

**Supplementary Table 1.** Large-scale quantitative phosphoproteomic profiling was performed on paired vehicle- and hormone-treated mTAL-enriched suspensions (n=3). A total of 654 unique phosphopeptides corresponding to 374 unique phosphoproteins were identified. The peptide sequence, phosphorylation site(s), and the corresponding protein name, gene symbol, and RefSeq Accession number are reported for each phosphopeptide identified in any one of three experimental pairs. For those 414 phosphopeptides that could be quantified in all three experimental pairs, the mean Hormone:Vehicle abundance ratio and corresponding standard error are also reported.

Peptide Sequence column: \* = phosphorylated residue

Site(s) column: ^ = ambiguously assigned phosphorylation site

Log<sub>2</sub>(H/V) Mean and SE columns: H = hormone-treated, V = vehicle-treated, n/a = peptide not observable in all 3 experimental pairs

Sig. column: \* = significantly changed Log<sub>2</sub>(H/V), p<0.05

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (H/V) Mean	Log <sub>2</sub> (H/V) SE	Sig.
1	Aak1	AP2-associated protein kinase 1	NP_001166921	VGSLT*PPSS*PK	T622 <sup>^</sup> , S626 <sup>^</sup>		0.24	0.95
2	Abca12	PREDICTED: ATP-binding cassette, sub-family A (ABC1), member 12	XP_237242	GLVQVLS*FFSQVQQQR	S251 <sup>^</sup>	1.24	2.13	
3	Abcc10	multidrug resistance-associated protein 7	NP_001101671	LMT*ELLS*GIRVLK	T464, S468	-2.68	2.48	
4	Abcf1	ATP-binding cassette sub-family F member 1	NP_001103353	QLSVPAS*DEDEVPVPR	S109	n/a	n/a	
5	Ablim1	actin-binding LIM protein 1	NP_001037859	PGSSIPGS*PGHTIYAK	S51	-3.55	1.81	
6	Ablim1	actin-binding LIM protein 1	NP_001037859	RSS*GREDEEELLR	S236	n/a	n/a	
7	Ablim1	actin-binding LIM protein 1	NP_001037859	S*SGREDEEELLR	S235 <sup>^</sup>	n/a	n/a	
8	Ablim1	actin-binding LIM protein 1	NP_001037859	SGLHRPVST*DFAQNSYGDVSGGVR	S318 <sup>^</sup>	1.43	1.17	
9	Ablim1	actin-binding LIM protein 1	NP_001037859	SGLHRPVST*DFAQNSYGDVSGGVR	T319 <sup>^</sup>	1.18	1.24	
10	Ablim1	actin-binding LIM protein 1	NP_001037859	STS*QGSINSYVYSR	S136	0.45	0.09	*
11	Ablim1	actin-binding LIM protein 1	NP_001037859	T*LSPTSAEGFDQGR	T113 <sup>^</sup>	n/a	n/a	
12	Ablim1	actin-binding LIM protein 1	NP_001037859	T*SSSEIYSRPGSSIPGS*PGHTIYAK	T35 <sup>^</sup> , S51 <sup>^</sup>	n/a	n/a	
13	Ablim1	actin-binding LIM protein 1	NP_001037859	TLS*PTSAEGFDQGR	S115	-0.13	0.13	
14	Ablim1	actin-binding LIM protein 1	NP_001037859	TS*ESIYSRPGSSIPGS*PGHTIYAK	S37 <sup>^</sup>	n/a	n/a	
15	Ablim1	actin-binding LIM protein 1	NP_001037859	TSSEIYSRPGSSIPGS*PGHTIYAK	S51 <sup>^</sup>	n/a	n/a	
16	Abp10	PREDICTED: annexin V-binding protein ABP-10	XP_001060944	KLS*SQPSTDSTDKER	S237	-6.36	3.15	
17	Acin1	apoptotic chromatin condensation inducer 1	NP_001163939	GLS*PLSSTADTK	S479	3.68	3.76	
18	Acsc2	acetyl-coenzyme A synthetase, cytoplasmic	NP_001101263	VRGWS*PPPEVR	S30	-0.62	0.15	
19	Adcy6	adenylate cyclase type 6	NP_036953	NVEPPSPT*PAAR	S53	-0.95	1.15	
20	Adcy6	adenylate cyclase type 6	NP_036953	NVEPPSPT*PAAR	T55 <sup>^</sup>	-0.30	1.60	
21	Add1	alpha-adducin	NP_058686	SPPDQSAVPNT*PPS*TPVK	T610, S613 <sup>^</sup>	n/a	n/a	
22	Add1	alpha-adducin	NP_058686	SPPDQSAVPNT*PPS*TPVKLEGLPQEPSR	T610, S613 <sup>^</sup>	n/a	n/a	
23	Add1	alpha-adducin	NP_058686	SPPDQSAVPNT*PPS*TPVK	T610 <sup>^</sup> , T614 <sup>^</sup>	n/a	n/a	
24	Add1	alpha-adducin	NP_058686	SPPDQSAVPNT*PPS*TPVKLEGLPQEPSR	T610, T614 <sup>^</sup>	n/a	n/a	
25	Add1	alpha-adducin	NP_058686	VVTS*PPPTTAPHK	S12	n/a	n/a	
26	Add1	alpha-adducin	NP_058686	YSDVEVPASVTGHFSFADGDS*GTCSPLR	S427	-0.21	0.17	
27	Add1	alpha-adducin	NP_058686	YSDVEVPASVTGHFSFADGDS*GTCSPLR	S431	-0.93	0.53	
28	Add3	gamma-adducin isoform 2	NP_113740	DRTEEVLSPDGS*PSK	S648	-0.73	0.16	*‡
29	Add3	gamma-adducin isoform 2	NP_113740	DRTEEVLSPDGS*PSK	S650 <sup>^</sup>	n/a	n/a	
30	Add3	gamma-adducin isoform 2	NP_113740	TEEVLSPDGS*PSK	S644 <sup>^</sup>	n/a	n/a	
31	Add3	gamma-adducin isoform 2	NP_113740	TEEVLSPDGS*PSK	S648	-0.34	2.45	
32	Ahnak	PREDICTED: AHNAK nucleoprotein	XP_574618	EFSA*PT*PTGTLFAGGEGK	T2934	n/a	n/a	
33	Ahnak	PREDICTED: AHNAK nucleoprotein	XP_574618	FKAEALPS*PK	S2257	-0.67	0.15	*‡
34	Ahnak	PREDICTED: AHNAK nucleoprotein isoform 1	XP_001078032	KGDRS*PEPGQTWAHEVFSSR	S94	-0.19	0.10	
35	Ahnak	PREDICTED: AHNAK nucleoprotein isoform 1	XP_001078032	KGDRS*PEPGQTWAHEVFSSR	T100 <sup>^</sup>	-0.42	0.42	
36	Ahsg	alpha-2-HS-glycoprotein precursor	NP_037030	VLHAQCHSTPDS*AEDVR	S138	-1.00	0.99	
37	Ahsg	alpha-2-HS-glycoprotein precursor	NP_037030	VLHAQCHSTPDS*AEDVR	S138	n/a	n/a	
38	Akap12	A-kinase anchor protein 12 isoform alpha	NP_476444	S*PWSIASVTEPLEHTAGEAMPVVEVTEK	S890 <sup>^</sup>	n/a	n/a	
39	Akap12	A-kinase anchor protein 12 isoform alpha	NP_476444	TEPASEEQEPAEDTQARLS*ADYEK	S350 <sup>^</sup>	n/a	n/a	
40	Akap12	A-kinase anchor protein 12 isoform alpha	NP_476444	TEPASEEQEPAEDTQARLS*ADYEK	Y353 <sup>^</sup>	n/a	n/a	
41	Akap2	A-kinase anchor protein 2	NP_001011974	TLS*MIIEEIR	S730	0.41	0.32	
42	Aldoa1	aldolase A-like 1	NP_001013965	LQS*IGTENTEENR	S46	n/a	n/a	
43	Aldoa1	aldolase A-like 1	NP_001013965	KELSDIAHRIVAPKGLAIDES*TGSIK	S36 <sup>^</sup>	n/a	n/a	
44	Ank2	PREDICTED: ankyrin 2, neuronal	XP_342338	AS*PIVQPEEASEPK	S1726	n/a	n/a	
45	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	AEEPVS*PLTAYQK	S2544	-0.31	0.10	
46	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	LSDGEYIS*DGEEGEDAITGDTKYLGPQDLK	S875	n/a	n/a	
47	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	MNVPETMNEVLDMDS*DDEVGK	S855	0.43	0.13	
48	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	RIT*GGLLR	T2465	2.64	0.45	*‡
49	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	RQS*FTSLALR	S1458	0.88	0.20	*‡
50	Ank3	ankyrin 3, epithelial isoform 2	NP_001029156	SFADENN*VHDPV*VQNET*PGSLES*PAQAR	S2457	-0.52	0.12	*
51	Ankhd1-Eif4ebp3	PREDICTED: multiple ankyrin repeats, single KH-domain homolog	XP_001054207	AVITTT*S*K	T1619 <sup>^</sup> , T1620 <sup>^</sup> , S1621 <sup>^</sup>	n/a	n/a	
52	Ankrd12	ankyrin repeat domain-containing protein 12	NP_001101708	S*STGEGSS*KTQHEK	S972 <sup>^</sup> , S979 <sup>^</sup>	n/a	n/a	
53	Ankrd12	ankyrin repeat domain-containing protein 12	NP_001101708	SST*GEGSS*KTQHEK	T974 <sup>^</sup> , S979 <sup>^</sup>	n/a	n/a	
54	Ankrd54	ankyrin repeat domain-containing protein 54	NP_001020456	S*KLNILQEGHS*OCLAEVRLVKQIHMRLR	S217, S227	0.57	1.07	
55	Ap2a2	AP-2 complex subunit alpha-2	NP_112270	EMAEAFAGEIFKLVAGDT*MDS*VK	T160, S163	n/a	n/a	
56	Ap3d1	AP-3 complex subunit delta-1	NP_001094189	NAETVKS*PEKEGVPVGEK	S825	1.85	2.05	
57	Ap3d1	AP-3 complex subunit delta-1	NP_001094189	VDIITEEMPENALPS*DEDDKDPNDPYR	S784	n/a	n/a	
58	Apbb1	amyloid beta A4 precursor protein-binding family B member 1	NP_536726	INGALES*VLSSS*SR	S569 <sup>^</sup> , S574 <sup>^</sup>	n/a	n/a	
59	Apoc2	apolipoprotein C-II	NP_001078821	AAAGELYQKTY*LTVDKLRDMY*S*K	Y60 <sup>^</sup> , Y72 <sup>^</sup> , S73 <sup>^</sup>	n/a	n/a	
60	Aqp1	aquaporin-1	NP_036910	VWT*SGQVEEYDLADDDINSR	T246 <sup>^</sup>	1.29	0.42	
61	Aqp1	aquaporin-1	NP_036910	VWT*SGQVEEYDLADDDINSR	S262	1.35	0.57	
62	Aqp1	aquaporin-1	NP_036910	VWT*SGQVEEYDLADDDINSR*RVEMKPK	S262	-0.60	1.51	
63	Aqp2	aquaporin-2	NP_037041	RQS*VELHS*POSQSLPR	S256, S261	1.05	1.10	
64	Aqp2	aquaporin-2	NP_037041	RQS*VELHS*POSQSLPR	S256, S264	2.67	2.64	
65	Aqp2	aquaporin-2	NP_037041	RQS*VELHS*POSQSLPR	S256	1.60	0.17	*‡
66	Aqp2	aquaporin-2	NP_037041	RQS*VELHS*POSQSLPR	S261 <sup>^</sup> , S264 <sup>^</sup>	2.00	1.98	
67	Aqp2	aquaporin-2	NP_037041	RQS*VELHS*POSQSLPR	S261	n/a	n/a	
68	Aqp2	aquaporin-2	NP_037041	RRQS*VELHS*POSQSLPR	S256, S261	n/a	n/a	
69	Aqp2	aquaporin-2	NP_037041	RRQS*VELHS*POSQSLPR	S256	1.70	0.24	*‡
70	Arfgap2	ADP-ribosylation factor GTPase-activating protein 2	NP_001028879	HGTDLWIDMNSAPSHS*PEK	S145	n/a	n/a	
71	Arfgef2	brefeldin A-inhibited guanine nucleotide-exchange protein 2	NP_851597	ELEKPIQSKPOS*PVIQATAGS*PK	S218, S227	-0.90	0.12	*‡
72	Arfgef2	brefeldin A-inhibited guanine nucleotide-exchange protein 2	NP_851597	ELEKPIQSKPOS*PVIQATAGS*PK	S227	n/a	n/a	
73	Arhgap24	rho GTPase-activating protein 24	NP_001012032	RCS*WIDKPEPQSR	S283 <sup>^</sup>	-0.70	1.44	
74	Arhgef11	rho guanine nucleotide exchange factor 11	NP_076472	S*SCTAEK	S509	n/a	n/a	
75	Arhgef12	rho guanine nucleotide exchange factor 12	NP_001013264	VEHDL*SVAGLQS*PDR	S1176 <sup>^</sup>	n/a	n/a	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (H/V) Mean	Log <sub>2</sub> (H/V) SE	Sig.
76	Arl6ip6	ADP-ribosylation factor-like protein 6-interacting protein 6	NP_001019481	IGDGS*PVLDPKR	S77	0.33	0.46	
77	Armc10	armadillo repeat-containing protein 10	NP_001100046	S*AEDLTEGSDAILSAEQLEK	S43*	n/a	n/a	
78	Atp1a1	sodium/potassium-transporting ATPase subunit alpha-1 precursor	NP_036636	S*PDTNENPLETR	S228	1.82	1.74	
79	Atp1a3	sodium/potassium-transporting ATPase subunit alpha-3	NP_036638	VDNSS*LTGESEPTQR	S207^	n/a	n/a	
80	Atn2l	ataxin 2-like	NP_001123569	EVDGLLTDSPMG*PVSSK	S347	0.68	1.38	
81	B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	NP_001012134	KKDNKYY*IPAVMYSK	Y279^	0.97	2.04	
82	Bad	bcl2 antagonist of cell death	NP_073189	RMS*DEFEGSFK	S156	0.97	1.80	
83	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	IGHHS*TSDDSSAYR	S338^	n/a	n/a	
84	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	IGHHS*TSDDSSAYRS*VDEVNYWDK	S338^, S348^	0.47	0.62	
85	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	IGHHST*SDSSAYR	T339^	n/a	n/a	
86	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	IGHHSTS*DDSSAYR	S340	n/a	n/a	
87	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	S*VDEVNYWDK	S348	0.68	0.54	
88	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	NP_036914	S*VDEVNYWDKQDHPISR	S348	1.88	2.45	
89	Bckdk	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial precursor	NP_062117	S*TSATDTHVELAR	S31^	n/a	n/a	
90	Bckdk	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial precursor	NP_062117	ST*SATDTHVELAR	T32^	n/a	n/a	
91	Bckdk	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial precursor	NP_062117	STS*ATDTHVELAR	S33^	n/a	n/a	
92	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	FHDSS*EGDDTETEDYR	S397	n/a	n/a	
93	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	IDIS*PSALR	S658	0.50	0.51	
94	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	LKELFDYS*PPLHK	S512^	-0.13	0.14	
95	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	RIDISPS*ALR	S660	-0.73	0.42	
96	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	YS*PSQNS*PIHHIPSR	S284, S289	-3.55	4.58	
97	Bclaf1	bcl-2-associated transcription factor 1	NP_001041317	YS*PSQNS*PIHHIPSR	S284^	-0.04	0.27	
98	Bsnd	barttin	NP_620435	LWEEAAYDQSL*LPDFTHIQMK	S107	-0.55	0.96	
99	Bsnd	barttin	NP_620435	MKEETVQAGAEPEEQEEDLYGLPDS*PGDPLPK	S290	n/a	n/a	
100	Bsnd	barttin	NP_620435	S*PPDRDEAHLQVPWASR	S206^	-0.20	0.23	
101	Bsnd	barttin	NP_620435	S*PQSPDRDEAHLQVPWASR	S202^	-0.25	0.33	
102	Bsnd	barttin	NP_620435	SQSS*PPACSGQSAPLASFHDDLDVGSSEGR	S175^	n/a	n/a	
103	Cad	CAD protein	NP_001099180	IHRAS*DPGLPAEPEK	S1859	0.40	0.09	*
104	Camta2	calmodulin-binding transcription activator 2	NP_001099271	KDGY*LWKKR	Y121	n/a	n/a	
105	Canx	calnexin precursor	NP_742005	AEDEILNRS*PR	S582	0.37	0.66	
106	Carhsp1	calcium-regulated heat stable protein 1	NP_690003	TFS*ATVR	S52	0.37	0.76	
107	Carhsp1	calcium-regulated heat stable protein 1	NP_690003	TFSAT*VR	T54	0.67	1.23	
108	Cbx5	chromobox protein homolog 5	NP_001100267	KSS*FNSASDDIK	S93	3.18	2.78	
109	Ccar1	cell division cycle and apoptosis regulator protein 1	NP_001102005	NLS*TMVDIHTVLKK	S1117^	n/a	n/a	
110	Cdk5rap2	CDK5 regulatory subunit-associated protein 2	NP_775157	AVEKHYKSLPGESS*SKFHSQEQVVK	S467^	1.48	1.76	
111	Cgnl1	cingulin-like protein 1	NP_001101634	EGVGEETLS*PR	S251	-0.50	0.82	
112	Cgnl1	cingulin-like protein 1	NP_001101634	NCFKPCGS*QPN*PTPEDLAK	S198, S202^	n/a	n/a	
113	Cgnl1	cingulin-like protein 1	NP_001101634	NCFKPCGS*QPN*PTPEDLAK	S202	1.52	1.77	
114	Cgnl1	cingulin-like protein 1	NP_001101634	RKS*PTAPS*PQAYSETK	S256, S261	-0.51	0.75	
115	Cgnl1	cingulin-like protein 1	NP_001101634	RKS*PTAPS*PQAYSETK	S256, S261	2.87	0.56	*‡
116	Cgnl1	cingulin-like protein 1	NP_001101634	RKS*PTAPS*PQAYSETK	S256	-0.40	0.50	
117	Cgnl1	cingulin-like protein 1	NP_001101634	RKS*PTAPS*PQAYSETK	S256	n/a	n/a	
118	Cgnl1	cingulin-like protein 1	NP_001101634	RKSPT*APS*PQAYSETK	T258, S261	3.19	0.74	*‡
119	Cgnl1	cingulin-like protein 1	NP_001101634	RKSPT*APS*PQAYSETK	T258^	2.46	2.30	
120	Cgnl1	cingulin-like protein 1	NP_001101634	RQDS*AGPILDGAR	S283	1.15	1.28	
121	Cgnl1	cingulin-like protein 1	NP_001101634	S*PTAPS*PQAYSETK	S256^	n/a	n/a	
122	Cgnl1	cingulin-like protein 1	NP_001101634	S*SEHLRPSQVFLQR	S413^	-0.07	0.11	
123	Cgnl1	cingulin-like protein 1	NP_001101634	SRS*VDSAFPGLQGNTEYLTEFSR	S387^	-3.95	3.29	
124	Cgnl1	cingulin-like protein 1	NP_001101634	SS*EHLRPSQVFLQR	S414	-0.08	0.11	
125	Clasp2	CLIP-associating protein 2	NP_446174	GRSRTKMVS*QSQPSGR	S459, S465	n/a	n/a	
126	Cldn10	claudin 10	NP_001099528	MGYTYNGPTS*VMSSR	S256	n/a	n/a	
127	Clmn	calmin	NP_001100225	SHSEGLDFKPS*PPLSK	S722	-0.28	0.14	
128	Clmn	calmin	NP_001100225	SHSEGLDFKPS*PPLSK	S726^	-0.38	0.23	
129	Clmn	calmin	NP_001100225	VFVCDQLES*PTGFSLGAPSHK	S358	n/a	n/a	
130	Cobl1	Cobl-like 1	NP_001101203	ASPES*PSESSAQPPAIIQDGK	S115	1.64	1.73	
131	Cobl1	Cobl-like 1	NP_001101203	ASPESPS*EDSSAQPPAIIQDGK	S117^	n/a	n/a	
132	Cobl1	Cobl-like 1	NP_001101203	QSS*LNFGSSDPEHIR	S180	-0.14	0.03	
133	Comt	catechol O-methyltransferase	NP_036663	AIYQGPSS*PKDS	S260^	n/a	n/a	
134	Coq9	ubiquinone biosynthesis protein COQ9, mitochondrial precursor	NP_001030334	YTDQS*GEEEDYESEEQIQHR	S80	n/a	n/a	
135	Cpeb1	cytoplasmic polyadenylation element-binding protein 1	NP_001099746	SY*LKAVT*AAFVEIKTKFTK	Y483^, T488^	n/a	n/a	
136	Ctdsp2	CTD small phosphatase-like protein 2	NP_001014070	KYS*EVDDSLPSGGEKPSK	S28^	1.16	0.83	
137	Ctnna1	catenin alpha-1	NP_001007146	TPEELDD*DFETEDFDVR	S643	n/a	n/a	
138	Ctnna1	catenin alpha-1	NP_001007146	SRTS*VQTEDDQLIAGQSAR	S657	n/a	n/a	
139	Ctnnb1	catenin beta-1	NP_445809	RLS*VELTSLFR	S675	-0.38	0.81	
140	Ctnnb1	catenin beta-1	NP_445809	RTS*MGTTQQQFVEGVR	S552	2.15	0.15	*‡
141	Ctnnb1	catenin beta-1	NP_445809	T*SMGGTQQQFVEGVR	T551^	2.04	0.46	*‡
142	Ctnnb1	catenin beta-1	NP_445809	TS*MGTTQQQFVEGVR	S552^	2.04	0.46	*‡
143	Ctnnd1	catenin delta-1	NP_001101210	LRS*YEDMIGEVPDDQYYWAPLAQHR	S320	0.47	0.43	
144	Ctnnd1	catenin delta-1	NP_001101210	S*MGYDLDLYGMMSDYGTAR	S288^	n/a	n/a	
145	Ctnnd1	catenin delta-1	NP_001101210	S*RDQVYGPQVQR	S252^	-2.47	0.95	
146	Ctnnd1	catenin delta-1	NP_001101210	VGSS*SVDLHR	S268	2.14	2.79	
147	Ctnn	cortactin isoform B	NP_068640	KQT*PPAS*PSPQPAEDRPPS*SPIYEDAAPLK	T364, S368^, S380^	n/a	n/a	
148	Ctnn	cortactin isoform B	NP_068640	KQT*PPAS*PSPQPAEDRPPS*PIYEDAAPLK	T364, S368, Y384^	n/a	n/a	
149	Ctnn	cortactin isoform B	NP_068640	KQT*PPAS*PSPQPAEDRPPS*SPIYEDAAPLK	T364^, S380^	n/a	n/a	
150	Ctnn	cortactin isoform B	NP_068640	KQT*PPAS*PSPQPAEDRPPS*PIYEDAAPLK	T364, Y384^	n/a	n/a	
151	Cul1	culin-1	NP_001102097	LIEKERNGETINT*R	T198^	0.46	0.10	*
152	Cyba	cytochrome b-245 light chain	NP_077074	KKPS*EAEAEAASAGPQVNPPIVTDEVV	S168	1.34	0.26	*‡
153	Cys1	cystin 1	NP_001103067	TAAVQEECGDPRPAT*PPGGR	T55	1.51	2.15	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (H/V) Mean	Log <sub>2</sub> (H/V) SE	Sig.
154	Cys1	cystin 1	NP_001103067	VTGNPEDESCASEAPGSS*PK	S116	-1.62	2.33	
155	Dap	death-associated protein 1	NP_071971	DKDDQEWESTS*PPKPTVYISGVIAIR	S51^A	-0.49	0.50	
156	Dbln	drebrin-like protein	NP_112642	LRS*PFLQK	S288	-0.53	0.11	*
157	Ddi2	protein DD11 homolog 2	NP_001029321	TQALLS*PGER	S121	5.15	5.04	
158	Disc1	disrupted in schizophrenia 1 homolog	NP_783186	LLALSS*RNTRRLGS*VK	S623^A, S631^A	-0.77	0.17	*‡
159	Dixdc1	dixin	NP_001032743	QAY*VAWVNAQLKK	Y31	n/a	n/a	
160	Dnajc5	dnaJ homolog subfamily C member 5	NP_077075	SLS*TSGESLYHVLGLDK	S10	0.77	0.39	
161	Dnm1l	dynamain-1-like protein	NP_446107	SKPIPIPAS*PQK	S596	-0.33	0.74	
162	Dock8	dedicator of cytokinesis 8	NP_001032882	VMSS*NPDLAGTHCAADEEVK	S904^A	n/a	n/a	
163	Dtnb	dystrobrevin beta	NP_001012191	VLDS*PSRLDEEHR	S394	n/a	n/a	
164	Dync1h1	cytoplasmic dynein 1 heavy chain 1	NP_062099	TDSTS*DGPRPAAWMR	S4368^A	-0.20	0.18	
165	Dync1l1	cytoplasmic dynein 1 light intermediate chain 1	NP_665715	DFQEYVEGEDFPAS*PQR	S207	n/a	n/a	
166	Dync1l1	cytoplasmic dynein 1 light intermediate chain 1	NP_665715	KPASV*SPTTPTS*PTEGEAS	S510, S516^A	n/a	n/a	
167	Dync1l1	cytoplasmic dynein 1 light intermediate chain 1	NP_665715	KPASV*SPTTPTS*PTEGEAS	S516	n/a	n/a	
168	Dync1l1	cytoplasmic dynein 1 light intermediate chain 1 dual specificity tyrosine-phosphorylation-regulated kinase 1B	NP_665715	KPASV*SPTTPTS*PTEGEAS	T518^A	n/a	n/a	
169	Dyrk1b	kinase 1B	NP_001100966	IYQY*IQSR	Y273	0.58	0.99	
170	Edc4	enhancer of mRNA-decapping protein 4	NP_001028240	TRS*PDVISSASTALSQDPIEIAEALSR	S734^A	4.68	5.16	
171	Eef1d	elongation factor 1-delta	NP_001013122	GATPAEDDEDNDILFGS*DEEEDKEAAR	S531	n/a	n/a	
172	Egf	pro-epidermal growth factor precursor	NP_036974	KDDQLAGDNADLS*KEVASLDSNPK	S799	-0.23	0.14	
173	Ehbp1f1	EH domain-binding protein 1-like protein 1 isoform 1	NP_001020288	LKPKS*VKVVAELSL*TLTS*GVLLREGR	S141^A, S150^A, S154^A	0.97	0.98	
174	Eif3b	eukaryotic translation initiation factor 3 subunit B	NP_001026810	AKPAAQSEETAA*PAAS*PTPQSAQEPSAPGK	S75, S79	n/a	n/a	
175	Eif3b	eukaryotic translation initiation factor 3 subunit B	NP_001026810	AKPAAQSEETAA*PAAS*PTPQSAQEPSAPGK	S75^A, T81^A	n/a	n/a	
176	Eif3c	eukaryotic translation initiation factor 3 subunit C	NP_001094132	LLLS*EDEEDTKR	S39^A	-0.22	0.38	
177	Eif4b	eukaryotic translation initiation factor 4B	NP_001008325	SLENELNKEDCHS*PTSCKPKPDQPLK	S459	-1.35	0.07	*‡
178	Eif4g2	eukaryotic translation initiation factor 4 gamma, 2	NP_001017374	FDKLCLELLNVGES*K	S107	1.23	2.18	
179	Eif5b	eukaryotic translation initiation factor 5B	NP_001103611	SVPTIDS*GNEDDSSFK	S215	n/a	n/a	
180	Epb4.1	PREDICTED: erythrocyte membrane protein band 4.1	XP_232771	RLS*THSPFR	S890^A	0.96	1.09	
181	Epb4.1f1	band 4.1-like protein 1 isoform L	NP_067713	SLDGAEFSPAS*VSENHADAGPDGDKR	S441	-0.15	0.57	
182	Epb4.9	dematin	NP_001101855	DSSVPGS*PSNIVAK	S26	2.60	2.42	
183	Epb4.9	dematin	NP_001101855	DSSVPGSPS*NIVAK	S28	1.81	1.64	
184	Epb4.9	dematin	NP_001101855	STS*PPPS*PEVWAEER	S92, S96	n/a	n/a	
185	Epn3	epsin-3	NP_001019962	TPVLPSPGPIIDPWAPSSPT*PK	T361	1.45	1.46	
186	Eps15l1	epidermal growth factor receptor substrate 15-like 1	NP_001025092	STPSHGVSSSLNLTGSL*PK	S255	n/a	n/a	
187	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	HS*LSSEPOQVEDVAPPGSSPHANR	S421^A	n/a	n/a	
188	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	HSL*SEPOQVEDVAPPGSSPHANR	S423^A	n/a	n/a	
189	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	HSL*SEPOQVEDVAPPGSS*PHANR	S437	n/a	n/a	
190	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	HSL*SEPOQVEDVAPPGSS*PHANR	S438	-0.19	0.10	
191	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	RAEDYSNVHTS*PEAEGAPHL	S675	n/a	n/a	
192	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	YWGPAS*PTHK	S528	0.82	1.32	
193	Eps8l2	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_001101978	YWGPASPT*HK	T530^A	-0.83	0.47	
194	ErbB2	receptor tyrosine-protein kinase erbB-2	NP_058699	RHRSS*TR	S1055	n/a	n/a	
195	Esam	endothelial cell-selective adhesion molecule precursor	NP_001004245	AAPRRPGTFTPTPSVQALS*SPR	S347^A	-2.99	1.81	
196	Esam	endothelial cell-selective adhesion molecule precursor	NP_001004245	AAPRRPGTFTPTPSVQALS*PR	S348	-1.08	0.20	*‡
197	Exosc2	exosome complex exonuclease RRP4	NP_001102422	Y*KLGQAGALVQVSPALVK	Y163	-0.99	1.34	
198	Fam129b	niban-like protein 1	NP_001103355	TVLEAS*PPAS*PLR	S693, S697	0.84	0.48	
199	Fam169a	PREDICTED: family with sequence similarity 169, member A	XP_226706	TILGS*SDNVATLSNEEK	S522	0.17	0.43	
200	Fam21c	WASH complex subunit FAM21	NP_954677	GQPAQGPVSEES*PPSPKPKG	S384^A	0.00	0.55	
201	Fam21c	WASH complex subunit FAM21	NP_954677	TS*PDSEQPPASEPWVERPWSVEEIR	S5^A	n/a	n/a	
202	Fam54b	hypothetical protein LOC298549	NP_001013957	AS*FETLNPDLCLK	S38	4.83	0.60	*‡
203	Fam54b	hypothetical protein LOC298549	NP_001013957	ASS*FADMMGLK	S235	0.52	0.47	
204	Fam54b	hypothetical protein LOC298549	NP_001013957	NAS*VFNLR	S100	1.54	1.59	
205	Fam82a2	regulator of microtubule dynamics protein 3	NP_001014068	S*QSLPNSLDYAQTSEER	S44	1.18	0.06	*‡
206	Fam82a2	regulator of microtubule dynamics protein 3	NP_001014068	SQS*LPNSLDY*YAQTSEER	S46^A	1.18	0.06	
207	Farp1	FERM, RhoGEF and pleckstrin domain-containing protein 1	NP_001100757	LGAPENSGIS*TLER	S23	3.12	3.08	
208	Farp1	FERM, RhoGEF and pleckstrin domain-containing protein 1	NP_001100757	LGAPENSGIS*TLER	T24	3.11	3.08	
209	Farp1	FERM, RhoGEF and pleckstrin domain-containing protein 1	NP_001100757	SPDEATAADQES*EDDLASAR	S893	n/a	n/a	
210	Fcho2	PREDICTED: Fcho2 isoform 2	XP_219503	LSGNEIPRPF*PPITSNTS*PPPTAPLAR	S533, S541^A	n/a	n/a	
211	Fkbp15	PREDICTED: FK506 binding protein 15	XP_342847	RLS*LTPDPEKK	S1094^A	2.24	2.50	
212	Fkbp2	peptidyl-prolyl cis-trans isomerase FKBP2	NP_001127900	VDCPIKS*R	S44	n/a	n/a	
213	Fkbp8	peptidyl-prolyl cis-trans isomerase FKBP8	NP_001032257	LEPS*NKTHIAELSKLVK	S329	n/a	n/a	
214	Flna	filamin-A	NP_001128071	RAPS*VANVGSCHDSLK	S2144	0.27	0.16	
215	Fnbp1l	formin-binding protein 1-like	NP_001034698	RHS*SDINHLV*YQGR	S488	1.75	0.45	
216	Foxp1	forkhead box protein P1	NP_001029303	ERLQAMMT*HLHV*STEPKAAPOPLNLV*SV*VTLSK	T401, S421, S422^A	0.67	1.03	
217	G3bp1	GTPase activating protein (SH3 domain) binding protein 1	NP_598249	SAS*PAPADVAPAQEDLR	S231	0.17	0.27	
218	G3bp1	GTPase activating protein (SH3 domain) binding protein 1	NP_598249	YQDEVFGVFTPEQEE*EEEEVEEPEER	S149^A	n/a	n/a	
219	Gbf1	PREDICTED: golgi-specific brefeldin A-resistance factor 1	XP_219953	ADAPDAGAQSDS*ELPSYHQNDVSLDR	S1301^A	n/a	n/a	
220	Gck	glucokinase	NP_036697	VMLVKVGEAGQW*VKTK	S100^A	-0.57	0.11	*
221	Gck	glucokinase	NP_036697	VMLVKVGEAGQW*VKTK	T103^A	-0.57	0.12	*
222	Gng12	PREDICTED: guanine nucleotide binding protein (G protein), gamma 12	XP_001067408	ASADLMS*YCEEHARSPLLMGIPTSENPFK	S41^A	0.38	0.24	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (HV) Mean	Log <sub>2</sub> (HV) SE	Sig.
223	Gng12	PREDICTED: guanine nucleotide binding protein (G protein), gamma 12	XP_001067408	S'DPLLMGIPTSENPFK	S49	0.63	0.14	*‡
224	Golga5	golgin subfamily A member 5	NP_001028237	KKS*EPDDELLFDLNSQK	S116	1.25	1.15	
225	Golgb1	Golgin subfamily B member 1	NP_620240	DQHGLEAGLNDTGMELNS*PQPDGVDK	S614	0.64	0.05	*‡
226	Grif1	PREDICTED: glucocorticoid receptor DNA-binding factor 1	XP_001053554	KVS*AVSKPVLRY	S1046	0.22	0.18	
227	Gsk3a	glycogen synthase kinase-3 alpha	NP_059040	GEPNVS*YICSR	S278^	-1.61	1.94	
228	Gsk3a	glycogen synthase kinase-3 alpha	NP_059040	GEPNVS*YICSR	Y279	0.12	0.44	
229	H3f3b	histone H3.3	NP_446437	FQS*AAIGALQEASEAIVLVGLFEDTNLCIAHAK	S87^	1.39	2.99	
230	Hdac2	histone deacetylase 2	NP_445899	MLPHAPGVQMAIPEDAVHEDS*GDEDGEDPDKR	S394	3.95	4.21	
231	HdGF	hepatoma-derived growth factor	NP_446159	AGDMLEDSP*PKRPK	S165	-0.27	0.28	
232	HdGF	hepatoma-derived growth factor	NP_446159	S*CAEEPEVEPEAHEGDGDK	S107	n/a	n/a	
233	Hist1h1d	histone H1.2	NP_579819	KAS*GPPVSELITK	S36	-0.04	0.02	
234	Hist1h1d	histone H1.2	NP_579819	RKAS*GPPVSELITK	S36	0.35	0.75	
235	Hist1h1d	histone H1.2	NP_579819	S*GPPVSELITK	S36^	0.26	0.54	
236	Hist1h2ail	histone H3.1	NP_001013074	FQSSAVMALQEAACEAY*LVGLFEDTNLCIAHAK	Y100	0.98	2.19	
237	Hist1h4b	histone H4	NP_073177	RIS*GLIYEETR	S48	-0.34	0.07	*
238	Hmgn1	high-mobility group nucleosome binding domain 1	NP_001013202	QAEVADQQTDLPAENGETENQSPAS*EEEK	S87^	n/a	n/a	
239	Hn1	hematological and neurological expressed 1 protein	NP_001005876	S*NSSAEASSGDFLDLK	S80^	0.42	0.25	
240	Hn1fa	hepatocyte nuclear factor 1-alpha	NP_036801	MVS*KLS*QLQTELLAALLES*GLS*K	S3^, S6^, S19^, S22^	1.57	1.64	
241	Hnrnpa1	heterogeneous nuclear ribonucleoprotein A1	NP_058944	SES*PKPEQLRK	S6	n/a	n/a	
242	Hnrnpa1	heterogeneous nuclear ribonucleoprotein A1	NP_058944	SES*PKPEQLRK	S6	n/a	n/a	
243	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3 isoform a	NP_937765	SSGS*PYGGYGSGGGSGGGYGSR	S359	-0.50	0.25	
244	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3 isoform a	NP_937765	SSGSPY*GGYGSGGGSGGGYGSR	Y361	n/a	n/a	
245	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3 isoform a	NP_937765	SSGSPYGGYG*GSGGGSGGGYGSR	Y365	-0.72	1.00	
246	Hnrmpc	heterogeneous nuclear ribonucleoprotein C	NP_001020804	GDDQLELKDDKEPEEGEDDRDS*ANGEDDS	S291	n/a	n/a	
247	Hnrmpk	heterogeneous nuclear ribonucleoprotein K	NP_476482	SG*YDGLGPITTVQTIK	S379	1.22	0.81	
248	Hnrmpk	heterogeneous nuclear ribonucleoprotein K	NP_476482	IIPTEELGQLPS*PTATSQLPLESDAVECLNYQHYK	S116	n/a	n/a	
249	Hnrmpu	heterogeneous nuclear ribonucleoprotein U	NP_476480	AKS*PQPVVEEEDHFDDTVCLDYNCDLHFK	S245	-0.34	0.42	
250	Hnrph1	heterogeneous nuclear ribonucleoprotein H	NP_543172	HTGPN*PDANDGFVR	S27	0.51	0.60	
251	Hnrph1	heterogeneous nuclear ribonucleoprotein H	NP_543172	HTGPN*PD*ANDGFVR	T30	-0.43	0.29	
252	Hsd11b2	corticosteroid 11-beta-dehydrogenase isozyme 2	NP_058777	ALRPGQPGVHDTQDPNPS*PTVSAL	S394	0.46	0.98	
253	Hsp90aa1	heat shock protein HSP 90-alpha	NP_786937	ESDDKPEIEDVGS*DEEEEEK	S263	n/a	n/a	
254	Hsp90aa1	heat shock protein HSP 90-alpha	NP_786937	ESDDKPEIEDVGS*DEEEEEK	S263	n/a	n/a	
255	Hsp90aa1	heat shock protein HSP 90-alpha	NP_786937	ESDDKPEIEDVGS*DEEEEEKDGDK	S263	n/a	n/a	
256	Hsp90ab1	heat shock protein HSP 90-beta	NP_001004082	IEDVGS*DEEDDSGK	S255	n/a	n/a	
257	Hsp90ab1	heat shock protein HSP 90-beta	NP_001004082	IEDVGS*DEEDDSGKDK	S255	n/a	n/a	
258	Hsp90ab1	heat shock protein HSP 90-beta	NP_001004082	IEDVGS*DEEDDSGKDKDK	S255	n/a	n/a	
259	Hspa4	heat shock 70 kDa protein 4	NP_705893	MQVDQEEPTHEEQPQT*PAENK	T538	0.97	0.44	
260	Hspa9	stress-70 protein, mitochondrial	NP_001094128	EAAEKAKCELSVQ*DNLPYLTMDASGPK	T325^	0.00	0.45	
261	Hspb1	heat shock protein beta-1	NP_114176	QLS*SGVSEIR	S85	1.37	1.57	
262	Hspc159	galectin-related protein	NP_001128202	LDDGHLNLSLGS*PVQADVYFPR	S25	n/a	n/a	
263	Htatsf1	HIV-1 Tat specific factor 1	NP_001101729	VFDD*DEKDEEDTDVIR	S698	n/a	n/a	
264	Inad1	PREDICTED: InaD-like (Drosophila) isoform 2	XP_001055452	KTLSAS*PPEQPSR	S459^	0.37	1.08	
265	Jph1	junctophilin-1	NP_001100100	SESKSS*IS*S*KR	S231^, S233^, S234^	n/a	n/a	
266	Kif26a	kinesin-like protein KIF26A	NP_001163819	LLPS*PAPPPP	S942	2.42	0.53	*‡
267	Ktn1	PREDICTED: kinectin 1	XP_341306	EIQNGTLHES*DSEHVQDFK	S75	1.34	1.66	
268	Ktn1	PREDICTED: kinectin 1	XP_341306	EIQNGTLHESD*EHVQDFK	S77^	1.35	1.63	
269	Lad1	ladinin	NP_001101412	ALPGKS*PPSSAEQSPDPPTK	S320^	-0.04	0.30	
270	Lad1	ladinin	NP_001101412	GRPEETAQQQS*PVSEK	S181	n/a	n/a	
271	Lad1	ladinin	NP_001101412	LPS*VEEAESVSKPSPAS*K	S62, S76^	1.10	0.59	
272	Lad1	ladinin	NP_001101412	LPS*VEEAESVSKPSPAS*KDEGEFFQAILR	S62^, S76^	0.68	1.07	
273	Lad1	ladinin	NP_001101412	LPS*VEEAESVSKPSPASK	S62	0.34	0.21	
274	Lad1	ladinin	NP_001101412	LPS*VEEAESVSKPSPASKDEGEFFQAILR	S62	n/a	n/a	
275	Lad1	ladinin	NP_001101412	NLS*STTEDESPK	S38	n/a	n/a	
276	Lad1	ladinin	NP_001101412	S*VEEAESVSKPSPASK	S62	-0.15	0.24	
277	Lad1	ladinin	NP_001101412	S*VEEAESVSKPSPASKDEGEFFQAILR	S62	n/a	n/a	
278	Larp1	PREDICTED: la related protein	XP_220446	ESPRPPAAEAAPGS*DGEDGGR	S132	n/a	n/a	
279	Larp7	la-related protein 7	NP_001037755	ELVDS*SS*SGVSKATK	S166	-0.62	0.30	
280	Lcp1	plastin-2	NP_001012044	GS*VSEEMMLER	S5^	n/a	n/a	
281	Lig4	ligase IV, DNA, ATP-dependent	NP_001099565	AAEIVPS*DMYKTGSTRFPRIK	S567^	0.66	1.24	
282	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	FGS*RPEAVTQCR	S132	2.88	0.51	*‡
283	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	GENEETLGRPAQPSPAGET*PHSPGVDAPIAK	T485	n/a	n/a	
284	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	GENEETLGRPAQPSPAGETPHS*PGVEDAPIAK	S488	0.59	0.81	
285	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	GWSEPEPEQSEFFGGGT*VQT*ESPRPSR	T634^	n/a	n/a	
286	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	KGWSEPEPEQSEFFGGGT*VQT*ESPRPSR	S640	n/a	n/a	
287	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	PAQPSPAGETPHS*PGVEDAPIAK	S488	3.77	3.39	
288	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	RLS*ENSCSLDDLLEIGAGHLSAFAFNSEK	S225	0.74	0.79	
289	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	RLENSCS*LDLLEIGAGHLSAFAFNSEK	S230^	0.46	0.50	
290	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	S*PLEPESPGWPGFGDTTAK	S697	1.13	0.47	
291	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	SEAQQPIYTKPLS*PDAR	S360	0.76	0.92	
292	Lima1	PREDICTED: LIM domain and actin binding 1	XP_217039	TSSVKS*PKPLSPSLR	S603^	-1.42	1.04	
293	Llg2	lethal(2) giant larvae protein homolog 2	NP_001121021	SQS*DGAETKPGVMEHALLSDAWVLK	S970^	-0.88	0.93	
294	Lmna	lamin-A isoform C2	NP_001002016	LRLS*PSPTQR	S389	-0.74	0.17	*‡
295	Lmo7	LIM domain only protein 7	NP_001001515	EVSR*PDQFSDMR	S1061	-1.13	1.18	
296	Lmo7	LIM domain only protein 7	NP_001001515	S*KLSLSDVSAEDVQSLR	S650	-0.86	0.56	
297	Lmo7	LIM domain only protein 7	NP_001001515	S*LSDVSAEDVQSLR	S652	1.21	1.15	
298	Lmo7	LIM domain only protein 7	NP_001001515	SKS*LDVSAEDVQSLR	S652^	n/a	n/a	
299	Lmo7	LIM domain only protein 7	NP_001001515	SLS*DVSAEDVQSLR	S654	1.20	1.14	
300	Lmo7	LIM domain only protein 7	NP_001001515	RGES*LDNLSQRPQSWR	S1563	0.01	0.12	
301	LOC360570	myosin 18a	NP_001165608	RFS*FSQR	S140	0.12	0.41	
302	LOC360570	myosin 18a	NP_001165608	SLAPDLS*DEHDVDPVDSISRPR	S2020	0.12	0.30	
303	LOC360713	PREDICTED: pleckstrin homology-like domain, family B, member 2-like	XP_001066275	KGS*LQVDIAGFGLGHSASFAPR	S510	1.22	0.17	*‡
304	LOC360713	PREDICTED: pleckstrin homology-like domain, family B, member 2-like	XP_001066275	RLS*AGTTVADVQK	S465	2.66	2.56	
305	LOC361100	topoisomerase II beta	NP_001094328	KTSFDQDS*DVIDFSDTSEPPALPR	S1570	n/a	n/a	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (HV) Mean	Log <sub>2</sub> (HV) SE	Sig.
306	LOC361346	hypothetical protein LOC361346 precursor	NP_001017462	SKKY*IGRQDSLDIK	Y155 <sup>^</sup>	0.25	1.06	
307	LOC366669	PREDICTED: similar to Nesprin-2 (Nuclear envelope spectrin repeat protein 2) (Synne-2) (Synaptic nuclear envelope protein 2) (Nucleus and actin connecting element protein) (NUANCE protein)	XP_001080795	LTSHPTGLDDEKEAS*ENETDIEDPR	S6383 <sup>^</sup>	n/a	n/a	
308	LOC366669	PREDICTED: similar to Nesprin-2 (Nuclear envelope spectrin repeat protein 2) (Synne-2) (Synaptic nuclear envelope protein 2) (Nucleus and actin connecting element protein) (NUANCE protein)	XP_001080795	SISEGHPWHVPDS*PSHSK	S6483 <sup>^</sup>	0.15	1.11	
309	LOC366669	PREDICTED: similar to Nesprin-2 (Nuclear envelope spectrin repeat protein 2) (Synne-2) (Synaptic nuclear envelope protein 2) (Nucleus and actin connecting element protein) (NUANCE protein)	XP_001080795	TEEGDT*PIEALLDFPR	T4207	n/a	n/a	
310	LOC680758	PREDICTED: rCG41835-like	XP_001058748	DGIHT*PVRERPEE	T120	-1.69	1.46	
311	LOC681101	PREDICTED: hypothetical protein	XP_001060309	WPPGPAAGS*APSGDGR	S125	-0.27	0.19	
312	LOC684097	sorting nexin-3	NP_001037748	RYS*DFEWLR	S72	3.47	0.34	*‡
313	LOC684233	PREDICTED: spenito-like	XP_001068152	SLS*PGGAALGYR	S293	0.72	0.68	
314	LOC685179	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform 2	XP_001055673	DMDEPS*PVPNVEEVTLPK	S347	n/a	n/a	
315	LOC688084	PREDICTED: similar to COLLAGEN family member (col-183)	XP_001081078	NPS*APGP	S55	n/a	n/a	
316	LOC688230	PREDICTED: hypothetical protein	XP_001081555	LREEEFKAVS*KDLPVDY*DDK	S3575, Y3582	0.91	1.07	
317	LOC688292	PREDICTED: caspase recruitment domain family, member 14-like	XP_001081765	EENEKLRSMT*FSLVEK	T278 <sup>^</sup>	4.47	0.42	*‡
318	LOC688717	SRA stem-loop-interacting RNA-binding protein, mitochondrial	NP_001102977	VLHGAQTS*DEEKDF	S105	0.17	0.58	
319	LOC690284	PREDICTED: rCG64368-like	XP_001073960	VIS*GPS*DOVRK	S441, S444	n/a	n/a	
320	Lpp	lipoma-preferred partner homolog	NP_001013886	RS*SLDAEIDSLTSLADLECCSSPYKPR	S116 <sup>^</sup>	1.15	1.47	
321	Lpp	lipoma-preferred partner homolog	NP_001013886	RSS*LDAAEIDSLTSLADLECCSSPYKPR	S117 <sup>^</sup>	0.97	1.31	
322	Lrba	lipopolysaccharide-responsive and beige-like anchor protein	NP_001102025	KES*LISPHFTTNSDENSSIGK	S898	4.45	0.17	*‡
323	Lrba	lipopolysaccharide-responsive and beige-like anchor protein	NP_001102025	VEGIEGS*PAEEAR	S1037	-0.08	0.98	
324	Lrrc47	leucine rich repeat containing 47	NP_001129138	RES*GEGEEEVADARS	S292	n/a	n/a	
325	Lrrfp1	leucine-rich repeat flightless-interacting protein 1	NP_001014291	AENQRPVEDSALS*PGPLAGAK	S302	0.08	0.22	
326	Lsm14a	protein LSM14 homolog A	NP_001121024	RS*PVPARPLPPTSQK	S216	-0.88	0.35	
327	Lsm14a	protein LSM14 homolog A	NP_001121024	S*SPQLDLPLRK	S182 <sup>^</sup>	0.70	0.98	
328	Macf1	microtubule-actin crosslinking factor 1	NP_001129230	KLANSEPVGTQ*AK	T3419 <sup>^</sup>	-0.32	0.30	
329	Map2	microtubule-associated protein 2	NP_037198	KVAIRT*PPKSPAT*PK	T1647, T1654	0.59	1.68	
330	Map2	microtubule-associated protein 2	NP_037198	VDHGAETIOS*PSR	S1780	-1.99	0.46	
331	Map3k9	PREDICTED: mitogen-activated protein kinase kinase 9	XP_576071	S*S*PALPGFTSLMEIGK	S655 <sup>^</sup> , S656 <sup>^</sup>	0.19	0.49	
332	Map4	microtubule-associated protein 4	NP_001019449	ATS*PSTLVSTGSSSR	S786	0.14	0.24	
333	Map4	microtubule-associated protein 4	NP_001019449	RTS*PSKPPSAPALRPGPK	S761 <sup>^</sup>	n/a	n/a	
334	Map4	microtubule-associated protein 4	NP_001019449	RTSPS*KPPSAPALRPGPK	S763 <sup>^</sup>	n/a	n/a	
335	Map4	microtubule-associated protein 4	NP_001019449	VGS*LDNVGHLPAAGTVK	S978	1.50	2.50	
336	Mapt	microtubule-associated protein tau	NP_058908	KVAVVRT*PPKS*PSASK	T164, S168 <sup>^</sup>	n/a	n/a	
337	Mapt	microtubule-associated protein tau	NP_058908	VAVVRT*PPKSPAS*K	T164, S172 <sup>^</sup>	-1.55	1.93	
338	Marcks	PREDICTED: myristoylated alanine-rich C-kinase substrate	XP_002729011	EAAEAPEAGPSPS*AEETEGASASSTSSPK	S115	n/a	n/a	
339	Matr3	matrin-3	NP_062022	RDS*FDDRGPSLNPVLDYDHGSR	S188	-1.59	1.04	
340	Mgll	monoglyceride lipase	NP_612511	NKS*EVDLYNSDPLICHAGVK	S189	-0.09	0.05	
341	Mllr4	afadin	NP_037349	PENLT*FRERQR	T1795	1.88	1.83	
342	Mme	nephrysin	NP_036740	GRS*ESQMDITDINAPKPK	S4	1.31	0.17	*‡
343	Mme	nephrysin	NP_036740	GRSES*QMDITDINAPKPK	S6 <sup>^</sup>	1.71	0.35	
344	Mmm1	PREDICTED: rCG55340-like	XP_001065496	YVSVLQET*ASKOGLMLLQMLSDLHVQESK	T522 <sup>^</sup>	1.52	0.73	
345	Mrp147	39S ribosomal protein L47, mitochondrial	NP_001032260	KSS*TV	S250 <sup>^</sup> , T251 <sup>^</sup>	-0.57	1.84	
346	Myh9	myosin-9	NP_037326	KGTGDCS*DEEVGKADGADAK	S1944	n/a	n/a	
347	Myi9	myosin regulatory light polypeptide 9	NP_001094355	ATS*NVFAMFDQSQIQEFK	S20	n/a	n/a	
348	Myi9	myosin regulatory light polypeptide 9	NP_001094355	AT*SNVFMFDQSQIQEFK	T19 <sup>^</sup>	n/a	n/a	
349	Nap114	nucleosome assembly protein 1-like 4	NP_001012170	EFITGDVEPTDAEASAWHS*EENEEDDLKAGDMK	S125	0.23	0.28	
350	Ncbp1	nuclear cap-binding protein subunit 1	NP_001014785	KTS*GANETEDHLESICK	S22	n/a	n/a	
351	Nck1	cytoplasmic protein NCK1	NP_001100321	RKPS*VPDTASPADDSFVDPGER	S85	1.11	0.85	
352	Ndrg1	protein NDRG1	NP_001011991	T*AGSSVTSLEGTR	T328	0.80	1.08	
353	Ndrg1	protein NDRG1	NP_001011991	TAS*GSSVTSLEGTR	S330	-0.16	0.13	
354	Ndrg2	protein NDRG2	NP_598267	T*ASLTSAAIDGSR	T316 <sup>^</sup>	1.52	0.30	*‡
355	Ndrg3	protein NDRG3	NP_001013945	SVTSNQSDGTQESCES*PDVLDLDR	S361	n/a	n/a	
356	Nfib	nuclear factor 1 B-type	NP_113754	KPEKPLFSST*PODSSPR	S328 <sup>^</sup>	-0.30	0.23	
357	Nid2	nidogen-2	NP_001012005	SFSLIS*GS*INOTRSYR	S705, S707	6.24	6.81	
358	Nkapl	NKAP-like protein	NP_001025084	IGELGAPEVWGLS*PK	S139	-0.19	0.24	
359	Nop56	nucleolar protein 56	NP_001020903	EELAS*DEEEMATSSISVPK	S517	n/a	n/a	
360	Nop56	nucleolar protein 56	NP_001020903	KFS*EEPEAAASCTK	S561	0.48	0.11	
361	Nop58	nucleolar protein 58	NP_068522	HIKEEPLS*EEEPCTSTAVPSPEK	S507	n/a	n/a	
362	Nop58	nucleolar protein 58	NP_068522	HIKEEPLS*EEEPCTSTAVPSPEK	S507	-1.08	0.38	
363	Npat	protein NPAT	NP_001101617	HTT*VKEVQSEKK	T1130 <sup>^</sup>	n/a	n/a	
364	Npm1	nucleophosmin	NP_037124	CGSGPVHISGQHLVAVEEADAE*EDEEEDVVK	S125	n/a	n/a	
365	Nsd1	histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific	NP_001100807	SLS*EDVSDSGTSK	S564 <sup>^</sup>	n/a	n/a	
366	Nsfl1c	NSFL1 cofactor p47	NP_114187	KKS*PNELVDLFLK	S114	n/a	n/a	
367	Nsfl1c	NSFL1 cofactor p47	NP_114187	RHS*GQDVHVVLK	S176	0.76	0.98	
368	Nucb1	nucleobindin-1 precursor	NP_445915	SGKLS*QELDFVSHNVR	S85	-0.26	0.18	
369	Nucks1	nuclear ubiquitously casein and cyclin-dependent kinases substrate	NP_073636	KVVDYSQFQES*DDADEDYGR	S19	n/a	n/a	
370	Nucks1	nuclear ubiquitously casein and cyclin-dependent kinases substrate	NP_073636	VVDYSQFQES*DDADEDYGR	S19	n/a	n/a	
371	Numa1	PREDICTED: nuclear mitotic apparatus protein 1	XP_218972	AAQLQGS*PAPEKGEVLGDALQLDLTK	S416	1.07	0.66	
372	Numa1	PREDICTED: nuclear mitotic apparatus protein 1	XP_218972	TQPDGTSVPGEPAS*PISQR	S1769	-0.13	0.40	
373	Numa1	PREDICTED: nuclear mitotic apparatus protein 1	XP_218972	VPSTYPTSLSEELS*PPSHQAK	S185	-0.14	0.36	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (HV) Mean	Log <sub>2</sub> (HV) SE	Sig.
374	Nup98	nuclear pore complex protein Nup98	NP_112336	NLNNSNLFSPVNHDESLAS*PSEYPENGER	S623^	n/a	n/a	
375	Olr1061	olfactory receptor Olr1061	NP_001000065	MSNS*GLR	S4	n/a	n/a	
376	Osbp	oxysterol-binding protein 1	NP_001102397	GDMS*DEDDNEFFDAPEIITMPENLGHK	S226	1.08	1.39	
377	Palm	paralemin	NP_570842	LNGS*AAELPATK	S345	0.66	0.90	
378	Palm	paralemin	NP_570842	SETMVNAQQTPLGT*PK	T145	-1.09	0.17	*‡
379	Palmd	palmdelphin	NP_001020859	SNGLAHTS*PTRPTPOQR	S322^	n/a	n/a	
380	Pard3	partitioning defective 3 homolog	NP_112514	RSS*DPALTGLSTVSDNFSSEEPSR	S144	n/a	n/a	
381	Pclo	protein piccolo isoform 2	NP_001104267	KLAAVAAT*VT*STTIVTHV/DALTMVEAAAAAR	T2394^, T2396^	0.29	1.14	
382	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	Y*HGHSMSDPGVSY*YR	Y289, S300	n/a	n/a	
383	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YGMGT*SVER	T231	0.80	0.76	
384	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YGMGTS*VER	S232	-0.14	0.07	
385	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHS*MSDPGVSY*YR	S293, S300	-0.25	0.08	
386	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHS*MSDPGVSY*R	S293, Y301	0.51	0.79	
387	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHS*MSDPGVSYR	S293	-0.97	1.07	
388	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHSMS*DPGVSY*YR	S295^, S300^	-1.45	0.88	
389	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHSMS*DPGVSY*R	S295^, Y301^	n/a	n/a	
390	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHSMS*DPGVSYR	S295	-0.07	0.15	
391	Pdha1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	NP_001004072	YHGHSMSDPGVSY*YR	S300^	-0.11	0.18	
392	Pds5b	sister chromatid cohesion protein PDS5 homolog B isoform 1	NP_001095853	AESPETS*AVESTQSTPQK	S1364^	n/a	n/a	
393	Pdxd1	pyridoxal-dependent decarboxylase domain-containing protein 1	NP_001128433	VQGTGVT*PPPTPSGTR	T687	0.80	0.06	
394	Pebp1	phosphatidylethanolamine-binding protein 1	NP_058932	VLTPQVMNRPSS*SIWDGLDPGK	S51	0.15	0.28	
395	Pebp1	phosphatidylethanolamine-binding protein 1	NP_058932	VLTPQVMNRPSS*SIWDGLDPGK	S52	0.14	0.28	
396	Pebp1	phosphatidylethanolamine-binding protein 1	NP_058932	FKVES*FR	S153	-0.50	0.12	*
397	Pex19	peroxisomal biogenesis factor 19 isoform 2	NP_001128249	AKPS*PAPS*PTISAPDASGPQK	S35, S39^	n/a	n/a	
398	Pex19	peroxisomal biogenesis factor 19 isoform 2	NP_001128249	AKPS*PAPSPT*ISAPDASGPQK	S35, T41	n/a	n/a	
399	Pgm1	phosphoglucomutase-1	NP_058729	AIGIILTAS*HNPGGPNGDFGIK	S117	0.28	0.13	
400	Pgrmc2	membrane-associated progesterone receptor component 2	NP_001008375	LLKPGEPESEY*DEEDTK	Y204	1.21	0.79	
401	Pgrmc2	membrane-associated progesterone receptor component 2	NP_001008375	LLKPGEPESEY*DEEDTKDHSKQD	Y204^	-4.78	2.49	
402	Pgrmc2	membrane-associated progesterone receptor component 2	NP_001008375	LLKPGEPESEY*DEEDTK	T205	2.48	1.16	
403	Pgrmc2	membrane-associated progesterone receptor component 2	NP_001008375	LLKPGEPESEY*DEEDTKDHSK	T205	0.24	0.57	
404	Pgrmc2	membrane-associated progesterone receptor component 2	NP_001008375	LLKPGEPESEY*DEEDTKDHSKQD	T205	-4.82	2.48	
405	Phactr1	phosphatase and actin regulator 1	NP_999622	RLS*QRPTAELEQR	S467	2.16	2.53	
406	Phlpp1	PH domain leucine-rich repeat protein phosphatase 1	NP_067689	GKMLPLVNRWTR	T521	n/a	n/a	
407	Pi4kb	phosphatidylinositol 4-kinase beta	NP_112345	S*VENLPEGGITHEQR	S428^	n/a	n/a	
408	Pkn2	serine/threonine-protein kinase N2	NP_001099225	AS*SLGEIDDSSELR	S581^	n/a	n/a	
409	Pkp2	plakophilin-2	NP_001093969	TSS*VPEYVYK	S82	0.91	2.12	
410	Plec	plectin isoform 1c	NP_001157768	SSS*VGSSSSYPISSAVPR	S4275	0.82	0.23	
411	Plekha6	PREDICTED: pleckstrin homology domain containing, family A member 6	XP_341119	YIDLEPVAPLS*PEELK	S1167	n/a	n/a	
412	Plekha6	PREDICTED: pleckstrin homology domain containing, family A member 6	XP_341119	HRS*IHVDISNLEAALR	S1094	0.45	1.03	
413	Plekha6	PREDICTED: pleckstrin homology domain containing, family A member 6	XP_341119	S*IHVDISNLEAALR	S1094	1.45	0.17	*‡
414	Plekha6	PREDICTED: pleckstrin homology domain containing, family A member 6	XP_341119	T*KSPAEEITPSAVVR	T1001	1.79	2.16	
415	Plekha6	PREDICTED: pleckstrin homology domain containing, family A member 6	XP_341119	TKS*PAEEITPSAVVR	S1003	0.25	0.60	
416	Plekha6	PREDICTED: pleckstrin homology domain containing, family G (with RhoGef domain) member 3 isoform 2	XP_234320	RRES*LSYIPK	S1064	3.34	3.05	
417	Plixdc2	plexin domain-containing protein 2	NP_001101892	RGSG*GHPVAEVEPVGEK	S507	1.69	0.32	*‡
418	Pnn	pinin	NP_001102493	QES*DPEDDVKKPALQSSVAVTSK	S100^	n/a	n/a	
419	Pnn	pinin	NP_001102493	S*LSPGKENINSLEVEK	S440^	-2.58	1.26	
420	Pnn	pinin	NP_001102493	SLS*PGKENINSLEVEK	S442	-2.58	1.26	
421	Pp1b1	liprin-beta-1	NP_001101366	RRPS*DENISITPSEQQWTHNR	S713	0.36	0.23	
422	Ppm1g	protein phosphatase 1G	NP_671742	KLEEALST*EGAENGNSDK	T525^	n/a	n/a	
423	Ppp1r1a	protein phosphatase 1 regulatory subunit 1A	NP_073167	RPT*PATLVLTSDDSSPEVEDRIPNPLLK	T35	1.53	0.20	*‡
424	Ppp1r1a	protein phosphatase 1 regulatory subunit 1A	NP_073167	RPTPATLVL*SDQSSPEVEDR	T42^	n/a	n/a	
425	Ppp1r1a	protein phosphatase 1 regulatory subunit 1A	NP_073167	RRPT*PATLVLTSDDSSPEVEDR	T35	n/a	n/a	
426	Ppp1r1a	protein phosphatase 1 regulatory subunit 1A	NP_073167	RRPTATLVLTSDDQSS*PEVEDRIPNPLLK	S47^	-0.16	0.14	
427	Ppp1r1a	protein phosphatase 1 regulatory subunit 1A	NP_073167	STLSMS*PR	S67	n/a	n/a	
428	Ppp1r1b	protein phosphatase 1 regulatory subunit 1B	NP_612530	IAESHLOTISNISENQAS*EEDELGELR	S102	0.20	0.08	
429	Ppp1r1b	protein phosphatase 1 regulatory subunit 1B	NP_612530	RRPT*PALLFR	T34	6.20	0.49	*‡
430	Ppp1r2	protein phosphatase inhibitor 2	NP_620178	IDEPDTPYHNMIGDDEDVCS*DSEGENVMTPEILAK	S87^	n/a	n/a	
431	Ppp2r5d	PREDICTED: delta isoform of regulatory subunit B56, protein phosphatase 2A	XP_001062510	RKS*ELPDQVYTIK	S632	2.11	0.46	*‡
432	Ptcp	enhanced at puberty protein 1	NP_001012488	KAS*PEPPDSEASALK	S534	-1.06	1.22	
433	Prkab1	5'-AMP-activated protein kinase subunit beta-1	NP_114182	CSDVSELSSS*PPGPHYHQEPIYSKPEER	S182^	-0.20	0.44	
434	Prkab2	cAMP-dependent protein kinase catalytic subunit beta	NP_001071113	T*WLCGTPEYLAEILSK	T196^	0.87	1.71	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (H/V) Mean	Log <sub>2</sub> (H/V) SE	Sig.
435	Prkacb	cAMP-dependent protein kinase catalytic subunit beta	NP_001071113	TWT*LCGTPEYLPEILSK	T198^	0.84	1.76	
436	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory subunit	NP_037313	EDEIS*PPPPNPVK	S83	2.23	1.49	
437	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory subunit	NP_037313	TDSREDEIS*PPPPNPVK	S83	0.61	1.86	
438	Prkar2a	cAMP-dependent protein kinase type II-alpha regulatory subunit	NP_062137	RVS*VCAETFPNDEEDNDPR	S97	0.38	0.63	
439	Prkar2b	cAMP-dependent protein kinase type II-beta regulatory subunit	NP_001025191	RAS*VCAEAYNPDEEDDAESR	S112	n/a	n/a	
440	Prkod	protein kinase C delta type	NP_579841	SPSDYSNFDPEFLNEKPLQLS*FSDK	S643	0.26	0.11	
441	Prkod	protein kinase C delta type	NP_579841	SPSDYSNFDPEFLNEKPLQLS*DK	S645^	n/a	n/a	
442	Prkocbp	protein kinase C delta-binding protein	NP_604444	KGS*EAAQPTPVKPPR	S199^	-0.08	0.27	
443	Prpsap1	phosphoribosyl pyrophosphate synthase-associated protein 1	NP_071990	LGLVAIHGEAQCTELMDDGRHS*PPMVK	S244	n/a	n/a	
444	Psap	sulfated glycoprotein 1 isoform A preproprotein	NP_037145	NGGFCEVCKLVII*LEHLEKNSTK	Y448	-0.10	0.47	
445	Ptpn18	tyrosine-protein phosphatase non-receptor type 18	NP_001013129	IQRPVVS*HTENAQGTALGR	S393	n/a	n/a	
446	Ptpn21	tyrosine-protein phosphatase non-receptor type 21	NP_598229	RNS*IEIAGLTHGFEGLR	S637	0.28	0.53	
447	Ptfr	polymerase I and transcript release factor	NP_001099311	ATEEPPSGTS*DELIK	S42	1.44	1.27	
448	Pum1	pumilio homolog 1	NP_001102154	RDS*LTGSSDLTK	S710	1.52	0.13	‡
449	Pxn	paxillin	NP_001012147	TGS*SSPPGGLSKPGSQDMLGSLQSDLNK	S315	1.00	0.19	‡
450	Pxn	paxillin	NP_001012147	TGSS*PPGGLSKPGSQDMLGSLQSDLNK	S317^	0.97	0.13	
451	Pxn	paxillin	NP_001012147	YAHQQPPS*PSPIYSSSTK	S83	-0.09	0.20	
452	Qdpr	dihydropteridine reductase	NP_071785	SLFKNCDLMMWQSIWTS*TISSHLATKHLK	S112^	n/a	n/a	
453	Rai1	PREDICTED: retinoic acid induced 1	XP_220520	SCT*APSAQPHDRPMSANASLAPGQR	T232	n/a	n/a	
454	Raly	RNA-binding protein Raly	NP_001011958	GRLS*PVVPPVR	S119	-0.90	0.57	
455	Ranbp2	PREDICTED: RAN binding protein 2 isoform 2	XP_215401	QNQPTSVAVSAPASS*ETSKSPK	S1638^	n/a	n/a	
456	Ranbp2	PREDICTED: RAN binding protein 2 isoform 2	XP_215401	QNQPTSVAVSAPASSETS*KSPK	S1641^	n/a	n/a	
457	Ranbp2	PREDICTED: RAN binding protein 2 isoform 2	XP_215401	QNQPTSVAVSAPASSETS*PK	S1643	0.58	2.15	
458	Rap1gap	PREDICTED: Rap1 GTPase-activating protein	XP_233609	RGS*ALGIGAVEESLIVPGKS*PTR	S557, S574	4.98	0.66	‡
459	Rap1gap	PREDICTED: Rap1 GTPase-activating protein	XP_233609	RSS*AIENIQEVEQEK	S589	2.40	0.30	‡
460	Rap1gap	PREDICTED: Rap1 GTPase-activating protein	XP_233609	RGS*MDAMGLSNK	S505	5.36	0.67	‡
461	Raver1	ribonucleoprotein PTB-binding 1	NP_001013961	HKMS*PPPSFSEPR	S626	-0.23	0.11	
462	Rbm14	PREDICTED: RNA binding motif protein 14	XP_001072105	RLS*ESQLSFR	S618	2.10	0.24	‡
463	Rbm14	PREDICTED: RNA binding motif protein 14	XP_001072105	T*PPFFGR	T206	-0.32	0.16	
464	Rbm39	RNA-binding protein 39	NP_001013225	DKS*PVREPIDNLTPEER	S136	-0.05	0.17	
465	Rbm39	RNA-binding protein 39	NP_001013225	KDKS*PVREPIDNLTPEER	S136	0.67	0.87	
466	RGD1304931	hypothetical protein LOC313776	NP_001101471	YS*GSPDAAIQMSSPOLTEARPK	S196^	2.05	1.80	
467	RGD1305269	PREDICTED: LIM and calponin homology domains 1 isoform 4	XP_223397	SINHOIES*PGER	S1118	n/a	n/a	
468	RGD1306410	hypothetical protein LOC360768	NP_001014148	HIEPELAGRDS*PYR	S264	1.95	2.20	
469	RGD1308601	hypothetical protein LOC307249	NP_001100844	RDS*SESQLASTESDKPTTGR	S66	-0.09	0.56	
470	RGD1308601	hypothetical protein LOC307249	NP_001100844	RDS*ESQLASTESDKPTTGR	S67	n/a	n/a	
471	RGD1308601	hypothetical protein LOC307249	NP_001100844	RDSSES*QLASTESDKPTTGR	S69^	n/a	n/a	
472	RGD1309108	PREDICTED: hypothetical protein	XP_236102	T*IPKPKPNLKY*QT*MK	T715, Y726, T728	n/a	n/a	
473	RGD1309922	hypothetical protein LOC306007	NP_001163943	VSKDEVQNGETAEAADS*PLKEDGLLPK	S612	-0.70	0.41	
474	RGD1310230	mitochondrial fission factor	NP_001034104	VLTLSERPLDFLDERPPPT*POSEEIR	T112^	n/a	n/a	
475	RGD1311728	PREDICTED: RIKEN cDNA 9130221D24-like	XP_227688	RKT*DTVDDSSVGDHSGSLR	T23	-1.47	1.36	
476	RGD1560083	PREDICTED: myosin IIIA similar to DNA segment, Chr 4, ERATO Doi 22, expressed isoform 1	XP_574090	QLVNHPLTKT*GNLPLS*K	T1124^, S1130^	n/a	n/a	
477	RGD1560286	PREDICTED: transcription elongation factor B (SIII), polypeptide 2	NP_001108071	ILGSAS*PEEEQEKPILRPTR	S107	-0.10	0.21	
478	RGD1561118	hypothetical protein LOC500552	XP_220759	KTTIFAEAQESS*T*VLELK	S22, T23	n/a	n/a	
479	RGD1561149	hypothetical protein LOC500552	NP_001128101	QPS*SGGTAESVSDTASIR	S403	n/a	n/a	
480	RGD1561149	hypothetical protein LOC500552	NP_001128101	LQLERPVS*PEAQADLQR	S914	-0.46	0.10	*
481	RGD1561445	PREDICTED: hypothetical protein	XP_233277	SST*TFNLEEK	T1543, T1544	n/a	n/a	
482	RGD1561963_predicted	PREDICTED: similar to Dedicator of cytokinesis protein 10 (Protein zizimin 3)	XP_001060744	S*YKERT*THEELAK	S1158, Y1159, T1163	n/a	n/a	
483	RGD1562952_predicted	PREDICTED: similar to ErbB2 interacting protein isoform 1	XP_001072232	TSEPEAETNAGNS*PVTTNR	S580^	n/a	n/a	
484	RGD1563245	PREDICTED: G protein-coupled receptor 161	XP_222837	EAAKNS*ILHVK	S495	n/a	n/a	
485	RGD1563437	PREDICTED: enhancer trap locus 4-like	XP_001069190	HQEETHAPGQPLHCS*TGSPGDVK	S918^	0.43	0.63	
486	RGD1563437	PREDICTED: enhancer trap locus 4-like	XP_001069190	HQEETHAPGQPLHCS*TGSPGDVK	S921^	-0.22	0.11	
487	RGD1563437	PREDICTED: enhancer trap locus 4, partial	XP_214519	LGKGS*PPPPPPPR	S92	0.03	0.27	
488	RGD1564174	PREDICTED: tensin 3	XP_341257	WDS*YENMSADGEVLTQGPVDSGLYAK	S409^	n/a	n/a	
489	RGD1564748	PREDICTED: mortality factor 4 like 2-like	XP_228426	RS*NPS*EEGHS*VK	S336, S339, S344	n/a	n/a	
490	RGD1565496	hypothetical protein LOC300783	NP_001100301	WLDES*DAEMELR	S114	0.22	0.40	
491	Rims1	regulating synaptic membrane exocytosis protein 1	NP_439894	S*LTKPGS*K	S1423, S1430	n/a	n/a	
492	Rnmt	mRNA cap guanine-N7 methyltransferase	NP_001008300	GGGSEDEPS*PGGLTER	S99	n/a	n/a	
493	Rpl35	60S ribosomal protein L35	NP_997676	QLDLKVELS*QLR	S29	0.15	0.38	
494	Rps3	40S ribosomal protein S3	NP_001009239	DEILPT*PISEOK	T220^	2.53	2.35	
495	Rps3	40S ribosomal protein S3	NP_001009239	DEILPT*PISEOK	T221	2.53	2.35	
496	Rras2	ras-related protein R-Ras2	NP_001013452	FQEQECPSS*PEPTR	S186	0.22	0.37	
497	Rras2	ras-related protein R-Ras2	NP_001013452	FQEQECPSS*PEPTRK	S186	-0.96	0.73	
498	Rras2	ras-related protein R-Ras2	NP_001013452	KFQEQECPSS*PEPTR	S186	-0.96	0.75	
499	Rras2	ras-related protein R-Ras2	NP_001013452	KFQEQECPSS*PEPTRK	S186	-0.18	0.20	
500	Rtn4	reticulon-4	NP_114019	GPLPAAPPAAPERQPS*WER	S107	-1.05	0.71	
501	Rtn4	reticulon-4	NP_114019	LPAAPPAAPERQPS*WER	S107	0.62	0.65	
502	Rtn4	reticulon-4	NP_114019	RRGS*GSVDLTFALPAASEPVPSSAEK	S169^	-1.33	0.43	
503	Rtn4	reticulon-4	NP_114019	RRGSGS*VDLTFALPAASEPVPSSAEK	S171^	1.26	0.97	
504	Rtn4	reticulon-4	NP_114019	SKDKEDLVCSAALHS*PQESPVGK	S329	4.81	2.54	
505	Sccpdh	probable saccharopine dehydrogenase	NP_001014007	SVS*NLKPVVIGSK	S217	-0.42	0.50	
506	Scd1	sec1 family domain-containing protein 1	NP_062237	VNLEESTGVENS*PTGARPK	S298^	4.06	4.14	
507	Scrib	PREDICTED: scribbled homolog isoform 5	XP_343267	MQS*PELPAPER	S1483	n/a	n/a	
508	Scrib	PREDICTED: scribbled homolog isoform 5	XP_343267	MVEPENAVITITLPRPDDY*SPR	Y818	-0.41	0.09	*
509	Sec22b	vesicle-trafficking protein SEC22b	NP_001020857	NLGS*INTELQDVQR	S137	4.74	0.77	‡
510	Sec23ip	SEC23-interacting protein	NP_001128331	KLS*VGAYVSVR	S749	-0.49	0.09	*
511	Sec61b	protein transport protein Sec61 subunit beta	NP_001100124	PGPTPATNVGSSGRS*PSK	S17	-1.09	0.25	‡
512	Sec62	translocation protein SEC62	NP_001029301	ELEEQQT*DGDCDEDDDKDGMPEK	T582	n/a	n/a	
513	Sept2	septin-2	NP_476489	IYHLPDAES*DEDEDFKQETR	S218	-0.17	0.20	

#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (HV) Mean	Log <sub>2</sub> (HV) SE	Sig.
514	Sep14	septin 4	NP_001011893	IYQFFDCDS*DEDEDFKLDQALK	S206	n/a	n/a	
515	Sfrs3	splicing factor, arginine/serine-rich 3	NP_001041372	SLS*RRRR	S130^	n/a	n/a	
516	Sfrs6	splicing factor, arginine/serine-rich 6	NP_001014207	SHS*PLPAPPSK	S303	-1.08	0.86	
517	Sgta	small glutamine-rich tetra-ricopeptide repeat-containing protein alpha	NP_073194	GPDRT*PPESEDESAEER	T81	n/a	n/a	
518	Sh3g2	PREDICTED: endophilin-A1	XP_342858	S*GVQMDQPCCR	S400	n/a	n/a	
519	Shank2	SH3 and multiple ankyrin repeat domains protein 2 isoform c	NP_597684	RAPS*PVVS*PTELSK	S1119, S1123	-0.21	0.60	
520	Shank2	SH3 and multiple ankyrin repeat domains protein 2 isoform d	NP_597685	SNS*DNLNAGAPEWAVCSAATSHR	S43^	n/a	n/a	
521	Slc12a1	solute carrier family 12 member 1	NP_062007	KDS*NIHQSMHVGFEFNQK	S874	3.05	0.71	*‡
522	Slc12a1	solute carrier family 12 member 1	NP_062007	TDTFHAYDSHT*NTYYLQTFGHNTMDAVPK	T89^	1.31	0.23	*‡
523	Slc12a1	solute carrier family 12 member 1	NP_062007	VNRPS*LOEIHQLAK	S126	5.90	0.24	*‡
524	Slc16a7	monocarboxylate transporter 2	NP_058998	VSNTHNPPSDDRKDESS'I	S488	n/a	n/a	
525	Slc25a46	solute carrier family 25 member 46	NP_001093985	SFGSGTELGHWVTT*PPDIPGSR	T45	0.16	0.13	
526	Slc2a4	solute carrier family 2, facilitated glucose transporter member 4	NP_036883	RTPS*LLEQEVKPESTEVLVGPDEND	S488^	0.97	0.22	*‡
527	Slc43a2	large neutral amino acids transporter small subunit 4	NP_001099282	LCLST*TVDLEVK	S297	-1.50	0.16	*‡
528	Slc43a2	large neutral amino acids transporter small subunit 4	NP_001099282	LCLST*VDLEVK	T298^	n/a	n/a	
529	Slc43a2	large neutral amino acids transporter small subunit 4	NP_001099282	REDS*KLFLK	S552	3.05	3.00	
530	Slc43a2	large neutral amino acids transporter small subunit 4	NP_001099282	RLS*VGSMMR	S274	0.88	0.18	*‡
531	Slc4a2	anion exchange protein 2	NP_058744	RRPGAS*PTGETPTIEEGEEDDEVGAEGR	S113	0.21	0.06	
532	Slc4a2	anion exchange protein 2	NP_058744	RRPGASPT*GETPTIEEGEEDDEVGAEGR	T115	0.24	0.08	
533	Slc4a2	anion exchange protein 2	NP_058744	TS*PSPPTQTPHQEAAPR	S171^	0.08	0.17	
534	Slc5a3	solute carrier family 5 (inositol transporters), member 3	NP_446167	EEGNPVASMGHSEAE*PVDAYSNGQAALMGER	T626	n/a	n/a	
535	Slc9a1	sodium/hydrogen exchanger 1	NP_036784	IGS*DPLAYEPK	S707	1.47	1.66	
536	Slc9a1	sodium/hydrogen exchanger 1	NP_036784	SKEPSSPGTDVDFTPGSDS*PGSQR	S790^	n/a	n/a	
537	Slc9a3	sodium/hydrogen exchanger 3	NP_036786	RGS*LAFIR	S552	2.07	0.30	*‡
538	Slc9a3	sodium/hydrogen exchanger 3	NP_036786	VQIPNS*PSNFR	S791	-0.73	0.32	
539	Slc9a3r1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	NP_067605	EALVEPASES*PRPALAR	S277^	-0.06	0.22	
540	Slc9a3r1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	NP_067605	SAS*SDTSEELNAQDPSK	S287	n/a	n/a	
541	Slc9a3r1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	NP_067605	SASS*DTSEELNAQDPSK	S288^	n/a	n/a	
542	Slc9a3r1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	NP_067605	SASSDT*SEELNAQDPSK	T290	-0.20	0.40	
543	Sik	STE20-like serine/threonine-protein kinase	NP_062222	RDS*FIGTPYWMAPAEVMCETSK	S189	-0.91	0.78	
544	Smarca2	probable global transcription activator SNF2L2	NP_001004446	GRPPAEKLS*PNPKK	S1384	-1.13	0.43	
545	Smpx	small muscular protein	NP_445847	RKES*TPGTAEGAPAT*PEEK	S36, T47	n/a	n/a	
546	Smpx	small muscular protein	NP_445847	RKES*TPGTAEGAPAT*PEEK	S36	4.47	0.42	*‡
547	Smpx	small muscular protein	NP_445847	RKESTPGT*AEGAPAT*PEEK	T40	4.65	0.74	*‡
548	Snap23	synaptosomal-associated protein 23	NP_073180	ATWGDGDDSS*PSNVVSK	S110	0.08	0.26	
549	Snb1	beta-1-syntrophin	NP_001124014	GSQGTGPGTGVQAPDS*PAGVR	S88	-0.34	0.19	
550	Snb2	syntrophin, beta 2	NP_001162145	GLGPPS*PPAPPR	S77	1.66	1.74	
551	Snb2	syntrophin, beta 2	NP_001162145	KPS*LVSDLPWEGASPOSPFSGSEDS*GSPK	S190^, S213 ^	n/a	n/a	
552	Snb2	syntrophin, beta 2	NP_001162145	KPSLVSDLPWEGAS*POSFSGSEDS*GSPK	S201^	0.45	0.45	
553	Snb2	syntrophin, beta 2	NP_001162145	KPSLVSDLPWEGASPOS*PSFSGSEDS*GSPK	S204^, S215^	n/a	n/a	
554	Snb2	syntrophin, beta 2	NP_001162145	KPSLVSDLPWEGASPOS*PSFSGSEDS*GSPK	S204	0.08	0.11	
555	Snb2	syntrophin, beta 2	NP_001162145	KPSLVSDLPWEGASPOS*PSFSGSEDS*GSPK	S208^	0.08	0.11	
556	Snb2	syntrophin, beta 2	NP_001162145	KPSLVSDLPWEGASPOS*PSFSGSEDS*GSPK	S215^	0.21	0.09	
557	Sort1	sortilin precursor	NP_113955	YS*VLQHAEDGV*EALDTASHAK	S791	3.87	0.46	*‡
558	Sphk2	sphingosine kinase 2	NP_001012066	AKS*ELALAPAPAPA*HSLPHR	S364, T377^	n/a	n/a	
559	Sphk2	sphingosine kinase 2	NP_001012066	AKS*ELALAPAPAPA*HSLPHR	S364, S379^	n/a	n/a	
560	Spint2	serine protease inhibitor, Kunitz type 2 isoform b	NP_954518	NSCS*SFYGGCR	S100	n/a	n/a	
561	Spna2	spectrin alpha chain, brain	NP_741984	WRS*LQQLAER	S1217	-0.60	0.26	
562	Spp1	osteopontin precursor	NP_037013	ISHELESS*SEVN	S313	0.66	0.80	
563	Sptbn1	spectrin beta chain, brain 1	NP_001013148	GDQVS*QNGLP*AEQGS*PR	S2122	0.93	0.83	
564	Sptbn1	spectrin beta chain, brain 1	NP_001013148	GDQVS*QNGLP*AEQGS*PR	S2132	0.06	0.33	
565	Sptbn1	spectrin beta chain, brain 1	NP_001013148	VSEEAESQQWDT*SKGDQVS*QNGLP*AEQGS*PR	S2122	n/a	n/a	
566	Sptbn1	spectrin beta chain, brain 1	NP_001013148	VSEEAESQQWDT*SKGDQVS*QNGLP*AEQGS*PR	S2132	n/a	n/a	
567	Srrm1	serine/arginine repetitive matrix protein 1	NP_001101456	RRS*PS*PAPPPPPPPR	S558, S560	n/a	n/a	
568	Srrm1	serine/arginine repetitive matrix protein 1	NP_001101456	RYS*PPIQR	S601^	0.08	0.18	
569	Srrm2	PREDICTED: serine/arginine repetitive matrix 2	XP_220207	DKFS*PTQDRPESSTVLK	S1153	1.22	1.39	
570	Srrm2	PREDICTED: serine/arginine repetitive matrix 2	XP_220207	ELSHS*PPRDNFSFESLEFR	S1280^	-0.28	0.41	
571	Srrm2	PREDICTED: serine/arginine repetitive matrix 2	XP_220207	S*PVPSAFSDQSR	S2407	n/a	n/a	
572	Srrm2	PREDICTED: serine/arginine repetitive matrix 2	XP_220207	SSS*PVTLETAR	S1070	1.85	1.67	
573	Ssr1	translocon-associated protein subunit alpha	NP_001008891	VEMTSSNDVDM*WIPQET*LNQINKASPR	T261^	n/a	n/a	
574	Ssrp1	FACT complex subunit SSRP1	NP_112383	EGINPGYDDYADS*DEQHDAYLER	S444	n/a	n/a	
575	St14	matrilysin	NP_446087	GGGS*QDFGAGLK	S13	3.73	0.86	*‡
576	Stat1	signal transducer and activator of transcription 1 isoform alpha	NP_116001	LQSTENLLPMS*PEEFDMSK	S727	1.60	2.41	
577	Stat3	signal transducer and activator of transcription 3	NP_036879	YCRPESQHEPADPGSAAPY*LK	Y705	-0.11	0.09	
578	Stk40	serine/threonine-protein kinase 40	NP_898879	LSERET*VIFY*DVVR	Y179^	n/a	n/a	
579	Stx4	syntaxin-4	NP_112387	QGDNIS*DDDEVR	S15	n/a	n/a	
580	Stxbp5	syntaxin-binding protein 5 isoform m	NP_110470	DPYRREPRS*PR	S685^	n/a	n/a	
581	Suv420h1	histone-lysine N-methyltransferase SUV420H1	NP_001101982	DSIDIDIS*RRR	S871^	n/a	n/a	
582	Tacc2	transforming acidic coiled coil 2 isoform 1	NP_001004415	LDNTPAS*PPRS*PAEPSDPIAK	S2207, S2211	n/a	n/a	
583	Tceb3	transcription elongation factor B polypeptide 3	NP_058799	S*PEMDQEPVISHPKPKG	S195	0.07	0.19	
584	Tcfap2d	transcription factor AP-2-delta	NP_001100365	QHMEQKEQT*ARKK	T166	n/a	n/a	
585	Tgfb11	PREDICTED: transforming growth factor beta-1-induced transcript 1 protein	XP_341935	VQNHLPASGPPQPAV*PTR	S186^	n/a	n/a	



#	Gene Symbol	Protein Name	Refseq Accession	Peptide Sequence	Site(s)	Log <sub>2</sub> (H/V) Mean	Log <sub>2</sub> (H/V) SE	Sig.
586	Tgfb11	PREDICTED: transforming growth factor beta-1-induced transcript 1 protein	XP_341935	VQNHLPASGGPPQAVSPT*R	T188	n/a	n/a	
587	Tgoln1	trans-Golgi network integral membrane protein TGN38 precursor	NP_620195	VLGPSS*SENGEQLTDSMKDEK	S271^	0.76	0.98	
588	Thoc2	PREDICTED: THO complex 2	XP_233081	GGEKPPVSGSLKS*PVPR	S1393	0.54	0.44	
589	Thrap3	thyroid hormone receptor-associated protein 3	NP_001009693	ERS*PALKS*PLQSVVVR	S248, S253	0.25	0.59	
590	Thrap3	thyroid hormone receptor-associated protein 3	NP_001009693	IDIS*PSTFR	S679	-0.03	0.07	
591	Tjp1	tight junction protein ZO-1	NP_001099736	AVPVS*PSAVEEDEDGHTVVATAR	S1602	-0.08	0.13	
592	Tjp1	tight junction protein ZO-1	NP_001099736	FNHLLPSETVHKPELS*SKPPSPK	S1549^	0.63	1.24	
593	Tjp1	tight junction protein ZO-1	NP_001099736	FNHLLPSETVHKPELSKPPSPK	S1555	1.38	1.90	
594	Tjp1	tight junction protein ZO-1	NP_001099736	MSKPGAVS*TPVKHVDHTPK	S341^	-0.58	0.54	
595	Tjp1	tight junction protein ZO-1	NP_001099736	S*REDLSAQPVQTK	S605	n/a	n/a	
596	Tjp1	tight junction protein ZO-1	NP_001099736	SREDS*AOVPQTK	S610	-0.08	0.10	
597	Tjp2	tight junction protein ZO-2	NP_446225	KVQVAPLQGS*PPLSHDDR	S107	-0.62	0.13	*‡
598	Tjp3	tight junction protein ZO-3	NP_001101543	AIAPES*PGEGR	S348	n/a	n/a	
599	Tmem139	PREDICTED: transmembrane protein 139-like	XP_002726399	VVST*APDLQSLR	T171	0.32	1.11	
600	Tmem143	transmembrane protein 143	NP_001100983	VWLVLPALLGT*PRALSS*LENRMGAY*R	T37^, S43^, Y51^	-1.18	3.35	
601	Tmpo	lamina-associated polypeptide 2, isoform beta	NP_037019	QNGSNDSDRY*DNDESKIELK	S183^	n/a	n/a	
602	Tmpo	lamina-associated polypeptide 2, isoform beta	NP_037019	SST*PLPTVSSAENR	T159	0.26	0.14	
603	Tmx1	thioredoxin-related transmembrane protein 1	NP_001019971	KVEEQEADEEDV*EEETENR	S245	n/a	n/a	
604	Tmx1	thioredoxin-related transmembrane protein 1	NP_001019971	VEEQEADEEDV*EEETENR	S245	n/a	n/a	
605	Tnks1bp1	PREDICTED: tankyrase 1 binding protein 1	XP_215763	RAS*VSTNQNTDENDQELR	S883	n/a	n/a	
606	Tnks1bp1	PREDICTED: tankyrase 1 binding protein 1	XP_215763	RFS*EGVLRPPSODQEK	S423	0.54	0.65	
607	Tnks1bp1	PREDICTED: tankyrase 1 binding protein 1	XP_215763	S*SGSLSPGLETDPLEAR	S1355^	n/a	n/a	
608	Tnks1bp1	PREDICTED: tankyrase 1 binding protein 1	XP_215763	SSGSL*PGLTDPLEAR	S1360	n/a	n/a	
609	Tns1	PREDICTED: tensin 1	XP_237286	AINPTMAAPGSPSL*HR	S1467	-2.04	0.06	*‡
610	Tns1	PREDICTED: tensin 1	XP_237286	ET*TSRTPEEPLNLEGLVAHR	T1108	0.04	0.04	
611	Tns1	PREDICTED: tensin 1	XP_237286	ETTSRT*PEEPLNLEGLVAHR	T1115	0.01	0.07	
612	Tns1	PREDICTED: tensin 1	XP_237286	HLGGSGSVPGS*PSLDR	S1568	-0.86	0.15	*‡
613	Tns1	PREDICTED: tensin 1	XP_237286	HLGGSGSVPGS*LDR	S1570^	-1.15	0.12	
614	Tns1	PREDICTED: tensin 1	XP_237286	HPVQSHQVPLHSGVVTTPGS*PSLGR	S1523	-2.02	0.28	*‡
615	Tns1	PREDICTED: tensin 1	XP_237286	HVAYGGYST*PEDR	T1582	-0.98	0.12	*‡
616	Tns1	PREDICTED: tensin 1	XP_237286	KKDS*LNSSGPIITAR	S628	1.17	0.25	*‡
617	Tns1	PREDICTED: tensin 1	XP_237286	MAAPGS*PSLSHR	S1463^	n/a	n/a	
618	Tns1	PREDICTED: tensin 1	XP_237286	QVMGSPGPGFHGNVSGHPTSATVAPGS*PSLGR	S1497^	-2.34	0.28	*‡
619	Tns1	PREDICTED: tensin 1	XP_237286	S*QSPDVEPOLQAPAR	S873^	0.26	0.17	
620	Tns1	PREDICTED: tensin 1	XP_237286	SQS*FPDVEPOLQAPAR	S875	0.70	0.59	
621	Tns1	PREDICTED: tensin 1	XP_237286	SYS*PYDQLHPAASNGSFRPK	S1052	n/a	n/a	
622	Tns1	PREDICTED: tensin 1	XP_237286	T*PEEPLNLEGLVAHR	T1115	n/a	n/a	
623	Tns1	PREDICTED: tensin 1	XP_237286	TVGTNTPPS*PGFGR	S1446	-0.68	0.16	*‡
624	Tns1	PREDICTED: tensin 1	XP_237286	VGSHQVPLHSGVVTTPGS*PSLGR	S1523	-2.89	0.60	*‡
625	Tns1	PREDICTED: tensin 1	XP_237286	WDS*YDNFNHGR	S592	1.88	1.49	
626	Tomm34	mitochondrial import receptor subunit TOM34	NP_001037709	NRVPS*AGDVER	S186	-0.38	0.20	
627	Tomm70a	mitochondrial import receptor subunit TOM70	NP_997684	AS*PALGSGPDGSGDSLEMSLDR	S94	n/a	n/a	
628	Tor1aip1	torsin-1A-interacting protein 1	NP_659560	LEOHSQQAQQQLS*PATSGR	S142	-3.11	2.63	
629	Tpr	translocated promoter region	NP_001100655	TDGFAEIH*POVAVVPR	S2152	-0.30	0.16	
630	Tra2a	transformer-2 protein homolog alpha	NP_001119768	HT*PTPIYMGRR	T200	0.00	0.04	
631	Trim23	GTP-binding protein ARD-1	NP_001094107	MEIRVVT*LLDGGAGK	T409	n/a	n/a	
632	Trim28	transcription intermediary factor 1-beta	NP_446368	SRS*GEGEVGLMR	S474	1.02	1.61	
633	Ttn	PREDICTED: titin	XP_001065955	DT*STT*AWQIVSAT*VAR	T22251^, T22254^, T22262^	n/a	n/a	
634	U2af2	PREDICTED: U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 isoform 6	XP_001060115	NRDORSAS*RRRRR	S55^	1.57	3.18	
635	Ubxn4	UBX domain-containing protein 4	NP_001012025	NTELCET*PTTSDPK	T156	n/a	n/a	
636	Ugdh	UDP-glucose 6-dehydrogenase	NP_112615	RIPYT*PGEIPK	T474	-0.27	0.12	
637	Uhrf1	E3 ubiquitin-protein ligase UHRF1	NP_001008882	KS*TPGATT*SPR	S696^, T697^, T702^	n/a	n/a	
638	Utrn	utrophin	NP_037202	NVRPQPPT*SPGGR	T1404	0.48	0.78	
639	Utrn	utrophin	NP_037202	NVRPQPPTS*PEGRR	S1405	-0.49	0.28	
640	Vcl	vinculin	NP_001100718	S*LLDASEEAIKK	S721	-0.49	0.11	*
641	Wbp11	WW domain-binding protein 11	NP_001009661	RRDEDMLYS*PELAQR	S237	-0.28	0.19	
642	Wdr20a	WD repeat domain 20a	NP_001094364	RNS*TDSRPVSVTYR	S357	-2.83	1.99	
643	Wdr20a	WD repeat domain 20a	NP_001094364	SNS*LPHSAVSNAGSK	S434	-0.82	2.15	
644	Wdr20a	WD repeat domain 20a	NP_001094364	SNSLPHS*AVSNAGSK	S438^	1.62	1.25	
645	Xpo1	exportin-1	NP_445942	EKVY*IGK	Y126	n/a	n/a	
646	Zc3h18	zinc finger CCH domain-containing protein 18	NP_958819	VQSQEEIHS*DEEDQASEPK	S63	n/a	n/a	
647	Zdhhc5	probable palmitoyltransferase ZDHHC5	NP_001034427	GDS*LKEPTSIADSSR	S380	1.03	1.35	
648	Zfp64	zinc finger protein 64	NP_001012093	THMR	T192	-2.28	1.65	
649	Zfr	PREDICTED: zinc finger RNA-binding protein	XP_345170	RRDS*DGVDGFEAEKG	S1027	n/a	n/a	
650	Znf574	zinc finger protein 574	NP_001019429	KS*HVRNHLR	S509	n/a	n/a	
651	Zranb2	zinc finger Ran-binding domain-containing protein 2	NP_113804	ENVEIEREES*DGEYDEFGR	S120^	n/a	n/a	
652	Zranb2	zinc finger Ran-binding domain-containing protein 2	NP_113804	EVEDKES*EGEEDEDEDLSK	S153	n/a	n/a	
653	Zranb2	zinc finger Ran-binding domain-containing protein 2	NP_113804	YNLDAS*EEEDSNK	S188	n/a	n/a	
654	Zyx	zyxin	NP_446213	S*PGGGLTLK	S336	-0.30	0.21	