

Supplementary table 3

Master_id_first	PsitelnProtein	diff	FDR
Q14667	T1269	-3.108141116	3.64E-04
Q12986	NYSSPPPCHLSR	-2.817871942	0.005560233
Q8TF76	S147	-2.481805893	4.08E-04
Q6GQQ9	T547	-2.066624751	8.80E-10
Q9ULF5	T540	-2.012049272	1.68E-08
P55196	T566	-1.904127051	6.70E-06
Q96B97	T354	-1.864841922	3.65E-06
P55010	PPENSDSGTGKK	-1.724806875	1.05E-08
Q9Y490	T144	-1.708470042	4.50E-08
Q14008	T569	-1.701629405	6.30E-08
O60716	T916	-1.564088716	3.96E-07
Q96PY5	T467	-1.504990335	2.55E-08
O60716	T177	-1.497759427	1.31E-07
Q9HBI1	T28	-1.449898751	6.70E-06
Q9HAU0	S855_T868	-1.448978882	1.05E-08
Q96PY5	T450	-1.439540452	3.99E-06
Q5VWQ0	S92	-1.401106769	0.005932397
Q9UBT7	S538	-1.388417033	2.33E-08
P55010	T153	-1.37072482	1.68E-08
Q7L4E1	S276	-1.358098142	0.002070713
O15355	S527	-1.320544943	1.05E-08
Q8NHQ8	PFQSGSLKRPGS	-1.299050452	2.26E-08
Q9HAU0	T868	-1.279379983	1.68E-08
Q5HYJ3	S227	-1.247831063	2.98E-06
Q6WCQ1	S269	-1.221617265	4.64E-04
Q8TEH3	T923	-1.203429085	3.19E-05
Q9BYN0	T8	-1.167116736	4.96E-05
Q15058	S272	-1.165446493	9.74E-06
Q86SQ0	T898	-1.160435859	3.96E-07
Q6IQ23	T472	-1.133086137	1.82E-04
Q9NV70	T445	-1.123674943	2.54E-08
Q5T5P2	T1760	-1.120340964	1.85E-05
Q04721	S2093	-1.09596714	1.22E-06
O75146	S1045	-1.094187269	1.09E-05
Q15059	S542	-1.091349078	1.98E-05
Q8IVL1	S1215	-1.0731331	2.03E-05
Q6R327	T1332	-1.041692126	1.05E-05
O75122	S360	-1.033839303	9.18E-06
Q99959	T118	-1.026275863	3.22E-06
Q7Z2Z1	S1045	-0.991101049	0.009564698
Q16181	T426	-0.987232757	3.65E-06
Q9UQC2	T385	-0.98559854	1.40E-05
Q6ZT07	S267	-0.983842651	1.18E-04
Q8IVT5	T425	-0.983087558	2.19E-07
Q9NXV6	S151	-0.971312438	3.96E-07
Q9HAU0	T438	-0.966190493	2.76E-07
P23508	S681	-0.963527723	6.81E-06
Q9BTT6	T474	-0.962871739	2.06E-04
Q92556	S344	-0.958543954	5.66E-08
Q9Y448	T153	-0.958136504	1.49E-05
Q7Z460	S1091	-0.956730721	7.10E-06
Q07157	T589	-0.948760819	3.65E-06
Q15811	S559	-0.946586015	0.001867503
Q96QZ7	S1361_T1365	-0.93753858	0.001590938

Q13435	S883	-0.935934566	6.70E-06
Q9HAU0	S382	-0.93276788	1.82E-04
Q5T5P2	S1084	-0.925159608	4.06E-05
Q99501	T376	-0.924542471	2.52E-04
Q9BQ39	HHYDSDEKSETF	-0.91727353	0.024921716
P84098	S189	-0.907679996	0.033723097
Q96MU7	T148	-0.878887347	0.037829431
Q9UBP0	S268	-0.87864525	3.19E-05
P38432	S271	-0.877882717	2.36E-05
Q12923	T320	-0.875361226	6.47E-05
Q9UHV9	S14	-0.867535695	0.01846624
Q9C0D5	S214	-0.864768775	0.003689508
Q6NSI4	S39	-0.864481975	8.28E-04
Q13177	T134	-0.861904323	1.98E-05
Q6ZVF9	S526	-0.858466865	4.26E-04
Q9Y2I1	S467	-0.853827107	1.98E-05
O60716	T59	-0.851516547	2.50E-06
Q9H0B6	S539	-0.850899358	6.01E-05
Q9UNL2	S105	-0.849638511	7.10E-06
Q9UQB8	T340	-0.841768662	1.98E-05
Q96F86	S161	-0.835192327	0.027103985
Q86VW2	S490	-0.834038972	9.40E-05
Q6UB98	S1143	-0.833942879	1.09E-05
Q13136	T1159	-0.829502195	0.003240581
Q8TEW0	S1312	-0.827854685	0.005932397
Q9P2M7	T34	-0.820859584	7.22E-06
Q7Z4S6	S853	-0.807412946	2.71E-05
O95490	YSSGTQSR	-0.806154668	2.29E-04
P35658	S1023	-0.803412654	0.036413724
P53801	Y174	-0.802538375	0.026440093
Q15181	S250	-0.791148671	0.012922115
Q9Y2J4	S661	-0.788388981	6.70E-06
P35611	S135	-0.784012053	5.13E-05
Q9Y5A9	S394	-0.783342619	8.07E-05
Q07157	T1167	-0.782506262	0.001519252
Q04637	S704	-0.779217567	4.92E-05
Q8NEY1	T942	-0.775370459	8.50E-06
Q8TEW0	S1223	-0.773775296	0.007082264
P35568	S794	-0.773038275	1.40E-05
O14646	S1677_S	-0.770864253	0.001041057
Q5SYE7	S662	-0.765006156	6.44E-05
P35241	S533	-0.758105065	0.032165945
Q8NHQ8	S387	-0.753901899	1.58E-05
P49006	S119_S/T	-0.750664741	0.008382431
Q76L83	SSLTQEEAPVSW	-0.747317101	1.76E-04
O43491	QPPPAAESQSSI	-0.744424857	0.022572892
O00192	S203	-0.743203841	7.96E-05
Q96T37	S58	-0.741300775	4.06E-05
Q9C0D5	T687	-0.741016038	3.56E-05
Q92609	S522	-0.732813312	4.87E-04
Q8NFC6	S1017	-0.731311408	3.50E-05
P35711	S424	-0.72351618	3.65E-04
P20290	T82	-0.722701934	3.56E-04
O60749	S226	-0.713993177	9.74E-06
P53367	S132	-0.713359032	0.001745391
Q9HAU0	T460	-0.709642163	1.58E-05

O43491	SDPEEEKGSQP	-0.70374801	3.83E-05
Q6ZVF9	S460	-0.697277545	3.22E-06
Q9Y4D1	T675	-0.692897914	2.10E-04
Q8TEW0	S201	-0.675576314	0.001127271
P25098	S685	-0.674065557	0.015128319
Q92551	S197	-0.673421144	3.19E-04
Q4VC05	S207	-0.666631503	1.07E-05
Q9Y4K1	S410	-0.66589918	5.95E-04
P05412	S63	-0.661607607	0.002195488
Q04637	S1209	-0.658995596	1.98E-05
Q12767	S668	-0.658440952	3.13E-04
O60716	S230	-0.658377386	1.58E-05
Q9UHY8	S65	-0.65650915	4.96E-05
Q93052	S609	-0.651039959	0.001759769
Q96F81	S1350	-0.646940701	6.59E-05
Q9Y2J4	S166	-0.642205639	8.55E-05
Q6DN90	T901	-0.634836063	0.006958044
O96013	T207	-0.634461386	2.03E-05
Q5VZ46	S518	-0.62945503	0.045452161
Q01082	T2187	-0.628269648	0.008566303
P49815	GPLPSSSPRSPS	-0.625526601	0.005117384
Q6R327	T1103	-0.623297144	5.30E-04
P06730	S209	-0.623207968	2.01E-04
Q9UQB8	T360	-0.622140051	6.14E-04
Q8WUH6	S77	-0.621976805	0.003452289
Q9UIW2	T1615	-0.619758382	8.28E-04
Q96CW1	S236	-0.618851269	5.86E-05
Q96NL6	S656	-0.61873091	0.015050147
Q04637	S1097	-0.618253492	1.41E-04
P55196	S1275	-0.616017966	1.07E-05
P13073	S56	-0.613448061	0.001514523
O95819	T834	-0.610065352	0.018095709
Q9Y5S2	S524	-0.604367641	0.001354977
P60468	S49	-0.603939988	2.71E-05
Q9BRK4	S570	-0.602871106	3.37E-05
Q8IZP0	T196	0.600332281	0.004231049
P62753	S235_S236	0.607886321	0.015647504
Q16513	S21	0.611142248	6.67E-04
Q96T88	ASATSSSQRDW0	0.621837233	0.004516747
Q9UGH3	S639_S/T	0.63015119	0.021939966
Q03111	S209	0.632054136	0.00974682
Q04637	SSLSRER	0.639810501	0.001966976
Q14241	S322	0.640312185	0.009564698
Q9Y6G9	T408	0.643604984	0.002710202
P62753	S236_S240	0.644408149	0.017151429
Q5VSY0	S360	0.653167884	0.006739153
O15040	S408	0.655953223	0.008208954
Q9H4M7	T296	0.667004206	0.029726219
P27448	SVSSSQKQR	0.673577433	0.001071305
Q13233	S252	0.695203491	3.53E-06
P49023	Y118	0.698254049	0.007966093
P17096	S9	0.708053041	0.006462963
Q13233	S250_S252	0.711410445	3.94E-04
P62753	S244_S247	0.717066182	0.001757042
Q07157	S1124	0.720974107	4.76E-04
O75694	S992	0.758641103	2.52E-04

Q9Y4I1	S600	0.77882986	7.64E-04
Q05D32	S9	0.809866775	1.98E-05
Q9UPW6	S39	0.82928638	5.08E-04
Q5QJE6	S245	0.831169048	0.001645587
Q9Y2I9	S787	0.836173338	0.019605992
Q8TBZ3	S347	0.851679974	0.013861972
O95819	S710_S715	0.865250429	5.62E-06
O60238	EHVPSSSSIHNG	0.91091649	0.017864016
O95819	S550	0.956989147	1.98E-05
O15550	S829	0.966406805	2.10E-04
Q99502	S314	0.999118334	0.036974231
P15927	S174	0.999549223	7.64E-04
Q9H9D4	S346	1.052553265	4.68E-04
Q8NC56	S138_S/T	1.0911335	0.013560244
Q92917	T138	1.14968258	0.027583976
Q5SW79	S807	1.150341015	3.94E-04
Q96B36	S203	1.168131014	0.007942145
Q07157	S144	1.248523138	0.045642212
Q9NS37	S50	1.28098435	2.01E-04
O14668	S158	1.321636135	1.40E-05
Q9Y4K4	T168	1.411432511	2.26E-08
P62491	S182	1.41861915	5.52E-04
Q9Y520	S867	1.77222641	1.98E-05
Q9NYZ3	S303	1.838108759	5.70E-05
P17544	T326	2.311651391	7.84E-06
Q9H000	S365	2.366027162	1.09E-05
Q8TCN5	S195	3.429181246	2.03E-05