00578	0.00688	FGFR4_B	-1.48215	-1.57827	-2.47815	-2.36201	-0.98696	-0.99394	-0.84080	-0.76675
CNKN1G3_A	0.78512	0.80698	0.82804	0.84444	0.50463	0.28581	0.72310	0.91203	FLJ11149_A	-2.15128	-2.60133	-1.01601	-1.41343	-0.50167	-1.78843	-0.60613	-0.19272
CNKN1G3_B	1.07181	0.96192	1.14529	1.24621	0.93311	1.04428	0.95455	1.18175	FLJ11149_B	1.25490	1.31275	0.42518	0.50875	0.88591	0.79060	0.77542	0.88996
CNKN2A1_A	0.26286	0.34062	0.75726	0.62408	0.72175	0.68927	0.85975	0.88473	FLJ13052_A	1.08495	1.28804	0.93408	1.04774	1.17674	1.09936	0.91387	0.98461
CNKN2A1_B	1.18166	1.12018	0.94808	0.99430	1.37273	1.24901	1.14346	1.21255	FLJ13052_B	-0.64428	-0.68064	-0.30366	-0.18506	-0.66098	-0.68738	-0.11900	-0.22593
CNKN2A2_A	1.05516	1.05211	0.96767	1.02501	1.12632	1.13088	0.77055	0.63815	FLT1_A	0.08739	-0.04113	-0.03166	0.05830	0.28987	0.24556	-0.02246	-0.23124
CNKN2A2_B	0.23287	-0.02716	0.65732	0.75699	-0.11791	-0.16379	0.19744	0.06739	FLT1_B	0.37269	0.27384	-1.18611	-0.91166	-1.36571	-1.35667	-0.73850	-0.86690
CNKN2B_A	-0.11367	-0.01827	-0.19209	-0.55679	-0.59071	-0.53916	-0.27962	-0.40095	FLT3_A	-1.36409	-1.32858	-1.66361	-1.15424	-1.42230	-1.13758	-0.17739	-1.30781
CNKN2B_B	0.73724	0.62687	0.24652	0.26685	-0.61451	-0.29707	0.08033	0.24956	FLT3_B	0.05981	-0.22819	0.15111	0.04436	-0.30639	-0.09831	0.07177	-0.21286
DAPK1_A	1.06501	0.85866	1.04634	0.99727	0.87714	0.82185	0.63546	0.71204	FLT3LG_A	0.57228	0.64015	0.77316	0.73617	0.81584	0.63480	0.66230	0.29714
DAPK1_B	-0.63775	-1.38364	-0.05190	-0.02942	-0.84278	-0.87890	-0.66526	-0.75617	FLT3LG_B	-0.05680	-0.02123	-1.90933	-1.81502	-0.03958	-0.12556	-0.23875	-0.27137
DAPK2_A	-0.51393	-1.71527	-1.83558	-1.69870	-0.00173	0.01471	-0.45798	-0.35491	FLT4_A	0.07080	0.10130	-0.86151	-0.92654	-0.67060	-0.75723	-0.21441	-0.31495
DAPK2_B	-1.75618	-1.63194	-0.92191	-1.21606	-1.21264	-1.36245	-1.19739	-0.97127	FLT4_B	-0.60894	-0.60319	-0.09259	-0.15397	1.01730	0.77429	0.19233	0.28492
DAPK3_A	-0.16042	-1.31588	-0.59460	-0.56456	-0.08227	-0.21002	0.56582	0.54499	FNK3_A	-0.34632	0.04546	0.75773	0.47455	0.22122	0.05480	0.70497	0.44614
DAPK3_B	0.76931	0.91859	-0.47075	-0.41030	0.11731	0.08410	0.48127	0.50920	FNK3_B	-1.72369	-1.66320	-0.27211	-0.31781	-1.26727	-1.55714	-1.30335	-1.50429
DCAMKL1_A	0.10939	0.13706	0.41057	0.60705	0.43256	0.54838	0.39883	0.22476	FRK_A	-1.37023	-1.39698	0.47421	0.39711	-0.06558	0.22593	-0.32848	-0.37903
DCAMKL1_B	1.05691	1.06955	0.87702	0.98332	0.39670	0.16611	0.45691	0.45512	FRK_B	-0.27963	-0.26047	0.86617	0.89262	0.50216	0.31948	0.59495	0.62856
DCK_A	1.02658	1.14277	0.48515	0.27016	-0.06768	0.29534</											

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells (cont)

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b	siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b
IBTK_A	0.07249	-0.12889	-0.11693	-0.12300	-0.10370	-0.108621	-0.82995	-0.82687	MAP2K4_A	-0.14311	-0.03627	0.61218	0.43118	0.10798	0.21811	0.42521	0.62976
IBTK_B	0.03981	-0.09382	0.41614	0.40389	0.31020	0.08927	0.01997	-0.08682	MAP2K4_B	0.43511	0.53679	0.53924	0.47834	0.83845	0.73188	1.04980	1.06386
ICK_A	0.34691	0.44613	0.76266	0.71048	0.97388	0.76857	0.91074	0.61497	MAP2K5_A	-0.03831	0.06306	-0.77631	-0.79700	-0.17948	-0.14878	-0.02563	-2.85121
ICK_B	0.66939	0.73207	0.57334	0.30286	0.36845	0.51998	0.41658	0.32543	MAP2K5_B	0.36419	0.41635	0.15006	0.30727	-0.81848	-0.86367	-0.35801	-0.26931
IHPK1_A	0.83026	1.06528	0.23492	0.36917	0.81831	0.93344	0.52051	0.38231	MAP2K6_A	-0.62408	-0.64009	-0.38985	-0.28003	-0.08108	-0.20078	-1.06993	-1.10081
IHPK1_B	-0.13320	-0.24666	0.70762	0.66046	0.54463	0.57566	0.03605	-0.17459	MAP2K6_B	0.61378	0.66578	0.41039	0.43702	0.28634	0.13920	-0.02813	0.14933
IHPK2_A	0.08929	-0.00537	0.46253	0.13733	-0.00403	0.02537	0.15860	0.16588	MAP2K7_A	-0.86934	-0.97239	-1.05434	-0.89214	-1.00901	-1.05433	-0.18213	-0.02355
IHPK2_B	-1.43057	-1.59597	0.20304	-0.04826	-0.29422	-0.47587	-0.67560	-0.72120	MAP2K7_B	-2.60933	-2.37084	-0.66762	-0.30631	-0.99979	-0.87442	-0.47381	-0.62541
IHPK3_A	-1.28567	-0.94235	-0.43257	-0.27090	-0.08999	-0.03708	0.47790	0.47602	MAP3K10_A	-0.45379	-0.58540	-1.73125	-1.77344	-1.25077	-1.26390	-2.70421	-2.55558
IHPK3_B	-0.80271	-0.29890	-0.22655	-0.12961	-0.17130	-0.11404	0.43513	0.37835	MAP3K1_B	0.64579	0.64180	0.42907	0.44622	1.18157	1.10854	0.80719	0.74136
IKBKAP_A	0.42839	0.18693	0.19021	0.15217	-0.02161	0.12175	0.09763	0.05605	MAP3K10_B	1.37404	1.47669	0.89260	1.14160	1.44083	1.48543	1.10412	1.11435
IKBKAP_B	0.60305	0.68103	0.31055	0.45653	-0.50484	-0.25642	-0.83459	-0.99050	MAP3K11_A	0.38867	0.32770	-0.29670	-0.19287	0.47003	0.38436	0.55305	0.46538
IKBK_E	-1.49185	-1.36150	-0.15902	-0.19297	-0.35296	-0.25103	-0.74356	-0.52977	MAP3K11_B	-0.77778	-0.88297	-1.37119	-1.46762	-0.38644	-0.34258	-0.55005	-0.63462
IKBK_G	-0.29287	-2.33197	-1.37093	-1.00321	-0.69786	-0.73793	-1.20132	-1.08269	MAP3K13_A	0.72496	0.78874	0.56995	0.65859	1.09437	0.90895	0.66044	0.71443
ILK_A	-1.35593	-1.28489	-2.08064	-2.20024	-1.17343	-0.89080	-0.60930	-0.59434	MAP3K13_B	0.90645	0.71645	0.27116	0.23135	0.63849	0.53515	0.70981	0.63026
ILK_B	0.44661	0.50639	0.83995	0.92096	0.77189	0.86332	0.50423	0.37422	MAP3K2_A	0.64672	0.74983	0.47622	0.65570	-0.26278	-0.06114	0.09571	0.01811
ILKAP_A	-1.15762	-1.28405	0.12159	-0.10943	-0.49047	-0.51960	0.01330	-0.07231	MAP3K2_B	-0.55835	-0.52585	-0.19070	-0.12452	-0.67007	-0.44125	-1.02343	-0.93449
ILKAP_B	-0.85244	-0.80699	0.44981	0.20693	0.41451	0.37199	0.48667	0.36420	MAP3K3_A	0.43313	0.53683	0.53964	0.47106	0.40182	0.33396	0.53880	0.54973
IRAK1_A	0.11763	0.96674	0.55057	0.44636	0.15394	0.12392	0.32240	0.23451	MAP3K3_B	-0.10024	-0.24579	0.14302	0.04064	0.79902	0.83156	-0.10975	-0.26969
IRAK1_B	-0.25364	-0.11524	0.06711	0.01571	0.36445	0.23668	-0.02533	0.06588	MAP3K4_A	0.43458	0.33951	0.16509	0.08038	-0.73152	-0.84308	-0.54819	-0.55012
IRAK2_A	0.14161	-0.22279	0.00928	-0.06727	0.57970	0.49982	0.59349	0.45822	MAP3K4_B	0.92278	0.80218	0.67406	0.84450	0.87057	0.83309	0.78072	0.63143
IRAK2_B	-0.01569	-0.09314	-1.49280	-1.55016	-1.63887	-1.67562	-0.61542	-0.79209	MAP3K5_A	-1.08864	-1.11942	-0.51036	-0.44998	-0.49007	-0.52488	-0.21018	-0.18017
IRAK3_A	0.25099	0.44448	-0.11076	-0.05071	-0.06627	0.00072	0.40413	0.42657	MAP3K5_B	0.80213	0.92744	0.63963	0.76344	0.55533	0.60137	0.61793	0.79318
IRAK3_B	1.24628	0.91639	0.82863	0.82946	0.19495	0.14284	0.89017	0.94942	MAP3K6_A	-1.51388	-1.34103	0.12996	0.55579	-0.94432	-0.92209	-0.82834	-0.43956
IRAK4_A	0.92726	1.12685	1.06336	1.01605	0.73313	0.75501	0.88573	0.80654	MAP3K6_B	0.55577	0.64536	-0.11884	0.04699	-0.81304	-0.89632	-1.49753	-1.27368
IRAK4_B	-0.01007	-0.05506	-0.02127	-0.10925	-0.13601	-0.00303	0.27116	0.11853	MAP3K7_A	-0.24738	-0.07993	0.69684	0.84075	-0.02893	-0.10343	0.00708	-0.19014
ITK_A	1.54669	1.54340	1.03821	1.11242	1.25607	1.35475	1.17336	1.25216	MAP3K7_B	-0.08855	-0.12463	-1.53448	-1.66583	-1.60161	-1.62243	-1.23335	-1.23136
ITK_B	1.16254	1.16609	0.59835	0.53186	0.61310	0.30233	0.67599	0.93081	MAP3K7IP1_A	-0.67590	-0.56952	-1.25075	-1.18009	-0.82267	-0.70963	-0.66242	-0.74832
ITPK1_A	0.41824	0.53785	0.77219	0.63218	0.72266	0.69076	-0.11602	0.08599	MAP3K7IP1_B	0.47431	0.53351	0.72066	0.45318	0.76815	0.74364	0.63157	0.49972
ITPK1_B	0.95129	0.91802	0.84685	0.82661	1.01524	0.99340	0.31144	0.40919	MAP3K7IP2_A	-2.13320	-2.35374	-0.52305	-0.38807	-1.44822	-1.16382	-1.05892	-0.99132
ITPKA_A	-1.53885	-1.21272	-0.24890	-0.36260	-0.10275	-0.07450	-0.99285	-1.01518	MAP3K7IP2_B	0.83837	0.94909	1.15981	1.21063	0.98535	1.13995	1.14709	1.06888
ITPKA_B	-0.65092	-0.44020	-0.58458	-0.82436	-0.97112	-0.93198	-1.73688	-1.60906	MAP3K9_A	1.47608	1.40434	1.11317	1.14104	1.33693	1.52666	1.01038	1.15812
ITPKB_A	0.43517	0.68762	0.94433	0.92371	0.91451	1.00880	0.10330	0.46293	MAP3K9_B	0.101697	0.71660	1.00300	1.03874	1.15875	1.19926	0.64594	0.73004
ITPKB_B	0.85245	1.10831	0.36589	0.36491	0.77522	0.86628	0.53056	0.55200	MAP3K10_A	-2.05338	-2.06844	-2.23757	-1.78136	-2.53744	-2.36924	-3.88397	-3.80200
ITPKC_A	-0.62516	-0.62641	-1.66382	-1.46448	-0.92954	-0.91856	-0.94689	-0.96402	MAP3K10_B	0.72114	0.65710	0.04710	0.02584	0.18896	0.13917	0.11849	0.25546
ITPKC_B	0.83043	0.66938	0.86570	0.91542	0.67048	0.60102	0.35722	0.27850	MAP4K1_A	-0.07536	-0.13787	-0.63190	-0.57723	-0.29967	-0.35602	0.01305	0.05484
JAK1_A	1.50932	1.52286	1.12011	1.20689	1.34333	1.38309	1.35163	1.31589	MAP4K1_B	-0.52308	-0.64775	0.44510	0.49124	0.48559	-0.48021	0.00522	0.01266
JAK1_B	-0.93397	-0.97706	-1.83294	-1.70757	-1.14784	-1.15493	-1.19815	-1.34577	MAP4K2_A	0.41614	0.17605	0.45883	0.62657	-0.25210	-0.27026	0.49250	0.27895
JAK2_A	0.46504	0.40959	1.03623	1.08165	1.06027	1.05846	0.92723	0.82961	MAP4K2_B	-0.47706	-0.62330	0.13581	0.27842	-0.46712	-0.32462	-0.30447	-0.76028
JAK2_B	0.67391	0.76590	0.68437	0.74241	0.74253	0.64427	0.52399	0.42100	MAP4K4_A	-1.02602	-0.90141	-0.14363	-0.22767	-0.35874	-0.33657	-0.30859	-0.06305
JAK3_A	1.12893	1.30460	1.13906	1.12958	1.15579	1.23366	1.14169	1.16251	MAP4K4_B	-1.75145	-1.60959	-0.47850	-0.66547	-0.51210	-0.32846	-0.41995	-0.32780
JAK3_B	-0.53672	-0.75080	-0.04277	0.06296	0.27348	0.39090	0.34334	0.39813	MAP4K5_A	0.93186	0.84001	0.62048	0.68643	0.60917	0.69338	0.46038	0.29213
KDR_A	1.35280	1.28061	1.09191	1.06032	1.30386	1.13740	0.94388	1.02141	MAP4K5_B	-1.27998	-1.50213	-0.25472	-0.07360	-1.20931	-1.06418	-0.15966	-0.25865
KDR_B	-0.84516	-0.97368	-2.14640	-2.01490	-2.57391	-2.54575	-1.07101	-0.91004	MAPK1_A	1.37645	1.46878	1.33014	1.13553	1.34022	1.39161	1.01050	1.08148
KHK_A	-1.00200	-1.21933	-0.69421	-0.65685	-0.09390	-0.12018	-0.03764	-0.20351	MAPK1_B	0.61025	0.70908	0.78395	0.78877	1.01118	0.95730	0.84755	1.02843
KHK_B	1.02381	0.79259	0.87302	0.58662	0.49675	0.56304	0.44508	0.27444	MAPK10_A	1.27145	1.22811	1.27584	1.17817	1.32688	1.34133	0.65311	1.11225
KIAA1446_A	0.07683	0.05951	0.64620	0.61547	0.41973	0.53914	0.40777	0.17590	MAPK10_B	1.23430	0.99668	1.00931	0.74406	1.02890	0.98809	0.81955	0.86774
KIAA1446_B	0.43110	0.26847	0.21641	0.23440	0.88073	0.87000	0.42139	0.20078	MAPK11_A	-2.58749	-2.35856	-2.50905	-2.68682	-1.74276	-1.62432	-1.31228	-1.36708
KIAA1804_A	-0.21502	-0.30055	-1.40093	-0.94313	-0.75614	-0.71297	0.16698	0.12176	MAPK11_B	1.16502	1.07388	0.92583	0.79121	1.11382	0.86521	0.87364	0.79046
KIAA1804_B	0.43319	0.11968	0.99453	0.82521	0.82100	0.70416	0.34461	0.73513	MAPK12_A	-2.07072	-1.98540	-3.67337	-3.74326	-2.33911	-2.38534	-3.75546	-3.87022
KIDINS220_A	1.26632	1.29660	1.03589	1.01611	1.32934	1.26094	1.06623	1.10050	MAPK12_B	0.80798	0.87143	0.88580	0.93917	0.40544	0.36202	0.67304	0.65773
KIDINS220_B	0.05368	-0.01663	0.86742	0.79989	0.69800	0.63154	0.83230	0.83914	MAPK13_A	0.09842	0.39594	0.17713	0.15544	-0.47631	-0.61400	-0.05556	-0.16235
KIP2_A	-0.26686	-0.21464	-0.01261	0.09275	0.44175	0.43563	0.37452	0.36609	MAPK13_B	-0.98087	-0.65144	-0.82418	-0.93109	-2.35967	-1.88591	-1.87552	-1.80568
KIP2_B	-0.33546	0.01983	0.41654	0.27253	0.76531	0.98253	-0.35411	-0.17362	MAPK14_A	-0.07772	-0.01823	-0.26596	-0.21193	0.45325	0.32594	0.35371	0.33716
KIS_A	0.38677	0.15734	0.44314	0.41022	0.57421	0.89861	0.50802	0.53134	MAPK14_B	0.38155	0.25341	-0.48035	-0.77248	0.12347	0.04122	-0.37174	-0.27703
KIS_B	0.38494	0.44136	0.28333	0.05926	-0.24318	-0.21683	0.82165	0.61649	MAPK3_A	0.63806	1.38771	0.47870	0.38815	0.96299	0.81017	0.72372	0.07640
KIT_A	0.40113																

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells (cont)

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b	siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b
MK-STYX_A	-1.99800	-1.77542	-1.49910	-1.65761	-2.00015	-2.18751	-3.07840	-3.24853	PDK4_A	0.52254	0.35894	0.59625	0.48560	0.72009	0.85094	0.77117	0.82724
MK-STYX_B	0.48836	0.34927	0.71070	0.69265	0.63973	0.57842	0.27684	0.18180	PDK4_B	-0.82230	-1.00310	-1.88738	-2.02252	-2.43935	-1.99084	-1.59045	-1.61757
MOS_A	0.80442	0.75642	0.27002	0.68821	1.17162	1.01763	0.52603	0.71734	PDPK1_A	-2.29275	-2.15094	-0.97090	-1.04647	-1.40497	-1.41934	-1.16444	-1.11799
MOS_B	0.64238	0.71302	0.50609	0.59478	0.22451	0.19125	0.06470	0.09374	PDPK1_B	0.77997	0.78592	0.49914	0.64650	0.87052	0.95248	0.51915	0.49334
MST1R_A	0.38672	0.57387	0.43570	0.51411	0.42454	0.36852	0.55646	0.64907	PDXK_A	-1.85474	-1.57099	-1.18284	-1.01921	-1.30343	-0.49751	0.15040	0.47483
MST1R_B	0.77896	0.79670	0.12730	0.26764	0.52858	0.48895	0.26903	0.20857	PDXK_B	-0.26327	-0.04093	-0.36070	-0.27273	-0.89115	-0.90241	0.10358	0.15641
MST4_A	0.66812	0.65692	0.29676	0.26472	-0.11847	-0.01670	0.16089	0.17828	PFKFB2_A	-0.37539	-0.06082	0.35351	0.21441	-1.18233	-0.94289	0.30901	0.02289
MST4_B	1.12524	0.92195	0.71491	0.54630	1.08346	0.95162	0.31514	0.37307	PFKFB2_B	-0.89620	-0.89364	-1.86517	-2.02101	-0.28830	-0.37245	-0.07269	-0.07187
MVK_A	0.20485	-0.08932	0.73613	0.38279	0.38384	0.37517	0.74981	0.91496	PFKFB3_A	0.55213	0.61938	0.38883	0.26896	0.66910	0.76281	0.98118	0.99585
MVK_B	0.03973	-0.09349	-1.44367	-1.48763	-0.94742	-1.05737	-1.15957	-0.94962	PFKFB3_B	1.07010	1.29878	0.72165	0.76505	0.57689	0.67175	1.02414	0.90052
MYLK_A	1.20698	1.03037	0.83954	0.97553	0.47357	0.58927	0.79343	0.65149	PFKM_A	-0.30489	-0.73612	-1.73579	-1.21220	-0.89722	-0.63003	0.38323	0.44014
MYLK_B	-0.14395	-0.19680	-0.18955	0.08971	0.54107	-0.43339	0.32342	0.25081	PFKM_B	-0.27431	-0.47433	-0.07945	0.04055	0.79143	0.91161	-0.39048	-0.71122
MYLK2_A	0.26869	0.45395	0.74070	0.69144	0.18346	0.22510	0.01769	0.05779	PFTK1_A	0.15925	0.32938	-0.09588	0.13063	0.19639	0.15500	0.38323	0.44014
MYLK2_B	1.20537	1.19050	0.32433	0.46939	1.01675	1.03129	0.71071	0.96295	PFTK1_B	-0.28018	-0.26156	-0.50471	-0.68288	-1.17451	-1.04744	-0.71399	-0.92742
NAGK_A	-1.01219	-0.80073	-0.76518	-0.69842	-1.28082	-1.26410	-1.13732	-1.12305	PGK1_A	0.22179	-0.05319	-0.28978	-0.25888	-0.31497	-0.29968	-1.62060	-1.58832
NAGK_B	-0.42344	-0.54874	-1.75544	-2.09107	-0.64760	-0.72621	-0.74581	-0.86774	PGK1_B	0.98981	0.85003	0.88879	0.65609	1.18845	1.06217	0.86183	0.72643
NEK1_A	-0.12852	-0.77497	0.20228	0.16861	-0.74345	-0.69997	0.09859	-0.12114	PHKA1_A	-0.36426	-0.34422	0.40239	0.62370	-0.02618	-0.08903	0.53164	0.43950
NEK1_B	0.88067	0.86873	0.74848	0.71858	0.48388	0.72558	0.77282	0.42925	PHKA1_B	-1.39401	-1.44473	-0.78993	-0.73350	-1.41431	-1.24786	-1.04401	-0.43178
NEK11_A	0.73818	0.68965	0.92063	0.88513	0.73805	0.83604	0.24892	0.16951	PHKA2_A	-1.51034	-1.38948	-0.30333	-0.37420	-0.66394	-0.79578	-0.00109	0.00446
NEK11_B	-1.37543	-1.76535	-0.43266	-0.51904	-1.26331	-1.24479	-0.19274	-0.48552	PHKA2_B	-2.48232	-2.41487	-2.77780	-3.41309	-1.45387	-1.67410	-1.88883	-1.03194
NEK2_A	0.42730	0.52448	0.06662	0.15115	0.35448	0.48397	0.59417	0.89597	PHKB_A	0.22610	0.34587	-0.38212	-0.26076	0.06558	0.06611	-0.57755	-1.25338
NEK2_B	0.55331	0.81411	0.45572	0.64933	0.09657	0.37921	0.94325	0.94142	PHKB_B	0.66594	0.61746	0.73422	0.60324	0.11391	0.02638	0.21133	0.71505
NEK3_A	-2.39169	-2.55468	-4.37074	-3.34780	-2.10575	-2.24684	-4.22688	-4.19102	PHKG1_A	-0.80934	-0.57327	-0.31928	-0.13909	0.86975	1.06063	0.32232	0.31850
NEK3_B	1.35025	1.38241	1.15302	1.08194	1.54483	1.40773	1.08496	1.19881	PIK3AP1_A	0.95543	0.94226	0.34360	0.45306	0.67732	0.75805	0.75928	0.90309
NEK4_A	-0.00564	-0.15293	0.15682	-0.08874	-1.51982	-1.46300	-0.91002	-0.58833	PIK3AP1_B	0.30399	0.23629	0.98399	0.95661	0.18870	0.39658	0.63380	0.47896
NEK4_B	1.12036	1.23984	1.14172	1.04244	1.65663	1.28027	0.89386	0.92755	PIK3C2A_A	0.74635	0.71309	0.34779	0.45188	-0.18946	-0.00502	0.33404	0.17032
NEK6_A	0.68959	0.71321	0.14529	0.16207	0.35687	0.27699	0.82444	0.67915	PIK3C2A_B	0.94086	0.67297	0.69820	0.65472	1.02893	0.87867	1.00232	0.90652
NEK6_B	0.86762	0.89118	0.33392	0.00942	0.50016	0.54989	0.70473	0.51625	PIK3C2B_A	-0.03282	-0.07749	0.50850	0.48247	0.92378	0.50084	0.90734	0.94536
NEK7_A	0.47069	0.50814	0.27995	-0.26886	0.57981	0.57769	0.99144	0.74937	PIK3C2B_B	-0.66647	-0.57092	-2.14523	-2.04440	0.36449	0.16008	-0.28974	-0.29568
NEK7_B	-0.74512	-0.78651	-0.17446	-0.30459	-1.19486	-1.23911	-0.20811	-0.59478	PIK4I1_A	-0.55828	-0.45008	0.27394	0.39866	0.41782	0.55092	0.23232	0.13639
NEK8_A	-0.59580	-0.34683	-0.05951	0.16890	0.47153	0.66030	-0.60825	-0.60041	PIK3AP1_B	-2.53960	-2.52615	-2.48296	-2.29178	-2.11575	-2.17769	-1.60296	-1.78094
NEK8_B	-1.45044	-1.65461	-1.45179	-1.47188	0.71937	0.70803	0.42559	0.37454	PIK3C2A_A	-0.20027	-0.51305	0.26391	0.04511	0.44423	0.40323	-0.41593	-0.43473
NEK9_A	-3.22990	-1.49934	-4.11148	-3.47465	-2.09111	-2.96414	-2.19894	-2.28717	PIK3C2A_B	0.98671	0.95952	0.52937	0.62756	0.56027	0.55796	0.41511	0.25635
NEK9_B	0.39757	0.41995	0.46121	0.44637	0.52522	0.55003	0.60564	0.83801	PIK3C2B_A	1.39658	1.34876	1.01681	1.16086	1.33275	1.25245	1.22336	0.99494
NIPA_A	0.29438	0.11821	0.16983	0.34387	0.52854	0.59796	-0.48275	-0.56345	PIK3C2B_B	-0.65006	-0.76675	0.31736	0.17907	-0.58024	-0.31359	-0.41474	-0.37026
NIPA_B	-2.14184	-1.11239	-0.49030	-0.55168	-1.20557	-1.12797	-0.39367	-0.42486	PIK3C2G_A	1.38927	1.45641	1.10572	1.16946	1.05886	1.30739	0.98467	1.02758
NJMU-R1_A	-0.94903	-0.95529	-1.64932	-1.57249	0.06205	-0.34515	0.35599	0.35496	PIK3C2G_B	1.03721	1.16241	1.04013	1.13535	1.03581	0.87999	0.44821	0.50505
NJMU-R1_B	1.09716	0.92075	0.08736	-1.53207	0.51877	0.20614	0.39855	0.33817	PIK3C3_A	1.54994	1.43979	1.08356	1.14052	1.08028	0.99963	0.84048	0.75327
NLK_A	-1.12997	-0.73165	-1.85427	-1.72811	-1.60536	-1.49758	-2.54539	-3.05968	PIK3C3_B	1.05507	1.11750	0.97506	0.99911	1.14836	1.03845	0.68708	0.61454
NLK_B	-0.40330	-0.55593	0.10815	0.03315	0.22796	0.32384	0.05273	0.00124	PIK3CA_A	1.18601	1.26622	1.10959	1.09173	1.21474	1.21961	0.66823	0.78923
NME1_A	1.22455	1.21293	0.90695	0.97682	0.80655	0.71784	0.61665	0.74566	PIK3CA_B	0.65586	0.58343	0.71412	0.58502	0.54484	0.53147	0.41859	0.75035
NME1_B	-0.02923	0.15300	0.25169	0.26523	1.01845	0.96266	-0.49133	-0.47913	PIK3CB_A	1.51028	1.30629	1.03428	1.09778	1.33441	1.32712	1.05718	1.29271
NME2_A	-1.32082	-1.29836	-0.63998	-0.27357	0.86747	0.56720	-0.79449	0.82538	PIK3CB_B	1.34620	1.27428	0.86553	0.69716	0.65318	0.54798	0.63939	0.68570
NME2_B	-0.32131	-0.40655	-0.01533	0.10048	-0.13426	-0.45069	0.27272	0.37663	PIK3CD_A	1.49758	1.29115	1.13207	1.07063	1.00561	1.05436	1.13568	0.93361
NME3_A	-3.89748	-3.19996	-2.39187	-2.56734	-2.54342	-2.55492	-1.14684	-1.25904	PIK3CD_B	-0.99022	-0.72720	-1.36323	-1.83807	-1.63944	-1.60687	-0.54482	-0.52232
NME3_B	0.26454	0.62922	0.32627	0.26608	0.54504	0.31980	0.01199	-0.02621	PIK3CG_A	1.32667	1.61608	0.95861	1.07825	1.40164	1.47879	1.24249	1.38076
NME4_A	0.78298	0.89901	1.00910	0.82308	0.79449	0.61830	0.05635	0.26052	PIK3CG_B	1.02528	0.91705	0.59216	0.63744	0.93232	0.88273	0.90271	1.05772
NME4_B	-1.02482	-0.99324	0.77419	0.57265	1.18834	0.06171	0.10027	0.09524	PIK3R1_A	1.42915	1.34474	1.11452	1.08327	1.44306	1.44022	1.11024	1.20913
NME5_A	0.31120	-0.38593	0.50486	0.35399	-0.56858	-0.60002	0.35909	0.23449	PIK3R1_B	-1.83246	-1.92829	-1.02259	-0.68962	-1.52669	-1.61130	-1.14159	-1.23641
NME5_B	-0.24664	-0.36382	0.50519	0.27183	0.30962	0.07600	0.39930	0.28911	PIK3R2_A	1.25805	1.38812	1.09013	1.15997	1.32728	1.30685	1.05444	0.98988
NME6_A	-1.83506	-1.68784	-1.37296	-0.82663	-0.90444	-0.80916	-0.32448	-0.96750	PIK3R2_B	-0.56689	-0.60613	0.29872	0.19578	0.22992	0.30014	-0.31922	-0.24408
NME6_B	0.93334	1.08951	0.84433	0.99951	0.97553	0.93131	0.82190	0.80565	PIK3R3_A	1.44421	1.31835	0.74205	1.04968	1.11889	1.29305	0.98897	1.08223
NME7_A	-1.96014	-1.85721	-2.04045	-2.09747	-1.07643	-0.87914	-1.07929	-0.89482	PIK3R3_B	0.47925	0.35495	0.06583	0.28390	0.41410	0.40055	-0.63407	-0.80937
NME7_B	0.16701	0.15747	0.37913	0.42055	0.85810	0.61684	0.42413	0.33852	PIK3R4_A	0.43137	0.55178	-0.01176	0.16837	-0.26071	-0.05076	0.14418	0.14785
NRBP_A	0.61086	0.41315	-0.36080	-0.13329	0.41029	0.40589	0.57590	0.43635	PIK3R4_B	-0.88898	-1.08080	-0.20291	0.00506	-0.44119	-0.74053	-1.46685	-1.45426
NRBP_B	-0.34102	-0.57923	-1.71538	-1.77167	-1.33533	-1.42635	-0.76652	-0.83964	PIK4C1_A	0.10647	1.18803	-1.02382	0.80041	0.92325	0.90360	0.77919	0.67641
NRGN_A	-1.38570	-1.35481	-2.17243														

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells (cont)

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b	siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b
PRKAB1_A	0.51283	0.51348	-1.81940	-1.95920	-0.57717	-0.36568	-0.16123	-0.29014	ROR2_A	-1.32935	-1.47466	-0.03018	0.21033	0.07050	0.23280	0.50693	0.46005
PRKAB1_B	-1.12395	-1.06100	-1.64826	-1.55789	-1.53363	-1.39971	-1.32731	-1.48331	ROR2_B	-1.60932	-1.67689	-0.93919	-0.91986	-0.83962	-0.70747	-0.33329	-0.43859
PRKAB2_A	-0.08419	0.41056	0.18436	0.18570	-0.74504	-0.45279	-0.18954	-0.03600	ROS1_A	0.92386	0.92332	1.04168	1.13468	1.07890	0.97321	0.84865	1.14176
PRKAB2_B	1.45229	1.59555	1.06600	1.16265	0.86641	1.10278	1.05112	1.15145	ROS1_B	1.21339	1.17531	0.86962	0.99457	0.56036	0.37554	0.86162	0.94849
PRKACA_A	0.54492	0.54305	0.70761	0.71311	0.50422	0.58411	0.71257	0.56501	RPS6KA1_A	0.59748	0.71468	0.31531	0.61122	1.26640	1.18922	0.91731	1.15698
PRKACA_B	0.26764	0.08718	-0.48162	-0.49956	-0.78249	-0.89128	-0.23231	-0.59136	RPS6KA1_B	-0.32396	-0.02907	0.05853	0.08149	-0.04774	-0.23944	-0.09422	0.00479
PRKACB_A	-0.10557	-0.29482	-0.84389	-0.87859	-1.11157	-1.04675	-0.15629	-0.42549	RPS6KA2_A	0.59414	0.59698	-0.44583	-0.21803	0.24503	0.45795	0.66843	0.75000
PRKACB_B	-0.26625	-0.44398	-0.09198	-0.07433	-0.101303	-0.10870	-0.29073	-0.22521	RPS6KA2_B	0.21317	0.06577	0.57718	0.65314	0.40708	0.62340	0.03908	0.17001
PRKACG_A	-0.40842	-0.31388	-1.10810	-1.17854	-0.18569	-0.22993	-0.17278	-0.30662	RPS6KA3_A	0.49373	0.46529	0.94415	0.96135	0.67906	0.71863	0.49003	0.53557
PRKACG_B	-0.17752	-0.51529	-0.71778	-0.90824	-0.35502	-0.21804	-0.34914	-0.43554	RPS6KA3_B	0.29863	0.19617	0.46913	0.56835	-0.08853	0.14339	-0.11917	-0.32617
PRKAG1_A	-0.93465	-0.94974	0.11219	0.25613	0.61789	0.61227	0.18508	0.26912	RPS6KA4_A	-0.21092	-0.24700	0.22694	-0.19115	-0.59836	-0.49578	-0.17427	-0.71877
PRKAG1_B	0.32968	0.58858	-0.70688	-0.95170	0.30525	0.33466	0.81719	1.02570	RPS6KA4_B	0.52413	0.14143	0.40818	0.69146	0.48250	0.54187	0.40778	0.43761
PRKAG2_A	0.74236	0.61338	0.39589	0.62526	0.12535	-0.00304	0.17561	0.05606	RPS6KA5_A	0.06304	0.08719	-0.10997	-0.87197	-1.24576	-1.09141	-0.47753	-0.58128
PRKAG2_B	0.04160	-0.32871	0.69146	0.53999	0.12796	0.06962	0.18023	0.31914	RPS6KA5_B	0.41135	0.50077	0.56836	0.73706	0.58775	0.45244	0.31226	0.43915
PRKAG3_A	-0.80102	-1.03565	-0.84296	-0.61942	-1.77397	-1.56212	-0.99594	-1.01012	RPS6KA6_A	-0.18420	-0.20233	-0.41821	-0.37017	-1.59453	-1.47364	-1.01929	-1.05249
PRKAG3_B	0.27609	0.14403	-0.77409	-0.54157	-1.31899	-1.11646	-0.42599	-0.50494	RPS6KA6_B	1.22298	1.05722	0.99285	0.98067	0.57524	0.46773	0.26189	0.32408
PRKAR1A_A	0.58690	0.29201	-0.16265	-0.14310	-0.65898	-0.51973	0.15082	0.23594	RPS6KB2_A	-1.27733	-0.97371	0.20973	0.12673	-0.35421	-0.09144	-0.80190	-0.86303
PRKAR1A_B	1.39894	1.13006	0.80560	0.87054	0.67743	0.73856	0.86505	0.83760	RPS6KB2_B	-1.02058	-0.90471	-1.46084	-1.03190	-1.46253	-1.42147	-0.71410	-1.00603
PRKAR2A_A	1.05623	1.08477	1.26317	1.06759	1.43448	1.34929	1.20367	1.11956	RPS6K1_A	0.78378	0.99163	0.87742	1.00741	0.36603	0.68761	0.30347	0.66709
PRKAR2A_B	-1.90247	-2.22404	-1.86355	-1.92566	-1.07419	-1.17078	-1.15984	-1.72028	RPS6K1_B	-0.94969	-0.91056	-2.30611	-2.14083	-1.58221	-1.50204	-0.44665	-0.74099
PRKAR2B_A	0.69508	0.59151	-0.08833	0.05987	-0.94644	-0.98294	-0.72738	-0.72059	RPS6K1_L_B	-2.71717	-2.71971	-0.49063	-0.46766	-0.55892	-0.46534	-0.78168	-0.97110
PRKAR2B_B	-0.93534	-0.99369	-0.53163	-0.93819	-0.38199	-0.43883	0.83992	0.89521	RPS6K1_B	-1.72040	-1.69327	-2.12139	-1.76906	-4.46118	-4.21207	-3.76879	-3.23123
PRKCA_A	-0.17346	-0.57366	-1.15085	-0.60819	-1.25296	-1.29719	-0.84220	-0.78962	RYK_A	0.38192	0.24948	0.90164	0.85428	0.80604	0.72666	0.82609	0.95604
PRKCA_B	-2.68409	-2.70458	-4.59873	-4.63488	-3.38698	-3.43753	-0.40543	-1.13332	RYK_B	-1.05434	-0.89957	-0.80960	-1.11443	-0.10782	-0.84164	-1.39092	-1.30130
PRKCABP_A	1.15783	1.20812	1.01794	1.22567	1.06387	1.06723	0.81658	0.95969	SGK_A	-0.01640	0.08654	0.33949	0.46081	-0.41265	-0.25455	-0.69123	-0.82880
PRKCABP_B	-0.19253	-0.00072	-0.21026	-0.43128	-0.21683	-0.27999	-1.22724	-1.17385	SGK_B	0.74767	0.68693	0.56357	0.74203	-0.44766	-0.27145	-0.25705	0.50569
PRKCB1_A	0.02519	0.14401	-0.03815	0.10856	-0.18001	-0.14762	0.35774	0.26045	SGK2_A	-1.70517	-1.45685	0.69051	0.71967	-0.50595	-0.29826	-0.40920	-0.23469
PRKCB1_B	0.62818	0.53298	1.12748	1.04211	1.22877	1.42362	1.05709	1.12797	SGK2_B	-0.47623	-0.34481	-0.11172	-0.05359	-1.26264	-0.90525	-1.39552	-1.15602
PRKCBP1_A	0.93611	0.86928	0.63031	0.64623	0.99492	0.88595	0.17145	1.09799	SGKL_A	0.22255	0.44054	0.77201	0.86209	0.74848	0.76861	0.68076	0.62768
PRKCBP1_B	0.17024	0.66873	0.66317	0.71958	0.98864	0.85040	0.41146	0.62909	SGKL_B	0.86287	1.11127	0.87110	0.96959	0.81868	0.97455	0.77863	0.71612
PRKCD_A	0.39689	0.48747	0.01256	0.19200	-0.04155	0.03935	-0.56569	-0.70503	SH3KBP1_A	0.96839	1.00681	0.71209	0.97144	0.81287	0.55325	0.67475	0.46067
PRKCD_B	-0.38318	-0.13782	-1.85033	-1.35945	-0.73218	-0.29181	0.30640	0.25318	SH3KBP1_B	0.74836	0.83444	0.88936	0.71505	1.25245	1.21946	0.91643	0.80778
PRKDCBP_A	-0.33663	-0.01621	-0.53842	-0.81366	-0.69671	-0.76890	-0.37519	-0.52979	SKP2_A	-1.94658	-2.16800	0.05713	0.29477	0.07551	0.06764	0.10118	0.21188
PRKDCBP_B	0.14175	0.29636	0.03633	-0.05734	0.43868	0.54205	-0.20820	-0.06237	SKP2_B	0.53961	0.76101	0.02170	0.19128	0.39456	0.39222	-0.32241	-0.18413
PRKCE_A	0.91760	0.74858	0.85922	0.70405	0.32641	0.38128	0.56899	0.44446	SLK_A	0.74542	0.61138	0.51951	0.23789	0.86745	0.69508	0.40947	0.40800
PRKCE_B	0.71293	-1.50397	-0.89519	-0.91760	-0.64684	-0.71832	-0.19262	-0.21818	SLK_B	-0.91328	-0.86634	-3.66640	-3.62982	-2.46937	-2.57620	-2.23739	-2.26540
PRKCH_A	-0.70291	0.37533	0.53797	0.62835	-0.04507	-0.06656	-0.14569	-0.12306	SMG1_A	0.23162	0.22652	0.18892	0.03362	-0.03409	-0.04347	-0.03987	0.12250
PRKCH_B	-0.36642	-0.29705	0.90453	0.81117	-0.06015	0.06825	-0.17070	-0.13863	SMG1_B	0.99915	0.90117	0.61426	0.39078	1.06518	1.16464	0.74244	0.83348
PRKCI_A	1.47207	1.23830	1.10454	1.00336	0.92920	1.13936	1.07953	1.06694	SNARK_A	0.47164	0.37174	0.89179	1.20473	0.31444	0.37253	0.69899	0.57625
PRKCI_B	-0.60420	-0.16786	-0.09816	-0.06836	-0.57000	-0.22220	-0.67798	-0.74247	SNARK_B	0.61448	0.71599	0.54061	0.85062	0.45144	0.52648	0.51756	0.61241
PRKCL1_A	-0.62484	-0.42377	-2.67579	-2.61435	-1.55672	-1.74940	-1.48516	-1.34042	SNF1LK_A	-1.43810	-1.76340	-0.78159	-0.77293	-1.67178	-1.62214	-1.37561	-1.74049
PRKCL1_B	-1.06079	-0.56383	-2.67524	-2.48017	-2.65126	-2.56552	-1.24224	-1.33888	SNF1LK_B	0.42124	0.67637	0.47517	0.63587	0.49807	0.54820	0.22247	0.13879
PRKCL2_A	1.26605	1.23103	1.08218	1.11305	0.87076	0.98879	0.93938	0.91250	SNF1LK2_A	0.98484	0.97727	1.05583	0.92753	0.68991	0.41879	0.72623	0.86901
PRKCL2_B	-0.76085	-0.66835	-0.46723	-0.27443	-0.79341	-0.69958	-0.17355	-0.02534	SNF1LK2_B	1.07738	0.96287	1.01489	1.04989	0.91250	0.78449	0.72824	1.11754
PRKCN_A	0.30619	0.47106	-0.11509	-0.32610	0.09974	0.17355	0.98951	0.89401	SNRK_A	0.01753	-0.05729	0.20139	0.31834	-0.42752	-0.46154	0.05656	-0.04763
PRKCN_B	-1.51825	-1.44994	0.08523	0.06956	-1.18698	-1.14362	-0.17878	-0.12867	SNRK_B	0.78807	0.60533	0.51976	0.65732	0.22406	0.22098	0.13845	0.29732
PRKCQ_A	0.78557	0.83265	0.85572	0.72705	0.92932	1.01098	1.00273	1.10484	SPEC2_A	0.05135	-0.03875	0.07706	-0.11121	-0.97631	-0.75768	-0.36697	-0.07892
PRKCQ_B	0.19094	-0.36682	-1.55553	-1.66238	-1.05679	-0.90371	-1.31618	-1.42120	SPEC2_B	-0.02268	0.20093	-0.53598	-0.13419	-1.06925	-0.96388	-0.43034	-0.36257
PRKCZ_A	0.34518	0.13164	0.92219	0.74398	0.83400	1.00583	0.85586	0.80193	SPHK1_A	0.22684	0.33446	0.20041	-0.05802	-0.07344	0.02728	-0.36088	-0.48985
PRKCZ_B	1.06027	1.07260	0.99597	1.06224	0.96378	1.19545	0.97871	0.98288	SPHK1_B	-1.33993	-0.82808	0.15425	0.30492	-0.28293	-0.40703	-0.68758	-0.72368
PRKD2_A	-1.05545	-1.10774	-1.60732	-1.37328	-1.57299	-1.59294	-0.07458	0.17158	SPHK2_A	-1.08001	-0.83378	-0.47000	-0.46024	0.22867	0.13262	-0.93576	-0.64722
PRKD2_B	0.53986	0.42329	0.51758	0.73872	-0.30628	-0.01261	-0.37305	-0.21301	SPHK2_B	0.70805	0.85292	0.45531	0.42373	0.43905	0.28389	0.74289	0.63257
PRKDC_A	0.55064	0.57082	0.87784	0.90475	0.95802	0.96804	0.69775	0.53177	SRC_A	0.92437	1.03174	1.03306	1.11121	0.98677	1.07271	0.67376	0.75350
PRKDC_B	-0.23935	-0.08692	-0.40893	-0.61027	0.39754	0.24541	-0.00370	-0.56886	SRC_B	0.19238	0.09931	0.36831	0.42364	-0.57654	-0.58069	-0.09868	-0.02947
PRKG2_A	1.02782	1.10607	0.32353	0.44764	0.40527	0.65602	0.65922	0.73592	SRPK1_A	-1.36746	-1.25320	0.54767	0.41430	0.64719	0.64937	0.36151	0.18782
PRKG2_B	1.05335	1.29244	0.88890	1.04088	0.71344	0.83271	0.55719	0.68076	SRPK1_B	0.39781	0.63072	-0.72129	-0.89702	0.19494	0.26770	0.36596	0.36704
PRKRA_A	1.30475	1.															

Additional File 2: Z-score values for kinase siRNA library screen of Ewing's sarcoma cells (cont)

siRNA	TC-32_a	TC-32_b	TC-71_a	TC-71_b	SK-ES-1_a	SK-ES-1_b	RD-ES_a	RD-ES_b
TBK1_A	-0.38917	-0.37902	0.72730	0.79508	-0.70343	-0.58038	0.16441	0.15303
TBK1_B	0.72731	0.88761	0.99230	1.11196	1.17098	1.18047	1.04720	0.89210
TEC_A	0.60531	0.70916	0.50766	0.78818	0.80114	0.93412	0.58075	0.73027
TEC_B	0.07848	-0.01292	-0.56495	-0.63293	0.43622	0.68843	0.50105	0.58876
TEK_A	1.03892	1.14032	1.09116	1.00605	1.19961	1.23048	1.03514	1.20181
TEK_B	1.11671	0.45095	0.95532	0.67979	0.75848	0.88764	0.54064	0.51901
TESK1_A	1.36376	1.48123	1.17500	1.07476	1.42639	1.30893	0.84996	0.93785
TESK1_B	0.29520	0.37667	-0.21080	-0.21476	0.46010	0.21993	-0.01575	-0.01112
TESK2_A	1.23806	0.79946	0.88601	1.02259	0.91594	0.75897	0.80110	0.69458
TESK2_B	-1.04812	-1.26237	0.01158	0.00294	-1.16185	-1.10944	-0.82450	-0.73271
TGFBR1_A	1.26753	1.41133	1.33468	0.79157	1.58073	1.44541	1.24785	1.31335
TGFBR1_B	0.38295	0.53091	0.06202	0.08500	1.06986	0.93996	0.78677	0.71417
TGFBR2_A	1.44904	1.41578	1.15817	1.09973	1.32192	1.29946	1.10243	1.18306
TGFBR2_B	-1.40712	-0.91559	-1.79059	-2.85801	-1.68037	-1.97780	-2.45560	-2.18375
TK1_A	0.65995	0.83036	-0.06946	0.25267	0.62814	0.65739	0.47960	0.63097
TK1_B	-2.61750	-1.63656	-0.59023	-0.37114	-1.91392	-1.77207	-2.79068	-2.79438
TK2_A	-3.73204	-3.31600	-1.07047	-1.22204	-1.76741	-2.19718	-0.70923	-0.35839
TK2_B	-0.37063	-0.23426	-1.65454	-1.39653	0.23526	0.24206	0.26374	0.28924
TLK1_A	0.72665	0.74381	0.06271	-0.13400	0.10849	0.46341	0.36114	0.23402
TLK1_B	0.84296	0.86166	0.13589	-0.01513	0.23614	0.23545	-0.05582	-0.03095
TNIK_A	0.78239	0.64295	0.33300	0.27542	0.43669	0.41707	0.48063	0.54384
TNIK_B	-0.04980	-0.02722	-1.77583	-2.17841	-1.57213	-1.47000	-1.11717	-1.21588
TNK1_A	-0.31541	-0.22667	0.43332	0.39894	-0.17370	0.04429	0.37559	0.50176
TNK1_B	-0.97217	-1.08471	-1.19302	-1.14548	-2.23816	-1.85695	-1.15551	-1.13821
TNK2_A	-2.44889	-2.55809	-1.80730	-1.64313	-2.26008	-2.17356	-2.05721	-2.02896
TNK2_B	-1.50292	-1.78361	-2.12661	-1.98065	-1.52617	-1.50663	-1.89872	-2.54192
TNNI3K_A	0.75738	1.08991	1.23495	1.36891	0.90882	1.00995	0.77436	0.67682
TNNI3K_B	-1.72508	-1.66169	-0.10174	-0.64054	-0.46710	-0.26771	0.05086	0.07822
TPK1_A	-0.03321	-0.27614	-0.59675	-0.58554	-0.94786	-1.26754	-0.44637	-0.39649
TPK1_B	-0.03123	-0.04296	-0.39272	-0.35328	0.34351	-0.13587	-0.01319	-0.17248
TRAD_A	1.02416	1.09977	0.62086	0.73282	0.45478	0.52392	0.34631	0.16073
TRAD_B	0.86299	0.78642	1.05353	1.09825	0.34057	0.41807	0.44918	0.55354
TSKS_A	-0.68314	-0.79367	-2.42791	-1.12529	-1.51606	-1.58299	-1.48336	-1.48175
TSKS_B	-0.13159	-0.15846	-0.05992	-0.09114	0.04731	0.15825	0.10588	0.21225
TTBK1_A	0.96648	1.03264	0.54592	0.78584	0.61255	0.64349	0.91713	0.69448
TTBK1_B	0.67206	0.73362	0.82626	0.98367	0.64809	0.73551	0.76318	0.70024
TTBK2_A	-0.57411	-0.26567	0.52358	0.48025	0.87961	0.79130	0.60381	0.52000
TTBK2_B	0.88310	1.03686	0.81566	0.84413	0.20269	0.00654	0.30223	0.30400
TTK_A	-0.24602	0.07578	-0.12884	-0.24941	-0.56782	-0.41384	0.09244	0.21054
TTK_B	1.26094	1.31798	1.17475	1.10223	1.38859	1.43626	1.21221	1.44752
TYK2_A	0.85958	0.84526	0.46329	0.54037	0.38352	0.44316	0.69832	0.50437
TYK2_B	0.76552	0.56727	-0.06234	-0.06403	0.24806	0.12562	0.08330	0.14753
TYRO3_A	-0.95042	-0.87209	-1.76768	-1.68097	-1.44958	-1.20369	-1.70159	-1.75167
TYRO3_B	0.47898	0.53677	0.55032	0.35887	0.49270	0.71848	-0.28198	-0.44094
UCK1_A	-1.44152	-1.21318	-1.19733	-1.14125	-1.31263	-1.44440	-0.71204	-0.96027
UCK1_B	-1.85893	-1.57671	-1.34059	-1.73710	-1.20544	-1.43812	-1.88856	-2.13579
UGP2_A	1.18066	1.31497	0.91231	0.70900	0.97678	1.06256	0.85794	0.73861
UGP2_B	0.34071	0.18675	-0.16101	-0.27995	-0.16552	0.04602	-0.00421	0.04433
ULK1_A	0.02642	-0.00329	-0.45458	-0.61250	-2.05145	-2.03096	-0.67577	-0.64991
ULK1_B	0.00946	-0.04053	1.15045	1.28431	0.31886	0.41880	0.16674	0.35751
ULK2_A	0.10851	-0.14602	-0.68339	-0.61043	-1.54581	-1.62524	-0.81032	-0.97249
ULK2_B	-1.32086	-1.04877	-0.33240	-0.26238	-0.26604	0.13201	0.15211	0.18735
UMP-CMP_A	-0.51721	-0.29135	0.20966	0.31712	-0.03139	-0.11836	0.46861	0.45104
UMP-CMP_B	-0.17662	-0.07479	0.21383	0.41226	-0.98839	-1.04957	-0.58945	-0.39414
UMPK_A	1.22295	1.22386	0.91841	1.16854	1.27551	1.32474	1.03861	1.15583
UMPK_B	-0.88720	-0.75017	-0.36683	-0.19886	-1.21660	-1.28749	-1.11050	-1.19310
URKL1_A	-0.70301	-0.53523	0.09497	0.06383	-1.51675	-1.61817	-0.49611	-0.53967
URKL1_B	0.78264	0.78569	0.65268	0.57310	0.11743	0.23722	0.34981	0.38755
VRK1_A	1.27797	1.26348	0.64938	0.26682	0.51507	1.12572	0.59997	0.66362
VRK1_B	1.47578	1.55928	1.00136	1.00394	0.81961	0.59557	0.97161	0.99177
VRK2_A	1.07123	0.73354	0.28500	0.21308	0.49483	0.43402	0.41770	0.42639
VRK2_B	1.17138	1.13272	0.73209	0.61990	0.45504	0.72079	0.87989	0.79574
VRK3_A	-0.62447	-0.46915	-0.71277	-0.80662	-0.51506	-0.59435	-0.77920	-0.99130
VRK3_B	0.42274	0.57037	-1.09015	-0.94686	0.54787	0.49974	0.05643	-0.20490
WNK1_A	1.50862	1.23819	1.09125	1.18413	1.32629	1.33563	1.27068	1.09278
WNK1_B	0.34106	-0.00237	0.21094	0.18993	0.77942	0.63167	1.19306	0.96318
WNK3_A	0.90576	0.82852	0.57351	0.48872	1.10336	1.07008	0.64885	0.63672
WNK3_B	0.77653	0.71518	0.79130	0.80358	0.96950	0.83212	0.33590	0.25951
WNK4_A	-0.12310	-0.27231	-0.08358	-0.12139	-0.70540	-0.53908	-0.75417	-0.72373
WNK4_B	-2.05354	-2.30386	0.04115	-0.02268	0.89880	0.97059	0.32768	0.20846
XYLB_A	1.59484	1.38478	0.83475	0.97715	1.29051	1.12568	1.16549	0.99902
XYLB_B	0.55768	0.58559	0.62083	0.45708	0.45825	0.20079	1.12203	1.08883
YES1_A	0.33046	0.29023	0.67904	0.69747	1.01271	0.84129	0.21321	0.27608
YES1_B	-0.84846	-0.84879	0.70788	0.71962	0.41409	0.14251	-0.08586	-0.07541
ZAK_A	0.83247	0.37254	-0.18219	-0.14222	-1.62640	-1.62933	-0.30195	-0.50048
ZAK_B	1.24950	1.27568	0.34021	0.76111	0.63730	0.85090	0.73959	0.55250