

Supplementary Table 1

Master_id_first	PsitelnProtein	diff	FDR
P84098	S189	-1.601285935	5.34E-04
O15318	S157	-1.099746365	1.48E-06
Q9NRR4	S217_S221	-1.084820763	0.05335353
P11388	S1377	-0.906680414	4.94E-04
Q9UHB7	SSPRPTAEK	-0.790739696	0.008201779
Q9UET6	S328	-0.787862448	0.020411503
Q96RK0	S436	-0.725815166	0.03996628
Q9UQ35	S222	-0.647954614	9.28E-04
Q9UGJ0	S71	-0.623054246	1.05E-04
Q12830	S1310	-0.61198994	1.64E-04
O75152	S758	0.600581432	1.08E-04
Q9NW75	S129	0.603346356	0.025396568
O95239	S801	0.608402004	7.23E-04
Q9BW71	S269	0.612583742	0.015086008
P23588	S230	0.617812509	0.002774465
Q2LD37	S4124	0.620432603	0.002919652
Q96RK0	S173	0.621975348	0.00325839
Q07352	S92	0.622425044	0.00170609
P47974	S123	0.625429989	5.13E-04
Q5T3J3	T389	0.626906056	8.35E-04
Q9C0B5	S585	0.630533702	1.62E-05
Q14980	S2047	0.631751766	0.030072138
P50548	T526	0.632349172	6.68E-05
O14686	S2726	0.634112153	0.00316626
Q86SQ0	S212	0.634453806	0.025782168
O43765	S305	0.636390615	7.41E-04
Q14687	S140	0.647659414	0.042091274
P29966	T143_S/T	0.650991426	0.005211092
Q7Z333	S1366	0.654912206	0.002210316
Q9Y618	T1891	0.655328979	5.93E-05
O94854	S578	0.662045104	7.44E-04
Q15691	S155	0.667176558	1.60E-05
Q5TCQ9	S225	0.668281716	0.003311399
Q9UPP1	S1021	0.671320468	0.003214663
P15822	T815	0.677893992	0.032612107
Q9HCH0	S1295	0.678682301	0.017665654
Q9NZJ0	S557	0.680741726	0.001317333
Q9UKA4	S433	0.687767512	0.01083684
Q9Y6Y0	T330	0.688945771	7.36E-06
Q9NPR2	S830	0.690385117	2.79E-05
Q09666	S5110	0.691529262	0.007446374
Q6PKG0	T376	0.693030694	1.05E-05
O43395	T172	0.706961962	9.69E-04
Q8TF72	S285	0.715513557	5.41E-04
Q9UBH6	S676	0.731256273	6.05E-04
A6H8Y1	S100	0.742657482	8.49E-04
Q9UGU5	S197	0.742826356	2.09E-04
P0CAP2	S179	0.744699706	0.04100589
P55196	T1352	0.744821371	1.62E-05
Q9C0A6	RSSQAGDIAAEK	0.747945513	0.011160463
Q86SQ0	KSSISSISGRDDLMDYHR	0.755708695	0.001935992
Q5SW79	S1160_S1165	0.760147348	3.02E-06
Q5VZL5	S1181	0.760613334	0.00649768
P20794	Y159	0.76152212	0.0092259

Q9C0B5	S409	0.764737033	4.32E-06
P15056	S429	0.765237995	2.56E-04
P19634	S703	0.765531499	0.00336638
Q8IY17	S372	0.768346763	0.00172905
P30260	S364	0.77178388	9.03E-04
P51812	S369_S375	0.77284535	7.10E-06
O76039	S407	0.784799619	1.06E-06
Q5T5P2	S474	0.805447723	9.92E-06
Q765P7	S601	0.814822492	1.78E-06
Q6EEV4	LRAPSSR	0.816925808	7.16E-04
P49327	S831	0.830290237	0.01081861
Q07889	S1134	0.831732501	8.35E-05
Q2LD37	S3653	0.844740204	2.72E-05
Q02880	S1466_S1476	0.860430005	0.01247716
Q9Y6J0	T1927	0.865531602	0.00144142
Q14160	T1342_S1348	0.873953214	5.69E-04
P09884	T219	0.88199901	2.99E-07
P10398	T181	0.882434715	2.01E-05
O94804	T952	0.904594386	2.13E-05
Q7L804	S388	0.905983072	1.61E-05
O60934	T497	0.90645826	2.06E-04
O14924	S172	0.907228951	4.45E-04
P47974	S125	0.908337559	8.78E-04
Q14934	S272	0.927758926	0.00124733
O15357	T958	0.92990858	1.88E-05
P78536	S819	0.937365009	0.04174181
Q9BY44	S526	0.94387581	2.47E-04
Q5VT52	S581	0.950257319	2.67E-04
P35658	S430_S433	0.967176553	4.29E-06
O43379	S49	0.978846214	2.35E-05
Q5TKA1	S65	0.987942275	2.09E-04
O75151	S1056_S/T	0.99804248	0.00353474
Q8N5U6	S128	1.001813291	5.35E-07
Q32P44	S156_S	1.022239865	0.01709590
Q9BY84	S501	1.029517509	0.03618943
Q8NG27	S265	1.045478351	9.74E-05
P41162	TESSPGSR	1.056013312	0.00179812
Q9UKJ3	T293	1.060143047	2.70E-07
P53367	T361	1.077303313	9.25E-06
Q8TF72	S1173	1.083112256	5.18E-06
O43295	S858	1.087697647	1.45E-04
Q6ZSZ5	T1345	1.090282824	1.99E-08
Q92609	S558_T/S	1.091240871	6.04E-06
Q6Y7W6	S26_S30	1.110548473	1.99E-08
P23443	T444	1.111601402	9.88E-07
Q9UHI6	S500	1.113680257	1.99E-06
Q9NUL3	S440	1.114938608	6.24E-06
Q6ZRI6	T364	1.118541397	4.77E-07
P78536	T735	1.122244157	6.92E-09
Q8N5C8	S645	1.140803328	5.37E-04
O14974	S507	1.145085025	5.42E-06
Q86SQ0	S415	1.153948522	4.25E-05
Q15418	S363_S369	1.158902881	2.70E-07
Q9HCM7	S487	1.15983313	5.65E-05
Q7RTP6	RKTSQSEEEEAPR	1.160156936	8.13E-06
Q92995	S40	1.171179592	5.40E-05

Q15418	S732	1.174621426	2.06E-04
Q8TF72	S1279	1.1846569	1.08E-04
P30307	T48	1.211040686	2.99E-07
Q9UJY4	S400	1.22029939	9.03E-04
Q14680	T428	1.282646332	5.06E-08
Q8TF72	S816	1.341870967	2.70E-07
Q15418	S380	1.341896167	5.35E-07
P15056	S151	1.355292094	2.00E-07
Q8IWC1	S524	1.362640637	2.70E-07
Q15154	S1283	1.378095071	3.91E-05
P12270	S2155	1.426634142	3.58E-08
Q7Z5J4	T1068	1.433040868	1.88E-07
Q5SW79	S1160	1.495906705	6.04E-08
P17544	T326	1.513289333	6.89E-04
Q8TF72	S403	1.543404534	7.41E-07
Q9UQC2	S543	1.573349361	1.13E-07
P12270	T2116	1.586348409	1.28E-07
P27361	Y204	1.676090111	2.70E-07
P28482	T185	1.695007092	9.67E-08
Q9UJY4	S177	1.816177669	1.62E-05
Q9UDY2	S163	1.88550839	9.88E-07
Q9NZN5	T703	2.151653105	0.00171603
P28482	Y187	2.434053769	5.06E-08
P27361	T202_Y204	2.990318021	1.86E-09
P28482	T185_Y187	3.267982367	1.86E-09