Type 1 Diabetes Cadaveric Human Pancreata Exhibit a Unique Exocrine Tissue Proteomic Profile

Chih-Wei Liu, Mark A. Atkinson and Qibin Zhang

Supplementary Figures

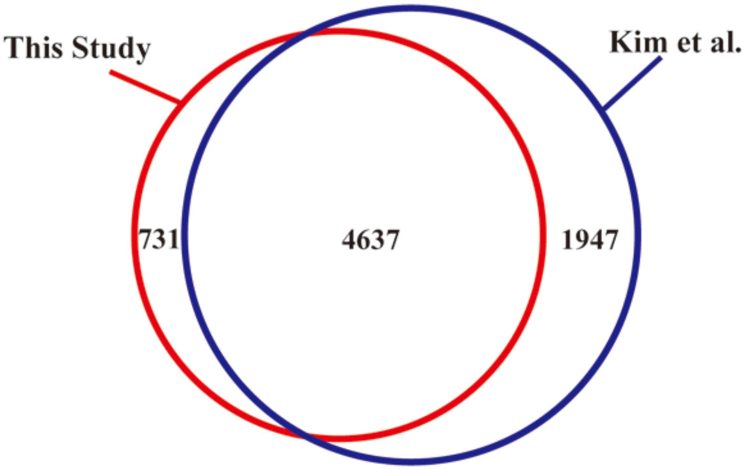

Figure S1. Venn diagram showing pancreatic head proteome identified in this study and pancreatic proteome by Kim et al. [1] Raw datasets in the latter were re-searched using MaxQuant under the same parameters used in our study. The calculation was based on gene name information in those two datasets.

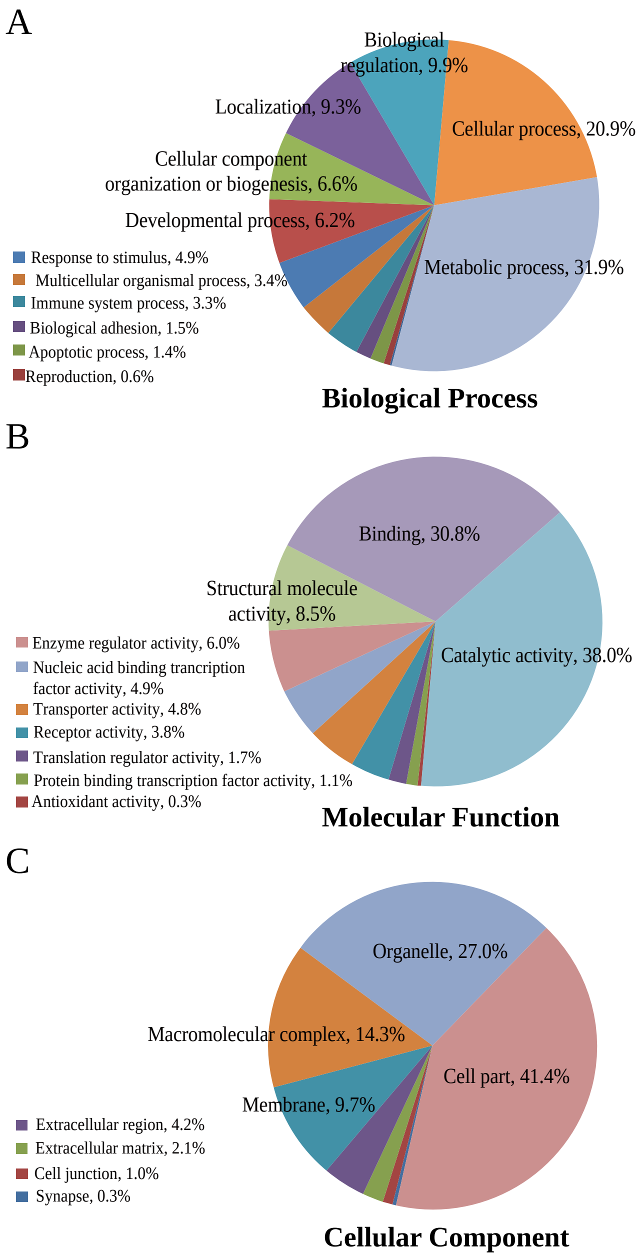

Figure S2. Gene Ontology (GO) functional classification of the pooled isolated human pancreatic islets proteome identified in Schrimp-Rutledge et al.[2] In total, 6649 “Entrez Gene Symbol” provided in that report of Schrimp-Ruledge et al. were analyzed by PANTHER software, and 9834, 5809, and 3032 annotation hits were found in the categories of biological process (A), molecular function (B), and cellular component (C), respectively.

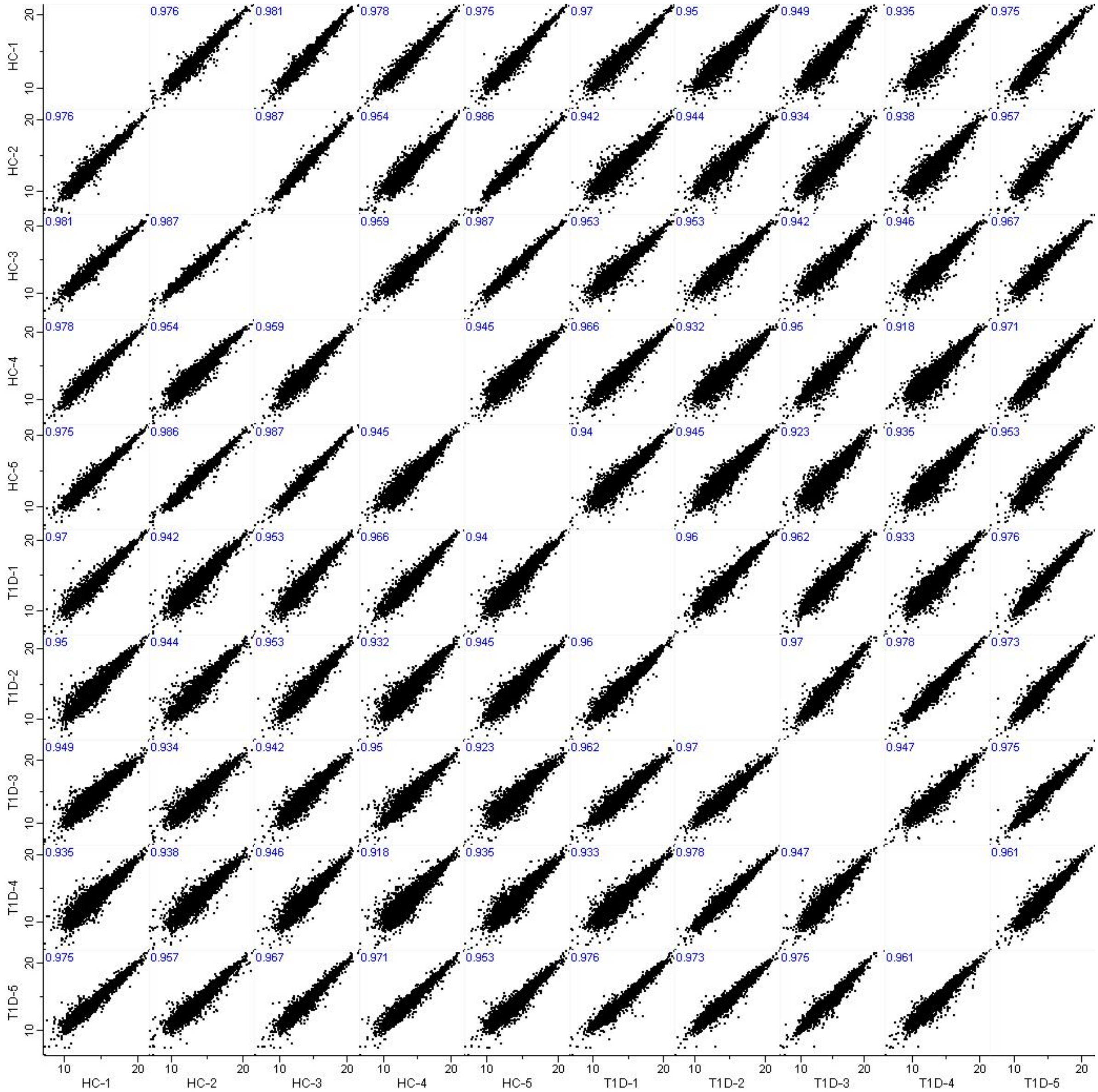

Figure S3. Multi-scatter plot of pancreatic tissue proteome from samples of Type 1 diabetes and healthy subjects.

The plot exhibits a good correlation among the biological replicates with an average Pearson's correlation coefficient of 0.96. T1D and HC in the plot indicate samples belonging to type-1 diabetes and healthy control subjects, respectively.

REFERENCES

[1] Kim, M. S., Pinto, S. M., Getnet, D., Nirujogi, R. S., *et al.*, A draft map of the human proteome. *Nature* 2014, *509*, 575-581.
[2] Schrimpe-Rutledge, A. C., Fontes, G., Gritsenko, M. A., Norbeck, A. D., *et al.*, Discovery of novel glucose-regulated proteins in isolated human pancreatic islets using LC-MS/MS-based proteomics. *Journal of proteome research* 2012, *11*, 3520-3532.

Table S1. 5368 protein groups identified in pancreatic tissue.

Majority protein ID	Protein names	Gene names	Mol. weig	Sequence	Peptides	Unique pe	Score	Q-value	HC 1 rep	HC 2 rep	HC 3 rep	HC 4 rep	HC 5 rep	T1D 1 re	T1D 2 re	T1D 3 re	T1D 4 re	T1D 5 re	BCGA m	BCGA m	BCGA m	BCGA m	Identified in Kim et a	Pancreas e	Pancreas enriched proteins in Uhlén et al (2015)
A0A024QZX5;A0A	Serpin B6	SERPINB6	43.024	58.9	51	51	320.18	0	325270	169730	224560	452610	190380	324570	410490	398040	200690	392420	Enriched	Enriched	Enriched	Enriched	YES		
A0A024R4E5;Q00	Vigilin	HDLBP	141.44	46.4	111	111	323.31	0	919610	791870	761150	706840	1240200	792490	851600	729320	404430	692570	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WZA9;A0A	Transmembrane prote	TMPIT;TMEM120A	20.459	5.7	1	1	1.8299	0.00975	1525	1752.5	1540.3	867.99	2379.2	1166.8	1435.2	1205.2	1661.6	1328.1	Low	Enriched	Enriched	No expres	YES		
A0A024R571;Q9H	EH domain-containin	EHD1	61.927	30.8	21	12	63.24	0	85759	60600	80353	73419	81948	124490	110810	95612	71560	104740	Enriched	Moderate	Enriched	Moderate	YES		
A0A024R644;O75	Ceroid-lipofuscinosis	CLN5	46.339	7.6	2	2	3.3613	0.00078	7382.8	5543.4	5162.3	7796.4	5162	8237.9	7587.3	11461	4582.5	8210.3	Enriched	Enriched	Enriched	Low			
K7EN05;K7EPC8;	Transcription elongat	ELOF1	8.6531	23.7	3	3	24.207	0	28863	19035	19414	29983	25020	16584	14934	14331	8583.7	19801	Enriched	Enriched	Enriched	No expres	YES		
A0A024R7W5;A0A	YTH domain-contain	YTHDF3;YTHDF1	58.311	12.9	6	4	11.248	0	34484	35364	35776	28403	44008	28248	44116	39072	34801	37726	Enriched	Moderate	Enriched	Moderate			
A0A024RAC6;Q14	Transcription elongat	TCEB3	87.229	9.3	8	8	19.858	0	47036	34439	45651	45885	52841	43559	71649	156890	37757	57869	Moderate	Enriched	Enriched	Enriched	YES		
A0A024RBT2;Q9N	Diablo homolog, mit	hCG_1782202;DIABLO	18.919	19.9	3	3	49.348	0	4565.4	3382.7	4525.1	6968.1	5007.7	7266.2	38993	15134	36102	27545	Enriched	Enriched	Enriched	No expression			
E7EWF5;G5E9M9;	Transcription cofacto	VGLL4	24.223	11.6	2	2	10.015	0	4516.1	4299	7266.6	4578.5	7005.7	2411.4	14206	11539	15990	7919.2	Enriched	Enriched	Enriched	Moderate			
A0A075B6F6;Q8T	Minor histocompatib	HM13	30.162	11.4	6	6	12.874	0	58451	49287	48116	55659	44808	82769	69108	59484	24909	61108	Moderate	Enriched	Enriched	No expres	YES		
A0A075B797;M0R	Nitric oxide synthase	NOSIP	25.62	11.6	2	2	6.4528	0	8004.7	4930	6758.7	10117	6313.2	9597.8	11587	10168	6025.8	8872.3	Enriched	Enriched	Enriched	No expres	YES		
A0A075B6I8;P017	Ig lambda chain V-I r	IGLV1-47	12.283	23.9	5	2	6.3799	0	3504.5	3697.8	5825.2	2932.3	3949.3	4368.3	6547.7	36632	4033.1	6417					YES		
A0A075B6J4;A0A075B6K0;A0A075B6		IGLV3-25;IGLV3-16;IG	12.011	19.6	5	4	8.1467	0	728.35	670.38	1376.8	418.96	868.84	1219.2	1585.1	12964	1186.1	2020.2	Moderate	Moderate	Moderate	No expression			
A0A075B6J7		IGLV3-21	12.446	30.8	5	3	11.073	0	7507.5	8929.5	15604	6978.9	12137	7045.5	10282	8184.7	7302.4	7221.1							
A0A075B6L0;A0A	Ig lambda-3 chain C r	IGLC3;IGLC2;IGLC6	11.208	82.1	19	2	60.719	0	54756	54540	72731	61156	58660	58536	78463	296130	39770	66826	Low	Moderate	Moderate	Low	YES		
A0A075B730;A0A	Epiplakin	EPPK1	553.12	20.5	29	22	89.569	0	108770	43522	61944	93943	62085	75471	98604	101650	56467	100500	Moderate	Moderate	Moderate	No expres	YES		
A0A075B746;P829	28S ribosomal protei	MRPS21	10.688	14.9	1	1	3.3013	0.00078	7629.7	3088.1	2219.9	7083.2	7408.9	6303.8	4106.2	4050.7	2095	6905.2	Enriched	Enriched	Enriched	No expres	YES		
E9PKH0;M3ZCP1;	Receptor-type tyrosin	PTPRC	67.887	4.2	2	2	4.0424	0.00062	5286.2	3330.1	3707.8	5911.5	3813.7	5289.5	3504.6	6050.6	1445.9	5728.6	Moderate	No expres	Low	Low	YES		
A0A087WT45;A0A	GRIP1-associated pro	GRIPAP1	90.856	17.1	14	14	37.435	0	24548	21741	26008	22499	30595	25194	30337	32280	16363	29388	Moderate	Enriched	Moderate	No expres	YES		
A0A075B7B1;O15	Synemin	SYNM	140.16	5.2	6	6	21.837	0	18742	18514	15682	14097	19540	13860	12887	13034	8695	22169	Enriched	Moderate	Moderate	Moderate	YES		
A0A075B7D6		TAF15	3.5044	56.2	2	2	4.8462	0.00043	11801	12037	13801	8013	13971	7561.3	8971.9	5471	5391.6	10526	Moderate	Enriched	Enriched	Enriched	YES		
A0A075B7F2		TAF15	26.158	7.5	2	2	24.547	0	1055.6	1205.2	1182.9	1462.2	1683.1	1377.8	1540	1428.7	703.36	1713.5	Moderate	Enriched	Enriched	Enriched	YES		
A0A075B7F8;A8C	Nuclear envelope por	POM121C;POM121	125.09	6.4	7	7	43.508	0	13520	11184	12415	7210.6	17258	10021	21059	8900.6	12298	17214	No expres	No expres	Moderate	No expres	YES		
V9HW75;A0A087V	Nucleobindin-2;Nesfa	HEL-S-109;NUCB2;DC	50.222	58.8	55	54	323.31	0	509590	455890	339880	411640	498360	460240	490680	345030	246500	315300	Enriched	Enriched	Enriched	Enriched			
A0A087WSW9;A0	Thioredoxin reductas	TXNRD1;GML	60.078	29	14	12	33.257	0	39977	33128	34291	41393	39523	33877	38378	36885	23498	34271	Enriched	Enriched	Enriched	Enriched			
K7ERP4;A0A087X	Glutathione peroxida	GPX4	17.629	38.1	8	8	27.026	0	29431	22551	29324	37222	32228	33109	49036	39127	38374	36845	Enriched	Enriched	Enriched	No expres	YES		
A0A087WT38;Q96	Williams-Beuren syn	WBSCR16	17.209	19.6	2	2	7.5446	0	3603.9	2214.5	1786.3	3935.1	1727.2	3913.5	2401.3	3671.7	816.77	4233.9	Enriched	Enriched	Enriched	No expres	YES		
A0A087WT44;P30	Heme oxygenase 2	HMOX2	41.669	23.5	10	10	24.315	0	15043	13684	15898	25280	17489	20318	16712	20398	8736.6	18768	Enriched	Enriched	Enriched	Low	YES		
A0A087WTA8;P08	Collagen alpha-2(I) c	COL1A2	129.15	15	46	46	323.31	0	146810	220980	343100	152900	293960	99036	447760	271330	145660	178110	Enriched	Enriched	Enriched	Enriched	YES		
Q5T985;A0A087W	Inter-alpha-trypsin in	ITIH2	105.21	10.1	11	11	25.042	0	32192	33551	34869	41527	28629	28770	35212	53960	22278	38178	Moderate	Low	Low	No expres	YES		
A0A087WTL2;Q9P	Armadillo repeat-con	ARMCX1	39.004	11.5	4	4	8.1985	0	17428	11364	17668	5736.8	26133	3263.8	7584.3	3419.4	3318.4	9365	Low	Moderate	Enriched	No expres	YES		
A0A087WTL4;A0A	Bcl-2-like protein 13	BCL2L13	48.871	10	5	5	13.978	0	31582	12994	16843	43031	21809	41651	37831	43550	14829	41064	Moderate	Enriched	Enriched	No expres	YES		
A0A087WTP3;Q92	Far upstream element	KHSRP	73.027	31.9	26	25	323.31	0	138970	114180	136700	133820	159210	122260	209670	178020	110460	152700	Enriched	Enriched	Enriched	Moderate	YES		
E7EQ49;A0A087W	WD repeat-containin	WDR37	27.438	30.1	7	7	35.424	0	26143	18726	20951	22670	22417	28564	31473	32463	14996	28190	Enriched	Enriched	Enriched	Moderate	YES		
A0A087X0S7;A0A	Leucine-rich repeat-c	LRRC41	56.4	6.1	2	2	31.839	0	871.09	199.62	215.46	222.35	269.56	134.8	196.74	242.44	520.73	535.69	Enriched	Moderate	Enriched	Moderate	YES		
A0A087WTV1;Q9P	Oxysterol-binding pro	OSBPL2	20.362	7.2	2	2	8.7559	0	6882.8	6418.2	6034.9	3379.1	5456.2	8056.5	19595	13365	9683.2	11924	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WTV6;J3KR12			25.868	34.1	11	1	29.387	0	44117	37978	41446	33334	52322	37859	76758	53594	52991	60709							
A0A087WTX2;Q92	Zinc transporter SLC	SLC39A7	46.393	5.8	4	4	12.695	0	40878	24424	21264	42337	45834	22209	22958	15044	7572.3	31779	Moderate	Moderate	Moderate	Moderate	YES		
A0A087WTX5;A0A	Ig kappa chain C regi	IGKC	25.624	55.1	34	31	323.31	0	176780	177700	214890	234430	182340	180300	205320	723270	107240	192920	Moderate	Enriched	Moderate	No expres	YES		
A0A087WWB5;A0	Gamma-tubulin comp	TUBGCP3	48.983	4.6	2	2	33.669	0	10786	8886	8224.7	10370	10320	9481.2	13081	19336	8688.8	15202	No expres	Moderate	Enriched	Moderate	YES		
Q13030;E9PH25;E	Glycophorin-A	GPErik;GYPA	9.3318	15.3	1	1	4.0301	0.00062	2399.2	6094	3584.8	1860.3	4310.3	2096.9	4075.1	2534.9	2548.1	3217.2	No expres	Low	Low	Low			
A0A087WU53;Q9P	Magnesium transport	MAGT1	41.531	10.6	4	4	5.5618	0	17484	10496	13815	26943	13852	34101	18989	14204	6757.9	14804	Enriched	Enriched	Enriched	No expres	YES		
A0A087WU62;A0A	39S ribosomal protei	MRPL45	29.348	19.1	6	6	12.308	0	41740	31337	31447	41663	38176	39901	27907	44795	14337	41462	Enriched	Enriched	Enriched	No expres	YES		
A0A087WUA5;Q9	EH domain-containin	EHD4	61.113	40.2	31	26	323.31	0	156090	102920	142300	138460	137790	184380	211830	150350	107050	163430	Moderate	Enriched	Enriched	No expres	YES		
A0A087WUB9;Q8	Beta-catenin-like pro	CTNNBL1	65.702	14.1	11	11	55.084	0	41211	29477	38351	38727	40335	43953	49701	52746	34515	57603	Enriched	Moderate	Moderate	No expres	YES		
A0A087WUC6;Q1	Signal peptidase com	SPCS2	25.09	50.7	25	25	100.72	0	156800	98986	109240	125880	147570	190860	183830	156430	72985	119900	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WUD1;Q6	Zinc finger protein 78	ZNF787	40.428	22.5	6	6	66.094	0	11881	13248	13295	11535	17448	10187	18601	11895	12499	12796	Enriched	Low	Low	Moderate	YES		
A0A087WUD3;Q9	Oligosaccharyltransfe	OSTC	9.369	15.7	4	4	6.142	0	7446.4	2677	4149.2	7882.9	3807.9	10039	7514.3	12021	3209.3	8415.9	Enriched	Enriched	Enriched	No expres	YES		
A0A087WUH0;R4	DNA repair protein c	BIVM-ERCC5;ERCC5	133.11	1.5	2	2	3.7556	0.0006	5743.7	6146.5	7329.4	5225	8889.1	5495.7	18853	15640	11420	9630.7	Enriched	Moderate	Enriched	Moderate			
J3QTS8;A0A087W	Tryptase alpha/beta-1	TPSAB1;TPSB2	31.282	35.8	21	17	77.207	0	70685	64467	85574	84281	101740	127530	126590	236660	54308	106060	Low	Moderate	Moderate	Low	YES		
A0A087WUK0;Q2	AP2-associated prote	AAK1	85.759	15.3	9	7	32.593	0	60974	52003	55592	56119	60411	45441	45791	63991	30529	66692	Enriched	Enriched	Enriched	Low	YES		
A0A087WUK2;O1	Heterogeneous nucle	HNRNPDL	40.04	27	14	12	129.89	0	117740	83231	119260	159550	112350	112190	191320	146690	92842	137650					YES		
A0A087WUL0;Q3	Bifunctional ATP-de	DAK	59.057	41.5	30	30	91.521	0	111120	85127	89742	125250	102560	106630	136700	164340	66525	118980	Low	Low	Moderate	No expres	YES		
A0A087WZG9;B4	Retrotransposon-deri	hCG_1642748;PEG10	40.471	6.7	2	2	3.2116	0.00077	1541.8	1609.2	2765.8	1379.7	3489.7	1470.2	2210.6	2056.5	1828.2	2095.9	Moderate	Enriched	Enriched	Enriched	YES		
A0A087WUM0;P5	Synaptojanin-2-bindi	SYNJ2BP	20.774	32.3	9	9	22.054	0	45070	28168	35186	48263	32013	47086	32763	30535	19869	50416	Enriched	Enriched	Enriched	No expres	YES		
Q9UDT1;A0A087V	Rhomboid domain-co	WUGSC:H_RG122E10.	8.3796	17.7	2	2	4.0627	0.00062	17099	9668.1	13885	14563	13262	23067	19288	20520	7967.5	14789	Low	Enriched	Enriched	No expression			
A0A087WUQ1;E5	PDZ and LIM domai	PDLIM2	7.7495	15.3	2	2	2.8011	0.00222	4414.5	4408.2	4520.7	5175.5	4481.9	4317.3	7462.3	5167.4	4986.6	5133	Enriched	Moderate	Enriched	No expres	YES		
A0A087WUQ6;P07	Glutathione peroxida	GPX1	21.938	56.9	17	17	126.24	0	91226	61590	66401	91164	76503	110010	110590	151220	63033	144570	Enriched	Enriched	Enriched	Enriched	YES		
E7ETK0;A0A087W	40S ribosomal protei	RPS24	15.197	35.1	13	13	17.799	0	47465	32831	31494	41566	38848	38090	101790	59449	46190	48128	No expres	Enriched	Enriched	Enriched	YES		
A0A087WUT6;O60	Eukaryotic translatio	EIF5B	138.68	24.3	35	35	148.25	0	142310	93446	111190	108220	151850	121350	160740	120490	79387	116800	Enriched	Moderate	Enriched	Enriched	YES		
A0A087WUW5			9.1322	68.3	9	3	10.685	0	6891.6	3564.4	4299.3	3345.2	5948.9	6727.1	9921.4	3890.7	9641.7	7811.8							
A0A087WV30;C9J	NF-kappa-B essential	IKBKG	12.981	24.3	2	2	7.9853	0	14046	17629	12644	17996	16258	13970	11430	16273	8873.9	14096	Enriched	Moderate	Moderate	Moderate	YES		
A0A087WV05;Q9	C-Myc-binding prote	MYCBP	12.755	33.6	6	6	22.859	0	33266	27579	35407	20283	32790	41635	51851	39373	23857	46079	Moderate	Enriched	Enriched	Moderate	YES		
A0A0A0MSA0;A0	Laminin subunit alph	LAMA3	360.18	1.6	4	3	7.3297	0	4352.7	4052	5289.5	4298	4517.1	3352.7	4727.4	3875.7	3316.7	4990.4	Enriched	Low	Moderate	Moderate	YES		
F8WER1;H7BZF7;	Aromatic-L-amino-ac	DDC	24.757	7.9	2	2	2.2714	0.00494	2188.1	1881.8	2266.9	1554.7	2074	5851.8	11092	10546	4785.6	10523	Moderate	Moderate	Enriched	Enriched	YES		
A0A087WV25;O95	FGFR1 oncogene par	FGFR1OP	38.099	7.1	2	1	8.0418	0	8115.7	6189.3	7259	6480.8	7429.9	6400.6	8380.9	5486.2	5322.6	6545.9	Moderate	Low	Moderate	Low	YES		
A0A087WV47;A0A	Ig gamma-1 chain C r	IGHG1	51.153	45.3	63	1	323.31	0	326070	315520	358170	482300	349450	352520	406830	1138000	247800	356980	Low	No expres	Moderate	No expres	YES		
A0A087WV52;Q9	28S ribosomal protei	MRPS30	38.893	10.4	4	4	71.088	0	7914.3	10689	10671	9456.1	12010	8476.5	12030	10507	10918	13378	No expres	Enriched	Enriched	No expres	YES		
A0A087WV73;P46	Probable 28S rRNA (	NOP2	94.095	9.4	7	7	26.258	0	21994	19766	22552	24466	25452	23591	36086	32613	22047	31459	Enriched	Enriched	Enriched	No expres	YES		
I3L405;I3L261;I3L	Mannose-P-dolichol	MPDU1;HBEBP2BPA	5.736	53.7	3	3	8.3692	0	6373.5	3129.2	4538.3	5762.2	4820.6	4355	5793	5438.4	2317.4	7774.7	Low	Low	Enriched	No expres	YES		
A0A087WV97;Q8	Stromal membrane-a	SMAP2	46.382	15.1	6	6	9.1319	0	4262.3	3659.7	3474.6	3669.6	4587.7	6091.1	3309.5	3763.8	2092.1	3685.2	Moderate	Moderate	Enriched	No expres	YES		
A0A087WVA8;Q8	Testis-expressed sequ	TEX2	125.38	2.9	3	3	5.6148	0	3833.7	2797.1	3110.5	7421.5	2981.5	5000	2752.3	3616.1	1820.3	3782.4	Enriched	Enriched	Enriched	No expression			
A0A087WVC1;A0	ATP-dependent RNA	DDX50	82.226	8.1	8	4	3.35	0.00078	19331	16159	14408	14925	18133	12703	11069	13600	6369.7	14948	Low	Enriched	Enriched	No expression			
A0A087WVD1;Q9	Leukocyte receptor c	LENG9	50.766	5.9	2	2	15.961	0	3932.2	3621.1	4169.8	9014.1	3134.3	5584.9	4727	8158.9	3052.4	7459.6	Enriched	Enriched	Enriched	No expres	YES		
A0A087WVD4;Q9	Arsenite methyltransf	AS3MT	37.969	3	1	1	1.8987	0.00829	9925.7	5259.5	7213.8	10243	7607.3	7648.6	23631	12637	9992.1	10164	Low	Enriched	Moderate	No expres	YES		
A0A087WVF7;Q9	Intersectin-2	ITSN2	191.6	2.6	4	3	6.4625	0	14829	10896	11030	9732.7	16526	5691.1	10444	8959.2	5034.5	8424	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WVG2;Q5	Ras-interacting protei	RASIP1	103.53	4.3	3	3	5.6551	0	4915.2	3897.3	5139.2	3765.9	6581.7	4760.1	6283.6	5052.4	5218	6365.3	Low	Moderate	Moderate	No expres	YES		
A0A087WVI4;Q7Z	Transmembrane chan	TMC4	78.737	7.5	5	5	19.129	0	15657	10147	17462	19416	13906	17421	14688	16758	8613.7	14943	Enriched	Enriched	Enriched	No expres	YES		
A0A087WVJ0;B1A	Mucin-1;Mucin-1 sul	MUC1	25.565	20.6	5	5	16.378	0	42391	24236	53313	35780	52640	31236	47907	31234	28899	37441	Moderate	Enriched	Enriched	Enriched			
A0A087WVM4;B7	Monofunctional C1-t	MTHFD1L	99.31	5.6	5	4	4.8735	0.00043	4739.3	3581.6	5227.4	7007.9	6292.1	4338.9	4179.9	3181.3	2013.9	4254.9	Low	Enriched	Enriched	No expres	YES		
A0A087WVM5;B4	Coiled-coil domain-c	CCDC28A	17.792	28	5	5	44.184	0	27547	23095	30174	27510	33470	22910	27294	25443	16791	24893	Enriched	Enriched	Enriched	Moderate	YES		
A0A087WVP4;A0A	Smoothelin	SMTN	104.84	3.1	3	3	47.815	0	4936.5	5933.7	4815.9	3872.9	9347.2	5614.7	10774	5677.9	7450	13826	No expres	Moderate	Moderate	Low	YES		
A0A087WXJ9;A0A	Probable serine carbo	CPVL	26.648	14.8	3	2	6.9078	0	2345.3	1709.6	1337.3	1166.7	1077.9	770.41	1220.8	3453.4	2097	3124.2	Low	Low	Moderate	Low	YES		
A0A087WVS8;Q7	MOB kinase activato	MOB2	26.879	9.3	3	3	3.5841	0.00079	26989	19783	24009	25090	28025	21883	29791	23853	15383	26361							
A0A087WVW8;A0	Sodium-coupled neu	SLC38A3	10.275	16.7	1	1	5.4402	0	12941	13089	14011	11291	14473	9358	10850	9576.7	5177.2	10856	Moderate	Low	Low	Low			
A0A087WVZ9;A0A	DNA-directed RNA p	POLR2E	21.459	17.4	3	2	6.5844	0	4424.2	3610.1	3744.6	2775	6736.5	2638.9	4797.6	3240.1	4314.7	3504.3	Moderate	Enriched	Enriched	Enriched	YES		
F8W0M9;C9JID8;	Secernin-3	SCRN3	23.602	5.3	2	2	3.434	0.00079	21093	15596	18968	20879	12207	21798	20755	24006	9368.9	19254	No expres	Moderate	Enriched	No expres	YES		
A0A087WW23;P2	Arachidonate 5-lipox	ALOX5AP	24.208	9.6	3	3	5.5894	0	696.22	934.27	1020.4	453.28	1100.2	1389.2	5304	8432.7	3241.6	2320.6	Low	Moderate	Enriched	Low	YES		
A0A087WW32;Q9	Interleukin-1 recepto	IRAK4	24.285	18.3	2	2	20.09	0	4264.9	3895.8	4296.1	3762	4079.3	2876.4	2906.4	2823.3	1721.3	3447.5	Moderate	Moderate	Moderate	No expres	YES		
A0A087WW36;A0	Lysophosphatidic aci	ACP6	16.314	12.6	1	1	3.175	0.00077	3368.3	2429.6	1828.5	5422.6	1544.6	2727.6	2378	5145.1	1096.9	5496.4	Enriched	Enriched	Enriched	No expression			
A0A087WW40;Q9	Endophilin-B1	SH3GLB1	44.26	27.7	15	7	28.044	0	68012	50610	59494	65360	57129	66369	101990	87825	63432	79760	Moderate	Enriched	Enriched	Enriched	YES		
A0A087WW55			26.622	46.6	65	0	323.31	0	1667100	1254600	1925300	1557700	1674600	1546400	1965300	1263400	1619300	1348200							
C9JAG1;A0A087W	Ethanolaminephosph	EPT1	20.557	5	1	1	1.8595	0.00878	7217.4	8199.9	8222.8	6109.4	10058	7112.2	6806.2	4257.7	3692	5281.9							
S4R460;A0A087W	Ig heavy chain V-III r	IGHV3OR16-9	10.429	30.2	6	3	29.436	0	14529	12280	12121	15071	13770	13640	16105	32649	12925	13185							
A0A087WWA7;P5	Putative segment pola	DVL1P1;DVL1	47.716	2.3	1	1	2.3001	0.00478	2482.9	1590.2	2038.4	2136	2668.2	2278.5	3562.5	2803.1	2771.4	3258.2	Enriched	Enriched	Enriched	Low	YES		
A0A087WWF1;Q8	Selenoprotein M	SELM	16.081	34	9	9	25.926	0	54206	32425	38349	52579	44806	52685	46228	50632	26009	45996	No expres	Enriched	Enriched	No expression			
A0A087WWI0;Q9	Leucine-rich repeat-c	C10orf11	25.689	15.5	2	2	13.844	0	1138.3	1018.1	924.84	556.45	1370.6	1243.3	3838.9	3155.2	4355.4	2024.4	Enriched	Enriched	Enriched	No expression			
A0A087WWK8;Q6	IQ motif and SEC7 d	IQSEC1	124.48	3.1	3	3	9.1867	0	4975.4	3649.4	3832.1	4421.4	4029.8	3489	3751.8	3837.5	4536.2	3798.5	Enriched	Moderate	Enriched	Enriched	YES		
A0A087WYS5;A0A	Trafficking protein pa	TRAPPC3	12.778	21.9	2	2	10.662	0	20448	16887	21210	24621	21418	18762	23171	22672	13971	22242	Moderate	Enriched	Enriched	Enriched	YES		
H0YMB3;A0A087	GMP reductase 2;GM	GMPR2	33.921	25.1	10	9	18.562	0	34254	29309	29759	27937	47815	22476	31154	23839	17124	27834	Moderate	Enriched	Enriched	No expres	YES		
A0A087WWP4;Q9	Putative RNA-bindin	RBM15	102.13	7.1	6	6	50.625	0	10844	7855.3	13095	16980	10437	13219	13928	15791	8162.6	14913	Enriched	Moderate	Enriched	No expres	YES		
V9GYP5;A0A087V	Ribosomal RNA smal	EMG1	23.79	16.6	3	3	6.1382	0	30312	28053	29285	19167	35212	20893	32000	24672	19677	24177	Low	Enriched	Enriched	Moderate			
A0A087WWS1;Q9	THO complex subuni	THOC1	75.651	11	8	8	11.779	0	41051	45786	39186	42588	44482	35224	30474	28372	19545	34587	Enriched	Enriched	Enriched	No expres	YES		
A0A087WWW9;O	B-cell lymphoma/leu	BCL10	18.073	12.2	2	2	2.3317	0.00462	8855.9	6659.2	7528.3	8129.7	9402	6760.7	7862.2	7943.5	3083.8	8436.3	Enriched	Moderate	Enriched	No expres	YES		
F5H5L8;F5GXV3;	Folate receptor beta;	FOLR2;FOLR3	16.899	16.9	3	3	41.636	0	10547	13945	12297	16405	17224	9226.1	13348	20327	8797.9	14626	Enriched	Low	Low	Moderate			
A0A087WWY3			245.85	45.1	174	2	3.3128	0.00078	7459.1	5891.3	5870.3	3834.9	10106	2582	7941.8	5234.1	3588.4	5903.3							
A0A087WWZ2;Q9	Phosphorylated CTD	PCIF1	34.458	10.9	3	3	5.8153	0	2635	3069.3	2763.3	2524	3576.5	2128.8	2316.4	2480.5	1542.2	2742.1	Enriched	Moderate	Moderate	No expres	YES		
A0A087WXC5;E7	NADH dehydrogenas	NDUFA10	40.836	22	12	12	38.603	0	115390	93905	112310	87791	137300	98457	70993	89818	44636	85826	Low	Enriched	Enriched	No expres	YES		
A0A087WXI5;P12	Cadherin-1;E-Cad/C	CDH1	100.03	21	27	27	135.73	0	217810	152000	161420	208150	203390	183920	163100	166370	103150	178850	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WXK9;Q1	Thyroid receptor-inte	TRIP11	227.42	14.9	28	28	130.18	0	101760	70628	74923	112810	103100	78608	78637	80799	48357	97283	Moderate	Moderate	Enriched	Moderate	YES		
B7Z879;A0A087W	Vacuolar protein sort	VPS11	107.37	6.2	5	5	35.145	0	25813	15920	18451	26567	19487	20391	15733	20967	9788.4	21297	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WXL8;A0A	Ig gamma-3 chain C r	IGHG3	56.889	37.3	42	16	114.63	0	75647	69433	92326	71199	72936	65903	77399	243410	62543	75046	Moderate	Moderate	Low	Moderate	YES		
A0A087WXM6;J3	60S ribosomal protei	RPL17	19.586	54.4	24	24	91.537	0	290990	196480	175890	180060	295860	185400	171670	234380	70820	170240	No expres	Enriched	Enriched	Enriched	YES		
C9JDP3;C9J0M6;E	Integrator complex su	INTS12	9.4947	22.7	2	2	4.2201	0.00063	25365	20615	25406	22102	34754	19011	33374	18969	15649	26901	Low	Moderate	Enriched	No expres	YES		
A0A087WXP3;E9	Integrin beta;Integrin	ITGB6	75.849	1.3	2	2	3.2402	0.00077	19319	18001	22044	18689	17163	20638	26224	25432	10140	23317	Moderate	Enriched	Enriched	Low			
F5H1Z6;A0A087W	PCTP-like protein	STARD10	29.043	46.4	12	12	61.052	0	63129	45035	47360	70782	69990	47791	61699	57298	40449	50180	Low	Enriched	Enriched	No expres	YES		
A0A087WXS7;O4	ATPase ASNA1	ASNA1	37.119	16.6	8	8	23.838	0	46769	22820	28283	55786	34485	42894	43495	38620	27055	44218	Low	Enriched	Enriched	No expres	YES		
S4R399;G3V328;A	Ataxin-3	ATXN3	23.002	10.1	2	2	3.2143	0.00077	3702.6	2248.4	3691	3327.6	3499.9	2597.9	1733.4	1316.9	822.81	2905.8	Moderate	No expres	Moderate	Low	YES		
A0A087WXZ3;Q9	YTH domain-contain	YTHDF2	61.163	5.1	3	1	5.015	0.00044	25276	18836	20088	21400	25060	15987	17683	17261	12084	20486	Moderate	Enriched	Enriched	No expres	YES		
A0A087WY55;Q9	Vacuolar protein sort	VTA1	31.102	18.6	5	5	10.364	0	17444	13960	17127	14672	21593	14320	44650	23685	26763	21912	Moderate	Enriched	Enriched	No expres	YES		
A0A087WY71;E9	AP-2 complex subun	AP2M1	49.526	26.7	15	15	49.965	0	97593	74569	86527	105800	82206	95807	107690	116090	51544	103100	Low	Enriched	Enriched	Enriched	YES		
D6RAW0;D6RFM	Ubiquitin-conjugatin	UBE2D3;UBE2D2;UBE	8.2133	36.1	3	3	15.492	0	24638	22833	21068	22758	29308	18813	47503	59930	16277	19811	Enriched	Enriched	Enriched	Enriched			
A0A087WY88;Q8	Protein jagunal homo	JAGN1	20.791	14.4	7	7	32.266	0	58308	44059	47657	42933	55557	45674	44793	41078	27290	45754	Moderate	Enriched	Enriched	No expres	YES		
A0A087WYC5			52.426	43.6	63	1	8.4881	0	5568.2	6856.8	6866.7	5734.2	6758.4	5167	9436.3	4692.9	6440.8	7126.1							
A0A087WYC8;Q9	Regulator of nonsens	UPF3B	25.232	6.5	1	1	3.179	0.00077	5932.1	5563.8	5660.3	6673.7	4741	5273.7	3223.6	4486.7	2831.7	4468.3	Moderate	Moderate	Enriched	No expression			
A0A087WYD6;Q0	Antigen peptide trans	TAP2	77.596	7.4	4	3	26.136	0	16540	13103	15617	15812	17562	11416	12795	15293	6666.7	14151	Enriched	Moderate	Enriched	Low	YES		
A0A087WYF7;Q6	MICOS complex sub	APOOL	29.205	37.7	11	11	48.065	0	51093	37903	46952	41295	62100	31772	36545	33296	19419	47946	Low	No expres	Moderate	No expres	YES		
A0A087WYF8;A0A	PDZ and LIM domai	PDLIM3	21.754	26.9	5	5	24.691	0	9207.8	6859.6	7521.2	6294.3	8471	7341.6	8789.1	6339.6	3170.7	7823.2	No expres	Moderate	Enriched	Low	YES		
A0A087WYN9;Q7	ATP-dependent RNA	DHX29	155.29	12.9	15	15	63.621	0	53274	42531	42282	42668	56525	46785	39660	44401	24390	47123	Moderate	Enriched	Enriched	Moderate	YES		
A0A087WYP2;Q8	Selenoprotein H	SELH;C11orf31	13.303	29.8	5	5	12.469	0	25556	33772	39595	16378	58979	21294	51940	63536	24191	30864	Enriched	Enriched	Enriched	No expression			
A0A087WYR3;O4	Tumor protein D54	TPD52L2	23.764	47.7	19	19	79.585	0	88558	78860	84714	83902	87766	96900	98195	103250	71950	98792	No expres	Moderate	Enriched	Enriched	YES		
A0A087WYR4;A0	Ig lambda-1 chain C r	IGLC1	24.83	46	21	0	299.55	0	131640	114930	160990	222780	119890	154370	170890	701830	87216	155640	Low	Moderate	Moderate	Moderate	YES		
A0A087WYS1;E7	UTP--glucose-1-phos	UGP2	56.967	47	46	46	323.31	0	137100	94368	110750	146150	117900	151880	181150	252050	92211	161710	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WYS3;H7	Protein kinase C-bind	ZMYND8	121.25	2	2	2	7.9639	0	11094	8595.5	10619	9371.8	12252	7553.5	6430.8	7396.2	4694.4	9984	Enriched	Moderate	Enriched	Moderate	YES		
A0A087WYT3;Q1	Prostaglandin E synt	PTGES3	19.155	42.7	15	15	45.024	0	87310	56282	79468	60114	74541	102560	115830	127840	65248	105980	Enriched	Enriched	Enriched	Low	YES		
A0A087WYU1;Q9	Sorting nexin-9	SNX9	66.476	16.7	13	13	29.996	0	60348	42063	54975	71660	57705	61822	55231	71511	28226	75776	Moderate	Moderate	Enriched	Low	YES		
A0A087WYV5;X6	Slit homolog 2 protei	SLIT2	159.98	2	2	2	15.296	0	23323	18315	19525	22507	25004	21596	18193	18671	7427.9	20037	Low	Moderate	Moderate	Moderate	YES		
A0A087WYV8;P3	Fibrillin-2	FBN2	314.67	1.9	6	2	17.314	0	10987	8092.9	10131	9496.5	11237	10898	13092	23329	3011.3	17839	No expres	No expres	Low	Moderate	YES		
A0A087WYW3;P3	NK-tumor recognitio	NKTR	131.82	2	2	2	3.0995	0.00095	5282.6	4047.4	4883.7	4800.8	6538.1	5175.7	5075.6	5855.1	3852.7	7622.3	Moderate	Moderate	Enriched	No expression			
H7BYV1;E9PS44;	Interferon-induced tr	IFITM2;IFITM3;IFITM1	8.0866	13.5	1	1	2.1818	0.00561	1275.4	1587.9	1701.1	997.5	2051.8	1938.3	2618.9	1363.6	2916.5	1912.5	Enriched	Enriched	Enriched	Low			
E9PKS4;B3KUF4;	Transcription factor (	GATA4	19.013	29.7	6	4	28.525	0	27302	22166	22595	24076	33457	13627	20532	19588	16108	21992	Enriched	Moderate	Low	Low	YES		
A0A087WZ13;E9P	Ribonucleoprotein P	RAVER1	77.843	14.3	9	9	31.324	0	15029	11857	13025	13070	13040	15849	22510	23990	12399	17608	No expres	No expres	Moderate	No expres	YES		
B7Z385;A0A087X	Adenylyl cyclase-ass	CAP2	39.911	12.6	7	6	8.0071	0	14261	14149	13924	14636	17703	12064	12757	11735	8120.7	14287	Moderate	Low	Moderate	Moderate	YES		
A0A087WZ38;Q86W51		PDCD6	13.958	19.5	5	3	8.3762	0	4252	4956.3	5104.8	4587.5	5047.3	2766.7	5481	4806.8	5954.4	5587.5	Low	Moderate	Enriched	Enriched			
H0YCW6;A0A087	Alpha-1,2-mannosylt	ALG9	24.198	40.6	9	9	20.085	0	106200	77806	71121	75325	85644	63364	68210	74281	41014	68579	No expres	Enriched	Enriched	No expres	YES		
A0A087WZD8;Q8	General transcription	GTF3C2	63.874	7.2	3	3	9.5841	0	13994	11273	13074	9401.3	17241	10134	16262	13474	12180	13837	Enriched	Enriched	Enriched	Moderate	YES		
A0A087WZG4;M0	Rho guanine nucleoti	ARHGEF18	116.32	2.1	2	2	9.4826	0	1369.9	1308.5	2247.5	666.07	2268.3	1498	4078.3	2201.8	2668.4	2937.9	Enriched	Enriched	Enriched	Enriched	YES		
A0A087WZH7;P29	Myristoylated alanine	MARCKS	31.595	42.7	30	29	323.31	0	191770	210290	278190	139950	282470	144850	434210	323440	275590	296440	Moderate	Enriched	Enriched	Enriched	YES		
A0A087WZH9;P01	Ig kappa chain V-I region Roy;Ig kappa chain V		11.842	39.8	9	0	190.17	0	34619	36531	46696	34164	38842	31338	34478	124050	27538	35308							
H0YAE9;D6REQ6;	Ribonuclease T2	RNASET2	21.772	20.5	3	3	16.685	0	2704.8	1485.8	2036.3	3055.3	2522.5	2064.2	2016.4	1838.5	2819	2088.7	Moderate	Enriched	Enriched	No expres	YES		
A0A087WZN1;O4	Isocitrate dehydrogen	IDH3B	42.41	24	12	11	44.861	0	34612	23782	27472	31516	35054	31935	29509	31767	16941	32672	Enriched	Enriched	Enriched	Enriched	YES		
A0A087X0T8;A0A	Cell adhesion molecu	CADM1	38.78	9	5	5	5.4408	0	22347	19833	31338	18935	35527	16003	21194	14836	21585	20191	Enriched	Moderate	Enriched	Enriched	YES		
A0A087WZV0;O4	Inositol hexakisphosp	PPIP5K2	144.36	8.1	8	6	15.008	0	6234	6908.7	8254.7	4439.2	8794.5	7211.3	6009.4	5372.8	3258.4	5122.5					YES		
B5MD00;A0A087V	Mitochondrial import	TOMM7	5.6718	21.6	2	2	3.5629	0.00079	5737.5	5111.6	6006.2	2899.6	8734.1	2501.1	5241.9	4028.6	3618.9	4548.9	Enriched	Enriched	Enriched	Enriched			

A0A087WZZ5;E9F	Splicing factor 3B sul	SF3B2	97.584	21.7	28	28	243.54	0	154310	120000	145030	123900	183430	118790	152960	145820	97264	149230	Moderate	Enriched	Enriched	Enriched	YES	
J3KPF9;A0A087X	Kinesin-like protein I	KIF3A	80.354	10	7	7	13.044	0	15431	13798	16110	16491	16735	13228	13756	16092	8897	17267	Low	Enriched	Enriched	No expres	YES	
A0A087X014;Q7Z	Zinc finger protein 8	ZNF804A	126.92	1.8	2	1	1.9518	0.00799	4943.2	6268.1	6966.7	4601	7895.3	3224.9	8490.3	4653.9	10610	5245.1	Low	No expres	Low	Low		
A0A087X082;Q14	Caprin-1	CAPRIN1	72.755	12.5	8	8	43.962	0	48175	33672	32549	78444	35177	39535	44563	78099	26451	61342	Enriched	Enriched	Enriched	Moderate	YES	
A0A087X0C8;E7E	Calpain-5	ASB2;CAPN5	72.984	4.2	2	2	2.9612	0.00169	9393.7	4493.2	5585.9	16753	4785	9373.7	7178.3	13297	3814.6	12534	Low	Moderate	Low	No expres	YES	
A0A087X0D2			4.0674	36.1	1	1	7.3815	0	10171	6455.7	16088	3720.2	14800	8840.2	6118.5	3750.7	3003	11077						
A0A087X0D5;P09	Pro-cathepsin H;Cath	CTSH	36.269	9.6	5	5	16.314	0	16732	14319	19434	15245	15918	32301	30531	30403	10303	27337	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X0H9;Q5T	RNA-binding protein	RBM26	113.79	8.1	8	8	17.893	0	38155	28712	29295	32537	33372	32637	32387	28988	20739	38869	Low	Moderate	Enriched	No expres	YES	
A0A087X0I9;Q047	Protein kinase C thet	PRKCQ	77.969	1.2	1	1	2.2925	0.00496	2256.1	18572	6468.6	3938.6	8601.4	2748.8	23867	7814.2	4825.1	5200.3	No expres	Moderate	Moderate	Moderate	YES	
A0A087X0K0;P39	Collagen alpha-1(XV	COL15A1	140.06	10.5	18	18	139.79	0	129140	120460	130570	118640	138760	121760	237430	198880	94005	138490	No expres	Moderate	Enriched	Moderate	YES	
A0A087X0M4;Q9	Kanadaptin	SLC4A1AP	82.89	7.1	6	6	16.636	0	12716	14057	18883	12332	21949	17639	21768	16034	15053	16774	Moderate	Moderate	Enriched	No expres	YES	
A0A087X0M8;O0	Neural cell adhesion	CHL1	130.79	3.9	4	4	8.7661	0	31222	23970	31467	29508	34908	30653	19361	44099	7826.2	39996	No expres	No expres	Moderate	Low	YES	
A0A087X0P4;H0Y	Pre-B-cell leukemia t	PBX1	28.859	15.4	3	1	21.796	0	27365	16103	17583	20754	18659	22907	22335	30114	10722	27991	Enriched	Enriched	Enriched	Enriched		
A0A087X0P6			11.192	44.1	6	2	4.6022	0.00043	7655.7	6743.5	7113.1	8006.6	7318.8	5864.6	6249.3	9480.5	3537.3	7791.8						
A0A087X0R6;Q9U	Sorting nexin-12	SNX12	19.825	20.3	8	6	23.934	0	11961	10805	13924	10384	14572	12606	15954	16953	7023.9	14829	Moderate	Enriched	Enriched	No expres	YES	
A0A087X0R9;B8Z	Neutral and basic am	SLC3A1	63.514	5.1	2	2	2.1846	0.00543	4766.3	2677.4	3377.4	5493.6	3642.5	5274.6	7690.3	10007	3874	5981.8	Enriched	Moderate	Enriched	Low		
A0A087X0S5;P121	Collagen alpha-1(VI)	COL6A1	108.34	36.5	80	80	323.31	0	453610	357440	415940	602480	444190	558720	779450	1746900	282280	647040	Enriched	Enriched	Enriched	Enriched	YES	
Q2TAM5;A0A087	Transcription factor p	RELA	42.868	17.8	7	4	23.687	0	33994	28652	35315	26789	40928	36773	61200	44904	49259	45968	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X0W9;Q8	OTU domain-contain	OTUD6B	37.325	7.7	2	2	2.3321	0.00462	23347	22816	18486	19885	22301	22769	29128	27423	15916	21554	No expres	Low	Moderate	No expression		
V9GY49;A0A087X	Arf-GAP with SH3 d	ASAP3	17.385	9.6	1	1	16.536	0	5629.4	6257.9	6906.8	4042.4	9154.1	4255.7	8950.9	5655.2	7033.2	5577.5	Enriched	Moderate	Moderate	No expres	YES	
A0A087X0Z7;H0Y	Dehydrogenase/reduc	DHRS7	42.619	22.6	10	1	26.528	0	16092	12727	16221	12375	16568	21969	37604	44742	12218	21934	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X117;Q15	Nodal modulator 1	NOMO1	139.47	44	78	2	5.5183	0	9436.6	9488.8	9692.1	12236	10488	8561.9	9085	8409.9	6847.7	10072	No expres	Enriched	Moderate	Moderate		
A0A087X142;A6N	Septin-8	SEPT8	49.355	16.7	9	5	8.2462	0	5146.2	3849.3	6574.9	5659.6	5282.7	3811.2	11878	8311	8780.4	10139	Moderate	Enriched	Enriched	Enriched	YES	
A0A087X176;Q6Z	Sulfhydryl oxidase 2	QSOX2	77.249	8.5	5	5	9.0128	0	12895	11326	8623.3	18713	8991.3	9302.8	10818	15606	8559.3	14199	Low	Enriched	Enriched	No expres	YES	
A0A087X1A5;Q5J	Double-stranded RN	STAU1	54.945	15.4	8	8	84.427	0	21680	17345	14910	28612	18236	20579	23969	27793	19910	23970	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X1E4;P53	Arfaptin-2	ARFIP2	41.595	15.5	6	6	16.346	0	44236	30713	31826	40114	42699	44305	42974	36717	27188	37078	Moderate	Enriched	Enriched	Moderate	YES	
A0A087X1G1;H7B	NADH dehydrogenas	NDUFA5	11.965	53.5	12	5	43.033	0	97917	65748	82414	107590	101080	96873	113190	96765	67730	112750	Moderate	Enriched	Enriched	Enriched	YES	
A0A087X1G7;O60	15 kDa selenoprotein	SEP15	17.942	32.9	10	10	216.85	0	85968	46993	51810	120320	45084	96678	142120	217870	43955	124100	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X1H5;Q15	Arf-GAP with coiled-	ACAP2	88.02	6.9	6	6	45.013	0	18500	14386	18256	13338	20679	20379	49116	24714	38650	31469	Low	Moderate	Enriched	Low	YES	
A0A087X1J7;P223	Glutathione peroxida	GPX3	25.402	18.7	5	5	31.002	0	15575	16480	13269	18095	14201	10806	17543	17512	8691.3	14501	Enriched	Enriched	Enriched	Moderate	YES	
A0A087X1L7;O75	Left-right determinati	LEFTY1;LEFTY2	41.727	7	2	2	42.496	0	37936	21448	34612	31716	41646	50157	40131	86723	18594	42844	Enriched	Enriched	Moderate	Enriched	YES	YES
A0A087X1N2;Q03	CCAAT/enhancer-bi	CEBPZ	114.16	4.4	4	4	11.416	0	2064.7	1053.7	1380	2963.2	1444.6	2137.6	926.74	1945.7	618.97	2679.2	Moderate	Moderate	Enriched	Moderate	YES	
F8W8P5;C9IYE1;	Calcium-dependent s	CADPS2	136.58	5.1	7	2	15.72	0	32705	27822	26093	20595	32165	16197	30963	21358	17681	24630	Enriched	Enriched	Enriched	No expres	YES	
A0A087X1P5;J3K	COP9 signalosome c	COPS7B	23.556	18.7	8	8	98.22	0	51480	45459	46262	39020	52710	44741	50882	41463	33628	47932	Moderate	Moderate	Moderate	No expres	YES	
A0A087X1R5;Q13	Protein Red	IK	65.654	19.7	16	16	40.175	0	45687	33275	39682	41524	54123	36637	38393	36451	28785	42855	No expres	Moderate	Enriched	Enriched	YES	
A0A087X1S2;P67	Nuclease-sensitive el	YBX1	34.028	39.5	18	10	166.38	0	55182	33632	37735	31243	50562	50093	50228	59142	19975	47309	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X1V9;A0A	Ig kappa chain V-II re	IGKV2D-40;IGKV2D-2	11.043	52	9	5	47.867	0	20306	19952	25744	37311	21480	29679	24460	86525	14140	25816						
A0A087X1X9;Q8	Stromal membrane-a	SMAP1	49.219	4.6	2	2	4.6447	0.00043	4118.9	4230.9	4948.9	4760.2	6044.8	2555.1	2870.8	3251.5	2086.9	3518.2	Moderate	Enriched	Enriched	No expres	YES	
A0A087X1Z3;Q9U	Proteasome activator	PSME2	29.126	42.5	22	21	100.2	0	101210	56220	64462	114740	78237	106030	115140	144590	61433	102110	Enriched	Enriched	Enriched	Enriched	YES	
A0A087X232;F8W	Complement C1s sub	C1S	75.905	10.7	7	7	9.9028	0	15494	17428	21057	21214	18570	19818	29037	40762	27774	23047	Moderate	Enriched	Enriched	Enriched	YES	
A0A087X256;Q2M	WASH complex subu	KIAA1033	136.5	4.4	7	7	11.005	0	28916	14019	20300	34013	16929	34868	24698	34089	13412	26772	Moderate	Enriched	Enriched	Moderate	YES	
A0A087X271;B4D	Calponin-2	CNN2	19.757	35.8	10	7	12.534	0	18374	10733	18510	15445	16830	13348	13276	11078	11217	14061	Enriched	Enriched	Enriched	No expres	YES	
A0A087X2C0;A0A	Ig mu chain C region:	IGHM	64.106	28.7	19	16	167.66	0	51365	63226	52063	54792	64015	43651	94388	179270	47544	55207	Moderate	Moderate	Low	Low	YES	
A0A087X2D8;O60	C-Jun-amino-termina	SPAG9	145.17	18.7	26	26	259.95	0	130420	101260	114620	115670	153180	120890	138200	113290	58163	136850	Enriched	Enriched	Enriched	Low	YES	
A0A087X2H1;Q9U	E3 ubiquitin-protein	HECTD1	289.63	2.2	4	4	12.624	0	2318.2	2520.9	3292.7	2219.1	2769.6	1379.1	1368.6	1490.4	1530.5	2074.1	Enriched	Enriched	Enriched	No expres	YES	
A0A087X2I1;P623	26S protease regulato	PSMC6	45.796	42.2	25	25	76.566	0	84945	59281	66861	92448	81173	104140	95561	105750	57920	92846	Moderate	Enriched	Enriched	Moderate	YES	
Q5JXX1;Q5JXX2;	Mortality factor 4-lik	MORF4L2	17.617	20.3	2	2	14.3	0	17903	12081	17529	14076	30695	12540	30353	16774	24043	22400	Enriched	Enriched	Enriched	Enriched	YES	
A0A088AWN2;Q8	WD repeat-containin	WDR20;ANO6	67.475	4.4	3	3	3.2537	0.00077	453.71	195.97	632.37	122.29	586.14	2078.1	6757.4	4924.8	3851.4	3243.9	Low	Moderate	Moderate	No expression		
A0A0A0MT38;A0	Dedicator of cytokine	DOCK9	22.13	11.3	3	3	4.3864	0.00063	10559	5719.9	5282.7	13547	5908.7	7581.4	5004.6	10597	3445.8	8666.4	Enriched	Enriched	Enriched	Low	YES	
A0A096LNH6;Q14	Dedicator of cytokine	DOCK1	217.75	4.1	7	7	10.706	0	6228.8	5458.4	5643.9	6504.4	5565.2	7468.3	5691.2	6428.3	2181.7	8024.7	Moderate	Moderate	Enriched	Moderate	YES	
A0A096LNV3;A0A	E3 ubiquitin-protein	RNF114	20.885	12.2	3	3	10.164	0	7031.9	4753.5	3887.6	7448.5	5653.8	4550.6	8071.7	9504.8	6082.5	6365.4	Enriched	Enriched	Enriched	Low	YES	
A6XMV8;A0A096	Trypsin-2	PRSS2	26.67	35	52	4	100.52	0	398770	145200	264920	297410	303020	318360	217630	262010	76116	275870	Enriched	Enriched	Enriched	Enriched	YES	YES
A0A096LP10;Q9N	Putative bifunctional	ALG13	17.801	17.9	2	2	5.1486	0.00044	20329	6492.4	10273	25524	9676.9	29879	19761	19831	8867.2	19470	Enriched	Moderate	Enriched	No expres	YES	
A0A096LP25			54.448	7.6	3	1	3.1742	0.00077	2907.9	1572.5	1590.9	4699.5	1295	2748.5	2010.7	4171.4	1414.9	4187.3						
A0A096LP26;A0A	Putative WAS protein	WASH3P;WASH2P;WA	49.236	13.4	5	3	14.451	0	17164	14883	16249	13547	20520	18739	25335	18380	21835	18030	Enriched	Enriched	Enriched	No expression		
A0A096LPI6;P300	ES1 protein homolog	C21orf33	25.64	54.2	20	19	95.739	0	128500	66298	86780	118010	105950	99429	104360	128690	71908	120340	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MQR1;Q9	Mitogen-activated pro	MAP4K5	95.023	3.7	2	2	4.0909	0.00062	26551	844.55	2667.6	20892	766.34	30828	2277	7529.5	995.29	21378	Moderate	Low	Enriched	Low	YES	
A0A0A0MQR4;I3L	Protein capicua homo	CIC	163.68	1.7	2	2	31.793	0	2724.1	3471	4251.5	2046.4	4934.6	2006.6	3316.3	2995.9	2330.5	3205.3	Enriched	Moderate	Enriched	Moderate	YES	
A0A0A0MQS1;Q5	Pyrroline-5-carboxyla	PYCRL	29.892	10.5	3	3	5.6028	0	7519.7	5959.7	7844.1	5692.1	8448	11311	15050	7570	8769.2	10078	Low	No expres	No expres	No expres	YES	
A0A0A0MTC7;A0	Laminin subunit alph	LAMA4	201.82	25.9	55	55	323.31	0	238480	200990	225780	245470	240660	233140	245720	281310	158780	299230	Low	No expres	Moderate	Moderate	YES	
A0A0A0MQT0;P0	Retinol-binding prote	RBP1	22.31	43.1	29	29	323.31	0	400230	278440	257050	256790	204160	293090	271080	339750	197480	379660	Enriched	Enriched	Enriched	Enriched	YES	
U3KQC1;A0A0A0	WD repeat-containin	WDR18	43.237	10.9	4	4	9.4596	0	21444	16689	22734	16511	22861	11734	21245	16915	28332	22552	No expres	Moderate	Moderate	Enriched	YES	
A0A0A0MQU4;Q9	Selenocysteine lyase	SCLY	48.793	46.1	34	34	105.52	0	135720	96908	115700	138370	130620	132250	143020	207380	86594	130940	Moderate	Enriched	Moderate	No expres	YES	
A0A0A0MQW0;A	Myelin expression fa	MYEF2	61.957	14.2	11	8	12.872	0	9868.3	9125.1	10097	7910.5	11765	7273	9667.4	7635.1	7068.9	8340.3	Moderate	Enriched	Enriched	Moderate	YES	
H7C4T5;C9JP00;A	Muscleblind-like pro	MBNL1;MBLL;MBNL3	35.71	10.9	4	4	6.3617	0	20641	15204	18442	13132	19584	15679	14673	14020	10595	18648	Enriched	Moderate	Enriched	Moderate		
A0A0A0MR40;F5	Actin-binding LIM p	ABLIM2	71.286	3.9	2	2	6.4328	0	10494	7064.6	8428	11064	10746	7648.1	8853.5	8948.1	5340.6	11025	Moderate	Enriched	Moderate	No expres	YES	
A0A0A0MR66;P98	RNA-binding protein	RBM10	110.36	11.7	11	11	84.235	0	24957	17240	20030	26837	26773	24542	26910	26767	14083	28508	Low	Enriched	Enriched	Enriched	YES	
A0A0A0MR85;Q0	Glutathione S-transfe	GSTM4	25.563	41.7	22	1	2.9414	0.00169	19551	15727	15946	7159.4	10541	5915.5	10761	7175.3	8944.4	6988.6	Enriched	Enriched	Moderate	Enriched		
A0A0A0MRA5;B7	Heterogeneous nucle	HNRNPUL1	85.939	30.9	37	37	154.11	0	230520	172130	198980	193970	233990	218540	241380	235020	164530	228880	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRC4;A0	G-protein-signaling m	GPSM1	72.135	5.1	2	2	3.9669	0.00062	5052.3	2306.9	4184.7	6127.1	3500.3	5883.9	4563.8	6433.3	2830.7	5342.7	Enriched	Enriched	Enriched	No expres	YES	
A0A0A0MRE1;B4	Exocyst complex con	EXOC7	70.2	23.7	12	12	86.663	0	50029	33554	41742	51750	46102	49515	52711	53343	27034	55902	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRF6;Q9	A-kinase anchor prot	AKAP9	453.49	4.2	17	17	91.339	0	50612	36885	48341	45713	57272	51572	52917	45533	30758	51024	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRF9;P16	1-phosphatidylinosito	PLCG2	146.06	2.6	3	3	2.2665	0.00494	6651	16944	16859	3300.4	27287	1702.4	6810.8	2416.3	6464.8	4415.9	Enriched	Moderate	Moderate	Enriched	YES	
A0A0A0MRI1;Q8I	GPALPP motifs-cont	GPALPP1	37.971	6.2	3	3	4.5714	0.00043	4054.9	2698.4	4329.2	4415.1	5104.7	4224.1	1887	2121.7	789.66	3449.1					YES	
A0A0A0MRI2;Q9U	Sorting nexin-6;Sorti	SNX6	47.804	17	10	9	25.977	0	25161	25612	25658	23143	27160	38429	70008	95512	27963	41617	Enriched	Enriched	Enriched	No expres	YES	
A0A0A0MRJ6;H7	Protein-L-isoaspartat	PCMT1	30.315	28.1	14	10	41.46	0	28426	24354	21327	25996	30304	24086	31510	22641	18419	25217	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRK6;Q1	Metaxin-1	MTX1	51.462	13.5	6	6	16.356	0	52476	44229	53961	50744	62845	33500	52140	48342	32629	53373	Enriched	Enriched	Enriched	Enriched	YES	
Q5SVL2;A0A0A0	Caspase-7;Caspase-7	CASP7	24.79	15.8	4	4	170.18	0	18399	21677	39657	16945	64701	12471	22983	15551	10649	14992	Moderate	Moderate	Enriched	Moderate	YES	
A0A0A0MRM8;Q9	Unconventional myo	MYO6	145.01	25.3	43	43	211.24	0	167270	109840	117060	137030	146450	195720	177270	159690	95251	149220	Low	Moderate	Enriched	Moderate	YES	
A0A0A0MRM9;Q1	Nucleolar and coiled-	NOLC1	74.543	18.1	19	19	49.166	0	41746	30321	35787	41929	42290	51011	96379	56095	52726	59402	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRP6;B7	Probable global trans	SMARCA1	122.86	2.9	3	2	2.0881	0.0069	4365.4	2912.2	2780.7	3458.3	2873.3	2868.5	2783.7	3908.8	1274.7	3257.3	Moderate	Enriched	Enriched	Enriched	YES	
A0A0A0MRR7;P0	U1 small nuclear ribo	SNRPC	19.687	11.7	2	2	22.375	0	7012.3	3691.5	6372.9	4134.1	3931.3	14937	34367	11700	10871	19269	Moderate	Enriched	Enriched	Moderate	YES	
B6VEX4;A0A0A0	Abl interactor 1	ABI1	43.294	30.8	12	10	50.247	0	87982	61545	69558	64570	82195	63450	63689	65077	31746	72147	Moderate	Moderate	Enriched	Moderate	YES	
A0A0A0MRV0;Q9	Ribosome-binding pr	RRBP1	152.45	71	239	9	323.31	0	1751600	1325900	1298100	1571800	1786700	2106900	3027600	1944600	1184100	1552700	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MRV3;Q9	WD repeat-containin	WRAP73	48.874	2.5	1	1	2.1163	0.00626	7021.5	4571.3	9742.5	10216	7104.1	8955.6	10272	10951	5008.5	8997.8						
J3QKK8;A0A0A0	Prostamide/prostagla	FAM213B	16.549	16.2	2	2	4.7974	0.00043	7509.8	5508.8	8488.4	7938.2	8206.3	8917	9327.2	8293.1	6179.9	7537.3					YES	
A0A0A0MRX8;Q5	Nuclear factor 1;Nuc	NFIB	50.29	7.2	4	2	3.1845	0.00077	2411.1	2678.6	2894.5	3413.9	3876.2	5422.8	3559.6	3189.8	2018	3165.5	Enriched	Enriched	Enriched	Moderate	YES	
B0QYI1;A0A0A0	TBC1 domain family	TBC1D22A	53.04	5.7	3	1	3.3799	0.00078	5506.9	5380.6	4265.4	6139.4	4966.3	4933.6	4327.2	5045.2	1994.6	4862	Enriched	Enriched	Enriched	Enriched		
E7EMV7;A0A0A0	TNFAIP3-interacting	TNIP1	55.697	3.7	2	2	2.7888	0.00222	4826.1	5100.8	4927.4	3800.4	5173.1	2580.6	2746.3	2533.2	2011.1	3481.7	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MS13			13.917	28	4	1	15.559	0	32172	50298	39169	32545	32946	20087	27450	49088	20763	26198						
A0A0A0MS37;Q8	Spermatogenesis-assc	SPATA20	89.237	7.1	4	4	11	0	11217	8400.9	9276.4	18354	8975.7	10271	12283	13789	6892.8	13745	Enriched	Enriched	Enriched	No expres	YES	
A0A0A0MS41;Q9	Sideroflexin-3	SFXN3	35.503	41.7	12	11	45.909	0	45992	31574	36861	56299	39871	52186	44539	60799	28520	54428	Enriched	Moderate	Enriched	Enriched	YES	
A0A0A0MS45;J3K	Conserved oligomeric	COG4	87.183	13.9	10	10	36.644	0	41116	35755	39710	47782	49723	41071	39985	46477	23396	41256	Moderate	Moderate	Enriched	Moderate	YES	
Q5SWX3;A0A0A0	Calcium/calmodulin-	CAMK2G;CAMK2B	57.796	22.1	9	6	23.509	0	16823	13864	16780	32082	14320	20259	17876	64086	16172	24670	Enriched	Enriched	Enriched	Enriched		
A0A0A0MS59;Q6	Helicase SRCAP	SRCAP	315.61	0.9	3	3	6.6464	0	1425.9	991.05	1458.7	3141.1	1391.7	1408.6	1461.5	1587.7	920.23	1607.2	Moderate	Moderate	Enriched	Moderate	YES	
A0A0A0MS87;Q9	Protein NDRG2	NDRG2	39.544	26.7	9	6	25.616	0	32829	33531	44050	24254	45285	30197	55631	36907	44153	35838	Enriched	Enriched	Enriched	Low	YES	
A0A0A0MSA6			19.545	45	28	2	3.8899	0.00061	22773	25268	14562	18256	16463	28133	30358	18818	25648	25351						
A0A0A0MSA7;O4	Eukaryotic translatio	EIF4G3	180.5	5.5	11	3	4.5245	0.00043	7584.6	4952.1	5884.6	6346.7	7736.4	5956.9	7175.1	5594.1	4477	6755.3	Moderate	Moderate	Enriched	Moderate	YES	
A0A0A0MSB3;Q5	cGMP-dependent pro	PRKG1	51.897	5	2	2	4.8622	0.00043	1446.9	1259.4	1401.2	1752.6	1773.1	2077.7	1540.8	1917.4	713.96	1701.5	Moderate	Low	Moderate	Low	YES	
A0A0A0MSC4;H7	Platelet-derived grow	PDGFA	9.7552	18.6	1	1	3.1059	0.00095	4594.7	2770.8	3636.5	5936.1	4421.2	4949.6	3466.8	3639.9	2614.3	3680	Moderate	Enriched	Enriched	Moderate		
A0A0A0MSD7;E7	Receptor-type tyrosir	PTPRN2	49.455	8.8	3	3	6.4983	0	3623.3	4858.7	5959.2	2933.1	4825.9	1930.2	2766.8	2109.5	3092.9	3198.2	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MSE2;Q1	Hydroxyacyl-coenzy	HADH	42.123	29.7	20	20	105.36	0	153780	102560	136150	172730	167670	152760	275220	291700	110170	196050	Enriched	Enriched	Enriched	Enriched	YES	
J3KNW4;A0A0A0	Four and a half LIM	FHL2	44.205	8.2	2	2	16.456	0	5302.8	4873.5	7313.2	5932	5413.3	8549.5	21496	11380	10067	15766	Enriched	Moderate	Enriched	Low	YES	
A0A0A0MSI6;B7Z	F-box only protein 4	FBXO44	19.214	9.7	1	1	2.2009	0.00544	2945.5	1453.4	1754.7	4606.9	1952.8	3105.9	2951.1	3329.7	1232.3	3391.9	Enriched	Moderate	Moderate	No expression		
A0A0A0MSI8;O00	Exocyst complex con	EXOC5	82.118	7.3	5	5	9.2512	0	16463	8337.5	12123	19568	11729	20972	16650	17272	8772.8	17381	Moderate	Enriched	Enriched	No expres	YES	
A0A0A0MSK6;Q1	Rho GTPase-activatir	ARHGAP5	171.68	3.3	4	4	18.618	0	9478.3	3837.6	5808.3	13686	4933.8	10144	8183.3	9485	3145	10320	Low	Enriched	Enriched	No expres	YES	
A0A0A0MSM4;Q9	Protein TANC1	TANC1	50.847	3	1	1	9.9397	0	4621.5	4535.7	6215	3261.5	5591.8	4254.7	5807.3	5132.7	3780.1	5775.9	Moderate	Enriched	Enriched	No expres	YES	
H7C1X5;E7EUA2;	SH3 and multiple anl	SHANK2	121.22	1.4	2	2	1.9501	0.00799	23148	17264	23785	16101	26273	21456	18695	11502	5214.1	22272	Enriched	Enriched	Moderate	Moderate	YES	
A0A0A0MSS8;P42	Aldo-keto reductase	AKR1C3	36.867	36.8	19	4	139.73	0	119490	106980	81091	115150	97990	105720	88976	102750	50906	131380	Enriched	Enriched	Enriched	Enriched		
A0A0A0MST9;A0	MAP/microtubule aff	MARK3	74.09	13.7	8	7	16.032	0	26993	22563	24453	22483	34358	21066	23608	21164	14692	24338	Moderate	Enriched	Enriched	Moderate	YES	
A0A0A0MSU4;O9	ATP-binding cassette	ABCA8	183.06	6.2	12	12	40.005	0	34618	31899	40448	43530	38952	53581	92280	45936	32445	67107	No expres	Low	Low	Low	YES	
A0A0A0MTN9;A0	NADPH:adrenodoxin	FDXR	48.027	17.1	7	7	11.16	0	21716	21266	22447	20959	22935	22659	19991	27515	23143	25125	Enriched	Moderate	Moderate	Moderate	YES	
A0A0A0MSZ9;Q0	Cleavage stimulation	CSTF1	38.448	3.8	1	1	3.7211	0.0008	4312.3	4929.2	3871.8	4201.8	4487.7	2720.4	3443.4	3232.9	4542.8	3164.9	No expres	Low	Moderate	Moderate	YES	
A0A0A0MT30;Q0	Aldo-keto reductase	AKR1C1	37.115	27.5	13	0	16.907	0	21518	33218	18621	32049	26467	33157	34250	23363	13904	39247	Enriched	Enriched	Enriched	Enriched		
A0A0A0MT32;Q5T	Lysosomal acid lipas	LIPA	32.57	11	4	4	7.82	0	8956.1	4827.6	7477.8	7195.6	8757.7	8114.1	5189.7	4283.3	2935.3	5606.9	Enriched	Enriched	Enriched	Enriched		
A0A0A0MT33;Q9U	Protein SCAF8	SCAF8	148.86	4.8	8	8	33.088	0	48035	41221	48920	50144	58918	43065	70835	56679	38971	54180					YES	
Q9HBD4;A0A0A0	Transcription activato	SMARCA4	188.15	5.8	8	5	13.024	0	10605	6798.7	8536.1	8356	9409.9	7994.1	7625.9	9375.9	5100.2	9026.7	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MT60;Q5T	FK506-binding prote	FKBP15	136.27	6.8	8	8	70.391	0	35179	31539	33185	24643	37146	36716	43793	53032	21585	36778	Enriched	Enriched	Enriched	Moderate	YES	
A0A0A0MT66			32.406	50.2	24	1	3.0684	0.00114	3983.1	3965.7	14095	1655.2	11952	2002.6	4456.9	1555.1	3684.6	2264.6						
A0A0A0MT83;P26	Isovaleryl-CoA dehy	IVD	46.65	30.5	17	17	34.309	0	22508	18286	20087	24411	19845	21855	20421	23331	10495	25332	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MTB8;Q8	WD repeat-containin	WDR36	99.365	5.9	5	5	23.925	0	22075	24378	24000	16932	29046	17465	20157	19834	15367	21883	Low	Enriched	Enriched	No expres	YES	
A0A0A0MTR7;A0	E3 ubiquitin-protein	RNF213	591.4	3	14	14	28.66	0	32325	36378	53949	19622	56338	22203	33272	17387	24737	23321	Moderate	Enriched	Enriched	No expres	YES	
G5EA18;E5RJN7;	Double-stranded RN	STAU2	31.723	6.2	2	2	2.1025	0.00675	1204.7	1414	1433.8	1422.3	1220.9	1566.3	1225	1326.4	787.11	1658.7	Moderate	Moderate	Moderate	Moderate	YES	
A0A0A0MTL4;A0	Neuron navigator 2	NAV2	261.86	1.1	2	2	2.0106	0.00771	16649	51255	22713	7219.3	40706	2687.3	18153	20499	23579	13214	Moderate	Enriched	Enriched	No expression		
A0A0A0MTH3;Q1	Integrin-linked protei	ILK	54.611	24	15	15	31.405	0	75468	45485	64084	74096	87539	93723	82779	86098	44637	94300	Low	Enriched	Enriched	Moderate	YES	
B8ZWD1;A0A0A0	Acyl-CoA-binding pr	DBI	11.15	59.8	20	20	315.19	0	220090	213000	238120	248190	291790	238680	288360	294170	144140	245030	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MTJ5;Q01	Tyrosine-protein kina	ROR1	98.363	3.5	3	3	4.9319	0.00044	12274	9927.7	11686	11563	14679	10190	10469	12572	5456.2	11861	Moderate	Moderate	Moderate	Moderate	YES	
A0A0A0MTJ9;Q6P	Neutral cholesterol e	NCEH1	49.881	7.4	3	3	5.6701	0	26536	23471	23454	27052	31802	19215	17398	16613	10507	24173					YES	
A0A0A0MTP0;A0	Coiled-coil domain-c	CCDC91	40.705	4.7	2	2	3.1368	0.00095	8748.9	7399.6	4143.3	7518.6	7341.5	7274	3067	5449.1	941.67	5104.3	No expres	Moderate	Enriched	No expres	YES	
A0A0A0MTM7;Q0	Retinoblastoma-like p	RBL2	95.247	4.4	3	3	7.121	0	4321.2	5997.1	5477.2	3076.5	5941	4608.5	6881.4	4956.1	5363.1	6060.8	Enriched	Enriched	Enriched	Enriched	YES	
Q5T2B5;A0A0A0	Cullin-2	CUL2	82.358	9.5	8	8	23.102	0	47546	31576	37662	44031	38931	37332	41127	40386	22540	43521	Moderate	Moderate	Enriched	Moderate	YES	
H0YB18;H0YB70;	Hydroxypyruvate iso	HYI	17.588	31.1	5	5	22.503	0	8474.5	4592.7	5804.2	14409	5347	11554	12298	16557	6977.1	13152	Enriched	Enriched	Enriched	No expres	YES	
A0A0A0MTS2;P06	Glucose-6-phosphate	GPI	64.824	41.5	57	3	323.31	0	335460	288470	312120	356120	370460	435330	479500	581180	233680	420890	Enriched	Enriched	Enriched	Enriched	YES	
A0A0A0MTS6;K7	Methyl-CpG-binding	MBD3	20.6	11.9	2	2	5.1616	0.00044	5825.6	3940.7	4689.2	8245.6	5769.6	5607.8	4649.5	5233.4	2716.4	6757.1	Moderate	Enriched	Enriched	Moderate		
A0AV02-5;A0AV0	Solute carrier family	SLC12A8	34.799	6.2	3	3	5.2984	0	4725.3	3885.5	4505.1	8263.1	5483.5	6961.2	6194	6143.3	2385.4	6109.3	Enriched	Moderate	Moderate	No expression		
B7Z8Z7;A0AV96;	RNA-binding protein	RBM47	60.567	20.7	14	12	27.352	0	66761	55757	61668	66325	68468	62827	66994	65538	36226	60899	Enriched	Enriched	Enriched	No expres	YES	
A0AVT1;A0AVT1-	Ubiquitin-like modifi	UBA6	117.97	19.3	26	26	118.04	0	99909	63865	88572	115490	90101	90781	82458	112300	50958	85216	Moderate	Moderate	Enriched	No expres	YES	
A0MZ66;A0MZ66-	Shootin-1	KIAA1598	71.639	29.5	23	23	82.166	0	104800	62822	69880	108750	74316	111890	88877	89863	46601	89019	Enriched	Enriched	Enriched	No expres	YES	
A1IGU5	Rho guanine nucleoti	ARHGEF37	76.277	5.8	3	3	4.7748	0.00043	35629	20750	26913	11339	26124	48331	14801	14167	5439.7	11985					YES	
A1L0T0;M0R026;	Acetolactate synthase	ILVBL	67.867	14.1	7	7	14.444	0	20217	12911	12889	32455	13104	22553	15770	25770	7122.5	17681	Enriched	Enriched	Enriched	Enriched	YES	
G3V311;A1L390-2	Pleckstrin homology	PLEKHG3	77.752	3.2	2	2	2.0562	0.0074	3169	3445.2	3866	1841.5	4696.2	3310.8	4100	3141	2636.2	3400.4	Moderate	Moderate	Moderate	Enriched	YES	
A1X283	SH3 and PX domain-	SH3PXD2B	101.58	8.2	6	6	15.153	0	34084	29816	23394	24875	31456	21921	18189	16958	8298	26529	Moderate	Enriched	Enriched	No expres	YES	
A2A274;Q99798	Aconitate hydratase,	ACO2	87.819	51.8	80	80	323.31	0	523690	470480	410770	498850	628800	555240	687650	723610	250400	653930	Moderate	Enriched	Enriched	Low	YES	
A2A2F0;Q86X10-2	Ral GTPase-activatin	RALGAPB	147.39	5.3	6	6	10.188	0	15679	17833	20961	11385	23542	14229	20123	15608	12024	16931					YES	
A2A2Q9;Q9Y312	Protein AAR2 homol	AAR2	45.034	15.1	6	6	50.6	0	26483	19547	20433	30117	19440	24371	23142	34094	14764	28484					YES	
A2A3R5	40S ribosomal protei	RPS6	24.968	39.4	29	2	40.893	0	39004	13040	12718	14139	42456	7671.7	7479.9	7376.8	3406.6	9677.5	Enriched	Enriched	Enriched	Enriched	YES	
A2ABF8;A2ABF9;	Histone-lysine N-met	EHMT2	135.42	0.8	1	1	2.585	0.00308	1517.5	1560.5	1808.4	1207.2	2200.1	1362.7	2290.2	1263.7	1704.4	2060.4	No expres	Low	Moderate	Moderate		
A2ACR1;P28065-2	Proteasome subunit b	PSMB9	20.96	20.4	4	4	7.1975	0	28983	24892	32122	30356	30871	27463	30643	38437	19702	30886	Enriched	Moderate	Enriched	Moderate	YES	
A2AE48;Q12899;	Tripartite motif-conta	TRIM26	28.666	19.4	3	3	25.674	0	18325	15918	16315	13619	18511	10338	13373	12501	8554.4	16510	Moderate	Enriched	Enriched	Enriched	YES	
Q4TT37;A2IDC6;	39S ribosomal protei	MRPL28	25.895	17	4	4	7.1043	0	8370.3	5703.9	7320.3	6179	8526	9788.8	6351.1	5954.5	3896.8	8538.7	Enriched	Moderate	Enriched	Enriched	YES	
A2RRP1;A2RRP1-	Neuroblastoma-ampl	NBAS	268.57	7	20	20	29.172	0	47079	38412	42726	37337	54353	51077	44220	41303	25617	41340	Enriched	Enriched	Enriched	Enriched	YES	
A2RUB6-2			32.307	5.6	1	1	3.0469	0.00132	2273.9	1968.5	1707.5	2686.5	1668	3519.4	2050	33339	0	5257.4						
A3KFL4;A3KFL2;	Exosome complex co	EXOSC2	29.408	8.7	3	3	5.17	0.00044	27770	14311	24724	16359	30600	14133	32264	26510	12522	21783	Moderate	Low	Moderate	Enriched	YES	
A3KMH1-2;A3KM	von Willebrand facto	VWA8	116.94	9	9	9	13.749	0	12002	8406	10000	15386	10904	12040	11391	15785	4650.7	13705					YES	
C9J1X0;A4D1P6;A	WD repeat-containin	WDR91	79.239	9	8	8	12.343	0	17941	15204	19033	16359	24461	13929	23557	18273	15884	19265	Low	Moderate	Moderate	No expres	YES	
Q86UF2;A4D2H0;	cTAGE family memb	CTAGE6;CTAGE15;CT	87.899	8.5	7	1	4.4531	0.00042	35205	24845	26648	25797	30587	24800	18700	18655	8391.7	20819						
A4UGR9-2;A4UG	Xin actin-binding rep	XIRP2	377.34	0.8	2	2	2.6509	0.00274	9281.2	83227	28311	10563	19481	5705.9	12540	5669.3	21225	8691.3	No expres	Low	No expres	No expres	YES	
F5H4Q5;A5D8V6	Vacuolar protein sort	VPS37C	17.143	31.8	5	5	7.0959	0	30589	14653	24471	45688	19476	35073	27773	50737	16184	40172	Enriched	Enriched	Enriched	No expres	YES	

A5PLN9-2;A5PLN	Trafficking protein pa	TRAPPC13	45.934	5.8	2	2	3.4688	0.00079	3755.2	1742.3	2467	5499	2267.3	5655.4	2456.8	3479.8	1383.6	4449.2							
A5YKK6;A5YKK6	CCR4-NOT transcrip	CNOT1	266.94	8.5	21	21	38.876	0	35363	26997	32434	28654	37374	22685	30426	30722	20170	29385	Enriched	Enriched	Enriched	Enriched	YES		
H3BMP0;H3BV12;	Golgin subfamily A n	GOLGA8N;GOLGA8Q;	67.096	2	1	1	5.0121	0.00044	2394.7	1712.9	1559.4	1822.4	2953.7	1718.6	1629.3	1669.1	1309.3	1873.9							
H3BTL1;Q9H492;	Microtubule-associat	MAP1LC3B;MAP1LC3.	9.0115	16	1	1	2.2765	0.00495	13870	8773.8	9923.4	15630	12213	12309	13848	15879	7628.1	13990	No expres	Enriched	Enriched	Enriched			
A6NDB9	Paralemmin-3	PALM3	71.695	22.6	13	13	138.7	0	89388	53262	46035	46336	63697	60551	66133	64771	48326	74819	Moderate	Enriched	Moderate	No expres	YES		
A6NDG6;H3BV17	Phosphoglycolate ph	PGP	34.006	12.5	4	4	7.6972	0	7856.3	2384.3	4491.8	11741	2972.2	8156.5	7606.1	9249.6	8809.3	10875					YES		
A6NDU8	UPF0600 protein C5	C5orf51	33.62	4.4	1	1	3.7211	0.0008	3008.6	2199.3	2877	4321.9	2773	3184.6	4295.2	3988.4	4648.8	3314.8	Moderate	Enriched	Enriched	No expression			
G3V2I3;A6NED2	RCC1 domain-contai	RCCD1	39.906	6.4	2	2	11.001	0	2436.6	1681.1	1650.8	2002.5	2731.2	1743.5	2554.1	2106.2	1698.4	2681.8	Enriched	Enriched	Enriched	No expres	YES		
A6NEM2;P51610-	Host cell factor 1;HC	HCFC1	213.47	6.4	15	15	47.469	0	33302	23577	26924	26647	29334	32679	49362	47411	29361	45446	Enriched	Enriched	Enriched	No expres	YES		
A6NER6;H3BN14;	Calretinin	CALB2	22.155	6.2	3	3	14.56	0	18958	22278	46689	94872	19598	83960	21766	59403	14220	58872	Moderate	Moderate	Moderate	Moderate	YES		
A6NFI3;A0A087X	Zinc finger protein 31	ZNF316;KLF14;SALL1;	108.44	3	2	1	4.8971	0.00044	3633.2	2290.3	3927.2	3249.3	5927.1	2992.3	4844.6	3038.2	3226.1	3805.8	No expres	Moderate	Low	No expression			
A6NJU6;A6NFX8;	ADP-sugar pyrophos	NUDT5	20.629	32.3	10	10	58.396	0	138160	38579	51198	109000	58215	106140	79137	90701	37454	89034	Enriched	Enriched	Enriched	No expres	YES		
K7EIJ0;B4DFG2;K	WW domain-binding	WBP2	18.224	14.4	3	3	5.0648	0.00044	1260	998.41	1249.4	1140.8	1569.9	628.49	797.93	1136.6	756.31	964.83	Moderate	Enriched	Enriched	Enriched	YES		
H3BU16;A6NGP5;	Hematological and ne	HN1L	17.603	34.1	5	5	18.969	0	21087	20653	22500	19525	29803	17360	25829	21805	15786	22915	Enriched	Enriched	Enriched	Low	YES		
A6NGV6;P27540-2	Aryl hydrocarbon rec	ARNT	45.924	6.2	2	2	3.0333	0.00132	15596	9507.9	13893	8731.5	12156	18463	10994	9339.1	5194.2	11413	Moderate	Moderate	Enriched	Low			
A6NGW1;O95070;	Protein YIF1A	YIF1A	26.377	10.4	3	3	20.166	0	4737.6	4282	8596.6	24152	7031.4	2965.6	3767.2	4127.6	1842.7	7028.1	Enriched	Enriched	Enriched	Enriched	YES		
A6NHN7;A6NHB5	Zinc finger MYM-typ	ZMYM3	141.79	2	2	2	8.8048	0	17285	15461	16143	14119	20501	8844.7	11209	11201	6818.5	12043	Enriched	Enriched	Enriched	Moderate	YES		
A6NHL2-2;A6NHL	Tubulin alpha chain-	TUBAL3	45.517	14	12	4	28.119	0	18298	17906	22567	23950	22415	16068	20243	21141	12330	19869	Low	No expres	Low	No expression			
A6NHR9-2;A6NHF	Structural maintenan	SMCHD1	215.74	5.3	9	9	22.865	0	49851	38878	43256	50691	55454	34970	31381	30298	21073	39777	Low	Moderate	Moderate	Moderate	YES		
A6NHT5	Homeobox protein H	HMX3	37.824	4.5	2	2	52.042	0	888.48	1179.8	1020.5	4300.1	1666.1	0	34551	1514.4	2014	19703					YES		
A6NIH7	Protein unc-119 hom	UNC119B	28.136	7.6	2	2	4.4468	0.00042	12495	8963.6	10425	9546.7	10309	19522	18625	26528	6549.8	19149	Enriched	Enriched	Enriched	No expres	YES		
A6NIR2;X6R7Y7;	Intraflagellar transpo	HSPB11	13.028	18.8	2	2	5.1536	0.00044	27159	21471	25194	16692	19356	15134	19748	28864	7583.6	22474	Enriched	Enriched	Enriched	Enriched	YES		
A6NIT2;A6NMN0;	Phosphorylase b kina	PHKA1	132.63	1.2	2	2	6.0741	0	6079.6	3861.4	5776.6	9952.3	5659.3	7480.4	5388.4	7279.3	3167.8	7328.4	Low	Moderate	Moderate	Moderate	YES		
A6NJX6;Q96BP2	Coiled-coil-helix-coil	CHCHD1	10.957	9.3	1	1	2.106	0.00675	8175.3	4576.9	8193.6	6524.9	10395	8626.4	13162	6890.2	9065.3	12698	Enriched	Enriched	Enriched	No expression			
A6NLH6;Q9P003	Protein cornichon ho	CNIH4	15.771	13.9	1	1	3.3407	0.00078	23541	12260	14371	11515	16290	31265	39122	49830	17856	32729	Enriched	Enriched	Enriched	No expres	YES		
A6NLJ0	C2 calcium-dependen	C2CD4B	38.768	3.8	1	1	5.3793	0	4192.9	8304.4	5740.3	4488.9	7583.6	2695.5	6681.7	7757.2	2345.6	5145.8							
A6NLN1;P26599;P	Polypyrimidine tract-	PTBP1	56.51	36.4	45	36	290.59	0	233550	161260	195000	200020	213650	250680	346000	291140	189430	234210	Enriched	Enriched	Enriched	Enriched	YES		
C9J6F6;Q8IXF9;A	Aquaporin-12A;Aqua	AQP12A;AQP12B	32.645	14	5	5	7.055	0	12186	12887	12123	14432	13645	19498	26012	10510	7139.4	12477	No expres	No expres	Enriched	No expres	YES	YES	YES
E9PJK1;E9PRJ8;H	CD81 antigen	CD81	17.963	30.9	11	11	108.02	0	51381	40918	51184	60733	59376	77228	141430	131820	49464	88184	Enriched	Enriched	Enriched	Enriched	YES		
A6NML8;K4DI95;	Protein diaphanous h	DIAPH2	124.85	7.8	9	9	23.548	0	50894	40632	44969	59078	50951	44241	37433	50954	19722	50119	Enriched	Moderate	Enriched	Enriched	YES		
A6NMQ3;Q5T5H1	Alpha-endosulfine	ENSA	15.634	50.7	9	9	27.838	0	46841	38733	48301	36410	50107	37467	61413	64777	30227	49396	Enriched	Enriched	Enriched	Enriched	YES		
A6NMZ7;A6NMZ7	Collagen alpha-6(VI)	COL6A6	247.17	8.2	22	22	67.158	0	94245	72194	90988	103610	75522	98783	166260	123460	46895	77337	Low	Low	Low	No expres	YES		
A6NNI4;G8JLH6;P	CD9 antigen	CD9	17.764	35.2	11	11	185.49	0	217500	121650	182520	193060	186480	234780	236220	241830	79862	228850	Moderate	Enriched	Enriched	Enriched	YES		
A6NNK5;Q12888;	Tumor suppressor p5	TP53BP1	209.02	7.3	11	11	53.897	0	53581	44986	53575	42825	60702	49932	58563	69473	32566	57960	Enriched	Enriched	Enriched	Enriched	YES		
A6PVH9;F2Z2V0;I	Copine-1	CPNE1	53.046	16.2	7	7	21.67	0	16004	8939	9522.5	25975	16693	24321	13226	18341	9081.5	18518	Enriched	Enriched	Enriched	Enriched	YES		
A6PVN5;Q15257-2	Serine/threonine-prot	PPP2R4;DKFZp781M17	37.375	25.5	11	6	21.488	0	65475	49411	54094	44884	65218	78788	47718	81078	24803	47086	Enriched	Enriched	Enriched	Enriched			
A6PWM2;Q6UXH1	Cysteine-rich with E	CRELD2	25.129	31	15	2	2.7802	0.0024	1876.9	894.81	1274.5	2286.2	1876	9794.8	1472	1889.5	594.79	2632.5	Enriched	Enriched	Enriched	No expres	YES		
A6XGL2;P01308	Insulin;Insulin B chai	INS	10.959	29.6	12	12	30.876	0	54817	57981	56953	144690	61852	61542	40661	42476	22228	38619	Enriched	Enriched	Enriched	Enriched		YES	YES
A8CTZ0;F8W7U0;	Intersectin-1	ITSN1	100.7	2.1	2	1	2.7263	0.00239	11295	10922	14501	13932	14228	10506	8396.2	11633	3670.6	10108	Enriched	Moderate	Moderate	Enriched	YES		
D6RAR2;D6RFL2;	LYR motif-containin	LYRM9	9.9534	23.3	2	2	3.8897	0.00061	12843	13160	17730	11387	21287	12122	14754	14819	8759.5	13997							
J3QLE5;A8MT02;	Small nuclear ribonu	SNRPN;SNRPB	17.546	11.8	2	2	42.612	0	10645	3427.5	4314.9	19863	3944.1	8379	5061.2	23283	5243.5	13540	Enriched	Enriched	Enriched	Enriched	YES		
H3BQG3;A8MT40	Pyruvate dehydrogen	PDPR	54.79	7.1	3	3	8.6873	0	22726	18522	23698	17846	20335	22518	26782	24210	26504	24209	Moderate	Enriched	Enriched	No expres	YES		
A8MTY9;O14972-	Down syndrome criti	DSCR3	27.958	16.1	5	5	10.694	0	18706	12553	15659	27416	15856	20881	15133	20830	7698	26081	Moderate	Moderate	Enriched	Moderate	YES		
A8MUA9;A8MU27	Small ubiquitin-relat	SUMO3	15.317	28.9	5	3	40.305	0	26448	14773	16640	20483	20987	8608.3	15867	13494	16005	20243	Enriched	Enriched	Enriched	Enriched	YES		
A8MUM1;Q53HC	Protein TSSC1	TSSC1	46.319	9.9	5	5	41.564	0	9880.5	9838.4	11466	8754.5	14148	8490.9	12432	8967.6	8365.6	9150.5	Low	Moderate	Enriched	No expres	YES		
A8MV65-2;A8MV	Transcription cofacto	VGLL3	35.171	3.8	2	2	3.5626	0.00079	1750.2	1111.2	1226.6	638.6	1115.4	600.37	223.51	0	101.48	183.83	No expres	Moderate	Moderate	No expression			
A8MWD9;Q49AN	Putative small nuclea	SNRPGP15;SNRPG	8.544	27.6	4	4	13.894	0	9028.4	4976.1	6103.2	9566.6	8243.3	34805	25480	30925	6683	13024	Enriched	Enriched	Enriched	Enriched			
M0R275;J3KRI8;A	RAC-beta serine/thre	AKT2	14.409	7.8	1	1	2.1841	0.00543	6937	6414.1	6960.8	4816.7	8741.6	2490	4561.1	3619.8	3271.6	6218.1	Moderate	Low	Low	Low	YES		
A8MZH8;A8MXQ	Pituitary tumor-trans	PTTG1IP	11.598	15.9	1	1	3.3333	0.00078	4016.1	3452.6	4066.5	3917.2	4159	4213.7	2382.6	3011.2	1871.9	3147.7	Enriched	Enriched	Enriched	Enriched	YES		
A8MXU7;F5GYS3	Bcl2-associated agon	BAD	16.867	20.2	2	2	27.08	0	16312	13916	15056	11116	22078	14180	15404	13001	5716.5	15186	Low	Moderate	Moderate	No expres	YES		
A8MXV4	Nucleoside diphosph	NUDT19	42.233	11.2	5	5	29.174	0	19639	12591	10647	18302	15529	14326	15495	14808	8246.7	17470	Low	Enriched	Enriched	No expression			
A8MYT4;Q8NEB9	Phosphatidylinositol	PIK3C3	94.399	3.8	3	3	8.7331	0	4222.7	2980.2	3072.5	5491.5	2935.5	3592.4	2277.5	4476.8	1028.4	4910.1	Moderate	Moderate	Enriched	Moderate	YES		
A9X3U0;Q96GF1	E3 ubiquitin-protein	RNF185	16.786	8.9	1	1	2.5657	0.00344	1573.6	1803.1	1978.7	1226	2759.6	1520	4623.2	2275.5	3018.8	3467.6	Low	Enriched	Enriched	No expres	YES		
M0R088;E9PCT1;	Serine/arginine repeti	SRRM1	78.139	6.6	7	7	12.539	0	25742	29468	31646	19025	39491	24687	66451	38938	21796	24554	Moderate	Enriched	Enriched	Moderate	YES		
B0QY60		SUN2	21.772	40.4	8	1	3.0288	0.00132	1774.2	1247.1	1792.7	2104.6	1078.6	1198.1	3026.6	1632	3602.9	2669.4					YES		
B0QY67		SUN2	15.711	25	2	1	7.2105	0	3792.1	2663.2	3588.8	2834.2	4364.2	2125.3	3666.9	2653.9	2361.9	3362.5					YES		
B0QY89;Q9Y262;	Eukaryotic translatio	EIF3L	70.901	24.5	20	20	50.63	0	90958	77514	87377	80386	93447	118070	213190	171930	94972	114480	Enriched	Enriched	Enriched	No expres	YES		
B0QYK0;Q01844-	RNA-binding protein	EWSR1	64.929	15.4	13	13	46.9	0	88848	60161	77217	70482	81799	63661	57076	58097	31897	70527	Enriched	Enriched	Enriched	Moderate	YES		
H3BQQ9;B0QYN7	SUMO-conjugating e	UBE2I	15.516	21.9	5	5	15.923	0	33592	20790	29567	24608	29887	29798	35211	32826	15361	32938	Moderate	Enriched	Enriched	Enriched	YES		
B0QYZ7;B1AKL4;	Eukaryotic translatio	EIF4ENIF1	26.034	4.2	2	2	3.5886	0.00079	2931.5	2060.6	2639.9	3271.2	3462.9	2398.5	2004.3	2535.7	1338.8	3298.4	Moderate	Moderate	Enriched	No expression			
B0QZK5		HP1BP3	4.4418	52.5	4	1	10.694	0	10390	3858.8	7588	2847.1	8324.3	2287.9	7727.4	6897.8	4945.8	5711.3	Enriched	Enriched	Enriched	No expres	YES		
B0QZK9		HP1BP3	8.2371	61.8	8	0	20.224	0	17400	45499	42791	9109.8	58576	7406.3	20835	12628	12866	9466.5	Enriched	Enriched	Enriched	No expres	YES		
B0YIW2;P02656	Apolipoprotein C-III	APOC3	12.815	20.5	5	5	16.938	0	4953.6	6288.6	7752.6	4228.1	7208.2	4851.5	6064.1	4765.2	3637.7	4705.9	Enriched	No expres	No expres	No expres	YES		
B0YIW6;P48444;P	Coatomer subunit de	ARCN1	61.626	38	46	46	198.28	0	386470	254540	277890	391670	389430	392030	336100	367560	145310	344860	Moderate	Enriched	Enriched	Enriched	YES		
B1AH56		IFT27	5.7065	56.9	3	2	11.828	0	45247	27467	29730	48408	27763	43882	48470	54146	23007	56333					YES		
B1AH78;P15153;B	Ras-related C3 botul	RAC2;RAC3	18.502	35.5	14	0	3.6514	0.0008	7369	9343.4	7453.3	7933.3	8393.3	4129	5960.9	6105.3	4338.3	6482.2	Enriched	Moderate	Moderate	Moderate			
B1AHD1;P55769	NHP2-like protein 1;	NHP2L1	14.627	28.8	10	10	83.741	0	63636	34187	45679	58034	57587	77145	82913	81620	44464	77366	Enriched	Enriched	Enriched	Enriched	YES		
B1AHJ6		TPST2	15.639	28.9	11	2	17.877	0	12656	7383.7	10454	15748	9347.7	14067	12030	16953	9076.5	16332	Moderate	Enriched	Enriched	Enriched	YES		
B1AHM9		FBLN1	20.471	30.2	9	1	7.4037	0	1483.4	1696.2	1673.5	1148.8	2101.6	1099.8	9404	4512	3391.4	1788.7	Moderate	Moderate	Moderate	Moderate	YES		
B1AJU4;O14896-2	Interferon regulatory	IRF6	31.356	8.7	4	4	8.2956	0	7504.5	7003.3	7748.1	8337.3	7656.5	7923.4	7817.3	8151.6	2972.3	6952.7	Enriched	Enriched	Enriched	Enriched	YES		
B1AJY7;O75832;O	26S proteasome non-	PSMD10	20.808	33.7	9	9	39.962	0	14322	12096	14560	10580	18062	14721	18986	18847	9807.5	14480	Low	Enriched	Enriched	Enriched	YES		
B1AK63;Q9HAF1-	Chromatin modificati	MEAF6	19.164	5.9	1	1	2.7367	0.00239	13089	10157	17490	5957.5	19311	8569.6	8694.5	3886.8	4604.4	7756.3							
B1AK87;B1AK88;	F-actin-capping prote	CAPZB	29.295	58.5	22	22	71.365	0	237990	191950	236360	278610	272590	262250	231970	239980	128980	246100	Enriched	Enriched	Enriched	Enriched	YES		
Q6NVW1;B1AKC	Ephrin type-B recept	EPHB2	53.252	3.1	1	1	3.9086	0.00061	3591.9	2425	3048.9	2950.3	4825.2	4327.9	4295.7	4027.5	2384.3	7639.2	Enriched	Moderate	Moderate	Moderate			
B1AKK6;Q9H246	Uncharacterized prot	C1orf21	10.192	11.5	1	1	2.665	0.00256	1809.7	1149.6	1924.9	1024.6	2584.6	1193.8	1908.9	1564	1199.9	1410.3	Moderate	Enriched	Enriched	No expres	YES		
B1AKN7;B1AKN5	Nuclear factor 1;Nuc	NFIA;NFIX	51.451	13.5	7	5	20.82	0	33847	27877	34077	24753	44321	18186	18537	14259	9227.9	19420	Enriched	Enriched	Enriched	No expression			
B1AKR6;Q9NP97	Dynein light chain ro	DYNLRB1	16.253	38.5	9	9	20.298	0	65567	79990	77751	41511	96954	66800	35877	36418	23417	38236	Enriched	Enriched	Enriched	No expres	YES		
H0Y6Y8;B1AL05;	39S ribosomal protei	MRPL43	18.657	18.3	3	3	7.2805	0	4359.6	2867	4153.6	745.47	6545.7	2124.2	5319.9	3124	3765.1	4499.6	Enriched	Enriched	Enriched	No expres	YES		
B1ALA9		PRPS1	24.084	45.9	15	2	3.2731	0.00078	7698.5	4465.4	5322.7	9669.6	6048.2	9254.2	7364	7168	4378.4	9113.1	Moderate	Enriched	Enriched	Enriched			
B1ALC0;O15511;	Actin-related protein	ARPC5	14.807	45.9	10	10	73.248	0	109700	93158	117410	97623	133650	130570	116890	124240	58994	97411	Enriched	Enriched	Enriched	Enriched	YES		
B1ALK7;Q14155-1	Rho guanine nucleoti	ARHGEF7	79.831	18	13	13	50.954	0	39228	29550	34501	65795	40359	46177	48858	54603	33848	55341	Moderate	Enriched	Enriched	Enriched	YES		
B1AM15;Q9H503;	Barrier-to-autointegr	BANF2	4.6984	47.6	2	2	5.0094	0.00044	27182	16882	16040	11982	27185	14367	17814	10360	6540.8	14282	Low	Moderate	Low	No expression			
B1AMS2;Q14141-	Septin-6	SEPT6	49.303	17.6	11	2	5.9989	0	10494	5574.9	6925.3	23044	5560.2	9618.8	14047	12892	6068.7	18464	Moderate	Low	Enriched	Low	YES		
B1AMX9;Q12933-	TNF receptor-associa	TRAF2	46.566	6.2	3	3	3.8253	0.00061	1375.1	1109	1164.2	1593.6	2924	1193.4	3012.1	2749.6	1933	1382.8	Moderate	No expres	Low	Moderate	YES		
B1ANH0;B1ANG9	Guanylate kinase	GUK1	23.711	18.9	4	4	5.9598	0	14080	13834	27345	13062	23181	11441	23349	21562	20516	21941	No expres	Enriched	Enriched	Enriched	YES		
B1ANM7;Q9UNN	FAS-associated facto	FAF1	55.998	14.9	7	7	11.304	0	24540	17940	21632	29455	26756	21895	25719	27595	16212	24768	Low	Enriched	Enriched	No expres	YES		
B1AP13;H3BLV0;	Complement decay-a	CD55	49.338	9.9	4	4	32.612	0	17138	12920	16069	14689	15564	20240	21789	28143	13439	18926	Enriched	Moderate	Enriched	Enriched	YES		
B1AQT1;D6RBY7;D6RFK6;A0A087WZ		ANK3	21.501	39.5	6	2	11.769	0	12613	10269	19366	5978.4	19470	12920	12925	4519.2	5289.3	8652.6	Enriched	Enriched	Enriched	Enriched	YES		
C9JIZ6;B1AVU8;P	Prosaposin;Saposin-	PSAP	58.44	30.4	30	30	64.458	0	121080	78058	95175	94625	94734	152790	239130	233930	103540	128160	Enriched	Enriched	Enriched	Enriched	YES		
H7C1Q6;H7BXF4;	Sphingomyelin phosp	SMPD4	83.146	15.4	9	9	20.058	0	20980	9845.3	13361	22379	13255	22351	17009	22013	8714.7	18489	Moderate	Moderate	Moderate	Moderate	YES		
B2WTI3;B2WTI4;	Bifunctional arginine	JMJD6	39.241	9	2	2	19.006	0	10653	5300	6744.7	10560	9055.3	9184.3	7056.2	9641.6	3108.4	9584.2	Enriched	Enriched	Enriched	Enriched			
B3KN26;Q9NWW	Nicotinamide ribosid	NMRK1	11.938	13.2	2	2	6.118	0	3646.1	3312.6	3367.7	3437.4	3490.7	3652.7	3676	2634.1	2358	2961.7					YES		
B3KNX7;Q13153;	Serine/threonine-prot	PAK1	58.202	23.6	16	4	23.344	0	25429	19280	19612	20346	25572	37560	38540	32679	20897	24644	Enriched	Enriched	Enriched	Moderate	YES		
F5H5N2;B4DNC9;	Iron-sulfur cluster as	ISCU	16.64	11	2	2	4.0142	0.00062	10987	10295	10232	9185.4	10285	12672	13305	12994	7846.6	13869	Enriched	Enriched	Enriched	Enriched	YES		
B3KS98;O15372;A	Eukaryotic translatio	EIF3S3;EIF3H	41.581	32.8	16	16	52.464	0	37078	30982	36850	36115	37929	32622	41718	40086	32111	41401	Enriched	Enriched	Enriched	Enriched	YES		
H0YNX3;H0YLV1	Mortality factor 4-lik	MORF4L1	8.1452	16.2	1	1	3.798	0.00061	4217	3686.3	6055.8	2133.3	7359.9	1547.5	3638.6	2483.4	3176.6	2628.5	Enriched	Enriched	Enriched	No expression			
B3KUB4;O43570-	Carbonic anhydrase	CA12	31.857	15.5	4	4	7.5997	0	13427	12303	10821	17359	10293	11494	9153.4	11895	4244.6	12101	Enriched	Enriched	Enriched	Enriched			
B3KW70;F5GYX4	Microfibrillar-associa	MFAP5	17.114	20.9	5	5	10.34	0	19679	20692	20011	23092	28355	26192	44587	70581	26408	46593	Moderate	Low	Low	No expres	YES		
B3KY94;O14735-3	CDP-diacylglycerol--	CDIPT	25.946	13.1	5	5	10.346	0	23981	15108	14784	17147	17528	26513	31525	37635	12226	26811	Enriched	Enriched	Enriched	Enriched	YES		
B4DDD8;P12081-4	Histidine--tRNA ligas	HARS	48.569	48	31	27	111.19	0	170590	122040	151500	225850	156970	200040	264410	241260	104490	185370	Moderate	Enriched	Enriched	Moderate	YES		
F8WAK5;B4DDH2	Serine/threonine-prot	STK33	37.084	7.6	2	2	8.1159	0	6820.7	5853.1	9297.1	6217.3	9596.1	5515.7	6636	7123.4	4238	6468.8	Low	Low	Moderate	No expres	YES		
B4DE15;P78381-5	UDP-galactose transl	SLC35A2	42.226	2.7	1	1	3.2261	0.00077	22512	22556	17685	19238	26710	21909	15964	16314	7442.6	16518	Moderate	Enriched	Enriched	Enriched			
B4DE85;P48651-2	Phosphatidylserine sy	PTDSS1	34.579	7.6	3	3	5.8852	0	25846	20881	26147	28398	29073	46415	33572	30245	14964	26240	Enriched	Enriched	Enriched	Enriched	YES		
B4DEB1;K7ES00;	Histone H3	H3F3A;H3F3B	14.052	34.1	12	3	22.603	0	131450	81267	76546	129670	100250	86784	130310	158660	61158	150030	Enriched	Enriched	Enriched	Enriched			
B4DEK9;Q13214-2	Semaphorin-3B	SEMA3B	45.038	3.9	1	1	3.2042	0.00077	5087.6	3346.8	4017.4	4799.7	4509	5776.1	4279.5	4808.2	2571.4	6462.5	Enriched	Enriched	Moderate	Moderate	YES		
F8WEE4;B8ZZ56;	AN1-type zinc finger	ZFAND2B	10.578	10.4	1	1	2.6818	0.00256	6522.7	5961.6	6916.6	4933.2	8564	4745.4	11483	6714.1	8445.4	7871.3	Low	Enriched	Enriched	No expres	YES		
H3BPN6;H3BT78;	Serine/threonine-prot	ULK3	9.2547	15.5	2	2	4.5481	0.00043	4223.8	2376.4	3305.2	5839	3035.7	4570.6	2947.4	4098.3	2139.5	3686.8	Enriched	Enriched	Moderate	No expression			
B4DGJ5;Q8N7H5-	RNA polymerase II-a	PAF1	32.92	14.2	4	4	6.3942	0	30722	24380	30625	27818	32008	27987	29571	27482	13941	29441	Enriched	Moderate	Moderate	Enriched	YES		
B4DGM3;Q969G3-	SWI/SNF-related ma	SMARCE1	44.77	12.2	7	7	26.435	0	26000	18965	26045	26670	28590	27469	33202	33287	16275	27482	Enriched	Enriched	Enriched	Enriched	YES		
B4DGU4;P35222	Catenin beta-1	CTNNB1	84.765	32.9	39	26	114.15	0	149710	138220	160670	151260	203310	134350	201960	169500	143550	171980	Enriched	Enriched	Enriched	Enriched	YES		
B4DGW9;Q9UM1	Hippocalcin-like prot	HPCAL4	13.854	15.1	1	1	3.711	0.0008	4565.8	2211.6	2870.4	4552.1	2621	3992.8	2035.7	2390.5	1643	3635.7	Moderate	Moderate	Low	No expression			
B4DHE8;Q96DH6-	RNA-binding protein	IGSF9B;MSI2	34.812	18.8	5	4	12.99	0	29365	17050	23144	27571	30327	26654	21703	23527	10098	22116	Moderate	Low	Low	Enriched	YES		
B4DHJ7;Q12983	BCL2/adenovirus E1	BNIP3	19.943	6.7	1	1	104.65	0	2100.5	1002.4	2583.2	1492.7	1598.5	16530	15450	6324.1	7659.1	9535.2	Enriched	Enriched	Enriched	Enriched	YES		
C9JM82;B4DJ62;G	Septin-5	SEPT5	34.672	12.3	3	3	7.4399	0	13375	10188	15915	8265.6	16360	12379	15741	13576	9103.3	13432	Moderate	No expres	Low	No expres	YES		
B4DJC3	Histone H2A	H2AFY	21.548	52.5	15	5	5.9314	0	14594	11086	20627	21511	13882	17929	20512	23541	10497	19033	Enriched	Enriched	Enriched	Enriched	YES		
B4DJV2;O75390	Citrate synthase;Citra	CS	50.431	23.2	18	10	86.54	0	71917	62069	68520	61062	98156	87330	68004	85585	38456	69867	Enriched	Enriched	Enriched	Enriched	YES		
B4DJV5;Q13610	Periodic tryptophan	PWP1	49.038	10.9	5	5	11.738	0	28502	18699	27431	17219	18644	34530	38805	23913	16315	31166	Enriched	Enriched	Enriched	Enriched	YES		
B4DLN1		MRPL12	48.099	15.2	12	0	56.135	0	72684	61240	76471	73066	76501	108580	96969	88631	56970	81413	Low	Moderate	Enriched	No expression			
H0YBZ9;B4DP61;	Survival motor neuro	SMN1	8.5333	22.8	1	1	3.0927	0.00095	5787.8	4984.8	5731.5	4969.5	5882.7	5296	5551.7	4960	2942.2	4774.3	Low	Low	Enriched	No expression			
F5H2D0;B4DPQ0;	Complement C1r sub	C1R	76.613	5.8	5	5	14.505	0	33778	35155	36528	40569	34066	34147	34977	51498	22753	34325	Moderate	Enriched	Enriched	Enriched	YES		
B4DQI6;Q13595-3	Transformer-2 protei	TRA2A	20.589	22.8	5	3	3.4082	0.00079	3499.2	3150.4	3160.4	3488.6	4497.9	4977.4	22136	9222.8	17857	7414.9	Moderate	Moderate	Enriched	Enriched	YES		
B4DR61;P61619;P	Protein transport pro	SEC61A1	52.949	28.4	30	23	56.347	0	174140	117000	137050	151990	190370	180560	188790	168120	69074	149260	No expres	Enriched	Enriched	Low	YES		
B4DR80;Q9Y6E0-	Serine/threonine-prot	STK24	45.835	27.4	15	4	51.227	0	81731	64648	69555	78618	79612	63383	72510	80636	43545	74874	Enriched	Enriched	Enriched	Enriched	YES		
B4DTL2;E9PGC0;	Ras GTPase-activatin	RASA1	101.54	3.5	4	4	10.064	0	6194.3	3212.4	4015	5946.3	5762.6	5053.7	5057.7	5968.9	2339	6146.4	Enriched	Enriched	Enriched	Enriched			
F5H6D8;B4DTN4;	N6-adenosine-methyl	METTL3	26.266	9.4	2	2	2.4608	0.00413	9880.6	10582	12260	7244.6	17030	4631.8	7366.1	4383.1	4913.8	7284.3	Moderate	Enriched	Enriched	Enriched	YES		
B4DUC8;Q13126;	S-methyl-5-thioaden	MTAP	33.186	55	21	21	200.41	0	138630	108960	120680	122620	151850	143870	180470	174440	79604	137080	Moderate	Moderate	Low	Low	YES		
R4GNC0;B4DVL2;	N-acylethanolamine-	NAAA	24.725	17.1	5	5	15.057	0	14805	14342	19506	19446	18050	17219	14717	15486	8171.9	16892	Enriched	Enriched	Enriched	No expression			
B4DWR3;P61758	Prefoldin subunit 3	VBP1	22.254	10.4	3	3	6.4862	0	11750	10889	12090	11873	14206	7307.2	10035	8976.2	9109.9	9752.6	Enriched	Enriched	Enriched	Enriched	YES		
B4DXW4;Q9H078-	Caseinolytic peptidas	CLPB	57.663	17.6	7	7	19.19	0	22830	20698	20352	20355	26618	22680	27305	23330	15690	25716	Low	Moderate	Moderate	No expres	YES		
B4DXZ6;E7EU85;	Fragile X mental reta	FXR1	68.326	11.8	10	8	44.315	0	50884	40268	46688	56627	47204	47384	102600	100070	28964	59298	Enriched	Enriched	Enriched	No expres	YES		
B4DYY6;Q75T13-	GPI inositol-deacylas	PGAP1	34.404	8.6	2	2	2.8204	0.00223	11111	9106.1	10613	11000	13344	9499.4	11815	11063	8790.8	10291	No expres	Low	Moderate	Enriched	YES		
B4E0E3;G3V1M5;	Transmembrane prot	TMEM134	11.318	9.1	1	1	2.7169	0.00238	14019	10685	13456	13676	18850	18144	11931	12896	6262.7	14322	Enriched	Enriched	Enriched	No expression			
B4E0K5;Q16539-2	Mitogen-activated pr	MAPK14	32.357	13.1	4	4	16.266	0	36103	21213	25825	27055	23575	43892	47603	57447	29890	36173	Low	Enriched	Enriched	Enriched	YES		
B4E0T2;P50542-2;	Peroxisomal targetin	PEX5	73.182	4.2	2	2	9.6487	0	8148.5	4377.1	6724.3	8161.2	6410.6	9800.4	8375.7	9147.7	4449.5	8445	Enriched	Enriched	Enriched	Moderate	YES		
Q8NBY1;B4E0Y9;	Serine/threonine-prot	RBM4B;MST4;STK25	43.867	19.6	12	0	11.925	0	11380	7989.6	7884	7027.8	6207.5	15338	19796	21651	8752.3	15391	Enriched	Enriched	Enriched	Moderate			
B4E107;F5GXE4;	Arginyl-tRNA--prote	ATE1	47.834	14.9	7	7	26.543	0	20597	14300	19898	22515	24339	21133	15769	16252	9153.8	18377	No expres	Enriched	Enriched	No expres	YES		
B4E1Z4;E7ETN3;	Complement factor B	CFB	140.94	18.8	24	13	90.488	0	67170	64294	69726	163100	61998	69962	70009	233620	49677	76171	Enriched	Enriched	Enriched	Moderate	YES		
B4E2Q0;P98194-2	Calcium-transporting	ATP2C1	104.71	5.5	5	5	13.089	0	9825.1	7815.3	9328.2	12771	10283	10576	8251.1	11189	4653.6	10117	Enriched	Moderate	Enriched	Moderate	YES		
B4E3S0;Q9ULV4;	Coronin;Coronin-1C	CORO1C	41.603	28.5	13	12	21.636	0	29271	26341	27387	40404	32779	25725	25740	28580	29598	35682	Low	Enriched	Enriched	No expres	YES		
B5MC20;P0C870	JmjC domain-contain	JMJD7	24.796	10.6	3	3	17.299	0	19608	8808.3	10913	14799	14030	15584	11416	13115	3932.8	15749							
B5MC59;P35244	Replication protein A	RPA3	9.1703	32.9	3	3	7.1649	0	15600	18782	11568	12225	12480	21320	19965	29353	10318	19262	Low	Enriched	Enriched	Moderate	YES		
B5MCA4;P16422	Epithelial cell adhesi	EPCAM	37.893	37.4	27	27	261.13	0	145450	82793	100160	192110	117930	156120	130160	180550	78344	284350	Enriched	Enriched	Enriched	Enriched	YES		
B5MCW2		RPL3	31.243	50	34	2	56.007	0	2674.6	1678.5	2075	2484.4	3034.5	4952.8	28432	1262.7	21646	3996.7	Enriched	Enriched	Enriched	Enriched	YES		
B5MCX3;Q15019;	Septin-2	SEPT2	36.94	59.5	28	25	186.68	0	139020	99634	119640	153740	111350	107330	130390	207980	58996	142610	No expres	Enriched	Enriched	Enriched	YES		
V9GYU2;B5MCX7	Ankyrin repeat doma	ANKRD54	12.704	15	2	2	3.3618	0.00078	2431.7	1592.1	2821.6	3903.8	2860.5	7895	3360.4	4490	2414.9	4039.4	Moderate	Enriched	Enriched	No expression			
B5MD17;J3KS05;	Chromobox protein h	CBX1	19.325	24.4	10	6	11.427	0	30491	31011	34867	20749	42300	20014	25941	15571	22523	21219	Enriched	Moderate	Enriched	Enriched	YES		
B5MD46;Q9BXI6;	TBC1 domain family	TBC1D10A	47.913	3.1	1	1	2.3866	0.00429	892.16	1134	1116.9	892.89	1624.3	692.09	913.08	695.85	825.19	867.7	Moderate	Enriched	Enriched	No expres	YES		
B5MDU6;Q9H6V9	UPF0554 protein C2	C2orf43;FLJ21820	42.668	8.6	4	4	5.7289	0	14202	10384	14867	10045	9440.7	20785	19885	20562	10438	16771	Low	Low	Moderate	No expres	YES		
E7EW69;E7EX04;	Septin-10	SEPT10	52.145	19.6	11	7	20.295	0	9326.9	11810	7879.4	8563.2	9973.4	8911.4	7488.9	8965.5	5280.6	9902.9	Moderate	Enriched	Enriched	Enriched	YES		
E7EST9;B5MEG5;	Ubiquitin carboxyl-te	USP19	145.56	2	2	2	22.962	0	7826.8	8624.9	9773.1	6000.8	11544	6527.3	7276	5168.4	3995.7	6761	Enriched	Enriched	Enriched	Enriched	YES		
B7WPD9;Q2KJY2-	Kinesin-like protein	KIF26B	184.68	1.3	2	2	3.5164	0.00079	8825.8	4919.5	7041.1	2921.3	13688	6641.9	6805.3	3646.9	4536.4	5223.7	Low	No expres	Low	No expression			
G3V1D0;B7WPE2;	Echinoderm microtub	EML3	95.024	4.6	3	3	7.316	0	12667	11428	12812	12195	18136	9347	15647	11755	9634.3	13249	Moderate	Moderate	Moderate	Enriched	YES		
B7WPG3;C9JYN3;	Heterogeneous nucle	HNRPLL;HNRNPLL	56.45	21.5	10	10	34.615	0	29071	16605	20419	23658	25144	25456	19555	25746	11765	28472	Moderate	Enriched	Enriched	No expres	YES		
F8W9A8;B7WPL9;	Inositol hexakisphos	PPIP5K1	156.65	3.8	4	2	4.2264	0.00063	7569.3	30977	17300	4837.4	20560	2376	7484	3944.9	6198	6262.3							
B7Z2R7;Q5T8D3-	Acyl-CoA-binding do	ACBD5	58.792	5.7	2	2	4.3492	0.00063	4455.5	3959.4	4734.8	4918.7	5090.9	4791.4	3859.6	4710.1	2535	5734.7	Moderate	Enriched	Enriched	No expression			
B7Z2Y2;Q14746-2	Conserved oligomeric	COG2	76.078	18.1	9	9	28.486	0	46516	37686	43498	47849	58329	53799	59718	53433	35826	58343	Enriched	Enriched	Enriched	Moderate	YES		
B7Z3R2;Q9ULQ1;	Two pore calcium ch	TPCN1	87.317	3.3	2	2	5.0188	0.00044	6118.7	3737.6	4972	6109.2	6264.2	7622.1	4902.1	5852.7	3301.8	6938.9	Enriched	Enriched	Enriched	No expres	YES		
B7Z493;E9PJX4;	FYVE, RhoGEF and	FGD4	95.45	9.5	7	7	13.564	0	5017.8	3868.7	4347.3	5296.2	4150.7	4495.1	4994.1	5271.6	3755.2	5331.9	Enriched	Enriched	Enriched	No expres	YES		

E7EPW5;G3XAH9	Suppressor of tumori	ST7;ST7L	58.067	8.7	4	4	6.6413	0	3662.3	4475.4	4691.3	2743.5	6085.2	3510.7	3977.3	2825.1	2889	3063.3	Enriched	Moderate	Moderate	Enriched	
B7Z4M1;O95197-6	Reticulon;Reticulon-	RTN3	12.747	8.9	2	2	4.4508	0.00042	3128.3	1196	1947.6	2166.4	1972	1058.5	2454.9	1955.1	1307.3	1654.1	Enriched	Enriched	Enriched	No expres	YES
B7Z637;Q8IUR7-8	Armadillo repeat-con	ARMC8	67.185	8.8	5	5	11.304	0	8018	5842.3	6429.7	5699.6	8676.5	5746	4574.8	6546.3	2463.5	6692.8	Low	Moderate	Enriched	Low	YES
B7Z651;E9PHW9;(	Ankyrin-2	ANK2	119.9	5	5	3	5.7298	0	8342.3	9924.3	10492	8597.4	13235	7342	7174.3	6291.4	3390	7191.8	Low	No expres	Moderate	No expres	YES
B7Z685;D6RC99;E	Guanylate cyclase so	GUCY1B3	62.761	2.2	1	1	5.0115	0.00044	5232.4	4620.9	5047.3	4652.7	4552.2	5038	5416.4	9616.7	1736.9	6578.2	Low	Moderate	Enriched	Low	YES
B7Z6D5;Q96GQ7	Probable ATP-depen	DDX27	86.604	7.7	7	7	21.995	0	17268	13964	19891	15825	19186	16997	21236	22911	12507	23414	Enriched	Enriched	Enriched	No expres	YES
B7Z7V6;Q6PJI9-2;	WD repeat-containin	WDR59	52.462	3.5	1	1	15.065	0	11066	7575.7	8376	9081.3	10009	7166.2	9542	10857	6925.1	9207.2	Enriched	Moderate	Enriched	No expres	YES
C9JWE6;E7ENB6;	E3 ubiquitin-protein	PDZRN3	55.408	2.2	1	1	2.1768	0.0056	5202.8	4352.7	6527.6	3517.1	7105.3	4999.5	8107.1	5597.5	5275.4	7433.2	Enriched	Moderate	Low	Moderate	
B7ZAQ6-2;B7ZAQ	Golgi pH regulator A	GPR89A;GPR89B;GPR8	38.484	17	9	9	21.259	0	10385	8238.8	8765.5	11519	9148.8	14596	27731	45151	10485	16942	Moderate	Enriched	Enriched	No expres	YES
B7ZBJ4;Q9H9S4;C	Calcium-binding prot	CAB39L	22.957	20.2	3	3	11.406	0	5692.1	2348.7	3501.3	6795.6	3081.6	6310.4	5431.7	5412.4	2295.9	4633.6	Low	Moderate	Enriched	No expres	YES
Q96NX8;F8W9Z6;	Syntaxin-16	STX16;STX16-NPEPL1	23.021	17.8	3	3	6.8833	0	14437	11241	11173	16044	12594	16024	14938	13623	8520.5	13646	Enriched	Enriched	Enriched	Enriched	YES
B7ZBR7;Q6DHV5-2		CC2D2B	44.196	2.9	1	1	2.0551	0.0074	3956.3	2291.1	2885.1	2871.4	2979.9	7750.2	5220.8	22139	3981.4	12717	Moderate	Moderate	No expres	No expression	
B7ZC38;Q9NR46;I	Endophilin-B2	SH3GLB2	44.361	19.8	10	8	20.729	0	15296	22345	27482	12628	17224	11853	42565	32273	17575	15171	Enriched	Enriched	Moderate	No expres	YES
B7ZKJ8;Q14624-4;	Inter-alpha-trypsin in	ITIH4	103.88	12.3	16	16	78.95	0	47896	90029	88661	57415	57142	29946	43157	67400	55801	46843	Low	Moderate	Moderate	Moderate	YES
Q5QPR3;J3QKR5;I	Cyclin-dependent kin	CDK11A;CDK11B;CDC	91.006	8.1	8	8	15.756	0	39681	31325	36322	30159	39985	22706	24994	34620	21482	32624	No expres	Moderate	Moderate	Moderate	YES
E7ENR5;B8ZZ47;I	U3 small nucleolar ri	IMP4	27.091	4.7	1	1	3.3005	0.00078	11456	8265.9	9119.1	9829.2	11674	7758.2	12915	10238	6961.3	12061	Enriched	Enriched	Enriched	Moderate	
C9JEL3;B9A044;B	Eukaryotic translatio	EIF4E2	24.602	25.4	9	9	16.106	0	27834	21220	14367	13390	26066	16291	24150	20582	11768	19013	Enriched	Enriched	Enriched	Moderate	YES
B8ZZA8		GLS	18.634	31.4	7	1	4.2281	0.00063	8367.6	7631.4	6687.2	6095.3	8119.6	5156.5	4537.5	4524.6	2462.3	5890.8	Moderate	Enriched	Enriched	Enriched	YES
B8ZZF2;Q8N9V3-2	WD repeat, SAM and	WDSUB1	47.567	2.3	1	1	2.3697	0.00428	3582.4	2415.7	2004.2	2792	3061.2	3148.8	2265.6	1608	2212.2	2205	Low	Enriched	Enriched	No expression	
B8ZZF5;Q9H8M9;	Protein eva-1 homolo	EVA1A	16.163	16.4	2	2	3.8356	0.00061	1263.3	655.51	1106.4	932.74	985.25	1089.2	471.63	558.24	214.55	740.23					YES
B8ZZG1;Q9NZW5	MAGUK p55 subfam	MPP6	48.757	10.3	6	6	16.519	0	5096.2	4093.3	4359.5	6600.2	5664.7	5066	5452.8	5358.3	2235.6	5341.8	No expres	Low	Enriched	Low	YES
B8ZZJ0;B9A032;B	Small ubiquitin-relate	SUMO1	6.6846	19	2	2	4.692	0.00043	1700.5	1125.8	887.35	1410.2	2039.8	1855.5	2460.9	1823.7	1396.3	2122.7	Enriched	Enriched	Enriched	Moderate	YES
B8ZZJ1;B8ZZA2;H	Hyccin	FAM126A	46.919	5.5	2	2	2.1246	0.00609	7925.8	5910	10161	10933	12102	9408	13472	15338	9736.3	12005	No expres	Enriched	Enriched	No expression	
B8ZZQ6;P06454-2	Prothymosin alpha;Pr	PTMA	11.758	37.4	11	11	102.68	0	36084	27298	34197	31624	49484	48364	214270	122850	230640	102190	Enriched	Enriched	Enriched	Enriched	YES
B8ZZS4;Q9H8Y5	Ankyrin repeat and zi	ANKZF1	57.572	7.6	4	4	8.3114	0	19813	15188	17677	22780	18948	21436	22366	22030	14654	21628	Moderate	Low	Moderate	No expres	YES
B8ZZU8;Q15370;C	Transcription elongat	TCEB2	12.527	38.1	6	6	36.936	0	88284	74372	80168	75614	121600	58221	44710	59713	21083	57406	No expres	Enriched	Enriched	Enriched	YES
B8ZZV5;Q8TCC3-	39S ribosomal protei	MRPL30	11.935	10.9	1	1	3.0664	0.00114	4867.1	4403.9	5114.3	4177.5	5792.6	5566.4	5835.6	5327.5	2889	6503.8	Enriched	Enriched	Enriched	No expression	
B8ZZX6;Q658P3-4	Metalloreductase STI	STEAP3	50.628	5.9	2	2	4.3723	0.00063	3466.2	2316.6	2310	3498.7	3229.2	4223.8	4935.5	4017.3	1668.7	4519.9	Moderate	Enriched	Enriched	No expres	YES
C9J2I0;B8ZZY2;P5	Arf-GAP domain and	AGFG1	25.497	18.5	7	6	14.933	0	44120	52750	46630	50282	56987	27657	35630	41095	22808	38657	Enriched	Moderate	Enriched	No expres	YES
B9A018;Q53GS9;C	U4/U6.U5 tri-snRNP	USP39	62.043	18.8	11	11	46.122	0	54939	33507	46316	56052	38360	51073	51767	58898	28837	58499	Low	Low	Moderate	No expres	YES
B9A067;Q16891-2	MICOS complex sub	IMMT	78.973	46.8	46	33	230.71	0	195860	146680	190910	190020	227930	247100	389640	338130	190060	256850	Enriched	Enriched	Enriched	Enriched	YES
J3QWB6;J3KMX2;	SWI/SNF-related mat	SMARCD2	26.714	16.9	5	5	11.029	0	12685	9602.7	9771.9	8928.3	11831	16175	18694	20648	12526	16193	Moderate	Enriched	Enriched	Enriched	YES
B9ZVT1;Q8IXT5	RNA-binding protein	RBM12B	102.7	6.2	4	4	8.4393	0	11689	8175.1	14890	15584	14288	12021	13884	13630	7329.7	12046	Low	No expres	Moderate	No expres	YES
B9ZVU2		DNPEP	29.865	23.3	11	3	10.493	0	11624	11698	11552	5062	10356	6286.8	26108	27232	7661.4	16596	Enriched	Enriched	Enriched	Enriched	YES
C9J7B4;I3L2Y3;C9	E3 ubiquitin-protein	RNF13;RNF167	17.299	6.7	1	1	2.6086	0.00273	7294.9	6441.5	10359	4861.9	10339	2904.1	10330	7432.4	5905	7912.6	Enriched	Enriched	Enriched	Moderate	
C9JKT3;C9IYB4;Q	[Pyruvate dehydroger	PDK1	17.75	15.6	3	3	3.0828	0.00114	11612	8335.5	8611	11523	11539	10523	9860.8	7285	7021.5	9980.7	Low	Moderate	Enriched	No expres	YES
C9IZ65		CTNNB1	6.526	35.6	4	3	15.576	0	19240	8005.2	11284	9800.5	17329	6115.1	13610	12901	6542.9	13059	Enriched	Enriched	Enriched	Enriched	YES
C9JF62;C9JSK8;C9	NEDD8-conjugating	UBE2F	15.674	25.2	3	3	6.0131	0	3131	3299.6	3040.5	2036.1	4701.7	1466.2	1355.8	1578.8	1050.7	1230	Enriched	Enriched	Enriched	No expression	
C9IZF9		PDCD6IP	17.064	44.4	7	1	2.7018	0.00238	8745.8	5392.2	9382.2	4056.3	6325.6	10430	22897	11805	7746.1	14957	Enriched	Enriched	Enriched	No expres	YES
C9JMG3;C9JWL4;	AP-4 complex subun	AP4M1	29.685	10.2	2	2	3.2239	0.00077	9607.8	8427.7	8937.5	9652.4	11119	10872	12141	10932	6149.1	10861	Moderate	Low	Moderate	Low	YES
C9IZN5		NDUFA5	10.694	43	10	3	20.83	0	9315.6	5138.1	7471.2	4841.6	7072.6	10032	6177.1	4776	3042.7	7035.4	Moderate	Enriched	Enriched	Enriched	YES
C9J3L8;C9J5W0;E	Translocon-associate	SSR1	29.573	30.6	13	13	101	0	38145	28395	31384	29062	50271	51166	109840	107230	31692	43743	Enriched	Enriched	Enriched	Moderate	YES
C9J9T0;C9IZU8;Q9	Ribulose-phosphate 3	RPE;RPEL1	20.972	15.7	6	3	32.774	0	21625	19787	18450	20001	19196	15652	18689	18990	16080	19751	Moderate	Moderate	Enriched	No expression	
C9IZW8;C9JXM4;I	NADH dehydrogenas	NDUFB2	9.3942	12.8	2	2	2.1423	0.0061	2474.2	2084.7	2216.7	1678.1	3647.7	2414.9	3288.5	1926	2920.1	2776.1	Enriched	Enriched	Enriched	No expres	YES
C9J0I9;Q86WB0;Q	Nuclear-interacting p	ZC3HC1	50.562	11.8	4	4	8.3188	0	17997	19524	20647	15235	31234	14261	16890	12175	11453	15031	Low	Enriched	Enriched	No expres	YES
C9J0J0;Q96EE4	Coiled-coil domain-c	CCDC126	12.768	9.9	2	2	3.9585	0.00061	6335.8	2265.7	2806	7102.6	2900	3626.1	3781.9	5206.8	2124	5919	Low	Moderate	Enriched	No expression	
C9J0K6;P30626-2;	Sorcin	SRI	17.605	62.6	16	16	46.551	0	81407	70287	62806	61377	85309	55686	81865	102230	33319	56875	Enriched	Enriched	Enriched	No expres	YES
C9JLK8;C9JQE9;C	NLR family member	NLRX1	14.716	22	2	2	6.257	0	11939	11755	9181.5	15084	15669	7463.7	7980.9	11196	4523	11705	Enriched	Moderate	Moderate	No expres	YES
C9J0X4;C9J481;P5	Histone deacetylase 4	HDAC4	14.689	17.9	2	2	4.6617	0.00043	8700.1	6956	7751.7	9296.5	8119.5	6871.6	7435.2	8629.7	4691.5	8822	Low	Moderate	Moderate	Moderate	YES
C9J111;C9J8A7;Q8	Polypeptide N-acetyl	GALNT11	18.34	13.1	2	2	1.8578	0.00878	12548	9968.4	11539	15745	12227	13212	11768	11291	3936.6	21736	Enriched	Enriched	Enriched	No expression	
F8WF15;F8W8F0;(	Ubiquitin-conjugatin	UBE2E2	9.7027	16.9	1	1	15.962	0	10130	8840.2	8995.9	9661.1	8533.6	7665.4	12842	13095	7436.3	13815	Moderate	Enriched	Enriched	No expression	
C9J1Z8;P84085	ADP-ribosylation fac	ARF5	17.107	62	26	2	25.871	0	18175	3109.3	4865	8905.6	6140.4	9546.4	3494.2	14448	1245.8	10795	Low	Enriched	Enriched	Enriched	YES
C9J296		LAMB1	20.037	24	4	1	30.469	0	6633.7	6935.3	8205.4	5442.6	13676	6454	8529.9	5832.8	4085.7	6502.5	No expres	Enriched	Enriched	Moderate	YES
C9J2C3;Q14435;Q	Polypeptide N-acetyl	GALNT3	53.375	11.2	5	5	32.877	0	41967	30466	27896	43586	45037	27418	36051	33704	20842	48772	Enriched	Enriched	Enriched	Moderate	YES
G5E9D8;C9J2H1;C	Inter-alpha-trypsin in	ITIH5	78.437	18.9	16	16	34.536	0	29810	26450	39646	37126	41428	30172	38211	34982	23736	38001	Low	Moderate	Moderate	No expres	YES
C9J2Q2;Q8N5M1	ATP synthase mitoch	ATPAF2	23.152	15.1	3	3	6.3579	0	7308.8	4928.7	5325.2	6208.6	5423.5	8490.4	8364.8	10359	6299.4	9087	Low	No expres	Moderate	Moderate	YES
C9J2Y9;P30876;C9	DNA-directed RNA p	POLR2B	133.06	19.3	25	25	54.016	0	66654	59765	67292	57271	74757	56283	75841	68605	51882	66148	Enriched	Enriched	Enriched	Enriched	YES
C9J3D7;Q9UKG9;(	Peroxisomal carnitine	CROT	65.883	5.1	2	2	3.4945	0.00079	7889.9	5194.1	7894.3	7957.3	5602.7	7472.8	6222.8	10766	4059.3	7735.9	Enriched	Moderate	Moderate	No expression	
C9J3F6;Q92609;Q9	TBC1 domain family	TBC1D5	67.534	8.4	4	4	27.391	0	4837.3	4646.2	4337.7	4110.4	5366.3	3446.9	5707.2	5076	3131.2	4785.5	Enriched	Enriched	Enriched	Low	YES
C9JRH2;C9JMJ4;C	Regulator of chromos	RCC1	24.465	38.3	9	9	73.059	0	56193	43698	49400	46128	66096	39062	51839	54922	30277	52382	Moderate	Moderate	Moderate	Moderate	YES
C9J494;Q9H000-2;	Probable E3 ubiquiti	MKRN2	46.68	13.3	6	6	7.6098	0	24372	15945	19658	13298	26592	21253	36416	20066	23287	23702	Low	Moderate	Enriched	No expres	YES
C9J4Z3;P61513	60S ribosomal protei	RPL37A	7.624	52.9	12	12	111.28	0	88888	54844	67152	52205	94514	67444	133750	108050	47018	59302	Enriched	Enriched	Enriched	Enriched	YES
C9J932;H7C5M9;C	Programmed cell dea	PDCD10	9.0495	39.2	3	3	7.8893	0	18422	15265	15862	14603	19320	29327	29826	30217	11824	23587	Enriched	Enriched	Enriched	Moderate	YES
C9JJV6;C9JZL8;C9	Myeloid-associated d	MYADM	15.935	15.6	2	2	162	0	12077	8792.1	12470	8794.3	18608	8069.3	10451	11632	6390.5	15078	Enriched	Enriched	Enriched	No expres	YES
C9J5N1;Q9BTE6;C	Alanyl-tRNA editing	PTGES3L-AARSD1;AA	55.065	13.1	7	7	23.827	0	31375	19475	23776	26473	28283	42015	41107	32198	21532	34731	Moderate	Enriched	Enriched	No expres	YES
C9J5P6;P29475-2;I	Nitric oxide synthase	NOS1	161.02	2.2	3	3	6.6543	0	1339.1	892.51	1898.9	1287.7	1473.8	1698.2	2561	1833.5	1251.2	1320.9	Enriched	Moderate	Moderate	Low	
C9J5X1;P08069	Tyrosine-protein kina	IGF1R	154.79	3.5	6	2	2.2935	0.00496	9786	7617.9	10399	6338.2	12923	6786.2	12802	9643.1	18660	11986	Moderate	Enriched	Enriched	Low	YES
C9J719;C9JJ78;Q1	3-beta-hydroxysteroi	EBP	16.721	14.4	2	2	2.1577	0.00611	1607.2	1763.6	1991.9	2382.2	2396.8	1035	3458.7	1480.3	891.61	1620.7	Low	Enriched	Enriched	Enriched	YES
C9J7H8		LDHB	14.833	78.1	37	1	2.1965	0.00544	11684	6705.4	7899.6	7862.1	10686	50370	17371	11586	5772	8949.1	Enriched	Enriched	Enriched	Enriched	YES
C9J7K9;O15162-2;	Phospholipid scrambl	PLSCR1	34.217	11.3	3	3	17.744	0	5601.5	3847.3	6102.5	8403.4	5667.3	9509.7	5604.4	8239.6	3570.8	8742.4	Enriched	Enriched	Enriched	Moderate	YES
C9J7U9		SCRN1	15.329	38.3	9	3	8.4219	0	10288	5810.1	8386.3	14987	8402.3	19154	12641	13250	8118.4	13649	Enriched	Enriched	Enriched	Enriched	YES
C9J880;Q68CQ7-2	Glycosyltransferase 8	GLT8D1	19.42	5.7	2	2	2.5787	0.00326	6046.8	3790.3	4801	6076.8	5410.9	6666.7	5894.3	5345.2	3616.7	5110	Enriched	Enriched	Enriched	Enriched	YES
C9J8E1;P49137-2;(	MAP kinase-activated	MAPKAPK3;MAPKAPI	37.389	5.7	2	2	2.4533	0.00412	11164	4209.9	6037.3	13645	7765.5	10978	5050.5	8129.7	2370.8	11807	Enriched	Enriched	Enriched	Enriched	
C9J8T0		EEFSEC	47.876	21.8	9	1	77.948	0	85075	60961	61421	66927	86856	57147	51396	48307	29917	57653	Enriched	Enriched	Moderate	No expres	YES
C9J9K3;P08865;A(	40S ribosomal protei	RPSA;RPSAP58	29.505	55.3	42	42	266.17	0	268780	206330	252910	203490	288420	232190	219430	193500	103770	181420	Enriched	Enriched	Enriched	Enriched	YES
C9J9P7;C9JFQ5;P5	RNA-binding protein	RBM5	14.526	9.2	1	1	2.5601	0.00344	4933.6	5163.8	4041	5189.3	5813.6	4041.8	3632.2	3381.2	2457.5	4256.5	Enriched	Enriched	Enriched	Enriched	YES
C9JA08;Q96D46	60S ribosomal export	NMD3	60.125	18.1	9	9	59.994	0	35123	26238	26044	27279	47499	30967	28489	25738	15958	29354	Enriched	Enriched	Enriched	No expres	YES
C9JA28;Q9UNL2;(	Translocon-associate	SSR3	20.161	17.8	6	6	16.681	0	20960	14584	18666	30609	19165	37400	85839	73431	23264	28846	Enriched	Enriched	Enriched	No expres	YES
C9JAB2;Q16629-3	Serine/arginine-rich s	SRSF7	26.928	37	15	12	100.13	0	77776	47858	66641	80632	75475	77785	197160	124040	85199	85370					YES
C9JAJ9		RBBP7	4.5342	29.7	3	3	3.0957	0.00095	2279.3	979.23	1166.7	2192.8	1877.1	1495.3	1118.2	2141.9	515.97	2225.3	Enriched	Enriched	Enriched	Low	YES
C9JAX1;Q16595;Q	Frataxin, mitochondr	FXN	14.91	38.5	6	6	15.426	0	9124.7	9504.8	10194	9928.5	12101	6305.1	6547.5	7322	3911.3	9115.6	Low	Moderate	Moderate	Low	YES
H7C613;H7C5T6;C	Dehydrogenase/reduc	DHRSX	6.7737	19	1	1	3.1387	0.00095	4253.3	3298.1	4353.4	2906.4	5536.2	2484	5874.3	2746.1	2145.7	2876.1	Low	Enriched	Enriched	No expres	YES
C9JBE1		DNPEP	36.567	20.5	9	2	21.024	0	8429.2	15172	15767	6609.3	17055	10066	12471	7872.6	11073	12240	Enriched	Enriched	Enriched	Enriched	YES
C9JBG5;Q8NBJ9;C	SID1 transmembrane	SIDT2	96.728	3.2	3	3	4.8384	0.00043	5136.5	2325.9	3188.4	6405.4	3766	3931.5	5217.3	9363.7	1948.4	4082.9	Enriched	Enriched	Enriched	No expression	
C9JBI8;O75030-12	Microphthalmia-asso	MITF;TFE3;TFEB;TFEC	40.819	4.7	2	2	2.1065	0.00676	1622.1	2679.6	1886.7	1534.8	2871.6	2441	4237.6	3157.3	3103.6	3329.2	Enriched	Enriched	Enriched	Low	
C9JBU1;O43819	Protein SCO2 homol	SCO2	15.086	22.1	2	2	6.518	0	2412.5	3543.4	4612.5	2503.8	6113.3	1649.2	3421.9	2986.7	2702.6	3278.6	Enriched	Moderate	Enriched	Low	
C9JC84;P02679;C9	Fibrinogen gamma ch	FGG	52.337	49.5	57	57	323.31	0	310600	190000	243460	466190	176370	225930	214330	804330	173110	298270	Enriched	Enriched	Enriched	No expres	YES
E9PNC7;E9PQX9;(	Dr1-associated corep	DRAP1	16.658	12.2	2	2	1.9565	0.008	10481	7175.9	7791.1	10059	8600	10976	9441.3	9841.6	5388.6	8922.4	Moderate	Moderate	Enriched	Moderate	YES
C9JCD9;P41223;P4	Protein BUD31 homo	BUD31	11.905	50.5	7	7	76.632	0	34059	21835	24269	30624	28420	31978	62851	43326	52021	43465	Moderate	Enriched	Enriched	Enriched	YES
C9JDE9;P09110;H7	3-ketoacyl-CoA thiol	ACAA1	40.269	25.8	12	12	34.035	0	18469	13552	13615	19868	13625	11722	10983	12974	9120.9	17083	Enriched	Enriched	Enriched	Enriched	YES
C9JDR0;Q15738	Sterol-4-alpha-carbo	NSDHL	28.146	27.6	6	6	19.917	0	25884	14510	18196	26897	21523	25792	15881	25853	9024.2	28611	Enriched	Low	Moderate	Enriched	YES
C9JE79		CALD1	9.0317	37.5	6	1	3.2426	0.00077	4970.1	4144.9	4021.4	5172.3	6520.8	3297.2	4171.6	3147.8	1904	3828.4	Low	Enriched	Enriched	Moderate	YES
C9JG97;C9JEH3;Q	Angio-associated mig	AAMP	44.693	11.6	4	4	12.965	0	6238.9	6741.3	8309.6	6022.8	9242.8	5759.2	21623	20092	7303.5	7287.3	Moderate	Enriched	Enriched	Low	YES
C9JEH7;P22090	40S ribosomal protei	RPS4Y1	29.383	43.9	28	2	61.584	0	5001.5	16224	4639.8	8907.2	34795	25687	24837	5898.8	3010.2	29924	Enriched	Moderate	Enriched	Enriched	
C9JEJ2;P49585;C9	Choline-phosphate cy	PCYT1A	43.263	19.5	7	6	35.953	0	51934	38227	43756	65099	51030	43102	51769	61100	26964	56224	Enriched	Enriched	Enriched	No expres	YES
C9JF17;P05090;C9	Apolipoprotein D	APOD	24.158	36.7	11	11	96.584	0	73761	65593	91631	80709	87297	85637	88020	75179	60446	70065	Moderate	Enriched	Enriched	Moderate	YES
C9JF50;E9PLU1;E	Mitochondrial fission	MTFR1L	16.733	30.3	3	3	10.038	0	2980.5	3128.5	3120.9	5158.9	3223.7	3228.4	2822.1	3014.3	2267.9	4380.3					YES
C9JF58;Q8WVF1-3	Protein OSCP1	OSCP1	38.19	3.6	1	1	4.7498	0.00043	12085	9516.7	10005	10515	9402.8	10103	8992	10682	5291.5	10489					
F8WEJ3;H7C0F2;C	Phosphatidylinositol-	PIGX	9.3557	11.4	1	1	1.9585	0.00801	7583.1	7085.1	6426.9	4258.3	9190.6	5495.1	5719.5	3391.6	4149.9	4961.2	No expres	No expres	Moderate	No expression	
C9JFA1		STK25	9.9652	23.6	3	3	13.669	0	20529	9351.4	13833	32405	9939.8	26783	22414	25928	10719	27085	Enriched	Enriched	Enriched	Enriched	
C9JFE4;Q13098-5;	COP9 signalosome co	GPS1	53.371	17.8	10	9	24.347	0	12953	11024	11244	11678	12343	9769.1	9716.7	11578	4832.1	10764	Moderate	Moderate	Enriched	No expres	YES
C9JFR7;P99999	Cytochrome c	CYCS	11.333	42.6	15	15	229.71	0	178360	123540	144550	214660	215300	127350	192570	222340	67720	189310	Enriched	Enriched	Enriched	Enriched	YES
C9JFV4;Q8IZL8	Proline-, glutamic aci	PELP1	124.94	6.2	6	6	26.806	0	19873	17857	21560	14774	26305	23968	31390	26237	18015	27842	Enriched	Low	Moderate	No expres	YES
E9PLG6;C9JFX4;C	Single Ig IL-1-related	SIGIRR	21.79	12.2	2	2	4.9207	0.00044	1998.7	2001.8	2276.9	2081.3	1743.8	2101.2	1767.2	1747.8	1321.3	2365.2	Moderate	Enriched	Enriched	No expres	YES
J3KPK1;C9JFZ1;J3	Synaptojanin-1	SYNJ1	139.91	1.9	2	2	2.9665	0.00169	3342.6	6773.7	8308.3	1717.1	4856.5	1409.1	6371.8	6077.1	14571	4357.1	No expres	Low	Enriched	Low	
C9JG87;Q9NYK5;(	39S ribosomal protei	MRPL39	34.032	8.8	3	3	11.82	0	3225.6	2944.9	4389	2420.2	4516	3161.4	4160	2199.8	2296.1	3257.9	Low	Enriched	Enriched	No expres	YES
C9JG93		SEPT2	2.5679	69.6	1	1	3.0687	0.00114	4971.6	4767.8	3920.9	2408.6	6287.6	1945.1	4598.6	4964	2840.2	2579.5	No expres	Enriched	Enriched	Enriched	YES
C9JGI3;P19971;P1	Thymidine phosphor	TYMP	46.087	17.8	6	6	14.031	0	8614	8586.3	9230.1	8494.8	10277	6355.2	7281.7	7484.4	5592.2	7777.3	Low	Low	Moderate	Enriched	YES
F5GZZ9;C9JHR8;C	Scavenger receptor cy	CD163	120.32	15.7	19	19	154.03	0	60547	69020	61795	81677	67564	53721	88502	108180	94890	103340	Low	Moderate	Moderate	Low	YES
C9JI87		VDAC1	20.374	77.2	30	1	5.4751	0	6428.8	4490.2	5035.1	7724.6	6435.5	7605.5	21542	7660.3	6349.5	12065	Low	Enriched	Enriched	Enriched	YES
C9JI98	Transmembrane prote	TMEM238	18.04	10.2	2	2	18.705	0	2446.8	2625.8	3036.8	1712.8	3614.3	1684.8	3382	3354.8	1710.3	2769.2					
C9JIF9;P13798;H7	Acylamino-acid-relea	APEH	81.673	3.4	3	3	3.7417	0.0006	6522.9	10124	21102	5789.5	11644	10082	10699	21268	10181	28619	Enriched	Enriched	Enriched	No expres	YES
C9JIK8;Q9Y4P1-6;	Cysteine protease AT	ATG4B	24.833	14.6	2	2	4.2215	0.00063	13517	9415.8	9983.4	20293	8353.4	18110	13956	14002	7326.8	17157	Enriched	Enriched	Enriched	Moderate	YES
C9JIS1;C9JXA5;C9JZN1		GNB2	25.538	33.2	14	2	3.7336	0.0006	2784.8	2088.9	2024.2	1198.2	2563.7	3673.4	4923.7	2737.3	1208.5	1921	Enriched	Enriched	Enriched	Enriched	YES
C9JJN9;Q8N3P4-3;	Vacuolar protein sort	VPS8	161.8	1.7	2	2	3.0374	0.00132	4245.7	2332.6	3107.1	6261.6	2993.6	4732.7	4247.6	6121	2664.1	4717.7	Moderate	Moderate	Moderate	Enriched	YES
C9JJX6;E9PDC3;O	Armadillo repeat pro	ARVCF	96.827	5.4	4	4	7.8844	0	6749	4630.4	9153.4	5397.3	8734.6	5005.3	4830.2	4907.5	4308	5008.5	Enriched	Moderate	Moderate	Enriched	YES
C9JK83;O95630-2;	STAM-binding prote	STAMBP	36.156	3.5	3	3	6.3966	0	1874	1841.9	2051.1	1467.2	2786.7	1473.7	1660.2	1592.6	1029.9	1586.5	Enriched	Enriched	Enriched	Enriched	YES
C9JKG1		BGN	26.744	24.4	13	1	2.7388	0.00239	7099.5	7728.2	7277.4	6455.6	9023.5	5285.4	22797	4800.9	38082	8322.2	Enriched	Moderate	Enriched	Enriched	YES
C9JKQ2;O43676	NADH dehydrogenas	NDUFB3	7.5855	16.9	2	2	19.22	0	13189	7614.4	8511.2	7447.2	7552.8	18618	12753	16942	4293.9	18231	Enriched	Enriched	Enriched	Enriched	YES
U3KQU8;C9JLB7;(	Oxidoreductase NAD	OXNAD1	34.725	7.7	2	2	2.0481	0.00739	8018.8	5675.1	5977.2	7607.4	5327.4	6748.7	6185.6	7924.5	2539.7	6695	Moderate	Enriched	Moderate	No expression	
C9JLI6;H0YMV8;C	40S ribosomal protei	RPS27L	10.886	25.8	7	2	4.0275	0.00062	12527	10017	12124	10297	19258	11278	10200	9313.5	4991.3	8995.3	Enriched	Enriched	Enriched	No expres	YES
C9JLU1;P52434-3;	DNA-directed RNA p	POLR2H	16.996	20.1	2	2	10.43	0	11739	8084.4	8640.5	10996	11082	9784	12848	12232	8889.3	10038	Enriched	Enriched	Enriched	Enriched	YES
C9JM46		GPD1L	18.642	59.5	13	1	2.8458	0.00204	10969	4560	6922.2	5321	8381.7	6173.5	7650.3	5140.7	4103.9	7727.1	Moderate	Enriched	Enriched	Enriched	YES
F5H0H6;F5GWT0;	Pepsin A-5;Pepsin A-	PGA3;PGA5;PGA4	13.306	8.6	2	2	3.8129	0.00061	4779.4	2907.2	4690.3	4662.5	5173.6	4142	4602.1	2977.9	10081	4549.7	Low	Moderate	Moderate	No expression	
C9JMV9;Q03154-3	Aminoacylase-1	ABHD14A-ACY1;ACY	56.435	11	6	6	16.032	0	25792	20898	23489	26392	28456	40781	31330	32439	19697	33531	Enriched	Moderate	Moderate	Moderate	
F8WCQ4;C9JNP8;(	Presenilins-associatec	PARL	19.605	22.5	3	3	8.0699	0	11858	10507	12519	13822	12535	11936	10995	15370	6657.3	13636	Enriched	Enriched	Enriched	No expression	
C9JQ41;H7C525;Q	Coiled-coil domain-c	CCDC58	15.296	33.8	5	5	6.8235	0	16994	17936	16891	13669	27899	11668	16859	14282	8767.1	15382	Low	Moderate	Moderate	No expres	YES
E7EUY3;E7ETT1;I	Propionyl-CoA carbo	PCCB	55.708	30.4	23	21	323.31	0	83245	43735	58430	77494	66582	76166	72324	84212	39511	80995	Enriched	Moderate	Enriched	Enriched	YES
F5H7J8;C9JQZ6;J3	Uncharacterized prot	C7orf57	17.48	11.5	1	1	2.0217	0.00771	9407.7	21234	8834.5	5099	50215	886.19	5755.4	3351.9	3995.3	4104.9	No expres	No expres	No expres	No expression	
C9JRJ5;Q9UGP4	LIM domain-containi	LIMD1	65.534	9.2	4	4	14.064	0	13816	7044.9	9278.3	19907	11191	11002	16445	17261	6341	18364	Enriched	Enriched	Moderate	No expres	YES
C9JRL4		MDH1	13.044	70.8	22	6	7.9431	0	23957	17863	22862	24364	26547	25326	21186	23468	11628	22089	Enriched	Enriched	Enriched	Enriched	YES
C9JRV9		UBA5	12.652	56.8	14	2	9.2735	0	12490	10585	9791.3	6934.6	14994	8492.5	12031	9632.3	9082	8225.9	Moderate	Enriched	Enriched	No expres	YES
C9JRZ6;Q9NX63;F	MICOS complex sub	CHCHD3	26.694	44.8	15	15	53.984	0	53811	43411	54956	45626	64586	66473	82676	97919	46615	80654	Enriched	Enriched	Enriched	No expres	YES
C9JS50;Q687X5;Q	Metalloreductase STI	STEAP4	38.579	11.5	4	4	5.9546	0	8225.7	10116	7572.6	7972.3	9379.6	6182.3	8256.3	6086.9	4118.9	6624.7	Enriched	Enriched	Enriched	No expres	YES
C9JTV6;C9JBJ1;H7C366		GART	25.188	35.3	9	2	7.3831	0	5835.7	8200.6	7498.6	4584.5	8296.3	3798.3	4942	4170.6	4159.9	4045.1	Moderate	Enriched	Enriched	No expres	YES
F8WFC3;C9JUD5;(	Regulator of microtul	RMDN2	18.157	16.9	2	2	8.4364	0	25751	11244	19446	28032	20228	25513	21200	22259	12426	30511					YES
S4R3N0;C9JUV8;F	Butyrophilin subfami	BTN3A2;BTN3A3;BTN	12.932	8.7	1	1	2.6916	0.00238	3410.5	1028.7	1550.4	2679.8	1703.4	3023.5	1933.4	2746.9	1447.5	3051.7	Low	Moderate	Moderate	Low	
C9JV50		SACM1L	21.43	42.8	10	1	18.147	0	12999	6256.1	10056	6364.5	18652	9819.6	7468.6	4970.4	3876.4	7559.5	Moderate	Enriched	Enriched	Enriched	YES
C9JV77;P02765	Alpha-2-HS-glycopro	AHSG	39.411	17.7	7	7	24.804	0	26638	29310	50962	20841	34730	20848	32621	54039	20100	32751	Low	No expres	No expres	Low	YES
C9JVN9;Q9H9P8-2	L-2-hydroxyglutarate	L2HGDH	48.475	12.2	6	6	10.907	0	2247	1485.4	1486.9	1538.9	1999	1395.5	1300.7	1316.8	878.68	1725.9	No expres	Low	Moderate	No expres	YES
C9JVY5;Q9Y2D5;(	A-kinase anchor prot	AKAP2	85.282	7.7	6	6	19.218	0	8598.9	6993.1	7763.9	7531.7	10892	7305.4	8237.4	7546.4	3200.7	7643.5					YES
H7C0G7;C9JWV4;	Non-homologous end	NHEJ1	24.751	5.8	1	1	3.5372	0.00079	4179	4147.2	4318	3653.9	4722.5	3189.9	4185.5	5011.6	2322.6	4032.1	Moderate	Enriched	Moderate	Low	
C9JXC3;Q9Y530	O-acetyl-ADP-ribose	OARD1	12.782	36.3	6	6	12.062	0	16758	12512	13443	11279	13869	15619	22697	22745	12089	18969					YES
C9JXC6		SEC61A1	10.817	53.5	9	2	3.7661	0.0006	2474.5	5266.4	4179.5	1792.8	7761.4	1460.8	2380.1	1160.6	1960.6	1908.7	No expres	Enriched	Enriched	Low	YES
H0Y329;C9JYH8;C	WD repeat domain pl	WDR45	31.781	7.3	3	2	2.3709	0.00428	7343	5264.5	5948	5817.4	7817.3	5338.7	5938.7	5011.3	3002.4	6031.4	Moderate	Enriched	Enriched	Moderate	YES
C9JYQ9;H0Y8C2;(	60S ribosomal protei	RPL22L1	14.478	25.6	3	3	12.969	0	6957.3	7205.3	6985.3	7571.5	6313.8	5530.7	8021.5	8698.5	3652.3	7355.9	Enriched	Enriched	Enriched	No expres	YES
C9JYY6;F8W775;C	Neuronal cell adhesic	NRCAM	133.81	22.3	28	28	109.92	0	129400	89563	105160	98529	140770	119130	100940	92230	56334	102910	Enriched	Enriched	Enriched	Enriched	YES
C9JZ87;Q9NUM4;I	Transmembrane prote	TMEM106B	12.201	21.8	2	2	4.5702	0.00043	8930.4	8445.6	9465.8	7490.6	10637	12819	10606	11682	3708.6	8330.1	Moderate	Enriched	Enriched	No expres	YES
H7C4M9;C9JZG9;(	Ubiquitin-conjugatin	UBE2H	7.0801	40.3	3	3	4.9658	0.00044	7251.2	9069.4	7941.5	9080.5	9343.9	5635.7	5198.3	6212.2	3153.6	7379.5	Moderate	Enriched	Enriched	No expression	
C9JZP6;Q13268;Q	Dehydrogenase/reduc	DHRS2	23.818	16.9	4	4	4.5679	0.00043	1960.5	1977.5	2136.6	1939.3	3162.2	1593.7	1575.8	1301.2	751.27	1739.6	No expres	Moderate	Enriched	Enriched	YES
C9JZR2;O60716-5;	Catenin delta-1	CTNND1	104.85	44.2	65	65	297.14	0	310320	246070	274740	354870	310530	291250	375180	352460	224780	338810	Enriched	Enriched	Enriched	Enriched	YES
C9K025;P18077	60S ribosomal protei	RPL35A	10.645	39.4	7	7	16.91	0	71461	55524	52722	28787	63386	63477	113950	68764	64300	62949	Enriched	Enriched	Enriched	No expres	YES
C9K0E9		AADAC	23.061	22.1	4	2	58.46	0	14070	14311	13735	14023	17250	13905	18579	13432	8624.9	12939	Enriched	Enriched	Enriched	Enriched	
C9K0G7		BDH1	18.444	7.2	1	1	2.9796	0.00169	4544.1	4214	4640.3	4009.8	4503.1	2834.3	3330.3	2989.7	2037.7	3681.1	Enriched	Enriched	Enriched	Low	
C9K0H3;P17035-2	Zinc finger protein 28	ZNF28;ZNF154;ZNF70	63.673	3.5	4	1	3.1187	0.00095	6560.4	4961.1	6734.5	5013.3	11278	6474.8	5108.3	4955.4	2465.4	6964.3	No expres	No expres	Low	No expression	
C9K0J5;Q70E73	Ras-associated and pl	RAPH1	141.18	3	3	3	5.5915	0	14606	14011	17693	16421	19141	12405	17372	17389	10356	14028	Enriched	Enriched	Enriched	No expres	YES
CON P48668;CO	Keratin, type II cytos	KRT6C;KRT6B;KRT6A	60.024	13.1	15	0	33.208	0	12112	11094	12329	14219	16297	13749	174100	31927	35092	17666	No expres	No expres	No expres	Moderate	
CON P02768-1;P	Serum albumin	ALB	69.366	78	281	281	323.31	0	3217800	3180300	3687100	4403500	2499100	3131900	4702100	1.2E+07	2943800	4223400	Low	Enriched	Enriched	Enriched	YES

CON	P05787;P05	Keratin, type II cytos	KRT8	53.704	68.3	159	32	323.31	0	2083000	1388100	1639200	2016600	1893400	2171400	3596300	4311000	2107700	2982200	Enriched	Enriched	Enriched	Enriched	YES		
CON	P07477;E7I	Trypsin-1;Alpha-tryp	PRSS1	26.558	44.5	52	1	3.3086	0.00078	60079	32914	18305	11699	54288	11205	14205	5774.9	34735	18007	Moderate	Enriched	Enriched	No expression		YES	YES
CON	P08727;P08	Keratin, type I cytosk	KRT19	44.091	71.2	69	24	323.31	0	242340	187240	234500	411490	300610	314630	715130	844200	455620	434330	Enriched	Moderate	Enriched	No expres	YES		
CON	P13645;P13	Keratin, type I cytosk	KRT10	59.51	11.6	9	6	20.367	0	10619	9462.7	12454	8774.7	14856	9650.8	36108	11664	17548	10644	Enriched	Enriched	Enriched	Enriched	YES		
CON	P21752;P63	Thymosin beta-10	TMSB10	4.8054	31	2	2	20.561	0	30717	19506	29560	45420	15218	27482	66650	47689	65497	61822	Enriched	Enriched	Enriched	Low			
CON	P35527;P35	Keratin, type I cytosk	KRT9	62.129	6.7	3	2	10.902	0	255.58	184.51	227.15	167.13	459.5	226.38	1258	207.06	2032.9	208.61	Low	Low	Low	Low	YES		
CON	P35908;P35	Keratin, type II cytos	KRT2	65.865	12.1	11	2	3.0127	0.00132	6221.3	6367.1	6483.9	7061.5	8628	6099.1	8234.2	6179.7	6067.9	5990	Moderate	Low	Low	Moderate	YES		
CON	Q3KNV1;P(	Keratin, type II cytos	KRT7	51.385	60.6	54	5	175.78	0	149570	142260	178470	137420	202620	146220	448750	591320	254740	423490	Moderate	Enriched	Moderate	Moderate	YES		
CON	Q6NXH9;C	Keratin, type II cytos	KRT73	58.911	12.1	9	1	7.8854	0	21848	20049	19362	12590	28914	15589	57700	13045	27452	21851	No expres	No expres	No expres	No expression			
CON	Q9NSB4;Q(	Keratin, type II cuticu	KRT82	56.682	1.6	1	1	3.1514	0.00076	4634.4	2538	4076.6	2037.1	7599.7	4997.8	3854.5	2190.1	1974.1	2061.1	Moderate	Moderate	Moderate	No expression			
CON	Q9QWL7;C	Keratin, type I cytosk	KRT17	48.161	20.8	13	2	8.2817	0	26365	11281	21482	26940	31894	31112	56034	37382	24151	46132	Enriched	Low	Enriched	Enriched	YES		
D3DQ30;Q5SRH9-		Tetratricopeptide rep	TTC39A	63.18	3.8	2	2	3.3549	0.00078	4035.5	3797	4187	4763.3	4926.6	4247.5	4043.3	3992.4	2522.5	5171	Enriched	Moderate	Enriched	Moderate			
E5RK62;F5GY03;I		SPARC	SPARC	13.379	13	1	1	7.0849	0	6282.3	4869.7	6385.4	10337	5970.1	8793.8	8023.5	8041.6	8092.1	8281.3	No expres	Enriched	Enriched	Enriched			
D3DQV9;P78344;I		Eukaryotic translatio	EIF4G2	102.33	25.4	29	29	93.237	0	160340	103190	126730	134930	146850	146350	116440	126960	58707	135950	No expres	Enriched	Enriched	Enriched	YES		
D3DRR9;Q86WR7		Proline and serine-ric	C10orf47;PROSER2	24.792	6.3	1	1	5.8993	0	5924.7	5518.7	5306.4	4408.9	6969.5	4425.8	15483	8317	13420	9295.3	Enriched	Enriched	Enriched	No expres	YES		
D3DSM0;P05107		Integrin beta;Integrin	ITGB2	78.354	4.1	3	3	5.4647	0	8782.4	8870.8	10882	8693.5	12234	8497.4	17702	23918	16604	14857	Moderate	Low	Moderate	No expres	YES		
D3DT44;P48507;P		Glutamate--cysteine l	GCLM	28.615	13.8	3	3	7.9444	0	14218	13902	14402	11432	16040	10223	11290	10995	14048	15248	Enriched	Low	Enriched	Moderate	YES		
D3DTX6;Q96SB3		Neurabin-2	PPP1R9B	89.333	6.5	5	4	9.6097	0	7274.3	5563	6823.2	9059.9	9050.5	6325.7	8700.9	7677.9	5746.9	9253	Moderate	Moderate	Moderate	No expres	YES		
D3DVS1;Q5BJH2		Transmembrane prot	TMEM128	18.822	8.5	1	1	5.2636	0.00022	11639	7936.5	11838	9980.4	12524	11260	9050.5	8625.6	6319.9	12469	Moderate	Enriched	Enriched	No expres	YES		
D3YTB1;F8W727;l		60S ribosomal protei	RPL32	15.616	37.6	15	15	68.23	0	107730	89733	94921	102730	110170	128060	182990	152500	74323	92852	Enriched	Enriched	Enriched	Enriched	YES		
E7ENA2;D3YTF9;		Thioredoxin reductas	TXNRD2	53.567	32.2	19	17	60.225	0	104080	88207	97145	73861	119260	89029	105760	98415	64313	91988	Enriched	Moderate	Moderate	Low	YES		
D3YTG3;Q7Z7G0;		Target of Nesh-SH3	ABI3BP;DKFZp667H21	195.32	5.8	8	8	36.496	0	24826	23981	31836	26731	35180	28624	32372	36517	16669	34942	Moderate	Moderate	Moderate	No expression			
D6R934;P02746;A		Complement C1q sub	C1QB	26.459	17.1	3	3	34.434	0	22256	30978	25776	29407	19479	19168	14035	47472	9854.9	24025	Low	Low	Moderate	Low	YES		
D6RGV8;D6RHG2		[Pyruvate dehydroger	PDK2	11.509	15.3	2	2	3.4903	0.00079	5733.9	2784.4	3113.7	5210	3768.2	3003	3153.3	4683	1608.8	3467	Moderate	Enriched	Moderate	Enriched	YES		
D6R9X5;D6R9A4			G3BP2	6.4503	32.1	1	1	10.079	0	3819.3	12991	9484.2	3129.4	15645	959.4	6393.4	2350.9	4586.9	2669.8	Moderate	Enriched	Enriched	Enriched	YES		
D6R9M0;O00139-2		Kinesin-like protein I	KIF2A	32.692	9.9	2	2	4.9779	0.00044	2642.3	2153.9	2696.8	2167.8	3330	1280.6	1417.5	1888.6	583.67	1481.1	Moderate	Moderate	Enriched	Moderate	YES		
D6RD48;D6RAZ7;		Claudin domain-cont	CLDND1	10.329	15.7	1	1	10.175	0	10925	9852.3	8560.1	9634.3	8905.7	7876	7597.9	8997.1	3437.3	9009.3	No expres	Low	Enriched	Enriched			
D6R9Z7;P15954		Cytochrome c oxidas	COX7C	6.3824	55.4	5	5	9.2996	0	33111	28029	30169	37148	30711	40097	56268	61973	26568	37162	Enriched	Enriched	Enriched	Enriched	YES		
D6RA51;O15455		Toll-like receptor 3	TLR3	39.33	3.4	1	1	5.1979	0.00022	6761.9	6132.4	6887.5	5644.6	8346.3	4247.9	7025.9	10618	5950	7780.1	Moderate	Moderate	Enriched	No expression			
D6RA57;H0Y9X1;		Translation machiner	TMA16	17.155	15.3	3	3	6.297	0	3411.2	2862.4	4722	3987.3	3250.2	2801.7	3175.8	3956.4	2663.8	3306							
D6RA77;Q9BPZ3		Polyadenylate-bindin	PAIP2	11.385	15.1	3	3	83.803	0	13837	10258	12954	12243	8838.1	15404	11511	14074	4229.8	12104	Enriched	Enriched	Enriched	No expression			
D6RAW2;Q9BW91		ADP-ribose pyrophos	NUDT9	22.979	33	8	8	89.92	0	76016	39807	50927	44673	63655	53125	43318	30455	19643	53462	Low	Enriched	Enriched	No expres	YES		
H0Y9F5;D6RAX3;		Protocadherin-1	PCDH1	13.98	9.5	1	1	2.7173	0.00238	3929.9	3242	3680	3976.3	4662.7	2907.5	3392	3460.5	1605.4	4114.8	Moderate	Moderate	Moderate	Enriched	YES		
D6RAY1;D6REQ3;		Mothers against deca	SMAD1;SMAD5	10.819	25.3	2	2	5.1627	0.00044	10301	7856.8	9913.8	8794.1	11356	8468.4	9370.5	6916.1	5425.7	8357	Moderate	Enriched	Enriched	Low			
D6RBP5;Q9BZM1		Group XIIA secretory	PLA2G12A	7.6769	28.6	4	4	8.7729	0	13605	7133.5	16269	23360	12185	16565	14270	17793	7215	15701	Low	Enriched	Enriched	No expres	YES		
D6RBS5;Q8IZ81;D		ELMO domain-conta	ELMOD2	20.204	32.7	6	6	14.413	0	23185	15311	13291	20921	19671	18187	12324	17957	9271.5	16727	Enriched	Enriched	Enriched	No expres	YES		
D6RBX6;Q99643-2		Succinate dehydroge	SDHC	7.6228	35.8	4	4	7.8584	0	2943.9	3233.9	4483.4	1138.8	6965.2	8808.4	33024	16662	26437	12967	Enriched	Enriched	Enriched	Enriched	YES		
D6RC04;D6RJ90;C		COMM domain-cont	COMMD10	15.911	15.8	2	2	59.892	0	10949	9625.7	11636	6840.8	12607	3399.1	5443.1	6709.9	3075.9	6053.1	Moderate	Enriched	Enriched	No expression			
E5RIJ3;D6RCM8;C		Tumor necrosis facto	TNFAIP8	7.935	26.5	1	1	3.5053	0.00079	957.05	591.63	304.29	1938.4	875.77	877.91	970.43	2286.5	595.75	1399.7	Moderate	Moderate	Enriched	Moderate	YES		
D6RCP5;Q8N264-3		Rho GTPase-activatir	ARHGAP24	69.48	5.3	3	3	3.5272	0.00079	5935.2	7747.7	6397.3	5117	9713.9	4288.2	9021.6	6237.4	4881.3	7058.2	Enriched	Enriched	Enriched	No expression			
D6RCQ8;D6RF77			PGM3	16.086	51	9	4	6.7676	0	1958.3	1084.5	2169.7	1626.8	2698.1	791.38	1379	843.37	527.4	1166.4	Low	Enriched	Enriched	Moderate	YES		
D6RD44;Q96EI5;C		Transcription elongat	TCEAL4	14.328	44.2	5	5	12.252	0	7376.3	7404.2	8609.8	6229.6	10236	4436.5	9815.1	7411.7	7946.3	8656	Enriched	Enriched	Enriched	Enriched	YES		
D6RD47;P62266;D		40S ribosomal protei	RPS23	14.837	29.1	10	10	17.512	0	47425	41648	46756	22909	60449	36974	90705	54740	52587	37350	Enriched	Enriched	Enriched	Enriched	YES		
D6RDU9;D6REA0;		Glutamyl-tRNA(Gln)	PET112	39.539	4.2	1	1	8.1379	0	4599.6	4486.3	4600.5	3818.2	5478	4957.4	4245.8	3118.4	1750.7	3362					YES		
D6RE83;P09936;D		Ubiquitin carboxyl-te	UCHL1	23.174	32.4	6	6	15.626	0	25568	26117	36575	28866	26153	23358	31784	26780	22970	37732	Low	Enriched	Enriched	Enriched	YES		
D6REB4;Q9H074-3		Polyadenylate-bindin	PAIP1	39.908	12	6	6	14.711	0	50324	32836	38976	35156	32242	42469	40907	45637	19227	45779	Moderate	Enriched	Enriched	Enriched	YES		
D6RGI3;D6RER5;C		Septin-11	SEPT11	49.005	42.8	27	15	80.265	0	104080	70846	82926	87551	111050	99243	140460	121540	64775	99469	Enriched	Enriched	Enriched	Moderate	YES		
D6REX3;O94979-4		Protein transport prot	SEC31A	136.22	30.8	54	54	249.16	0	293180	227920	249740	195060	334180	246840	344430	255440	169830	258460	Enriched	Enriched	Enriched	Enriched	YES		
D6RF01			OCIAD1	3.2896	55.2	2	2	11.171	0	3474	3846.8	3559.7	2433.8	4517.9	2406.1	3517.8	1652.8	1314.9	2628.1	Enriched	Enriched	Enriched	No expres	YES		
D6RF30;H3BQL2;l		Golgin subfamily A n	GOLGA8K;GOLGA8T;(	68.877	3.6	2	2	5.9253	0	31590	22520	13475	23649	29666	13192	16596	16605	7314.6	21841							
D6RF48;Q9P2W9;l		Syntaxin-18	STX18	35.42	26.6	7	7	67.972	0	25655	15042	20023	23096	26430	22609	27169	25572	17225	26902	Enriched	Enriched	Enriched	No expres	YES		
D6RGG3;Q99715;C		Collagen alpha-1(XII	COL12A1	333.2	8.3	24	24	48.47	0	74977	68332	80960	83329	86641	71088	86121	134680	39356	89889	Low	Enriched	Enriched	No expres	YES		
D6RGX2;Q9NUQ7		Ufm1-specific protea:	UFSP2	44.162	21.4	12	12	39.646	0	102250	58923	74824	75330	79679	101560	75212	87283	43535	78620	Moderate	Enriched	Enriched	No expres	YES		
D6RHH4;D6RBD0;D6RFZ9			GNB2L1	25.869	56.7	35	3	4.9371	0.00044	1867.7	1119.8	1343.3	1866.7	1642.4	8897.6	2348	1877.9	884.45	1383.4	Enriched	Enriched	Enriched	Enriched	YES		
D6RIT2;D6RAM1;D6R9T0;D6RDU3;D6			HNRNPH1	18.366	61	19	2	5.1298	0.00044	28280	15563	19731	22672	18881	51575	17289	22255	6913.1	36001	Enriched	Enriched	Enriched	Enriched	YES		
D6RIY6;Q06265-3;		Exosome complex co	EXOSC9	46.977	5.2	2	2	4.6087	0.00043	3225.1	3068.1	3618.1	2304.3	4888	3081.9	4808.9	3702.8	2576.4	3233	Low	Moderate	Moderate	No expres	YES		
D6RJA0;Q8WTS6		Histone-lysine N-met	SETD7	40.127	9.4	4	4	8.5991	0	10879	11876	12887	6585.2	10127	20286	31921	37407	15335	22623	Moderate	Enriched	Enriched	No expres	YES		
D6W648;Q9P1Y5;(		Calmodulin-regulatec	hCG_2004001;CAMSAI	136.18	7.2	8	8	17.722	0	12696	11201	13946	8609.5	18312	10527	13044	11338	11666	13527					YES		
E2QRB3;P32322;P		Pyrroline-5-carboxyl:	PYCR1	30.213	51.4	23	22	90.783	0	86021	71989	78964	74022	142260	69718	92737	80662	62351	76541	Enriched	Enriched	Enriched	Moderate	YES		
E2QRG1			PLD3	19.421	11.3	2	1	3.7578	0.0006	7148.2	8125.1	16693	4680.6	21891	7394.7	6937.1	3489.9	4094.1	5741.6	Low	Moderate	Enriched	Low	YES		
E3W994;J3KR49;E		CLIP-associating prot	CLASP2	138.86	9.3	11	9	82.431	0	14726	17819	16873	12355	22858	9883.5	21653	13417	12668	15594	No expres	Moderate	Enriched	Enriched	YES		
E5G745;G5E9X4;C		Glutaminase liver iso:	GLS2	31.199	8.6	3	3	10.104	0	10607	6045	7970.7	17943	8560.7	14309	10507	12439	7586.6	15494	Moderate	Enriched	Moderate	Low	YES		
E5RJ08;E5RHM5;I		Coiled-coil-helix-coil	CHCHD7	5.2317	25	2	2	8.4379	0	4498.3	3019.5	5269.1	4649.4	6607.9	4804.2	1491.8	2032.6	1278.8	5315.8	Enriched	Moderate	Enriched	No expres	YES		
E5RFU2;P34913;P		Bifunctional epoxide	EPHX2	58.855	37.3	27	27	162.57	0	134080	79269	80596	190370	74182	193580	106410	199710	50943	167280	No expres	Enriched	Moderate	Enriched	YES		
E5RG17;Q6P1N9;C		Putative deoxyribonu	TATDN1	36.418	40.4	18	18	110.22	0	126310	80133	87957	105590	88025	95390	114770	90861	56839	108370	Moderate	Enriched	Enriched	No expres	YES		
E5RG44;E5RIT1;E		Triple QxxK/R motif-	TRIQK	6.0772	22.2	2	2	6.1796	0	24704	15368	22013	24567	24193	102150	26013	25123	8386.3	19263							
E5RGL4;E5RHV6;		CMP-N-acetylneuran	ST3GAL1	5.0096	23.9	1	1	7.2014	0	4473.5	3220	4484.9	4106	7622.2	4914.6	6476.8	4837.8	3840.3	4597	Moderate	Low	Moderate	Moderate	YES		
E5RGM3			SKP1	11.575	21.6	9	6	23.663	0	38898	34160	34469	32653	36168	57382	57715	39788	47530	38829	Enriched	Enriched	Enriched	Moderate	YES		
E5RGM5			NDRG1	18.158	35.8	7	2	4.2742	0.00063	4822	5478.7	5710.7	3380.6	5461	5117.6	4974	5477.1	2315.1	4001.5	Enriched	Enriched	Enriched	Enriched	YES		
E5RGN3;E5RIM7;(		Copper transport pro	ATOX1	6.3304	35.6	3	3	5.7457	0	11717	5287.2	16074	19118	7871.9	11032	5978.2	5376.7	7756.6	17513	Moderate	Enriched	Enriched	Moderate	YES		
E5RGQ3;Q9H446-3		RWD domain-contair	RWDD1	8.5618	27.8	3	3	6.2852	0	15704	9982.8	9333.9	11760	7854	20993	17871	23381	6640.8	19668	Enriched	Enriched	Enriched	No expression			
E5RGR0;O75608-2		Acyl-protein thioeste	LYPLA1	20.861	31	8	8	34.82	0	66567	61477	74850	56919	79884	73911	113100	87870	64093	65383	Enriched	Enriched	Enriched	Moderate	YES		
E5RGS4;O60925		Prefoldin subunit 1	PFDN1	13.466	17.1	3	3	4.3406	0.00063	13996	9165.5	8221	8987.3	9413.8	11465	11933	21526	10077	12520	Moderate	Moderate	Enriched	Moderate	YES		
E5RGW4			NPM1	6.8625	52.5	14	8	28.883	0	43790	39900	30451	48738	39891	32772	36829	53604	36318	47866	No expres	Enriched	Enriched	Enriched	YES		
E5RH41;P29084		Transcription initiatic	GTF2E2	22.139	9.6	4	4	15.744	0	8554.3	6768.8	8526.1	10688	7921	9429.6	12579	12799	9125.3	9530.7	Enriched	Enriched	Enriched	Enriched	YES		
E5RHE7			HDAC2	10.384	44.2	9	5	23.981	0	28682	26789	28579	32738	30642	27182	30289	32745	17043	34111	Enriched	Enriched	Enriched	Enriched	YES		
E5RIW3;E5RJD8;E		Tubulin-specific char	TBCA	10.08	58.3	13	13	41.731	0	75919	72075	80074	72498	83190	66390	58485	50671	38648	56603	Enriched	Enriched	Enriched	Enriched	YES		
E5RHG8;Q15369;C		Transcription elongat	TCEB1	9.9601	56.2	9	9	30.144	0	20490	14524	15368	15843	19695	9871.2	14355	11837	9372.9	15614	Enriched	Enriched	Enriched	Enriched	YES		
E5RHG9			UQCRB	9.2397	32.9	8	1	16.73	0	3597.9	4023.7	4617.6	2819.1	4814.9	14416	22077	4555.9	3514.5	4595.4	Enriched	Enriched	Enriched	Enriched	YES		
E5RHK3			ARMC1	13.504	12.2	4	4	11.479	0	23992	13958	25023	30683	21947	23287	24018	28571	16461	27757	Enriched	Enriched	Enriched	No expres	YES		
E5RHP7;P00915;E		Carbonic anhydrase 1	CA1	27.754	24.3	8	8	38.356	0	37607	88328	28829	28333	37343	47050	51333	41760	24091	39518	Enriched	Moderate	Low	Low	YES		
E5RJB8;E5RHU3;I		Syndecan;Syndecan-2	SDC2	14.905	16.8	2	2	7.4181	0	19548	10016	12121	9269.7	13098	10876	11702	13041	3411.5	16153	Moderate	Enriched	Enriched	Enriched	YES		
E5RHX8;Q9NPA8-		Transcription and mF	ENY2	11.315	26	4	4	11.909	0	13097	35753	32240	9514.7	31258	11348	21577	10196	19724	11780	Enriched	Enriched	Enriched	No expres	YES		
E5RHY5;E5RHR7			CTNNA1	3.7994	59.4	4	2	31.783	0	9178	6382.1	6585.1	7450.2	8254.7	7440.3	9518.9	8038.5	6208.5	9628.6	Enriched	Enriched	Enriched	Enriched	YES		
E5RHZ7			EYA1	4.7885	26.8	1	1	2.1032	0.00675	15775	5666	13337	2909.6	37636	23666	23037	4190.3	2998.3	10683	Low	No expres	Low	Low			
E5RI06			GSR	15.788	26.9	6	1	2.9235	0.00168	7168.4	3970.7	9789.8	4188.3	5635	30685	33340	7494.6	5169.2	16524	Enriched	Enriched	Enriched	No expres	YES		
E5RI98			NPM1	11.865	42.3	16	4	9.9568	0	30056	31379	41299	39709	35325	18714	63496	20517	51482	53028	No expres	Enriched	Enriched	Enriched	YES		
E5RIH5;Q6NXR4		TELO2-interacting pı	TTI2	53.305	4.4	1	1	22.92	0	3967.3	2716.4	2805.8	3275.9	3523.7	4375.9	8238.5	9577.5	6176.2	9026.3					YES		
E5RIS3;Q8TCF1-4		AN1-type zinc finger	ZFAND1	18.847	7.9	1	1	3.3951	0.00078	1820.4	1205.2	1412.8	2677.7	1880.1	2346.2	1556.4	1419.5	776.58	2009.2	Moderate	Enriched	Enriched	No expres	YES		
E5RJ98			NDRG1	10.425	31.6	5	3	8.4625	0	3585.8	985.43	1882.8	3085.2	2684.3	4903	2588.3	4127.8	653.32	2568.3	Enriched	Enriched	Enriched	Enriched	YES		
E5RJI7;Q9BYD1		39S ribosomal protei	MRPL13	17.076	28.4	4	4	8.6859	0	9987.1	7640.3	9120.6	11086	10263	8459.2	7141	6483.5	3670.5	9528.4	Low	Moderate	Enriched	No expres	YES		
E5RJW1;E5RJK5			RAD21	13.782	11.7	2	2	5.0998	0.00044	12505	6296.4	7836.3	15528	7850.1	8118	13253	14834	7071.3	13236	Enriched	Enriched	Enriched	Enriched	YES		
E5RJU4			TACC1	14.75	24.6	3	1	3.9889	0.00062	4473.9	5541.8	5575.5	4997	7135.6	3907.3	4158.8	3586.4	2417.3	3975.7	Enriched	Enriched	Enriched	Enriched	YES		
E5RJZ1;H0YBD2;C		Cytochrome c oxidas	COX7A2L	8.8399	32.9	2	2	11.186	0	7661.1	5794.8	6250.6	5378.9	8407.9	7883.6	11729	7575.6	4701.1	8303.3	Enriched	Enriched	Enriched	Enriched	YES		
E5RK64;O95292-2		Vesicle-associated me	VAPB	7.8009	40.8	3	1	3.1504	0.00076	4153.9	11944	10287	2737.7	16220	1922.3	3687	1469.1	1714.6	2140.7	Enriched	Enriched	Enriched	Enriched	YES		
E5RK69;E7EMC6		Annexin	ANXA6	51.776	58.7	62	3	106.29	0	40767	19043	24644	38403	24171	23157	16887	21983	7672.8	23750	Low	Enriched	Enriched	Moderate	YES		
E7EM64;Q7L5N1		COP9 signalosome co	COPS6	36.064	37.7	11	11	93.908	0	65405	56515	63616	63531	72266	43813	71771	57339	43336	66789	Enriched	Enriched	Enriched	Enriched	YES		
E7EM93;Q9BQG2		Peroxisomal NADH p	NUDT12	50.051	7.2	3	3	5.3047	0	15558	9724.4	10431	16723	10873	17403	12056	13373	6466.7	16634	No expres	Low	Moderate	No expres	YES		
E7EMA9;Q32M88;		Acid trehalase-like pı	ATHL1	83.379	7.3	4	4	5.5391	0	12616	6404.2	9615.3	15112	10034	9014.8	9515	10829	7394.1	13711	Enriched	Enriched	Moderate	No expres	YES	YES	
E7ETZ0;H0Y7A7;I		Calmodulin	CALM1;CALM2;CALM	16.966	42	22	13	117.31	0	144950	130230	160830	407310	150900	144160	153970	119430	59636	171270	Enriched	Enriched	Enriched	Enriched	YES		
E7EMF1;E7ESP4;I		Integrin alpha-2	ITGA2	88.561	6.9	3	3	48.718	0	7190.5	6567.8	5413.5	7719.6	5501.9	7257.3	5677.5	7837.7	3561.9	8030.9	No expres	Moderate	Enriched	No expres	YES		
E7EMJ5			CTNNB1	16.638	22	5	1	2.483	0.00395	1918.1	1379.8	1650.1	1976	2497.4	2662.1	4110	2676.5	1067.3	2086.1	Enriched	Enriched	Enriched	Enriched	YES		
J3QLD9;E7EMK3;		Flotillin-2	FLOT2	47.142	23.4	14	14	71.565	0	56475	46626	54668	61767	61770	62874	56305	75412	27211	72373	Enriched	Enriched	Enriched	Moderate	YES		
E7EMM4;Q13510;		Acid ceramidase;Acic	ASAH1	41.796	23.2	14	14	46.92	0	66748	38186	52976	45131	62791	119590	89923	133820	54975	70664	Enriched	Enriched	Enriched	Enriched	YES		
E7EMN6;Q6NXS1		Protein phosphatase i	PPP1R2;PPP1R2P3	19.245	15.3	3	3	52.499	0	30315	23243	32383	30197	33721	20677	36874	25994	26486	31479	No expres	Moderate	Enriched	Low	YES		
E7EMV2;E7ESP9;		Neurofilament mediu	NEFM	78.881	6.2	4	3	3.0483	0.00133	2041.1	4689	3628.9	773.06	4236.3	0	284.81	640.06	244.37	287.09	Low	Moderate	Moderate	Low			
E7EMW7;O95071-		E3 ubiquitin-protein	UBR5	308.57	1.9	4	4	8.2541	0	10928	5730.7	7936.6	8094.8	9522	11441	7450.5	7154.3	6567.4	8202.3	Moderate	Enriched	Enriched	Enriched	YES		
H0Y612;E7EN20;C		E3 ubiquitin-protein	TRIM33	98.891	2.9	2	2	3.817	0.00061	8015	5078.5	5821.1	7764	6843.5	4576	4231.3	5641.2	1683.1	7001.1	Enriched	Moderate	Enriched	Enriched	YES		
E7EN65;P15502-2;		Elastin	ELN	61.923	11.3	6	6	12.276	0	42413	36142	39620	42711	51534	38696	41515	37470	22870	42204	Enriched	Low	Low	Moderate	YES		
E7EN86;P52747-2;		Zinc finger protein 14	ZNF143	65.885	4.4	3	1	2.0357	0.00755	3348.1	5631.4	4087.4	3785.5	4424	2611.8	4720.1	2902	4222.2	3308.2	Enriched	Moderate	Enriched	Moderate			
E7END6;P04070;P		Vitamin K-dependent	PROC	55.389	2.4	1	1	1.8625	0.00878	1239.4	1239.7	1465.9	1131.6	1489.1	1006.6	1222.3	941.28	1345.1	1359.3	Enriched	No expres	Low	Low			
E7ENL6;P12111-4		Collagen alpha-3(VI)	COL6A3	278.11	49.6	311	0	9.1366	0	23475	23360	25971	20160	30093	31496	100880	122130	53310	57827	No expres	Enriched	Enriched	Enriched	YES		
E7EV99;E7ENY0;l		Alpha-adducin	ADD1	70.055	41	34	34	228.38	0	210290	172010	190310	169580	213090	180570	260700	252540	133850	197430	Enriched	Enriched	Enriched	Enriched	YES		
E7ENZ3;P48643-2		T-complex protein 1	CCT5	53.848	45.3	47	3	25.308	0	12661	9843.2	12828	15388	13439	14372	43352	46562	23457	14577	Low	Enriched	Enriched	Moderate	YES		
E9PEZ7;E7EW77;l		Abl interactor 2	ABI2	49.25	9.2	4	2	3.6949	0.0008	9215.2	4973.6	8110.6	8562.3	8551.3	7840.2	7993.7	8471.5	4272.3	11380	Moderate	Enriched	Enriched	Low	YES		
E7EPB6;P13569;P		Cystic fibrosis transm	CFTR	163.35	13.9	19	19	142.27	0	86391	82926	70446	111760	86255	85636	80562	138390	42483	98461	Low	Low	Low	Enriched	YES		
E7ES33;E7EPK1;C		Septin-7	SEPT7	48.715	37.6	21	2	237.58	0	96319	71938	87531	98257	106780	106930	192490	123720	120940	133260	Enriched	Enriched	Enriched	Enriched	YES		
E7EPN9;Q9Y520-2		Protein PRRC2C	PRRC2C	308.77	5.1	12	12	41.531	0	43367	40437	43815	35654	56509	32739	54474	55377	35623	49104					YES		
E7EPT4;P19404		NADH dehydrogenas	NDUFV2	27.907	25	11	11	44.781	0	41607	29983	35052	92065	36702	62778	71012	94045	31374	80117	Moderate	Enriched	Enriched	Enriched	YES		
E7EPU2;Q9Y2E4		Disco-interacting pro	DIP2C	168.64	2.3	4	1	6.9717	0	21530	13705	18951	21665	19963	19778	16836	15121	9838.9	21058	Enriched	Enriched	Enriched	Enriched	YES		
E7EPZ9;P22105-3		Tenascin-X	TNXB	458.38	17.4	54	1	2.1646	0.00611	3432.5	5129.1	5751.8	3097.8	6943.9	2587.2	3238.7	1958.1	1800.5	2597.4	Enriched	Low	Low	Moderate	YES		
I3L0K1;E7EQ34;O		Golgi SNAP receptor	GOSR2	23.136	25.6	5	5	17.216	0	27623	20654	28421	38811	25123	25724	27223	30634	18426	27529	Enriched	Enriched	Enriched	Enriched	YES		
E7EQ45;Q9H0R1-2		AP-5 complex subun	AP5M1	56.465	2.2	1	1	2.1354	0.00609	10976	9662.9	9299.8	10255	10292	9363.6	9034.5	8354.3	4471.1	7777.4							
E7EQ69;Q9GZZ1;(		N-alpha-acetyltransfe	NAA50	19.311	32.1	6	6	7.1181	0	19116	16124	17515	17510	18802	19785	20104	19085	13612	16744					YES		
E7EQB2;E7ER44;I		Lactotransferrin;Lact	LTF	76.625	11.9	9	8	17.087	0	7567.7	7021.1	7591	9017.4	8050.5	9448.5	6609.4	8110.8	3313.8	7701.6	No expres	Moderate	Low	Enriched	YES		
E7EQB3;Q9BSV6		tRNA-splicing endon	TSEN34	34.317	4.1	1	1	1.9142	0.00814	3176.8	1852.1	2898.1	3630	2372.2	2742.9	3877.9	4162	3401.5	3285.7	Enriched	Enriched	Enriched	No expression			
E7EQI7;Q12768		WASH complex subu	KIAA0196	117.06	6.3	7	7	13.038	0	12863	9451.1	12042	15902	12449	10462	10440	12480	6112.9	13361	Enriched	Moderate	Enriched	Low	YES		
E7EQR4;P15311		Ezrin	EZR	69.371	49.7	74	55	323.31	0	412470	320770	365770	378380	454400	440450	857840	672070	525930	532500	Enriched	Enriched	Enriched	Enriched	YES		
E7EQR8;Q9GZM5		Protein YIPF3;Protei	YIPF3	38.889	9.8	3	3	4.6114	0.00043	13447	8946.7	9294	14055	11032	14290	7077.4	11119	4510.8	12080	Low	Enriched	Enriched	Low			
S4R3H4;E7EQT4;C		Apoptotic chromatin	ACIN1	145.44	18.1	25	25	64.734	0	83395	62840	72462	78432	85944	120240	93563	101860	58791	109050	Moderate	Moderate	Moderate	Moderate	YES		
E7EQU1;E9PES6;I		High mobility group ı	HMGB3	22.09	24.4	5	3	5.844	0	6734.9	8107.2	7279.6	5034.5	9430.3	5574.3	18046	18214	5315.5	5702.6	Moderate	Moderate	Enriched	No expres	YES		
E7EQY1;Q96C01;C		Protein FAM136A	FAM136A	26.776	24.5	9	9	21.785	0	16309	12921	13142	15891	15330	20585	19679	16905	10999	18745					YES		
E7ER68;Q658Y4;C		Protein FAM91A1	FAM91A1	88.986	8.1	6	6	41.262	0	21360	30158	20528	17225	27612	15121	19041	22908	10776	16354	Moderate	Enriched	Enriched	No expres	YES		
E7ER77;Q7Z2K6;C		Endoplasmic reticulu	ERMP1	93.159	2.6	3	3	4.8527	0.00043	2645.5	1183.5	1571.5	2220.1	1657.1	1904.7	2335.6	2304.8	564.72	1975.1	Moderate	Moderate	Enriched	No expres	YES		
E7ERA5			MYH10	21.553	34	8	1	3.2654	0.00077	3410.4	11199	6323.5	1987.7	5863.4	2089	14604	1203	79521	5209.4	Moderate	Enriched	Enriched	Moderate	YES		
E7ERH1			TNS1	85.658	11.4	9	3	5.2201	0.00022	13679	10536	12410	7565.4	15557	11084	12727	11438	7904	15144	Enriched	Enriched	Enriched	No expres	YES		
E7ERK6			CLU	23.712	37.7	14	1	5.4227	0	5969.5	4791.3	5717.7	8755.5	5301.8	7210	10651	9067.3	48094	10686	Enriched	Enriched	Enriched	Enriched	YES		
E7ERN9			GGT1	8.2568	17.5	2	2	5.3863	0	2071.3	1019.7	1736.4	2201.8	1581.2	3843.9	1927.1	1826.1	851.01	2047.7	Enriched	Enriched	Enriched	Enriched			
E7ERQ4;Q8NHS3		Major facilitator supe	MFSD8	52.268	2.5	1	1	3.4329	0.00079	2854.5	3616.9	4874.5	3112.3	3927.5	8167.1	8427.2	6943.4	3941.7	5692	Low	Enriched	Enriched	No expres	YES		
E7ERS3;Q86VM9;		Zinc finger CCCH do	ZC3H18	108.94	5.3	4	4	7.8932	0	6859.5	6575.7	7309.2	5441.8	9527.8	4446.7	6852.4	6428.2	4800.7	6459.4	Moderate	Enriched	Moderate	No expres	YES		
E7ERU0;E9PHM6;		Dystonin	DST	615.65	1.6	7	6	14.12	0	9119.7	6212.2	11192	10704	9853.3	10791	12053	12330	6308.1	12340	Enriched	Enriched	Enriched	Moderate	YES		
E7ES19;P35443		Thrombospondin-4	THBS4	96.005	3	2	2	3.1379	0.00095	2357.5	2705	5091.6	1450.3	5881.9	2486.7	5739.1	2196.1	2678.7	2402.5	Low	Moderate	Enriched	No expres	YES		
H0YBP1;E7ESA6;(		Focal adhesion kinas	PTK2	115.45	8.5	11	11	30.635	0	17662	13980	17403	18141	16893	22915	28077	29721	12945	24586	Enriched	Enriched	Enriched	Enriched	YES		
E7ESA8;Q8WWY3		U4/U6 small nuclear	PRPF31	54.909	10.6	7	7	13.964	0	10941	8275	9372.5	15451	10012	11941	12628	15932	6701.5	10758	Enriched	Enriched	Enriched	Moderate	YES		
F8VX32;E7ESB2;H0Y304;P11532-5;P1			DMD	141.77	13.7	18	3	58.01	0	68390	34485	48700	56967	52840	67781	69812	66464	38159	61691	No expres	Enriched	Enriched	Enriched	YES		
E7ESC6;Q9UIA9		Exportin-7	XPO7	124.07	19.3	19	19	56.206	0	64288	52690	61073	53423	71865	57248	65979	75351	37854	66565	Enriched	Moderate	Enriched	Enriched	YES		
F8W7U3;E7ESD2;		WASH complex subu	FAM21A;FAM21C;FAM	136.86	17.7	21	21	93.167	0	67593	47583	53126	75229	58098	59111	46549	61959	28578	55588	Enriched	Enriched	Enriched	No expression			
E7ESE0			RPL9	18.9	71.1	32	8	272.38	0	262740	162210	189090	191650	252030	209850	264340	244360	105690	187180	No expres	Enriched	Enriched	Low	YES		
E7ESG2;Q9HAW4		Claspin	CLSPN	145.31	1.6	2	2	1.9546	0.008	13228	6125.7	9498.9	5781.8	19811	7605.9	18328	8827.5	8714	6846.3	Moderate	No expres	No expres	No expression			
E7ESG8		Serine/threonine-prot	PPP2CA	16.854	35.9	7	2	5.1106	0.00044	4053.1	1810.4	5072	4491.3	2931.1	3217.6	2404.3	3800.8	1404.8	3150.1	Low	Enriched	Enriched	Enriched			
E7ESJ7;Q9NRY5		Protein FAM114A2	FAM114A2	47.956	19.5	8	8	67.905	0	9241.9	7868.3	8889.2	22932	8337.4	13943	11397	19920	9870.9	14450	Moderate	Moderate	Enriched	No expres	YES		
E7ESY4;Q13330-2		Metastasis-associated	MTA1;MTA3	79.372	7.1	4	3	6.7339	0	10401	12487	16857	9743.3	16521	7138.1	10261	10597	4985.8	9697	Enriched	Enriched	Enriched	Moderate			
E7ET49;Q8NCG7-		Sn1-specific diacylgly	DAGLB	68.951	2.9	2	2	3.9405	0.00061	13309	10094	11309	9140.2	17051	10874	9682	9924.7	7033.9	11466	Enriched	Enriched	Moderate	No expression			
E7ET67;Q9H313-5		Protein tweety homol	TTYH1	30.378	4.6	1	1	6.9126	0	5112.8	3208.9	3950.2	11860	4168	6528	4928	8894.3	2823.2	8192.5	No expres	No expres	No expres	No expression			
H0YBA1;E7ETA6;		Pericentriolar materia	PCM1	85.715	1.4	1	1	3.0558	0.00114	2162.4	1613.8	1690.9	2579	2660.6	2424.2	2184.2	2006.5	1669.3	3068.7	Enriched	Enriched	Enriched	Low	YES		
E7ETB3;Q9ULA0;		Aspartyl aminopeptic	DNPEP	54.502	26.2	19	10	54.638	0	71800	74126	83948	61011	95368	53828	77770	80621	41389	70440	Enriched	Enriched	Enriched	Enriched	YES		
F5GXF5;E7ETD6;C		Nucleosome-remodel	BPTF	271.53	0.9	3	3	4.2176	0.00063	5651.1	6547.5	5379.9	6703.1	5547	4959.1	6249.3	6232.2	2977	5760.8	Enriched	Enriched	Enriched	Moderate	YES		
G3XAM2;E7ETH0		Complement factor I;	CFI	65.059	12	6	6	11.579	0	14021	13021	15486	28434	15162	13795	12351	18860	10037	17126	Enriched	Enriched	Enriched	Enriched	YES		

E7ETK5		IMPDH2	30.611	38	18	5	27.638	0	9574.3	7952	7977.8	9678.1	10219	11347	9639.5	10445	5462.1	8899.1	Moderate	Enriched	Enriched	Enriched	YES
E7ETM6;Q8N2H4	Protein SYS1 homol	SYS1	15.183	6.7	1	1	2.1541	0.00611	9156.7	7164.4	6461.8	10923	11089	6957.7	8017.6	9955.3	4984.8	7859.6					
E7ETZ4;Q9Y6E2;(	Basic leucine zipper a	BZW2	46.913	18.1	8	8	23.938	0	68158	52062	84088	85619	70150	59803	112690	96934	66867	84399	Enriched	Enriched	Enriched	No expres	YES
E7EU05;P16671-4;	Platelet glycoprotein	CD36	52.062	15.8	15	15	74.869	0	93592	72886	112320	95710	116500	110060	94340	96183	45090	141410	Enriched	Enriched	Moderate	No expres	YES
E7EU96;Q5U5J2;P	Casein kinase II subu	CSNK2A1;CSNK2A3	45.31	33	17	16	65.718	0	75688	57818	59963	67620	70813	61265	65649	64050	43173	71000	Enriched	Enriched	Enriched	Moderate	YES
E7EUC4;Q9NRH2	SNF-related serine/th	SNRK	61.086	3.8	1	1	5.4662	0	6277.5	5146	5960.5	6825.8	5854.5	4730.8	6723.4	8019.5	3194.1	6216.9	Enriched	Enriched	Enriched	Enriched	YES
E7EUI6	Integrin beta	ITGB1	17.063	38.2	11	1	4.5719	0.00043	439.46	1720.5	1174	209.24	1620.3	0	922.2	158.95	615.98	0	Enriched	Enriched	Enriched	Enriched	YES
I3L0K0;H3BMK6;I	tRNA-dihydrouridine	DUS2	8.2518	23.3	1	1	3.2787	0.00078	6514.6	3279.1	5872.1	7937.6	5361	8714.5	6687.9	7957.6	3157.9	8194.7					
E7EX73;E9PGM1;	Eukaryotic translatio	EIF4G1	158.64	35.3	72	64	323.31	0	291160	212870	216530	311180	264810	270900	363270	354830	184820	308170	Enriched	Enriched	Enriched	Enriched	YES
E7EV43;K4DI92;Q	RWD domain-contai	RWDD4	14.012	11.2	1	1	2.2762	0.00495	6763.2	5344.5	7172.7	5608.7	5679.4	22977	6235.2	7179	4439.8	6353.6					YES
E7EVB6;O60941;E	Dystrobrevin;Dystrob	DTNB	70.512	25.6	16	7	45.63	0	36121	33971	32334	34471	43896	28106	28732	28832	16660	28823	Low	Low	Low	Moderate	
E7EVG2;Q86U86-(	Protein polybromo-1	PBRM1	168.5	4.9	5	5	12.98	0	11268	8646.9	11235	19513	11895	11803	10516	10003	5163.9	13069	Enriched	Enriched	Enriched	No expres	YES
E7EVJ5;Q96F07-2;	Cytoplasmic FMR1-i	CYFIP2	142.58	10.2	17	1	5.4283	0	5184.5	4536.4	6764.5	7036.7	7037.4	5607	9581.6	7823.9	4295.7	7723.2	Enriched	Moderate	Enriched	Enriched	YES
E7EVK2;U3KQ69;	Mitochondrial GTPas	MTG1	31.677	3.5	1	1	1.8705	0.00845	5165.1	3952.3	3938.7	5550.4	4413.7	5084.8	3562.3	3314.2	2264.9	5428.3	Enriched	Moderate	Moderate	Moderate	
I3L3R2;E7EVS6		ACTG1;ACTB	18.031	59.8	39	5	68.498	0	63357	58758	63976	59508	85836	47740	73397	42491	38162	56630	Enriched	Enriched	Enriched	Enriched	
E7EVW7;P14317	Hematopoietic lineag	HCLS1	49.704	10.7	5	5	8.4403	0	16510	22710	16049	15982	18817	25917	14858	13124	11642	16228	Moderate	Moderate	Moderate	Moderate	YES
E7EVY0;S4R3Q9;	Mitochondrial inner	OXA1L	45.165	5.4	2	2	5.4855	0	8417.2	7186.2	8514.9	6403.2	8957.1	6317	9239.4	9085.3	4859	8045.8	Moderate	Enriched	Enriched	Enriched	
E7EW05;Q9NVU7	Protein SDA1 homol	SDAD1	75.44	3.7	2	2	3.2721	0.00077	20317	9018.2	11594	17086	14722	16940	15704	19017	7270.4	20419	Low	Moderate	Enriched	No expres	YES
E7EW32;Q7L1V2-	Vacuolar fusion prot	MON1B	47.836	8.7	3	3	5.7204	0	2517.2	1359.7	1985.8	4097.2	1041.5	2888.2	0	3954.4	1014.7	3127.2	No expres	Enriched	Enriched	No expres	YES
E7EW84;Q8TAG9-	Exocyst complex con	EXOC6	81.851	2.9	3	3	6.0417	0	2742.3	3266.3	4210.4	1802.9	4536.4	1804.7	4102.6	2792.9	2278.1	2932.2	Enriched	Enriched	Enriched	No expres	YES
Q5JRJ2;Q5JRJ0;E7	TSC22 domain famil	TSC22D3	8.6727	26	2	2	3.3815	0.00078	15082	12631	15820	9863.8	17173	18107	23548	23392	11999	21338	Enriched	Enriched	Enriched	Enriched	YES
E7EWE1		UBA5	38.753	27.7	18	2	7.6689	0	14644	8606.2	12926	8771.9	16179	12030	10519	8493.9	6306.7	8898.4	Moderate	Enriched	Enriched	No expres	YES
E7EWP0;H0Y886;(	NADH dehydrogenas	NDUFB5	20.038	26	7	7	32.492	0	79960	44293	58458	69169	63349	70906	51611	61696	25322	81762	Enriched	Enriched	Enriched	Enriched	
E7EWP2;O75962-5	Triple functional don	TRIO	262.68	1.9	4	4	6.5945	0	18982	10852	13838	26146	13653	18846	15135	14702	12513	19698	Moderate	Moderate	Enriched	Low	YES
E7EWP3;P25189;P	Myelin protein P0	MPZ	27.879	15.2	5	5	11.39	0	15394	18534	47831	13396	57342	10586	14557	11747	8361.3	20065	Moderate	No expres	Low	Moderate	YES
F5H7K1;E7EWW0	UPF0505 protein C1	C16orf62	107.94	8.8	8	8	13.196	0	11136	8786.3	10028	14369	12582	9488.8	8083.1	8856.5	4674.4	10447	Moderate	Enriched	Enriched	Moderate	YES
E7EX17;P23588;P	Eukaryotic translatio	EIF4B	69.697	44.2	40	26	153.87	0	163850	129190	149170	126690	225430	166370	264220	162470	176750	157370	Enriched	Enriched	Enriched	Moderate	YES
E7EX53;P61313-2	Ribosomal protein L	RPL15	15.722	38.3	11	1	3.5237	0.00079	13663	11507	10616	18614	11392	11424	17734	12912	6405.8	16869	Enriched	Enriched	Enriched	Enriched	YES
E7EX82;Q8NDX5-	Polyhomeotic-like pr	PHC3	89.139	2.4	2	2	1.8566	0.00877	1868.3	1843.6	2113.9	1947.6	2634.7	1790.8	1286.8	1336.3	780.96	1527.2	Enriched	Enriched	Enriched	No expression	
E9PAK5;O75064	DENN domain-conta	DENND4B	133.41	1	1	1	4.745	0.00043	4664.7	4644	5497.8	3221.8	6726.4	3391.3	6301.1	3707.1	6953.7	4819.9	Moderate	Enriched	Enriched	Enriched	YES
E9PAM4;Q9BTU6	Phosphatidylinositol	PI4K2A	51.218	6.7	3	2	2.7597	0.0024	4788.3	4927.5	5364.5	4394.5	5717.1	2371.3	2834.7	2372.9	2039.6	4196.5	Enriched	Moderate	Enriched	Low	YES
E9PAQ1;P27918	Properdin	CFP	45.147	2.9	1	1	1.9925	0.00787	2997.2	3087.2	3935.1	2541.7	4367.2	1854.4	3266.8	3659.1	2614.3	2484.7	Low	No expres	No expres	No expression	
F8VZJ2;H0YHX9;(	Nascent polypeptide-	NACA	15.016	52.9	18	7	230.5	0	141670	73456	94090	170380	90647	179310	163270	169290	97381	148920	Enriched	Enriched	Enriched	Enriched	YES
E9PB61;Q86V81	THO complex subuni	ALYREF	27.557	29.9	15	14	152.14	0	90773	75784	112720	64241	128550	88049	107980	77123	43965	73172					YES
E9PBS1;P22234;P	Multifunctional prote	PAICS	45.651	25.7	16	16	29.912	0	55631	43394	47221	55139	51464	72598	117580	141660	43322	70026	Enriched	Enriched	Enriched	Enriched	YES
E9PC15;Q53H12;E	Acylglycerol kinase,	AGK	43.796	13.2	6	6	17.327	0	19879	15210	16948	20447	16289	24676	22155	36072	13180	31597	Moderate	Moderate	Enriched	No expres	YES
E9PC52;Q16576;Q	Histone-binding prot	RBBP7	46.938	16.8	7	7	10.383	0	25648	16903	23789	18565	28852	28589	36654	46408	14693	29713	Enriched	Enriched	Enriched	Low	YES
E9PC66;P17029;B	Zinc finger protein w	ZKSCAN1	59.674	8.3	4	3	11.693	0	16017	13263	19441	14367	23140	10790	13693	12255	8979.6	14262	Enriched	Enriched	Enriched	Low	YES
E9PC69;Q7KZI7-1	Serine/threonine-prot	MARK2	86.69	9.9	7	6	29.967	0	19112	19899	22082	15512	28773	12883	33640	20478	25149	21467	No expres	No expres	Low	No expres	YES
E9PC74;Q13144	Translation initiation	EIF2B5	78.346	7.9	6	6	25.657	0	13321	9548.5	8462	6157.9	17010	11568	11384	13051	3669.5	10328	Low	Enriched	Enriched	Moderate	YES
F5H7V9;E9PC84;J	Tenascin	TNC	201.14	3.2	5	5	13.324	0	13854	17005	11640	8674.3	17242	10614	16144	20415	6974.7	20708	No expres	No expres	Moderate	No expres	YES
H0YA68;E9PCD7;(	Epididymis-specific a	MAN2B2	107.51	4	3	3	3.8221	0.00061	4782.3	4262.3	4517.8	7334.9	5289.3	5399.1	4416.9	4693.3	2235.1	5414.1	Enriched	Enriched	Enriched	Low	YES
E9PCN5;Q9H9A5-	CCR4-NOT transcrip	CNOT10	67.091	4.3	2	2	5.082	0.00044	3550	3241.2	4437.6	2797.8	4952.7	2590.4	4354.7	4089.1	4603.2	4187.1	No expres	Moderate	Moderate	No expres	YES
E9PCT3;P51636-2;	Caveolin;Caveolin-2	CAV2	12.953	31	6	6	26.736	0	32957	33315	41643	31794	44768	36534	43603	34960	37657	52938	Enriched	Enriched	Enriched	Moderate	YES
E9PCX7		NNT	99.728	27.1	36	1	3.4634	0.00079	4029.4	4043	3493.8	3611.7	5696.5	1746	1603.6	3311.2	955.16	3280.8	No expres	Moderate	Enriched	Low	YES
H7C529;H7C4W2;	PX domain-containin	PXK	5.1604	22	1	1	3.2457	0.00077	3307.3	1980.1	3367.1	3511.8	3837	3578	3354.6	3318.3	4345.4	4654.3	Low	Moderate	Enriched	No expression	
E9PD68;Q14194;Q	Dihydropyrimidinase	CRMP1	62.029	23.2	16	5	143.6	0	19080	25024	31979	15179	30344	11223	17181	16327	13048	16555	Enriched	Moderate	Enriched	Enriched	YES
E9PDE8;O95757	Heat shock 70 kDa p	HSPA4L	91.953	15.9	15	8	94.423	0	37533	27243	26467	32502	36933	43913	37093	42226	25788	38924	Moderate	Low	Moderate	Low	YES
E9PDF6;O43795-2	Unconventional myo	MYO1B	128.48	21.3	32	32	77.196	0	95333	63029	78978	95757	90395	80477	86071	102890	52095	101880	Enriched	Enriched	Enriched	Enriched	YES
E9PDL4;Q05084-3	Islet cell autoantigen	ICA1	53.242	7	3	3	5.1982	0.00022	1709.9	148.2	472.21	476.18	430.28	2363.3	978.45	774.49	665.38	990.58	Low	Enriched	Enriched	Moderate	YES
E9PDP5;Q8IWZ3;(	Ankyrin repeat and K	ANKHD1	166.74	7	9	3	27.164	0	21065	19390	21986	19826	24933	17430	22242	16246	19835	19898	Moderate	Enriched	Enriched	No expres	YES
H0YG13;H0YFL1;	cGMP-dependent 3,5	PDE2A	18.834	11	2	2	3.3914	0.00078	13285	6175.1	4508.2	12345	5685.6	11393	11700	24027	5958.9	13546	No expres	Low	Moderate	Enriched	YES
E9PEH0;Q9NQV8-	PR domain zinc finge	PRDM8	45.082	2.3	1	1	2.2195	0.00545	8386.3	7902.5	6027.2	1868.2	5928.8	3436.8	17451	14705	17339	10395	Moderate	Low	No expres	No expression	
E9PEP6;O14786;Q	Neuropilin-1	NRP1	101.3	6.4	4	4	17.268	0	9134.2	8085	11725	9730.1	14678	9863.9	10555	11973	4664.1	11751	No expres	Low	Enriched	Low	YES
E9PEQ6;Q9UNP9-	Peptidyl-prolyl cis-tr	PPIE	27.698	14.8	3	3	8.122	0	16275	11676	13926	16037	16368	11469	10453	16658	5451.8	17859	Low	Enriched	Enriched	Low	YES
E9PER6;Q6A1A2;(	Putative 3-phosphoin	PDPK1;PDPK2	60.328	4.3	2	2	5.2119	0.00022	8706.5	5159.4	7612.5	7729.6	10387	7520.3	9215.2	7176.6	3964.7	7908.5	Enriched	Enriched	Enriched	Enriched	YES
E9PEW8		HBD	11.346	92.3	30	1	1.9926	0.00787	2574.7	2354.1	2581.3	2889.7	3838.6	73125	12782	6492.2	1699.8	4444.9	Low	Low	Low	Low	YES
E9PHQ0;E9PEZ3;(	Protein diaphanous h	DIAPH1	140	20.2	32	32	108.85	0	176520	134160	139110	181880	180990	133630	139090	144940	68202	163020	Enriched	Enriched	Enriched	Enriched	YES
E9PF10;O75694-2;	Nuclear pore comple	NUP155	148.09	9.6	14	14	41.873	0	31756	30918	44002	30716	41077	25189	60775	48015	36206	38523	No expres	Low	Moderate	Low	YES
E9PF16;Q96CM8-	Acyl-CoA synthetase	ACSF2	63.652	4.4	2	2	12.35	0	15790	14437	16108	13787	17053	18428	29732	28316	15183	30174	Low	Moderate	Moderate	No expres	YES
E9PF17;P13611-4;	Versican core protein	VCAN	176.83	2.9	4	4	23.959	0	18241	17926	17136	13954	22150	14890	17854	42795	8007	26491	Moderate	Low	Enriched	Moderate	YES
E9PF19;Q9Y4P3;C	Transducin beta-like	TBL2	45.935	48.4	34	33	299.72	0	211970	169060	211610	159460	248210	245360	270190	248000	120590	195070	Enriched	Enriched	Enriched	Moderate	YES
E9PF42;Q8N398-2	von Willebrand facto	VWA5B2	108.61	1.3	1	1	3.466	0.00079	6591	7369.9	11330	6375.7	11265	7086.7	12162	12701	7302.1	10473	Low	Low	Low	No expres	YES
E9PGF5;E9PF55;Q	Tensin-1	TNS1	183.22	19.9	37	30	285.49	0	146800	113860	145500	138780	177090	122230	178190	160090	108930	153610	Enriched	Enriched	Enriched	No expres	YES
Q5T9S2;E9PFB9;J	Coiled-coil domain-c	CCDC18	84.35	1.2	1	1	2.709	0.00238	4386.3	4115.5	3914	6575.9	4557.4	142770	0	11608	2543.1	4647.5	No expres	No expres	Low	No expression	
E9PFH4;Q9Y5L0-3	Transportin-3	TNPO3	96.669	6.9	5	5	7.7835	0	27533	20081	23574	21931	29454	19770	20723	20826	14938	23647	Enriched	Enriched	Enriched	Enriched	YES
Q3HKR1;E9PFK9;	Rab5 GDP/GTP exch	RABGEF1	46.983	7.6	4	4	5.5204	0	3930.8	2920.6	2982.4	3707.2	3213.8	4523.8	4432.4	3897.4	2197.1	4128.2	Moderate	Enriched	Enriched	No expres	YES
E9PFR3;Q14738-2	Serine/threonine-prot	PPP2R5D	69.116	10.8	6	4	12.059	0	1802	2560.2	3139.1	1532.9	3855.3	1381.4	2034.9	1817.9	1042.4	2138.5	Moderate	Enriched	Enriched	Enriched	YES
E9PFW8		SQSTM1	18.379	25.7	3	1	2.2895	0.00495	2936.3	1764.1	1503.2	3611.1	2326	3163.4	2147.9	2418.1	1044.7	2641.9	Enriched	Enriched	Enriched	Enriched	YES
H7C0V9;E9PG40;I	Amyloid beta A4 pro	APP	54.981	15.3	7	7	15.867	0	28258	25963	24551	22390	32119	23321	32157	21686	27457	26569	Enriched	Enriched	Enriched	Enriched	YES
Q5TG12;E9PGC5;(	Receptor-type tyrosi	PTPRK	164.2	5.3	9	8	18.001	0	25040	19682	30499	30413	30262	32647	45591	33650	26154	38567	Enriched	Enriched	Enriched	Enriched	YES
E9PGC8;P78559;P	Microtubule-associat	MAP1A	331.25	1.5	5	3	3.2379	0.00077	15100	13741	22497	10704	22719	14501	19539	12376	8830.9	17204	Enriched	Enriched	Enriched	Enriched	YES
E9PGM9;P78332;(	RNA-binding protein	RBM6	113.93	3.7	3	3	3.2902	0.00078	10470	8999.2	10567	8533.1	15868	6500.7	6145.2	5752	3459.2	10141	Enriched	Enriched	Enriched	Enriched	YES
E9PGN7;P05155-2	Plasma protease C1 i	SERPING1	59.491	17.3	13	13	48.004	0	61883	50293	58366	94424	51672	59593	63205	110140	39448	65434	Enriched	Enriched	Enriched	Enriched	YES
E9PGT1;Q15631;H	Translin	TSN	25.572	34.1	14	14	35.808	0	17110	15593	14574	21856	17386	12858	24966	22858	14670	19767	Enriched	Enriched	Enriched	Moderate	YES
E9PRI4;E9PGT3;Q	Ribosomal protein S	RPS6KA1	81.146	18.6	12	6	18.966	0	30391	20218	22987	29715	27706	25745	35244	41608	17222	36706	Enriched	Moderate	Moderate	Moderate	YES
E9PGT6;Q99627-2	COP9 signalosome c	COPS8	19.344	28.3	5	5	17.923	0	8233.1	6190.4	6685.9	7633.3	7301.3	6515.4	8429.8	10127	4607.2	9300.6	Enriched	Enriched	Enriched	Enriched	YES
E9PH64;Q9Y6M9	NADH dehydrogenas	NDUFB9	20.383	46.4	7	7	14.842	0	981.22	465.37	1177.8	2127.2	564.34	5068.4	757.9	1489.8	183.49	2325.4	Enriched	Enriched	Enriched	No expres	YES
E9PHF7;Q96RQ3;I	Methylcrotonoyl-Co	MCCC1	68.331	43.3	29	29	184.23	0	233480	155220	184460	148560	177980	210330	140520	176770	70937	205550	Enriched	Enriched	Enriched	No expres	YES
E9PHG5;Q6UW02;	Cytochrome P450 20	CYP20A1	53.448	24.5	15	15	76.438	0	82301	60213	70478	78345	81044	63700	117590	123210	49005	75228	Moderate	Enriched	Moderate	No expres	YES
E9PHK0;P05452	Tetranectin	CLEC3B	17.794	40.6	9	9	26.818	0	35602	34288	41539	27865	46370	24035	26476	34232	21280	28869	Enriched	No expres	Low	Moderate	YES
E9PHM2;Q15031	Probable leucine--tR	LARS2	96.93	3	2	2	3.6355	0.0008	4188.4	3791.2	3038.2	7398.2	2674.1	5022.4	2726.3	4988.6	1475.4	5045.6	Low	Low	Moderate	Moderate	YES
E9PHN6;F6XZQ7;	Glutathione S-transf	GSTM2	22.876	64.2	26	10	59.043	0	131770	84298	91300	106690	98444	73086	62075	83591	40944	79401	Enriched	Enriched	Enriched	No expres	YES
E9PHV4;O15514	DNA-directed RNA p	POLR2D	12.777	13.6	1	1	4.4024	0.00063	3938.5	3257.4	2718.8	3939.4	3210.6	3025.2	2620.8	3705.3	1395.5	3822.1	Enriched	Enriched	Enriched	Moderate	YES
E9PHV5;P28290-2	Sperm-specific antige	SSFA2	136.14	9.1	10	10	86.823	0	67879	58012	68842	57809	80782	80423	114550	113430	57700	82375	Moderate	Enriched	Enriched	Moderate	YES
E9PHY8;Q8NDA8;	Maestro heat-like rep	MROH1	180.28	3.6	6	4	12.346	0	6283	4137.1	6364.3	14061	4335.1	6023.9	4184.9	9244.1	1837.9	8584.7					YES
E9PI21		HSD17B12	17.715	31.7	13	1	2.2184	0.00545	4776.4	3827.7	5371.8	5002.1	4428.9	6575.4	6517	5097.2	5647.7	5300.2	Enriched	Enriched	Enriched	No expres	YES
E9PI65		HSPA8	17.916	70.2	34	5	9.3081	0	25045	15399	16888	44030	16640	33209	31411	41573	17364	32331	Enriched	Enriched	Enriched	Enriched	YES
E9PI87;Q9BUP3;Q	Oxidoreductase HTA	HTATIP2	21.976	14.3	3	3	5.1208	0.00044	1987.3	1504	2224.8	1681.8	2261.9	5138.3	8934	30374	12732	10057	Enriched	Enriched	Enriched	Enriched	YES
E9PI99;Q5T6K7;Q	Nuclear transcription	NFYC	16.202	27	4	4	10.593	0	3702.1	3049	3083.4	2584.8	5013.5	2161.1	2266.8	1636.6	1916.5	2520.4	Moderate	Moderate	Enriched	Enriched	
E9PIB2;G3V1A6;P	Gasdermin-D	GSDMD	30.824	8.7	2	2	4.7509	0.00043	11218	8919.7	6846.2	8561.5	11711	6281.6	5941.6	6330.1	2132.3	7091.7	Enriched	Enriched	Moderate	No expres	YES
E9PJW1;E9PQU9;I	Syntaxin-17	STX17	4.9858	41.5	3	3	3.0913	0.00095	2062.4	1524.2	1736.7	975.93	1782.2	3553.7	7385.7	5949.7	3928.3	4221.5	Enriched	Enriched	Enriched	No expression	
E9PIE3;Q969G5	Protein kinase C delt	PRKCDBP	31.088	14	5	5	8.7656	0	3092.9	3679.2	4986.2	2986	4674.7	3446.2	5112	6861.3	4135.1	4704.6	Enriched	Moderate	Enriched	No expres	YES
E9PIE4;Q9Y6C9	Mitochondrial carrier	MTCH2	28.662	30	7	7	27.848	0	13852	10067	16313	15473	16380	14039	19177	18782	9371.4	15958	Moderate	Enriched	Enriched	No expres	YES
E9PN66;E9PKN9;I	Tumor protein p53-ir	TP53I11	6.8649	40.3	3	3	18.695	0	7012.2	7018.8	7471.1	5240.4	10696	5130.8	7131.3	7514.8	3109.8	6647.8	Low	Moderate	Low	Moderate	YES
E9PIM6;E9PNQ8;I	Thy-1 membrane gly	THY1	17.041	17	3	3	10.744	0	19336	17228	23850	14454	21987	13913	22595	22976	11838	15962	Enriched	Low	Moderate	Enriched	YES
E9PIN3;Q9UBU9;I	Nuclear RNA export	NXF1	68.106	8.5	6	6	10.63	0	8854.9	7123.8	6995.6	7640.8	8617.3	9935.2	11885	7949.7	12461	8233.7	Moderate	Enriched	Enriched	Enriched	YES
E9PIT3;P00734	Prothrombin;Activati	F2	65.408	23.5	12	11	139.89	0	66429	78053	88854	89915	45949	46279	39797	101340	24111	58616	Low	Low	No expres	Low	YES
E9PIZ8;K9J7I2;E9I	NADH dehydrogenas	NDUFB8	7.913	31	2	2	4.1176	0.00062	25547	21435	26124	16084	34599	16629	14863	15157	7457	16252	Enriched	Enriched	Enriched	Enriched	YES
E9PJ24;F8WEF5;C	PHD and RING finge	PHRF1	178.22	0.9	1	1	13.961	0	1951.3	1546.2	3172.9	547.43	1738.2	1292.6	1993.6	2089.7	1100	1440.4	Moderate	Low	Moderate	No expression	
E9PJ42;Q5BJD5-3;	Transmembrane prote	TMEM41B	21.72	9.2	1	1	3.9646	0.00062	4507.7	5172.8	5226.1	2883.2	6956.6	2775.2	4548.6	4058.8	3193.8	4311.9	Enriched	Enriched	Enriched	Enriched	YES
E9PJ55;Q9NUJ3	T-complex protein 1	TCP11L1	67.238	5	5	5	9.1675	0	72385	18350	72255	15381	48553	44767	26133	13731	7409.6	24078	Low	Moderate	Moderate	No expres	YES
E9PJ81;Q04323-2;	UBX domain-contain	UBXN1	32.611	16.6	6	6	20.41	0	24940	19519	23826	26555	29035	22325	34826	24300	29243	34422	Enriched	Enriched	Enriched	Enriched	YES
E9PJB8;E9PN30;Q	Selenoprotein S	VIMP	18.494	22.9	4	4	16.544	0	9994.2	9529.4	10795	11746	17338	6692.3	5321	5079.6	4490.2	10012					YES
E9PJL5;Q96N23;Q	Uncharacterized prot	C12orf55;C12orf63	351.97	0.5	2	2	2.3568	0.00445	7729.7	5479.9	9019.4	7000.8	8098.4	8711.4	8057.8	9913.9	3835.5	10517	No expres	No expres	No expres	No expression	
E9PK06		EEF1D	15.327	44.3	9	2	18.822	0	32251	18462	30796	23812	26490	27951	45808	22869	18324	31697	Enriched	Enriched	Enriched	Enriched	YES
E9PK25;P23528;G	Cofilin-1	CFL1	22.728	61.3	29	8	94.846	0	104880	73347	88180	146160	98928	153490	169660	213380	93823	157940	No expres	Enriched	Enriched	Enriched	YES
E9PQR3;E9PKM5;	Ferritin;Ferritin heav	FTH1	5.6423	26	2	2	11.603	0	1766.7	2167.5	2065.9	1914.6	3563.4	1351	3406.4	3369.9	1916.8	9746.6	Enriched	Enriched	Enriched	Enriched	YES
E9PK47;P06737-2;	Phosphorylase;Glyco	PYGL	94.069	15.5	14	10	76.121	0	85980	73088	64988	91003	65050	70730	56851	73875	37672	84529	Moderate	Low	Moderate	No expres	YES
E9PS17;E9PK59;Q	N-terminal kinase-lik	SCYL1	85.718	6.6	5	5	10.445	0	35197	21970	22346	29835	26172	34914	25665	28724	12797	25649	Moderate	Enriched	Moderate	No expres	YES
E9PK67;E9PNI7;Q	Poly [ADP-ribose] p	PARP10	109.1	1	1	1	2.3504	0.00445	2329.3	2443.2	2565	2351.9	3906.4	1289	3633.5	2550.6	2055.2	2681.4	Enriched	Moderate	Moderate	No expres	YES
E9PK68	Serine/threonine-prot	PPP3CA	17.027	36.1	6	1	2.9174	0.00187	4237.4	1765.5	2363.6	5061.3	2382.2	3220.8	2006.7	4629.2	1143.4	3739.5	Enriched	Enriched	Enriched	No expres	YES
E9PK91;Q9NYF8-	Bcl-2-associated tran	BCLAF1	100.4	20.8	25	2	157.8	0	74681	58421	73755	68997	94364	81111	153370	112240	83038	95091	Moderate	Enriched	Enriched	Enriched	YES
E9PKC0;Q6IQ23;C	Pleckstrin homology	PLEKHA7	144.42	16.7	20	20	57.032	0	50622	41297	48696	50464	52219	90945	57191	45992	31056	48702	Low	Low	Moderate	No expres	YES
E9PKF3		ACAT1	5.4194	85.2	6	3	5.7091	0	6771.1	7998.9	9611.1	4761.1	11407	3868.3	8939.2	4483.4	4112	6338.3	Moderate	Enriched	Enriched	Moderate	YES
H7BXH2;E9PKF6;	Serine/threonine-prot	PPP6R3	92.407	11.7	9	9	17.772	0	38704	32240	34237	34121	46237	29412	27317	31871	16703	29756					YES
E9PKG1;H7C2I1;C	Protein arginine N-m	PRMT1	37.709	41.5	16	16	53.653	0	92660	84906	90108	103030	103350	74563	60535	69273	32264	94776	Low	Enriched	Enriched	Enriched	YES
E9PKT9;O96033	Molybdopterin synth	MOCS2	9.2145	13.3	1	1	3.0699	0.00114	3160.6	2200	2215.1	1553.9	2602	5523	8358	7679.4	3253.1	4317.9	Low	Moderate	Enriched	No expres	YES
E9PQK4;E9PSH0;I	CUGBP Elav-like fan	CELF1;CELF2	9.9402	23	4	4	6.3794	0	18962	17976	19521	16914	20041	14705	21444	20430	11913	21383					
E9PL10;Q96K17	Transcription factor I	BTF3L4	15.779	20	4	1	6.5333	0	20801	17991	21215	16076	23139	18221	18605	14858	12475	15910	Enriched	Enriched	Enriched	No expres	YES
E9PPR1;E9PL12		EEF1D	18.157	62	20	0	10.57	0	56169	39108	57630	27552	67880	53065	47313	40045	33502	43438	Enriched	Enriched	Enriched	Enriched	YES
E9PL19		PUF60	24.757	27.6	8	3	5.7569	0	14092	8195.8	9256.7	16613	10146	12599	10143	9791	6109.7	13278	Enriched	Enriched	Enriched	Enriched	YES
E9PL24;Q5VU43-2	Myomegalin	PDE4DIP	126.95	2	2	2	2.4467	0.00412	6629.4	4227.5	5250.3	6705.1	6705.8	9510.4	5106.1	5812.1	2922.1	7891.5	Enriched	Enriched	Enriched	Moderate	YES
E9PL57;F8VSA6;E9PS38		NEDD8-MDP1;NEDD8	19.536	27.1	9	4	15.615	0	10656	8544.4	8892.3	13220	8500.5	8460.6	7754	17386	7043.9	12435	Enriched	Enriched	Enriched	Enriched	YES
E9PL71;E9PN91		EEF1D	20.819	52.4	22	2	5.5966	0	34901	68188	112910	15491	103860	11006	19335	10279	21021	12777	Enriched	Enriched	Enriched	Enriched	YES
E9PS47;E9PLE4;Q	Phosphatidylserine s	PTDSS2	6.3166	58.3	2	2	3.8417	0.00061	2626.9	2542.6	3422.2	1671.8	3736.9	1623.7	2102.4	1573.8	1276.3	2070.8	Enriched	Low	Moderate	No expres	YES
E9PQD0;E9PS30;E	Probable RNA-bindi	EIF1AD	7.3314	23.4	1	1	3.9802	0.00062	3502.7	3445.2	4234.9	2588.9	5209.5	2101.5	3182.6	2112.4	1597.9	3235.2	Enriched	Enriched	Enriched	No expres	YES
E9PLK3;P55786;P	Puromycin-sensitive	NPEPPS	102.99	31.3	47	46	151.6	0	238030	165600	193190	201180	206760	181580	237870	241240	126590	203910	Enriched	Moderate	Enriched	Moderate	YES
E9PLL0		MVB12A	12.987	8.3	1	1	2.3474	0.00445	4635.5	5048.2	4857.9	2866.7	6679.9	3171.5	5065.2	5070.3	4845.4	3694					YES
E9PLL6;P46776;E	60S ribosomal protei	RPL27A	12.201	38.9	11	11	205.83	0	220430	111370	169330	119770	182260	163620	96310	109920	44814	123410	Enriched	Enriched	Enriched	Enriched	YES
E9PLX0;E9PJJ3;E9PLC9;E9PMC6;E9PJ		CAPN1	13.559	51.6	13	4	6.9795	0	21495	12812	15964	19509	17942	20572	18348	17419	10683	18091	Enriched	Moderate	Enriched	Enriched	YES
R4GMU8;E9PLX3;	Ragulator complex p	LAMTOR5	8.2153	29.1	2	2	9.1484	0	7617.1	4597.7	5111.4	11786	7576.6	8060.5	8012	7601.2	2125.4	6369.6					
E9PMC5;E9PM12;	V-type proton ATPas	TCIRG1	19.44	33.3	6	6	12.11	0	19269	20234	21210	19110	20842	20776	14374	12916	8297	17935	Enriched	Enriched	Enriched	Enriched	YES
E9PMG1;H0YDT0;	RalBP1-associated E	REPS1	80.435	5.7	3	3	8.5378	0	10413	10034	9958.4	10262	11067	8737.4	7813.1	8137.5	3254.8	8738	Moderate	Enriched	Enriched	Low	YES
E9PMI6;J3KN38;P	Methylosome subuni	CLNS1A	18.259	25.1	4	4	6.7152	0	14904	11836	14944	9974.9	17091	8065.6	18618	15145	11097	13375	Moderate	Enriched	Enriched	Enriched	YES
E9PMP2		PAK1	9.8951	29.2	2	1	3.5858	0.00079	4439.3	13122	8566.6	4292.2	10616	2524.7	8519.6	5302.2	6471.9	4002.8	Enriched	Enriched	Enriched	Moderate	YES
E9PMR4;P48509;E	CD151 antigen	CD151	28.067	6.8	2	2	2.9254	0.00168	6196.3	4297.6	5196.9	9547.4	6186	6340.1	6848.2	8145.6	2966.2	7304.7	Enriched	Enriched	Enriched	Moderate	YES
E9PMR6;Q9NZN5-	Rho guanine nucleoti	ARHGEF12	161.91	3.9	4	4	63.915	0	19458	14279	17323	14539	18281	14245	14613	15948	11277	16484	Enriched	Enriched	Enriched	Low	YES
E9PMS6;E9PMT2;	LIM domain only pr	LMO7	145.42	8.4	10	10	115.66	0	55660	58110	66603	35669	90302	38181	54600	52201	50324	52180	Enriched	Low	Enriched	No expres	YES
E9PMX6		PNLIPRP1	20.504	61.1	23	9	67.178	0	64765	53786	34882	51318	41165	48334	36113	34093	25061	41985	Low	Enriched	Enriched	Enriched	YES
Q5JR06;E9PN11		RHOC	10.277	82.6	21	6	13.289	0	16977	9736	13320	36774	11356	15364	17857	36171	10121	17664	No expres	No expres	No expres	Enriched	YES
E9PN57;H0YEK1;(	Sjoegren syndrome/s	SSSCA1	6.7918	21.7	1	1	3.1646	0.00077	7893	7553.4	7817.7	5948.8	10822	6182.8	5080.6	4328	2173	4758.7	Enriched	Enriched	Enriched	Moderate	YES
E9PNL2;Q9UNH6-	Sorting nexin-7	SNX7	45.03	4.8	2	2	3.5066	0.00079	11579	8464.8	8311	12228	8993.6	13550	13597	10529	5955.8	11898	Enriched	Enriched	Enriched	Moderate	YES
E9PNM1;P37268-4	Squalene synthase	FDFT1	47.285	4.4	2	2	6.3356	0	5112.9	2973.9	4291.3	9993.5	3493	7069.2	6013.9	7866.6	3966.3	7796.7	Enriched	Enriched	Enriched	Enriched	YES
E9PNP3;Q9H7C9;I	Mth938 domain-cont	AAMDC	15.588	27.7	7	7	54.624	0	22415	26753	34514	36719	46146	26748	44981	44307	30594	46582					YES
E9PNU4;Q13190-3	Syntaxin-5	STX5	27.842	25.2	9	9	42.29	0	33608	16322	19595	43859	18401	42166	49357	41043	31628	44311	Enriched	Moderate	Moderate	Enriched	YES
E9PNW4;E9PR17;	CD59 glycoprotein	CD59	11.985	30.6	8	8	16.834	0	64084	42165	60309	84023	62263	49392	52042	52318	52755	71786	Enriched	Enriched	Enriched	Enriched	YES
H0YCC7;E9PP81;(	Putative deoxyribonu	TATDN3	15.822	17.4	3	3	15.023	0	11068	2919.1	2891.8	15764	3005.6	18315	2716.8	6807.8	2056.8	12259	Moderate	Moderate	Enriched	No expres	YES
E9PPB1		MPZL3	7.5789	21.5	1	1	2.3708	0.00428	4562.2	2000.7	3344.1	3976.1	3790.7	5597.7	4316.5	8836	2287.4	7592.8	Low	Enriched	Enriched	No expression	
E9PPJ9;G5E9D4;Q	Elongator complex p	ELP4	19.976	15.1	3	3	8.5049	0	5138.5	2726.9	2776.7	9530.4	1881.6	4319.1	3445.8	11390	1318.5	7891	Low	Enriched	Enriched	Enriched	YES
E9PQ14		DPP3	19.819	57.1	14	2	5.5406	0	7859.7	5622	5626.7	4346.5	9521.6	4252.2	6524.5	4114.1	4534.4	5360.5	Enriched	Enriched	Enriched	No expres	YES
E9PQD6;E9PR14;(	Serum amyloid A pro	SAA1;SAA2	13.546	59.8	17	0	3.5318	0.00079	5377.6	4872.1	6724.4	4186.1	6399.2	3349.1	8092.3	9939.6	2214.8	5794.9	Moderate	No expres	No expres	Moderate	
E9PQH6;Q5JR08;P	Rho-related GTP-bin	RHOC	19.224	53.8	22	3	38.737	0	29655	26029	26711	16181	25977	30556	43676	31976	37982	39191	No expres	No expres	No expres	Enriched	YES
E9PQT8;O43189-2	PHD finger protein 1	PHF1	45.694	6	2	2	6.7933	0	25995	18719	21024	24610	21305	28135	26803	35000	12192	28316	Enriched	Enriched	Enriched	Enriched	YES
E9PQY3;P11117;E	Lysosomal acid phos	ACP2	45.306	25.6	14	14	52.315	0	78843	57016	80200	67058	82010	116800	80351	58380	37381	63047	Moderate	Enriched	Enriched	Enriched	YES
E9PR30;P62861	40S ribosomal protei	FAU	10.905	12.2	7	7	14.079	0	13110	10578	11619	12191	13660	10172	39426	26988	8629.1	11957	No expres	Enriched	Enriched	Enriched	YES
E9PR38;H0YEH2;(	Pumilio homolog 1	PUM1	100.5	3.9	3	1	5.9244	0	1287.9	1365.6	1619.8	1010.8	2292.4	1430.2	1644.2	1201.1	899.04	1669	Enriched	Enriched	Enriched	Enriched	YES
E9PR44;P02511;A	Alpha-crystallin B ch	CRYAB	20.03	37.9	9	9	13.941	0	17245	19689	18545	15927	24141	18362	42282	44253	25004	34942	Low	Enriched	Enriched	Moderate	YES

E9PRK2;Q96I59;H	Probable asparagine-	NARS2	27.205	12	3	3	19.929	0	4192.6	3356.3	3972.8	2978.7	4609.7	4629.1	10982	7521.4	7682.9	8477.8	Moderate	Moderate	Enriched	No expres	YES
E9PRL3;E9PI70;E9PIP0;E9PPH0		CHID1	14.852	50	12	1	2.1968	0.00544	4392.8	2419.4	1893	1545.3	2450.8	1317.9	2179.1	1292.9	1069.8	2153.3	Enriched	Enriched	Enriched	No expres	YES
E9PRY8;P29692;P	Elongation factor 1-d	EEF1D	76.569	23.4	36	0	323.31	0	661900	439100	497840	554530	675610	782720	594390	424880	258760	410540	Enriched	Enriched	Enriched	Enriched	YES
E9PSI1;E9PQY7;E	Transmembrane 9 su	CHMP4A;TM9SF1	92.386	9.1	8	8	16.816	0	22466	16432	20810	24966	29524	17159	18738	14524	13508	19014	Enriched	Enriched	Enriched	No expression	
F1LLU7		ECI2	22.007	44.7	15	2	2.4204	0.00412	21634	11411	12120	6158.3	20789	4385.3	14043	4740.9	16015	12245					YES
F1T0I1;J3KNL6;O	Protein transport pro	SEC16A	249.48	14.1	36	36	204.78	0	222840	175460	194820	188620	324810	182530	217680	179360	107160	197180	Enriched	Enriched	Enriched	Enriched	YES
F2Z2B9;Q9BSJ2;Q	Gamma-tubulin comp	TUBGCP2	82.603	8.2	6	6	9.01	0	15408	10557	11500	13179	8898.6	12432	11185	17598	8518.1	14948	Moderate	Enriched	Enriched	Enriched	YES
F2Z2Y6;O95777;C	U6 snRNA-associate	LSM8	7.3713	58.2	6	6	82.389	0	16753	13081	17278	35699	16729	17478	12891	15028	7399.4	18667	Low	Moderate	Enriched	No expres	YES
F2Z357;J3KPC5;X	Rap1 GTPase-activat	RAP1GAP	66.98	7.5	5	5	19.402	0	34367	32403	30583	37141	36312	23737	26925	34798	24142	31805	Enriched	Enriched	Enriched	Enriched	YES
Q5STR5;Q4VX54;	Death domain-associ	DAXX	14.205	16.2	2	2	2.1342	0.00609	4041.6	2250.8	4114.2	7837.6	2823.2	5880.6	4839.4	6739.4	1929.4	5956.9	Low	Moderate	Moderate	Moderate	YES
F5GWI4;P00813;F	Adenosine deaminase	ADA	38.292	10.9	4	4	7.2047	0	9837.5	9324.2	10028	10309	8245.8	10141	12400	13063	5038.5	12643	Enriched	Moderate	Moderate	Moderate	YES
H0YGN0;F5GWI9;	WASH complex subu	CCDC53	11.414	12.1	1	1	2.6445	0.00274	15693	11301	12190	26750	11464	17769	15858	21799	10688	17336	No expres	Moderate	Enriched	No expres	YES
F5GWT4;Q9H4A3-	Serine/threonine-pro	WNK1	225.5	2.4	4	4	23.23	0	17685	12902	14907	15432	17818	15152	17203	17100	10345	17251	Enriched	Enriched	Enriched	Moderate	YES
F5GWX5;Q14839;	Chromodomain-helic	CHD4	217.1	15.1	29	20	93.961	0	129270	100330	115060	121860	134920	130680	180890	164020	94375	162820	Enriched	Enriched	Enriched	Enriched	YES
F5H479;F5GX19;F	Ragulator complex p	LAMTOR1	11.076	51.5	4	4	45.077	0	28947	27724	27825	27112	35825	25966	26326	21456	18930	24934					YES
F5GX88;P17813-2;	Endoglin	ENG	51.139	5.9	2	2	5.5753	0	3386	3265.9	3138	2683.4	4600.7	1526.1	2552.4	2587.9	1143.8	4049.1	Moderate	Low	Moderate	Low	YES
F5GXJ9;Q13740-2;	CD166 antigen	ALCAM	59.528	31.4	25	25	64.789	0	161750	79843	114200	138860	142830	113700	96631	101890	54104	122050	Enriched	Enriched	Enriched	Enriched	YES
F5GXW5;Q99622;	Protein C10	C12orf57	9.9953	50.5	3	3	4.329	0.00063	1126.8	1031.2	1434.4	2204.5	917.91	1121.1	1048.8	1677.9	832.04	1540.9	Enriched	Enriched	Enriched	No expres	YES
F5GXX5;P61803	Dolichyl-diphosphoo	DAD1	9.5541	50.6	6	6	14.456	0	44106	30907	40282	41373	38217	43237	40121	41667	19464	42451	No expres	Enriched	Enriched	Enriched	YES
F5GY80;F5H7G1;F	Complement compon	C8B	60.04	15.7	7	7	58.656	0	18991	23605	19930	21065	25155	24452	18529	35542	11153	23270	Moderate	Moderate	Low	Low	YES
H0YGR4;F5GYG5;	Oligoribonuclease, m	REXO2	22.006	42.2	9	9	74.637	0	62532	44229	55091	67678	45190	60700	88031	91574	75202	94034	Enriched	Enriched	Enriched	No expres	YES
F5GYK2;Q9NRL3;	Striatin-4	STRN4	68.584	6.5	4	4	26.763	0	13833	15764	17930	11902	19913	9056.9	10955	9463.4	7200.6	10036	Moderate	Moderate	Moderate	No expres	YES
F5GYN4;J3KR44;C	Ubiquitin thioesteras	OTUB1	28.05	51	24	11	59.313	0	82361	51679	65312	136400	71215	87128	80201	141390	53169	98712	Enriched	Enriched	Enriched	Enriched	YES
F5GYQ1;P61421;R	V-type proton ATPas	ATP6V0D1	44.659	12	6	6	106.8	0	37388	30646	38804	36943	41457	46544	39802	34637	19641	42894	Moderate	Enriched	Enriched	Enriched	YES
F5GYQ2;Q9UI30-2	Multifunctional meth	TRMT112	9.2555	48.1	4	4	9.0124	0	14993	11256	12281	13440	13627	16900	11515	13231	5319.2	13465	Enriched	Enriched	Enriched	No expres	YES
F5GYV5;H7BZV4;	ADP-ribosylation fac	ARL6IP4	23.687	19.4	3	3	6.05	0	23401	18357	26268	19288	21395	25084	60447	38619	39182	42560	Moderate	Enriched	Enriched	No expres	YES
F5H324;F5GYY5;F	Arylsulfatase E	ARSE	61.077	18	10	8	21.358	0	19555	15107	20502	13213	22434	16049	64679	21646	32795	35324	Enriched	Enriched	Enriched	Enriched	YES
M0R0Q7;F5GZ28;	DNA ligase;DNA liga	LIG1	88.386	1.6	2	2	3.7302	0.0008	7721.1	3622	5507.4	6970.7	4803.2	6738	5146	5741.5	3810.1	6826.5	No expres	Moderate	Moderate	Low	YES
F5GZ78;P49023-2;	Paxillin	PXN	64.232	19.2	11	11	51.042	0	55632	44040	52859	46876	67375	34051	58844	47532	37387	53248	Moderate	Enriched	Enriched	Moderate	YES
F5GZG1;F5H823;B7ZB78		RAP1B	13.889	54.9	21	6	45.055	0	42095	21372	24694	57397	25240	37640	25193	36696	12057	47442	Enriched	Enriched	Enriched	Enriched	YES
F8WCM7;F8VRJ6;	Thiamin pyrophosph	TPK1	14.085	15.7	1	1	50.793	0	8851.2	5674.9	7023.1	11593	5913.7	7806.6	4732.9	9481.5	2510.9	9267.5	Moderate	Low	Moderate	No expression	
F5GZS6;J3KPF3;P	4F2 cell-surface anti	SLC3A2	64.872	13.4	9	9	49.859	0	25973	23080	29148	28150	30621	25930	31305	31048	13740	25287	Moderate	Enriched	Enriched	Enriched	YES
F8VWA9;F5H5T2;	Putative Dol-P-Glc:G	ALG10B;ALG10	8.7901	18.2	2	2	8.759	0	3010	2233.1	2281.4	4616.9	2625.4	2564.9	2590.4	2861.8	1870.1	3573.2	No expres	Low	Moderate	No expression	
F5H004		RAP1B	14.293	42.5	13	1	4.8084	0.00043	1477.2	1352.8	2995.3	4379.7	1684.8	5256.1	10517	2806.6	15884	15089	Enriched	Enriched	Enriched	Enriched	YES
F5H039;Q9NQX3;	Gephyrin;Molybdopt	GPHN	84.733	31.2	23	23	194.26	0	207980	128400	143670	147540	188870	154870	170580	228660	103570	188700	Enriched	Enriched	Enriched	No expres	YES
F5H0R1;Q9H6E5	Speckle targeted PIP	TUT1	98.434	2.9	3	3	5.9939	0	1179.8	1370.6	1318.8	415.63	1923.2	470.15	1565.4	971.56	1338.8	854.71	Moderate	No expres	Low	No expres	YES
F5H145;Q6N063-4	2-oxoglutarate and ir	OGFOD2	17.534	9.4	1	1	2.525	0.00379	750.5	851.68	1024	858.33	1228.7	1232.4	2457.9	1850.1	1599.6	1814.6	Enriched	Enriched	Moderate	No expression	
F5H157;Q15286	Ras-related protein R	RAB35	21.214	45.9	9	9	23.9	0	49673	30121	35365	62061	45262	54525	44321	38756	23865	54274	Enriched	Enriched	Enriched	Low	YES
F5H1F7;P29375-2;	Lysine-specific deme	KDM5A	195.74	0.9	1	1	2.5476	0.00362	0	128.64	118.27	0	222.1	0	8428.9	4308.1	428.26	196.22	Enriched	Moderate	Enriched	No expression	
F5H1Y4;Q9HD26-	Golgi-associated PD	GOPC	44.79	17	7	7	30.692	0	39430	31141	28596	42909	39463	27883	24915	31412	15503	32360	Enriched	Low	Moderate	No expres	YES
F5H2U8;F5H2A4;F	High mobility group	HMGA2	10.767	21.2	1	1	5.4236	0	1835.2	1930.4	2320.3	979.47	3114.5	1176.1	1824.8	1133.6	1706.6	1879.4	Moderate	Low	Low	Moderate	
F5H2T0;O95163	Elongator complex p	IKBKAP	111.47	2.8	3	3	5.3318	0	9189.1	10300	8665.9	9133.2	13252	8797.1	9010.3	7595.2	6072.4	8350.5	Moderate	Enriched	Enriched	Moderate	YES
H0Y5D5;F5H2X7;	Cip1-interacting zinc	CIZ1	91.124	6.2	3	3	40.733	0	6681.9	5680.3	6841.1	8190.9	6472.9	6066.6	8733.1	11179	6453.5	9102.2	Low	Enriched	Enriched	Moderate	YES
F5H345;P08397-2;	Porphobilinogen dea	HMBS	35.761	12.1	6	6	21.305	0	26950	16300	20169	33642	23595	23681	28019	28627	15074	36499	Enriched	Enriched	Enriched	Low	YES
F5H365;Q15436;Q	Protein transport pro	SEC23A	82.968	21.1	22	15	51.783	0	68398	60252	69859	57777	78304	61089	73941	66732	49172	66253	No expres	Low	Enriched	Enriched	YES
F5H3F0		OTUB1	19.432	51.2	14	1	2.7388	0.00239	14378	14664	14681	5442	10596	12778	22981	15618	38010	12208	Enriched	Enriched	Enriched	Enriched	YES
F5H3P3;F5H6Q0;F5H2R5		ARHGDIB	17.936	45.3	7	1	21.344	0	6742.6	25651	18885	4798.7	16368	2598.1	9138.9	5070.9	6349.9	3453.3	Enriched	Moderate	Enriched	No expres	YES
F5H442;Q99816-2;	Tumor susceptibility	TSG101	40.917	14.2	5	5	11.364	0	31923	16705	20071	31228	28089	29534	61541	60030	29444	28673	Enriched	Enriched	Enriched	Moderate	YES
I3L3M4;K7EP40;K	Claudin;Claudin-7	CLDN7	8.8353	19.3	1	1	3.8681	0.00061	22743	15324	16987	20609	19638	21019	16703	17882	8812.5	17666	Enriched	Enriched	Enriched	Enriched	
F5H4Z7;Q96EY8;	Cob(I)yrinic acid a,c-	MMAB	18.795	39.3	6	3	94.053	0	6234.6	7064.3	5238.9	3060.9	7246.3	6057.8	38045	13540	19224	13386	Enriched	Enriched	Enriched	No expres	YES
F5H5D3;Q9BQE3;	Tubulin alpha-1C ch	TUBA1C;KLK9	57.73	55.1	86	3	55.435	0	19596	15309	17325	14192	21966	9103.1	12862	13305	5901.3	12106	Enriched	Enriched	Enriched	No expression	
F5H5F3;Q9Y487;C	V-type proton ATPas	ATP6V0A2	38.051	14	4	4	9.4166	0	20231	14544	17707	21515	18039	19960	22599	24572	12137	20356	No expres	Low	Moderate	Moderate	YES
F5H5N1;O75251-2	NADH dehydrogenas	NDUFS7	19.77	22.5	4	4	84.964	0	28627	18329	23557	21287	24555	39578	53659	75945	21247	49087	Enriched	Enriched	Enriched	Low	YES
F5H5P2;P12694;P1	2-oxoisovalerate deh	BCKDHA	54.202	28.6	16	16	35.691	0	47991	43524	42467	55673	46379	51904	46317	47358	25935	49516	Enriched	Enriched	Enriched	Enriched	YES
F5H5V4;F5GX23;C	26S proteasome non-	PSMD9	16.913	51	7	1	17.437	0	21241	16543	18747	20992	23551	27785	52394	49313	25680	29143	Enriched	Enriched	Enriched	Moderate	YES
H7C5W6;F5H619;	HEAT repeat-contain	HEATR5A	174.02	0.8	1	1	3.2388	0.00077	2664.8	1443.4	1690.7	3556	1634.3	4360.9	1788.8	2732.6	940.64	2680.3	Low	Enriched	Enriched	No expres	YES
F5H669;Q8N684-2	Cleavage and polyad	CPSF7	41.265	18.4	9	8	35.261	0	18720	12584	16311	27159	15707	14195	19247	20301	9677.1	20738	Enriched	Enriched	Enriched	No expres	YES
F5H6C5		DDB1	29.939	30.1	12	2	7.3585	0	12143	7860.8	8971.2	21707	11261	11167	7050.7	11159	3387	12608	Enriched	Enriched	Enriched	Moderate	YES
F5H6E2;O00159-2	Unconventional myo	MYO1C	118.99	32.9	57	57	323.31	0	226610	154230	181560	205840	211710	213560	207590	205790	123610	250220	Enriched	Enriched	Enriched	Enriched	YES
F5H6G8;Q9H8J5	MANSC domain-con	MANSC1	6.2572	24.6	2	2	3.2255	0.00077	1300	551.5	912.02	1795.3	737.07	1395	639.36	1228.8	491.12	1204.2	Enriched	Enriched	Enriched	No expres	YES
H0YLF3;F5H6I0;H	Beta-2-microglobulin	B2M	8.4984	43.7	5	5	8.8996	0	20526	21483	28318	19923	28530	18668	29463	33651	15602	22562	Enriched	Enriched	Enriched	Enriched	YES
J3QS47;J3QRH5;J	Cytochrome b561	CYB561	24.68	8.6	3	3	27.662	0	15803	23195	17413	10787	19730	10918	16803	11949	11963	16241	Enriched	Enriched	Enriched	Moderate	YES
F5H7V8;Q7Z2W9	39S ribosomal protei	MRPL21	16.268	13.3	1	1	4.2059	0.00062	4885.4	2977.3	3909.6	5927.6	5186.7	5901.8	9273.4	5537.2	12119	5953.9	Moderate	Enriched	Enriched	No expres	YES
M0QYS5;F5H8D7;	DNA repair protein X	FOXH1;XRCC1	31.386	13.7	5	5	37.78	0	31942	18235	19041	40139	19726	23008	33562	38027	25882	39272	Enriched	Low	No expres	Low	
F6QDS0;I3L352;Q	ATP-dependent RNA	DDX19A	54.017	28	19	0	172.82	0	96211	79842	91389	103360	108270	77133	87914	80658	60836	92091	Moderate	Moderate	Enriched	Enriched	
G3V4N6;G3V5T1;	Epimerase family pro	SDR39U1	13.318	19	2	2	2.9761	0.00169	1964.5	1286.2	2817.3	3302	1874.8	3131.5	3106.8	5318.9	1566.4	3074.2	Enriched	Enriched	Enriched	Enriched	YES
H7C3P4;F6S8M0;F	N-acetylglucosamine-	GNS	56.374	8.3	6	6	12.794	0	10042	10129	10906	8506.3	12010	10565	10818	8898.9	7420.1	9673.7	Enriched	Enriched	Enriched	Enriched	YES
F6T1Q0;Q6L8Q7-2	2,5-phosphodiesteras	PDE12	52.175	18.2	10	10	22.828	0	26938	33899	23301	28463	26867	21358	20306	25341	17755	22434	Enriched	Enriched	Enriched	No expres	YES
F6TLX2;Q9HC38-	Glyoxalase domain-c	GLOD4	54.719	32.5	32	32	117.09	0	281030	238290	227120	250680	248590	399690	508890	389700	198820	306610	Moderate	Enriched	Enriched	Enriched	YES
F6U236;Q9BY11	Protein kinase C and	PACSIN1	46.146	2.7	2	2	5.689	0	6555.3	11963	10845	7720.6	13783	31341	10793	9816.6	4819	8057.1	Low	No expres	Moderate	No expression	
F6UT28;B1AKQ8;F6X3N5		GNB1	18.426	37.6	11	3	4.5884	0.00043	4541.5	5720	6236.4	3998.3	6645.5	4107.5	4099.8	2905.6	2629.8	3108.7	Enriched	Enriched	Enriched	Enriched	YES
F6VRR5;Q9BY77-	Polymerase delta-inte	POLDIP3	48.103	15.5	8	8	23.012	0	23888	23780	28270	19731	33482	21395	25129	21638	16008	23328	Enriched	Enriched	Enriched	Moderate	YES
F6WQW2;P43487-	Ran-specific GTPase-	RANBP1	31.904	14.7	9	9	92.772	0	73385	53554	72713	55051	70924	60651	160130	144190	58366	85804	No expres	Enriched	Enriched	Moderate	YES
J3KTF9;F6WST4;F	ORM1-like protein 3	ORMDL3;ORMDL1;OR	11.796	11.8	1	1	1.8236	0.00975	13327	8939.1	11024	12545	14322	4151.5	5877	5234.3	4860.7	8941.2	Enriched	Enriched	Enriched	No expression	
F6X2W2;Q7Z3B1;	Neuronal growth reg	NEGR1	32.85	13	4	4	13.422	0	47548	47494	55633	38335	62184	48310	78610	74672	33257	49789	Low	Moderate	Moderate	No expres	YES
F6XEV2;Q9BPX6-	Calcium uptake prot	MICU1	54.578	4.2	2	2	3.4173	0.00079	5976.9	6397.5	7592.1	4326.5	9190.7	3028.9	4323.3	4567.4	2983.5	4379.1					YES
F8WAX7;F6XHT0;	Selenoprotein K	SELK	8.2912	15.3	1	1	1.9252	0.00814	3055.6	1896.9	2249.7	2266.6	2397.1	4855.6	4393.4	3994.2	1371.2	3001.1	Enriched	Enriched	Enriched	No expression	
F8W145;F8VP97;F	CCR4-NOT transcrip	CNOT2	33.265	7.4	2	2	5.6996	0	13988	19044	16410	12001	22991	10021	14028	10409	10328	13757	Enriched	Enriched	Enriched	Enriched	YES
F8VPD4;P27708	CAD protein;Glutam	CAD	236.02	7.9	21	21	76.633	0	72714	57498	63852	71093	69917	74729	78803	95747	35528	75779	Low	Moderate	Moderate	Moderate	YES
F8VPF3;F8VZU9;F8W180		PDE6H	14.436	76.2	28	2	10.386	0	4863.7	4309.5	4549	6068.3	9251.9	2797	3046.7	2343.4	1449.5	2621	No expres	No expres	No expres	No expression	
F8VPF7;Q96D96-4	Voltage-gated hydro	HVCN1	24.833	7	1	1	7.2856	0	7596	10423	10010	7891.7	12689	7458.4	10243	8433.6	5965.4	8775.8	Low	Moderate	Moderate	No expres	YES
F8VQD4;Q8TAD7	Overexpressed in col	C12orf75;OCC1	9.3362	13.5	1	1	104.02	0	10506	9979.5	12647	9156.6	10001	8961.3	10045	11618	6409.4	19849	Enriched	Enriched	Enriched	No expres	YES
F8VQD9;Q9BSB4	Autophagy-related p	ATG101	21.926	7.9	1	1	4.4334	0.00042	2115.9	1318	1893.1	1974	1554.5	2535.4	2282.3	2183.9	1277.5	2687.6					YES
H0YH87;F8WB06;	Ataxin-2	ATXN2	98.004	7.2	5	5	13.909	0	18814	14771	17691	16280	17775	18793	20795	16680	18570	18526	Moderate	Moderate	Enriched	Moderate	YES
F8VRL4;F8VRR0;	Diphosphoinositol p	NUDT4;NUDT11;NUD	11.014	45.3	6	6	17.62	0	41323	35756	46757	37458	43476	42807	59798	69352	36944	52783	Enriched	Enriched	Enriched	No expression	
F8VRZ4		TUBA1A	12.219	86.6	39	0	17.904	0	41204	26793	31790	21585	52202	32178	31019	29258	20505	25496	Enriched	Enriched	Enriched	No expression	
F8VW54;F8VS78;F	Tetraspanin-31	TSPAN31	9.9004	14	2	2	5.6909	0	13975	7502.7	8316.6	7949.3	13482	10110	20157	15142	15647	18914	Enriched	Enriched	Enriched	Enriched	YES
F8VSL3;P25208	Nuclear transcription	NFYB	14.548	9.2	1	1	2.4238	0.00412	2338.6	1806	3169.2	2532.5	2119.6	1910.8	4311.3	3902.7	2368.2	3319.4	Low	Moderate	Enriched	Enriched	YES
J3KPG5;F8VU39;C	Bromodomain adjace	BAZ2A	208.07	1.4	3	3	3.9789	0.00062	32567	15964	33535	8303.3	15481	9256.9	10109	7141.9	5520.2	18300	Moderate	Moderate	Enriched	Enriched	YES
F8VU56;P23467-4;	Receptor-type tyrosi	IGFL2;PTPRB	239.56	0.8	2	2	2.8186	0.00222	1774.4	922.74	1663.4	1619.3	1543.2	950.08	3421.6	3077.7	1561.2	2907.6	No expres	Low	No expres	No expression	
F8VUY8;Q96QD8	Sodium-coupled neu	SLC38A2	10.027	13.6	2	2	4.341	0.00063	1897.9	1511.8	2393.4	1098.2	3694.9	762.93	3471.7	1336.5	1592.6	2260.5	Enriched	Enriched	Enriched	No expres	YES
F8VV56;F8W022;F	CD63 antigen	CD63	16.021	34.5	5	5	11.775	0	17310	16431	18002	9846.8	20957	14876	35246	18496	29335	24561	Enriched	Enriched	Enriched	Enriched	YES
F8VV61		TBC1D15	13.672	22.5	4	2	4.2221	0.00063	873.5	223.45	399.74	502.17	403.24	726.91	444.95	408.27	107.31	591.53	Enriched	Enriched	Enriched	No expres	YES
F8VVA7;P61923;P	Coatomer subunit ze	COPZ1	22.34	24.7	21	12	144.75	0	127040	112130	113180	140550	143330	163090	176620	144870	79383	125720	Enriched	Enriched	Enriched	No expres	YES
F8VVI9;J3KTP3;Q	Cadherin-19	CDH19	48.84	2.5	1	1	3.846	0.00061	8390.2	5868.5	10900	6954.5	8439.3	10578	11553	11231	5446	12117	No expres	No expres	Moderate	No expression	
F8VW41;Q86VP3-	Phosphofurin acidic	PACS2	94.426	3.1	4	4	9.8316	0	2656.9	3632.3	3633.9	1609	4730.3	1387.3	3091.9	1286	2866.5	2068.3	Low	Enriched	Enriched	Moderate	YES
F8W1U7;F8VWH9	ADP-ribosylation fac	ARFGAP1	29.571	28.8	8	8	25.781	0	8294.6	5042.9	5806.2	7729.3	7804.5	9579.8	5306.6	5382.6	2592.9	6484.6	Enriched	Enriched	Moderate	No expres	YES
F8VWL0;F8VX55;	Alpha-globin transcri	TFCP2	43.933	4.2	1	1	5.7994	0	5378.3	2276.1	2596.4	7181	2905	4654.4	3004.8	4389.2	1283.8	4648.3	Low	Enriched	Enriched	Moderate	YES
F8VWQ5		CS	14.439	30.3	7	3	2.9206	0.00187	12083	12187	12296	9514.7	16920	11553	16672	8895	11487	12519	Enriched	Enriched	Enriched	Enriched	YES
J3KPF0;F8VWT9;C	Probable E3 ubiquiti	HECTD4	468.65	0.6	2	2	4.1376	0.00062	9991.8	8499.9	8195.1	10160	9909.7	7174.5	8032.7	9038.7	5650.1	11374					YES
F8VXC8;Q8TAQ2-	SWI/SNF complex su	SMARCC2	136.18	14.1	15	11	44.489	0	58903	43530	55990	64834	52081	73103	85378	86914	58030	89794	Moderate	Moderate	Enriched	Low	YES
F8VXG7;Q99590-2	Protein SCAF11	SCAF11	142.6	3.1	4	4	10.59	0	32602	17575	28258	27253	25932	24777	20728	19359	15097	26657					YES
F8VXU5;Q9UBQ0;	Vacuolar protein sort	VPS29	23.98	25.2	6	6	16.691	0	36690	28596	31484	25786	35295	40576	54907	68949	24292	37588	Enriched	Enriched	Enriched	No expres	YES
H3BU82;F8VZ44;C	Aladin	AAAS	38.518	2.8	1	1	1.8317	0.00976	6256.2	3502.2	5786	7564.6	4792.8	5943.7	5008.1	6438.2	3066.9	6485.7	Enriched	Moderate	Moderate	No expres	YES
F8VZ58		NACA	13.597	20.6	6	2	6.349	0	9839.7	7205.1	7931.1	8367.9	9874.2	8471	9121	6677.7	5334.2	8459.9	Enriched	Enriched	Enriched	Enriched	YES
F8W026		HSP90B1	5.5824	81.6	14	3	11.3	0	8644	7722.1	9895.3	14026	12697	6614.8	8465.9	9576.5	7165.5	9575.9	Low	Enriched	Enriched	Low	YES
F8W031;F8VXJ7;F8W1K5		CNPY2	29.224	50.6	26	0	147.66	0	163910	91336	104770	148770	107450	191660	155820	139840	82953	159140	Enriched	Enriched	Enriched	Enriched	YES
F8W038;Q8IXM2;	Chromatin complexe	C17orf49;BAP18;RNAS	16.29	27.4	5	2	17.395	0	2573.2	2111.2	2670.5	2404.8	2684.3	1830.4	1556.1	2715.1	1111	3148.3	No expres	Enriched	Enriched	No expression	
H0YHR7;F8W061;	Iron-sulfur protein N	NUBPL	13.317	16.2	2	2	16.942	0	5296.4	5548.4	8249.4	2933.5	8074.8	4599.5	4281.4	2535.6	1930.9	4792.2	Low	Low	Moderate	No expres	YES
F8W0P7		ATP5B	28.392	55.9	37	3	6.2043	0	10499	10078	10528	5720.7	14043	17371	32932	37838	13349	20150	Enriched	Enriched	Enriched	Low	YES
F8W0Q9;Q8NEY8	Periphilin-1	PPHLN1	44.682	4.7	2	2	3.6014	0.0008	2046.2	2516.4	2152.7	1814.1	3061.8	2815.5	4250.2	3826	2925.6	3610.8	Enriched	Enriched	Enriched	No expres	YES
F8W0W8;P36873;	Serine/threonine-pro	PPP1CC	38.25	34	21	2	3.1326	0.00095	4580.6	4068.8	3936.1	4235.3	4775.1	2653.8	4010.9	5001.4	2685.7	3634.9	Enriched	Enriched	Enriched	Enriched	YES
H0YHN7;F8W111;	Carboxypeptidase M	CPM	22.595	7.6	2	2	8.9816	0	19167	12569	12742	22128	14935	21046	19217	24282	11327	24660	Moderate	Enriched	Enriched	No expression	
F8W118;H0YHC3;	Nucleosome assemb	NAP1L1	24.694	31.6	10	9	82.535	0	76320	58308	56481	85349	59942	73867	85917	103830	44541	81231	Enriched	Enriched	Enriched	Enriched	YES
F8W1A4;P54819-5	Adenylate kinase 2,	AK2	25.63	72.8	33	33	198.37	0	366700	251650	288080	408680	301160	392800	362380	535200	151420	513770	Enriched	Enriched	Enriched	Enriched	YES
F8W1I5;P14649	Myosin light chain 6	MYL6B	19.036	20.6	7	1	4.3812	0.00063	14247	11565	14639	16261	14559	19690	20469	20023	8995.4	21241	Enriched	Enriched	Enriched	Enriched	YES
F8W1R7;G3V1V0;	Myosin light polyper	PDE6H;MYL6	16.29	71	29	3	110.69	0	299870	268050	284610	329790	311890	261330	376550	432700	171240	330580	No expres	No expres	No expres	No expres	YES
F8W1U3		KRT8	32.548	60.6	89	10	162.75	0	99113	87301	89685	110480	88875	66587	109400	73539	137830	131080	Enriched	Enriched	Enriched	Enriched	YES
F8W642		CS	7.3535	75.8	12	7	13.221	0	15307	15783	23869	16042	24224	20616	34505	18734	31301	27192	Enriched	Enriched	Enriched	Enriched	YES
F8W6A4;Q9BQ90	Kelch domain-conta	KLHDC3	28.032	6	1	1	7.1769	0	5896.7	4748.7	7166.9	2947.7	7826.1	3961.7	7435.8	4267.3	4539	6530.7	Low	Enriched	Enriched	Low	
F8W6I7;P09651-2;	Heterogeneous nucle	HNRNPA1;HNRNPA1L	33.155	66.4	46	45	323.31	0	251820	189510	235670	246830	278800	324670	494080	427080	247620	314450	No expres	Enriched	Enriched	Enriched	YES
F8W6P5		HBB	9.67	86.7	42	2	11.594	0	17295	69212	9905.9	21186	11585	13718	28538	22419	22735	21715	Moderate	Moderate	Moderate	Moderate	YES
F8W717;O00423;C	Echinoderm microtu	EML1	88.716	14.8	11	11	18.723	0	2236.5	2078.6	1982.3	2917.1	3049.4	2945.2	3693.7	1908.8	1657.8	2518.9	Low	Moderate	Moderate	Low	YES
F8W733;Q9NXR7-	BRCA1-A complex s	BRE	31.972	15.1	4	4	7.4143	0	27287	20389	27202	25007	29443	19524	63182	28108	21053	24309	Enriched	Enriched	Enriched	Moderate	YES
F8W785;O00461	Golgi integral memb	GOLIM4	78.759	6.4	4	4	15.738	0	6217.9	7491.5	7630.5	8303.8	7738.2	3843.4	8438.3	8444.3	8814.7	9728.8	Moderate	Moderate	Enriched	No expres	YES
F8W7C6;A0A087WV22;X1WI28		RPL10	18.565	52.1	21	7	52.739	0	191400	158120	200860	191770	226510	370560	309070	280410	162980	256360	Enriched	Enriched	Enriched	Enriched	
F8W7Q4;Q96A26;	Protein FAM162A	FAM162A	16.515	31.2	8	8	16.335	0	56323	43975	65671	42353	80843	61577	52436	59299	35034	48039	Enriched	Enriched	Enriched	No expres	YES
F8W881;Q9NX05-	Constitutive coactiva	FAM120C	99.351	1.2	2	2	4.2422	0.00063	5292	4375.7	4203.6	7701.9	5184.1	5076.8	5402.3	3954.9	2077.2	4973.8	Moderate	Low	Low	No expres	YES
F8W8I6;P31483;C	Nucleolysin TIA-1 is	TIA1	42.835	16.4	9	3	7.4127	0	3620.3	3506.7	3237.5	3990.3	3596.7	3386.9	3324.5	3680.4	1830.3	2826.6	Enriched	Moderate	Enriched	Enriched	
F8W8V9;Q12756;	Kinesin-like protein	KIF1A;KIF1Bbeta;KIF1	165.98	2.9	4	2	10.495	0	28504	23524	24678	21786	28400	20305	23310	25153	12118	23697	Enriched	Low	Moderate	No expression	
J3KQ45;F8W8W7;	Trans-Golgi network	TGOLN2	47.879	20.5	9	9	106.93	0	36105	37321	34333	30591	56449	26324	38032	39930	24061	50461	Enriched	Enriched	Enriched	Enriched	YES
F8W8Z9;Q8N4H5;	Mitochondrial impor	TOMM5	10.976	13.3	1	1	2.1558	0.00611	3454.2	2819.3	4166.4	4126.3	2621.4	3785.8	4555.6	2916.6	4767.3	7722.6					
F8W914;Q9NQC3-	Reticulon;Reticulon-	RTN4	37.144	18.3	11	11	26.179	0	19835	20740	18452	18766	22431	16652	17909	17449	10957	19224	Enriched	Enriched	Enriched	Enriched	YES
F8W9E7;Q96BJ8-2	Engulfment and cell	ELMO3	85.332	4.4	3	3	6.5745	0	8380	5610.5	7141.2	11007	6851.8	10419	7679.1	10448	4748	8813.8	Moderate	Enriched	Enriched	No expres	YES
F8W9F8;Q9NQ94-	APOBEC1 complem	A1CF	65.97	12.8	8	6	14.227	0	9028.8	9081.8	8899.7	8811.5	9382.4	8107	9058	11277	6777.3	10213	Moderate	Enriched	Enriched	No expres	YES
F8W9F9;H0Y7T5;	Serine/threonine-pro	WNK2	234.38	7.5	14	14	63.456	0	74179	63895	67846	67805	76322	50814	64966	63006	43561	73295	Moderate	Enriched	Moderate	No expres	YES
F8W9P7;C9J8Q1;F	NFU1 iron-sulfur clu	NFU1	10.799	45.5	4	4	8.3796	0	17734	22536	18209	15823	23996	15526	16443	14504	9004.1	14501	Moderate	Moderate	Enriched	No expres	YES
F8W9S7;Q14C86-	GTPase-activating pr	GAPVD1	157.46	2	2	2	4.2723	0.00063	4975.4	2411.4	3727.6	7913.4	2973.2	5082.9	3077	4854.5	1680.8	5025.5	Enriched	Enriched	Enriched	Moderate	YES
F8W9X7;Q567U6	Coiled-coil domain-c	CCDC93	73.041	12.2	8	8	40.665	0	25488	16248	22108	33546	22690	47004	42631	44250	18518	36500	Moderate	Moderate	Enriched	Enriched	YES
F8W9Y0;Q13277-	Syntaxin-3	STX3	29.636	5	2	2	8.2652	0	9785	5275.1	6078.2	15503	5380.7	6695	2795.9	3977.7	2171.2	6852	Enriched	Enriched	Enriched	Enriched	YES
J3QRU4;F8WCA0;	Vesicle-associated m	VAMP2;VAMP3	12.251	43.4	10	4	39.856	0	31815	23495	27715	34373	29380	28304	132220	37539	45132	36187	Moderate	Enriched	Enriched	Enriched	YES
F8WCF6;P59998;P	Actin-related protein	ARPC4-TTLL3;ARPC4	21.058	38.1	9	9	16.295	0	20455	18579	22924	30720	31506	25813	46794	46677	23318	32227	Enriched	Enriched	Enriched	Moderate	YES
H0Y5I5;F8WCX2;	Zinc finger protein 6	ZNF687	75.56	2	1	1	8.1561	0	5236.7	4350.5	6034.1	4199.9	7249.7	4033.7	9102.2	8669.7	4690.6	5214.8	Low	Moderate	Moderate	No expres	YES
F8WCZ3;Q96NT0	Coiled-coil domain-c	CCDC115	21.09	16.6	4	4	8.9462	0	23697	16907	20182	18987	19087	24804	22229	18852	10713	23650	Enriched	Enriched	Enriched	No expres	YES
F8WDN7		SACM1L	33.081	32.4	10	2	2.4324	0.00412	10845	4968.2	6495.2	18638	6951.2	14443	9349.5	15474	4788.5	15842	Moderate	Enriched	Enriched	Enriched	YES
F8WE88;Q9Y4I1-2	Unconventional myo	MYO5A	215.36	7.3	13	8	26.391	0	37035	31149	31588	33379	28611	28843	36324	29352	35274	38380	Low	Moderate	Enriched	Low	YES
F8WEL9;Q49B96	Cytochrome c oxidas	COX19	13.798	9.8	1	1	20.467	0	2839.1	4086.1	3631.8	2903.9	3884.3	2798.3	3553.5	4045.6	2668.5	3318.1	Enriched	Enriched	Moderate	No expression	
F8WF65		EEF1B2	3.1045	75.9	8	1	2.6279	0.00273	20890	23565	14735	18687	16060	16720	20806	18766	12488	17255	Enriched	Enriched	Enriched	Enriched	YES
F8WF69;P09496-2	Clathrin light chain	CLTA	27.818	13.5	4	4	5.0804	0.00044	4437.8	4411.2	5190.7	4198.9	5621.4	9303.8	41550	18433	40773	18089	Enriched	Enriched	Enriched	Enriched	YES
F8WJN3;Q16630-3	Cleavage and polyad	CPSF6	52.269	31.2	20	19	145.87	0	63916	48603	58677	71637	63632	72032	74643	77312	43265	71221	Moderate	Moderate	Enriched	Low	YES
G0XQ39;Q13586;E	Stromal interaction m	STIM1	88.645	19.1	15	15	53.187	0	43988	42211	42711	35638	61106	44431	55840	39400	26014	40252	Moderate	Moderate	Moderate	Moderate	YES
G3V0E4;O75439	Mitochondrial-proce	PMPCB	54.191	13.1	8	8	163.23	0	38574	18922	27738	57911	25890	40045	42833	60485	23465	49090	Enriched	Enriched	Enriched	Moderate	YES
G3V126;Q9UI12-2	V-type proton ATPas	ATP6V1H	51.57	11.7	10	10	35.407	0	36234	26330	30009	35604	34881	35443	41158	36051	22841	37059	No expres	Enriched	Enriched	Enriched	YES
G3V160;Q969H4-2	Connector enhancer	CNKSR1	50.189	2	1	1	2.7096	0.00238	1375.2	2111.5	1618.6	1244.3	2523.2	1818.4	6422.5	3830.3	7373.4	3734.7	Enriched	Moderate	Moderate	Enriched	YES
G3V1D4;Q9NUP9	Protein lin-7 homolo	LIN7C	19.186	44.5	13	13	34.218	0	96297	76006	129680	78014	130910	75633	95585	44759	46725	72906	Moderate	Enriched	Enriched	No expres	YES
G3V1L9;Q07157;A	Tight junction protei	TJP1	197.46	21.8	42	40	252.38	0	187290	129500	147810	155790	174300	136080	181280	203370	106750	204690	Enriched	Enriched	Enriched	Moderate	YES
G3V1P3;Q969J3	Loss of heterozygosi	LOH12CR1	20.247	16.9	3	3	4.4695	0.00042	9063.1	5802.6	7094.1	7032.7	8054.9	6656.9	5854.6	4982.6	4609.1	6334.3	No expres	Moderate	Moderate	No expression	
H7C308;G3V1P5;C	Mediator of RNA pol	MED15	22.035	8.8	2	2	31.81	0	2393.7	2158.9	2833.6	1751.8	3998.3	1181.8	3286.6	2479.7	1579.4	2550	Enriched	Moderate	Enriched	No expression	

G3V1U5;Q9Y3E0;	Vesicle transport pro	GOLT1B	8.2139	35.1	8	8	19.507	0	26102	23159	29559	32455	29225	14573	17671	19742	12711	24504	Enriched	Enriched	Enriched	No expression		
G3V234		RDH11	20.592	17.1	4	1	2.096	0.00674	3793	2866.1	3586	2497.9	4048.6	1568.1	2520.1	3252.4	1380	2634	Enriched	Enriched	Enriched	Enriched	YES	
G3V2D5;G3V2P5;	Zinc finger protein 3	ZFP36L1	19.527	30.7	5	5	9.4309	0	2863.6	2175.5	2551.6	2346.5	3615.4	1868.1	5213.4	2671	5316.3	3262	Enriched	Enriched	Enriched	Enriched	YES	
Q6V3B1;G3V563;	Protein max	MAX	11.026	10.6	1	1	2.7988	0.00222	3862.7	2941.8	3818.5	3388.7	4616.2	2968.1	4807.4	5169.2	2985.9	5310.9	Enriched	Enriched	Enriched	Moderate	YES	
G3V2S6;Q9Y5K8;	V-type proton ATPas	ATP6V1D	21.921	32.8	5	5	19.478	0	9151.8	7861.8	8837.8	8678.7	12754	10887	24642	23375	7595.7	13069	Enriched	Enriched	Enriched	Enriched	YES	
H0YJN9;G3V2T4;	Legumain	LGMN	9.658	12.1	2	2	5.9819	0	3573.4	5993.3	4903.8	5182.8	6903.9	1913.3	3787.4	11932	4882.5	4433.8	Moderate	Moderate	Enriched	Low	YES	
G3V2U4;Q9P2D8-	Protein unc-79 homo	UNC79	290.78	0.7	2	2	1.9257	0.00815	16666	25404	34236	11926	29949	4900.9	11089	6427.3	1569.5	10218						YES
G3V2U7;P07311	Acylphosphatase;Acy	FBN3;ACYP1	14.125	27.9	3	3	14.536	0	3195.1	3375.5	4321.5	3215.3	3956	2649.3	4109.4	2683.6	2767.5	2982.8	Low	Low	No expres	No expres	YES	
G3V325;C9JJT5;C	ATP synthase subuni	ATP5J2-PTCD1;ATP5J2	84.109	4.1	7	7	12.632	0	27900	14707	22225	37915	23831	26952	23178	27015	13317	28696	Enriched	Enriched	Enriched	Enriched	YES	
G3V387		SERPINA1	12.722	32.5	7	3	5.5365	0	3165.2	2581.5	2374.7	6137.8	3742	3730.4	4892.4	6499.9	2372.2	3961.2	Enriched	Enriched	Enriched	Low	YES	
G3V3G9;V9GY54;	DDB1- and CUL4-as	DCAF8	84.752	6.8	4	3	25.818	0	22293	15072	15960	23716	20801	11072	14466	17091	14995	20950					YES	
G3V3K6		HNRNPC	13.337	66.9	18	2	30.131	0	4645.6	3643.1	3908.1	10430	4642.1	13462	28798	10528	31654	21853	Enriched	Enriched	Enriched	Enriched	YES	
G3V511;G3V3X5;	Latent-transforming	LTBP2	189.24	1.4	3	3	17.585	0	9446.3	11014	11010	6469	17914	7912.1	16578	36952	6208.7	15274	Enriched	Moderate	Enriched	Moderate	YES	
G3V4C1;P07910-2	Heterogeneous nucle	HNRNPC	32.238	50	28	12	181.77	0	287560	186510	216990	259860	214810	259540	225660	354720	114080	289130	Enriched	Enriched	Enriched	Enriched	YES	
G3V4F2;Q86TX2;	Acyl-coenzyme A thi	ACOT1;ACOT2	43.733	34.4	15	15	149.3	0	76133	63962	73703	75230	80720	70332	83049	75419	46892	98753	Low	Moderate	Enriched	Enriched	YES	
G3V4K3;Q9H9C1-	Spermatogenesis-defe	VIPAS39	59.718	9.6	4	4	10.904	0	12703	11213	12892	12463	13935	11488	11087	17982	7085	13391					YES	
G3V4P8;P60983	Glia maturation facto	GMFB	17.512	28.7	8	7	238.02	0	29869	20107	20088	37112	24220	38252	36728	89362	20291	57006	Enriched	Enriched	Enriched	Enriched	YES	
G3V4T6;O43708-2	Maleylacetoacetate is	GSTZ1	24.232	16.6	3	3	4.2594	0.00063	7987.5	5467.5	5931.3	6104.2	7071	5221.5	3786	3849.5	2663.4	6518.9	Low	Moderate	Moderate	Moderate	YES	
G3V4U0;Q9UBX5;	Fibulin-5	FBLN5	50.881	17.4	8	8	22.523	0	13619	18796	21679	8898.1	27886	12531	26601	62560	17305	20013	No expres	Enriched	Moderate	Moderate	YES	
G3V4V8		NSFL1C	4.0004	28.6	2	2	2.1976	0.00544	6998.1	9171.1	9360	7222.1	9800.5	6845.4	6470.3	7354.1	2926	6572.7	Enriched	Enriched	Enriched	Moderate	YES	
G3V529;Q9GZR7;	ATP-dependent RNA	DDX24	91.48	10.4	8	8	26.251	0	16949	15122	20748	17609	22087	13437	19416	16434	9836.9	16477	Enriched	Enriched	Enriched	No expres	YES	
G3V583;Q8N128;C	Protein FAM177A1	FAM177A1	16.322	27.9	4	3	5.861	0	16037	14448	18123	13997	17554	13806	17506	16331	14260	13342	Moderate	Enriched	Enriched	No expres	YES	
G3V5D7;G3V239;G3V420;G3V2S0;G3V		NDRG2	12.145	48.1	5	2	19.255	0	7704.9	7386.3	7209	7144.6	10066	6612.1	6407.6	6324.2	4697.5	5780.7	Enriched	Enriched	Enriched	Low	YES	
G3V5V3;O60524-4	Nuclear export media	NEMF	114.02	7.3	7	7	14.854	0	9179.5	9369.2	6575	15304	7062.1	12322	7444.1	10261	4852.5	9823.3					YES	
G3V5Z3;Q6IN85-2	Serine/threonine-prot	SMEK1	82.03	7.4	5	2	6.4072	0	4265.3	3522.3	4849.8	4886.9	6083.3	3919.8	3903.4	4703.5	2755.8	4349.6	Moderate	Enriched	Enriched	No expres	YES	
G3V5Z7;P60900;P	Proteasome subunit a	PSMA6	28.147	52.4	22	22	45.086	0	75668	45195	52574	67659	66661	79997	83318	83535	37300	80070	Enriched	Enriched	Enriched	Enriched	YES	
G3XA86;Q9Y2Z9-	Ubiquinone biosynth	COQ6	50.705	11.1	7	7	11.809	0	24835	20990	22533	20318	25710	24231	24334	22045	15512	24805	Enriched	Enriched	Moderate	No expres	YES	
G3XAG1;Q96ME7	Zinc finger protein 51	ZNF512	64.594	12.5	7	7	21.754	0	26625	27221	34184	23938	36589	22534	41985	43034	21810	35061	Moderate	Enriched	Enriched	No expres	YES	
G3XAH6;P51003;	Poly(A) polymerase	PAPOLA;PAPOLB	80.625	7	6	6	10.831	0	34083	20104	25095	34338	29267	41535	28669	25894	16215	29139	Enriched	Enriched	Enriched	Moderate		
G3XAI2;P07942	Laminin subunit beta	LAMB1	200.48	38.1	124	120	323.31	0	555270	437470	507670	609110	572910	693090	880810	931110	407930	724970	No expres	Enriched	Enriched	Moderate	YES	
G3XAJ6;Q14699;C	Raftlin	RFTN1	58.762	7.2	3	3	28.875	0	3695.6	4394.5	5080.1	2485.4	4839.6	5137.7	5260.5	7084.3	3774.8	7396.5	Moderate	Moderate	Enriched	No expres	YES	
G3XAL9;P55011-3	Solute carrier family	SLC12A2	124.59	4.5	3	3	16.117	0	15461	15406	13333	12028	18694	14730	18794	15597	11271	14773	Moderate	Moderate	Enriched	No expres	YES	
G3XAN4;Q15629-	Translocating chain-a	TRAM1	33.435	15.3	11	11	246.59	0	87397	77770	74773	76862	108730	61866	77457	60781	47157	69995	Enriched	Enriched	Enriched	Enriched	YES	
G3XAP0;Q86U06-	Probable RNA-bindi	RBM23	28.636	9.3	2	1	2.1149	0.00643	2249.7	2043.8	2227.1	3156.6	2194.8	1831.9	1286.3	2593.3	737.73	2943.1	Moderate	Enriched	Enriched	No expression		
G5E933;O95248;O	Myotubularin-related	SBF1	208.44	2.9	6	6	11.754	0	8366.3	5311.7	7382	9748.6	8473.6	8579.2	8434.2	7931.3	5076.5	8557.7	Low	Moderate	Moderate	No expres	YES	
G5E975;Q12824-2;	SWI/SNF-related ma	SMARCB1	45.05	13.2	5	5	30.64	0	36326	24045	25507	17974	25376	28210	29355	20513	16989	33093	Enriched	Enriched	Enriched	Enriched	YES	
G5E994;Q5VW38-	Protein GPR107	GPR107	63.984	3.3	2	2	4.3468	0.00063	4575.3	3187.8	3157.8	4034.1	5751.3	2207.4	3330.3	2008	1376	3237.2	Enriched	Moderate	Enriched	Enriched	YES	
I3L4X3;G5E9C2;Q	NF-kappa-B inhibito	NFKBIB	25.176	9	2	2	3.7385	0.0006	2530.6	2411.2	3064.5	2440.1	3427.9	3018.4	6479.2	3550.7	5577.1	4098.3	Enriched	Moderate	Moderate	Low	YES	
G5E9C5;O76074-2	cGMP-specific 3,5-cy	PDE5A	93.629	13.1	9	9	51.791	0	22485	19435	19990	41446	16840	24489	36659	34699	26912	32859	No expres	Moderate	Moderate	No expres	YES	
G5E9C8;Q07889;C	Son of sevenless hom	SOS1;SOS2	150.86	2.4	3	3	4.8577	0.00043	7389.6	9629.8	10401	6496.6	9877.1	4844.5	10960	10571	4891.8	9888.8	Enriched	Enriched	Enriched	Moderate		
G5E9D5;Q9BQ52-	Zinc phosphodiestera	ELAC2	90.036	2.7	2	2	3.6518	0.0008	6839.6	5428.3	5406.5	7799.5	6374.1	5799.7	3729.7	5280.8	2060.2	5533	Low	Moderate	Moderate	Enriched	YES	
G5E9L0;Q8N6H7;I	ADP-ribosylation fac	ARFGAP2	53.476	25.2	12	10	90.275	0	66097	42079	51046	69639	53275	79701	53730	98615	29989	71731	Moderate	Enriched	Enriched	Enriched	YES	
G5E9Q6;P35080-2	Profilin;Profilin-2	PFN2	20.787	38.8	13	3	24.241	0	32785	33606	37335	36054	46524	31643	29972	22887	19484	27790	Enriched	Enriched	Enriched	Enriched	YES	
G5E9S7		ARPC2	4.1457	86.8	5	2	20.906	0	23091	36583	30643	13479	37028	9298.3	13079	12745	5347.9	12557	Enriched	Enriched	Enriched	Enriched	YES	
G5E9T8;O95249;K	Golgi SNAP receptor	GOSR1	28.972	19.6	7	7	16.619	0	16508	15028	16348	12319	22932	18698	28204	28115	16412	21593	Enriched	Enriched	Enriched	Enriched	YES	
G5E9W7;G5E9V5;	28S ribosomal protei	MRPS22	36.805	19.1	8	8	11.961	0	11230	11396	12988	9551.7	9923.7	5222.5	9380	7695.3	5425.7	12869	Enriched	Enriched	Enriched	Moderate	YES	
G5E9W3;Q9UKF6	Cleavage and polyad	CPSF3	73.476	5.1	4	4	16.165	0	6886.8	4084	6374	7107.1	6584.6	14302	11050	6612.7	5026.4	7778.1	Moderate	Enriched	Enriched	No expres	YES	
G5E9W9;Q9NUV9	GTPase IMAP family	GIMAP4	39.033	15.5	6	5	28.495	0	12613	11500	13216	13161	17474	12842	19957	31283	16112	18998	No expres	Low	Low	No expres	YES	
G5EA09;O00560-2	Syntenin-1	SDCBP	34.819	20.1	6	6	7.1662	0	21561	16339	18629	23807	20756	20597	34995	34795	17383	33287	Enriched	Enriched	Enriched	Enriched	YES	
G5EA31;P53992	Protein transport pro	SEC24C	111.98	20.5	33	31	236.07	0	122230	97140	109590	102910	126440	111780	118710	138340	66045	111200	Moderate	Enriched	Enriched	Moderate	YES	
G5EA36;P30260;P	Cell division cycle pr	CDC27	91.737	5.5	4	4	10.148	0	11232	10076	10675	15467	10739	16236	31768	46387	11386	22086	Moderate	Moderate	Enriched	Moderate	YES	
G8JLB3;Q9Y606-2	tRNA pseudouridine	PUS1	42.92	15.1	5	5	8.3829	0	12137	12517	15134	11114	19286	7686.6	13684	13217	8878.9	15684	Enriched	Moderate	Moderate	No expres	YES	
G8JLB6;P31943;E	Heterogeneous nucle	HNRNPH1	51.229	38.3	35	1	323.31	0	141300	93598	112840	142820	147260	141330	240780	279530	123930	193680	Enriched	Enriched	Enriched	Enriched	YES	
G8JLD5;O00429-4	Dynamin-1-like prote	DNM1L	79.621	30.5	26	1	137.93	0	86260	84217	105630	107180	116020	79652	89194	96878	62255	92255	Enriched	Enriched	Enriched	Low	YES	
H0UI06;P14406;D	Cytochrome c oxidas	COX7A2	12.844	31.3	6	6	15.764	0	37734	24882	29803	44744	40561	40257	44802	41234	21147	41847	Enriched	Enriched	Enriched	Enriched	YES	
X6RLT1;H0UI80;C	Negative elongation f	NELFCD;TH1L	66.432	6.7	5	5	58.41	0	6999.7	2332.8	1815.3	6326.9	1582.1	8234.3	3312.3	8130.7	1184.3	11362	Moderate	Enriched	Enriched	No expres	YES	
H0Y2Q1;Q96FX7	tRNA (adenine(58)-N	TRMT61A	20.421	7.3	2	2	10.661	0	9480.7	7849.2	6419.9	10282	8866.7	10347	6831.1	9134.1	4098.1	10222	Enriched	Moderate	Moderate	No expres	YES	
H0Y2Y8;Q15942;C	Zyxin	ZYX	57.643	19.8	11	10	47.015	0	24303	24248	25585	21777	32889	21456	37066	35348	35442	32946	Enriched	Enriched	Enriched	Low	YES	
Q5QPK2;H0Y368;	Dolichol-phosphate	DPM1	32.426	42.2	21	21	140.45	0	98439	61081	76569	80187	82497	143140	113170	101160	56056	93473	Moderate	Enriched	Enriched	Moderate	YES	
H0Y3A3;Q5VWQ8	Disabled homolog 2-	DAB2IP	118.06	1.7	2	2	2.1804	0.0056	5612.1	5221.4	6342.7	8351.6	6372.2	5245.9	4690.1	5073	2495.1	4709.1	Enriched	Enriched	Enriched	No expres	YES	
H0Y3K4;Q96EV2	RNA-binding protein	RBM33	100.24	3	2	2	10.951	0	17822	16476	18558	14195	22494	10264	10931	8338	8449.4	14434	Moderate	Enriched	Enriched	No expres	YES	
H0Y589;H0Y3N9;	Histone lysine demet	PHF8	72.831	3	2	2	2.3777	0.00429	12063	66038	9685.3	9963.2	18843	4243.4	5941.8	2450.9	2841.7	7306.3	Moderate	Low	Moderate	Moderate	YES	
H0Y3V5;Q6YHU6-	Thyroid adenoma-ass	THADA	133.85	1.3	1	1	3.5402	0.00079	2747.9	1093.8	1385.2	3135.7	1646.3	4575.6	3590.3	3618.4	1459.8	3539.9	Enriched	Enriched	Enriched	No expres	YES	
H0Y400		DDX39B	21.679	47.6	25	2	13.92	0	15377	8842.2	10184	7441.3	12443	4716.7	47105	19699	15683	14824					YES	
J3KRT8;J3QQN8;J	Neurofibromin;Neur	NF1	23.54	10.2	1	1	41.954	0	2984.5	925.06	1379.1	5466.8	694.54	2160.8	1324.5	2668.3	750.09	3011.8	Moderate	Moderate	Enriched	Low	YES	
H0Y494;J3KPC8;H	Serine/threonine-prot	SIK3	138.58	1.2	1	1	2.1432	0.0061	11598	5263.6	6612.7	4023.5	13317	15386	7450.3	5527.8	3095.2	6421.9					YES	
H0Y4J5		PDIA2	25.03	61.7	44	7	119.98	0	15748	13458	34939	14196	25246	23120	20062	10002	7144.4	11983	Low	Enriched	Enriched	Enriched	YES	
H0Y4R1;P12268	Inosine-5-monophos	IMPDH2	50.957	47.4	34	21	245.88	0	240790	187190	176650	194050	238770	279390	242100	271540	115240	229610	Moderate	Enriched	Enriched	Enriched	YES	
H0Y517;H7C1U3;	Coiled-coil and C2 d	CC2D1B	69.548	10.7	6	6	11.159	0	27489	17418	20947	20990	23567	23811	23875	28676	14798	30978	Moderate	Moderate	Enriched	No expres	YES	
H0Y7H7;H0Y599;	Dedicator of cytokine	DOCK4	158.93	2.7	3	3	10.57	0	9552.2	11466	7957.6	12032	12530	12994	16520	25999	7949.3	18416	Moderate	Low	Moderate	Enriched	YES	
H0Y5B4;H7BZ11;J	60S ribosomal protei	RPL36A;RPL36A-HNR	13.228	35.7	8	8	14.129	0	66022	43626	65162	47689	72148	88794	179540	106260	61967	83141	Enriched	Enriched	Enriched	Enriched		
H0Y614;P61960	Ubiquitin-fold modifi	UFM1	8.5507	29.6	9	9	34.204	0	35269	29425	25956	28250	37077	28305	51315	53356	16185	28814	Enriched	Enriched	Enriched	No expres	YES	
H0Y621;H0Y5K5;	Endoplasmic reticulu	ERGIC3	36.851	11.7	4	4	5.8786	0	6498.9	6991.4	4572.7	6775.2	7583.4	3155.3	2646.2	2505.7	1758.7	3251.2	Enriched	Enriched	Enriched	No expres	YES	
H0YE12;H0Y679;	Proline-rich protein	PRCC	22.543	4.5	1	1	2.1179	0.00626	8676	7268.4	11384	13354	11945	11100	15573	9791.6	10463	13788	No expres	Low	Moderate	Low	YES	
H0Y695;P48728-4;	Aminomethyltransfer	AMT	41.364	16.4	8	2	18.027	0	52531	37860	30357	45403	49247	34338	43753	56436	23373	54526	Enriched	Enriched	Enriched	Enriched	YES	
H0Y6D8;Q32MN6;	TATA-box-binding p	TBP	11.502	12.9	1	1	6.1376	0	5477.8	5156.4	5010.4	7721.3	4155.9	5606.5	2890.8	5134.5	1775.2	6698.3	Enriched	Moderate	Moderate	Moderate		
H0Y6I0;Q13439-3;	Golgin subfamily A n	GOLGA4	246.6	12.6	28	27	111.96	0	119030	97772	102090	106620	142330	105640	121490	108180	78382	115670	Moderate	Enriched	Enriched	Moderate	YES	
H0Y6K2;P25440-4	Bromodomain-contai	BRD2	88.288	3.3	2	2	4.2264	0.00063	8599.3	5839.5	7762.4	8549.5	6964.7	6127.4	9910.1	8654.4	5218.5	8770	Enriched	Enriched	Enriched	Enriched	YES	
H0Y6K5;H0Y7L6;	Transcription factor	SP3	75.311	3.5	3	3	50.553	0	9018.2	5760.8	7277.2	8257.9	10557	7813.1	8102.3	5702.3	5217	10163	Moderate	Moderate	Enriched	Low		
H0Y6T7;Q92542-2	Nicastrin	NCSTN	30.045	9.1	3	3	8.7623	0	4744.1	4676.5	4803.6	2672.8	6973.3	3227.9	4592.8	2426.5	3733.9	4253.3	Moderate	Enriched	Enriched	Enriched	YES	
R4GMW6;H0Y6Z9	COMM domain-cont	COMMD3-BMI1;COMM	18.133	9.4	1	1	18.926	0	20948	8254.3	15040	25536	17487	11422	3796	5389.5	2282.6	13695	Enriched	Enriched	Enriched	No expres	YES	
H0Y8D0;H0Y870;	Transmembrane prot	TMEM222	8.8913	23.8	1	1	3.7607	0.0006	15325	6274.2	7272.2	11707	9210.4	11048	6671.9	8108.3	3877.5	11383	Enriched	Enriched	Enriched	No expression		
H0Y8C3;Q9NZJ7-	Mitochondrial carrier	MTCH1	43.121	11.4	4	4	3.6609	0.0008	3918.1	1922	2314.3	3948.4	1830.4	3778.2	2694.4	3710.3	2411.7	5081.4	Enriched	Enriched	Enriched	No expres	YES	
H0Y8D1		PRSS1	15.421	69	46	6	31.769	0	27461	18429	25402	14645	39135	27395	46937	23797	36351	19316	Moderate	Enriched	Enriched	No expression		
H0Y8G2		COPG1	8.3562	63.2	5	2	40.002	0	11594	12672	10292	6981.3	22983	1917.4	4028.1	3080.8	2172.7	5524.7					YES	
H0Y8N7;Q9BYD6	39S ribosomal protei	MRPL1	26.614	9.5	3	3	8.253	0	6135.2	5576.7	5644	4408	7542.6	9019.1	14512	19256	4030.3	7920.5	Low	Enriched	Enriched	No expres	YES	
H0Y8P4;Q8TED0-	U3 small nucleolar R	UTP15	61.32	6.4	3	3	15.969	0	14014	11040	13485	12330	14723	12997	11676	13159	7812.9	14057	No expres	Low	Moderate	No expres	YES	
H0Y8Q7;H0YA20;	Diacylglycerol kinase	DGKQ	16.964	7.6	1	1	2.9666	0.00169	3570.9	3262.7	4062.5	3040.4	4884.5	4089.2	5402.1	3709.7	6119.9	6122.8	No expres	No expres	Moderate	No expression		
H0Y8W2;H0YAM7;H0YAF8		GNB2L1	30.152	57.3	43	0	11.253	0	27930	14539	18879	18617	21996	15753	20469	16744	18585	19204	Enriched	Enriched	Enriched	Enriched	YES	
H0Y8X4;O43598;C	2-deoxynucleoside 5-	DNPH1	25.868	29.2	17	17	41.852	0	108800	78585	90461	123290	106310	82064	81772	100350	50752	95401					YES	
H0Y9Q7		CANX	18.719	62.9	27	1	9.1938	0	10707	6978.3	9211.9	13392	10643	11047	46866	16515	20768	30982	No expres	Enriched	Enriched	Enriched	YES	
H0Y9Y1		BTF3	9.3894	67.4	10	2	43.761	0	39178	48127	58368	24460	68335	24210	42275	25676	31157	25117	Enriched	Enriched	Enriched	Enriched	YES	
H0Y9Y3;Q9UMS6;	Synaptopodin-2	SYNPO2	125.25	5.7	8	8	12.698	0	23581	26256	24982	17492	34644	21233	57794	55167	27760	40111	Enriched	Enriched	Moderate	No expres	YES	
H0Y9Z3;Q9HAD4-	WD repeat-containin	WDR41	18.462	14.7	2	2	9.6657	0	5479.1	3895.9	4889.4	7663.1	4845.5	5301.1	6249.4	8016.9	4951	6561.1	Moderate	Enriched	Enriched	No expression		
H0YA44		PAIP1	5.6249	20.4	1	1	2.6063	0.00273	6444.5	6440.2	8554.9	2399.4	8228.1	8363	13824	9596.6	13135	10264	Moderate	Enriched	Enriched	Enriched	YES	
H0YAK9;Q6UXI9;	Nephronectin	NPNT	49.791	27.4	13	3	79.61	0	40956	68344	46226	29283	58684	45703	73505	89539	30097	66353	Enriched	Enriched	Enriched	No expres	YES	
H0YAV1;Q7LG56;	Ribonucleoside-diph	RRM2B	46.966	12	5	5	10.423	0	18278	9464.3	13432	22368	12022	16330	19540	25766	11253	18733	Low	Enriched	Enriched	No expres	YES	
H0YAW6		PABPC1	20.698	12.3	3	2	5.1434	0.00044	2279	3430.2	4045.4	1400.4	9204.2	1389.4	2607.5	1553.3	1172	1574.2	Enriched	Enriched	Enriched	Enriched	YES	
H0YBI6;H0YBQ0;	Thioredoxin reductas	TXNRD3	66.536	1.8	1	1	2.9774	0.00169	5404.6	3891.2	4031.2	4987.8	4731.5	4776.3	3746.8	3442	2331.8	3657.8	Low	Low	Moderate	No expres	YES	
H0YBN4		PABPC1	19.655	56.6	20	1	14.479	0	4491.4	2654.1	3611.1	3120.5	3815.5	9102.7	15095	46826	9939.7	14219	Enriched	Enriched	Enriched	Enriched	YES	
H0YBV6;Q9BXY0	Protein MAK16 hom	MAK16	16.552	22.6	3	3	60.052	0	32353	19324	20536	26899	21763	27679	27313	33096	13646	31307	Enriched	Enriched	Enriched	Moderate	YES	
H0YC35	Clusterin	CLU	33.419	49.3	23	1	2.4926	0.00378	11490	10583	11245	12612	11996	8927	8954.3	8456.9	9891.9	9201.5	Enriched	Enriched	Enriched	Enriched	YES	
H0YCE7;O43427-	Acidic fibroblast gro	FIBP	15.538	6.6	1	1	1.9588	0.00801	7054.1	5354.2	5365.3	5591.6	4367.2	4856.1	3912	5642.5	2084.7	4422.8	Enriched	Enriched	Enriched	Enriched	YES	
H0YD13;P16070-1	CD44 antigen	CD44	22.683	33.5	9	9	41.077	0	31275	26505	29136	34711	32665	39524	37709	61428	17612	46694	Enriched	Enriched	Enriched	Moderate	YES	
H0YF19;H0YD68;	Outer dense fiber pro	ODF2L	17.984	7.8	1	1	2.3086	0.00479	10309	5505.4	6265	9076	8111.7	20051	7116.9	5891.1	5115.5	8284.8	No expres	No expres	Moderate	No expression		
H0YDA6;H0YF31		NAPRT	13.697	10.2	2	2	10.934	0	3922.2	5431.1	6940.8	2971.4	10233	2796	10332	3534.4	6169.7	7358.2					YES	
H0YDD3;Q9BVK2	Probable dolichyl py	ALG8	25.483	13.7	3	3	2.8522	0.00186	1958.7	1159.7	1546.9	2299.8	1796.1	1471.7	1316.9	1991.5	1538.9	1874.2	Enriched	Enriched	Enriched	Enriched		
H0YDU8;P53041;	Serine/threonine-prot	PPP5C	55.096	22.5	11	11	46.322	0	32786	23880	26754	20914	41086	25218	44854	25915	22601	29018	Moderate	Low	Moderate	Low	YES	
H0YE57;Q9UBM7	7-dehydrocholesterol	DHCR7	25.479	5.4	1	1	4.774	0.00043	4401.6	2881.7	2923.3	3569.8	4400	3549.9	3144.6	3222.6	1167.9	2758.2	Enriched	Moderate	Enriched	Enriched		
H0YE58		EEF1D	13.387	68.1	19	1	27.584	0	23313	4729.7	5635.8	11770	9036.9	12417	5292.6	15038	2078.9	9168.8	Enriched	Enriched	Enriched	Enriched	YES	
H0YFT4		SYNE1	7.0438	17.7	1	1	2.2233	0.00545	1855.4	4705	2568.4	8121.4	2434.1	3298.8	6447.4	35162	2134.5	4492	No expres	Moderate	Moderate	Enriched	YES	
H0YG47;Q96PU8;	Protein quaking	QKI	25.789	21	5	5	15.334	0	19928	17938	22518	14079	25810	18848	26241	25264	17883	23391	Enriched	Enriched	Enriched	Low	YES	
H0YG79;Q9H6F5	Coiled-coil domain-c	CCDC86	9.1349	12.5	1	1	2.5856	0.00309	7474.9	5897.7	7796.5	5917.7	11946	6067.7	8661.1	6799.9	3582.1	9152.6	Enriched	Enriched	Enriched	No expres	YES	
H0YH86		APPL2	21.16	6.9	1	1	2.6445	0.00273	8638.5	5405.5	6603.4	7553.1	6969.9	6783	6344.6	7725	4241.4	7180.3	Enriched	Enriched	Enriched	No expres	YES	
H0YHA7;J3QQ67;	60S ribosomal protei	RPL18	18.863	49.7	19	19	90.4	0	168530	89076	111020	135680	149200	125280	144060	115100	73470	109110	No expres	Enriched	Enriched	Enriched	YES	
H0YHG0;P82979;	SAP domain-containi	SARNP	59.075	12.8	8	8	55.242	0	46320	35227	36787	41962	62673	42467	56187	88009	27577	46650	Low	Enriched	Enriched	No expres	YES	
H0YHG9		KIF21A	15.319	9.4	2	2	5.7656	0	4241.3	2985.6	3238.9	8100.8	3241.6	7896.5	8339.3	11006	3363.5	6470.3	Low	Enriched	Enriched	No expres	YES	
H0YHL1		DCTN2	14.207	46.1	8	1	2.8717	0.00186	16190	17795	20486	9303.9	17150	19288	19574	18495	6988.2	18431	Enriched	Enriched	Enriched	Enriched	YES	
H0YHM7		FKBP11	6.7608	44.4	9	3	7.1479	0	11395	6528.4	16538	5438.7	10175	8335.9	6715.2	5149.9	2912.1	7542.4	Enriched	Enriched	Enriched	No expres	YES	YES
H0YI09;Q9H8H3;	Methyltransferase-lik	METTL7A	28.188	29.5	20	20	145.17	0	311360	317210	265790	142090	224210	198490	295500	242060	188110	185000	Enriched	Enriched	Enriched	Enriched	YES	
H0YJ02;H0YJH0;C	Protein salvador hom	SAV1	8.0375	29.9	2	2	4.7776	0.00043	2545.3	1039.1	971.63	1329.7	1867.2	825.78	1105.4	886.63	709.08	1162.7	Low	Moderate	Enriched	No expression		
H0YJ34;Q96AC1;C	Fermitin family homo	FERMT2	73.352	28.6	31	27	111.86	0	113880	85237	114890	103490	114230	154350	146620	118660	69527	134940	Low	Enriched	Enriched	Enriched	YES	
Q96B13;H0YJ75;Q	Serine/threonine-prot	PPP2R5C	44.878	16.4	8	3	23.386	0	35269	24293	27654	46326	28441	34748	26371	43957	13292	38005	Enriched	Enriched	Enriched	Enriched		
H0YJA2;Q6PJT7-5	Zinc finger CCCH do	ZC3H14	73.206	14.6	9	9	48.937	0	9981	9555.9	10800	6374.7	9939.7	6865.9	10311	8337	5865.8	10803	Moderate	Enriched	Enriched	Moderate	YES	
H0YJE4		DHRS7	17.851	26.9	6	3	5.9986	0	14250	9381.4	9415.6	13095	12065	9919.3	8732.1	9404.6	5574.5	10977	Enriched	Enriched	Enriched	Enriched	YES	
H0YJG0		CKB	20.147	55.9	20	5	15.627	0	71877	89641	98886	50812	100740	87719	85729	55067	52801	69294	Enriched	Enriched	Enriched	Enriched	YES	
H0YJG4;Q9HCK8-	Chromodomain-helic	CHD8;CHD6;CHD7	101.62	3.7	3	2	7.0437	0	10536	7122.7	10760	12790	8416.5	30955	13707	13562	8394.2	13752	Moderate	Enriched	Enriched	Moderate		
H0YJV7;P25490	Transcriptional repre	YY1	20.732	23.7	4	3	47.122	0	55973	23607	45695	25569	39556	21226	25411	25774	20893	35272	No expres	Enriched	Enriched	Enriched	YES	
H0YJY4;Q8N806;	Putative E3 ubiquitin	UBR7	14.322	20.2	3	3	12.336	0	9856.1	6135.8	7616.6	19638	6250.9	9327.8	10289	12759	9024.3	12763	Moderate	Enriched	Enriched	No expres	YES	
H0YJZ8		KTN1	17.309	50.3	15	1	4.9507	0.00044	14406	12066	21754	4329.2	36280	7825.3	12059	2820.3	3375.4	6207.4	Enriched	Enriched	Enriched	Enriched	YES	
H0YK10		GALK2	22.669	4.3	2	2	2.5248	0.00379	6797.3	5620.3	5737.4	6375.2	7501	4989.1	5832.7	4381.6	2521.8	6099	Moderate	Moderate	Moderate	Low	YES	
H0YK61;Q5J8M3;	ER membrane protei	EMC4	8.3403	61.5	5	5	15.282	0	14995	10995	14641	12695	12453	22789	22599	17780	7044.8	17782					YES	
H0YN04;H0YKC9;	Ceramide synthase 4	CERS4	35.73	11.4	5	5	9.9961	0	26272	21037	22441	42197	46106	15153	15920	11800	8727.6	19553					YES	
J3KPH4;H0YKD5		SNX1	10.464	12.7	1	1	8.9495	0	1976	1649.4	1896.5	1561.6	2756.2	1420.6	1882.6	1616.5	592.65	1815.1	Moderate	Enriched	Enriched	Moderate	YES	
H0YLP6;H0YMF4;	60S ribosomal protei	RPL28	9.657	37.1	16	16	144.83	0	110330	47775	79275	84610	103250	175360	334300	189980	128570	138090	No expres	Enriched	Enriched	Moderate	YES	
H0YKF0		ETFA	30.22	40.5	23	2	3.8625	0.00061	1770.9	1669.5	2568.8	1013.6	2505.6	1264.5	1255.4	1396.8	531.17	1536.3	Moderate	Enriched	Enriched	Moderate	YES	
H0YKW5;Q9C002	Normal mucosa of es	C15orf48;NMES1	14.693	11.4	1	1	4.1591	0.00062	4795.1	5111.5	6575.4	4159.6	6060.8	2803.7	2777.3	2548	4542.7	3806.1	Enriched	Low	Enriched	No expression		
H0YKW8;H0YMK	Death-associated pro	DAPK2;DAPK3	9.4457	11.1	1	1	2.1072	0.00676	4735.5	4961.4	5831.9	4701	6767.5	5299.1	19819	8217.4	14274	8660.2	Moderate	Low	Moderate	Moderate		
H0YKX0;Q96EP0-	E3 ubiquitin-protein	RNF31	102.29	4.7	3	3	11.644	0	24249	19324	18054	21343	16506	18677	16785	19296	10992	20264	Moderate	Low	Moderate	No expres	YES	
H0YL91;Q15650	Activating signal coi	TRIP4	42.052	2.7	1	1	2.7388	0.00239	4889.5	4970.8	5674.8	3118.8	8756.7	2209.5	2755.5	1794.3	3201.9	3657.9	Enriched	Enriched	Enriched	No expres	YES	
H0YLA2;P37108	Signal recognition pa	SRP14	13.058	30.4	11	11	35.097	0	79298	53958	64588	80590	96871	62703	61019	76191	28828	74248	No expres	Enriched	Enriched	Enriched	YES	
H0YN43;H0YLC6		GATM	3.6401	67.7	5	2	3.444	0.00079	29209	11540	16300	31887	11770	29581	36360	13238	15763	43839	Moderate	Enriched	Enriched	Enriched	YES	
H0YLH3;Q92696	Geranylgeranyl trans	RABGGTA	49	9.4	3	3	8.7065	0	14747	8330.9	8493.2	17572	10347	14322	13151	14246	6371.6	13129	Low	Enriched	Moderate	Enriched	YES	
H0YNU2;H0YNW	CTD small phosphata	CTDSPL2	10.444	13	1	1	4.8318	0.00043	10673	9246.8	11554	8842.6	13336	5996.7	8752.1	8493.1	4719.7	8680.6	Low	Moderate	Enriched	No expres	YES	
H0YMY5		IDH3A	5.2061	33.3	1	1	5.5654	0	5608	4828	4216	3555.4	5808.9	3590.5	3394.7	3227.3	1573.7	4389.7	Low	Moderate	Enriched	Moderate	YES	
H0YNX7;P30047-	GTP cyclohydrolase	GCHFR	7.7668	38.8	3	3	22.891	0	10757	10646	11279	14595	11578	11391	10882	15733	5446.7	13625	Enriched	Low	Moderate	Moderate	YES	
H3BLS7;Q5THJ4-2	Vacuolar protein sort	VPS13D	356.92	1	4	4	7.2044	0	19013	7917.2	10534	13768	15689	17178	9356	8209.7	5347.1	10818	Enriched	Enriched	Enriched	Moderate	YES	
H3BLV9;Q5R363;	SRSF protein kinase	SRPK1	76.039	16.2	10	6	21.757	0	28892	24416	32197	28021	41436	25686	32748	30599	16422	28369	Enriched	Enriched	Enriched	Low	YES	
H3BLZ8;Q92841;C	Probable ATP-depen	DDX17	80.439	38.6	53	39	185.41	0	295940	206360	244830	320140	269620	253440	295880	383980	164060	319630	Enriched	Enriched	Enriched	Enriched	YES	
H3BM14;H3BM74	NEDD8 ultimate bus	NUB1	71.921	16	8	8	41.868	0	35358	25272	32679	33547	50979	31388	37205	44607	22677	44267	Enriched	Enriched	Enriched	No expres	YES	
H3BM67;H3BUP2;H3BUN4;O60936-2;		NOL3	15.022	14.4	1	1	10.214	0	5989.5	4694.8	4898.4	5921	6060.1	5779.2	3016.3	2177.6	2764.7	4098.6	Enriched	Moderate	Enriched	Low	YES	
H3BM79;Q9H8T0;	AKT-interacting prot	AKTIP	28.004	8.4	1	1	3.7317	0.0008	10711	3694.4	5869.2	12860	4923.6	8960.2	7234.6	8952.8	3403.9	10642	No expres	Moderate	Enriched	No expres	YES	
H3BM91;Q9H0A8;	COMM domain-cont	COMMD4	22.763	11.8	2	2	3.8685	0.00061	13236	14565	12772	9263.4	16533	12573	15225	13550	6021.5	10135	No expres	Moderate	Enriched	Enriched	YES	
H3BMM5;Q96AX1	Vacuolar protein sort	VPS33A	61.238	16.9	9	9	17.939	0	29963	21269	25342	42001	25415	26254	24735	31684	14668	31437	Moderate	Moderate	Moderate	No expres	YES	
H3BPG5;H3BV80;	RNA-binding protein	RNPS1	15.108	23.4	5	5	78.775	0	32282	32685	38520	25704	32754	33842	38325	39470	19975	38835	No expres	Enriched	Enriched	Enriched	YES	
H3BQF7;H3BMU1	IST1 homolog	IST1	19.013	35.5	10	10	29.856	0	40361	30986	31188	37425	42382	20683	38334	25456	17159	27832					YES	
H3BQQ6;H3BTI2;	Protein FAM192A	FAM192A	11.814	14.6	1	1	3.0186	0.00132	3538.9	2840.9	3583.5	5969	3295.6	3752.9	3799.4	5098.1	1449.9	4639.6					YES	
H3BMY1		CTRB2	18.032	63.1	38	4	13.728	0	10224	7798.5	8355.5	8134.1	16814	7021.4	6091.9	3866.3	4054.1	5732.1	No expres	No expres	Enriched	No expres	YES	

H3BNX3			31.769	36	14	1	5.4359	0	20193	6985.4	4407.2	11569	2832.6	18855	14580	8277.3	6945.3	27552							
H3BNY8;H3BN01		MPI	20.431	53	16	3	50.463	0	21918	5222.1	5345.4	10450	4332.7	20004	25225	27003	16072	15343	No expres	Moderate	Moderate	Enriched	YES		
H3BS10;H3BP20;F	Beta-hexosaminidase	HEXA	58.44	9.2	6	6	8.7392	0	8846.8	6355.8	7821.2	7678.3	7869.3	13383	10708	10898	6221.4	8809.7	Moderate	Enriched	Enriched	Enriched	YES		
H3BSZ3;H3BS11;I	Ubiquinone biosynth	COQ7	11.273	20.4	3	3	3.5209	0.00079	5456.6	5187.2	6965.8	3592.8	7771.8	4189.6	7358	4412.7	4088.7	6425.5	Enriched	Low	Moderate	No expres	YES		
H3BP92		CTRB2	14.699	53.3	39	13	85.457	0	137690	162220	148560	106010	197600	113650	125630	95423	81512	114060	No expres	No expres	Enriched	No expres	YES	YES	YES
H3BPB8;P34949;F	Mannose-6-phosphat	MPI	44.45	37.5	21	8	94.016	0	96055	55631	72013	114240	73279	99114	108610	117450	68334	103200	No expres	Moderate	Moderate	Enriched	YES		
H3BPD5;P78549-3	Endonuclease III-like	NTHL1	25.744	8.5	2	2	4.7216	0.00043	2757.2	2222.4	2775.7	2138.5	3682.2	2739.3	5004.9	4163.7	3109.1	4992.7	Moderate	Low	Moderate	Moderate	YES		
J3KSE6;J3KTR0;H	Cirhin	CIRH1A	8.7729	15.2	1	1	2.9396	0.00168	29626	18801	20639	21929	22709	26293	18050	19320	8456.4	23689	Enriched	Enriched	Enriched	No expres	YES		
H3BPE1;H3BQK9;	Microtubule-actin cro	MACF1	856.87	5.1	35	27	108.59	0	121920	131400	129590	118360	145540	110810	125790	130890	74298	130240	Enriched	Enriched	Enriched	Enriched	YES		
H3BPE7;P35637-2	RNA-binding protein	FUS	53.496	17.1	22	17	204.16	0	241920	169740	220120	222510	239400	195220	238610	310410	127810	300500	Enriched	Moderate	Enriched	Enriched	YES		
H3BPU4;Q9UGJ1-:	Gamma-tubulin comp	TUBGCP4	44.905	8.1	4	4	7.3791	0	4472.5	1356.2	2703.5	3925.8	2711.3	4130	3193.4	3494.6	827.56	4275.9	Enriched	Moderate	Enriched	Enriched			
H3BU63;H3BSE3;I	Phosphopantothenoy	PPCDC	8.9964	25.9	2	2	4.9092	0.00044	10969	10804	11515	9047.6	14314	8222.2	10919	10897	8917.7	10123	Moderate	Moderate	Moderate	No expression			
H3BQQ2;Q86UK7-	Zinc finger protein 5!	ZNF598	93.287	8.4	7	7	11.498	0	9264.8	10282	10354	9861.4	13652	8338.9	9100.1	8339.3	5534.9	7913.9	Moderate	Enriched	Moderate	No expres	YES		
H3BR29;H3BSM7;	UPF0420 protein C1	C16orf58	46.342	31.4	11	11	25.637	0	13389	7026.2	11732	15714	9842.1	15636	13874	18051	7689.7	15911	Low	Enriched	Enriched	No expres	YES		
H3BRD2;P55789;F	Sulfhydryl oxidase;F	GFER	15.795	26.6	2	2	4.3773	0.00063	4760.2	4661.8	4812.5	9846.8	5974.9	2865.8	3585.3	4556.5	2908.8	6211.9	Enriched	Moderate	Moderate	Low	YES		
H3BRF9;H3BUW6	Abscission/NoCut ch	ZFYVE19	49.203	5.6	2	2	1.8568	0.00878	8238.6	15011	12188	4111.6	17397	3204.9	4965.3	7260.3	2235.5	6263.3	Low	Enriched	Moderate	No expres	YES		
H3BRL3;O14562;F	Ubiquitin domain-co	UBFD1	32.64	24.3	6	6	20.977	0	41128	20518	25759	37774	34005	29943	27932	26096	18705	31780	Low	Moderate	Moderate	Low	YES		
H3BRN4;P80404;F	4-aminobutyrate ami	ABAT	58.14	58.8	73	73	323.31	0	597820	452450	463120	515200	643440	586690	613100	541720	273040	469270	Enriched	Enriched	Enriched	Enriched	YES		
H3BRR0;Q9NZD8-	Maspardin	SPG21	17.258	12.3	3	3	7.6057	0	16681	9862.6	14553	25694	12291	21219	16809	25941	9147.3	20252	Enriched	Enriched	Enriched	No expres	YES		
H3BSA1;P19784;H	Casein kinase II subu	CSNK2A2	27.025	30.4	8	7	21.606	0	54799	32923	39379	54731	41772	39088	43794	56018	28825	51275	Moderate	Enriched	Enriched	Low	YES		
H3BSM0;Q53FZ2;	Acyl-coenzyme A sy	ACSM3	65.42	11.5	7	7	15.809	0	47496	28268	33103	30501	62611	39101	28798	29092	11152	36443	Moderate	Moderate	Moderate	Moderate	YES		
H3BST1;Q9UL45;I	Biogenesis of lysoson	BLOC1S6	20.265	20.9	3	3	69.647	0	10892	5354.9	9088	19037	8049.4	17144	16532	17591	6226.5	17307							
H3BST5;Q8IXI1;I3	Mitochondrial Rho G	RHOT2	23.086	21.2	3	3	8.3066	0	17769	13780	17826	15751	32039	15656	15055	12911	10244	15325	Low	Enriched	Moderate	No expres	YES		
H3BSW6;Q2VPK5	Cytoplasmic tRNA 2-	CTU2	63.681	4.6	3	3	8.2365	0	7136.4	5185.4	5307.9	7141.4	5160.3	7253.6	5924.5	6635.2	3878.4	7051.3							
H3BTA3;Q9UNE7-	E3 ubiquitin-protein	STUB1	18.378	19.1	3	3	5.8729	0	4517.1	5892.7	7342.4	3955.5	7449.1	4715.4	7825.5	4613	6764.8	4811.9	Enriched	Enriched	Enriched	No expres	YES		
H3BTB7;Q5JPH6;C	Probable glutamate--t	EARS2	56.825	12.1	7	7	17.987	0	3305.2	3029	4384.6	2939	6498.4	4708	7851	4669	6666.4	6508	Enriched	Enriched	Enriched	No expression			
H3BTW5;Q7Z401;	C-myc promoter-binc	DENND4A	112.61	2.4	2	2	9.6542	0	9550.3	3908.4	5183.3	8971.9	8172.3	11902	11418	9190.3	3523.4	8649.1	No expres	Low	Moderate	Moderate	YES		
H3BUF6;Q8WWM	Ataxin-2-like protein	ATXN2L	112.71	6.4	5	5	37.413	0	20608	21118	20445	13829	27110	17382	32697	20062	16920	24141	Enriched	No expres	Moderate	Enriched	YES		
H7BXD5;P28676;C	Grancalcin	GCA	22.109	23.2	3	3	15.997	0	7735.4	3336.4	3989.7	4521.6	5151.2	8785.3	4360.3	10277	3662.1	6876.2	Enriched	Moderate	Enriched	Moderate	YES		
H7BXF5;Q9H0E3;	Histone deacetylase c	SAP130	111.28	1.1	1	1	5.3269	0	2805.3	2796.4	2633.5	3191.5	4053.4	2408.4	4054.9	3431.8	3037	3542.2	Moderate	Enriched	Enriched	No expres	YES		
H7BXF7		AOX1	21.217	34.7	10	1	3.9497	0.00061	1268.4	1842.9	1420.6	1762.4	2482.1	1254.7	1227.2	1505.7	574.12	1140.2	Enriched	Enriched	Enriched	Enriched	YES		
H7BXI1;A0FGR8-2	Extended synaptotag	ESYT2	98.008	11.5	11	11	42.062	0	27591	18183	17550	22753	20265	22738	26396	34694	14689	25660	Enriched	Enriched	Enriched	No expres	YES		
H7BXJ4;Q0JRZ9-2	FCH domain only pro	FCHO2	43.42	13.8	6	6	10.97	0	1263.7	1099.1	1571	1104.5	1920	1117.5	2093	1426.8	1612.2	1061.5	Low	Enriched	Enriched	No expression			
H7BXR3;O94875-5	Sorbin and SH3 dom	SORBS2	70.174	44	41	2	17.781	0	2997.1	6108.6	4558.7	2043.7	6669.5	1654.3	3250.1	2432.2	3244.4	2988.6	Enriched	Enriched	Enriched	Low	YES		
H7BXY3;Q7L2E3-	Putative ATP-depend	DHX30	130.55	13.3	15	15	33.911	0	36701	34694	40125	45059	41883	36456	44887	42771	23873	41279	Enriched	Enriched	Enriched	Enriched	YES		
H7BXY5;Q0ZGT2-	Nexilin	NEXN	68.814	15.6	10	10	31.125	0	33527	40024	38719	27286	50548	17847	19621	17158	13411	29235	No expres	Low	Moderate	Enriched	YES		
H7BY35;Q92736;C	Ryanodine receptor 2	RYR2	562.6	0.4	2	2	2.0501	0.00739	10746	13018	12739	5277.4	18060	8064.4	13436	9606.3	7589.4	7734.1	No expres	No expres	Low	No expression			
H7BYC8;Q8TCX1-	Cytoplasmic dynein 2	DYNC2LI1	35.501	3.5	1	1	2.9705	0.00169	14653	12630	14103	14226	9023.6	11516	7766.6	14556	4312	13956	Enriched	Low	Moderate	Enriched			
Q5JRG1;H7BYF2;(	Nucleoporin p58/p45	NUPL1	49.095	2.6	2	2	2.8823	0.00186	5440.5	4856.6	5319.4	4873.7	6029.5	5402.1	4947.5	4382.1	3162	5704.9	Low	Low	Moderate	Moderate	YES		
H7C051;H7BYI2;C	SWI/SNF-related ma	SMARCAL1	35.349	4.6	1	1	2.7236	0.00239	383.48	296.1	714.25	310	958.85	307.28	997	798.21	681.59	1225.2	Moderate	Low	Moderate	No expres	YES		
H7BYP9;O15068-5	Guanine nucleotide e	MCF2L	88.995	3	2	2	8.9132	0	10319	13434	15151	8171.9	19704	5204.2	10951	9275	8040.9	10277	Low	Enriched	Enriched	Enriched	YES		
H7BYR8;P02686-6	Myelin basic protein	MBP	25.742	17.8	4	1	4.7697	0.00043	8856.1	11292	35449	7140.1	45351	6110.3	10196	6206.7	11984	8439.7	Enriched	Moderate	Enriched	Low	YES		
H7BYT1;P48730-2	Casein kinase I isofor	CSNK1D	49.064	7.7	4	2	3.1825	0.00077	5751.7	5209.6	5593.6	5697.4	7366.1	3417.7	5244.7	4315.6	2558	4951.7	Enriched	Enriched	Enriched	Enriched			
H7BYU9;Q9GZN8;	UPF0687 protein C2	C20orf27	14.249	13.4	2	2	2.2936	0.00496	2088.7	2202.8	3283.5	825.48	3420.9	2569.1	3238.4	1036.6	1387.7	3100.5	Enriched	Moderate	Moderate	No expres	YES		
H7BYV6;Q9NQY0	Bridging integrator 3	BIN3	23.928	8.8	1	1	3.1353	0.00095	7742.5	6739.4	5261.5	7444.1	8197.4	5900.5	4849.1	4774.1	2383.3	5802.2	Enriched	Moderate	Enriched	No expres	YES		
H7BYX6		NCAM1	80.282	19.3	12	1	44.749	0	21547	14835	21913	20819	18743	16555	23505	21094	12324	27132	Enriched	Moderate	Enriched	Enriched	YES		
H7BYY1;P09493-2;F5H7S3;B7Z596		TPM1	28.747	66.9	50	0	49.412	0	15876	14236	18811	10830	24042	20669	41001	32483	24837	28263	Enriched	Enriched	Enriched	Enriched	YES		
H7BZ14;Q9H2H8;I	Peptidyl-prolyl cis-tr	PPIL3	20.272	33.9	9	9	89.015	0	53523	49410	28904	90786	54603	48787	57874	31394	30433	25864	Enriched	Enriched	Enriched	No expres	YES		
H7BZD2;Q8N7R7-	Cyclin-Y-like protein	CCNYL1	13.501	17.6	2	2	3.191	0.00077	5265.5	4475.4	4546.5	3288.6	4600.5	4087.5	7979.5	4022.4	4621.8	3988.8	Low	Enriched	Enriched	No expression			
H7BZJ3		PDIA3	13.519	66.7	22	2	5.0021	0.00044	15357	10358	10391	19830	12163	12486	11935	13107	5088.2	14301	Moderate	Enriched	Enriched	Enriched	YES		
H7BZK0;Q14BN4-	Sarcolemmal membra	SLMAP	50.263	4.2	2	2	3.1081	0.00095	1070	1647.8	1427.2	1457.4	1435.9	2880.6	2414.8	2094	1221.4	2915.2	Moderate	Enriched	Enriched	No expres	YES		
H7BZL0;Q9BYG3;	MKI67 FHA domain-	NIFK	11.741	25.5	2	2	12.689	0	10491	8492.7	10600	7435.8	14808	6643.2	9604.3	9401.4	4596.7	9870.3					YES		
H7BZN7;Q9NY93-	Probable ATP-depen	DDX56	20.842	9.3	2	2	2.2746	0.00494	6703.3	6200.6	7398.1	8128.5	8650.1	6642.9	6713.8	6906.6	3404	7642.4	Enriched	Moderate	Enriched	No expres	YES		
H7BZS7;Q96PE7	Methylmalonyl-CoA	MCEE	8.4148	43.6	6	6	8.301	0	10386	10773	18579	8304.5	18720	15339	28517	17463	12266	16527	Moderate	Enriched	Enriched	No expres	YES		
H7C2R6;H7BZW1;	UPF0769 protein C2	C21orf59	13.334	13.7	1	1	3.9225	0.00061	6480.8	5149.7	6997.9	5819.5	7621.6	3622.6	3314	2793.5	2968	5310.6	Enriched	Enriched	Enriched	No expres	YES		
H7BZW6;X6RAL5	Histone deacetylase c	SAP18	16.036	26.6	5	5	24.116	0	33550	21869	27100	41447	32412	36628	62674	51100	37354	50947	Enriched	Enriched	Enriched	Enriched	YES		
H7C190;H7C052;F	Melanophilin	MLPH	15.96	9	1	1	2.3115	0.00479	2012	561.54	970.82	724.74	764.37	513.77	877.62	610.79	562.22	1177.2	Enriched	Enriched	Enriched	No expres	YES		
H7C069		SEC61A2	15.726	42.1	17	10	30.063	0	68660	50289	70164	93387	72634	91574	75808	68449	44555	62261	Low	Enriched	Enriched	No expression			
H7C070;Q2LD37-6	Uncharacterized prot	KIAA1109	180.5	1.5	2	2	2.2296	0.00545	21295	15150	13852	21783	17355	13095	8640.8	22472	2577.6	26801	Low	Moderate	Enriched	Enriched			
H7C078;Q4VXZ8;(	Peroxisomal 2,4-dien	DECR2	9.9005	18.1	1	1	2.4856	0.00396	15748	5664.5	12011	14028	7189.4	13085	13650	20776	6522.2	16755	Enriched	Enriched	Enriched	No expres	YES		
H7C0D5		YIPF4	6.447	44.8	2	1	3.614	0.0008	2078.4	1956.4	2087.2	2317.8	2353.5	11274	2930.3	2852.7	1046.7	2928.1	No expres	Low	Moderate	Low			
H7C0E5;O75312;F	Zinc finger protein ZI	ZPR1	42.542	13	4	4	9.7588	0	11249	6482.1	7595	13630	6892.4	10299	7900.9	12783	5299.4	10867					YES		
H7C0N7		HEBP2	4.5923	35.6	1	1	3.0834	0.00114	5936.6	12318	5121.4	5029.5	7937.6	4218.3	3670.9	4939.3	4189.7	5008.1	Enriched	Enriched	Enriched	Enriched	YES		
H7C0Q6;Q9C037-3	Tripartite motif-conta	TRIM4	23.413	23.3	4	4	12.539	0	21646	16662	20965	20486	22184	18950	25064	18977	11413	27885	Enriched	Enriched	Enriched	No expres	YES		
H7C189;Q13107-2	Ubiquitin carboxyl-te	USP4	69.447	6.4	3	2	4.6666	0.00043	407.63	176.63	559.95	366.02	603.4	429.27	492.6	360.34	614.7	412.26	Enriched	Enriched	Enriched	Enriched	YES		
H7C1J4;Q6BDS2	UHRF1-binding prot	UHRF1BP1	154.72	0.9	2	2	3.8482	0.00061	10355	7600.7	8711.6	13553	10021	12122	7624.3	13062	4913.2	12632	Moderate	Enriched	Enriched	No expression			
H7C1N3;O15155-2	BET1 homolog	BET1;DKFZp781C0425	14.872	18.8	3	3	5.9152	0	7889.1	7542.3	9640.5	10274	8787.4	6779.5	7672.2	8407.7	2802.5	8890.5	Moderate	Enriched	Enriched	Low			
H7C1U8;Q9BUR5;	Apolipoprotein O	APOO	20.08	35.4	7	7	31.264	0	21175	14878	18544	26547	18221	17500	22357	24523	13467	19569	Moderate	Enriched	Enriched	No expres	YES		
H7C218		CPVL	16.486	14.9	2	1	8.2613	0	32661	7914.2	12046	20268	13097	19097	14572	23157	7563.6	19430	Low	Low	Moderate	Low	YES		
H7C2E3		LANCL1	16.962	20.3	6	5	12.022	0	26773	17456	18386	63534	15037	28160	20873	35812	12753	36492	Moderate	Enriched	Enriched	Enriched	YES		
H7C2F9;Q15032-2	R3H domain-contain	R3HDM1	33.121	5.6	1	1	6.3898	0	5083	4036	4621.6	5740.8	4268.7	5174	3670.8	5949.5	2292.8	5493.4	Moderate	Enriched	Enriched	Enriched			
H7C2Q8;Q99848	Probable rRNA-proc	EBNA1BP2	40.684	8.3	4	4	8.6552	0	22366	23441	23243	21088	26040	14904	19522	19793	10871	20616	Moderate	Low	Enriched	Enriched	YES		
H7C2T1;P46527;E	Cyclin-dependent kir	CDKN1B	11.94	33.7	4	4	114.63	0	20533	14051	17744	13834	21161	18138	22080	19281	10010	17816	Moderate	Enriched	Enriched	Moderate	YES		
H7C2U8;Q9H0X4	Protein ITFG3	ITFG3	20.934	7.3	1	1	4.1155	0.00062	7498.7	5686.2	7884	6979.5	11936	3735.7	4526.9	2937.8	3134	5049.3	Enriched	Enriched	Enriched	No expres	YES		
H7C335;P16383-2;	GC-rich sequence DN	GCFC2	22.824	12.6	2	2	9.6087	0	16847	10178	16007	16417	15476	13296	11613	14214	6828.9	12874							
H7C3F4;Q9NWH9	SAFB-like transcripti	SLTM	70.491	18.8	12	12	25.474	0	24799	21615	26837	17711	31069	24367	45176	31457	37167	37121	Moderate	Moderate	Enriched	No expres	YES		
H7C3F5;O75175-3	CCR4-NOT transcrip	CNOT3	58.866	7	4	4	6.1318	0	19707	18182	19323	16557	23566	18626	20384	15158	13238	17498	Moderate	Low	Moderate	Low	YES		
H7C3P9;Q9UNS2-:	COP9 signalosome cc	COPS3	39.036	28.4	10	10	75.83	0	59137	46666	54964	40601	68611	49032	56377	48003	33541	50036	Low	Enriched	Enriched	Moderate	YES		
H7C488;Q9NQ48-:	Leucine zipper transc	LZTFL1	26.795	24.7	5	5	25.441	0	22176	18101	17262	20757	19372	12962	13691	12560	10611	16507	Low	Moderate	Enriched	No expres	YES		
H7C4Y9		RAB3GAP2	19.048	7.6	2	2	9.1578	0	1939.2	1212	1416.7	1290.4	1392	1756.5	946.5	1002.1	251.45	1614.9	Enriched	Enriched	Enriched	Low	YES		
H7C5E3;Q6I9Y2	THO complex subuni	THOC7	3.3108	40	1	1	3.6028	0.0008	5656.1	3841.7	5224.4	3505.9	3095.9	5435	8014.2	7044.9	5012.6	7070.7	Moderate	Enriched	Enriched	No expression			
H7C5H1		CFB	34.581	35.1	13	3	7.6508	0	16595	11374	17925	26987	10886	15994	8989.2	19913	4568	16355	Enriched	Enriched	Enriched	Moderate	YES		
H7C5R8;Q460N5-3	Poly [ADP-ribose] po	PARP14	171.15	1.8	2	2	3.7411	0.0006	178.36	217.99	183.97	103.09	113.08	245.14	0	140.85	121.87	193.79	Enriched	Enriched	Enriched	No expres	YES		
P0CAP1-11;H8Y6F	DNA-directed RNA p	GCOM1;POLR2M	64.045	1.8	1	1	2.7658	0.0024	1447.6	1593	1926.3	1266.2	2643.4	4160.1	11376	7224.4	11157	5640.2	Enriched	Enriched	Enriched	No expression			
H9KV50;Q9NZV5-	Selenoprotein N	SEPN1	62.066	4.3	2	2	7.1253	0	5143.9	6168.5	7522.6	4892.6	8734.1	4155.2	8210.6	7219.6	7075.9	6594.4	Enriched	Enriched	Enriched	No expression			
H9KV77;Q9NQ92	Coordinator of PRMT	COPRS	18.911	7.6	1	1	2.7061	0.00238	5820.4	4586.8	3704.7	6323.2	5464.8	6940	3794.4	4416.1	2419.2	5275							
H9KVA9;P46736;A	Lys-63-specific deubi	BRCC3	36.239	8.8	4	4	4.417	0.00063	12836	8639.7	14291	6993.9	13725	6269.1	17201	14643	23103	14063	Moderate	Enriched	Enriched	No expres	YES		
H9KVC7;H9KVC9	Interferon-induced G	MX1;MX2	20.898	14.2	2	2	6.8903	0	2647	1869.6	3050.9	8989.2	2086.5	7669.3	3331.3	9132.4	1595.4	4782	Enriched	Moderate	Enriched	Low			
I3L0A0;Q13404;Q	Ubiquitin-conjugating	UBE2V1	42.208	25.9	15	6	92.038	0	105390	81279	85432	91154	106360	96813	107390	111690	46801	90438	Low	Low	Low	No expression			
I3L0N3;P46459	Vesicle-fusing ATPas	NSF	82.091	46.7	58	7	217.91	0	423020	300320	362060	316230	377300	550530	399410	418480	240930	344110	Enriched	Enriched	Enriched	Enriched	YES		
I3L0S0		P4HB	16.215	70.3	40	13	212.62	0	148970	132240	109500	95212	206080	76402	71517	56716	37604	61305	Enriched	Enriched	Enriched	Enriched	YES		
I3L0T3;P45381	Aspartoacylase	ASPA	8.9382	16.5	1	1	3.4585	0.00079	6690.9	5384.5	8746.9	8659.1	8268.9	6236.7	9858.4	9344.1	4288	10646	Moderate	Low	Low	Low	YES		
I3L0W4;Q96F10	Diamine acetyltransfe	SAT2	15.056	27.9	3	3	22.443	0	11174	8085.4	6471.4	6245	9796.2	7095.5	8968	5703.1	3127.7	7933.7	Enriched	Enriched	Enriched	No expression			
I3L0W5		YWHAE	4.5157	81.6	7	1	4.01	0.00062	6361.1	5135.6	9390.2	3383.4	8289.8	5802.4	15585	2882.1	3898.1	6813.6	Enriched	Enriched	Enriched	Low	YES		
I3L0X5;I3L4C3;O7	Sperm-associated ant	SPAG7	20.083	29	6	6	15.195	0	23186	18831	20738	23374	19226	20851	42759	38237	31905	44469	No expres	Enriched	Enriched	Enriched	YES		
I3L112;P52429	Diacylglycerol kinase	DGKE	51.101	2.9	1	1	2.3866	0.00429	2048.7	1675.1	1653.8	2386.5	2361.6	2916.7	2699.9	2947.9	1186.3	2095.3	No expres	Enriched	Moderate	No expression			
I3L161;I3L3X5;Q9	Phospholipid scrambl	TMEM256-PLSCR3;PL	18.276	17.6	3	3	18.207	0	8928.5	6691	9548.2	10201	8914	9391.5	12026	11481	7707.2	10456	Enriched	Enriched	Enriched	No expres	YES		
I3L1T3;Q9GZP9	Derlin-2	DERL2	18.038	7	1	1	2.6142	0.00273	4947.2	5046	5879.7	2981.4	9772.5	2609.6	2466.2	3151.5	1801.5	2350.6	Moderate	Enriched	Enriched	No expres	YES		
I3L4I0;I3L1Y9;Q9	FLYWCH family mer	FLYWCH2	9.56	20.9	1	1	10.102	0	12182	9811.8	12543	7208.6	17139	12917	12488	10572	5742.3	12020	Moderate	Low	Low	No expression			
I3L2B0		CLUH	138.23	13.4	13	4	36.383	0	42451	38489	41902	42085	57410	39711	44101	32623	31444	37929					YES		
I3L2K5;Q8IWR0;I3	Zinc finger CCCH do	ZC3H7A	83.647	4.8	4	4	19.165	0	4465.1	3524.7	3242.9	4168.3	4079.2	4402.2	2930.6	3500.6	1984.6	3040.6	Moderate	Moderate	Enriched	No expres	YES		
I3L2Z7		GP2	13.899	34.4	9	2	3.3398	0.00078	2780.1	2397.9	2639.7	2746.7	4254.9	9036.2	4288	3382.1	1756.4	2558.5	Enriched	Enriched	Enriched	Enriched	YES		
I3L362;Q86W50-2;	Methyltransferase-lik	METTL16	18.98	13.1	2	2	3.3951	0.00078	7830.8	4595.9	5972.4	13490	5505.8	8399.2	7946.8	10775	7355	9215.6					YES		
I3L397;I3L504		EIF5A	16.118	61.9	38	2	191.78	0	242330	174430	215970	271040	220470	341580	392360	332900	127570	263660	Enriched	Moderate	Enriched	Enriched			
I3L3B4;F8W9H0;E	Vitamin K epoxide re	VKORC1	11.082	19.2	5	5	9.6905	0	4281.9	6002.7	5235.3	2077	5191.6	2148	3957.2	3439.6	2016	2514.1	Low	Enriched	Enriched	No expres	YES		
I3L3P5		P4HB	16.876	51.3	32	4	9.9363	0	52911	25747	25344	26287	23310	16608	21174	18086	11691	26925	Enriched	Enriched	Enriched	Enriched	YES		
I3L3U6		P4HB	20.689	67.6	51	2	7.0409	0	10675	2014.7	4097.6	8602.3	3405.7	41910	8478.5	12145	3056.8	14058	Enriched	Enriched	Enriched	Enriched	YES		
I3L3X8		CARHSP1	10.103	20.2	3	3	8.4039	0	24657	20092	19819	19551	22193	21540	38784	20705	15972	22621	Enriched	Enriched	Enriched	No expres	YES		
I3L4G8;I3L4A1;Q9	Charged multivesicul	CHMP6	20.167	14.5	2	2	5.2729	0.00022	6887.2	5362.6	8463.9	5833.7	8445.8	5724.2	5530	5025.4	2793.2	5268.7	Enriched	Low	Moderate	No expres	YES		
I3L4A2;Q9UIC8;Q	Leucine carboxyl me	LCMT1	18.052	10.1	2	2	2.4662	0.00413	11818	6694.2	8538.6	8707.4	10825	12168	11931	17446	4040	8551.5	Enriched	Enriched	Enriched	No expres	YES		
J3KQU4;I3L4I4;O7	TOM1-like protein 1	TOM1L1	51.686	10.3	4	4	13.028	0	10095	11493	14793	8280.4	19073	5519.8	15026	14687	12102	11674	Moderate	Enriched	Enriched	Low	YES		
I3L4J1			48.07	17.5	12	0	13.035	0	22697	28444	25805	18809	31895	35340	50832	52301	22339	34273							
J3KMX1;Q99567	Nuclear pore comple	NUP88	78.77	15.5	11	11	31.717	0	35221	31743	38431	27252	42240	34308	39319	33287	22767	35273	Moderate	Moderate	Enriched	Moderate	YES		
J3KMY5;G3V3E8;	Epididymal secretory	NPC2	16.23	56.1	11	11	42.232	0	120250	88662	100080	100680	115170	94724	81398	75283	44621	97488	Enriched	Enriched	Enriched	Enriched	YES		
J3KN01;P55196;P5	Afadin	MLLT4	207.62	21.5	39	1	256.97	0	148260	121890	131880	161720	167200	134790	153970	156870	86630	153920	Enriched	Enriched	Enriched	Moderate	YES		
J3KN10;P42356;P4	Phosphatidylinositol	PI4KA	236.83	4.1	8	8	19.841	0	24950	16031	22676	28062	24651	23287	26633	27884	13960	26653	Enriched	Enriched	Enriched	Enriched	YES		
J3KN16;Q5VYK3	Proteasome-associate	KIAA0368;ECM29	223.69	18.9	31	31	91.324	0	149400	114120	116140	137510	145240	124650	161270	148920	100710	138590	Moderate	Enriched	Enriched	Low	YES		
J3KN32;Q9UKL0;F	REST corepressor 1;I	RCOR1;RCOR3	53.327	7	2	2	3.7849	0.0006	1669.8	992.96	1555.8	2729.2	1521	1840.5	1574.4	2723.7	1037.5	2868.2	Moderate	Low	Enriched	Enriched			
J3KN75;Q0IIM8;D	TBC1 domain family	TBC1D8B	128.11	3.5	4	4	26.17	0	3299.3	2687.6	2065.9	5790.2	1893.9	2557.1	2030.4	2662.8	1362.9	3377.8	Low	Moderate	Enriched	No expres	YES		
J3KNF4;O14618;E	Copper chaperone fo	CCS	27.086	8.2	2	2	2.3268	0.00462	1619	1087.7	1265.4	1225.5	1841.7	1855.4	1886.4	1811.2	1150	2187.8	Moderate	Moderate	Enriched	Enriched	YES		
J3KNG9;P04920-2;	Anion exchange prot	SLC4A2	127.65	2.3	2	2	5.5611	0	2207	1778.8	1465.9	1446.5	1565.6	1600.1	4707.1	2527.5	6796.3	4204.9	Moderate	Moderate	Moderate	Moderate			
J3KNL2;Q8WYJ6-2	Septin-1	SEPT1	46.918	5.1	4	3	3.902	0.00061	2856.3	2092.5	3114.9	2111.4	3543.8	2765.9	2021.4	1716.2	1078	1659.3	Low	No expres	Low	No expres	YES		
J3KNN5;Q9UJV9;F	Probable ATP-depen	DDX41	71.648	8	4	4	9.1808	0	26699	16316	19075	24455	20320	28841	22872	31672	12326	30961	Moderate	Enriched	Enriched	No expres	YES		
J3KNQ4;Q9NVD7;	Alpha-parvin	PARVA	46.589	18.7	14	11	77.823	0	47184	33735	34667	44359	31918	61017	64390	82821	26115	57891	Moderate	Enriched	Enriched	No expres	YES		
J3KNV4;Q13683-1	Integrin alpha-7;Integ	ITGA7	123.63	3.6	4	4	13.024	0	17855	20341	19444	18013	24005	21090	31470	34538	17808	34521	Moderate	No expres	Low	Enriched	YES		
J3QL05;J3KP15;Q(	Serine/arginine-rich s	SRSF2	15.156	28.5	10	10	127.45	0	47179	30828	37148	40009	39962	25163	45771	48632	17328	37403					YES		
J3KP58;P30622-2;I	CAP-Gly domain-con	CLIP1	148.13	13.6	16	16	182.13	0	34578	27489	25121	28056	33656	20865	26169	28536	17436	27936	Moderate	Enriched	Enriched	Low	YES		
J3KPP4;O95232	Luc7-like protein 3	LUC7L3	58.22	14.5	7	7	171.41	0	45617	34612	34246	44150	35434	31369	64081	65148	36180	64077					YES		
J3KPS0;Q9NXW2;	DnaJ homolog subfar	DNAJB12	45.489	8.8	3	3	16.682	0	4121.1	2745.9	3808.3	2685.9	3758.7	2405.9	3509.9	2884.6	2792.9	3699.9	Enriched	Enriched	Enriched	Enriched	YES		
J3KPS2;Q6ZRV2	Protein FAM83H	FAM83H	96.337	6.4	4	4	20.592	0	17531	16786	21170	13148	28217	20042	26820	27605	12741	23424	Enriched	Enriched	Enriched	No expres	YES		
J3KPS3;P04075;P0	Fructose-bisphosphat	ALDOA	39.817	58.2	51	50	323.31	0	207470	167970	189630	196690	265110	245840	395060	371520	166500	235450	Enriched	Enriched	Enriched	Enriched	YES		
J3KSW2;J3KQ09;X	DNA polymerase iota	POLI	71.806	1.6	1	1	2.2752	0.00495	8702.2	6494.9	7733.6	8648.3	9255.1	8188.9	8157.3	6177.7	3044.3	7642.8	No expres	Low	Enriched	No expres	YES		
J3KQ32;Q9NTK5;(	Obg-like ATPase 1	OLA1	46.937	53.8	33	26	129.63	0	277190	198800	216540	188860	278450	205530	186070	193860	90957	171140	Enriched	Enriched	Enriched	No expres	YES		
J3KQ40;O95759-2;	TBC1 domain family	TBC1D8	132.42	1.4	1	1	2.8642	0.00186	6610.9	3846.4	6590.8	11471	4871.1	6901.5	7050.8	8182.1	5049.9	8656.6	Enriched	Enriched	Enriched	Moderate	YES		
J3KQ48;Q9Y3E5	Peptidyl-tRNA hydro	PTRH2	19.325	32.8	7	7	51.422	0	5641.8	4842.2	6013.7	9710.6	7741.5	6297.6	5507.4	7461.5	3253	5293.2	Enriched	Enriched	Enriched	No expres	YES		
J3KQ61;O95696;O	Bromodomain-contai	BRD1	57.893	2.2	1	1	2.5232	0.00379	1582.5	2016.7	2691.6	722.95	2598.4	1168.7	1537.2	917.51	946.63	1326.3	Low	Moderate	Enriched	Moderate			
J3KQA9;Q5JR59-3	Microtubule-associat	MTUS2	151.17	1.5	2	2	2.3874	0.00429	4654.7	5585	6323.1	4663.9	8120	2839.1	5898.8	5565.2	4690.5	4791							
J3KQE5;P62826;B	GTP-binding nuclear	RAN	26.816	39.7	23	23	97.438	0	153410	73153	111190	144410	122580	257380	194250	194830	77846	174610	No expres	Enriched	Enriched	Enriched	YES		
J3KQJ1;Q8NBJ7;Q	Sulfatase-modifying f	SUMF2	35.922	27.8	13	13	25.843	0	46402	38760	41989	33576	62930	28149	37890	28597	22893	34689	Enriched	Enriched	Enriched	No expres	YES		
J3KQL8;Q9BQE5	Apolipoprotein L2	APOL2	48.915	7.1	3	3	5.2586	0.00022	8244.7	8556.4	10254	8191.3	13129	9702.5	29437	15729	20242	13750	Low	Low	Moderate	No expres	YES		
J3KR05;O75128-6;	Protein cordon-bleu	COBL	122.45	5.1	6	6	21.67	0	10113	16039	12628	13860	19007	11764	15428	14751	10969	15697	Low	Enriched	Enriched	Enriched	YES		
J3KR58;Q99611	Selenide, water dikin	SEPHS2	51.313	14.3	5	4	8.1336	0	1774.4	1158.1	1232.7	1039.5	1905.9	1167.9	1323	1440.8	617.65	1474.4	Enriched	Enriched	Enriched	Enriched	YES		
J3KR72;P49848;P4	Transcription initiatic	TAF6	78.948	6.1	4	4	9.3403	0	6317.8	6855.6	6990.3	7581.5	8823	4073.4	10308	8180.2	5753.2	7565.2	Enriched	Enriched	Enriched	Low	YES		
J3KR97;Q9BTW9;(	Tubulin-specific chap	TBCD	136.55	3.9	4	4	9.63	0	10462	11311	10048	5809	12196	6111.6	13734	8753	7191	6545	Enriched	Moderate	Moderate	Enriched	YES		
J3QLE8;J3QL53;J3KRE8		GPS1	18.153	13.3	2	1	2.3037	0.00479	3341.9	3204.7	4153.6	2493.4	5998.7	2778.3	3461.1	2668.7	1712.9	2309.1	Moderate	Moderate	Enriched	No expres	YES		
J3KRG2;Q96QA5	Gasdermin-A	GSDMA	17.892	7.5	1	1	3.3277	0.00078	2353.2	1564.1	1773	4521.7	1503.8	3468.1	2341.7	2598.1	2104.9	2440.5							
J3KRW7;J3KS81;C	Transmembrane prot	TMEM199	9.743	25.8	2	2	23.575	0	10914	7781.1	9934.7	9399.6	11635	7415.3	8461.4	6086.6	6431.6	7666.5	Enriched	Enriched	Enriched	No expression			
J3QLB2;J3KRX2;J	Zinc transporter ZIP1	SLC39A11	19.35	17.7	2	2	4.4527	0.00042	8202.6	5831.7	5878.3	7682.5	8353.4	6973.4	7708.3	7158.6	7136.5	10424	Enriched	Enriched	Enriched	No expres	YES		
J3KSH8;J3KT51;Q	Hematological and ne	HN1	9.6032	14.9	1	1	16.575	0	7286.2	3656.1	4718.7	8022.1	7780.6	6739.4	10996	10240	7642.2	9406.5	Enriched	Enriched	Enriched	No expres	YES		
J3QS53;J3QRZ2;J3	Uncharacterized prot	C17orf62	9.8514	14.1	1	1	3.2922	0.00078	10738	5651.2	12155	5030.2	5694.3	14165	7762.2	9892.8	5483.1	11870	Enriched	Moderate	Moderate	No expres	YES		
J3KSL8;Q9Y2L5-2	Trafficking protein pa	TRAPPC8	104.24	4	4	4	7.4954	0	5502.8	4592.3	5384.5	4176	6512.4	4537.9	6120.2	4629.2	2892.1	4137.6					YES		
J3KSW8;Q6WCQ1	Myosin phosphatase	MPRIP	95.928	16.2	12	12	51.089	0	35923	28954	30828	28673	32692	30343	20038	26299	13597	25319	Enriched	Enriched	Enriched	Enriched	YES		
J3KSY7;O15234	Protein CASC3	CASC3	25.651	9.9	2	2	5.7183	0	23906	18335	20479	16556	23304	21458	38549	27304	36489	34116	Moderate	Enriched	Enriched	Enriched			
J3QRW8;J3KT08;C	Transmembrane emp	TMED6	11.915	18.5	3	3	6.3803	0	1684.7	2502.1	1955	1880.8	3811.8	3569.6	4844.2	3244.4	4508.6	4219.2	No expres	Enriched	Enriched	No expres	YES	YES	
J3KTD8;Q13951-2		CBFB	6.8585	28.3	2	2	24.314	0	10690	10650	9558.5	7455.6	15966	5673.7	6633.5	5282.3	5283.6	7254.2	Enriched	Enriched	Enriched	Enriched	YES		
J3QR09;J3KTE4;P	Ribosomal protein L1	RPL19	23.134	23.8	15	15	35.68	0	113100	58454	72084	69597	92974	116260	151470	123760	71367	95850	No expres	Enriched	Enriched	Enriched	YES		
J3KTL2;Q07955;Q	Serine/arginine-rich s	SRSF1	28.329	31.2	17	14	46.828	0	94671	71355	80985	92390	97272	87507	93266	108050	50802	88586					YES		
J3KTN0		EIF4A1	13.906	66.7	19	3	4.4687	0.00042	5574.4	5069.6	5346.2	4896.3	7881	7240	8047.7	9374.7	4605.4	6081.7	Enriched	Enriched	Enriched	Moderate	YES		

J3QK89;Q8IWX8	Calcium homeostasis	CHERP	104.93	11.5	10	10	25.761	0	27799	27546	29563	28474	34465	18763	20024	18892	14874	23575	Enriched	Enriched	Enriched	Enriched	YES
J3QKV4		SF3B3	10.175	23.1	3	2	10.05	0	13375	6024.2	9849.7	27130	8251.8	17774	5753.4	6644.7	5015.8	16393	Enriched	Enriched	Enriched	Enriched	YES
J3QKW2;J3QLS3;	28S ribosomal protei	MRPS7	20.838	25.1	4	4	8.6391	0	34501	41108	49192	30001	66308	7172.2	17107	13723	10795	42739	Enriched	Enriched	Enriched	No expres	YES
J3QL56;O75880	Protein SCO1 homol	SCO1	30.178	13	3	3	7.8794	0	19342	18495	19746	10173	25019	15540	19525	18357	13652	15757	No expres	Moderate	Enriched	No expres	YES
J3QL71;Q96FV2;J	Secernin-2	SCRN2	47.493	14.8	7	6	25.854	0	15493	10360	12097	36820	12414	19109	22001	14793	14417	22873	Enriched	Enriched	Moderate	No expres	YES
J3QLG5;Q8NFI3-2;	Cytosolic endo-beta-	ENGASE	16.881	36.3	4	4	30.815	0	9893.1	5982	7574.2	6611.7	11050	5264.8	5173.3	4908.4	4687.8	5487.9	Enriched	Enriched	Enriched	No expres	YES
J3QLK7;Q9BZF2-2	Oxysterol-binding pr	OSBPL7	47.037	2.4	1	1	1.8317	0.00976	3292.8	2179.3	2882.5	2303.9	2815.7	2569.4	2340.6	2934.4	1188.6	2517	Enriched	Enriched	Moderate	No expres	YES
J3QLU9;P04626-5;	Receptor tyrosine-pr	ERBB2	117.1	4.3	5	5	8.0509	0	12193	12975	12405	14117	13325	12020	19898	19814	18055	14534	Enriched	Enriched	Enriched	No expres	YES
J3QQU5		FLII	13.134	10.3	2	2	4.7054	0.00043	19400	24954	18527	14551	25343	15373	16683	14872	12526	15533	Enriched	Enriched	Enriched	Moderate	YES
J3QQY2;J9JIE6;Q9	Transmembrane and	TMCO1	11.372	41.3	8	8	34.882	0	41103	22497	29954	37781	27314	47230	45776	48710	22288	37312	Enriched	Enriched	Enriched	Enriched	YES
J3QR04;P63272	Transcription elongat	SUPT4H1	6.7146	25.4	1	1	2.6578	0.00256	5231.1	4449.4	4648.3	3954.8	5590.2	1672.3	2164.1	3150.8	1830.5	3929.5	Enriched	Enriched	Enriched	Low	YES
J3QRK9;Q96CD0	F-box/LRR-repeat pr	FBXL8	15.662	7.6	1	1	3.2897	0.00078	4006.9	3435.3	3061.5	3237.1	3578.9	3393.7	3317	3278.3	1515.6	3651.4	Enriched	Low	Low	No expres	YES
J3QRN2		APOH	19.907	53.6	11	2	4.9749	0.00044	13998	18216	22673	9521	15662	9278.1	13590	12431	10769	10862	Moderate	Enriched	Enriched	Enriched	YES
J3QRP2;Q8IZR5-3;	CKLF-like MARVEL	CMTM4	15.77	6.4	1	1	1.8542	0.00877	3875.4	3108.9	3654.6	2579.1	5616.2	3536.3	3172	2503	2271.3	3321	Enriched	Enriched	Enriched	No expres	YES
J3QRS3;P19105;O	Myosin regulatory lig	MYL12A;MYL12B	20.457	58.2	25	6	151.16	0	151400	121620	126640	225260	113810	142720	173150	253650	92062	199920	Enriched	Enriched	Enriched	Enriched	YES
J3QRS9;X6R4W8;	BUB3-interacting and	ZNF207	52.541	6.7	3	3	5.1227	0.00044	9197.1	6772.8	10943	6042.8	14100	7856	7470.5	5995.1	3687.6	7200.2	Enriched	Enriched	Enriched	Enriched	YES
J3QRU1;P07947	Tyrosine-protein kina	YES1	61.386	10.4	5	3	4.9578	0.00044	15767	11057	12916	15149	16871	14089	11815	12094	4501.7	11677	Enriched	Enriched	Enriched	Moderate	
J3QRV5;Q6P1M3;	Lethal(2) giant larvae	SPATS2;LLGL2	113.38	14.6	17	14	60.276	0	55766	42427	50297	39604	52684	32805	61404	50009	32021	52132	Moderate	Enriched	Enriched	No expres	YES
J3QSB8;Q9BXW6-	Oxysterol-binding pr	OSBPL1A	33.003	4.9	1	1	13.345	0	17012	11151	12631	12324	14953	14877	14191	15380	8586.4	18127	Moderate	Enriched	Enriched	Moderate	YES
J3QT38;Q9Y2D4-2	Exocyst complex con	EXOC6B	79.368	4.1	3	3	4.4563	0.00042	4472.3	3574.4	4582.6	3813.2	5890.1	7252.7	6627.9	6006.2	5694.1	5801.6	Low	Enriched	Enriched	Moderate	YES
J3QT77;Q15165-3;	Serum paraoxonase/a	PON2	37.98	17.5	5	5	21.416	0	15469	16928	16183	21013	17208	24152	19574	17353	10722	16518	Enriched	Enriched	Enriched	Enriched	YES
J3QT87;Q96SW2-2	Protein cereblon	CRBN	45.341	5.6	2	2	6.6003	0	13749	12114	12577	10017	14937	8817.6	15353	18630	6897.5	12044	Enriched	Enriched	Enriched	No expres	YES
J3QTA2;Q99933;Q	BAG family molecula	BAG1	38.76	20.9	9	9	23.099	0	23924	15266	21657	22651	24163	25287	27704	25414	18897	30684	Enriched	Enriched	Enriched	Moderate	YES
J3QTA6;Q9BRQ6;	MICOS complex sub	CHCHD6	28.817	25.4	8	8	53.884	0	34391	31717	34546	25964	44543	23063	30211	25987	19721	28096	Moderate	Enriched	Moderate	No expres	YES
J3QTJ6;Q5CZC0;Q	Fibrous sheath-intera	FSIP2	789.88	0.3	2	2	1.9627	0.00801	19276	48424	21280	62156	34809	16828	16854	28830	12465	19104					YES
J9JIC5;Q9HAS0;J3	Protein Njmu-R1	C17orf75	44.609	11.6	7	7	13.367	0	7086.8	4400.7	8077.5	10919	6318.8	11160	11728	8407.2	3879.3	8704.7	No expres	No expres	Moderate	No expres	YES
J9JID7;Q03252	Lamin-B2	LMNB2	69.948	50	57	48	206.52	0	142770	100500	121120	148380	141070	227240	284000	276200	150940	182040	No expres	Low	Low	Moderate	YES
K4DI93;Q13620-1;	Cullin-4B	CUL4B	102.75	18.9	15	11	93.872	0	35371	23711	33376	39054	38343	35459	49021	38784	34022	43833	Low	Enriched	Enriched	Moderate	YES
K7EII6		EML2	18.888	42	9	2	49.327	0	13913	12346	12869	12680	15248	12620	10714	12587	5786.3	11641	Enriched	Enriched	Enriched	Moderate	YES
K7EM02;K7EIJ8;	Katanin p60 ATPase-	KATNAL2	13.999	9.4	2	2	7.6317	0	35156	26238	31481	35088	34196	37629	36913	35643	20019	34239	Low	Moderate	No expres	No expres	YES
K7EIK7;O95834;O	Echinoderm microtul	EML2	84.729	20.4	18	11	45.041	0	83553	64949	73073	64978	85634	62126	108480	75789	93832	70998	Enriched	Enriched	Enriched	Moderate	YES
K7ENA3;W4VSQ8	Protein syndesmos	NUDT16L1	18.944	5.3	1	1	1.8595	0.00878	6472.7	5072.3	4717.8	5209.1	5348.8	4976.7	6717.9	6160.4	3684.4	5456.2	Enriched	Enriched	Moderate	No expres	YES
K7EIU8;Q13485	Mothers against deca	SMAD4	50.052	7	4	4	7.5463	0	10534	5094.7	6155.1	7958.9	8030	9533.1	10534	11007	6235.5	10980	Enriched	Enriched	Enriched	Enriched	
K7EIV2;Q9BU89;	Deoxyhypusine hydr	DOHH	24.385	10.3	2	2	5.8399	0	5479.8	4578.9	5916.7	2879.8	7914	3011	5239.6	2879.2	3477.2	3326.8	Enriched	Moderate	Moderate	Low	
K7EIY6;Q9BV68-2	E3 ubiquitin-protein	RNF126	30.872	4.6	1	1	3.8082	0.00061	14771	8587.2	11205	9756.7	17072	7627.1	6830.5	5098.3	2992.6	7876.5	Enriched	Moderate	Moderate	Low	YES
K7ESQ3;K7EJ64;K7EJZ4;K7EPE5;K7E		TUBB6	10.688	57.3	6	2	6.0023	0	23730	28658	24537	19312	38293	28153	21591	18105	12292	18538	Moderate	Enriched	Enriched	No expres	YES
K7EJE6;K7EK60;	Formin-like protein 1	FMNL1	55.091	6.4	2	2	5.5935	0	9706.6	3752.7	5223.4	14033	4539	7404.3	8406.7	13325	3830.2	9938.1	Enriched	No expres	Low	Moderate	YES
K7EJE8;K7EKE6;	Lon protease homolo	LONP1	93.296	31.1	34	34	152.24	0	205790	152970	193870	211750	210990	198330	220970	312830	109730	250240	Enriched	Enriched	Enriched	Enriched	YES
K7EK09;K7EMM5	Kynurenine formamic	AFMID	12.595	9	1	1	1.9702	0.00802	2892.1	2133.6	2309.3	2386	3629	1370.1	2460.2	2250.6	2599.4	2346.7	Low	Low	No expres	No expres	YES
K7EQ55;K7EK33;	DAZ-associated prot	DAZAP1	43.312	15	7	7	13.336	0	37673	27322	32110	42651	39888	50045	36474	39213	21380	40197	Enriched	Enriched	Enriched	No expres	YES
K7EK56;Q9UFG5;	UPF0449 protein C1	C19orf25	17.116	31.9	3	3	17.003	0	10788	4801.2	6817	15494	5595.4	12721	11366	12722	4475.9	13343	Enriched	Moderate	Moderate	No expres	YES
K7EK91;Q9UFH2-	Dynein heavy chain 1	DNAH17	508.78	0.2	1	1	2.7312	0.00239	5389.9	17100	7672	3782.4	7489.6	4066.9	26799	20032	12394	7025.9	Moderate	No expres	Low	Low	
K7EKI4;K7ELF1;	39S ribosomal protei	MRPL4	14.056	26	2	2	7.0234	0	12685	10151	9898.5	11535	13646	11612	7461.5	8433.1	4068.3	10997	Low	Low	Moderate	No expres	YES
K7EKI8;O60437;K	Periplakin	PPL	204.49	18.1	36	36	80.835	0	145020	111470	127020	184020	137280	135260	141540	157100	89023	183300	Enriched	Enriched	Enriched	Enriched	YES
K7EKP8;O00154-2	Cytosolic acyl coenz	ACOT7	30.849	7.1	3	3	2.8189	0.00223	11253	9324.1	16744	11147	14719	19648	19175	16215	13313	14810	Enriched	Moderate	Moderate	Moderate	YES
K7EKY5		CA4	20.71	34.2	10	3	25.127	0	64795	55182	73693	71433	70596	97776	62276	51721	30047	77507	No expres	Enriched	Moderate	Moderate	YES
K7EL21;Q13938;K	Calcyphosin	CAPS	30.24	16	4	4	11.764	0	18128	17530	16957	21073	19861	18049	9607.2	14462	4397.4	13051	Enriched	Enriched	Moderate	No expres	YES
K7ELC2;P62841;K	40S ribosomal protei	RPS15	17.723	60.5	38	22	198.8	0	636160	443680	579690	734520	625700	734820	696620	695670	320940	583010	Enriched	Enriched	Enriched	Enriched	YES
K7ELC7;P61353	60S ribosomal protei	RPL27	16.359	45.8	23	23	165.6	0	196410	134690	178470	181870	198890	215430	209620	152950	116690	178900	No expres	Enriched	Enriched	Enriched	YES
K7ELH8;Q6ZPD9	Probable C-mannosy	DPY19L3	79.509	4.2	3	3	4.049	0.00062	8768.5	6414	7671.8	6468.7	11701	6872.7	10105	8129.3	7712.4	8968.3	No expres	Enriched	Enriched	No expres	YES
K7ELL7;P14314-2;	Glucosidase 2 subuni	PRKCSH	60.192	37	29	29	323.31	0	208260	163790	174870	151540	220960	178490	210250	186320	135250	180840	Enriched	Enriched	Enriched	Low	YES
K7ELQ9;Q6UW68;	Transmembrane prot	TMEM205	19.27	31.8	10	10	56.607	0	59742	53061	54086	43850	71905	54508	145650	87330	94597	90216	Enriched	Enriched	Enriched	No expres	YES
K7ELV2;Q96EE3;	Nucleoporin SEH1	SEH1L	29.541	25.9	5	5	64.633	0	18219	7554.9	8708	11756	9964.5	11802	14556	19055	6887.7	19468	Moderate	Enriched	Enriched	No expres	YES
K7ELW0;Q99497;	Protein DJ-1	PARK7	17.91	75.7	37	37	262.8	0	259410	163480	209290	257290	218710	280080	406750	475610	142540	286030	No expres	Enriched	Enriched	Enriched	YES
K7EM11;O14908-2	PDZ domain-contain	GIPC1	13.988	35.2	6	6	44.117	0	25533	25655	35179	26410	32260	20180	27081	28990	18680	27528	Enriched	Enriched	Enriched	Enriched	YES
K7EM18;P41567;	Eukaryotic translatio	EIF1;EIF1B	13.607	59.5	17	17	234.41	0	154880	92624	106030	135960	131450	146180	122850	127420	62031	130070	Enriched	Enriched	Enriched	Moderate	YES
K7EM96		VMP1	5.0465	44.4	2	2	33.397	0	22899	13838	19076	24296	23368	22842	22050	19155	10595	23153					
K7EML0		PPY	8.6261	26.6	6	2	3.7461	0.0006	1613.6	1201.5	1934.9	665.82	2634.1	944.91	1432.2	1001.8	1336.4	1069.8	No expres	Moderate	Enriched	Low	
K7EMM8;Q49A26	Putative oxidoreduct	GLYR1	57.215	14.1	8	8	17.823	0	1184.5	747.49	1075.6	1954.7	930.24	6656.2	1583.4	1882.6	824.91	1310.9					YES
K7EN45;Q13526	Peptidyl-prolyl cis-tr	PIN1	9.8329	50	5	5	47.931	0	29843	18938	23693	35425	28520	23261	23002	28861	16758	29037	Enriched	No expres	Moderate	Enriched	YES
K7ENH2;K9J957;P	Proteasome activator	PSME3	20.593	30.2	5	2	56.075	0	82686	46866	54380	87084	58960	76832	64176	81330	38680	86918	Enriched	Enriched	Enriched	Moderate	YES
K7ENJ4		ATP5A1	21.339	51.3	19	1	3.7436	0.0006	5565.6	2566.5	3325.4	3714.5	4722.7	2961.8	4017.6	4369.3	1741.7	5282.3	Enriched	Enriched	Enriched	Moderate	YES
K7ENL9;Q96DM3;	Uncharacterized prot	C18orf8	69.389	7.1	4	4	10.762	0	15314	13113	16393	11601	22530	10972	17706	14349	14583	18833	Moderate	Moderate	Enriched	No expres	YES
K7ERV8;K7ENQ8;	Cytohesin-1	CYTH1	22.388	10.3	1	1	5.1985	0.00022	2017	644.06	1202.3	3590.7	1042.2	2071.8	1325.7	1263.9	1044.2	2277.2	Enriched	Moderate	Moderate	Enriched	
K7ENV7;K7EKW4		ISOC2	19.005	29.1	8	4	10.785	0	1848.6	2186.5	2020.2	838.66	3347.2	641.74	1035.3	916.87	860	932.71	Moderate	Enriched	Enriched	No expres	YES
K7EP46;P52888;K	Thimet oligopeptidas	THOP1	65.119	8.8	4	4	11.888	0	12937	8665.7	10878	14065	15262	14499	21312	15444	10995	17444	Moderate	Low	Moderate	Enriched	YES
K7ER08;K7EQ03;	RNA-binding protein	RBM42	39.897	8.8	4	4	11.285	0	2707.2	2136.2	3950.9	2610.9	3145.8	3544.3	3869.3	3912.7	2255.9	3799.4	Moderate	Enriched	Enriched	Moderate	YES
K7EPI1		QTRT1	13.434	21.8	2	1	18.275	0	11345	8285.1	10208	6365.3	15000	7223.6	8496.6	4887.9	5811.4	9369.4	Enriched	Enriched	Moderate	No expres	YES
K7EPK2		NARS	18.728	17.8	5	1	5.4417	0	14670	7551.8	11887	4629.1	16376	7421	5189.8	4783.6	4479.1	7488.8	No expres	Enriched	Enriched	Enriched	YES
K7EPV5;Q02386	Zinc finger protein 4	ZNF45	15.201	14.7	2	1	3.2912	0.00078	9171.4	8802.2	14571	3950.7	9075.1	15341	41360	11945	39721	9848.8	Enriched	Low	Moderate	No expression	
Q08E86;K7EQ86;	UPF0378 protein KI	KIAA0100	237.31	1.1	2	2	4.912	0.00044	9689.7	12526	12397	9078.3	15302	7326.6	15244	10898	22460	14356	Moderate	Moderate	Enriched	Enriched	YES
K7EQN7		DDX39A	28.832	16.9	7	1	5.8568	0	10895	11229	10854	6965.6	11506	15004	42129	34487	9693.5	16228					
K7EQX8;P84157-2;Q6ZR64		MXRA7	1.9121	100	2	2	19.313	0	14517	13335	14647	19778	16614	19426	24694	39513	14629	29963	No expres	No expres	Low	Enriched	YES
K7ER00;Q9Y285;	Phenylalanine--tRNA	FARSA	62.395	18.1	15	15	41.767	0	121630	91263	100130	93722	132180	107830	107560	92831	70365	96374	Enriched	Enriched	Enriched	Moderate	YES
K7ER74;P02655;V	Apolipoprotein C-II	APOC4-APOC2;APOC2	20.049	18.5	3	3	28.465	0	4712.2	3482.5	12479	3607.8	3611.9	6308.3	4766.7	10200	4707.1	6010.7	Enriched	Enriched	Moderate	No expression	
K7ERC8;Q06136;	3-ketodihydrosphing	KDSR	22.62	12.8	4	4	30.121	0	49179	31313	34488	41043	58810	27290	34841	27215	30588	33415	Enriched	Moderate	Enriched	Enriched	YES
K7ERG9;P00746	Complement factor D	CFD	27.862	26.2	7	6	50.89	0	21595	20614	23711	20662	31227	18130	23277	47146	13366	24710	Enriched	Low	Moderate	Moderate	YES
K7ERI7;P35268;K	60S ribosomal protei	RPL22	11.168	65.3	21	21	79.977	0	123130	89223	109910	85843	135120	88542	221540	121110	151090	105990	Enriched	Enriched	Enriched	No expres	YES
K7ERI9;P02654	Apolipoprotein C-I;T	APOC1	8.647	23.4	3	1	6.4313	0	6488.7	2366.8	2699.5	23034	4697	10439	5728.7	5520.1	1292.3	4225.6	Enriched	Low	Moderate	No expression	
K7ERP3		JUP	11.432	24	5	2	2.2318	0.00528	8524	5739.3	7227.7	7225.1	7713.8	4644.5	6306.8	5988.6	4021.7	6947.6	Enriched	Enriched	Enriched	Moderate	YES
K7ERU7;Q9BQ61;	Uncharacterized prot	C19orf43	13.369	36.8	4	4	23.697	0	15526	13887	16035	14643	20726	11983	17267	15485	8579.8	14407	Enriched	Enriched	Enriched	No expres	YES
K7ES63		TUBB6	12.585	38.8	10	3	5.4871	0	5474.8	5512.3	5067.2	6349.7	5810.3	4595.1	5879.5	6580.9	4344.2	8094.4	Moderate	Enriched	Enriched	No expres	YES
K7ES70;P55083;P	Microfibril-associate	MFAP4	31.326	11.4	6	6	17.062	0	30990	23735	25612	43252	23963	25784	28626	71408	15004	36259	Low	No expres	No expres	Low	YES
K7ESP4;Q8WVC6;	Dephospho-CoA kin	DCAKD	24.177	24.9	5	5	9.8903	0	6765.1	4969.8	5740.7	9238.1	5927	9487.2	6205.6	8830.5	3050.3	8014.4	Moderate	Enriched	Moderate	No expression	
K7N7A8;P29972-4	Aquaporin-1	AQP1	48.685	6.2	4	4	11.132	0	5023.9	3957.3	4490.8	6878.9	4372.8	7887.4	5854.1	9934.9	2890.5	8119.3	Moderate	Enriched	Enriched	Enriched	YES
L0R6Q1		SLC35A4	11.133	11.7	1	1	17.993	0	2014.4	3294.6	4033.7	2272.3	4940	1540	2482.8	1349.1	1180.4	3022.3	Moderate	Enriched	Enriched	No expres	YES
L0R819		ASNSD1	11.25	20.8	2	1	4.7766	0.00043	4420.2	3052.9	3722.4	8511.8	3676.6	6920.8	3928.7	4351.9	3346	5293.5	Enriched	Enriched	Enriched	No expres	YES
M0QWZ7;Q9NP81	Serine--tRNA ligase,	SARS2	58.182	40.2	19	19	132.54	0	61443	49197	58100	53605	67441	65525	91583	103510	46395	76159	Moderate	Moderate	Moderate	No expres	YES
M0QXB4;O14579;	Coatomer subunit ep	COPE	36.923	43.8	27	27	184.73	0	187580	89374	103310	155330	106730	242310	260140	321160	105810	227040	No expres	Enriched	Enriched	Low	YES
M0QXF7		C19orf10	9.5594	41.7	5	1	2.2728	0.00494	3244.6	2916.1	3139.6	1900.7	4120.8	4590.8	26008	10882	21799	4469.7	Enriched	Enriched	Enriched	Enriched	YES
M0QXF9;O15382;	Branched-chain-amin	BCAT2	49.967	31.5	27	27	141.27	0	399890	334640	315600	213920	299790	264270	220730	208380	117850	211820	Moderate	Enriched	Enriched	Moderate	YES
M0QY37		TUBB4A	12.031	57.8	16	1	15.404	0	12506	13015	10469	6649.4	19922	1770.4	2060.4	1400.4	1281.6	4734.9					YES
M0QY77;Q9BQD3	KxDL motif-containi	KXD1	21.864	5.6	1	1	2.7138	0.00238	581.58	246.7	553.94	440.25	669.55	578.32	731.23	209.73	597.41	693.04					
M0QY97;Q9UPT8	Zinc finger CCCH do	ZC3H4	95.425	10.5	6	6	66.452	0	19886	20383	23048	13788	29861	14672	27266	26007	20842	23906	Enriched	Enriched	Enriched	Moderate	YES
M0QYS1;P40429;	60S ribosomal protei	RPL13A;RPL13a;RPL1	24.104	37.6	20	20	74.353	0	191580	104390	127230	131360	160380	337610	218880	213400	107600	135790	Enriched	Enriched	Enriched	Enriched	YES
M0QYT9;Q14653;	Interferon regulatory	IRF3	30.779	31.3	8	8	15.664	0	25807	21049	23380	29783	25480	24181	25750	27332	15606	29852	Enriched	Enriched	Enriched	Moderate	YES
M0R0N4;X6R390;	AP-2 complex subun	AP2S1	17.303	24.3	4	4	10.085	0	23453	27932	25967	16761	20777	10895	10006	20876	5047.1	20673	Enriched	Enriched	Enriched	Moderate	YES
M0QZ52		CALM3	9.3542	62.7	14	5	10.82	0	8829.6	7915.5	8704.3	14218	10125	7045.7	9522.9	6026.5	6263.2	7465.9	Moderate	Enriched	Enriched	Moderate	
M0QZM1		HNRNPM	39.933	47	26	1	8.3231	0	3464.1	3864.1	5482.3	2283.6	3425.3	7985.5	12030	11423	6358.5	9264.8	No expres	Enriched	Enriched	Enriched	YES
M0QZR4;Q92888-	Rho guanine nucleoti	ARHGEF1	108.32	13.1	11	11	48.471	0	34052	31645	32926	34052	39397	36178	47633	36790	25029	41098	Enriched	Moderate	Moderate	Enriched	YES
M0QZS6		SAE1	29.422	52.5	16	2	68.858	0	46091	56137	54042	50939	74944	35043	48071	51710	31323	47481	Enriched	Moderate	Enriched	No expres	YES
M0R0F0;P46782;	40S ribosomal protei	RPS5	22.391	53.5	29	29	117.87	0	126820	93708	121150	127400	134440	155580	253400	237040	168030	130920	No expres	Enriched	Enriched	Enriched	YES
M0R300;M0R0P8;	Unconventional myo	MYO9B	234.23	1.2	2	2	7.9898	0	12304	10709	12984	11107	15503	11839	14806	14671	10249	17905	Enriched	Moderate	Moderate	Moderate	YES
M0R105		SUPT5H	6.2669	29.6	4	3	8.4093	0	11409	11008	14604	6413.1	15972	4304.4	5443.3	5065.2	3325.7	7396.8	Enriched	Enriched	Enriched	Enriched	YES
M0R140		RPS19	11.051	49	11	2	1.8049	0.00989	5055.2	8712.6	5924.2	3329.6	9757.3	4429.7	7340.1	6121.3	7872.2	4815.5	Enriched	Enriched	Enriched	Enriched	YES
M0R3D6;M0R1A7	60S ribosomal protei	RPL18A	16.714	56.7	16	16	33.196	0	43813	27128	35137	33092	45345	35978	90271	61575	33738	38994	Enriched	Enriched	Enriched	Enriched	YES
M0R1I1		TUBB4A	7.7774	35.1	9	5	11.384	0	32082	22506	27430	36510	32461	40454	30279	18856	18746	30224					YES
M0R1Q1		C3	11.239	35.9	4	2	4.2991	0.00063	1303	1937.8	2366.3	732.9	2486.5	1464.8	4575	7742.3	6800.7	2124.6	Enriched	Enriched	Enriched	No expres	YES
M0R1T5;O43633	Charged multivesicul	CHMP2A	24.781	15.9	8	8	77.49	0	11831	12669	17997	13625	17919	14923	24773	35759	17251	22760	Moderate	Enriched	Enriched	Enriched	YES
M0R208;Q16740	ATP-dependent Clp	CLPP	20.568	21.6	4	4	14.318	0	6180.6	4167.6	4737.9	8939.3	5830.1	7213.1	10383	17560	7097.1	9768.1	Low	Enriched	Enriched	Low	YES
M0R248		ECH1	29.139	35.2	20	2	3.162	0.00077	2978.3	2259.8	2310.7	1724	3638.6	1998.7	2558.3	2027.7	2092.7	3014.7	Moderate	Enriched	Enriched	Enriched	YES
M0R268;P09012;	U1 small nuclear rib	SNRPA	28.388	10.5	3	2	2.0153	0.00771	7106.4	9257.9	7968.9	3935.3	10906	3962.8	8942.2	9117	8066.8	7075.4	Low	Enriched	Enriched	Enriched	YES
M0R2A0;Q5UCC4	ER membrane protei	EMC10	38.975	8.4	4	4	3.818	0.00061	10906	7851.9	8839.2	10062	12044	8274.7	7703.3	8332.5	4289.5	8186.7					
M0R2B0;M0R2U2;M0R1H0		FBL	18.198	34.6	11	2	27.289	0	8467	5858.7	6133.2	4886.4	8674.2	7303.7	5853.1	5030.5	2432.2	7249.8	Enriched	Enriched	Enriched	Enriched	YES
M0R2K9;Q14318;	Peptidyl-prolyl cis-tr	FKBP8	27.527	11.3	2	2	75.56	0	5456.9	7092.8	6178.7	6193.7	7310.8	6911.8	11804	14762	6161.6	9219.3	Enriched	Moderate	Moderate	Low	YES
M0R2T0		HNRNPM	38.226	52.9	39	1	2.772	0.0024	16735	18211	27767	7046.7	34691	13594	15796	7059	6123.1	10169	No expres	Enriched	Enriched	Enriched	YES
M0R2X2;Q7Z3K3-	Pogo transposable el	POGZ	11.203	11.9	2	2	4.5132	0.00042	2690	3242.4	4511	1469.8	4534.6	849.98	2231.7	1943.5	2510.3	2616.7	Enriched	Enriched	Enriched	Enriched	YES
O00115-2;O00115	Deoxyribonuclease-2	DNASE2	33.615	3.6	1	1	2.1163	0.00625	3098.1	3036	3323.5	2284	4269.2	1899.7	2807.9	2182.9	2140.7	2281	Enriched	Enriched	Enriched	Low	YES
O00116	Alkyldihydroxyaceto	AGPS	72.911	16.4	9	9	115.03	0	23776	16894	16244	22243	18001	14440	18335	24773	11568	26450	Moderate	Enriched	Moderate	Moderate	YES
O00148	ATP-dependent RNA	DDX39A	49.129	23.4	22	1	2.2756	0.00495	7065.3	3543.6	3642.9	5260.2	5082.4	4425.2	5642.8	6261.9	2094.3	5877.2					
O00151	PDZ and LIM domai	PDLIM1	36.071	36.5	17	17	55.037	0	25377	20575	21653	19755	25353	14442	25874	22223	32526	23772	Enriched	Enriched	Enriched	Enriched	YES
O00160	Unconventional myo	MYO1F	124.84	5	6	4	4.4534	0.00042	6376.9	4650.1	6554.9	9839.2	5170.3	7207.9	9283.4	11696	6500.1	9650.4	Enriched	Low	Low	Moderate	YES
O00161;O00161-2;	Synaptosomal-assoc	SNAP23	23.354	52.1	12	12	103.25	0	76770	65392	74658	71105	72129	86399	112960	98192	49564	116770	Enriched	Enriched	Enriched	No expres	YES
O00165-5;O00165;	HCLS1-associated pr	HAX1	26.099	35.1	8	8	15.045	0	17489	9477.1	12341	13498	14512	25142	13602	10639	6528.9	12873	Enriched	Enriched	Enriched	Enriched	YES
O00170;E9PMH2	AH receptor-interacti	AIP	37.636	17.3	5	5	12.706	0	26365	22579	24843	28676	29270	22988	22777	39275	12843	28112	Enriched	Enriched	Enriched	Moderate	YES
O00178	GTP-binding protein	GTPBP1	72.453	14.9	9	9	23.412	0	31791	23529	24660	27341	29826	33353	41316	42562	20878	37528	Moderate	Enriched	Enriched	Moderate	YES
O00182-2;O00182	Galectin-9	LGALS9	35.888	3.7	1	1	3.0053	0.00151	6249	4676.3	4577.8	6971.7	5713.9	4986	4805	3319.5	1621.8	4832.7	Enriched	Low	Moderate	Enriched	YES
O00186	Syntaxin-binding pro	STXBP3	67.764	18.2	13	13	59.118	0	49193	32202	36134	42656	41100	45853	38362	48316	21780	49701	Moderate	Moderate	Enriched	Enriched	YES
O00193;E9PM92	Small acidic protein	SMAP;C11orf58	20.332	35.5	17	17	181.21	0	78852	61620	95617	50525	109080	70268	92311	106750	48513	75666	No expres	Enriched	Enriched	Moderate	
O00203;O00203-3	AP-3 complex subun	AP3B1	121.32	25.3	33	30	113.68	0	142300	95474	103330	115340	139620	133120	110850	121090	57917	114830	Low	Enriched	Enriched	Enriched	YES
O00217;E9PPW7;	NADH dehydrogenas	NDUFS8	23.705	26.2	8	8	26.21	0	85699	54868	56567	51745	70951	69759	76829	106930	30730	64567	Enriched	Enriched	Enriched	Moderate	YES
O00231;O00231-2	26S proteasome non-	PSMD11	47.463	47.6	32	32	94.046	0	109370	85298	103440	97230	132920	118070	130860	118690	68103	101360	Low	Enriched	Enriched	No expres	YES
O00232;O00232-2	26S proteasome non-	PSMD12	52.904	31.4	26	26	144.25	0	138150	110450	136280	139300	148440	126890	125340	144940	62057	131540	Moderate	Enriched	Enriched	Moderate	YES
O00264;O00264-2	Membrane-associate	PGRMC1	21.671	15.9	5	5	9.0516	0	10188	17903	15071	8024.6	12258	11596	20735	29544	12233	13688	Enriched	Enriched	Enriched	Enriched	YES
O00267-2;O00267;	Transcription elongat	SUPT5H	120.5	11.6	11	11	30.051	0	47687	32048	40530	38209	44569	53134	69731	65869	31876	53625	Enriched	Enriched	Enriched	Enriched	YES
O00273;O00273-2	DNA fragmentation f	DFFA	36.521	18.7	5	5	11.625	0	31780	20959	29668	21530	31986	29060	37364	17567	23548	31265	Moderate	Enriched	Enriched	Moderate	YES
O00299	Chloride intracellula	CLIC1	26.922	51.5	22	22	206.42	0	116470	80714	96116	138910	94864	113400	130830	163670	86188	135510	Enriched	Enriched	Enriched	Enriched	YES
O00303;H0YDT6	Eukaryotic translatio	EIF3F	37.563	31.1	12	12	30.365	0	85711	44675	70384	61407	74267	80317	69210	70506	32202	61957	No expres	Enriched	Enriched	Enriched	YES
O00308-2;O00308;	NEDD4-like E3 ubiq	WWP2	86.307	4.4	3	2	6.0151	0	7491.2	6610.8	6713.7	6241.3	7958.3	6942.2	7389.3	7810.4	5202.3	8001.9	Enriched	Enriched	Enriched	Low	
O00330-3;O00330	Pyruvate dehydrogen	PDHX	51.459	20.4	9	9	43.353	0	23249	19038	21422	20550	24573	27973	23822	25828	12604	27576	Moderate	Moderate	Enriched	Moderate	YES
O00339-3;O00339-	Matrilin-2	MATN2	102.23	5.2	4	4	7.4792	0	2485.8	2418.7	4842.4	2421.1	5403.8	5117.4	6233.4	2671.1	2368	3287.3	Enriched	Low	Moderate	No expres	YES
O00391-2;O00391	Sulfhydryl oxidase 1	QSOX1	66.86	5.1	3	3	4.1996	0.00062	14420	13053	14275	16315	13809	11517	12161	12436	5964.4	14230	Enriched	Enriched	Enriched	Moderate	YES
O00399	Dynactin subunit 6	DCTN6	20.747	14.2	6	6	12.621	0	26198	26198	24057	18945	37411	15268	25941	14942	33820	26028	Moderate	Enriched	Enriched	Enriched	YES
O00400;H7C562	Acetyl-coenzyme A t	SLC33A1	60.908	9.5	5	5	8.0287	0	36798	26801	29445	34779	43849	30608	28640	30784	14644	32347	Moderate	Enriched	Enriched	Enriched	YES
O00401	Neural Wiskott-Aldri	WASL	54.826	11.3	4	4	11.717	0	34484	19122	24067	34433	24110	41024	48946	33036	25155	38864	Moderate	Enriched	Enriched	No expres	YES
O00410;O00410-3;	Importin-5	IPO5	123.63	22.2	31	30	212.86	0	134390	80155	102860	144600	117050	141000	132190	168380	60048	125740	Enriched	Enriched	Enriched	Moderate	YES
O00418;H3BRH4	Eukaryotic elongatio	EEF2K	82.143	3	2	2	5.3881	0	6823.9	6661.3	7011.9	5127.4	10220	5997.8	12677	8733.1	18873	8846.5	Enriched	Enriched	Enriched	No expres	YES
O00429;O00429-6;	Dynamin-1-like prot	DNM1L	81.876	32.5	26	1	92.923	0	8320.4	8919.1	10923	7981.1	11297	6333.1	7743.8	7190.6	9358.4	8257.4	Enriched	Enriched	Enriched	Low	YES
O00442;O00442-2	RNA 3-terminal phos	RTCA	39.336	32.8	21	21	46.902	0	109190	65185	95116	92128	99542	108380	108300	104760	60445	91931					YES
O00458;C9JA65;O	Interferon-related de	IFRD1	50.268	10	4	4	88.299	0	3782.8	3847.4	3918.3	3548.4	5937.5	3333.5	5428.6	4230.9	4540	5352.7	Enriched	Enriched	Enriched	Enriched	
O00468-6;O00468-	Agrin;Agrin N-termin	AGRN	214.84	27.5	65	65	323.31	0	300850	272290	367340	271380	448860	236660	363600	334710	193550	296850	Enriched	Enriched	Enriched	Enriched	YES
O00479	High mobility group	HMGN4	9.5388	31.1	7	7	69.543	0	7067.7	5055.3	7648.9	5697.7	9789.1	10015	108990	29096	91102	37481	Enriched	Enriched	Enriched	Enriched	YES
O00483	Cytochrome c oxidas	NDUFA4	9.3697	44.4	5	5	10.318	0	14679	9882.2	11515	13671	10872	12933	39465	19045	17633	17919	Enriched	Enriched	Enriched	No expres	YES
O00487	26S proteasome non-	PSMD14	34.577	18.4	7	7	37.828	0	17919	17291	23792	11150	29265	21139	56436	47701	18145	19383	Enriched	Enriched	Enriched	Enriched	YES
O00488	Zinc finger protein 5	ZNF593	15.199	13.4	1	1	3.0842	0.00114	2359.9	967.74	1662	2198.8	1803.2	4343.9	1797.8	1520.8	523.35	1911.7	Enriched	Enriched	Enriched	No expres	YES
O00499-9;O00499-	Myc box-dependent-	BIN1	45.563	17.8	7	7	60.093	0	55214	47779	49189	49008	51091	60716	88547	91971	30525	56227	Enriched	Enriched	Moderate	Moderate	YES
O00505	Importin subunit alp	KPNA3	57.81	8.1	6	2	3.0505	0.00133	2049.9	1889.7	1239.7	1457.2	2211.6	379.71	1039.5	771.11	1140.3	1506.2	Enriched	Enriched	Enriched	Low	YES
O00515;E9PDI4	Ladinin-1	LAD1	57.13	29.2	19	19	168.27	0	57964	55724	53658	70419	70889	52953	84698	71484	57476	79790	Enriched	Enriched	Enriched	Enriched	YES

O00519	Fatty-acid amide hyd	FAAH	63.065	11.7	7	7	18.537	0	16627	11693	13628	12770	23287	14448	9992.4	8324	6522.7	8433.3	No expres	Moderate	Moderate	Low		YES	
O00534	von Willebrand facto	VWA5A	86.488	13.2	12	12	55.873	0	31708	27860	36320	33525	42237	18227	25803	19997	17749	25537	Enriched	Enriched	Enriched	Enriched		YES	
O00566;U3KQ48	U3 small nucleolar ri	MPHOSPH10	78.863	4.1	2	2	6.0618	0	6608.5	4384.6	6013.5	6547.9	5903.3	6170	18031	6590	21234	12762	Enriched	Moderate	Moderate	Enriched		YES	
O00567	Nucleolar protein 56	NOP56	66.049	41.2	45	45	224.22	0	296290	188800	245280	279440	312140	281730	232280	260400	112630	275280	Enriched	Enriched	Enriched	Enriched		YES	
O00571;O00571-2	ATP-dependent RNA	DDX3X	73.243	42	41	10	185.47	0	248190	130170	165560	243560	180330	224560	322300	348210	155340	235230	Enriched	Enriched	Enriched	Moderate		YES	
O00592-2;O00592	Podocalyxin	PODXL	55.385	5.9	4	4	8.9108	0	14302	9880.6	14079	11227	24814	15048	15060	13539	5546.3	15644	Low	Enriched	Enriched	Enriched		YES	
O00625	Pirin	PIR	32.113	7.9	2	2	3.6349	0.0008	3238.6	2798.5	3263.8	6848.9	3567.3	3141.7	4155.4	5296.9	3159.4	6231	No expres	No expres	Moderate	Moderate		YES	
O00629	Importin subunit alpl	KPNA4	57.886	12.1	8	0	23.136	0	55956	61791	55561	48624	65610	29376	40501	42279	22451	42926	Enriched	Enriched	Enriched	Enriched		YES	
O00743-2;O00743;	Serine/threonine-prot	PPP6C	32.532	20.5	5	4	5.8629	0	22358	19610	23198	12593	18965	12324	32521	18899	21701	17583	Enriched	Enriched	Enriched	Enriched		YES	
O00754-2;O00754	Lysosomal alpha-mar	MAN2B1	113.61	9.9	11	11	56.635	0	43131	35807	37167	47005	36933	39662	33443	44803	18930	42026	Enriched	Enriched	Enriched	Moderate		YES	
O00763-3;O00763-	Acetyl-CoA carboxyl	ACACB	255.09	3.3	6	2	12.156	0	18661	14702	16748	24199	18550	17254	16309	18896	9951.2	24412	Moderate	Enriched	Enriched	Moderate		YES	
O00764;F2Z2Y4;O	Pyridoxal kinase	PDXK	35.102	38.5	25	25	102.72	0	125220	102350	134790	111930	164190	117350	155160	136240	81447	119030	Enriched	Enriched	Enriched	Moderate		YES	
O00767	Acyl-CoA desaturase	SCD	41.522	3.6	1	1	11.147	0	4108.5	5685.5	4952.7	11207	5475.4	3252.1	3158.6	4160	2752.1	36672	No expres	No expres	Enriched	Low			
O14495	Lipid phosphate phos	PPAP2B	35.116	11.6	4	4	14.128	0	12777	9144.8	11177	10584	9645.6	12231	11396	12638	12608	15337	Enriched	Enriched	Enriched	Moderate		YES	
O14497-3;O14497;	AT-rich interactive do	ARID1A	205.92	3.8	5	4	23.997	0	19497	16435	19754	18712	21045	16960	22383	20384	14311	19965	Enriched	Enriched	Enriched	Enriched		YES	
O14558;K7EP04	Heat shock protein be	HSPB6	17.135	40	11	11	31.917	0	29775	24659	33662	59940	31241	35483	44175	47594	25857	47219	Low	Moderate	Moderate	No expres		YES	
O14561;H3BNK3	Acyl carrier protein, i	NDUFAB1	17.417	30.8	11	11	67.667	0	117040	64638	69973	90681	70502	118020	79728	182250	35171	128210	Enriched	Enriched	Enriched	Enriched		YES	
O14617-5;O14617-	AP-3 complex subun	AP3D1	136.65	21.1	30	30	80.683	0	92330	81646	80675	103320	101490	76300	82806	71997	62395	78499	Enriched	Enriched	Enriched	Enriched		YES	
Q5T6N4;O14639-2	Actin-binding LIM pi	ABLIM1	95.526	19.9	15	4	50.266	0	29028	23944	28135	30372	32398	49969	35839	36896	29778	39799	Enriched	Enriched	Enriched	Enriched		YES	
O14647-2;O14647	Chromodomain-helic	CHD2	200.56	0.6	1	1	2.0937	0.00673	3321.2	2858.3	3009.2	2474.3	3494.3	1805.3	2772	2212.4	1287.4	1777.6	Moderate	Enriched	Enriched	No expres		YES	
O14656	Torsin-1A	TOR1A	37.808	7.8	4	4	15.006	0	16989	9658.2	17962	33273	13882	15305	15933	22136	10238	22039	Moderate	Enriched	Enriched	Enriched			
O14657	Torsin-1B	TOR1B	37.978	6.8	3	3	5.7458	0	3435.7	3677.2	3739.6	3590.7	3518.8	3505.7	11420	5178.1	9043.9	7823.3	Moderate	Enriched	Enriched	Moderate		YES	
O14672;O14672-2	Disintegrin and metal	ADAM10	84.141	13.8	11	11	26.375	0	12026	11787	11888	7708.6	14854	8219.3	14154	12344	7730.9	12393	Enriched	Enriched	Enriched	Moderate		YES	
O14732-2;O14732	Inositol monophosph	IMPA2	28.511	46.4	24	24	240.25	0	133210	56214	92578	103650	104080	124670	137380	149300	67755	150830	Enriched	Enriched	Enriched	Enriched		YES	
O14737;K7EQA1;(	Programmed cell dea	PDCD5	14.285	36	7	7	14.667	0	9812.9	6541.3	7264.4	13174	7613.1	12330	13056	35826	7926.9	12532	Moderate	Moderate	Enriched	No expres		YES	
O14744-5;O14744;	Protein arginine N-m	PRMT5	67.673	17	13	13	61.086	0	36450	18713	22236	27570	25424	70292	59019	78323	18910	44243	No expres	Enriched	Enriched	No expres		YES	
O14745;J3QRP6	Na(+)/H(+) exchange	SLC9A3R1	38.868	39.7	20	19	109.43	0	59106	55752	69032	72810	78006	73181	120650	116160	64877	92866	Enriched	Enriched	Enriched	Enriched		YES	
O14773-2;O14773	Tripeptidyl-peptidase	TPP1	34.463	19.7	10	10	28.627	0	49373	43109	44859	55292	51756	57257	46818	48468	28187	39562	Enriched	Enriched	Enriched	Enriched		YES	
O14776-2;O14776;	Transcription elongat	TCERG1	121.69	13.8	16	15	50.693	0	87628	67400	99956	61300	101300	75282	54760	73146	29887	80213	Low	Enriched	Enriched	Moderate		YES	
O14791-3;O14791;	Apolipoprotein L1	APOL1	42.158	7.9	2	2	24.667	0	1869.9	2458.1	2725.5	2108.4	2941.8	3680.1	4258.2	23973	3103.5	5305.6	Moderate	Low	Moderate	No expres		YES	
O14802	DNA-directed RNA p	POLR3A	155.64	3.2	4	4	17.178	0	12864	15676	12450	11622	20951	11193	13522	10374	6278.3	14077	Low	Enriched	Enriched	No expres		YES	
O14818;O14818-2;	Proteasome subunit a	PSMA7	27.887	46	24	24	243.97	0	159790	118320	136600	135670	151070	150860	129060	140020	55444	139510	Enriched	Enriched	Enriched	Moderate		YES	
O14828;O14828-2	Secretory carrier-assc	SCAMP3	38.287	17.3	7	7	18.424	0	14208	13772	11172	22126	11666	14005	11245	17536	6860.8	11302	Moderate	Enriched	Enriched	Enriched		YES	
O14841	5-oxoprolinase	OPLAH	137.46	18.9	19	19	88.114	0	58315	33392	39551	61382	44009	44802	40762	41818	22492	49516	Enriched	Low	Low	Enriched		YES	
O14874-2;O14874-	[3-methyl-2-oxobuta	BCKDK	37.767	25.1	6	6	23.454	0	38423	31731	43743	77864	33220	36535	59078	62193	35480	58316	Enriched	Enriched	Enriched	Low		YES	
Q5VV89;O14880;(	Microsomal glutathio	MGST3	18.416	23.5	7	7	13.492	0	24562	33742	32696	13944	39858	46430	40772	29116	26014	29762	Enriched	Enriched	Enriched	No expres		YES	
O14907	Tax1-binding protein	TAX1BP3	13.735	13.7	1	1	107.2	0	16901	10126	8760.9	18876	6699.2	10713	9280.5	17792	4985.7	17680	Enriched	Enriched	Enriched	Enriched		YES	
O14920-4;O14920-	Inhibitor of nuclear f	IKBKB	79.508	7.6	4	4	14.97	0	21406	18503	19617	19931	22310	18744	23696	33141	20901	26661	Enriched	Moderate	Enriched	Low		YES	
O14925;Q5SRD1;E	Mitochondrial impor	TIMM23;TIMM23B	21.943	12.9	3	3	8.8577	0	13318	10946	11399	12536	15095	12151	14842	14321	8404.3	15661	Enriched	Enriched	Enriched	No expres		YES	
O14933-2;O14933	Ubiquitin/ISG15-con	UBE2L6	10.086	19.5	2	2	4.8724	0.00043	2124	720.47	1098.2	3309.2	921.81	2254.6	2010	5031	955.69	2504.2	Enriched	Enriched	Enriched	Moderate			
O14936-3;O14936;	Peripheral plasma me	CASK	102.11	22.1	22	22	52.264	0	88681	54864	62697	104290	77856	77935	87727	104650	37084	76495	Enriched	Enriched	Enriched	Moderate		YES	
O14939-4;O14939;	Phospholipase D2	PLD2	104.66	2.4	2	2	2.5532	0.00344	4251.8	2143.3	3467.8	3357.4	4038.7	3805.8	5095.7	4639	2969.5	3808.2	Enriched	Moderate	Moderate	Moderate		YES	
O14949	Cytochrome b-c1 cor	UQCRQ	9.9062	23.2	3	3	5.7846	0	13237	8584.9	11624	13912	15279	13949	10701	10782	5176.2	14208	Enriched	Enriched	Enriched	Enriched		YES	
O14964-2;O14964;	Hepatocyte growth fa	HGS	76.375	14.9	11	11	19.172	0	30209	19144	27144	27176	25474	29880	44088	40601	20230	46983	Enriched	Enriched	Enriched	Enriched		YES	
O14974-4;O14974;	Protein phosphatase 1	PPP1R12A	109.1	19.4	23	22	86.478	0	112130	89796	83190	106310	109240	105410	119180	124510	64646	110170	Low	Low	Enriched	Low		YES	
O14975-2;O14975;	Very long-chain acyl-	SLC27A2	64.615	8.8	6	6	8.2069	0	22001	22050	24507	17010	25977	14686	16769	16453	10036	16656	No expres	Low	Moderate	Low		YES	
O14976;O14976-2	Cyclin-G-associated l	GAK	143.19	11.6	18	18	36.745	0	47518	35215	40168	42543	49546	53467	83227	65306	61147	84648	Enriched	Enriched	Enriched	Enriched		YES	
O14980	Exportin-1	XPO1	123.38	30.2	41	41	209.27	0	209510	144860	197540	195630	178950	199130	220060	306880	104940	244750	Enriched	Enriched	Enriched	Enriched		YES	
O15020-2;O15020	Spectrin beta chain, r	SPTBN2	268.31	17	50	36	126.63	0	147650	107010	126660	118740	154580	141640	134790	140040	86419	120250	No expres	Low	Low	No expres		YES	
O15031	Plexin-B2	PLXNB2	205.12	12	19	19	42.56	0	52601	43260	50172	54100	57234	49343	48468	46061	31859	51400	Enriched	Enriched	Enriched	Enriched		YES	
O15037	Protein KHNYN	KHNYN	74.533	4.3	3	3	6.3251	0	6897	6612.2	6228.1	5654.5	7313.8	4379.8	6810.1	8633	6275.4	7573.4						YES	
O15042-2;O15042;	U2 snRNP-associatec	U2SURP	118.23	17	18	16	118.77	0	66811	54180	65542	61457	72358	51104	64196	69814	37041	69187						YES	
O15066-2;O15066	Kinesin-like protein I	KIF3B	43.269	12.9	5	5	8.743	0	15109	14758	13584	12956	20381	10519	12688	10160	8612.1	13000	Enriched	Enriched	Enriched	Low		YES	
O15067	Phosphoribosylformy	PFAS	144.73	14.3	20	20	63.022	0	51814	41117	52217	48751	59033	41964	51148	41259	28667	47941	Low	Low	Moderate	Moderate		YES	
Q5VZY9;O15075-2	Serine/threonine-prot	DCLK1;DCX	40.456	6.9	2	2	6.7523	0	2574.5	1651.2	2612.3	4287.4	2023.6	4329.8	2163.8	2434.2	1808.5	3522	Low	Moderate	Low	Moderate			
O15084;O15084-4;	Serine/threonine-prot	ANKRD28	112.96	6.5	7	6	19.521	0	19228	14811	17930	16815	19282	18616	16688	17393	9137.3	19076	Moderate	Enriched	Enriched	No expres		YES	
O15116;E5RJ47;E5	U6 snRNA-associatec	LSM1	15.179	12	2	2	3.0464	0.00132	21450	40047	39703	11426	38790	7577.7	16761	9785.7	11629	12153	Enriched	Enriched	Enriched	Moderate		YES	
O15118;K7EQ23;C	Niemann-Pick C1 prc	NPC1	142.17	1.9	2	2	6.9313	0	12612	7643.4	9547.4	10039	9559.8	12812	16296	18406	9671.8	12252	Moderate	Moderate	Enriched	Enriched			
O15120;O15120-2	1-acyl-sn-glycerol-3-	AGPAT2	30.914	12.6	4	4	32.794	0	9841.3	9603	10994	10461	12745	7231.7	10491	9819.7	6429	10218	Enriched	Enriched	Enriched	Moderate		YES	
O15121	Sphingolipid delta(4)	DEGS1	37.866	9.9	4	4	9.9151	0	17386	9986.7	15826	22927	13452	20034	15141	19588	8744	20606	Enriched	Moderate	Enriched	Enriched			
O15126;A0A087W	Secretory carrier-assc	SCAMP1	37.92	17.8	7	7	19.478	0	18376	12305	15606	13964	24750	14034	16440	14185	11805	15716	Enriched	Enriched	Enriched	Moderate		YES	
O15127	Secretory carrier-assc	SCAMP2	36.648	13.7	8	8	43.167	0	28271	26022	27670	31019	31293	22388	31456	29967	21370	29546	Enriched	Enriched	Enriched	No expres		YES	
O15143;C9JBJ7;C9	Actin-related protein	ARPC1B	40.949	32.8	16	16	158.68	0	66696	44696	50183	82013	57518	68139	75177	69900	74194	99045	Enriched	Enriched	Enriched	Moderate		YES	
O15144	Actin-related protein	ARPC2	34.333	38.3	18	15	66.928	0	109430	73774	90896	107860	99349	123390	180840	200190	61406	112420	Enriched	Enriched	Enriched	Enriched		YES	
O15145;C9JZD1;F	Actin-related protein	ARPC3	20.546	36	10	10	26.88	0	48053	39558	40382	51628	53818	56700	132180	114610	71781	68466	Moderate	Enriched	Enriched	Low		YES	
O15160;E7EQB9;C	DNA-directed RNA p	POLR1C	39.249	21.7	8	8	14.192	0	24524	13479	18740	19129	18229	18865	14583	17650	9379.4	22739	Enriched	Moderate	Enriched	Enriched		YES	
O15173;O15173-2;	Membrane-associatec	PGRMC2	23.818	36.8	19	18	319.94	0	96622	86233	104220	82001	163200	79115	81888	54936	37820	65116	Enriched	Moderate	Enriched	Enriched		YES	
O15212;A2AB88	Prefoldin subunit 6	PFDN6	14.582	25.6	4	4	9.578	0	19255	18166	13970	16197	19343	10825	9199.4	10731	6749.4	10785	Low	Enriched	Enriched	Moderate		YES	
O15213	WD repeat-containing	WDR46	68.07	4.3	3	3	8.7446	0	4598.2	3911.1	6065.6	2686.2	6694.1	2105.8	6129	3025.4	2918.6	2966.1	Moderate	Low	Moderate	Moderate		YES	
O15230	Laminin subunit alph	LAMA5	399.73	27.4	136	135	323.31	0	509730	445290	538070	498270	606530	471440	741840	679010	349000	675660	Enriched	Enriched	Enriched	Moderate		YES	
O15231-4;O15231-	Zinc finger protein 18	ZNF185	67.281	14.3	8	8	51.313	0	9584.5	7977.4	8418.9	8482.2	7348.6	8854.6	11059	12138	6476.2	12555	Enriched	Moderate	Moderate	No expres		YES	
O15235	28S ribosomal protei	MRPS12	15.173	15.2	2	2	4.1416	0.00062	16151	13057	14720	11106	24978	8682.4	16213	11648	13982	16832	Low	Enriched	Enriched	Enriched			
O15240	Neurosecretory prote	VGF	67.257	28.3	20	20	86.303	0	43704	47159	64696	34331	80578	33772	80373	58769	103280	108770	Enriched	Moderate	Enriched	Enriched		YES	
O15247	Chloride intracellulai	CLIC2	28.356	24.3	6	5	24.348	0	17516	17445	21375	16325	26373	15154	17197	17333	9340.9	15195	No expres	No expres	Low	No expres		YES	
O15254-2;O15254	Peroxisomal acyl-coe	ACOX3	69.574	3.7	2	2	11.054	0	11430	7325.7	11910	17477	7627.3	8406.8	9584.7	16866	5330.8	13271	Enriched	Moderate	Moderate	No expression			
Q9P0H9;O15258;Q	Protein RER1	RER1	24.817	21	5	5	24.525	0	18335	14965	13495	18232	19734	32681	35317	35010	10666	17373	Enriched	Enriched	Enriched	Enriched		YES	
Q5T8U5;O15260-2	Surfeit locus protein	SURF4	21.127	26.9	12	12	86.948	0	83995	57984	69484	111020	78070	154800	89236	107910	41760	77453	Low	Enriched	Enriched	No expres		YES	
O15264;O15264-2	Mitogen-activated pr	MAPK13	42.089	11.8	4	4	7.0298	0	11815	10875	9983.4	10930	11961	10341	8277.3	6667.7	5434.4	9855.1	Enriched	Enriched	Enriched	Moderate		YES	
O15269	Serine palmitoyltrans	SPTLC1	52.743	16.7	7	7	16.804	0	26484	19346	22650	19320	24402	20974	25419	21886	15799	20478	Moderate	Enriched	Enriched	Enriched		YES	
O15294-3;O15294;	UDP-N-acetylglucosa	OGT	115.7	10	10	10	18.301	0	37200	34087	36071	31064	42569	42197	49296	35804	33556	36357	Enriched	Enriched	Enriched	Enriched		YES	
O15305;H3BV55;I	Phosphomannomutas	PMM2	28.082	50	18	18	106.21	0	180300	100600	120040	144060	142540	240820	199010	139550	73502	147990	Enriched	Enriched	Enriched	Moderate		YES	
O15320-8;O15320-	cTAGE family memb	CTAGE5	81.84	28.2	24	1	69.411	0	55003	43708	47734	46879	63901	47481	65296	33182	37681	41584	Enriched	Low	Moderate	Enriched		YES	
O15355	Protein phosphatase 1	PPM1G	59.271	19.2	10	10	42.769	0	21985	15216	17271	27478	19633	31717	67257	92526	21725	32266	Low	Enriched	Enriched	Enriched		YES	
O15371-2;O15371-	Eukaryotic translation	EIF3D	58.14	40.1	26	26	84.249	0	135810	106730	111610	140020	132620	113250	110950	111670	53372	113310	No expres	Enriched	Enriched	Enriched		YES	
O15381-2;O15381;	Nuclear valosin-conta	NVL	82.745	5.3	3	3	10.089	0	3041.9	2110.8	2318.1	10703	1856.8	9780.3	3137.5	8618.9	1475.7	5443.1	No expres	No expres	Low	No expres		YES	
O15400-2;O15400	Syntaxin-7	STX7	27.4	25.1	6	6	19.958	0	26812	24170	30232	31254	36509	35020	25612	23401	11276	28205	Enriched	Moderate	Enriched	Moderate		YES	
O15438;O15438-4	Canalicular multispec	ABCC3	169.34	2.8	3	3	11.501	0	4187.8	2635.1	2981.9	4292.5	3572.3	3557.1	2722.7	3812.4	1405.3	4544.8	Enriched	Enriched	Enriched	Moderate		YES	
O15460-2;O15460	Prolyl 4-hydroxylase	P4HA2	60.632	3.8	2	2	4.7917	0.00043	15864	15178	17655	13388	18171	9026.3	11209	8845.1	7806.4	12985	Moderate	Enriched	Enriched	Enriched		YES	
O15498-2;O15498	Synaptobrevin homol	YKT6	18.58	25	5	5	8.4013	0	14634	10920	11064	14571	15690	10341	10542	9703	7687.2	11587	Low	Moderate	Moderate	No expres		YES	
O15523-2;O15523	ATP-dependent RNA	DDX3Y	72.931	34.7	33	2	12.187	0	4234.9	6442.3	3487.7	4740.8	7243.2	5958.9	6117.7	5453.8	3267.5	6843.8	Enriched	No expres	Moderate	Enriched		YES	
O15541	RING finger protein 1	RNF113A	38.787	5.8	2	2	4.0639	0.00062	3914.1	3390.7	3669.8	2562.5	5002.4	3630.8	4232.9	3424.1	3138.9	4294.7	Low	Enriched	Enriched	Moderate		YES	
O15551	Claudin-3	CLDN3	23.318	15.9	5	4	50.954	0	5409.9	4736.6	4850.3	4071.2	7041.8	20855	38007	25869	20988	24726	Moderate	Enriched	Enriched	No expres		YES	
O43143	Putative pre-mRNA-s	DHX15	90.932	24.8	32	32	132.56	0	92022	76775	92921	84405	93792	89555	142440	163170	74921	110900	Enriched	Enriched	Enriched	Enriched		YES	
O43148;O43148-2;	mRNA cap guanine-N	RNMT	54.843	7.1	3	3	10.198	0	2825.5	2743	2909.1	4788.7	3020.8	2703.1	3420.5	5589.5	3624.1	5903.9	Enriched	Moderate	Enriched	Moderate		YES	
O43149	Zinc finger ZZ-type a	ZZEF1	331.07	2.5	8	8	15.534	0	43389	43061	44379	42113	54642	43178	62653	42057	28316	44224	Enriched	Enriched	Enriched	Moderate		YES	
O43159;E9PPP6;E9	Ribosomal RNA-proc	RRP8	50.714	3.7	2	2	2.9123	0.00187	3412.7	3417.7	3040.7	2490.5	6262.1	2886.4	2572	2787.8	1420.1	3281.7	Moderate	Moderate	Moderate	No expres		YES	
O43172-2;O43172	U4/U6 small nuclear	PRPF4	58.32	15.7	9	9	57.242	0	32126	24663	28355	29309	36890	35015	55078	42999	29802	41035	No expres	Enriched	Enriched	Enriched		YES	
O43175;Q5SZU1	D-3-phosphoglycerat	PHGDH	56.65	46.7	66	66	323.31	0	527290	290360	415520	499850	436020	464970	583840	591820	256300	434510	Enriched	Enriched	Enriched	Enriched		YES	
O43181;H0Y9M8	NADH dehydrogenas	NDUFS4	20.108	30.3	7	7	28.825	0	48730	26281	28778	50902	35792	50314	39749	75814	17281	63867	Enriched	Enriched	Enriched	Moderate		YES	
O43237;O43237-2;	Cytoplasmic dynein 1	DYNC1LI2	54.099	35.2	30	28	103.57	0	154590	104170	124560	128600	146440	125700	155520	148980	97489	148510	Enriched	Enriched	Enriched	Moderate		YES	
O43242;O43242-2	26S proteasome non-	PSMD3	60.977	35.6	32	32	323.31	0	142380	88943	108880	166700	101870	118600	130850	139240	73236	147990	No expres	Enriched	Enriched	Enriched		YES	
O43252	Bifunctional 3-phosp	PAPSS1	70.832	27.4	21	18	118.95	0	90055	67880	76266	81697	95910	81864	89232	102990	42046	70650	Moderate	Enriched	Enriched	Enriched		YES	
O43264;O43264-2	Centromere/kinetoch	ZW10	88.828	14.8	12	12	136.48	0	78388	67298	73722	59207	81528	56289	61037	72950	32060	60444	Moderate	Enriched	Enriched	No expres		YES	
O43278-2;O43278	Kunitz-type protease	SPINT1	56.885	2.5	1	1	6.8493	0	654.75	421.53	578.33	700.24	1195.9	1061.9	2818.1	192.08	2123.8	1840.9	Moderate	Enriched	Enriched	Enriched		YES	
O43290	U4/U6.U5 tri-snRNP	SART1	90.254	24.5	19	19	291.52	0	65375	44471	59964	68143	73111	56434	60320	70503	37498	61934	No expres	Enriched	Moderate	Moderate		YES	
O43294-2;O43294	Transforming growth	TGFB1I1	47.941	13.1	5	5	16.005	0	14356	13270	13616	11909	14961	11898	13166	14344	6937.7	16135	Enriched	Moderate	Enriched	Enriched		YES	
O43301	Heat shock 70 kDa pi	HSPA12A	74.977	9	7	7	15.827	0	18729	14070	19814	18134	24252	20549	59335	27499	14788	23977	Moderate	Moderate	Moderate	Low		YES	
O43318-4;O43318-	Mitogen-activated pr	MAP3K7;DKFZp586F0	53.739	9.6	4	4	6.7568	0	23343	19557	23717	22116	23956	27178	23354	23993	12724	22265	No expres	Moderate	Enriched	Moderate		YES	
O43324;H0YAL7;I	Eukaryotic translation	EEF1E1;EEF1E1-BLOC	19.81	32.8	7	7	89.955	0	72200	58564	56675	57171	65526	59255	48951	46977	23612	56805	Low	Enriched	Enriched	Moderate		YES	
O43353;E7ERW9;I	Receptor-interacting	RIPK2	61.194	4.4	2	2	1.9144	0.00814	1097	569.66	599.1	642.54	1298.5	843.5	428.97	142.06	141.74	175.48	Low	Enriched	Enriched	Low		YES	
O43390;O43390-3;	Heterogeneous nucle	HNRNPR	70.942	48.3	54	3	11.541	0	19316	2192.5	4933.6	18008	3939.9	20908	7693.8	10019	2817.8	17806	Enriched	Enriched	Enriched	Enriched		YES	
O43390-2;O43390-	Heterogeneous nucle	HNRNPR	71.214	48.6	54	3	275.07	0	230330	150490	179500	223490	185910	203090	281490	393030	136660	244000	Enriched	Enriched	Enriched	Enriched		YES	
O43395	U4/U6 small nuclear	PRPF3	77.528	17.9	9	9	22.652	0	57600	36439	50371	45547	56044	56796	63249	54866	34628	58654	Low	Moderate	Moderate	Enriched		YES	
O43396;K7ER96;K	Thioredoxin-like prot	TXNL1	32.251	47.8	19	19	156.63	0	160360	134390	125060	151480	182370	156720	197870	268760	94728	167280	Enriched	Enriched	Enriched	Moderate		YES	
O43402;M0R1B0	ER membrane protei	EMC8	23.773	22.9	5	5	16.543	0	31916	21069	23212	23498	26315	40586	35326	42949	14284	28932						YES	
O43414-3;H0Y4B0	ERI1 exoribonucleas	ERI3	14.542	41.4	5	5	6.84	0	9320.1	6026	7856.4	7846.1	11129	10684	7710.6	8703.7	5413.7	7911.9	No expres	Moderate	Moderate	Moderate			
O43422	52 kDa repressor of t	PRKRIR	87.703	1.8	1	1	4.9006	0.00044	3015.8	3501	4282.1	3061.5	5463.5	1644.6	3944.4	2456.9	970.53	2515	Moderate	Enriched	Enriched	Low			
O43464-3;O43464;	Serine protease HTR.	HTRA2	46.381	15.4	6	6	30.188	0	30784	16801	25749	33223	25198	40112	44465	57678	23413	56244	No expres	Moderate	Enriched	Enriched		YES	
O43488;H3BLU7	Aflatoxin B1 aldehyc	AKR7A2	39.589	30.1	21	10	24.973	0	22291	22668	24810	18687	31720	18558	31860	27407	27747	26817	Enriched	Enriched	Enriched	Enriched		YES	
O43490-5;O43490-	Prominin-1	PROM1	92.74	2.7	1	1	8.4709	0	3370.9	2171.6	2891.7	5735.8	2970.7	3436.7	5714.3	6440.4	2477.8	4687.7	Enriched	Enriched	Enriched	Enriched		YES	
O43491;E9PHY5;C	Band 4.1-like protein	EPB41L2	112.59	30.8	43	33	169.25	0	208910	175680	242340	184060	291460	203010	324620	232430	183910	250050	Moderate	Moderate	Enriched	Moderate		YES	
O43505	N-acetyllactosaminid	B3GNT1	47.119	13	7	7	18.465	0	61852	40342	45507	56718	54265	64586	54633	37912	41000	54261	Enriched	Enriched	Enriched	Enriched			
O43520;K7ERI0	Phospholipid-transpo	ATP8B1	143.69	5.4	6	6	14.608	0	29738	20828	25841	19655	28523	28955	30989	25984	11819	32743	Enriched	Moderate	Enriched	Low		YES	
O43524-2;O43524	Forkhead box protein	FOXO3	48.406	6.8	2	2	8.5195	0	10728	7375.3	8782	11215	9521.4	11940	11311	9311.8	8793.2	12045	Enriched	Enriched	Enriched	Enriched		YES	
O43583;F8VVL1	Density-regulated pro	DENR	22.092	37.9	10	10	186.9	0	70509	57687	55205	66392	83563	60872	85721	62853	43899	73203	Low	Enriched	Enriched	No expres		YES	
O43592	Exportin-T	XPOT	109.96	5.8	6	4	7.4788	0	8057.4	4845.1	10502	19399	10408	11386	9564.6	15222	5682.1	12970	Moderate	Enriched	Enriched	Moderate		YES	
O43615;M0QXU7	Mitochondrial impor	TIMM44	51.355	29.9	20	20	62.081	0	71147	62083	70777	80528	97385	65222	62426	58973	29367	68653	Moderate	Low	Moderate	Moderate		YES	
O43639	Cytoplasmic protein 1	NCK2	42.915	8.9	3	3	8.709	0	10463	6450.4	8023.1	10592	6896.9	4369.3	9157.3	18023	4490.8	15596	Enriched	Enriched	Enriched	Moderate		YES	
O43660-2;O43660	Pleiotropic regulator	PLRG1	56.289	18.8	8	8	14.427	0	14528	11234	12932	12449	14821	15350	14496	13536	7379.6	13968	Low	Enriched	Enriched	Moderate		YES	
O43665-2;O43665;	Regulator of G-protei	RGS10	19.608	9	1	1	15.557	0	5288.8	4044.3	4312.1	10712	3740.7	4324.6	3415.3	5646.3	2271.4	5814.5	Low	Low	Moderate	Low		YES	
O43678	NADH dehydrogenas	NDUFA2	10.921	40.4	8	8	12.39	0	28421	20963	27372	28586	37784	27554	34430	28832	18160	27805	Enriched	Enriched	Enriched	Enriched		YES	
O43684-2;O43684;	Mitotic checkpoint pi	BUB3	36.954	26.7	9	9	29.639	0	18915	15230	16915	12726	19626	20115	35760	46384	16666	24587	Enriched	Enriched	Enriched	Moderate		YES	
O43687;J3KN37;O	A-kinase anchor prot	AKAP7	11.464	24	2	2	10.759	0	4846.2	5863.5	3587.5	6520.7	5650.3	9893.8	7779.5	23900	4856.2	9363.6	Enriched	Enriched	Enriched	Low		YES	
O43707;O43707-2	Alpha-actinin-4	ACTN4	104.85	67.9	153	40	323.31	0	941830	703160	795310	1065800	887540	930830	1165500	1375800	616840	1165800	Enriched	Enriched	Enriched	Enriched		YES	
O43709;H7C0G4;C	Probable 18S rRNA (	WBSCR22	31.88	7.5	2	2	4.6801	0.00043	13887	8599.2	13409	14964	14871	13774	13435	10413	6693.6	17268	Enriched	Enriched	Enriched	Low		YES	
O43715	TP53-regulated inhib	TRIAP1	8.7858	39.5	4	4	19.216	0	35363	33508	27269	43283	31676	36668	27651	31516	12533	36070	Enriched	Enriched	Enriched	No expres		YES	YES
O43719	HIV Tat-specific facto	HTATSF1	85.852	10.2	7	7	66.632	0	24169	17894	21696	21173	22730	19863	27394	22176	15107	27244	Enriched	Moderate	Enriched	Enriched		YES	
O43747;O43747-2	AP-1 complex subun	AP1G1	91.35	16.9	19	18	41.179	0	65204	37262	53362	82077	50696	94912	77416	79759	43239	85719	Enriched	Enriched	Enriched	Enriched		YES	
O43765;K7EMD6	Small glutamine-rich	SGTA	34.063	18.5	6	6	12.506	0	22800	15534	16689	15681	24838	16463	18049	18480	10328	16731	Moderate	Low	Moderate	Enriched		YES	
O43772;C9JPE1	Mitochondrial carniti	SLC25A20	32.943	33.6	12	12	25.455	0	54596	49241	53591	41056	65516	57017	60468	51043	28645	53958	Enriched	Enriched	Enriched	No expres		YES	
O43776	Asparagine--tRNA lig	NARS	62.942	36.7	35	29	323.31	0	263640	127110	163450	275330	197090	263210	280530	264430	121960	255300	No expres	Enriched	Enriched	Enriched		YES	
O43809	Cleavage and polyade	NUDT21	26.227	30	8	8	18.436	0	57635	47379	52909	51017	52399	73890	93414	88899	57413	73075	Low	Enriched	Enriched	Low		YES	
O43813	LanC-like protein 1	LANCL1	45.283	13.8	7	6	12.372	0	29162	21616	25712	25011	34066	24234	38512	43319	22996	34827	Moderate	Enriched	Enriched	Enriched		YES	
O43815;O43815-2	Striatin	STRN	86.131	9.4	6	6	15.77	0	22733	19520	21680	22914	27240	18287	22563	19488	13707	21124	Moderate	Moderate	Moderate	No expres		YES	
O43823;M0QYL4	A-kinase anchor prot	AKAP8	76.107	3.5	2	2	2.5501	0.00362	8797.3	2874.1	4450.9	2339.2	7415.2	2269.8	5819	2675.8	2377.4	3470	Enriched	Moderate	Enriched	Enriched		YES	
U3KPU7;U3KQS2;	Glucose-6-phosphate	SLC37A4	46.443	10.7	4	4	8.1075	0	22823	13959	21929	34941	20025	27268	24714	26098	12410	34651	Enriched	Enriched	Enriched	Enriched		YES	
O43852;O43852-3;	Calumenin	CALU	37.106	54	30	9	129.99	0	201150	152260	125350	181290	188330	152180	144060	190860	66232	150400	Enriched	Enriched	Enriched	Moderate		YES	
O43852-2;O43852-	Calumenin	CALU	37.134	47.9	23	2	7.9487	0	48721	18233	17338	31267	6515.4	50899	7314.2	21040	10897	35466	Enriched	Enriched	Enriched	Moderate		YES	
O43865;O43865-2	Putative adenosylhon	AHCYL1	58.951	30	24	17	73.555	0	116230	89738	89018	126930	112960	200460	128950	142290	62876	137650	Enriched	Enriched	Enriched	Enriched		YES	
O43920	NADH dehydrogenas	NDUFS5	12.517	54.7	9	9	16.102	0	13172	12436	17413	14934	12986	19816	31610	25212	17715	30144	Enriched	Enriched	Enriched	Enriched		YES	
O43924	Retinal rod rhodopsir	PDE6D	17.42	7.3	1	1	2.7666	0.0024	2687.7	1425.7	1825.2	2573.9	1894.4	2239.5	2183.7	2392	976.99	2141.5	Low	Low	Moderate	Moderate		YES	
O60216	Double-strand-break	RAD21	71.689	11.3	7	7	12.103	0	19981	13654	16782	25300	19106	19394	19816	30247	9436.9	22044	Enriched	Enriched	Enriched	Enriched		YES	
O60220	Mitochondrial impor	TIMM8A	10.998	48.5	5	5	19.71	0	37519	26252	35218	28716	39112	30077	39609	47318	19182	46011	Low	Low	Low	No expres		YES	
O60231;A2AB15	Putative pre-mRNA-s	DHX16	119.26	6	4	4	12.398	0	17429	12277	13445	15781	17682	12647	17027	14392	11103	20126	Enriched	Enriched	Enriched	Moderate		YES	
O60240	Perilipin-1	PLIN1	55.99	28.9	15	15	66.912	0	73912	67260	63856	138080	72371	57386	44518	44392	33361	105940						YES	
O60256;I3L0S1;O6	Phosphoribosyl pyroj	PRPSAP2	40.925	25.5	11	8	26.625	0	77729	68889	81590	76293	124070	68880	77516	66042	42002	65820	Enriched	Moderate	Enriched	Moderate		YES	
O60262	Guanine nucleotide-b	GNG7	7.5217	22.1	2	2	4.0567	0.00062	18018	6403.6	7929.2	13091	6347.2	9531.5	7020.3	10215	4038	8944.4	Enriched	Enriched	Enriched	Moderate		YES	
O60264	SWI/SNF-related ma	SMARCA5	121.9	10.4	10	9	55.852	0	69165	49590	66216	57019	61225	73254	82808	80849	46349	70831	Low	Moderate	Enriched	Moderate		YES	

O60268-2;O60268-	Uncharacterized prot	KIAA0513	33.717	4.3	1	1	8.9879	0	10159	11572	10355	11081	12952	7409.3	6530.1	8721.2	4493.2	12827	Moderate	Enriched	Moderate	Enriched	YES		
O60292	Signal-induced prolif	SIPA1L3	194.61	2.2	4	4	9.0957	0	10129	8235.7	10553	15025	10149	8913.8	7803.8	10768	5430.1	9894.1	Moderate	Moderate	Enriched	Enriched	YES		
O60306	Intron-binding protei	AQR	171.29	7.1	12	12	25.619	0	46123	34996	40502	53856	43129	44526	36723	45718	20836	47501	Moderate	Enriched	Enriched	Low	YES		
O60313;O60313-2;	Dynamin-like 120 kD	OPA1	111.63	34.2	38	38	118.84	0	181390	147370	201950	175310	198100	149340	204560	189280	117390	214110	Enriched	Moderate	Enriched	Moderate	YES		
O60318;O60318-2	Germinal-center asso	MCM3AP	218.4	1.6	2	2	3.7897	0.0006	8411	6279.3	8558.6	8211.2	9008.1	7593.5	7640	6862.5	4540	8860.4	Low	Moderate	Enriched	Enriched	YES		
O60341;O60341-2	Lysine-specific histor	KDM1A	92.902	11.9	9	9	9.5455	0	32850	31590	29713	30812	31967	46049	27782	34948	18645	31199					YES		
O60343-2;O60343-	TBC1 domain family	TBC1D4	139.55	7.3	8	7	17.892	0	23568	20412	27928	23292	25214	25938	26435	28052	13495	27121	Enriched	Moderate	Enriched	Low	YES		
O60344;O60344-4	Endothelin-convertin	ECE2	99.772	5	3	2	6.7939	0	4082.5	2187.9	2739.7	6570.2	1864.6	4557.5	3751.5	3529.2	1165.2	5504.7	Moderate	Enriched	Moderate	Enriched			
O60356;O60356-2	Nuclear protein 1	NUPR1	8.8727	20.7	3	3	61.81	0	15565	7135.9	12418	5681.1	16299	16928	30475	10398	13703	11497	Moderate	Enriched	Enriched	Enriched	YES	YES	
O60476	Mannosyl-oligosacch	MAN1A2	73.003	18.6	12	12	30.092	0	39928	28561	43182	56600	39056	48059	67139	54766	57849	52574	Enriched	Enriched	Enriched	Low	YES		
O60486	Plexin-C1	PLXNC1	175.74	1.2	2	2	3.1974	0.00077	4200.5	1955.7	2471	2699.6	2090.2	4575.5	3958.1	7700.9	1724.9	5313.1	Moderate	Low	Enriched	Enriched	YES		
O60493-2;O60493-	Sorting nexin-3	SNX3	14.766	37.7	11	9	41.292	0	76283	73875	86286	63858	83280	64683	68088	73622	50261	73083	Enriched	Enriched	Enriched	Enriched	YES		
O60502-3;O60502-	Bifunctional protein	MGEA5	76.192	7.4	4	4	83.501	0	1826.4	1547.7	1312	2565.7	2015	1936.4	1043.4	1588.8	548.36	1636.7	Moderate	Enriched	Enriched	Moderate	YES		
O60504;O60504-2;	Vinexin	SORBS3	75.34	13.7	8	8	41.122	0	32533	29178	31747	24142	38945	28247	45034	42699	17818	33399	Enriched	Enriched	Moderate	Moderate	YES		
O60506;O60506-2	Heterogeneous nucle	SYNCRIP	69.602	49.3	64	2	323.31	0	453620	247520	305530	385700	335700	414230	472550	709240	229940	432430	Enriched	Low	Enriched	Enriched	YES		
Q5SRN1;O60508	Pre-mRNA-processin	CDC40	60.83	5.9	2	2	6.8278	0	6562.3	1769.6	4331.2	8814.8	3075.8	7331.9	6058	8689.9	2649.1	6928.4	Moderate	Enriched	Enriched	No expres	YES		
O60518	Ran-binding protein (	RANBP6	124.71	2.8	3	2	12.471	0	7349.6	2778.8	4135.1	11296	3359.9	8697.5	6224.9	9302.7	2587.6	8743.2	Enriched	Moderate	Enriched	Moderate	YES		
O60547;O60547-2	GDP-mannose 4,6 de	GMDS	41.949	42.7	22	22	68.955	0	98933	74012	81583	88562	103210	88037	74834	85265	50184	83673	Enriched	Enriched	Moderate	Low	YES		
O60568	Procollagen-lysine,2-	PLOD3	84.784	4.6	3	3	9.0504	0	9236.6	13789	11116	8830.4	11708	9448.1	11188	12032	6080.2	8410.4	Enriched	Enriched	Enriched	Enriched	YES		
O60645-2;O60645-	Exocyst complex con	EXOC3	73.796	18.4	12	12	52.561	0	44250	38916	45761	45347	46339	43509	49344	40040	27259	53826	Moderate	Low	Moderate	Moderate	YES		
O60664-4;O60664;	Perilipin-3	PLIN3	45.803	37.4	22	12	112.58	0	98504	74814	97169	97648	99937	101820	147960	150500	87119	131080					YES		
O60669	Monocarboxylate tra	SLC16A7	52.2	5.6	3	3	4.6197	0.00043	3541.3	1938.8	2210	3340.6	3800.6	2767.3	2353.3	2069.8	1898.4	2445	Enriched	Moderate	Enriched	No expres	YES		
O60684;Q5TFJ7	Importin subunit alpl	KPNA6	60.029	12.3	5	3	8.4439	0	18165	15660	12925	20646	21989	14363	10211	10281	10036	12181	Moderate	Enriched	Enriched	Enriched	YES		
O60701;O60701-2;	UDP-glucose 6-dehy	UGDH	55.023	46.8	37	26	184.38	0	208990	154810	144670	144890	192090	154950	242350	231460	93163	172390	Enriched	Enriched	Enriched	Enriched	YES		
O60704	Protein-tyrosine sulfo	TPST2	41.911	27.6	17	8	49.679	0	85595	59011	74577	91983	77631	85317	65969	110990	42050	89219	Moderate	Enriched	Enriched	Enriched	YES		
O60711;O60711-2;	Leupaxin	LPXN	43.332	5.7	2	2	3.8908	0.00061	3482	4841.4	4087.4	5310.5	3288.4	6141.6	18002	3904.4	2794.5	13479	Enriched	Moderate	Enriched	Enriched	YES		
O60749;O60749-2	Sorting nexin-2	SNX2	58.47	31.4	25	22	64.43	0	94207	82390	89088	81071	105900	81894	98838	82145	46617	86400	No expres	Enriched	Enriched	Moderate	YES		
O60763;O60763-2	General vesicular trar	USO1	107.89	35.7	64	64	323.31	0	458390	355450	359770	442890	502300	430660	468140	448950	251270	439340	Moderate	Enriched	Enriched	Moderate	YES		
O60783	28S ribosomal protei	MRPS14	15.139	27.3	3	3	62.254	0	14460	7861.9	10025	15054	16092	13591	13160	12784	7303.9	16614	Enriched	Enriched	Enriched	Enriched	YES		
O60784;O60784-3;	Target of Myb protei	TOM1	53.818	12.4	9	7	47.614	0	91015	72864	71218	78971	96579	85027	95226	95907	44195	68109	Low	Moderate	Moderate	No expres	YES		
P62807;P57053;O6	Histone H2B type 1-(	HIST1H2BC;H2BFS;HI!	13.906	51.6	27	0	237.67	0	343830	223470	286210	440930	336730	436560	914980	1047200	371920	467470	Moderate	Enriched	Moderate	Enriched	YES		
O60825-2;O60825	6-phosphofructo-2-ki	PFKFB2	54.406	7.9	3	2	3.4585	0.00079	12035	9616.7	13045	14481	13178	10590	13220	10011	7220.6	12713	Low	Moderate	Enriched	Moderate	YES		
O60826	Coiled-coil domain-c	CCDC22	70.755	18.2	11	11	23.374	0	10295	6665	7774.4	10124	9970.8	9425.7	9303.3	8311.5	5076.2	8611.2	Moderate	Low	Moderate	Low	YES		
O60828-2;O60828;	Polyglutamine-bindir	PQBP1	30.401	20.1	5	5	54.506	0	30248	18078	24710	20047	28369	20395	39829	27616	41012	42040	No expres	Enriched	Enriched	Moderate	YES		
O60831;A6NP52	PRA1 family protein	PRAF2	19.258	12.9	2	1	4.965	0.00044	4230.7	3600.9	4489.9	4698.8	4487.9	4069.6	4421.3	5553	4058.3	4414.8	Low	Moderate	Enriched	Moderate	YES		
O60832;O60832-2;	H/ACA ribonucleopr	DKC1	57.673	27.2	24	24	259.51	0	120440	77546	101390	113190	114400	90540	106770	94427	62648	130280	Enriched	Enriched	Enriched	Enriched	YES		
O60869;O60869-2;	Endothelial differenti	EDF1	16.368	30.4	6	6	6.8652	0	48705	22462	21920	50654	30532	38720	20187	28119	13334	45642	Enriched	Enriched	Enriched	No expres	YES		
O60884	DnaJ homolog subfar	DNAJA2	45.745	22.1	13	13	53.869	0	92540	74518	84430	70360	107520	93257	88060	73551	47617	89851	Enriched	Enriched	Enriched	Low	YES		
O60885-2;O60885-	Bromodomain-contai	BRD4	80.462	2.5	1	1	8.8576	0	6384.7	4342.4	5715.8	5189.4	5312.8	2179.2	5135.6	5999.6	2146.5	5603.2	Enriched	Enriched	Enriched	Enriched	YES		
O60888-3;O60888;	Protein CutA	CUTA	16.832	31.4	8	8	24.345	0	23321	18493	28770	30641	22607	27875	27786	23782	13077	25695	Enriched	Enriched	Enriched	No expres	YES		
O60927;Q5SRK2	Protein phosphatase	PPP1R11	13.952	19	2	2	20.207	0	5090.9	4832.2	5687	5832	7312.6	6730	5999.3	4183.8	3693	5929.6	Enriched	Enriched	Enriched	Enriched	YES		
O60934;E5RGN7;I	Nibrin	NBN	84.958	6.1	4	4	6.4553	0	23261	25439	27375	17316	27562	14006	28467	14853	19959	17098	Enriched	Enriched	Enriched	Enriched	YES		
O60938	Keratocan	KERA	40.508	4.5	1	1	3.3539	0.00078	21939	1985.5	4119.1	36660	5143.8	51857	4713.4	12843	1694.1	18990	No expres	No expres	No expres	No expression			
O75051	Plexin-A2	PLXNA2	211.1	7.7	15	13	28.374	0	39791	27897	32503	55144	39272	42184	54897	65845	27413	50593	Moderate	Enriched	Enriched	Enriched	YES		
O75063	Glycosaminoglycan x	FAM20B	46.432	7.1	3	3	4.8092	0.00043	22209	16622	16241	20706	53493	13707	15791	13648	8451	13078	Enriched	Moderate	Enriched	Enriched	YES		
O75071	EF-hand calcium-bin	EFCAB14	55.031	6.3	3	3	3.5986	0.0008	8543	7406.7	6703.7	7151.7	12050	7031	4519.5	6563.8	2180.5	5726.8							
O75083;O75083-3;	WD repeat-containin	WDR1	66.193	25.9	23	23	170.06	0	124840	83645	117840	88690	102120	110190	155000	125830	81504	102440	Enriched	Enriched	Enriched	Enriched	YES		
O75116;E9PF63;Q	Rho-associated prote	ROCK2	160.9	10.2	12	10	100.76	0	65265	42719	53493	66391	58074	48710	49549	89387	28743	61142	No expres	Moderate	Enriched	Moderate	YES		
O75131	Copine-3	CPNE3	60.13	24.4	17	5	157.46	0	140940	69474	96324	108260	106200	128240	135520	119630	59356	130210	Low	Enriched	Enriched	Moderate	YES		
O75146;O75146-2	Huntingtin-interactin	HIP1R	119.39	18.8	20	19	62.579	0	42651	34528	33947	46829	35424	37617	49241	49035	34784	58955	Enriched	Enriched	Enriched	Enriched	YES		
O75152;E9PQ61	Zinc finger CCCH do	ZC3H11A	89.13	9	5	5	53.487	0	22788	20708	19510	20080	20367	19942	16320	20996	10467	20060	Enriched	Enriched	Enriched	Enriched	YES		
O75155;O75155-2	Cullin-associated NE	CAND2	135.25	8.9	14	5	12.223	0	22405	21337	23681	18244	22243	16928	26083	23619	20560	21830	Moderate	Moderate	Enriched	Enriched	YES		
O75165	DnaJ homolog subfar	DNAJC13	254.41	6.9	17	17	38.297	0	38728	35624	40363	39941	41251	36131	36326	38363	20592	39729	Enriched	Moderate	Enriched	Moderate	YES		
T1ECW5;O75170-(	Serine/threonine-prot	PPP6R2	72.856	2.3	1	1	21.606	0	5770.6	4844.7	4080.9	7163.7	5197.4	3417.2	3229.7	3940.7	2180.6	6314.5					YES		
O75190-3;O75190;	DnaJ homolog subfar	DNAJB6	35.714	17.8	6	1	24.375	0	11871	8936.5	10098	8351	9833.9	20521	26587	37756	9767.4	23979	Low	Low	Enriched	Enriched	YES		
O75191;O75191-2	Xylulose kinase	XYLB	58.382	9.1	4	4	14.047	0	6428.1	5609.7	5476.6	6317.9	6056.5	4403.5	4471.2	3727.8	2813.1	5901.8	No expres	No expres	Low	Low	YES		
O75208;H3BSJ5;H	Ubiquinone biosynth	COQ9	35.509	22.6	9	7	40.961	0	22003	16939	20999	20607	23204	20967	27823	28086	14723	25815	No expres	Enriched	Enriched	Enriched	YES		
O75223;M0QZK8;(	Gamma-glutamylcycl	GGCT	21.007	46.8	15	15	187.53	0	66362	49624	48175	58874	54087	74252	109380	98928	54801	80372	Enriched	Enriched	Enriched	Enriched	YES		
O75306-2;O75306	NADH dehydrogenas	NDUFS2	51.851	29.5	15	15	48.055	0	56296	34684	39841	69877	47886	52677	38217	63111	16977	56353	Enriched	Enriched	Enriched	Enriched	YES		
O75319	RNA/RNP complex-1	DUSP11	38.938	4.8	1	1	5.4883	0	5334.6	1704.8	3674.9	4289	2578.7	4358.8	4065	3781.7	2751.2	5792.3	Moderate	Enriched	Enriched	Enriched			
O75323;O75323-2	Protein NipSnap hor	GBAS	33.742	26.6	8	7	25.636	0	87069	51790	66082	78208	80063	68067	96689	65993	57926	75662	Low	Enriched	Enriched	Enriched	YES		
O75340-2;O75340;	Programmed cell dea	PDCD6;hCG_1985580	21.664	29.1	10	8	24.828	0	42977	36677	50842	31770	57999	32591	33941	31637	20754	33725	Low	Moderate	Enriched	Enriched	YES		
O75348	V-type proton ATPas	ATP6V1G1	13.757	39	7	7	55.982	0	31726	21391	30864	47251	41394	20738	20913	28474	34584	23925	Enriched	Enriched	Enriched	Enriched	YES		
O75351	Vacuolar protein sort	VPS4B	49.301	24.3	17	12	43.843	0	57245	35840	49979	54835	61009	62534	40873	38529	23579	49607	Enriched	Enriched	Enriched	No expres	YES		
O75355-2;O75355	Ectonucleoside triph	ENTPD3	50.761	9.7	3	3	21.053	0	7857.6	8149.1	10674	9116.1	12445	9689.3	8625.5	12061	5348.6	9627.9	Moderate	Enriched	Enriched	Enriched	YES		
O75367-3;O75367;	Core histone macro-I	H2AFY	39.488	44.7	30	14	171.69	0	155420	121400	143780	130970	159460	167540	183640	188460	80811	164140	Enriched	Enriched	Enriched	Enriched	YES		
O75368	SH3 domain-binding	SH3BGRL	12.774	51.8	15	15	68.971	0	66595	37148	49508	73853	46275	62859	119230	116210	53951	83930	Enriched	Enriched	Enriched	Moderate	YES		
O75369-8;O75369-	Filamin-B	FLNB	281.63	54	207	189	323.31	0	1095600	896180	1026100	1045200	1134200	1107100	1366200	1465600	688510	1223100	Enriched	Enriched	Enriched	Enriched	YES		
O75380;D6RBT3	NADH dehydrogenas	NDUFS6	13.711	47.6	7	7	34.697	0	40473	26057	34714	29883	44865	36726	33223	29764	20199	39101	Enriched	Enriched	Enriched	Enriched	YES		
O75387;O75387-2	Large neutral amino a	SLC43A1	61.476	8.6	6	6	16.66	0	38822	29147	36584	25213	56154	45580	53677	38544	27332	30167	Enriched	Enriched	Enriched	Enriched	YES		
O75396	Vesicle-trafficking pr	SEC22B	24.593	52.1	25	25	144.09	0	91797	78547	83721	76842	101740	106300	200320	149850	75189	100810	Enriched	Enriched	Enriched	Enriched	YES		
O75400-3;O75400-	Pre-mRNA-processin	PRPF40A	106.91	14.2	16	16	112.53	0	114570	81682	102110	100930	120820	118450	162640	163260	82153	146400	Enriched	Enriched	Enriched	Low	YES		
O75410-7;O75410;	Transforming acidic c	TACC1	79.871	8.9	5	3	32.089	0	11435	10106	9867.3	11625	10488	7181.8	8017.1	8776.8	5319.1	9714.2	Enriched	Enriched	Enriched	Enriched	YES		
O75427	Leucine-rich repeat a	LRCH4	73.449	10.2	6	6	27.427	0	42911	32542	41457	40703	45314	37487	44279	39120	31625	44666	Enriched	Moderate	Moderate	Moderate	YES		
O75431-2;O75431;	Metaxin-2	MTX2	28.823	28.1	6	6	28.461	0	29595	21119	27154	20947	31326	31330	36784	54879	16764	37683	Low	Enriched	Enriched	Enriched	YES		
O75436;S4R3Q6;O	Vacuolar protein sort	VPS26A	38.169	39.4	13	12	86.745	0	41502	33796	39208	42713	46768	33662	45303	46691	19376	41147	Enriched	Enriched	Enriched	Enriched	YES		
O75438;O75438-2	NADH dehydrogenas	NDUFB1	6.9611	36.2	4	4	5.4834	0	4547.2	4950.2	4499.3	3091	6467.2	6227.7	3678.3	2430.9	2225.5	3126.8	Enriched	Enriched	Enriched	Enriched	YES		
O75460	Serine/threonine-prot	ERN1	109.73	4.2	4	4	6.2376	0	1712.4	727.42	1335.9	2961.6	1390.8	2165.1	2021.6	1570.3	895.96	2575.3	Moderate	Moderate	Moderate	No expression			
O75475;O75475-3;	PC4 and SFRS1-inte	PSIP1	60.103	22.8	13	12	162.53	0	121200	88924	125130	93054	139950	81052	130170	134590	66428	115420	Low	Moderate	Enriched	Enriched	YES		
O75477;B0QZ43	Erlin-1	ERLIN1	38.925	26	14	5	23.805	0	19779	24048	22735	16122	24623	13278	18973	27350	14827	23258	Enriched	Enriched	Enriched	Low	YES		
O75487;O75487-2	Glypican-4;Secreted	GPC4	62.411	10.1	4	3	12.391	0	21253	13525	16974	19152	19163	16379	15291	17128	9194.2	18843	No expres	Moderate	Moderate	Low	YES		
O75489	NADH dehydrogenas	NDUFS3	30.241	49.2	24	24	77.588	0	109940	69471	82481	97468	108020	87500	103370	108490	56260	117500	Enriched	Enriched	Enriched	Moderate	YES		
Q5JRI1;O75494-5;(	Serine/arginine-rich s	SRSF10;FUSIP1	20.913	14	4	4	6.4737	0	7671.1	5090.2	7510.6	17340	7108.1	7508.3	7134.6	17600	4585.6	12240	Moderate	Moderate	Enriched	No expres	YES		
O75506	Heat shock factor-bin	HSBP1	8.5435	65.8	5	5	44.499	0	29970	22610	25327	26539	26037	38355	71250	40160	30778	34554	Moderate	Enriched	Enriched	Enriched	YES		
O75521-2;O75521;	Enoyl-CoA delta isor	ECI2	39.609	37.3	19	6	62.619	0	77931	50067	53250	47629	82120	59953	64396	43201	25884	52973					YES		
O75525-2;O75525	KH domain-containir	KHDRBS3	30.249	7	4	1	9.5343	0	9866.9	5057.6	4020.8	12239	5796.3	4334.2	5990.8	11073	8010.5	11155	Low	Moderate	Enriched	Moderate	YES		
O75531	Barrier-to-autointegra	BANF1	10.058	59.6	13	13	51.52	0	56002	105010	67207	64127	94133	43100	81611	78213	41836	67728	Low	Enriched	Enriched	Enriched	YES		
O75533	Splicing factor 3B sul	SF3B1	145.83	36.6	63	63	323.31	0	273080	238840	261000	246280	313140	320460	342810	385540	200570	283760	Enriched	Enriched	Enriched	Moderate	YES		
O75534-2;O75534;	Cold shock domain-c	CSDE1	85.746	20.6	18	18	75.932	0	53869	48348	51500	46995	63635	47397	57939	56156	37679	60668	Enriched	Enriched	Enriched	No expres	YES		
O75554-2;O75554	WW domain-binding	WBP4	40.03	4.2	1	1	5.1979	0.00022	7186	6994.2	7387.5	7762.6	8556.4	4718.6	8201.6	6086.9	4095.5	6597.7	Low	Moderate	Moderate	Moderate			
O75569;O75569-3;	Interferon-inducible (	PRKRA	34.404	25.6	9	9	83.269	0	55920	50671	47213	38562	65933	41855	41649	36330	25744	39780	Moderate	Enriched	Enriched	Enriched	YES		
O75592-2;O75592	E3 ubiquitin-protein	MYCBP2	509.7	1.7	7	7	11.078	0	19110	15195	17832	20476	19568	10751	14675	19426	7041.4	18619	Enriched	Enriched	Enriched	Enriched	YES		
O75600;O75600-2	2-amino-3-ketobutyra	GCAT	45.285	21.2	13	13	36.445	0	75206	47116	54050	58979	52641	56411	51675	60065	35409	57824	Moderate	Enriched	Moderate	Moderate			
O75643	U5 small nuclear ribo	SNRNP200	244.5	21.8	59	59	323.31	0	291470	194410	244420	315140	268510	319100	279750	352290	172730	317240	No expres	Enriched	Enriched	Enriched	YES		
O75663;O75663-2	TIP41-like protein	TIPRL	31.444	25	7	7	20.595	0	34989	18235	23091	34531	26661	31879	16771	31811	10262	36340	Enriched	Moderate	Enriched	Low	YES		
O75683	Surfeit locus protein	SURF6	41.45	4.2	1	1	2.3067	0.00479	5809.8	6505.9	7113.9	4080.5	9190.5	4714.9	7591	5441.5	3920.4	6828.7	Enriched	Moderate	Moderate	No expres	YES		
O75688;B8ZZF0;C	Protein phosphatase	PPM1B	52.642	14.6	7	4	6.374	0	541.89	191.67	450.61	475.13	239.38	110.63	0	94.196	73.204	233.13	Enriched	Enriched	Enriched	Low	YES		
O75691	Small subunit proces	UTP20	318.38	2.8	9	9	16.209	0	36002	30214	40648	26593	41737	50833	60757	58987	26634	50318	Moderate	Moderate	Moderate	No expres	YES		
O75746-2;O75746	Calcium-binding mito	SLC25A12	62.72	19.1	11	6	6.0404	0	21633	10934	14654	23261	15709	21247	21169	22080	12501	23224	No expres	Low	Enriched	Moderate	YES		
O75764	Transcription elongat	TCEA3	38.971	24.4	10	8	20.913	0	34737	27717	30457	25122	35779	42533	30186	31946	18645	32684	Enriched	Enriched	Enriched	No expres	YES		
O75781-2;O75781	Paralemmin-1	PALM	37.157	8.2	3	3	3.9044	0.00061	4730.7	4196.4	5466.8	6427.4	4995	3286	3351	5726.5	3331.6	4921.8	Moderate	Moderate	Moderate	Moderate	YES		
O75792	Ribonuclease H2 sub	RNASEH2A	33.395	11.4	3	3	5.1369	0.00044	2127.6	2106.6	1943.5	1704	1944.5	1724.9	1746.2	1660	1176.2	2288.4	Moderate	Enriched	Moderate	Moderate	YES		
P54855;O75795	UDP-glucuronosyltra	UGT2B15;UGT2B17	61.036	4	2	2	2.9478	0.00169	14384	12983	16608	11760	20456	25316	23138	10417	12544	20475	Enriched	Enriched	Enriched	Low			
O75808;O75808-2	Calpain-15	CAPN15	117.31	1.8	2	2	3.8674	0.00061	11964	12867	13378	10324	18332	11641	27382	9566.5	15516	13947					YES		
X6RLL4;O75818-2	Ribonuclease P prote	RPP40	34.676	6.3	2	2	2.9989	0.00151	322.98	184.8	370.95	201.61	355.11	150.82	451.24	451.71	472.87	418.16	Moderate	Moderate	Moderate	Low			
O75821;K7ENA8;I	Eukaryotic translatio	EIF3G	35.611	53.4	24	24	129.15	0	191890	112580	135110	143470	156010	148030	127090	113410	70013	144560	Enriched	Enriched	Enriched	Enriched	YES		
O75822;O75822-3;	Eukaryotic translatio	EIF3J	29.062	51.2	24	24	62.707	0	164040	170110	151450	148440	220420	219290	172920	156020	89298	145960	Moderate	Enriched	Enriched	Low	YES		
O75828	Carbonyl reductase [	CBR3	30.85	22.7	10	3	6.418	0	19185	17813	20176	17255	22841	14151	15782	13479	10803	17953	Low	No expres	Low	Low	YES		
O75830;C9J7N5	Serpin I2	SERPINI2	46.144	43.5	31	31	204.03	0	224670	158400	184250	136740	206720	223940	281700	156350	164730	183500	Low	Enriched	Enriched	Enriched	YES		YES
O75843	AP-1 complex subun	AP1G2	87.116	5.2	4	3	3.7826	0.0006	905.87	530.19	700.78	1154.9	614.43	737.35	608.29	907.43	517.33	1086.7	Low	No expres	Moderate	Enriched			
O75844	CAAX prenyl protea	ZMPSTE24	54.812	21.1	14	14	98.232	0	99489	64286	83247	100570	97063	121740	127960	96113	71723	109680	Enriched	Enriched	Enriched	Enriched	YES		
O75874	Isocitrate dehydrogen	IDH1	46.659	51.9	57	55	323.31	0	674290	457230	558790	625070	532610	618000	602360	602720	395930	623410	Enriched	Enriched	Enriched	Enriched	YES		
O75881	25-hydroxycholester	CYP7B1	58.255	9.7	5	5	9.4385	0	5835.9	4370.8	5351.1	3730.5	6513.7	5403.6	6240.1	3532.4	3621	4654.3	Low	Low	Low	No expres	YES		
O75882-2;O75882;	Attractin	ATRN	141.43	3	3	3	13.137	0	4743.8	4704.3	4047.7	3633.8	4414.9	4340.3	8130.7	10357	6545.9	6168.4	Moderate	Moderate	Enriched	No expres	YES		
O75884;A0A087W	Putative hydrolase RI	RBBP9	21	46.2	8	8	21.888	0	57884	44865	53478	52361	61206	50818	48740	40420	35645	47418	Enriched	Enriched	Enriched	No expres	YES		
O75886;O75886-2	Signal transducing ad	STAM2	58.164	13	7	6	9.5879	0	17100	14420	14276	19859	18291	19959	21080	26642	9143.1	21031	Enriched	Enriched	Enriched	No expres	YES		
O75891;O75891-3;	Cytosolic 10-formylt	ALDH1L1	98.828	24.8	33	22	84.503	0	118750	95143	105180	120390	105780	125820	191470	132760	81470	141630	No expres	Enriched	Moderate	Moderate	YES		
O75907;A0A0A0M	Diacylglycerol O-acy	DGAT1	55.278	11.1	5	5	20.011	0	21219	17684	19574	27630	25607	26101	20463	19246	10041	22845	Moderate	Moderate	Moderate	Low	YES		
O75911;O75911-2	Short-chain dehydrog	DHRS3	33.548	7.9	2	2	4.1635	0.00062	19710	23898	23815	18349	32254	16876	40246	40275	17136	19693	Enriched	Enriched	Enriched	Enriched			
O75915;F8WF90;C	PRA1 family protein	ARL6IP5	21.614	17	10	10	51.275	0	56137	30570	42993	59542	35907	59005	68802	85084	27220	65560	Enriched	Enriched	Enriched	Enriched	YES		
O75923-15;O7592:	Dysferlin	DYSF	222.31	7.5	13	11	22.247	0	25438	20428	23311	19280	28713	25235	21052	21920	11002	21188	Enriched	Low	Moderate	No expres	YES		
O75925;O75925-2;	E3 SUMO-protein lig	PIAS1	71.835	4.5	2	2	6.9324	0	13780	10965	13912	12868	13142	10707	11485	12544	5885.9	12173	Enriched	Moderate	Enriched	Enriched			
O75934	Pre-mRNA-splicing f	BCAS2	26.131	25.3	7	7	53.409	0	22291	15012	17612	19328	18195	27263	46654	45329	24693	38771	Enriched	Enriched	Enriched	Moderate	YES		
X6RCK5;O75935-:	Dynactin subunit 3	DCTN3	17.299	25.8	5	5	10.753	0	30714	27238	37809	22100	30097	40997	51308	39489	31603	40852	Enriched	Enriched	Enriched	Moderate	YES		
O75937	DnaJ homolog subfar	DNAJC8	29.841	17.8	9	9	31.104	0	43106	29820	43450	37694	47678	26205	62193	56730	19506	40618	Enriched	Enriched	Enriched	Enriched	YES		
O75943-3;O75943-	Cell cycle checkpoin	RAD17	57.244	2	1	1	2.1149	0.00643	4741.8	4749.4	4312.7	6006.4	4476.9	4395.5	4310.1	5058.8	2227.8	5594.4	Low	Enriched	Enriched	Enriched			
O75947;O75947-2	ATP synthase subuni	ATP5H	18.491	75.8	23	23	63.936	0	205580	147550	183020	281270	184860	192310	244370	274820	107260	257040	Enriched	Enriched	Enriched	Enriched	YES		
O75955;O75955-2	Flotillin-1	FLOT1	47.355	23.9	10	10	51.028	0	39760	32156	33860	45211	34285	38640	47229	51223	26958	51854	Enriched	Enriched	Enriched	Enriched	YES		
O75964;E9PN17	ATP synthase subuni	ATP5L	11.428	46.6	8	8	43.966	0	50490	43968	49135	77612	65220	75732	78073	60493	40257	81653	Enriched	Enriched	Enriched	Enriched	YES		
O75976;O75976-2	Carboxypeptidase D	CPD	152.93	4.9	6	6	10.102	0	8986.6	12237	10398	10037	12663	7980.3	7472.6	5847.3	4957.8	6808.7	Enriched	Enriched	Enriched	Enriched	YES		
O76003	Glutaredoxin-3	GLRX3	37.432	21.8	9	9	14.943	0	28039	23875	29594	25163	32507	28297	31083	26641	18370	24210	Enriched	Enriched	Enriched	Low	YES		
O76021;J3QSV6;O	Ribosomal L1 domai	RSL1D1	54.972	27.3	15	15	25.702	0	59298	55129	60313	35093	76690	40774	45162	40828	27382	52005	Moderate	Enriched	Enriched	Enriched	YES		
O76024	Wolframin	WFS1	100.29	12.6	11	11	38.373	0	22923	21905	24546	30929	29327	25182	42115	27160	44871	30298	Enriched	Enriched	Enriched	Enriched	YES		
O76027	Annexin A9	ANXA9	38.363	15.9	5	5	8.5843	0	21755	20718	24806	27297	27761	28953	29058	27997	14248	25603	Enriched	Moderate	Moderate	Enriched	YES		
O76031	ATP-dependent Clp	CLPX	69.223	24.3	13	13	46.018	0	56067	41251	41989	54549	50145	38201	38618	49026	21653	49509	Enriched	Enriched	Enriched	Low	YES		
O76038	Secretagogin	SCGN	32.039	35.5	14	14	40.504	0	51947	53963	56296	48320	68914	33332	42817	32689	43863	41661	Low	Enriched	Enriched	Enriched	YES		
O76041-2	Nebulette	NEBL	31.196	34.4	11	7	18.936	0	11055	6985	7942.4	10984	7828.4	9156.5	9539.1	10086	7758.7	12724	Enriched	Enriched	Enriched	Enriched	YES		
O76070;F8W754	Gamma-synuclein	SNCG	13.331	36.2	6	4	10.343	0	17369	19617	21045	13484	28780	14964	26366	15200	25006	29765	No expres	No expres	No expres	Low	YES		
O76094;O76094-2	Signal recognition pa	SRP72	74.605	36.1	46	46	297.57	0	231920	161750	173150	181590	224670	266240	415220	347500	172890	252640	Enriched	Enriched	Enriched	Moderate	YES		
O94760;O94760-2	N(G),N(G)-dimethyla	DDAH1	31.121	59.3	30	30	170.99	0	156510	109740	115060	117380	139540	148300	245260	190150	117020	147800	Enriched	Enriched	Enriched	No expres	YES		
O94763-2;O94763-	Unconventional pref	URI1	51.246	6.8	2	2	5.9759	0	5309.7	7242.8	5710.1	6158.8	6129.2	3595.6	2821.2	6088.4	2446.7	6160.8					YES		
O94776;O94776-2	Metastasis-associated	MTA2	75.022	9.3	5	4	30.989	0	16997	11063	14052	14755	19286	11328	18648	16249	9440.9	17161	No expres	No expres	No expres	Moderate	YES		
O94778	Aquaporin-8	AQP8	27.381	6.9	2	2	4.8033	0.00043	12499	7456.9	8164	4449.9	13778	9035.1	6155.1	4511.7	3929.4	10143	Enriched	Enriched	Enriched	Enriched		YES	
O94804	Serine/threonine-prot	STK10	112.13	7.2	7	7	11.091	0	15323	16020	16801	18429	18653	15585	17183	16049	14496	17395	Enriched	Low	Moderate	Moderate	YES		
O94811	Tubulin polymerizati	TPPP	23.693	17.8	6	6	20.474	0	12363	6583.4	8732.2	16863	7331.7	16491	12492	17583	6551.6	15044	Enriched	Enriched	Enriched	Low	YES		
O94819	Kelch repeat and BT	KBTBD11	65.719	21.5	11	11	150.22	0	27521	20154	26127	15403	31032	13994	20574	20613	11529	19388	Moderate	Moderate	Moderate	Moderate	YES		
O94822;O94822-3;	E3 ubiquitin-protein	LTN1	200.55	3.3	6	6	12.968	0	27106	21441	22462	29636	30487	32459	20091	20501	10917	24062					YES		
O94826	Mitochondrial impor	TOMM70A	67.454	18.8	16	16	62.16	0	39276	31529	33778	40845	44759	25553	31609	27687	18635	37225	Enriched	Enriched	Enriched	Enriched	YES		
O94832;J3QRN6;K	Unconventional myo	MYO1D	116.2	18.2	26	26	53.047	0	77946	56990	73682	78216	81950	67584	86565	70492	55236	81409	No expres	Low	Enriched	Enriched	YES		
O94855;O94855-2;	Protein transport pro	SEC24D	113.01	22.8	45	43	218.07	0	174770	141010	155090	150500	207250	177990	171490	157700	85830	149520	Low	Moderate	Enriched	Moderate	YES		
O94874;O94874-2;	E3 UFM1-protein lig	UFL1	89.594	36.9	51	51	151.11	0	214490	171280	187140	228810	214980	238150	255630	252530	148260	210750					YES		
O94875-11;O9487!	Sorbin and SH3 dom	SORBS2	134.59	25.1	48	2	194.86	0	247710	207100	242850	261540	275270	251940	400780	307980	172620	315680	Enriched	Enriched	Enriched	Low	YES		
O94875-12;O9487!	Sorbin and SH3 dom	SORBS2	80.965	40.5	46	0	6.52	0	12055	11528	11120	8067.7	20403	7369.3	15042	11322	5752.5	12787	Enriched	Enriched	Enriched	Low	YES		
O94875-7	Sorbin and SH3 dom	SORBS2	113.55	25.1	43	3	8.8072	0	2630.9	2954.8	7020.9	7447.8	4906.9	687.94	1044.2	781.46	660.32	3146.4	Enriched	Enriched	Enriched	Low	YES		
O94886	CSC1-like protein 1	TMEM63A	92.125	4.5	5	5	6.8351	0	4285.6	4360.3	4015	3773.3	4173.6	3589.3	2833	3290.7	1658.7	3737.4	Low	Moderate	Moderate	Enriched	YES		
O94887;O94887-3;	FERM, RhoGEF and	FARP2	119.89	2.3	3	3	3.3986	0.00078	6563.2	5628.4	5230.7	4365.9	7241.1	4862.1	4776.7	6143.8	4886.3	7422.2	Moderate	Enriched	Moderate	Moderate	YES		
O94888;C9JAT7	UBX domain-contain	UBXN7	54.862	18.8	7	7	20.445	0	15032	11502	8473.4	15095	8848.1	9643.7	7444.5	13822	3105.1	11480	Moderate	Moderate	Enriched	No expres	YES		
O94901-9;H0Y742	SUN domain-contain	SUN1	101.93	13.1	12	12	68.846	0	41398	36411	44591	39682	50408	40157	36421	37335	21212	42711					YES		

O94903;E5RG77;E	Proline synthase co-t	PROSC	30.344	37.5	18	18	96.673	0	119320	67957	71315	105200	83286	127940	116750	135510	59264	119350	Enriched	Enriched	Enriched	Moderate	YES		
O94905;E5RHW4	Erlin-2	ERLIN2	37.839	48.1	25	15	317.45	0	220390	97487	133480	232520	153020	199250	215770	205570	128450	252610	Enriched	Enriched	Enriched	Low	YES		
O94906-2;O94906	Pre-mRNA-processin	PRPF6	102.43	16.9	14	14	59.246	0	35918	27717	35494	25863	44219	30625	35475	31148	25095	31281	Moderate	Enriched	Enriched	Enriched	YES		
O94915;H0Y9X0;F	Protein furry homolo	FRYL	339.59	1.1	3	3	4.8872	0.00044	6095.8	4707.1	6396.9	5581.2	4646.5	5172.5	3338.7	5521.2	2310.2	6539.8	Moderate	Enriched	Enriched	Enriched			
O94919	Endonuclease domai	ENDOD1	55.016	9.8	5	5	28.657	0	10838	10848	14828	10186	14030	12945	33427	20501	27881	14871	Moderate	Moderate	Enriched	Moderate	YES		
O94925	Glutaminase kidney i	GLS	73.46	24.4	21	2	5.5941	0	6976.9	6366.8	5708.3	5771.9	8582.7	5676.1	7096.3	5834.4	2704	5108.7	Moderate	Enriched	Enriched	Enriched	YES		
O94925-3	Glutaminase kidney i	GLS	65.459	29.8	25	0	259.75	0	171600	118940	128830	131250	180420	145670	164800	141470	75743	170170	Moderate	Enriched	Enriched	Enriched	YES		
O94964-2;X6R3R3	Protein SOGA1;N-te	SOGA1	183.86	1.7	2	2	1.9529	0.008	10670	5164.5	4501.6	22784	7328.7	5605.4	2798.1	7612.8	1457.5	5986.2							
O94973;O94973-2	AP-2 complex subun	AP2A2	103.96	26.4	30	7	105.68	0	155220	129040	144970	166900	160130	123840	136030	162630	73653	163480	Enriched	Enriched	Enriched	Enriched	YES		
O94973-3	AP-2 complex subun	AP2A2	73.127	29.4	21	1	8.438	0	2553.1	4546.5	5662.2	1892.9	6772.4	2042.7	2740.2	2032.2	1416.9	2581	Enriched	Enriched	Enriched	Enriched	YES		
O94992;K7ERG7;	Protein HEXIM1;Pro	HEXIM1;HEXIM2	40.623	5.8	2	2	3.5899	0.00079	5337.7	7752.1	4641.9	5110.1	6101.2	3561.1	4214.7	5324.4	2910.8	3984.6	Enriched	Moderate	Enriched	Enriched			
O95049-5;O95049;	Tight junction protei	TJP3	97.486	4.4	3	3	130.48	0	3831	2648	2703.6	3299.1	4300.1	3671.4	6854.9	4510.2	4012	5258.9	Moderate	Low	Moderate	No expres	YES		
O95081;O95081-2	Arf-GAP domain and	AGFG2	48.962	9.1	3	2	5.9459	0	10665	13004	12266	15090	12611	10116	16045	11609	18568	12246	Moderate	Moderate	Moderate	No expres	YES		
O95104;O95104-2;	Splicing factor, argini	SCAF4	125.87	4.1	4	4	8.1961	0	12993	10373	13592	12089	12566	11967	15005	17184	7764.6	11797					YES		
O95139;A0A087W	NADH dehydrogenas	NDUFB6	15.489	35.9	5	5	25.828	0	37982	24757	30657	38748	38475	73216	35449	31605	16805	35688	Enriched	Enriched	Enriched	Low	YES		
O95140	Mitofusin-2	MFN2	86.401	4.4	3	3	4.4268	0.00042	10375	7900.3	7780.3	11202	9431	13841	16781	19412	8047.4	14106	Enriched	Enriched	Enriched	Moderate	YES		
O95154	Aflatoxin B1 aldehyd	AKR7A3	37.206	44.4	35	15	166.19	0	197240	164940	164620	164670	243700	213250	181290	562070	96827	299020	Enriched	Enriched	Enriched	Enriched	YES		
O95155-3;O95155-	Ubiquitin conjugatior	UBE4B	121.82	4.2	4	4	17.661	0	6468.6	4003.3	5959.3	6866	6147.3	8998.8	10064	11084	11455	11500	Enriched	Enriched	Enriched	Moderate	YES		
O95159	Zinc finger protein-lil	ZFPL1	34.114	9.4	3	3	10.491	0	5542.7	3790.4	3829.6	3728.1	8688.5	4769	6502	4171.1	3444.7	5328.7	Moderate	Low	Moderate	Enriched			
S4R3I5;O95167	NADH dehydrogenas	NDUFA3	4.6462	75.6	2	2	7.0056	0	9380.3	11721	8799.4	8050.1	12994	8229.1	9002.7	7115.3	5192.9	10999	Enriched	Enriched	Enriched	No expres	YES		
O95168;O95168-2;	NADH dehydrogenas	NDUFB4	15.208	44.2	7	7	22.453	0	42747	34293	38240	34210	45386	31031	32477	29762	17745	32493	Enriched	Enriched	Enriched	No expres	YES		
O95182;M0R0N0	NADH dehydrogenas	NDUFA7	12.551	63.7	9	9	16.648	0	44089	30379	34243	44192	56721	22674	25364	18162	21316	29932	Moderate	Moderate	Enriched	Enriched	YES		
O95202	LETM1 and EF-hand	LETM1	83.353	18.8	21	21	101.26	0	88155	89822	81245	70041	106120	78410	104750	92494	59152	110620	Low	Moderate	Moderate	No expres	YES		
O95218-2;O95218	Zinc finger Ran-bindi	ZRANB2	36.318	19.7	8	8	48.697	0	51222	43526	48283	29445	50553	48313	83748	65838	71879	76387	Moderate	Enriched	Enriched	No expres	YES		
O95219;F8W9T3	Sorting nexin-4	SNX4	51.908	10.9	4	4	10.392	0	6996.8	6675.3	7370	5681.4	9474.8	5503.1	5644.7	5970.6	3972.6	5876.4	Enriched	Enriched	Enriched	Moderate	YES		
O95251-2;O95251-	Histone acetyltransfe	KAT7	58.135	7	3	3	12.385	0	7588.1	4671.2	5978.9	10805	4746.1	9246.7	8139.9	10138	4533.2	9266					YES		
O95292	Vesicle-associated m	VAPB	27.228	26.7	8	6	52.987	0	57711	41871	61001	47689	65854	47238	91121	70274	37758	61287	Enriched	Enriched	Enriched	Enriched	YES		
O95295	SNARE-associated p	SNAPIN	14.874	16.2	2	2	4.7511	0.00043	18062	15536	18071	17276	21224	15337	17824	12002	9983.1	14315	Enriched	Enriched	Enriched	No expres	YES		
O95298;O95298-2	NADH dehydrogenas	NDUFC2	14.187	27.7	5	5	9.3578	0	56889	39998	66603	42846	38467	64441	47647	61532	19789	63809	Enriched	Enriched	Enriched	No expression			
O95302;O95302-3	Peptidyl-prolyl cis-tr	FKBP9	63.083	11.6	9	9	14.047	0	13984	11339	13703	14354	13884	11070	24907	17087	17687	13682	Enriched	Enriched	Enriched	Enriched	YES		
O95336;M0R261;N	6-phosphogluconolac	PGLS	27.547	43.8	19	19	73.294	0	70729	59132	59214	63086	70954	70081	62693	64677	39114	63172	Enriched	Enriched	Enriched	No expres	YES		
O95340;O95340-2	Bifunctional 3-phosp	PAPSS2	69.5	34.2	22	19	65.69	0	105440	98914	106120	96648	140940	105430	119410	96942	75111	99329	Enriched	Enriched	Enriched	No expres	YES		
O95352-3;O95352-	Ubiquitin-like modifi	ATG7	68.617	11.6	7	7	29.286	0	20470	11721	16739	23193	17882	20871	22822	52611	16582	26294	No expres	Low	Moderate	No expres	YES		
O95363	Phenylalanine--tRNA	FARS2	52.356	6.7	3	3	3.9151	0.00061	15300	9417.5	14225	19764	11775	15270	17217	21967	10770	19087	Enriched	Moderate	Moderate	Moderate	YES		
O95372;Q5QPQ0;	Acyl-protein thioeste	LYPLA2	24.737	26.8	11	11	58.138	0	58346	41474	56845	23497	92429	30894	30600	20810	18503	38189	Enriched	Enriched	Enriched	Enriched	YES		
O95373	Importin-7	IPO7	119.52	9.4	9	9	24.01	0	27502	22672	25106	30536	26810	23808	25168	28499	18965	26677	Enriched	Enriched	Enriched	Enriched	YES		
O95376	E3 ubiquitin-protein	ARIH2	57.818	5.5	3	3	7.8732	0	14478	8688.5	10611	14777	10617	18845	12627	14561	5776.6	13834	Moderate	Enriched	Enriched	Enriched	YES		
O95391	Pre-mRNA-splicing f	SLU7	68.386	2.6	1	1	2.4788	0.00395	4309.4	4297.6	5636.4	4199.6	6342.9	2923.9	3984.1	3207	1282.1	3153.3	Moderate	Enriched	Enriched	No expres	YES		
O95394;O95394-3;	Phosphoacetylglucos	PGM3	59.851	36.2	29	24	80.249	0	113250	101180	111280	115890	148810	127240	180050	123070	135480	163120	Low	Enriched	Enriched	Moderate	YES		
O95396	Adenylyltransferase a	MOCS3	49.669	10.2	5	5	9.7622	0	33518	26311	29348	31187	36046	32694	33979	28376	23886	31358	No expres	Low	Moderate	Low	YES		
Q5H8X8;O95399;	Urotensin-2	UTS2	16.276	5.8	1	1	3.1239	0.00095	425.1	233.37	1030.3	232.13	490.87	8205	8903.3	6478	3850.8	4245.9	No expres	No expres	No expres	No expression			
O95400	CD2 antigen cytoplas	CD2BP2	37.646	15	4	4	8.2482	0	12881	11550	11122	11219	13878	9253.9	8673.9	10457	5603.8	10934	Enriched	Moderate	Moderate	Low	YES		
O95425-2;O95425-	Supervillin	SVIL	200.84	5	7	7	19.921	0	27878	28618	28490	24918	29324	22992	32028	33182	15788	29216	Enriched	Enriched	Enriched	Moderate	YES		
O95427;K7EM62	GPI ethanolamine ph	PIGN	105.81	4.7	5	5	8.1544	0	9730.4	6691.7	6182.8	7114.9	8687.4	7118.1	6095.4	6913.1	3002.1	7565.2	Moderate	Enriched	Enriched	No expres	YES		
O95428-6;O95428-	Papilin	PAPLN	134.84	6.3	8	8	14.936	0	19518	17569	25063	15086	30419	17652	23207	24654	15495	23054	Moderate	Moderate	Low	No expres	YES		
O95433;O95433-2;	Activator of 90 kDa h	AHSA1	38.274	28.4	14	14	44.19	0	43570	33940	38765	39979	45238	51182	93831	62318	50495	60316	Moderate	Enriched	Enriched	Enriched	YES		
O95453-2;O95453-	Poly(A)-specific ribo	PARN	66.574	9.9	5	5	13.041	0	49859	40715	41180	30538	45512	38536	40457	34068	18469	37253	Enriched	Enriched	Enriched	Enriched	YES		
O95456-2;O95456;	Proteasome assembly	PSMG1	30.288	12	5	5	226.38	0	12186	10397	11251	7682.3	13247	14957	18447	14882	14888	22027	Moderate	Enriched	Enriched	Enriched	YES		
O95470	Sphingosine-1-phosp	SGPL1	63.523	17.6	12	12	57.753	0	35328	25485	36574	30457	31815	31393	62232	90011	42369	52709	Enriched	Enriched	Enriched	Moderate	YES		
O95477	ATP-binding cassette	ABCA1	254.3	0.6	1	1	2.5143	0.00379	6437.8	4201.8	5494.6	7525.6	5994.8	6559.6	5541	4073.9	3372.3	6191.4	Enriched	Moderate	Enriched	Enriched			
O95486	Protein transport pro	SEC24A	119.75	10.4	11	10	27.117	0	46953	35162	41336	43991	58347	36355	31316	26093	20257	33978	Enriched	Enriched	Enriched	Moderate	YES		
O95487-2;O95487;	Protein transport pro	SEC24B	133.63	12.9	12	11	35.725	0	47052	28754	41490	45592	38216	43183	43430	43351	22514	42273	Low	Moderate	Enriched	Enriched	YES		
Q5TIH2;O95562	Vesicle transport pro	SFT2D2	11.756	9.3	1	1	2.6658	0.00256	4192.5	4434.4	5585.1	2579.1	4357.2	8484.5	13897	10183	12175	10607	Moderate	Moderate	Moderate	Low	YES		
Q5R3B4;O95563	Mitochondrial pyruva	MPC2	11.681	35.2	5	5	11.456	0	17467	13486	16567	18147	19029	17994	16501	14847	11174	17207					YES		
O95571;M0QXB5	Persulfide dioxygena	ETHE1	27.873	20.5	7	7	25.185	0	22563	17839	19433	17857	24088	20424	27007	18476	16061	25742	Enriched	Enriched	Enriched	Moderate	YES		
O95573;H7BYZ7	Long-chain-fatty-acid	ACSL3	80.419	13.6	12	8	30.296	0	31168	27813	27092	32934	34004	34309	25711	28877	14576	29773	Enriched	Moderate	Enriched	Enriched	YES		
O95671-2;O95671;	N-acetylserotonin O-	ASMTL	67.192	17.5	11	11	39.1	0	18837	18479	23648	21788	25440	31443	18838	19814	11549	20854	Enriched	Enriched	Enriched	Enriched	YES		
O95674	Phosphatidate cytidyl	CDS2	51.417	15.1	6	6	13.863	0	29964	22852	28106	29207	39126	21705	42623	24355	25073	32870	Enriched	Moderate	Enriched	Enriched	YES		
O95685	Protein phosphatase	PPP1R3D	32.559	10.4	3	3	15.805	0	9050.9	9392.6	9142.1	9102.7	11336	8326.6	6338.5	7990.6	4574.5	8808.3	Low	Low	Moderate	Moderate	YES		
O95716	Ras-related protein R	RAB3D	24.267	50.2	31	22	279.76	0	247880	186900	205630	264830	201980	309730	403310	382040	170430	334340	Low	Low	Low	No expres	YES		
O95721;C9JAF7	Synaptosomal-associ	SNAP29	28.97	26	5	5	33.218	0	42668	38041	43185	34747	60783	34894	50636	51576	32263	48392	Enriched	Moderate	Enriched	No expres	YES		
O95747;C9JIG9	Serine/threonine-prot	OXSR1	58.022	19.2	12	11	99.017	0	52600	34851	45150	54677	58721	61854	54766	61577	27012	58935	Moderate	Enriched	Enriched	Moderate	YES		
O95758-1;O95758-	Polypyrimidine tract-	PTBP3	56.501	18	10	5	12.431	0	14274	12526	16035	17960	16247	14988	42142	24227	22962	23690					YES		
O95782-2;O95782	AP-2 complex subun	AP2A1	105.36	17	21	14	26.51	0	42628	30205	32165	38096	39127	45207	67892	59252	30971	46273	Enriched	Enriched	Moderate	No expres	YES		
O95786;O95786-2;	Probable ATP-depen	DDX58	106.6	11.9	12	12	16.375	0	54737	31636	48326	51419	49256	45256	42315	51018	20901	38599	Enriched	Moderate	Enriched	No expres	YES		
O95810	Serum deprivation-re	SDPR	47.173	23.8	18	18	53.554	0	66959	48982	51781	60670	60051	79470	68973	86629	39723	73464	No expres	Moderate	Low	No expres	YES		
O95816	BAG family molecula	BAG2	23.772	4.7	2	2	4.8944	0.00044	4970.3	4281	4940.7	6160.5	4905.7	5430.6	4785.5	9844.7	2253.7	6472	No expres	No expres	Moderate	Moderate	YES		
O95817;C9JFK9	BAG family molecula	BAG3	61.594	17.9	12	12	26.56	0	42861	33705	44183	26150	53090	25618	38127	28651	24495	28714	Enriched	Enriched	Enriched	No expres	YES		
O95822-2;O95822	Malonyl-CoA decarb	MLYCD	50.945	16.7	7	7	91.403	0	33821	24733	25752	27126	32402	25370	27588	25551	18964	26751	Enriched	Enriched	Enriched	No expres	YES		
O95831-3;O95831;	Apoptosis-inducing f	AIFM1	66.294	32.5	33	33	219.62	0	311730	169940	181860	268670	218030	254610	250900	337850	141030	308990	Moderate	Moderate	Enriched	Moderate	YES		
O95841;Q9UKU9	Angiopoietin-related	ANGPTL1;ANGPTL2	56.719	2.6	1	1	1.9576	0.00801	14360	8047.6	11943	7982.6	14424	8652.3	10518	4015.5	6864	10105	Moderate	Moderate	Moderate	No expression			
O95861-4;O95861;	3(2),5-bisphosphate	BPNT1	29.188	34.2	12	12	34.576	0	58069	52638	57074	54794	66087	48724	62086	51794	37938	52027	Moderate	Moderate	Moderate	No expres	YES		
O95865;Q5SSV3;	N(G),N(G)-dimethyla	DDAH2	29.644	43.5	17	17	127.28	0	70064	55768	68477	68439	65586	72887	90294	107570	64337	95473	Enriched	Enriched	Enriched	Enriched	YES		
O95870-2;O95870	Abhydrolase domain-	ABHD16A	59.382	9.9	4	4	5.9009	0	15017	10244	11893	16282	16993	16045	18158	19030	8236.1	14778					YES		
O95881	Thioredoxin domain-	TXNDC12	19.206	37.8	11	11	53.192	0	89911	65837	63811	74768	95173	59702	53671	54112	30790	56095	Enriched	Enriched	Enriched	No expres	YES		
O95926;O95926-2	Pre-mRNA-splicing f	SYF2	28.722	9.1	2	2	4.3089	0.00063	3294.6	3410.8	3449	2436.3	4692.8	2897.5	6018.8	5408.2	4603.8	5921	Enriched	Enriched	Enriched	Moderate			
O95967;E9PRU1	EGF-containing fibul	EFEMP2	49.405	9.9	4	4	6.8452	0	4401.2	5543	6502.4	2850	7721.7	4208.7	11481	8975.4	9042.1	4412.6	Enriched	Enriched	Enriched	Moderate	YES		
O95980	Reversion-inducing c	RECK	106.46	6.7	6	6	10.077	0	23663	20498	26793	23785	24621	30040	39758	41273	21969	31179	Enriched	Moderate	Enriched	Moderate	YES		
O95994;B5MC07;I	Anterior gradient pro	AGR2	19.979	33.7	9	7	26.888	0	70811	28183	58590	26123	39486	27725	36938	47500	17595	35023	Enriched	Moderate	Moderate	No expres	YES		
O96000-2;O96000;	NADH dehydrogenas	NDUFB10	20.143	51.8	19	19	98.358	0	133910	97202	107810	124350	122280	166210	160420	160720	80074	152950	Low	Enriched	Enriched	No expres	YES		
O96005;O96005-4;	Cleft lip and palate tı	CLPTM1	76.096	14.9	11	11	39.548	0	36752	28005	33778	39776	39001	29735	34332	36149	18252	39847	Low	Moderate	Enriched	Low	YES		
O96007	Molybdopterin synth	MOCS2	20.944	14.4	2	2	5.0335	0.00044	6234.7	4489.1	4953.5	7253	6311	7383.6	5871.7	6275.4	3442.6	7001.4	Low	Moderate	Enriched	No expres	YES		
O96008;K7EKG4;	Mitochondrial impor	TOMM40	37.893	7.2	3	3	2.8553	0.00186	7253.1	7136.3	6831	7713.6	9216.2	4999.8	6443.6	5912.4	4291	6308.1	Enriched	Enriched	Moderate	Moderate	YES		
O96013;O96013-2;	Serine/threonine-prot	PAK4;NRBP2	64.071	8	4	4	8.2719	0	5908.2	12309	10877	6741	14952	5256.1	8165.5	5351.2	4201.7	5777.9	Enriched	Enriched	Enriched	Enriched			
O96019;H7C5S0;C	Actin-like protein 6A	ACTL6A	47.46	18.4	7	7	102.24	0	29717	17348	19302	22946	28827	21883	19975	25091	10157	27714	Moderate	Low	Enriched	Enriched	YES		
P00167-2;P00167;I	Cytochrome b5	CYB5A	11.268	68.4	16	16	241.38	0	200450	137830	168960	122430	158010	206270	178530	186390	83282	194350	Enriched	Enriched	Enriched	Enriched	YES		
P00325;P00325-2	Alcohol dehydrogena	ADH1B	39.854	59.7	60	11	323.31	0	299930	263700	355690	308620	408790	295150	612930	673970	270540	385460	Low	Enriched	Low	Enriched	YES		
P00338;P00338-3;I	L-lactate dehydrogen	LDHA	36.688	60.5	48	43	249.75	0	192430	151980	173870	237480	231580	203290	532640	540710	296670	282820	Enriched	Enriched	Enriched	Enriched	YES		
P00352;Q5SYQ9;C	Retinal dehydrogenas	ALDH1A1	54.861	65.5	114	42	323.31	0	1575400	1221800	1315900	1497200	1423000	1902200	1476600	1243000	787890	1377100	Moderate	Enriched	Enriched	Enriched	YES		
P00367;P00367-3;I	Glutamate dehydroge	GLUD1;GLUD2	61.397	48.7	63	63	323.31	0	724410	544080	669970	558270	786730	594440	743910	732390	422040	744490	Enriched	Enriched	Enriched	Enriched			
P00387-2;P00387;I	NADH-cytochrome b	CYB5R3	31.628	57.9	26	25	143.55	0	138800	103070	129920	147850	140970	108650	118720	111730	48706	133560	Enriched	Enriched	Enriched	Enriched	YES		
P00390-2;P00390;I	Glutathione reductas	GSR	51.7	40.7	32	27	102.42	0	181160	148320	156030	167580	213820	161320	192100	193880	117970	176430	Enriched	Enriched	Enriched	No expres	YES		
P00403	Cytochrome c oxidas	MT-CO2	25.565	23.8	9	9	56.218	0	48794	46195	31417	48568	49422	31465	31214	41793	17940	39766					YES		
P00414	Cytochrome c oxidas	MT-CO3	29.95	5.4	2	2	7.3028	0	909.04	778.8	778.15	3040.1	1118.6	1159.7	1339.9	2142.6	861.19	1685.3					YES		
P00441;H7BYH4	Superoxide dismutas	SOD1	15.936	68.8	22	22	101.27	0	134020	100180	112560	149750	128080	122880	215330	166850	149460	191220	Enriched	Enriched	Enriched	Enriched	YES		
P00450;E9PFZ2;H7	Ceruloplasmin	CP	122.2	30.6	34	34	310.65	0	113280	129410	134590	184950	87046	94742	81018	354260	41936	123020	Moderate	Moderate	Moderate	Low	YES		
P00451	Coagulation factor V	F8	267.01	0.6	2	2	4.8698	0.00043	14212	11651	14627	20565	11085	25888	24259	20413	9078.5	16806	Moderate	Enriched	Enriched	Enriched			
P00488	Coagulation factor X	F13A1	83.266	40.7	37	37	163.6	0	109990	155370	111060	185530	132790	118250	123120	190410	106810	170130	Moderate	Low	Moderate	Moderate	YES		
P00491	Purine nucleoside ph	PNP	32.118	57.4	18	18	46.229	0	49758	50244	45914	56116	56259	78154	77053	87911	41259	61600					YES		
P00492	Hypoxanthine-guanir	HPRT1	24.579	46.3	21	21	114.66	0	168680	76902	113950	108150	113230	109240	144270	166160	63591	116030	Moderate	Enriched	Enriched	Enriched	YES		
P00505;P00505-2	Aspartate aminotrans	GOT2	47.517	46.5	32	32	131.05	0	226300	160520	163010	225670	211090	267190	151420	152380	87241	173510	Enriched	Enriched	Enriched	Enriched	YES		
P00533-4;P00533-	Epidermal growth fac	EGFR	69.227	12.4	8	8	47.098	0	18090	15226	14175	19199	18111	13566	18476	16896	11726	18221	Moderate	Enriched	Enriched	Low	YES		
P00558;P00558-2	Phosphoglycerate kin	PGK1	44.614	83	93	93	323.31	0	585490	435560	541980	643910	586410	676170	942470	1135200	479710	659820	Enriched	Enriched	Enriched	Enriched	YES		
Q5T9B7;P00568;H	Adenylate kinase isoe	AK1	23.411	57.1	23	23	80.324	0	96372	93531	122550	103930	121500	145350	208960	192510	124140	151090	Moderate	Moderate	Enriched	Moderate	YES		
P00738;J3QLC9;J3	Haptoglobin;Haptogl	HP	45.205	44.6	32	15	218.56	0	153460	205820	298920	526790	152160	134490	108690	227140	134170	166300	Enriched	No expres	No expres	No expres	YES		
P00739;P00739-2;	Haptoglobin-related	HPR	39.029	28.7	18	1	2.2201	0.00545	2892.6	2836.5	2665.9	3258.6	2845.7	3028.7	2797.2	5653.6	1441.8	2581.1	Moderate	No expres	No expres	Low	YES		
P00740-2;P00740	Coagulation factor IX	F9	47.617	9.9	5	5	75.503	0	13035	11993	12967	13139	14983	14806	15690	13366	8955.4	13401	Low	No expres	No expres	No expres	YES		
P00747	Plasminogen;Plasmin	PLG	90.568	17.8	14	14	34.751	0	28150	32006	35307	50630	27893	24034	34319	37805	31214	37104	Moderate	Moderate	Low	No expres	YES		
P00918	Carbonic anhydrase 2	CA2	29.246	52.3	34	34	306.12	0	169430	255060	175940	227440	220700	196190	280620	360990	153920	202890	Enriched	Enriched	Enriched	Low	YES		
P00966	Argininosuccinate syı	ASS1	46.53	29.1	26	26	83.924	0	138920	107140	123140	152670	137780	130290	138040	106260	85321	136720	Enriched	Enriched	Enriched	Enriched	YES		
P00995;D6RIU5	Pancreatic secretory t	SPINK1	8.5067	53.2	15	15	88.157	0	116190	107720	88397	102980	120890	176630	300410	128310	112870	98136	Enriched	Enriched	Enriched	Enriched	YES		YES
P01008	Antithrombin-III	SERPINC1	52.602	29.1	19	19	83.864	0	96850	111880	104920	106760	79473	82717	78963	114970	58509	103230	No expres	No expres	Low	No expres	YES		
P01009;P01009-2;I	Alpha-1-antitrypsin;S	SERPINA1	46.736	64.1	80	76	323.31	0	383610	301070	705280	872380	331080	395620	552990	2261000	682910	668580	Enriched	Enriched	Enriched	Low	YES		
P01011;G3V3A0;G	Alpha-1-antichymotr	SERPINA3	47.65	50.8	49	49	202.69	0	161410	166460	209220	246820	147640	135260	165760	233750	103320	158260	Moderate	Enriched	Enriched	Enriched	YES		
P01019	Angiotensinogen;Ang	AGT	53.154	21.6	15	15	66.191	0	47590	30747	41037	67536	27017	52625	36072	85863	20496	42556	Enriched	Moderate	Enriched	No expres	YES		
P01023	Alpha-2-macroglobul	A2M	163.29	38.9	77	77	323.31	0	331360	419360	423940	435870	292440	357250	298700	985050	185050	390410	Low	Enriched	Enriched	No expres	YES		
P01024	Complement C3;Con	C3	187.15	55	137	123	323.31	0	660860	767120	1020500	1194900	615980	626800	682390	1741800	595220	779090	Enriched	Enriched	Enriched	No expres	YES		
P01031	Complement C5;Con	C5	188.3	11	21	21	56.958	0	65212	62787	63797	83773	73407	96242	93858	208590	61187	105050	Low	Enriched	Moderate	Low	YES		
Q5H9A7;P01033;H	Metalloproteinase inl	TIMP1	16.057	35	5	5	23.321	0	7771.4	6503.9	10174	8394	8054.3	5972.6	14652	11949	11319	9120.9	Enriched	Enriched	Enriched	Enriched	YES		
P01034	Cystatin-C	CST3	15.799	34.9	10	10	58.394	0	50786	59241	51998	47589	63815	40633	61786	54537	35297	38779	Moderate	Enriched	Enriched	Enriched	YES		
P01042-2;P01042-	Kininogen-1;Kininog	KNG1	47.883	37.5	22	22	157.37	0	95808	110200	130200	143620	87371	93122	85975	215160	91700	106620	Moderate	No expres	No expres	Low	YES		
P01116-2;P01116	GTPase KRas;GTPas	KRAS	21.424	22.3	5	1	16.094	0	18029	11912	16588	15007	18158	21937	25070	22932	14954	20455	Enriched	Moderate	Enriched	Enriched	YES		
P01275	Glucagon;Glicentin;	GCG	20.909	67.2	28	28	153.77	0	53441	68413	59382	98808	72287	87409	122510	75845	42155	132500	Low	Enriched	Enriched	Enriched	YES	YES	
P01298;K7EKP2	Pancreatic prohormo	PPY	10.445	23.2	9	5	22.578	0	95939	85797	144130	39626	137810	36617	61254	40839	124130	46459	No expres	Moderate	Enriched	Low		YES	YES
P01303	Pro-neuropeptide Y;I	NPY	10.851	19.6	2	2	3.0998	0.00095	2176.2	2457.6	2093.2	3975.4	1956.3	5664.8	7756	3230.2	14254	3121.7	Enriched	Moderate	Enriched	Enriched			
P01591;D6RD17;C	Immunoglobulin J ch	IGJ	18.098	25.2	4	4	18.938	0	10847	21999	12869	12469	17318	9035.4	37806	51310	16773	13794	No expres	No expres	No expres	No expres	YES		
P01596;P01598	Ig kappa chain V-I region CAR;Ig kappa chain		11.346	26.2	5	0	153.31	0	10957	11574	15199	12534	13646	9889.4	7810.1	31361	3872	8054.9							
P01613;P01605	Ig kappa chain V-I region Ni;Ig kappa chain V-		11.745	29.5	5	1	77.054	0	3579.1	3663.2	4737.1	3245.2	3103.5	2497.4	1942.3	17681	1053.4	3472.9							
P01621	Ig kappa chain V-III region NG9		10.729	48	5	2	7.72	0	8144	9828.9	11577	10973	10203	7242.7	11074	12699	6410.2	9239.6							
P01625	Ig kappa chain V-IV region Len		12.64	24.6	7	4	11.339	0	10523	16446	15024	7326.5	16565	7710.9	16303	11223	20824	9716.7							
P01714;A0A075B6	Ig lambda chain V-III	IGLV3-19	11.392	26.9	6	5	6.5105	0	9026.9	12650	15746	11027	13286	8734.8	10038	12695	8445.4	7812.3							
P01742	Ig heavy chain V-I region EU		12.472	16.2	2	1	1.9252	0.00814	6474.3	8236.8	9532	4324.2	10060	5608	8553.1	6119	5877.5	6215.4							
P01765;P01779;P0	Ig heavy chain V-III region TIL;Ig heavy chain		11.612	24.3	4	1	14.124	0	2537.6	3292.4	1352	1828.9	1798	1217.3	1437.3	5555.9	534.14	1866.5							
P01780	Ig heavy chain V-III region JON		12.32	25.2	4	1	3.6849	0.0008	7231.4	6584	11164	9074.2	8398.8	7278.9	6683.5	18122	3407.6	7390.9							
P01859	Ig gamma-2 chain C r	IGHG2	35.9	39.6	25	15	313.34	0	116030	86212	96976	132380	80464	110080	88421	301380	45655	112190	Moderate	Low	Low	Moderate	YES		
P01861	Ig gamma-4 chain C r	IGHG4	35.94	42.5	36	5	61.12	0	26283	36861	150910	40305	49765	27767	43240	47110	49045	40316					YES		
P01876	Ig alpha-1 chain C re	IGHA1	37.654	32.3	18	6	137.53	0	82434	71287	94577	102050	71507	76985	123000	313100	52300	77506	Enriched	Enriched	Moderate	Moderate	YES		
P01877;A0A075B6	Ig alpha-2 chain C re	IGHA2	36.526	20.9	14	2	53.53	0	33846	21570	31226	38441	24451	22785	23724	85149	6609.1	24003					YES		
P01891;P10316	HLA class I histocom	HLA-A	40.908	33.7	11	0	3.0375	0.00132	2264.8	2339.9	2979.7	4049.7	2722.1	3113.9	2691.3	3127.8	2052.2	5143.7	Enriched	Enriched	Enriched	Enriched	YES		
P02042;E9PFT6	Hemoglobin subunit	HBD	16.055	80.3	36	1	144.05	0	46636	240000	35191	46370	60955	52079	38428	42195	16308	38713	Low	Low	Low	Low	YES		
P02452	Collagen alpha-1(I) c	COL1A1	138.94	22.5	54	47	323.31	0	413690	621350	905500	528630	841890	287740	768640	575780	257630	430400	Enriched	Enriched	Enriched	Moderate	YES		
P02458;P02458-1	Collagen alpha-1(II)	COL2A1	141.78	4.9	6	3	9.0758	0	2626.9	6740.6	6822.6	3173.2	14798	1576.2	6621.2	2832.2	2239.2	3069.6	Moderate	No expres	No expres	Moderate	YES		
P02461	Collagen alpha-1(III)	COL3A1	138.56	13.3	24	17	208.85	0	148110	221340	391280	144620	333390	102150	220420	239280	62692	193930	Moderate	Moderate	Enriched	Moderate	YES		
P02462-2;P02462	Collagen alpha-1(IV)	COL4A1	127.98	5.9	16	11	65.676	0	48866	39302	50651	53729	54049	70168	100790	130500	49141	90895	Moderate	Enriched	Enriched	Enriched	YES		
P02545;P02545-3;I	Prelamin-A/C;Lamin-	LMNA	74.139	66.6	119	114	323.31	0	653510	508260	561870	758630	672720	888690	1210500	1596900	594970	1027400	Enriched	Enriched	Enriched	Enriched	YES		
P02647;F8W696	Apolipoprotein A-I;P	APOA1	30.777	70.4	50	50	278.3	0	261530	226810	232250	364760	188950	273720	257750	629770	159940	308320	Enriched	Low	Low	No expres	YES		
P02649;H0Y7L5	Apolipoprotein E	APOE	36.154	42.9	18	15	118.16	0	48601	41079	48943	55095	46815	62894	62605	134640	43762	67147	Enriched	Enriched	Moderate	No expres	YES		
V9GYM3;P02652;	Apolipoprotein A-II;I	APOA2	14.914	50.4	17	17	158.6	0	82798	63626	126200	112410	74343	145770	121800	201530	64104	128960	Moderate	Moderate	Low	No expression			
P02671-2;P02671	Fibrinogen alpha cha	FGA	69.756	43.8	53	53	323.31	0	318940	234950	330820	428310	205640	197200	224380	546990	336410	327420	Enriched	Enriched	Moderate	No expres	YES		
P02675;D6REL8	Fibrinogen beta chair	FGB	55.928	51.5	51	51	323.31	0	442790	241630	335610	515670	206100	229050	214870	797610	218830	377030	Moderate	No expres	Moderate	No expres	YES		
P02730	Band 3 anion transpc	SLC4A1	101.79	4.2	3	3	6.359	0	3632.9	3639.3	1561.9	3540.6	1807.7	3693	2690.4	23973	1168.4	5243.6	Low	No expres	Low	No expres	YES		
P02741;Q5VVP7;P	C-reactive protein;C-	CRP	25.038	18.3	7	7	27.523	0	24277	26225	35160	56292	16676	27369	24238	185990	7678.5	37855	No expres	No expres	Enriched	No expres	YES		
P02743	Serum amyloid P-cor	APCS	25.387	19.7	5	5	25.24	0	8569.6	7313.5	6505.2	7875.2	9246.4	8850	10340	15460	5231.7	24762	Enriched	Moderate	Enriched	Low	YES		
P02745;X6RLJ0	Complement C1q sul	C1QA	26.016	13.9	4	4	8.4602	0	16737	16968	16836	17204	17811	23466	24362	68675	18915	25503	Low	Low	Low	No expression			
P02747	Complement C1q sul	C1QC	25.773	11	3	3	4.6321	0.00043	5921.1	7599.8	6335.4	8988.5	5845.5	3508.9	3102	6803.2	3064.9	4774.3	Low	Moderate	Moderate	No expres	YES		
P02748	Complement compon	C9	63.173	19.9	16	16	89.846	0	54743	53142	52975	68038	64270	112100	123020	271010	57467	116320	No expres	No expres	No expres	Low	YES		
P02749	Beta-2-glycoprotein	APOH	38.298	50.7	21	9	57.302	0	116610	117710	138190	193430	70279	91589	75343	192330	64476	145000	Moderate	Enriched	Enriched	Enriched	YES		
P02750	Leucine-rich alpha-2-	LRG1	38.177	23.9	11	11	45.548	0	33811	32923	33411	50535	30792	39662	53701	71905	49218	39878	Enriched	Enriched	Enriched	No expres	YES		

P02751-10;P02751	Fibronectin;Anastelli	FN1	239.62	21.8	48	1	305.92	0	199960	189430	207150	201110	221860	152470	201780	289780	116750	291820	No expres	Moderate	Enriched	Moderate	YES		
Q5VY30;P02753	Retinol-binding prote	RBP4	22.974	36.7	9	9	16.526	0	24887	19609	23254	30023	22042	33631	27346	40256	14110	30332	No expres	Moderate	Enriched	Enriched	YES		
P02760;S4R3Y4	Protein AMBP;Alpha	AMBP	38.999	37.8	17	17	102.5	0	49800	59153	69035	48569	70767	56754	77383	315370	30044	90655	Low	Moderate	Moderate	Enriched	YES		
P02763	Alpha-1-acid glycopr	ORM1	23.511	39.8	19	13	77.22	0	95806	113520	105620	286510	76079	117310	88622	325920	56302	111590	Moderate	No expres	Low	Low	YES		
P02766;A0A087W	Transthyretin	TTR	15.887	59.9	17	17	87.506	0	98371	114270	110560	96351	132190	138070	152330	111090	62358	161010	No expres	Enriched	Enriched	Enriched	YES		
P02774;P02774-3;I	Vitamin D-binding pr	GC	52.963	54.4	39	1	217.41	0	185950	222200	272250	322890	165150	173900	185280	373800	222940	225780	Enriched	Enriched	Enriched	Enriched	YES		
P02786;G3V0E5	Transferrin receptor p	TFRC	84.87	5.4	4	4	7.1287	0	10736	7791.8	11615	8952.1	12260	10531	15355	10553	16722	12636	Enriched	Enriched	Enriched	Enriched	YES		
P02787	Serotransferrin	TF	77.063	55.3	90	88	323.31	0	543640	443410	605810	589380	421230	471360	567510	1314400	375320	552370	Enriched	Low	Low	Low	YES		
P02790;Q9BS19	Hemopexin	HPX	51.676	31	25	25	143.36	0	172660	200960	164000	253270	133730	152320	152140	245670	101440	151970	Moderate	Low	Moderate	Low	YES		
P03905	NADH-ubiquinone o	MT-ND4	51.58	4.6	4	4	8.6864	0	22976	17720	29301	31953	23912	28752	34195	33911	20694	28216					YES		
P03915	NADH-ubiquinone o	MT-ND5	67.026	5.6	3	3	10.972	0	15147	9729.6	11109	18086	12003	16328	16062	13647	8318.7	14889					YES		
P03950	Angiogenin	ANG	16.55	28.6	4	4	7.8478	0	4069.8	3385.5	4323.6	3828.8	5142	3424.6	9308.4	4877.8	5687.3	6900.4	Enriched	Moderate	Enriched	Low	YES		
P04003	C4b-binding protein	C4BPA	67.033	13.2	9	9	40.261	0	33974	47690	51636	59718	41715	26030	33501	105310	38897	39679	Low	Moderate	Enriched	Low	YES		
P04004	Vitronectin;Vitronect	VTN	54.305	33.7	26	26	82.567	0	154030	151020	150550	193750	161240	219680	233540	407660	151680	256710	Enriched	Moderate	Moderate	Low	YES		
P04040	Catalase	CAT	59.755	46.1	41	41	283.4	0	149330	158680	122160	142970	151580	158990	135340	143840	87206	152000	Enriched	Enriched	Enriched	Enriched	YES		
P04054;F8W062	Phospholipase A2	PLA2G1B	16.36	49.3	41	41	323.31	0	614600	208690	281600	292580	325800	733810	1537300	330370	682130	355170	Low	Enriched	Enriched	Enriched	YES	YES	YES
P04062-4;P04062-2	Glucosylceramidase	GBA	50.316	14.7	8	8	20.289	0	16987	11881	13703	17184	16153	20265	16856	14857	9598.1	14735	Moderate	Enriched	Enriched	Moderate	YES		
P04066	Tissue alpha-L-fucosi	FUCA1	53.688	6.4	4	4	6.1481	0	8783.2	5593.8	6302.2	12847	6083.5	9987.1	7099.9	8560.9	3517.6	8935.6	Enriched	Enriched	Enriched	Enriched	YES		
P04080	Cystatin-B	CSTB	11.139	53.1	13	13	39.447	0	50826	41402	46771	46531	53175	58646	102280	115630	40334	70805	Enriched	Enriched	Enriched	Enriched	YES		
P04083;Q5T3N1	Annexin A1;Annexin	ANXA1	38.714	54	36	36	309.31	0	166590	172440	195050	193410	179470	228590	318060	302090	159170	248200	Enriched	Moderate	Enriched	Low	YES		
P04114;A0A087W	Apolipoprotein B-10	APOB	515.6	3	13	12	27.345	0	62747	94159	90032	86903	65508	57725	66525	95304	48827	65357	Enriched	Low	Low	No expres	YES		
P04118;A0A087W	Colipase	CLPS	11.954	73.2	40	40	323.31	0	477570	582060	380970	375200	575080	397950	549540	730190	480490	370530	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P04150-7;P04150-5	Glucocorticoid recep	NR3C1	60.601	9.7	5	5	24.308	0	13181	8984.9	13249	13269	15394	16831	13673	14352	7654.5	14078	Enriched	Enriched	Enriched	Enriched	YES		
P04179-4;P04179;I	Superoxide dismutase	SOD2	19.73	60.2	19	19	181.77	0	121890	95623	113430	96983	144850	109720	177580	163750	142640	142050	Enriched	Enriched	Enriched	Low	YES		
P04181	Ornithine aminotrans	OAT	48.534	19.8	10	2	64.799	0	53284	19285	26295	58274	31983	76854	48347	57476	18398	57339	Enriched	Enriched	Enriched	Enriched	YES		
P04181-2	Ornithine aminotrans	OAT	32.853	23.3	9	1	3.2926	0.00078	11263	7137.1	7487.6	4818.3	11510	8870.3	7110.6	4992.8	4649.4	7139.4	Enriched	Enriched	Enriched	Enriched	YES		
P04196	Histidine-rich glycopr	HRG	59.578	12.4	9	9	63.193	0	39418	31701	42336	61827	37797	54909	42236	229760	20069	58254	Moderate	Low	Low	Low	YES		
P04206	Ig kappa chain V-III region GOL		11.83	45.9	11	1	95.938	0	22422	25713	26194	29552	22736	22190	26724	81934	13960	26413							
P04207	Ig kappa chain V-III region CLL		14.275	19.4	5	5	13.642	0	10256	8186.5	12070	8472.4	11720	7012.3	8508.8	10905	4521.7	7116.6							
P04208	Ig lambda chain V-I region WAH		11.725	24.8	6	3	8.6529	0	2837.1	2624.8	4172.2	2004.3	3339.5	4725.3	7386.2	36250	5121.9	6047.6							
P04217;M0R009;P	Alpha-1B-glycoprote	A1BG	54.253	25.7	9	9	25.156	0	35912	25551	38723	46542	31073	31496	31833	41395	18566	36447	Low	Moderate	Moderate	No expres	YES		
P04264;CON__P04	Keratin, type II cytosl	KRT1	66.038	21.1	19	8	53.704	0	44774	29851	34807	45001	36426	55322	151940	54669	44787	43066	Moderate	No expres	Low	Moderate	YES		
P04271;A8MRB1	Protein S100-B	S100B	10.713	31.5	4	4	9.1637	0	21067	17655	22701	22856	23076	29646	21635	18591	16226	22551	No expres	No expres	Low	No expression			
P04275	von Willebrand facto	VWF	309.26	10.7	31	31	93.525	0	98316	84239	95663	81472	117950	98171	93129	99945	57941	109760	No expres	Enriched	Moderate	Low	YES		
P04350	Tubulin beta-4A chai	TUBB4A	49.585	50.2	62	1	81.587	0	46806	38330	70984	33800	58192	44113	52468	35367	28347	42208					YES		
P04406-2;E7EUT5	Glyceraldehyde-3-ph	GAPDH	31.548	75.8	80	3	323.31	0	797480	583480	659000	749150	738020	918190	973710	1061700	504640	909160	No expres	Enriched	Enriched	Enriched	YES		
P04424-2;P04424;I	Argininosuccinate lya	ASL	49.509	29.7	17	17	49.713	0	62853	41186	47640	67204	55611	60752	56900	67765	28796	75571	Enriched	Enriched	Enriched	Low	YES		
P04430;A0A0A0M	Ig kappa chain V-I re	IGKV1D-37	11.84	16.7	4	2	5.3938	0	4215.5	6443.8	4631.1	4270.1	7588.9	2501.9	3746.1	6445.4	1937.6	3596.4					YES		
Q5SRN7;Q5SRN5;	HLA class I histocom	HLA-A	34.211	35.8	12	2	11.615	0	28805	18448	25828	53503	20962	18982	29079	41858	20015	15149	Enriched	Enriched	Enriched	Enriched	YES		
P04632;K7ELJ7;K7	Calpain small subuni	CAPNS1	28.315	48.9	30	30	271.43	0	120820	129880	151410	120120	165900	118600	186290	165820	88291	122070	No expres	Enriched	Enriched	Enriched	YES		
P04733	Metallothionein-1F	MT1F	6.0863	19.7	5	2	3.7691	0.0006	8835.3	9623.3	9374.7	5860.8	10093	6473.3	9631.6	11281	10705	8954.2	Enriched	Enriched	Enriched	Enriched			
P04746	Pancreatic alpha-amy	AMY2A	57.706	69.9	142	6	323.31	0	1627200	2224100	1316700	2451100	1701200	2222600	1287300	871130	877760	1128100					YES	YES	YES
P04792	Heat shock protein be	HSPB1	22.782	50.7	25	25	128.24	0	139390	104570	110070	161060	115340	116450	271080	158030	163420	160060	Moderate	Enriched	Enriched	Moderate	YES		
P04839	Cytochrome b-245 he	CYBB	65.335	7.4	4	4	41.804	0	21275	20164	21073	21596	19999	25376	31637	43905	42641	36867	Enriched	Low	Low	No expres	YES		
P04843;B7Z4L4	Dolichyl-diphosphoo	RPN1	68.569	61.4	90	90	323.31	0	655650	441550	537250	684140	586970	722470	775640	684930	419650	625270	Enriched	Enriched	Enriched	Moderate	YES		
P04844-2;P04844	Dolichyl-diphosphoo	RPN2	67.723	45.9	74	74	323.31	0	609960	486370	542100	718430	550090	591000	615440	561560	281760	532830	Enriched	Enriched	Enriched	Enriched	YES		
P04899;P04899-4;I	Guanine nucleotide-b	GNAI2	40.45	51.5	25	12	52.501	0	72032	49828	71853	74384	64772	87000	84242	81458	52635	77378	Moderate	Low	Enriched	Enriched	YES		
P05023-4;P05023;I	Sodium/potassium-tra	ATP1A1	113	36.7	72	49	323.31	0	329350	281580	284080	319550	355420	337690	537390	520260	214410	384680	Enriched	Enriched	Enriched	Enriched	YES		
P05026-2;P05026;V	Sodium/potassium-tra	ATP1B1	34.893	45.8	22	22	218.77	0	156660	142450	133280	164350	216890	146140	170640	194860	68698	158730	Enriched	Enriched	Enriched	Enriched	YES		
P05060	Secretogranin-1;GAV	CHGB	78.275	42.5	47	24	323.31	0	260230	235510	539960	139440	394840	102770	129410	117310	127450	137420	Moderate	Moderate	Enriched	Enriched	YES		
P05062;A0A087W	Fructose-bisphosphat	ALDOB	39.473	25	10	10	85.482	0	31301	39872	31907	28361	39639	93544	101660	59234	52488	45163	Enriched	Moderate	Moderate	Enriched	YES		
P05091	Aldehyde dehydroger	ALDH2	56.381	49.7	51	1	223.91	0	218720	180510	214130	218660	235920	190350	276530	269560	142990	230960	Enriched	Enriched	Enriched	Enriched	YES		
P05091-2	Aldehyde dehydroger	ALDH2	50.989	53.2	50	2	5.1229	0.00044	9425.4	12010	16690	6848.7	25893	4916.4	19440	7045.4	9226.9	19790	Enriched	Enriched	Enriched	Enriched	YES		
P05109	Protein S100-A8;Pro	S100A8	10.834	17.2	2	2	2.7597	0.0024	12455	10865	12878	23431	11934	16522	11972	13109	7210.4	12641	Enriched	Moderate	Enriched	No expres	YES		
P05114;A6NL93;A	Non-histone chromos	HMGN1	10.659	51	9	9	104.04	0	72523	47430	61978	67818	63916	57610	102520	93550	71117	102590	Enriched	Enriched	Enriched	Enriched	YES		
P05129-2;P05129	Protein kinase C gam	PRKCG	62.029	4.4	3	2	2.8754	0.00186	2025.4	2581.7	3240.9	1799.8	3890.9	1699.1	2179.4	1829.7	1615.9	2031.2	Enriched	Enriched	Moderate	Moderate			
P05141	ADP/ATP translocase	SLC25A5	32.852	33.2	24	9	31.959	0	89540	44401	53090	95223	78693	97860	104030	140130	27410	71460	Enriched	Enriched	Enriched	Enriched	YES		
P05162	Galectin-2	LGALS2	14.644	73.5	17	17	140.88	0	125100	94282	66216	66154	79844	41079	65692	56247	37240	55197	Enriched	Enriched	Enriched	Enriched	YES		
P05164-2;P05164;I	Myeloperoxidase;My	MPO	73.853	9.7	6	6	30.712	0	6297.4	4959.3	6431.2	4107.8	5368.2	6418.7	16188	13460	11333	13189	Low	Low	Low	Low	YES		
P05165;P05165-2;I	Propionyl-CoA carbo	PCCA	80.058	29.8	27	27	216.78	0	98271	86609	91690	93780	104360	120660	140860	145900	58104	119850	Moderate	Moderate	Enriched	Moderate	YES		
P05186-2;P05186-3	Alkaline phosphatase	ALPL	48.908	3.1	2	2	46.803	0	7515.6	6644.3	9018.7	7624.1	10071	15023	12190	22349	10913	16267	Moderate	No expres	Low	Low	YES		
P05198;H0YJS4;G3	Eukaryotic translation	EIF2S1	36.112	45.4	28	28	213.05	0	105070	70324	87710	73302	113020	89964	92959	170150	46193	88039	Enriched	Enriched	Enriched	Moderate	YES		
P05204	Non-histone chromos	HMGN2	9.3926	38.9	7	6	73.15	0	61123	42154	57133	32377	40157	59006	87748	117110	48675	122790	Enriched	Enriched	Enriched	Enriched	YES		
P05362	Intercellular adhesion	ICAM1	57.825	13.9	7	3	55.433	0	27702	23586	27128	23548	35448	22114	29573	24745	20474	32548	Enriched	Moderate	Enriched	No expres	YES		
P05386	60S acidic ribosomal	RPLP1	11.514	13.2	4	4	10.128	0	13225	8058.8	9445	15809	9770.1	45544	23280	16233	12603	15255	Enriched	Enriched	Enriched	Enriched	YES		
P05387	60S acidic ribosomal	RPLP2	11.665	48.7	25	25	323.31	0	276760	167260	204040	277910	250910	314130	433490	331550	169720	254820	Enriched	Enriched	Enriched	No expression			
P05388;F8VU65;F8	60S acidic ribosomal	RPLP0;RPLP0P6	34.273	37.9	33	33	289.58	0	549190	348050	431510	385310	569400	447720	425450	435660	188070	380680	Enriched	Enriched	Enriched	Enriched			
P05408;C9JNY7;H	Neuroendocrine prot	SCG5	23.729	32.1	6	2	15.607	0	21930	23874	24922	18542	29143	19434	18003	10089	13949	20797	Low	Enriched	Enriched	Enriched	YES	YES	
S4R3A2;S4R371;P	Fatty acid-binding pr	FABP3	10.17	14.6	1	1	28.484	0	5129.1	5617.5	5584.9	2986.9	4713.2	5485.8	8819.4	8011.8	5192.7	10383	Moderate	No expres	No expres	Low	YES		
P05423	DNA-directed RNA p	POLR3D	44.395	2.5	1	1	2.1149	0.00642	4102	3198.7	2644.7	3124.7	4247.4	3190.6	3804.2	3414.6	1754.3	4334.9	Low	Moderate	Moderate	Enriched	YES		
P05451	Lithostathine-1-alpha	REG1A	18.731	40.4	43	30	202.51	0	1007000	631110	576870	1221900	755380	929720	1742400	845950	911750	866130	Enriched	Enriched	Enriched	Enriched	YES	YES	
P05455;E7ERC4	Lupus La protein	SSB	46.836	51.2	36	36	248.15	0	266900	178530	189900	240170	205000	218380	294300	384810	143650	297410	Moderate	Moderate	Enriched	Enriched	YES		
P05543;CON__Q9	Thyroxine-binding gl	SERPINA7	46.324	5.1	2	2	5.0141	0.00044	9359.7	7126.8	8643	29697	8147.4	8605.2	8235	16264	4164.2	10521	Low	Low	No expres	No expression			
P05556;P05556-2;I	Integrin beta-1	ITGB1	88.414	27.9	34	24	121.52	0	142280	120370	150060	144960	175300	151330	229710	210020	87934	202850	Enriched	Enriched	Enriched	Enriched	YES		
P05783	Keratin, type I cytosk	KRT18	48.057	61.9	102	19	323.31	0	911310	674130	734780	1147800	911590	1057500	1322300	1949900	635600	1224700	Enriched	Enriched	Enriched	Enriched	YES		
P05937;P05937-2	Calbindin	CALB1	30.025	8	2	2	2.3283	0.00462	11252	9504.9	18947	5886	15300	6178	6405.1	5064.7	6031.6	4630.6	Low	No expres	Low	Low			
P05976-2;P05976;I	Myosin light chain 1/	MYL1;MYL3	16.684	10	5	2	9.2899	0	66542	46787	53045	70526	64094	61324	62121	72782	29312	76392	Low	No expres	No expres	No expression			
P05997	Collagen alpha-2(V)	COL5A2	144.91	5.7	12	11	115.33	0	58632	79603	120240	51978	96789	46328	84484	59995	41794	51398	Low	Moderate	Enriched	Moderate	YES		
P06213-2;P06213	Insulin receptor;Insul	INSR	155.14	13.9	21	17	59.682	0	33712	24150	34687	26626	47114	35863	52493	38391	32066	43285	Enriched	Enriched	Enriched	Moderate	YES		
P06280	Alpha-galactosidase	GLA	48.766	10.5	3	3	6.5253	0	15988	7508.3	13569	32023	12103	18250	13405	18530	6881.3	23976	Enriched	Moderate	Enriched	Low	YES		
P06396;A0A0A0M	Gelsolin	GSN	85.696	37.2	57	24	323.31	0	302320	251860	277450	304080	289060	290030	330040	410220	178960	359160	Enriched	Enriched	Enriched	Moderate	YES		
P06576;H0YH81	ATP synthase subuni	ATP5B	56.559	53.1	72	20	323.31	0	436830	405310	457220	422340	549990	455840	582720	721860	298710	453060	Enriched	Enriched	Enriched	Low	YES		
P06702	Protein S100-A9	S100A9	13.242	21.9	3	3	6.6533	0	16826	14433	17274	27957	15423	15808	15908	17519	10270	16974	Enriched	Low	Moderate	No expres	YES		
P06727	Apolipoprotein A-IV	APOA4	45.398	43.4	24	24	172.32	0	54946	50481	52505	80710	54202	100610	70266	238910	52333	86889	Enriched	No expres	No expres	Low	YES		
P06730-2;D6RBW	Eukaryotic translation	EIF4E	28.777	26.6	9	9	44.181	0	36358	24989	14816	23762	20362	23162	18209	35608	11537	22705	Moderate	Enriched	Enriched	Low	YES		
P06733	Alpha-enolase	ENO1	47.168	69.1	93	21	323.31	0	777360	522690	463520	901260	798460	805710	1418900	819790	674020	628740	Enriched	Enriched	Enriched	Enriched	YES		
P06733-2	Alpha-enolase	ENO1	36.928	67.7	66	2	4.9543	0.00044	66277	52954	43177	58283	93271	40320	55409	20456	70497	33710	Enriched	Enriched	Enriched	Enriched	YES		
P06744-2	Glucose-6-phosphate	GPI	64.324	41.1	56	2	8.8568	0	12250	4358.4	13593	9044.2	19622	17335	8820.3	8350.1	4767.1	16789	Enriched	Enriched	Enriched	Enriched	YES		
P06748;P06748-2;I	Nucleophosmin	NPM1	32.575	48	35	17	80.706	0	163130	108620	129200	123260	150480	179810	251540	195210	192170	194130	No expres	Enriched	Enriched	Enriched	YES		
P06753-2;A0A087WWU8;Q5VU59;P067		TPM3	29.032	64.5	60	0	323.31	0	237540	192350	213560	236660	228060	287730	443870	497370	234300	378200	Enriched	Enriched	Enriched	Moderate	YES		
P06753-6			28.922	60.9	55	0	7.2668	0	3067.7	1837.6	3373.9	2222	3641.8	2274.5	2181.1	2340	1798.7	2820.3							
P06756-3;P06756-2	Integrin alpha-V;Integ	ITGAV	111.13	11.3	12	12	25.065	0	60387	40270	46652	69393	50498	64647	58813	78387	24913	67029	Enriched	Enriched	Enriched	Enriched	YES		
P06870;P06870-2	Kallikrein-1	KLK1	28.889	21.8	11	11	50.393	0	66721	38483	29012	62705	35701	58304	51255	33229	21622	30987	Enriched	Enriched	Enriched	Enriched	YES		
P07099	Epoxide hydrolase 1	EPHX1	52.948	50.1	52	52	178.27	0	340590	217330	351970	525540	292660	291710	600280	365130	243670	394770	Low	Enriched	Enriched	No expres	YES		
P07101-6;P07101-5	Tyrosine 3-monooxy	TH	44.897	5.2	2	2	2.8051	0.00222	5631.5	3706.6	5047.6	2785.3	8482.3	3419.3	1463.2	1172.3	1301.8	3593.7	Low	No expres	No expres	Low			
P07195;A8MW50	L-lactate dehydrogen	LDHB	36.638	67.1	70	30	323.31	0	552380	413220	512570	545670	520160	542460	808610	733390	553570	557930	Enriched	Enriched	Enriched	Enriched	YES		
P07237;H7BZ94;F5	Protein disulfide-ison	P4HB	57.116	69.3	153	81	323.31	0	2294300	1427800	1684600	1855700	2394700	3004300	3683700	2628900	1713900	1849600	Enriched	Enriched	Enriched	Enriched	YES		
P07305;P07305-2	Histone H1.0;Histone	H1F0	20.863	33.5	19	19	173.93	0	257580	74138	113580	222220	104940	246890	290570	387900	187060	333950	Enriched	Enriched	Enriched	Moderate	YES		
P07327	Alcohol dehydrogena	ADH1A	39.858	46.9	47	1	15.231	0	5069.4	5395.2	16082	11500	11088	7941.2	10316	11530	6599.4	21587	Enriched	Low	Low	Moderate			
P07339;C9JH19;H7	Cathepsin D;Catheps	CTSD	44.552	47.6	39	39	236.82	0	381310	288660	344450	353310	333410	406080	521770	422700	282330	396820	Moderate	Moderate	Enriched	Enriched	YES		
P07355;P07355-2;I	Annexin A2;Annexin	ANXA2;ANXA2P2	38.604	75.8	96	96	323.31	0	687510	509760	649640	830900	586950	615780	1046600	1129100	594360	858750	Enriched	Enriched	Enriched	Enriched	YES		
P07357	Complement compon	C8A	65.163	22.8	12	12	50	0	23777	24734	25543	23337	31908	22218	21800	34416	13859	31722	Low	No expres	No expres	Low	YES		
P07360	Complement compon	C8G	22.277	29.7	5	5	11.812	0	14736	11407	12181	23784	12837	25935	19433	44615	11555	23106	Moderate	No expres	No expres	Low	YES		
P07384	Calpain-1 catalytic su	CAPN1	81.889	30.8	31	21	121.43	0	148940	107340	121900	126510	132790	184110	190970	183250	93505	154730	Enriched	Moderate	Enriched	Enriched	YES		
P07437;Q5JP53;Q5	Tubulin beta chain	TUBB	49.67	52.5	73	10	62.557	0	89295	49655	58475	109450	80964	89432	137380	162560	40062	95147	Enriched	Enriched	Enriched	Enriched	YES		
P07585;F8VWU0	Decorin	DCN	39.746	55.7	50	1	323.31	0	322290	342120	596150	447580	470360	343460	754030	778860	359680	496870	Enriched	Enriched	Enriched	No expres	YES		
P07585-2	Decorin	DCN	27.353	42.4	25	1	2.2932	0.00496	24834	25226	30526	21077	31932	26651	132410	86155	49114	32392	Enriched	Enriched	Enriched	No expres	YES		
Q5URX0;P07686;H	Beta-hexosaminidase	HEXB	38.258	35.3	20	20	82.947	0	75717	47352	57134	91621	56470	73114	63400	76319	37046	83478	Enriched	Enriched	Enriched	No expres	YES		
P07711	Cathepsin L1;Cathep	CTSL	37.564	11.1	6	6	10.83	0	6245.5	6493	7586	4870.6	7141.8	4422.4	5070.1	7953.5	2383	5055.2					YES		
P07737;K7EJ44;I3I	Profilin-1	PFN1	15.054	67.1	27	27	251.37	0	197360	143400	160560	211920	184490	214490	406830	440950	236100	249640	Moderate	Enriched	Enriched	Moderate	YES		
P07741;H3BQZ9;P	Adenine phosphoribo	APRT	19.608	67.2	37	37	76.41	0	225790	193010	177720	219500	237360	365510	231060	228030	129440	206250	Enriched	Enriched	Enriched	Moderate	YES		
P07814;V9GYZ6	Bifunctional glutamat	EPRS	170.59	40.7	113	112	323.31	0	756420	518170	608940	694440	805460	731750	827210	714510	376610	633390	Enriched	Moderate	Enriched	Enriched	YES		
P07858	Cathepsin B;Catheps	CTSB	37.821	34.8	20	20	127.69	0	86870	64904	94913	97415	90444	82007	172360	172010	69695	112540	Enriched	Enriched	Enriched	Moderate	YES		
P07900;P07900-2	Heat shock protein H	HSP90AA1	84.659	52	107	57	323.31	0	840880	817960	677670	1014900	841990	666190	1015400	1201000	556310	909480	Enriched	Enriched	Enriched	Enriched	YES		
P07902;P07902-2	Galactose-1-phospha	GALT	43.363	16.9	8	8	22.467	0	19484	15748	15889	15727	21515	14186	20994	15283	15700	19008	Moderate	Moderate	Moderate	Enriched	YES		
P07919;A0A096LP	Cytochrome b-c1 cor	UQCRH	10.739	35.2	8	8	34.101	0	29501	24319	26380	28072	33661	33768	47995	38366	32878	42355	Enriched	Enriched	Enriched	Enriched	YES		
P07948;E5RJ37	Tyrosine-protein kina	LYN	58.573	14.1	8	2	26.504	0	22370	14874	19230	24400	23507	29403	18382	20322	7801.3	20748	Low	Moderate	Enriched	Moderate	YES		
P07951	Tropomyosin beta ch	TPM2	32.85	56.3	40	0	3.9408	0.00061	4362.3	3343.8	3129.5	3749.9	3289.1	3712.4	5195.6	4401.6	2914	4053.1	No expres	Low	Moderate	Low	YES		
P07951-2;P07951-3	Tropomyosin beta ch	TPM2	32.989	58.5	46	0	90.078	0	123060	118780	108440	89642	134270	208990	340940	245130	163750	395870	No expres	Low	Moderate	Low	YES		
P07954-2;P07954	Fumarate hydratase,	FH	50.212	44.1	44	44	323.31	0	357950	305930	333890	288260	435700	365710	339630	386660	158130	359510	Enriched	Enriched	Enriched	Enriched	YES		
P07996;P07996-2	Thrombospondin-1	THBS1	129.38	10.9	16	5	36.94	0	55892	53763	52124	53062	75121	59044	87392	91081	42467	69785	Enriched	Moderate	Enriched	Moderate	YES		
P07998;G3V357	Ribonuclease pancrea	RNASE1	17.644	55.8	20	20	201.49	0	180250	133610	114020	116190	154660	102620	131130	84609	74897	105100	Enriched	Enriched	Enriched	Moderate	YES		
P08047-3;P08047-2	Transcription factor S	SP1	75.823	5.7	4	4	4.1447	0.00062	6962.7	5891.6	6788.4	5124.6	10114	5035.4	5774.9	5144	3753.8	8188.7	Moderate	Enriched	Enriched	No expression			
P08107;P08107-2;V	Heat shock 70 kDa pr	HSPA1A	70.051	56.2	94	38	323.31	0	449160	321180	372180	409490	449640	377950	756700	701030	473740	439390	Enriched	Enriched	Enriched	No expres	YES		
P08133;P08133-2	Annexin A6	ANXA6	75.872	59.1	92	33	323.31	0	712500	528870	687780	761700	663420	744230	893530	757520	446820	719680	Low	Enriched	Enriched	Moderate	YES		
P08138-2;P08138	Tumor necrosis facto	NGFR	35.766	8.1	2	2	4.5715	0.00043	2244.9	2656.8	3059.4	1942.9	4934.1	1654	2720.1	2543.8	1646.7	2172.1	Low	No expres	Low	Enriched	YES		
P08217	Chymotrypsin-like el	CELA2A	28.887	53.9	56	49	323.31	0	606520	303470	462220	338170	733940	559640	707700	266750	173910	305490	Enriched	Enriched	Moderate	Enriched	YES	YES	YES
P08218	Chymotrypsin-like el	CELA2B	28.809	27.5	21	14	31.954	0	104570	87082	83000	87080	98458	86491	137500	88886	43227	93137	Low	Moderate	Moderate	Enriched	YES	YES	YES
P08237;P08237-3;I	ATP-dependent 6-ph	PFKM	85.182	15	12	9	37.459	0	26949	15211	20824	27660	21205	25380	24996	31659	15562	28833	Enriched	Enriched	Enriched	Enriched	YES		
P08238	Heat shock protein H	HSP90AB1	83.263	51.4	101	39	323.31	0	229840	215950	234500	312250	276440	234000	365080	412750	186280	281910	No expres	Enriched	Enriched	Enriched	YES		
P08240;P08240-2	Signal recognition pa	SRPR	69.81	45.8	52	52	323.31	0	346110	239670	269550	292570	342090	350190	339630	338820	149470	241180	Enriched	Enriched	Enriched	Enriched	YES		
P08243-2;P08243;I	Asparagine synthetas	ASNS	62.168	25.6	14	14	29.345	0	63742	39249	43162	42148	83891	78920	43093	52211	19880	46704	Low	Enriched	Enriched	Moderate	YES		
P08253-2;P08253-3	72 kDa type IV colla	MMP2	65.764	3.6	2	2	2.9461	0.00169	5264.6	5978	6960.6	5169.6	13431	4912.9	8082.2	6097.8	3520	5316.7	Enriched	Enriched	Enriched	Moderate	YES		
P08294	Extracellular superox	SOD3	25.851	36.7	16	16	194.13	0	60935	61369	77334	65639	87614	72978	71919	72088	41257	68261	Moderate	Enriched	Moderate	Enriched	YES		
P08311	Cathepsin G	CTSG	28.837	40	16	16	64.123	0	48592	42544	55484	40731	53932	45241	149750	116350	83752	79773	Moderate	Low	Low	Moderate	YES		
P08559;P08559-2;I	Pyruvate dehydrogen	PDHA1	43.295	27.2	16	16	92.273	0	42362	28939	36862	49668	43306	60096	61880	78149	26875	77084	Enriched	Enriched	Enriched	Low	YES		
P08571;D6RFL4	Monocyte differentiat	CD14	40.076	14.4	6	6	44.524	0	9643.3	5485.7	8456.6	15979	9085	11367	13343	21168	8906.6	11584	Low	Moderate	Enriched	Low	YES		
P08572	Collagen alpha-2(IV)	COL4A2	167.55	13.7	34	34	321.19	0	188610	173750	214720	136310	262960	179620	287530	340150	107730	224790	Moderate	Enriched	Enriched	Enriched	YES		
P08574	Cytochrome c1, hem	CYC1	35.422	33.5	13	13	33.625	0	114800	98990	133340	94004	152530	106230	109760	88955	56393	117920	Enriched	Enriched	Enriched	Enriched	YES		
P08579	U2 small nuclear ribo	SNRPB2	25.486	23.6	6	5	11.572	0	11709	9087.9	8078.3	8895.4	10129	6352.5	5981.7	7012.7	4001.7	9340.4	Enriched	Enriched	Enriched	Moderate	YES		
P08603	Complement factor H	CFH	139.09	34.4	40	34	182.09	0	153020	204320	183560	202220	149190	128930	128610	356530	111900	177060	Enriched	Low	Moderate	Moderate	YES		
P08621;P08621-2;I	U1 small nuclear ribo	SNRNP70	51.556	28.6	21	21	34.965	0	68504	56687	61970	51901	70199	56271	67441	72245	39506	61360	Enriched	Enriched	Enriched	Enriched	YES		
P08648	Integrin alpha-5;Integ	ITGA5	114.54	4.7	4	4	10.148	0	10121	8470.5	9319.6	9882.1	8809.5	11468	10299	19004	5841	15674	Moderate	Moderate	Enriched	Moderate	YES		
P08651-4;P08651-5	Nuclear factor 1 C-ty	NFIC	45.412	22.2	11	9	41.84	0	57392	42571	54727	32691	59704	57028	86136	80857	48398	61547	Enriched	Enriched	Enriched	Moderate	YES		
P08670;B0YJC4	Vimentin	VIM	53.651	79.6	127	113	323.31	0	1229500	657900	797830	1256000	836180	1106600	1411500	1560600	1084300	1187100	No expres	Enriched	Enriched	Enriched	YES		
P08684;A0A087W	Cytochrome P450 3A	CYP3A4;CYP3A7	57.343	10.3	5	4	8.9226	0	33032	14524	20517	10882	16844	31127	11904	12070	14288	12463	Enriched	Enriched	Moderate	Enriched			
P0CW22;P08708;H	40S ribosomal protei	RPS17L;RPS17	15.55	54.8	19	19	237.08	0	220750	131240	146380	214840	153610	268130	359990	275940	138030	228740	Enriched	Enriched	Enriched	Enriched	YES		
P08754	Guanine nucleotide-b	GNAI3	40.532	37.6	16	7	56.025	0	49621	31166	33743	22426	46002	27428	46958	34456	35069	31867	Enriched	Enriched	Enriched	Low	YES		
P08758;D6RBL5;D	Annexin A5;Annexin	ANXA5	35.936	84.7	89	89	323.31	0	820060	573140	871680	753790	702860	961380	1168800	998720	718110	904760	Enriched	Enriched	Enriched	Enriched	YES		
P08861	Chymotrypsin-like el	CELA3B	29.263	53.3	55	0	149.84	0	173130	111940	116580	151260	142800	182380	411080	233430	185700	140770	Enriched	Enriched	Enriched	No expres	YES	YES	YES
P08913	Alpha-2A adrenergic	ADRA2A	48.956	14.7	6	6	37.711	0	13960	21352	19516	14865	19189	15237	15868	14842	13591	19244	Enriched	Enriched	Enriched	No expres	YES		
P09093;B1AQ54	Chymotrypsin-like el	CELA3A	29.488	53.7	65	34	323.31	0	856570	703210	559470	647420	650160	898090	856160	539450	655850	485460	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P09104;P09104-2;I	Gamma-enolase;Enol	ENO2	47.268	35.5	28	7	20.52	0	6914	7508.8	8761.9	7194.8	11792	6041.4	7391.1	4659.3	4036.1	5683.2	No expres	Low	Enriched	Enriched			
P09132;A0A087W	Signal recognition pa	SRP19	16.156	53.5	11	11	81.308	0	35691	21310	29514	21505	31762	43310	105100	65060	52148	51212	Enriched	Enriched	Enriched	Enriched	YES		
P09210;P08263;Q1	Glutathione S-transfe	GSTA2;GSTA1;GSTA3	25.664	51.8	45	23	323.31	0	1715600	482620	649960	1021600	547060	1320700	1643400	1196800	786530	995860	Moderate	Enriched	Moderate	Enriched			
P09211;A8MX94	Glutathione S-transfe	GSTP1	23.356	67.1	45	45	323.31	0	368550	321790	348960	419930	487990	478820	409500	457890	198810	538600	Enriched	Enriched	Enriched	Enriched	YES		
P09327;B4DV78	Villin-1	VIL1	92.694	20.6	18	12	119.09	0	88383	88269	94824	74038	120580	71420	116380	108600	63687	90387	Enriched	Low	Moderate	Moderate	YES		
P09382	Galectin-1	LGALS1	14.716	53.3	17	17	37.692	0	88731	81146	93181	118730	97039	84460	244710	251690	92070	108040	Moderate	Enriched	Enriched	Low	YES		

P09417;P09417-2	Dihydropteridine red	QDPR	25.789	55.3	20	20	67.999	0	60698	45621	42598	56001	56571	55292	58249	63232	29976	51601	Enriched	Enriched	Enriched	Enriched	YES		
Q5T7C4;Q5T7C6;F	High mobility group	HMGB1	18.311	63.9	31	21	300.44	0	403800	259970	372590	302680	415880	319260	655660	457120	310200	411510	Enriched	Enriched	Enriched	Moderate			
P09467	Fructose-1,6-bisphos	FBP1	36.842	54.1	35	30	135.32	0	149640	122210	110660	129280	128130	145440	233720	194490	111190	144180	Enriched	Enriched	Enriched	Enriched	YES		
P09471-2;P09471	Guanine nucleotide-b	GNAO1	40.086	21.5	9	4	24.731	0	38577	42332	44248	37056	46502	29929	31268	28557	17226	37257	Moderate	Enriched	Enriched	Moderate	YES		
P09488;P09488-2;I	Glutathione S-transfe	GSTM1	25.712	51.4	26	4	199.82	0	512720	258980	254400	109210	115350	87891	239370	205700	119430	98213	Enriched	Enriched	Enriched	Enriched			
P09493-3;P09493-4;P09493-10;H0YKX5		TPM1	32.876	68	54	0	5.7069	0	4617.8	1945.1	3102.9	6841.4	2998.2	8762.3	7883.5	6109.7	2960.4	11144	Enriched	Enriched	Enriched	Enriched	YES		
P09493-8			32.816	68.3	55	0	16.421	0	36429	29394	16133	31808	48860	9132.5	6370.3	3948.5	2258.7	7090.1							
P09497-2;P09497;I	Clathrin light chain E	CLTB	23.181	23.2	10	10	29.245	0	61871	37185	61778	61881	49761	92704	107590	106680	39230	90328	Enriched	Enriched	Enriched	Low	YES		
P09525	Annexin A4	ANXA4	35.882	69.9	78	0	323.31	0	414820	356540	457900	621820	475230	558150	962930	915850	531130	550230	Enriched	Enriched	Enriched	Enriched	YES		
P09525-2	Annexin A4	ANXA4	27.062	77.2	64	4	4.9708	0.00044	14840	12342	13845	24140	17297	16500	17599	20086	8865.2	19190	Enriched	Enriched	Enriched	Enriched	YES		
P09543-2;P09543;I	2,3-cyclic-nucleotide	CNP	45.098	32.2	21	21	59.806	0	105250	89318	96757	107650	106300	106750	96562	116100	53150	117630	Enriched	Moderate	Enriched	Enriched	YES		
P09619;P09619-2	Platelet-derived grow	PDGFRB	123.97	4.2	7	7	22.395	0	13622	8882.6	12435	16964	12003	17699	22866	29263	9287.4	19123	Enriched	Low	Enriched	Moderate	YES		
P09622;E9PEX6;P	Dihydrolipoyl dehyd	DLD	54.177	37.3	30	30	135.98	0	170440	145090	123630	181210	175670	166230	266910	294180	107830	183550	Moderate	Enriched	Enriched	Enriched	YES		
P09661;H0YMA0;I	U2 small nuclear ribo	SNRPA1	28.415	40	16	16	49.745	0	41810	31676	39615	39110	47291	31011	28839	28606	17188	31608	Enriched	Moderate	Enriched	Enriched	YES		
P09669	Cytochrome c oxidas	COX6C	8.7813	37.3	4	4	8.1641	0	96712	62021	124730	123000	69807	145670	108920	121420	53212	152500	Enriched	Enriched	Enriched	Moderate	YES		
P09758	Tumor-associated cal	TACSTD2	35.709	18	9	9	27.755	0	31186	26671	31335	23776	39672	25453	53494	58914	42806	43644	Enriched	Enriched	Enriched	Enriched	YES		
P09874	Poly [ADP-ribose] po	PARP1	113.08	41.2	76	76	323.31	0	724370	485070	535720	563050	691680	449710	488370	528170	278700	539810	Enriched	Enriched	Enriched	Enriched	YES		
P09917-3;P09917	Arachidonate 5-lipox	ALOX5	74.634	3.7	4	4	30.272	0	4211.7	2834.9	3534.7	5973.8	3008.7	3711.1	8476.7	16170	3049	6391.7	Enriched	Enriched	Enriched	Moderate	YES		
P09960;P09960-4;I	Leukotriene A-4 hyd	LTA4H	69.284	40.1	43	43	203.04	0	188730	142150	147820	144140	179590	145270	266000	279690	113410	159960	Enriched	Enriched	Enriched	Enriched	YES		
P09972;K7EKH5;C	Fructose-bisphosphat	ALDOC	39.455	10.7	4	3	39.642	0	12343	12790	14607	9283.3	20655	8097.8	16923	9396.4	7797.4	10680	Moderate	Low	Enriched	Enriched	YES		
P0C0L4-2;P0C0L4	Complement C4-A;C	C4A	187.7	26	56	1	213.78	0	192560	180540	210640	299360	156290	147510	161760	584780	142050	208660	Enriched	Enriched	Enriched	No expression			
Q71UI9;P0C0S5;Q	Histone H2A.V;Histo	H2AFV;H2AFZ	13.509	27.3	10	9	75.313	0	60995	53350	61317	63291	70514	100140	231350	272030	80695	101910	Enriched	Enriched	Enriched	Enriched	YES		
Q99878;Q96KK5;C	Histone H2A type 1-.	HIST1H2AJ;HIST1H2AI	13.936	37.5	20	9	25.076	0	77327	47253	56833	195100	52194	139430	266250	164780	91266	173740	Enriched	Moderate	Moderate	No expression			
P0C2W1	F-box/SPRY domain-	FBXO45	30.632	3.5	1	1	2.2529	0.00511	5091.2	5076.5	8409.6	3398.4	7438.5	2896.4	7147.4	5171.7	5468.7	6052	Moderate	Enriched	Enriched	No expression			
P0C7P0	CDGSH iron-sulfur d	CISD3	14.215	9.4	2	2	3.8856	0.00061	11553	15345	13499	8172.9	21557	6022.7	11754	9820.8	5756.6	13710	Enriched	Enriched	Enriched	No expres	YES		
P0CG12	Chromosome transmi	CHTF8	51.391	4.6	2	2	5.0589	0.00044	7743	6995.2	7797.8	4846.1	9852.3	6228.8	9992.2	7307.6	10081	9043.5	No expres	Low	No expres	No expres	YES		
P0CG24;A0A087W	Zinc finger protein 88	ZNF883;ZNF689;ZNF27	43.966	14.8	4	0	5.9369	0	7175.5	4529.1	5667	5251.9	8006.7	4195.2	2771.8	2361.8	2184.4	5155.9	Enriched	Enriched	Enriched	No expression			
P0CG37;A0A087W	Cryptic protein;Crypt	CFC1;CFC1B	24.612	9.9	3	3	6.4813	0	4659.3	6704.7	6189	5172.1	7628.2	4525.1	7942.9	4580.8	5226.1	6366.7	Moderate	Moderate	Enriched	No expres	YES	YES	
P0DJ93	Small integral memb	SMIM13	10.351	13.2	2	2	5.2852	0	1537.8	1457.2	1492.1	1124.1	2773	1148.4	2805	2150.2	1869.9	1422.4					YES		
P0DJI8	Serum amyloid A-1 p	SAA1	13.532	62.3	17	2	51.271	0	78525	82267	84049	115620	61466	71159	61733	98043	43172	69794	Moderate	No expres	No expres	Moderate	YES		
P0DJI9	Serum amyloid A-2 p	SAA2	13.527	58.2	16	5	33.145	0	45701	46677	58418	47607	33896	29702	29765	34023	27732	37318	Moderate	Low	Low	No expression			
P0DMN0;P0DMN9	Sulfotransferase 1A4	SULT1A4;SULT1A3	34.196	27.8	9	5	32.962	0	34215	19299	31448	36144	26153	47891	51059	88996	25787	44671	Enriched	Enriched	Enriched	Moderate	YES		
P10109	Adrenodoxin, mitoch	FDX1	19.393	5.4	1	1	2.1078	0.00676	3034	1857.2	1737.3	1940	3234.9	2994.8	7429.1	2274	6298.2	5637.4	Low	Enriched	Enriched	No expression			
P10114	Ras-related protein R	RAP2A	20.615	15.8	3	1	2.1288	0.00609	2747	1222.6	2567.6	3976.7	2495.5	4231.5	2881.3	4045.8	1426.1	3119.5	Enriched	Moderate	Enriched	Low	YES		
P10155;P10155-3;I	60 kDa SS-A/Ro ribo	TROVE2	60.67	21	12	12	22.047	0	43202	32437	37904	37555	41893	46413	61046	59047	42370	54396	Enriched	Enriched	Enriched	Moderate	YES		
P10253	Lysosomal alpha-gluc	GAA	105.32	22.8	31	31	81.091	0	151240	130290	163160	149910	157010	142290	123970	123400	66571	127360	Moderate	Moderate	Enriched	Moderate	YES		
P10301	Ras-related protein R	RRAS	23.48	40.8	17	9	97.574	0	53081	57574	61780	47194	61541	40405	53278	54403	34770	60204	Low	Low	Moderate	Enriched	YES		
Q96II5;P10398	Serine/threonine-prot	ARAF	67.925	10.5	7	7	14.263	0	26065	16938	20493	18768	20906	25697	32444	35828	14532	27974	Moderate	Enriched	Enriched	Enriched	YES		
P10412	Histone H1.4	HIST1H1E	21.865	43.4	36	7	323.31	0	594840	327410	523920	413860	563440	402920	528290	651400	206520	520630	Moderate	No expres	Low	Low	YES		
P10515;E9PEJ4	Dihydrolipoyllysine-r	DLAT	68.996	20.1	18	2	47.959	0	39898	22130	26599	48856	24422	48006	33410	52467	21834	49165	Low	Moderate	Enriched	Moderate	YES		
P10586-2;P10586;I	Receptor-type tyrosir	PTPRF	211.68	7.7	13	10	37.465	0	58085	48624	50396	41515	57472	36521	46664	42823	37723	48410	Enriched	Enriched	Enriched	Enriched	YES		
P10599;P10599-2	Thioredoxin	TXN	11.737	59	19	19	72.251	0	185150	124600	162750	175150	175860	187690	241550	219030	308050	198240	Enriched	Enriched	Enriched	Moderate	YES		
P10606	Cytochrome c oxidas	COX5B	13.696	55	12	12	203.08	0	50279	43374	52124	34833	59244	63607	131680	147980	56619	75673	Enriched	Enriched	Enriched	Enriched	YES		
X6R5C5;X6R8A1;I	Carboxypeptidase;Ly	CTSA	54.255	7.5	4	4	9.6454	0	13098	11399	14870	13282	15090	15409	30846	31080	9964.7	14497	Moderate	Enriched	Enriched	Enriched	YES		
P10620;F5H7F6;F5	Microsomal glutathio	MGST1	17.598	26.5	7	7	44.549	0	63487	31102	40706	45148	51000	48846	25694	22034	14292	37626	Enriched	Enriched	Enriched	No expres	YES		
P10636;P10636-9;I	Microtubule-associat	MAPT	78.927	8.8	6	3	98.247	0	12584	12942	16316	14849	14467	14818	19980	15699	12188	15273	Low	Low	Moderate	Low	YES		
P10636-2;P10636-4	Microtubule-associat	MAPT	36.76	10.8	4	1	2.6807	0.00256	11678	10039	15457	10696	15006	11382	10548	10398	5151.4	12544	Low	Low	Moderate	Low	YES		
P10643	Complement compon	C7	93.517	36.7	39	39	323.31	0	123830	109780	134770	124900	131890	131420	193260	376040	123530	163160	Low	Enriched	Enriched	Enriched	YES		
P10644;P10644-2;I	cAMP-dependent pro	PRKAR1A	42.981	29.4	19	19	91.813	0	72874	46065	51756	72074	60898	60851	57779	84009	36072	70353	Enriched	Enriched	Enriched	Enriched	YES		
P10645;G5E968	Chromogranin-A;Vas	CHGA	50.688	29.1	20	20	131.4	0	38293	62200	64625	67987	54649	51296	161290	91190	77758	121030	Enriched	Enriched	Enriched	Moderate	YES		
P10768;X6RA14;H	S-formylglutathione I	ESD	31.462	66	31	31	125.33	0	191380	151740	190600	141860	206730	165500	263140	242750	105820	151080	Enriched	Enriched	Enriched	Enriched	YES		
P10809	60 kDa heat shock pr	HSPD1	61.054	72.1	125	125	323.31	0	1130900	815720	874930	1369400	1172500	954980	1044400	1624800	591940	1139900	Enriched	Enriched	Enriched	Enriched	YES		
P10909-4;P10909;I	Clusterin;Clusterin bo	CLU	48.803	44.2	32	4	323.31	0	119550	96626	120010	112720	119410	140830	216900	359730	203000	175310	Enriched	Enriched	Enriched	Enriched	YES		
P11021	78 kDa glucose-regul	HSPA5	72.332	69	145	131	323.31	0	1665900	1176800	1469100	1463700	1749500	1978200	2372000	1703400	1016000	1430200	Enriched	Enriched	Enriched	Enriched	YES		
P11047	Laminin subunit gam	LAMC1	177.6	39.5	137	133	323.31	0	916770	675200	818570	908000	905010	993940	1340600	1387600	545270	1254500	Enriched	Enriched	Enriched	Moderate	YES		
P11137-3;P11137;I	Microtubule-associat	MAP2	199.08	3.9	7	1	12.056	0	29344	30295	38840	23357	47301	20511	33112	25726	25771	30233	No expres	Enriched	Enriched	Low	YES		
P11142;E9PKE3;P	Heat shock cognate 7	HSPA8	70.897	59.3	104	44	323.31	0	954850	612350	641860	756600	802150	750270	1147000	1248000	686500	807660	Enriched	Enriched	Enriched	Enriched	YES		
P11166;C9JIM8	Solute carrier family	SLC2A1	54.083	5.7	2	2	5.8172	0	5738.6	11169	14766	6171.3	18058	6587.9	5945.4	5321.3	3200.8	6666.7	Enriched	Moderate	Enriched	Moderate	YES		
P11171-4;Q4VB86	Protein 4.1	EPB41	66.398	30.6	18	16	87.471	0	77393	66052	66961	69766	88962	70307	73295	63974	42837	73379	Enriched	Enriched	Enriched	Low	YES		
P11172;P11172-3;I	Uridine 5-monophosp	UMPS	52.221	12.3	8	8	28.941	0	15046	11714	12706	16052	16180	13286	14420	15983	6136.9	15721	Moderate	Moderate	Enriched	Enriched	YES		
P11177-2;P11177;I	Pyruvate dehydrogen	PDHB	37.2	49.6	30	30	180.2	0	141840	117190	130020	138290	153550	149450	189260	210590	99441	175550	Enriched	Enriched	Enriched	Enriched	YES		
P11182;Q5VVL7	Lipoamide acyltransf	DBT	53.486	35.3	22	22	79.941	0	92743	74145	74693	75323	105460	57576	77109	59381	42352	86978	Enriched	Enriched	Enriched	No expres	YES		
P11215;P11215-2	Integrin alpha-M	ITGAM	127.18	2.1	2	2	7.3769	0	4912.5	6751	8406.6	5123.4	2415	7273.4	7618	21153	5966	12330	Moderate	Low	Low	No expres	YES		
P11216	Glycogen phosphoryl	PYGB	96.695	32.9	41	37	214.13	0	164990	140210	158770	180020	169390	208960	316180	279280	153220	216190	No expres	No expres	Moderate	Enriched	YES		
P11233;H7C3P7	Ras-related protein R	RALA	23.567	36.9	11	5	19.546	0	30884	17331	26144	28925	24709	25310	26568	23208	19287	32138	Enriched	Enriched	Enriched	Low	YES		
P11279;P11279-2	Lysosome-associated	LAMP1	44.882	12	13	13	192.99	0	35197	24573	30530	40579	29776	44203	55868	44731	30962	38927	Enriched	Enriched	Enriched	Enriched	YES		
Q5T4U5;P11310;P	Medium-chain specif	ACADM	50.27	37.9	26	26	141.66	0	160000	119730	129900	127820	166350	217370	336170	306390	93011	193850	Enriched	Enriched	Enriched	Enriched	YES		
P11387	DNA topoisomerase	TOP1	90.725	18.8	14	14	64.071	0	63101	48509	57021	54492	65247	61871	96273	92929	45657	76983	Enriched	Enriched	Enriched	Enriched	YES		
P11413;P11413-3;I	Glucose-6-phosphate	G6PD	59.256	18.8	11	11	16.423	0	25198	22654	24124	27160	28729	29042	73424	65788	28629	33362	No expres	Moderate	Moderate	Moderate	YES		
P11498	Pyruvate carboxylase	PC	129.63	12.9	12	12	34.59	0	27541	24246	28959	24361	38033	18859	29921	23829	16839	34187	No expres	Moderate	Moderate	Low	YES		
P11586;F5H2F4	C-1-tetrahydrofolate	MTHFD1	101.56	47.4	62	61	303.8	0	400010	299590	355950	332810	386960	331290	372910	294100	211450	325040	Enriched	Enriched	Enriched	Enriched	YES		
P11717	Cation-independent r	IGF2R	274.37	2.6	5	5	10.793	0	23685	22963	23648	24926	27345	14420	24571	26230	17055	26217	Moderate	Enriched	Enriched	Moderate	YES		
P11766	Alcohol dehydrogena	ADH5	39.724	33.7	23	23	132.67	0	211990	154950	187600	158440	209780	168090	291220	226570	136990	178640	Enriched	Enriched	Enriched	Moderate	YES		
P11908;P11908-2;I	Ribose-phosphate py	PRPS2	34.769	28.9	15	6	37.586	0	29495	17516	22697	28454	23545	31264	28640	27297	16705	30112	Enriched	Enriched	Enriched	Moderate	YES		
P11940;A0A087W	Polyadenylate-bindin	PABPC1;PABPC3	70.67	42	59	7	115.54	0	149430	168490	153530	134280	196390	176490	211000	150100	131780	160210	Enriched	Enriched	Enriched	Enriched	YES		
P12004	Proliferating cell nuc	PCNA	28.768	36.4	14	14	81.148	0	59103	46688	51062	60703	51387	63575	99158	84803	58275	65926	Moderate	Moderate	Enriched	Low	YES		
P12110;P12110-3	Collagen alpha-2(VI)	COL6A2	108.58	28.8	62	12	323.31	0	301200	238770	317770	377330	303870	417040	698280	904960	234900	444100	No expres	Moderate	Enriched	Moderate	YES		
P12111-2;P12111;I	Collagen alpha-3(VI)	COL6A3	321.35	46	319	8	323.31	0	1562400	1242200	1534600	1786500	1539500	1903600	2628600	4705800	1195400	2236200	No expres	Enriched	Enriched	Enriched	YES		
P12235;V9GYG0	ADP/ATP translocase	SLC25A4	33.064	35.9	20	3	5.7706	0	5744.2	4305.8	4028.8	2392.4	4844.7	5685.9	2790	4872.5	860.32	5103	Enriched	Enriched	Enriched	Enriched			
P12236;I7HJJ0	ADP/ATP translocase	SLC25A6	32.866	38.9	28	10	148.96	0	266410	140650	176600	334260	193510	313150	333820	338570	155990	269830	Enriched	Enriched	Enriched	Enriched	YES		
P12270	Nucleoprotein TPR	TPR	267.29	21.4	59	59	323.31	0	228110	157090	181000	239560	206340	239640	354340	371690	217830	318490	Enriched	Enriched	Enriched	Moderate	YES		
P12277	Creatine kinase B-typ	CKB	42.644	44.1	28	13	323.31	0	92451	93850	106680	131240	90099	150230	104690	187440	54203	142280	Enriched	Enriched	Enriched	Enriched	YES		
P12429;D6RA82;D	Annexin A3;Annexin	ANXA3	36.375	44	25	25	101.22	0	145810	133640	142690	147040	148000	225220	296820	243890	142630	159270	Low	Enriched	Enriched	Moderate	YES		
P12532;P12532-2;C	Creatine kinase U-typ	CKMT1A;CKMT1B	47.036	8.6	4	4	50.656	0	23177	16493	24369	24257	23921	15955	29392	22276	25227	25359	Moderate	Enriched	Moderate	No expres	YES		
P12814;P12814-3;I	Alpha-actinin-1	ACTN1	103.06	55.9	114	59	323.31	0	522130	449540	456860	520400	509970	466240	551210	640690	297490	613710	Enriched	Enriched	Enriched	Enriched	YES		
P12821;A0A0A0M	Angiotensin-converti	ACE	149.71	8.8	12	12	17.156	0	42034	49502	62933	44388	61079	37186	50042	51743	36675	49618	Moderate	Moderate	Low	Low	YES		
P12931;P12931-2	Proto-oncogene tyros	SRC	59.834	17.5	8	6	29.606	0	40307	41624	38764	37433	45439	27828	34158	34308	17559	36067	Low	Low	Low	Moderate	YES		
P12955-3;P12955;I	Xaa-Pro dipeptidase	PEPD	47.261	22.4	9	9	29.595	0	41400	31910	30233	48310	37052	38159	33965	43621	21103	40225	Enriched	Enriched	Enriched	Moderate	YES		
P12956;B1AHC9;P	X-ray repair cross-co	XRCC6	69.842	49.9	71	71	323.31	0	570500	295440	389750	562670	362230	605490	603280	1002000	223420	640710	Enriched	Enriched	Enriched	Enriched	YES		
P13010	X-ray repair cross-co	XRCC5	82.704	38.4	55	55	152.43	0	246440	183920	223980	231790	237670	310160	488320	484160	201160	330840	Enriched	Enriched	Enriched	Enriched	YES		
P13073;H3BN72;H	Cytochrome c oxidas	COX4I1	19.576	43.8	17	17	171.97	0	113040	68473	73172	139240	81274	113560	117900	177160	101630	179790	Enriched	Enriched	Enriched	Enriched	YES		
P13284	Gamma-interferon-in	IFI30	27.963	9.2	2	2	3.0833	0.00114	4765.3	9833.5	6236.6	8795.9	8098.9	4159.4	5346.9	4911.8	3477.7	4878.8	Enriched	Enriched	Enriched	Enriched	YES		
P13473-2;P13473;I	Lysosome-associated	LAMP2	44.955	7.3	5	5	10.03	0	17977	11324	13977	12030	14887	19352	23551	37892	7138.7	14145	Enriched	Enriched	Enriched	Enriched	YES		
P13489	Ribonuclease inhibito	RNH1	49.973	44.9	31	31	176.02	0	169910	124080	135900	176240	161710	131570	160390	136530	105980	136420	Moderate	Enriched	Enriched	Moderate	YES		
P13498	Cytochrome b-245 li	CYBA	21.012	12.3	2	2	4.7618	0.00043	8142.5	8127.1	7708.6	8379.8	8404.8	6229.2	8691.7	11579	5462.4	9924.7	Moderate	Moderate	Enriched	Moderate			
P13521	Secretogranin-2;Secr	SCG2	70.94	23.2	13	13	29.066	0	69437	80136	120150	72690	111860	56523	72365	49857	51094	70674	Low	Low	Enriched	Enriched	YES		
P13639	Elongation factor 2	EEF2	95.337	54.5	142	142	323.31	0	1253400	894720	975700	1181000	1138600	1351500	1600200	1458700	783490	1116400	No expres	Enriched	Enriched	Enriched	YES		
P13667	Protein disulfide-ison	PDIA4	72.932	66.2	140	137	323.31	0	1442400	1082300	1508100	1232300	1907600	1745000	1724200	1504800	785120	1312700	Enriched	Enriched	Enriched	Enriched	YES		
P13671	Complement compon	C6	104.79	17.2	14	14	162.78	0	43294	44249	48092	52657	43895	73396	59436	112400	37143	72832	Enriched	Enriched	Enriched	Enriched	YES		
P13674-3;P13674-2	Prolyl 4-hydroxylase	P4HA1	58.957	6	3	3	5.5237	0	7713.6	8218	7885.6	7823	9426.1	5736	7174.6	7584.3	3487.7	7211.9	Enriched	Enriched	Enriched	Moderate	YES		
P13693;Q5W0H4;J	Translationally-contr	TPT1	19.595	41.3	25	21	137.6	0	195500	124820	166980	172470	201290	281060	280470	187730	169450	201630	Enriched	Enriched	Enriched	Enriched	YES		
P13716;P13716-2;I	Delta-aminolevulinic	ALAD	36.294	38.5	18	18	94.244	0	82202	46050	50300	51395	58266	60713	69309	55892	31193	59356	Enriched	Enriched	Enriched	Low	YES		
P13761;Q9TQE0;C	HLA class II histocor	HLA-DRB1;HLA-DRB5	29.822	7.5	2	2	3.0672	0.00114	9123.3	7987.3	11490	7880.4	13662	7264.2	12181	9724.2	6362.8	21153	Enriched	Enriched	Enriched	No expression			
P13796	Plastin-2	LCP1	70.288	38.4	30	23	128.54	0	80705	82958	78781	122950	74022	75847	115080	224880	71111	107450	Moderate	Low	Moderate	Low	YES		
P13797;A0A0A0M	Plastin-3	PLS3	70.81	42.2	42	31	314.41	0	233670	199700	192980	292450	237210	296200	269440	390040	129120	281740	Moderate	Enriched	Enriched	Moderate	YES		
P13804;P13804-2;I	Electron transfer flav	ETFA	35.079	43.8	26	5	323.31	0	172560	117130	134450	122350	158130	173770	178760	190980	92723	200820	Moderate	Enriched	Enriched	Moderate	YES		
P13861-2;P13861	cAMP-dependent pro	PRKAR2A	43.066	63.6	41	34	323.31	0	179260	119970	159150	189640	172950	196850	242000	240390	125980	201710	Enriched	Enriched	Enriched	Low	YES		
P13984	General transcription	GTF2F2	28.38	7.6	2	2	3.601	0.0008	13457	23545	22299	9923.3	25126	3272.3	7990.1	8935.3	6009.2	9543.3	Low	No expres	Moderate	Low	YES		
P14174	Macrophage migratio	MIF	12.476	53	26	26	102.03	0	179700	150330	162380	188890	187660	193410	190620	171300	102910	163610	Enriched	Enriched	Enriched	Enriched	YES		
P14209;A0A096LP	CD99 antigen	CD99	18.848	22.7	6	6	105.63	0	52641	55528	57941	31625	101050	41835	55080	36292	29822	28666	Enriched	Enriched	Enriched	Enriched	YES		
P14324-2;P14324;A	Farnesyl pyrophosph	FDPS	40.532	14.4	7	7	25.86	0	73281	73143	68739	61716	92919	68753	81644	84812	48656	85802	Enriched	Enriched	Enriched	Enriched	YES		
P14543;P14543-2	Nidogen-1	NID1	136.38	32.9	73	72	323.31	0	319740	234260	287510	377430	311140	343630	413880	482470	205610	443740	Low	Low	Moderate	Enriched	YES		
P14550	Alcohol dehydrogena	AKR1A1	36.573	60	44	27	206.43	0	224310	157240	179120	223960	199440	210910	501840	324830	228650	232920	Enriched	Enriched	Enriched	Enriched	YES		
P14555	Phospholipase A2, m	PLA2G2A	16.083	25.7	7	7	19.006	0	19246	21151	21161	18481	27850	22011	36062	200250	20113	35021	Moderate	Low	Moderate	Low	YES		
P14618;P14618-3;I	Pyruvate kinase PKM	PKM	57.936	65.3	97	97	323.31	0	692700	523080	624500	801950	764150	752760	972360	1029600	445060	691340					YES		
P14625	Endoplasmin	HSP90B1	92.468	66.6	204	193	323.31	0	2183100	1527300	1792400	1971100	2097100	2548300	2542500	2665000	1075800	2142000	Low	Enriched	Enriched	Low	YES		
P14735	Insulin-degrading enz	IDE	117.97	19.8	23	23	63.009	0	105550	74899	79520	97883	121110	109560	97920	122200	40372	106340	Moderate	Enriched	Enriched	Low	YES		
P14854	Cytochrome c oxidas	COX6B1	10.192	70.9	13	13	25.179	0	58357	38884	42841	74750	45887	66277	76795	71622	32720	68724	Enriched	Enriched	Enriched	Moderate	YES		
P14866;M0QXS5;F	Heterogeneous nucle	HNRNPL	64.132	34	29	13	102.47	0	155010	102630	140220	126570	164050	151270	220440	166220	160760	167370	Enriched	Enriched	Enriched	Enriched	YES		
P14868;P14868-2	Aspartate--tRNA liga	DARS	57.136	50.5	37	37	323.31	0	221960	161920	170130	184540	185800	242120	241870	233440	123460	227410	Enriched	Enriched	Enriched	Moderate	YES		
P14923	Junction plakoglobin	JUP	81.744	33.6	37	25	154.28	0	91707	65207	78275	83551	88315	57876	81871	81270	47945	83647	Enriched	Enriched	Enriched	Moderate	YES		
P14927;B7Z2R2;P	Cytochrome b-c1 cor	UQCRB	13.53	40.5	11	4	53.745	0	98651	72836	91073	98043	92657	153070	82736	99905	33675	104990	Enriched	Enriched	Enriched	Enriched	YES		
P15085;C9JUF9;C	Carboxypeptidase A1	CPA1	47.14	64.2	126	123	323.31	0	1986900	1575100	1414700	1987400	1591300	1890200	1820800	1691200	1000700	1382600	No expres	Enriched	Enriched	Enriched	YES	YES	YES
P15086	Carboxypeptidase B	CPB1	47.367	69.1	123	111	323.31	0	1678400	1588800	1323900	1552000	1774800	1171600	1424200	966700	784290	940740	Moderate	Enriched	Enriched	Enriched	YES	YES	YES
P15088	Mast cell carboxypep	CPA3	48.669	17.7	12	12	48.238	0	107990	45118	74173	94421	39922	51773	103720	95934	45868	92384	Low	Enriched	Moderate	Moderate	YES		
P15090	Fatty acid-binding pr	FABP4	14.719	56.1	20	20	301.33	0	60096	80643	54088	98655	57977	108440	116800	97391	136230	197410	Low	Low	Moderate	Low	YES		
P15104	Glutamine synthetase	GLUL	42.064	14.7	6	6	11.453	0	14317	13488	15640	19664	15653	25106	48950	17086	38813	27273	Enriched	Enriched	Enriched	Enriched	YES		
P15121;E9PCX2	Aldose reductase	AKR1B1	35.853	37.7	18	18	129.6	0	148160	71630	76420	93657	86373	202090	278680	182460	130520	168830	Moderate	Enriched	Enriched	Enriched	YES		
P15144	Aminopeptidase N	ANPEP	109.54	32.5	41	41	145.64	0	244030	262570	192800	236590	279570	225610	183690	199750	109960	228370	Enriched	Enriched	Enriched	Enriched	YES		
P15170-2;P15170-3	Eukaryotic peptide cl	GSPT1	68.6	31	24	12	140.74	0	130990	99506	109430	109060	135310	137020	171400	142360	84323	137510	Enriched	Enriched	Enriched	Low			
P15259	Phosphoglycerate mu	PGAM2	28.766	31.2	21	2	5.0626	0.00044	3402.4	3043.1	3709.2	3111.5	5700.4	2765.8	6158.9	2918.8	4083.8	4474	Moderate	No expres	No expres	No expression			
P15289;P15289-2	Arylsulfatase A;Aryls	ARSA	53.588	8.9	5	5	8.2501	0	11797	10130	11626	15199	12084	15351	12984	15218	8425.3	14922	Low	Moderate	Moderate	Moderate	YES		
P15374;A0A087W	Ubiquitin carboxyl-te	UCHL3	26.182	49.1	19	19	104.46	0	97755	84821	113770	70398	119120	98877	95673	79938	51553	90988	Low	Enriched	Enriched	Moderate	YES		
P15529-16;P15529	Membrane cofactor p	CD46	36.826	11.6	6	6	11.052	0	14953	9859.5	12963	16652	16910	14758	26504	25358	14512	17683	Low	Enriched	Enriched	Enriched	YES		
P15531;P15531-2;I	Nucleoside diphosph	NME1	17.149	63.8	19	2	35.837	0	14200	11841	13512	10116	15917	15367	15571	21040	4900.8	13962	Moderate	Enriched	Enriched	Moderate	YES		
P15848-2;P15848	Arylsulfatase B	ARSB	45.995	2.4	1	1	2.7901	0.00222	3729.6	3693.8	4658.3	2746.1	6191.1	4595	6947.6	4784.1	5704.9	6501.5	No expres	No expres	Moderate	No expression			
P15880;H0YEN5;E	40S ribosomal protei	RPS2	31.324	51.2	32	32	146.67	0	397350	218490	276580	401710	280210	277790	396320	460120	164030	334020	Enriched	Enriched	Enriched	Enriched	YES		
P15924;P15924-3;I	Desmoplakin	DSP	331.77	38.3	163	160	323.31	0	748430	579140	660450	731020	765480	689420	884290	713500	550440	744200	Enriched	Enriched	Enriched	Enriched	YES		
P15927;P15927-2;I	Replication protein A	RPA2	29.247	10.7	5	5	11.947	0	9940.1	11761	10449	9364.3	13254	6666.2	6247.8	6939.8	3507.9	6790.5	Moderate	Enriched	Enriched	Moderate	YES		
P16035;B4DFW2	Metalloproteinase inl	TIMP2	24.399	20	3	3	7.9981	0	19757	20111	26247	23431	24957	15324	16340	18588	10514	16563	Enriched	Enriched	Enriched	Enriched	YES		
P16104;Q96QV6;C	Histone H2AX;Histo	H2AFX;HIST1H2AA;HI	15.144	46.2	21	10	150.36	0	75226	53728	64506	52388	77593	64729	197190	116270	105260	120410	Enriched	Moderate	Enriched	No expression			
P16144-4;P16144-2	Integrin beta-4	ITGB4	194.46	15	24	24	67.509	0	59538	49465	68395	69026	65807	58966	50313	51624	29718	70714	Enriched	Moderate	Moderate	No expres	YES		
P16152;E9PQ63;A	Carbonyl reductase [I	CBR1	30.375	43.7	28	21	286.56	0	115850	99217	103270	136670	124800	124020	110140	176240	73649	106880	Moderate	Moderate	Enriched	Low	YES		
P16219;E9PE82	Short-chain specific a	ACADS	44.297	32.5	17	17	45.336	0	56770	43504	48526	60826	50964	81435	94366	81029	53699	90322	Enriched	Moderate	Moderate	Moderate	YES		
P16220-3;P16220-2	Cyclic AMP-responsi	CREB1	25.444	10.4	3	3	33.323	0	12616	13746	14454	10812	14361	15564	34661	27943	22572	22283	Moderate	Enriched	Enriched	Moderate			
P16233	Pancreatic triacylglyc	PNLIP	51.156	53.8	108	101	323.31	0	1803700	1843300	1160700	1734100	1526900	1559400	1762300	947920	677140	1050500	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P16278-3;P16278;I	Beta-galactosidase	GLB1	72.75	13.4	9	9	22.012	0	16526	14780	10102	11265	16008	9896.7	7570.2	11379	3339.3	10503	Moderate	Enriched	Enriched	Enriched	YES		
P16284-5;P16284-3	Platelet endothelial c	PECAM1	79.26	20.6	15	15	74.1	0	15175	9802.6	11886	17770	12931	33153	19323	17615	9999.6	24746	Enriched	Enriched	Enriched	Enriched	YES		
Q5F2F8;P16298-2;	Serine/threonine-prot	PPP3CB	56.014	14.7	6	2	33.304	0	8108.7	7139.6	7214.8	11810	5549.8	7983.8	7975.1	10377	4294.1	9368.4	Enriched	Enriched	Enriched	Enriched	YES		
P16401	Histone H1.5	HIST1H1B	22.58	24.8	11	6	55.054	0	41358	33029	46267	34861	34378	27174	44987	105310	26257	42218	Low	No expres	No expres	No expres	YES		
P16402	Histone H1.3	HIST1H1D	22.35	25.8	28	1	1.9513	0.00799	6402.1	9012.5	11352	5567.6	8246.6	8521	10652	17838	4514	9681.7	No expres	Low	Low	Low	YES		
P16403	Histone H1.2	HIST1H1C	21.364	44.6	33	5	10.032	0	28093	26700	27790	18682	30183	17659	18849	27861	11399	23066	Low	Enriched	Enriched	No expres	YES		
P16435;H0Y4R2;E	NADPH--cytochrome	POR	76.689	18.9	12	12	34.873	0	51078	46288	46533	54135	51891	63452	52351	65375	28717	58112	No expres	Moderate	Moderate	Low	YES		
P16444	Dipeptidase 1	DPEP1	45.673	32.8	26	26	97.513	0	191740	111510	164340	227400	109690	245730	255840	161510	94425	161450	Moderate	Enriched	Enriched	Enriched	YES		
P16455	Methylated-DNA--pr	MGMT	21.646	41.5	7	7	19.875	0	31269	19796	21485	34591	28991	14725	15049	16587	9232.2	24612	Low	Moderate	Moderate	Moderate	YES		
P16519-3;P16519;I	Neuroendocrine conv	PCSK2	68.579	11.5	9	9	58.229	0	29658	27023	24272	27050	26313	18012	25301	20027	33632	31358	Low	Low	Enriched	Low	YES		
P16615;P16615-5;I	Sarcoplasmic/endopl	ATP2A2	114.76	28.6	48	30	281.45	0	341280	208100	260730	322910	278990	385210	384750	409780	179640	329570	Enriched	Enriched	Enriched	Enriched	YES		
P16870-2;P16870	Carboxypeptidase E	CPE	49.885	38.9	17	17	94.613	0	70576	65626	96128	64509	91035	45944	60435	45768	69155	58907	Low	Moderate	Enriched	Enriched	YES		

P16930;P16930-2	Fumarylacetoacetase	FAH	46.374	25.1	16	16	36.855	0	81840	54103	70010	74805	69668	79952	91419	95577	48470	80546	Moderate	Low	Moderate	Low	YES		
P16949;A2A2D0;P	Stathmin	STMN1	17.302	22.8	4	2	9.9382	0	6378.8	7738.9	7519.4	5688.1	6801.6	5667.1	7453.5	7014.2	7856.5	9819.9	Enriched	Moderate	Moderate	Enriched	YES		
P16989-2;P16989;I	Y-box-binding protei	YBX3	31.947	42.9	23	15	282.8	0	110770	80052	104790	89879	127920	76879	123710	120310	54433	94684					YES		
P17026	Zinc finger protein 22	ZNF22	25.915	26.8	6	3	14.646	0	42336	24188	33809	25666	43259	40245	32403	25782	19562	33752	Moderate	Enriched	Enriched	Moderate	YES		
P17028	Zinc finger protein 24	ZNF24	42.155	6	3	2	7.0649	0	9558.7	5620.6	4523.7	10519	4601.3	5599.1	7067.9	6707.9	5670.8	9671.3	Enriched	Enriched	Enriched	Enriched	YES		
P17050	Alpha-N-acetylgalact	NAGA	46.564	10.2	5	5	10.34	0	34396	29139	33151	24991	33371	35259	38820	52493	23756	47474	Enriched	Moderate	Enriched	Moderate	YES		
P17066	Heat shock 70 kDa p	HSPA6	71.027	26	43	3	14.197	0	22874	19339	22086	19518	35244	21241	35455	46700	10550	18417	Moderate	Low	Enriched	Low			
P17096;P17096-3	High mobility group	HMGA1	11.676	33.6	4	4	15.992	0	18645	12202	16407	16140	19644	16827	26776	15691	13216	15792	Low	Enriched	Enriched	Low	YES		
P17152	Transmembrane prote	TMEM11	21.541	13.5	5	5	10.968	0	15191	17440	29738	13111	22742	17651	32603	20082	20523	24822	Enriched	Moderate	Enriched	Moderate	YES		
P17174;P17174-2	Aspartate aminotrans	GOT1	46.247	49.6	36	36	131.55	0	156990	104760	132430	175320	134630	191820	184980	220510	94745	176030	Enriched	Moderate	Enriched	Enriched	YES		
P17252;J3KRN5	Protein kinase C alph	PRKCA	76.749	15.6	9	6	32.957	0	37728	30642	39818	32220	46981	40426	66077	45274	36623	43201	Enriched	Moderate	Enriched	Moderate	YES		
P17480;E9PKP7;P	Nucleolar transcriptic	UBTF	89.405	17.7	17	17	78.398	0	99437	60181	69787	93883	74572	80224	76213	102460	51970	105540	Enriched	Enriched	Enriched	Enriched	YES		
P17568	NADH dehydrogenas	NDUFB7	16.402	12.4	2	2	2.693	0.00238	12891	11663	11332	9330.3	14960	10564	12567	10918	5843	11728	No expres	Low	Enriched	Enriched	YES		
P17612-2;P17612;(	cAMP-dependent prc	PRKACA;KIN27	39.821	42.3	14	6	43.072	0	60363	53141	61946	63188	63491	56288	70920	80505	36461	64834	Enriched	Enriched	Enriched	Moderate	YES		
P17655;P17655-2	Calpain-2 catalytic su	CAPN2	79.994	30.7	21	20	100.71	0	99041	61371	76612	99093	94404	136760	124210	142980	60155	126510	Enriched	Enriched	Enriched	Enriched	YES		
P17661	Desmin	DES	53.535	24.7	21	11	124.22	0	36319	61931	35193	28918	53797	40522	42949	39792	22869	62683	Enriched	No expres	Low	Low	YES		
P17677;P17677-2	Neuromodulin	GAP43	24.802	23.1	3	3	9.8077	0	9001.4	6701.9	10215	6258.7	12452	6861.4	11158	8529.9	6774.2	13573	Enriched	Moderate	Moderate	Enriched	YES		
P17812;P17812-2	CTP synthase 1	CTPS1	66.69	7.3	6	4	5.0842	0.00044	1285.7	1845.4	2016.1	1537.4	1675.7	1686.9	2222.3	1998.8	1102.6	1956.6					YES		
P17844;J3KTA4;P1	Probable ATP-depen	DDX5	69.147	30.9	27	13	23.428	0	50587	37061	41564	55926	45447	40496	38915	39136	17328	46158	No expres	Enriched	Enriched	Enriched	YES		
P17858;P17858-2	ATP-dependent 6-ph	PFKL	85.018	22.3	24	20	284.28	0	115610	83906	80236	112780	95234	122090	201410	180770	70817	129410	Enriched	Enriched	Enriched	Enriched	YES		
P17900	Ganglioside GM2 act	GM2A	20.838	23.8	7	7	18.684	0	20204	10108	15240	29899	11295	40986	19912	32342	12130	25966	Enriched	Enriched	Enriched	Enriched	YES		
P17931	Galectin-3	LGALS3	26.152	34.8	17	17	58.461	0	161060	104990	124920	191320	125210	151700	257150	284110	107140	189150	Enriched	Enriched	Enriched	Moderate	YES		
R4GNH3;P17980;E	26S protease regulato	PSMC3	47.352	49.4	31	31	155.35	0	274650	205350	244250	237930	257490	253210	302850	252130	150790	250860	Moderate	Moderate	Enriched	Enriched	YES		
P17987;E7EQR6;E	T-complex protein 1	TCP1	60.343	43.7	42	35	148.25	0	201630	146050	174530	186220	191950	227320	278660	328500	125810	217450	Moderate	Enriched	Enriched	Enriched	YES		
P18031	Tyrosine-protein pho	PTPN1	49.966	9	5	5	7.6978	0	4703.9	5246.6	6296.5	5607.7	16367	4576.1	6154.1	5083.1	2667.5	4476.9	Enriched	Moderate	Enriched	Moderate	YES		
P18065	Insulin-like growth fa	IGFBP2	34.814	24.6	8	8	22.986	0	64703	80438	58309	67116	78409	53555	41145	35319	24237	42761	No expres	Enriched	Enriched	Moderate	YES		
P18084;V9GZ57;H	Integrin beta-5;Integr	ITGB5	88.053	6.1	3	3	17.394	0	30114	17431	24263	36900	20554	34964	30356	32344	12344	36002	Enriched	Enriched	Enriched	Enriched	YES		
P18085;C9JPM4;C	ADP-ribosylation fac	ARF4	20.511	63.9	32	12	68.041	0	107510	48448	49988	137330	66713	100320	87447	189660	36920	117040	Enriched	Enriched	Enriched	Enriched	YES		
P18124;A8MUD9	60S ribosomal protei	RPL7	29.225	51.2	37	37	239.61	0	255050	156340	176440	247780	239680	256150	221310	203970	95440	183800	Enriched	Enriched	Enriched	Enriched	YES		
P18206-2;P18206;(	Vinculin	VCL	116.72	60	120	120	323.31	0	446680	389190	416560	419730	446060	569720	928550	905850	413250	635760	Enriched	Enriched	Enriched	Enriched	YES		
P18428	Lipopolysaccharide-b	LBP	53.383	14.6	9	9	13.614	0	6693.5	5501.7	10114	11353	5285.9	5617.7	5132.9	13707	3059.9	9708.3	Enriched	Moderate	Moderate	Enriched	YES		
P18583-2;P18583-	Protein SON	SON	232.3	5.7	11	11	33.938	0	25825	27488	30781	25038	35403	22928	25324	24241	16692	25681	Enriched	Enriched	Enriched	Enriched	YES		
P18615;P18615-3;I	Negative elongation f	NELFE	43.239	24.7	7	7	23.208	0	26309	18373	23286	22858	24435	24675	28642	27005	18257	29657					YES		
P18669;Q8N0Y7	Phosphoglycerate mu	PGAM1;PGAM4	28.804	65.7	42	23	296.43	0	427190	282640	304940	367980	362210	383420	496710	474190	270510	392830	Enriched	Enriched	Enriched	Enriched			
P18827	Syndecan-1	SDC1	32.461	3.9	1	1	4.1226	0.00062	1732.1	1694.1	1711	1329.7	2291.3	1321.8	2456.8	1426.1	3930.9	2227.1	Enriched	Enriched	Enriched	Enriched	YES		
P18859;P18859-2;	ATP synthase-coupli	ATP5J	12.587	55.6	19	19	323.31	0	151730	143500	169480	127710	218830	118260	132210	138560	56482	142290	Enriched	Enriched	Enriched	Moderate	YES		
P19021-2;P19021-	Peptidyl-glycine alph	PAM	96.257	4.5	4	4	6.7359	0	23215	20328	26769	17049	29103	17393	24851	15338	19866	16437	Enriched	Enriched	Enriched	Enriched	YES		
P19075	Tetraspanin-8	TSPAN8	26.044	14.3	6	6	20.533	0	9425.4	7645.7	11115	7590.6	10346	22020	47753	20456	29622	25822	Enriched	Enriched	Enriched	Enriched	YES		
P19320-2;P19320-	Vascular cell adhesio	VCAM1	71.254	2.3	1	1	4.0129	0.00062	6988.6	5477.3	5181.9	6904.2	7031.7	6893.4	8310.7	19582	4211.2	8308.1	Moderate	Enriched	Enriched	Low	YES		
P19338;H7BY16	Nucleolin	NCL	76.613	38.2	78	78	323.31	0	761400	512500	673820	671950	736090	662850	1008800	996980	477960	843970	Enriched	Enriched	Enriched	Enriched	YES		
P19367-4;P19367-	Hexokinase-1	HK1	101.08	13.6	12	10	22.762	0	43128	43314	52662	44342	54245	45309	60242	67718	24452	63504	Enriched	Enriched	Enriched	No expres	YES		
P19387	DNA-directed RNA p	POLR2C	31.441	24	7	7	14.67	0	14532	12376	14428	11424	18483	11003	15017	12164	8083.5	11721	Enriched	Enriched	Enriched	Enriched	YES		
P19440;E7ET76;P1	Gamma-glutamyltran	GGT1;GGT3P	61.409	14.8	10	10	19.827	0	39336	34928	38005	36414	42253	28058	35595	31496	25805	29034	Enriched	Enriched	Enriched	Enriched			
P19474	E3 ubiquitin-protein	TRIM21	54.169	6.9	3	3	5.1125	0.00044	3846.5	2901.1	3592.2	8034.6	4044.6	4953.8	5695.9	5689.6	5826.7	6260.1	Moderate	Enriched	Moderate	Moderate	YES		
P19525;P19525-2	Interferon-induced, d	EIF2AK2	62.094	9.6	6	6	20.461	0	50520	39927	41077	35980	53251	33021	28959	37326	16017	34299	Moderate	Low	Enriched	Enriched	YES		
P19526	Galactoside 2-alpha-l	FUT1	41.251	3.8	1	1	1.8113	0.0099	6720.3	4526.9	5710.6	7266	6145.3	7423.6	8963.4	6727.9	6701.7	7037.2	Moderate	Enriched	Moderate	Enriched			
P19623	Spermidine synthase	SRM	33.824	48	25	25	80.661	0	113340	88242	88432	69134	109670	115810	116050	84214	51195	75253	Moderate	Enriched	Enriched	Enriched	YES		
P19634	Sodium/hydrogen exc	SLC9A1	90.762	1.7	1	1	3.4915	0.00079	2780.9	1991.8	2241.3	3333.2	2460.8	2483.4	2660.2	2587.9	1290.7	2713.2	Enriched	Low	Moderate	Enriched	YES		
P19652	Alpha-1-acid glycopr	ORM2	23.602	32.8	14	8	84.92	0	91094	70811	55265	140870	47818	67843	57063	181540	39091	67595	Low	No expres	No expres	No expres	YES		
P19827;P19827-2;I	Inter-alpha-trypsin in	ITIH1	101.39	11.6	14	14	27.612	0	46593	34866	43270	65004	33510	52940	57233	88255	36324	65627	Low	No expres	No expres	Moderate	YES		
X6R868;P19835;P1	Bile salt-activated lip	CEL	79.666	29.2	90	90	323.31	0	833940	987500	585250	912470	857650	1173800	1537900	1116800	928340	773530	Low	Enriched	Enriched	Enriched	YES	YES	YES
P19838;P19838-2;I	Nuclear factor NF-ka	NFKB1	105.35	12.6	16	16	55.661	0	34937	28425	30348	32706	35193	28820	26497	28386	13914	29352	Low	Enriched	Enriched	Enriched	YES		
P19961;P04745;P1	Alpha-amylase 2B;A	AMY2B;AMY1A	57.709	68.9	136	5	46.655	0	145340	124230	74127	479240	78119	92578	65934	85418	47446	78193	Moderate	Enriched	Enriched	Enriched	YES	YES	YES
P20020-5;P20020-	Plasma membrane cal	ATP2B1	129.15	9.1	15	5	19.377	0	15955	10012	11304	13963	16112	13673	11886	11756	7383.8	13425	Enriched	Low	Enriched	Moderate	YES		
P20042	Eukaryotic translatio	EIF2S2	38.388	58.9	38	38	323.31	0	430800	289600	387660	334200	470350	407590	488060	349620	218550	328190	Moderate	Enriched	Enriched	Enriched	YES		
P20073-2;P20073	Annexin A7	ANXA7	50.315	29.2	21	20	48.123	0	56487	50996	47241	60880	52773	57983	94401	98465	58326	75954	Moderate	Enriched	Enriched	Enriched	YES		
P20290;P20290-2	Transcription factor I	BTF3	22.168	41.3	11	3	29.204	0	69975	41552	50781	81183	47836	77022	59546	79887	30904	78488	Enriched	Enriched	Enriched	Enriched	YES		
P20338	Ras-related protein R	RAB4A	24.389	21.1	6	4	6.0192	0	3100.2	2153.7	1948.9	3050.7	1811.8	2657.7	3313.5	3518.4	1489.8	3341.1	Enriched	Enriched	Enriched	Moderate	YES		
P20339-2;P20339;I	Ras-related protein R	RAB5A;RAB5B	22.178	47.3	11	5	6.1679	0	4128	4543.4	4055.5	2599.5	6146.6	2480.7	2252.4	1607	1513.4	2653.7	Enriched	Enriched	Enriched	Enriched			
P20340-2;H0YGL6	Ras-related protein R	RAB6A	23.548	49	17	12	79.575	0	60065	52931	56876	46647	64207	68037	92056	84964	39805	66430	Enriched	Enriched	Enriched	Enriched	YES		
P20618	Proteasome subunit b	PSMB1	26.489	51.9	22	22	115.54	0	95229	75723	95655	100800	94674	107370	138230	145280	83318	120520	Enriched	Enriched	Enriched	Enriched	YES		
P20645;H0YGT2	Cation-dependent ma	M6PR	30.993	10.8	5	5	14.551	0	23089	15503	19711	20032	25825	27823	25550	30726	11125	32162	Enriched	Enriched	Enriched	Enriched	YES		
P20674;H3BV69;H	Cytochrome c oxidas	COX5A	16.762	40	13	13	76.949	0	127540	63815	117450	326360	100900	215630	129580	130930	51786	189850	Enriched	Enriched	Enriched	Moderate	YES		
P20700;E9PBF6	Lamin-B1	LMNB1	66.408	53.1	68	59	323.31	0	335010	199280	254050	340640	282220	326290	546230	549710	396700	391550	No expres	No expres	Low	Low	YES		
P20774;Q5TBF5	Mimecan	OGN	33.922	23.8	25	25	323.31	0	137440	124510	185410	216960	146870	187520	346120	455710	129840	209660	No expres	Low	Low	No expres	YES		
P20810-9;P20810-	Calpastatin	CAST	80.264	23.9	21	21	323.31	0	172550	152830	156890	170350	240360	191890	204070	209850	118790	194000	Enriched	Enriched	Enriched	Moderate	YES		
P20815	Cytochrome P450 3A	CYP3A5	57.108	4.4	2	1	2.3077	0.00479	10653	2846.3	14410	2584.4	2905.7	908.89	4629	2549.9	7272	2870.4	No expres	Moderate	Moderate	Enriched	YES		
P20839-2;C9J029	Inosine-5-monophos	IMPDH1	52.597	8.6	4	2	14.032	0	14236	9510.1	11543	11703	13625	13869	11417	12188	6188.2	13381	Enriched	Enriched	Moderate	Enriched	YES		
P20908;A0A087W	Collagen alpha-1(V)	COL5A1	183.56	2	4	4	5.4282	0	18483	25263	29254	17650	40610	15604	28305	28578	13986	19249	No expres	Low	Enriched	Moderate	YES		
P20933;H0Y9C7	N(4)-(beta-N-acetylg	AGA	37.208	6.9	2	2	10.52	0	2594.6	1640.5	2931.8	2727.9	2983.8	3770.6	3579.3	2092.6	1496.3	4414.7	Enriched	Enriched	Enriched	Moderate	YES		
P20962	Parathymosin	PTMS	11.53	22.5	3	3	11.095	0	19403	19154	21301	11240	20935	19143	48076	45075	40768	30523	Low	No expres	Moderate	Enriched	YES		
P21266;A0A0A0M	Glutathione S-transfe	GSTM3	26.559	65.8	29	28	145.45	0	318330	241980	273960	424500	230550	294120	229530	285820	124620	234490	Enriched	Enriched	Enriched	Enriched	YES		
P21281	V-type proton ATPas	ATP6V1B2	56.5	50.9	30	23	105.06	0	111570	83748	96986	128260	116590	124850	163940	111270	95392	119320	Moderate	Enriched	Enriched	Enriched	YES		
P21283;E7EV59	V-type proton ATPas	ATP6V1C1	43.941	18.3	8	8	22.954	0	41654	32392	44623	36581	52219	37752	44247	35591	22510	34577	Moderate	Moderate	Enriched	Moderate	YES		
P21291;E9PP21;E	Cysteine and glycine-	CSRP1	20.567	66.3	31	29	323.31	0	162680	150990	159240	132430	223160	124180	157250	131560	84906	187370	Enriched	Enriched	Enriched	Enriched	YES		
P21397;P21397-2	Amine oxidase [flavir	MAOA	59.681	35.5	33	27	139.69	0	113770	91616	102680	95161	102040	136830	137290	183180	77765	161370	Moderate	Enriched	Enriched	Enriched	YES		
P21399	Cytoplasmic aconitat	ACO1	98.398	41.7	66	36	323.31	0	405310	326650	331560	376030	456150	367310	488070	555460	169700	377800	Enriched	Enriched	Enriched	Enriched	YES		
P21589-2;P21589;(	5-nucleotidase	NT5E	57.948	15.1	8	5	35.095	0	28252	15345	19614	41185	20331	28940	46168	75488	14242	38309	Low	No expres	Moderate	No expres	YES		
P21695-2;P21695	Glycerol-3-phosphate	GPD1	35.139	21.5	9	9	11.883	0	8414.5	24176	6449.3	21127	10914	8934.7	5705.7	8158.8	4798.4	21415	Enriched	No expres	Low	Enriched	YES		
P21796	Voltage-dependent an	VDAC1	30.772	79.9	44	12	248.48	0	327940	220610	236680	356320	320130	322670	481830	435690	173870	342540	Low	Enriched	Enriched	Enriched	YES		
P21810	Biglycan	BGN	41.654	33.4	28	14	116.66	0	76093	72745	69033	90274	80903	96324	278920	297540	72838	103170	Enriched	Moderate	Enriched	Enriched	YES		
P21912;A0A087W	Succinate dehydroge	SDHB	31.629	43.6	20	6	47.962	0	89966	68188	86803	86060	99782	89271	100200	77181	61098	98307	No expres	Enriched	Enriched	Moderate	YES		
P21953	2-oxoisovalerate deh	BCKDHB	43.122	23.7	10	10	73.513	0	100320	51506	78040	94287	101410	78501	62210	71379	28479	87365	No expres	Low	Moderate	Low	YES		
P21964-2;P21964;I	Catechol O-methyltra	COMT	24.449	60.6	21	21	90.545	0	165760	104940	96940	177300	111980	150090	153950	180710	94814	187940	Enriched	Enriched	Enriched	No expres	YES		
P21980;P21980-2	Protein-glutamine ga	TGM2	77.328	29.8	27	27	117.44	0	106500	94696	105080	130960	127160	108070	291800	148860	111510	132350	Enriched	Moderate	Enriched	Enriched	YES		
P22033	Methylmalonyl-CoA	MUT	83.134	29.3	28	28	203.42	0	271380	195090	184520	204740	230030	199740	238850	254420	111330	229090	Enriched	Enriched	Enriched	Enriched	YES		
P22059	Oxysterol-binding pr	OSBP	89.42	18.6	19	19	138.41	0	102710	72074	73266	81197	111900	75681	81100	74617	41502	87876	Enriched	Enriched	Enriched	Low	YES		
P22087;M0QXL5;	rRNA 2-O-methyltra	FBL	33.784	38.9	22	11	143.56	0	180170	151720	186700	122950	233030	118770	165390	171250	96640	171670	Enriched	Enriched	Enriched	Enriched	YES		
P22102;P22102-2	Trifunctional purine l	GART	107.77	21.2	25	18	82.17	0	106320	83093	98230	88208	113110	93952	116120	129960	68431	111780	Moderate	Enriched	Enriched	No expres	YES		
P22105	Tenascin-X	TNXB	464.32	17.5	55	2	309.49	0	179420	159360	205450	143480	236430	131690	177140	223170	97892	194290	Enriched	Low	Low	Moderate	YES		
P22307-4;P22307-	Non-specific lipid-tra	SCP2	50.341	23.8	13	13	78.535	0	73261	57591	63701	60659	62937	66795	66346	100560	44929	93076	Enriched	Enriched	Enriched	Enriched	YES		
P22314-2;P22314	Ubiquitin-like modifi	UBA1	113.8	47.2	102	93	323.31	0	721220	513920	647450	738270	655000	678650	790490	854050	438560	691170	Moderate	Enriched	Enriched	Low	YES		
Q32Q12;P22392-2;	Nucleoside diphosph	NME1-NME2;NME2;N	32.642	58.9	32	15	275.02	0	425700	330500	305650	509050	381690	384940	378000	561580	234050	340960	Enriched	Enriched	Enriched	Enriched			
P22413	Ectonucleotide pyro	ENPP1	104.92	20.9	24	24	273.18	0	53937	47340	42035	71414	64357	57528	66659	58921	18021	69378	Moderate	Enriched	Enriched	Moderate	YES		
P22466	Galanin peptides;Gal	GAL	13.302	11.4	1	1	7.4385	0	9394.2	14864	14130	10270	22500	19919	8752.2	12133	5394.7	13616	No expres	Low	Moderate	No expression			
P22626;P22626-2;	Heterogeneous nucle	HNRNPA2B1	37.429	59.8	66	65	323.31	0	639460	491500	691070	643550	688100	617970	1015200	872150	555900	785450	Enriched	Enriched	Enriched	Enriched	YES		
P22670	MHC class II regulato	RFX1	104.76	2.6	4	4	9.7392	0	11784	9367.6	9614.8	11178	10325	7637	6709.2	8304.9	4790.9	9881.3	Enriched	Enriched	Enriched	No expres	YES		
P22681	E3 ubiquitin-protein	CBL	99.632	2.8	2	2	2.4786	0.00395	9496.3	6995.8	7532.7	8649.3	8515.8	9684	11725	12956	5334	9505.3	Moderate	Moderate	Enriched	No expression			
P22694;A0A0A0M	cAMP-dependent prc	PRKACB	40.622	36.5	13	1	60.772	0	31403	22667	28673	29211	30681	26281	33425	49034	19290	30939	Enriched	Enriched	Enriched	Moderate	YES		
P22695;H3BRG4;F	Cytochrome b-c1 cor	UQCRC2	48.442	44.4	40	40	272.08	0	148950	115370	127000	151980	167160	138240	206450	216800	95150	160730	Enriched	Enriched	Enriched	Enriched	YES		
P22830;P22830-2;I	Ferrochelatase, mitoc	FECH	47.862	19.6	8	8	21.983	0	23058	24765	23840	24619	36706	25569	30171	20800	18465	26844	Moderate	Moderate	Enriched	No expres	YES		
P22897	Macrophage mannose	MRC1	166.01	5.5	8	8	16.05	0	18113	23188	23323	27464	19487	23959	17562	27494	10797	29955	No expres	Low	Enriched	Enriched	YES		
P23141-3;P23141;I	Liver carboxylesteras	CES1	62.392	24	23	23	58.579	0	53589	39273	60265	108910	52344	42927	42517	53342	19336	49756	Moderate	Moderate	Moderate	Moderate	YES		
P23142	Fibulin-1	FBLN1	77.213	20.3	25	5	126.85	0	92654	93430	107520	93172	123630	94384	126180	222110	82952	102030	Moderate	Moderate	Moderate	Moderate	YES		
P23193;P23193-2	Transcription elongat	TCEA1	33.969	31.9	12	10	64.958	0	43945	33135	40040	41794	38672	47146	48730	57160	25142	51836	Low	Enriched	Enriched	Enriched	YES		
P23229-4;P23229-	Integrin alpha-6;Inte	ITGA6	119.09	27.4	35	3	80.891	0	166920	148080	168940	189140	192440	148060	139600	140640	87739	153540	Moderate	Moderate	Enriched	Enriched	YES		
P23246;P23246-2	Splicing factor, proli	SFPQ	76.149	34.5	51	48	323.31	0	328860	259240	336460	312800	332210	314080	522770	564360	263600	428230	Moderate	Enriched	Enriched	Enriched	YES		
Q9NRH3;P23258;K	Tubulin gamma-2 cha	TUBG2;TUBG1	51.091	10.2	7	7	18.258	0	30737	25720	43033	21088	29454	27195	31403	22523	17684	27677	Enriched	Moderate	Moderate	No expression			
P23284	Peptidyl-prolyl cis-tr	PPIB	23.742	56	43	37	278.27	0	533650	409120	409200	467650	482980	722960	664910	479870	364290	377650	Enriched	Enriched	Enriched	Enriched	YES		
Q5T7Y6;P23297	Protein S100;Protein	S100A1	15.895	16.3	4	4	9.8601	0	1681.4	1332.1	1689.9	4990.6	1450.4	2968.8	2095.3	2746.2	1252.7	2522	Enriched	Moderate	Low	Low	YES		
P23368;P23368-2	NAD-dependent mali	ME2	65.443	13.2	10	9	49.654	0	30463	36208	31583	28464	37675	24508	27724	26793	18032	29973	Moderate	Enriched	Enriched	Moderate	YES		
P23381;P23381-2	Tryptophan--tRNA li	WARS	53.165	58	51	51	254.64	0	310630	191310	230460	281850	266870	349800	418380	452570	187100	304390	Enriched	Enriched	Enriched	Enriched	YES		
P23396;P23396-2;I	40S ribosomal protei	RPS3	26.688	77.4	47	47	175.74	0	342260	266290	315900	348350	355900	380100	511870	452310	255150	374790	Enriched	Enriched	Enriched	Enriched	YES		
P23434	Glycine cleavage syst	GCSH	18.884	18.5	9	9	133.7	0	46753	48974	46537	41689	43674	69187	89207	64622	60811	68451	Moderate	Enriched	Enriched	Moderate	YES		
P23443-4;P23443-	Ribosomal protein S6	RPS6KB1	51.016	3.5	1	1	3.0458	0.00132	5154	3192.5	3646.2	6486.5	5226.1	5017.3	4178.3	4038.2	1869.4	4693.1	Low	Enriched	Enriched	No expression			
P23458	Tyrosine-protein kina	JAK1	133.28	2	2	2	2.1075	0.00676	12486	11293	15410	10025	16038	9196.3	12293	9441.9	8217.3	11632	No expres	No expres	Enriched	Moderate	YES		
P23497	Nuclear autoantigen	SP100	100.42	9.9	15	7	28.736	0	55228	31373	32207	57355	32075	67361	48658	66355	22901	60516	Enriched	Moderate	Enriched	Moderate	YES		
P23511-2;P23511	Nuclear transcription	NFYA	33.939	4.4	1	1	2.0663	0.00724	3172.3	2163.3	2685.4	5011.8	2163.2	3061.8	2890.1	3612.4	1473.4	3685.2	No expres	Moderate	Moderate	Low	YES		
P23526;P23526-2	Adenosylhomocystei	AHCY	47.716	45.4	33	33	156.26	0	256440	165860	186090	237520	227720	229490	259430	245620	119870	243670	Moderate	Enriched	Enriched	Enriched	YES		
P23634-7;P23634-(	Plasma membrane cal	ATP2B4	132.59	16.9	21	11	51.448	0	111090	92055	105860	130840	114030	118400	107150	111420	62750	110580	Moderate	Enriched	Enriched	No expres	YES		
P23786	Carnitine O-palmitoy	CPT2	73.776	39.5	37	37	118.28	0	146720	113400	137460	141530	161620	202120	104360	159390	62047	115700	Low	Moderate	Moderate	No expres	YES		
P23919;G5E9E9;P	Thymidylate kinase	DTYMK	23.819	9.4	4	4	8.72	0	2535.8	1899.6	1934.3	2971.5	2294.9	2084.6	1190	1878.6	951.15	2536	Moderate	Low	Moderate	Moderate	YES		
P23946;P23946-2	Chymase	CMA1	27.324	41.7	12	12	87.657	0	139700	62088	102470	123090	62867	71384	105050	114380	50536	112120	Moderate	No expres	No expres	Low	YES		
P24043;A0A087W	Laminin subunit alph	LAMA2	343.9	37.1	172	172	323.31	0	847090	659640	732380	830780	814660	885700	1022800	1039100	505950	931870	Enriched	Moderate	Moderate	Moderate	YES		
P24298	Alanine aminotransfe	GPT	54.636	12.1	5	4	21.171	0	16354	7796.3	4748.7	10656	11905	4482.9	6124.3	5228.2	3204.6	8173.8	Enriched	Low	Low	Moderate	YES		
P24310	Cytochrome c oxidas	COX7A1	9.1174	15.2	2	2	2.6007	0.00273	4645.8	3163.6	5286.3	12084	4181.8	15013	5540.1	9244.4	2046.2	6568.7	No expres	Enriched	Enriched	Moderate			
P24390;M0R1Y2;P	ER lumen protein-ret	KDELR1	24.542	14.2	3	2	4.6035	0.00043	7468.4	6834.2	7937.5	4561.2	12527	6990.6	14056	7590	8911	10160	Moderate	Moderate	Enriched	Enriched			
P24534	Elongation factor 1-b	EEF1B2	24.763	42.2	26	12	200.03	0	184090	108790	120940	170160	110910	311890	166400	251040	57694	179530	Enriched	Enriched	Enriched	Enriched	YES		
P24539;Q5QNZ2	ATP synthase F(0) cc	ATP5F1	28.908	50.4	23	23	139.22	0	253300	186620	211410	260630	257510	224260	220100	276740	101910	269290	Enriched	Enriched	Enriched	Moderate	YES		
P24666;P24666-3	Low molecular weigh	ACP1	18.042	59.5	14	2	32.737	0	60724	48329	52082	57033	65096	74240	102810	136090	50598	71632	Moderate	Enriched	Enriched	Enriched	YES		
P24666-2	Low molecular weigh	ACP1	17.977	57	13	1	4.2163	0.00063	2426.5	1070.1	1345.9	2812.2	995.92	2561.1	1985.2	2902.5	1540	3007.6	Moderate	Enriched	Enriched	Enriched	YES		
P24752	Acetyl-CoA acetyltra	ACAT1	45.199	61.1	56	41	261.47	0	507970	333120	417720	463730	467290	437520	519010	515680	253920	519480	Moderate	Enriched	Enriched	Moderate	YES		
P24752-2	Acetyl-CoA acetyltra	ACAT1	17.175	58	16	0	8.2734	0	16244	7288.9	9823.7	16926	10339	11055	9950.8	8857.1	6025.8	13608	Moderate	Enriched	Enriched	Moderate	YES		
P24844;P24844-2	Myosin regulatory lig	MYL9	19.827	58.7	23	4	43.736	0	2398.6	734.8	550.73	3559.1	934.19	8392.6	8055.4	7750.2	1431.6	16371	No expres	Low	Enriched	Low	YES		
P24928;A0A087W	DNA-directed RNA p	POLR2A	217.17	12	21	21	124.28	0	91863	73176	86754	97498	99083	68080	74845	86896	48667	96053	Enriched	Enriched	Enriched	Enriched	YES		
P25311;C9JEV0	Zinc-alpha-2-glycopr	AZGP1	34.258	45.3	28	28	97.483	0	217380	158900	180050	195640	178180	214220	198140	230650	147870	167840	Moderate	Enriched	Moderate	Low	YES		
P25325;P25325-2;I	3-mercaptopyruvate s	MPST	33.178	44.8	21	21	49.894	0	93166	53992	84437	67785	84747	92595	89599	70549	50320	83708	Enriched	Enriched	Enriched	Enriched	YES		
P25398	40S ribosomal protei	RPS12	14.515	58.3	19	19	66.185	0	159650	81103	104520	244750	126700	162190	276940	281950	161390	193890	Low	No expres	No expres	Enriched	YES		
P25685;P25685-2	DnaJ homolog subfar	DNAJB1	38.044	20.9	6	5	12.428	0	10920	6137.7	6387.2	7878.5	8790.9	7945	6957.4	8244.3	4287.7	8853.7	Enriched	Enriched	Enriched	Moderate	YES		
P25686;P25686-2;(	DnaJ homolog subfar	DNAJB2	35.58	17.6	5	4	13.733	0	18348	17030	15775	14730	22137	16339	15104	14963	9983.4	16303	Moderate	Enriched	Enriched	Enriched	YES		
P25705;P25705-3	ATP synthase subuni	ATP5A1	59.75	55.7	75	8	323.31	0	482670	361680	420780	480480	458520	502410	697070	771460	319940	618880	Enriched	Enriched	Enriched	Moderate	YES		
P25705-2;K7EK77	ATP synthase subuni	ATP5A1	54.493	59.6	68	1	1.9207	0.00814	1517	1099.7	2566.7	974.83	2043.5	7888.4	9345.3	3240.8	2774.2	5106.3	Enriched	Enriched	Enriched	Moderate	YES		
P25786;P25786-2;I	Proteasome subunit a	PSMA1	29.555	47.5	26	26	120.58	0	98947	75605	98246	84790	106270	88464	114830	85373	72203	94715	Enriched	Enriched	Enriched	Enriched	YES		
P25787	Proteasome subunit a	PSMA2	25.898	49.1	23	23	119.46	0	139030	96606	124110	105980	131690	148750	172870	129120	88042	129750	Moderate	Enriched	Enriched	Moderate	YES		
P25788-2;P25788	Proteasome subunit a	PSMA3	27.647	34.3	13	6	30.752	0	56858	31869	44589	36573	48449	67551	67813	53468	41863	50751	No expres	Enriched	Enriched	Moderate	YES		
P25789;H0YMZ1;I	Proteasome subunit a	PSMA4	29.483	42.5	23	23	72.638	0	127970	73238	88672	132860	93640	148400	132160	156030	50139	121800	Enriched	Enriched	Enriched	Enriched	YES		
P25940	Collagen alpha-3(V)	COL5A3	172.12	1.7	2	2	3.821	0.00061	6908.3	7250.9	10783	5778.4	7550.9	9659.7	12754	8725	4332.4	8743.6	Moderate	Moderate	Moderate	No expres	YES		
P26006;P26006-1	Integrin alpha-3;Integ	ITGA3	116.61	3.9	4	4	7.5788	0	12469	12163	12262	11267	13371	8014.5	18977	17095	9950.6	15025	Moderate	Low	Moderate	Moderate	YES		
P26022	Pentraxin-related pro	PTX3	41.975	12.6	4	4	8.3199	0	2329.9	2668.8	1727.1	4028.4	2242.3	4016.4	5683.4	12614	4859.4	7431.8	No expres	Low	Moderate	No expres	YES		
P26038	Moesin	MSN	67.819	54.9	73	42	150.43	0	258170	262510	308230	269480	310660	289510	450250	400320	274530	405470	Moderate	Moderate	Enriched	Enriched	YES		
P26196	Probable ATP-depen	DDX6	54.416	34.2	23	23	145.58	0	154240	148780	171150	126340	214180	124960	222130	168160	115720	172730	Enriched	Enriched	Enriched	No expres	YES		
P26232-3;P26232-	Catenin alpha-2	CTNNA2	95.557	11.5	15	1	5.1768	0.00044	5562.2	1620.6	2855.5	5470	3177	6622.1	3853.4	3768.6	1840.1	4986.3	No expres	No expres	Moderate	Moderate			
P26368-2;P26368;I	Splicing factor U2AF	U2AF2	53.12	21.2	17	17	86.21	0	91174	63809	74928	77819	88194	91966	115900	122130	61600	92466	Enriched	Moderate	Enriched	Enriched	YES		
P26373;P26373-2;	60S ribosomal protei	RPL13	24.261	51.2	29	29	67.642	0	236600	161720	200480	166480	215210	283960	338420	225380	216390	253880	Enriched	Enriched	Enriched	Enriched	YES		
P26447	Protein S100-A4	S100A4	11.728	27.7	4	4	8.113	0	12377	10384	11808	13142	14589	13187	25105	26848	10110	14474	No expres	Moderate	Enriched	Moderate	YES		
P26572	Alpha-1,3-mannosyl-	MGAT1	50.878	13.9	6	6	6.1577	0	3735.7	4160.2	4783.7	3520.4	4127.8	3223.4	2579.1	2291	2673.1	4391	Enriched	Enriched	Enriched	Enriched	YES		
P26583;D6R9A6	High mobility group	HMGB2	24.033	31.1	13	11	27.143	0	30084	26199	32847	24082	43245	33998	91117	107060	39520	40694	Moderate	Enriched	Enriched	Enriched	YES		
P26639;P26639-2	Threonine--tRNA lig	TARS	83.434	47.3	56	48	323.31	0	400480	210180	276880	323400	349570	405370	333780	302630	117830	317750	Moderate	Enriched	Enriched	Moderate	YES		

P26640	Valine--tRNA ligase	VARS	140.47	36.9	72	72	323.31	0	545540	400440	475190	468830	566910	690630	535630	476270	284450	505050	Low	Moderate	Moderate	Enriched	YES		
P26641;P26641-2	Elongation factor 1-g	EEF1G	50.118	54.2	61	61	177.36	0	480570	320660	383320	449990	501020	489230	530580	408340	258370	367110	Enriched	Enriched	Enriched	Enriched	YES		
P26885	Peptidyl-prolyl cis-tr	FKBP2	15.649	38	16	16	60.701	0	173740	122290	118930	217100	129800	162510	132210	148880	108810	141090	Enriched	Enriched	Enriched	Enriched	YES		
P27105;P27105-2	Erythrocyte band 7 ir	STOM	31.73	31.2	8	8	55.695	0	41680	26416	30899	40387	31886	42657	64323	69485	28898	63803	Enriched	Enriched	Enriched	Enriched	YES		
P27169	Serum paraoxonase/a	PON1	39.731	10.1	3	3	12.87	0	11614	13073	13085	11296	11742	10334	11350	11938	7148.9	10419	No expres	No expres	Moderate	No expres	YES		
P27338;P27338-2	Amine oxidase [flavir	MAOB	58.762	35.4	24	18	78.243	0	62959	47927	45812	74169	57463	61930	52811	75113	25856	77741	Moderate	Moderate	Enriched	Moderate	YES		
P27348	14-3-3 protein theta	YWHAQ	27.764	64.1	41	29	323.31	0	109510	92498	103580	96225	128590	111820	223380	297500	94582	128120	Enriched	Enriched	Enriched	Enriched	YES		
P27361;E9PQW4;F	Mitogen-activated pr	MAPK3	43.135	26.4	11	1	18.769	0	22902	18954	25347	23596	28239	18020	20180	20587	9459	24636	Enriched	Low	Enriched	Moderate	YES		
P27635	60S ribosomal protei	RPL10	24.604	32.7	16	2	2.5586	0.00344	5350.9	3455.7	13428	3931.5	5637.9	14820	5025.5	16909	32902	5183.1	Enriched	Enriched	Enriched	Enriched			
P27694	Replication protein A	RPA1	68.137	24.5	18	18	91.191	0	63329	63423	67989	53722	75773	50644	62459	64231	52805	64564	Enriched	Moderate	Enriched	Moderate	YES		
P27695;G3V3M6;C	DNA-(apurinic or apy	APEX1	35.554	55.3	35	17	192.41	0	145340	113360	156710	120520	152910	143060	191840	152810	96386	129010	Enriched	Enriched	Enriched	Low	YES		
P27797;K7EJB9	Calreticulin	CALR	48.141	53	58	58	323.31	0	881640	744610	798570	637830	1113200	719350	933430	838240	363650	589420	Enriched	Enriched	Enriched	Enriched	YES		
P27816;E7EVA0;P	Microtubule-associat	MAP4	121	41	72	31	323.31	0	356940	302980	343070	326590	373910	289080	452120	438710	284490	422440	Enriched	Enriched	Enriched	Enriched	YES		
P27816-5;H7C4C5	Microtubule-associat	MAP4	85.251	35.4	43	2	6.9081	0	8127.4	7416.2	8672.1	8904.7	11287	7277	11368	9939.9	8458.8	10523	Enriched	Enriched	Enriched	Enriched	YES		
P27824;P27824-2;I	Calnexin	CANX	67.567	50	71	45	323.31	0	752300	661850	609470	584910	825920	533170	711010	784380	302670	606500	No expres	Enriched	Enriched	Enriched	YES		
P28062-2;P28062;(	Proteasome subunit b	PSMB8	29.769	19.5	5	4	7.3505	0	5477.1	3617.7	4079.8	7688.4	3483.7	11576	6603.8	9497.5	2858.8	8949.6	Moderate	Low	Enriched	Low	YES		
P28066;P28066-2	Proteasome subunit a	PSMA5	26.411	56.4	26	26	217.07	0	183100	92357	104110	161270	115670	267180	156430	204830	60026	156630	Enriched	Enriched	Enriched	Moderate	YES		
P28070	Proteasome subunit b	PSMB4	29.204	38.3	15	15	304.94	0	104130	64100	63312	90398	74747	113180	132670	114840	72749	99693	Enriched	Enriched	Enriched	Enriched	YES		
P28072	Proteasome subunit b	PSMB6	25.357	25.1	9	9	17.71	0	35893	26447	30246	26918	43175	53108	55793	44289	29514	41610	Enriched	Enriched	Enriched	Enriched	YES		
P28074;P28074-3	Proteasome subunit b	PSMB5	28.48	42.6	17	16	67.46	0	54977	44805	51247	53162	56804	70393	91765	81484	33212	62742	Enriched	Enriched	Enriched	Enriched	YES		
P28288;P28288-2	ATP-binding cassette	ABCD3	75.475	15.8	11	11	47.812	0	61217	53694	57931	70600	49131	66932	53936	71825	36025	67907	Enriched	Enriched	Enriched	Enriched	YES		
P28289;P28289-2	Tropomodulin-1	TMOD1	40.569	16.7	6	6	13.178	0	18978	15137	19662	16433	20374	16581	23215	22578	14282	25909	Enriched	Enriched	Enriched	Low	YES		
P28330	Long-chain specific a	ACADL	47.655	24.9	16	16	88.282	0	66944	43552	48337	19847	78049	20489	41305	42510	24696	37599	No expres	Enriched	Moderate	Enriched	YES		
P28331-4;P28331;I	NADH-ubiquinone o	NDUFS1	73.527	46.6	48	48	323.31	0	237530	173250	194950	225490	238950	200530	264470	266780	133520	245300	Enriched	Moderate	Enriched	Moderate	YES		
P28482-2	Mitogen-activated pr	MAPK1	36.432	35.4	13	0	19.849	0	71669	36132	45129	65807	50107	57676	55337	67605	28057	67808	Enriched	Enriched	Enriched	Low	YES		
P28799-2;P28799;I	Granulins;Acrogranir	GRN	46.991	11.2	6	6	15.302	0	9547	6459.9	10723	5373.7	10065	8397.8	26887	10089	20351	10937	Enriched	Enriched	Enriched	Enriched	YES		
P28838-2;P28838;I	Cytosol aminopeptida	LAP3	52.771	40.2	18	18	108.64	0	93495	67233	85035	120380	84599	170140	96985	152290	65885	133830	Enriched	Enriched	Enriched	No expres	YES		
P28906-2	Hematopoietic proger	CD34	35.01	12.2	7	1	25.974	0	17057	20848	33751	18994	24581	15051	30955	19849	11978	26240	Low	Moderate	Moderate	Moderate	YES		
P29083;C9IYL4	General transcription	GTF2E1	49.452	12.1	5	5	17.543	0	11118	12035	14535	4709.9	19652	7047.7	14010	7669.5	9765.6	9383	Moderate	Moderate	Moderate	Moderate			
P29120-2;P29120	Neuroendocrine conv	PCSK1	79.009	8.5	5	5	9.2003	0	7070.1	6540.5	5945	8895.4	7549.6	6932.2	6524.9	7403.3	5104.7	7374.7	No expres	No expres	Enriched	Enriched	YES		
Q5VZU9;P29144	Tripeptidyl-peptidase	TPP2	139.76	13.7	19	19	53.412	0	96557	86565	92211	89490	118630	73436	111640	91600	62021	93701	Enriched	Low	Moderate	Low	YES		
P29218;P29218-3;I	Inositol monophosph	IMPA1	30.188	34.3	11	11	95.597	0	77041	40472	45702	56950	46175	49829	64841	74788	47950	81123	Enriched	Enriched	Enriched	Moderate	YES		
P29350;P29350-3;I	Tyrosine-protein pho	PTPN6	67.56	23.9	15	14	189.97	0	40221	35332	37809	46048	44024	30146	42155	48088	27149	47660	Enriched	Moderate	Moderate	Low	YES		
P29353-3;P29353-;	SHC-transforming pr	SHC1	46.668	18.5	5	5	18.979	0	52046	44129	45000	51445	58188	33654	36637	59995	20813	53342	Enriched	Enriched	Enriched	Enriched	YES		
P29400;P29400-2	Collagen alpha-5(IV)	COL4A5	161.04	2.3	6	1	5.2761	0	16330	8278.2	9304	16427	11763	24385	13806	18423	4995.1	17877	Low	No expres	Low	Low			
P29401;P29401-2;I	Transketolase	TKT	67.877	47.2	70	70	323.31	0	595980	504770	557950	461340	714920	526000	977580	1128600	396370	542190	Enriched	Enriched	Enriched	Enriched	YES		
P29466-2;P29466;(	Caspase-1;Caspase-1	CASP1	42.888	12.5	5	5	13.491	0	15816	15689	15996	15378	16155	14522	20773	14465	11423	15657	Enriched	Moderate	Moderate	No expres	YES		
P29536-2;P29536	Leiomodin-1	LMOD1	63.783	6.8	3	3	6.9174	0	3747.3	5370.2	3998.7	4209.4	5869	2442.3	2587.8	3707.9	1985.6	4413.4	No expres	Low	No expres	Low	YES		
P29590-4;P29590-;	Protein PML	PML	62.006	15.2	9	9	30.864	0	18719	14969	17611	17117	18600	12260	14026	13296	7873.8	15844	Enriched	Moderate	Moderate	Enriched	YES		
P29622	Kallistatin	SERPINA4	48.541	18.3	8	8	17.852	0	15179	14477	16910	12934	14000	11699	14881	11917	8511.4	12923	Moderate	Enriched	Enriched	Enriched	YES		
P29692-3	Elongation factor 1-d	EEF1D	28.558	61.5	34	0	102.97	0	7436.9	6231.2	8795.6	6538.5	16239	3581.8	11646	6871.6	5835.7	9935.3	Enriched	Enriched	Enriched	Enriched	YES		
P29992;K7EL62	Guanine nucleotide-b	GNA11	42.123	37.3	17	7	50.571	0	83275	57696	74064	90842	74316	76209	107880	94225	51605	97582	Enriched	Enriched	Enriched	Moderate	YES		
P30038;P30038-2;I	Delta-1-pyrroline-5-c	ALDH4A1	61.719	20.6	14	14	31.749	0	51762	52612	49452	44331	68773	64491	70983	61022	33245	51677	Enriched	Low	Low	Enriched	YES		
P30039;P30039-2	Phenazine biosynthes	PBLD	31.785	55.2	33	33	323.31	0	336780	132220	197320	242410	204090	422650	309160	271920	139010	279760	Enriched	Enriched	Enriched	No expres	YES		
P30040;F8VY02	Endoplasmic reticulu	ERP29	28.993	44.4	25	25	73.87	0	264900	219840	213740	215130	252100	255020	242030	192970	117380	162760	Moderate	Enriched	Enriched	Enriched	YES		
P30041	Peroxiredoxin-6	PRDX6	25.035	61.2	45	45	323.31	0	352840	218700	250770	324950	299480	331120	446730	399250	276870	312330	Enriched	Enriched	Enriched	Moderate	YES		
P30043;M0R192;M	Flavin reductase (NA	BLVRB	22.119	49.5	11	11	64.266	0	83358	108280	99678	46061	128440	61959	79549	60146	51494	60243	Moderate	Enriched	Enriched	Moderate	YES		
P30044-2;P30044;I	Peroxiredoxin-5, mito	PRDX5	17.031	74.7	36	36	248.41	0	208710	137830	147140	180170	180260	207910	277760	356850	94224	187860	Enriched	Enriched	Enriched	No expres	YES		
P30046;B5MC82;P	D-dopachrome decarl	DDT;DDTL	12.712	58.5	16	16	190.87	0	153070	108440	150560	207870	143180	181560	233770	223660	112930	178870	Low	Enriched	Enriched	Enriched	YES		
P30048-2;P30048	Thioredoxin-depende	PRDX3	25.838	37	19	19	46.402	0	129200	118660	137120	104900	145020	132750	220030	207650	99025	131470	Moderate	Enriched	Enriched	Moderate	YES		
P30049	ATP synthase subuni	ATP5D	17.49	20.2	5	5	39.718	0	11308	3870.6	5749.1	13876	5077.4	13971	7969.2	6741	3923.2	11246	Enriched	Enriched	Enriched	Enriched	YES		
P30050;P30050-2	60S ribosomal protei	RPL12	17.818	64.2	23	23	185.92	0	171450	118140	136220	129800	199420	150040	213480	144410	143760	136500	No expres	Enriched	Enriched	Enriched	YES		
P30084	Enoyl-CoA hydratase	ECHS1	31.387	61.7	33	33	323.31	0	248620	158130	174110	289230	203110	314930	301560	396700	172990	451970	Enriched	Enriched	Enriched	Enriched	YES		
P30085;P30085-2;(	UMP-CMP kinase	CMPK1	22.222	73	28	28	252.76	0	209970	133260	163900	302160	188010	264260	330330	308240	225170	296650	Moderate	Enriched	Enriched	No expres	YES		
P30086	Phosphatidylethanola	PEBP1	21.057	58.3	34	34	323.31	0	517900	427630	524830	566120	567540	540490	647360	518190	287780	461650	Enriched	Enriched	Enriched	Enriched	YES		
P30101	Protein disulfide-ison	PDIA3	56.782	68.1	99	76	323.31	0	820260	531430	657520	772750	746230	765970	1270300	1095200	543340	832500	Moderate	Enriched	Enriched	Enriched	YES		
P30153;B3KQV6	Serine/threonine-prot	PPP2R1A	65.308	40.9	34	8	184.4	0	258550	155300	211940	243610	224930	296760	367740	252310	154870	263470	Moderate	Enriched	Enriched	Low	YES		
P30154;P30154-3;I	Serine/threonine-prot	PPP2R1B	66.213	18.1	15	3	5.5602	0	11136	9227.2	10793	11320	13807	17934	29209	20460	12706	20348	Enriched	Enriched	Enriched	Enriched	YES		
P30405;R4GN99;P	Peptidyl-prolyl cis-tra	PPIF	22.04	37.2	13	13	163.22	0	93442	86384	86275	73409	113860	69125	123690	75407	70716	90539	Enriched	Enriched	Enriched	Enriched	YES		
P30419;P30419-2	Glycylpeptide N-tetra	NMT1	56.806	26.6	15	15	44.208	0	139700	95761	108130	118240	135190	120390	120750	114520	60201	121130	Enriched	Enriched	Enriched	Enriched	YES		
P30460	HLA class I histocom	HLA-B	40.33	33.4	14	0	23.527	0	13589	10397	53858	10597	71303	33512	20754	14173	12636	13804	Enriched	Enriched	Enriched	Enriched	YES		
P30475;Q95365;Q	HLA class I histocom	HLA-B	40.328	35.6	15	0	121.33	0	51252	36064	41071	51709	50086	56558	100400	90269	40973	88204	Enriched	Enriched	Enriched	Enriched	YES		
P30479	HLA class I histocom	HLA-B	40.539	30.1	12	0	1.8268	0.00975	4611	25363	6482.3	4938	23997	5292.1	10667	4457.9	27493	26448	Enriched	Enriched	Enriched	Enriched	YES		
P30520	Adenylosuccinate syr	ADSS	50.097	19.7	12	12	28.689	0	43004	32020	35074	44275	41561	51048	37792	41527	25567	41865	Moderate	Moderate	Enriched	Low	YES		
P30533	Alpha-2-macroglobul	LRPAP1	41.465	23.8	8	8	28.068	0	49873	50645	66789	51185	63521	39325	46797	48766	27391	49257	Enriched	Enriched	Enriched	Enriched	YES		
P30566;P30566-2;	Adenylosuccinate lya	ADSL	54.889	24.8	14	14	44.405	0	113320	80579	94308	104610	89925	93846	115620	107550	60146	107910	Enriched	Enriched	Enriched	Enriched	YES		
P30711	Glutathione S-transfe	GSTT1	27.335	31.7	12	12	34.681	0	69710	55482	57449	68222	78908	60412	66224	75466	39290	72650	Moderate	Moderate	Moderate	Enriched			
P30740;P30740-2	Leukocyte elastase in	SERPINB1	42.741	43.5	30	30	148.48	0	92500	76888	135700	115280	102800	140180	290010	349100	90720	173790	Enriched	Enriched	Enriched	Enriched	YES		
P30837	Aldehyde dehydroger	ALDH1B1	57.206	37.7	36	26	150.49	0	161880	129300	156630	169480	179420	220900	273740	313300	141330	244590	Enriched	Moderate	Moderate	No expres	YES		
P31040-2;P31040;I	Succinate dehydroger	SDHA	67.299	28.2	30	30	130.71	0	177750	143500	165330	129700	214180	126530	170660	146410	81333	156780	Enriched	Enriched	Enriched	Enriched	YES		
P31146;H3BRY3	Coronin-1A;Coronin	CORO1A	51.026	16.1	8	8	15.667	0	35229	36103	40251	34474	45539	36259	56061	63815	46718	51910	Low	No expres	No expres	No expres	YES		
P31150	Rab GDP dissociation	GDI1	50.582	58.6	50	26	138.02	0	123800	112840	137740	108760	163280	147390	187860	192810	99533	133160	Enriched	Enriched	Enriched	Enriched	YES		
P31153;P31153-2	S-adenosylmethionin	MAT2A	43.66	42.3	19	12	95.824	0	102860	78197	77844	86786	96214	102430	131950	102190	59708	105800	Enriched	Enriched	Enriched	No expres	YES		
P31323	cAMP-dependent pro	PRKAR2B	46.302	33	18	11	37.406	0	23156	17847	21346	31016	19944	28750	43259	97515	23159	38476	No expres	Moderate	Enriched	Moderate	YES		
P31431-2;P31431	Syndecan-4	SDC4	16.545	28.1	4	4	11.615	0	34542	32404	26792	22795	32665	17599	32038	22025	32079	33665	Enriched	Enriched	Enriched	Low	YES		
P31689;P31689-2	DnaJ homolog subfar	DNAJA1	44.868	55.7	18	18	69.259	0	79226	52838	62778	79120	80288	70986	78504	93320	48085	89096	Enriched	Enriched	Enriched	Enriched	YES		
P31930	Cytochrome b-c1 cor	UQCRC1	52.645	44.2	37	37	323.31	0	134000	97487	102200	164740	141190	139720	115520	209770	66179	161180	Low	Enriched	Enriched	Moderate	YES		
P31937	3-hydroxyisobutyrate	HIBADH	35.329	34.2	16	16	75.149	0	63892	40399	51998	59685	62295	61305	62185	52817	37987	63092	Moderate	Enriched	Enriched	No expres	YES		
P31939-2;P31939	Bifunctional purine b	ATIC	64.523	41.3	43	43	323.31	0	266560	177180	215250	264000	241850	230040	258100	282820	150520	255960	Low	Enriched	Enriched	Moderate	YES		
P31942-2;P31942;I	Heterogeneous nucle	HNRNPH3	35.238	30.8	13	10	45.401	0	38444	35268	42927	61783	50252	46831	72309	69657	44747	50504	Enriched	Enriched	Enriched	Enriched	YES		
P31946-2;P31946	14-3-3 protein beta/a	YWHAB	27.85	70.1	40	23	323.31	0	119160	100300	113310	145010	113870	129170	195090	374440	100320	169720	Enriched	Enriched	Enriched	Enriched	YES		
P31947-2;P31947	14-3-3 protein sigma	SFN	24.336	16.2	6	2	3.9503	0.00061	2792.3	1340.6	2732.4	2005.3	3090.3	7687.5	28471	18861	12439	8151.6	Enriched	Enriched	Enriched	Enriched	YES		
P31948;P31948-2;I	Stress-induced-phosp	STIP1	62.639	40.1	48	48	242.45	0	350900	288650	321220	350990	335230	392670	377710	340930	217660	361110	Moderate	Moderate	Enriched	Moderate	YES		
P31949	Protein S100-A11;Pr	S100A11	11.74	55.2	11	11	36.858	0	55255	45104	59274	90299	53936	78210	159740	212400	111420	115410	Enriched	Enriched	Enriched	Low	YES		
P32004-3;P32004-;	Neural cell adhesion	L1CAM	138.91	6.2	7	7	29.485	0	18787	16110	22234	12707	23492	12568	19947	13514	10659	23273	Low	No expres	Moderate	No expres	YES		
P32119;A6NIW5	Peroxiredoxin-2	PRDX2	21.892	51	34	28	111.92	0	208790	145830	176660	230900	170730	241590	246920	225550	125690	216210	Enriched	Enriched	Enriched	Enriched	YES		
P32321;P32321-2;I	Deoxycytidylate dear	DCTD	20.016	28.1	3	3	7.4167	0	6529	2740.8	3434.8	6877.2	4477	2529	1459.6	1772.7	1683	3556	Moderate	Enriched	Enriched	Enriched	YES		
P32455	Interferon-induced gu	GBP1	67.93	5.6	5	1	5.9693	0	3526.4	3350.3	4270	4530	3568.9	2274.6	3717.8	3140.8	2789.1	3954.5	Enriched	No expres	Enriched	No expres	YES		
P32519-2;P32519;(	ETS-related transcrip	ELF1;DKFZp686H0575	64.928	9.1	4	4	16.905	0	11957	8163.7	11751	8160.1	14242	7597.5	10324	11079	5766	9796.5	Enriched	Low	Enriched	No expres	YES		
P32929;P32929-3;I	Cystathionine gamma	CTH	44.508	40.2	22	22	142.56	0	127860	82517	107430	103760	108050	127960	231740	211220	85711	121850	Low	Low	Moderate	No expres	YES		
P32969;D6RAN4;F	60S ribosomal protei	RPL9	21.863	58.3	31	7	20.409	0	97812	48488	64415	74388	69245	85427	64390	52275	139300	67017	No expres	Enriched	Enriched	Low	YES		
P33121-2;P33121;I	Long-chain-fatty-acid	ACSL1	76.87	17.3	11	11	35.459	0	84895	73227	68148	114460	73219	87025	62557	75337	38700	150730	Enriched	Enriched	Enriched	Enriched	YES		
P33176	Kinesin-1 heavy chai	KIF5B	109.68	39.3	49	49	245.54	0	217520	147550	181490	200570	215750	231300	323250	277860	154800	227180	Enriched	Enriched	Enriched	No expres	YES		
P33241;P33241-3;(	Lymphocyte-specific	LSP1	37.191	11.8	4	4	21.046	0	5724.4	6930	7530.9	5303	6841	5387.9	13469	7408.3	6587.1	8051.7	Enriched	Low	Low	Low	YES		
P33316;H0YNW5;I	Deoxyuridine 5-triph	DUT	26.563	17.1	5	5	16.243	0	15589	19059	17329	13581	19725	16772	16799	12013	13780	15699	Enriched	Enriched	Enriched	Enriched	YES		
P33402;P33402-3;I	Guanylate cyclase so	GUCY1A2	81.749	4.2	3	3	3.4253	0.00079	4118.2	4497.2	5110.2	6786.6	6402.2	4128.2	3117.3	8612.4	1977.7	5132.8	Low	No expres	Low	Moderate	YES		
P33908;P33908-2	Mannosyl-oligosacch	MAN1A1	72.968	16.7	12	12	23.606	0	45903	33750	41524	51070	46201	46368	45220	51979	22503	45600	Enriched	Enriched	Enriched	Low	YES		
P33947;O43731;O	ER lumen protein-ret	KDELR2;KDELR3	24.422	9	2	1	2.5527	0.00344	1667.4	950.57	1120	1076.6	2515	1261.2	5068.1	906.57	2289.6	2534.3	Enriched	Enriched	Enriched	Enriched			
P34059;H3BP66	N-acetylgalactosamin	GALNS	58.025	9.8	6	6	13.88	0	27520	24699	24611	26699	26670	28991	23611	24846	16885	26727	Enriched	Low	Moderate	Enriched	YES		
P34096	Ribonuclease 4	RNASE4	16.84	34.7	4	4	9.3557	0	8804.6	7081.9	7055.2	8374.7	6507.3	6090.7	7704.6	7724.2	5788.7	7984.5	Enriched	Enriched	Enriched	Enriched	YES		
P34896-2;P34896;I	Serine hydroxymethy	SHMT1	49.027	24.1	15	14	35.141	0	32944	30578	35534	34298	41881	32788	45078	32089	27876	33818	Enriched	Enriched	Enriched	Low	YES		
P34897-3;P34897;I	Serine hydroxymethy	SHMT2	53.454	40	27	26	101.39	0	68067	60643	78502	59794	114180	68842	108940	91710	53236	86887	Enriched	Enriched	Enriched	Moderate	YES		
P34932;A0A087W	Heat shock 70 kDa pr	HSPA4	94.33	48.3	62	55	193.64	0	336050	238950	263330	287560	309620	294860	336920	342900	178450	257270	Moderate	Enriched	Enriched	Low	YES		
P35030-5;P35030-;	Trypsin-3	PRSS3	25.924	53.8	54	28	323.31	0	236550	202150	188790	302810	288570	541180	280070	183720	110040	300960	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P35221;P35221-2;(	Catenin alpha-1	CTNNA1	100.07	40.2	65	40	323.31	0	350060	276290	321160	298930	309600	321320	403520	475180	193500	398460	Enriched	Enriched	Enriched	Enriched	YES		
P35232;C9JW96;E	Prohibitin	PHB	29.804	72.1	36	36	102.99	0	201010	137700	156860	195460	201710	245020	251850	256890	123730	263310	Moderate	Enriched	Enriched	Enriched	YES		
P35241;P35241-5;I	Radixin	RDX	68.563	43.2	54	23	100.45	0	238010	118730	136340	151930	158920	151640	177240	169610	90593	180250	Low	Enriched	Enriched	Enriched	YES		
P35249;C9JXZ7;C	Replication factor C	RFC4	39.681	10.2	3	3	16.674	0	8964.5	3895	4290.3	7089.8	4227.9	5788.8	3943.2	9621.2	2766.3	6942.6	Low	Moderate	Enriched	Enriched	YES		
P35250;A0A087W	Replication factor C	RFC2	39.157	12.7	4	4	13.504	0	9126.9	7011.3	7643.4	7722.1	10278	8409.5	6345	8345.6	3001.3	7667.3	Low	Low	Moderate	No expres	YES		
P35251-2;P35251;I	Replication factor C	RFC1	128.18	5.9	8	8	22.933	0	1484.5	1141	1291.1	3180.9	1305.9	7560.7	1928.1	3058.9	1863.6	2648.6	Moderate	Enriched	Enriched	Moderate	YES		
P35269;M0QXD6	General transcription	GTF2F1	58.24	8.5	3	3	21.273	0	10415	9509	8061.2	9838.1	10024	6057.3	6590	8236	6491.8	8997	Enriched	Moderate	Enriched	Enriched	YES		
P35270	Sepiapterin reductase	SPR	28.048	57.9	27	27	87.954	0	120530	89877	96107	125150	112210	144620	155630	179560	76291	132810	Enriched	Enriched	Enriched	Enriched	YES		
P35475;D6REB5;I	Alpha-L-iduronidase	IDUA	72.669	7.7	4	4	16.027	0	29580	24632	30420	26878	22487	27853	22940	15573	14979	22430	Enriched	Enriched	Moderate	Moderate	YES		
P35520;P35520-2	Cystathionine beta-sy	CBS	60.586	16.9	10	10	41.115	0	58237	38834	39518	23633	35479	34782	58996	29455	18212	23775	Low	Enriched	Enriched	No expres	YES		
P35555	Fibrillin-1	FBN1	312.24	35.7	161	156	323.31	0	900770	891770	958860	819590	1130500	923770	1312800	2313100	527700	1348600	No expres	Low	Enriched	Low	YES		
P35558	Phosphoenolpyruvate	PCK1	69.194	7.2	6	2	2.2698	0.00494	1987.7	1502.6	1639.3	1088.9	2778.5	665.42	1659.5	1091.3	420.5	1201.9	Moderate	No expres	Moderate	Moderate	YES		
P35573-2;P35573-;	Glycogen debranchin	AGL	172.62	11.5	13	13	24.468	0	64343	50757	60760	80186	64926	69163	66302	63351	34573	70888	Low	Moderate	Enriched	Enriched	YES		
P35579;P35579-2	Myosin-9	MYH9	226.53	64.5	332	261	323.31	0	2048000	1530100	1661100	2179000	1834500	1900100	3306100	3505400	2008400	2714300	Enriched	Enriched	Enriched	Enriched	YES		
P35580-2;P35580-	Myosin-10	MYH10	230.78	44.4	124	1	323.31	0	340830	309350	345270	397110	383820	343140	483710	552350	304470	502630	Moderate	Enriched	Enriched	Moderate	YES		
P35606-2;P35606	Coatomer subunit bet	COPB2	99.045	41.8	66	66	323.31	0	479030	418420	409550	426500	518030	533100	590890	558910	300660	508390	Enriched	Enriched	Enriched	Enriched	YES		
P35610;B1APM4	Sterol O-acyltransfer	SOAT1	64.734	13.6	10	10	105.72	0	77731	70155	70913	90035	74507	66748	83353	104530	54062	100360	No expres	Moderate	Enriched	No expres	YES		
P35612-2;P35612-(	Beta-adducin	ADD2	62.466	1.8	1	1	2.3643	0.00428	2438.4	1874.3	1546.4	2034.2	1954.9	1572.8	1378.6	1929.9	620.94	1810.6	Enriched	Moderate	Moderate	Moderate	YES		
P35613;P35613-2;I	Basigin	BSG	42.2	18.4	8	3	20.114	0	54801	61312	51300	47729	67407	34207	44900	30472	41519	38032	Low	Enriched	Enriched	Moderate	YES		
P35613-3;R4GMX	Basigin	BSG	19.438	33.5	7	2	9.316	0	1071.7	2713.8	2474.3	485.16	3046.4	474.03	1469.6	691.58	789.41	741.06	Low	Enriched	Enriched	Moderate	YES		
P35658-2;P35658-	Nuclear pore comple	NUP214	212.57	9.7	19	19	54.915	0	54689	38601	46742	52479	54743	40858	35096	36769	19367	48211	Enriched	Enriched	Moderate	Enriched	YES		
P35659;B4DFG0;P	Protein DEK	DEK	42.674	23.7	15	15	76.617	0	48590	23880	38530	43226	37829	48375	75566	80522	42946	70347	Enriched	Enriched	Enriched	Enriched	YES		
P35749;B1PS43	Myosin-11	MYH11	227.34	48.2	166	0	35.911	0	3363.1	3761.6	2528	1704.8	6424.7	2172.5	2574.3	2399.5	1036.5	4230.3	Enriched	Moderate	Moderate	Low	YES		
P35749-3	Myosin-11	MYH11	224.33	49	165	0	9.6878	0	7928.1	12024	7732.6	5710.1	7931.9	12124	11999	7671.6	4321.9	9440.4	Enriched	Moderate	Moderate	Low	YES		
P35749-4	Myosin-11	MYH11	223.57	48.9	167	0	323.31	0	511860	571620	379330	363490	586350	599420	773260	655750	310850	1006200	Enriched	Moderate	Moderate	Low	YES		
P35754	Glutaredoxin-1	GLRX	11.776	33	5	5	10.284	0	23090	38534	27911	27666	28203	15235	21438	20179	13332	22471	Enriched	Moderate	Enriched	Moderate	YES		
P35813;P35813-3;I	Protein phosphatase	PPM1A	42.447	22.3	11	8	27.637	0	54496	34811	40992	47373	48707	42999	31583	38241	17737	42181	Enriched	Enriched	Enriched	Moderate	YES		
P35858;P35858-2	Insulin-like growth fa	IGFALS	66.034	5	3	3	3.523	0.00079	3253.7	2722.1	3025.1	2334.9	4206.2	3843.5	3642.6	3313.1	1689	2866.4	Moderate	Moderate	Low	Low			
P35914;P35914-3;I	Hydroxymethylglutar	HMGCL	34.36	35.1	16	16	29.261	0	66962	57504	61604	56567	72055	55911	70635	65860	53641	67432	Enriched	Enriched	Enriched	Moderate	YES		
P35998;P35998-2	26S protease regulato	PSMC2	48.633	49.9	28	27	87.343	0	153310	108010	136490	119830	145510	113330	115540	123650	62245	124720	Enriched	Enriched	Enriched	Enriched	YES		
P36021	Monocarboxylate tra	SLC16A2	59.511	6.5	3	3	10.426	0	12578	13477	13428	10991	17933	8691.9	12499	10807	6614.3	11465	Low	Moderate	Moderate	No expres	YES		
P36269-2;P36269;I	Gamma-glutamyltran	GGT5	58.992	15	12	12	72.377	0	31980	26758	30609	40851	33148	35905	61727	59309	21406	42636	No expres	No expres	No expres	Moderate	YES		
P36404;V9GYD0;F	ADP-ribosylation fac	ARL2;ARL2-SNX15	20.878	19	5	5	13.104	0	18085	12196	12919	13918	13510	31013	44707	49999	15346	29386	Moderate	Enriched	Enriched	Enriched	YES		
P36405	ADP-ribosylation fac	ARL3	20.455	29.7	5	5	9.2782	0	18680	13732	17257	27561	18893	22632	18943	24769	9855.8	19705	Enriched	Enriched	Enriched	Moderate	YES		
P36507;G5E9C7	Dual specificity mito	MAP2K2	44.424	32.5	14	5	17.325	0	15376	11089	12312	20825	14288	13104	14347	17560	10819	14492	Moderate	Enriched	Enriched	Enriched	YES		
P36542;P36542-2	ATP synthase subuni	ATP5C1	32.996	33.2	16	16	51.126	0	66735	44904	54205	56738	58540	110170	117660	199230	58845	100790	Enriched	Enriched	Enriched	Enriched	YES		
P36543;P36543-2;(	V-type proton ATPas	ATP6V1E1	26.145	27.9	13	8	76.57	0	102860	84441	101180	103940	114790	107840	111040	143010	57013	92808	Enriched	Enriched	Enriched	Enriched	YES		
P36551	Oxygen-dependent co	CPOX	50.151	11.7	5	5	58.05	0	16909	15723	17015	22034	22161	14987	18483	16658	13237	24233	Low	Low	Moderate	Low	YES		
P36578;H3BM89	60S ribosomal protei	RPL4	47.697	49.4	58	58	323.31	0	548190	292460	367610	538060	435050	736750	584890	476100	257990	507750	Enriched	Enriched	Enriched	Enriched	YES		
P36871;P36871-2;I	Phosphoglucomutase	PGM1	61.448	63.9	64	64	323.31	0	458030	332110	377460	494630	403640	402270	489370	548390	245480	458360	Enriched	Enriched	Enriched	Enriched	YES		
P36915;A2AB27	Guanine nucleotide-b	GNL1	68.66	14.8	12	12	32.708	0	54557	45358	55061	44979	60174	45353	60288	62987	38655	55074	Enriched	Moderate	Moderate	Enriched	YES		
P36955	Pigment epithelium-d	SERPINF1	46.312	31.3	16	16	49.449	0	47719	37043	43242	50519	43856	48974	78488	190920	38433	72890	Low	Enriched	Enriched	Enriched	YES		
P36957;P36957-2;(	Dihydrolipoyllysine-r	DLST	48.755	24.1	18	18	68.924	0	63204	47004	57616	66357	77794	70015	87015	100460	50484	76316	No expres	No expres	No expres	Moderate	YES		
P36959	GMP reductase 1	GMPR	37.418	17.4	7	6	13.375	0	7056.4	17498	10392	8388.5	13700	10609	6136.5	3814.1	3372.5	5942.5	Moderate	Moderate	Moderate	Enriched	YES		
V9GYE7;P36980-2	Complement factor H	CFHR2	28.912	20.9	5	3	4.6956	0.00043	9092.6	11345	10132	11194	12248	13142	11006	51880	7375.5	13941	Moderate	No expres	Low	Low	YES		
P37059	Estradiol 17-beta-del	HSD17B2	42.785	8.5	3	3	11.318	0	14469	17419	14625	12065	18371	12998	19056	16750	9366.1	14489	Enriched	Enriched	Enriched	Low	YES		
P37198;M0QXN5	Nuclear pore glycopr	NUP62	53.254	10.5	13	13	32.53	0	22562	17920	22556	29947	22952	26998	26402	35300	16230	26173	Enriched	Low	Enriched	Moderate	YES		
P37235;E9PC71;P	Hippocalcin-like prot	HPCAL1;HPCA	22.313	48.7	10	10	38.777	0	49093	41414	49964	51450	55089	46836	78196	52389	50405	55433	Enriched	Enriched	Enriched	Enriched	YES		
P37802;P37802-2;	Transgelin-2	TAGLN2	22.391	79.9	43	40	323.31	0	325920	222810	241510	403280	288030	396510	467990	522850	202440	418940	Moderate	Enriched	Enriched	Enriched	YES		
P37837;F2Z393	Transaldolase	TALDO1	37.54	54	34	34	159.32	0	255010	153030	196450	197380	222060	262740	497540	389410	233910	314280	Enriched	Enriched	Enriched	Moderate	YES		
P38117;P38117-2;I	Electron transfer flav	ETFB	27.843	46.7	20	20	45.413	0	116090	121870	120010	98928	133440	74390	101340	136320	50091	102670	Enriched	Enriched	Enriched	Enriched	YES		
P38159;H0Y6E7;H	RNA-binding motif p	RBMX	42.331	48.8	35	7	208.81	0	174800	112170	155000	183710	174060	148480	219590	186400	128530	205550	Enriched	Enriched	Enriched	Moderate	YES		
P38606-2;P38606	V-type proton ATPas	ATP6V1A	64.735	37.7	36	36	133.14	0	191830	147710	168680	172610	182360	155320	181470	160300	123590	162420	Enriched	Enriched	Enriched	Enriched	YES		
P38646	Stress-70 protein, mit	HSPA9	73.68	62.3	89	86	323.31	0	529580	453260	479880	534710	653450	543050	977770	990460	412690	713440	Enriched	Enriched	Enriched	Enriched	YES		

P38919	Eukaryotic initiation	EIF4A3	46.871	35.8	24	18	105.06	0	86695	62294	76533	85433	79648	89862	183120	183010	90037	103870	Enriched	Enriched	Enriched	Moderate	YES		
P39019;A0A075B6	40S ribosomal protei	RPS19	16.06	64.8	22	12	100.85	0	71849	46518	61604	66519	71478	144600	166000	131860	72340	92218	Enriched	Enriched	Enriched	Enriched	YES		
P39023;G5E9G0;H	60S ribosomal protei	RPL3	46.108	50.1	49	17	263.54	0	333120	253740	315210	277860	349580	334650	482340	324420	336360	328830	Enriched	Enriched	Enriched	Enriched	YES		
P39060-2;P39060-	Collagen alpha-1(XV	COL18A1	135.76	14.2	41	41	207.3	0	180780	113840	153430	217000	180930	249630	256010	320830	125130	217870	Enriched	Enriched	Enriched	Moderate	YES		
P39656;P39656-2;I	Dolichyl-diphosphoo	DDOST	50.8	25.9	30	18	141.54	0	130780	75959	89881	106830	107550	111220	100180	94714	32268	76841	Moderate	Enriched	Enriched	Enriched	YES		
P39687;H0YN26	Acidic leucine-rich n	ANP32A	28.585	39	20	13	176.91	0	130310	82882	69500	174450	76429	89686	137210	183090	65758	108100	Enriched	Enriched	Enriched	Enriched	YES		
P39748	Flap endonuclease 1	FEN1	42.592	13.9	5	2	47.675	0	12476	8402	10088	7208.4	13626	8524.1	10944	6628.4	5767.8	9807.3	Moderate	Moderate	Enriched	Enriched	YES		
P40121;E7ENU9;P	Macrophage-capping	CAPG	38.498	32.8	15	15	121.01	0	100690	91698	88610	87398	97299	87656	114760	94486	96217	118040	Moderate	Moderate	Moderate	Low	YES		
P40222	Alpha-taxilin	TXLNA	61.89	10.6	6	6	50.542	0	23392	21399	23619	24854	22688	22511	31266	24779	33055	34508	Moderate	Low	Enriched	Low	YES		
P40227;P40227-2	T-complex protein 1	CCT6A	58.024	42.2	33	33	95.561	0	221120	161550	195840	218140	243710	147200	152680	156680	79312	159790	Enriched	Enriched	Enriched	Moderate	YES		
P40261	Nicotinamide N-meth	NNMT	29.574	19.3	5	5	23.911	0	7518.1	18497	8985.5	10346	10492	5315.4	7801.1	10990	7836.5	10606	Enriched	Enriched	Enriched	Moderate	YES		
P40313;I3NI28	Chymotrypsin-like pr	CTRL	28.002	16.7	12	11	15.965	0	38521	29021	30112	39357	34901	33831	29498	28345	19120	27612	Moderate	Enriched	Enriched	Enriched	YES	YES	YES
P40616-2;P40616;I	ADP-ribosylation fac	ARL1	18.565	39	10	10	64.004	0	59526	38743	45021	85499	50349	55101	73904	112980	31402	68152	Enriched	Enriched	Enriched	Moderate	YES		
P40763-3;P40763;I	Signal transducer and	STAT3	83.125	28.9	25	25	64.286	0	109220	78277	100690	122180	95939	84061	92859	141350	56335	111020	Enriched	Enriched	Enriched	Enriched	YES		
P40818;P40818-2	Ubiquitin carboxyl-te	USP8	127.52	7.5	7	7	15.884	0	10961	11040	9843.5	10556	12879	9410.7	10198	10980	7815	12215	No expres	Moderate	Enriched	Low	YES		
Q5QNY5;P40855-5	Peroxisomal biogenes	PEX19;DCAF8	26.137	17.9	3	2	8.5151	0	9627.3	6373.5	8943.3	13582	10179	10313	12301	12086	7501.5	14656	Low	Moderate	Enriched	Moderate	YES		
P40925;P40925-3;I	Malate dehydrogenas	MDH1	36.426	49.4	42	26	178.2	0	285270	191210	229060	418180	222020	445950	427340	477540	164960	366980	Enriched	Enriched	Enriched	Enriched	YES		
P40926;P40926-2;(	Malate dehydrogenas	MDH2	35.503	60.7	50	50	273.69	0	355230	255410	315030	370840	328030	499700	659700	808580	294560	491160	Enriched	Enriched	Enriched	Enriched	YES		
P40937-2;P40937;I	Replication factor C	RFC5	36.104	17.2	6	6	7.259	0	26175	25354	29743	24854	29183	29162	25836	24375	12497	24759	Moderate	Moderate	Moderate	No expression			
P40939	Trifunctional enzyme	HADHA	82.999	51	94	94	323.31	0	624410	461750	535210	846590	590700	604580	737860	983570	367270	766270	No expres	Enriched	Enriched	Enriched	YES		
P41091;Q2VIR3;F8	Eukaryotic translatio	EIF2S3;EIF2S3L	51.109	35.6	20	20	170.96	0	200290	145310	147800	155390	259860	122810	73421	82630	39406	103090	Enriched	Enriched	Enriched	Low	YES		
P41208	Centrin-2	CETN2	19.738	43	9	9	27.75	0	37047	41417	42242	36982	48882	23740	29849	30315	16612	30846	Enriched	Enriched	Enriched	Enriched	YES		
P41214;Q5SY38;P4	Eukaryotic translatio	EIF2D	64.706	13.9	6	6	40.501	0	75298	45823	54454	56411	67228	50502	46056	40640	24066	49564					YES		
P41219;P41219-2;I	Peripherin	PRPH	53.65	37.2	28	21	50.859	0	113950	75072	95980	112670	95603	100510	110050	126780	81989	160950	Low	Low	Moderate	Enriched	YES		
P41222	Prostaglandin-H2 D-i	PTGDS	21.029	16.3	3	3	7.7308	0	24689	22321	26902	25215	23112	24198	26725	55176	14038	26962	No expres	Moderate	Enriched	Enriched	YES		
P41227;P41227-2	N-alpha-acetyltransfe	NAA10	26.458	35.3	11	11	42.132	0	47969	38408	35335	25464	48789	44312	42033	42018	22677	35369					YES		
P41240	Tyrosine-protein kina	CSK	50.704	7.1	3	3	6.7236	0	8259.7	5983.8	7787.8	5979.2	6904.9	8551.9	8592.6	7289.2	5644.2	6599.6	Enriched	Moderate	Moderate	Enriched	YES		
P41250	Glycine--tRNA ligase	GARS	83.165	34.8	47	47	197.78	0	320520	211620	277810	267590	331810	445450	498430	414700	237440	297090	Enriched	Enriched	Enriched	Enriched	YES		
P41252;A0A0A0M	Isoleucine--tRNA lig	IARS	144.5	28.1	55	55	178.26	0	273440	166480	215920	198930	270270	309320	307150	240550	112450	212180	Enriched	Enriched	Enriched	Enriched	YES		
P41743;Q05513-2;	Protein kinase C iota	PRKCI;PRKCZ	68.262	2.7	2	2	20.106	0	1417.2	883.78	1257.5	2872.2	817.48	1605.1	1432.6	2534.7	1016.9	1758.2	Enriched	Moderate	Enriched	Low			
P42025	Beta-centractin	ACTR1B	42.293	24.2	15	8	161.59	0	93612	62394	76564	64460	76840	98318	69504	53143	34643	72552	Enriched	Enriched	Enriched	Enriched	YES		
P42126;P42126-2;(	Enoyl-CoA delta isor	ECI1;DCI	32.816	29.8	19	19	96.852	0	89395	55303	75065	95216	109700	75582	108310	115330	46431	128220	Enriched	Enriched	Enriched	Enriched	YES		
P42166	Lamina-associated pc	TMPO	75.491	21	18	5	5.8692	0	18533	12994	15939	20941	17744	14494	15621	21501	14264	20567	Moderate	Enriched	Enriched	No expres	YES		
P42167	Lamina-associated pc	TMPO	50.67	37.4	27	1	95.53	0	167550	127330	181060	117490	221240	124470	170410	180380	114350	149420	Moderate	Enriched	Enriched	No expres	YES		
P42167-2;P42167-3	Lamina-associated pc	TMPO	38.737	41.7	23	2	7.0049	0	2863.1	1701.4	1797.4	1977.2	2050.8	1351	1254.6	1247.2	1026.3	3053.3	Moderate	Enriched	Enriched	No expres	YES		
P42224;J3KPM9;P4	Signal transducer and	STAT1	87.334	17.9	14	14	33.244	0	65667	67122	77750	76572	80086	60157	77831	86722	42080	71554	Enriched	Enriched	Enriched	Enriched	YES		
P42226-2;P42226-3	Signal transducer and	STAT6	74.456	9.1	5	4	8.049	0	28437	28464	28755	22666	30669	21403	30394	28602	21149	23961	Enriched	Enriched	Enriched	Enriched	YES		
P42285	Superkiller viralicidic	SKIV2L2	117.8	15.8	16	15	29.395	0	43448	29623	39431	50449	38479	41297	48358	56864	22905	51338	Moderate	Enriched	Enriched	Low	YES		
P42330-2	Aldo-keto reductase f	AKR1C3	23.364	39.7	14	2	45.156	0	34089	36021	17699	16569	27517	24126	14388	20934	4079.1	30331	Enriched	Enriched	Enriched	Enriched			
P42338;H0Y871;Q	Phosphatidylinositol	PIK3CB;DKFZp779K12	122.76	3.5	4	4	10.276	0	14253	6592	8288	10828	13211	13818	13172	12388	6600.1	11382	Moderate	Enriched	Enriched	Moderate			
P42345	Serine/threonine-prot	MTOR	288.89	2.8	7	7	15.312	0	15540	16071	14646	14559	14547	14408	14151	22135	7738.1	14716	Moderate	Low	Moderate	Moderate	YES		
P42566;B1AUU8;P	Epidermal growth fac	EPS15	98.655	7.5	5	5	18.607	0	25055	25914	21507	20062	27444	19424	20898	20898	11712	20389	Low	Enriched	Enriched	Enriched	YES		
Q5T4L4;P42677	40S ribosomal protei	RPS27	7.3564	37.9	7	2	38.086	0	80532	65691	72788	67357	94227	78957	116050	92600	45960	65900	Enriched	Enriched	Enriched	Enriched	YES		
P42704	Leucine-rich PPR mo	LRPPRC	157.9	38.3	76	76	323.31	0	502740	386810	447040	428880	508530	404070	439210	516740	219000	477270	Enriched	Enriched	Enriched	Enriched	YES		
P42765;K7EME0	3-ketoacyl-CoA thiol	ACAA2	41.924	43.8	28	28	282.26	0	187970	136400	140080	191850	186350	147230	273550	325010	106590	210050	No expres	Enriched	Enriched	Enriched	YES		
P42766;F2Z388	60S ribosomal protei	RPL35	14.551	51.2	17	17	261.68	0	312480	171990	209270	256200	293710	489590	287550	222120	222360	228370	No expres	Enriched	Enriched	Enriched	YES		
P42773	Cyclin-dependent kir	CDKN2C	18.127	28	4	4	23.805	0	5487.6	2552.7	3471.5	7223.4	2747.8	4556.8	4274.3	5700.5	3671.2	5802	Low	Moderate	Moderate	Enriched	YES		
P42785;P42785-2;I	Lysosomal Pro-X car	PRCP	55.799	4.8	2	2	24.61	0	18003	10380	16612	10431	23667	11292	12673	14689	5009.1	11781	Enriched	Enriched	Enriched	Moderate	YES		
P42892-2;B4DKB2	Endothelin-convertin	ECE1	85.807	11.2	6	5	21.62	0	12811	7821	6317.9	14073	7784	7711.4	5469.9	9073.6	2756	12092	Enriched	Moderate	Enriched	Low			
P43004-3;P43004-2	Excitatory amino acid	SLC1A2	61.007	10.8	6	6	12.163	0	9118.7	6844.3	7965.4	6623.8	11209	9121.5	13303	9100.1	5636.8	11602	Low	Enriched	Moderate	No expres	YES		
P43007	Neutral amino acid tr	SLC1A4	55.722	8.5	4	4	62.185	0	27710	24228	20013	23431	28347	27417	21869	14428	15073	21683	Enriched	Enriched	Enriched	Enriched	YES		
P43034	Platelet-activating fac	PAFAH1B1	46.637	38.8	30	30	163.79	0	183810	143370	178670	138290	189540	180770	293500	234660	128640	188570	Low	Enriched	Enriched	Enriched	YES		
P43121	Cell surface glycopro	MCAM	71.607	11.3	10	10	25.874	0	32752	33647	39116	26668	42341	32393	44548	29110	23794	50942	Enriched	Moderate	Moderate	No expres	YES		
P43155-2;P43155;I	Carnitine O-acetyltra	CRAT	68.568	35	34	26	131.08	0	129360	182680	107030	113730	150410	115020	129280	91117	97274	124820	Enriched	Enriched	Enriched	Enriched	YES		
P43243;A8MXP9;I	Matrin-3	MATR3	94.622	33.9	50	50	231.66	0	230150	211620	254480	222890	286800	203820	307870	252940	193120	256150	Enriched	Enriched	Enriched	Low	YES		
P43246-2;P43246;	DNA mismatch repair	MSH2	97.321	9.9	10	10	15.765	0	21121	10437	14378	38116	12525	28932	22977	22878	11606	29197	No expres	Low	Moderate	Moderate	YES		
P43304;P43304-2	Glycerol-3-phosphate	GPD2	80.852	23.5	22	22	80.82	0	30600	23741	29687	28095	34411	35230	70565	54380	44261	41633	Low	Enriched	Enriched	Low	YES		
P43405-2;P43405	Tyrosine-protein kina	SYK	69.509	3.6	3	3	4.3934	0.00063	10715	7822.9	9073.9	6463.7	10230	6712.4	14589	9812.7	16006	11216	Enriched	Enriched	Moderate	Moderate	YES		
P43490	Nicotinamide phosph	NAMPT	55.52	33.6	30	30	255.28	0	130400	132020	120790	149300	149670	130100	178450	218430	109980	166920	Enriched	Enriched	Enriched	Low	YES		
P43652	Afamin	AFM	69.068	11	5	5	15.177	0	42093	28172	34934	54589	24462	37118	30765	53974	19878	43833	Low	Low	Low	No expres	YES		
P43686;P43686-2	26S protease regulato	PSMC4	47.366	44.7	28	27	50.116	0	114070	93145	113010	115890	127890	120130	146030	179220	84088	117420	No expres	Moderate	Enriched	Moderate	YES		
P45880;P45880-2;I	Voltage-dependent an	VDAC2	31.566	53.7	30	11	323.31	0	109600	75477	97418	93129	118730	182250	266310	226460	92172	128520	Enriched	Enriched	Enriched	Enriched	YES		
P45954;P45954-2	Short/branched chain	ACADSB	47.485	36.3	14	14	31.558	0	30695	22994	30261	33042	33586	38937	32740	34480	15633	33305	Moderate	Moderate	Enriched	Moderate	YES		
P45973	Chromobox protein h	CBX5	22.225	25.1	9	9	56.421	0	60755	42822	60283	67346	80384	51475	65107	52832	43257	63043	Enriched	Enriched	Enriched	No expres	YES		
P45974-2;P45974	Ubiquitin carboxyl-te	USP5	93.307	31.4	38	38	147.39	0	158550	126350	151340	173350	180690	153680	181220	167870	99417	155990	Moderate	Moderate	Moderate	Enriched	YES		
P45984-3;P45984-2	Mitogen-activated pro	MAPK9	44.223	20.2	9	8	23.019	0	24971	13672	18852	22129	21269	19777	23342	22326	15495	24322	Enriched	Enriched	Enriched	Moderate	YES		
P45985;P45985-2	Dual specificity mitog	MAP2K4	44.287	13.5	5	4	8.1539	0	14348	11817	16582	16344	14400	21089	19892	24092	10692	19625	Moderate	Moderate	Enriched	Enriched	YES		
P46019	Phosphorylase b kina	PHKA2	138.41	2	3	3	11.494	0	7044.8	3473.5	4427.9	14718	3705.8	8707.8	4952.7	16311	3666.3	9704.8	Enriched	Enriched	Enriched	Enriched	YES		
P46060	Ran GTPase-activatin	RANGAP1	63.541	14.8	13	13	30.334	0	100700	91220	109140	78371	115930	69484	100460	101400	65446	99212	Moderate	Moderate	Enriched	Enriched	YES		
P46063	ATP-dependent DNA	RECQL	73.457	6	6	6	32.181	0	44983	36575	39463	37742	45504	31801	50653	58741	21909	42520	Moderate	Enriched	Enriched	Moderate	YES		
P46100-4;P46100;I	Transcriptional regula	ATRX	278.23	2.6	5	4	19.304	0	8156.3	6773.3	9584.4	7576.1	12251	15898	27223	30076	19389	25439	Enriched	Enriched	Enriched	Enriched	YES		
P46108;P46108-2	Adapter molecule crk	CRK	33.83	43.4	17	16	66.387	0	79713	56115	71777	100140	70894	96506	84976	94984	43412	88511	Moderate	Moderate	Enriched	No expres	YES		
P46109	Crk-like protein	CRKL	33.777	40.3	16	15	32.428	0	92664	71756	77903	86867	86453	87451	110960	121800	52318	90223	Moderate	Enriched	Enriched	Enriched	YES		
P46199	Translation initiation	MTIF2	81.316	4	2	2	124.55	0	13829	9418.5	10504	11634	13047	11083	9664.9	9977.1	3925.1	12149	Enriched	Enriched	Enriched	Moderate	YES		
P46379-2;P46379;I	Large proline-rich pro	BAG6	118.69	9.2	11	11	22.65	0	28718	27740	26483	27731	32445	33230	26133	28607	13014	25752					YES		
P46734-2;P46734;I	Dual specificity mitog	MAP2K3	36.172	25.5	12	7	22.169	0	28923	22194	26919	32315	32615	31085	28428	33764	12321	27991	Enriched	Enriched	Enriched	Moderate	YES		
P46777	60S ribosomal protei	RPL5	34.362	40.4	32	32	159.97	0	325890	227830	277130	266070	335170	369990	606090	457550	281960	352670	Enriched	Enriched	Enriched	Enriched	YES		
P46778;G3V1B3;M	60S ribosomal protei	RPL21	18.565	41.2	18	18	69.279	0	143730	116470	134380	111980	164990	167100	203430	196280	81517	129850	No expres	Enriched	Enriched	Enriched	YES		
P46781;B5MCT8;(	40S ribosomal protei	RPS9	22.591	50	22	22	42.592	0	146320	91560	114030	88117	134390	138690	251860	139480	98246	118380	Enriched	Enriched	Enriched	Enriched	YES		
P46783;S4R435;F6	40S ribosomal protei	RPS10;RPS10-NUDT3	18.898	56.4	25	25	69.652	0	124860	101570	130260	85808	125460	128670	184880	133770	120790	128650	No expres	Enriched	Enriched	Enriched			
P46821	Microtubule-associat	MAP1B	270.63	11.5	28	26	102.52	0	59208	63609	98256	58865	76612	48620	67063	55392	38711	71907	No expres	Moderate	Enriched	Moderate	YES		
P46926;D6RAY7;I	Glucosamine-6-phosp	GNPDA1	32.668	22.8	9	2	21.038	0	30764	28537	32865	27854	33196	42021	57205	73629	29118	41889	Moderate	Moderate	Enriched	Enriched	YES		
P46934-4	E3 ubiquitin-protein	NEDD4	104.22	9.3	10	0	22.065	0	15268	12161	15754	20516	17514	13825	12818	20215	6788	16368	Moderate	Low	Moderate	No expression			
P46937-2;P46937-8	Yorkie homolog	YAP1	52.747	6.6	3	2	4.7674	0.00043	6385.2	5500.8	7889.3	5343.1	6537.1	5303.8	6081.4	6333.7	3682.5	5115.7	Moderate	Enriched	Enriched	No expres	YES		
P46939;P46939-2	Utrophin	UTRN	394.46	36.4	171	131	323.31	0	1031000	635060	744660	860420	905470	844520	851900	862520	452740	865250	Enriched	Enriched	Enriched	Moderate	YES		
P46940;H0YLE8	Ras GTPase-activatin	IQGAP1	189.25	44.2	114	110	323.31	0	599710	448860	557260	642270	561790	567220	684490	766360	372090	683640	Enriched	Enriched	Enriched	Enriched	YES		
P46952;C9IY88;P4	3-hydroxyanthranilat	HAAO	32.556	22.4	9	9	20.017	0	12904	8886.2	9071	14162	10776	13838	11660	15842	5739.8	14861	Moderate	Moderate	Moderate	Enriched	YES		
P46976-2;P46976;(	Glycogenin-1	GYG1	37.478	15.9	6	6	17.574	0	22728	10194	14471	12283	13625	30311	62066	28000	19593	20890	Enriched	Enriched	Enriched	Enriched	YES		
P46977;P46977-2	Dolichyl-diphosphoo	STT3A	80.529	24.7	36	30	81.715	0	233840	138880	177970	230250	202010	214110	207180	168960	107130	201150	Low	Enriched	Enriched	Enriched	YES		
P47755;F8W9N7;C	F-actin-capping prote	CAPZA2	32.949	39.5	11	10	53.254	0	45227	33104	33060	39586	42175	47495	53819	68794	24554	49555	Enriched	Enriched	Enriched	Enriched	YES		
P47813;O14602;X(	Eukaryotic translatio	EIF1AX;EIF1AY	16.46	42.4	19	19	56.189	0	168260	79523	96163	174770	118850	163550	220770	161030	130110	158230	Enriched	Enriched	Enriched	Enriched			
P47897;P47897-2	Glutamine--tRNA lig	QARS	87.798	40.4	38	37	112.51	0	150830	126100	148540	141850	173440	213930	172960	133730	90648	148760	Enriched	Enriched	Enriched	No expres	YES		
P47914	60S ribosomal protei	RPL29	17.752	22.6	7	7	39.319	0	50790	25331	37436	36809	95239	56043	45858	27556	17141	35630	Enriched	Enriched	Enriched	Moderate	YES		
P47985;P0C7P4	Cytochrome b-c1 cor	UQCRFS1;UQCRFS1P1	29.668	31.8	16	16	37.466	0	73922	85263	91550	84849	110820	60946	89020	80350	48717	72628	Enriched	Enriched	Enriched	Enriched	YES		
P48047;H7C0C1	ATP synthase subuni	ATP5O	23.277	71.4	33	33	138.46	0	149610	116580	145700	146510	141990	123420	214190	195150	115050	166670	Enriched	Enriched	Enriched	Moderate	YES		
P48052	Carboxypeptidase A2	CPA2	47.03	47.3	69	69	323.31	0	593440	652820	661800	919230	659600	682930	860870	479410	545970	408690	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P48059;P48059-4;I	LIM and senescent ce	LIMS1	37.251	38.2	13	10	24.513	0	32667	27527	32436	31243	41785	26231	50375	59293	21928	32123	Enriched	Moderate	Enriched	Low	YES		
P48061-2;P48061-5	Stromal cell-derived	CXCL12	10.103	23.6	3	3	2.9572	0.00169	6212	4437.6	5425.4	5282.5	6831.1	4481.4	6224.8	4595.2	3323	4197.2	Enriched	Enriched	Enriched	Enriched	YES		
P48147	Prolyl endopeptidase	PREP	80.699	42.5	40	40	86.41	0	126280	80966	96818	111450	106070	135820	116170	103510	61655	114560	Enriched	Moderate	Moderate	Moderate	YES		
P48163-2;P48163	NADP-dependent ma	ME1	55.165	14.9	7	7	67.757	0	44519	34119	43790	65793	48624	61236	57292	109380	32313	100180	Moderate	Low	Enriched	Moderate	YES		
P48304;H7BZ24	Lithostathine-1-beta	REG1B	18.665	46.4	40	27	323.31	0	286240	121880	176960	106870	176830	133140	587320	359520	564120	208230	Enriched	Enriched	Enriched	Enriched	YES	YES	
P48426-2;P48426;(	Phosphatidylinositol	PIP4K2A	39.802	11.5	3	2	4.7726	0.00043	19417	19018	17689	16888	22395	16515	16361	17499	8646.5	18852	Moderate	Moderate	Moderate	Moderate	YES		
P48436	Transcription factor S	SOX9	56.136	6.1	3	3	5.3807	0	7232.9	5197.1	5704.9	11685	5325.3	7801	8121.3	10686	5871.4	7958.3	Enriched	Enriched	Enriched	Moderate			
P48449;P48449-2;I	Lanosterol synthase	LSS	83.308	16	12	12	23.887	0	42194	33661	38685	36072	41932	41315	52272	57195	23694	47047	Enriched	Enriched	Enriched	Enriched	YES		
P48506;E1CEI4	Glutamate--cysteine l	GCLC	72.765	28.1	23	16	71.818	0	97823	73168	165150	79628	119620	93827	102980	97637	50436	82160	Moderate	Enriched	Enriched	Moderate	YES		
P48544	G protein-activated ir	KCNJ5	47.667	7.4	3	3	6.4199	0	4864.1	4261	4864.3	5217.8	5953.5	3792.6	5228.4	5640.7	5478.5	5522.9	Enriched	Low	Low	Low	YES		
R4GMR5;P48556;I	26S proteasome non-	PSMD8	32.551	18.5	6	6	10.226	0	19692	12764	15012	25688	18075	17501	19032	23845	9930.1	19583	Enriched	Enriched	Enriched	Enriched	YES		
P48634;P48634-2;I	Protein PRRC2A	PRRC2A	228.86	4.6	7	7	25.916	0	29967	25356	27298	26665	37617	20394	31970	29835	22358	32544					YES		
P48637;P48637-2	Glutathione syntheta	GSS	52.384	28.5	14	14	72.326	0	40139	33373	32043	37767	37018	42453	47914	44118	25805	43418	Enriched	Enriched	Enriched	Moderate	YES		
P48643;B7ZAR1;E	T-complex protein 1	CCT5	59.67	44.5	49	5	178.07	0	404090	219700	251590	349730	267650	439320	362240	468690	171370	383940	Low	Enriched	Enriched	Moderate	YES		
P48681	Nestin	NES	177.44	14.3	21	21	56.629	0	61141	51417	57890	60594	66264	58017	92724	106620	39367	65015	Low	Moderate	Enriched	No expres	YES		
P48723	Heat shock 70 kDa pr	HSPA13	51.927	10.2	7	7	99.085	0	49856	33236	36447	58569	45867	85992	48868	44007	20415	46069	Low	Moderate	Enriched	Moderate	YES		
P48729;P48729-2;I	Casein kinase I isofor	CSNK1A1	38.914	15.1	6	2	23.811	0	49146	53085	50601	29945	56837	26809	30387	36224	17911	35035	Enriched	Enriched	Enriched	Enriched	YES		
P48735;P48735-2;I	Isocitrate dehydrogen	IDH2	50.909	46.5	56	54	231.93	0	713890	547240	626580	722010	792210	692880	672200	874430	368690	755000	Enriched	Enriched	Enriched	Moderate	YES		
P48739;P48739-2;I	Phosphatidylinositol	PITPNB	31.54	20.3	8	8	22.546	0	82653	62806	74933	75319	93174	59365	103360	110530	49614	102940	Enriched	Enriched	Enriched	Low	YES		
P49006	MARCKS-related pro	MARCKSL1	19.529	17.9	3	2	15.665	0	1493.7	1450.7	1801.2	1389.8	1970.1	883.47	1339.4	1115.2	1080.1	1763.5	Enriched	Enriched	Enriched	Moderate	YES		
P49189;P49189-2	4-trimethylaminobuty	ALDH9A1	53.801	50.8	45	43	163.25	0	364490	229610	232780	263360	329260	310160	257260	173910	170290	221700	Enriched	Enriched	Enriched	Enriched	YES		
P49207	60S ribosomal protei	RPL34	13.293	37.6	11	11	35.383	0	69685	34677	52810	47758	77758	92201	134850	84079	61412	74476	No expres	Enriched	Enriched	Enriched	YES		
P49257	Protein ERGIC-53	LMAN1	57.548	28.2	46	46	323.31	0	356170	282850	271580	285130	396010	312450	452740	451290	187310	314440	Enriched	Enriched	Enriched	Low	YES		
P49321-2;P49321;I	Nuclear autoantigeni	NASP	48.804	10.2	6	0	16.869	0	11321	9651.3	8962.4	10698	12375	10019	16383	13522	11637	13304	No expres	Moderate	Enriched	Moderate	YES		
P49326;P49326-3	Dimethylaniline mon	FMO5	60.22	9	5	5	7.4199	0	14871	9115.3	12509	12318	8649.4	8496.2	8415.7	4551.6	15185	20968	Enriched	Enriched	Moderate	Moderate	YES		
P49327	Fatty acid synthase;[A	FASN	273.42	24.1	63	63	248.12	0	142910	195640	138400	188730	193610	134720	146570	142250	143140	260990	No expres	Moderate	Moderate	Enriched	YES		
P49354-2;P49354;I	Protein farnesyltransf	FNTA	36.492	26.3	9	9	46.647	0	13066	4804	7772.3	13847	6740.5	17039	21945	46371	7380.9	16399	No expres	Enriched	Enriched	Enriched	YES		
P49368;B4DUR8;P	T-complex protein 1	CCT3	60.533	50.1	54	54	317.28	0	302000	207680	210250	280330	237630	285270	311940	358680	174040	289880	Enriched	Enriched	Enriched	Enriched	YES		
P49406;A0A0A0M	39S ribosomal protei	MRPL19	33.535	9.9	3	3	5.9568	0	12828	11002	12319	11174	14102	11877	13860	11816	7028.4	13868	No expres	Low	Enriched	Moderate	YES		
P49407;P49407-2;I	Beta-arrestin-1	ARRB1	47.065	21.1	12	12	73.092	0	41669	32215	36926	42430	55614	37551	49081	63921	24596	52190	Enriched	Enriched	Moderate	No expres	YES		
P49411	Elongation factor Tu,	TUFM	49.541	52.7	59	59	323.31	0	336890	258080	265530	350690	323500	381830	401060	425580	192820	411400	Low	Enriched	Enriched	Enriched	YES		
P49419-2;P49419;I	Alpha-aminoadipic se	ALDH7A1	55.366	47	40	40	218.27	0	218630	151710	179730	204490	208240	317040	434350	667850	190230	328930	Moderate	Enriched	Enriched	Moderate	YES		
P49441;B8ZZF6;E	Inositol polyphospha	INPP1	43.998	17	9	3	63.892	0	23243	17802	25669	25984	21722	45221	44227	53824	23561	44916	Enriched	Enriched	Enriched	Enriched	YES		
P49458;E9PE20;P4	Signal recognition pa	SRP9	10.112	43	4	4	7.1725	0	24520	12775	16631	40358	15711	25971	25993	21427	12688	23421	Moderate	Enriched	Enriched	Enriched	YES		
P49459;H0Y9V2;P	Ubiquitin-conjugatin	UBE2A;UBE2B	17.315	15.8	2	2	3.9351	0.00061	12587	10079	11357	10853	11443	6418.1	9992.1	7118	4795.8	9946.4	Enriched	Enriched	Enriched	Moderate			
P49588;P49588-2	Alanine--tRNA ligase	AARS	106.81	46.4	79	79	323.31	0	425450	298040	363600	535640	421320	488420	662840	698590	272040	514090	Enriched	Enriched	Enriched	Enriched	YES		
P49589-3;P49589;I	Cysteine--tRNA ligas	CARS	94.637	35.1	42	42	190.83	0	226800	160900	190690	199160	197230	266510	219110	217730	105080	240240	Enriched	Enriched	Enriched	Enriched	YES		
P49590-2;P49590;I	Probable histidine--tI	HARS2	54.114	16.4	8	4	10.19	0	9107.9	7704	8475	7432.7	11091	9464.8	10315	8125.1	9419.4	7699.7	Moderate	Moderate	Enriched	Low	YES		
Q5T5C7;P49591	Serine--tRNA ligase,	SARS	61.312	41.2	39	39	169.33	0	268310	167410	227280	274570	242130	307560	387080	432340	175140	306270	Enriched	Enriched	Enriched	Enriched	YES		
P49593;P49593-2;I	Protein phosphatase 1	PPM1F	49.83	17.8	7	7	17.213	0	22629	19514	23610	23136	26592	22813	25372	21169	17264	21260	Enriched	Moderate	Moderate	Moderate	YES		
P49662;E9PMT1;A	Caspase-4;Caspase-4	CASP4	43.262	13.5	4	4	8.2165	0	16989	10910	14338	22700	14262	16503	12602	18360	9644.4	17250	Enriched	Enriched	Enriched	Moderate	YES		
P49711;P49711-2	Transcriptional repre	CTCF	82.785	12	8	6	12.503	0	18485	13890	18428	10800	21904	12176	18715	16261	18258	17345	Enriched	Enriched	Enriched	Enriched			
P49720;A0A087W	Proteasome subunit b	PSMB3	22.949	40	10	10	33.692	0	108130	65310	80692	91867	96026	117520	111170	132210	57818	92625	Enriched	Enriched	Enriched	Moderate	YES		
P49721	Proteasome subunit b	PSMB2	22.836	42.3	13	13	44.173	0	65149	45534	55324	49131	61325	64556	73940	66887	45503	61995	No expres	Enriched	Enriched	Enriched	YES		
P49748;P49748-3;I	Very long-chain spec	ACADVL	70.389	60.6	74	74	323.31	0	379930	283530	286830	382830	321400	335210	430780	699660	247890	390180	Enriched	Enriched	Enriched	Enriched	YES		
P49750-4;P49750;I	YLP motif-containin	YLPM1	241.64	8	15	15	43.644	0	73847	51894	62854	81695	71399	62836	67682	83446	34067	80640	Enriched	Enriched	Enriched	No expres	YES		
P49755;G3V2K7	Transmembrane emp	TMED10	24.976	52.5	34	34	181.8	0	169280	130730	131430	185130	147070	210750	200000	173830	150530	173420	Moderate	Enriched	Enriched	Enriched	YES		
P49756	RNA-binding protein	RBM25	100.18	16.8	15	15	42.762	0	49735	40477	56826	49380	63496	52128	60677	54892	36365	57067	Moderate	Enriched	Enriched	Moderate	YES		
P49757-4;P49757-2	Protein numb homolo	NUMB	64.526	3.2	2	2	2.5428	0.0038	5964.3	5912.7	5435.8	4650.6	6603.4	5271.8	6817	5865.8	3613.8	5200.8	Moderate	Moderate	Enriched	Moderate	YES		
P49770	Translation initiation	EIF2B2	38.989	21.4	13	13	60.465	0	36014	23496	29041	44838	30598	48060	41708	51544	17458	46332	Enriched	Enriched	Enriched	Enriched	YES		
P49773	Histidine triad nucleo	HINT1	13.802	68.3	16	16	85.548	0	102820	66680	89159	90534	114750	79259	74344	61526	43377	83985	Enriched	Enriched	Enriched	Enriched	YES		
P49790-2;P49790;I	Nuclear pore comple	NUP153	149.39	6.8	8	8	18.12	0	46742	35375	41652	37509	49726	45408	50282	45904	33264	50802	Enriched	Enriched	Enriched	Enriched	YES		
P49792	E3 SUMO-protein lig	RANBP2	358.2	14.7	43	30	191.6	0	106010	76549	86631	103220	107090	89668	96457	137470	58868	115380	Enriched	Moderate	Enriched	Enriched	YES		
P49821;G3V0I5;P4	NADH dehydrogenas	NDUFV1	50.817	31.2	21	21	60.597	0	111990	81422	90564	74077	126920	101380	116930	133770	54423	105290	Enriched	Enriched	Enriched	Moderate	YES		
P49841;P49841-2	Glycogen synthase ki	GSK3B	46.744	14.3	6	6	66.045	0	18753	20426	24113	14287	30083	11453	21819	15708	15311	15651	Enriched	Enriched	Enriched	Moderate	YES		
P49902;P49902-2;(	Cytosolic purine 5-nu	NT5C2	64.969	8.9	6	6	18.373	0	28758	25162	27713	18003	28327	16300	11977	18793	4872.3	17181	Enriched	Moderate	Enriched	Low	YES		
P49903;P49903-2;I	Selenide, water dikin	SEPHS1	42.91	23.2	10	9	82.121	0	82014	57460	57807	68257	67478	65389	74753	97091	41688	82132	Moderate	Moderate	Enriched	Moderate	YES		
P49914;P49914-2	5-formyltetrahydrofo	MTHFS	23.255	44.3	8	8	24.426	0	40968	16461	26865	43667	28808	41363	32322	37752	14447	37783	Enriched	Enriched	Enriched	Moderate	YES		
P49915;P49915-2	GMP synthase [glutai	GMPS	76.715	19.5	16	16	75.807	0	69973	60928	54649	64445	70970	71147	79119	90153	51839	65467	Enriched	Enriched	Enriched	Moderate	YES		
P49916;P49916-2;I	DNA ligase 3	LIG3	112.91	10.5	10	10	40.725	0	14533	9419.7	12499	12843	13677	12711	12765	12564	8294.6	14434	Low	Low	Moderate	Moderate	YES		
P49959;P49959-3;I	Double-strand break	MRE11A	80.592	17.8	11	11	129.36	0	35299	13810	20191	33737	17871	43398	24778	36741	14333	39586	Low	Low	Moderate	Low	YES		
P49961-4;P49961-5	Ectonucleoside triph	ENTPD1	42.73	10.2	3	3	6.0805	0	22343	17747	20146	19614	19584	19956	14355	17406	7234.5	21201	Moderate	Low	Low	Moderate	YES		

P50135	Histamine N-methylt	HNMT	33.295	21.6	10	10	27.644	0	25856	18424	25619	25364	26263	20121	58839	90564	28473	37514	Moderate	Enriched	Enriched	Low	YES		
P50148;B1AM21	Guanine nucleotide-b	GNAQ	42.142	27.3	14	5	16.179	0	15184	12296	16063	16868	21288	19560	23327	22508	12833	19233	Enriched	Enriched	Enriched	Low	YES		
P50213;H0YL72;P	Isocitrate dehydrogen	IDH3A	39.591	30.1	17	12	62.77	0	36362	31950	35368	37746	50064	32348	37415	38244	25739	41095	Low	Moderate	Enriched	Moderate	YES		
P50225;H3BRY5;P	Sulfotransferase 1A1	SULT1A1	34.165	23.7	6	2	16.188	0	20523	16107	25166	17026	15893	17485	27330	36449	17380	20389	Enriched	Enriched	Enriched	Moderate	YES		
P50238;K4DIB9;H	Cysteine-rich protein	CRIP1	8.5328	32.5	2	1	3.1206	0.00095	6427.3	2481.4	4098.3	1181.8	5663.7	1332.9	8047.2	4769.3	6658.5	1589.5	Enriched	No expres	Low	Low			
P50336;F5H1I5;F5	Protoporphyrinogen	PPOX	50.765	8.2	5	5	7.392	0	19090	19637	20401	20284	23617	14136	22141	26906	15509	22386	Moderate	Moderate	Moderate	Moderate	YES		
P50395;P50395-2;(	Rab GDP dissociation	GDI2	50.663	73.7	78	54	323.31	0	783940	545220	606350	758620	731630	697610	939970	918670	458230	724430	No expres	Enriched	Enriched	Enriched	YES		
P50402;Q5HY57	Emerin	EMD	28.994	23.6	7	7	10.791	0	18837	15026	20904	17566	22819	14148	17230	19826	10448	18955	Enriched	Moderate	Moderate	Enriched	YES		
P50416;P50416-2	Carnitine O-palmitoy	CPT1A	88.367	18.2	15	15	26.641	0	53964	42031	46332	46378	55101	49711	61260	56440	28575	58005	Enriched	Enriched	Enriched	Moderate	YES		
P50440;P50440-3	Glycine amidinotrans	GATM	48.455	75.9	125	1	2.0143	0.00771	2057.4	2014.6	2858.8	2234.8	3289.7	1362.4	2863.1	2334.6	1445.9	2022.5	Moderate	Enriched	Enriched	Enriched	YES		
P50440-2	Glycine amidinotrans	GATM	44.883	81.3	126	2	323.31	0	1562900	1190700	1147700	1788200	1577300	1579700	1854900	2112500	821040	1523200	Moderate	Enriched	Enriched	Enriched	YES		
P50453	Serpin B9	SERPINB9	42.403	6.4	2	2	2.7747	0.0024	1180.6	1195	1453.9	967.43	1312.2	1390.9	1194	1374.1	470.98	1107.8	Enriched	Low	Moderate	Moderate	YES		
P50454;E9PPV6;E	Serpin H1	SERPINH1	46.44	31.3	18	11	87.453	0	78507	72056	78417	91684	78611	67415	75934	115360	38743	85070	No expres	Low	Enriched	Moderate	YES		
P50479;P50479-2	PDZ and LIM domai	PDLIM4	35.398	11.2	3	3	12.011	0	17720	11904	16287	11796	20660	10997	27759	22805	13390	22306	Enriched	No expres	Moderate	No expres	YES		
P50502;Q3KNR6;C	Hsc70-interacting pro	ST13;ST13P5;ST13P4	41.331	22.5	15	15	61.779	0	60101	43367	44956	70777	56883	83588	84880	102610	27284	52192	Enriched	Enriched	Enriched	Enriched			
P50552	Vasodilator-stimulate	VASP	39.829	28.7	10	10	16.134	0	25764	19653	23388	35563	27754	19917	19495	23295	13784	23789	Enriched	Moderate	Enriched	Low	YES		
P50570-5;P50570;I	Dynamin-2	DNM2	97.976	20.8	26	2	82.345	0	107740	73002	90146	96621	100370	141880	206630	153080	102570	138700	Moderate	Low	Moderate	Enriched	YES		
P50579;P50579-3;I	Methionine aminopep	METAP2	52.891	41.2	27	27	141.98	0	150230	115100	120060	112630	162610	114600	167320	131970	144620	124480	Low	Enriched	Enriched	No expres	YES		
P50583	Bis(5-nucleosyl)-tetra	NUDT2	16.829	33.3	5	5	12.221	0	2486.1	3478.9	3335.1	1428.5	4247.3	853.29	1397.4	1338.6	795.98	2098.8	Moderate	Low	Moderate	No expres	YES		
P50851	Lipopolysaccharide-r	LRBA	319.1	14.3	47	0	258.86	0	228470	187070	229550	177370	310520	188890	209780	176940	105610	198340	Enriched	Enriched	Enriched	Enriched	YES		
P50895;A0A087W	Basal cell adhesion m	BCAM	67.404	30.6	22	20	79.408	0	68104	49739	60916	63834	69265	69024	75597	86966	42486	86253	Low	Enriched	Moderate	Moderate	YES		
P50897;E9PIA8;E9	Palmitoyl-protein thi	PPT1	34.193	34.6	17	17	101.17	0	86062	55586	63567	75138	87460	96338	94946	73416	91004	114120	Enriched	Enriched	Enriched	Moderate	YES		
P50914;E7EPB3	60S ribosomal protei	RPL14	23.432	39.1	18	18	46.282	0	65561	34083	42347	41508	60928	61877	106260	124940	114090	60424	Enriched	Enriched	Enriched	Enriched	YES		
P50990-2;P50990;I	T-complex protein 1	CCT8	57.645	53.1	51	51	323.31	0	202630	181020	186050	232410	222320	230950	383910	369120	195330	251290	Enriched	Enriched	Enriched	Enriched	YES		
P50991;P50991-2	T-complex protein 1	CCT4	57.924	39.7	37	36	98.433	0	101500	75733	92575	92254	110040	88826	112330	73627	95574	87015	Enriched	Enriched	Enriched	Enriched	YES		
P50995-2;P50995	Annexin A11	ANXA11	51.242	33.9	23	21	150.32	0	120370	88986	111000	126960	113800	145790	188000	259260	92468	185410	Enriched	Enriched	Enriched	Enriched	YES		
P51116	Fragile X mental reta	FXR2	74.222	8	7	5	49.718	0	13221	11564	11229	10054	15779	13185	19288	12067	20426	17351	Moderate	Moderate	Enriched	Enriched	YES		
P51148;P51148-2;I	Ras-related protein R	RAB5C	23.482	54.2	21	14	81.531	0	86096	70827	71999	70219	74577	84155	113990	126960	61348	98797	Enriched	Moderate	Enriched	Moderate	YES		
P51149;C9J4V0;C9	Ras-related protein R	RAB7A	23.489	63.3	24	24	161.65	0	136410	103540	119590	124560	124200	153060	202750	229380	88829	159890	Enriched	Enriched	Enriched	No expres	YES		
P51151;Q9NP90	Ras-related protein R	RAB9A;RAB9B	22.837	9.5	3	3	3.986	0.00062	16215	12636	13799	19067	15937	20127	24036	15770	12563	15600	Enriched	Enriched	Enriched	Enriched			
P51153	Ras-related protein R	RAB13	22.774	34.5	11	8	13.767	0	18951	11459	14250	14970	15632	27477	19529	31258	8877.3	24798	Enriched	Enriched	Enriched	Enriched	YES		
P51178;P51178-2	1-phosphatidylinosito	PLCD1	85.664	9.3	7	6	12.316	0	45089	40774	44494	39974	63106	44097	68857	47847	29184	51461	Moderate	Enriched	Enriched	Moderate	YES		
P51397	Death-associated pro	DAP	11.164	31.4	3	3	21.097	0	50735	39134	38371	31730	61549	27966	25839	30151	12246	31103	Moderate	Enriched	Enriched	Enriched	YES		
P51398-3;P51398;I	28S ribosomal protei	DAP3	41.673	13.7	7	7	16.584	0	12573	8397.8	10172	10701	13615	7671.5	14014	12437	6401.3	12190	Enriched	Enriched	Enriched	Enriched	YES		
P51452;P51452-2;I	Dual specificity prote	DUSP3	20.478	31.4	6	6	24.414	0	31186	22996	23429	24627	27640	24820	23462	23102	13513	23976	Enriched	Enriched	Enriched	Moderate	YES		
P51531-2;P51531	Probable global trans	SMARCA2	179.28	7.2	10	7	34.928	0	60550	50270	65678	69083	88415	39565	52777	50240	31248	55345	Enriched	Enriched	Enriched	Enriched	YES		
P51553-2;P51553;I	Isocitrate dehydrogen	IDH3G;hCG_2004980	41.468	19.2	9	8	23.523	0	28539	25242	27774	25059	35481	22730	37925	29648	20076	29362	Low	Enriched	Enriched	Enriched	YES		
P51570;P51570-2;I	Galactokinase	GALK1	42.272	33.2	16	16	50.953	0	56910	38549	42531	63294	52572	54022	57030	54530	36748	56995	No expres	Low	Low	No expres	YES		
P51571;A6NLM8	Translocon-associate	SSR4	18.998	29.5	12	12	44.582	0	89017	56335	83534	178190	88020	85673	84743	120010	38217	92740	Enriched	Enriched	Enriched	Enriched	YES		
P51572;P51572-2;(	B-cell receptor-assoc	BCAP31	27.991	48	28	28	126.72	0	214260	186880	230860	220880	238670	306780	692810	482490	290270	365350	Enriched	Enriched	Enriched	Enriched	YES		
P51580	Thiopurine S-methylt	TPMT	28.18	14.7	5	5	6.288	0	16555	12687	15029	13364	16410	28089	35635	50556	15249	20645	Enriched	Moderate	Enriched	Enriched	YES		
P51608-2;A0A087	Methyl-CpG-binding	MECP2	53.323	50	28	28	259.51	0	174620	113860	153820	128280	190620	134540	210120	221530	101660	184590	No expres	Low	Moderate	Enriched	YES		
P51648;P51648-2;.	Fatty aldehyde dehyd	ALDH3A2	54.847	22.3	13	12	37.77	0	85385	61771	72459	110190	73108	99777	77724	120150	43167	108170	Enriched	Enriched	Enriched	Enriched	YES		
P51649;P51649-2;(	Succinate-semialdehy	ALDH5A1	57.214	22.2	14	14	163.77	0	86162	69465	82621	66883	91336	72410	96552	94185	51365	107870	No expres	Low	Moderate	Moderate	YES		
P51659;E7EWE5;F	Peroxisomal multifun	HSD17B4	79.685	36.3	33	33	217.02	0	208610	167420	150300	204330	158850	163410	153150	207040	97670	223380	Enriched	Enriched	Enriched	Enriched	YES		
P51665;H3BNT7;H	26S proteasome non-	PSMD7	37.025	17.9	8	8	23.104	0	66732	66703	76694	56372	71988	68120	75846	56263	48075	61905	Moderate	Enriched	Enriched	Enriched	YES		
P51687	Sulfite oxidase, mitoc	SUOX	60.282	9.2	4	4	21.01	0	8795.9	8779.7	9094.1	5175.1	11653	9182.8	12200	11135	5351.4	10352	Enriched	Enriched	Enriched	Moderate	YES		
P51689;P51689-3	Arylsulfatase D	ARSD	64.859	9.9	6	4	6.1122	0	19876	14047	18447	12165	19761	11997	22966	18914	11287	13975	Enriched	Enriched	Enriched	Low	YES		
P51692	Signal transducer and	STAT5B	89.865	7.2	7	2	82.911	0	30516	17674	23539	29952	27451	32035	33660	43440	21458	37376	Enriched	Enriched	Enriched	Enriched			
P51812	Ribosomal protein S6	RPS6KA3	83.735	20.8	14	7	42.035	0	68733	48329	49431	60748	52657	69923	73109	92514	39227	72869	Enriched	Enriched	Enriched	Low	YES		
P51858-2;P51858;I	Hepatoma-derived gr	HDGF	25.537	66.5	39	38	274.44	0	314210	233990	334780	246800	341500	325230	558040	525020	247300	372020	Enriched	Enriched	Enriched	Enriched	YES		
P51884	Lumican	LUM	38.429	47	42	26	267.18	0	216420	188940	246930	300450	233240	227930	509640	768230	236890	325130	No expres	Moderate	Enriched	Moderate	YES		
P51888	Prolargin	PRELP	43.809	34	27	27	57.525	0	152350	181800	267740	237820	243660	240640	285490	281190	134600	258250	Enriched	Moderate	Moderate	Enriched	YES		
P51911;P51911-2;I	Calponin-1	CNN1	33.17	38	19	19	61.988	0	53051	70614	41545	39138	72037	64110	85171	60432	40359	119830	No expres	No expres	Low	No expres	YES		
P51948;H0YJ92;H(	CDK-activating kinas	MNAT1	35.823	8.4	2	2	2.9134	0.00187	5181.4	6137.7	3881.2	6717.2	3823.6	6979.7	4416.2	3711.2	2911.4	4535.3	No expres	No expres	Moderate	Low			
P51970	NADH dehydrogenas	NDUFA8	20.105	44.8	15	15	122	0	86744	70781	76851	83830	99525	73883	73707	70319	42169	86470	Moderate	Enriched	Enriched	No expres	YES		
P51991;P51991-2	Heterogeneous nucle	HNRNPA3	39.594	43.4	35	35	290.27	0	330600	230880	291100	356700	307620	383370	450620	499960	225560	423710	Enriched	Enriched	Enriched	Enriched	YES		
P52209-2;P52209;I	6-phosphogluconate	PGD	51.872	42.8	32	32	124.98	0	206880	160300	188000	231590	216880	201490	219030	231350	116870	198340	Low	Moderate	Enriched	Enriched	YES		
P52272-2;P52272;/	Heterogeneous nucle	HNRNPM	73.62	55.3	64	8	319.43	0	338310	267560	296030	287600	373190	306620	574020	585030	282420	389450	No expres	Enriched	Enriched	Enriched	YES		
P52294;C9JYI4	Importin subunit alph	KPNA1	60.221	14.3	9	7	19.543	0	18335	10578	17779	28833	17252	16685	17764	23772	9581	22676	Enriched	Enriched	Enriched	Low	YES		
P52298-3;P52298;(	Nuclear cap-binding	NCBP2	11.932	32	3	3	6.6673	0	23351	16488	23474	25473	23977	21414	24084	20798	15294	26427	Enriched	Moderate	Enriched	Enriched	YES		
P52306-4;P52306;I	Rap1 GTPase-GDP d	RAP1GDS1	66.316	13.5	7	7	28.128	0	24138	18331	21083	22730	25392	20082	22341	27699	12907	25726	Low	Enriched	Enriched	Moderate	YES		
P52564;P52564-2	Dual specificity mito	MAP2K6	37.492	24.6	8	4	17.922	0	4166.8	3818.2	5674	3861.9	5074.7	5679.9	5667.5	5231.7	2890.1	3967.1	Moderate	Moderate	Moderate	Moderate	YES		
P52565;J3KRE2;J3	Rho GDP-dissociatio	ARHGDIA	23.207	42.6	19	16	249.12	0	254900	130930	175260	234060	233840	284840	322560	263920	180180	227460	Enriched	Enriched	Enriched	Moderate	YES		
P52566;H0YGX7	Rho GDP-dissociatio	ARHGDIB	22.988	38.3	10	1	113.53	0	56892	52215	55727	36079	69823	63920	116750	166830	42009	87897	Enriched	Moderate	Enriched	No expres	YES		
P52597	Heterogeneous nucle	HNRNPF	45.671	29.9	26	18	212.27	0	124270	77249	98115	91700	112850	155620	271770	234410	152580	186210	Low	Moderate	Enriched	Moderate	YES		
P52630-4;P52630	Signal transducer and	STAT2	97.456	8.1	7	7	11.991	0	27731	24075	24692	29151	26780	23744	25516	35425	17815	30592	Enriched	Enriched	Enriched	Moderate	YES		
P52701-3;P52701;I	DNA mismatch repair	MSH6	137.96	10.2	13	13	64.96	0	56959	42642	48462	37149	56552	38292	60083	61691	32264	49216	Moderate	Enriched	Enriched	Moderate	YES		
P52735-3;P52735-2	Guanine nucleotide e	VAV2	97.031	17.5	17	17	125.93	0	64035	60875	57745	76239	67522	53759	59440	54065	29212	58655	Enriched	Enriched	Enriched	Low	YES		
P52757;P52757-9;I	Beta-chimaerin	CHN2	53.923	11.3	4	4	8.9148	0	5027.1	3738.9	5444.5	4762.7	5282.8	2749.3	4388.8	4410.4	1835.9	4312.5	Moderate	Moderate	Moderate	Moderate	YES		
P52758;H0YB34;H	Ribonuclease UK114	HRSP12	14.494	54	12	12	32.307	0	58006	39177	51426	64026	59293	69831	70184	68603	44797	63965	Low	Moderate	Enriched	Enriched	YES		
P52788;H7C2R7;P	Spermine synthase	SMS	41.268	20.5	7	7	21.029	0	56342	36301	45168	52926	60606	50418	36583	47888	27304	48516	Enriched	Low	Enriched	Enriched	YES		
P52815	39S ribosomal protei	MRPL12	21.348	17.7	6	2	4.7716	0.00043	6038.2	5044.7	4108.1	5217.6	6030.4	3034.2	2701.1	4670.4	1631.6	4084.8	Low	Moderate	Enriched	No expression			
P52895;S4R3P0;B4	Aldo-keto reductase	AKR1C2	36.735	22.6	11	2	5.584	0	32519	36172	20542	46268	29034	39388	36946	42713	27406	62607	Enriched	Enriched	Enriched	No expression			
P52907	F-actin-capping prote	CAPZA1	32.922	28.7	12	11	82.218	0	74101	59920	74389	69466	87504	87060	95413	84227	50059	78582	Enriched	Enriched	Enriched	Enriched	YES		
P52943;P52943-2;I	Cysteine-rich protein	CRIP2	22.492	47.6	13	12	229.96	0	105590	92277	121280	91541	136550	123840	216490	143980	142330	158050	Low	Low	Enriched	Enriched	YES		
P52948-5;P52948;I	Nuclear pore comple	NUP98	195.82	8.2	17	17	37.806	0	31824	24787	29519	27629	33023	36396	38942	42672	20815	34764	Moderate	Moderate	Moderate	Enriched	YES		
P53004	Biliverdin reductase	BLVRA	33.428	39.5	15	15	37.404	0	38850	27255	30728	27446	33778	61691	88363	55724	27068	51828	Enriched	Enriched	Enriched	Moderate	YES		
P53007;B4DP62	Tricarboxylate transp	SLC25A1	34.012	26.4	11	11	32.222	0	60503	45340	55673	53578	72823	61429	65857	65350	29303	68977	Moderate	Enriched	Enriched	Moderate	YES		
P53367;P53367-2	Arfaptin-1	ARFIP1	41.738	21.7	9	9	34.564	0	29468	23824	26760	30140	31348	34452	45738	46746	17734	27759	Enriched	Moderate	Enriched	Low	YES		
P53384-2;P53384;I	Cytosolic Fe-S cluste	NUBP1	33.412	15.2	5	5	110.94	0	38130	13630	18009	27091	17698	39449	28472	22481	18416	37382	Low	Moderate	Enriched	Moderate	YES		
P53396;P53396-2;I	ATP-citrate synthase	ACLY	120.84	41.2	61	61	252.94	0	305620	250540	275510	257040	287500	264980	373490	280830	226030	294280	Enriched	Enriched	Enriched	Enriched	YES		
P53582	Methionine aminopep	METAP1	43.215	31.1	13	13	42.151	0	60761	37953	42782	35472	55436	47619	81507	60950	46921	51614	Enriched	Enriched	Enriched	Enriched	YES		
P53597	Succinyl-CoA ligase	SUCLG1	36.249	33.8	15	15	67.552	0	91503	74402	83433	71939	88380	73408	117920	122570	62053	102180	Enriched	Enriched	Enriched	No expres	YES		
P53602	Diphosphomevalonat	MVD	43.404	2.8	1	1	3.2093	0.00077	2673.4	1654.6	1654.8	3136.7	1726	3657.3	1533.8	2109.1	920.63	2541	Moderate	No expres	Low	No expres	YES		
P53609-2;P53609	Geranylgeranyl transf	PGGT1B	33.829	12	5	5	12.582	0	8986.4	7228.5	10337	6642.7	12122	4304.5	7221.1	8068.7	4752.2	8935.5	Moderate	Moderate	Enriched	Enriched	YES		
Q5T4U8;P53611	Geranylgeranyl transf	RABGGTB	17.318	7.2	1	1	2.0996	0.00674	3388.6	2293.3	2832.4	2263.5	2033.1	6037.6	7274.9	8422.3	1981.2	5529.4	Enriched	Enriched	Enriched	Enriched	YES		
P53618	Coatomer subunit bet	COPB1	107.14	43.2	82	82	323.31	0	333930	302140	301650	367890	363840	364640	297480	313060	170110	324020	Enriched	Enriched	Enriched	Enriched	YES		
P53621;P53621-2	Coatomer subunit alp	COPA	138.34	44.8	103	103	323.31	0	592330	437260	493180	524520	630470	657930	637300	614420	291770	519820	Enriched	Enriched	Enriched	Moderate	YES		
P53634	Dipeptidyl peptidase	CTSC	51.853	18.1	8	6	18.014	0	17261	19548	18370	11422	24803	9950.4	25545	14922	29636	14574	Enriched	Enriched	Enriched	Low	YES		
P53677;E7ER80;P5	AP-3 complex subun	AP3M2	46.977	13.2	5	1	35.659	0	14913	10325	11485	13503	17234	10368	9483.2	9678.6	4961.2	12377	Moderate	Moderate	Enriched	Moderate	YES		
P53999	Activated RNA polyr	SUB1	14.395	51.2	13	13	101.92	0	101160	67328	87103	111550	91375	121320	198450	215800	82188	138740	Enriched	Enriched	Enriched	Enriched	YES		
P54136;P54136-2	Arginine--tRNA ligas	RARS	75.378	49.4	55	55	232.83	0	296270	215140	249680	279360	267610	316960	341510	330960	123470	269360	Low	Enriched	Enriched	Enriched	YES		
P54274	Telomeric repeat-bin	TERF1	50.245	3	1	1	2.2184	0.00545	3528.8	2903.4	3540	1756.1	6443.5	1256.2	2129.4	1633.5	1726.3	1887.9	Moderate	Moderate	Enriched	Low			
P54289-4;P54289-5	Voltage-dependent ca	CACNA2D1	121.89	2.2	2	2	15.459	0	4679.7	4877.1	6846.3	4629.2	8896.1	3452.8	3766.7	3452.2	1694.8	5371.6	No expres	No expres	Enriched	No expres	YES		
P54315;E9PRT6	Inactive pancreatic li	PNLIPRP1	51.847	68.3	69	54	323.31	0	544660	714460	283760	634060	349280	324280	328010	239410	328080	315950	Low	Enriched	Enriched	Enriched	YES	YES	YES
P54317;A0A087W	Pancreatic lipase-rela	PNLIPRP2	51.946	42.2	55	50	287.78	0	1168500	1147700	687720	305120	359470	447080	790230	315790	505300	377450	No expres	Enriched	Enriched	Enriched	YES	YES	
P54577	Tyrosine--tRNA ligas	YARS	59.143	63.3	61	61	323.31	0	462100	310370	378380	389590	477480	534940	572470	495880	255600	421080	Enriched	Enriched	Enriched	Enriched	YES		
P54578-2;P54578;/	Ubiquitin carboxyl-te	USP14	52.385	38.8	27	27	112.82	0	164890	118770	134580	118680	140090	141670	127300	144090	61822	130770	Enriched	Enriched	Enriched	Moderate	YES		
P54619-2;P54619;I	5-AMP-activated pro	PRKAG1	34.083	21.7	7	7	11.639	0	20569	12972	13979	16381	15972	16798	14769	17267	6528.4	18019	Low	Enriched	Enriched	Moderate	YES		
P54652	Heat shock-related 7(	HSPA2	70.02	47.4	59	20	64.599	0	86725	51781	53231	64573	65876	98820	104920	118340	86755	96829	Low	Enriched	Enriched	Moderate	YES		
P54687-4;P54687;I	Branched-chain-amin	BCAT1	42.837	32.7	27	27	178.75	0	211640	125560	119380	226050	200740	239990	172710	176830	67133	165190	No expres	Enriched	Enriched	Low	YES		
P54709	Sodium/potassium-tr	ATP1B3	31.512	15.8	4	4	6.5475	0	6916.3	5705.7	7188.8	4835.9	8677.6	5679.3	17215	19543	4611.8	7841.6	Moderate	Enriched	Enriched	Enriched	YES		
P54710	Sodium/potassium-tr	FXYD2	7.2832	18.2	1	1	7.8448	0	20460	17958	27613	24279	39454	18063	27405	24279	14325	27371	Enriched	Enriched	Enriched	Enriched	YES		
P54725-2;P54725-3	UV excision repair pr	RAD23A	33.433	16.9	7	2	9.1431	0	39310	29156	29836	21828	31666	35199	57300	67225	21092	34271	Enriched	Enriched	Enriched	Enriched	YES		
P54727;Q5W0S5	UV excision repair pr	RAD23B	43.171	28.4	20	12	40.019	0	89621	54825	75137	83733	85723	95134	130380	125890	69970	106060	Moderate	Enriched	Enriched	Enriched	YES		
P54753	Ephrin type-B recept	EPHB3	110.33	6.9	5	5	24.318	0	12469	8523	9653.3	13609	12632	8834.6	8646.1	14494	6074.5	17648	Enriched	Moderate	Low	Low	YES		
Q96L35;P54760-4;	Ephrin type-B recept	EPHB4	102.56	1.3	1	1	3.8382	0.00061	3878.3	3630.1	4465.2	3908.1	6977.7	4027.7	5369.1	5153	3917.7	5187.2	Enriched	Moderate	Moderate	Moderate			
P54802	Alpha-N-acetylgluco	NAGLU	82.265	4.6	3	3	6.3982	0	6452.7	3995.7	8753.1	12378	5768.3	7341.5	8821.5	10329	5115.2	9678.1	Enriched	Moderate	Moderate	Moderate	YES		
P54826	Growth arrest-specifi	GAS1	35.693	4.6	1	1	3.2947	0.00078	2536.3	3225.2	4069.7	2436.8	4794.8	2549.5	3187.9	2719.8	1898.4	2769.2	No expres	Moderate	Moderate	Enriched	YES		
P54868-2;P54868;I	Hydroxymethylglutar	HMGCS2	52.481	36.5	20	20	120.83	0	134860	99544	130940	140540	79529	522610	74358	90838	41642	134780	Enriched	Enriched	Moderate	Moderate			
P54886-2;P54886	Delta-1-pyrroline-5-c	ALDH18A1	87.088	42.1	44	44	157.62	0	190910	197090	209820	165270	245150	211550	271270	174080	142780	189080	Moderate	Enriched	Enriched	No expres	YES		
P54920;M0R0Y2;N	Alpha-soluble NSF a	NAPA	33.232	30.8	11	11	50.598	0	34577	22018	25115	32911	35570	33034	53718	60372	18473	34185	No expres	Moderate	Enriched	Low	YES		
P54922;C9JZW7	[Protein ADP-ribosyl	ADPRH	39.506	8.7	2	2	5.6232	0	23378	15516	17910	26450	18611	15988	19935	25281	11287	21756	Moderate	Enriched	Moderate	Moderate	YES		
Q5STX8;P55008;P	Allograft inflammato	AIF1	18.038	21.1	3	3	82.952	0	23329	38446	22151	49289	21463	12769	8037.9	13870	3868.9	19165	Moderate	No expres	Low	Moderate	YES		
P55010	Eukaryotic translatio	EIF5	49.222	41.3	30	30	161.22	0	169710	111370	118560	100650	174050	114230	113180	104170	58640	111600	Enriched	Enriched	Enriched	Moderate	YES		
P55039;A8MZF9	Developmentally-reg	DRG2	40.746	19	6	6	15.673	0	29333	24365	25809	32270	29075	42655	38822	28322	17879	31772	Moderate	Moderate	Moderate	Moderate	YES		
P55058;P55058-3;I	Phospholipid transfer	PLTP	54.739	16.8	10	10	47.401	0	24675	10484	14328	32824	14915	25144	21339	29085	17673	25124	Low	Enriched	Enriched	Moderate	YES		
P55060-3;P55060;I	Exportin-2	CSE1L	107.78	25.8	37	37	204.69	0	176380	133500	159120	179940	169450	168810	162930	192300	91699	178220	Low	Enriched	Enriched	Moderate	YES		
P55072	Transitional endoplas	VCP	89.321	58.6	99	98	323.31	0	924260	593120	650990	976420	867170	1012000	1167700	1257000	542620	929870	Moderate	Enriched	Enriched	Enriched	YES		
P55081	Microfibrillar-associa	MFAP1	51.958	17.5	7	7	36.678	0	18912	14349	16511	14331	20430	15995	24481	21441	15984	19987	Moderate	Enriched	Enriched	Moderate	YES		
P55084-2;P55084;I	Trifunctional enzyme	HADHB	48.879	38.3	38	7	206.49	0	262880	180670	199890	355430	219480	267990	347740	377680	222580	315250	Enriched	Enriched	Enriched	Enriched	YES		
P55145	Mesencephalic astroc	MANF	20.7	53.3	30	29	123.51	0	207430	176020	186870	219580	226450	317970	227790	268340	105450	173850	Enriched	Enriched	Enriched	Enriched	YES		
P55201-4;P55201-3	Peregrin	BRPF1	127.36	1.1	1	1	2.7071	0.00238	3546.2	5646.4	5204	4762.7	4822.8	3769.7	3290	3921.4	2776.9	3856.5	Moderate	Low	Moderate	No expression			
P55212	Caspase-6;Caspase-6	CASP6	33.31	18.1	7	7	28.445	0	32534	33243	43941	18355	32983	17958	28219	26701	13577	27924	Enriched	Moderate	Moderate	No expres	YES		
P55259;P55259-2;I	Pancreatic secretory g	GP2	59.48	36.7	54	6	323.31	0	287100	283820	210720	320350	300000	499350	415610	325880	245360	327110	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
P55259-3	Pancreatic secretory g	GP2	59.127	36.3	52	4	47.694	0	78133	47002	45656	103910	46821	65145	105540	46761	80068	96926	Enriched	Enriched	Enriched	Enriched	YES		
P55263-2;P55263;I	Adenosine kinase	ADK	38.703	28.1	15	15	276.2	0	132000	82294	125380	83479	121840	129790	115300	101160	68125	98332	No expres	Enriched	Enriched	Low	YES		
P55265;P55265-4;I	Double-stranded RN	ADAR	136.06	17.4	20	20	55.84	0	100810	68492	97047	78637	104420	96598	90246	103330	49921	106910	Enriched	Enriched	Enriched	Enriched	YES		
P55268	Laminin subunit beta	LAMB2	195.98	35.6	78	72	323.31	0	307250	251800	293790	289510	369600	321380	401090	421120	190530	397290	Moderate	Enriched	Moderate	Enriched	YES		
P55327-2;P55327;I	Tumor protein D52	TPD52	19.863	51.6	29	1	109.09	0	131050	100120	119700	143110	138750	158760	320130	259510	133400	164580	Enriched	Enriched	Enriched	Enriched	YES		
P55735-2;P55735;I	Protein SEC13 homo	SEC13	34.011	33.1	19	19	123.15	0	92670	65591	66361	78474	101560	70426	54449	51779	29564	59440	Low	Enriched	Enriched	Enriched	YES		
P55795	Heterogeneous nucle	HNRNPH2	49.263	35	34	11	64.599	0	67559	48278	64436	74687	60343	84909	73587	68519	32061	84689	No expres	Enriched	Enriched	Low	YES		
P55809;E9PDW2	Succinyl-CoA:3-keto	OXCT1	56.157	21.2	12	12	34.062	0	22724	13350	17244	17326	19685	14002	13061	19309	10139	20656	No expres	Moderate	Enriched	Moderate	YES		
P55884;P55884-2	Eukaryotic translatio	EIF3B	92.48	31.9	36	25	249.65	0	310070	184080	229220	265240	254580	266400	322430	317530	140310	291950	Enriched	Enriched	Enriched	Enriched	YES		
P55957;P55957-2	BH3-interacting dom	BID	21.994	19.5	4	4	21.802	0	5622.8	4036.2	4989.2	7509.8	4903.9	4269.9	7820.9	7828.2	4841.9	6550.1	Enriched	Enriched	Enriched	Low	YES		
P56181-2	NADH dehydrogenas	NDUFV3	50.983	18.4	9	9	32.606	0	47753	39599	47002	43131	62215	36566	38312	37267	21310	57343	Enriched	Enriched	Enriched	No expres	YES		
P56182	Ribosomal RNA proc	RRP1	52.839	5.9	2	2	3.2292	0.00077	5568.2	5554.3	7035.4	4647.8	6717.8	3850.6	9775	8384.4	5107.6	5409.7	Enriched	Moderate	Moderate	No expres	YES		
P56192;P56192-2	Methionine--tRNA li	MARS	101.11	31.7	32	32	234.54	0	159050	112130	122990	150100	159100	141790	133730	128690	73344	133460	Enriched	Enriched	Enriched	Enriched	YES		
P56199	Integrin alpha-1	ITGA1	130.85	7.5	11	11	20.474	0	35418	25883	41818	26980	38482	40867	61341	41781	23703	49438	No expres	No expres	Low	Low	YES		
P56277	Cx9C motif-containi	CMC4	7.7469	23.5	3	3	20.29	0	36518	29497	51839	23977	39368	24386	30587	31479	16451	29186					YES		
P56378;P56378-2;/	6.8 kDa mitochondri	MP68;C14orf2	6.662	34.5	5	5	7.1284	0	69349	31811	24312	18578	62786	42560	40232	54002	20882	28316	No expres	No expres	Low	No expression			
P56385	ATP synthase subuni	ATP5I	7.9331	27.5	3	3	5.0148	0.00044	26376	21331	24830	20729	22159	32856	37674	40269	20257	34351	Enriched	Enriched	Enriched	Enriched	YES		
P56470;M0QZ93	Galectin-4;Galectin	LGALS4	35.941	34.7	15	14	80.264	0	87203	77329	78488	70596	80564	95596	152180	127130	70858	119700	Enriched	Enriched	Enriched	Moderate	YES		
P56537;P56537-2	Eukaryotic translatio	EIF6	26.599	55.5	22	22	200.84	0	86909	84647	82678	105240	101170	78358	95922	111700	73653	90353	Enriched	Enriched	Enriched	Enriched	YES		
P56556;R4GN43	NADH dehydrogenas	NDUFA6	17.871	41.6	7	7	24.516	0	17859	15064	17171	13322	22679	16208	16964	15443	10438	15988	Enriched	Enriched	Enriched	Enriched	YES		
P57088;D6RAA6;H	Transmembrane prot	TMEM33	27.978	19.4	7	7	10.374	0	17638	16858	14659	12443	19004	21142	18344	17864	8923.8	14557	Enriched	Moderate	Enriched	No expres	YES		
P57735	Ras-related protein R	RAB25	23.495	27.2	6	5	8.997	0	11105	13695	14889	9488.3	21562	8080.1	12709	8776.7	8694.1	9454	Enriched	Enriched	Enriched	No expres	YES		
P57737-3;P57737-2	Coronin-7	CORO7	114.16	6.4	4	4	19.237	0	6488	3563.9	4975.4	4706	5814.9	5060.4	5420.4	5338.2	3621.1	4997.9	Low	No expres	Low	No expres	YES		
P57740;P57740-2;I	Nuclear pore comple	NUP107	106.37	10.6	8	8	154.24	0	55948	43037	51976	60118	53374	56578	49835	58028	24365	65823	Moderate	Moderate	Enriched	No expres	YES		
P58546;C9JL85	Myotrophin	MTPN	12.895	54.2	11	11	52.571	0	100610	83988	102670	119650	122050	98686	101420	97055	55233	106460	Enriched	Enriched	Enriched	No expres	YES		
P60022	Beta-defensin 1	DEFB1	7.4197	19.1	2	2	41.934	0	3676.7	2868.1	3577.7	2040.3	11131	5579.9	18355	2061.6	4060.4	3997.2	Enriched	Enriched	Enriched	Enriched	YES	YES	
P60174-1;P60174;I	Triosephosphate isor	TPI1	26.669	81.5	74	74	323.31	0	721360	471070	561470	657230	586470	822240	1021100	1035100	517700	889200	Enriched	Enriched	Enriched	Enriched	YES		
P60228;E5RGA2	Eukaryotic translatio	EIF3E	52.22	45.4	29	29	114.39	0	153520	103530	136450	113770	133910	156040	173200	177760	81738	151420	Enriched	Enriched	Enriched	Enriched	YES		
P60468;S4R3B5	Protein transport prot	SEC61B	9.9743	36.5	8	8	92	0	47349	47524	48357	44885	60450	55978	183630	100770	98361	64773	Enriched	Enriched	Enriched	Enriched	YES		
P60510;H3BTA2;H	Serine/threonine-prot	PPP4C	35.08	21.2	5	4	5.4773	0	4591.5	3125.8	3606.9	3721.1	4602.5	3045.4	2704.8	3545.5	1460.9	3301.5	Moderate	Enriched	Enriched	Moderate	YES		
P60602-2;P60602	Reactive oxygen spec	ROMO1	5.8998	27.1	1	1	2.7461	0.0024	2932.2	3464.8	3272.8	2631.1	3215.9	2688.8	2074.8	1684.7	774.83	2311.8	Enriched	Enriched	Enriched	No expres	YES		
P60604-2;P60604	Ubiquitin-conjugatin	UBE2G2	15.614	27	2	2	4.3477	0.00063	9360	6950.6	8352.9	9827	9328.6	10273	12210	10855	5945.3	9919.5	Low	Moderate	Enriched	Enriched	YES		

P63261;P60709;I3I	Actin, cytoplasmic 2;	ACTG1;ACTB	41.792	62.9	101	14	323.31	0	1435200	1095900	1435000	1421700	1453600	1680200	2568400	2592200	1606200	2036100	Enriched	Enriched	Enriched	Enriched		
P60842;J3KT12;P6	Eukaryotic initiation	EIF4A1	46.153	51.2	41	16	220.83	0	335970	152500	191070	316030	231910	317100	319740	335310	167910	343810	Enriched	Enriched	Enriched	Moderate	YES	
P60866;P60866-2;I	40S ribosomal protei	RPS20	13.373	47.1	14	14	40.096	0	142980	111430	148590	94716	157960	122650	104000	98007	59004	94142	Enriched	Enriched	Enriched	Enriched	YES	
P60891;P60891-2	Ribose-phosphate py	PRPS1	34.834	36.8	18	4	43.069	0	70112	53239	63808	65758	77650	91665	116290	85810	78283	86639	Moderate	Enriched	Enriched	Enriched		
P60903	Protein S100-A10	S100A10	11.203	50.5	15	15	143.45	0	233240	243670	398060	349420	251700	199280	271110	281270	114480	280730	Enriched	Enriched	Enriched	Moderate	YES	
P60953;P60953-1	Cell division control	CDC42	21.258	43.5	19	15	99.94	0	144320	100360	125320	182630	164520	159670	232590	224200	115690	176800	Enriched	Enriched	Enriched	Moderate	YES	
P60981-2;P60981;I	Destrin	DSTN	16.62	82.4	28	27	103.44	0	184790	149940	195880	211570	218240	183040	244210	217120	118210	184150	Enriched	Enriched	Enriched	Enriched	YES	
P61006;P61006-2	Ras-related protein R	RAB8A	23.668	42	13	9	65.698	0	40525	29772	47515	31855	43401	33798	40987	47864	23252	42597	Enriched	Enriched	Enriched	Moderate	YES	
P61009	Signal peptidase com	SPCS3	20.313	39.4	18	18	139.76	0	172520	89498	119650	146660	119680	234440	206330	171980	77315	151880	Enriched	Enriched	Enriched	No expres	YES	
P61011;P61011-2;(	Signal recognition pa	SRP54	55.704	50	45	45	323.31	0	402640	198320	200300	315850	282740	491330	344540	313700	139760	317520	Enriched	Enriched	Enriched	Enriched	YES	
P61018;P61018-2;(	Ras-related protein R	RAB4B	23.586	15.5	4	2	4.6082	0.00043	3888.9	8567.5	5692	2421.4	4873.7	5795.3	5973.8	8444.7	3259.9	5684.5	Enriched	Enriched	Moderate	Low		
P61019;P61019-2	Ras-related protein R	RAB2A	23.545	51.9	19	17	107.28	0	92812	88812	91964	65094	119370	97056	130320	130880	59888	93718	Enriched	Enriched	Enriched	Low	YES	
P61020;P61020-2	Ras-related protein R	RAB5B	23.707	39.1	12	5	7.9229	0	18948	12986	13517	18069	17282	11639	13931	11353	9966.1	14734	Enriched	Enriched	Enriched	Enriched	YES	
P61026	Ras-related protein R	RAB10	22.541	34	11	8	26.701	0	31348	21635	26375	32824	26640	33618	42208	53247	26171	32254	Enriched	Enriched	Enriched	No expres	YES	
P61081;M0QYI6	NEDD8-conjugating	UBE2M	20.9	19.1	4	4	11.972	0	30250	22809	21721	24850	29985	20293	20340	19866	11767	19845	Enriched	Low	Enriched	Enriched	YES	
P61086;P61086-3;I	Ubiquitin-conjugatin	UBE2K	22.406	32	10	10	37.206	0	77300	63017	71692	66303	89245	77238	72543	67738	37168	67163	No expres	Enriched	Enriched	Low	YES	
P61088;F8VSD4;F	Ubiquitin-conjugatin	UBE2N;UBE2NL	17.138	52	14	14	50.115	0	163650	141180	145050	145660	137330	158680	151510	154830	72554	154240	Enriched	Enriched	Enriched	Enriched	YES	
P61106;X6RFL8	Ras-related protein R	RAB14	23.897	60	22	22	80.129	0	96352	83401	90260	90459	104590	108030	259040	278660	75404	125350	Moderate	Moderate	Enriched	Enriched	YES	
P61158;B4DXW1	Actin-related protein	ACTR3	47.371	43.8	32	24	99.81	0	143910	120620	138060	159770	159610	166260	182580	207020	88874	145520	Enriched	Enriched	Enriched	Enriched	YES	
P61160;P61160-2;I	Actin-related protein	ACTR2	44.76	30.2	17	17	109.02	0	129350	89832	102640	113790	120810	129520	94429	90861	49369	102370	No expres	Enriched	Enriched	Low	YES	
P61163;R4GMT0	Alpha-centractin	ACTR1A	42.613	36.2	19	12	242.37	0	116430	60518	82263	76869	94007	117200	111600	72982	44032	94554	Moderate	Enriched	Enriched	Enriched	YES	
P61201;B4DIH5;P(	COP9 signalosome cc	COPS2	51.596	37.2	20	20	102.11	0	86970	71642	74215	76002	78303	83796	108540	116710	52023	76811	Enriched	Enriched	Enriched	Enriched	YES	
P84077;P61204;F5	ADP-ribosylation fac	ARF1;ARF3	20.697	63	37	14	323.31	0	434460	225540	253060	366520	297940	392310	338540	394480	180280	368600	No expres	Enriched	Enriched	Enriched	YES	
P61221;D6R9I9	ATP-binding cassette	ABCE1	67.314	38.4	30	30	76.802	0	117130	88606	93122	89616	110730	128090	134420	113950	75678	121990	Enriched	Enriched	Enriched	Moderate	YES	
P61225	Ras-related protein R	RAP2B	20.504	25.7	5	3	8.8166	0	25893	23864	33937	20165	24472	21378	31491	38426	17926	35911	Enriched	Enriched	Enriched	No expres	YES	
P61247;D6RAT0;D	40S ribosomal protei	RPS3A	29.945	58.3	41	41	116.46	0	377810	212760	278470	341000	306310	368500	459990	342710	380010	363760	Enriched	Enriched	Enriched	Enriched	YES	
P61254;J3QRI7;J3(	60S ribosomal protei	RPL26;KRBA2	17.258	57.9	19	3	38.971	0	132990	93801	123030	134010	143590	178330	318640	160730	173700	170470	Enriched	Enriched	Enriched	Enriched	YES	
P61278	Somatostatin;Somato	SST	12.735	21.6	9	9	35.209	0	30276	43360	91450	56114	65574	60059	125720	62114	111110	120380	Enriched	Enriched	Enriched	Enriched	YES	YES
P61313;E7EQV9;E	60S ribosomal protei	RPL15	24.146	39.2	20	10	65.594	0	142370	94615	133870	109280	178190	143510	158940	121160	71456	126990	Enriched	Enriched	Enriched	Enriched	YES	
P61326;Q96A72;F5	Protein mago nashi h	MAGOH;MAGOHB	17.163	39	7	7	58.444	0	28082	15345	25303	19033	25562	33360	73086	56883	33606	54323	Moderate	Moderate	Enriched	Low		
P61457	Pterin-4-alpha-carbin	PCBD1	11.999	67.3	13	13	32.156	0	22762	12426	18950	30467	19488	20493	33798	31900	15428	34625	Low	Enriched	Enriched	Low	YES	
P61586;C9JNR4;C	Transforming protein	RHOA	21.768	47.2	26	6	106.27	0	229070	169900	198960	186850	229700	227500	347660	529060	161470	320400	No expres	Enriched	Enriched	Enriched		
P61604;B8ZZL8	10 kDa heat shock pr	HSPE1	10.932	72.5	18	10	77.547	0	163080	113830	149840	181530	166490	407150	269070	235780	163560	208980	Enriched	Enriched	Enriched	Enriched	YES	
P61626	Lysozyme C	LYZ	16.537	25	5	2	7.947	0	6710	5656.8	7411.5	5339.5	6577.9	8666.3	15305	33247	8589.7	16543	No expres	No expres	Enriched	No expres	YES	
P61764;P61764-2	Syntaxin-binding pro	STXBP1	67.568	10.1	5	5	14.73	0	19116	19733	23702	13416	28923	19814	31173	30293	18962	25697	Moderate	Enriched	Enriched	Enriched	YES	
P61927	60S ribosomal protei	RPL37	11.078	19.6	5	5	8.5116	0	25425	13688	18317	12572	21012	22710	59887	40080	22525	19018	No expres	Enriched	Enriched	Enriched	YES	
P61956-2;P61956	Small ubiquitin-relat	SUMO2	8.1111	35.2	6	4	12.239	0	7032.3	4530.4	6256.5	7234.1	6704.5	7808	23329	10325	8137.2	10739	Enriched	Enriched	Enriched	Enriched	YES	
P61962	DDB1- and CUL4-as	DCAF7	38.926	6.7	2	2	3.0099	0.00151	4679.4	2602.1	3049.6	4621.3	3627.5	4544.1	5861	5513.4	2089.3	4900.8					YES	
P61964	WD repeat-containin	WDR5	36.588	16.8	6	6	22.069	0	6605.6	5118.7	5693.4	8601.1	6575.9	13004	6931.5	6892.5	3098.5	6219.5	Low	Enriched	Enriched	No expres	YES	
P61966;H7C1E4	AP-1 complex subun	AP1S1	18.733	26.6	7	6	91.664	0	24169	16749	29670	14423	29490	16579	23926	17016	7691.8	19533	Enriched	Moderate	Enriched	Moderate	YES	
P61970;H3BRV9	Nuclear transport fac	NUTF2	14.478	34.6	8	8	13.993	0	33915	28130	28816	42390	34124	35551	51613	57884	22960	38681	Enriched	Moderate	Enriched	Low	YES	
P61978-3;Q5T6W5	Heterogeneous nucle	HNRNPK	48.562	60.2	56	41	323.31	0	295450	231210	298840	239330	314230	304110	523440	453650	267940	329980	Enriched	Enriched	Enriched	Enriched	YES	
P61981	14-3-3 protein gamm	YWHAG	28.302	64.4	32	28	323.31	0	123120	91694	112490	124430	125920	159590	183380	220650	121030	153230	Enriched	Enriched	Enriched	No expres	YES	
P62070;P62070-4;I	Ras-related protein R	RRAS2	23.399	19.6	9	1	2.0802	0.00707	3992.6	4349.4	5093.9	6465.9	6624.9	3297.4	4730	6147.3	2849.3	5252.2	Moderate	Moderate	Enriched	Moderate	YES	
P62072	Mitochondrial impor	TIMM10	10.333	38.9	6	6	18.451	0	19285	14134	12885	27629	14703	16449	31250	40318	14824	28314	Moderate	Enriched	Enriched	No expres	YES	
P62081;B5MCP9	40S ribosomal protei	RPS7	22.127	51	37	37	175.89	0	225090	139810	153990	180690	164790	432940	613740	444740	211370	303470	Enriched	Enriched	Enriched	Enriched	YES	
P62136;P62136-2;I	Serine/threonine-prot	PPP1CA	37.512	34.5	22	3	29.462	0	35187	29023	28742	46683	28942	19728	26140	26451	20052	27496	Moderate	Enriched	Enriched	Low	YES	
P62140;E7ETD8	Serine/threonine-prot	PPP1CB	37.186	40.7	26	10	91.903	0	129370	86608	98854	138520	102250	126530	138470	159480	68879	127810	Enriched	Enriched	Enriched	Low	YES	
P62191;P62191-2	26S protease regulatc	PSMC1	49.184	40	28	28	202.92	0	181940	143720	168010	170250	194060	187790	203360	206800	105880	194280	Enriched	Enriched	Enriched	Enriched	YES	
P62195-2;P62195;I	26S protease regulatc	PSMC5	44.784	32.2	17	15	76.656	0	86183	75025	88228	108020	106380	75514	100070	119410	49316	70171	Enriched	Enriched	Enriched	Enriched	YES	
P62241;Q5JR95	40S ribosomal protei	RPS8	24.205	55.8	29	29	193.67	0	266510	159110	179240	201990	242500	345680	487120	352410	183850	256490	Enriched	Enriched	Enriched	Enriched	YES	
P62244;I3L3P7	40S ribosomal protei	RPS15A	14.839	56.9	13	2	71.934	0	63471	37522	43448	66819	53997	73469	71703	62812	30238	56688	Enriched	Enriched	Enriched	Enriched	YES	
P62249;M0R3H0;N	40S ribosomal protei	RPS16	16.445	43.2	15	7	58.696	0	31495	21186	25525	21724	33435	35307	180660	54075	59802	35476	Enriched	Enriched	Enriched	Enriched	YES	
P62253;I3L0Q0;I3I	Ubiquitin-conjugatin	UBE2G1	19.509	18.2	2	2	10.435	0	3519.4	2161.9	2292	7843.4	1829.5	3279.6	4249	10762	3278.1	8198.3	Enriched	Enriched	Enriched	Low		
P62258;P62258-2	14-3-3 protein epsilo	YWHAE	29.174	83.5	59	50	323.31	0	476170	339530	387660	405900	408720	449750	624530	741120	282420	425540	Enriched	Enriched	Enriched	Low	YES	
P62263;H0YB22;E	40S ribosomal protei	RPS14	16.273	35.1	23	23	66.152	0	91218	64917	79842	66697	89780	135090	155160	86007	87038	108700	Enriched	Enriched	Enriched	Enriched	YES	
P62269	40S ribosomal protei	RPS18	17.718	50.7	24	24	169.79	0	183330	123580	147310	140100	180590	211720	318080	191150	152770	187290	Enriched	Enriched	Enriched	Enriched	YES	
P62273;A0A087W	40S ribosomal protei	RPS29	6.6767	33.9	2	2	4.2056	0.00062	23529	12185	17761	15251	18563	24944	19643	15771	8789.7	17211	Enriched	Enriched	Enriched	Enriched	YES	
P62277;J3KMX5	40S ribosomal protei	RPS13	17.222	44.4	27	27	76.325	0	195460	147440	190310	180290	202970	324500	407860	238380	150420	205710	No expres	Enriched	Enriched	Enriched	YES	
P62280;M0QZC5	40S ribosomal protei	RPS11	18.431	46.2	24	24	202.06	0	277130	140710	195420	198850	249850	270110	373820	256250	115390	205800	No expres	Enriched	Enriched	Enriched	YES	
P62304;A6NHK2	Small nuclear ribonu	SNRPE	10.803	54.3	10	10	14.475	0	31618	20398	23818	37329	23263	36531	45989	48830	24186	42393	Moderate	Enriched	Enriched	Enriched	YES	
P62306	Small nuclear ribonu	SNRPF	9.7251	17.4	4	4	75.209	0	44407	38436	58071	45587	61060	51272	79986	66068	49646	62488	No expres	Moderate	Enriched	Low	YES	
P62310	U6 snRNA-associate	LSM3	11.845	13.7	2	2	5.9003	0	1614.7	1273.3	1465.6	1672.2	1356.4	1894.2	1088.7	1455	1431.1	1520.8	Moderate	Enriched	Enriched	No expres	YES	
P62314;J3QLI9	Small nuclear ribonu	SNRPD1	13.281	32.8	10	10	22.775	0	32668	16300	26921	42730	24167	37177	38123	38874	15857	35661	No expres	Enriched	Enriched	Low	YES	
P62316;K7ERG4;P	Small nuclear ribonu	SNRPD2	13.527	54.2	14	14	71.865	0	59236	43267	61856	60166	86863	58772	62956	80086	31378	60352	Enriched	Enriched	Enriched	Moderate	YES	
P62318-2;P62318;I	Small nuclear ribonu	SNRPD3	13.291	29.2	5	5	18.732	0	25467	16951	20311	15724	23628	19557	17787	19172	10545	21071	Enriched	Enriched	Enriched	Moderate	YES	
P62328	Thymosin beta-4;Her	TMSB4X	5.0526	79.5	13	13	171.29	0	185980	195130	198980	136700	341670	92923	198370	155050	151360	156570	Enriched	Enriched	Enriched	Enriched	YES	
P62330	ADP-ribosylation fac	ARF6	20.082	41.7	11	11	27.495	0	78732	57948	65735	46286	88275	50209	54596	62655	28895	62166	Enriched	Enriched	Enriched	Low	YES	
P62424;Q5T8U2	60S ribosomal protei	RPL7A	29.995	51.1	37	15	290.31	0	371300	251550	270080	256990	380270	266400	370860	303830	138350	232860	Enriched	Enriched	Enriched	No expres	YES	
P62487	DNA-directed RNA p	POLR2G	19.294	10.5	2	2	2.2391	0.00528	12160	12276	12282	9114.7	14452	12605	11951	12116	4962.1	8402.8	Enriched	Enriched	Enriched	Enriched	YES	
P62495;B7Z7P8;P(	Eukaryotic peptide cl	ETF1	49.03	34.8	21	21	112.77	0	89854	72843	67589	70215	78301	76131	75945	64929	40385	70902	Moderate	Enriched	Enriched	Enriched	YES	
P62633-2;P62633;I	Cellular nucleic acid-	CNBP	18.742	41.2	15	3	10.496	0	7881	4227.9	5767.9	8029.3	8487.1	8007.8	4373.9	6060.1	2370.5	5835.9	Enriched	Enriched	Enriched	Enriched	YES	
P62633-8;P62633-	Cellular nucleic acid-	CNBP	18.871	40.4	15	3	57.779	0	88153	38786	70122	75164	83712	81773	74505	70021	44248	80798	Enriched	Enriched	Enriched	Enriched	YES	
P62701;A6NH36	40S ribosomal protei	RPS4X	29.597	66.5	63	33	323.31	0	490540	266860	348780	443150	391220	546010	529930	503410	236760	396220	Enriched	Enriched	Enriched	Enriched	YES	
P62750;H7BY10;K	60S ribosomal protei	RPL23A	17.695	52.6	34	34	190.19	0	283420	160470	188670	263980	251510	301770	368780	223480	205150	257740	Enriched	Enriched	Enriched	Enriched	YES	
P62753;A2A3R7	40S ribosomal protei	RPS6	28.68	43.8	37	10	323.31	0	419110	208890	262530	485740	299500	434920	543540	469160	229200	459250	Enriched	Enriched	Enriched	Enriched	YES	
P62805	Histone H4	HIST1H4A	11.367	62.1	41	41	323.31	0	526980	310170	510400	525520	547000	463820	969540	1118200	396250	778930	No expres	Low	No expres	No expres	YES	
P62820;E7END7;P	Ras-related protein R	RAB1A	22.677	65.9	43	20	323.31	0	213570	161740	184170	240210	219310	331330	545610	538520	232890	335430	Enriched	Enriched	Enriched	Enriched	YES	
P62829;J3KT29;C9	60S ribosomal protei	RPL23	14.865	65	21	21	248.43	0	186210	85994	123080	127510	131490	213700	283250	225370	87193	146210	Enriched	Enriched	Enriched	Enriched	YES	
P62834;A0A075B6	Ras-related protein R	RAP1A	20.987	43.5	21	4	30.288	0	137300	127470	157890	126260	154190	127690	160480	151400	60258	152060	Enriched	Enriched	Enriched	Moderate	YES	
P62851	40S ribosomal protei	RPS25	13.742	42.4	8	8	27.631	0	53753	31195	24308	89953	34831	48653	17984	20166	8261.3	31005	No expres	Enriched	Enriched	Enriched	YES	
P62854;Q5JNZ5	40S ribosomal protei	RPS26;RPS26P11	13.015	43.5	10	10	89.281	0	199390	65154	85779	228690	137830	385910	93525	155060	57463	168710	Enriched	Enriched	Enriched	Moderate	YES	
P62857	40S ribosomal protei	RPS28	7.8409	52.2	7	7	47.979	0	29204	20565	25167	22577	27878	50506	73904	59674	51390	35237	Enriched	Enriched	Enriched	Enriched	YES	
P62873-2;P62873;I	Guanine nucleotide-t	GNB1	36.297	26.2	13	1	22.721	0	17861	14038	13555	15411	17199	30876	45779	73258	17708	24549	Enriched	Enriched	Enriched	Enriched	YES	
P62877	E3 ubiquitin-protein	RBX1	12.274	14.8	2	2	1.8109	0.0099	13384	15669	19767	13716	19526	11749	33765	30768	34586	22112	Enriched	Enriched	Enriched	No expression		
P62879;E7EP32;P(	Guanine nucleotide-t	GNB2	37.331	31.8	19	3	76.551	0	109750	53083	77429	85811	82790	91053	69682	94307	42791	87395	Enriched	Enriched	Enriched	Enriched	YES	
P62888;E5RI99	60S ribosomal protei	RPL30	12.784	62.6	12	12	42.769	0	106880	92796	103290	72578	108770	124860	192180	127250	118130	118760	No expres	Enriched	Enriched	Enriched	YES	
Q96EH5;Q59GN2;I	60S ribosomal protei	RPL39L;RPL39P5;RPL3	6.2924	21.6	2	2	4.5491	0.00043	4797	1965.7	2672.6	2170.5	3132.6	2324.8	6526.8	2556.6	7093.8	5238.1	No expres	No expres	Low	No expression		
P62899;H7C2W9;C	60S ribosomal protei	RPL31	14.463	50.4	17	17	47.097	0	127720	82706	100700	89531	113640	130750	134030	113080	93552	95675	Enriched	Enriched	Enriched	Enriched	YES	
P62906	60S ribosomal protei	RPL10A	24.831	52.1	34	34	165.61	0	256280	176480	186420	190740	246970	368570	399010	350370	176480	226910	Enriched	Enriched	Enriched	No expres	YES	
P62913-2;P62913;(	60S ribosomal protei	RPL11	20.124	47.5	22	22	294.44	0	153400	115700	136390	124430	183370	141470	170300	90405	109210	100920	No expres	Enriched	Enriched	Enriched	YES	
P62917;E9PKZ0;G	60S ribosomal protei	RPL8	28.024	33.5	23	23	128.53	0	79223	51878	63066	57095	76485	81119	191790	135370	72941	81457	Enriched	Enriched	Enriched	Enriched	YES	
P62937;F8WE65;C	Peptidyl-prolyl cis-tra	PPIA	18.012	66.1	33	11	145.35	0	565580	289870	352690	521660	400100	939040	886990	926960	516330	747220	Enriched	Enriched	Enriched	Enriched	YES	
P62942;Q5W0X3;(	Peptidyl-prolyl cis-tra	FKBP1A;FKBP12-Exip2	11.951	38.9	7	7	20.871	0	16120	12936	16122	16446	15411	17154	36444	39385	30513	25026	Moderate	Enriched	Enriched	Moderate		
P62979	Ubiquitin-40S ribosc	RPS27A	17.965	55.8	29	15	323.31	0	209630	143360	187710	285520	229120	246410	378580	320340	187440	374160	No expres	Enriched	Enriched	Enriched	YES	
P62987;M0R2S1	Ubiquitin-60S ribosc	UBA52	14.728	49.2	17	3	6.9933	0	13009	8568.2	8062.8	6785	12993	12855	31058	9725.9	34741	16495	Enriched	Enriched	Enriched	No expression		
P62993;P62993-2	Growth factor recept	GRB2	25.206	26.7	6	6	17.823	0	14635	13320	13884	9505.3	18918	9669.6	9501.4	12306	4050.3	9278.7	Enriched	Enriched	Enriched	Moderate	YES	
P62995-3;P62995;I	Transformer-2 protei	TRA2B	21.935	47.9	16	14	28.719	0	78034	60095	70944	85858	77940	90233	116700	90675	75543	99928	Enriched	Enriched	Enriched	Enriched	YES	
P63000;P63000-2	Ras-related C3 botuli	RAC1	21.45	43.8	22	9	47.595	0	106550	79887	109290	82169	115440	167430	202070	157560	80060	147220	Enriched	Enriched	Enriched	Enriched		
P63010;P63010-2;/	AP-2 complex subun	AP2B1	104.55	20.6	26	11	20.432	0	48624	35105	52357	36667	52351	57255	45508	51829	26077	42081	Low	Enriched	Enriched	Moderate	YES	
P63092;P63092-4;(	Guanine nucleotide-t	GNAS	45.664	37.1	17	1	87.076	0	55957	35199	48838	69608	45701	55642	57839	72535	32755	61993	Enriched	Enriched	Enriched	Enriched	YES	
P63104;E7EX29;B	14-3-3 protein zeta/d	YWHAZ	27.745	74.3	53	35	323.31	0	177380	129180	178270	179950	191140	217740	467910	538510	197050	229720	Enriched	Enriched	Enriched	Enriched	YES	
P63151;P63151-2	Serine/threonine-prot	PPP2R2A	51.691	26.4	13	6	72.592	0	94941	64471	77861	93932	86226	99056	112150	120200	58400	94690	Enriched	Enriched	Enriched	Enriched	YES	
P63167;F8VXL2;F	Dynein light chain 1,	DYNLL1	10.366	51.7	12	8	59.753	0	118190	60278	96167	97163	64583	140590	137030	110950	61503	161020	Enriched	Enriched	Enriched	Enriched	YES	
Q5VTU3;P63172	Dynein light chain Tc	DYNLT1	10.2	34.8	3	3	21.635	0	15346	11282	11947	17771	14561	9632.7	9239.4	15168	5518.1	13047	Enriched	Enriched	Enriched	Enriched	YES	
P63173;J3KT73;J3(	60S ribosomal protei	RPL38	8.2178	52.9	16	16	92.071	0	106610	63226	87124	141490	84090	75046	59589	63417	44982	63761	Enriched	Enriched	Enriched	Enriched	YES	
P63208;F8W8N3;P	S-phase kinase-associ	SKP1	18.658	35	17	14	49.484	0	124460	72806	93410	102760	102910	112690	95933	88946	52232	103420	Enriched	Enriched	Enriched	Moderate	YES	
P63220;Q8WVC2;(	40S ribosomal protei	RPS21	9.1113	68.7	16	16	45.831	0	59646	38750	43434	49493	74683	51394	45536	44479	25829	44908	Enriched	Enriched	Enriched	Enriched	YES	
P63241;P63241-2	Eukaryotic translatio	EIF5A	16.832	61	37	1	8.7477	0	16960	10197	12543	9664	17605	33418	72248	73284	11431	19804	Enriched	Moderate	Enriched	Enriched		
P63244;J3KPE3;D(	Guanine nucleotide-t	GNB2L1	35.076	57.1	50	0	293.66	0	391640	227140	303380	298220	322450	506640	422620	498510	197560	391170	Enriched	Enriched	Enriched	Enriched	YES	
P67775;P67775-2	Serine/threonine-prot	PPP2CA	35.594	49.8	26	2	301.99	0	104000	71299	75762	97151	96302	98896	81648	124050	41309	96200	Low	Enriched	Enriched	Enriched		
P67812;P67812-2;I	Signal peptidase com	SEC11A	20.625	39.1	9	9	18.676	0	20931	13055	19505	36955	13858	23977	21704	20600	11585	24492	Enriched	Enriched	Enriched	Enriched	YES	
Q5SRQ6;P67870;C	Casein kinase II subu	CSNK2B;CSNK2B-LY6	26.925	27.8	9	9	24.746	0	41779	39785	42693	28446	50589	33290	40113	30670	18795	33457	Enriched	Enriched	Enriched	Low	YES	
P67936	Tropomyosin alpha-4	TPM4	28.521	64.1	42	6	145.93	0	66867	65328	85918	93822	88723	65999	168200	139010	127410	107350	Low	Moderate	Enriched	No expres	YES	
P68032;P62736;P6	Actin, alpha cardiac r	ACTC1;ACTA2;ACTG2	42.019	65.5	87	28	323.31	0	485370	373820	271170	466900	353090	516080	486140	680170	194530	780590	Moderate	Low	Moderate	Low		
P68036;P68036-3;I	Ubiquitin-conjugatin	UBE2L3	17.861	53.9	15	15	58.538	0	113190	88307	97576	116110	121890	99200	111060	136870	46773	112550	Enriched	Enriched	Enriched	Enriched	YES	
Q5VTE0;P68104;A	Putative elongation fa	EEF1A1P5;EEF1A1	50.184	50.6	72	45	266.11	0	690190	607230	676190	519780	870540	830460	1251700	763490	556830	605150	Enriched	Enriched	Enriched	Enriched		
P68363;P68363-2	Tubulin alpha-1B ch	TUBA1B	50.151	67.8	96	0	323.31	0	829040	557160	694900	755500	708040	890230	983530	974490	509560	810510	Enriched	Enriched	Enriched	Enriched		
P68366-2;P68366	Tubulin alpha-4A ch	TUBA4A	48.328	70	95	21	114.77	0	166070	150670	274410	99515	219010	140910	197100	157750	82320	144750	Enriched	Enriched	Enriched	Enriched	YES	
P68371	Tubulin beta-4B chai	TUBB4B	49.83	53.5	76	1	323.31	0	760060	556730	667520	788320	806290	728290	915860	998530	473640	704310					YES	
P68402;P68402-3;I	Platelet-activating fac	PAFAH1B2	25.569	35.4	14	13	53.677	0	104510	77511	95789	76767	106330	80467	82099	82220	45968	88931	Moderate	Enriched	Enriched	Low	YES	
P68871	Hemoglobin subunit	HBB	15.998	94.6	62	15	323.31	0	483900	2306700	321850	469560	580670	698890	703910	522110	236560	473950	Moderate	Moderate	Moderate	Moderate	YES	
P69892;P69891;E9	Hemoglobin subunit	HBG2;HBG1	16.126	33.3	5	2	6.0818	0	16279	17436	7358.4	8395.3	8528.5	17416	13358	12377	4664.6	10192	Moderate	Low	No expres	No expression		
P69905;G3V1N2	Hemoglobin subunit	HBA1;HBA2	15.257	50	26	26	145.97	0	154810	578630	127770	147430	192310	255860	346340	253750	110920	167510	Enriched	Low	Low	No expres	YES	
P78310-2;P78310-(	Coxsackievirus and a	CXADR	38.123	22.7	8	8	31.984	0	67532	56850	62421	60640	76442	62741	47751	43242	25859	54342	Enriched	Enriched	Enriched	Low	YES	
P78345	Ribonuclease P prote	RPP38	31.834	9.5	2	2	48.256	0	38700	35656	41299	29026	47510	26703	20209	29770	6450.2	30879	Enriched	Moderate	Enriched	Moderate		
P78346;P78346-2;(	Ribonuclease P prote	RPP30	29.321	13.8	3	3	6.6432	0	11336	9897.1	8265.9	8307.3	10572	11990	6505.6	6419.4	4501.1	9668.6	Enriched	Moderate	Enriched	No expres	YES	
P78347-2;P78347-	General transcription	GTF2I	107.97	21.5	23	23	54.395	0	102600	98727	97351	103130	117520	90759	112100	115420	64529	96058	Enriched	Enriched	Enriched	Enriched	YES	
P78356	Phosphatidylinositol	PIP4K2B	47.377	15.1	5	4	9.9987	0	19148	16515	17677	16124	21384	12977	16585	14975	7684.1	14856	Moderate	Moderate	Moderate	Enriched	YES	
P78362;P78362-2	SRSF protein kinase	SRPK2	77.526	7.6	5	0	3.4191	0.00079	7510.2	7941.2	8095.8	6324.1	9849.3	6263	7263.7	5607.4	3330.5	5781.5	Moderate	Moderate	Enriched	Low	YES	
P78369;P78369-3;I	Claudin-10	CLDN10	24.488	26.3	6	6	27.697	0	17695	15643	17230	26480	19948	18426	26729	33930	11939	27514	Enriched	Enriched	Enriched	Enriched	YES	
P78371;P78371-2;I	T-complex protein 1	CCT2	57.488	59.4	69	69	323.31	0	549660	312920	363580	506900	430210	626050	513330	636940	285640	550360	Enriched	Enriched	Enriched	Enriched	YES	
P78406;E9PQ57;E	mRNA export factor	RAE1	40.968	11.7	5	5	10.08	0	17648	11892	14702	18810	19732	11763	9232.2	10938	5057.1	11866	Moderate	Moderate	Enriched	Enriched	YES	
P78417	Glutathione S-transfe	GSTO1	27.566	44.8	25	3	13.253	0	7762.9	9234.5	10970	6236.2	12171	5438.9	27289	35178	8409.3	9271.4	Enriched	Enriched	Enriched	Enriched	YES	
P78504-2;P78504	Protein jagged-1	JAG1	116.58	0.9	1	1	1.8299	0.00975	9609.7	7140.2	7164.1	10051	7748.5	6905.9	10173	7650.9	7326.9	7675.3	Enriched	Enriched	Enriched	Enriched		
P78527;P78527-2	DNA-dependent prot	PRKDC	469.08	28.9	150	150	323.31	0	639550	425160	526350	653120	523140	746260	805700	872550	402350	731510	No expres	Moderate	Enriched	Moderate	YES	
P78560;F8VV49;F	Death domain-contai	CRADD	22.745	19.6	6	6	17.296	0	3806.2	3166.1	3918.7	6216.5	3465.2	4457	5269.4	7336.8	3076.1	5933.9	Moderate	Moderate	Enriched	Enriched	YES	
X6R8F3;P80188;P(	Neutrophil gelatinase	LCN2	22.788	14.5	2	2	2.591	0.00272	4286	3590.6	3995	5952.7	3741.9	7177.1	3800.9	6185.8	2776.3	5000.9	Enriched	Low	Enriched	Low	YES	
P80217;P80217-2	Interferon-induced 3	IFI35	31.546	3.1	1	1	2.5984	0.00273	12629	13449	11393	6273.1	9067.4	2991.5	7584.7	6310.1	6711.3	11532	Enriched	Moderate	Enriched	Moderate	YES	
P80294;P0DM35	Metallothionein-1H;I	MT1H;MT1HL1	6.0393	31.1	3	2	4.3206	0.00063	1320.6	2664.3	1364.3	917.01	1854.3	850.3	1683.6	2336.2	986.56	1069.2	Enriched	Enriched	Enriched	Enriched		
P80297;P13640-2;I	Metallothionein-1X;I	MT1X;MT1G;MT2A;M	6.0683	65.6	10	6	39.325	0	45667	35528	35452	21392	51085	45116	183000	430330	91389	59025	Enriched	Enriched	Enriched	Moderate		
P80723	Brain acid soluble pr	BASP1	22.693	52.9	9	9	75.912	0	26612	21637	36546	21400	39438	16030	46558	42160	31036	34189	Enriched	Moderate	Enriched	Moderate	YES	
P80748	Ig lambda chain V-III	region LOI	11.935	27.9	3	0	6.3864	0	14550	13812	29991	25808	12229	13369	14072	58404	12831	15690						
P82094;P82094-2;/	TATA element modu	TMF1	122.84	12	11	11	35.494	0	12698	7667.9	9516.9	20035	9288.2	13011	10679	13205	6415.7	17281	Low	Moderate	Enriched	No expres	YES	
P82663	28S ribosomal protei	MRPS25	20.116	39.9	5	5	11.853	0	12596	9478.7	9823.2	9978.9	18877	10186	11906	10245	6430.9	13716	Low	Enriched	Enriched	No expres	YES	
P82664	28S ribosomal protei	MRPS10	22.999	12.4	2	2	6.3715	0	6626.1	2947.2	4064.6	9532.7	3589.7	14792	6406.2	9322.7	1866.7	10233	Enriched	Enriched	Enriched	No expres	YES	
P82909	28S ribosomal protei	MRPS36	11.466	62.1	6	6	36.607	0	36514	33344	36105	21198	41353	29014	47254	35007	23870	45607	Enriched	Enriched	Enriched	No expres	YES	
P82914	28S ribosomal protei	MRPS15	29.842	12.5	4	4	14.924	0	23608	19968	22580	20917	37020	12251	15181	18932	8340.4	23337	Enriched	Enriched	Enriched	No expression		
P82932	28S ribosomal protei	MRPS6	14.226	18.4	2	2	3.9843	0.00062	7228.2	4499	5478.4	4888	7978	4894.6	7472.3	5813.7	9287	10732	Moderate	Enriched	Enriched	Low	YES	
P82933	28S ribosomal protei	MRPS9	45.834	7.8	3	3	5.4575	0	19282	15728	18696	15081	21292	24194	41332	50305	13685	20704	Low	Enriched	Enriched	No expres	YES	
Q5JSL0;Q5JSK6;Q	High mobility group	HMGN5	16.496	36.5	6	6	10.82	0	11372	10711	13954	8245.8	19092	7729.7	15474	8263.8	8382.9	8731.8					YES	
P83111;P83111-2	Serine beta-lactamase	LACTB	60.693	12.1	6	6	9.4544	0	11766	8561.2	10844	12096	10048	12773	10765	12603	5405.8	11379	Moderate	Enriched	Enriched	No expres	YES	
P83436	Conserved oligomeric	COG7	86.343	11.9	10	10	23.91	0	20703	15203	16209	27754	17962	19695	16044	21414	8803.4	20626	No expres	Moderate	Moderate	No expres	YES	
P83731;C9JXB8;C	60S ribosomal protei	RPL24	17.779	31.2	8	8	19.534	0	29115	19305	20579	33815	23238	32375	66298	60875	16787	27387	Enriched	Enriched	Enriched	Enriched	YES	
P84022	Mothers against deca	SMAD3	48.08	7.3	3	3	8.927	0	5967.6	6400.5	9512.7	4813	7820.3	11289	18778	18184	7702.4	14920	Enriched	Enriched	Enriched	Moderate	YES	
P84090	Enhancer of rudimen	ERH	12.259	28.8	7	7	48.04	0	50386	31963	24635	51618	37534	38188	50333	69115	18505	52267	No expres	Enriched	Enriched	Enriched	YES	
P84095	Rho-related GTP-bin	RHOG	21.308	42.9	12	9	23.908	0	38536	36337	33257	39127	36311	43510	57549	66236	26422	45788	Enriched	Enriched	Enriched	Enriched	YES	
P84101-4;P84101;I	Small EDRK-rich fac	SERF2	5.2159	42.2	4	4	6.7838	0	6065	4681.8	5312.6	6292.7	6562	5022.2	8590.6	4147.8	10782	10359	Enriched	Enriched	Enriched	No expression		

P84103-2;P84103;	Serine/arginine-rich s	SRSF3	14.203	44.4	12	9	136.36	0	86942	59725	70382	64532	101810	65809	89259	94615	41060	86479						YES			
P98082-2;P98082-	Disabled homolog 2	DAB2	58.86	13	7	7	18.382	0	14151	14134	13267	15330	17909	11315	21692	27786	12966	16719	Low	Enriched	Enriched	Moderate		YES			
P98095;P98095-2	Fibulin-2	FBLN2	126.57	5.8	7	7	22.643	0	5127.8	6648	5906.4	4663.1	7431.5	5448.3	5853.6	8891.5	2467.7	7183.8	Moderate	No expres	No expres	Moderate		YES			
P98160	Basement membrane-	HSPG2	468.83	37.4	263	263	323.31	0	1255700	1071200	1276600	1126100	1524000	1347600	1661300	1659900	710350	1507900	Low	Moderate	Enriched	Moderate		YES			
P98172	Ephrin-B1	EFNB1	38.006	7.5	2	2	4.6195	0.00043	7099.1	5673.6	5804.1	5955.9	7164.9	10569	11231	9669.7	4889	7545.3	Enriched	No expres	Low	Moderate		YES			
P98179	Putative RNA-bindin	RBM3	17.17	38.2	8	8	34.981	0	37204	24209	40354	46396	37152	58199	100180	55703	86528	69176	No expres	Moderate	Enriched	Enriched		YES			
Q00013-2;Q00013;	55 kDa erythrocyte m	MPP1	49.074	15.6	8	8	8.0082	0	7838.9	8206.7	6577.5	7966.4	8586.2	7355.5	6657.8	9688.8	4028.7	8101.9	Enriched	Enriched	Enriched	Moderate		YES			
Q00059;Q00059-2;	Transcription factor	TFAM	29.096	40.7	16	16	37.833	0	75554	54612	65763	71955	84236	67683	109590	88614	67933	92756	Enriched	No expres	Moderate	Low		YES			
Q00169;F5GWE5;	Phosphatidylinositol	PITPNA	31.806	30.4	9	9	25.945	0	89248	85850	76701	64893	99091	58317	64433	65492	40770	71750	Enriched	Enriched	Enriched	Moderate		YES			
Q00266	S-adenosylmethionin	MAT1A	43.647	28.1	11	4	13.322	0	18505	15004	16630	22341	21304	17262	13836	13842	6570.6	14574	Moderate	Low	Low	Moderate		YES			
Q00325-2;Q00325	Phosphate carrier pro	SLC25A3	39.958	28	18	2	64.832	0	70932	42680	120670	38465	67005	60656	113340	119240	50555	75941	No expres	Enriched	Enriched	Enriched		YES			
Q00403;B1APE1	Transcription initiatio	GTF2B	34.833	25	5	5	27.258	0	20071	14802	16436	18179	15320	19471	19012	26251	8704.4	25721	Enriched	Moderate	Enriched	Moderate		YES			
Q00534	Cyclin-dependent kin	CDK6	36.938	18.7	8	8	30.474	0	35416	18993	23911	41964	26334	50611	37720	48377	15224	40840	Moderate	Moderate	Enriched	Moderate		YES			
Q00535;Q00535-2	Cyclin-dependent-lik	CDK5	33.304	20.9	5	4	7.072	0	20236	16244	14032	18163	20379	15819	17393	19362	8817.3	15794	No expres	Moderate	Moderate	No expres		YES			
Q00577	Transcriptional activa	PURA	34.91	23	18	18	55.664	0	160750	120220	157140	139670	151550	155750	150860	153540	100800	162500	Moderate	Enriched	Enriched	Moderate		YES			
Q00587-2;Q00587	Cdc42 effector protei	CDC42EP1	39.686	6.8	2	2	11.717	0	10496	9771.7	10536	5918.7	9915.7	13872	18117	13239	14747	14235	Moderate	Moderate	Moderate	Enriched		YES			
Q00610-2;A0A087	Clathrin heavy chain	CLTC	187.89	45.8	167	167	323.31	0	1018200	812310	832730	1139200	937170	974880	1111800	1247400	587490	1057900	Enriched	Enriched	Enriched	Enriched		YES			
Q00653-4;Q00653	Nuclear factor NF-ka	NFKB2	96.677	4	3	3	24.509	0	10319	7153.7	8670.6	9015.4	11226	11698	28256	21971	16284	17466	Enriched	Low	Moderate	No expres		YES			
Q00688	Peptidyl-prolyl cis-tra	FKBP3	25.177	35.7	14	14	51.268	0	57093	33826	42602	57882	59261	56985	61206	48675	25489	52999	Enriched	Enriched	Enriched	No expres		YES			
Q00765	Receptor expression-	REEP5	21.493	19.6	7	7	15.883	0	23742	13305	18960	17511	25822	18516	26468	16852	21016	20916	Enriched	Enriched	Enriched	Enriched		YES			
Q00796;H0YLA4	Sorbitol dehydrogena	SORD	38.324	34.7	14	14	37.856	0	47029	36952	42029	37951	47112	63102	63399	57737	40448	47886	Enriched	Moderate	Enriched	Moderate		YES			
Q00839	Heterogeneous nucle	HNRNPU	90.583	35	61	3	255.22	0	479880	351210	411250	425240	435620	414430	548290	599390	343900	540610	Enriched	Enriched	Enriched	Enriched		YES			
Q00839-2	Heterogeneous nucle	HNRNPU	88.979	33.7	59	1	10.176	0	3320.6	2637.7	3167.7	1550.6	2151.7	1341.6	1233.6	1150.7	866.39	2037.9	Enriched	Enriched	Enriched	Enriched		YES			
Q00G26	Perilipin-5	PLIN5	50.791	5.8	3	3	9.5247	0	8925	4543.7	6112.9	7702.7	5630.7	8234	8772.6	11825	6742	8429.5						YES			
Q01081;Q01081-2	Splicing factor U2AF	U2AF1	27.872	20.8	5	2	3.6109	0.0008	23685	15299	20333	11849	34625	21603	15962	11812	7321.8	12869	No expres	Enriched	Enriched	Enriched		YES			
Q01081-4	Splicing factor U2AF	U2AF1	19.715	26.9	5	2	23.011	0	35965	19750	31036	44236	24646	33355	35580	32945	21560	38400	No expres	Enriched	Enriched	Enriched		YES			
Q01082;A0A087W	Spectrin beta chain,	SPTBN1	274.61	50.4	197	182	323.31	0	935500	707340	858020	940130	994380	766930	1063600	1301900	563110	1021300	Enriched	Enriched	Enriched	Moderate		YES			
Q01085;Q01085-2;	Nucleolysin TIAR	TIAL1	41.59	18.4	10	4	33.757	0	27836	21552	26410	24901	31442	23253	23520	24583	12192	25887	Enriched	Enriched	Enriched	Enriched		YES			
Q01105;A0A087X	Protein SET;Protein	SET;SETSIP	33.488	29	18	2	2.1553	0.00611	408.63	409.73	572.74	483.23	750.56	869.78	7626	1283.5	8493.3	2749.1	Enriched	Enriched	Enriched	Enriched		YES			
Q01105-2;Q01105-	Protein SET	SET	32.103	30	18	2	116.75	0	106270	75275	98432	110110	84567	95474	234620	167940	104840	138220	Enriched	Enriched	Enriched	Enriched		YES			
Q01118;F8WD82;	Sodium channel prot	SCN7A	193.49	2.4	4	4	21.349	0	24645	17472	42594	18705	27649	30977	30394	22227	13884	30719	No expres	Moderate	Low	No expres		YES			
Q01415;B7ZAX5;	N-acetylgalactosamin	GALK2	50.378	12.7	8	8	25.124	0	37591	31762	38403	35362	51067	26335	28986	23784	21972	30213	Moderate	Moderate	Moderate	Low		YES			
Q01459	Di-N-acetylchitobias	CTBS	43.759	3.4	1	1	6.8316	0	19761	24178	20593	18536	23599	23414	17019	18934	11076	18172	Moderate	Moderate	Enriched	Enriched		YES			
Q01469;I6L8B7	Fatty acid-binding pr	FABP5	15.164	71.1	27	27	323.31	0	327350	347780	277720	397380	365930	242560	225540	204230	185230	428180	Low	Enriched	Enriched	Moderate		YES			
Q01518;Q01518-2	Adenylyl cyclase-ass	CAP1	51.901	53.3	52	43	157.12	0	213930	169650	181810	172000	206480	229280	332960	402620	175000	238290	Enriched	Enriched	Enriched	Enriched		YES			
Q01780;Q01780-2	Exosome component	EXOSC10	100.83	5.5	5	5	7.9489	0	9285.8	6661.7	7028.9	7984.3	7913	6837.9	5554.8	6663.1	3122	8009.6	Enriched	Moderate	Moderate	Moderate		YES			
Q01804-5;Q01804-	OTU domain-contain	OTUD4	116.95	3.1	2	2	8.7236	0	24038	19674	20486	23315	26006	18589	20864	18339	12049	21290	Enriched	Moderate	Enriched	Enriched		YES			
Q01813;Q01813-2	ATP-dependent 6-ph	PFKP	85.595	15.6	15	11	31.206	0	22912	19474	20706	30655	22620	23898	24222	33745	13167	29940	Enriched	Moderate	Enriched	Moderate		YES			
Q01831;Q01831-2	DNA repair protein c	XPC	105.95	10.5	7	7	39.546	0	21092	15231	21048	15220	19480	12846	13497	12739	9663.6	20588	Enriched	Enriched	Enriched	Enriched		YES			
Q01970-2;Q01970	1-phosphatidylinosit	PLCB3	131.2	8.3	9	9	53.232	0	23429	15759	17032	41747	13577	23904	18983	30565	11345	32667	Enriched	Low	Moderate	Low		YES			
Q01995;H0YCU9	Transgelin	TAGLN	22.611	60.7	34	31	211.09	0	189780	162970	121610	151430	201120	214970	322370	318240	141870	461950	Moderate	Enriched	Enriched	Enriched		YES			
Q02108-2;Q02108;	Guanylate cyclase so	GUCY1A3	70.184	2.6	2	2	2.1391	0.0061	4876.4	3880	4426.2	3334.4	6083.7	3695.2	4068.5	4205.5	2151.9	4732.6	Enriched	Enriched	Enriched	Moderate		YES			
Q02218;E9PDF2;E	2-oxoglutarate dehyd	OGDH	115.93	32.8	43	36	155.91	0	142770	134070	142640	131850	194480	126670	119830	132090	63879	137890	Low	Moderate	Moderate	Low		YES			
Q02252;Q02252-2;	Methylmalonate-sem	ALDH6A1	57.839	44.9	39	39	268.17	0	247430	224500	242100	162420	288950	177560	268320	204250	138320	181540	Moderate	Enriched	Enriched	Moderate		YES			
Q02318	Sterol 26-hydroxylas	CYP27A1	60.234	2.1	1	1	2.9126	0.00187	3580	3708.9	3510.1	4501	3171.4	3875.6	2189.7	4759	1225.5	4005.2	Enriched	No expres	Low	No expres		YES			
Q02338;C9JEB9;C	D-beta-hydroxybutyr	BDH1	38.157	5	2	2	1.8217	0.00974	2392.4	1711.2	2119.9	3104.1	1820	5637.6	2301.2	2781.3	1578.7	2467.6	Enriched	Enriched	Enriched	Low					
Q02388-2;Q02388	Collagen alpha-1(VII	COL7A1	292.26	0.6	2	2	2.3267	0.00462	3257	2950.4	5574.1	1369.2	4728.4	5572.5	6498	4693.9	1788.3	2656	Enriched	No expres	Moderate	Moderate					
Q02446	Transcription factor	SP4	81.984	1.1	1	1	2.0159	0.00771	832.22	703.71	773.54	547.03	898.56	664.46	1134.3	806.17	798.11	912.16	Moderate	Enriched	Enriched	No expression					
Q02487;Q02487-2	Desmocollin-2	DSC2	99.961	13.1	12	11	143.02	0	55185	30912	35835	47443	40183	35518	43942	42391	20115	42765	Enriched	Enriched	Enriched	No expres		YES			
Q02750;Q02750-2	Dual specificity mito	MAP2K1	43.439	28.5	14	5	37.898	0	76150	70818	72220	72708	119740	51057	102710	86207	50858	55584	Moderate	Enriched	Enriched	Enriched		YES			
Q02790	Peptidyl-prolyl cis-tra	FKBP4	51.804	51.4	26	26	275.2	0	210700	187830	169780	200560	243060	150280	212530	247700	103960	202130	Enriched	Enriched	Enriched	Enriched		YES			
Q02809;Q02809-2	Procollagen-lysine,2-	PLOD1	83.549	3.2	3	3	3.2474	0.00077	2611.9	4451.3	3749.7	2265.7	4003.9	1662	2784	2281.1	1659.6	1821.5	Moderate	Enriched	Enriched	Enriched		YES			
Q02818;C9JKZ2;H	Nucleobindin-1	NUCB1	53.879	26.7	18	17	56.555	0	27792	28955	27426	40155	26474	24303	25744	27980	16601	29531	Low	Enriched	Enriched	No expres		YES			
Q02878	60S ribosomal protei	RPL6	32.728	40.6	36	36	271.04	0	258970	192590	232330	210190	346580	196460	255690	206220	130190	195820	No expres	Enriched	Enriched	Enriched		YES			
Q02880-2;Q02880;	DNA topoisomerase	TOP2B	182.66	11.7	19	19	77.403	0	56955	41006	50746	57376	57754	47199	52629	63363	33173	54364	Enriched	Enriched	Enriched	Enriched		YES			
Q02952-3;Q02952-	A-kinase anchor prot	AKAP12	180.99	19.6	38	38	300.28	0	191240	162240	263460	185650	262690	169510	369150	391030	190510	277080	Moderate	Moderate	Enriched	Low		YES			
Q02978;I3L1P8;Q	Mitochondrial 2-oxo	SLC25A11	34.061	39.8	22	22	62.946	0	72788	77115	91794	62234	101180	81196	144160	131580	71214	90434	Moderate	Enriched	Enriched	Moderate		YES			
Q03111	Protein ENL	MLLT1	62.055	2.1	1	1	4.1866	0.00062	6316.7	4510.7	7133.3	4595.3	8645.3	4647.1	7529	6729.2	4883.3	6963.2	Enriched	Enriched	Enriched	Moderate					
Q03135;E9PCT5;C	Caveolin-1;Caveolin	CAV1	20.471	39.3	10	10	36.939	0	86687	81260	103630	114850	114570	96656	145210	122390	53805	167090	Moderate	Moderate	Enriched	Enriched		YES			
Q03169	Tumor necrosis facto	TNFAIP2	72.66	8.3	5	5	7.4325	0	8911.8	7893.1	9719.4	10660	10281	7839.5	9698.8	9785.4	9294.8	9653	Enriched	Moderate	Enriched	Moderate		YES			
Q03591;B1AKG0	Complement factor H	CFHR1	37.65	26.1	9	3	281.3	0	68624	58594	33405	81560	65593	68077	51739	165460	64344	32665	No expres	No expres	No expres	Moderate		YES			
Q03692	Collagen alpha-1(X)	COL10A1	66.157	1.5	3	2	3.2225	0.00077	605.18	1349.5	1212.8	897.29	3118	701.71	999.08	625.77	799.05	610.84	Moderate	Low	Low	Low		YES		YES	
Q04446;E9PGM4	1,4-alpha-glucan-bra	GBE1	80.473	25.6	25	25	74.798	0	72272	53631	62987	87151	76491	90233	72810	70802	31382	75888	Enriched	Enriched	Enriched	Enriched		YES			
Q04656-5;Q04656;	Copper-transporting	ATP7A	154.36	2.9	4	4	28.773	0	23202	20408	20698	18629	26288	17013	15092	10704	11229	18666	Moderate	Low	Moderate	Moderate					
Q5T3G3;Q5T7A9;	Transducin-like enha	TLE1	27.064	9.5	2	2	1.9049	0.0083	3069.4	2727.2	4472.6	2817.8	5006.6	3720.3	5946.7	3347.6	3126.9	3724.2	Enriched	Enriched	Enriched	Enriched					
Q04760-2;Q04760	Lactoylglutathione ly	GLO1	19.043	47.9	16	16	94.073	0	44920	36677	37305	48061	46388	58925	90260	117310	34706	62318	Enriched	Enriched	Enriched	Enriched		YES			
Q04837;E7EUY5	Single-stranded DNA	SSBP1	17.259	50.7	17	17	65.589	0	86887	59884	65109	91572	82026	97640	99167	129840	31233	88313	Low	Enriched	Enriched	Enriched		YES			
Q04917	14-3-3 protein eta	YWHAH	28.218	59.8	29	25	323.31	0	131340	99845	122090	114560	132290	127430	217770	286430	102560	162160	Low	Enriched	Enriched	Enriched		YES			
Q04941	Proteolipid protein 2	PLP2	16.691	16.4	6	6	13.258	0	17810	15464	16549	16081	23413	15754	20732	15994	13967	16957	Enriched	Enriched	Enriched	Enriched		YES			
Q05086-2;Q05086-	Ubiquitin-protein lig	UBE3A	97.967	12.9	10	10	22.388	0	27119	16991	21024	23948	26110	25219	24042	22796	10165	26996	Enriched	Enriched	Enriched	Enriched		YES			
Q05193-5;Q05193-	Dynamin-1	DNM1	95.894	9.9	10	0	5.0172	0.00044	4521.8	5213.3	5839.4	3742.8	7990.1	4777.6	7117.1	3774	4177.7	4229	Enriched	Enriched	Moderate	Enriched		YES			
Q05209;H0YC15;	Tyrosine-protein pho	PTPN12	88.105	3.2	2	2	68.436	0	11929	7488.7	9235.4	9425.3	9318.2	10222	12140	10331	7044	14310	No expres	Moderate	Enriched	Enriched		YES			
Q05315	Galectin-10	CLC	16.453	8.5	1	1	1.8022	0.00989	2965.4	3473.6	2811.2	6228.9	3610.5	4679	3500.4	7875.5	2272.2	5216.6	No expres	No expres	No expres	No expression					
Q05469-2;Q05469;	Hormone-sensitive li	LIPE	84.127	4.1	2	2	5.2735	0.00022	767.86	665.74	1473.6	2855.3	1144.4	1493.7	947.68	1418.2	853.36	2719.8	Low	No expres	Low	Enriched		YES			
Q5T760;Q05519-2;	Serine/arginine-rich s	SRSF11	42.316	18.3	8	8	15.347	0	39222	39169	40448	38935	49984	45959	114150	58941	60451	52582						YES			
Q05639	Elongation factor 1-a	EEF1A2	50.47	30.9	28	1	3.0895	0.00095	7938.2	8557.8	13497	6567.7	11945	7602.9	9646.9	7522.6	5085	6619.5	Enriched	Moderate	Enriched	Enriched		YES			
Q05655;Q05655-2	Protein kinase C delt	PRKCD	77.504	13.5	9	9	84.071	0	40420	27871	33704	27269	38419	31216	40658	41296	20281	44846	No expres	Low	Moderate	Low		YES			
Q05682;E7EX44;Q	Caldesmon	CALD1	93.23	35.8	49	6	315.37	0	195390	248420	249700	179650	326310	193830	437000	394900	249650	382000	Low	Enriched	Enriched	Moderate		YES			
Q05682-5;Q05682-	Caldesmon	CALD1	61.212	45.7	44	1	4.2753	0.00063	2704.8	4138.1	3136.3	3575.3	5894.7	2168.4	5173.8	3885.6	4228.6	7264.3	Low	Enriched	Enriched	Moderate		YES			
Q05707-2;Q05707;	Collagen alpha-1(XI	COL14A1	191.9	27.6	64	64	316.55	0	225250	207540	319750	293490	273310	263560	409240	497220	150000	267170	No expres	No expres	Low	Low		YES			
Q06124-2;Q06124;	Tyrosine-protein pho	PTPN11	68.01	12.5	9	8	21.532	0	51377	44327	48507	47524	59199	36706	41002	41104	24926	45929	Enriched	Enriched	Enriched	Enriched		YES			
Q06141	Regenerating islet-de	REG3A	19.395	43.4	19	19	243.45	0	77266	72102	72739	93874	82701	59642	97843	114330	502120	101020	Enriched	Moderate	Enriched	Low		YES		YES	
Q06203	Amidophosphoribosy	PPAT	57.398	13.2	6	6	10.487	0	15710	10891	11910	12433	19633	10061	8307.4	6050	4550.1	9123.4	Moderate	Moderate	Moderate	No expres		YES			
Q06210-2;Q06210	Glutamine--fructose-	GFPT1	76.758	52.9	69	69	323.31	0	451670	266370	332830	314660	446120	406290	429000	495130	176420	354590	Enriched	Enriched	Enriched	Enriched		YES			
Q06278	Aldehyde oxidase	AOX1	147.92	39	75	66	323.31	0	409850	252120	339580	363630	398380	282580	411450	338020	207430	303570	Enriched	Enriched	Enriched	Enriched		YES			
Q06323;Q06323-3;	Proteasome activator	PSME1	28.723	59.8	28	27	194.66	0	193850	186700	170370	168340	202090	121580	178680	217880	73675	149650	Enriched	Enriched	Enriched	Moderate		YES			
Q06587;Q06587-2	E3 ubiquitin-protein	RING1	42.429	9.9	3	3	12.439	0	2704.8	2326.6	2833.3	3145.5	4457.6	2397	3478.9	4065.1	1512.3	3265.2	Enriched	Enriched	Enriched	Enriched		YES			
Q06787-6;Q06787-	Fragile X mental reta	FMR1	66.459	15.9	11	1	52.993	0	52621	32383	42604	58837	38804	50281	51011	63897	25276	60840	Moderate	Moderate	Enriched	Low		YES			
Q06830;A0A0A0M	Peroxiredoxin-1	PRDX1	22.11	66.3	27	19	101.21	0	86088	70647	66061	131260	87956	81040	214010	244100	103790	126860	Enriched	Enriched	Enriched	Enriched		YES			
Q07021;I3L3Q7;I3	Complement compon	C1QBP	31.362	23	12	12	155.75	0	71174	50621	66883	48239	72648	50571	55706	93516	34534	76839	Moderate	Enriched	Enriched	Enriched		YES			
Q07065	Cytoskeleton-associa	CKAP4	66.022	60	76	76	323.31	0	306080	231010	239920	317830	289670	390500	474000	557890	278510	370150	Enriched	Enriched	Enriched	Enriched		YES			
Q07075	Glutamyl aminopepti	ENPEP	109.24	3.9	6	6	6.7931	0	14093	10696	13113	15138	14133	12429	14876	14721	8214	13470	No expres	No expres	Moderate	Low		YES			
Q07092-2;Q07092	Collagen alpha-1(XV	COL16A1	157.56	2.6	4	4	7.1859	0	18105	17625	18974	12403	22482	20696	56826	39129	22074	23696	Enriched	Low	Moderate	Moderate		YES			
Q07283	Trichohyalin	TCHH	253.92	0.6	1	1	1.9033	0.0083	599.93	2086.4	1531.9	527.42	2467.5	686.3	5205.6	926.6	13470	1333.1									
Q07507	Dermatopontin	DPT	24.005	34.8	16	16	54.299	0	82670	90127	117250	115210	115740	94706	95952	84890	46375	101190	No expres	Low	Moderate	Enriched		YES			
Q07666;Q07666-2;	KH domain-containi	KHDRBS1	48.227	22.3	18	15	73.271	0	55710	47840	58089	127940	64371	58033	103690	111380	79983	94833	No expres	Enriched	Enriched	Enriched		YES			
Q07812-5;Q07812-	Apoptosis regulator	BAX	18.129	29.9	4	4	18.994	0	8697.6	8478.8	10845	7119.6	11996	7627.8	12318	8648.7	10301	9423.9	Moderate	No expres	Moderate	Moderate		YES			
Q07866-7;Q07866-	Kinesin light chain 1	KLC1	66.291	20.4	13	10	46.054	0	79129	64737	69421	47854	80263	72897	79892	82117	53084	79172	Enriched	Enriched	Enriched	Enriched		YES			
Q07954	Prolow-density lipop	LRP1	504.6	13	57	57	200.15	0	192510	175940	202710	225360	218790	187310	225630	257670	118320	244880	Moderate	Moderate	Moderate	Low		YES			
Q07960;H0YE29;E	Rho GTPase-activati	ARHGAP1	50.435	39.6	20	20	106.21	0	76301	82242	85381	81169	101480	77271	90266	100450	42437	81622	Enriched	Enriched	Enriched	Enriched		YES			
Q08170	Serine/arginine-rich s	SRSF4	56.678	15.2	10	4	8.9305	0	10786	7849.1	11282	8181.8	11413	9712	11293	11743	7006.5	12036						YES			
Q08209-3;Q08209-	Serine/threonine-pro	PPP3CA	52.671	24.9	11	4	61.932	0	30045	26477	27678	26976	31980	27720	35197	33274	20033	28858	Enriched	Enriched	Enriched	No expres		YES			
Q08211	ATP-dependent RNA	DHX9	140.96	27.2	53	53	212.85	0	251700	179840	217640	237450	273360	247180	382130	334310	218680	276830	Enriched	Enriched	Enriched	Enriched		YES			
Q08257;Q08257-3;	Quinone oxidoreduct	CRYZ	35.206	54.7	40	40	151.92	0	175210	150390	160970	141500	227710	238280	234990	222760	98846	189160	Enriched	Enriched	Enriched	Moderate		YES			
Q08345-2;Q08345-	Epithelial discoidin d	DDR1	97.173	3.4	3	3	5.1101	0.00044	718.36	541.48	423.5	494.85	1069.2	458.72	1864.5	671.57	1568.4	954.52	Enriched	Enriched	Enriched	Enriched		YES			
Q08378;Q08378-2;	Golgin subfamily A m	GOLGA3	167.35	17.1	25	25	139.89	0	73341	46434	58886	112290	70105	67581	62040	70305	41997	77548	Moderate	Enriched	Enriched	Enriched		YES			
Q08379;B7ZC06;Q	Golgin subfamily A m	GOLGA2	113.08	13.2	14	14	118.98	0	51367	47968	48924	49036	82744	45461	48769	39378	28174	40289	Enriched	Enriched	Enriched	Moderate		YES			
Q08380;K7ESM3;	Galectin-3-binding p	LGALS3BP	65.33	9.7	6	6	32.499	0	17514	14445	14728	25891	12720	18363	18102	27153	22102	23883	Enriched	Enriched	Enriched	Enriched		YES			
Q08426-2;Q08426	Peroxisomal bifuncti	EHHADH	69.153	5.4	3	3	10.626	0	14155	14550	15755	12905	16351	14704	15395	10719	6809.4	11280	No expres	No expres	Moderate	Low		YES			
Q08431;X6R3G6;	Lactadherin;Lactadh	MFGE8	43.122	26.6	12	12	30.11	0	39665	40054	34552	38064	38624	44646	40632	49887	25913	40385	Moderate	Low	Moderate	Enriched		YES			
Q08623;Q08623-2;	Pseudouridine-5-mo	HDHD1	25.249	21.9	4	4	22.771	0	18819	8882.8	12098	24302	9654.7	16858	16133	23216	10001	20944						YES			
Q08722-2;Q08722-	Leukocyte surface an	CD47	31.742	6.5	3	3	6.0567	0	9475.8	9359.2	9986	9093.3	11256	15727	33911	44943	8317.1	17308	Enriched	Enriched	Enriched	Moderate					
Q08752	Peptidyl-prolyl cis-tra	PPID	40.763	12.4	6	6	10.993	0	5363.9	4166.8	4934.7	6596.2	5470.2	7682.5	14809	12248	14661	9463.8	Moderate	Moderate	Enriched	Moderate		YES			
Q08830	Fibrinogen-like prote	FGL1	36.379	14.4	6	6	12.178	0	11856	14906	36837	33944	27628	17096	51664	29506	12884	23526	Moderate	Enriched	Enriched	Enriched		YES			
Q08945	FACT complex subu	SSRP1	81.074	23.7	20	20	47.174	0	43337	36628	42948	51164	48545	50113	53721	54264	46149	49733	Moderate	Enriched	Enriched	Enriched		YES			
Q08AM6	Protein VAC14 hom	VAC14	87.972	12.7	9	9	132.54	0	33716	22460	26313	39696	32147	26542	27206	23933	14575	26817	Low	Low	Moderate	No expres		YES			
Q08J23-2;Q08J23;	tRNA (cytosine(34)-	NSUN2	82.392	23	19	19	104.87	0	53471	32874	44182	51808	56854	59588	59479	50640	26936	65818	Enriched	Enriched	Enriched	No expres		YES			
Q09161	Nuclear cap-binding	NCBP1	91.838	8.4	6	6	19.247	0	6940.2	5922.2	7715.5	5002.2	3890.7	11124	12649	17206	5746.5	11372	No expres	Low	Moderate	No expres		YES			
Q09666	Neuroblast differenti	AHNAK	629.09	62.6	375	375	323.31	0	2752700	2682700	3340600	2557700	3337500	2374700	3319600	3479900	1595500	3199100	Moderate	Enriched	Enriched	Enriched		YES			
Q0VAF6	Syncollin	SYCN	14.405	26.9	16	16	46.845	0	51296	43509	46956	43441	42535	64080	95934	49050	46034	44065	Low	Enriched	Enriched	No expres		YES		YES	YES
Q0VF96;Q0VF96-2	Cingulin-like protein	CGNL1	149.08	11.3	13	13	45.146	0	27918	25495	30905	30756	28975	22361	37385	36878	32743	38298	Moderate	Enriched	Enriched	No expres		YES			
Q10469	Alpha-1,6-mannosyl-	MGAT2	51.55	10.7	4	4	7.2001	0	58060	40586	45222	38489	68744	46192	34164	25589	19541	41789	No expres	Enriched	Enriched	Low		YES			
Q10471;Q10471-2	Polypeptide N-acetyl	GALNT2	64.732	21.9	15	15	28.419	0	104410	69142	54082	73454	97746	75847	67075	52872	33554	64377	Enriched	Enriched	Enriched	No expres		YES			
Q10472	Polypeptide N-acetyl	GALNT1	64.218	11.4	6	6	9.1309	0	16445	10864	11714	14492	14257	13463	10536	9987.4	5721.4	12087	Enriched	Enriched	Enriched	Moderate		YES			
Q10567-3;Q10567-	AP-1 complex subun	AP1B1	103.56	27.5	35	20	86.512	0	125440	101270	116700	127830	138370	156700	177810	187470	84397	148110	Enriched	Moderate	Enriched	Enriched		YES			
Q10570;A0A087X	Cleavage and polyad	CPSF1	160.88	8	14	14	68.889	0	36487	27913	38458	47691	38361	38400	44013	50743	30554	48500	Moderate	Enriched	Enriched	Moderate		YES			
Q12765;Q12765-2;	Secernin-1	SCRN1	46.382	27.1	16	10	104.79	0	94420	52459	82889	95382	101180	81430	74160	83650	54614	84692	Enriched	Enriched	Enriched	Enriched		YES			
Q12769;G3V198;E	Nuclear pore comple	NUP160	162.12	9.9	13	13	24.746	0	51815	32185	40440	51372	50435	38838	29457	44622	13818	44076	No expres	Low	Moderate	Low		YES			
Q12774	Rho guanine nucleoti	ARHGEF5	176.8	2.9	3	2	15.157	0	8658.4	13617	7131.2	7504.9	10776	7291	8423.7	6937.9	5559.8	8661.1	Enriched	Enriched	Moderate	Enriched		YES			
Q12778	Forkhead box protei	FOXO1	69.661	2.3	1	1	5.1055	0.00044	10348	5824.8	10888	4432.5	10746	5447	7620.5	5960.7	4132.7	6066.3	Enriched	Enriched	Enriched	Enriched					
Q12789-3;Q12789	General transcription	GTF3C1	236.28	2.9	5	5	24.906	0	12458	8956.7	10033	14112	9316.4	8984.5	10017	11418	10483	11674	Enriched	Enriched	Enriched	Enriched		YES			
Q12792;Q12792-3;	Twinfilin-1	TWF1	40.282	24.9	11	11	25.353	0	53591	48562	53388	44009	66117	33854	50775	40759	37395	51277	Enriched	Enriched	Enriched	Moderate		YES			
Q12797;Q12797-1	Aspartyl/asparaginyl	ASPH	85.862	16.6	11	11	37.067	0	16190	17147	19576	17968	18936	15140	24278	25270	14505	22901	Enriched	Moderate	Enriched	No expres		YES			
Q12802-4;Q12802;	A-kinase anchor prot	AKAP13	305.28	4.3	10	10	33.916	0	41673	32284	36523	38200	45008	33957	32773	32644	17230	37278	Enriched	Enriched	Enriched	Moderate		YES			
Q12805-2;Q12805-	EGF-containing fibul	EFEMP1	53.722	19.4	12	8	25.126	0	13214	19755	19162	14748	21986	14588	17199	43167	9547	18676	Moderate	Enriched	Enriched	Low		YES			
Q12846;Q12846-2;	Syntaxin-4	STX4	34.18	15.5	5	5	11.206	0	13634	11787	14915	12680	14687	16897	16030	17855	6105.8	17180	Moderate	Moderate	Enriched	Moderate		YES			
Q12873;Q12873-3;	Chromodomain-helic	CHD3	226.59	5	9	1	1.9694	0.00802	4628.1	3833.4	4118.3	3457.6	5891.7	3725.5	5477.2	3691.2	3878	5427	Enriched	Enriched	Enriched	Moderate		YES			
Q12874	Splicing factor 3A su	SF3A3	58.848	20	12	12	37.539	0	38671	30609	30763	40281	26310	40347	55281	82678	26095	44987	Low	Moderate	Enriched	Moderate		YES			
Q12882	Dihydropyrimidine d	DPYD	111.4	6.8	7	7	28.25	0	8829.6	3544.4	3564.6	7970.4	3471.4	5268.9	6138.3	9859.8	1356.2	9617.8	Enriched	Moderate	Moderate	Low		YES			
Q12893	Transmembrane prot	TMEM115	38.197	9.1	2	2	10.702	0	16277	11985	10348	10537	18746	9089.6	9084.7	8652	5969.5	11835	Moderate	Moderate	Enriched	Enriched					
Q12904;Q12904-2	Aminoacyl tRNA syn	AIMP1	34.352	54.8	24	24	131.28	0	129980	108700	106930	113460	160510	115280	117930	88588	68449	112170	Enriched	Enriched	Enriched	Moderate		YES			
Q12905;B4DY09;	Interleukin enhancer-	ILF2	43.062	40	27	27	107.14	0	96158	82131	89492	94977	101700	121660	114000	119770	58795	91853	No expres	Enriched	Enriched	Enriched		YES			
Q12906;Q12906-7;	Interleukin enhancer-	ILF3	95.337	32.2	49	44	222.55	0	286780	210540	267200	287700	271830	294120	433440	407500	243340	369070	Enriched	Enriched	Enriched	Enriched		YES			
Q12907;D6RBV2;	Vesicular integral-me	LMAN2	40.228	32.9	24	24	168.8	0	256580	254070	174970	217390	284520	273930	235520	234110	92048	197720	Moderate	Enriched	Enriched	Enriched		YES			
Q12912-2;Q12912;	Lymphoid-restricted	LRMP	56.212	23.4	10	10	38.236	0	19310	13860	18944	15790	23082	21703	17933	12729	12294	17399	No expres	Enriched	Moderate	Low		YES			
Q12929;Q12929-2	Epidermal growth fac	EPS8	91.88	9.1	6	6	28.255	0	2692	489.2	1082.6	2498.1	934.54	3802.2	2756.7	5516.3	633.31	5422.4	Moderate	Moderate	Enriched	Low		YES			
Q12931-2;Q12931	Heat shock protein 7	TRAP1	74.267	24.9	24	9	221	0	147510	96199	121900	104110	115040	121060	167800	271810	71658	147250	Enriched	Enriched	Enriched	Enriched		YES			
Q12955-5;Q12955-	Ankyrin-3	ANK3	202.59	15.5	29	22	248.24	0	100230	80368	86522	96616	102430	90592	106690	105410	60537	101220	Enriched	Enriched	Enriched	Enriched		YES			
Q12959-5;Q12959-	Disks large homolog	DLG1	95.165	17.6	13	11	44.118	0	38961	28850	35391	38899	40576	46620	65074	44114	41097	44866	No expres	Low	Moderate	Moderate		YES			
Q12965	Unconventional myo	MYO1E	127.06	9.7	10	8	25.101	0	39128	35895	33019	46104	38527	33659	36624	58353	16384	51738	Enriched	Enriched	Moderate	Moderate		YES			
Q12972;A0A0A0M	Nuclear inhibitor of	PPP1R8	38.478	25.4	8	8	57.178	0	52119	38796	49112	35190	63533	37895	41372	30554	22184	41788	Low	Moderate	Enriched	Enriched		YES			
Q12974-4;Q12974;	Protein tyrosine phos	PTP4A2	16.367	26.8	5	5	11.711	0	29729	24659	30804	20912	39832	21810	27939	22505	13451	23323	Enriched	Enriched	Enriched	Moderate		YES			
Q12981;Q12981-1;	Vesicle transport pro	BNIP1	26.132	16.2	3	3	7.1257	0	4418.5	3102.3	3519.7	5514.2	3679.6	5389.8	4123.4	4396.7	2536.8	4167.8	Enriched	Moderate	Moderate	Moderate		YES			
Q12996	Cleavage stimulation	CSTF3	82.921	11.7	8	8	15.556	0	17685	12584	14340	14173	19423	13566	13528	14260	9071.2	16286	Enriched	Enriched	Enriched	Moderate		YES			
Q13011	Delta(3,5)-Delta(2,4)	ECH1	35.816	38.1	31	13	86.763	0	225410	212520	185050	173770	191000	178520	190460	235980	133200	153670	Moderate	Enriched	Enriched	Enriched		YES			
Q13033-2;Q13033	Striatin-3	STRN3	77.744	6	4	4	5.6346	0	22122	21922	24224	24009	29853	14931	18568	17909	10784	18651	Low	Moderate	Enriched	Moderate		YES			
Q13042-3;Q13042-	Cell division cycle pr	CDC16	65.859	7.9	4	4	65.167	0	2080.8	1240.2	1993.3	2364.8	2149.2	2104.8	1559.5	1933	655.57	1928	Enriched	Enriched	Enriched	Enriched		YES			
Q13043;Q13043-2;	Serine/threonine-pro	STK4	55.63	18.7	10	6	13.266	0	17108	13435	14305	21264	14296	23092	16134	20899	9654.6	18692	Enriched	Enriched	Enriched	Low		YES			

Q13045-2;Q13045;	Protein flightless-1 h	FLII	138.49	14	19	19	61.838	0	73591	55509	67644	73112	82323	70342	86807	88942	48145	80516	Enriched	Enriched	Enriched	Moderate	YES		
Q13049	E3 ubiquitin-protein	TRIM32	71.988	1.7	1	1	2.1359	0.0061	11777	3494.9	3974.2	13852	5068.1	52389	6323	5027.9	2174.3	6272.1	Low	Moderate	Enriched	Moderate	YES		
Q13057;Q13057-2	Bifunctional coenzyn	COASY	62.328	29.1	19	19	100.74	0	69260	56220	59037	80839	65339	66732	65438	71951	40175	69284	Enriched	Enriched	Enriched	Enriched	YES		
Q13087-2;Q13087	Protein disulfide-ison	PDIA2	57.849	41.4	60	13	323.31	0	474810	471090	676820	591850	990660	584030	1242700	602290	488750	633160	Low	Enriched	Enriched	Enriched	YES	YES	YES
Q13103;C9J6K0	Secreted phosphopro	SPP2	24.337	13.3	3	3	4.6528	0.00043	3108.8	3646.1	4199.1	2502.2	4814.2	4604	4577	12732	2668.1	4627.4	No expres	No expres	No expres	No expres	YES		
Q13112	Chromatin assembly	CHAF1B	61.492	1.8	1	1	2.1818	0.0056	8341.8	5151.3	6877.5	9268.8	6872.6	7474.1	9165.6	9394.9	6196.8	8019.8	Low	No expres	Moderate	Low			
Q13131;Q13131-2	5-AMP-activated pro	PRKAA1	64.009	21.1	12	12	43.37	0	55204	48694	49923	46366	67473	41947	42909	37978	27704	48116	No expres	Low	Moderate	No expres	YES		
Q13148;B1AKP7;C	TAR DNA-binding p	TARDBP	44.739	32.9	21	21	83.898	0	131100	107130	99500	112350	127760	121700	134070	163380	82444	124360	No expres	Enriched	Enriched	Enriched	YES		
Q13151	Heterogeneous nucle	HNRNPA0	30.84	43	21	21	117.36	0	72344	60765	90722	68320	78864	97656	133530	152010	89657	127150	Enriched	Enriched	Enriched	Moderate	YES		
Q13155;F8W950;A	Aminoacyl tRNA syn	AIMP2	35.348	24.7	11	11	47.832	0	22477	19795	21423	18981	30475	22080	26558	20328	13440	19426	Enriched	Enriched	Enriched	Enriched	YES		
Q13158	FAS-associated death	FADD	23.279	4.8	1	1	2.5804	0.00326	3361.6	3316.6	3934.4	3196.3	3673.5	2837	3997.7	3608.9	2113.4	3981.7	Enriched	Moderate	Enriched	Enriched			
Q13162;H7C3T4	Peroxiredoxin-4	PRDX4	30.54	64.2	31	23	89.867	0	214240	163210	144630	177660	179120	173420	308410	166650	186810	177150	Enriched	Enriched	Enriched	Enriched	YES		
Q13177	Serine/threonine-prot	PAK2	58.042	32.6	20	10	169.26	0	103420	96279	92255	82773	117920	113750	81634	80148	44255	83383	Moderate	Moderate	Enriched	Moderate	YES		
Q13185;C9JMM0;I	Chromobox protein h	CBX3	20.811	21.9	10	6	52.452	0	47860	32318	44599	50428	43976	35546	62289	73106	38207	61125	No expres	Enriched	Enriched	Enriched	YES		
Q13188;Q13188-2;	Serine/threonine-prot	STK3	56.3	18.9	10	6	22.194	0	17554	12875	13289	13102	14391	20325	24108	35252	10947	22365	Enriched	Enriched	Moderate	Low	YES		
Q13200;Q13200-3;	26S proteasome non-	PSMD2	100.2	36.3	44	35	184.11	0	162690	95178	124220	238490	131690	196030	141370	235170	114570	180050	Enriched	Enriched	Enriched	Enriched	YES		
Q13206;E9PIF2	Probable ATP-depen	DDX10	100.89	3.4	2	2	15.19	0	6403.9	7379	6248.7	5842	9807	4599	9804.3	15937	14995	9041.2	Enriched	Enriched	Enriched	Moderate			
Q13217;X6R9L0	DnaJ homolog subfar	DNAJC3	57.579	26.8	25	25	150.28	0	148030	102750	108570	131270	149870	181360	141480	94196	115970	129930	Enriched	Enriched	Enriched	Low	YES		
Q13228;Q13228-4;	Selenium-binding pro	SELENBP1	52.39	55.1	40	40	265.35	0	252850	197100	212960	277640	224940	250230	437530	268480	224450	240670	Enriched	Enriched	Enriched	Enriched	YES		
Q13232;H3BPR2	Nucleoside diphosph	NME3	19.015	27.8	8	8	20.794	0	59736	58771	65107	56409	84715	51346	58168	56569	32406	57893	Low	Moderate	Enriched	Moderate	YES		
Q13242;H0YIB4	Serine/arginine-rich s	SRSF9	25.542	26.7	6	5	11.009	0	21968	16742	16379	23132	19238	11610	15477	17923	7740.6	13581					YES		
Q13243;B4DJK0;B	Serine/arginine-rich s	SRSF5	31.263	22.4	7	6	19.47	0	44024	26177	40803	38810	37452	30506	19511	32777	8332.7	30880					YES		
Q13247-3;Q13247	Serine/arginine-rich s	SRSF6	38.418	26.6	14	8	40.521	0	69673	53914	58941	78360	72497	65449	109090	97342	76090	95104					YES		
Q13263-2;Q13263;	Transcription interme	TRIM28	79.473	26.4	28	28	241.72	0	167420	146090	175620	171910	189450	190260	216500	220090	143650	211720	Moderate	Enriched	Enriched	Low	YES		
Q13283	Ras GTPase-activatin	G3BP1	52.164	21	12	10	35.665	0	71163	47380	61005	88861	69514	70743	97349	88944	56459	90504	Enriched	Enriched	Enriched	Low	YES		
Q13287	N-myc-interactor	NMI	35.056	8.1	2	2	5.9856	0	8586.7	7829.1	8526.4	8271.8	11129	5784.4	8059.9	8527.3	3397.4	11189	Enriched	Moderate	Enriched	Moderate	YES		
Q13308-5;Q13308-	Inactive tyrosine-prot	PTK7	89.763	3.8	2	2	9.8343	0	6394.1	4279.6	5296.4	6414	3910.7	4873.4	6095.6	6878.8	2917.8	5981.7	Moderate	Low	Moderate	No expres	YES		
Q13310-2;Q13310-	Polyadenylate-bindin	PABPC4	69.578	44.4	69	42	323.31	0	582830	293060	360810	491150	377690	704890	805560	552740	382580	573060	Moderate	Enriched	Enriched	Enriched	YES		
Q13315	Serine-protein kinase	ATM	350.68	2.8	10	10	11.226	0	30425	20125	26744	26652	25854	23935	22551	27579	13056	28298	Moderate	Moderate	Enriched	Moderate	YES		
Q13322-2;Q13322-	Growth factor recepto	GRB10	62.026	9.7	6	6	23.935	0	24379	18922	23552	19077	30074	14611	22060	16641	13000	18389	Enriched	Enriched	Enriched	Enriched	YES		
Q13325-2;Q13325	Interferon-induced pr	IFIT5	50.519	3.2	2	2	4.7225	0.00043	17840	10069	14395	22574	13293	18813	16498	22959	8839	20462	Moderate	Moderate	Enriched	Moderate	YES		
Q13332-6;Q13332-	Receptor-type tyrosir	PTPRS	212.48	4.8	8	4	14.928	0	25823	23575	24457	30662	29637	19712	22010	26252	12056	23825	Enriched	Enriched	Enriched	Moderate	YES		
Q13347	Eukaryotic translatior	EIF3I	36.501	40	20	20	65.643	0	123900	74861	78527	93579	117840	81501	126230	110030	84039	107540	Enriched	Enriched	Enriched	Moderate	YES		
Q13363-2;Q13363;	C-terminal-binding pr	CTBP1	46.404	16.6	10	5	18.268	0	31215	21620	24032	38516	25039	30289	39004	47376	30880	37731	Enriched	Enriched	Enriched	Enriched	YES		
Q13393-4;Q13393-	Phospholipase D1	PLD1	112.18	3.4	3	3	11.452	0	9654	7923.9	8737.4	11489	7409.9	11325	8343.7	12041	5109.1	9740.4	Enriched	Moderate	Moderate	Moderate	YES		
Q13405;E9PI78;E9	39S ribosomal protei	MRPL49	19.198	20.5	4	4	26.673	0	11197	8687.6	10517	10896	15477	9943	12938	9955.1	8415.1	13525	Enriched	Enriched	Enriched	Moderate	YES		
Q13409-3;Q13409-	Cytoplasmic dynein 1	DYNC1I2	68.426	19.3	21	2	208.18	0	100210	68330	79115	85330	102550	100700	105140	94498	62115	109340	Enriched	Enriched	Enriched	Enriched	YES		
Q13423	NAD(P) transhydroge	NNT	113.89	29.7	50	15	123.86	0	219260	178360	198700	183280	226070	184050	219860	235900	103120	218800	No expres	Moderate	Enriched	Low	YES		
Q13425	Beta-2-syntrophin	SNTB2	57.949	19.1	12	10	16.717	0	20366	17369	17874	17660	23600	20281	17453	14238	8479.4	16675	Moderate	Enriched	Enriched	Low	YES		
Q13426	DNA repair protein X	XRCC4	38.286	3.9	1	1	6.9078	0	8052.9	8890.4	8478.9	9998.2	17946	7465.6	4747.3	3990.8	2560.1	10494	Low	No expres	Moderate	Low	YES		
Q13427-2;Q13427;	Peptidyl-prolyl cis-tra	PPIG	40.299	23.2	9	6	36.424	0	66484	50510	59856	75974	58906	54074	73849	67463	38715	73234	Moderate	Low	Enriched	Moderate	YES		
Q13428-8;Q13428-	Treacle protein	TCOF1	144.41	14.7	19	19	79.209	0	46281	37178	44630	35299	47711	41853	91333	55192	73656	65849	Enriched	Moderate	Moderate	Enriched	YES		
Q13438;Q13438-2;	Protein OS-9	OS9;OR7D2	75.561	21.7	16	16	76.08	0	43060	40749	42659	44757	69984	34888	26278	35575	21371	46629	Enriched	Enriched	Enriched	Enriched	YES		
Q13442	28 kDa heat- and acid	PDAP1	20.63	49.2	14	14	160.62	0	87303	55345	51925	86579	61156	74264	109850	103550	87713	118510	Moderate	Moderate	Enriched	Enriched	YES		
Q13444-8;Q13444-	Disintegrin and metal	ADAM15	86.139	5.1	3	3	47.052	0	4893.6	3565.3	4225.3	5161.4	4737.7	4837.8	5556.3	5463.7	3361.7	5615.4	Moderate	No expres	Moderate	Enriched			
Q13445	Transmembrane emp2	TMED1	25.206	21.1	9	9	20.728	0	38039	26552	27990	22240	36791	21686	27866	26651	18527	28630	Low	Moderate	Enriched	Enriched	YES		
Q13451	Peptidyl-prolyl cis-tra	FKBP5	51.212	38.1	27	27	145.72	0	153090	151700	137880	124180	136380	108420	180840	154300	137810	185360	Moderate	Enriched	Enriched	Moderate	YES		
Q13464	Rho-associated prote	ROCK1	158.17	9.5	12	10	22.036	0	35864	30298	40251	30883	43202	35703	52249	51417	30314	47283	Enriched	Enriched	Enriched	Low	YES		
Q13469-3;Q13469-	Nuclear factor of acti	NFATC2	97.691	6	4	4	24.172	0	13098	11755	11876	12290	13440	14056	11203	14019	5889	11913	No expres	Moderate	Moderate	No expres	YES		
Q13492-3;Q13492-	Phosphatidylinositol-	PICALM	66.392	13.8	9	9	66.661	0	83910	81754	88187	72661	82111	80861	89157	112050	60614	105450	Moderate	Enriched	Enriched	Enriched	YES		
Q13496;Q13496-2	Myotubularin	MTM1	69.931	8	4	4	8.3808	0	11912	7117.6	9623.9	12697	11331	22674	12261	8532.4	5451.8	10606	No expres	No expres	Low	Low	YES		
Q13501;E7EMC7;I	Sequestosome-1	SQSTM1	47.687	22.5	12	10	83.938	0	34528	25614	33805	27857	48038	26454	27504	27268	13905	25603	Enriched	Enriched	Enriched	Enriched	YES		
Q13509;Q13509-2	Tubulin beta-3 chain	TUBB3	50.432	40.9	51	4	31.64	0	20737	23615	25353	20338	22390	25698	23994	36798	19074	25722	Moderate	Enriched	Enriched	Moderate	YES		
Q13523;H0YDJ3	Serine/threonine-prot	PRPF4B	116.99	8.4	11	11	28.034	0	17582	6615.7	9427	27075	8804.4	24598	14580	21676	6233.7	22093	Moderate	Enriched	Enriched	Moderate	YES		
Q13541	Eukaryotic translatior	EIF4EBP1	12.58	11	5	5	8.1249	0	13238	10294	13298	14018	14807	13421	13671	15976	7967.6	16741	Moderate	Enriched	Enriched	Low			
Q13542	Eukaryotic translatior	EIF4EBP2	12.939	10.8	1	1	15.337	0	8464.3	9167.1	4916.2	6750.9	9575	3538.9	2635.4	2232.8	1244.2	3514.8	Enriched	Enriched	Enriched	Enriched			
Q13546;Q13546-2	Receptor-interacting	RIPK1	75.93	10.1	7	7	20.92	0	47349	30992	40592	53377	40746	33733	48205	46238	44465	62017	Moderate	Enriched	Enriched	Moderate	YES		
Q13547	Histone deacetylase 1	HDAC1	55.102	13.9	7	2	61.486	0	5605.7	4605.3	4741.5	3366.2	4409.2	5752.4	8561.4	11178	4521	7357.3	Enriched	Enriched	Enriched	Enriched	YES		
Q13557-12	Calcium/calmodulin-	CAMK2D	54.113	27	14	1	71.382	0	42781	34619	40745	58644	48149	65739	83014	155170	33444	62678	Enriched	Enriched	Enriched	No expres	YES		
Q13561;Q13561-3;	Dynactin subunit 2	DCTN2	44.23	43.6	29	12	193.14	0	148920	102050	133890	136030	143300	135210	142540	121700	73538	134880	Enriched	Enriched	Enriched	Enriched	YES		
Q13563-2;Q13563-	Polycystin-2	PKD2	53.685	4.8	2	2	4.2892	0.00063	3679.1	2083.9	2563.9	6364	2923.4	5837.3	6787.6	6635.2	1899.3	4539.8	Low	Enriched	Enriched	Moderate			
Q13564-3;Q13564-	NEDD8-activating en	NAE1	50.624	29.2	11	11	41.664	0	24363	12071	15431	23196	18442	14475	9808	13478	5532.7	14067	Low	Enriched	Enriched	Enriched	YES		
Q13573;G3V3A4;C	SNW domain-contair	SNW1	61.494	28	16	16	110.98	0	65936	61476	71058	65701	76539	62256	72884	77704	43489	70144	Enriched	Enriched	Enriched	Moderate	YES		
Q13574-6;Q13574-	Diacylglycerol kinase	DGKZ	101.23	4.4	3	3	10.849	0	26523	21980	24445	18960	24318	21052	25354	22142	19344	26325	Enriched	Enriched	Enriched	Enriched	YES		
Q13576;F5H7S7;E	Ras GTPase-activatin	IQGAP2	180.58	45.7	124	120	323.31	0	615960	377960	482010	501900	517290	526240	668800	644020	379290	610800	Moderate	Enriched	Enriched	Moderate	YES		
Q13596-2;Q13596;	Sorting nexin-1	SNX1	51.812	26	14	11	28.464	0	33039	24813	26834	30031	26798	31606	27439	34569	14067	33700	Moderate	Enriched	Enriched	Moderate	YES		
Q13601-2;Q13601;	KRR1 small subunit	KRR1	36.788	10.2	4	4	11.048	0	7777.2	4541.5	5273.2	7400.4	5333.1	6486	6034.8	6419.4	1910	7299.9	Enriched	Moderate	Enriched	Moderate	YES		
Q13616	Cullin-1	CUL1	89.677	7.1	5	5	14.979	0	21217	16227	17245	20150	23295	30360	46243	47838	18425	26805	No expres	Moderate	Enriched	Enriched	YES		
Q13618-2;Q13618;	Cullin-3	CUL3	86.233	27.8	24	24	247.51	0	90982	52198	59394	84460	72287	78102	67206	93674	33566	86584	Enriched	Enriched	Enriched	No expres	YES		
Q13619;A0A0A0M	Cullin-4A	CUL4A	87.679	9.2	7	3	5.4756	0	1902.6	2126.9	2930	1480.8	2736.3	5015.4	10699	9428.7	6471.7	7914.1	No expres	Enriched	Enriched	No expres	YES		
Q13625-2;Q13625;	Apoptosis-stimulatin	TP53BP2	111.43	3.6	3	3	6.5546	0	10717	5948.8	7150.7	12129	8245.4	12098	11320	16390	5903.9	12004	Moderate	Moderate	Enriched	Low	YES		
Q13630;E9PKL9;E	GDP-L-fucose syntha	TSTA3	35.892	41.1	24	24	111.32	0	61672	47358	46144	62245	65636	95551	116500	87632	40010	75692	Enriched	Enriched	Enriched	Moderate	YES		
Q13642-1;Q13642-	Four and a half LIM	FHL1	31.895	46.1	17	17	86.297	0	61589	52169	61556	65999	68306	56646	170000	140700	60055	94702	Moderate	Enriched	Enriched	Moderate	YES		
Q13724-2;Q13724;	Mannosyl-oligosacch	MOGS	80.702	41.7	43	43	266.41	0	260380	198400	225580	262200	265200	244120	259340	238930	125040	240640	Low	Enriched	Moderate	Enriched	YES		
Q13769;H7C441;C	THO complex subuni	THOC5	78.507	4.4	3	3	4.5177	0.00042	9613.1	7671.2	6235.9	6533.7	9896	5418.1	5143.4	5601.8	3213.5	6893.2	Moderate	Moderate	Moderate	No expres	YES		
Q13796	Protein Shroom2	SHROOM2	176.41	3.2	5	5	9.9461	0	3899.9	2712.9	2374.8	3685.1	4212.2	2597.8	2305.5	2224.4	1329	2820.6	Moderate	Enriched	Enriched	Enriched	YES		
Q13813	Spectrin alpha chain,	SPTAN1	284.54	58.7	279	0	7.401	0	3047	1913.1	1933.6	14578	2261.5	3799	2584.9	31542	1482.3	4216.7	Low	Enriched	Enriched	Moderate	YES		
Q13813-2	Spectrin alpha chain,	SPTAN1	285.09	58.6	279	1	3.1635	0.00077	7346.4	2674.5	3416.2	8527.3	6667.5	6825.6	4696.7	7554.5	1143.8	10415	Low	Enriched	Enriched	Moderate	YES		
Q13813-3	Spectrin alpha chain,	SPTAN1	282.28	59.2	281	3	323.31	0	1625000	1133300	1351800	1479800	1574700	1489700	1867000	1798700	1066700	1620700	Low	Enriched	Enriched	Moderate	YES		
Q13823	Nucleolar GTP-bindi	GNL2	83.654	5.7	3	3	23.282	0	5665.7	2974.6	4122.5	4089.7	3844.3	6255.3	5065.4	7519	2724.6	6772.2	Moderate	Low	Moderate	Enriched	YES		
Q13825;Q13825-2	Methylglutaconyl-Co	AUH	35.608	19.5	6	6	42.669	0	15086	3769.4	9454.8	18326	9616	11076	2728.4	5069.4	1304.4	14333	Enriched	Enriched	Enriched	Enriched	YES		
Q13838;Q13838-2;	Spliceosome RNA he	DDX39B	48.991	39.7	38	9	226.69	0	288080	153730	191440	274250	204010	408210	323340	394920	155070	312020					YES		
Q13867;J3KSD8;K	Bleomycin hydrolase	BLMH	52.562	40.2	18	18	51.118	0	64520	43625	56351	63247	61029	57206	47081	64783	26783	58330	No expres	Moderate	Enriched	Enriched	YES		
Q13884;Q13884-2	Beta-1-syntrophin	SNTB1	58.06	48	44	44	283.32	0	242370	184250	207700	176570	267520	218950	310540	264920	149990	219840	Low	Enriched	Enriched	No expres	YES		
Q13885	Tubulin beta-2A chai	TUBB2A	49.906	50.6	68	5	69.22	0	114930	52125	76650	167990	92074	121080	112120	129220	67034	156180	Enriched	Enriched	Enriched	Enriched	YES		
Q13895;H7BY94	Bystin	BYSL	49.601	12.8	7	7	23.548	0	35811	31016	31550	30299	37713	35754	33359	34341	16397	39523	Moderate	Moderate	Moderate	Moderate	YES		
Q13907;Q13907-2	Isopentenyl-diphospl	IDI1	26.319	20.3	6	6	17.715	0	45707	39754	44544	35026	64661	39024	39893	34474	18620	39990	Enriched	Enriched	Enriched	Enriched	YES		
Q13948-9;Q13948-	Protein CASP;Homeo	CUX1	72.84	7.4	6	6	14.571	0	7843.1	3115	4324.2	15709	5067.2	13716	6342.7	10696	3255.7	11556	Enriched	Moderate	Enriched	Moderate	YES		
Q14005-3;Q14005-	Pro-interleukin-16;In	IL16	66.646	3	2	2	2.7199	0.00239	21254	15907	17124	12068	44903	16090	15802	16800	10349	15011	Enriched	Low	Moderate	Low	YES		
Q14008-2;Q14008;	Cytoskeleton-associa	CKAP5	218.52	10.5	19	19	60.928	0	74443	55215	66709	67146	66794	59002	66268	57540	36706	66922	Moderate	Enriched	Enriched	Moderate	YES		
Q14011;K7EPM4;I	Cold-inducible RNA-	CIRBP	18.648	57	22	21	187.05	0	115640	58550	72297	170350	83499	141430	209540	204040	126790	183720	Enriched	Enriched	Enriched	Enriched	YES		
Q14019;H3BT58	Coactosin-like protei	COTL1	15.945	38	7	7	21.408	0	25314	11425	16375	28419	14688	26392	77623	71614	27873	53914	No expres	Low	Enriched	No expression			
Q14061;H7C4E5;C	Cytochrome c oxidas	COX17	6.9151	55.6	5	5	35.708	0	36255	31606	42029	31411	50037	30591	39335	29035	18012	41802	Moderate	Enriched	Enriched	Moderate	YES		
Q14103-3;Q14103;	Heterogeneous nucle	HNRNPD	32.834	46.4	39	5	323.31	0	480820	294490	438240	545920	451710	614560	743910	789840	293460	644370	Enriched	Enriched	Enriched	Enriched	YES		
Q14103-4;Q14103-	Heterogeneous nucle	HNRNPD	30.672	43.2	35	1	2.9396	0.00168	6425.5	4504.2	4267.9	2779.4	4802.3	6094.7	4141.7	9432.4	2300	8226.8	Enriched	Enriched	Enriched	Enriched	YES		
Q14108;Q14108-2	Lysosome membrane	SCARB2	54.29	20.1	13	13	28.166	0	42710	32638	34702	42725	37213	75733	61081	50481	28120	48722	Enriched	Enriched	Enriched	Moderate	YES		
Q14112-2;A0A0A0	Nidogen-2	NID2	140.86	28.3	60	59	323.31	0	272290	195150	267000	293630	294350	280040	409550	419270	197630	381990	Low	Moderate	Enriched	Low	YES		
Q14116-2;Q14116	Interleukin-18	IL18	21.896	5.8	1	1	3.262	0.00077	4171.1	3772.4	4605.3	2819.2	8957.6	6586.2	4123.7	3120.2	2053.4	3543.5	Low	No expres	Low	Low	YES		
Q14118	Dystroglycan;Alpha-	DAG1	97.44	24.2	29	29	126.55	0	84564	68015	75745	61379	87751	59539	79165	74313	41736	73158	Enriched	Enriched	Enriched	Enriched	YES		
Q14126	Desmoglein-2	DSG2	122.29	25.8	35	35	323.31	0	150330	108760	112470	112830	126120	147140	175420	203570	81562	155800	Enriched	Enriched	Enriched	No expres	YES		
Q14137;Q14137-2	Ribosome biogenesis	BOP1	83.629	12.7	8	8	36.327	0	45968	36895	39763	42189	41473	40462	43527	48603	28200	47430	Enriched	Moderate	Moderate	Moderate	YES		
Q14139;Q14139-2;	Ubiquitin conjugatior	UBE4A	122.56	5.6	5	5	11.976	0	19546	12708	20772	31826	18272	21865	30671	36049	19000	26544	Enriched	Enriched	Enriched	Enriched	YES		
Q14151	Scaffold attachment f	SAFB2	107.47	19.7	22	11	29.813	0	26022	23155	24206	18805	38612	19326	33288	34788	24496	29197	Enriched	Enriched	Enriched	Enriched	YES		
Q14152;Q14152-2	Eukaryotic translatior	EIF3A	166.57	40.9	90	90	299.27	0	535070	385850	436470	549020	509190	541330	612540	570750	381440	572760	Enriched	Enriched	Enriched	Low	YES		
Q14156-3;Q14156;	Protein EFR3 homolo	EFR3A	87.579	8.8	6	6	38.332	0	29843	30450	33919	26917	37364	34134	43147	36047	22796	32121	Enriched	Enriched	Enriched	Enriched	YES		
Q14157;Q14157-5;	Ubiquitin-associated	UBAP2L	114.53	14.1	15	15	47.424	0	55957	51600	56026	48801	73503	63648	96619	74876	53685	68042	Enriched	Enriched	Enriched	Low	YES		
Q14160;Q14160-3;	Protein scribble homo	SCRIB	174.88	13.1	20	16	141.04	0	46897	30811	32379	43569	37737	33017	32157	35667	17146	42884	Enriched	Moderate	Enriched	Enriched	YES		
Q14165;F5H1S8	Malectin	MLEC	32.233	43.2	28	26	311.75	0	273720	155130	194210	231890	203890	240020	216780	208420	97165	234950	Enriched	Enriched	Enriched	Enriched	YES		
Q14166	Tubulin--tyrosine liga	TTLL12	74.403	20.2	12	12	55.621	0	35155	24333	30400	34618	27755	35986	27333	49021	13584	38938	Enriched	Enriched	Enriched	Enriched	YES		
Q14195-2;Q14195	Dihydropyrimidinase-	DPYSL3	73.91	44.7	37	27	127.27	0	110520	98265	126780	114810	132920	118970	194370	219930	96054	141700	Moderate	Moderate	Moderate	Moderate	YES		
Q14203-6;Q14203;	Dynactin subunit 1	DCTN1;DKFZp686E07	140.89	31.2	45	45	309.83	0	108800	87552	92429	118310	110350	193850	205780	259200	88865	139620	Enriched	Enriched	Enriched	No expres	YES		
Q14204	Cytoplasmic dynein 1	DYNC1H1	532.4	41.2	273	273	323.31	0	1536200	1083800	1262600	1540000	1342300	1542000	1718000	1720800	867450	1504000	Enriched	Enriched	Enriched	Enriched	YES		
Q14232;F5H0D0	Translation initiation	EIF2B1	33.712	23	8	8	18.321	0	31946	21923	26792	25799	32115	32370	37923	28868	23302	28540	Low	Enriched	Enriched	No expres	YES		
Q14240;Q14240-2;	Eukaryotic initiation	EIF4A2	46.402	47.7	36	17	98.775	0	175830	104540	111620	137050	125760	169310	147800	177550	73260	154090	Enriched	Enriched	Enriched	Enriched	YES		
Q14244-3;Q14244-	Ensconsin	MAP7	72.413	6.7	4	4	13.635	0	23563	20106	28866	31032	25760	33295	45747	29236	39007	42709	Enriched	Enriched	Enriched	Moderate	YES		
Q14247;Q14247-3;	Src substrate cortacti	CTTN	61.585	43.5	36	36	84.179	0	79957	70776	83244	75910	94843	72764	133150	112180	77088	101500	Enriched	Enriched	Enriched	Enriched	YES		
Q14257;Q14257-2;	Reticulocalbin-2	RCN2	36.876	16.7	4	4	11.461	0	13529	6254.1	7385.5	14670	5621.6	16255	11306	31254	4180	11059	No expres	Moderate	Enriched	Low	YES		
Q14258	E3 ubiquitin/ISG15 l	TRIM25	70.973	27.8	23	23	170.74	0	172070	111170	131930	176010	171240	155120	139400	159980	78252	156540	Enriched	Enriched	Enriched	Low	YES		
Q14314	Fibroleukin	FGL2	50.228	3.2	1	1	11.26	0	2582.2	2718.5	3642.5	2987.6	3520.5	1809.5	4213.3	3804.9	2730.2	3938.6	Enriched	Low	Low	No expres	YES		
Q14315;Q14315-2	Filamin-C	FLNC	291.02	9.2	26	9	15.404	0	20058	28212	24573	17566	35486	19971	31436	29803	16585	35997	Enriched	Low	Moderate	No expres	YES		
Q14320;B0S8I6	Protein FAM50A	FAM50A	40.241	23.3	6	6	21.842	0	21414	21321	25796	21472	21532	20395	26871	30586	19571	29161	Moderate	Enriched	Enriched	Enriched			
Q14344;Q14344-2	Guanine nucleotide-b	GNA13	44.049	10.3	4	4	6.7936	0	18694	14966	18024	12927	19607	15079	23295	22401	12192	19560	Enriched	Enriched	Enriched	Low	YES		
Q14353;Q14353-2	Guanidinoacetate N-r	GAMT	26.318	48.3	22	22	64.517	0	277120	177750	229220	233340	248880	272300	263330	239820	168420	217770	Moderate	Enriched	Enriched	Enriched	YES		
Q14376;Q14376-2;	UDP-glucose 4-epime	GALE	38.281	23.3	8	8	21.859	0	46158	28048	37543	34460	33514	54216	87182	74860	51910	57781	Enriched	Moderate	Moderate	No expres	YES		
Q14432	cGMP-inhibited 3,5-	PDE3A	124.98	1	1	1	3.2894	0.00078	10456	12335	14161	11927	22197	12235	21131	18639	12991	15822	No expres	Enriched	Enriched	No expres	YES		
Q14498-3;Q14498-	RNA-binding protein	RBM39	57.089	13.8	8	7	199.76	0	42116	33101	32515	56325	39833	43809	43121	55980	23210	47903	Enriched	Enriched	Enriched	Enriched	YES		
Q14515-2;Q14515	SPARC-like protein	SPARCL1	61.759	11.9	4	4	108.54	0	79894	88649	50547	133590	94340	37691	19673	23045	7816.4	29563	Low	Enriched	Enriched	Enriched	YES		
Q14527-2;Q14527	Helicase-like transcri	HLTF	99.918	2.1	3	3	4.7849	0.00043	2889	2082.1	2055	2042.9	2754.7	2099.3	3361.9	2789.2	3914.2	3917.9	Enriched	Enriched	Enriched	Moderate			
Q14554;Q14554-2	Protein disulfide-ison	PDIA5	59.594	37.6	25	25	58.098	0	152140	101990	125970	115970	146300	204070	150160	109020	83394	113720	Enriched	Enriched	Enriched	Moderate	YES		
Q14558;Q14558-2;	Phosphoribosyl pyro	PRPSAP1	39.393	25.8	9	6	15.021	0	19467	12534	14115	16440	17849	17480	14303	14190	8702.9	14054	Enriched	Enriched	Enriched	Enriched	YES		
Q14571	Inositol 1,4,5-trispho	ITPR2	308.06	8.6	21	17	73.038	0	62573	48729	55630	56121	70555	57903	78886	68081	41635	62041	Moderate	Enriched	Moderate	Enriched	YES		
Q14573	Inositol 1,4,5-trispho	ITPR3	304.1	2.6	7	4	6.5768	0	4066.1	3055.3	3355.7	4856.3	3470.6	4443.1	3606.2	3557.1	1856.5	4878.2	Enriched	Enriched	Enriched	Enriched	YES		
Q14651;C9JAM8	Plastin-1	PLS1	70.253	16.5	15	9	28.381	0	35878	26784	36745	40472	38087	44250	55895	60285	36814	52480	Enriched	Enriched	Enriched	Moderate	YES		
Q14657	EKC/KEOPS comple	LAGE3	14.804	34.3	5	5	68.979	0	16390	11579	13549	10731	15183	13312	9722.2	12221	5807.8	13655	Enriched	Enriched	Enriched	Enriched	YES		
Q14669;Q14669-2;	E3 ubiquitin-protein	TRIP12	220.43	2.9	6	6	9.5185	0	16802	16986	15685	15356	23379	13621	19517	14955	13090	18693	Low	Enriched	Enriched	Enriched	YES		
Q14676-4;Q14676-	Mediator of DNA dai	MDC1	116.63	2.5	2	2	3.8598	0.00061	2539.1	1078.7	3115.1	725.54	3812.1	2243	770.54	557.89	135	622.96	Moderate	Moderate	Enriched	Enriched	YES		
Q14677;Q14677-3;	Clathrin interactor 1	CLINT1	68.259	27	23	23	106.96	0	126940	95928	111150	110580	161420	130210	180720	211050	63110	125570	Enriched	Enriched	Enriched	Low	YES		
Q14683;G8JLG1	Structural maintenan	SMC1A	143.23	23.4	34	34	239.99	0	247860	177120	226950	234060	219970	208510	269680	281640	156010	297830	Moderate	Enriched	Enriched	Enriched	YES		
Q14684-2;Q14684	Ribosomal RNA proc	RRP1B	82.175	4.2	4	4	11.864	0	3387.6	3031.5	3216.3	3534.9	3804.1	2902.4	2223.8	3398.3	1262.8	2379.5	Enriched	Enriched	Enriched	Enriched	YES		
Q14690	Protein RRP5 homolo	PDCD11	208.7	6.1	9	9	21.329	0	38679	33884	37150	32340	47498	34077	46155	42952	20992	49689	Enriched	Moderate	Moderate	Low	YES		
Q14692	Ribosome biogenesis	BMS1	145.81	1.6	2	2	3.375	0.00078	4012.5	3448.9	5042.8	3942.3	7448.1	1977.4	5094.6	1950.2	4405.3	3014.4	Moderate	Moderate	Enriched	Moderate	YES		
Q14694;Q14694-3;	Ubiquitin carboxyl-te	USP10	87.133	8.4	6	6	12.237	0	26675	21515	23491	22102	31966	25293	30575	26020	19413	28431	Low	Moderate	Enriched	Moderate	YES		
Q14696	LDLR chaperone ME	MESDC2	26.076	42.3	18	18	121	0	148840	103830	111820	117550	130710	135410	104920	100760	51118	109600	Enriched	Enriched	Enriched	No expres	YES		
Q14697;F5H6X6	Neutral alpha-glucosi	GANAB	106.87	43	69	1	323.31	0	482800	412500	408990	408770	525600	458190	488110	457330	239280	395580	Moderate	Enriched	Enriched	Enriched	YES		
Q14697-2;E9PKU7	Neutral alpha-glucosi	GANAB	109.44	41.8	69	1	3.6257	0.0008	5715.4	6185.1	6135.7	6507.4	17295	2080.1	2983.4	1434.1	1175.9	3054.8	Moderate	Enriched	Enriched	Enriched	YES		
Q14739;C9JXK0	Lamin-B receptor	LBR	70.702	11.9	12	12	27.33	0	50471	33401	32980	69896	44196	33536	36708	70551	20035	57214	Moderate	Enriched	Enriched	Enriched	YES		
Q14749	Glycine N-methyltrar	GNMT	32.742	44.1	20	20	117.04	0	208290	118910	106060	86411	118060	224070	124010	114580	80573	82746	Moderate	Enriched	Moderate	Enriched	YES		
Q14764	Major vault protein	MVP	99.326	36.5	49	49	323.31	0	212350	160480	167120	208580	182270	192210	268740	492060	142830	285000	Moderate	Enriched	Enriched	Moderate	YES		
Q14789;F1T0J2;Q1	Golgin subfamily B n	GOLGB1	376.01	25.8	94	94	323.31	0	399250	298810	324780	389060	445390	382120	460420	424710	236500	432350	Enriched	Enriched	Enriched	Low	YES		
Q14790-9;H7C0E2	Caspase-8;Caspase-8	CASP8	61.835	6.5	4	4	4.1951	0.00062	56701	38128	47115	31446	41701	48100	48284	43021	20742	38059	Moderate	Low	Moderate	Moderate	YES		
S4R445;Q14802;Q	FXYD domain-contai	ZFYVE21;FXYD3	12.43	16.4	1	1	3.5179	0.00079	3860.5	3617.3	4637.6	2641	5622.2	2385.9	3857.4	2573.3	1775.3	3325	Enriched	Enriched	Enriched	No expres	YES		
Q14847;Q14847-2;	LIM and SH3 domair	LASP1	29.717	47.1	25	21	63.997	0	159000	118700	149950	139390	163740	153890	220150	195910	133730	207310	Enriched	Enriched	Enriched	Enriched	YES		
Q14914;Q14914-2	Prostaglandin reducta	PTGR1	35.869	32.8	20	20	41.858	0	66029	68354	86561	65519	69916	100250	111780	88474	51906	85910	Enriched	Enriched	Enriched	No expres	YES		
Q14956-2;Q14956	Transmembrane glyco	GPNMB	62.642	4.6	5	5	10.829	0	17035	7252.5	10346	27920	9325.7	19652	15760	22826	7699.5	20863	Moderate	Moderate	Enriched	Moderate			
Q14964	Ras-related protein R	RAB39A	25.006	9.7	5	2	4.5032	0.00042	25894	19840	21120	29039	20271	17875	25939	15705	20656	27557							
Q14966;Q14966-3;	Zinc finger protein 63	ZNF638	220.62	5.7	12	12	54.671	0	32370	28780	31861	24222	43450	25320	32541	26378	17575	31320	Enriched	Enriched	Enriched	Enriched	YES		
Q14974;Q14974-2;	Importin subunit beta	KPNB1	97.169	30.9	36	28	76.496	0	157660	140570	165920	139680	187390	141930	197250	185970	117430	155680	Enriched	Enriched	Enriched	Enriched	YES		
Q14980-2;A0A087	Nuclear mitotic appar	NUMA1	236.51	40.3	107	1	323.31	0	446260	312300	373680	504090	412980	440390	585240	589730	393350	584870	Enriched	Enriched	Enriched	Enriched	YES		

Q14CX7-2;Q14CX	N-alpha-acetyltransfe	NAA25	99.268	6.4	5	5	16.65	0	8831.9	5172.9	7727.2	9964.4	7176.5	11428	11708	10332	6583.2	9985.9					YES
Q15006	ER membrane protei	EMC2	34.833	24.9	7	7	22.334	0	16608	11316	13964	25458	14173	19663	14265	26810	9749	22477					YES
Q15007	Pre-mRNA-splicing r	WTAP	44.243	4.8	1	1	3.6508	0.0008	1891.4	1083.2	1209.1	1075.6	1722.1	806.84	1662.2	1489.5	1271.7	1761	Enriched	Enriched	Enriched	Enriched	YES
Q15008;Q15008-4;	26S proteasome non-	PSMD6	45.531	27	15	15	83.704	0	142260	103370	119430	136960	148770	120180	109790	102860	61705	120150	Moderate	Enriched	Enriched	Enriched	YES
Q15011-3;Q15011-	Homocysteine-respor	HERPUD1	26.22	11.6	2	2	3.8868	0.00061	14303	11831	14417	20513	15151	11908	12514	9669.8	7533.1	12710	Enriched	Enriched	Enriched	Enriched	
Q15018	BRISC complex subu	FAM175B	46.9	12.8	6	6	16.309	0	23384	20981	22937	16955	30541	16526	33056	22860	19803	20991	Enriched	Moderate	Enriched	Moderate	YES
Q15020-4;Q15020;	Squamous cell carcin	SART3	105.58	11.3	12	12	103.77	0	32399	29999	43538	42570	50803	46262	49428	51371	40575	63453	Enriched	Moderate	Enriched	Enriched	YES
Q15024	Exosome complex co	EXOSC7	31.821	5.5	3	3	6.6638	0	1526.4	835	961.11	2003.9	927.02	2232.6	1173.4	1694.1	903.03	2124.6	Low	Enriched	Enriched	Moderate	YES
Q15029-2;Q15029;	116 kDa U5 small nu	EFTUD2	105.38	28.3	32	32	88.775	0	148580	96517	115640	124470	128430	153540	154240	187970	76521	147780	Low	Enriched	Enriched	No expres	YES
Q15036-2;Q15036	Sorting nexin-17	SNX17	49.998	3.6	1	1	2.9021	0.00186	4182.1	3443.7	6487.1	2699.3	6588.7	1640.7	3353.1	2512.1	2656.9	3389.1	Low	Enriched	Enriched	Enriched	YES
Q15042;Q15042-3;	Rab3 GTPase-activat	RAB3GAP1	110.52	7.1	7	7	12.282	0	32971	18083	22205	42566	20144	33032	23001	30654	13551	34050	No expres	No expres	Moderate	Enriched	YES
Q15043-2;Q15043-	Zinc transporter ZIP1	SLC39A14	52.838	16.4	13	13	56.157	0	65273	38828	37761	72353	45965	79745	55687	55268	31269	64921	Enriched	Enriched	Enriched	Enriched	YES
Q15046;Q15046-2	Lysine--tRNA ligase	KARS	68.047	38	44	44	156.02	0	245210	191070	219060	218310	293410	238730	327810	280920	168550	230510	Enriched	Enriched	Enriched	Enriched	YES
Q15050	Ribosome biogenesis	RRS1	41.193	22.5	10	10	27.894	0	52056	26557	38605	47462	46592	52828	54909	50457	25932	57050	Low	Enriched	Enriched	Moderate	YES
Q15056-2;Q15056	Eukaryotic translatio	EIF4H	25.2	43.9	24	24	226.83	0	115400	90084	122850	108570	110090	166120	270640	201150	118730	182070	Enriched	Enriched	Enriched	Enriched	YES
Q15059	Bromodomain-contai	BRD3	79.541	3.9	2	2	4.1582	0.00062	14708	19168	21160	13195	21157	14886	20944	15894	10426	15595	Enriched	Enriched	Enriched	Enriched	YES
Q15061	WD repeat-containin	WDR43	74.89	5.9	5	5	9.9799	0	1553.2	1303.8	1724.4	1134.2	2123.8	4829.9	11781	9097.6	5348.7	6699.1	Moderate	Moderate	Moderate	Low	YES
Q15063-3;Q15063-	Periostin	POSTN	87.253	36.4	29	29	146.9	0	80730	52883	56044	66900	66056	66745	110540	241210	42381	126070	Low	Low	Enriched	Low	YES
Q15067-2;Q15067	Peroxisomal acyl-coe	ACOX1	74.667	13.6	11	3	24.205	0	68420	52410	52889	70658	56356	53337	99546	97049	57068	69046	Moderate	Enriched	Enriched	Moderate	YES
Q15067-3	Peroxisomal acyl-coe	ACOX1	70.135	13.5	11	3	8.2582	0	21354	16506	17132	18130	17442	20906	20572	15987	13419	22132	Moderate	Enriched	Enriched	Moderate	YES
Q15075	Early endosome anti	EEA1	162.46	30.7	49	48	323.31	0	162940	118420	134750	180510	159970	154300	203340	187140	109520	198880	Low	Moderate	Enriched	No expres	YES
Q15084-3;Q15084;	Protein disulfide-ison	PDIA6	47.837	55.4	81	81	323.31	0	732000	479790	511610	682170	584300	1052500	923080	858740	388510	639610	Enriched	Enriched	Enriched	Enriched	YES
Q15102;M0R389;N	Platelet-activating fac	PAFAH1B3	25.734	44.2	10	9	24.763	0	16546	17061	22337	17800	17032	15443	29603	24272	16310	21764	Moderate	Moderate	Enriched	Moderate	YES
Q15113	Procollagen C-endop	PCOLCE	47.972	10	3	3	15.268	0	7055.2	9089.7	8061.1	8784.3	13357	6127.9	5047.9	9534.8	2925.9	5335.8	Moderate	Low	Moderate	Moderate	YES
Q15121;Q15121-2;	Astrocytic phosphopr	PEA15	15.04	68.5	11	11	74.515	0	42341	28994	41444	76002	44686	51599	132290	82790	64341	64890	Enriched	Enriched	Enriched	Enriched	YES
Q15124;Q15124-2	Phosphoglucomutase	PGM5	62.224	14.8	8	8	47.588	0	27005	25729	26203	24039	32872	28149	23477	27739	12031	35015	Low	Low	Low	Low	YES
Q15126	Phosphomevalonate l	PMVK	21.995	16.1	5	5	7.3834	0	8239.3	7395.5	6106	7635.9	7998.3	9131	10118	8487.4	5040.9	8534.4	Enriched	Enriched	Enriched	Enriched	YES
Q15149-8	Plectin	PLEC	513.7	42.2	275	1	323.31	0	1012300	772840	907840	1075900	1006000	1066000	1336500	1301800	781090	1203700					YES
Q15172;Q15172-2	Serine/threonine-prot	PPP2R5A	56.193	14.8	8	6	19.085	0	21436	13880	20640	29461	18265	19378	19797	28917	10983	23120	Enriched	Enriched	Enriched	Enriched	YES
Q15181;Q5SQT6	Inorganic pyrophospl	PPA1	32.66	68.2	38	36	260.13	0	320920	234300	243160	277510	324470	305870	353620	400450	194250	271040	Enriched	Enriched	Enriched	No expres	YES
Q15208	Serine/threonine-prot	STK38	54.19	2.4	1	1	2.1528	0.00611	10317	11771	9105.9	11331	12187	7644.3	5496.3	5292.2	2499.7	7779.9	Enriched	Moderate	Enriched	Enriched	YES
Q15233;Q15233-2;	Non-POU domain-co	NONO	54.231	46.7	36	34	161.84	0	209900	161170	189440	218470	185630	208230	350510	324410	272330	299840	No expres	Enriched	Enriched	Enriched	YES
Q15269	Periodic tryptophan p	PWP2	102.45	5	4	2	4.3	0.00063	10091	7929.7	7705.9	8424	9128.4	8302.4	6499.2	9336.1	3302.8	9019.9	Low	Moderate	Moderate	Moderate	YES
Q15274;C9JCJ5	Nicotinate-nucleotide	QPRT	30.845	12.8	4	4	8.434	0	9988	7638.9	9590.9	7483.8	13701	10151	12320	7313	7744.3	9619.4	Moderate	Enriched	Moderate	Moderate	YES
Q15276-2;Q15276	Rab GTPase-binding	RABEP1	95.478	10	6	6	15.992	0	11881	9104	9614.8	14708	12664	11232	11242	11525	8691.6	15726	Low	Enriched	Enriched	Moderate	YES
Q15291-2;Q15291	Retinoblastoma-bind	RBBP5	55.071	4.4	1	1	18.297	0	2759.2	2660.4	1795.5	6135.1	1560.1	3947.3	2742.2	5529.4	1385.6	3571.9	No expres	Low	Moderate	No expres	YES
Q15293;Q15293-2	Reticulocalbin-1	RCN1	38.89	28.1	15	15	60.581	0	77000	60739	62669	81747	78060	70954	70698	82013	40405	75863	Enriched	Moderate	Enriched	Moderate	YES
Q15311	RalA-binding protein	RALBP1	76.063	9.8	7	7	18.498	0	21549	18184	21782	14910	31389	17045	29659	20037	28033	24786	Enriched	Enriched	Enriched	Enriched	YES
Q15363;E7EQ72;F	Transmembrane emp2	TMED2	22.761	47.8	16	16	30.549	0	69766	57227	59136	95875	77739	60505	81085	68927	44885	62535	No expres	Enriched	Enriched	Enriched	YES
Q15365	Poly(rC)-binding pro	PCBP1	37.497	58.1	46	28	323.31	0	206540	160410	173980	168160	241060	250540	436450	346920	187180	235100	Moderate	Enriched	Enriched	Enriched	YES
Q15366-6;Q15366-	Poly(rC)-binding pro	PCBP2	38.15	52.6	40	22	122.98	0	200650	142650	139160	161720	182760	178070	145450	162990	73948	150470	Enriched	Enriched	Enriched	Enriched	YES
Q15386;Q15386-2	Ubiquitin-protein lig	UBE3C	123.92	3.9	4	4	7.6299	0	6946.4	4309.3	6149	6734.1	6350.8	8181.9	8124.8	8801.8	5201.3	7981.1	Moderate	Enriched	Enriched	Enriched	YES
Q15388	Mitochondrial impor	TOMM20	16.298	10.3	3	3	5.1925	0.00044	7716.6	5743.7	5272.3	9124.4	4653.6	8868.5	8842.1	11468	4447	9081.9	Moderate	Enriched	Enriched	Enriched	YES
Q15393	Splicing factor 3B su	SF3B3	135.58	21.5	32	31	193.2	0	120900	92647	110670	106910	124780	104060	122750	122890	71501	115490	Enriched	Enriched	Enriched	Enriched	YES
Q15397	Pumilio domain-cont	KIAA0020	73.584	12.7	8	8	29.138	0	64897	61788	85366	44496	104320	28565	66408	57055	41327	49323	Enriched	Enriched	Enriched	Moderate	YES
Q15404;Q15404-2	Ras suppressor prote	RSU1	31.54	36.8	15	15	73.966	0	96805	64783	84301	127620	104690	100940	104970	130210	53292	111150	Moderate	Enriched	Enriched	Enriched	YES
Q15417;Q15417-3;	Calponin-3	CNN3	36.413	46.5	23	20	85.652	0	123870	110640	127370	108460	161490	118870	139320	172550	92016	128290	Low	Enriched	Enriched	Moderate	YES
Q15424;Q15424-4;	Scaffold attachment f	SAFB	102.64	18.5	24	13	92.052	0	66202	49157	59356	50090	71771	74833	95558	80874	65862	88629	Enriched	Moderate	Enriched	Low	YES
Q15427;Q5SZ64	Splicing factor 3B su	SF3B4	44.385	21.9	10	10	94.647	0	78723	95551	108050	56756	118010	65186	109700	84605	45863	74987	Enriched	Enriched	Enriched	Moderate	YES
Q15428;K7EMT0	Splicing factor 3A su	SF3A2	49.255	21.1	13	13	137.35	0	90673	51806	57796	76005	84468	75523	64948	62376	37043	80148	Enriched	Enriched	Moderate	Enriched	YES
Q15435;C9J177;H7	Protein phosphatase 1	PPP1R7	41.564	45.3	28	28	134.01	0	97296	65824	75719	117360	88330	111640	112970	140390	56092	116640	Enriched	Enriched	Enriched	Moderate	YES
Q15437	Protein transport pro	SEC23B	86.478	33.9	34	27	170.95	0	227910	145680	166580	263710	215750	246930	203780	188440	96322	203280	Enriched	Enriched	Enriched	Moderate	YES
Q15459;Q15459-2	Splicing factor 3A su	SF3A1	88.885	35.4	31	31	159.69	0	215090	156920	187860	185350	235250	202340	262420	281740	133530	232190	Enriched	Enriched	Enriched	Moderate	YES
Q15477	Helicase SKI2W	SKIV2L	137.75	11.5	16	15	53.094	0	67641	39014	57745	55393	45594	45275	60242	46912	31711	62769	Enriched	Enriched	Enriched	Enriched	YES
Q15493;Q15493-2	Regucalcin	RGN	33.252	44.5	18	18	121.53	0	126960	61747	101910	118380	83525	129550	210930	110880	58581	105420	Low	Enriched	Enriched	Enriched	YES
Q15526-2;Q15526;	Surfeit locus protein	SURF1	31.978	11.8	3	3	3.7839	0.0006	8643	18964	12701	12114	20690	10699	9832.6	10698	5567.9	12542	Moderate	Enriched	Enriched	Moderate	YES
Q15527	Surfeit locus protein	SURF2	29.647	4.7	1	1	2.0492	0.00739	8743	9097.9	7948.3	6039	11548	9556.4	11911	8867.5	8320.2	10100	Low	Moderate	Moderate	Enriched	YES
Q15554;Q15554-4	Telomeric repeat-bin	TERF2	59.593	8.9	5	5	11.751	0	13352	10252	11461	13724	13378	12912	12531	13546	10131	12875	Moderate	Enriched	Enriched	Enriched	YES
Q15555-4;Q15555-	Microtubule-associat	MAPRE2	30.691	27	9	8	22.025	0	23967	13166	18543	25760	29989	28076	16923	15710	10937	24038	Enriched	Enriched	Enriched	Enriched	YES
Q15582;H0Y8L3	Transforming growth	TGFBI	74.68	36.2	49	49	323.31	0	207620	222390	318630	213740	270110	242910	361630	441400	143120	336580	No expres	Moderate	Enriched	Low	YES
Q15599-2;Q15599	Na(+)/H(+) exchange	SLC9A3R2	36.153	12.9	6	3	11.613	0	6683.9	6299.2	9218.8	6918.6	8465.4	5054.1	8848.1	7674.1	5443	8521.5	Low	No expres	No expres	Moderate	YES
Q15628-2;Q15628	Tumor necrosis facto	TRADD	27.904	9.1	2	2	3.4839	0.00079	6036.9	4518.3	6237	4494.1	7101.1	3442.1	4171.2	4539.5	1285	4516.4	Enriched	Moderate	Enriched	Moderate	YES
Q15637-5;Q15637-	Splicing factor 1	SF1	71.751	18.4	20	20	89.847	0	95832	73773	75792	95874	102800	86960	93754	90232	52475	90024	Enriched	Enriched	Enriched	Enriched	YES
Q15642;W4VSQ9;	Cdc42-interacting pro	TRIP10	68.351	26.6	10	10	57.944	0	51773	45256	54546	48628	56151	38224	59004	51145	44442	53969	Enriched	Enriched	Moderate	No expres	YES
Q15648	Mediator of RNA pol	MED1	168.48	0.6	1	1	2.1215	0.00609	6083.3	5965.2	7687.4	4066.2	9260.4	4923.1	8091	5359.5	4760.2	6901.1	Low	Moderate	Enriched	Low	YES
Q15651;A0A087W	High mobility group	HMGN3	10.666	36.4	5	4	116.42	0	13738	10986	15218	9017	16576	14496	23652	13559	10964	22318	Enriched	Enriched	Enriched	Enriched	YES
Q15654	Thyroid receptor-inte	TRIP6	50.287	21	9	9	31.357	0	17793	14494	19444	13939	25047	11730	23272	21868	14701	16786	Enriched	Enriched	Enriched	Enriched	YES
Q15691	Microtubule-associat	MAPRE1	29.999	33.2	22	20	110.31	0	119490	99187	121540	83787	121920	87202	98489	95440	61495	98715	Enriched	Enriched	Enriched	Enriched	YES
Q15717;Q15717-2;	ELAV-like protein 1	ELAVL1	36.091	32.8	16	16	46.304	0	61064	59723	70207	51138	73733	45683	92508	79274	114650	71093	Moderate	Enriched	Enriched	No expres	YES
Q15746-11;Q1574(	Myosin light chain ki	MYLK	110.07	15.9	16	16	40.509	0	62910	41255	42603	50261	53223	69096	84643	81296	34399	80693	No expres	Moderate	Enriched	No expres	YES
Q15750-2;Q15750	TGF-beta-activated k	TAB1	49.917	9.3	6	6	24.945	0	24127	17224	20323	21935	11715	25597	24458	30355	13192	27984					YES
Q15758	Neutral amino acid tr	SLC1A5	56.598	5.2	4	4	8.079	0	15377	7474.4	13424	18990	21044	16992	17522	19737	6267.6	21689	Enriched	Moderate	Moderate	Low	YES
Q15785	Mitochondrial impor	TOMM34	34.559	12.6	3	3	22.243	0	24079	18669	21503	23770	22502	18057	19617	22446	11853	20324	Enriched	Enriched	Enriched	Enriched	YES
Q15813;Q15813-2	Tubulin-specific chap	TBCE	59.345	14.8	7	7	12.436	0	33508	30360	27772	19223	26621	37942	45538	38361	26037	34559	Enriched	Moderate	Enriched	Enriched	YES
Q15814	Tubulin-specific chap	TBCC	39.248	16.2	4	4	7.1081	0	8753.9	10440	8641.8	5788.8	11464	2937.4	6184.5	5556.9	4136.7	6723.2	Moderate	Moderate	Enriched	Moderate	YES
Q15819;G3V113	Ubiquitin-conjugatin	UBE2V2	16.363	57.2	12	3	8.8097	0	18965	17423	16891	16773	23216	16003	20099	18353	10287	20445	Moderate	Moderate	Enriched	Low	YES
Q15833-2;Q15833;	Syntaxin-binding pro	STXBP2;ZNF14	66.137	24.2	16	13	58.06	0	52343	39126	47769	55636	48065	49222	42307	53459	20577	57189	Moderate	Enriched	Enriched	Low	YES
Q15836	Vesicle-associated m	VAMP3	11.309	49	9	3	30.424	0	11458	8505.1	7805.6	8821.1	9979.3	9047.9	10944	10261	6957.8	10181	Enriched	Enriched	Enriched	Enriched	YES
Q15843;S4R3E9	NEDD8	NEDD8;NEDD8-MDP1	9.0714	66.7	10	5	61.613	0	25074	20037	28530	23558	34951	31971	168540	69502	89380	53761	Enriched	Enriched	Enriched	Enriched	
Q15847	Adipogenesis regulat	ADIRF	7.8547	28.9	9	7	320.89	0	78324	69265	78228	36484	87963	52317	98256	67336	54767	116200					YES
Q15907;Q15907-2	Ras-related protein R	RAB11B	24.488	52.3	17	4	72.295	0	58757	49297	50139	61230	57502	65099	78500	108340	38134	78402	Moderate	Moderate	Moderate	Low	
Q16134;Q16134-3	Electron transfer flav	ETFDH	68.495	34.8	31	31	135.34	0	141110	123110	116390	126190	143480	155320	152750	128480	85148	156800	Low	Low	Moderate	Moderate	YES
Q16186;A0A087W	Proteasomal ubiquitin	ADRM1	42.153	20.4	8	8	21.345	0	80512	48797	62703	41292	63298	75457	59735	59984	31704	56605	Moderate	Enriched	Enriched	Low	YES
Q16204	Coiled-coil domain-c	CCDC6	53.29	16.9	9	9	21.557	0	27181	21373	24167	23624	31175	30222	45585	41440	26729	45278	No expres	Enriched	Enriched	Enriched	YES
Q16222-3;Q16222;	UDP-N-acetylhexosa	UAP1	58.681	18.2	8	8	46.117	0	32409	23934	27860	40968	32771	35071	38365	37140	21597	33679	Moderate	Enriched	Enriched	Moderate	YES
Q16270-2;Q16270	Insulin-like growth fa	IGFBP7	28.86	36.2	9	9	36.942	0	17016	14136	17759	17993	18809	14007	15111	18723	10275	17724	No expres	Enriched	Enriched	Enriched	YES
Q16401;Q16401-2	26S proteasome non-	PSMD5	56.195	33.7	25	25	120.46	0	40665	23402	30826	48839	33075	59735	61392	60331	47845	44196	Moderate	Enriched	Enriched	Enriched	YES
Q16513-2;Q16513;	Serine/threonine-prot	PKN2	110.34	10.8	9	9	16.389	0	31094	26321	30199	34767	29492	28676	36489	33139	29559	30387	Enriched	Low	Enriched	Moderate	YES
Q16527;F8VW96;F	Cysteine and glycine-	CSRP2	20.954	50.3	13	11	116.19	0	42724	33875	37195	25254	58912	43087	67932	58166	24198	69373	Moderate	Moderate	Enriched	Moderate	YES
Q16531;F5GY55	DNA damage-binding	DDB1	126.97	23.9	35	25	323.31	0	144800	138040	134280	141540	160460	122830	155140	165430	86603	131180	Enriched	Enriched	Enriched	Moderate	YES
Q16537-3;Q16537-	Serine/threonine-prot	PPP2R5E	46.179	10.7	5	2	4.2714	0.00063	5562.5	4118.5	4958.3	8077.5	6033.4	5516.3	5757.4	6379.2	2704.7	7422.1	Moderate	Enriched	Enriched	Moderate	YES
Q16543;K7EQA9;F	Hsp90 co-chaperone	CDC37	44.468	31	17	17	133.17	0	116890	92079	98599	122910	108630	116080	185650	190360	103580	144380	No expres	Moderate	Enriched	Enriched	YES
Q16555;Q16555-2	Dihydropyrimidinase	DPYSL2	62.293	55.4	53	39	323.31	0	269030	237100	266230	268870	279260	247560	320480	407440	186710	305760	Enriched	Enriched	Enriched	Enriched	YES
Q16610;Q16610-4;	Extracellular matrix p	ECM1	60.673	4.6	2	2	3.7811	0.0006	5207.4	5959.1	5685.4	5750.6	6517.6	6033.5	5383.6	7734.4	2289.5	6230	Low	Moderate	Moderate	Moderate	YES
Q16625-4;Q16625-	Occludin	OCLN	31.602	29.5	8	8	81.585	0	50480	38100	42899	34673	48269	30014	42661	48870	25103	44072	Enriched	Enriched	Enriched	Moderate	YES
Q16643;Q16643-3;	Drebrin	DBN1	71.428	12.2	10	10	39.174	0	27897	24236	26615	26317	31499	27484	42349	37344	39753	40223	Low	Moderate	Enriched	Moderate	YES
Q16647	Prostacyclin synthase	PTGIS	57.103	18.4	11	11	61.517	0	35354	29344	31055	42000	33944	37411	42717	52015	24926	46726	Low	Low	Moderate	No expres	YES
Q16654	[Pyruvate dehydroge	PDK4	46.469	8.8	6	6	29.639	0	42260	32883	50718	63007	73332	122470	66947	87334	36468	57640	Enriched	Enriched	Enriched	No expres	YES
Q16658	Fascin	FSCN1	54.529	31.6	20	20	39.335	0	27803	21994	25273	32592	31548	32875	36583	40560	25348	34009	Low	No expres	Moderate	Enriched	YES
Q16666-3;Q16666-	Gamma-interferon-in	IFI16	75.935	22.9	18	18	35.093	0	41768	31443	41296	39723	45289	33774	43438	47874	21918	45319	Enriched	Moderate	Enriched	Low	YES
Q16698-2;Q16698;	2,4-dienoyl-CoA red	DECR1	34.994	49.7	28	28	323.31	0	259840	223040	262850	289630	273360	241770	302250	294240	143650	282900	Enriched	Enriched	Enriched	Moderate	YES
Q16706	Alpha-mannosidase 2	MAN2A1	131.14	14.1	17	17	149.91	0	82597	57566	57312	73324	64356	50677	59335	61198	35150	82239	Enriched	Enriched	Enriched	Moderate	YES
Q16762	Thiosulfate sulfurtrar	TST	33.429	48.1	19	19	300.88	0	126600	92372	109170	152960	131950	145110	186270	226930	84860	173810	Enriched	Enriched	Enriched	Moderate	YES
Q16775-2;Q16775;	Hydroxyacylglutathic	HAGH	28.86	58.5	25	25	73.361	0	81462	73822	83188	109210	86120	83913	92869	92268	57698	83436	Enriched	Enriched	Enriched	Enriched	YES
Q16795	NADH dehydrogenas	NDUFA9	42.509	44.3	25	25	63.49	0	155890	121220	138080	169490	150920	154660	145470	182690	83517	166980	Enriched	Enriched	Enriched	Moderate	YES
Q2NKQ5;Q16799	Reticulon;Reticulon-	RTN1	76.244	6.1	4	4	25.513	0	14626	10190	11677	11981	15577	12368	40959	34938	15469	19475	No expres	Low	Enriched	Enriched	YES
Q16822;B4DW73;I	Phosphoenolpyruvate	PCK2	70.729	51.2	46	42	287.67	0	200850	146280	175090	216740	212940	236980	204640	241470	95123	217710	Enriched	Enriched	Enriched	Enriched	YES
Q16849-3;Q16849-	Receptor-type tyrosin	PTPRN	96.26	3.5	2	2	5.8578	0	28139	19521	22607	16490	29172	22842	22148	18813	12345	18146	Enriched	Low	Enriched	Enriched	YES
Q16850-2;Q16850	Lanosterol 14-alpha	CYP51A1	46.312	16.1	8	8	21.378	0	33861	21784	32874	41153	27999	47736	54368	68677	24945	52689	Moderate	Moderate	Enriched	Enriched	YES
Q16853-2;Q16853	Membrane primary a	AOC3	70.674	32.6	37	29	189.77	0	137910	103450	133240	168980	164960	152050	146090	129170	78391	183150	Low	Low	Low	Moderate	YES
Q16854-2;Q16854;	Deoxyguanosine kina	DGUOK	21.438	11.1	2	2	2.8593	0.00186	20926	21899	17949	9324	15136	7252.9	8203	7348.8	12034	13269	Enriched	Enriched	Enriched	Low	YES
Q16864;Q16864-2	V-type proton ATPas	ATP6V1F	13.37	31.9	5	5	5.5847	0	4730.7	1758.8	3107.4	2846.4	3337.4	3588.1	4397.5	4432.2	2426.4	3989	Enriched	Enriched	Enriched	Enriched	YES
Q66S35;Q16877-2;	6-phosphofructo-2-ki	PFKFB4;PFKFB3	53.284	5.2	2	1	4.048	0.00062	3450.9	5717.9	4938.7	2296.6	7598.6	1560.6	3282.4	1984	2010.4	1988.3	Enriched	Enriched	Enriched	Low	
Q16890-5;E9PPQ1	Tumor protein D53	TPD52L1	19.456	20	3	3	6.0741	0	4544.4	2887.7	3281.7	4618.2	5412.1	4184.8	4058.3	4462.6	2529.7	3557	Enriched	Enriched	Enriched	No expression	
Q17RN3;Q17RN3-	Protein FAM98C	FAM98C	37.329	10.6	5	5	14.183	0	29917	24287	25067	22187	29716	20877	24282	21809	11471	22107	Moderate	Enriched	Enriched	No expres	YES
Q1KMD3;H3BQZ7	Heterogeneous nucle	HNRNPUL2;HNRNPUL	85.104	32.3	35	35	119.99	0	202180	157590	181130	136480	229290	142410	168680	168410	111810	170330	Enriched	Enriched	Enriched	No expres	YES
Q1RLN5;Q8IWW6	Rho GTPase-activatin	ARHGAP12	90.873	3.9	2	2	5.1512	0.00044	10329	7922.3	9967.5	12329	12876	14136	10413	10893	4080.8	9030.2	Low	Moderate	Enriched	Enriched	YES
Q27J81-2;Q27J81;	Inverted formin-2	INF2	134.62	3.6	6	6	13.061	0	22666	18198	28959	22765	24365	11178	15993	15041	13989	23336	Enriched	Moderate	Moderate	No expres	YES
Q29963;Q29865;A	HLA class I histocom	HLA-C	40.968	27.6	13	0	17.426	0	3884.5	4586.7	6527.8	3233.6	4574	2285.2	3384.9	3498.5	8523.5	4032	Enriched	Enriched	Enriched	No expres	YES
Q29RF7	Sister chromatid coh	PDS5A	150.83	11.4	18	15	229.4	0	62087	57539	65657	56048	74175	53633	80576	81416	47973	67102	Enriched	Enriched	Enriched	Moderate	YES
Q2NL82	Pre-rRNA-processing	TSR1	91.809	5.8	4	4	13.025	0	22889	20724	19578	22805	25937	19763	20072	25450	8926.7	22605	Enriched	Moderate	Moderate	Low	YES
Q2PPJ7-3;Q2PPJ7-	Ral GTPase-activatin	RALGAPA2	206.43	5.1	8	8	43.289	0	25401	20072	25209	22304	31146	22700	28248	27172	16661	25920					YES
Q2QGD7-2;Q2QGI	Zinc finger protein Z	ZXDC	74.817	1.7	1	1	2.9633	0.00169	1715.3	1727.9	1678.4	1140.5	1743.6	994.95	1481.8	1306.4	1723.4	1385.1	Moderate	Enriched	Enriched	No expression	
Q2TAA2;H7C5G1;	Isoamyl acetate-hydr	IAH1	27.598	22.2	8	8	43.742	0	22646	7379.1	12276	25944	9329.8	20846	15411	21350	10286	23202	Enriched	Enriched	Enriched	No expres	YES
Q2TAL8	Glutamine-rich prote	QRICH1	86.435	2.3	2	2	2.2579	0.00493	9951.5	7485.6	9508.6	10664	9986.5	8200.4	6669.6	7491.2	4597.4	7337.6	Enriched	Enriched	Enriched	Low	YES
Q2TAY7;Q2TAY7-	WD40 repeat-contain	SMU1	57.543	12.5	6	6	23.82	0	39737	30078	34011	32636	35420	29685	63036	44550	39916	45391	Low	Enriched	Moderate	No expres	YES
Q2TB90;Q2TB90-2	Putative hexokinase I	HKDC1	102.54	8.5	9	7	13.303	0	19803	25117	21120	21585	23343	40515	41700	49829	17446	39352	Low	Enriched	Moderate	No expres	YES
Q2UY09;Q2UY09-	Collagen alpha-1(XX	COL28A1	116.66	6.3	6	6	16.585	0	12594	22030	40257	12846	38328	18168	15181	15599	10031	22786					YES
Q32MZ4-3;Q32MZ	Leucine-rich repeat fl	LRRFIP1	82.688	21.4	17	16	122.25	0	114390	83701	104380	103610	134710	96361	149470	122780	78076	122990	Enriched	Enriched	Enriched	Low	YES
Q32P28-4;Q32P28;	Prolyl 3-hydroxylase	LEPRE1	78.921	2.4	2	2	3.8972	0.00061	20823	16502	19180	31142	18264	22831	22963	26522	14654	25308	No expres	Low	Moderate	No expres	YES
Q3KQU3-2;Q3KQU	MAP7 domain-conta	MAP7D1	88.725	2.5	2	2	3.1981	0.00077	7510.1	7652.6	8071.5	5330	10821	5405.4	11616	7081.8	11108	10515	Moderate	Moderate	Enriched	No expres	YES
Q3KQV9;Q3KQV9	UDP-N-acetylhexosa	UAP1L1	57.03	9.3	6	6	8.6033	0	6002.7	11399	6572.2	7802.4	7196.6	5665	8353.2	5534.7	8680.7	10514	Low	Low	Moderate	No expres	YES
Q3MHD2;Q3MHD	Protein LSM12 homo	LSM12	21.701	17.9	3	3	11.977	0	8908.1	8817.2	8717.4	9177.6	14315	8218.4	22991	14480	19698	14097	Enriched	Enriched	Enriched	Low	YES
Q3MIP1	Inositol 1,4,5-trispho	ITPRIPL2	58.446	2.8	1	1	7.6016	0	13659	6458.5	8865.2	16734	9027	10439	8605.9	15319	5077.1	13757	Enriched	Enriched	Enriched	No expression	
Q3MIR4	Cell cycle control pro	TMEM30B	38.941	3.7	1	1	4.0588	0.00062	6947.7	3485.8	5098.6	4851.6	7644.3	5624.9	6987.5	5064.5	3800.6	6501.3	Moderate	Enriched	Enriched	Enriched	YES
Q3SY69;Q3SY69-3	Mitochondrial 10-for	ALDH1L2	101.74	60.8	98	88	323.31	0	629990	324130	443070	580840	589830	535500	482980	397250	215590	562080	No expres	Enriched	Moderate	No expres	YES
Q3YEC7;Q3YEC7-	Rab-like protein 6	RABL6	79.548	20.4	17	17	45.595	0	86202	73872	74228	74369	101550	49854	55824	55012	28402	58102					YES
Q3ZCQ8;Q3ZCQ8-	Mitochondrial impor	TIMM50	39.646	14.2	7	7	28.317	0	16591	16211	20308	16589	23664	11631	55118	18407	91069	20398	Low	Enriched	Enriched	No expres	YES
Q3ZCW2;U3KQ88	Galectin-related prot	LGALSL	18.986	15.7	2	2	5.9832	0	3997.2	3213.5	2236.6	4002.7	4833	3372.9	2051.9	3210.1	878.92	3089.3					YES
Q495G5;Q8IVH4	Methylmalonic acidu	MMAA	47.135	3.5	3	3	4.4422	0.00042	10538	7884.5	8678.7	11458	8213.5	18418	16376	13612	10151	10419	Enriched	Enriched	Enriched	No expres	YES
Q4G0F5	Vacuolar protein sort	VPS26B	39.154	25.6	10	9	29.408	0	53648	50774	54218	45336	71527	43490	46556	42443	22750	47641	Moderate	Enriched	Enriched	No expres	YES
Q4G0J3;Q4G0J3-3;	La-related protein 7	LARP7	66.898	20.8	14	14	37.587	0	31586	26508	29043	35144	31277	29108	28965	31314	17238	36067	Enriched	Moderate	Enriched	Moderate	YES
Q4G0N4-2;Q4G0N	NAD kinase 2, mitoc	NADK2	45.972	31	15	12	87.084	0	73445	53872	59591	93840	72311	59839	71625	53727	35891	62847					YES
Q4G148-2;Q4G148	Glucoside xylosyltrar	GXYLT1	46.8	5.9	2	2	16.342	0	1347.7	1908.4	2735.9	1280	2390.4	1778.2	3277.2	2892.4	2537.1	2603.6					
Q4G176;F5H5A1;F	Acyl-CoA synthetase	ACSF3	64.129	16.7	12	12	33.512	0	59808	37307	55779	61039	53411	52726	69260	78331	36128	68533	Low	Moderate	Moderate	No expres	YES
Q4J6C6-4;Q4J6C6-	Prolyl endopeptidase	PREPL	73.351	1.9	1	1	2.3327	0.00462	6666.8	6880.1	5816.4	9091.2	5937.5	6461	8736.2	15662	7931.2	10733	Low	Moderate	Enriched	Enriched	YES
Q4KMP7	TBC1 domain family	TBC1D10B	87.198	2.5	1	1	22.759	0	7985.5	8037	8543.9	5811.3	10312	4964.7	4560.1	6247.7	2103.5	7991.8	Enriched	Enriched	Enriched	No expression	
Q4KMQ1	Taperin	TPRN	75.555	6.9	4	4	6.9044	0	2317.7	2129.2	2809.6	2021.8	3530.1	3157	5145.6	2576.3	3254.5	3811.3					YES
Q4KMQ2-3;Q4KM	Anoctamin-6	ANO6	103.96	10.2	9	9	75.491	0	57980	41523	49934	41377	64983	36775	31799	26077	12252	32042	Enriched	Enriched	Enriched	No expres	YES
Q4TT65		PDIA2	17.239	37	11	1	3.2906	0.00078	42578	97708	92622	42390	40939	23251	45700	32830	31949	26934	Low	Enriched	Enriched	Enriched	YES
Q5JTY5-2;Q9BRT8	COBW domain-conta	CBWD3;CBWD1;CBWI	41.896	9.6	5	5	31.982	0	8698	9632.4	9326.3	9997.4	9762.5	12218	12129	9724.5	5294.1	8886.2	Enriched	Moderate	Enriched	No expression	
Q4V9L6	Transmembrane prot	TMEM119	29.203	7.4	1	1	22.975	0	7381.1	4969.1	5399.4	7861.5	3957.8	4668.9	10385	6950.2	4099.6	8322.2	Low	Moderate	Moderate	No expres	YES
Q4VC05-2;Q4VC0	B-cell CLL/lymphom	BCL7A	25.029	10	2	2	3.8485	0.00061	19411	26586	26262	17358	35941	15381	18969	14823	9835.8	16174	Enriched	Moderate	Moderate	Low	
Q4VXN7		EPB41L1	12.398	18.4	2	1	2.3504	0.00445	7615.7	7915.6	8733.6	8127	13129	3792.7	6451.2	6414.6	3859.3	6203.1	Enriched	Enriched	Moderate	Low	YES
Q52LJ0-2;Q52LJ0	Protein FAM98B	FAM98B	45.547	22.2	10	9	66.226	0	67490	55179	65233	47865	76441	52200	76796	61957	37470	57809	No expres	Enriched	Enriched	No expres	YES
Q53EL6-2;Q53EL6	Programmed cell dea	PDCD4	50.576	58.7	62	62	323.31	0	472750	225250	280440	375550	280260	370490	351110	315630	270880	381460	Enriched	Enriched	Enriched	Moderate	YES
Q53FA7;H7BZH6;	Quinone oxidoreduct	TP53I3	35.536	14.5	5	5	14.876	0	45605	42754	51245	39689	56232	82538	35270	30167	19738	31488	Enriched	Enriched	Enriched	Moderate	YES
Q53GQ0	Estradiol 17-beta-del	HSD17B12	34.324	35.9	31	19	281.82	0	314710	248910	282930	297950	381400	359540	290440	293560	113240	248250	Enriched	Enriched	Enriched	No expres	YES

Q53H47-3;Q53H47	Histone-lysine N-met	SETMAR	62.123	11.9	8	8	11.576	0	24422	20503	24051	19247	41035	28013	22750	18009	12416	22216	Moderate	Low	Moderate	No expres	YES		
Q53H82	Beta-lactamase-like p	LACTB2	32.805	32.3	12	12	39.015	0	69252	52748	55572	62952	66848	63761	54043	58345	35524	64704	Low	Moderate	Enriched	No expres	YES		
Q53LP3	Ankyrin repeat doma	SOWAHC	55.671	4.2	2	2	4.1252	0.00062	1186.5	1365.1	1616.6	863.66	2645.1	1134.9	1884.6	1716.1	1597.2	2089.2					YES		
Q53SF7-4;Q53SF7	Cordon-bleu protein-	COBLL1	123.87	26.2	30	30	102.23	0	111500	85758	102670	94087	119160	101650	124230	100240	63643	99868	Enriched	Enriched	Enriched	Enriched	YES		
Q53T59;F6TR53;B	HCLS1-binding prote	HS1BP3	42.78	21.4	8	8	27.267	0	47376	33400	34784	53312	39760	40368	41709	55409	33580	49845	Enriched	Enriched	Enriched	No expres	YES		
Q53TN4-3;Q53TN	Cytochrome b reduct	CYBRD1	25.087	8.3	2	2	4.0998	0.00062	2502.6	2082.7	2919.1	2224.3	3414.9	2898.9	13732	18128	3175.6	4028.2	Enriched	Moderate	Enriched	No expres	YES		
Q562E7-4;Q562E7	WD repeat-containin	WDR81	197.99	2.3	4	4	57.309	0	22166	9939.9	13977	28114	10703	27364	23049	36256	9140.8	28148	Enriched	Enriched	Moderate	No expres	YES		
Q56VL3	OCIA domain-contai	OCIAD2	16.953	23.4	3	3	5.9268	0	4065.6	4440.4	4568.3	3397.6	7040.1	3755.3	12239	6209	8636.3	9112.7	Enriched	Enriched	Enriched	No expres	YES		
Q580Q6		EFEMP1	18.424	23.3	5	1	2.5591	0.00344	2216	3977.3	2358.9	1740.7	3666	1847.1	3187.3	3076.3	2996.2	2511.7	Moderate	Enriched	Enriched	Low	YES		
Q58FF6	Putative heat shock p	HSP90AB4P	58.264	16.4	22	3	36.533	0	8032.6	4987.3	7822.7	6986.4	7923.7	27121	41425	53732	7686.4	14710							
Q58FF8	Putative heat shock p	HSP90AB2P	44.348	27	23	2	4.866	0.00043	9032.5	9869.1	7669.7	6538	9690.9	11719	10536	9773	6096.3	8900					YES		
Q5BJF2;Q86XC5;J	Transmembrane prote	TMEM97	20.848	17	8	8	15.61	0	40756	39500	43944	63567	50882	33205	52031	37733	21972	53927	Enriched	Enriched	Enriched	Enriched	YES		
Q5BKZ1;A0A0A0	DBIRD complex sub	ZNF326	65.653	13.6	7	7	14.435	0	65728	53606	56338	66709	68273	47751	47604	49770	34757	57846	Moderate	Enriched	Enriched	No expres	YES		
Q5EBL8;Q5EBL8-	PDZ domain-containi	PDZD11	16.131	24.3	4	4	3.9497	0.00061	6668	5653.6	6380.3	5788.5	7740.5	4872.2	6272.7	5298.4	3123.5	5935.9	Enriched	Enriched	Enriched	No expression			
Q5EBM0-3;Q5EBM	UMP-CMP kinase 2,	CMPK2	39.561	7.7	3	3	4.1051	0.00062	2008	1979.6	2053.2	2154.2	2753.5	1772.9	2556	1527.2	3761.8	2031.7	Moderate	Enriched	Enriched	No expression			
Q5F1R6;Q5F1R6-3	DnaJ homolog subfa	DNAJC21	62.027	3	2	2	5.3006	0	8659.7	5522	8104.5	6988.6	7015.9	5342.7	7401.6	6862.1	4092.8	8550.3	Low	Enriched	Enriched	No expres	YES		
Q5GFL6-2;Q5GFL	von Willebrand facto	VWA2	78.4	5.2	4	3	5.3643	0	12403	15608	16040	11005	19816	11503	16679	11952	12014	14072					YES		
Q5GLZ8-6;Q5GLZ	Probable E3 ubiquiti	HERC4	106.71	4	3	3	10.144	0	6247.8	4598.2	5526.6	5766.8	5512.8	3563.7	3647.1	5252	2118.2	4628.6	Low	Enriched	Enriched	No expres	YES		
Q5HY54		FLNA	276.55	47.6	203	2	323.31	0	788830	847060	781270	722960	1081100	791830	1291200	1183700	584110	1115000	Enriched	Enriched	Enriched	Enriched	YES		
Q5HYI7-5;Q5HYI7	Metaxin-3	MTX3	28.608	13.5	2	2	6.4052	0	23179	14725	15591	24889	61649	12525	11377	21236	3016.5	19114	Low	Enriched	Enriched	No expres	YES		
Q5HYI8;C9JXM3	Rab-like protein 3	RABL3	26.422	30.9	7	7	31.434	0	54245	38788	54337	53507	38484	70430	111450	61206	52306	68423	Enriched	Moderate	Moderate	Low	YES		
Q5HYK3;F8VVX6;	2-methoxy-6-polypre	COQ5	37.14	26.6	8	8	17.843	0	40352	31725	32178	45284	31768	26694	39000	44656	19189	41448	Moderate	Enriched	Enriched	No expres	YES		
Q5JPE7-2;Q5JPE7;	Nodal modulator 2;N	NOMO2;NOMO3	134.19	48.2	82	6	323.31	0	424250	303630	350510	445720	368800	568070	574940	552950	248940	447560	Enriched	Enriched	Enriched	No expression			
Q5JPF3	Ankyrin repeat doma	ANKRD36C	199.75	1.8	3	3	3.2658	0.00077	18070	31141	33294	8008.6	36118	31481	36690	25170	14929	15628							
Q5JRA6;Q5JRA6-2	Melanoma inhibitory	MIA3	213.7	25.9	52	52	313.21	0	269340	179360	216730	224440	232980	225640	219350	255780	137480	275380	Moderate	Moderate	Enriched	Moderate	YES		
Q5JRS1;Q5JRS3;Q5JRS2		UBA1	18.604	48	13	4	5.8942	0	13909	8230.4	9213	15662	9251.6	16209	11349	18347	5674.1	16005	Moderate	Enriched	Enriched	Low	YES		
Q5JRU4		CELA2B	13.736	19	3	2	5.8034	0	12862	13906	14833	9214.5	17205	8022.2	9927.4	5160.6	5749.3	7411.8	Low	Moderate	Moderate	Enriched	YES		
Q5JRX3;Q5JRX3-2	Presequence protease	PITRM1	117.41	21	20	16	104.44	0	90010	94231	120930	69827	147750	75172	102940	94975	66450	91532	Enriched	Enriched	Enriched	Enriched	YES		
Q5JSD1;Q5JSD2		VDAC2	22.159	45.1	16	1	2.175	0.0056	811.74	2787.9	2543.6	1344.9	2444.9	154.36	424	219.46	170.36	427.6	Enriched	Enriched	Enriched	Enriched	YES		
Q5JSH3-4;Q5JSH3	WD repeat-containin	WDR44	91.271	9	9	9	34.648	0	42947	34235	34640	37981	36457	42443	52880	64801	25145	47323	Low	Low	Moderate	No expres	YES		
Q5JSP0-2;Q5JSP0-	FYVE, RhoGEF and	FGD3	68.793	3	2	2	4.2283	0.00063	7338.7	6885.4	6824.8	4848.7	6874.7	5586.4	7334.3	6615.3	6161.2	6209.5	Enriched	Enriched	Moderate	No expression			
Q5JSZ5-5;Q5JSZ5;	Protein PRRC2B	PRRC2B	165.53	2.2	3	3	4.9264	0.00044	12405	9257.6	10845	9880.1	15371	7669.8	13589	9969.7	6827.4	13389					YES		
Q5JTB4;Q5JTB6	Placenta-specific pro	PLAC9	6.0329	38.2	3	3	7.596	0	20508	19095	21937	9672.3	19963	17246	22147	30308	9558.8	22332	Low	Low	No expres	No expression			
Q5JTC4;Q9Y6N6	Laminin subunit gam	LAMC3	172.46	12.6	28	24	117.14	0	37894	43004	47450	37075	65841	60962	124280	115880	34505	69880	Moderate	No expres	Moderate	No expres	YES		
Q5JTH9-2;Q5JTH9	RRP12-like protein	RRP12	132.71	13.5	16	16	129.79	0	87803	58174	75210	80167	85327	81721	87577	94845	50944	97417	No expres	Low	Moderate	No expres	YES		
X6R5Z6;Q5JTJ3-3;	Cytochrome c oxidas	COA6	18.006	26.5	10	10	38.061	0	37909	42906	51684	35214	63975	28308	38740	32432	22530	38200					YES		
Q5JTV1;Q9UKD1	Glucocorticoid modu	GMEB2	51.233	4	2	2	7.9995	0	14170	5671.8	9361.9	12986	9560.9	15575	13294	17534	7615.1	14796	Enriched	Enriched	Enriched	No expression			
Q5JTV8;Q5JTV8-3	Torsin-1A-interacting	TOR1AIP1	66.248	25.6	16	16	29.485	0	34566	32918	40449	29661	48090	26241	43185	34001	31367	35476	Enriched	Enriched	Enriched	Enriched	YES		
Q5JTZ9	Alanine--tRNA ligase	AARS2	107.34	11.1	11	11	38.072	0	16704	23094	24494	13525	27102	18121	19967	17334	14329	17758	Enriched	Moderate	Moderate	No expres	YES		
Q5JUW8;Q92796;	Disks large homolog	DLG3	93.605	7.5	6	4	35.39	0	24562	14569	14939	22034	17479	19658	18217	16465	10816	18471	Enriched	Enriched	Enriched	Moderate	YES		
Q5JVD5;Q5JVD6;	Centriolin	CNTRL	16.875	6.9	1	1	2.5991	0.00273	410	407.38	398.48	220.86	810	1110.1	4396.5	4982	1625.1	2154.9					YES		
Q5JVF3-3;Q5JVF3	PCI domain-containi	PCID2	43.374	6.1	2	2	16.707	0	15175	10743	10930	14531	14854	10841	16655	12952	7171.3	14936	Moderate	Enriched	Enriched	No expression			
Q5JW84		GSTA3	12.529	41.7	14	2	4.6495	0.00043	4958.7	6480.3	5854.7	4632.1	4401.4	5362.7	4494.6	4496.7	2999.5	5081.7	Moderate	Low	Moderate	No expression			
Q5JW85	Glutathione S-transfe	GSTA3	19.742	39.5	20	0	4.6427	0.00043	10907	7811.1	7325.6	5777.7	6692.2	10258	5250.3	4445.7	2513.4	6505.2	Moderate	Low	Moderate	No expression			
Q5JY65;Q9BZJ0-2;	Crooked neck-like pr	CRNKL1	99.172	7.5	7	7	29.905	0	51961	39203	54874	54899	49882	66184	68635	66434	41751	61964	Moderate	Moderate	Enriched	No expres	YES		
X6R3N0;Q5K4L6-	Long-chain fatty acid	SLC27A3	87.323	9.4	5	5	32.773	0	28253	20957	25685	29276	21643	17130	20135	22511	10400	25161	Low	Moderate	Moderate	No expres	YES		
Q5LJA5;Q5LJA9;	Ubiquitin carboxyl-te	UCHL5	40.423	22.5	9	9	20.073	0	27018	26492	35535	25386	27606	32064	36025	30086	16229	25108	Moderate	Enriched	Enriched	No expres	YES		
Q5NDL2;Q5NDL2-	EGF domain-specific	EOGT	62.01	7	4	4	4.3428	0.00063	8985.2	9084.7	9339.9	6058.6	8289.8	3048.1	5500.1	5881.5	4007.2	6684.9					YES		
Q5QJ74;E9PP54	Tubulin-specific chap	TBCEL	48.194	10.8	4	4	5.1174	0.00044	13180	9708.4	14581	12832	16554	16532	14746	10898	7868.4	11215	Moderate	Moderate	Moderate	No expres	YES		
Q5QJE6;J3KP30	Deoxynucleotidyltra	DNTTIP2	84.468	4.6	3	3	3.9032	0.00061	2690.9	1901.3	2697.8	2703.7	4472.2	2392.5	3339	2624.3	1868.6	2637.8	Enriched	Enriched	Enriched	Moderate	YES		
Q5QPM7;Q92530;	Proteasome inhibitor	PSMF1	28.956	31.9	8	8	43.78	0	50990	33196	36292	49105	45341	36397	39393	46445	21667	43229	Enriched	Enriched	Enriched	Enriched	YES		
Q5R3I4;A9UJP8;H	Tetratricopeptide rep	TTC38	52.787	24.3	16	16	40.514	0	78493	43964	52470	62427	71380	73808	53585	63669	25034	55781	Enriched	Enriched	Moderate	No expres	YES		
Q5RI15;Q5RI15-2	Cytochrome c oxidas	COX20	13.291	19.5	2	2	4.329	0.00063	5024	5585.7	4511.3	4473.1	6013.6	2385.1	1890.4	2708.5	1160.1	3667.8					YES		
Q5RKV6	Exosome complex co	EXOSC6	28.235	11.8	2	2	3.3572	0.00078	11018	5147.6	8235	6853.2	21887	4567.9	6547.1	7129.7	3269.8	7497.2	Moderate	Enriched	Enriched	No expres	YES		
Q5SGD2-4;Q5SGD	Protein phosphatase	PPM1L	22.474	6.2	1	1	2.0466	0.00738	2171.3	1124.9	1525.9	2138.9	1540.2	2031.3	1297.3	1571.4	547.49	1533.4	Low	Moderate	Enriched	No expression			
Q5SRE5-2;Q5SRE	Nucleoporin NUP18	NUP188	182.29	3.6	5	5	28.311	0	14871	10085	12109	13693	14314	17684	14493	15218	6188.3	18136	Moderate	Low	Moderate	Enriched	YES		
Q5SRE7-2;Q5SRE	Phytanoyl-CoA diox	PHYHD1	30.047	41.5	15	15	63.647	0	48650	25468	35074	56298	41650	67321	40841	35610	15684	41444	Moderate	Enriched	Moderate	No expres	YES		
Q5SSJ5;Q5SSJ5-2;	Heterochromatin pro	HP1BP3	61.206	40.5	48	43	221.33	0	342130	245290	311860	267990	348120	312730	480700	443130	274620	383540	Enriched	Enriched	Enriched	No expres	YES		
Q5SW96	Low density lipoprot	LDLRAP1	33.885	9.7	4	4	5.8886	0	14959	11026	15864	13171	24864	10347	14284	10528	7044.7	13354	Enriched	Enriched	Enriched	No expres	YES		
Q5SWX8-4;Q5SW	Protein odr-4 homolo	ODR4	47.592	34.8	21	21	61.821	0	102660	83037	84061	74613	105250	95724	108740	110940	51182	86324					YES		
Q5SY16	Polynucleotide 5-hyd	NOL9	79.322	2.3	2	2	2.0922	0.00673	13954	10769	12181	10110	12690	12900	23070	24230	11797	13876	Enriched	Enriched	Enriched	No expres	YES		
Q5SY74;Q96IY1-2	Kinetochore-associat	NSL1	19.511	7.6	1	1	3.6647	0.0008	8529.4	5082.9	6790.7	6206.6	7048.2	3474.1	7133.6	5505.5	4585.9	8548.1	Enriched	Moderate	Enriched	Enriched			
Q5SYQ7		ALDH1A1	22.654	87.7	69	5	58.802	0	94806	131510	134930	47907	209980	63751	85883	42391	45539	48014	Moderate	Enriched	Enriched	Enriched	YES		
Q5SYV1;A0A087X242		SARDH	67.113	40.5	35	4	115.65	0	60306	46922	56044	27711	82488	25308	36140	38699	21394	42318	Moderate	Moderate	Low	No expres	YES		
Q5SZK8;Q5SZK8-	FRAS1-related extra	FREM2	351.15	14.1	39	39	127.36	0	90035	92394	103660	90332	109440	111750	119820	120600	79867	126900	No expres	No expres	Moderate	No expres	YES		
Q5T063;Q9NZJ6	Hexaprenyldihydroxy	COQ3	34.647	16.1	4	4	26.141	0	22525	12681	15687	21777	17347	24336	22814	29848	11700	27253	Low	Enriched	Enriched	No expres	YES		
Q5T0D9-2;Q5T0D	Tumor protein p63-re	TPRG1L	23.346	13.1	2	2	7.465	0	9438.9	9339.1	10132	5910.1	10177	3865.7	5570.2	4649	3309.8	4898.7	Enriched	Enriched	Enriched	No expression			
S4R347;Q5T0N5-3	Formin-binding prote	FNBP1L	70.525	10.7	5	5	11.3	0	24615	17945	18258	26617	22676	21970	21204	22426	12752	24839	Moderate	Enriched	Enriched	Enriched	YES		
Q5T0R8;Q5T0S3	Adenylyl cyclase-ass	CAP1	6.2509	75.9	10	2	5.2435	0.00022	3848.7	1934.9	1988.7	4520.8	1878	3268.5	2863.7	5016.4	1146.5	5213.3	Enriched	Enriched	Enriched	Enriched	YES		
Q5T0Y8;Q92485-2	Acid sphingomyelina	SMPDL3B	29.529	13.8	4	4	12.632	0	14208	13933	16240	11582	19553	12831	23316	16183	18166	15804	No expres	Moderate	Moderate	Moderate	YES		
Q5T123;A0A087W	SH3 domain-binding	SH3BGRL3	9.3804	44.3	7	7	64.268	0	29802	15504	17300	47179	21570	22485	16535	35754	13519	31642	Moderate	Enriched	Enriched	No expres	YES		
Q5T160;H0Y450	Probable arginine--tR	RARS2	65.505	4.5	2	2	6.3452	0	4402.5	3005.7	2835.7	5938.8	2886.6	2974.2	3411.2	4499.4	2986.9	4043.7	Enriched	Enriched	Enriched	No expres	YES		
Q5T196;Q8NFF5-3	FAD synthase;Molyb	FLAD1	50.141	9.6	4	4	8.3851	0	14269	14249	16635	14311	15429	20868	19462	20347	14675	19485	Moderate	Moderate	Moderate	Moderate	YES		
Q5T1Z0;Q9H008-2	Phospholysine phosp	LHPP	22.909	29.7	8	1	1.8411	0.00943	5396.5	3373.6	4366.9	6319	4980.5	6532.2	4405.8	4479.1	2672.2	5096.8	Moderate	Moderate	Moderate	No expres	YES		
Q5T200-2;Q5T200	Zinc finger CCCH do	ZC3H13	184.87	1.8	3	3	5.5025	0	2420.3	1924.9	2543.4	2135.5	2934.6	1868.1	5535.9	1988.4	5263.4	3141.9	Low	Moderate	Enriched	Low	YES		
Q5T2E6;Q5T2E7	UPF0668 protein C1	C10orf76	78.71	6.7	3	3	6.4692	0	17512	11223	11739	18476	15972	14657	15120	23627	11002	20915	Low	Enriched	Enriched	No expres	YES		
Q5T2T1;S4R337;Q	MAGUK p55 subfam	MPP7	65.523	9.4	5	5	14.492	0	17743	16050	23398	23422	20823	25803	26711	26778	12368	26997	No expres	Moderate	Moderate	No expres	YES		
Q5T2W1-2;Q5T2W	Na(+)/H(+) exchange	PDZK1	44.665	12.5	4	4	7.4684	0	21177	22243	23152	15407	20039	16113	18299	17002	13958	21265	Moderate	Low	Moderate	Enriched			
Q5T440	Putative transferase C	IBA57	38.155	9.6	5	5	27.896	0	28894	27824	30492	25587	39395	23311	49073	46368	26599	37446					YES		
Q5T446;H0Y5R6		UROD	21.458	40.4	8	2	34.284	0	34805	23421	28270	44665	23544	31908	28437	37732	15831	42129	Enriched	Enriched	Enriched	Moderate	YES		
Q5T447	E3 ubiquitin-protein	HECTD3	97.112	9.8	8	8	14.323	0	9252.8	9535.3	10557	10476	13536	7241.7	10987	9526.4	8904.1	10325	Moderate	Enriched	Enriched	No expres	YES		
Q5T4F7	Secreted frizzled-rela	SFRP5	35.563	11	3	3	4.0335	0.00062	7135.4	8239.6	9591.3	6256.7	11506	5718.9	4744.8	3935.4	2301.6	4793.1	Low	Enriched	Moderate	No expression			
Q5T4S7-3;Q5T4S7	E3 ubiquitin-protein	UBR4	571.85	10.2	47	41	119.26	0	163930	111470	131360	166350	150980	159990	155410	178760	78846	164010	Enriched	Enriched	Enriched	Enriched	YES		
Q5T5C0-3;Q5T5C	Syntaxin-binding pro	STXBP5	121.6	5.4	5	5	8.3702	0	18994	16878	20803	15371	26209	14400	23740	18728	15309	20508	Moderate	Enriched	Enriched	No expres	YES		
Q5T5P2-3;Q5T5P2	Sickle tail protein ho	KIAA1217	162.36	10.9	15	15	43.692	0	36538	35287	39003	36807	48711	34885	33470	34637	21861	43688	Enriched	Enriched	Enriched	No expres	YES		
Q5T619;P28698-2;	Zinc finger protein 64	ZNF648;MZF1	62.34	4.4	3	0	4.2995	0.00063	2330.3	1613.8	2402	1402.9	3134.6	1982.2	3726.6	2329.2	1830.9	2330.9	Enriched	Enriched	Enriched	Enriched			
Q5T6F2;A2A306;F	Ubiquitin-associated	UBAP2	117.11	2.3	2	2	3.6919	0.0008	1923.8	1756.7	2458.9	2581.4	2527.6	1560.4	3933.7	1624.6	2344.1	2895.7	Enriched	Enriched	Enriched	No expres	YES		
Q5T6J8;Q5T6J7;Q	Probable gluconokin	IDNK	9.7719	13.3	1	1	3.4331	0.00079	5458.2	4969.9	5858.9	4760.6	6714.8	3710.4	4721	4610.5	3086.2	5141.3							
Q5T6V5;Q5T6V7	UPF0553 protein C9	C9orf64	39.028	10	4	4	6.944	0	10094	10815	8139.5	11672	11336	8401.7	6998.9	9061.2	5424.9	7565.5	Enriched	Enriched	Enriched	No expres	YES		
Q5T7N3	KN motif and ankyri	KANK4	107.34	10.6	9	9	41.708	0	64141	45879	50121	44382	74705	41877	58586	65333	33652	52279	No expres	Enriched	Moderate	No expres	YES		
Q5T948;Q5T949		PPP2R4	28.58	24	7	2	16.352	0	5686.9	5639.9	2946	7077.6	2730.5	6737.8	9717.4	20595	6566.6	6470.3	Enriched	Enriched	Enriched	Enriched	YES		
Q5TA02;P78417-3	Glutathione S-transfe	GSTO1	23.341	47	27	5	83.699	0	263920	140920	196330	312760	182450	252210	313250	336480	188010	196350	Enriched	Enriched	Enriched	Enriched	YES		
Q5TAQ0;V5IRT4;	Ubiquinol-cytochrom	UQCC2	11.909	9.9	1	1	2.7131	0.00238	3526.9	2936.4	3332.3	2836.7	3874	2625	2533.5	2236	1442.3	2078.5					YES		
Q5TBC7;I6LA81	Bcl-2-like protein 15	BCL2L15	17.725	37.4	6	6	17.079	0	24566	20502	20126	17297	26780	16699	16302	13741	8374.4	15480	Low	Enriched	Moderate	No expres	YES		
Q5TCQ9-3;Q5TCQ	Membrane-associate	MAGI3	123.34	2	2	2	6.1216	0	6376.7	5190.1	6590.1	3556	7897.5	4632	8402	4184.7	5826.4	5606.8	Enriched	Enriched	Enriched	No expression			
Q5TDH0;Q5TDH0-	Protein DDI1 homolo	DDI2	44.522	17.8	7	7	21.859	0	26908	21476	21915	26296	24888	19006	23830	22338	16216	25691	Low	Low	Low	No expres	YES		
Q5TEC6	Histone H3	HIST2H3PS2	15.43	36	12	11	62.064	0	133150	105710	58197	97751	142050	76606	168600	269010	33776	107690	No expres	No expres	No expres	No expres	YES		
Q5TFE4;Q5QPD0;	5-nucleotidase domai	NT5DC1	51.844	21.8	9	9	22.959	0	39710	33746	34356	35758	40040	33603	36526	34314	20874	41799	Enriched	Enriched	Enriched	No expres	YES		
Q5TH69	Brefeldin A-inhibited	ARFGEF3	240.65	3.4	8	8	17.412	0	15595	9701.6	13261	16504	12371	13456	11938	18256	7517	15033					YES		
Q5TZA2;Q5TZA2-	Rootletin	CROCC	228.52	5.2	10	10	15.509	0	10212	13221	13970	9511.2	16102	13781	22906	13345	20482	13258	Enriched	Low	Moderate	Moderate	YES		
Q5UIP0-2;Q5UIP0;	Telomere-associated	RIF1	271.69	2.1	6	6	14.44	0	17319	8426.5	11501	20587	10265	24822	16572	23574	10462	22425	Moderate	Low	Moderate	No expres	YES		
Q5VIR6-2;Q5VIR6	Vacuolar protein sort	VPS53	76.351	7	5	5	8.0957	0	7398.9	6401.3	6731.6	6821.6	8005.2	5870.7	4622.6	6241.3	1936.4	6723.6	Moderate	Enriched	Moderate	No expres	YES		
Q5VT52-5;Q5VT5	Regulation of nuclea	RPRD2	100.27	5.6	4	4	11.511	0	14393	11396	15388	19664	16304	15328	16897	15546	11998	14659	Enriched	Enriched	Enriched	Moderate	YES		
Q9Y6G2;Q5VT94;	Growth hormone-ind	GHITM	34.394	3.1	1	1	2.3766	0.00428	16953	10453	14007	8724.2	14995	13287	15554	15996	7326	19153	Enriched	Enriched	Enriched	Enriched	YES		
Q5VTI5;Q9Y2H5	Pleckstrin homology	PLEKHA6	119.29	6.3	7	7	12.788	0	29252	33277	33348	34711	41890	25395	35113	36755	23274	31829	Moderate	Enriched	Moderate	Moderate	YES		
Q5VTR2	E3 ubiquitin-protein	RNF20	113.66	8.9	11	10	39.657	0	73734	49250	44560	83439	45101	60505	65526	96378	32643	79093	Enriched	Enriched	Enriched	Moderate	YES		
Q5VUB5	Protein FAM171A1	FAM171A1	97.853	1.6	1	1	13.865	0	4539.3	3227.4	3088.5	3465.6	4655.2	4192.3	7239.1	4929.5	3946	4347.9	Enriched	Enriched	Enriched	Enriched	YES		
Q5VV41	Rho guanine nucleoti	ARHGEF16	80.104	10	5	5	15.161	0	70637	54113	57640	69492	67132	58960	69930	67012	40400	62179	Enriched	Moderate	Moderate	Low	YES		
Q5VV42-2;Q5VV4	Threonylcarbamoyla	CDKAL1	54.666	4.7	2	2	4.1011	0.00062	4416.6	3328.6	3227.2	4156.3	4054.8	3834	3172.1	5553	2377.8	5272.3	Low	Low	No expres	No expres	YES		
Q5VW32-2;Q5VW	BRO1 domain-contai	BROX	42.871	16.4	8	8	50.2	0	22763	7703.1	16378	35647	12603	21522	18802	40991	9106	27247					YES		
Q5VW36;S4R400	Focadhesin	FOCAD	200.07	3.9	7	7	16.481	0	40404	28889	38138	38280	44167	39879	41065	35892	25493	37204					YES		
Q5VW52;Q9HCL2	Glycerol-3-phosphat	GPAM	80.139	3.1	1	1	3.3051	0.00078	2735.1	1463.9	2612.1	4429.9	1578.4	2139.8	2545.7	3151.2	1725	4052.4	Moderate	Moderate	Moderate	No expres	YES		
Q5VWC4;P55036-	26S proteasome non-	PSMD4	41.079	27.1	12	5	89.493	0	55185	34706	40461	49383	42427	61889	59930	77194	30584	53135	Enriched	Enriched	Enriched	Enriched	YES		
Q5VWU8;Q8TEW	Partitioning defective	PARD3	110	9.1	9	9	22.471	0	37342	24554	31895	41620	34155	29920	28983	35784	18033	35226	Moderate	Enriched	Enriched	Moderate	YES		
Q5VWZ2;Q5VWZ	Lysophospholipase-li	LYPLAL1	26.316	12.7	5	5	11.972	0	11384	12998	14195	10195	16871	9940	13450	11506	6843.1	12143	No expres	Enriched	Enriched	No expres	YES		
Q5VXN0;Q9H7B2	Ribosome productio	RPF2	24.605	17.3	6	6	19.124	0	42526	25445	25189	38593	28533	36022	40932	46596	24736	47008					YES		
Q5VYW8;Q9Y2P8	RNA 3-terminal phos	RCL1	19.887	6.3	1	1	2.3711	0.00428	14626	9314.7	11539	20232	12769	12888	9495.2	10238	5316.5	15025	No expres	Enriched	Enriched	No expres	YES		
Q5VZA6		ACO1	48.576	45.6	31	2	9.5078	0	13943	10756	12053	7771.1	15288	16318	12724	7777.3	4611.5	10180	Enriched	Enriched	Enriched	Enriched	YES		
Q5VZE5	N-alpha-acetyltransfe	NAA35	83.638	1.4	1	1	2.7625	0.0024	3011.5	3943.6	4555	2356.4	4550.2	10889	11964	10337	8902	7360.4					YES		
Q5VZK9-2;Q5VZK	Leucine-rich repeat-c	LRRC16A	147.09	4.9	7	7	9.2775	0	32298	21508	21194	29177	22584	35400	26950	35439	13251	32752	Moderate	Moderate	Enriched	No expres	YES		
Q5W0S4		RAD23B	8.5388	62.5	9	1	5.0088	0.00044	2779	3852.8	6273	2743.5	9917	3385.4	4354.5	3165.4	5367.9	3276.3	Moderate	Enriched	Enriched	Enriched	YES		
Q5W0U4	B box and SPRY do	BSPRY	44.381	8.2	3	3	6.1262	0	2016.1	1044.9	1671.2	1199.2	1623.8	1795.7	1478.1	1446.7	930.33	1860.9	Moderate	Enriched	Enriched	No expression			
Q5W0V3-2;Q5W0	Protein FAM160B1	FAM160B1	83.734	6.5	4	4	7.796	0	10146	13308	13466	9753.1	15605	6356.4	10398	8863.4	7452	8736.1	Enriched	Enriched	Enriched	No expres	YES		
Q5XKP0	Protein QIL1	QIL1	13.087	44.9	7	7	32.344	0	59376	53193	74300	46039	64056	48952	69662	68647	26396	66474							
Q60FE5		FLNA	278.22	45.7	200	0	1.9754	0.00803	4445.5	3360.8	4396.3	5473.5	2323.9	5119.1	4634.3	3714	4047.5	7712.4	Enriched	Enriched	Enriched	Enriched	YES		
Q63HR2-6;Q63HR	Tensin-like C1 domai	TENC1	152.45	8.2	10	9	22.974	0	24223	21902	27268	27851	27683	24761	30689	25526	20990	31351	Moderate	Moderate	Moderate	Moderate	YES		
Q63ZY3-3;Q63ZY	KN motif and ankyri	KANK2	90.043	13.2	10	10	60.841	0	28687	27232	32741	27221	38543	22230	43258	35092	27700	36111	Enriched	Enriched	Enriched	No expres	YES		
Q659C4;Q659C4-9	La-related protein 1B	LARP1B	105.32	11.7	10	9	78.9	0	38012	26789	30466	29523	43505	30149	27103	25260	16066	24690	No expres	Enriched	Enriched	No expres	YES		
Q66K14-2;Q66K14	TBC1 domain family	TBC1D9B	138.67	9	12	11	28.717	0	54453	42892	50523	49985	48827	38242	34716	41717	21507	44942	Enriched	Enriched	Enriched	Moderate	YES		
Q66K74-2;Q66K74	Microtubule-associat	MAP1S	109.79	13.3	13	13	46.551	0	20232	13971	16231	16949	20428	19237	22152	21933	14332	24520	Moderate	Moderate	Moderate	No expres	YES		
Q66LE6;Q00005-6	Serine/threonine-prot	PPP2R2D;PPP2R2B	52.042	17.2	9	2	5.8662	0	39597	21544	23834	31851	26687	24316	19218	17912	14180	25359	Moderate	Enriched	Moderate	No expression			
Q684P5-3;Q684P5	Rap1 GTPase-activat	RAP1GAP2	77.897	9.4	8	1	21.913	0	13744	14615	15772	21306	16569	12397	10521	13365	7909	13110					YES		
Q68CP9-3;Q68CP	AT-rich interactive d	ARID2	191.42	1.9	4	4	6.1547	0	2076.6	1024.3	1743.2	2859.5	1612.4	2079.8	2251.4	2553.3	964.52	3009.8	Enriched	Enriched	Enriched	No expression			
Q68CZ2;E9PCX8;	Tensin-3	TNS3	155.26	13.6	22	21	111.46	0	83622	60713	73842	81963	86251	81857	129680	120550	65314	94985	Enriched	Enriched	Enriched	No expres	YES		
Q68D91;Q68D91-2	Metallo-beta-lactama	MBLAC2	31.371	15.1	3	3	18.28	0	14288	11443	12689	15515	13126	11513	11071	15276	6932.4	14201	No expres	Moderate	Moderate	No expres	YES		
Q68DH5	LMBR1 domain-cont	LMBRD2	81.171	1.6	1	1	3.032	0.00132	12159	12072	11237	12173	15073	9632.4	7562.8	11812	3044.2	10732	Low	Enriched	Enriched	No expres	YES		
Q68DQ2	Beta/gamma crystalli	CRYBG3	330.63	2.3	5	5	14.906	0	17748	10224	12246	19527	18399	68271	54624	24469	11935	23816	Enriched	Enriched	Enriched	Moderate	YES		
Q68E01-2;Q68E01	Integrator complex su	INTS3	118.01	4.3	4	4	12.667	0	3735.8	3856.4	3638.6	3845.5	4544.7	3350.5	3847.8	2571.7	2311.1	3156.8	Moderate	Enriched	Enriched	Low	YES		
Q68EM7-2;Q68EM	Rho GTPase-activati	ARHGAP17	87.608	8	8	8	33.226	0	38221	25592	28921	46634	30540	28594	23877	59683	13435	33196	Moderate	Enriched	Enriched	No expres	YES		
Q69YN2-3;Q69YN	CWF19-like protein	CWF19L1	45.536	22.2	9	9	26.634	0	43107	35497	44317	32522	49472	38660	45602	42837	25444	37650	No expres	Moderate	Moderate	No expres	YES		
Q6DD88;F5H6I7	Atlastin-3	ATL3	60.541	32.3	32	31	231.5	0	337650	241000	318300	263940	408370	238140	252250	228700	115910	241340	Low	Enriched	Enriched	No expres	YES		
Q6DKJ4;Q6DKJ4-	Nucleoredoxin	NXN	48.392	25.3	8	8	171.22	0	8727.6	8084.4	11277	8720.3	14380	9663.4	8665.9	7057.7	4774.9	7506.3					YES		
Q6DT37	Serine/threonine-prot	CDC42BPG	172.46	1	1	1	16.926	0	5828.1	5819.5	6094.7	4520.1	8932.5	3905.5	6536.5	4330.7	4620.2	5812.1	No expres	No expres	Low	No expres	YES		
Q6EEV4-2;Q6EEV	DNA-directed RNA p	POLR2M	8.8268	26.7	2	2	10.899	0	2608.4	3298.1	3330.5	1754.8	4658.2	1636.7	2066.2	2970.3	1734.2	2486.3					YES		
Q6FI81-3;Q6FI81;	Anamorsin	CIAPIN1	32.212	30.1	9	9	27.623	0	76440	70112	75901	57148	94416	64200	134590	63493	72562	92821	Enriched	Enriched	Enriched	Moderate	YES		
Q6GMV2	SET and MYND dom	SMYD5	47.34	5.3	2	2	3.561	0.00079	12442	9815	12216	13232	15087	8244	10791	11202	6924.1	11407	Moderate	Moderate	Moderate	Enriched	YES		
Q6GMV3	Putative peptidyl-tRN	PTRHD1	15.805	15	5	5	11.793	0	5322	2008.4	3227.6	5111.8	4315.1	1574.7	1439.4	1426.1	861.21	2548.3					YES		
Q6GPI1;P17538;J3	Chymotrypsinogen B	CTRB2;CTRB1	27.923	51.7	57	24	323.31	0	902380	649130	575740	813400	657910	838750	860390	724540	448110	743650	No expres	No expres	Enriched	No expres	YES	YES	YES
Q6GTS8	Probable carboxypep	PM20D1	55.741	15.9	7	7	12.263	0	53299	16906	37000	32489	14442	34871	28525	21823	20560	19427	Moderate	Enriched	Moderate	No expression			YES
Q6IA69;E9PNF5;H	Glutamine-dependen	NADSYN1	79.284	2.8	2	2	3.1037	0.00095	3310.4	1554.2	3063.6	1423.4	2459.8	2672.4	2498.5	2936.3	826.45	2383.2	Moderate	Enriched	Enriched	No expres	YES		
Q6IAN0;J3KRS1	Dehydrogenase/reduc	DHRS7B	35.119	25.2	12	12	51.12	0	49967	38187	47849	36102	44271	50548	48855	49671	24383	47745	No expres	Moderate	Enriched	No expres	YES		
Q6IBS0;D6RG15	Twinfilin-2	TWF2	39.548	27.2	9	9	119.06	0	41480	34354	31619	44660	38135	42010	54489	41500	39810	47611	Enriched	Moderate	Moderate	Moderate	YES		
Q6ICG6-3;Q6ICG6	Uncharacterized prot	KIAA0930	41.728	4.6	2	2	2.4577	0.00413	6576.1	6809.3	7940.7	5946	9684.5	5464.7	8279.3	7083.5	7948.6	7984.6					YES		
Q6ICJ4;A0A087W	Glutathione S-transfe	Em:AP000351.3;GSTT2	25.948	32.6	11	11	23.977	0	21400	16041	30805	31628	21176	29028	37363	114590	27619	49961	No expres	Enriched	Moderate	Moderate	YES		
Q6IQ22	Ras-related protein R	RAB12	27.248	15.2	3	3	6.2006	0	25000	27979	30245	27249	34781	32922	25640	28380	12536	26205	Moderate	Moderate	Enriched	No expres	YES		
Q6KC79-2;Q6KC7	Nipped-B-like protei	NIPBL	304.34	1.2	3	3	4.5972	0.00043	7513.8	6550.5	6859.5	4748.3	6736.1	5384.5	11471	8885.8	10994	10795	Enriched	Moderate	Enriched	Moderate	YES		
Q6N069;Q6N069-4	N-alpha-acetyltransfe	NAA16	101.46	16.6	16	14	28.712	0	65573	40566	45124	61571	51541	43834	41448	44517	21582	54969					YES		
Q6NUK1;Q6NUK1	Calcium-binding mit	SLC25A24	53.354	20.3	10	10	34.472	0	55243	46273	47324	40132	54791	54690	67343	70285	40037	62591	Moderate	Moderate	Enriched	Low	YES		

Q6NUM9-2;Q6NUI	All-trans-retinol 13,1	RETSAT	52.438	15.4	9	9	22.293	0	6166.9	4351.5	7403.3	5392.2	6159.1	6653.3	5402.5	3316.1	2784.6	7142.8	Enriched	Enriched	Enriched	No expres	YES	
Q6NUQ1	RAD50-interacting pi	RINT1	90.631	7.3	5	3	18.479	0	30527	16492	22723	17357	29809	20405	17557	15594	8995.4	17925	Low	Moderate	Moderate	No expression		
Q6NUQ4;Q6NUQ4	Transmembrane prot	TMEM214	77.15	31.3	29	29	88.069	0	170980	123850	136040	119310	204030	140040	148560	122580	77455	116470	Enriched	Enriched	Enriched	No expres	YES	
Q6NVY1;A0A087V	3-hydroxyisobutyryl-	HIBCH	43.482	50.3	36	36	160.37	0	153850	110830	114160	187900	162750	192290	166420	226690	72008	196560	Moderate	Enriched	Enriched	Moderate	YES	
Q6NW34-2;Q6NW	Uncharacterized prot	C3orf17	56.748	4.4	2	2	2.4761	0.00395	3617.2	3392.9	4593.4	3642.7	4841.8	3382.7	4775.7	4441.4	2413.2	4102.4	Enriched	Enriched	Enriched	No expression		
Q6NXG1-2;Q6NX(	Epithelial splicing re	ESRP1	67.664	21.1	12	12	52.744	0	38590	28563	32982	48632	33562	43388	37201	44874	22537	41708	Enriched	Enriched	Enriched	No expres	YES	
Q6NXR6;Q86TU7-	Histone-lysine N-met	SETD3	33.329	6.8	2	2	4.7399	0.00043	687.79	529.61	773.55	595.99	1177.5	1578.3	8055.4	5226	4065	3119	Enriched	Enriched	Enriched	Enriched	YES	
Q6NYC8;Q6NYC8	Phostensin	PPP1R18	67.942	4.4	2	2	46.629	0	3727.1	4604.1	4060.9	3769.5	3806.2	4423	13035	12434	9476.4	11290					YES	
Q6NZI2;Q6NZI2-2	Polymerase I and trar	PTRF	43.476	40	27	27	205.96	0	51171	41825	50778	61486	56970	149110	82200	92604	37735	85509	Enriched	Enriched	Enriched	Enriched	YES	
Q6NZY4;Q6NZY4-	Zinc finger CCHC do	ZCCHC8	78.576	8.9	6	6	15.726	0	36357	25968	29803	34036	29023	26101	31630	40348	17865	37092	Enriched	Enriched	Enriched	No expres	YES	
Q6P158;H7C109	Putative ATP-depend	DHX57	155.6	2.6	3	3	4.7661	0.00043	6548.6	5647.8	5244.8	8301	6810.5	5893.5	5937.8	8264.1	3942.2	8119.1	Enriched	Moderate	Moderate	Moderate	YES	
Q6P161	39S ribosomal protei	MRPL54	15.819	8	2	2	2.843	0.00204	4618.9	3058.9	5616.5	4845.2	5089.5	2402.1	6473.1	3645.4	3267.2	6898.8	Low	Enriched	Enriched	No expres	YES	
Q6P1A2-2;Q6P1A2	Lysophospholipid ac	LPCAT3	46.765	7.4	3	3	7.1448	0	8027.1	6495.1	6198.6	8101.1	7655.6	4766.7	5461.4	5683	3235.7	5424.7	Moderate	Moderate	Moderate	Enriched	YES	
Q6P1J9	Parafibromin	CDC73	60.576	13.7	7	7	28.696	0	25512	19573	23854	21373	27744	33469	31619	38877	14951	33211	Low	Enriched	Enriched	No expres	YES	
Q6P1L8	39S ribosomal protei	MRPL14	15.947	9	1	1	9.4607	0	2838.1	2179	2638.6	2809.5	4304.4	2698	3289	2301.4	1589.7	2639.5	Moderate	Enriched	Enriched	No expres	YES	
Q6P1M0;Q6P1M0-	Long-chain fatty acid	SLC27A4	72.063	8.6	5	5	11.066	0	28334	21306	24407	21837	24245	23449	15681	17606	8096.3	22811	Moderate	Enriched	Moderate	No expres	YES	
Q6P1N0-2;Q6P1N(	Coiled-coil and C2 d	CC2D1A	103.93	12.5	11	11	71.441	0	62069	50488	55048	59864	63800	44972	48742	47492	27713	48089	Low	Moderate	Moderate	No expres	YES	
Q6P1Q9-2;Q6P1Q9	Methyltransferase-lik	METTL2B	36.057	3.8	1	1	5.0186	0.00044	2942.1	1846.8	2489.3	3098.6	2483.2	2866	2958	2492.6	1494.9	2879	No expres	No expres	Moderate	No expression		
Q6P1X6;H0YF29;(	UPF0598 protein C8	C8orf82	23.889	33.3	8	8	18.093	0	44364	43660	47776	40654	50882	47355	38380	37935	22971	41444	Enriched	Enriched	Enriched	No expres	YES	
Q6P2E9;Q6P2E9-2	Enhancer of mRNA-(	EDC4	151.66	6.1	8	8	33.772	0	36097	24518	32323	37685	33715	31384	34605	37652	22090	33715	Moderate	Enriched	Moderate	Moderate	YES	
Q6P2P2;Q6P2P2-2	Putative protein argin	PRMT9	94.5	4.4	3	3	6.6578	0	20288	12722	18462	13007	25602	13856	18975	12033	6797.8	14565						
Q6P2Q9	Pre-mRNA-processin	PRPF8	273.6	21.9	60	60	323.31	0	234740	161980	186860	205110	207540	226360	267640	355550	119850	264710	No expres	Enriched	Enriched	Enriched	YES	
X6RAS2;Q6P3S1-5		DENND1B	45.783	3.9	1	1	3.5058	0.00079	3007.9	1427.3	1947.1	5785.9	2794	9477.5	2752.4	4419.9	924.47	2888.5	No expres	No expres	Low	No expression		
Q6P3W7;F8VSC5	SCY1-like protein 2	SCYL2	103.71	9.8	7	7	18.635	0	23187	17188	20020	24351	23082	13161	17644	17708	13734	21821	Enriched	Enriched	Enriched	No expres	YES	
Q6P4A7;Q6P4A7-2	Sideroflexin-4	SFXN4	37.998	8.6	4	4	7.752	0	3785.3	1807.1	3079.1	3779.2	2624.4	3929.8	3396.2	4126.8	2134.5	4603.4	Moderate	Enriched	Enriched	No expres	YES	
Q6P4A8	Phospholipase B-like	PLBD1	63.254	5.1	2	2	5.7473	0	3708.6	6832.5	5530.6	4488.7	10587	4502.5	5462.8	5054.5	2893	4036.5	Enriched	Enriched	Enriched	No expres	YES	
Q6P4Q7	Metal transporter CN	CNNM4	86.606	1.8	1	1	2.1999	0.00544	5135	2770.9	3678.5	5894	2610.5	5433.1	7168.9	5282.6	2353.8	7227.4	Enriched	Moderate	Moderate	No expression		
Q6P587;Q6P587-2;	Acylpyruvase FAHD	FAHD1	24.843	39.3	15	15	116.63	0	89823	58947	81104	50795	111300	79523	76495	51639	44102	64076	Enriched	Enriched	Enriched	No expres	YES	
Q6P597-2;Q6P597;	Kinesin light chain 3	KLC3	55.235	6.8	3	3	9.0107	0	10646	10402	9830.4	5727.1	17109	9347.5	10387	5858	5571.9	9683.9	No expres	Low	Moderate	No expres	YES	
Q6P6B1	Glutamate-rich protei	ERICH5	39.935	13.9	5	5	15.432	0	18675	14258	8991.4	22756	14441	5002.2	11280	20651	14165	19653					YES	
Q6P6C2-3;Q6P6C2	RNA demethylase AI	ALKBH5	43.048	8.4	3	3	5.1242	0.00044	14007	11754	13806	14309	19615	16010	15701	12894	8330.5	15980	Enriched	Enriched	Enriched	No expres	YES	
Q6P996-3;Q6P996-	Pyridoxal-dependent	PDXDC1	76.546	28.3	24	24	76.769	0	83305	69451	75567	89845	94812	72790	79008	75507	48616	78080	Enriched	Enriched	Enriched	Enriched	YES	
Q6P9B9	Integrator complex su	INTS5	107.99	2.3	2	2	3.0181	0.00132	4775	4145.5	5314.2	3640.9	7393.5	2011.2	4320.8	3505.4	2035.9	3567.9	Enriched	Enriched	Enriched	No expression		
Q6PCB0	von Willebrand facto	VWA1	46.804	28.3	12	6	45.308	0	51642	43961	50717	53374	60891	60299	83289	88509	60641	78843	Enriched	Moderate	Enriched	No expres	YES	
Q6PCB7-2;Q6PCB	Long-chain fatty acid	SLC27A1	51.78	11.1	5	5	10.794	0	19790	21229	25012	27216	23507	15001	22933	23832	12131	22741	Enriched	Enriched	Enriched	No expres	YES	
Q6PCE3	Glucose 1,6-bisphosp	PGM2L1	70.441	5.1	4	4	5.0103	0.00044	3953.1	1859.9	1987	5988.8	1553.9	2708.4	2346.9	4358.8	921.53	4619.9	Moderate	Moderate	Enriched	No expression		
Q6PD62	RNA polymerase-ass	CTR9	133.5	5.1	5	5	11.427	0	18529	14177	14122	16559	17535	11547	10981	15193	5432.3	14489	Moderate	Moderate	Enriched	Moderate	YES	
Q6PGP7;D6RCE2	Tetratricopeptide rep	TTC37	175.48	17.6	32	32	99.578	0	100770	85820	95748	106000	107520	109650	117570	87961	63816	94562	Moderate	Moderate	Enriched	Enriched	YES	
Q6PI48	Aspartate--tRNA liga	DARS2	73.562	7.6	5	5	14.768	0	25693	16948	19909	17777	23860	21908	29162	28655	13359	25935	Moderate	Moderate	Moderate	No expres	YES	
Q6PI78	Transmembrane prot	TMEM65	25.498	14.2	3	3	6.9414	0	15402	12079	14660	12616	15465	8942.4	9070.9	11255	5721.6	11610	Low	Enriched	Enriched	No expres	YES	
Q6PJF5-2;Q6PJF5	Inactive rhomboid pr	RHBDF2	93.378	2.9	2	2	4.6928	0.00043	2662.4	2779.3	2737.6	1558.6	3493.2	1266.4	2691.9	2592.5	2109.7	2757.1	Enriched	Low	Moderate	No expres	YES	
Q6PK81-2;Q6PK81	Zinc finger protein 77	ZNF773	50.373	3.2	3	1	2.1553	0.00611	8246.4	6762.3	12482	6035.3	15006	6008.6	5026.9	3832.3	3895.7	7343.7						
Q6PKG0;Q6PKG0-	La-related protein 1	LARP1	123.51	33	45	44	170.76	0	293330	195830	223590	238170	285180	281250	219660	201880	130020	236750	Enriched	Enriched	Enriched	Enriched	YES	
Q6PML9	Zinc transporter 9	SLC30A9	63.514	9	7	7	11.586	0	25994	16732	21417	19814	21633	21555	26529	24361	10520	24118	Enriched	Enriched	Enriched	Enriched	YES	
Q6QNY0	Biogenesis of lysosom	BLOC1S3	21.255	25.7	4	4	7.7386	0	11181	7462.2	9379	7932	14138	7500.3	9088.8	7964.8	5272.6	8720.3	Low	Enriched	Moderate	No expres	YES	
Q6QNY1	Biogenesis of lysosom	BLOC1S2	15.961	9.2	1	1	4.4085	0.00063	9046.6	9597.2	17216	3805.8	27938	4324.2	10616	5194.4	10694	5108.4	Moderate	Enriched	Enriched	No expression		
Q6ULP2-5;Q6ULP2	Aftiphilin	AFTPH	99.37	7.2	5	5	22.93	0	6077.9	3596.8	3829.8	5453.3	4666.3	4427.8	4640	5162.7	2454.9	4752.6	Enriched	Enriched	Enriched	No expres	YES	
Q6UN15;Q6UN15-	Pre-mRNA 3-end-pro	FIP1L1	66.526	15.8	8	8	13.003	0	9263.4	12241	18867	6604	13281	4973.2	26305	10128	39966	12328	Low	Low	Moderate	No expres	YES	
Q6UUV9-3;Q6UUV	CREB-regulated tran	CRTC1	62.529	3	1	1	2.0718	0.00724	4198.5	2086.1	3729.6	5960.7	4024.8	6123	7258.7	6937.8	3808.2	7497.3	Moderate	Low	Moderate	Low	YES	
Q6UW15	Regenerating islet-de	REG3G	19.33	32.6	8	8	49.645	0	32139	29867	37232	127790	37634	34455	37464	104640	40163	52868	Moderate	Enriched	Enriched	No expres	YES	YES
Q6UWP2;A0A087V	Dehydrogenase/reduc	DHRS11	28.308	31.2	9	9	15.669	0	12489	13721	15382	11273	13753	10364	10870	14606	8527.9	12006	Moderate	Moderate	Moderate	No expres	YES	
Q6UWP7-3;Q6UW	Lysocardiolipin acylt	LCLAT1	44.561	16	6	6	10.339	0	25449	13617	20641	25421	18584	23777	21718	22139	11864	22984	Enriched	Enriched	Enriched	No expres	YES	
Q6UWY5	Olfactomedin-like pro	OLFML1	45.95	36.6	19	19	79.464	0	95262	73518	111050	130030	111880	106070	183590	194660	51772	117100	Low	Low	Low	No expres	YES	
Q6UX06	Olfactomedin-4	OLFM4	57.279	26.7	21	21	105.96	0	68178	67186	64126	61202	71064	61332	102050	66245	512420	82701	Enriched	Enriched	Enriched	Enriched	YES	
Q6UX46;H0Y3U4	Protein FAM150B	FAM150B	16.915	13.8	2	2	3.6808	0.0008	6736.7	9659.8	10166	6217.9	12579	7322.1	10525	12838	7050.2	8240.5	No expres	Enriched	Enriched	No expression		
Q6UXG2;Q6UXG2	UPF0577 protein KIA	KIAA1324	111.38	16.8	27	23	99.601	0	123550	100420	94822	106620	121890	111450	132290	124800	55903	110290	Enriched	Enriched	Enriched	No expres	YES	
Q6UXH1-4;Q6UXI	Cysteine-rich with E(	CRELD2	35.288	23.7	17	4	62.372	0	79049	63321	73785	64609	79615	236440	52195	95600	39082	89443	Enriched	Enriched	Enriched	No expres	YES	
Q6UXN9	WD repeat-containin	WDR82	35.079	9.3	2	2	7.1655	0	3458.8	3339.8	3111	2346.7	2995	4314.6	5848.9	8759.2	3359.7	4905.1	Enriched	Enriched	Enriched	Low	YES	
Q6VY07;Q6VY07-	Phosphofurin acidic (	PACS1	104.9	14.5	11	11	54.607	0	38317	32388	34451	32777	39270	30478	54602	59120	24937	34072	Enriched	Enriched	Enriched	No expres	YES	
Q6W4X9	Mucin-6	MUC6	257.05	0.5	1	1	2.9174	0.00187	9777.6	7878.1	9722.3	10220	10420	7290.2	15585	21967	3233.5	9238.8	Low	Low	Low	Enriched	YES	
Q6W5P4-5;Q6W5P4-4			41.961	4.4	1	1	1.8192	0.00974	215.44	582.96	711.27	225.67	910.43	1249	2908.4	8171	1965.5	2949.5						
Q6WKZ4-3;Q6WK	Rab11 family-interac	RAB11FIP1	70.982	10.6	7	7	14.189	0	34767	24964	37806	39502	30324	42579	71402	50604	59557	45062	Enriched	Enriched	Enriched	No expres	YES	
Q6XQN6-3;Q6XQN	Nicotinate phosphori	NAPRT	56.099	15.8	9	9	24.293	0	16558	25440	36113	45719	40205	22470	21239	19481	17573	38781					YES	
Q6Y1H2	Very-long-chain (3R)	PTPLB	28.368	7.1	2	2	3.7961	0.00061	5107.8	3377.4	2594.2	4412.9	4692.3	3031.9	2446.7	2243.8	1562.7	3393.1	Enriched	Enriched	Enriched	Enriched	YES	
Q6Y7W6-4;Q6Y7V	PERQ amino acid-ric	GIGYF2	148.63	9.4	14	14	66.457	0	54305	42501	54385	45361	67633	43345	51791	37639	29559	53731	Enriched	Enriched	Enriched	Enriched	YES	
Q6YHK3-3;Q6YHI	CD109 antigen	CD109	74.41	2	2	2	3.8837	0.00061	4816.3	2269.2	3292.8	7417.9	3249.6	9575.2	3092.4	5581.4	1858.6	5078.6	Moderate	Low	Moderate	No expres	YES	
Q6YN16;Q6YN16-	Hydroxysteroid dehy	HSDL2	45.394	32.8	16	16	225.71	0	140970	78005	98130	153290	108680	241400	133280	150670	67369	179920	Enriched	Enriched	Enriched	Low	YES	
Q6YP21-3;Q6YP21	Kynurenine--oxoglut	CCBL2	47.752	20	10	10	22.822	0	76412	52090	57322	62353	74698	63699	53438	53581	26582	56244	Enriched	Enriched	Enriched	Moderate	YES	
Q6ZMI0-4;Q6ZMI(	Protein phosphatase	PPP1R21	42.132	10.5	3	3	9.1906	0	21211	15490	18852	24824	21002	18240	22892	19435	16659	22335					YES	
Q6ZMP0;Q6ZMP0-	Thrombospondin typ	THSD4	112.45	2.5	2	2	5.5005	0	4269.4	2069.2	3401	4322.7	5977.7	2292.9	4886.9	4671.5	3838.3	6507	Enriched	Enriched	Enriched	No expres	YES	
Q6ZN11-3;Q6ZN11	Zinc finger protein 79	ZNF793;ZNF76;ZNF77	35.863	7.7	3	0	3.4112	0.00079	3112.6	1479.2	2824	1942.5	3058.1	2924.6	3684.6	2378.3	2964.3	3299.3	Moderate	Low	Low	No expression		
Q6ZN40;P09493-7;P09493-6;H0YNC7		TPM1	37.452	68.4	61	0	323.31	0	249400	200440	222460	216660	239450	334080	582810	405860	287510	611520	Enriched	Enriched	Enriched	Enriched	YES	
Q6ZNB6;Q6ZNB6-	NF-X1-type zinc fing	NFXL1	101.34	21.1	19	19	108.06	0	60394	46260	57944	48573	86473	43030	55539	49958	36576	56868	Moderate	Enriched	Moderate	No expres	YES	
Q6ZSJ8	Uncharacterized prot	C1orf122	11.471	24.5	2	2	4.6037	0.00043	6608	6818.7	5549.8	5496.7	8351.3	4288.9	5461.7	5101.6	2538.8	4987.8	Enriched	Enriched	Enriched	No expression		
Q6ZT12;Q6ZT12-4	E3 ubiquitin-protein	UBR3	212.43	1.2	2	2	1.9647	0.00802	9331.2	4126.6	7198.6	14965	6645.6	12873	10662	15944	4699.1	10858	Moderate	Enriched	Enriched	No expres	YES	
Q6ZT21-2;Q6ZT21	Transmembrane prot	TMPPE	34.078	9.8	2	2	3.205	0.00077	3527.8	1086.6	1574.3	3194	1416.1	2672.2	2020.6	4298.5	1351.8	4414					YES	
Q6ZUJ8-2;Q6ZUJ8	Phosphoinositide 3-k	PIK3AP1	70.411	17.1	9	9	26.486	0	31141	22895	28301	35842	30720	26973	37907	36227	26460	29827	Enriched	Enriched	Enriched	No expres	YES	
Q6ZUS6-6;Q6ZUS(	Coiled-coil domain-c	CCDC149	44.314	13.2	4	4	24.701	0	15188	13019	12600	11125	17535	11721	27217	16570	19729	16721	Enriched	Enriched	Moderate	No expres	YES	
Q6ZUT6-2;Q6ZUT	Uncharacterized prot	C15orf52	34.763	3.1	1	1	2.2457	0.00511	4903.9	5099.2	4825	3825.2	5777.1	5274.1	11691	8213.1	15004	8973.5	Low	Enriched	Moderate	No expres	YES	
Q6ZVL6	UPF0606 protein KIA	KIAA1549L	199	0.5	2	2	2.1317	0.00609	16321	24738	46770	29311	50939	12182	34466	23684	6746.6	22962						
Q6ZVM7;Q6ZVM7	TOM1-like protein 2	TOM1L2	55.556	13.4	9	7	23.126	0	15245	10518	12018	17056	12502	23615	14013	15464	6237	16364	Enriched	Enriched	Enriched	Moderate	YES	
Q709C8-3;Q709C8	Vacuolar protein sort	VPS13C	417.27	11.5	43	43	142.02	0	143190	110360	128700	122370	152930	138060	135440	116820	70194	133710	Enriched	Enriched	Enriched	No expres	YES	
Q70CQ2-3;Q70CQ	Ubiquitin carboxyl-te	USP34	377.59	1.2	3	3	5.5193	0	2942.3	2132.7	2652.8	4078.3	1772.8	3259.4	3228.9	4974.9	1561.2	3799.3	Enriched	Enriched	Enriched	Low	YES	
Q70UQ0-4	Inhibitor of nuclear fa	IKBIP	43.083	5	2	2	4.5657	0.00043	17451	15716	15673	17041	16132	11607	11927	11061	7126.1	13219					YES	
Q712K3	Ubiquitin-conjugatin	UBE2R2	27.166	10.5	2	2	4.3301	0.00063	13407	12858	12293	7198.5	15957	4384.7	4263.9	4452.1	4164.5	6006.2	Enriched	Enriched	Enriched	No expres	YES	
Q71RC2-6;Q71RC2	La-related protein 4	LARP4	72.733	3.5	2	1	2.9393	0.00168	916.4	943.2	1020.3	1347.8	935.45	3279.5	1190.2	1097.4	771.35	862.92	Low	Enriched	Enriched	Enriched	YES	
Q71RC2-2	La-related protein 4	LARP4	67.279	3.8	2	1	6.3906	0	3206.4	5530.7	4517	2171.5	5755.7	2386.2	4165.2	3663.4	2130.7	2316.5	Low	Enriched	Enriched	Enriched	YES	
Q71U36-2;Q71U36	Tubulin alpha-1A ch	TUBA1A;TUBA3C;TUE	46.297	73.1	93	2	9.6695	0	30749	28377	32918	29355	33802	36238	38258	33085	21770	32263	Enriched	Enriched	Enriched	No expres	YES	
Q71UI9-5;E5RJU1	Histone H2A.V	H2AFV	6.8918	42.4	8	7	12.47	0	35283	20629	30392	45473	25799	34356	41759	55667	24206	43013	Enriched	Enriched	Enriched	Enriched		
Q7KZ85	Transcription elongat	SUPT6H	199.07	6.7	12	12	21.444	0	31201	28043	33463	29334	43951	26793	38709	36366	29406	40611	Moderate	Moderate	Moderate	Moderate	YES	
Q7KZF4	Staphylococcal nucle	SND1	102	48.7	96	96	323.31	0	639610	389520	515630	677240	582800	683240	751410	700800	355820	616720	Enriched	Moderate	Enriched	Enriched	YES	
Q7KZN9-2;Q7KZN	Cytochrome c oxidas	COX15	43.835	4.6	2	2	3.0946	0.00095	1677	1483.4	1678.2	1526	1806.4	1577.5	2089	2459.7	1932	2743.2	Enriched	Enriched	Enriched	No expression		
Q7L014	Probable ATP-depen	DDX46	117.36	20.6	23	23	52.886	0	98932	65983	82236	88425	78836	81725	66952	79642	41295	80842	Moderate	Enriched	Enriched	Enriched	YES	
Q7L0Y3;C9JVB6	Mitochondrial ribonu	TRMT10C	47.346	19.6	8	8	17.942	0	50651	38597	46240	42056	51732	54981	75438	73181	29360	61754					YES	
Q7L1Q6;Q7L1Q6-4	Basic leucine zipper a	BZW1	48.043	22	13	10	39.509	0	135660	46238	57625	95363	61221	89239	76921	71456	52763	115200	Moderate	Enriched	Enriched	Enriched	YES	
Q7L266;Q7L266-2	Isoaspartyl peptidase/	ASRGL1	32.054	15.3	3	3	12.385	0	8206.5	7090.4	8163.6	13419	8422.1	8568.8	9274.8	18901	5106.6	13397	Enriched	Enriched	Enriched	No expres	YES	
Q7L273	BTB/POZ domain-co	KCTD9	42.566	2.8	1	1	2.154	0.00611	5083.2	5235.8	6316.7	2551.1	9145.1	4532.9	6580.8	4752.3	4552.7	4701.7	Moderate	Moderate	Enriched	No expression		
Q7L2H7;J3KNJ2;Q	Eukaryotic translatio	EIF3M	42.502	32.1	21	21	74.438	0	134920	86014	97428	86978	98159	122830	135170	153540	61438	105010	Enriched	Enriched	Enriched	Enriched	YES	
Q7L2J0	7SK snRNA methylp	MEPCE	74.354	6.5	5	5	11.726	0	15151	12260	9415	7087.5	13955	16851	9712.8	8712.8	6333	25137	Moderate	Enriched	Enriched	No expression		
Q7L311	Armadillo repeat-con	ARMCX2	65.683	6	3	3	4.7799	0.00043	1857.9	1920.3	1926.1	1515.4	3220.5	1598.8	2080.9	1012.1	1591.1	1757.3	Low	Moderate	Enriched	Moderate	YES	
Q7L3S4;Q7Z7K2	Zinc finger protein 77	ZNF771;ZNF467	35.702	9.5	3	1	2.5399	0.00379	4538.9	5174.7	5312	4415.2	7139.8	3136.4	6239.8	6764	3293.2	5024.8	Low	Moderate	Low	No expression		
Q7L3T8	Probable proline--tRI	PARS2	53.262	7.4	4	4	8.7911	0	15301	14236	12714	15981	14200	12752	14370	13786	10335	13887	No expres	Moderate	Moderate	No expres	YES	
Q7L523	Ras-related GTP-binc	RRAGA	36.566	10.9	3	3	4.8749	0.00044	1163.4	716.51	1325.7	2889.2	1388.2	7895.6	1760.8	1459.6	996.94	1897.3	Low	Enriched	Enriched	Enriched	YES	
Q7L576;Q7L576-2	Cytoplasmic FMR1-i	CYFIP1	145.18	18.7	31	14	156.11	0	154800	100420	116420	146190	121060	139050	155570	209150	77031	170510	Enriched	Enriched	Enriched	Enriched	YES	
Q7L5D6-2;Q7L5D(	Golgi to ER traffic pr	GET4	30.522	12.4	4	4	9.1456	0	20636	11704	14919	22743	15212	18940	16255	23523	8324.3	19597					YES	
Q7L5Y1-2;Q7L5Y1	Mitochondrial enolas	ENOSF1	41.023	16.6	6	6	14.429	0	11693	9993.2	13201	15809	11271	16911	15285	16909	8440.9	13309	Moderate	Enriched	Enriched	Enriched	YES	
Q7L7V1-2;Q7L7V1	Putative pre-mRNA-s	DHX32	75.087	5.7	3	3	8.9954	0	11870	7890.1	10690	10370	9005	12646	8425.6	11902	3086	9995	Enriched	Enriched	Enriched	No expres	YES	
Q9H8S9;Q7L9L4;(	MOB kinase activator	MOB1A;MOB1B	25.079	15.3	3	3	7.8966	0	18275	14836	8845.8	24576	14609	13702	14921	26396	9442.5	21182					YES	
Q7LBR1	Charged multivesicul	CHMP1B	22.109	9	3	3	26.605	0	7884.4	5453.5	6290.1	6726.7	8996	6338.3	7884.3	5735.6	8641.9	7592.7	Enriched	Moderate	Enriched	No expres	YES	
Q7LGA3-3;Q7LGA	Heparan sulfate 2-O-	HS2ST1	26.757	7.4	1	1	5.0691	0.00044	12475	8278.2	8521.6	6536.8	9760.3	9153.3	9398.6	8414.6	7390.7	9417.3	Low	Moderate	Enriched	Low	YES	
Q7RTP6	Protein-methionine su	MICAL3	224.29	1.6	3	3	7.1762	0	7952.8	4708.7	6757.3	11779	6377.2	8195.1	7960.2	9485.1	4981.8	9628.4	Enriched	Enriched	Moderate	Moderate	YES	
Q7RTS1	Class A basic helix-lo	BHLHA15	20.818	19.6	7	7	11.749	0	23930	16604	23208	14398	22444	17557	34154	26210	16960	29710					YES	YES
Q7RTV0	PHD finger-like doma	PHF5A	12.405	44.5	6	6	39.931	0	31094	16745	21352	26900	29982	15981	19908	19211	10485	23489	Moderate	Enriched	Enriched	No expres	YES	
Q7Z2T5;Q7Z2T5-2	TRMT1-like protein	TRMT1L	81.746	5.7	4	4	14.3	0	24757	22222	29645	19629	38846	30102	41958	29602	12810	25087					YES	
Q7Z2W4;C9J6P4;(	Zinc finger CCCH-typ	ZC3HAV1	101.43	20.1	19	19	50.269	0	56635	46570	49154	61781	56471	47550	59055	72419	31213	48386	Enriched	Enriched	Enriched	Enriched	YES	
Q7Z2Z2-2;Q7Z2Z2	Elongation factor Tu	EFTUD1	119.89	9.8	8	8	19.158	0	55147	29286	31085	50027	36409	37878	34574	51432	21644	33742	Moderate	Enriched	Enriched	No expres	YES	
Q7Z304	MAM domain-contai	MAMDC2	77.555	2.9	2	2	4.0227	0.00062	10528	6361.7	9372.5	13593	10141	10203	6471.7	19153	4149.6	13603	Low	Moderate	Moderate	No expres	YES	
X6RI79;Q7Z333-3;	Probable helicase sen	SETX	107.93	1.2	2	2	2.2961	0.00496	4671.6	9484.9	9583.4	3821	22783	2224.5	3402.7	1613.3	1603.2	3294.3	Low	Moderate	Enriched	Enriched		
Q7Z392;D6RHE5	Trafficking protein pa	TRAPPC11	128.88	2.2	3	3	7.6848	0	19353	13428	13245	18453	13750	16266	14065	15008	8481	14124					YES	
Q7Z3B4-3;Q7Z3B4	Nucleoporin p54	NUP54	50.775	22.9	14	14	48.083	0	49130	39764	45713	47469	55118	42114	40083	38679	23449	43952	Moderate	Moderate	Enriched	No expres	YES	
Q7Z3D6-3;Q7Z3D(	UPF0317 protein C14	C14orf159	62.782	14.1	8	8	17.584	0	10187	11234	11267	8551.7	15270	12667	24963	36769	14205	14422	Enriched	Moderate	Moderate	No expres	YES	
Q7Z3E2;H0Y7V5	Coiled-coil domain-c	CCDC186	103.69	5.2	6	6	23.955	0	9807.6	4945.3	5408.3	8428.3	9461.3	12757	5541.5	6186.3	3429	7970.4					YES	
Q7Z3J3	RanBP2-like and GR	RGPD4	197.29	8.5	15	3	8.8976	0	8350.3	10017	9212.4	5265.3	13875	7572.3	5154.8	5978.5	2153.2	4639.6						
Q7Z3T8;Q7Z3T8-3	Zinc finger FYVE do	ZFYVE16	168.9	2	2	2	16.196	0	3332.6	1969.9	2090.9	5206	1352.6	3309.4	4282.4	4198.5	2467.7	3876.9	Enriched	Moderate	Moderate	Moderate	YES	
Q7Z3U7-2;Q7Z3U7	Protein MON2 homo	MON2	185.85	3.8	8	8	12.558	0	21566	13413	17221	23147	21845	21118	17007	19589	13858	17067	Enriched	Enriched	Enriched	Low	YES	
Q7Z406-6;Q7Z406	Myosin-14	MYH14	228.66	28	74	49	150.24	0	156830	139670	156550	150220	165410	127180	202310	160820	177250	180640	Enriched	Enriched	Enriched	No expres	YES	
Q7Z417	Nuclear fragile X me	NUFIP2	76.12	12.8	7	7	19.268	0	11227	10614	10652	9735.7	16069	8118	7080.5	5396.4	4905.6	7601.8	Enriched	Enriched	Enriched	No expres	YES	
Q7Z422-2;Q7Z422	SUZ domain-contain	SZRD1	14.604	25	2	2	22.824	0	6593.7	5438.9	6629.2	3517.1	6916.7	4174.1	6558.2	3635.3	6942.5	6791.2					YES	
Q7Z434-4;Q7Z434	Mitochondrial antivir	MAVS	40.467	6.3	3	3	7.4012	0	13052	14516	17288	13328	20630	12302	25037	19816	10682	15389	Low	Enriched	Enriched	No expres	YES	
Q7Z4G1;Q7Z4G1-2	COMM domain-cont	COMMD6	9.638	12.9	2	2	4.0811	0.00062	1441.2	892.3	899.52	1636.4	1052.8	1482.7	1265.5	1073.6	629.06	1385.6	Enriched	Enriched	Enriched	No expres	YES	
Q7Z4H3-2;Q7Z4H3	HD domain-containir	HDDC2	19.55	31.8	5	5	11.655	0	7785.3	5376.2	7086.1	6253	9018	8746.4	9079.3	12731	3404.6	9672.2	Enriched	Enriched	Enriched	Moderate	YES	
Q7Z4H8;Q7Z4H8-3	KDEL motif-containi	KDELC2	58.572	15.6	11	11	41.905	0	30634	27818	28937	33882	37133	21287	26252	26950	13922	33001	No expres	Enriched	Enriched	No expres	YES	
Q7Z4I7-3;Q7Z4I7;(	LIM and senescent ce	LIMS2	38.425	19	7	4	5.0047	0.00044	5630.2	3764.2	5663.9	5224.8	6409.1	9299.6	4534	5464.7	4536.7	5457.1	Enriched	Moderate	Moderate	No expres	YES	
Q7Z4S6-6;Q7Z4S6	Kinesin-like protein I	KIF21A	180.74	7.5	10	8	37.7	0	26338	23938	27402	20732	32471	22216	26119	23318	13850	22853	Low	Enriched	Enriched	No expres	YES	
Q7Z4V5-2;Q7Z4V5	Hepatoma-derived gr	HDGFRP2	74.229	12.4	10	9	51.865	0	15468	14878	18435	15795	23562	10171	21040	25889	12201	13369					YES	
Q7Z4W1;J3KS22;J	L-xylulose reductase	DCXR	25.913	41	14	14	22.58	0	40675	35638	46375	31155	47944	26214	43996	34416	30652	31919	No expres	Enriched	Enriched	No expres	YES	
Q7Z5G4-3;Q7Z5G4	Golgin subfamily A n	GOLGA7	15.578	15.7	2	2	2.5691	0.00344	15075	12440	13306	11753	19983	8322.9	9250.9	8533.3	5963.3	12652	Enriched	Enriched	Enriched	No expression		
Q7Z5K2;Q7Z5K2-2	Wings apart-like prot	WAPAL	132.94	2	3	3	4.6118	0.00043	6240.4	4215	6689.1	8465.4	4511.7	6035	5021	9838.1	1729.5	6107	Enriched	Moderate	Enriched	Moderate	YES	
Q7Z5L7;Q7Z5L7-2	Podocan	PODN	68.975	6	5	4	12.62	0	3653.8	6171.3	7527.6	4137.3	6994.2	4201.8	7164.8	10458	4664.2	7740.1	Moderate	Moderate	Moderate	No expres	YES	
Q7Z5L9-2;Q7Z5L9	Interferon regulatory	IRF2BP2	59.48	18.2	11	9	92.833	0	20848	23808	24944	12920	29868	13557	17751	20036	13310	17869	Enriched	Enriched	Enriched	No expres	YES	
Q7Z5R6	Amyloid beta A4 pre	APBB1IP	73.182	1.4	1	1	2.1179	0.00626	13300	15636	16584	19793	12620	15092	20574	31622	17338	23102	Enriched	Moderate	Moderate	No expres	YES	
Q7Z6E9-2;Q7Z6E9	E3 ubiquitin-protein	RBBP6	197.29	1.9	3	3	13.714	0	2607.3	1642.8	2188.6	1682.9	2648.5	1775.1	2961.7	2120.2	2532.5	2950	Moderate	Moderate	Moderate	Moderate	YES	
Q7Z6K5;Q7Z6K5-2	Arpin	ARPIN;C15orf38-AP3S2	24.943	35.8	8	8	21.615	0	26122	24209	28441	26114	37904	20388	27576	25080	24056	28465						
Q7Z6L1-3;Q7Z6L1	Tectonin beta-propel	TECPR1	86.696	5.9	3	3	4.2621	0.00063	3406.8	1492.1	2462.9	3127	2466.6	2437.9	2287.2	6414.6	1998	3493.4	Enriched	Enriched	Enriched	No expres	YES	
Q7Z6Z7-2;Q7Z6Z7	E3 ubiquitin-protein	HUWE1	480.19	11.8	48	48	139.31	0	158630	124270	133530	127980	155360	128720	175310	177620	92193	173760	Enriched	Enriched	Enriched	Moderate	YES	
X6R631;Q7Z7F7;Q	39S ribosomal protei	MRPL55	6.8487	41.8	2	2	7.9878	0	9411.3	4655.1	6156.9	10524	5140.3	9976.5	16379	11742	10207	13564	Low	Enriched	Enriched	No expres	YES	
Q7Z7H5;Q7Z7H5-3	Transmembrane emp2	TMED4	25.943	41	19	13	130.12	0	86213	81451	76804	105220	90832	111700	107640	80182	59247	86805	Enriched	Enriched	Enriched	No expres	YES	
Q7Z7K6-3;Q7Z7K(	Centromere protein V	CENPV	29.73	21.7	7	7	97.844	0	34846	30982	33768	32207	35251	36652	55777	56001	35907	53828	Low	Enriched	Moderate	No expres	YES	
Q86SK9-2;Q86SK9	Stearoyl-CoA desatu	SCD5	28.982	17.6	4	4	46.275	0	19509	21512	19795	21083	28878	15568	19336	20286	11495	20236	Low	Enriched	Enriched	No expres	YES	
Q86SQ7-2;Q86SQ7	Serologically defined	SDCCAG8	40.934	4.2	1	1	3.8745	0.00061	8142.7	8019	9936.5	9387.7	8543.4	10916	14295	10782	12865	11222	Low	Enriched	Moderate	No expres	YES	
Q86T03;Q86T03-2	Type 1 phosphatidyli	TMEM55B	29.469	15.2	4	4	5.7662	0	5171.5	4693.8	6102.3	3761.3	7847.6	3940.2	8601.3	6385.6	6445.9	5806.4	Enriched	Enriched	Enriched	No expres	YES	
Q86T13	C-type lectin domain	CLEC14A	51.635	3.3	1	1	3.047	0.00132	4509.6	3220.8	3220.9	5122.9	3060.6	5714.7	3183.4	5258.2	1615.7	5524	Moderate	No expres	Low	No expression		
Q86TI0-2;Q86TI0;I	TBC1 domain family	TBC1D1	131.38	8	7	6	20.905	0	7857.8	4915.2	8504.6	6083.3	13082	4942.2	6208.2	5641.7	2585.1	5823.8	Moderate	Enriched	Enriched	Low	YES	
Q86TM6-2;Q86TM	E3 ubiquitin-protein	SYVN1	61.731	8	8	8	21.032	0	12688	11274	12315	8331.3	19580	8221.2	9519.9	8011.1	6799.5	9632.5	Moderate	Enriched	Enriched	No expres	YES	
Q86TN4-3;Q86TN4	tRNA 2-phosphotran	TRPT1	23.566	14.8	2	2	3.7046	0.0008	12249	6675.7	9086.7	13196	7704.2	7833.1	9809.7	12909	4784.9	10475	Low	Enriched	Enriched	No expression		
Q86TP1;Q86TP1-2	Protein prune homol(	PRUNE	50.199	9.9	5	4	13.459	0	15122	13066	13877	18572	16274	24934	16032	16413	10106	15501	Enriched	Enriched	Enriched	Enriched	YES	
Q86U28;J3QSS7	Iron-sulfur cluster as	ISCA2	16.476	37.7	7	7	18.955	0	23145	18996	20949	20534	25777	19946	21413	20897	13695	22541	Moderate	Enriched	Enriched	No expres	YES	
Q92843-2;Q86U42	Polyadenylate-bindin	PABPN1	37.17	19.8	6	6	16.518	0	46263	41039	34627	30313	49083	20697	29400	38335	24706	41515	Enriched	Enriched	Enriched	Moderate	YES	

Q86UA1	Pre-mRNA-processin	PRPF39	78.429	2.7	2	2	4.2857	0.00063	5553.3	3155.3	3773.5	6623.5	4955	4811.8	4218.5	5289.7	2322.8	4647.3	Low	Moderate	Moderate	No expres	YES	
Q86UD1;E9PJ29	Out at first protein hc	OAF	30.688	9.2	2	2	2.0317	0.00755	4457.7	4250.3	4167.1	4984	3284.5	4368.2	3633.3	5110.6	1318.3	3360.2	Enriched	Enriched	Enriched	No expres	YES	
Q86UE4;E5RJU9	Protein LYRIC	MTDH	63.836	32.3	33	33	121.41	0	148930	119790	121960	212260	168520	124410	174050	160590	74746	150580	Enriched	Enriched	Enriched	Low	YES	
Q86UP2;Q86UP2-4	Kinectin	KTN1	156.27	42.1	84	70	323.31	0	396430	269760	302230	395370	395340	381980	467500	493740	245390	434420	Enriched	Enriched	Enriched	Enriched	YES	
Q86UP6	CUB and zona pelluc	CUZD1	68.152	34.3	42	42	323.31	0	260760	233310	270860	270490	358950	299350	634480	457520	254180	285220	Moderate	Moderate	Moderate	No expres	YES	YES
Q86UU1-2;Q86UU	Pleckstrin homology-	PHLDB1	144.74	4.3	7	6	9.5966	0	14344	14251	14439	16158	13819	19856	16926	16928	11175	16933	Enriched	Moderate	Moderate	Moderate	YES	
Q86UV5-2;Q86UV	Ubiquitin carboxyl-te	USP48	112.96	3.3	2	2	2.1537	0.00611	10491	6902.4	8614.7	15516	7564.1	10395	10850	13125	7758.6	10776	Enriched	Enriched	Enriched	No expres	YES	
Q86UX7-2;Q86UX	Fermitin family homc	FERMT3	75.429	8	4	3	43.7	0	12824	9636.8	10472	20108	11104	11221	12029	14910	5867.2	13417	Enriched	Low	Low	No expres	YES	
Q86UY0;Q8NBS9;	Thioredoxin domain-	TXNDC5	40.369	48.6	32	32	120.48	0	179030	150910	143370	188630	170190	226610	314520	284670	130430	186150	Enriched	Enriched	Enriched	No expres	YES	
Q86V21;Q86V21-3	Acetoacetyl-CoA syn	AACS	75.143	2.5	2	2	2.1128	0.00642	6157.3	5313.3	5447.4	4854	9499	6275.3	45271	35495	5654.1	8325.5	Enriched	Enriched	Enriched	No expres	YES	
Q86V48;Q86V48-2	Leucine zipper protei	LUZP1	120.27	4.2	5	5	26.125	0	5504	4887.4	5085.1	4655.7	6371.9	4847.3	6980.5	5427	5974.7	6785.9	Enriched	Moderate	Moderate	No expres	YES	
Q86V85	Integral membrane pr	GPR180	49.395	3.2	1	1	13.199	0	2142	2071.1	2889.7	1442	4405	2189.2	2455.3	2655.6	1714.7	2260.9	Low	Moderate	Moderate	No expression		
Q86VD7	Mitochondrial coenz	SLC25A42	35.409	7.5	3	3	7.8053	0	6018.5	5999.7	8734.3	6897.9	7777.6	7138.8	14860	13094	10411	11626	Enriched	Moderate	Moderate	Moderate		
Q86VI7;Q9UKR3-2	Kallikrein-13	KLK13	22.352	6.4	1	1	8.5032	0	4269.1	5595.1	5220.5	4673.5	6924.6	4086.2	5023.5	6412.7	3133.3	6194.3	Moderate	Moderate	Low	Moderate		
Q86VN1-2;Q86VN	Vacuolar protein-sort	VPS36	36.957	23.8	11	11	21.406	0	22083	14202	13172	15106	17556	16538	15181	17476	8885.8	16910	Enriched	Enriched	Enriched	No expres	YES	
Q86VP6;Q86VP6-2	Cullin-associated NE	CAND1	136.37	31	68	59	274.01	0	434400	309290	360520	454380	440120	374880	555260	460620	292070	422930	Moderate	Moderate	Enriched	Moderate	YES	
Q86VR2;K7ENZ6;	Protein FAM134C	FAM134C	51.396	5.8	3	3	4.6594	0.00043	2306.1	1251.1	1831.5	2913	1360.5	3666.1	2154.1	3474.3	986.29	2930.5	Enriched	Enriched	Enriched	Enriched	YES	
Q86VS8	Protein Hook homolc	HOOK3	83.125	7.5	5	5	21.823	0	2529.4	2951.1	3414.1	2589.6	3706.4	1808.1	2498.7	2340.2	1862.4	2649.2	No expres	Moderate	Moderate	No expres	YES	
R4GNF4;Q86VU5	Catechol O-methyltra	COMTD1	27.747	26.2	13	13	49.354	0	44248	35615	34070	48560	43398	33570	41169	36579	24479	51519	Enriched	Enriched	Enriched	No expres	YES	
Q86VX2-2;Q86VX	COMM domain-cont	COMMD7	22.412	13.6	2	2	8.6265	0	9621.3	10190	15327	7275.5	10743	8956.5	8512.6	9681.6	4264.3	7079.6	Enriched	Enriched	Enriched	No expres	YES	
Q86VY4	Testis-specific Y-enco	TSPYL5	45.143	15.3	5	5	27.94	0	6330.3	5430.1	5833.8	6489.2	7542	4659	7306.1	3774.7	4751	4595.4	Moderate	Moderate	Enriched	Enriched	YES	
Q86W42-3;Q86W4	THO complex subuni	THOC6	32.89	14.9	4	4	10.455	0	10559	10587	11139	8928.8	15336	11060	18576	19942	10393	12386	Moderate	Low	Moderate	No expres	YES	
Q86W56-5;Q86W5	Poly(ADP-ribose) gly	PARG	54.793	3.4	1	1	2.9408	0.00169	9857	7269.9	8174.7	9748.3	9753.4	8625.1	7782.1	11414	4599.4	8887.1	Moderate	Enriched	Enriched	Moderate		
Q86W92-2;Q86W9	Liprin-beta-1	PPFIBP1	113.18	13.1	11	11	34.854	0	53113	48343	61898	50341	62891	40061	48652	44815	38573	54938	Moderate	Moderate	Moderate	No expres	YES	
Q86WA6-2;Q86WA	Valacyclovir hydrola:	BPHL	31.106	13.9	5	5	13.94	0	35730	31686	30233	51402	37319	33534	52031	124890	37791	79292	Low	Moderate	Moderate	Enriched	YES	
Q86WA8;H3BQ67;	Lon protease homolo	LONP2	94.615	3.4	2	2	5.3384	0	2452.3	966.99	1685.5	2553	1263.7	2420.8	2349.3	3030.2	1131.2	2361.4	Enriched	Enriched	Enriched	Low		
Q86WQ0;Q86WQ0	Nuclear receptor 2C2	NR2C2AP	15.876	24.5	4	4	9.0029	0	10155	7055.1	8286.6	11924	8202.3	8997.8	8198.8	8978.7	3683.1	8699.5	Moderate	Enriched	Enriched	No expres	YES	
Q86WR0;Q86WR0	Coiled-coil domain-c	CCDC25	24.479	22.1	6	6	15.819	0	13167	7178.5	8612.4	8704.9	9818.4	8819.4	9018.4	8429.7	4043.9	7248.3	Low	Enriched	Enriched	No expres	YES	
Q86WU2-2;Q86WU	Probable D-lactate de	LDHD	52.144	13.4	11	11	23.021	0	12383	10012	9967	10366	13020	8480.4	8416.9	8959.8	5431.9	10386	Low	Low	No expres	No expres	YES	
Q86WV6;J3QTB1	Stimulator of interfer	TMEM173	42.192	8.7	3	3	16.014	0	15015	13953	12416	25801	13844	18524	17998	24222	8326	19956	Moderate	Enriched	Enriched	No expres	YES	
S4R3V8;Q86X29-6	Lipolysis-stimulated l	LSR	66.175	12.6	7	7	18.117	0	9385.7	8853	12791	9502.2	12175	11446	8938.4	6906.6	6266.3	9182.7	Enriched	Enriched	Enriched	Low	YES	
Q86X55-2;Q86X55	Histone-arginine metl	CARM1	41.884	10.2	3	3	27.085	0	8696.9	5739.4	6192.1	13420	5914.8	11630	15425	16130	7503.2	14086	Enriched	Enriched	Moderate	Enriched	YES	
Q86X76-2;Q86X76	Nitrilase homolog 1	NIT1	31.858	23.4	10	10	18.134	0	18552	14326	19235	11651	23718	27416	65243	42392	34798	28998	Enriched	Enriched	Enriched	Moderate	YES	
Q86XE5;Q86XE5-2	4-hydroxy-2-oxogluta	HOGA1	35.248	16.2	5	4	6.4608	0	18923	13545	17588	21600	17135	26312	33748	28704	17773	25230					YES	
Q86XL3;Q86XL3-3	Ankyrin repeat and L	ANKLE2	104.11	2.7	2	2	4.6473	0.00043	9225.7	8344	10047	7819.9	13377	7058	9883.9	8318.5	6460.8	10223	Low	Moderate	Moderate	Enriched	YES	
Q86XP3-2;Q86XP3	ATP-dependent RNA	DDX42	90.067	22.5	23	23	81.932	0	98567	82240	85211	88346	111440	65166	68174	57010	49957	67544	Enriched	Enriched	Enriched	Enriched	YES	
Q86XR7-2;Q9Y3B	Transmembrane emp2	TMED7	46.172	11.9	7	7	14.262	0	32814	23184	21497	28885	42434	38943	75791	48509	32075	36558	Enriched	Moderate	Enriched	Moderate	YES	
Q86XX4-2;Q86XX	Extracellular matrix p	FRAS1	443.63	12.4	48	48	323.31	0	124280	126780	153960	120320	178820	170360	240810	265780	148210	210180	Enriched	Enriched	Enriched	No expres	YES	
Q86Y39;K7EQ77;I	NADH dehydrogenas	NDUFA11	14.852	39.7	6	6	32.75	0	63927	32049	42508	59747	49650	53205	47080	61720	21590	54678	Enriched	Enriched	Enriched	No expres	YES	
Q86Y56;E9PGY2;I	HEAT repeat-contain	HEATR2	93.52	2.6	2	2	2.8061	0.00222	4816.3	4664.9	5671.5	3994.3	6754.3	5556.7	4325.3	5349.6	2583.6	4721.5	Enriched	Enriched	Enriched	No expres	YES	
Q86Y82;B1AJQ6	Syntaxin-12	STX12	31.642	17	4	4	9.7154	0	20815	16918	18301	17669	19326	31091	43530	50132	27966	34084	Enriched	Enriched	Enriched	Enriched	YES	
Q86Y97	Histone-lysine N-met	SUV420H2	52.112	5.4	2	2	2.9304	0.00168	8108.9	14368	11451	10069	11080	6036.2	5453.4	5942.1	4397.8	14190	Enriched	Enriched	Moderate	No expression		
Q86YB7;Q86YB7-2	Enoyl-CoA hydratase	ECHDC2	31.126	27.7	8	8	66.073	0	38302	27137	31274	45814	34163	34834	38245	51438	19291	45289	Enriched	Enriched	Enriched	No expres	YES	
Q86YB8;Q5TAE8	ERO1-like protein be	ERO1LB	53.543	35.3	22	20	183.7	0	135230	109630	110500	122090	148270	113320	282160	159180	100180	114350	Low	Enriched	Enriched	No expres	YES	
Q86YN1;Q86YN1-	Dolichyldiphosphata:	DOLPP1	27.03	12.6	2	2	3.7132	0.0008	1792	1790.1	1712.2	1551.9	1939.6	1378.6	1159	846.41	951.44	1288.3	Enriched	Enriched	Enriched	Low		
Q86YP4-2;Q86YP4	Transcriptional repre:	GATAD2A	65.225	5.4	3	2	4.7215	0.00043	6313.3	7457.3	6851.7	6601.4	8363.7	4506.8	5888.8	5436.2	4950	5962.9	Enriched	Enriched	Enriched	No expres	YES	
Q86YQ0;F6U1T9;(	Calcineurin subunit E	HZGJ;PPP3R1;DKFZp4	84.72	5.6	4	4	31.82	0	30453	27513	26065	28544	32513	19716	18701	21124	13549	25738	Enriched	Low	Moderate	Low		
Q86YS7;Q86YS7-2	C2 domain-containin	C2CD5	110.45	5.4	6	6	15.588	0	3082.5	1775.4	2278.8	2105.2	3803.2	6387	39507	43220	7214.2	6093.3					YES	
Q8IU81	Interferon regulatory	IRF2BP1	61.687	9.6	4	4	9.4732	0	2201.8	2419	2646.4	2366.8	2943.8	2117.5	2157.7	2853.4	1548.9	2239.6	Enriched	Moderate	Moderate	Moderate	YES	
Q8IU85-2;Q8IU85;	Calcium/calmodulin-	CAMK1D	40.189	20.7	8	8	72.003	0	41598	18586	20831	37932	25838	37937	26338	40241	11848	42783	Enriched	Enriched	Enriched	No expres	YES	
X6RLX0;Q8IUD2-2	ELKS/Rab6-interacti	ERC1	128.47	5.6	6	6	29.07	0	3888.7	3476.6	4744	3913.7	5355	1983.2	3877.1	3579.5	2544.2	3438.9	Moderate	Moderate	Moderate	No expres	YES	
Q8IUR6;Q8IUR6-3	CREB3 regulatory fa	CREBRF	72.148	2.7	2	2	2.2676	0.00494	4164.5	3931	6087.4	3077.1	6760.5	4679.2	8068.5	3315.9	3745.9	5797						
Q8IUX7-2;Q8IUX7	Adipocyte enhancer-l	AEBP1	82.182	2.3	1	1	67.231	0	1441	757.04	1387.5	2446.5	934.96	518.96	1525.4	5513.8	683.88	2131.8	Moderate	Low	Moderate	Enriched	YES	
Q8IUZ5;H7BYK2;(	5-phosphohydroxy-L	PHYKPL	49.71	7.6	5	4	9.1513	0	33475	15048	19662	34107	18811	30149	33726	30885	15057	35519					YES	
Q8IV03	Leucine rich adaptor	LURAP1L	24.583	4.3	1	1	2.4044	0.00411	2733.3	2680.1	3265.6	2432.4	3775.7	2332.2	5390.6	4485.2	4359.3	4167.8						
Q8IV36-2;Q8IV36;	Protein HID1	HID1	88.615	13.3	11	11	65.827	0	48422	43752	42691	51413	48368	48371	63072	62407	33472	51126					YES	
Q8IV38;G3V0G5	Ankyrin repeat and M	ANKMY2	49.298	7.9	3	3	5.2768	0	9444.6	8241.3	7462.1	5906.8	9326.6	8824.8	8056.7	8545.1	3666.6	5947.8	Enriched	Enriched	Enriched	Enriched	YES	
Q8IVF2-3;Q8IVF2	Protein AHNAK2	AHNAK2	605.64	10.3	5	5	17.685	0	37193	50357	76639	46061	63803	26645	36931	36599	35612	42059	Moderate	No expres	Moderate	No expres	YES	
Q8IVG5	Sterile alpha motif dc	SAMD9L	184.53	0.8	1	1	1.9528	0.008	6843.4	5269.4	5153.8	6458.8	6098.1	8008.2	7123	7774	3486.2	6256	Enriched	Enriched	Moderate	No expression		
Q8IVI9-3;Q8IVI9-2	Nostrin	NOSTRIN	48.875	14	5	5	10.921	0	15835	4723.2	9260.4	12100	8225	21516	28633	15931	12142	18972	Enriched	Enriched	Enriched	No expres	YES	
Q8IVM0-2;Q8IVM(	Coiled-coil domain-c	CCDC50	56.339	5	2	2	6.1005	0	8877.6	7938.9	8626.4	7528	12803	8199.8	11541	9333.9	8310.9	10121	Moderate	Enriched	Enriched	No expres	YES	
Q8IVN8	Somatomedin-B and	SBSPON	29.61	15.9	5	5	10.557	0	9030.5	10737	12162	5489.5	14864	7760.1	11785	10330	10407	11597					YES	
Q8IVP5	FUN14 domain-conta	FUNDC1	17.177	11	1	1	21.098	0	2289.5	2094.4	2302.6	3612.3	2713.3	3781.8	4834.8	11064	2005.7	4277.5	Moderate	Enriched	Enriched	No expression		
Q8IVS2	Malonyl-CoA-acyl ca	MCAT	42.961	5.9	1	1	44.844	0	1953.8	1081.8	991.06	3147.9	714.61	1660.3	2005.1	2905.4	329.83	2716.6	Moderate	Moderate	Moderate	Moderate	YES	
Q8IVT5-2;Q8IVT5;	Kinase suppressor of	KSR1	97.114	4.9	4	4	9.0903	0	12239	9879.3	13405	15175	14220	12891	13646	13940	8398.3	13367	Enriched	Enriched	Enriched	No expres	YES	
Q8IW45;Q8IW45-2	ATP-dependent (S)-N	CARKD	36.576	37.8	18	18	68.794	0	41984	35181	39332	47127	49558	36647	33872	46599	24992	40902	Enriched	Enriched	Enriched	No expres	YES	
Q8IWA4;Q8IWA4-	Mitofusin-1	MFN1	84.099	7.2	5	5	15.894	0	14464	18589	18310	14893	20597	19377	18377	14825	8569.3	15239	No expres	Enriched	Enriched	Moderate	YES	
Q8IWA5-3;Q8IWA	Choline transporter-l	SLC44A2	79.845	2.4	3	3	2.9092	0.00187	1813.1	1175.8	2199.2	1799.8	1827.7	2824.5	3224.8	2499.2	1172.4	3190.8	Enriched	Enriched	Moderate	No expres	YES	
Q8IWB7	WD repeat and FYVI	WDFY1	46.323	8.3	3	3	27.767	0	28859	20292	24106	23222	26720	46163	31849	57138	16522	44866	Low	Enriched	Enriched	No expres	YES	
Q8IWE2;Q8IWE2-2	Protein NOXP20	FAM114A1	60.741	20.6	12	12	65.519	0	69243	36380	39881	57744	49903	49716	60808	70583	31446	71411	Enriched	Enriched	Enriched	Enriched	YES	
Q8IWF2	FAD-dependent oxid	FOXRED2	77.79	1.9	1	1	2.2562	0.00493	5859.6	3779.9	5075.5	7349.6	4626.9	7147	5494.9	6354.8	4497.4	6170.4	No expres	Moderate	Moderate	No expression		
Q8IWJ2;B8ZZW2;/	GRIP and coiled-coil	GCC2	195.91	5.5	9	9	20.584	0	57248	43754	42081	48880	43867	48842	42906	38653	23223	48390	Enriched	Enriched	Enriched	No expres	YES	
Q8IWQ3-6;Q8IWQ	Serine/threonine-prot	BRSK2	68.739	4.1	2	2	219.8	0	20633	15296	16029	16330	18465	18376	14765	15980	7530.3	14012	No expres	Enriched	Low	No expres	YES	
Q8IWS0-5;Q8IWS(	PHD finger protein 6	PHF6	37.628	6.9	2	2	2.5996	0.00273	4196.7	3793.8	4704.8	4266.1	5039.6	1947.8	3150	2826.3	1644.6	2782.3	Moderate	Enriched	Enriched	No expres	YES	
Q8IWT6	Volume-regulated an	LRRC8A	94.198	3.6	2	2	4.6482	0.00043	8892.9	6482.2	8411	7188.2	7559.7	7997.2	10159	8412.7	7081.2	7366.3	Enriched	Enriched	Enriched	No expression		
Q8IWV7;A0A087V	E3 ubiquitin-protein	UBR1	200.21	3.2	6	6	9.5272	0	2597.8	2328.5	2922.8	1591.4	4436	1160.4	2153.7	1958	1299.5	2028.4	Enriched	Enriched	Enriched	No expres	YES	
Q8IWW8;Q8IWW8	Hydroxyacid-oxoacid	ADHFE1	50.307	15.4	7	7	19.363	0	13318	10932	13845	14264	16878	14792	17454	14810	9013.7	17422	Moderate	Enriched	Moderate	No expres	YES	
Q8IWZ8	SURP and G-patch d	SUGP1	72.47	7	5	5	7.8819	0	27739	21281	19696	23845	21479	27855	24249	19653	12223	23275					YES	
Q8IX12-2;Q8IX12;	Cell division cycle an	CCAR1	131.04	13.1	15	15	26.676	0	37042	28452	38162	35227	41428	43842	41745	39898	22550	40992	Enriched	Moderate	Enriched	No expres	YES	
Q8IXB1-2;Q8IXB1	DnaJ homolog subfar	DNAJC10	86.135	14.2	11	11	44.047	0	52335	34476	36955	51979	39665	38151	50069	52484	31576	49513	Moderate	Enriched	Enriched	No expres	YES	
Q8IXI2-4;Q8IXI2;(	Mitochondrial Rho G	RHOT1;TMEM91	66.54	8.8	6	6	14.069	0	17337	11954	11909	16265	16102	19862	14261	14007	9266.8	16283	Enriched	Enriched	Enriched	No expression		
Q8IXJ6-2;Q8IXJ6-3	NAD-dependent prot	SIRT2	39.515	13.4	5	5	15.965	0	819.18	153.05	191.97	1220.4	222.7	5574	384.31	822	199.73	442.31	Enriched	Enriched	Enriched	No expres	YES	
Q8IXM3	39S ribosomal protei	MRPL41	15.383	10.2	2	2	1.8997	0.0083	3472.6	2688.9	3336.5	4833.1	3101	4607.7	2840.6	3368.7	1999.9	3687.1	Enriched	Enriched	Enriched	No expression		
Q8IXQ6-3;Q8IXQ6	Poly [ADP-ribose] pc	PARP9	80.29	7.5	5	5	7.1277	0	16021	12170	15568	20019	14634	18593	19564	20413	13923	20626	No expres	Enriched	Enriched	No expres	YES	
Q8IXW5;Q8IXW5-	Putative RNA polyme	RPAP2	69.508	2.9	2	2	2.9082	0.00186	5428.6	3389.8	5199	5868.7	5731.6	5053.3	4672.8	5344	2900.8	5524.5	Low	Enriched	Enriched	No expression		
Q8IY17-5;Q8IY17-	Neuropathy target est	PNPLA6	143.35	1.5	2	2	4.0258	0.00062	13434	16658	15114	14352	16018	11154	16201	16868	9714.4	16007	Moderate	Enriched	Enriched	Moderate	YES	
Q8IY21;H0Y8Z7	Probable ATP-depen	DDX60	197.85	2.8	4	4	8.1563	0	3970.4	3198.8	5208.7	4127.8	4001	3253.1	3580.7	4614.8	2960.2	3702.1	Low	No expres	Enriched	No expression		
Q8IY63-2;Q8IY63	Angiomotin-like prot	AMOTL1	101.18	1.4	1	1	2.5154	0.00379	7814.6	6019.2	9424	6384.6	11121	7664.9	18070	10979	14116	14249	Low	Enriched	Enriched	No expression		
Q8IY81	pre-rRNA processing	FTSJ3	96.557	10.5	7	6	36.102	0	16560	13062	16337	14097	11948	9805.9	14530	19597	8236.1	21124	Enriched	Enriched	Enriched	No expres	YES	
Q8IY95-2;Q8IY95	Transmembrane prote	TMEM192	30.549	4.1	2	2	5.1994	0.00022	5732.3	4147.4	6089.4	4121.4	3189.6	9447.8	3999	5241.5	1328.5	4684.5	Moderate	Enriched	Enriched	No expres	YES	
Q8IYB8	ATP-dependent RNA	SUPV3L1	87.99	8.7	6	6	17.312	0	16251	13801	18031	13925	21108	16974	16211	14833	12407	17399	Enriched	Moderate	Moderate	Low	YES	
Q8IYD1	Eukaryotic peptide cl	GSPT2	68.882	17.8	13	1	5.0814	0.00044	4537.7	1924.2	3274.4	6270.5	2122.7	3565	3753.3	5429.4	4178.7	4840.9	Moderate	Moderate	Enriched	No expression		
Q8IYI6	Exocyst complex con	EXOC8	81.798	13	14	14	54.576	0	48787	22491	28103	44215	30863	178240	96158	45842	27965	60741	Low	Moderate	Enriched	No expres	YES	
Q8IYJ3;Q8IYJ3-2;/	Synaptotagmin-like p	SYTL1	61.856	21	11	11	22.493	0	49679	44332	46097	43647	58833	61729	76265	65531	37580	58611	Moderate	Enriched	Enriched	No expres	YES	
Q8IYK2	Coiled-coil domain-c	CCDC105	56.908	2	1	1	2.2076	0.00545	10703	12839	24771	8346.4	12654	8390.5	36555	26132	21525	11730	No expres	No expres	Low	No expression		
Q8IYL3	UPF0688 protein C1o	C1orf174	25.977	10.7	2	2	2.434	0.00412	156.67	189.95	79.832	89.201	162.77	157.68	145.99	176.96	62.26	84.001	Moderate	Moderate	Enriched	No expression		
Q8IYQ7	Threonine synthase-li	THNSL1	83.069	10.4	9	9	34.32	0	44403	28474	34276	33771	36505	30403	30722	33641	15331	35880	Enriched	Enriched	Enriched	No expres	YES	
Q8IYS1	Peptidase M20 doma	PM20D2	47.776	6.4	3	3	5.253	0.00022	11872	7977.4	8852.8	13179	13646	6011.2	12301	9064.3	6278.2	16182	Moderate	Enriched	Enriched	No expres	YES	
Q8IZ07;H0YIN8	Ankyrin repeat doma	ANKRD13A	67.618	8	4	4	7.3345	0	27301	16774	22391	17880	25352	28710	44311	26102	18241	33922	Enriched	Enriched	Enriched	No expres	YES	
Q8IZ52;F8W6H2;(	Chondroitin sulfate s	CHPF	85.466	4	2	2	7.1251	0	10698	8375.2	11527	11594	9533.7	6898.7	13493	9586.8	8354.2	8774.5	Enriched	Enriched	Enriched	Moderate		
Q8IZ73-2;Q8IZ73	RNA pseudouridylate	RPUSD2	54.097	2.9	1	1	3.2681	0.00077	6673.6	5136.9	6501.5	8295.1	6793.7	8596.7	5965.1	6748.5	3139.1	6240.5	Moderate	Low	Moderate	Moderate	YES	
Q8IZ83;Q8IZ83-3;I	Aldehyde dehydroger	ALDH16A1	85.126	16.7	13	13	25.346	0	64273	40180	39134	74781	59835	48606	49832	55520	28537	54840	Enriched	Enriched	Moderate	No expres	YES	
Q8IZC6;Q8IZC6-2	Collagen alpha-1(XX	COL27A1	186.89	1.7	2	2	2.4461	0.00412	3210.9	3128.5	5065.4	5239	4757.5	3300.3	25028	5849.5	4703.1	10344	Enriched	Enriched	Enriched	No expression		
Q8IZH2-2;Q8IZH2;	5-3 exoribonuclease	XRN1	192.84	2.8	4	4	8.5576	0	23113	11283	16427	37713	15087	30406	19546	30601	9742.6	30361	No expres	Enriched	Enriched	No expres	YES	
Q8N0U8;Q8N0U8-	Vitamin K epoxide re	VKORC1L1	19.835	10.2	2	2	2.8107	0.00222	3653.5	2215.3	3028.6	3558.5	3189	2339.9	4087.9	2782.6	2784.9	2574.9	Low	Enriched	Enriched	No expres	YES	
Q8N0W3;Q8N0W3	L-fucose kinase	FUK	117.62	5	4	4	8.1265	0	29494	13859	18440	39852	16773	31687	24715	28962	10717	33292	Moderate	Enriched	Enriched	No expres	YES	
Q8N0X4-2;Q8N0X	Citrate lyase subunit	CLYBL	33.408	34	9	9	82.715	0	25973	22663	26444	28607	33375	29163	33418	37917	15569	28404	Low	Enriched	Moderate	No expres	YES	
Q8N0X7	Spartin	SPG20	72.832	4.8	3	3	11.539	0	18307	20996	14985	23723	17712	16801	13818	16195	10626	19283	No expres	Low	Enriched	Moderate	YES	
Q8N0Z3	Spindle and centriole	SPICE1	96.263	2.5	2	2	3.2966	0.00078	6210.6	5142.6	4524.8	3924.5	8994	3934.1	5446	3411.7	5789.2	4452.9						
Q8N0Z6	Tetratricopeptide rep	TTC5	48.927	3.4	1	1	2.1432	0.0061	1948.5	998.62	1394.8	3627.8	1237.5	1728.4	1653.6	4256.6	1772.5	2274.5	Moderate	Moderate	Enriched	No expres	YES	
Q8N129	Protein canopy homo	CNPY4	28.309	9.7	2	2	5.6008	0	2989.4	2083	2116	3278.9	2961.9	2250.7	2378.9	2942.7	851.25	2631.5	Moderate	Enriched	Enriched	No expres	YES	
Q8N142;Q8N142-2	Adenylosuccinate syr	ADSSL1	50.208	8.3	4	4	7.43	0	17668	15511	15815	29395	22307	13800	12408	14025	9126.7	20795	Enriched	Enriched	Moderate	No expres	YES	
Q8N163;Q8N163-2	Cell cycle and apopto	CCAR2	102.9	23.3	20	20	82.706	0	80214	67586	69478	68173	87875	65453	77968	75197	43994	77993					YES	
Q8N183	Mimitin, mitochondri	NDUFAF2	19.856	38.5	8	8	26.119	0	46971	36240	48382	44420	63034	32937	40731	38223	22755	44011	Enriched	Enriched	Enriched	No expres	YES	
Q8N1B4;Q8N1B4-2	Vacuolar protein sort	VPS52	82.22	5.5	3	3	12.647	0	14019	11850	11343	11195	13851	12711	10695	12120	5445.1	12996	Enriched	Enriched	Enriched	Enriched	YES	
Q8N1F7;H3BVG0;	Nuclear pore comple:	NUP93	93.487	18.3	14	14	70.256	0	62286	44862	48977	61601	59077	55709	59704	73983	38575	69071	No expres	No expres	Moderate	Moderate	YES	
Q8N1G2	Cap-specific mRNA (	CMTR1	95.32	5.6	5	5	14.038	0	11596	8034.5	9429.5	9261.4	11324	13613	12291	9326.3	7331.4	9590.5					YES	
Q8N1G4	Leucine-rich repeat-c	LRRC47	63.472	38.9	38	38	179.9	0	112910	76730	91769	137830	104050	148310	154510	161370	90945	136020	Enriched	Enriched	Enriched	No expres	YES	
Q8N201	Integrator complex su	INTS1	244.29	3.3	7	7	16.945	0	13573	18399	15879	10631	15759	11060	13750	11997	10541	11664	Enriched	Enriched	Enriched	Moderate	YES	
Q8N2F6-6;Q8N2F6	Armadillo repeat-con	ARMC10	24.756	20.4	7	7	41.61	0	8083.5	9514.2	7177.8	4371	5967.3	7449.5	15624	23323	9610.6	9965.9	No expres	Enriched	Enriched	No expres	YES	
Q8N2K0;Q8N2K0-	Monoacylglycerol lip	ABHD12	45.096	21.6	9	9	15.57	0	18423	14632	18974	21719	16708	18065	16033	23326	12124	19432	Moderate	Enriched	Enriched	No expres	YES	
Q8N2S1-2;Q8N2S1	Latent-transforming g	LTBP4	165.74	4	7	7	22.759	0	16961	16847	19584	13037	27233	13271	19677	23690	9014.9	19695	Enriched	Low	Low	Enriched	YES	
Q8N335	Glycerol-3-phosphate	GPD1L	38.418	42.5	23	10	85.672	0	289340	153640	183320	202370	198510	269860	256570	176080	123800	192410	Moderate	Enriched	Enriched	Enriched	YES	
Q8N357	Solute carrier family	SLC35F6	40.214	3.2	2	2	8.2154	0	6744.4	5360.5	3219.6	8608.1	6457.1	5351.8	3088.9	2219.9	1608.7	4281					YES	
Q8N392-2;Q8N392	Rho GTPase-activatir	ARHGAP18	70.163	18.3	13	13	83.286	0	51288	30026	32272	43633	37539	55844	58036	116260	23533	64821	Enriched	Moderate	Enriched	No expres	YES	
Q8N3C0	Activating signal coin	ASCC3	251.46	5.4	13	13	126.97	0	75214	48386	58991	81192	67574	81412	68765	83558	32026	84001	No expres	Moderate	Enriched	Low	YES	
Q8N3D4;E9PSB0;I	EH domain-binding p	EHBP1L1	161.85	2.9	4	4	11.541	0	10219	6704.6	9731.2	20256	8920.3	10498	14692	20105	9450.1	16699	No expres	No expres	Moderate	No expres	YES	
Q8N3F8	MICAL-like protein 1	MICALL1	93.44	13.4	10	10	36.274	0	34116	33839	36668	28292	48017	26301	39589	26167	29700	33736	Moderate	Enriched	Moderate	No expres	YES	
Q8N3R9-2;Q8N3R	MAGUK p55 subfam	MPP5	73.421	3.1	2	2	3.0248	0.00132	1605	1796.7	1372.8	2403.3	1679.7	1273.9	1508.2	2156.4	868.28	2007	Moderate	Enriched	Enriched	No expres	YES	
Q8N3U4;Q8N3U4-	Cohesin subunit SA-2	STAG2	141.32	5.7	7	5	9.968	0	43281	24017	29573	52580	29513	41437	39438	53836	19502	47213	Enriched	Enriched	Enriched	Low	YES	
Q8N3V7-2;Q8N3V	Synaptopodin	SYNPO	96.395	16.7	12	12	45.352	0	48260	39961	47705	50915	54777	49578	75309	64397	44096	63215	Enriched	Enriched	Enriched	Enriched	YES	
Q8N3X1-2;Q8N3X	Formin-binding prote	FNBP4	110.45	2.3	2	2	28.843	0	5591.5	3918.2	3571.6	3167.3	5991.4	3186	7688.6	4045.7	20501	6306.7	Enriched	Enriched	Enriched	Enriched	YES	
Q8N442	Translation factor GU	GUF1	74.327	5.4	3	3	15.696	0	5099.8	3416.5	4277	4880.6	4532.9	5911.8	9300.5	6137.1	3896.5	4131.3	Moderate	Moderate	Moderate	No expres	YES	
Q8N465;H7C0N1;I	D-2-hydroxyglutarate	D2HGDH	56.415	5.4	2	2	5.3724	0	5627.9	4170.3	5871.5	7375.4	6636.9	5734.3	5804.1	6335.4	2912.2	7243.6						
Q8N490-2	Probable hydrolase P	PNKD	15.396	12	1	1	5.0691	0.00044	6325.7	6797.6	6222.1	4425.9	7136.7	2572.3	6406.6	5784.3	7655.2	5566.5	Enriched	Enriched	Enriched	No expres	YES	
Q8N4C8-5;Q8N4C	Misshapen-like kinas	MINK1;MAP4K4;TNIK	143.64	6.6	8	8	25.403	0	23338	17254	19640	21519	27027	22469	18071	16913	11966	22121	Enriched	Moderate	Moderate	No expression		
Q8N4P3;H0YNP9;I	Guanosine-3,5-bis(di	HDDC3	20.329	35.8	11	11	31.924	0	54682	39196	55734	30626	88867	32951	35503	35852	12890	36027	Low	Enriched	Enriched	No expres	YES	
Q8N4Q0;J3QQQ7;J	Zinc-binding alcohol	ZADH2	40.14	6.9	2	2	9.599	0	6673.9	4753.6	5232.1	5091.2	7265.3	6361.1	4416.1	6106.9	1534.8	5922.7	Moderate	Moderate	Enriched	No expres	YES	
Q8N4T8;Q8N4T8-2	Carbonyl reductase fa	CBR4	25.301	28.7	7	7	15.667	0	34586	28318	34254	30171	43961	30604	40480	26823	29433	35763	Enriched	Enriched	Moderate	Enriched	YES	
Q8N4V1;Q8N4V1-	Membrane magnesiur	MMGT1	14.686	16.8	1	1	13.168	0	8068.5	6197.5	5808.2	5460.2	7322.6	3292.6	5134.1	3602.6	2570.2	4707.4	Enriched	Enriched	Enriched	No expres	YES	
Q8N4X5-2;Q8N4X	Actin filament-associ	AFAP1L2	90.859	8.2	4	4	11.782	0	11257	8714.5	8732.9	13386	9518.3	6965.9	6617.9	9011.7	7856.1	9254.4	Low	Enriched	Moderate	No expres	YES	
Q8N573-2;Q8N573	Oxidation resistance p	OXR1	93.733	7.9	6	6	23.321	0	28816	27988	31399	26869	33286	27620	35308	28439	29011	30470	Low	Enriched	Enriched	No expres	YES	
Q8N5C6	S1 RNA-binding dom	SRBD1	111.77	6	5	5	21.117	0	26539	22278	22314	22140	23109	25857	19771	21814	13670	25173	Low	Moderate	Enriched	No expres	YES	
Q8N5G0-2;Q8N5G	Small integral membr	SMIM20	7.7019	19.4	2	2	2.8129	0.00222	8090.6	6016	6524.4	8430	7439.1	9378.8	8794.5	7720.2	3595.3	8716.1					YES	
Q8N5G2	Macoilin	TMEM57	76.177	5.1	3	3	9.8072	0	25677	24229	25705	18533	30558	28061	49818	38731	30668	36638	Low	Low	Moderate	No expres	YES	
Q8N5J2-2;Q8N5J2-	Protein FAM63A	FAM63A	36.458	6.1	2	2	2.7423	0.0024	1961	1776.2	1859.5	1403.4	2606.2	505.35	966.83	993.39	635.92	1254.3	Enriched	Enriched	Enriched	No expres	YES	
Q8N5K1;D6RCF4	CDGSH iron-sulfur d	CISD2	15.278	38.5	11	11	25.546	0	15859	14263	12914	14472	19682	11196	13459	11764	10052	12006	Enriched	Enriched	Enriched	No expres	YES	
Q8N5L8	Ribonuclease P prote	RPP25L	17.631	12.3	1	1	2.5406	0.00379	5920.3	3620.4	3442	5909.8	4366	9324.3	7798.5	5327.4	6759.1	6907						
Q8N5N7	39S ribosomal protei	MRPL50	18.325	20.9	4	4	9.036	0	15009	10564	11051	18875	16376	15719	9941	16831	4609.7	13379	Enriched	Enriched	Enriched	No expres	YES	
Q8N5X7	Eukaryotic translatio	EIF4E3	24.441	6.2	1	1	2.2392	0.00528	8508	10121	8571.6	11394	10412	8286.5	7095.5	8010.3	3656.2	9654.8	Low	Enriched	Enriched	No expres	YES	
Q8N668;Q8N668-2	COMM domain-cont	COMMD1	21.178	36.8	11	11	36.387	0	59072	51852	56636	62375	66369	58314	58427	59247	34091	56167	Enriched	Enriched	Enriched	No expres	YES	
Q8N6L1;Q8N6L1-2	Keratinocyte-associat	KRTCAP2	14.678	11.8	1	1	3.1899	0.00077	10921	10782	10526	14734	10087	7455.9	7080.7	4824.6	7258.4	8460.2	Enriched	Enriched	Enriched	No expression		
Q8N6M3	Fat storage-inducing t	FITM2	29.855	8	3	3	11.36	0	15777	11157	11469	7189.5	10752	22607	27661	34000	6797.6	17236	Moderate	Enriched	Enriched	No expression		
Q8N6R0-2;Q8N6R(	Methyltransferase-lik	METTL13	44.562	4.8	2	2	2.9825	0.00169	4498.7	2563	2968.6	4461.7	3506.9	5261	4554.4	4993.6	1571.8	4681.6	Enriched	Moderate	Moderate	Enriched	YES	
Q8N766-3;Q8N766	ER membrane protei	EMC1	111.69	22.3	19	19	81.123	0	119260	101970	108350	98110	116620	104240	128840	107740	75991	107540					YES	
Q8N8N7	Prostaglandin reducta	PTGR2	38.499	14.8	7	1	26.324	0	45834	32999	33906	47668	31790	42393	26898	44415	12966	43914	No expres	No expres	Low	No expres	YES	
Q8N8S7;Q8N8S7-3	Protein enabled homo	ENAH	66.509	20.3	14	14	42.976	0	33715	35869	35310	34615	41769	25332	68551	59536	40876	37728	Moderate	Enriched	Enriched	No expres	YES	
Q8N9B5-2;Q8N9B	Junction-mediating ar	JMY	110.28	3.3	2	2	201.82	0	14649	12366	12676	11593	17041	11389	14963	16620	9207.1	15319	Moderate	Enriched	Enriched	No expression		

Q8N9N7;H3BSW0	Leucine-rich repeat-c	LRRC57	26.754	17.6	5	5	6.2501	0	33434	22015	26957	29354	25248	23600	11736	16074	11468	27770	Moderate	Moderate	Moderate	No expres	YES	
Q8N9T8	Protein KRI1 homolc	KRI1	82.597	4.6	2	2	10.038	0	2956.6	1421.9	1411.8	7458.8	1630.2	3393.5	2088.7	5455.3	1398.1	4256.2	Enriched	Enriched	Moderate	No expres	YES	
Q8N9U0;Q8N9U0-	Tandem C2 domains	TC2N	55.284	27.8	15	15	34.549	0	105580	83335	102420	109500	160130	96102	133230	86843	55080	88226	Moderate	Enriched	Enriched	No expres	YES	
Q8NAT1	Protein O-linked-mar	POMGNT2	66.615	12.6	7	7	9.2345	0	32672	22256	24352	27111	30295	24865	30378	26630	17371	26992					YES	
Q8NB90-2;Q8NB9	Spermatogenesis-assc	SPATA5	86.076	16.6	15	13	28.544	0	86055	64181	74582	70559	83944	65207	74159	68181	40992	71888	No expres	Low	Low	No expres	YES	
Q8NBF2	NHL repeat-containi	NHLRC2	79.443	20.4	15	15	56.873	0	112860	97019	107750	92321	127740	112760	113660	97493	47977	91804	Low	Low	Moderate	No expres	YES	
Q8NBF6;H7C0I1;E	Late secretory pathw	AVL9	71.947	5.1	3	3	7.2808	0	13001	9291	9458.6	10664	11776	9768.4	13753	14755	7388.3	12434	Moderate	Moderate	Enriched	Low	YES	
Q8NBJ5	Procollagen galactosy	COLGALT1	71.635	4.5	3	3	2.6706	0.00256	12642	13785	15692	15569	14688	11060	17533	16048	15735	12248					YES	
Q8NBL1	Protein O-glucosyltra	POGLUT1	46.189	9.7	5	5	8.3253	0	36035	26178	37169	33602	41087	30688	30818	28400	15587	32945					YES	
Q8NBM8;D6R9J0;	Prenylcysteine oxidas	PCYOX1L	54.646	7.3	4	4	6.4789	0	24561	19271	17250	16510	17287	10400	5102.3	5474.9	2773	10879	Moderate	Low	Enriched	No expression		
Q8NBN3-3;Q8NBN	Transmembrane prote	TMEM87A	56.773	7.5	3	3	5.2011	0.00022	8464.8	7227.1	9656.3	7259.1	9715.4	5874.3	7027.4	7628.4	4586.7	7822.7	Enriched	Enriched	Enriched	Moderate	YES	
Q8NBN7;Q8NBN7	Retinol dehydrogena	RDH13	35.932	23.6	7	7	71.327	0	16572	15204	20205	17304	21238	25789	24979	44109	11203	39977	Enriched	Enriched	Enriched	No expres	YES	
Q8NBP0	Tetratricopeptide rep	TTC13	96.812	4.7	3	3	6.3954	0	2163.5	2218	2501.2	1877.6	2752.4	2169.8	1498	1593.5	875.11	1901.5	Moderate	Moderate	Enriched	No expres	YES	
Q8NBQ5;D6RCD0	Estradiol 17-beta-del	HSD17B11	32.935	33.3	16	16	97.255	0	83083	66403	73186	77831	84544	76889	151180	191370	57347	87023	Enriched	Enriched	Enriched	No expres	YES	
Q8NBX0	Saccharopine dehydr	SCCPDH	47.151	17.9	7	7	26.391	0	39622	47404	37318	48578	44773	36285	28114	37022	16104	42147	Low	Moderate	Enriched	Enriched	YES	
Q8NC51-2;Q8NC5	Plasminogen activato	SERBP1	44.256	57	48	48	323.31	0	378740	253050	291850	350200	389360	311720	473110	600840	260650	370450	Enriched	Enriched	Enriched	Enriched	YES	
Q8NC56	LEM domain-contain	LEMD2	56.974	18.7	10	10	26.535	0	38719	28139	38552	38816	43587	34264	45290	32737	33011	45096	No expres	Moderate	Moderate	Moderate	YES	
Q8NC96;F5H2U7	Adaptin ear-binding c	NECAP1	29.737	14.5	5	5	18.377	0	33773	33400	29737	25991	43053	35278	34375	39748	20445	36868	No expres	Enriched	Enriched	Enriched	YES	
Q8NCA5-2;Q8NCA	Protein FAM98A	FAM98A	55.272	12.9	5	4	20.243	0	7335.2	7918	9630.5	6480.3	12227	3908.7	5314.3	5434.9	3802.1	5487	Moderate	Enriched	Enriched	Enriched	YES	
Q8NCF5;H3BSZ7;(	NFATC2-interacting	NFATC2IP	45.816	11	3	3	5.3713	0	16660	16068	17512	13584	17077	14958	17408	15331	8906.9	19585	Enriched	Enriched	Enriched	Moderate	YES	
Q8NCN4	E3 ubiquitin-protein	RNF169	77.193	2.4	2	2	17.417	0	3856.7	4131.2	4291.6	2890.8	6286.9	2682.7	5318.3	4441.8	3566.4	5118.5	No expres	Moderate	Low	No expres	YES	
Q8NCW5-2;Q8NC	NAD(P)H-hydrate ep	APOA1BP	20.43	56.2	13	13	203.96	0	203730	130510	160760	149930	145700	182110	137280	176160	53382	149420	Enriched	Enriched	Enriched	No expres	YES	
Q8ND04;Q8ND04-	Protein SMG8	SMG8	109.68	3.7	3	3	7.7468	0	27521	22493	27787	27316	31858	19176	31093	41582	17816	34522					YES	
Q8ND24-2;Q8ND2	RING finger protein 2	RNF214	61.317	7.5	4	4	8.3889	0	36455	34105	34180	33976	50121	14415	23135	19290	16315	22467	Moderate	Enriched	Enriched	No expres	YES	
Q8ND56-3;Q8ND5	Protein LSM14 homc	LSM14A	46.411	16.4	11	11	140.12	0	40018	25063	29612	35508	29667	42893	36075	56668	16571	46728	Enriched	Enriched	Enriched	Enriched	YES	
R4GNF3;Q8ND76-	Cyclin-Y	CCNY	11.633	13.9	1	1	4.3457	0.00063	19947	8350.5	8891.6	23200	9838.4	18894	15865	27363	7020.2	20907	Enriched	Enriched	Enriched	No expres	YES	
Q8NDH3-5;Q8NDI	Probable aminopeptic	NPEPL1	50.53	12.2	6	6	18.179	0	15256	9710.8	13931	29534	14782	26115	12483	17940	6694.1	21409	Enriched	Moderate	Moderate	No expres	YES	
Q8NDI1-3;Q8NDI1	EH domain-binding p	EHBP1	132.32	2.4	3	3	4.4357	0.00042	2988.4	3948.9	3669.5	1684.5	3445.6	4090.8	9638.8	7811.5	11678	6058.5	Enriched	Enriched	Enriched	Enriched	YES	
Q8NE01-2;Q8NE0	Metal transporter CN	CNNM3	70.631	4.6	3	3	3.1196	0.00095	4118.7	6100.2	20096	2325.2	20534	3792.6	5371.9	2256.2	1210.3	3324.6	Enriched	Enriched	Enriched	No expres	YES	
Q8NE62	Choline dehydrogena	CHDH	65.358	30.1	20	20	112.57	0	114330	80241	89490	84710	138220	87073	122980	96325	64664	123830	Enriched	Enriched	Enriched	No expres	YES	
Q8NE71-2;Q8NE7	ATP-binding cassette	ABCF1	91.679	26.8	32	32	323.31	0	180100	110870	140330	136050	166890	149280	205840	171530	121710	178110	No expres	Enriched	Enriched	Enriched	YES	
Q8NE86-3;Q8NE8	Calcium uniporter pr	MCU	35.158	14.6	4	4	8.8376	0	17395	14046	17321	13754	16141	12984	26706	19217	20376	18761					YES	
Q8NEG4-2;Q8NEC	Protein FAM83F	FAM83F	36.795	5.1	1	1	2.7437	0.0024	6048.7	6713.3	6707.4	9389.4	6454.9	8623.5	8193.5	7841	3778.9	7897.9	Moderate	Enriched	Moderate	No expres	YES	
Q8NEN9	PDZ domain-containi	PDZD8	128.56	1.2	1	1	5.3946	0	15704	16239	16982	15616	20865	10107	11627	9814.3	7915.8	12197	Enriched	Enriched	Enriched	No expres	YES	
Q8NEU8;F8VXB0;	DCC-interacting prot	APPL2	74.493	9.3	7	7	16.991	0	11126	7446.2	7301.1	12901	8789.8	9184.4	9237.2	11975	4709.5	11843	Enriched	Enriched	Enriched	No expres	YES	
Q8NF91-4;Q8NF91	Nesprin-1	SYNE1	1005.2	2.5	19	18	53.928	0	33430	26726	32149	36730	35619	33238	32731	34645	19813	31498	No expres	Moderate	Moderate	Enriched	YES	
Q8NFC6	Biorientation of chro	BOD1L1	330.46	1.1	3	2	18.721	0	18590	17573	17944	18979	23605	16901	20256	20341	10658	17830					YES	
Q8NFD5;Q8NFD5-	AT-rich interactive do	ARID1B	236.12	2	3	2	4.4597	0.00042	14664	13079	15526	10577	18006	10855	14931	15574	11105	14416	Moderate	Enriched	Enriched	No expres	YES	
Q8NFH4;F8VTY2	Nucleoporin Nup37	NUP37	36.707	12.6	3	3	7.6171	0	7033.5	3746.3	6030.4	13535	4741.6	8703	8653.5	12516	3803.5	9663.5	Moderate	Moderate	Enriched	No expres	YES	
Q8NFH5-2;Q8NFH	Nucleoporin NUP53	NUP35	33.12	16.2	5	5	30.588	0	28735	23745	34718	27925	37102	23006	27217	28124	17435	28873	Moderate	Enriched	Enriched	No expres	YES	
Q8NFH8-4;Q8NFH	RalBP1-associated E	REPS2	71.405	5.6	3	3	11.48	0	11477	11466	13417	6097.5	16392	7685.7	11228	7130.3	8202.9	10011	Low	Enriched	Enriched	Low	YES	
Q8NFU3-3;Q8NFU	Thiosulfate sulfurtran	TSTD1	11.75	22	2	1	2.2139	0.00545	8852.7	7075.4	8033.2	8824.8	9942.7	8516.1	9366.1	9896.5	6764.3	9243.1					YES	
Q8NFV4;Q8NFV4-	Alpha/beta hydrolase	ABHD11	34.69	37.5	14	14	32.643	0	28703	19874	24402	44180	28306	26249	27782	32202	19176	34409	Enriched	Enriched	Enriched	No expres	YES	
Q8NFW8;Q8NFW8	N-acylneuraminate cy	CMAS	48.379	30	14	14	51.573	0	35832	30147	33356	33561	39701	28632	36548	31115	25162	32359	No expres	Low	Enriched	No expres	YES	
Q8NFX7-2;Q8NFX	Syntaxin-binding pro	STXBP6	23.587	10	4	4	9.3459	0	5784.5	5195.3	6534.5	4725.2	7772.8	9417.5	17872	15052	8490.7	11898	Moderate	Enriched	Enriched	No expres	YES	
Q8NFZ8	Cell adhesion molecu	CADM4	42.785	11.3	4	4	13.004	0	12975	12608	16890	11838	17324	11812	15497	10350	8827.3	11359	Moderate	Moderate	Low	Moderate	YES	
Q8NHG7	Small VCP/p97-inter	SVIP	8.4426	14.3	1	1	2.8263	0.00204	13964	5181.2	6805.8	9099.7	5917.5	14683	9216.5	13923	11162	17139	Enriched	Enriched	Enriched	No expres	YES	
Q8NHG8	E3 ubiquitin-protein	ZNRF2	24.115	14.5	3	3	6.2448	0	9301.4	6807.1	8109.7	11702	8515.5	9747	7742.2	10185	5010.6	8836.3	Low	Low	Moderate	No expres	YES	
Q8NHP1	Aflatoxin B1 aldehyc	AKR7L	36.963	35.3	23	0	26.749	0	19201	12939	16189	17723	17691	40347	76575	113400	28578	40187					YES	
Q8NHP8;Q8NHP8-	Putative phospholipa	PLBD2	65.471	9.8	6	6	7.7462	0	7319.6	9140.4	8162.5	8224.5	7743	6852	7537.1	5887.8	4394	6044.4	Low	Enriched	Enriched	No expres	YES	
Q8NHV1	GTPase IMAP family	GIMAP7	34.508	9.3	2	2	18.304	0	16123	5440.9	6174.5	21124	5222.1	15622	9427.9	24385	4666.3	18440	No expres	Moderate	Low	No expres	YES	
Q8NHV4-2;Q8NHV	Protein NEDD1	NEDD1	62.379	11	4	4	13.379	0	23499	16186	25004	23913	25450	24575	33260	34134	37376	37628	Low	Enriched	Enriched	No expression		
Q8NHY2-3;Q8NHY	E3 ubiquitin-protein	RFWD2	57.526	2	1	1	2.6765	0.00256	16109	9606.4	12054	12746	9493	16168	19319	42429	6631.3	18673	Enriched	Enriched	Enriched	No expres	YES	YES
Q8NI22;Q8NI22-2;	Multiple coagulation	MCFD2	16.39	64.4	18	11	110.49	0	204280	109000	130450	156290	175760	178280	120520	167290	60125	140780	Moderate	Enriched	Enriched	Enriched		
Q8NI27	THO complex subuni	THOC2	182.77	5	8	8	15.658	0	21092	16868	21064	21006	24225	13250	20157	16941	11963	20988	Enriched	Enriched	Enriched	Low	YES	
Q8NI35;Q8NI35-4;	InaD-like protein	INADL	196.37	2.9	4	4	10.214	0	13500	11194	13948	14577	16886	15452	13524	12041	9020.2	17073	Moderate	Enriched	Enriched	No expres	YES	
Q8NI60;Q8NI60-3	Chaperone activity of	ADCK3	71.949	20.4	18	18	42.597	0	51864	49581	55753	42381	60712	35801	49282	49900	32801	48538					YES	
Q8TAE8	Growth arrest and DN	GADD45GIP1	25.384	19.8	5	5	7.6931	0	7921.1	9618.3	9522.2	8650.7	14424	6910.4	9225.1	7411.5	6789.8	7172.8	Moderate	Moderate	Moderate	No expres	YES	
Q8TAT6;Q8TAT6-	Nuclear protein local	NPLOC4	68.119	17.4	14	14	32.202	0	67877	35884	42498	83796	46817	57916	45189	59730	28873	59750	Enriched	Enriched	Enriched	No expres	YES	
Q8TB45;Q8TB45-2	DEP domain-containi	DEPTOR	46.293	6.8	2	2	2.4099	0.00412	12500	4615.4	9218.4	14871	5525.1	13407	13287	28948	7737	16971					YES	
Q8TB61-3;Q8TB61	Adenosine 3-phosphc	SLC35B2	42.127	11.2	7	7	16.404	0	20301	16022	22846	17700	26890	32809	41837	32476	21208	27279	Enriched	Enriched	Enriched	No expres	YES	
Q8TBA6-2;Q8TBA	Golgin subfamily A n	GOLGA5	78.107	19	12	12	46.9	0	29513	28096	30237	28144	37319	29119	34205	28625	15891	32626	Moderate	Enriched	Enriched	No expres	YES	
Q8TBB5-3;Q8TBB	Kelch domain-contai	KLHDC4	54.495	7	3	3	4.492	0.00042	3867.4	2413.8	4857.4	2303	4650.8	1759	5254	3908.6	3282.2	4672.9	Moderate	Enriched	Moderate	No expression		
Q8TBC4;F8W8D4;	NEDD8-activating en	UBA3	51.852	9.3	4	4	13.631	0	11872	6010.1	7352.2	10202	8076.1	8971.1	10748	11086	4513.3	9915.1	Enriched	Enriched	Enriched	Moderate	YES	
Q8TBQ9	Protein kish-A	TMEM167A	8.0598	12.5	2	2	2.7403	0.00239	3903.4	3917.4	3963.6	3818	4601	3777.5	17278	13990	6106.9	10150	Moderate	Enriched	Enriched	No expres	YES	
Q8TBX8-3;Q8TBX	Phosphatidylinositol	PIP4K2C	45.053	10.4	7	7	16.545	0	18591	15310	13385	20007	22371	19190	17352	15810	9055.2	15567	Enriched	Enriched	Enriched	No expres	YES	
Q8TC07-2;Q8TC07	TBC1 domain family	TBC1D15	77.394	19.7	14	12	97.503	0	71459	57073	68392	94007	65375	108720	124820	109990	61401	89679	Enriched	Enriched	Enriched	No expres	YES	
Q8TC12;Q8TC12-3	Retinol dehydrogena	RDH11	35.386	18.2	10	7	97.986	0	29699	19104	21079	27196	22889	38926	28079	36600	11873	28413	Enriched	Enriched	Enriched	Enriched	YES	
Q8TCD5;J3KRC4;(	5(3)-deoxyribonuclec	NT5C	23.382	48.8	11	11	40.083	0	32522	19602	29743	39039	32405	24922	21982	34824	12003	33443	No expres	No expres	Moderate	No expres	YES	
Q8TCJ2	Dolichyl-diphosphoo	STT3B	93.673	14.6	14	13	49.396	0	66972	43309	48040	72199	50564	101360	94025	62227	41911	81235	Moderate	Enriched	Enriched	No expres	YES	
Q8TCS8	Polyribonucleotide n	PNPT1	85.95	21.8	20	20	55.243	0	108670	81324	90588	112130	108270	111450	117820	122800	63124	119990	Moderate	Enriched	Enriched	No expres	YES	
Q8TD16;Q8TD16-2	Protein bicaudal D hc	BICD2	93.532	4	3	3	5.1993	0.00022	944.52	1390.1	1925.4	1335.5	9936.3	1643.6	3914.5	3027.6	3128.1	2771.1	No expres	Moderate	Enriched	Enriched	YES	
Q8TD19	Serine/threonine-prot	NEK9	107.17	12	10	10	40.782	0	38454	33200	34676	35220	39980	35573	38275	40352	23821	38504	Enriched	Enriched	Enriched	Enriched	YES	
Q8TD30;Q8TD30-2	Alanine aminotransfe	GPT2	57.903	16.3	8	7	24.655	0	16489	14212	14028	19471	20879	24649	15032	11546	9713.2	17417	Low	Enriched	Enriched	No expres	YES	
Q8TD55-2;Q8TD55	Pleckstrin homology	PLEKHO2	47.785	4.8	1	1	7.8607	0	10708	6169.6	6408	13883	9460.9	8584.6	9137.5	10504	6436.8	10716	Enriched	Moderate	Moderate	Low	YES	
Q8TDB6	E3 ubiquitin-protein	DTX3L	83.553	6.9	7	7	29.681	0	17590	9114.5	11958	24962	13244	17859	21962	29394	19194	26705	Enriched	Enriched	Enriched	No expres	YES	
Q8TDD1-2;Q8TDD	ATP-dependent RNA	DDX54	98.665	4.5	4	4	7.9854	0	23046	21604	23162	18233	27026	19022	20885	24966	9879.7	23317	Enriched	Enriched	Moderate	No expres	YES	
Q8TDH9;A0A0A0I	Biogenesis of lysoson	BLOC1S5;BLOC1S5-T	21.609	12.3	2	2	4.3341	0.00063	3422.6	2386.9	2488.6	2260.6	4018.3	2624.7	2405.3	2421.6	1242.5	2933.1					YES	
Q8TDI0;K7EMY3	Chromodomain-helic	CHD5	223.05	4.8	9	0	2.1768	0.0056	2572.3	1460.6	2173.6	1922.3	1662.7	2134.4	2080.6	2323.4	706.89	2138.2	Enriched	No expres	Low	Low		
Q8TDN6	Ribosome biogenesis	BRIX1	41.401	14.7	6	6	12.911	0	10952	12844	16420	7911.5	19440	12581	28553	21323	11533	13568					YES	
Q8TDW0	Volume-regulated an	LRRC8C	92.448	2.1	1	1	3.0368	0.00132	1836.4	1136.6	2023.2	3117.7	2057.8	2191.7	2079	2372.8	1736.2	2672.1	No expres	Moderate	Moderate	No expression		
Q8TDX7;Q5TBH0;	Serine/threonine-prot	NEK7;NEK6	34.551	6.6	2	1	2.5744	0.00344	10911	9779.7	10750	10936	13524	9083.4	10074	11214	6448.2	10501	Moderate	Enriched	Enriched	Low	YES	
Q8TDY2-2;Q8TDY	RB1-inducible coiled	RB1CC1	182.85	1.3	3	3	4.8456	0.00043	32246	23372	23439	34409	23910	86074	45410	34682	14677	34099	Moderate	Enriched	Enriched	Low		
Q8TE77;Q8TE77-3	Protein phosphatase S	SSH3	72.995	12.1	9	9	20.14	0	6127.8	6236.7	7409.8	7205.2	7864.9	6091.4	6038.7	7134.9	4577	6898.4	Enriched	Enriched	Moderate	No expres	YES	
Q8TEA8	D-tyrosyl-tRNA(Tyr)	DTD1	23.423	7.7	2	2	98.061	0	8775.5	7105.7	7490.8	5094.7	11775	7646.8	9762.7	6484.9	7780.1	8458.3	Enriched	Enriched	Enriched	No expres	YES	
Q8TEB1;H0YL64;I	DDB1- and CUL4-as	DCAF11	61.669	15	8	8	17.872	0	17547	14743	16401	10775	18385	16269	16408	19002	12092	17873					YES	
Q8TEM1;Q8TEM1	Nuclear pore membra	NUP210	205.11	8.1	15	15	22.986	0	47732	33125	39960	38004	41494	46731	61244	56793	36513	54562	Low	Moderate	Moderate	Enriched	YES	
Q8TEQ8;Q8TEQ8-	GPI ethanolamine ph	PIGO	118.7	6.7	8	8	17.106	0	24405	24088	25394	24415	25379	24730	52279	41540	21107	26330	Enriched	Moderate	Enriched	No expres	YES	
Q8TEV9-2;Q8TEV	Smith-Magenis syndr	SMCR8	87.754	1.4	1	1	3.2357	0.00077	7665.7	5304.7	6679	7714.6	4825.4	8404.2	7184.9	7759.8	3644.7	7820.5	No expres	No expres	Low	No expression		
Q8TEX9;Q8TEX9-	Importin-4	IPO4	118.71	13.4	15	15	38.489	0	70651	55414	54760	50373	63401	51939	61943	63993	35720	55843	Low	Enriched	Enriched	No expres	YES	
Q8TF01;Q8TF01-2	Arginine/serine-rich p	PNISR	92.576	3.5	2	2	18.342	0	10478	11406	13496	11567	11425	7065.3	12859	10589	9607.2	10715						
Q8TF46-3;Q8TF46	DIS3-like exonucleas	DIS3L	86.259	3.2	2	2	2.7162	0.00238	13536	7796.1	14520	13336	11406	22152	15139	6780.1	3382.7	15404	Low	Enriched	Enriched	No expression		
Q8TF65	PDZ domain-containi	GIPC2	34.354	39	21	21	112.39	0	227180	104630	156930	243500	163230	226670	176860	203970	94194	210760	Moderate	Enriched	Moderate	No expres	YES	
Q8TF71;A0A087X	Monocarboxylate tra	SLC16A10	55.492	7.6	5	5	17.637	0	31352	22588	29012	23360	34047	56517	47728	25521	15757	29086	Low	Low	Moderate	No expres	YES	
Q8TF74	WAS/WASL-interact	WIPF2	46.288	21.8	7	7	50.47	0	37218	30247	33198	28959	48748	24732	33949	26774	21112	31086	Enriched	Enriched	Enriched	Moderate	YES	
Q8WTT2	Nucleolar complex p	NOC3L	92.547	2.8	4	4	12.873	0	15172	13422	14974	18215	15632	8678.4	8905.5	11442	4979.9	13131	Moderate	Moderate	Enriched	No expres	YES	
Q8WTW3;A0A087	Conserved oligomeric	COG1;ADCK1	108.98	10.7	9	9	42.238	0	40657	39767	43675	31961	56514	30795	53560	26506	26490	31952	Low	Enriched	Enriched	No expres	YES	
Q8WU76-2;Q8WU	Sec1 family domain-c	SCFD2	69.991	11.6	9	9	57.806	0	27891	18277	21007	31222	24649	30242	22932	24246	13540	27263	Enriched	Enriched	Enriched	No expres	YES	
Q8WU90	Zinc finger CCCH do	ZC3H15	48.602	11	7	4	11.491	0	16762	11042	15004	16423	18511	15434	11429	11200	4279.9	14361	Enriched	Moderate	Enriched	Enriched	YES	
Q8WUA2	Peptidyl-prolyl cis-tr	PPIL4	57.224	15.9	8	8	32.692	0	75029	61168	59589	67584	72417	55631	58427	85216	30057	75136	No expres	Low	Moderate	No expres	YES	
Q8WUF5	RelA-associated inhil	PPP1R13L	89.09	5.7	3	3	124.99	0	12590	10845	9923.9	10091	12678	8011	12232	12548	5941.3	12704	Enriched	Enriched	Moderate	No expres	YES	
Q8WUF8-2;Q8WU	Protein FAM172A	FAM172A	34.29	7.5	2	2	6.3851	0	3954.3	1266.5	2213.6	8456.2	1268.1	6186.7	2461.3	9678.9	1008.8	6583.2	Moderate	Enriched	Enriched	Enriched	YES	
Q8WUH2	Transforming growth	TGFBRAP1	97.157	2	2	2	5.0507	0.00044	17460	10865	16526	26930	15032	21746	19454	24840	11400	21655	Low	Enriched	Enriched	No expres	YES	
Q8WUH6	Transmembrane prote	TMEM263	11.748	46.6	5	5	12.807	0	10339	9726.2	11787	8986.9	16603	8602.4	11210	11453	4939.9	10070					YES	
Q8WUM0	Nuclear pore comple	NUP133	128.98	7.5	8	8	16.879	0	45012	35803	37910	37575	40345	35159	35420	42480	23671	40081	Moderate	Enriched	Enriched	Moderate	YES	
Q8WUM4;Q8WUM	Programmed cell dea	PDCD6IP	96.022	34	49	43	225.8	0	242160	165520	174500	242580	215840	206920	285630	286930	176350	254390	Enriched	Enriched	Enriched	No expres	YES	
Q8WUN7	Ubiquitin domain-co	UBTD2	26.189	5.6	1	1	3.5434	0.00079	5820.1	4910.1	5510.4	5398.7	6543.3	6382.4	7186.7	6833.8	6019.3	7396.1	Moderate	Enriched	Enriched	No expression		
Q8WUX1;C9JJU1;(	Sodium-coupled neu	SLC38A5	51.457	7.8	3	3	5.4458	0	9720.3	6990.1	7167.3	3902.6	10268	4877.3	5326.5	3196.1	2030.8	9313.9	Moderate	Enriched	Enriched	No expres	YES	YES
Q8WUX9	Charged multivesicul	CHMP7	50.91	9.1	3	3	24.35	0	22226	21791	27151	14004	27255	18687	51273	23807	19219	27047	Moderate	Enriched	Enriched	Moderate	YES	
Q8WUY1	Protein THEM6	THEM6	23.865	21.6	8	8	17.099	0	41653	21506	20956	54119	25132	37902	36725	63855	20740	50011					YES	
Q8WV41	Sorting nexin-33	SNX33	65.264	6.6	3	3	6.0114	0	4400.6	3715.1	4869	4637.4	5749.4	9112.3	5092.1	4527.3	2158.7	4052.1	Enriched	Enriched	Moderate	No expres	YES	
Q8WVJ2;E5RFP0	NudC domain-contai	NUDCD2	17.676	27.4	5	5	13.527	0	12828	8671.1	10932	14330	11774	12410	9140.9	9775.6	6322	11708	Low	Enriched	Enriched	No expres	YES	
Q8WVM7-2;Q8W	Cohesin subunit SA-	STAG1;DKFZp781D141	140.09	5.6	8	6	12.811	0	29390	24408	30996	29388	28679	32418	44626	55305	25018	42687	Low	Low	Low	No expres	YES	
Q8WVM8;Q8WVM	Sec1 family domain-c	SCFD1	72.379	43.5	42	38	323.31	0	217050	159930	184780	182900	246140	218880	211540	190550	107920	188320	Moderate	Enriched	Enriched	Enriched	YES	
Q8WVV4;Q8WVV	Protein POF1B	POF1B	68.064	16.3	7	7	36.319	0	10938	6876.4	8215.4	12531	8069.7	16187	16947	15187	12371	16100	Moderate	No expres	Moderate	No expres	YES	
Q8WVY7	Ubiquitin-like domai	UBLCP1	36.804	18.6	8	8	22.392	0	44131	30911	32914	41869	36811	48507	68329	63110	39071	52533	Moderate	Enriched	Enriched	No expres	YES	
Q8WW12;Q8WW1	PEST proteolytic sig	PCNP	18.925	42.7	10	10	102.15	0	102260	94518	103380	85953	139090	62352	131740	130200	74775	102970	Enriched	Enriched	Enriched	No expres	YES	
Q8WW59	SPRY domain-contai	SPRYD4	23.128	15	4	4	11.468	0	14406	13569	15283	6603.1	17047	9039.7	10719	14911	4381.2	16790	Enriched	Enriched	Enriched	No expres	YES	
Q8WWC4	Uncharacterized prot	C2orf47	32.544	7.6	2	2	6.731	0	14677	13028	12006	11559	16824	10637	8765	8050.1	3954.1	12157	Enriched	Enriched	Enriched	No expres	YES	
Q8WWI5;Q8WWI5	Choline transporter-l	SLC44A1	73.301	9.3	5	5	28.237	0	32476	22353	32931	19052	42232	26109	35690	24062	15972	24788	Enriched	Enriched	Enriched	No expres	YES	
Q8WWM9;K7EMC	Cytoglobin	CYGB	21.404	23.2	4	4	12.439	0	4938.5	5671.6	6782.8	5363.1	8496.1	5037.1	8638.6	6217.8	4151	7851.7	Low	Enriched	Moderate	No expres	YES	
Q8WWQ0	PH-interacting protei	PHIP	206.69	1.6	2	2	7.0104	0	7890.2	7918.3	9520.1	7173.8	11506	5078.6	7350.7	6335.7	5134.6	7442.7	Enriched	Enriched	Enriched	Enriched	YES	
Q8WX92	Negative elongation f	NELFB	65.697	7.9	4	4	7.1704	0	2246.3	1511	2401.1	3466	2370.1	4759	4052.1	3487.6	3302.4	3305.3					YES	
Q8WX93-4;Q8WX	Palladin	PALLD	73.321	7.6	5	5	8.6155	0	10405	10654	11685	9075.5	17396	10305	13000	7903.8	8800	10292	Moderate	Enriched	Enriched	Enriched	YES	
Q8WXA9-2;Q8WX	Splicing regulatory gl	SREK1	71.649	9.9	6	6	21.102	0	29704	24071	24246	31934	29048	29548	23069	23451	12995	31588					YES	
Q8WXC6	Myeloma-overexpres	MYEOV2	6.2107	35.1	2	2	10.088	0	25716	16433	21380	25295	22910	34662	24482	37677	12954	26035	Enriched	Enriched	Enriched	No expression		
Q8WXC6-1	Myeloma-overexpres	MYEOV2	27.664	3.6	1	1	2.1201	0.00626	16920	12733	9072.5	9349.4	13318	25509	25849	16408	9983.1	27412	Enriched	Enriched	Enriched	No expression		
Q8WXD2;Q8WXD	Secretogranin-3	SCG3	53.005	14.5	8	8	37.453	0	62594	73427	127030	53907	89228	37014	43948	28460	55439	44561	No expres	No expres	Enriched	No expres	YES	
Q8WXD5	Gem-associated prote	GEMIN6	18.824	6	1	1	2.5725	0.00344	7131.3	6898	8377.1	5841.5	7180	7582.3	9895.3	10022	7136.6	9625.2	Low	Moderate	Moderate	No expression		
Q8WXE0-2;Q8WX	Caskin-2	CASKIN2	118.16	4.4	3	3	9.8529	0	13959	8633.9	9865.7	12291	13883	9571.8	10878	11842	7770	13226	Moderate	Low	Moderate	No expres	YES	
Q8WXF1-2;Q8WX	Paraspeckle compone	PSPC1	45.57	20.4	11	10	53.458	0	77918	48629	65072	91484	71752	89009	116620	138880	56052	93641	Enriched	Enriched	Enriched	No expres	YES	
Q8WXF7-2;Q8WX	Atlastin-1	ATL1	63.054	8	5	3	7.3791	0	17622	13154	17384	20622	16127	15693	19056	20023	11810	19285	Enriched	Enriched	Enriched	No expres	YES	
Q8WXG6-8;Q8WX	MAP kinase-activatin	MADD	171	4	6	6	11.213	0	14570	90306	12953	18351	36525	8670.3	8101	7430.2	4815.5	8038.6	Enriched	Moderate	Enriched	Enriched	YES	
Q8WXH0;Q8WXH	Nesprin-2	SYNE2	796.43	6.4	37	36	323.31	0	115230	78666	101650	126060	100630	109490	125450	168660	72438	152710	Moderate	Enriched	Enriched	Moderate	YES	
Q8WXI9	Transcriptional repre	GATAD2B	65.26	9.9	5	4	12.816	0	27394	27608	33557	18439	42472	21694	32217	22193	22856	27727	Moderate	Moderate	Enriched	No expres	YES	
Q8WXQ8;H7C4Q6	Carboxypeptidase A5	CPA5	49.035	6.2	5	2	3.8866	0.00061	28113	27142	26532	35777	30176	21087	20998	17907	18174	19222	Moderate	Low	Moderate	No expression		
Q8WXX5	DnaJ homolog subfar	DNAJC9	29.909	21.2	7	7	25.045	0	12609	11926	14358	18080	11638	13853	32616	46618	15766	22466	Enriched	Enriched	Enriched	Moderate	YES	
Q8WY22	BRI3-binding protein	BRI3BP	27.835	13.9	3	3	13.718	0	9181.1	5080.9	5772.5	8722.5	9866.6	5139.1	6687.5	8221.8	4473.8	6289.4	Enriched	Enriched	Enriched	No expres	YES	
Q8WYP5;Q8WYP5	Protein ELYS	AHCTF1	252.5	5.6	11	11	33.075	0	57323	40550	51121	44447	65672	47061	50145	53004	25669	53969	No expres	Moderate	Moderate	Low	YES	
Q8WYQ5-3;Q8WY	Microprocessor comp	DGCR8	82.75	1.2	1	1	2.1104	0.00659	6049.2	5077.1	6845.8	7282.6	7532.6	5554.2	7847.6	6046.1	5824.2	6621.5	Enriched	Enriched	Moderate	No expression		
Q8WZ82	Ovarian cancer-assoc	OVCA2	24.418	5.7	1	1	9.1062	0	11220	5774.6	10338	9334.7	15563	9424	11766	6227.1	7971.6	11095					YES	
Q8WZA0;Q8WZA(	Protein LZIC	LZIC	21.494	37.4	8	8	95.478	0	65433	31277	40880	90872	38170	68647	47153	56102	29400	94396	No expres	Moderate	Enriched	No expres	YES	
Q8WZA9	Immunity-related GT	IRGQ	62.717	9.8	7	7	16.525	0	22528	21957	23870	22111	31657	19766	29730	24997	18227	25741	No expres	No expres	Low	No expres	YES	
Q92499;F1T0B3;A	ATP-dependent RNA	DDX1	82.431	50.3	65	65	309.24	0	419230	301870	353910	393910	463000	375440	368610	388140	193190	360110	Moderate	Enriched	Enriched	Enriched	YES	
Q92506	Estradiol 17-beta-del	HSD17B8	26.973	24.9	5	5	13.028	0	18201	17982	17236	15376	19004	25297	38578	43739	14077	24120	Enriched	Enriched	Enriched	Enriched	YES	
Q92520;C9JMN4;(	Protein FAM3C	FAM3C	24.68	55.5	20	20	84.695	0	106930	71144	72994	135610	100040	131730	145190	152430	69432	137630	Moderate	Enriched	Enriched	Moderate	YES	
Q92522	Histone H1x	H1FX	22.487	32.4	18	18	67.804	0	64539	56185	76372	54786	85918	65540	107030	118990	67881	73586	No expres	Enriched	Enriched	Enriched	YES	
Q92538	Golgi-specific brefeld	GBF1	206.44	10.9	21	21	104.11	0	87329	62512	66782	64004	77985	72213	58162	66902	32087	65576	Enriched	Moderate	Enriched	Enriched	YES	
Q92541	RNA polymerase-ass	RTF1	80.313	2.8	2	2	2.3838	0.00429	1479	1562.3	1289.9	1839.1	1851.1	1156.3	1341.3	1103.4	1055.9	1510.1	Moderate	Moderate	Enriched	Low	YES	
Q92544	Transmembrane 9 su	TM9SF4	74.518	10	6	6	34.043	0	25104	14278	20492	28560	26456	30847	25204	21527	11678	27745	Enriched	Enriched	Enriched	Low	YES	
Q92556;Q92556-2;	Engulfment and cell	ELMO1	83.829	6.1	4	4	37.232	0	6936	7228.9	8775.1	6925.5	9212.6	10345	8206.8	6783.4	3240.5	6531.2	Moderate	Low	Enriched	No expres	YES	
Q92562	Polyphosphoinositide	FIG4	103.63	1.3	1	1	5.1979	0.00022	7102.9	4671.2	3476	7246.9	4248	2972.9	5142.7	4476.6	2968.8	6254.2	Enriched	Moderate	Enriched	Enriched	YES	
Q92572	AP-3 complex subun	AP3S1	21.732	31.1	8	8	25.975	0	54334	41754	48905	57357	58016	44130	49305	38343	31933	49122	Enriched	Enriched	Enriched	Enriched	YES	
Q92575	UBX domain-contain	UBXN4	56.777	18.1	12	12	48.611	0	62407	41673	53518	59728	53671	69715	86920	97688	42988	67057	Enriched	Moderate	Enriched	Enriched	YES	
Q92597;Q92597-3;	Protein NDRG1	NDRG1	42.835	36.5	17	12	196.21	0	132000	80179	97458	75690	119270	91622	102120	82697	66156	84736	Enriched	Enriched	Enriched	Enriched	YES	
Q92598-2;Q92598-	Heat shock protein 1(	HSPH1	92.115	31.3	28	21	123.74	0	97382	79432	70700	81370	82378	83946	101080	142370	53922	106090	Enriched	Enriched	Enriched	Low	YES	
Q92614-3;Q92614-	Unconventional myo	MYO18A	226.69	12.5	24	24	170.68	0	108630	90085	103400	100560	113170	113210	114550	116800	65159	123370	No expres	No expres	Low	Low	YES	
Q92615	La-related protein 4E	LARP4B	80.551	7.2	4	4	89.002	0	54683	44639	45499	47001	59104	36778	43689	38461	27593	42500	Enriched	Moderate	Enriched	Enriched	YES	

Q92616	Translational activatc	GCN1L1	292.75	30	103	103	323.31	0	456800	314570	399580	457160	441360	482590	462670	485950	236040	474800	Enriched	Enriched	Enriched	Enriched	YES	
Q92621	Nuclear pore comple:	NUP205	227.92	8.7	18	18	59.626	0	39555	30265	37138	45018	40078	35311	33653	43003	18504	45137	Low	Moderate	Enriched	Moderate	YES	
Q92625	Ankyrin repeat and S	ANKS1A	123.11	3.4	3	3	11.183	0	12643	14721	20070	6707.5	24255	11210	15794	8541.2	10772	12282	Moderate	Moderate	Enriched	Enriched	YES	
Q92626;H7C1W1;(	Peroxidasin homolog	PXDN	165.27	2.8	3	3	7.6576	0	18096	12950	16645	15043	20777	11665	12461	9776.5	10109	20893	Enriched	Moderate	Enriched	Moderate	YES	
Q92629;Q92629-2;	Delta-sarcoglycan	SGCD	32.071	16.3	4	4	10.694	0	16987	15178	16566	17694	18817	13089	19366	20733	12321	18153	Enriched	Moderate	Moderate	No expres	YES	
Q92665	28S ribosomal protei	MRPS31	45.318	10.4	4	4	30.184	0	28307	23029	26380	29497	33923	23584	21064	29243	11480	28643	Enriched	Moderate	Enriched	Low	YES	
Q92673	Sortilin-related recep	SORL1	248.42	1.4	3	3	3.9596	0.00061	5689.4	6347.2	7817	5088.6	8517.5	5012	8021.1	7070.7	6099.9	7181.5	Enriched	Enriched	Enriched	Enriched	YES	
Q92688;Q92688-2;	Acidic leucine-rich n	ANP32B	28.787	29.5	15	8	34.176	0	77309	108880	73039	61195	80199	49691	48402	60640	27685	69112	Enriched	Enriched	Enriched	Enriched	YES	
Q92692-2;K7EKE8	Nectin-2	PVRL2	51.359	6.1	2	2	16.344	0	6627.8	5116.7	7709.4	6321.5	10452	3181.8	6651.1	5849	3219.5	6806.3	Enriched	Enriched	Enriched	Enriched	YES	
Q92734-2;Q92734;	Protein TFG	TFG	43.02	33.8	32	32	323.31	0	180860	118080	150390	142220	144160	256460	256980	218920	92875	214690	Enriched	Enriched	Enriched	No expres	YES	
Q92747;E9PF58;Q	Actin-related protein	ARPC1A	41.569	18.9	10	10	30.486	0	36972	19009	27736	29382	37775	24910	24339	22203	10450	25587	Low	Enriched	Enriched	Moderate	YES	
Q92766;Q92766-2;	Ras-responsive eleme	RREB1	181.42	3.3	5	4	22.065	0	9613.4	5241.5	7082.6	15532	5802.8	13417	8675.9	13857	6894.2	10937	Enriched	Enriched	Enriched	Moderate		
Q92769-3;Q92769;	Histone deacetylase 2	HDAC2;HDAC1	51.998	17.2	8	3	19.188	0	23923	15864	14967	21241	12354	20096	19451	22109	7853.7	19875	Enriched	Enriched	Enriched	Enriched		
Q92783-2;Q92783	Signal transducing ad	STAM	44.971	20.3	6	2	11.141	0	26263	16130	20384	23881	22296	35482	28754	25965	11854	31471	Low	Moderate	Enriched	Enriched	YES	
Q92797;A0A087W	Symplekin	SYMPK	141.15	4.8	5	5	17.996	0	21685	15074	19164	15346	12772	24993	31682	37839	20479	30372	Low	No expres	Moderate	No expres	YES	
Q92804-2;Q92804;	TATA-binding protei	TAF15	61.557	19.5	14	9	20.721	0	49127	31819	43597	63596	34059	53216	66654	50989	43253	64359	Moderate	Enriched	Enriched	Enriched	YES	
Q92851-7;Q92851-	Caspase-10;Caspase-	CASP10	28.363	5.3	1	1	3.9462	0.00061	5362.2	2882.9	3937.2	5669.3	4085	5344.3	4337	4205.8	4428.8	3512.6	Moderate	Low	Moderate	Moderate	YES	
Q92871	Phosphomannomutas	PMM1	29.746	6.9	2	2	3.1053	0.00095	10964	7694.6	11460	4879.7	6320.5	10599	4904.1	5621.7	2655.8	10713	Enriched	Moderate	Enriched	Enriched	YES	
Q92878;Q92878-2;	DNA repair protein R	RAD50	153.89	20.5	36	36	113.17	0	155280	82354	120720	155270	110820	161210	216770	217680	106790	192740	Enriched	Enriched	Moderate	Low	YES	
Q92882	Osteoclast-stimulatin	OSTF1	23.787	10.3	3	3	3.1982	0.00077	5765.6	3375.6	5529.1	15852	6155.7	4735.7	3324.5	3695.6	2673.6	5238.8	Moderate	Moderate	Moderate	No expres	YES	
Q92889	DNA repair endonucl	ERCC4	104.48	3.1	3	3	5.8724	0	1048.4	2099.2	1505.5	1228.3	2514	926.13	1853.2	1531.9	1108	1290.8	No expres	Low	Moderate	Low		
Q92890-3;Q92890;	Ubiquitin fusion degr	UFD1L	29.901	27.8	7	7	168.19	0	24880	19241	19520	22243	24238	18389	34090	22340	19280	26066	Low	Enriched	Enriched	Moderate	YES	
Q92896;Q92896-2;	Golgi apparatus prote	GLG1	134.55	24.7	35	35	103.09	0	147370	98868	117550	202440	116930	142730	145580	164410	81197	177600	Enriched	Enriched	Enriched	Enriched	YES	
Q92900-2;Q92900	Regulator of nonsens	UPF1	123.03	32.7	49	49	203.48	0	179510	138910	141460	163920	185960	144250	158110	168050	97650	167720	Enriched	Enriched	Enriched	Enriched	YES	
Q92905	COP9 signalosome cc	COPS5	37.578	19.8	8	8	24.937	0	38683	38728	40206	24113	50154	41433	42155	23733	21335	37844	Enriched	Enriched	Enriched	Enriched	YES	
Q92917	G patch domain and I	GPKOW	52.228	13.9	5	5	27.451	0	57282	41811	34974	77244	38526	40405	56012	76399	42769	78348	Enriched	Moderate	Enriched	Moderate	YES	
Q92922	SWI/SNF complex su	SMARCC1	122.87	8.3	9	5	11.149	0	18165	12372	13696	17199	16278	15497	24847	23638	16917	22334	Enriched	Enriched	Enriched	Enriched	YES	
Q92930;H0YNE9	Ras-related protein R	RAB8B	23.584	30.9	7	3	13.594	0	1314.6	1177.8	1153.1	614.76	1485.8	1810.5	3912.7	6057.3	3261.7	2667.2	Moderate	Enriched	Enriched	No expres	YES	
Q92947-2;Q92947	Glutaryl-CoA dehydr	GCDH	47.355	22.9	11	11	112.39	0	57689	48865	46472	51234	50641	57710	64706	75098	32719	63716	Moderate	Moderate	Moderate	Moderate	YES	
Q92973-2;Q92973;	Transportin-1	TNPO1	101.31	16.5	15	11	136.25	0	78450	45637	51379	48674	73622	57300	41126	51250	30749	64836	Enriched	Enriched	Enriched	Moderate	YES	
V9GYM8;Q92974-	Rho guanine nucleoti	ARHGEF2	116.07	4.1	3	3	10.085	0	11415	8927.2	10013	12236	8194.2	9226.7	9012.4	12563	5767.9	12577	Enriched	Enriched	Enriched	Enriched	YES	
Q92990;Q92990-2;	Glomulin	GLMN	68.207	5.6	4	4	6.6755	0	27015	4627.8	8334.1	17921	7042.9	18733	8450.1	11456	3993.3	17813	No expres	Low	Moderate	Moderate	YES	
Q93008-1;Q93008	Probable ubiquitin ca	USP9X	290.46	9.6	30	30	80.467	0	116970	78219	85822	123440	92674	119790	115620	128610	54697	114430	Enriched	Enriched	Enriched	Enriched	YES	
Q93009-3;Q93009;	Ubiquitin carboxyl-te	USP7	126.27	23.1	38	38	148.92	0	138620	94006	105590	149300	121490	128240	118350	144360	61483	133960	Enriched	Enriched	Enriched	Enriched	YES	
Q93015;Q93015-2	N-acetyltransferase 6	NAT6	31.445	4.2	1	1	3.3421	0.00078	7312.2	9452.7	8364.5	6945.6	14457	5575	9375.8	5535.7	7570.8	7571.9	Moderate	Low	Low	Low		
Q93034	Cullin-5	CUL5	90.954	15	12	12	32.811	0	31787	19991	27255	45923	29202	30040	25008	35550	15874	36900	Moderate	Enriched	Enriched	No expres	YES	
Q93050-1;Q93050;	V-type proton ATPas	ATP6V0A1	95.755	10	8	8	64.872	0	24344	19003	21662	26763	21769	23311	27052	26463	14915	25815	Enriched	Enriched	Enriched	Moderate	YES	
Q93052;A0A087W	Lipoma-preferred par	LPP	65.746	23.7	12	12	39.716	0	50624	43838	45028	41492	58875	42489	61738	52857	28848	54701	Enriched	Enriched	Enriched	No expres	YES	
Q93084-4;Q93084-	Sarcoplasmic/endopl	ATP2A3	109.13	18.6	23	13	42.679	0	54654	36205	51496	50224	41682	52998	47774	50434	27084	48374	Moderate	Moderate	Enriched	Enriched	YES	
Q93099	Homogentisate 1,2-di	HGD	49.963	24.7	10	10	51.288	0	44076	39943	46713	58327	57393	77699	61443	63489	24844	52080	Moderate	Moderate	Moderate	Moderate	YES	
Q93100-4;Q93100-	Phosphorylase b kina	PHKB	123.82	10.1	9	9	59.633	0	24352	20894	23615	20896	25322	22388	22161	22180	12249	20474	Moderate	Enriched	Enriched	Enriched	YES	
Q969E4;Q5H9L2;(	Transcription elongat	TCEAL3;TCEAL5;TCE	22.502	27.5	8	8	104.99	0	33043	24835	41762	34619	37071	39788	64548	50252	45155	58069	Enriched	Enriched	Enriched	No expression		
Q969E8	Pre-rRNA-processing	TSR2	20.894	6.3	1	1	1.945	0.00798	8327.7	5198.3	7194.1	7966.5	6919.9	7025.1	4349.2	5079	1900.9	6744.6	Enriched	Moderate	Enriched	Moderate		
Q969G6	Riboflavin kinase	RFK	17.623	12.3	1	1	3.5346	0.00079	4925.2	4603.1	3363.5	7246.2	3859.2	4616.3	4677.7	4879.3	2055	6502.5	Enriched	Enriched	Enriched	Moderate		
Q969H8;M0QYN0	UPF0556 protein C19	C19orf10	18.795	29.5	10	6	32.589	0	94436	76726	52064	93516	65545	99682	78872	70634	54803	79308	Enriched	Enriched	Enriched	Enriched	YES	
Q969N2-4;Q969N2	GPI transamidase cor	PIGT	54.118	12	5	5	7.5852	0	8975.8	9359.4	9097.2	8915.4	10094	10049	6356.2	5945.4	3551.8	7749.3	Enriched	Enriched	Enriched	No expres	YES	
Q969P0-3;Q969P0;	Immunoglobulin supe	IGSF8	55.807	4.9	3	3	2.6156	0.00273	1820.6	932.69	769.04	1400.1	1256.9	1878.7	1140.4	1842.1	424.11	2091.5	Moderate	Enriched	Moderate	No expres	YES	
Q969S3	Zinc finger protein 62	ZNF622	54.271	25.4	18	18	44.708	0	60936	59013	63114	58552	93253	84961	75629	66311	29032	59161	Enriched	Enriched	Enriched	No expres	YES	
Q969S9-2;Q969S9-	Ribosome-releasing f	GFM2	81.199	1.6	2	2	4.8729	0.00043	1944.2	879.17	2168.9	3496	1378.8	2790.5	1602	3270.2	596.91	3160.4	Moderate	Enriched	Enriched	No expres	YES	
Q969V3-2;Q969V3	Nicalin	NCLN	62.846	29.2	28	28	142.94	0	84177	58955	69779	88198	72872	74536	74820	66061	35660	76746	No expres	Moderate	Moderate	Enriched	YES	
Q969X5-2;Q969X5	Endoplasmic reticulu	ERGIC1	22.16	46.5	12	12	110.15	0	41301	37237	38621	52611	48928	38625	52989	73850	27427	43876	Enriched	Enriched	Enriched	No expres	YES	
Q969Y2-3;Q969Y2	tRNA modification G	GTPBP3	49.846	8.3	5	5	28.824	0	8468.1	5134.7	7114.6	13809	6596.7	10970	9088.2	9910	5695.4	10860	Enriched	Enriched	Enriched	No expression		
Q969Z3	Mitochondrial amido	MARC2	38.023	20.6	10	4	42.3	0	57164	51247	68803	38458	65586	37337	47810	31019	32185	54847	Low	Moderate	Moderate	No expres	YES	
Q96A00;K7EJB8;K	Protein phosphatase 1	PPP1R14A	16.693	33.3	6	6	13.025	0	20422	12812	15504	15133	15787	13698	19227	11480	16183	18419	No expres	Low	Low	No expres	YES	
Q96A33-2;Q96A33	Coiled-coil domain-c	CCDC47	55.317	37.1	27	27	185.18	0	212440	124360	151140	185400	203410	201710	184370	201170	75560	197850	Moderate	Enriched	Enriched	No expres	YES	
Q96A35	39S ribosomal protei	MRPL24	24.915	24.1	5	5	40.014	0	54055	37945	43423	58064	47135	51804	47688	57122	37068	76976	Moderate	Enriched	Enriched	No expres	YES	
Q96A49	Synapse-associated p	SYAP1	39.933	20.7	6	6	53.354	0	3631.7	1496.6	2187.9	5313.5	1970.5	4873.6	3472.1	4029.6	2773.6	2849.7	Moderate	Enriched	Enriched	No expres	YES	
Q96A57;Q96A57-2	Transmembrane prote	TMEM230	13.188	19.2	2	2	4.9326	0.00044	31368	26253	25985	29551	25105	23857	30761	27365	16741	29285					YES	
Q96A65;Q96A65-2	Exocyst complex con	EXOC4	110.5	16.5	14	14	56.472	0	91780	60485	72441	78825	79234	67495	50360	59413	29427	71042	Enriched	Enriched	Enriched	Low	YES	
Q96AB3;Q96AB3-	Isochorismatase dom	ISOC2	22.337	28.8	10	6	84.02	0	73702	52318	56292	75264	67512	54396	62026	70394	36251	73516	Moderate	Enriched	Enriched	No expres	YES	
Q96AE4;E9PEB5;(	Far upstream element	FUBP1	67.56	33.9	29	28	146.49	0	149160	120340	155610	142180	176230	140100	234360	231950	174300	201000	Moderate	Low	Enriched	Moderate	YES	
Q96AG3-3;Q96AG	Solute carrier family	SLC25A46	37.203	12.2	4	4	26.911	0	7083.3	5307.8	5566	9444.9	6455.5	9157.5	4830	7827.9	3282.9	7049.5	Low	Enriched	Enriched	Enriched		
Q96AG4	Leucine-rich repeat-c	LRRC59	34.93	56.4	48	48	323.31	0	289650	190420	235450	288910	256050	405310	408550	403030	218420	317750	Enriched	Enriched	Enriched	No expres	YES	
Q96AJ9-1;Q96AJ9	Vesicle transport thro	VTI1A	23.435	12.3	3	3	14.862	0	6456.5	6654.4	7143.9	5470	9151.6	6945.6	5431.9	5713.6	3515	6405.3	Enriched	Moderate	Moderate	No expres	YES	
Q96AP7;C9JIE7;F8	Endothelial cell-selec	ESAM	41.176	6.7	2	2	3.1846	0.00077	8508	4656.6	6500.8	12106	6835.4	8055	15380	9710	2537.3	9689.1	No expres	Moderate	Moderate	No expres	YES	
Q96AQ6-2;Q96AQ	Pre-B-cell leukemia t	PBXIP1	77.683	6.1	3	3	11.501	0	11040	9931.1	11673	10532	15174	7230.1	9902	12816	4869.5	11038	Enriched	Enriched	Enriched	Enriched	YES	
Q96AQ8;U3KQP8	Mitochondrial calciu	MCUR1	39.694	8.6	3	3	5.0237	0.00044	4312.3	4291.7	4448.7	4227.1	5145.3	3536.5	4864.1	5346.9	4481.3	4531.1					YES	
Q96AT1	Uncharacterized prot	KIAA1143	17.465	16.2	2	2	6.4484	0	8502.2	7571.2	12206	12197	12073	4383.2	8934.5	7390.2	8414.4	11031	Moderate	Enriched	Enriched	No expres	YES	
Q96AY3	Peptidyl-prolyl cis-tr	FKBP10	64.244	6.2	3	3	6.6659	0	10231	9052.7	12278	8433.6	10854	11274	10641	21892	6109.2	13810	No expres	Low	Low	No expres	YES	
Q96B36;Q96B36-3	Proline-rich AKT1 su	AKT1S1	27.383	14.1	3	3	8.234	0	23118	15077	15747	22077	24705	21325	19292	14557	10193	12531	Low	Moderate	Enriched	No expres	YES	
Q96B45	UPF0693 protein C1(	C10orf32	11.564	23.8	3	3	32.003	0	11940	8526.1	9844.6	9544.3	15773	7952	8356.3	7821.7	6910.9	9808.4	Moderate	Enriched	Enriched	No expres	YES	
Q96B49	Mitochondrial impor	TOMM6	8.0019	29.7	3	3	6.8939	0	3934.3	3229.9	5969.9	4850.8	3923.7	5770	5798.2	5153.4	3019.9	5592						
Q96BJ3-3;Q96BJ3	Axin interactor, dors	AIDA	25.913	19.6	3	3	13.533	0	7362.1	3475.6	3875.6	11632	3486.3	6176.5	5833.6	9634.7	6323.9	10977	No expres	Enriched	Enriched	No expres	YES	
Q96BM9	ADP-ribosylation fac	ARL8A	21.416	28	6	3	17.43	0	6603.9	5009.4	8515.3	4934.6	8277	5076.9	2947.3	4249.8	985.35	4336.3	Moderate	Moderate	Moderate	No expres	YES	
Q96BN8	Ubiquitin thioesteras	OTULIN	40.262	9.7	2	2	5.7216	0	7380	4847.8	5059.8	7878	6664.5	6518.8	4742.3	8325	2606.3	7554.2					YES	
Q96BS2;E9PQ58;(	Calcineurin B homol	TESC	24.75	23.8	5	5	17.047	0	35927	31259	35121	33627	39197	25259	28994	33360	21032	33931	Enriched	Enriched	Enriched	No expres	YES	
Q96BT7-3;Q96BT7	Alkylated DNA repai	ALKBH8	25.742	8.5	1	1	3.5892	0.00079	4709.6	1407.5	2245.5	2515.1	1701.2	3788.2	2880.7	2025.4	1300.7	4075.3	Low	Low	Moderate	No expression		
Q96BW5-2;Q96BW	Phosphotriesterase-re	PTER	33.435	47	19	19	94.947	0	81792	56275	68708	95180	72372	102450	121060	148710	63572	107000	Enriched	Enriched	Enriched	No expres	YES	
Q96BZ9;Q96BZ9-3	TBC1 domain family	TBC1D20	45.854	5.2	2	2	1.9412	0.00798	1288.9	1007.4	1954.6	986.8	1732.2	3581.4	4838.1	4448.4	2593.4	3086.1	Moderate	Enriched	Enriched	No expres	YES	
Q96C19;H0Y4Y4	EF-hand domain-con	EFHD2	26.697	47.5	22	20	144.4	0	171480	167650	132820	296080	196500	146260	216610	184820	106090	314430	Moderate	Moderate	Enriched	No expres	YES	
Q96C23;B8ZZ75	Aldose 1-epimerase	GALM	37.765	39.5	16	16	94.586	0	84977	69548	87948	65932	79749	68625	134220	104740	88605	89522	Enriched	Enriched	Enriched	No expres	YES	
Q96C45	Serine/threonine-prot	ULK4	142.44	1	1	1	1.9528	0.00799	14891	15889	12513	8280.2	13553	8396.4	5844	9828	3001.6	8520.6	No expres	No expres	Moderate	No expression		
Q96C86	m7GpppX diphospha	DCPS	38.608	29.1	13	13	72.746	0	37303	20502	26841	40927	31319	41610	29017	34633	16171	33093	Low	Moderate	Moderate	No expres	YES	
Q96C90	Protein phosphatase 1	PPP1R14B	15.911	38.1	7	7	21.657	0	54696	37358	40665	49004	60039	33839	32183	42116	18285	37054	Enriched	No expres	Low	No expression		
Q96CB9-3;Q96CB9	5-methylcytosine rRN	NSUN4	21.24	5.9	1	1	2.4449	0.00412	8189.6	7342.8	8546.4	7983.7	8527.2	6391.9	5134	4228.6	3177.3	6616.1	Moderate	Enriched	Enriched	No expres	YES	
Q96CF2	Charged multivesicul	CHMP4C	26.41	15.5	4	4	17.588	0	26468	16145	19713	27160	26866	23264	20928	24676	16256	22930	Enriched	Enriched	Enriched	No expression		
Q96CN7;D6RGE2	Isochorismatase dom	ISOC1	32.236	29.9	10	10	115.98	0	91132	51926	61322	77570	70850	149580	133990	127640	49374	83058	Low	Moderate	Enriched	No expres	YES	
Q96CS3	FAS-associated facto	FAF2	52.623	13	7	7	11.308	0	3019.6	2994.2	2952.6	1996.2	3892.5	4262.7	4497.1	3057.7	3736.8	2889.3	Enriched	Enriched	Enriched	Moderate	YES	
Q96CT7	Coiled-coil domain-c	CCDC124	25.835	40.4	11	11	40.734	0	23911	19949	22847	20994	25570	33554	42488	29439	27169	32623	Low	Moderate	Moderate	No expres	YES	
Q96CU9-3;Q96CU	FAD-dependent oxid	FOXRED1	52.104	7.8	3	3	7.7385	0	9200	6113.6	8565.2	11441	8489.1	7708.3	9504.6	10382	6133	11385	Moderate	Enriched	Moderate	No expres	YES	
Q96CX2	BTB/POZ domain-co	KCTD12	35.7	30.8	17	17	62.578	0	56764	46101	62423	61728	52999	44568	56925	66386	35490	67146	Low	Moderate	Enriched	Moderate	YES	
Q96D09	G-protein coupled re	GPRASP2	93.772	1.6	1	1	1.8512	0.0091	5004.6	2897.5	2759.9	6490.2	2933.3	4486.2	2860.5	4227.9	2874.7	4428.3	Moderate	Enriched	Enriched	No expres	YES	
Q96DA2	Ras-related protein R	RAB39B	24.622	7	1	1	3.755	0.0006	7356.5	2534.8	4472.8	5031	4439.8	6843	6088.7	6743	3046.5	6088.5	No expres	Low	Moderate	No expression		
Q96DC8;Q5W0J8;(	Enoyl-CoA hydratase	ECHDC3	32.633	35.3	11	11	44.336	0	53084	31698	37834	50942	43686	44994	65707	45043	49806	64374	No expres	Enriched	Enriched	No expres	YES	
Q96DE5;A0A087W	Anaphase-promoting	ANAPC16	11.667	23.6	2	2	2.7449	0.0024	9466.6	7335.1	11172	11351	11079	11448	15484	11542	7533.2	11487						
Q96DG6	Carboxymethylenebu	CMBL	28.048	31.8	8	8	28.347	0	57401	44784	42356	41477	71272	33580	39720	41065	15064	34429	Enriched	Enriched	Enriched	No expres	YES	
Q96DI7;Q96DI7-2;	U5 small nuclear ribc	SNRNP40;DKFZp434D	39.31	16.2	6	6	12.455	0	12908	10313	11628	7938.9	17997	11822	11815	10936	9403.2	12236	No expres	Moderate	Moderate	Low		
Q96DN0;F5GYS6	Endoplasmic reticulu	ERP27	30.48	22	19	19	323.31	0	447180	191990	269900	574840	296210	599860	606850	415600	326500	382430	Moderate	Enriched	Enriched	No expres	YES	YES
Q96DU7	Inositol-trisphosphate	ITPKC	75.207	2	1	1	2.3669	0.00428	4241.8	2472.9	2707.8	4540.5	2980.3	3781.1	4570.3	5168.1	1658.5	4037.2	Enriched	Enriched	Moderate	Moderate	YES	
Q96DV4	39S ribosomal protei	MRPL38	44.596	9.7	3	3	6.1006	0	5575.8	3985.3	4760.9	4882.2	5223.3	4144.1	5372.6	4238	3058.8	5113.4	No expres	Enriched	Enriched	No expres	YES	
Q96DZ1;Q96DZ1-3	Endoplasmic reticulu	ERLEC1	54.858	33.7	19	19	120.06	0	86596	71120	94961	65428	115160	78070	91047	57847	59184	77701					YES	
Q96E39	RNA binding motif p	RBMXL1	42.141	44.4	30	3	5.0613	0.00044	16408	12372	20054	10273	23347	13591	55997	78222	14983	16679					YES	
Q96E52;X6RL62;X	Metalloendopeptidas	OMA1	60.12	8.6	4	4	6.7471	0	4975.7	3639.9	3872.9	2899.6	6443.4	2773.3	4092.8	2374.8	2364	4091	No expres	Enriched	Enriched	No expres	YES	
Q96EC8	Protein YIPF6	YIPF6	26.256	12.3	5	5	9.6861	0	18876	19758	20373	20145	25355	16445	20334	16506	16423	18118	Enriched	Enriched	Enriched	Moderate	YES	
Q96ED9-2;Q96ED9	Protein Hook homolo	HOOK2	83.021	8.4	6	6	12.986	0	17313	12696	15261	25030	20783	27961	20472	22035	11415	18980	Enriched	Enriched	Enriched	No expres	YES	
Q96EK6;G3V4W4;	Glucosamine 6-phosp	GNPNAT1	20.749	27.7	10	10	65.393	0	54621	45396	49881	54052	64128	62824	49862	51527	26468	45503	Moderate	Enriched	Enriched	No expres	YES	
Q96EL2	28S ribosomal protei	MRPS24	19.015	7.8	1	1	8.4636	0	1376.3	1252.3	1644.1	1028.2	2008.3	2358	10436	2483	3926	2750.8	Enriched	Enriched	Enriched	No expression		
Q96ES6	Major facilitator supe	MFSD3	42.695	3.9	2	2	9.3737	0	3623.8	4535.5	2826.5	1767.3	5252.6	2808.3	3337.9	1857.9	1346	2409.3	Enriched	Enriched	Moderate	No expression		
Q96EY1-2;Q96EY	DnaJ homolog subfar	DNAJA3	49.611	8.2	4	4	6.5721	0	14154	12936	12850	10938	16470	15315	17519	22690	7584.2	16889	Enriched	Enriched	Enriched	No expres	YES	
Q96EY7	Pentatricopeptide rep	PTCD3	78.549	11.9	7	7	19.122	0	24706	19894	18933	23158	32636	17184	17153	18332	7655.9	21257	Moderate	Enriched	Enriched	No expres	YES	
Q96F25	UDP-N-acetylglucosa	ALG14	24.15	10.2	2	2	6.6151	0	18959	11505	15680	14945	22387	21167	19341	15193	10682	15323	Low	Moderate	Enriched	No expres	YES	
Q96F85;B8ZZB8;(	CB1 cannabinoid rec	CNRIP1	18.648	19.5	3	3	4.6133	0.00043	16969	10389	18319	21196	16280	17576	23592	21351	11648	25028	No expres	Moderate	Enriched	No expres	YES	
Q96F86;H3BSQ0;I	Enhancer of mRNA-c	EDC3	56.077	5.7	2	2	2.0386	0.00755	1482.7	1191.3	1667.7	966.41	1813.5	1075.8	1432.1	1417.3	1427.5	1519	Moderate	Enriched	Enriched	No expres	YES	
Q96FJ2	Dynein light chain 2,	DYNLL2	10.35	51.7	11	7	20.453	0	90593	43190	58069	46877	57782	98287	91617	96460	30452	105340	Enriched	Enriched	Enriched	No expres	YES	
Q96FQ6	Protein S100-A16	S100A16	11.801	22.3	3	3	8.1142	0	8138.4	7757.7	7586.6	7967.8	11513	6023.3	8392.8	8294.2	5761.1	8788.9	Enriched	Enriched	Enriched	No expres	YES	
Q96FX8	p53 apoptosis effecto	PERP	21.386	7.8	1	1	4.0481	0.00062	1339.4	1624.5	2159.6	457.7	2112.9	258.49	709.98	797.87	264.72	821.81	Enriched	Enriched	Enriched	No expression		
Q96G03	Phosphoglucomutase	PGM2	68.283	30.1	24	24	230.68	0	87967	64523	81007	83562	82113	89354	84694	116720	46031	98306	Enriched	Enriched	Enriched	No expres	YES	
Q96G25-3;Q96G25	Mediator of RNA pol	MED8	19.002	14	2	2	6.2543	0	16368	13265	15169	13077	18074	12746	15980	17432	11708	19045	Enriched	Moderate	Enriched	Moderate		
Q96G46;Q96G46-2	tRNA-dihydrouridine	DUS3L	72.593	11.1	6	6	39.176	0	15720	4555.1	10172	12291	9092.7	14205	9406	13681	5055	14320	Enriched	Enriched	Moderate	No expres	YES	
Q96GA3	Protein LTV1 homol	LTV1	54.854	3.8	1	1	5.347	0	2592.7	1339.9	1166.9	3896.5	1341.5	7292.5	1858.3	3526.9	377.46	3514.2	Enriched	Enriched	Enriched	No expression		
Q96GA7;F8VYZ3;	Serine dehydratase-li	SDSL	34.674	15.2	4	4	11.605	0	7270.4	6964.2	6876.8	4136.1	12769	4583.2	6521.5	6695.5	4378.1	5145.1	No expres	Low	Low	No expres	YES	
Q96GD0	Pyridoxal phosphate	PDXP	31.698	20.9	5	4	16.041	0	13442	8136.8	8995	11845	14514	11234	10155	9135.2	6813.1	8980.3	Moderate	Enriched	Enriched	No expres	YES	
Q96GG9;C9JVE2	DCN1-like protein 1;	DCUN1D1	30.124	13.9	5	2	30.94	0	37741	25911	28616	35316	38741	29394	37206	34175	19297	35200	Enriched	Enriched	Enriched	No expres	YES	
Q96GJ1-3;Q96GJ1-	tRNA (uracil(54)-C(5	TRMT2B	51.485	3.1	1	1	1.9485	0.00799	3826	2804.7	3008.1	5368.5	2851.3	4393.5	3573.4	4636.2	2116.5	4432.5	Moderate	Moderate	Moderate	No expression		
Q96GK7;Q6P2I3	Fumarylacetoacetate	FAHD2A;FAHD2B	34.596	28.3	12	12	37.106	0	24181	19673	21435	23129	26815	25080	22119	29318	9767	28349	Enriched	Enriched	Enriched	No expres	YES	
Q96GS4	Uncharacterized prot	C17orf59	37.226	12	4	4	53.463	0	2135.9	1730.2	2787.3	1830	3136.4	1739.9	2309.1	1778.9	1240.6	1762	Moderate	Moderate	Low	No expres	YES	
Q96GW9	Methionine--tRNA li	MARS2	66.59	2.5	1	1	17.767	0	5298.9	2688.6	4000.1	6979.3	4028.4	5366.6	4648.2	6424.7	2102.7	6149.4	Moderate	Enriched	Moderate	No expres	YES	
Q96GX9;S4R3D6;(	Methylthioribulose-1	APIP	27.125	41.3	11	11	31.558	0	56488	23858	30816	38401	37650	41414	28946	31673	16606	39476	Moderate	Enriched	Enriched	No expres	YES	
Q96GY0;H0YAP0	Zinc finger C2HC do	ZC2HC1A	35.092	8	2	2	8.2722	0	2708.5	1986.6	2858.5	1507	3307.1	1843.8	3134.7	1972.1	1413.2	2047.7					YES	
Q96H20-2;Q96H20	Vacuolar-sorting prot	SNF8	28.736	14	3	3	6.1258	0	27036	15700	17792	22825	19671	18890	20336	17174	11111	25815	Moderate	Enriched	Enriched	No expres	YES	
Q96H55-3;Q96H55	Unconventional myo:	MYO19	71.7	3.3	2	2	4.8641	0.00043	4799.9	4361.4	5310.4	3727.6	7710.5	4030.1	5496.1	3232.7	2851.9	5007.8	Enriched	Enriched	Enriched	No expres	YES	
Q96HC4;Q96HC4-	PDZ and LIM domai	PDLIM5	63.944	39.8	26	26	184.87	0	221450	121110	142560	136700	195180	165360	205320	160730	92216	195360	Enriched	Enriched	Enriched	Enriched	YES	
Q96HD1;Q96HD1-	Cysteine-rich with E(	CRELD1	45.439	9.3	3	3	9.2115	0	6216.1	4991.7	5958.3	9514.4	7286.9	5640.8	5552.4	5165.7	5216.7	6563.2	Moderate	Moderate	Moderate	Enriched	YES	
Q96HD9	N-acyl-aromatic-L-ar	ACY3	35.241	32	7	7	32.193	0	21116	17004	18269	20642	22264	21188	24151	20570	13393	24541	Low	Enriched	Low	No expres	YES	
Q96HE7;G3V3E6	ERO1-like protein al	ERO1L	54.392	35.5	21	19	132.73	0	106290	70213	90970	93715	79030	115680	95362	104000	47463	105480	Enriched	Enriched	Enriched	No expres	YES	
Q96HN2-2;Q96HN	Putative adenosylhon	AHCYL2	66.592	15.2	10	3	192.75	0	28659	21627	22393	19459	29570	21375	16966	21444	8859.1	19455	Enriched	Moderate	Enriched	Moderate	YES	
Q96HP0	Dedicator of cytokine	DOCK6	229.56	1.8	3	2	16.256	0	4437.3	3043.6	3884.1	7640.3	2322.7	9604.7	8338.3	11055	6555.8	6973.8	Enriched	Moderate	Moderate	No expres	YES	
Q96HR9	Receptor expression-	REEP6	20.733	22.8	5	5	20.01	0	37688	29339	31502	39806	34988	34705	76718	71750	62077	47591	Moderate	Enriched	Moderate	No expres	YES	
Q96HS1;F5GXG4;(	Serine/threonine-prot	PGAM5	32.004	15.9	4	4	16.21	0	30859	30783	32355	23870	37138	26102	27271	26084	20068	28435	No expres	No expres	Moderate	No expres	YES	
Q96HU1;Q96HU1-	Small G protein signa	SGSM3	85.353	9.1	8	8	20.175	0	9837	9390.9	9138.9	9097.4	11214	9090.1	21424	19870	11957	10168	Enriched	Enriched	Enriched	Enriched	YES	
Q96HY6;Q96HY6-	DDRGK domain-con	DDRGK1	35.61	47.1	29	29	276.29	0	134700	92813	102320	149420	108820	142570	137100	161140	79657	145570	Enriched	Enriched	Enriched	No expres	YES	
Q96HY7	Probable 2-oxoglutar	DHTKD1	103.08	18.5	14	14	57.649	0	31251	22758	35441	46990	29614	38728	42759	43869	28271	53833	Moderate	Enriched	Enriched	No expres	YES	
Q96I23	Protein preY, mitoch	PYURF	12.654	18.4	2	2	7.2703	0	3414.6	1596.7	1831	5685.1	2027.4	3778.9	3335.4	4366.4	3058.2	4060						
Q96I24	Far upstream element	FUBP3	61.64	31.1	17	16	62.941	0	72088	49051	60195	61158	79378	78455	116520	105660	64430	93215	Low	Moderate	Enriched	Enriched	YES	
Q96I25	Splicing factor 45	RBM17	44.961	15	6	6	19.665	0	17268	13224	18292	21926	19130	15327	46669	21084	17852	20850	Enriched	Enriched	Enriched	No expres	YES	
Q96I99;Q96I99-2;F	Succinyl-CoA ligase	SUCLG2	46.51	44.4	45	45	323.31	0	214490	143740	147750	173830	139370	195840	280480	284480	85480	225030	Enriched	Enriched	Enriched	No expres	YES	
Q96II8-3;Q96II8-4;	Leucine-rich repeat a	LRCH3	78.801	1.5	1	1	2.6336	0.00273	4823.8	5931.5	3431.7	7211.3	3474	6265.2	4368.6	7353.5	2221.9	4895.4	Enriched	Low	Moderate	No expression		
Q96IJ6;Q96IJ6-2;A	Mannose-1-phosphat	GMPPA	46.291	38.6	23	23	106.02	0	102750	80272	80028	83128	101050	126000	146060	143040	59725	99146	Moderate	Moderate	Moderate	No expres	YES	
Q96IU4;F8W9U3;E	Alpha/beta hydrolase	ABHD14B	22.345	36.7	12	12	52.589	0	27980	19575	21525	39851	27753	39458	32836	31737	12683	29931	Moderate	Enriched	Enriched	No expres	YES	
Q96IV0-3;Q96IV0-	Peptide-N(4)-(N-acet	NGLY1	63.827	10.9	7	7	26.042	0	12119	12059	12448	9463.4	15033	8804.8	13430	11325	8312.3	9927.4	Enriched	Enriched	Enriched	No expres	YES	
Q96IX5	Up-regulated during s	USMG5	6.4575	27.6	5	5	39.03	0	49738	34297	36639	32688	36102	46117	68612	74439	23167	56735	Enriched	Enriched	Enriched	No expres	YES	
Q96IZ0	PRKC apoptosis WT	PAWR	36.567	17.1	5	5	41.211	0	34746	28525	34345	24446	51395	21256	26802	23071	15857	23805	Moderate	Enriched	Enriched	Low	YES	
Q96J02-3;Q96J02-2	E3 ubiquitin-protein	ITCH	86.497	9.3	6	5	12.274	0	4785.9	3401.2	4604.5	4232.2	6725.3	3726.2	5257.3	3884.2	2508.3	5079.1	Moderate	Moderate	Moderate	Low	YES	
Q96JA1;Q96JA1-2	Leucine-rich repeats	LRIG1	119.11	3.1	2	2	43.786	0	6333.1	4942.3	5292.9	6506.9	9993.7	4921.8	6325.7	4964.4	2937.9	5481.5	Moderate	Enriched	Enriched	Enriched		
Q96JB2;Q96JB2-2	Conserved oligomeric	COG3	94.095	12.6	10	10	25.865	0	31934	28866	33796	29718	37237	32384	48283	45611	27007	35959	Moderate	Enriched	Enriched	No expres	YES	
Q96JB5;Q96JB5-4;	CDK5 regulatory sub	CDK5RAP3	56.92	34	26	26	181.56	0	168660	79337	96296	146810	120120	312650	219280	273920	92007	163750	Enriched	Enriched	Enriched	No expres	YES	
Q96JC1-2;Q96JC1	Vam6/Vps39-like prc	VPS39	100.77	5.3	5	5	12.463	0	4745.2	3051.6	4214	10152	3279	4126.7	2943.1	3830.1	1322	4410.6	Low	Moderate	Moderate	Enriched	YES	
Q96JE9-2;Q96JE9	Microtubule-associat	MAP6	47.376	8.4	3	3	3.7864	0.0006	2481.5	2403.1	3472.2	2716.3	3984.2	2547.6	3459.9	2665.6	3351.5	4428.1	Low	Moderate	Enriched	No expres	YES	

Q96JG6-3;Q96JG6;	Coiled-coil domain-c	CCDC132	107.92	5.4	4	4	9.3098	0	19512	19487	19080	21097	19809	11840	12908	16769	7130.7	18240	Low	Enriched	Enriched	No expres	YES		
Q96JH7	Deubiquitinating prot	VCPIP1	134.32	4.7	5	5	7.6697	0	19809	8648.4	11854	14753	13322	19884	13576	24493	9600.9	20707	No expres	Low	Moderate	No expres	YES		
Q96JJ7;H3BPB3;B	Protein disulfide-ison	TMX3	51.871	8.6	3	3	11.258	0	43396	26726	34041	29407	35382	25878	31824	30115	18539	39521	Moderate	Enriched	Enriched	No expres	YES		
Q96JM3	Chromosome alignme	CHAMP1	89.098	6.2	4	4	20.089	0	33944	24777	27156	27073	28804	28268	30217	41970	14660	33608					YES		
Q96JP5-2;Q96JP5;	E3 ubiquitin-protein	ZFP91;ZFP91-CNTF	59.57	8.9	4	4	27.404	0	6588.6	6483.7	7289.6	4339.3	10945	4201.3	7308.2	6095	4770.8	6267.9	Moderate	Enriched	Enriched	No expression			
Q96JQ2	Calmin	CLMN	111.65	6.1	4	4	31.779	0	9529.2	9647.6	15387	9377.9	17176	6050	11929	11088	4158.5	10396	Moderate	Enriched	Enriched	No expres	YES		
Q96JX3	Protein SERAC1	SERAC1	74.147	4.7	4	4	4.3055	0.00063	7275.2	4703	6514.3	6190.6	9211.4	9157.7	13483	9778.3	8255.2	7415.5	Low	Enriched	Enriched	No expression			
Q96K76-4;Q96K76	Ubiquitin carboxyl-te	USP47	154.7	11.2	16	16	39.606	0	44516	30143	35284	45870	40984	37708	37445	37275	28152	42181	Enriched	Enriched	Enriched	No expres	YES		
Q96KA5-2;Q96KA	Cleft lip and palate tr	CLPTM1L	58.355	11.2	8	8	15.015	0	23373	20723	24949	16382	27240	16752	25380	17146	12842	17443	No expres	Enriched	Enriched	No expres	YES		
Q96KC8	DnaJ homolog subfar	DNAJC1	63.882	19.3	15	15	53.552	0	102370	76438	97960	80217	126290	101590	142810	110200	66123	97559	Enriched	Enriched	Enriched	No expres	YES		
Q96KM6	Zinc finger protein 51	ZNF512B	97.263	4.8	4	4	8.2281	0	10699	11135	13400	9151.6	15823	5857.2	7689	8629.1	9762.7	8813.3	Moderate	Enriched	Enriched	No expres	YES		
Q96KN1	Protein FAM84B	FAM84B	34.474	14.5	4	4	13.391	0	24698	12855	17005	15647	18405	22524	25221	19592	13192	21115	Moderate	Enriched	Enriched	No expres	YES		
Q96KP1	Exocyst complex com	EXOC2	104.07	12.9	11	11	18.973	0	17788	13259	16530	20639	15433	16141	14585	15314	10996	17288	Low	Enriched	Moderate	No expres	YES		
Q96KP4;Q96KP4-2	Cytosolic non-specifi	CNDP2	52.878	56.6	64	39	323.31	0	503400	364250	335940	481570	398820	391290	487180	589070	276460	458800	Enriched	Enriched	Enriched	No expres	YES		
Q96KR1	Zinc finger RNA-bind	ZFR	117.01	10.2	11	11	99.924	0	59528	66174	68161	44314	82418	40086	38860	43077	23044	47123	Enriched	Enriched	Enriched	Enriched	YES		
Q96L12	Calreticulin-3	CALR3	44.995	2.9	3	3	5.6559	0	4170.1	7155.2	6296.1	2405.7	11207	8764.9	5364	3418.3	2341.5	2872.2	No expres	No expres	No expres	No expression			
Q96L91-3;Q96L91	E1A-binding protein	EP400	335.8	0.8	2	2	3.5414	0.00079	4249	3571.4	3916.8	4924.3	4770.6	5168.5	5498.6	5662.5	3599.4	4652.2	Moderate	Moderate	Moderate	Moderate	YES		
Q96LB3;Q96LB3-2	Intraflagellar transpo	IFT74	69.239	5.8	3	3	5.5893	0	2080.6	1956	2416.6	2163.1	1587.7	2215.8	1571.7	1922.3	746.06	1943.2	No expres	No expres	Moderate	No expres	YES		
Q96LD4-2;Q96LD4	Tripartite motif-conta	TRIM47	44.41	13	4	4	13.539	0	12329	15593	16632	13536	15667	10127	11204	14572	5590.6	14453	Low	Enriched	Moderate	No expres	YES		
Q96LJ7;H0YNC2	Dehydrogenase/reduc	DHRS1	33.909	13.7	3	3	11.576	0	13132	12567	14740	17582	15007	10854	10901	11817	11800	16645	Enriched	Enriched	Enriched	Enriched	YES		
Q96LJ8	UBX domain-contain	UBXN10	30.811	3.6	1	1	1.8265	0.00975	5237.5	5414.1	6273	4030.3	7040.4	2673.1	6907.7	5597.7	5286.8	6821.5	Low	Low	Low	No expression			
Q96M27;Q96M27-	Protein PRRC1	PRRC1	46.701	21.1	20	20	125.32	0	103380	43547	62526	106200	61294	157530	110050	137950	54559	119310	No expres	Enriched	Enriched	Moderate	YES		
Q96MG7	Melanoma-associated	NDNL2	34.308	3.9	1	1	3.1536	0.00076	2028.9	1811.9	2172.6	1379.4	1969.9	1467	2739.7	1950.1	2079.9	2505.4	Moderate	Moderate	Enriched	No expres	YES		
Q96MG8;F5H1M8;	Protein-L-isoaspartat	PCMTD1	40.675	14.3	4	4	6.3559	0	16495	11327	12652	20270	15095	16187	17493	17981	7338.7	17020	Enriched	Enriched	Enriched	No expression			
Q96MH6;Q49A68;	Transmembrane prote	TMEM68	37.424	14.2	4	4	6.0525	0	4285.9	5883.4	4866.2	4102.5	6053.7	2757.7	3490.3	3196.9	1837.7	2818.4	No expres	Moderate	Moderate	No expres	YES		
Q96MM6;Q5JX83	Heat shock 70 kDa pr	HSPA12B	75.687	9.6	7	7	11.874	0	22309	19263	27385	18299	31899	20187	34371	28036	21627	32785	Moderate	Low	Moderate	No expres	YES		
Q96MW5;H3BQV3	Conserved oligomeric	COG8	68.423	7.4	4	4	9.2775	0	8731.8	8151.8	7789.2	10304	10635	10293	8377.3	8241.9	4621	8770.9	Enriched	Enriched	Moderate	No expression			
Q96N11-2;Q96N11	Uncharacterized prot	C7orf26	39.027	6.2	2	2	8.9249	0	1588.3	1086.4	1440.8	1709	1755.9	1435	1851.7	962.17	1568.3	1272.1	Enriched	Enriched	Moderate	No expression			
Q96N66;Q96N66-2	Lysophospholipid ac	MBOAT7	52.764	15.3	7	7	155.05	0	77935	52731	61110	68558	74054	49007	62380	76186	32082	76831	Enriched	Enriched	Enriched	Enriched	YES		
Q96N67-4;Q96N67	Dedicator of cytokine	DOCK7	238.27	4.5	11	10	22.206	0	50356	28847	35502	34540	42025	34740	45066	36567	21735	35428	Low	Enriched	Enriched	No expres	YES		
Q96NB2	Sideroflexin-2	SFXN2	36.231	12.4	4	4	9.3215	0	11791	6303.2	9782.4	12993	8460	13382	9284.2	13063	4300.1	12879	Enriched	Enriched	Enriched	No expres	YES		
Q96NY7-2;Q96NY	Chloride intracellular	CLIC6	70.995	12.1	10	8	26.304	0	17968	16870	16407	23947	19178	28515	33103	41018	26082	23108	Moderate	Enriched	Moderate	No expres	YES		
Q96P11-2;Q96P11-	Probable 28S rRNA (	NSUN5	50.41	9	3	3	10.647	0	6437.5	7600.2	7864.1	5051	8785.8	4311.4	6890.3	4859.2	4336.1	6366.3	Enriched	Enriched	Enriched	No expression			
Q96P16-3;Q96P16	Regulation of nuclear	RPRD1A	31.625	12.7	3	2	3.8492	0.00061	3449.6	4934.8	7460.9	3592.3	7723.2	2124.6	3310.5	2772	2436.5	3715.9	Enriched	Enriched	Enriched	No expres	YES		
Q96P47;Q96P47-2;	Arf-GAP with GTPas	AGAP3	95.043	6.7	5	5	14.557	0	18538	20391	22029	14132	19973	15548	18708	19740	12490	19608	Enriched	Enriched	Enriched	No expres	YES		
Q96P48-3;Q96P48;	Arf-GAP with Rho-G	ARAP1	160.99	4.9	6	6	12.576	0	21695	23456	17491	22012	20228	17217	22794	25562	15723	20963	Low	Moderate	Enriched	Enriched	YES		
Q96P70	Importin-9	IPO9	115.96	5	5	5	22.277	0	12070	8150.6	8927.3	17526	11080	14459	16393	23994	11019	16384	Enriched	Enriched	Enriched	Moderate	YES		
Q96PC3-4	AP-1 complex subun	AP1S3	18.476	18.2	3	2	7.3669	0	10795	9201.4	10319	16297	12232	11900	10211	14009	5085.8	13391	Low	Low	Moderate	No expression			
Q96PE2	Rho guanine nucleoti	ARHGEF17	221.67	1.1	2	2	3.0209	0.00132	1617.8	1894.3	2052.1	1237.6	2821.7	1467.2	3309.2	1804.4	3143.5	1873.1	Moderate	Low	Moderate	Moderate	YES		
Q96PK6	RNA-binding protein	RBM14	69.491	25.3	21	17	53.787	0	59297	52294	58061	46811	81245	49417	73273	63879	46547	62938	Low	Enriched	Enriched	Moderate	YES		
Q96PU4;B1AL33;(	E3 ubiquitin-protein	UHRF2	89.984	2.7	2	2	3.8842	0.00061	5882.2	6623.9	6547.2	5250	6551.8	2709.1	5067.7	4793.7	5338.4	4725.4	Moderate	Enriched	Enriched	No expres	YES		
Q96PU5-3;Q96PU5	E3 ubiquitin-protein	NEDD4L;ZNF227	100.75	15	14	8	51.418	0	63565	48224	64323	67172	62249	72004	65232	70769	36317	58281	Moderate	Enriched	Moderate	Enriched	YES		
Q96PZ0;E7EUH7	Pseudouridylate syntl	PUS7	75.035	5.3	3	3	7.9125	0	4713.4	4627.6	5042	2834.4	7141.1	2878	9706.8	3142.9	4545.4	3995.7	Moderate	Enriched	Enriched	No expres	YES		
Q96Q06;Q96Q06-2	Perilipin-4	PLIN4	134.43	22.5	17	17	62.009	0	34194	37695	41990	66097	52898	30899	39676	29216	31758	53541					YES		
Q96Q11-2;Q96Q11	CCA tRNA nucleotic	TRNT1	47.828	22.9	8	8	11.537	0	26574	23734	25154	27193	26919	24802	33000	32612	17253	27232	Moderate	Moderate	Enriched	No expres	YES		
Q96QC0	Serine/threonine-prot	PPP1R10	99.057	3.6	3	3	4.4448	0.00042	9786.5	8739.8	11643	13107	10513	10402	13730	14469	8742.1	13648	Moderate	Enriched	Enriched	Moderate	YES		
Q96QG7-2;Q96QG	Myotubularin-related	MTMR9	53.796	2.6	1	1	2.9412	0.00169	5327.3	4736.1	4445	3497.5	9764.2	3479.9	5739.8	3713.6	2761.6	4446.1	Enriched	Enriched	Enriched	Moderate			
Q96QK1	Vacuolar protein sort	VPS35	91.706	26.9	31	31	287.05	0	149660	84514	115020	143470	114430	157650	137660	175990	80693	150170	Enriched	Enriched	Enriched	No expres	YES		
Q96QK8;D6R9U3	Small integral membr	SMIM14	10.71	23.2	2	2	2.2852	0.00495	5690.2	5649.6	5874	2885.5	6736	4518.3	3561.9	3448	3089.3	5257.6							
Q96QR8	Transcriptional activa	PURB	33.24	17.9	5	5	14.809	0	13246	10083	12322	15617	14637	14833	55948	16567	43164	25484	Enriched	Enriched	Enriched	No expres	YES		
Q96QU6	1-aminocyclopropane	ACCS	57.323	3.6	1	1	3.108	0.00095	3373.6	2350.9	2972.6	2315.8	4662.6	2678.8	3604.5	2163.2	2339.7	3823.8	Enriched	Enriched	Moderate	No expression			
Q96QZ7-7;Q96QZ7	Membrane-associated	MAGI1	157.78	10.4	13	12	32.076	0	12201	10355	12346	14047	13707	12809	11695	11333	7491.1	13012	Enriched	Enriched	Enriched	Enriched	YES		
Q96R05	Retinoid-binding prot	RBP7	15.536	11.9	2	2	7.9313	0	27381	20061	22730	20679	22434	16947	21438	11962	17555	24578	Low	Moderate	Moderate	No expres	YES		
Q96RF0-3;Q96RF0	Sorting nexin-18	SNX18	64.751	2.7	1	1	9.8654	0	3794	3539.9	4452.6	3228.2	5609.2	2262	3706.4	3793.7	3220.4	3379.4	Enriched	Enriched	Enriched	No expres	YES		
Q96RL7-4;Q96RL7	Vacuolar protein sort	VPS13A	347.67	2.3	5	5	12.179	0	12535	7885.3	9920.2	15835	9665.9	12783	14568	14349	10481	13674	Moderate	Enriched	Enriched	Moderate	YES		
Q96RP9;Q96RP9-2	Elongation factor G,	GFM1	83.471	22.5	21	21	62.1	0	141510	122410	118260	125100	160080	97728	102930	105360	57180	116240	Enriched	Enriched	Enriched	No expres	YES		
Q96RS6;Q96RS6-2	NudC domain-contai	NUDCD1	66.755	15.1	7	7	50.346	0	24405	15721	18611	18102	24578	13014	21591	14710	12260	22758	Moderate	Enriched	Enriched	No expres	YES		
Q96RT1-7;Q96RT1	Protein LAP2	ERBB2IP	146.08	4.7	6	6	15.276	0	13877	9798.4	10410	14434	12500	12560	9710.8	10471	7230.8	12215	Moderate	Moderate	Enriched	No expres	YES		
Q96RT7-2;Q96RT7	Gamma-tubulin comp	TUBGCP6	196.76	2	2	2	9.6407	0	4550.8	3906	3793.6	3610.6	5464.9	3794.6	5343.2	3523.8	3717.2	5193.1	Moderate	Enriched	Moderate	No expression			
Q96S06;H3BSB7;E	Lipase maturation fac	LMF1;LA16c-360B4.1	64.873	10.1	6	3	45.291	0	27000	25099	21086	19714	26730	17536	16117	18104	7792	19305	Enriched	Enriched	Moderate	No expression			
Q96S44;Q5JZ02	TP53-regulating kina	TP53RK	28.16	20.2	6	6	20.388	0	20187	19061	18051	14419	27301	11623	9446.2	10949	5931.1	14243	No expres	Enriched	Enriched	No expres	YES		
Q96S52;Q96S52-2	GPI transamidase cor	PIGS	61.655	15.5	7	7	17.273	0	20827	22160	22365	17240	26999	14066	19764	17035	9886.9	17175	Enriched	Enriched	Enriched	No expres	YES		
Q96S55-2;Q96S55;	ATPase WRNIP1	WRNIP1	69.458	12.5	8	8	71.654	0	15195	10537	13435	9309.9	13667	22466	27260	40976	11509	25010	Low	Enriched	Enriched	No expres	YES		
Q96S59;Q96S59-2;	Ran-binding protein 9	RANBP9	77.846	4	2	2	31.088	0	4747.7	5159.4	4454.6	3998.3	5552.8	3185.3	3412.8	3640.7	1814.4	3382.5	Enriched	Enriched	Enriched	Low	YES		
Q96S66-3;Q96S66-	Chloride channel CL	CLCC1	47.436	25.1	12	12	33.361	0	50002	36860	44360	38297	57457	31572	41328	31562	23590	38687	Low	Low	Moderate	Moderate	YES		
Q96SI9-2;Q96SI9	Spermatid perinuclea	STRBP	71.966	7.3	7	2	6.2479	0	11115	8679.4	8826.3	8783.9	12304	9007	11318	7471.9	7333.6	9736.9	Enriched	Enriched	Enriched	No expres	YES		
Q96SK2-3;Q96SK2	Transmembrane prote	TMEM209	58.194	6.4	2	2	5.4646	0	6946.3	3495.8	4734.2	6221.1	4026.6	15871	9349.9	7067.8	3409.3	9892.1	Low	Moderate	Enriched	No expres	YES		
Q96SL4	Glutathione peroxida	GPX7	20.996	16	2	2	10.812	0	3723.7	4966.5	4383.9	3223.8	4371.8	2544	3049.6	2756.2	2470.3	2848.2	Low	Moderate	Moderate	Moderate	YES		
Q96ST2-2;Q96ST2	Protein IWS1 homolo	IWS1	56.109	7.7	3	3	4.8176	0.00043	5961.3	4655.8	4383.4	4881.1	5239	3803.3	3074.3	3873.7	1514.2	4626.5	Moderate	Enriched	Enriched	No expres	YES		
Q96ST3	Paired amphipathic h	SIN3A	145.17	10.1	10	9	66.097	0	24957	16227	18150	14605	23141	17616	19885	22148	8313.8	23037	Moderate	Enriched	Enriched	No expres	YES		
Q96SU4-5;Q96SU4	Oxysterol-binding pro	OSBPL9	62.528	5.6	3	3	6.7502	0	21137	19368	22865	21315	25677	22945	20407	18480	15023	21351	Enriched	Enriched	Enriched	No expres	YES		
Q96SZ5	2-aminoethanethiol d	ADO	29.751	20.4	6	6	23.508	0	36133	19812	28080	27865	42243	26619	30115	24976	19684	31276	Enriched	Moderate	Enriched	Low			
Q96T23-2;Q96T23	Remodeling and spac	RSF1	160.13	2.8	4	4	15.989	0	5917	3211.1	3979.2	7581.3	4452.8	4432.5	3686.2	5910.6	3769.5	6444.9	Enriched	Moderate	Enriched	No expres	YES		
Q96T51;Q96T51-2	RUN and FYVE dom	RUFY1	79.817	12.9	8	8	15.179	0	9623.6	8207	9761.3	8370.4	9145	13945	22031	19143	10205	14613	Enriched	Enriched	Enriched	No expres	YES		
Q96T58	Msx2-interacting pro	SPEN	402.24	0.5	2	2	3.4791	0.00079	2006.5	1904.1	2257.1	1105.6	2694.5	1660.4	2326.8	2380.6	1670	2590.3	Enriched	Enriched	Enriched	Enriched	YES		
Q96T60-2;Q96T60	Bifunctional polynuc	PNKP	53.003	10.2	4	4	14.832	0	21551	11022	15627	23502	16534	14249	8991.6	12077	6046.3	14099	Low	Moderate	Moderate	No expres	YES		
Q96TA1-2;Q96TA1	Niban-like protein 1	FAM129B	82.682	32.3	33	33	224.94	0	181620	117470	138590	180890	154460	174470	203240	201210	107710	200270	Enriched	Enriched	Enriched	No expres	YES		
Q96TC7;H0YMB1;	Regulator of microtul	RMDN3	52.118	20	8	8	32.338	0	36457	47452	42914	33504	57035	35341	32249	36725	18199	35206					YES		
Q99426-2;Q99426;	Tubulin-folding cofac	TBCB	21.801	21.8	4	4	12.894	0	22755	34133	36092	23934	40830	14869	49467	36440	32928	27968	Moderate	Enriched	Enriched	Enriched	YES		
Q99436	Proteasome subunit b	PSMB7	29.965	35.4	16	16	51.817	0	130550	78183	106490	109970	135770	119910	121700	104660	51464	108930	Moderate	Enriched	Enriched	Enriched	YES		
Q99442;F8WF48;F	Translocation protein	SEC62	45.861	15.8	6	6	34.863	0	65959	36012	43882	43834	95070	61352	77895	54890	31309	56643	Enriched	Enriched	Enriched	Moderate	YES		
Q99447;Q99447-3;	Ethanolamine-phospl	PCYT2	43.835	22.6	11	11	64.816	0	64638	54315	61285	40675	56492	58989	75436	54572	47576	59577	Enriched	Moderate	Moderate	Enriched	YES		
Q99459	Cell division cycle 5-	CDC5L	92.25	22.6	19	19	59.076	0	113680	89103	114930	96684	98942	89138	113580	126650	56778	129520	Enriched	Enriched	Enriched	No expres	YES		
Q99460;Q99460-2;	26S proteasome non-	PSMD1	105.84	29.5	30	25	90.266	0	157590	116400	151110	146870	148940	115510	124610	112970	68547	123170	Enriched	Enriched	Enriched	Enriched	YES		
Q99470	Stromal cell-derived	SDF2	23.026	11.4	2	2	3.8734	0.00061	21354	21060	26208	29368	24890	18648	24071	34699	12518	29172	Enriched	Enriched	Enriched	Enriched			
Q99471;H3BPF6	Prefoldin subunit 5	PFDN5	17.328	21.4	3	3	6.4287	0	19130	11797	17211	15033	17759	26835	33220	23188	14994	26673	Moderate	Enriched	Enriched	Enriched	YES		
Q99523-2;Q99523	Sortilin	SORT1	77.374	1.9	1	1	2.3966	0.00411	6002.9	5911.4	6537.2	6379.3	6680.2	6769.3	5082.9	5012.6	3386.1	7180.9	Enriched	Enriched	Enriched	No expres	YES		
Q99536;Q99536-3;	Synaptic vesicle mem	VAT1	41.92	45.5	27	27	273.12	0	341530	290940	325180	281200	343780	338560	386140	435040	202090	425950	Enriched	Enriched	Enriched	Enriched	YES		
Q99543-2;Q99543	DnaJ homolog subfar	DNAJC2	65.913	8.1	4	4	10.362	0	10574	4180	6468.7	13389	5820.3	11418	8334.4	8480.4	3792.5	12354	Enriched	Enriched	Enriched	Moderate	YES		
Q99569-2;Q99569;	Plakophilin-4	PKP4	127.14	1.8	2	2	3.392	0.00078	1220.3	1090.8	1264.9	1177.1	1404.3	1301.5	932.4	919.25	433.51	770.97	Enriched	Moderate	Enriched	Low	YES		
Q99571-3;Q99571;	P2X purinoceptor 4	P2RX4	40.48	12.7	4	4	25.616	0	11426	10042	13054	12774	18629	11911	13986	9007.7	9143.8	12989	Low	Enriched	Enriched	Moderate	YES		
Q99574;H7C5T9	Neuroserpin	SERPINI1	46.426	4.9	2	2	2.6863	0.00238	8908	6126.1	7280.7	13894	6642.7	11723	7709	7814.2	5327	10390	No expres	Enriched	Enriched	Enriched	YES		
Q99575	Ribonucleases P/MR	POP1	114.71	5.7	5	5	39.245	0	11756	8174.2	9329.4	9873.2	14371	10714	13527	13378	9139.3	13320	Moderate	Low	Low	Moderate	YES		
Q99584	Protein S100-A13	S100A13	11.471	42.9	9	9	98.296	0	31826	32788	44866	58794	31054	45790	56394	86381	46688	72172	Enriched	Enriched	Enriched	Moderate	YES		
Q99598;C4P0D6;C	Translin-associated p	TSNAX;DISC1	33.112	50.3	19	19	323.31	0	112660	78169	99285	82795	107320	99706	116630	118100	59883	110970	Moderate	Moderate	Enriched	Enriched	YES		
Q99613;Q99613-2;	Eukaryotic translatio	EIF3C;EIF3CL	105.34	23.7	37	37	321.87	0	184380	133360	144290	131430	155300	175230	220510	181090	126930	193060	Enriched	Enriched	Enriched	Enriched	YES		
Q99614	Tetratricopeptide rep	TTC1	33.526	23.6	7	7	25.95	0	45438	47662	36068	41018	59405	16843	14391	15182	11668	18972	Moderate	Moderate	Enriched	Enriched	YES		
Q99615-2;Q99615	DnaJ homolog subfar	DNAJC7	50.096	12.3	5	5	29.321	0	13552	12925	14133	17461	16552	16011	12483	16356	6955.2	25849	No expres	Enriched	Enriched	Moderate	YES		
Q99623;J3KPX7;F	Prohibitin-2	PHB2	33.296	62.5	35	31	156.78	0	116550	74165	91594	143610	112180	131640	172350	186650	73450	145120	Enriched	Enriched	Enriched	Enriched	YES		
Q99653;H0YKE7;I	Calcineurin B homol	CHP1	22.456	12.3	2	2	14.278	0	9860.2	9652.2	9565.5	7738.4	12366	6849	8752	8607.7	5989.9	10034					YES		
Q99707;Q99707-2	Methionine synthase	MTR	140.53	5.1	8	8	23.844	0	46850	29376	43358	52597	39351	35604	34080	48502	17314	39473	Enriched	Moderate	Enriched	Moderate	YES		
Q99714;Q99714-2;	3-hydroxyacyl-CoA d	HSD17B10	26.923	61.7	30	30	209.82	0	227950	175570	214640	209910	258590	211250	234290	242810	136890	210780	Enriched	Enriched	Enriched	Moderate	YES		
Q99729-3;D6R9P3	Heterogeneous nucle	HNRNPAB	30.588	34.7	15	14	128.71	0	117370	71681	92683	82505	100700	117340	249140	214160	85609	148250	Moderate	Enriched	Enriched	Enriched	YES		
Q99733;Q99733-2;	Nucleosome assembl	NAP1L4	42.823	30.9	13	12	86.44	0	54743	42597	49011	62938	59889	56267	64863	111470	32321	67512	Moderate	Enriched	Enriched	Enriched	YES		
Q99735-2;Q99735	Microsomal glutathio	MGST2	8.3587	18.2	2	2	16.687	0	10833	10354	11133	12719	11998	13562	21344	25334	8419	13759	Enriched	Enriched	Enriched	Enriched	YES		
Q99747;Q99747-2	Gamma-soluble NSF	NAPG	34.746	22.1	7	7	41.752	0	31422	23565	24779	32743	27390	28700	25342	40433	11550	29502	Moderate	Enriched	Enriched	No expres	YES		
Q99757;M0QXH0;	Thioredoxin, mitocho	TXN2	18.383	34.9	9	9	67.732	0	85109	73244	73851	79405	72129	49662	52770	59697	28541	80567	Enriched	Enriched	Enriched	Enriched	YES		
Q99766;Q8WXQ4	ATP synthase subuni	ATP5S	24.866	13	3	3	2.9773	0.00169	6467.1	6071	8161.7	4561.1	11276	3078.3	5564.9	4504.6	3848.8	5333	Moderate	Moderate	Enriched	Low			
Q99805	Transmembrane 9 su	TM9SF2	75.775	20.7	25	25	196.22	0	288390	137700	151480	184410	176760	339950	193000	199440	86112	266260	Enriched	Enriched	Enriched	Enriched	YES		
Q99808;Q99808-2	Equilibrative nucleos	SLC29A1	50.219	6.4	3	3	33.275	0	1498.4	833	1471.6	766.9	2354.9	1096.6	1312.4	495.32	686.96	835.36	Enriched	Enriched	Enriched	Enriched	YES		
Q99828;Q99828-2	Calcium and integrin-	CIB1	21.703	47.6	12	12	51.246	0	49745	36359	46804	50644	61597	52207	41299	40427	18867	45509	Enriched	Enriched	Enriched	Moderate	YES		
Q99832-3;Q99832;	T-complex protein 1	CCT7	54.804	46.7	40	40	255.59	0	291440	189970	242860	231980	279660	253240	268060	279000	147370	264270	Low	Enriched	Enriched	Enriched	YES		
Q99895	Chymotrypsin-C	CTRC	29.483	53.4	51	51	323.31	0	597170	561210	326730	498880	428050	434000	319070	229530	201170	311150	Enriched	Enriched	Enriched	Enriched	YES	YES	YES
Q99943	1-acyl-sn-glycerol-3-	AGPAT1	31.716	7.8	2	2	4.3958	0.00063	8165.3	5320.5	7419.8	9781.6	7936.2	12336	7345.6	8909.9	3784.1	8417.6	Enriched	Enriched	Enriched	Enriched	YES		
Q99959-2;Q99959;	Plakophilin-2	PKP2	92.755	25.3	26	26	159.03	0	111860	95878	105950	93950	113720	92531	103460	102160	69835	97064	No expres	Low	Moderate	Low	YES		
Q99961;Q99961-2;	Endophilin-A2	SH3GL1	41.489	24.5	12	10	34.863	0	67367	45644	43522	117700	37963	69764	58287	88453	40413	80086	Enriched	Enriched	Enriched	Low	YES		
Q99969;C9J8S2	Retinoic acid recepto	RARRES2	18.617	31.9	5	5	7.5692	0	21552	9593	11256	26953	15499	17836	9878	13395	8017.3	13494	Enriched	Enriched	Enriched	Enriched	YES		
Q99986	Serine/threonine-prot	VRK1	45.476	3.3	1	1	2.5143	0.00379	12115	8947.9	11845	14236	12789	16608	13185	12959	6829.7	13704	No expres	Low	Moderate	Moderate	YES		
Q99988;A0A0A0M	Growth/differentiatio	GDF15	34.14	6.2	2	2	4.1823	0.00062	1874.1	2108.9	2958.2	2668.6	6430.9	8419.9	9548.4	4244.2	1624	3560.1	Enriched	Enriched	Enriched	Moderate			
Q9BPW8	Protein NipSnap hom	NIPSNAP1	33.31	25.7	11	10	41.284	0	57583	45012	52152	38024	58497	57693	49024	40992	21852	49219	Enriched	Enriched	Enriched	Enriched	YES		
Q9BPX5	Actin-related protein	ARPC5L	16.941	31.4	8	8	56.662	0	48149	51532	55986	31978	80470	24467	39837	26765	29041	31527	Enriched	Enriched	Enriched	No expres	YES		
Q9BQ13-2;Q9BQ1	BTB/POZ domain-co	KCTD14	26.188	46.2	21	21	78.058	0	166070	117780	125510	156410	138590	186700	136020	207800	63348	159140	Enriched	Enriched	Enriched	No expres	YES		
Q9BQ15-2;Q9BQ1	SOSS complex subur	NABP2	11.493	21.4	1	1	9.6193	0	3142.5	1688.8	1805.2	2985.9	2320.4	1888.3	2071.8	2149.3	1742.2	4001.2							
Q9BQ67;M0QX71	Glutamate-rich WD r	GRWD1	49.419	10.5	4	4	11.933	0	26766	11959	17941	15193	18007	20703	16520	15962	6898.2	29416	Enriched	Moderate	Moderate	No expres	YES		
Q9BQ69	O-acetyl-ADP-ribose	MACROD1	35.505	26.2	10	10	26.033	0	36295	30151	33459	36838	35783	29908	55698	33118	35584	43524	Enriched	Enriched	Moderate	No expres	YES		
Q9BQ70;H3BMJ8;	Transcription factor 2	TCF25;NULP1	76.666	8.6	4	4	21.6	0	2938.6	1758	2609.3	2162.9	3022.7	2210.6	3288.6	1955	1793	2730.6	Enriched	Enriched	Enriched	Enriched	YES		
Q9BQ95-4;Q9BQ9	Evolutionarily conser	ECSIT;ZNF428	33.938	9.5	2	2	2.7495	0.0024	3394.8	2703.7	3504.8	3963.6	4419.3	4579.6	3710.7	3580.9	2306.5	4222.8	Enriched	Enriched	Enriched	No expression			
Q9BQA1;H0Y711;	Methylosome protein	WDR77	36.724	7.6	2	2	6.4375	0	2705.7	1104.6	1566.1	1898.2	2127.7	2044.7	1816.4	2197.5	1424.3	2387.4	Moderate	Moderate	Enriched	Moderate	YES		
Q9BQC3;Q9BQC3-	Diphthamide biosynt	DPH2	52.082	9.4	3	3	4.8595	0.00043	5879.1	3636.2	4453.3	5915.5	4343.2	4230.3	4334.4	4067.2	3362.6	5208.1	Moderate	Moderate	Moderate	Enriched			
Q9BQC6	Ribosomal protein 63	MRPL57	12.266	20.6	4	4	6.9546	0	12079	10479	11230	8844.4	18762	10016	9369	7092.4	5349.9	8749.8							
Q9BQG0;Q9BQG0	Myb-binding protein	MYBBP1A	148.85	14.4	22	22	98.101	0	100880	79659	89765	107850	95676	90411	109120	106390	55014	116710	Enriched	Enriched	Enriched	No expres	YES		
Q9BQS8;Q9BQS8-	FYVE and coiled-coi	FYCO1	166.98	11.6	17	17	137.36	0	51922	31340	32976	39503	42842	35873	39227	38899	22342	40850	Moderate	Moderate	Enriched	No expres	YES		
Q9BR76;A0A087W	Coronin-1B;Coronin	CORO1B	54.234	17	13	12	29.334	0	76415	66567	72244	85549	76498	59789	91428	83649	76158	84074	Enriched	Enriched	Enriched	No expres	YES		
Q9BRA2;I3L2R6;I3	Thioredoxin domain-	TXNDC17	13.941	44.7	12	12	22.468	0	49113	38580	43025	49464	47419	93852	91472	95899	31098	62607	Enriched	Enriched	Enriched	No expres	YES		
Q9BRG1;K7EKV4	Vacuolar protein-sort	VPS25	20.747	39.2	8	8	12.364	0	48768	32793	36833	38535	47941	42505	42610	39760	25631	39600	Enriched	Enriched	Enriched	No expres	YES		
Q9BRK4	Leucine zipper putati	LZTS2	72.759	2.4	1	1	2.5274	0.00379	16973	7764.4	4078.7	29650	2492.7	10449	4467.2	10722	7503.4	13538	Moderate	Enriched	Enriched	No expres	YES		
Q9BRK5;H0Y3T6;	45 kDa calcium-bind	SDF4	41.806	12.4	4	4	10.953	0	24609	18231	22316	20250	30096	16570	17024	12037	10172	18913	Enriched	Enriched	Enriched	No expres	YES		
Q9BRP8-2;Q9BRP	Partner of Y14 and m	WIBG	22.704	52.7	17	17	235.32	0	153570	108730	131980	124570	168090	137970	193590	120730	111680	154990	Enriched	Enriched	Moderate	No expres	YES		
Q9BRR6-2;Q9BRR	ADP-dependent gluc	ADPGK	53.96	15.3	6	5	18.76	0	13618	7323.1	11279	22437	10163	11737	10656	19585	5792.8	14763	Enriched	Enriched	Enriched	No expres	YES		
Q9BRX2	Protein pelota homol	PELO	43.359	10.6	3	3	25.676	0	6628.2	2454	4690.6	7679.8	9138.7	12478	12374	5138.8	5768.8	8983.9	Low	Moderate	Enriched	No expres	YES		
Q9BRX8-2;Q9BRX	Redox-regulatory pro	FAM213A	24.462	29.4	10	10	51.428	0	63575	44415	55374	77394	50846	114550	124810	145700	36300	91517					YES		
Q9BRZ2	E3 ubiquitin-protein	TRIM56	81.487	12.5	8	8	20.431	0	22164	17800	19112	15351	18199	15074	23721	28196	14967	20024	Enriched	Enriched	Enriched	No expres	YES		
Q9BS26	Endoplasmic reticulu	ERP44	46.971	39.2	28	28	106.42	0	164750	131460	122230	139860	159080	181520	198550	179060	105030	153720	Enriched	Enriched	Enriched	No expres	YES		
Q9BS40	Latexin	LXN	25.75	11.7	3	3	4.2548	0.00063	1315.7	1488.1	1473.5	1259.7	1680.8	965.21	546.91	590.51	386.52	806.05	Enriched	Moderate	Enriched	No expres	YES		
Q9BSD7;Q5TDF0	Cancer-related nucle	NTPCR	20.713	49.5	10	10	21.92	0	13192	7008.3	11615	19310	8553.7	14271	11990	20546	8182	17492					YES		
Q9BSF4	Uncharacterized prot	C19orf52	29.233	22.3	4	4	17.032	0	24949	22956	19968	22643	28493	18612	16702	18506	6214.8	19729	No expres	Moderate	Moderate	No expres	YES		
Q9BSH4	Translational activato	TACO1	32.477	13.5	3	3	44.168	0	10466	22704	23917	5506.3	14904	3624.9	17781	20183	15753	13586	Moderate	Moderate	Moderate	No expres	YES		
Q9BSH5	Haloacid dehalogena	HDHD3	28	29.1	9	9	49.357	0	39758	34263	41629	23970	57473	33018	45944	50204	19863	37496	Moderate	Moderate	Moderate	No expres	YES		
Q9BSJ8;Q9BSJ8-2	Extended synaptotag	ESYT1	122.85	31.9	43	43	94.183	0	104600	82801	96490	141370	101300	121430	137610	155270	68349	133350	Low	Enriched	Enriched	Enriched	YES		
Q9BSY4;Q9BSY4-	Coiled-coil-helix-coil	CHCHD5	12.395	11.8	1	1	8.2923	0	13873	8343.7	9292	12157	15292	13149	13124	13106	8683.6	16236	Low	Enriched	Enriched	No expres	YES		
Q9BT09	Protein canopy homo	CNPY3	30.748	43.5	20	20	103.97	0	67017	72608	53232	60448	69728	57117	66093	75561	48650	58587	Moderate	Enriched	Moderate	No expres	YES		
Q9BT22;Q9BT22-2	Chitobiosyldiphosph	ALG1	52.518	16.2	9	9	25.852	0	23563	19235	24428	33154	28209	21853	28087	34211	13624	27325	No expres	Moderate	Moderate	No expres	YES		
Q9BT40-2;Q9BT40	Inositol polyphospha	INPP5K	42.783	5.9	4	4	6.078	0	6994.7	6338	7494.3	6004	8931.3	3892.4	5633.9	5877.3	3446.4	5228.2	Moderate	Moderate	Moderate	Enriched	YES		
Q9BT73	Proteasome assembly	PSMG3	13.104	9.8	1	1	3.2452	0.00077	13962	11570	11345	12860	11171	8501.3	9964.4	14228	8014.2	14034	Low	Enriched	Enriched	No expres	YES		
Q9BT78;D6RFN0;I	COP9 signalosome co	COPS4	46.268	51.5	22	22	82.989	0	86336	61006	67343	87539	74605	78900	78801	93940	49297	85264	Enriched	Enriched	Enriched	No expres	YES		
Q9BTC0	Death-inducer obliter	DIDO1	243.87	4.6	9	9	18.942	0	25350	31692	31046	24789	39981	19146	29735	24831	15943	28129	Moderate	Moderate	Enriched	Moderate	YES		
Q9BTE1-2;H3BUD	Dynactin subunit 5	DCTN5	16.633	28.9	4	4	5.7273	0	10421	5231.8	7694.1	12092	7808.6	11658	10093	14649	4366.7	12100	Low	Moderate	Enriched	Low	YES		
Q9BTE3-2;Q9BTE	Mini-chromosome ma	MCMBP	72.748	2.7	1	1	2.9406	0.00169	15645	13586	13237	14723	14140	12128	15611	15528	10659	17362					YES		

Q9BTT0-3;Q9BTT	Acidic leucine-rich n	ANP32E	25.125	25.9	8	8	24.985	0	11265	5549.7	6636.7	22548	6223.9	14399	7066.9	12577	4057.6	12628	Moderate	Moderate	Enriched	Moderate	YES	
Q9BTT6;Q5T0G3;	Leucine-rich repeat-c	LRRC1	59.241	9.4	5	2	3.9198	0.00061	14544	25062	18272	16566	19225	11261	11046	10452	8780.1	11793	Moderate	Moderate	Enriched	No expres	YES	
Q9BTV4	Transmembrane prote	TMEM43	44.875	24	13	13	62.845	0	89037	65324	76948	88381	77650	136970	129640	91180	63101	95846	Enriched	Enriched	Enriched	No expres	YES	
Q9BTX3-2			11.039	17	4	4	16.553	0	34279	27125	30252	24981	33093	32196	31167	23669	20068	29074						
Q9BTY2	Plasma alpha-L-fucos	FUCA2	54.066	7.3	3	3	6.4323	0	5328.7	5080.6	5198.8	8280.9	4094.2	5433.8	4989.1	11645	2518.6	6398.6	Moderate	Enriched	Enriched	No expres	YES	
Q9BTZ2-5;Q9BTZ	Dehydrogenase/reduc	DHRS4	21.036	16.6	5	5	7.7441	0	8588.5	10916	14537	7083.6	14173	9320.6	13920	13326	9968.4	12296	Enriched	Enriched	Enriched	No expression		
Q9BU23-3;Q9BU2	Lipase maturation fac	LMF2	67.155	15.3	11	11	76.675	0	111040	68847	81259	106270	97889	99864	107710	70132	50131	90154	Enriched	Enriched	Enriched	Enriched	YES	
Q9BU68	Proline-rich protein 1	PRR15L	11.705	26.2	2	2	23.983	0	12588	12087	10867	12064	13571	10855	8926.9	9216.5	6363.1	11904						
Q9BUB5-3;Q9BUE	MAP kinase-interacti	MKNK1;DKFZp686E14	39.103	17.9	5	5	10.124	0	40148	31429	27480	31387	30429	22948	21208	24016	10751	26862	Enriched	Enriched	Enriched	Enriched	YES	YES
Q9BUB7-2;Q9BUE	Transmembrane prote	TMEM70	18.57	11.2	2	2	5.8394	0	13488	8052.2	10822	11162	12063	16558	12798	11823	7974.4	12170	Moderate	Enriched	Enriched	No expression		
Q9BUF5	Tubulin beta-6 chain	TUBB6	49.857	40.6	43	1	10.85	0	14817	8846.2	10218	12157	14600	11314	11141	9430.5	4794.5	10773	Moderate	Enriched	Enriched	No expres	YES	
Q9BUF7	Protein crumbs homo	CRB3	12.854	13.3	1	1	20.856	0	2629.3	2268.1	2958.7	3051.8	3863.4	1990.8	2538.6	2882.4	1806.8	2883.4	Enriched	Enriched	Enriched	No expres	YES	
Q9BUH6	Uncharacterized prot	C9orf142	21.639	28.4	7	7	22.097	0	22376	14105	17477	12819	23193	11282	22741	21158	11316	21179	Moderate	Moderate	Moderate	No expres	YES	
Q9BUL9	Ribonuclease P prote	RPP25	20.632	6.5	1	1	2.1821	0.00561	2928.8	3647	4231.8	2247.9	6018.5	1758.2	4151.9	3201.7	2232.3	3632.6	No expres	Moderate	Moderate	No expres	YES	
Q9BUN8-2;Q9BUN	Derlin-1	DERL1	26.423	3.9	1	1	2.1073	0.00676	659.12	521.77	588.27	438.8	948.02	1044.7	6019.2	11138	1151.8	1446.8	Enriched	Enriched	Enriched	No expression		
Q9BUP0;A0A087X	EF-hand domain-con	EFHD1	26.927	20.9	5	3	7.0023	0	9727.3	7494.7	7974.9	9780.6	8494.8	8050	8577.6	9138.2	3851.9	10183	Moderate	Low	Moderate	Moderate		
Q9BUQ8	Probable ATP-depen	DDX23	95.581	16.6	15	15	61.042	0	43967	32529	45313	34871	46297	40322	63923	44614	44317	54194	Moderate	Moderate	Moderate	Moderate	YES	
Q9BUT1;Q9BUT1-	3-hydroxybutyrate de	BDH2	26.724	37.1	10	10	26.833	0	48162	37621	42367	49188	45143	64586	60601	80363	28685	62048	Enriched	Enriched	Enriched	No expres	YES	
Q9BUV8-4;Q9BU	Uncharacterized prot	C20orf24	9.53	16.1	2	2	4.5047	0.00042	11021	9455.3	14871	4958.7	16038	15946	12477	5475.2	9052.6	8500.6	Enriched	Enriched	Enriched	No expression		
Q9BV10;H7C5R7;	Dol-P-Man:Man(7)G	ALG12	54.654	10.7	6	6	21.174	0	8342.2	7535.1	8011.3	8846.4	9052.1	20507	16964	32862	5524.9	10779	Moderate	Low	Moderate	No expression		
Q9BV20-2;Q9BV2	Methylthioribose-1-p	MRI1	34.529	17.4	6	6	18.29	0	18532	14798	16935	18773	19679	29612	30476	16275	11295	19701	Enriched	Enriched	Enriched	No expres	YES	
Q9BV40;C9JXZ5;E	Vesicle-associated m	VAMP8	11.438	32	4	4	23.539	0	6757.8	3233.8	3767.3	6527.4	4199.1	7445.7	28261	22656	14485	13455	No expres	Enriched	Enriched	Enriched	YES	
Q9BV57	1,2-dihydroxy-3-keto	ADI1	21.498	27.9	5	5	18.044	0	19393	9453	18566	12504	9552.3	13694	22697	26437	7951.2	23919	Enriched	Enriched	Enriched	No expres	YES	
Q9BV79;H3BM30;	Trans-2-enoyl-CoA r	MECR	40.461	8.8	4	4	7.2124	0	2901.9	2204.7	1638.9	2847.6	3747.4	3155.3	3350.4	2650.9	1655.3	3123.6	Moderate	Low	Moderate	No expres	YES	
Q9BVC6	Transmembrane prote	TMEM109	26.21	13.2	8	8	21.511	0	12372	8773.7	8866.4	12127	12967	11868	32522	38392	5982.8	15558	Moderate	Enriched	Enriched	Enriched	YES	
Q9BVG4	Protein PBDC1	PBDC1	26.056	32.2	9	9	39.239	0	24575	19014	21556	24098	19796	28221	22862	39774	10373	29519					YES	
Q9BVI4	Nucleolar complex p	NOC4L	58.467	1.9	2	2	3.7643	0.0006	3508.7	1255.7	1810.8	2589.9	2258.4	3048.9	2597.2	3389	1026.1	3920.9	Enriched	Low	Low	No expres	YES	
Q9BVJ6-3;Q9BVJ6	U3 small nucleolar R	UTP14A	82.004	8.1	5	3	18.059	0	4237.7	1246.2	2721.8	5516.9	1780.5	6068.7	2537.2	4603.2	1590.1	4283.7	Moderate	Moderate	Moderate	No expres	YES	
Q9BVJ7	Dual specificity prote	DUSP23	16.588	20.7	3	3	3.8292	0.00061	1102.4	1014.2	1323.2	801.85	1000.2	1715.4	2674.9	2999	1222.3	1568.1	Enriched	Enriched	Enriched	No expres	YES	
Q9BVK6	Transmembrane emp	TMED9	27.277	47.7	27	21	170.68	0	202360	149630	149340	163850	181700	185620	241590	168980	105490	158430	Enriched	Enriched	Enriched	Enriched	YES	
Q9BVM4	Gamma-glutamylami	GGACT	17.328	15.7	3	3	8.4821	0	28138	20446	22632	29745	23424	32121	21182	23910	10864	22887					YES	
Q9BVP2-2;Q9BVP	Guanine nucleotide-b	GNL3	60.54	22.9	12	12	106.33	0	37060	28489	38581	39806	40559	38814	37775	38983	19803	40090	Moderate	Enriched	Enriched	No expres	YES	
Q9BVQ7-2;Q9BV	Spermatogenesis-asso	SPATA5L1	66.111	3.9	2	2	4.2323	0.00063	2629.8	3007.6	3144.8	3258.8	3435.4	2683.4	3027.6	2335.4	2097.2	2181.1	Low	Moderate	Enriched	No expres	YES	
Q9BW04;Q9BW04	Specifically androgen	SARG	63.964	6.8	3	3	19.736	0	20631	33476	23972	21837	28608	18500	28059	24095	20485	21680					YES	
Q9BW27-3;Q9BW	Nuclear pore comple	NUP85	69.799	16.9	10	10	37.853	0	37471	26671	34419	35235	39574	27897	39060	30440	27962	40709	Enriched	Enriched	Enriched	No expres	YES	
Q9BW30	Tubulin polymerizati	TPPP3	18.985	19.3	4	4	5.097	0.00044	5210.4	11032	7370	3260.6	9393.1	1725.9	2231.7	2677.6	1401.5	3018.9	Enriched	Moderate	Enriched	No expres	YES	
Q9BW60-2;Q9BW	Elongation of very lo	ELOVL1	29.485	4.4	1	1	2.8929	0.00186	3008.2	3182.7	3188.5	2616.4	3392	2338.4	3396.8	2946.4	1535.5	2699.2	Moderate	Enriched	Enriched	No expres	YES	
Q9BW85;M0R2S3	Coiled-coil domain-c	CCDC94	37.085	15.2	4	4	14.378	0	5258.5	5574	5694.1	3983.1	7917.9	3210.1	4172	3981	3804.7	5657.5	Moderate	Low	Moderate	Moderate	YES	
Q9BW92;F6S7Q7;	Threonine--tRNA lig	TARS2	81.035	5.4	3	3	8.5301	0	4735.4	3756.7	3430.4	4477	2879	5669.1	4521.2	5596.1	2929.8	5820.1	Enriched	Moderate	Moderate	No expres	YES	
Q9BWD1;Q9BWD	Acetyl-CoA acetyltra	ACAT2	41.35	14.1	5	5	15.982	0	2998.3	2847.1	3547.5	2487.2	4355.1	2765.2	3973.9	4435.8	2322.3	3007.7	Enriched	Moderate	Enriched	No expres	YES	
Q9BWE0;Q9BWE	Replication initiator	REPIN1;ZNF785	63.574	5.8	3	1	10.853	0	1057.4	649.29	668.19	789.77	1295.7	847.49	1653	995.01	821.52	932.83	Enriched	Enriched	Enriched	No expression		
Q9BWF3;E9PB51;	RNA-binding protein	RBM4;RBM4B	40.313	22	9	6	18.198	0	15053	10657	14625	13320	14972	14896	17879	15970	9373.1	17009	Enriched	Enriched	Enriched	Enriched	YES	
Q9BWH2;H7C0K8	FUN14 domain-conta	FUNDC2	20.675	17.5	6	6	59.09	0	53984	50705	53243	37735	83007	34215	37246	34846	17238	35642	Enriched	Enriched	Enriched	No expres	YES	
Q9BWJ5	Splicing factor 3B su	SF3B5	10.135	54.7	4	4	18.646	0	8110.4	4897.4	6024.7	7641.5	10831	4342.9	3256	4244.3	1756.6	4944.7	Enriched	Enriched	Enriched	No expres	YES	
Q9BWS9;Q9BWS9	Chitinase domain-co	CHID1	44.94	41	25	14	62.288	0	118250	86668	81805	115730	105340	109720	91133	90496	49604	97347	Enriched	Enriched	Enriched	No expres	YES	
Q9BX40-2;Q9BX4	Protein LSM14 homo	LSM14B	42.02	6.8	3	3	35.249	0	16512	14159	13927	13351	22171	10903	10796	13219	7279.2	13052	Moderate	No expres	Low	No expres	YES	
Q9BX66-12;Q9BX	Sorbin and SH3 dom	SORBS1	143.74	16	24	24	114.36	0	123430	120610	123620	119090	159550	121510	104120	119230	55652	134480	Moderate	Enriched	Enriched	No expres	YES	
Q9BX67-2;Q9BX6	Junctional adhesion r	JAM3	29.223	5	2	2	8.2221	0	3416.4	6018.6	6778.7	3487.1	8653.6	1915.2	6994.3	4024.8	2633.9	4685.7	Enriched	Moderate	Enriched	Enriched	YES	
Q9BX68	Histidine triad nuclec	HINT2	17.162	37.4	9	9	20.297	0	16843	18576	18614	12865	25925	14709	21679	16489	14121	17993	Enriched	Enriched	Enriched	No expres	YES	
Q9BX95	Sphingosine-1-phosp	SGPP1	49.107	9.5	5	5	21.223	0	11140	9471.1	11862	8458.1	17083	6888.8	9068	6960.1	5534	9307.4	Low	Enriched	Enriched	No expres	YES	
Q9BX97	Plasmalemma vesicle	PLVAP	50.594	25.8	15	15	37.582	0	130090	65446	98390	136270	108950	104470	93331	94214	57937	118340	No expres	Moderate	Moderate	No expres	YES	
Q9BXN1	Asporin	ASPN	43.417	31.1	15	15	47.669	0	62335	53296	89734	83701	71594	78690	191340	269530	63014	78208	No expres	Low	Moderate	No expres	YES	
Q9BXP5-4;Q9BXP	Serrate RNA effector	SRRT	100.15	19.2	19	19	87.531	0	43593	32652	42613	35723	47637	40645	66076	53343	38540	52114	Enriched	Enriched	Enriched	Moderate	YES	
Q9BXR0;K7ESP6;	Queuine tRNA-ribos	QTRT1	44.047	10.7	3	2	27.421	0	15333	14160	16414	12108	16292	11975	15740	13715	10417	15010	Enriched	Enriched	Moderate	No expres	YES	
Q9BXS5;Q9BXS5-	AP-1 complex subun	AP1M1	48.586	36.9	18	16	50.642	0	67444	62178	69218	61221	83777	72887	105550	85201	44972	80077	Low	Enriched	Enriched	No expres	YES	
Q9BXV9	Uncharacterized prot	C14orf142	10.859	38	7	7	82.579	0	35047	22994	22863	64551	28360	27934	23858	53555	17549	36363	Low	Moderate	Enriched	No expression		
Q9BXW7-2;Q9BX	Cat eye syndrome cri	CECR5	43.588	14	5	5	29.084	0	14326	13134	15860	13365	19101	13333	11282	11496	6056.8	11792	Enriched	Enriched	Enriched	No expres	YES	
Q9BXX0	EMILIN-2	EMILIN2	115.69	5.5	5	5	18.546	0	25760	56617	27753	23327	32378	22922	43328	58285	50182	38674	Enriched	Enriched	Moderate	No expres	YES	
Q9BY32;Q9BY32-	Inosine triphosphate	ITPA	21.445	20.1	4	4	8.3596	0	20109	16898	17352	24641	20877	18310	49936	56429	16856	21346	Moderate	Enriched	Enriched	Moderate	YES	
Q9BY44;Q9BY44-	Eukaryotic translatio	EIF2A	64.989	34.2	21	21	98.141	0	160390	110300	137910	117750	196050	127160	115270	95062	68421	111020	Enriched	Enriched	Enriched	Low	YES	
Q9BY50;B4DI03;K	Signal peptidase com	SEC11C;SEC11L3	21.542	49.5	17	17	91.307	0	127190	60692	85318	268130	74995	152420	132980	118050	54945	130310	Enriched	Enriched	Enriched	No expression		
Q9BY89	Uncharacterized prot	KIAA1671	196.71	1.9	3	3	6.7821	0	16653	11356	10135	11203	14994	41406	30304	12915	10419	15483					YES	
Q9BYB0-3;Q9BYE	SH3 and multiple an	SHANK3	171.15	2.4	2	2	31.609	0	4221.2	3338.6	3623.9	5987.9	3221.2	4045.8	3361.3	5194.6	1835.1	5353.9	No expres	Low	Moderate	No expression		
Q9BYC8	39S ribosomal protei	MRPL32	21.405	7.4	2	2	3.6955	0.0008	3177.2	3801.1	4449.7	2859.8	5424.7	3016.9	6097.2	5191.9	4293.1	4918.9	Enriched	Enriched	Enriched	No expres	YES	
Q9BYD2	39S ribosomal protei	MRPL9	30.243	15.7	5	5	7.909	0	10298	9814.5	10970	10801	11153	10436	12282	12144	9602.8	10451	Enriched	Enriched	Enriched	Moderate	YES	
Q9BYG5;Q9BYG5	Partitioning defective	PARD6B	41.182	5.1	2	2	3.1156	0.00095	16932	16081	21624	16749	20079	15757	26030	20973	16403	15197	Low	Moderate	Moderate	Low	YES	
Q9BYN8	28S ribosomal protei	MRPS26	24.211	25.9	5	5	6.3409	0	7005	4681	5986	7787	6719.6	6253.8	5768.2	6043.5	2312	6892.6	Enriched	Enriched	Enriched	No expres	YES	
Q9BYT8;E9PCB6	Neurolysin, mitochor	NLN	80.651	7.1	6	6	82.182	0	52789	36800	43101	51175	38849	60265	42027	56233	19089	54232	Enriched	Enriched	Enriched	No expres	YES	
Q9BYV8-3;Q9BY	Centrosomal protein	CEP41	14.544	12.6	1	1	4.0917	0.00062	376.96	604.74	568.44	605.17	737.72	663.43	955.07	815.32	993.5	945.1					YES	
V9GYZ0;Q9BZ23-	Pantothenate kinase	PANK2	17.217	12	1	1	21.637	0	1311.5	1404.3	2059.6	1150.5	1961.7	726	1353.2	735.65	759.39	1263.5	Enriched	Enriched	Enriched	No expres	YES	
Q9BZE1;S4R369	39S ribosomal protei	MRPL37	48.117	21.3	8	8	15.96	0	46164	28492	31250	32399	36000	28095	25935	34080	12759	35590	Enriched	Enriched	Enriched	No expres	YES	
Q9BZE4;Q9BZE4-	Nucleolar GTP-bindi	GTPBP4	73.964	19.4	14	14	57.583	0	85585	64569	73854	81644	95761	82096	94323	89012	51712	92461	Moderate	Moderate	Enriched	No expres	YES	
Q9BZE9-2;Q9BZE	Tether containing UB	ASPSCR1	69.989	25	17	17	90.067	0	42930	29951	35278	35306	51363	31683	38764	31949	25988	40844	Moderate	Low	Moderate	No expres	YES	
Q9BZF1-3;Q9BZF	Oxysterol-binding pr	OSBPL8	96.955	13.2	12	11	109.7	0	52216	38197	44190	53041	43120	38205	54977	48946	24134	49656	Enriched	Enriched	Enriched	Low	YES	
Q9BZF9;F5H2B9;	Uveal autoantigen wi	UACA	162.5	10.8	18	12	58.346	0	55456	45978	58583	48806	64115	49966	66510	57376	48697	62428	Enriched	Enriched	Enriched	No expres	YES	
Q9BZH6	WD repeat-containin	WDR11	136.68	12.3	13	13	56.876	0	84247	60022	68009	93050	77027	83967	79028	88171	41518	86167					YES	
Q9BZK7	F-box-like/WD repea	TBL1XR1	55.594	6.4	4	4	10.394	0	7590.4	5370.4	5310.7	5748.6	8447.2	5651.2	6285.3	7982	4768.3	7689	Enriched	Enriched	Enriched	No expres	YES	
Q9BZL4;K7EL81;	Protein phosphatase	PPP1R12C	84.88	6.3	6	5	9.9675	0	6494.6	7174.9	9099.6	6900	10946	6535.8	12226	11583	7866.3	12401	Enriched	Enriched	Moderate	No expres	YES	
Q9BZQ8	Protein Niban	FAM129A	103.13	36.3	56	56	323.31	0	370400	244290	299860	288600	351190	263400	380450	304450	273370	332160	Enriched	Enriched	Enriched	No expres	YES	
Q9BZV1;K7EP32;	UBX domain-contain	UBXN6	49.753	14.1	8	8	58.04	0	39364	36352	45273	29578	48596	53079	45719	34749	29839	36057	Enriched	Enriched	Enriched	No expres	YES	
Q9BZX2	Uridine-cytidine kina	UCK2	29.299	13.8	3	3	7.5987	0	4145.5	1676.9	3056.1	4193.1	2614.4	1750.2	1944.7	1948.3	747.1	3044.6	No expres	Moderate	Enriched	Moderate		
Q9BZZ2-2;Q9BZZ	Sialoadhesin	SIGLEC1	175.72	1.6	2	2	3.2857	0.00078	10278	18952	20086	11671	23745	6578.1	10996	7892.9	5710	9818.6	Enriched	Moderate	Low	No expres	YES	
Q9BZZ5-2;Q9BZZ	Apoptosis inhibitor 5	API5	56.769	29.2	22	22	129.11	0	114730	73046	90745	103160	105360	111400	126940	172610	59659	131450	Low	Enriched	Enriched	Low	YES	
Q9C005	Protein dpy-30 homo	DPY30	11.25	48.5	7	7	9.8769	0	20519	15438	18555	20878	18865	16240	17551	19630	9179.4	19977	Moderate	Enriched	Enriched	No expression		
Q9C040;Q9C040-2	Tripartite motif-conta	TRIM2	81.529	9.3	6	6	34.721	0	11481	10640	12539	8797.3	14323	13418	29745	28691	15478	16955	Low	Moderate	Enriched	Enriched	YES	
Q9C0B1	Alpha-ketoglutarate-	FTO	58.281	25.7	14	14	63.487	0	21279	18046	24844	23252	29570	28331	28710	28119	17095	24538	Enriched	Enriched	Enriched	Enriched	YES	
Q9C0B5-2;Q9C0B	Palmitoyltransferase	ZDHHC5	71.951	9.8	4	4	9.369	0	7931.6	7904.2	7325	6488.6	8008.4	8435.2	6235.6	6861.3	3256.2	5078.6	Enriched	Enriched	Enriched	No expres	YES	
Q9C0C2;Q9C0C2-	182 kDa tankyrase-1-	TNKS1BP1	181.79	26.1	45	45	198.29	0	156180	164000	174690	138680	206090	137890	230190	188760	174460	205990	Moderate	Enriched	Moderate	No expres	YES	
Q9C0C9;K7ES11	E2/E3 hybrid ubiquit	UBE2O	141.29	7	8	8	19.511	0	32474	23270	26574	33315	30524	31974	31103	36821	16501	31227	Moderate	Moderate	Moderate	No expres	YES	
Q9C0I1-3;Q9C0I1-	Myotubularin-related	MTMR12	73.231	11.5	8	8	15.631	0	19247	13480	14466	16704	16748	12203	12112	16169	9783.6	14194	Enriched	Enriched	Enriched	No expres	YES	
Q9C0J8	pre-mRNA 3 end pro	WDR33	145.89	2.2	2	2	5.271	0.00022	11783	10139	14229	9367.1	16442	14485	20965	17456	17223	16924	Enriched	Enriched	Enriched	No expres	YES	
Q9GZL7	Ribosome biogenesis	WDR12	47.707	14.4	5	5	10.405	0	8531.1	8068.8	8009.7	11520	8480.5	7976.8	7359.7	8169.8	2621.8	9347.6	Enriched	Enriched	Enriched	No expres	YES	
Q9GZM7;F6SDV2	Tubulointerstitial ne	TINAGL1	52.387	42.8	39	2	179.62	0	189100	174200	197470	175860	240860	206650	260360	301100	113700	203210	Moderate	Low	Moderate	No expres	YES	
Q9GZM7-3	Tubulointerstitial ne	TINAGL1	48.807	44	38	1	1.9826	0.00803	1782.8	1408.6	1577.8	1094.3	2412.9	2157.1	12563	13332	1677.5	2200.6	Moderate	Low	Moderate	No expres	YES	
Q9GZP4-2;Q9GZP	PITH domain-contain	PITHD1	24.121	41.9	9	7	27.375	0	45851	38463	43639	46371	43850	48087	63970	46250	45239	49946					YES	
Q9GZS3;H0YL19;	WD repeat-containin	WDR61	33.58	30.8	15	15	122.94	0	69739	36334	45057	78289	50008	85488	67389	88140	32740	69441	Moderate	Enriched	Enriched	Low	YES	
Q9GZT3-2;Q9GZT	SRA stem-loop-inter	SLIRP	12.122	24.3	5	5	36.076	0	32104	39414	37563	29101	46614	39064	76485	74091	39993	68922					YES	
V9GYE8;Q9GZT4	Serine racemase	SRR	12.442	23.7	2	2	197.03	0	17578	5925.8	11757	16779	10708	41964	42589	48399	12782	29778	Enriched	Moderate	Moderate	No expres	YES	
Q9GZT6-2;Q9GZT	Coiled-coil domain-c	CCDC90B	27.979	23.3	9	9	42.872	0	68186	50012	58344	66467	62922	84189	43142	62010	23254	65522	Enriched	Enriched	Enriched	No expres	YES	
Q9GZT8-2;Q9GZT	Putative GTP cycloh	NIF3L1	38.983	26	13	13	49.701	0	78617	37664	43983	73190	55279	89569	61854	62322	32345	67321	Moderate	Enriched	Enriched	No expres	YES	
Q9GZT9;Q9GZT9-	Egl nine homolog 1	EGLN1	46.02	21.4	8	8	47.404	0	27405	18355	23356	18992	25394	22856	25502	21021	13957	24745	Enriched	Enriched	Enriched	No expression		
Q9GZY8-5;Q9GZY	Mitochondrial fission	MFF	27.105	6.3	1	1	2.5753	0.00326	1412.3	1023.8	1657.5	837.64	2084.3	1657.7	2343.4	1352	2156.7	2003.9	Moderate	Enriched	Enriched	No expres	YES	
Q9GZZ9;E7EQ61;	Ubiquitin-like modifi	UBA5	44.863	28.2	25	9	101.87	0	312240	213520	228070	204380	362740	241130	228140	169660	105640	188370	Moderate	Enriched	Enriched	No expres	YES	
Q9H008	Phospholysine phosp	LHPP	29.165	31.1	13	6	63.92	0	54105	44014	54599	74287	68172	52364	44913	95015	23051	61464	Moderate	Moderate	Moderate	No expres	YES	
Q9H061;E9PI90	Transmembrane prote	TMEM126A	21.527	32.3	12	12	16.821	0	38641	19425	23915	33833	30248	37831	38139	48414	20993	32982	Low	Enriched	Enriched	No expres	YES	
Q9H082	Ras-related protein R	RAB33B	25.717	12.7	3	2	3.3553	0.00078	4913.5	3549.8	4325.1	3287.2	5415.5	5646.1	6857.1	5466.2	4228.6	6626.7	Moderate	Moderate	Moderate	No expression		
Q9H089;H7C2X7	Large subunit GTPas	LSG1	75.225	6.5	4	4	16.129	0	6287.1	7082.8	9074.7	7351.2	10964	5806.8	11744	7227.2	8416	8392.2	Enriched	Moderate	Moderate	No expres	YES	
Q9H098;Q9H098-2	Protein FAM107B	FAM107B	15.558	35.1	10	10	29.435	0	15779	10103	12019	18636	20515	10399	14952	21748	12002	21484	Enriched	Enriched	Enriched	No expres	YES	
Q9H0A0-2;Q9H0A	N-acetyltransferase 1	NAT10	107.3	15.4	14	14	26.718	0	17168	14660	16114	36809	17664	19072	15283	19944	9323.8	19920	Enriched	Enriched	Enriched	No expres	YES	
Q9H0B6;Q9H0B6-	Kinesin light chain 2	KLC2	68.934	9.8	6	2	7.4333	0	2439	2686.4	2318.7	3268.9	3057.2	2099.3	2042.5	2549	1750.6	2762.1	Enriched	Moderate	Enriched	No expres	YES	
Q9H0C8;F8SNU7;	Integrin-linked kinase	ILKAP;ILKAP3	42.906	9.2	4	4	6.1789	0	1999.6	1915.1	2158.7	1328.4	2683.6	1583.9	1927.7	1699.9	1713.4	1609	Low	Moderate	Moderate	No expres	YES	
Q9H0D6-2;Q9H0D	5-3 exoribonuclease	XRN2	99.96	24.8	26	26	133.03	0	97937	70444	79081	100310	84062	96261	103650	111870	74123	115970	No expres	Enriched	Enriched	No expres	YES	
Q9H0E2;E7EN89;	Toll-interacting prote	TOLLIP	30.281	26.6	7	7	11.867	0	40772	28557	35525	54063	33767	50156	36198	35367	18573	53303	Moderate	Enriched	Enriched	No expres	YES	
Q9H0J9;G5E9U9	Poly [ADP-ribose] po	PARP12	79.063	4.1	3	3	11.887	0	19562	14390	18477	14912	22510	20520	23776	23124	10317	19642	Enriched	Enriched	Enriched	No expres	YES	
Q9H0L4	Cleavage stimulation	CSTF2T	64.436	14.3	10	2	30.923	0	35131	26112	29166	30181	42549	29303	34212	30434	22618	33245	Moderate	Moderate	Enriched	Low	YES	
X6RM59;Q9H0P0-	Cytosolic 5-nucleotic	NT5C3A	37.405	28.4	12	12	33.81	0	44944	25205	37107	37180	29368	44108	49097	64957	33984	49307					YES	
Q9H0Q0;C9JPE5;	Protein FAM49A	FAM49A	37.312	6.8	2	1	13.294	0	9804.1	8642.4	9007.2	9779.7	8465	12335	16032	10631	8684.8	13426	Moderate	Moderate	Moderate	Low	YES	
Q9H0R4;Q9H0R4-	Haloacid dehalogena	HDHD2	28.536	32.8	8	8	21.755	0	16058	7614.9	8780.7	18152	9482.5	20961	13425	17162	7211.7	14137	Enriched	Enriched	Enriched	No expres	YES	
Q9H0S4-2;Q9H0S	Probable ATP-depen	DDX47	45.169	9.4	3	3	8.5234	0	8156.1	5422.9	6763.9	9502.2	8253.3	10875	15142	17915	6994.9	12790	Enriched	Enriched	Enriched	No expres	YES	
Q9H0U4;E9PLD0;	Ras-related protein R	RAB1B;RAB1C	22.171	57.2	35	12	129.39	0	69040	53247	60410	113390	80475	83485	146200	163420	56331	123170	Enriched	Enriched	Enriched	No expres	YES	
Q9H0U6	39S ribosomal protei	MRPL18	20.576	8.9	1	1	14.53	0	2151.9	1573	1839.5	1475.7	2002.4	2556.6	2707.8	2360.4	812.14	2340.5	Moderate	Enriched	Enriched	No expres	YES	
Q9H0V9;Q9H0V9-	VIP36-like protein	LMAN2L	39.71	11.5	4	4	13.444	0	13117	10146	10505	15330	12462	20067	26050	15619	11953	19789	Enriched	Enriched	Enriched	No expres	YES	
Q9H0W5	Coiled-coil domain-c	CCDC8	59.374	5.9	2	2	35.165	0	8924.2	7165.9	8581.1	9596.1	8130	9723.5	11986	10102	6742.3	11308	Moderate	Enriched	Enriched	No expres	YES	
Q9H0W9-2;Q9H0	Ester hydrolase C11o	C11orf54	33.098	44.3	16	16	36.797	0	64054	76388	77288	52665	92038	55503	190180	85072	118030	68792	Moderate	Moderate	Enriched	No expres	YES	
Q9H147	Deoxynucleotidyltran	DNTTIP1	37.013	5.2	3	3	5.9161	0	1332.4	1815.7	3172.5	2263.1	2024.3	1478.7	8489.6	1603.8	8620	3377.2	Enriched	Enriched	Enriched	No expres	YES	
Q9H173;D6REA1;	Nucleotide exchange	SIL1	52.084	12.4	6	6	17.467	0	7351.7	6053.1	6238	10086	8873	6582.6	4280.6	7422.1	2034	7689.5	Low	Enriched	Enriched	No expres	YES	
Q9H1A4;H0Y564	Anaphase-promoting	ANAPC1	216.5	2.8	4	4	7.787	0	10034	2924.4	4510.5	13144	5513.2	4120.6	4139.5	4611.5	2398.9	9831.4	Enriched	Enriched	Moderate	No expres	YES	
Q9H1B7	Interferon regulatory	IRF2BPL	82.658	9.3	7	5	14.94	0	31764	22623	28357	29325	38236	39992	47712	54965	24340	41575					YES	
Q9H1C7	Cysteine-rich and tra	CYSTM1	10.631	9.3	1	1	1.8241	0.00975	2256.6	1746.8	2187.6	3354.5	2515.3	1838.4	1850.3	1707.7	1432.5	2082.8						
Q9H1E3;Q9H1E3-	Nuclear ubiquitous c	NUCKS1	27.296	23.9	10	10	54.068	0	52360	52106	65666	44959	85975	43201	139300	96266	75580	68152	Enriched	Enriched	Enriched	No expres	YES	
Q9H1E5	Thioredoxin-related t	TMX4	38.952	13.5	6	6	17.081	0	15414	13714	20813	11683	19545	7275.9	10286	9886.6	6031.2	10431	Moderate	Enriched	Enriched	Enriched	YES	
Q9H1H9-3;Q9H1H	Kinesin-like protein	KIF13A	196.07	2.6	3	2	34.16	0	1451.8	2029.7	3350	1674.5	2168.1	2351.2	7326.2	6893.5	4381.3	4734.8	Enriched	Low	Low	No expres	YES	
Q9H1I8-3;Q9H1I8	Activating signal coi	ASCC2	77.368	8.7	5	5	8.4907	0	5093.6	2515.9	3726.1	8381.3	3975	9714.9	4756.6	6280	1827	4875	No expres	Low	Moderate	Enriched	YES	
Q9H1J1-3;Q9H1J1	Regulator of nonsens	UPF3A	17.112	9.3	1	1	5.7539	0	925.79	920.96	1504.7	637.73	1434.3	2053	5995.5	4327.4	3373.6	3643.1	Enriched	Enriched	Enriched	Enriched		
Q9H1K0;H7C204	Rabenosyn-5	ZFYVE20	88.869	3.7	3	3	4.1329	0.00062	6108.8	7396.5	6378.2	5146.9	9571.9	4558.3	6568.2	4377.5	3382.1	4476.3	Moderate	Enriched	Enriched	No expres	YES	
Q9H1X3	DnaJ homolog subfa	DNAJC25	42.403	10.3	4	2	22.779	0	25507	23424	25939	17463	36709	23361	31257	27901	17249	23217					YES	
Q9H1X3-3;F2Z3D	DnaJ homolog subfa	DNAJC25;GNG10	16.499	25.5	4	2	21.616	0	15688	11184	13680	12700	16275	19033	19799	17015	15329	16054	Moderate	Enriched	Enriched	Enriched	YES	
Q9H1Y0;Q9H1Y0-	Autophagy protein 5	ATG5	32.447	12.4	3	3	15.727	0	19775	12023	17548	21559	22966	15055	9197	8339.5	5733.2	13956	Enriched	Enriched	Enriched	Moderate	YES	
Q9H1Z4-2;Q9H1Z	WD repeat-containin	WDR13	43.036	8.7	3	1	17.524	0	5943.8	4688.1	5148.7	3979.2	5766.8	3827.4	3798.8	4315.5	1860.1	4301.2	Enriched	Enriched	Enriched	No expres	YES	
Q9H267;F5H008;Q	Vacuolar protein sort	VPS33B	70.584	7.5	4	4	4.8739	0.00044	21749	13279	15778	23001	18053	23659	21137	24723	10531	22551	Enriched	Moderate	Enriched	No expres	YES	
Q9H2D6-5;Q9H2D	TRIO and F-actin-bin	TRIOBP	68.04	14.8	10	10	19.19	0	21761	16206	20931	21005	22825	18832	28958	25824	16399	25596	Enriched	Enriched	Enriched	Enriched	YES	
Q9H2F3;I3L2H6;I3	3 beta-hydroxysteroi	HSD3B7	41.016	9.5	3	3	7.9421	0	8061.4	16435	17810	10764	18341	5660.7	16772	8684.1	16743	16921	Moderate	Enriched	Moderate	No expression		
Q9H2G2;Q9H2G2-	STE20-like serine/th	SLK	142.69	21.6	30	30	118.32	0	145280	111900	128170	115480	142050	130500	202490	153530	112540	151270	Enriched	Enriched	Enriched	Enriched	YES	
Q9H2K0	Translation initiation	MTIF3	31.725	14.4	4	4	6.7411	0	19879	21052	19275	14134	27388	13525	14631	12139	7069	13894	Moderate	Enriched	Enriched	No expres	YES	
Q9H2K8;G3V1Q8	Serine/threonine-pro	TAOK3	105.4	3.5	3	3	5.7146	0	3830.5	3338.5	3657.9	3471.1	5450.8	3416.1	5549	4984.4	3685	4776.8	Moderate	Moderate	Enriched	No expres	YES	
Q9H2M9	Rab3 GTPase-activat	RAB3GAP2	155.98	5.3	6	6	10.522	0	8914.2	29667	9990	6692.6	20382	5068.1	8455	6447.1	2269.2	5607	Enriched	Enriched	Enriched	Low	YES	
Q9H2P0	Activity-dependent n	ADNP	123.56	6.9	8	8	10.683	0	16265	15834	21021	12232	21338	21171	31612	26049	23186	25924	Moderate	Enriched	Enriched	Enriched	YES	
Q9H2U1-3;Q9H2U	ATP-dependent RNA	DHX36	111.48	8.7	8	8	22.815	0	59150	51683	46563	45271	76799	36598	37010	40575	14278	47461	Moderate	Enriched	Enriched	No expres	YES	
Q9H2U2;Q9H2U2-	Inorganic pyrophospl	PPA2	37.92	53	31	29	252.08	0	201410	127910	171620	181620	205790	182500	182400	272160	94510	205950	Moderate	Enriched	Enriched	No expres	YES	
Q9H2W6	39S ribosomal protei	MRPL46	31.705	14.7	4	4	8.281	0	3152.2	2734.8	3126.9	3331.2	2694	1848.2	1918.5	1977.6	1154.8	2565.8	Enriched	Moderate	Enriched	No expres	YES	
Q9H307;Q9H307-2	Pinin	PNN	81.613	24.7	21	21	103.61	0	70006	65256	64114	47631	66294	56246	82682	78951	55523	77968	Enriched	Enriched	Enriched	Enriched	YES	
Q9H329-2;Q9H32	Band 4.1-like protein	EPB41L4B	58.566	15.4	8	7	34.114	0	35140	16081	22111	34625	23824	31233	34683	33917	13524	31813	Enriched	Enriched	Enriched	No expres	YES	
Q9H330-4;Q9H33	Transmembrane prot	TMEM245	55.418	4.2	2	2	9.6359	0	5800.6	5233.5	5153	3092.4	6714.1	6001.3	10318	7191.7	6725.9	7642.9					YES	
Q9H3H3;Q9H3H3-	UPF0696 protein C1	C11orf68	27.354	8.8	3	3	6.3633	0	3050.1	2046.6	2107.1	4545.4	2289.8	9946.3	3933.5	3978.7	1523.1	3240.4	Moderate	Enriched	Enriched	No expres	YES	
Q9H3H5-3;Q9H3H	UDP-N-acetylglucos	DPAGT1	34.269	5.6	2	2	3.3439	0.00078	5270.1	2210.7	3264.3	3016.5	4488.1	4210	6145.1	3975.8	4401.9	4280.2	Enriched	Enriched	Enriched	Enriched		
Q9H3K6;H3BV85;	BolA-like protein 2	BOLA2;BOLA2B	10.116	31.4	2	2	14.049	0	13527	9321.1	9272.1	11598	13260	13204	10215	11310	6653.5	10348	Enriched	Moderate	Enriched	No expres	YES	
Q9H3M7-2;Q9H3	Thioredoxin-interacti	TXNIP	37.319	13.1	4	4	9.534	0	7009.9	8443.7	10260	7721.6	13528	8571.9	6317.8	5898.3	3857.5	8029.8	Enriched	Enriched	Enriched	Enriched		
Q9H3N1	Thioredoxin-related t	TMX1	31.791	24.6	11	11	24.651	0	87661	44419	53322	88096	55286	98361	69582	78274	40500	89198	Moderate	Enriched	Enriched	Enriched	YES	

Q9H3P2;H0Y3X6;(	Negative elongation f	NELFA	57.276	11.9	5	5	17.188	0	13468	9948.9	13109	13527	14850	12766	13652	14867	10432	12073					YES	
Q9H3P7	Golgi resident protei	ACBD3	60.593	36.2	23	23	110.98	0	104900	83875	85650	105010	125460	97270	132840	120240	56347	102510	Enriched	Enriched	Enriched	Enriched	YES	
Q9H3Q1;J3KRZ9;(	Cdc42 effector protei	CDC42EP4	37.979	24.7	7	7	148.45	0	20461	18792	22074	18999	27348	15336	23859	21190	12439	23222	Enriched	Enriched	Enriched	Enriched	YES	
Q9H3S7	Tyrosine-protein pho	PTPN23	178.97	9.8	19	19	51.69	0	17889	14753	16765	16840	22080	23610	43537	39120	25361	23255	Moderate	Enriched	Enriched	No expres	YES	
Q9H3U1-2;Q9H3U	Protein unc-45 homo	UNC45A	101.67	15	14	14	51.602	0	34301	27825	28642	26436	34403	37545	41805	38247	25969	39622	Enriched	Enriched	Enriched	No expres	YES	
Q9H3U7;Q9H3U7-	SPARC-related modu	SMOC2	49.674	2.7	1	1	1.8932	0.00829	6969.4	7041.8	6248.1	6985.7	9210.2	5189	5842.9	4606.6	8768.2	5099.4	Moderate	Enriched	Moderate	No expres	YES	
Q9H3Z4-2;Q9H3Z4	DnaJ homolog subfar	DNAJC5	18.801	24	4	4	12.746	0	14980	12485	19689	12846	32382	9916.6	12391	11240	7246.3	14757	Enriched	Enriched	Enriched	No expres	YES	
Q9H425-3;Q9H425	Uncharacterized prot	C1orf198	32.214	22.5	6	6	25.207	0	22222	21066	29491	19056	29348	22641	39263	38313	30169	33730	Enriched	Enriched	Enriched	No expres	YES	
Q9H444	Charged multivesicul	CHMP4B	24.95	21	8	8	18.63	0	10985	7571	9612.8	12524	10859	12181	8831.2	9371	5598.7	10610	Low	Enriched	Enriched	No expres	YES	
X6RCZ8;X6RJB2;	F-box/LRR-repeat pr	FBXL15	17.351	8.3	1	1	2.2707	0.00494	11467	5288.1	7593.6	13513	6712.7	9295	9077.1	12056	4055.4	12366	Low	Moderate	Moderate	No expression		
Q9H477-2;Q9H477	Ribokinase	RBKS	30.36	7.3	2	2	2.9806	0.00169	23702	13839	24368	17455	28715	7082.3	7152.1	9221.8	3720.2	10603	Moderate	Moderate	Enriched	No expres	YES	
Q9H479	Fructosamine-3-kinas	FN3K	35.171	22	6	6	9.9213	0	6500.8	7122.5	7168	7584.8	9836.2	9464.4	7002.2	6357.2	5020	6267.7	Low	No expres	No expres	No expres	YES	
Q9H488	GDP-fucose protein (	POFUT1	43.955	17	7	7	25.423	0	25833	23521	16838	19266	23394	20996	28487	29941	27655	25160	Moderate	Low	Moderate	Low	YES	
Q9H490-2;Q9H490	Phosphatidylinositol	PIGU	47.61	3.6	1	1	3.4271	0.00079	6157.6	2915.7	5073.7	14442	4140.7	7084.7	6829.4	10487	2442.4	8094.6	Moderate	Enriched	Enriched	No expression		
Q9H4A4;A6NKB8	Aminopeptidase B	RNPEP	72.595	39.8	48	43	323.31	0	295930	225480	287200	248000	299580	237090	353650	350380	169100	276500	Moderate	Enriched	Enriched	Enriched	YES	
Q9H4A5;Q5T5I6;Q	Golgi phosphoprotei	GOLPH3L	32.767	25.6	12	8	39.395	0	21121	12171	14411	26955	14391	33037	22238	31003	13713	23054	Enriched	Enriched	Enriched	No expres	YES	
Q9H4A6	Golgi phosphoprotei	GOLPH3	33.81	37.2	14	10	42.945	0	36567	27955	31037	42875	33614	62819	41929	42890	21361	36248	Enriched	Enriched	Enriched	No expres	YES	
Q9H4B0	Probable tRNA N6-a	OSGEPL1	45.122	6	3	3	4.5985	0.00043	6298.6	3529	7815.5	4023.6	3868.6	9306.8	18273	14980	6704.1	12070	Low	Moderate	Moderate	No expression		
Q9H4F8;Q9H4F8-2	SPARC-related modu	SMOC1	48.162	5.5	2	2	9.1933	0	5272.7	5162	7175.4	3029.9	10108	5855	8653.4	9373.1	5634.9	5636	Enriched	Enriched	Enriched	No expres	YES	
Q9H4G0-4	Band 4.1-like protein	EPB41L1	78.83	26.5	22	3	77.467	0	80853	82909	90009	66581	104930	67977	101140	131770	56629	94349	Enriched	Enriched	Moderate	Low	YES	
Q9H4G4;Q5VZR0;	Golgi-associated plan	GLIPR2	17.218	37	5	5	21.39	0	16515	8763.6	10955	16431	12006	12389	10728	11171	7774.1	18161	Enriched	Enriched	Enriched	No expres	YES	
Q9H4X1-2;Q9H4X	Regulator of cell cycl	RGCC	12.924	12.8	2	2	4.6115	0.00043	4298.3	1079.1	1916.4	8934.7	1453.6	3379.1	2980.1	9966.4	2083.6	7330.1						
Q9H553;A0A0A0M	Alpha-1,3/1,6-mannc	ALG2	47.091	15.1	14	14	24.38	0	37420	29962	34167	36700	42530	30535	66609	63067	27528	33143	Enriched	Enriched	Enriched	No expres	YES	
Q9H583;Q5T3Q7	HEAT repeat-contain	HEATR1	242.37	3.1	6	6	12.966	0	11771	8795.8	9911.7	14177	10094	12498	13759	15405	10113	12984	Enriched	Enriched	Enriched	No expres	YES	
Q9H5N1-2;Q9H5N	Rab GTPase-binding	RABEP2	59.316	11.1	5	5	41.105	0	6694.2	6809.2	8306	5128.8	9523.2	9508.3	16840	16451	10985	11327	Enriched	Enriched	Moderate	No expres	YES	
Q9H5Q4	Dimethyladenosine tr	TFB2M	45.348	4.5	2	2	2.3138	0.00479	1783.4	1489.4	1388	1986.1	1906.5	1880.8	2027.2	3975.3	971.89	1256.9	Moderate	Enriched	Enriched	No expression		
Q9H5V9-3;Q9H5V	UPF0428 protein CX	CXorf56	23.936	10.6	2	2	2.5985	0.00273	7046.9	6173	9730	7146.2	6583.4	12244	29699	13878	6789	10119	Enriched	Low	Moderate	No expres	YES	
Q9H6A0-2;Q9H6A	DENN domain-conta	DENND2D	53.148	7.5	3	3	7.9321	0	2449.1	1198.9	1280.3	5963.2	754.24	3732.6	1596.6	4259.4	338.68	3590.2	Moderate	Moderate	Enriched	No expres	YES	
Q9H6Q4-3;Q9H6Q	Cytosolic Fe-S cluste	NARFL	42.009	9.1	3	3	8.5833	0	9830.3	9927.6	10756	6845.8	12445	4603.5	5876.8	6884.2	3804.8	7215.8	Enriched	Moderate	Moderate	No expres	YES	
Q9H6R3	Acyl-CoA synthetase	ACSS3	74.777	7.4	5	5	11.928	0	14937	10857	16511	16143	13975	16885	13701	13650	7873.9	14791	Moderate	Moderate	Moderate	No expres	YES	
Q9H6R4-4;Q9H6R	Nucleolar protein 6	NOL6	127.32	8	9	9	38.878	0	69936	49914	64680	76602	72074	63279	73570	76477	40393	78393	Moderate	Moderate	Moderate	No expres	YES	
Q9H6S0	Probable ATP-depen	YTHDC2	160.25	2.3	3	3	4.4448	0.00042	4367.6	3158.4	4695.6	2670.9	5024.2	3323.5	3966.1	2435.6	2342.3	3020.9	Moderate	Moderate	Enriched	Moderate	YES	
Q9H6S3;Q9H6S3-3	Epidermal growth fac	EPS8L2	80.62	9.2	6	6	18.441	0	19143	19007	18312	16272	21864	16964	16541	18710	9036.8	17886	Enriched	Enriched	Enriched	No expres	YES	
Q9H6W3;Q9H6W3	Bifunctional lysine-sp	NO66	71.085	5.1	3	3	5.1739	0.00044	7017.3	12059	7587.9	5702.2	10489	6570.3	7009.9	5676.3	6507.8	6944.7					YES	
Q9H6Z4-2;B7Z7F3	Ran-binding protein	RANBP3;ZNF8	59.694	20.1	11	11	49.851	0	68264	60081	75380	56076	78727	64657	96146	85630	87037	73742	Moderate	Moderate	Moderate	Moderate	YES	
Q9H773	dCTP pyrophosphata	DCTPP1	18.681	20	3	3	13.612	0	10600	8735	10289	9857.5	11880	10224	11665	15064	5906.1	13813	Enriched	Enriched	Enriched	No expression		
Q9H788	SH2 domain-containi	SH2D4A	52.726	6.8	3	3	8.6227	0	8763	5152.9	4719.4	7647.3	5053.5	4249.4	4826.6	6000.8	3334.8	6689.3	Enriched	Moderate	Moderate	No expres	YES	
Q9H792;H3BUZ5;I	Pseudopodium-enricl	PEAK1	193.1	1	2	2	2.1648	0.00612	6862.6	4666.1	3849.7	5466.5	6792.1	8304.8	1506.1	2460.5	967.91	2630.2					YES	
Q9H7D7-2;Q9H7D	WD repeat-containin	WDR26	70.459	3.3	2	2	3.4891	0.00079	6585.8	7185.1	7142.7	6763	9806.2	4005.4	9394.6	7329.1	8735.6	7506.5	Moderate	Enriched	Enriched	No expres	YES	
Q9H7E2-3;Q9H7E2	Tudor domain-contai	TDRD3	83.102	7.5	4	4	23.325	0	14394	9747.9	13182	11218	21532	8680.8	16197	10120	9921.3	14501	Moderate	Moderate	Moderate	No expres	YES	
Q9H7L9	Sin3 histone deacetyl	SUDS3	38.136	7.3	2	2	6.1245	0	3620.2	2983	3528.1	3296.2	4588.2	3324.7	2735.1	2303.8	927.28	2797.7	Moderate	Enriched	Enriched	No expres	YES	
Q9H7N4	Splicing factor, argini	SCAF1	139.27	2.1	2	2	2.4398	0.00412	3573.8	3660.5	6072.7	2913.3	4766.4	10049	16518	5183.4	7529.4	9554	Low	Moderate	Low	No expres	YES	
Q9H7Z3	Protein NRDE2 homo	NRDE2	132.67	3.4	3	3	3.0123	0.00132	10954	10257	7194.7	3628.8	14745	4682.9	11253	10767	4247.8	4947.8					YES	
Q9H7Z7;A6NHH0;	Prostaglandin E synth	PTGES2	41.943	28.4	15	15	53.893	0	118220	73452	78437	125350	102690	91267	82366	103370	45254	113560	Moderate	Moderate	Moderate	No expres	YES	
Q9H813-2			46.467	2.2	1	1	2.11	0.00659	27818	27655	23939	12818	25057	9298.3	15834	11398	20234	39364						
Q9H814	Phosphorylated adap	PHAX	44.402	6.1	2	2	14.679	0	8127.8	6388.3	9187	6789.4	7864.8	10334	7457.2	10375	3234.3	9595.5	Moderate	Moderate	Enriched	No expres	YES	
Q9H832-2;Q9H832	Ubiquitin-conjugatin	UBE2Z	28.075	22	5	3	8.7126	0	9098.9	10368	11566	10818	11313	8123.5	10218	9214.3	6860.9	10466	Enriched	Enriched	Enriched	No expres	YES	
Q9H845;H0Y8Z9	Acyl-CoA dehydroge	ACAD9	68.76	28.8	25	24	73.332	0	118890	109900	114020	85876	164210	82347	145760	142510	57135	105080	Enriched	Enriched	Enriched	No expres	YES	
Q9H871;Q9H871-2	Protein RMD5 homo	RMND5A	43.992	5.4	2	2	3.3223	0.00078	2792.9	1012.7	2033.3	4077.6	2290.7	2821.9	1370	1784.8	996.46	2015.2	Enriched	Enriched	Enriched	Enriched		
Q9H8G2	Caspase activity and	CAAP1	38.367	4.2	1	1	3.2111	0.00077	3537.8	3879.4	4984.9	2459.9	5523.3	4271.5	4354.9	2795.9	2702	3005.2						
Q9H8L6	Multimerin-2	MMRN2	104.41	2.6	2	2	11.061	0	4687.3	4858	5091.9	3897.2	5670.1	16063	12365	17865	4547.8	15689	Moderate	Low	Moderate	No expres	YES	
Q9H8Y8;Q9H8Y8-	Golgi reassembly-stac	GORASP2	47.145	31	22	22	113.52	0	104360	132730	117780	111350	190640	115130	140400	115530	75792	104070	Enriched	Enriched	Enriched	Enriched	YES	
Q9H902-2;Q9H902	Receptor expression-	REEP1	18.936	6.9	1	1	4.7863	0.00043	1337.8	1114.8	1379.1	1409.5	1362.8	728.79	397.39	657.23	0	1401	Enriched	Enriched	Enriched	Moderate		
Q9H936;E9PJH7	Mitochondrial glutan	SLC25A22	34.47	26.3	13	11	48.043	0	81212	43782	60955	82504	69400	65196	73168	83775	42211	80705	Enriched	Moderate	Moderate	No expres	YES	
Q9H974-2;Q9H974	Queuine tRNA-ribosy	QTRTD1	33.471	6.5	2	2	2.8766	0.00186	19167	14781	18443	20422	17933	14571	19105	20817	9130.8	18785	Moderate	Low	Moderate	No expres	YES	
Q9H993;F5GZY1	UPF0364 protein C6	C6orf211	51.172	12.5	6	6	8.2675	0	26035	26110	28825	23871	29140	20572	20875	23174	11800	22031	No expres	Low	Enriched	No expres	YES	
Q9H9A6	Leucine-rich repeat-c	LRRC40	68.249	10.5	6	6	13.506	0	28765	28262	28212	31382	29985	30312	31034	36608	14131	27659	No expres	Moderate	Enriched	No expres	YES	
Q9H9B4	Sideroflexin-1	SFXN1	35.619	34.8	10	9	48.898	0	78057	46066	70995	50423	61722	84738	103400	115570	50400	77217	Enriched	Enriched	Moderate	No expres	YES	
Q9H9G7;Q9H9G7-	Protein argonaute-3;I	AGO3;AGO4	97.359	14.1	12	2	4.2127	0.00062	14200	9800.5	12605	12152	13793	11265	10656	8385.6	5063.4	10903						
Q9H9H4	Vacuolar protein sort	VPS37B	31.307	9.1	3	3	6.2207	0	3704	2608	2323.3	2846.8	2928.7	6570.5	5766	4986.7	3511.6	4222.2	Enriched	Moderate	Enriched	No expres	YES	
Q9H9T3-2;Q9H9T3	Elongator complex p	ELP3	60.647	5.1	3	3	99.401	0	12669	9129.2	9877	14099	10895	6118.7	5300.7	8743.3	3325.5	11096	Enriched	Enriched	Enriched	No expres	YES	
Q9HA64;I3L2G3;I3	Ketosamine-3-kinase	FN3KRP	34.412	20.4	14	14	32.943	0	25056	19709	22566	22925	33870	25702	31313	29228	19336	31592	Enriched	Enriched	Enriched	No expres	YES	
Q9HA65-3;Q9HA6	TBC1 domain family	TBC1D17	67.223	10.3	6	6	8.793	0	17913	10040	10580	17084	15472	15855	9589.2	13720	4773.4	12938	Moderate	Low	Moderate	No expres	YES	
Q9HA77;A0A087V	Probable cysteine--tR	CARS2	62.223	11.5	8	8	24.594	0	65997	63327	57902	57606	64808	57829	69736	54055	38175	66053	Enriched	Enriched	Enriched	No expres	YES	
Q9HAB8;Q9HAB8	Phosphopantothenate	PPCS	34.005	16.7	10	10	49.601	0	26386	23658	19677	17015	24232	17853	10333	16942	3344.2	17741	Enriched	Enriched	Enriched	No expres	YES	
Q9HAJ7-2;Q9HAJ7	Histone deacetylase c	SAP30L	15.436	8	1	1	3.6799	0.0008	10230	6249	9517.8	6148.5	12138	6569.4	7499.9	7711.6	4653.8	8017	Enriched	Enriched	Enriched	No expression		
Q9HAN9	Nicotinamide monon	NMNAT1	31.932	17.6	6	6	25.924	0	48188	31967	40378	59687	36169	40732	38871	60011	20200	53094	Low	Moderate	Moderate	No expres	YES	
Q9HAU0-5;Q9HAU	Pleckstrin homology	PLEKHA5	121.27	5.5	6	6	9.9174	0	3329.4	2393.8	2878.9	1103.7	4609	3235.1	2985	1380.9	1863.9	2613.9	Enriched	Enriched	Enriched	No expres	YES	
Q9HAU5	Regulator of nonsens	UPF2	147.81	6.4	6	6	17.678	0	16227	12720	14657	14752	17928	12358	15491	14537	8969.7	14285	Moderate	Enriched	Enriched	Moderate	YES	
Q9HAV4	Exportin-5	XPO5	136.31	8.2	11	11	18.81	0	9961.3	4256.5	6062.2	10050	6894.3	6425.5	4892.5	7074.4	3366.3	8205.9	Enriched	Enriched	Enriched	No expres	YES	
Q9HAV7	GrpE protein homolo	GRPEL1	24.279	29.5	8	8	22.545	0	54420	43153	44878	50202	62085	73023	67693	98962	27630	82955	Enriched	Enriched	Enriched	No expres	YES	
Q9HAZ2-2;Q9HAZ	PR domain zinc finge	PRDM16	138.18	1.5	2	1	1.9543	0.008	2362.1	2243.2	2785.9	1459.9	3312.8	5291.5	27971	7731	4486.1	4884	Moderate	Moderate	Moderate	No expression		YES
Q9HB07;F8VR84;I	UPF0160 protein MY	C12orf10	42.449	16.5	6	6	13.286	0	16556	17296	15944	16971	19846	13438	15540	14277	8860.3	13714	Enriched	Enriched	Enriched	No expres	YES	
Q9HB21;Q5RGS4;	Pleckstrin homology	PLEKHA1	45.553	5.7	2	2	3.6894	0.0008	1603.4	571.28	877.46	1984.4	1072.9	2477.7	1257.1	1614.9	616.07	1694.3	Enriched	Enriched	Enriched	No expres	YES	
Q9HB40;Q9HB40-	Retinoid-inducible se	SCPEP1	50.83	4.6	2	2	3.681	0.0008	6665.6	5761.1	6565.6	6266.6	5871.3	7712.2	7694.7	8256.4	4457.2	6466	Enriched	Moderate	Enriched	No expres	YES	
Q9HB66		MKKS	7.2634	39.7	2	2	3.9741	0.00062	3775.9	3945.9	3288.3	7239.7	4901.4	4725.5	4674.1	5409.2	2343.2	5138.7	Enriched	Enriched	Enriched	No expression		
Q9HB71;Q9HB71-	Calcyclin-binding pro	CACYBP	26.21	46.1	12	12	50.482	0	119970	126650	116630	115770	150590	82933	95161	95655	76069	118160	Enriched	Enriched	Enriched	Enriched	YES	
Q9HB90;A0A087X	Ras-related GTP-binc	RRAGC;RRAGD	44.223	11.3	5	5	12.729	0	15215	24083	29922	12052	25853	11060	18809	19846	9691.1	18032	Enriched	Enriched	Enriched	No expres	YES	
Q9HBG6-11;Q9HB	Intraflagellar transpo	IFT122	113.23	2.7	3	3	3.7262	0.0008	13979	8786.6	11568	15544	10998	10827	16067	17458	10699	14222	Moderate	Moderate	Moderate	No expres	YES	
Q9HBH5	Retinol dehydrogena	RDH14	36.864	11	3	3	5.4026	0	5260.8	6069.6	6291.9	9440.5	7533.1	13896	15347	8757.2	6280.9	8233.6	Moderate	Moderate	Enriched	No expres	YES	
Q9HBI6;V9GYP6;I	Cytochrome P450 4F	CYP4F11	60.145	4	2	2	2.9517	0.00169	21471	15305	18849	15340	15238	28352	32681	24018	12293	28420	No expres	No expres	Low	No expression		
Q9HBL7	Plasminogen recepto	PLGRKT	17.201	9.5	2	2	27.788	0	30895	24745	28086	24710	38187	20811	21175	21415	10511	34015					YES	
Q9HBL8	NmrA-like family doi	NMRAL1	33.344	12.4	3	3	7.2412	0	10150	8424.9	9470.6	10328	9751.2	11650	12003	9854.2	6860.4	9303.2	Enriched	Enriched	Enriched	No expression		
Q9HBR0;Q9HBR0-	Putative sodium-cour	SLC38A10	119.76	10.5	9	9	23.765	0	26888	23091	24033	30503	25473	21894	37130	28830	27431	39932	Enriched	Enriched	Enriched	Enriched	YES	
Q9HC07;V9GY93;	Transmembrane prote	TMEM165	34.905	16.4	4	4	52.677	0	6552.5	8539.3	6174.3	5533.3	8284.1	2871.4	2447.6	2029.7	1074	3831.5	Moderate	Enriched	Enriched	No expres	YES	
Q9HC35;Q9HC35-	Echinoderm microtul	EML4	108.91	37.6	69	69	269.92	0	393250	221850	283710	255900	386570	234830	262890	204820	147010	275970	Enriched	Enriched	Enriched	No expres	YES	
Q9HC78-2;Q9HC7	Zinc finger and BTB	ZBTB20;ZBTB45	73.4	2.8	2	2	4.2974	0.00063	10704	8524.8	10040	8367.8	18049	7624.8	9072.1	7529.5	5748.2	8366.1	Enriched	Enriched	Enriched	Moderate		
Q9HC84	Mucin-5B	MUC5B	596.33	0.3	1	1	4.5204	0.00042	1343.8	2424.2	2147	1146.9	2898.5	948.04	1814.8	6481.4	1237.1	1778.1					YES	
Q9HCB6	Spondin-1	SPON1	90.973	2.1	1	1	8.8307	0	11525	13156	12197	11300	11620	14123	20299	25761	11009	17194	Enriched	Enriched	Enriched	Moderate	YES	
Q9HCC0;Q9HCC0-	Methylcrotonoyl-Co.	MCCC2	61.332	41.4	33	33	274.72	0	218640	133080	177920	170310	193760	200460	164840	146920	93962	183440	Moderate	Enriched	Enriched	Low	YES	
Q9HCD5	Nuclear receptor coa	NCOA5	65.536	8.3	5	5	12.065	0	9749	6391.9	7956.7	9599.5	9865.4	28408	8539.6	7280.4	3583.3	8538.1	No expres	Enriched	Enriched	No expres	YES	
Q9HCE1-2;Q9HCE	Putative helicase MO	MOV10	101.6	11.7	11	11	23.622	0	44389	39412	43292	31798	52361	49842	62390	55099	37333	48508	Moderate	Low	Moderate	No expres	YES	
Q9HCE5;D6RBL4	N6-adenosine-methyl	METTL14	52.15	9.9	5	5	15.407	0	17966	15485	16641	14710	17782	11959	17807	15663	15214	18274	Low	Moderate	Enriched	No expres	YES	
Q9HCE6-3;Q9HCE	Rho guanine nucleoti	ARHGEF10L	135.18	11.7	14	2	31.622	0	46208	21415	22927	30773	27483	32560	22126	32343	10845	34304	Enriched	Enriched	Enriched	No expres	YES	
Q9HCG8;B7WP74	Pre-mRNA-splicing f	CWC22	105.47	5	3	3	46.107	0	12182	9194.4	9208.9	15575	9368.7	8296.7	7265.5	10213	8511.3	11124	Low	Moderate	Moderate	No expression		
Q9HCJ6	Synaptic vesicle mem	VAT1L	45.899	10.3	3	3	4.7545	0.00043	4243.7	1871.5	2981.6	5924.4	1937.4	3430.7	1780.8	3593.8	458.51	4352.4	Low	Low	Enriched	No expres	YES	
Q9HCM4-2;Q9HCI	Band 4.1-like protein	EPB41L5	57.885	8.9	5	4	34.584	0	24300	22131	24237	18562	30538	15770	18481	17244	13032	19677	Moderate	Enriched	Enriched	No expres	YES	
Q9HCN8	Stromal cell-derived	SDF2L1	23.598	43.9	13	13	85.117	0	55000	45657	51250	38709	67198	79540	74300	56188	43514	56670	Moderate	Enriched	Enriched	No expres	YES	
U3KQA5;U3KQB3	Casein kinase I isofor	CSNK1G1;CSNK1G2;C	47.172	4.5	2	2	1.8339	0.00976	2264.9	1989.5	1960.7	1755.6	3713.2	1640.6	2761.6	1979.7	1610.8	2719.1	Moderate	Enriched	Enriched	No expression		
Q9HCS7	Pre-mRNA-splicing f	XAB2	100.01	8.5	7	7	14.677	0	12251	8504.3	11793	13939	16209	11631	10074	8997.9	6807.8	12419	Low	Low	Low	No expres	YES	
Q9HCU0	Endosialin	CD248	80.858	2.5	2	2	2.089	0.0069	8976.8	9519.4	10102	10122	11428	7639.4	11312	11690	6010.6	9544.9	Enriched	Moderate	Moderate	No expres	YES	
Q9HCU5;B5MC98	Prolactin regulatory e	PREB	45.468	35.5	16	16	36.55	0	48854	47839	48473	35618	64237	37258	46242	39113	27088	43257	Moderate	Enriched	Enriched	No expres	YES	
Q9HD15	Steroid receptor RNA	SRA1	25.673	8.9	2	2	5.8244	0	7546.4	9045.5	11022	3959.9	11473	4890.2	20327	7357.8	29692	10668	Enriched	Enriched	Enriched	No expres	YES	
Q9HD20-2;Q9HD2	Manganese-transport	ATP13A1	121.11	16.9	26	26	91.342	0	143560	105970	107360	98799	131380	115260	100170	86840	54420	103160	Moderate	Enriched	Enriched	No expres	YES	
Q9HD33-2;Q9HD3	39S ribosomal protei	MRPL47	27.085	16.5	5	5	10.371	0	31715	29699	27547	28262	38834	45050	14676	22302	5781.4	26491	Enriched	Enriched	Enriched	No expres	YES	
Q9HD40-3;Q9HD4	O-phosphoseryl-tRN.	SEPSECS	55.41	16.2	6	6	15.602	0	29953	24613	29394	33337	35942	32986	41006	32426	27289	34723	No expres	Enriched	Moderate	No expres	YES	
Q9HD45;Q5TB53	Transmembrane 9 sul	TM9SF3	67.887	13.6	15	15	34.496	0	122920	99870	96768	84519	159850	141480	176670	178400	57398	105430	Enriched	Enriched	Enriched	No expres	YES	
Q9HDC9;H0Y512;	Adipocyte plasma me	APMAP	46.48	34.6	23	23	62.142	0	100110	83574	80317	95909	88272	79859	108370	121690	58241	97211					YES	
Q9NP58;H7BXK9;	ATP-binding cassette	ABCB6	93.884	6.3	5	5	6.8412	0	1407	1264.5	1479.3	1112.1	1650.7	2875.6	5272.6	2527.9	1083.7	1065.9	Moderate	Moderate	Moderate	No expres	YES	
Q9NP61-2;Q9NP61	ADP-ribosylation fac	ARFGAP3	51.989	35.4	28	28	323.31	0	186850	129870	150110	164520	188980	209000	199940	171180	114090	192400	Enriched	Enriched	Enriched	Enriched	YES	
Q9NP66;H0YKL0	High mobility group	HMG20A	40.143	9.8	3	3	35.867	0	18864	15349	17828	22718	20367	19767	39507	35159	22101	23816	Low	Moderate	Enriched	No expression		
Q9NP72;Q9NP72-2	Ras-related protein R	RAB18	22.977	57.8	14	13	75.939	0	110730	61558	75917	129030	92368	114520	108200	106610	74273	138190	Moderate	Enriched	Enriched	No expres	YES	
S4R313;Q9NP74;Q	Palmdelphin	PALMD	62.652	12.5	5	5	33.4	0	43768	35902	45973	40868	49668	40417	36732	29446	17343	38181	Low	Low	Moderate	No expres	YES	
Q9NP77;Q9NP77-2	RNA polymerase II su	SSU72	22.574	8.2	2	2	1.9253	0.00815	4650.8	2232.9	3871.9	4305.3	3849.1	3341.2	3131.7	4046.1	1880.5	3799.9	Enriched	Enriched	Enriched	No expres	YES	
Q9NPA0;H0YDT8	ER membrane protei	EMC7	26.47	15.3	6	6	13.866	0	66098	61306	60428	57474	77420	67059	56024	50795	30242	49273					YES	
Q9NPD3;E9PI41	Exosome complex co	EXOSC4	26.383	14.3	4	4	4.9868	0.00044	8964.6	8258.3	9104.8	8418.5	12665	7441.4	14166	13048	10735	10586	Enriched	Enriched	Enriched	No expres	YES	
Q9NPE3	H/ACA ribonucleopr	NOP10	7.7059	68.8	5	5	11.262	0	18017	11663	18536	12048	18479	15108	21239	17394	12202	16533	Enriched	Enriched	Enriched	No expres	YES	
Q9NPF4	Probable tRNA N6-a	OSGEP	36.426	12.2	6	6	11.463	0	24851	22826	26138	17992	30441	15055	20581	18921	17100	22357	Enriched	Moderate	Moderate	No expres	YES	
Q9NPF5;Q5TG38;(	DNA methyltransfera	DMAP1	52.992	8.1	3	3	5.9068	0	2959.5	2999.2	3840.7	2213.7	4718.6	2880	2935	2235.1	1110.1	2271.3	No expres	Moderate	Moderate	No expres	YES	
Q9NPH2;Q9NPH2-	Inositol-3-phosphate	ISYNA1	61.067	16.1	11	11	16.865	0	20235	18944	22529	19805	23264	19978	37063	28496	40680	28244	Low	Enriched	Enriched	No expres	YES	
Q9NPI1;Q9NPI1-2	Bromodomain-contai	BRD7	74.138	3.2	1	1	3.7478	0.0006	2666.9	1403.5	2939.5	5117.1	2007.8	4129.7	4012.9	5192.1	1478.4	4879.7	Enriched	Enriched	Enriched	No expres	YES	
Q9NPI6-2;Q9NPI6	mRNA-decapping en	DCP1A	59.361	5.1	2	2	5.1716	0.00044	5382.4	3836.9	4458.9	5567.5	4949	3477	3075.6	5386.1	1588.9	4203.4	Enriched	Enriched	Enriched	No expression		
Q9NPJ3-2;Q9NPJ3	Acyl-coenzyme A thi	ACOT13	12.366	18.8	5	5	22.294	0	14576	11993	9625.4	9402.6	12095	18622	20293	25715	11211	20878	Low	Enriched	Enriched	Moderate	YES	
Q9NPJ6	Mediator of RNA pol	MED4	29.745	9.3	2	2	4.4558	0.00042	2165.8	1154.6	1730.6	2523.1	1392.8	1679.5	2405.3	2725.8	1437.1	2119.6	Low	Low	Moderate	No expres	YES	
Q9NPQ8-4;Q9NPQ	Synembryn-A	RIC8A	59.612	17	9	9	20.628	0	37602	21763	25322	31775	32426	36955	32934	36681	20354	37677	Enriched	Enriched	Enriched	No expres	YES	
Q9NPY3	Complement compon	CD93	68.559	3.1	1	1	4.9911	0.00044	12769	11045	10264	10853	14499	13886	18646	15848	12438	13505	Moderate	Moderate	Enriched	No expres	YES	
Q9NQ29-2;Q9NQ2	Putative RNA-bindin	LUC7L	38.405	22.2	11	3	25.824	0	6484.5	6058	8145.2	5923.5	8165.9	8332.2	14630	13799	8713.2	11737	Enriched	Enriched	Enriched	No expres	YES	
Q9NQ50	39S ribosomal protei	MRPL40	24.49	24.3	4	4	5.1223	0.00044	18373	8920.6	19144	13565	18966	23773	14390	12754	7144.5	12945	Enriched	Enriched	Enriched	Moderate	YES	
Q9NQ66-2;Q9NQ6	1-phosphatidylinosito	PLCB1	133.7	10.3	13	13	57.761	0	35707	29195	35417	34406	49652	28132	35486	36808	18988	34596	Moderate	Enriched	Enriched	Enriched	YES	
Q9NQ88	Fructose-2,6-bisphos	TIGAR	30.062	5.9	1	1	2.9304	0.00168	3465.6	2805.4	2684.1	3890.3	2727.8	4752.1	2760.1	2913.9	1059.1	2972.9					YES	
Q9NQA3	WAS protein family l	WASH6P	47.989	9.6	3	1	57.041	0	7210	2971.8	7111.3	5813.1	7490.6	4634.9	6564.7	8070.4	4358.7	9289.6	No expres	Low	No expres	No expres	YES	
Q9NQE9	Histidine triad nuclec	HINT3	20.361	7.7	2	2	3.7457	0.0006	15624	13463	12312	11375	15116	15775	20604	25084	11141	16847	Moderate	Enriched	Enriched	No expres	YES	
Q9NQG1	Protein MANBAL	MANBAL	9.467	14.1	1	1	3.7371	0.0006	3349	2942.9	3350	1520.5	5088	2529.1	3523.2	2555.3	2009.3	2470.7	Enriched	Enriched	Enriched	No expression		
Q9NQG5;E9PIQ9	Regulation of nuclear	RPRD1B	36.899	21.5	12	11	126.29	0	105230	63773	73512	127310	74243	110620	109710	183590	55345	153100	Moderate	Enriched	Enriched	No expres	YES	
Q9NQP4;E9PQY2	Prefoldin subunit 4	PFDN4	15.314	36.6	7	7	23.698	0	1510.5	1100.8	1258.4	2367.8	1990.2	1403	2144	2059.8	1139.9	1500.8	Low	Moderate	Enriched	Enriched	YES	
Q9NQR4;H7C579	Omega-amidase NIT2	NIT2	30.608	47.5	16	16	143.57	0	138860	115810	122240	118100	121320	125990	148970	155070	82028	134980	Moderate	Enriched	Enriched	No expres	YES	
Q9NQS1	Cell death regulator	AVEN	38.506	4.7	1	1	3.5397	0.00079	14729	11362	10176	17059	11957	11245	10777	10107	7361.6	12820	No expres	Enriched	Enriched	No expres	YES	
Q9NQT8;E7ERX9	Kinesin-like protein	KIF13B	202.79	11.2	18	17	115.79	0	52845	46384	54642	50635	56486	40770	61485	61798	40003	64774	Enriched	Enriched	Enriched	Enriched	YES	
Q9NQW7-3;Q5T6F	Xaa-Pro aminopeptid	XPNPEP1	74.797	33.6	39	39	205.86	0	259890	151510	170640	249810	242250	254010	191310	222300	75907	218560	Enriched	Enriched	Enriched	Moderate	YES	
Q9NQX4	Unconventional myo	MYO5C	202.81	17.4	34	31	118.85	0	90451	68689	79658	89648	99357	121500	112960	104710	59841	109270	Enriched	Enriched	Enriched	No expres	YES	
Q9NQZ2	Something about siler	UTP3	54.557	7.7	3	3	16.062	0	12664	9804.9	10926	8857.5	12174	11974	16490	9983.9	12013	14254	Moderate	Moderate	Enriched	Enriched	YES	
Q9NQZ7	Ectonucleoside triph	ENTPD7	68.959	3	1	1	3.1547	0.00076	10477	5300	6965.3	14454	6344.5	14473	8397.6	11952	4026.8	10681	Low	Low	Moderate	No expression		
Q9NR09	Baculoviral IAP repe	BIRC6	530.25	1.7	8	8	16.396	0	17121	17827	17881	14255	25343	13260	18720	17905	10860	17947	Enriched	Enriched	Enriched	No expres	YES	
Q9NR12;Q9NR12-	PDZ and LIM domai	PDLIM7	49.844	17.5	7	7	20.562	0	35915	36730	30918	24861	37846	32973	46101	41916	17037	57582	Low	Low	Moderate	Moderate	YES	
Q9NR30;Q9NR30-	Nucleolar RNA helic	DDX21	87.343	22.1	19	15	75.975	0	92126	78426	82790	76509	108480	72109	105310	83225	60236	96624	Enriched	Enriched	Enriched	Enriched	YES	
Q9NR31;Q9NR31-	GTP-binding protein	SAR1A	22.367	51.5	15	10	188.55	0	76924	42866	47756	98239	49083	94445	97786	130750	33016	113940	Enriched	Enriched	Enriched	Enriched	YES	
Q9NR45	Sialic acid synthase	NANS	40.307	38.2	32	32	256.14	0	229880	149350	170100	178360	197540	251960	256970	267090	115760	185060	Enriched	Enriched	Enriched	No expres	YES	
Q9NR50;Q9NR50-	Translation initiation	EIF2B3	50.24	31	20	20	67.052	0	89354	66512	77940	88428	98491	66712	73546	67911	45538	69713	Moderate	Enriched	Enriched	No expres	YES	
Q9NR80-3;Q9NR8	Rho guanine nucleoti	ARHGEF4	71.13	1.5	1	1	2.1259	0.00609	1810.7	1689.5	1458.1	2261.4	1690.7	1681.6	1360.5	1394.3	434.44	1407.4	Low	Moderate	Low	Moderate		
Q9NRD1	F-box only protein 6	FBXO6	33.932	11.6	5	5	11.035	0	10726	5475.7	7013.4	13218	7218.3	12813	10443	12424	5521.6	12730	Moderate	Enriched	Enriched	No expres	YES	
Q9NRD5;F6V107;(	PRKCA-binding prot	PICK1	46.6	8.2	4	4	6.2405	0	13983	13214	13047	12005	16329	10784	15403	15349	12420	13635	Enriched	Moderate	Moderate	Enriched	YES	
Q9NRF8	CTP synthase 2	CTPS2	65.677	8.5	7	5	10.118	0	20814	20006	25777	19195	25782	14620	16637	14837	14047	19297	Moderate	Enriched	Enriched	No expres	YES	
Q9NRF9	DNA polymerase eps	POLE3	16.859	11.6	2	2	5.668	0	9920.9	4924.1	7296.4	12603	6131.8	10851	8327.2	11184	4863.6	12172	Low	Moderate	Enriched	Enriched		
Q9NRN5;B4DNG0	Olfactomedin-like pro	OLFML3	46.01	35.7	18	18	119.47	0	60429	65727	110640	62381	97557	61874	91893	83911	35672	60621	Low	Enriched	Moderate	No expres	YES	
Q9NRN7;E9PLW6	L-aminoadipate-semi	AASDHPPT	35.776	12.3	5	5	18.957	0	20403	10721	12494	21145	15769	21185	26698	22926	14864	26582	Low	Enriched	Enriched	Enriched	YES	
Q9NRR5	Ubiquilin-4	UBQLN4	63.852	17.8	11	6	68.089	0	36899	30057	29925	34103	41867	34802	28531	39953	14677	30749	Low	Enriched	Enriched	No expres	YES	
Q9NRV9;F5GWX2	Heme-binding protei	HEBP1	21.097	67.2	16	16	111.33	0	129810	86691	91210	170800	125050	157670	181250	158060	66386	126760	Moderate	Enriched	Enriched	No expres	YES	
Q9NRW7;A0A087	Vacuolar protein sort	VPS45	65.076	7.5	4	1	8.9437	0	1929.6	1621	1627.5	1432.4	2499.5	1940.5	1851.3	1073.7	1131.9	1424.3	Moderate	Moderate	Enriched	Enriched	YES	

Q9NRX4;Q9NRX4	14 kDa phosphohistic	PHPT1	13.832	72	11	11	25.225	0	91774	57844	72494	78037	72953	126870	169430	167210	47914	88810	Moderate	Enriched	Enriched	No expres	YES
Q9NRX5	Serine incorporator 1	SERINC1	50.494	6.2	2	2	15.238	0	9801.2	5540.2	6811.8	10953	9064.1	8008.9	8435.3	8466.5	4032.8	9333.8	No expres	Enriched	Enriched	Enriched	YES
Q9NRZ7-2;Q9NRZ	1-acyl-sn-glycerol-3-	AGPAT3	36.271	17.2	6	6	11.62	0	50558	44240	37393	33694	53327	37047	36184	48060	16458	39610	Moderate	Enriched	Enriched	No expres	YES
Q9NS56-2;Q9NS56	E3 ubiquitin-protein	TOPORS	112.34	1.2	1	1	2.7071	0.00238	3387	2605.6	3478.8	2206.2	6024.3	1961.7	2642.1	1475.6	1525.4	1640.6	Low	No expres	Moderate	Moderate	
Q9NS69	Mitochondrial import	TOMM22	15.521	59.9	7	7	28.474	0	55205	61207	70551	43643	101730	36674	65650	49530	43749	44261	Low	Enriched	Enriched	No expres	YES
Q9NS86	LanC-like protein 2	LANCL2	50.854	11.8	6	6	31.892	0	29636	15914	20355	40564	22089	38978	40569	44262	17145	45443	Enriched	Enriched	Enriched	No expres	YES
Q9NSD9;Q9NSD9-	Phenylalanine--tRNA	FARSB	66.115	36.3	37	37	159.97	0	231780	169490	163580	222010	184460	238410	167750	232550	76682	205670	Enriched	Enriched	Enriched	No expres	YES
Q9NSE4	Isoleucine--tRNA lig	IARS2	113.79	31	34	34	98.192	0	253120	152130	180570	230780	202090	227450	247850	271200	125030	231710	Moderate	Enriched	Enriched	Enriched	YES
Q9NSK0;Q9NSK0-	Kinesin light chain 4	KLC4	68.639	17.6	10	9	18.613	0	29349	27137	30030	19839	35753	27026	33990	26903	25766	27563	Enriched	Enriched	Enriched	No expres	YES
Q9NT62-2;Q9NT62	Ubiquitin-like-conjug	ATG3	35.467	19.6	8	8	18.615	0	15889	14405	15931	17649	18001	17730	12815	12838	8333.1	14782	Enriched	Enriched	Enriched	No expres	YES
Q9NTG7;E9PK80;I	NAD-dependent prot	SIRT3	43.573	13.5	5	5	13.112	0	22229	11335	14181	16722	16972	16626	15228	16605	7742.5	15119	No expres	Moderate	Moderate	No expression	
Q9NTI5-2;Q9NTI5	Sister chromatid cohe	PDS5B	158.28	10	18	15	79.353	0	56127	45774	61702	46522	63674	40415	47201	50294	23445	53098	Moderate	Moderate	Enriched	Low	YES
Q9NTJ4-3;Q9NTJ4	Alpha-mannosidase 2	MAN2C1	104.69	4.3	4	4	6.1109	0	6123.1	6901.5	6474.2	4328.5	7702.6	6375.6	8575.5	8331.9	5306.5	6790.1	Moderate	Moderate	Moderate	Enriched	YES
Q9NTJ5;E9PGZ4;C	Phosphatidylinositide	SACM1L	66.966	29.1	20	3	79.563	0	88201	66064	69911	67608	74464	93346	109030	106380	42950	91993	Moderate	Enriched	Enriched	Enriched	YES
Q9NTX5-6;Q9NTX	Ethylmalonyl-CoA d	ECHDC1	31.089	35.2	14	7	122.34	0	76150	57856	64158	61146	59295	86337	84816	119510	46393	79933	Enriched	Enriched	Enriched	No expres	YES
Q9NTZ6	RNA-binding protein	RBM12	97.394	7.5	8	8	13.272	0	20873	16311	21091	16207	21198	21831	29708	33701	13915	26524	Moderate	Moderate	Enriched	Low	YES
Q9NU19	TBC1 domain family	TBC1D22B	59.08	7.5	3	1	6.7841	0	6801.5	5358.7	6090.9	6077.1	7080.3	5134.5	4987.7	4414.7	2145.4	5976.5	Low	Enriched	Enriched	No expression	
Q9NU22	Midasin	MDN1	632.81	0.8	3	3	7.2718	0	6697	6382.5	6991.7	8971.9	7816.1	9261.5	20891	21593	8155.9	10766	Enriched	Enriched	Moderate	Enriched	YES
Q9NUB1;Q9NUB1	Acetyl-coenzyme A s	ACSS1	74.856	24.5	20	20	50.477	0	78938	56513	61530	62156	96267	51026	57140	62488	34646	63352	Enriched	Enriched	Moderate	No expres	YES
Q9NUJ1	Mycophenolic acid a	ABHD10	33.932	35.9	20	4	96.891	0	124950	75989	112980	149190	127990	214220	172580	215980	77933	129410	Enriched	Enriched	Enriched	No expres	YES
Q9NUL5-2;Q9NUL	UPF0515 protein C1	C19orf66	27.524	12.5	3	2	4.8385	0.00043	1655.3	2040	2176.9	1311.4	3267.6	1591.4	3824	3228.5	2488.7	2762.9	Moderate	Enriched	Enriched	No expres	YES
Q9NUL7	Probable ATP-depen	DDX28	59.58	5.9	3	3	3.1342	0.00095	5469.4	4092.6	4827.1	3866.9	5925.5	4193.3	4125.5	3931.1	2589.8	4781.4	Enriched	Moderate	Moderate	Low	YES
Q9NUN5-4;Q9NUN	Probable lysosomal c	LMBRD1	21.394	6.9	1	1	21.079	0	4610.2	4102.4	4528.1	4958.5	6601.8	5233.6	2736.1	2584	1021.3	4853.5	Enriched	Enriched	Enriched	No expres	YES
Q9NUP1	Biogenesis of lysoson	BLOC1S4	23.351	17.5	3	3	7.6935	0	9034.5	7175.1	6889.1	9076.6	9221.8	4234.8	6310.7	6983.2	3731.5	7952.5					YES
Q9NUQ2;H0YC22	1-acyl-sn-glycerol-3-	AGPAT5	42.072	9.6	3	3	4.6471	0.00043	9456.7	5367	5737.2	10253	6055.4	9076.3	6999.5	9284.3	3292.8	10888	Moderate	Low	Enriched	No expres	YES
Q9NUQ3-2;Q9NUQ	Gamma-taxilin	TXLNG	46.251	5.1	2	2	3.7123	0.0008	2313.9	2205.1	2835.9	1064.5	1688.5	1157.8	6310.3	5011.7	11273	5960.6					
Q9NUQ6-2;Q9NUQ	SPATS2-like protein	SPATS2L	54.178	15.1	6	6	117.46	0	23435	23525	22083	23625	28238	20098	23489	26066	12979	22546	Enriched	Enriched	Enriched	No expres	YES
Q9NUQ8;Q9NUQ8	ATP-binding cassette	ABCF3	79.744	12.1	9	9	35.05	0	69393	38026	62129	77717	55104	68101	51195	54729	32129	60849	Moderate	Moderate	Moderate	Enriched	YES
Q9NUQ9;E5RI16;E	Protein FAM49B	FAM49B	36.748	22.5	7	6	19.614	0	31757	29168	30042	24370	31348	27342	53538	61529	28843	33824	Enriched	Enriched	Enriched	No expres	YES
Q9NUY8-2;Q9NUY	TBC1 domain family	TBC1D23	76.5	11	9	9	114.31	0	33507	23579	22279	24825	38916	28082	19850	20001	8677	19918	Moderate	Enriched	Enriched	No expres	YES
Q9NV31	U3 small nucleolar ri	IMP3	21.85	13	2	2	3.928	0.00061	12829	8485.4	7143	10333	8790	13171	11305	10994	4225.8	11583	Enriched	Enriched	Enriched	No expres	YES
Q9NV35	Probable 8-oxo-dGTI	NUDT15	18.609	17.1	2	2	38.385	0	7373.1	5215.3	3513.3	10892	3578.5	5575.1	5145.5	8319.5	4734	9668.2	Moderate	Moderate	Moderate	No expression	
Q9NV70-2;Q9NV7	Exocyst complex con	EXOC1	100.28	12.3	12	12	24.847	0	30234	14584	22426	31719	22821	31345	35814	30430	26858	34447	Moderate	Enriched	Enriched	No expres	YES
Q9NV88-3;Q9NV8	Integrator complex su	INTS9	71.136	4.1	2	2	11.542	0	6788.6	4193	6310	11426	4936.7	9643.9	5916.4	8770.6	2471.9	8145.2	Moderate	Enriched	Enriched	Low	
Q9NV96;Q9NV96-	Cell cycle control pro	TMEM30A	40.683	12.2	5	5	30.595	0	16626	17764	19340	13411	26347	10092	10094	8432.7	4733.3	8710.1	Moderate	Enriched	Enriched	No expres	YES
Q9NVA4	Transmembrane prote	TMEM184C	50.141	3	1	1	15.6	0	12460	13136	15521	11693	16097	11576	5462.3	8470.5	2521.8	8397.5	Enriched	Moderate	Enriched	No expres	YES
Q9NVE5;Q9NVE5-	Ubiquitin carboxyl-te	USP40	140.13	1.6	2	2	3.275	0.00078	1446.4	1020.5	1158.9	1820.8	1510.2	1615.2	1327	1156.8	913.18	1227.4	Moderate	Enriched	Moderate	No expres	YES
Q9NVE7;E9PHT6;	Pantothenate kinase 4	PANK4	85.99	11	8	8	47.881	0	18339	16451	22294	18745	17319	24632	44195	46152	15318	26467	Enriched	Moderate	Enriched	No expres	YES
Q9NVH0;Q9NVH0	Exonuclease 3-5 don	EXD2	70.352	11.1	6	6	12.899	0	7643.1	3046	5381.1	10054	4150.6	5804.5	6005.9	8205.3	3976.1	7484.1	Moderate	Enriched	Enriched	Enriched	YES
Q9NVH1-3;Q9NVH	DnaJ homolog subfar	DNAJC11	57.196	15.6	6	6	40.957	0	28787	22017	22068	27519	26855	19873	11150	22097	3770.6	23260	Enriched	Enriched	Enriched	No expres	YES
Q9NVH6-7;Q9NVH	Trimethyllysine dioxy	TMLHE	41.537	7.1	2	2	3.9045	0.00061	7839.8	6191.5	8046.6	9402	8348.6	6841.9	6811.1	7450	3518.4	8408.2	Low	Moderate	Moderate	No expres	YES
Q9NVI7-2;Q9NVI7	ATPase family AAA	ATAD3A	66.217	30	18	18	125.35	0	112960	78816	109700	100730	132770	104520	138130	111360	83238	126230	Enriched	Enriched	Moderate	No expression	
Q9NVJ2;Q9NVJ2-2	ADP-ribosylation fac	ARL8B	21.539	33.9	6	3	43.62	0	74172	42895	60695	72983	63532	115860	87733	81687	36075	102240	Enriched	Enriched	Enriched	No expression	
Q9NVM6	DnaJ homolog subfar	DNAJC17	34.687	3.6	1	1	3.2395	0.00077	4016.7	5091.8	5246.9	2878.6	6248.9	2698.6	4007.6	3793.1	3864.2	4507.4	No expres	No expres	Low	No expres	YES
Q9NVM9-2;Q9NVM	Protein asunder homo	ASUN	68.494	5.3	3	3	3.9678	0.00062	17856	13285	15870	16245	16858	15083	15538	17753	8372.3	15155					YES
Q9NVN8	Guanine nucleotide-b	GNL3L	65.572	3.4	2	2	4.1263	0.00062	1478.6	1747.9	1794.6	1417.5	2505.6	1374.4	1613.8	1374.7	1331.5	1573.5	Moderate	Low	Moderate	No expres	YES
Q9NVP1	ATP-dependent RNA	DDX18	75.406	17.8	13	13	39.565	0	56263	43821	47978	51769	49498	51504	55186	65230	30018	61524	Enriched	Enriched	Enriched	Low	YES
Q9NVS2;Q5QPA5;	28S ribosomal protei	MRPS18A	22.184	12.8	2	2	3.1913	0.00077	2350	2933.5	2427	2047.7	4097.5	3041.4	3289	2963.6	2726.9	5245.3	Enriched	Moderate	Enriched	No expression	
Q9NVS9;Q9NVS9-	Pyridoxine-5-phosph	PNPO	29.988	29.9	12	12	85.567	0	21190	21738	23429	13204	31379	16727	21855	19659	15871	15074	Moderate	Enriched	Enriched	No expres	YES
Q9NVV4;Q5T851	Poly(A) RNA polyme	MTPAP	66.171	4.6	3	3	55.33	0	9528.2	9802.3	12477	6417	12111	6000.7	16556	11136	8207.9	15466	Enriched	Enriched	Enriched	No expres	YES
Q9NVZ3;D6RB24;	Adaptin ear-binding	NECAP2	28.338	15.2	4	4	7.9699	0	14453	14104	13542	12860	15705	14828	12547	10818	6886.2	13657	Moderate	Enriched	Enriched	No expres	YES
Q9NW13-2;Q9NW	RNA-binding protein	RBM28	69.922	16.8	9	9	27.529	0	31160	24944	31721	31361	42325	23902	35733	33725	27858	36309	Enriched	Moderate	Enriched	No expres	YES
Q9NW64-2;Q9NW	Pre-mRNA-splicing f	RBM22	41.151	22.4	7	7	27.366	0	23804	26195	26814	26835	37237	16819	24974	20560	16791	28142	Moderate	Enriched	Enriched	No expres	YES
Q9NW68;Q9NW68	BSD domain-contain	BSDC1	47.163	19.5	7	7	14.716	0	26742	20963	22680	29296	23031	25832	25477	28372	12637	26720	Enriched	Enriched	Enriched	No expres	YES
Q9NW97	Transmembrane prote	TMEM51	27.759	14.2	4	4	38.876	0	14107	12616	15408	15669	15643	11962	14672	24062	21387	17506	Enriched	Enriched	Enriched	No expres	YES
Q9NWB7	Intraflagellar transpo	IFT57	49.108	4.7	2	2	4.1903	0.00062	4723.6	2727.1	3846	3751.1	1997.3	4984	2942.1	7407.4	1729.3	6092.1	Moderate	Enriched	Enriched	No expression	
Q9NWF9;Q9NWF9	E3 ubiquitin-protein	RNF216	99.405	1.6	1	1	2.0813	0.00707	6336.8	4686	7360.4	15638	5758.3	6457	7207.4	11681	3343.3	9127.7	Enriched	Enriched	Enriched	No expression	
Q9NWQ8	Phosphoprotein asso	PAG1	46.98	2.5	1	1	3.1753	0.00077	11690	12487	14137	10114	14181	10621	7095.8	9672.4	1793.1	11960	Enriched	Enriched	Enriched	No expression	
Q9NWT6	Hypoxia-inducible fa	HIF1AN	40.285	5.2	1	1	3.4316	0.00079	4397.9	3615.7	3461.5	4907.5	4239	6173.9	2400	2822.4	1599.7	3814.2	Moderate	Moderate	Moderate	No expres	YES
Q9NWU1;C9J2G3;	3-oxoacyl-[acyl-carri	OXSM	48.842	10.2	6	6	16.264	0	26212	19550	24627	22704	27934	31006	21535	18885	8366.7	21221	Enriched	Moderate	Enriched	No expres	YES
Q9NWV4;B1ARP7	UPF0587 protein C1	C1orf123	18.048	43.8	7	7	93.381	0	103630	64653	60234	121310	71629	60564	69105	116020	41835	98687	Enriched	Enriched	Enriched	Low	YES
Q9NWV8;M0R193	BRISC and BRCA1-A	BABAM1	36.56	16.7	5	5	9.3635	0	25637	22034	25918	19039	28351	23075	28400	18130	21059	23188					YES
Q9NWY4	UPF0609 protein C4	C4orf27	39.436	6.1	2	2	6.4095	0	12917	13145	14656	11209	16085	13344	16158	11541	11493	15214	Moderate	Enriched	Enriched	No expres	YES
Q9NWZ5-3;Q9NW	Uridine-cytidine kina	UCKL1	44.567	13.2	5	5	6.5212	0	7791	5467.1	6390.8	5813	7648.3	4866	5111.1	5582.4	2933.5	5670.6	Low	Enriched	Enriched	Enriched	YES
Q9NX00	Transmembrane prote	TMEM160	19.657	5.3	1	1	2.6008	0.00273	1059	1206.1	1464	1094.3	1639.7	1017.4	1561.3	1342.4	1569.1	1742	Enriched	Moderate	Moderate	No expression	
Q9NX14;Q9NX14-	NADH dehydrogenas	NDUFB11	17.316	35.3	6	6	29.987	0	26972	16363	21238	21222	23497	29470	30685	30989	11954	27835	Enriched	Enriched	Enriched	No expres	YES
Q9NX24;J3QSY4;I	H/ACA ribonucleopr	NHP2	17.201	37.3	9	9	59.96	0	32165	25233	27753	31108	33797	21788	20599	18594	11073	27572	Enriched	Enriched	Enriched	Low	YES
Q9NX40;D6RDK6;	OCIA domain-contai	OCIAD1	27.626	27.3	8	8	16.998	0	47218	42225	43496	51715	51269	38501	53362	55686	35005	63835	Enriched	Enriched	Enriched	No expres	YES
Q9NX46	Poly(ADP-ribose) gly	ADPRHL2	38.946	10.2	4	4	26.155	0	11677	8092.8	7941.6	10272	14155	8362.9	6895.4	5017.5	2961.5	7590.1	Enriched	Enriched	Enriched	No expres	YES
Q9NX55	Huntingtin-interactin	HYPK	14.665	38	5	5	64.873	0	13064	7705.4	10851	15400	11462	26619	16520	26226	9818.6	27825					YES
Q9NX58	Cell growth-regulatin	LYAR	43.614	15.6	4	4	36.599	0	25601	19493	23737	22689	33654	21197	21708	23042	11201	23867	Enriched	Enriched	Moderate	No expres	YES
Q9NX62	Inositol monophosph	IMPAD1	38.681	12	4	4	10.295	0	13714	5898.3	8978.9	13090	10484	13984	9653.1	8386.5	5397.3	10961	Enriched	Enriched	Enriched	No expres	YES
Q9NXA8-4;Q9NXA	NAD-dependent prot	SIRT5	21.688	7.9	1	1	3.2631	0.00077	4019.1	3611.4	3624.8	3062.3	4373.2	2686.9	2466.2	3314.7	991.42	3042.9	Moderate	Moderate	Moderate	No expres	YES
Q9NXC5;Q9NXC5	WD repeat-containin	MIOS	98.583	7.4	8	8	37.768	0	16379	13545	14972	14835	16488	18619	18997	27786	10454	20754	Enriched	Enriched	Enriched	Moderate	YES
Q9NXF1-2;Q9NXF	Testis-expressed sequ	TEX10	103.91	4.3	3	3	12.999	0	5564.1	4472.5	6390.5	4860.7	6419.6	3796.6	4088.8	3520	3638.7	3915.4	Enriched	Moderate	Enriched	No expres	YES
Q9NXG2	THUMP domain-con	THUMPD1	39.315	28.6	14	14	79.36	0	37632	24898	35228	27762	28760	23859	31501	34161	22434	37710	Moderate	Moderate	Enriched	Enriched	YES
Q9NXJ5;U3KQ24;I	Pyroglutamyl-peptida	PGPEP1	23.138	16.3	5	5	9.2743	0	15644	13062	12869	16014	19573	11992	10156	14660	4598.2	12768	Moderate	Enriched	Enriched	No expression	
Q9NXN4-2;Q9NXN	Ganglioside-induced	GDAP2	56.048	5.6	2	2	2.292	0.00496	7303.3	5680.2	4668.8	6854	5563.2	9286.9	12226	10196	8787.1	7422.2	Moderate	Low	Moderate	No expres	YES
Q9NXS2-3;Q9NXS	Glutaminyl-peptide c	QPCTL	32.911	14.9	5	5	17.336	0	9472.1	8315.4	9154	6255	10821	6912.7	6963.1	6834.2	3802.6	6830.2	Low	No expres	No expres	No expres	YES
Q9NXV6	CDKN2A-interacting	CDKN2AIP	61.124	21.9	13	13	41.885	0	14277	15246	20474	13699	21925	14548	19151	15663	12602	18117	Low	Low	Enriched	No expres	YES
Q9NY12-2;Q9NY1	H/ACA ribonucleopr	GAR1	20.834	27.6	10	10	19.57	0	81631	44093	63924	64064	74076	103820	96039	72137	38780	73178	Moderate	Moderate	Enriched	No expres	YES
Q9NY15	Stabilin-1	STAB1	275.48	3.2	7	7	21.204	0	51294	54090	56979	39661	66637	24149	31128	31369	17171	36018	Moderate	Moderate	Moderate	Moderate	YES
Q9NY27-2;Q9NY2	Serine/threonine-prot	PPP4R2	40.175	16.4	6	6	13.35	0	9885.2	9102.2	11972	7772.7	14966	7628.5	14726	8869.7	10207	13696	Moderate	Enriched	Enriched	No expres	YES
Q9NY33-4;G3V1D	Dipeptidyl peptidase	DPP3	79.306	37.2	28	16	98.164	0	131660	97864	117270	131110	148060	104140	110130	111340	56616	109670	Enriched	Enriched	Enriched	No expres	YES
Q9NY61	Protein AATF	AATF	63.132	7.5	3	3	6.713	0	6473.6	4908.2	6705	8215.2	6067	7714.2	8249.7	12995	4293	9472.8	Enriched	Enriched	Enriched	Enriched	YES
Q9NYB0	Telomeric repeat-bin	TERF2IP	44.259	12	3	3	25.084	0	5654.9	5776.8	4720.8	5975.7	6340.1	5359.1	4467.9	4523.5	3144.4	4977.4	Moderate	Enriched	Enriched	Enriched	YES
Q9NYF8-2;Q9NYF	Bcl-2-associated tran	BCLAF1	105.95	19.5	24	0	3.6819	0.0008	18374	12379	12957	12960	20369	7795.3	4054	6470	1051.6	7022.4	Moderate	Enriched	Enriched	Enriched	YES
Q9NYJ1;Q9NYJ1-2	Cytochrome c oxidas	COA4	10.134	18.4	1	1	3.0947	0.00095	6348.2	4928.7	4447.9	6428.6	4427	5374.8	5539	7738.3	3989	7720.8					
Q9NYL4;F8VU90;	Peptidyl-prolyl cis-tr	FKBP11	22.18	30.8	24	18	254.41	0	408440	241990	253380	444690	289430	357050	249200	264450	141460	274290	Enriched	Enriched	Enriched	No expres	YES
Q9NYL9	Tropomodulin-3	TMOD3	39.594	46	28	27	63.773	0	123330	90215	107200	126640	119130	126500	122180	126020	56459	119950	Moderate	Enriched	Enriched	No expres	YES
Q9NYM9;E9PQJ6;	BET1-like protein	BET1L	12.388	45	4	4	36.215	0	13378	11413	12890	11645	10442	22959	23865	25361	20382	25415	Enriched	Enriched	Enriched	No expres	YES
Q9NYQ7;Q9NYQ7	Cadherin EGF LAG s	CELSR3;CELSR2	358.18	0.5	2	1	2.166	0.00612	3062	6571	6499.3	3057.8	8078	2794.3	3066.7	2669.6	2476.4	5506.8	Enriched	Moderate	Enriched	Enriched	
Q9NYU2-2;Q9NYU	UDP-glucose:glycopr	UGGT1	174.97	38.3	100	97	323.31	0	511120	359740	354570	500620	404950	511800	527130	468860	327190	427790					YES
Q9NZ01	Very-long-chain enoy	TECR	36.034	21.1	11	11	14.234	0	80500	25055	46724	73714	54687	85645	95500	85893	22580	68963					YES
Q9NZ08;Q9NZ08-2	Endoplasmic reticulu	ERAP1	107.23	23	22	22	83.031	0	140670	67190	79683	111390	84711	134640	108580	140000	62262	109680	Moderate	Low	Enriched	No expres	YES
V9GYX7;Q9NZ32;	Actin-related protein	ACTR10	33.201	26.2	6	6	120.5	0	26315	21374	23228	23328	24362	23291	21175	18439	8727.9	21330	Enriched	Enriched	Enriched	No expres	YES
Q9NZ43;G8JLK1;C	Vesicle transport pro	USE1	29.371	27	9	9	49.214	0	30757	21651	22962	29359	23744	33349	34646	26815	36080	35564	Low	Moderate	Moderate	No expres	YES
Q9NZ45	CDGSH iron-sulfur d	CISD1	12.199	48.1	12	12	73.319	0	66782	51942	56239	47584	77580	73878	76492	97033	38058	81086	Moderate	Moderate	Enriched	No expres	YES
Q9NZB2;Q9NZB2-	Constitutive coactiva	FAM120A	121.89	33.9	39	39	281.44	0	182540	131790	139630	191540	181460	159830	193220	190400	121000	185030	Enriched	Enriched	Enriched	Enriched	YES
Q9NZC3;H3BU22	Glycerophosphodiest	GDE1	37.718	10	4	4	4.238	0.00063	1931.4	560.85	611.63	1664.5	1444.9	2458.7	2086	1283.6	2222.2	1807.3	Low	Enriched	Enriched	Low	
Q9NZH0;Q9NZH0-	G-protein coupled re	GPRC5B	44.794	3	1	1	4.7498	0.00043	9049.7	7774.8	7826.8	7369.5	8175.3	7288.9	6950.9	7820.2	4395.6	8804	Enriched	Enriched	Enriched	Moderate	
Q9NZI7-4;Q9NZI7	Upstream-binding pro	UBP1	56.452	7.1	3	3	6.4183	0	7209.8	2875.5	4294.3	8939.4	3667.9	16187	8604.5	8934.1	2616.5	8538.5	Moderate	Enriched	Enriched	No expression	
Q9NZJ5;E7ER02;C	Eukaryotic translatio	EIF2AK3	125.21	6.5	6	6	20.172	0	22146	9519.3	13253	18655	14486	25430	15868	20398	7430.4	21843	Moderate	Enriched	Enriched	No expression	
Q9NZL9;Q9NZL9-	Methionine adenosyl	MAT2B	37.551	29.9	14	14	52.278	0	10548	11978	14189	7200.8	17877	6499.4	11403	7761.4	7606.4	9571.9	Enriched	Enriched	Enriched	No expres	YES
Q9NZM1-6;Q9NZM	Myoferlin	MYOF	233.47	11.2	21	19	41.198	0	31818	30436	32665	40814	34426	33822	28153	42896	14110	34566	Enriched	Moderate	Enriched	Enriched	YES
Q9NZM5	Glioma tumor suppre	GLTSCR2	54.389	8.4	3	3	10.19	0	13814	11777	13383	10437	13713	12717	14764	18289	7131.6	18559	Enriched	Enriched	Enriched	No expres	YES
Q9NZN3	EH domain-containin	EHD3	60.886	22.6	16	6	10.792	0	9177	5191.8	7068	9862.8	8141.4	13063	11933	11277	4457.7	11320	Low	Low	Moderate	No expres	YES
Q9NZN4;Q9NZN4-	EH domain-containin	EHD2	61.161	31.7	26	24	105.62	0	102440	104630	121120	142100	129040	122580	176250	172070	95783	171920	Low	Enriched	Moderate	No expres	YES
Q9NZQ3-5;Q9NZQ	NCK-interacting prot	NCKIPSD	64.195	6.9	4	4	6.4412	0	13278	9980	13840	14431	14288	11085	20063	15794	19294	17019	Enriched	Enriched	Enriched	Enriched	
Q9NZR1;G5EA42;	Tropomodulin-2	TMOD2	39.595	15.1	5	4	13.711	0	5093	4166.6	5138.2	5705.9	6599.2	4621.7	9610	6815.1	6272.4	6098	No expres	Low	Moderate	No expres	YES
Q9NZT2-2;Q9NZT	Opioid growth factor	OGFR	71.423	17.2	11	11	153.03	0	49787	37940	49561	35086	45098	42307	67763	57586	58810	61760	Enriched	Enriched	Moderate	Enriched	YES
Q9NZU5;Q9NZU5-	LIM and cysteine-ricl	LMCD1	40.832	34.8	13	13	31.814	0	72443	58729	57859	79509	76738	63899	97765	116990	57898	84326	Low	Enriched	Enriched	No expres	YES
Q9NZZ3	Charged multivesicul	CHMP5	24.57	15.1	5	5	14.694	0	36576	33063	32490	38440	38185	34780	31871	38497	17936	32250	Low	Enriched	Enriched	No expres	YES
Q9P000-2;Q9P000	COMM domain-cont	COMMD9	17.333	21.8	3	3	5.9727	0	2834.5	2712.7	3183.9	4233.7	3783.4	3448.2	3453.2	2829	2304.6	3314.8	Enriched	Enriched	Enriched	No expres	YES
Q9P013	Spliceosome-associat	CWC15	26.624	5.2	2	2	10.541	0	5345.7	2688.2	3874.5	4390.7	3974.4	4236	8836.2	3287.6	10562	8842.5	Enriched	Enriched	Enriched	No expres	YES
Q9P015;E5RHF4;E	39S ribosomal protei	MRPL15	33.419	16.6	4	4	9.3818	0	40316	30059	31211	39080	44963	28193	24557	23703	12792	30790	Enriched	Enriched	Enriched	No expres	YES
Q9P016;Q9P016-2	Thymocyte nuclear p	THYN1	25.697	32.9	8	8	23.008	0	53663	31956	42260	43970	40429	64532	122850	66264	98628	88630	Low	Enriched	Enriched	No expres	YES
Q9P032	NADH dehydrogenas	NDUFAF4	20.266	16	3	3	10.753	0	9880.4	16832	13949	5761.5	22387	2530.8	3524.5	2356.4	2870.2	6915.4	Low	Enriched	Enriched	No expres	YES
Q9P035;Q9P035-2;	Very-long-chain (3R)	PTPLAD1	43.159	20.2	14	14	98.065	0	51704	44111	49373	53227	59880	48652	65752	66767	32360	56974	Enriched	Enriched	Enriched	No expres	YES
Q9P0I2-2;Q9P0I2;S	ER membrane protei	EMC3	24.915	31.5	8	6	19.856	0	46137	30913	45704	40591	49659	34653	34896	35998	25660	41764					
Q9P0J0;Q9P0J0-2;I	NADH dehydrogenas	NDUFA13	16.698	47.2	10	10	20.088	0	29535	28832	32842	31454	36766	26216	24443	28866	16481	28796	Enriched	Enriched	Enriched	No expres	YES
Q9P0J1;Q9P0J1-2	[Pyruvate dehydroger	PDP1	61.053	17.3	9	9	58.128	0	13207	11264	13418	11088	15869	13096	26740	21191	17374	20193	No expres	Enriched	Enriched	No expres	YES
Q9P0J7	E3 ubiquitin-protein	KCMF1	41.945	9.2	5	5	13.585	0	11657	5962	8614.6	12639	7879.5	12149	9626.7	10001	5442.7	12269	Enriched	Enriched	Enriched	No expres	YES
Q9P0K7-4;Q9P0K7	Ankycorbin	RAI14	106.9	10.1	9	9	21.456	0	29066	18201	23813	30239	25139	27541	24499	28995	13632	30105	No expres	Moderate	Enriched	Low	YES
Q9P0L0;Q9P0L0-2	Vesicle-associated m	VAPA	27.893	43.4	16	16	67.739	0	138740	85164	100920	135350	115130	197850	191570	211910	79473	152760	Enriched	Enriched	Enriched	Enriched	YES
Q9P0M6;Q5SQT3	Core histone macro-I	H2AFY2	40.058	37.1	20	14	41.659	0	82350	64473	83617	90016	76242	96493	112710	109800	66030	118270	Enriched	No expres	Moderate	No expres	YES
Q9P0P8	Uncharacterized prot	C6orf203	27.941	12.9	4	4	13.232	0	20108	11994	13821	21216	11515	17731	24945	25695	15040	26015	Low	Moderate	Enriched	No expres	YES
Q9P0U4;Q9P0U4-2	CXXC-type zinc fing	CXXC1	75.711	6.6	4	4	8.8806	0	12617	9817.2	12338	11497	15212	8662.9	9920.7	9140.6	9335.7	11574	Enriched	Enriched	Enriched	No expres	YES
Q9P0V3;Q9P0V3-2	SH3 domain-binding	SH3BP4	107.49	4.2	5	5	4.6432	0.00043	8530.1	8090.2	10179	8121.2	9867.8	9897	10271	11391	6299.4	11193	Enriched	Enriched	Enriched	No expres	YES
Q9P1F3	Costars family protei	ABRACL	9.0564	40.7	5	5	16.938	0	7714.6	4915.1	5645	12876	4186.1	5541.1	5728.6	11911	4996.3	9307.7					YES
Q9P1Q0-4;Q9P1Q0	Vacuolar protein sort	VPS54	109.36	1.5	1	1	2.495	0.00378	4874.1	4335.6	3371.7	7146.3	4279.2	6570	4814.3	6582.6	2062.8	6399.2	Enriched	Enriched	Enriched	No expression	
Q9P1Z2-4;Q9P1Z2	Calcium-binding and	CALCOCO1	67.542	8.1	4	4	15.305	0	7564.1	4601.1	7201.9	4677.3	7122.9	10501	8919.9	5851.7	5377.4	6255.8	Enriched	Enriched	Enriched	Moderate	YES
Q9P206-2;Q9P206;	Uncharacterized prot	KIAA1522	113.06	13.4	12	12	47.963	0	25496	27925	22493	19504	38692	16377	28124	18795	22553	24204	Enriched	Enriched	Enriched	No expres	YES
Q9P253	Vacuolar protein sort	VPS18	110.18	6.3	5	5	9.5869	0	5971.4	2431	3142.6	6804.7	3095.3	2503.9	2011.4	4864.6	1784.8	5523.6	Enriched	Enriched	Enriched	No expres	YES
Q9P258	Protein RCC2	RCC2	56.084	17.4	12	12	45.355	0	22474	18085	23521	19988	27933	22497	25634	21886	12574	21547	Enriched	Enriched	Enriched	No expres	YES
Q9P260;Q9P260-2	LisH domain and HE	KIAA1468	134.63	3	3	3	7.3576	0	6701.6	3675.2	5890.2	8882.1	4739.7	8236.1	7956	10239	3931.9	8336.4	Enriched	Enriched	Enriched	No expres	YES
Q9P265	Disco-interacting pro	DIP2B	171.49	9.9	16	14	94.179	0	69419	58399	73753	62846	82514	83604	110460	120750	49729	92235	Moderate	Enriched	Enriched	No expres	YES
Q9P266	Junctional protein as	KIAA1462	148.35	11.1	12	12	49.305	0	36969	33844	45979	60377	47886	38867	54193	70311	26231	53796	Low	Moderate	Moderate	Enriched	YES
Q9P270	SLAIN motif-contain	SLAIN2	62.543	2.4	1	1	3.9643	0.00062	1052.4	1302.9	1227.7	865.78	1596.1	743.41	1470	1091	1031.4	1209.2	Moderate	Enriched	Enriched	No expres	YES
Q9P287;Q9P287-3;	BRCA2 and CDKN1	BCCIP	35.979	18.5	7	7	24.244	0	46262	30124	35270	30931	29494	37305	39491	41481	27872	41787	Enriched	Enriched	Enriched	No expres	YES
Q9P2B2	Prostaglandin F2 rece	PTGFRN	98.555	29.4	37	37	148.73	0	190360	101980	159600	137310	158480	203830	151860	137760	64189	181970	Enriched	Enriched	Enriched	No expres	YES
Q9P2D3;Q9P2D3-3	HEAT repeat-contain	HEATR5B	224.3	3.5	6	6	13.125	0	22012	26222	27323	17877	32136	16248	24406	24560	18432	24038	Moderate	Enriched	Enriched	No expres	YES
Q9P2E9-2;Q9P2E9	Ribosome-binding pr	RRBP1	152.19	70.7	234	4	20.439	0	21548	23491	26555	15446	36767	11083	16587	12582	10813	14759	Enriched	Enriched	Enriched	Enriched	YES
Q9P2H0;H0YF13	Uncharacterized prot	KIAA1377	125.87	1.6	2	2	2.1962	0.00544	39071	31038	38871	30768	41846	19031	19956	17479	16000	25796	Enriched	Moderate	Enriched	No expression	
Q9P2I0	Cleavage and polyade	CPSF2	88.486	2.3	2	2	3.9273	0.00061	4601.3	3795	3188	4190.1	4126.1	2721.1	3578.7	4757.5	2446	3762.3	Enriched	Enriched	Enriched	No expres	YES
Q9P2J5;Q9P2J5-2	Leucine--tRNA ligase	LARS	134.46	35.8	68	68	307.73	0	311270	200030	246240	298330	278640	352170	381820	384410	150450	296320	Enriched	Enriched	Enriched	No expres	YES
Q9P2M7;Q9P2M7-	Cingulin	CGN	136.38	18.5	27	27	108.05	0	114130	100400	89083	111170	101880	103880	128060	152700	101890	121460	Enriched	Enriched	Enriched	No expres	YES
U3KPZ7;Q9P2N5	RNA-binding protein	RBM27	114.54	2.4	3	3	5.3544	0	15116	5225	8709.7	19427	9143.2	16825	24930	20220	12609	17639	Moderate	Enriched	Enriched	No expres	YES
Q9P2P6;H3BN21	StAR-related lipid tra	STARD9	516.34	0.3	2	2	2.06	0.00724	8501.1	5209.8	8711.2	6383.6	15467	7965.2	6578.8	6230.5	2241.4	6043.6	Moderate	Moderate	Low	No expression	
Q9P2R3;Q9P2R3-2	Ankyrin repeat and F	ANKFY1	128.4	8.1	11	11	26.774	0	64307	54603	68220	66712	65096	59262	78395	90063	44134	78222	Moderate	Enriched	Enriched	No expres	YES
Q9P2R7-2;Q9P2R7	Succinyl-CoA ligase	SUCLA2	48.039	33.8	27	27	51.431	0	108870	87246	109770	102490	104910	126640	160960	164420	84146	134690	Moderate	Moderate	Enriched	Low	YES
Q9P2X0;Q9P2X0-2	Dolichol-phosphate r	DPM3	10.094	21.7	3	3	6.5952	0	19645	14679	11892	13259	22715	12911	13048	17809	9444.6	14516	Enriched	Enriched	Enriched	No expres	YES
Q9P2X3;J3KT25;J3	Protein IMPACT	IMPACT	36.476	9.1	3	3	4.3144	0.00063	4331.1	3664.6	4561.1	4762	4824.1	4438	3858.2	3664.3	2749	3464.9	Low	Low	Moderate	No expres	YES
Q9UBB4;Q9UBB4-	Ataxin-10	ATXN10	53.488	9.9	4	4	12.647	0	18777	18929	20626	18478	23348	10293	19447	17799	13453	20646	Enriched	Enriched	Enriched	Low	YES
Q9UBB5;X6RBL6;	Methyl-CpG-binding	MBD2	43.254	8	4	4	11.747	0	24548	19937	22311	16663	22115	20639	21069	16025	11721	23592	Enriched	Enriched	Enriched	Moderate	YES
Q9UBB9	Tuftelin-interacting p	TFIP11	96.819	3.9	3	3	6.2444	0	2364	856.13	1332.1	2531.9	1072.4	1879.4	1396.5	1544.5	1010.1	1867.4	Enriched	Moderate	Moderate	Moderate	YES
Q9UBC2-3;Q9UBC	Epidermal growth fac	EPS15L1;SPATA22	83.247	13.1	14	14	23.834	0	50449	59589	63710	61678	68952	52177	56042	56034	30448	56458	Enriched	Moderate	Moderate	No expres	YES
Q9UBE0;B3KNJ4;(	SUMO-activating enz	SAE1	38.449	40.8	16	2	3.1584	0.00077	8229.7	4631.6	7424.4	6076.7	8339.5	4817	14545	9449.4	6674.9	12675	Enriched	Moderate	Enriched	No expres	YES

Q9UBF2-2;Q9UBF	Coatomer subunit gar	COPG2	81.482	17.1	20	6	25.865	0	22587	10961	19416	37029	13947	36603	28520	58206	14944	32751	Low	Low	Moderate	No expres	YES	
Q9UBG0	C-type mannose recep	MRC2	166.67	5.1	9	9	106.81	0	18611	18169	24981	23458	31993	14650	33244	26290	21251	28144	Moderate	Moderate	Enriched	Moderate	YES	
Q9UBI6	Guanine nucleotide-b	GNG12	8.0061	66.7	7	7	51.11	0	43717	17978	17137	51067	37252	15544	13442	12202	11328	13141	Moderate	Enriched	Enriched	Enriched	YES	
Q9UBI9	Headcase protein hor	HECA	58.836	4.8	2	2	6.757	0	4233.1	3864.4	5065.2	2764.7	6149.7	2304.2	2197.8	1443.2	2468.1	3926.2	Enriched	Enriched	Enriched	No expression		
Q9UBK8-2;Q9UBK	Methionine synthase	MTRR	77.673	1.7	1	1	1.8367	0.00959	37368	14534	19225	28183	25635	53833	28077	23758	9796.7	27745	Enriched	Enriched	Enriched	Moderate		
Q9UBL3-3;Q9UBL	Set1/Ash2 histone me	ASH2L	60.207	12.9	8	8	17.471	0	34399	24203	33684	40323	61877	20892	21426	21058	11038	25108	Enriched	Enriched	Enriched	Moderate	YES	
Q9UBN7-2;Q9UBN	Histone deacetylase 6	HDAC6	114.36	1.7	2	2	2.4983	0.00378	2516.1	3168.5	2059.7	2574	2177.3	2385.9	2667.3	2190.5	1141.8	1873.3	Enriched	Enriched	Enriched	Moderate	YES	
Q9UBP6;F8VSD9;I	tRNA (guanine-N(7)-	METTL1	31.471	6.9	2	2	2.9432	0.00169	2561	2870.2	2759.7	1916.8	3056.3	2001.8	3590.5	2790.7	2912.4	3683.7	Enriched	Enriched	Moderate	Enriched	YES	
Q9UBP9-4;Q9UBP	PTB domain-containi	GULP1	33.333	10.7	3	3	6.5284	0	6412.2	3451.1	5694.8	5014.9	10724	3324.9	5000.6	3869.6	3035	5297.1	Enriched	Enriched	Enriched	Low	YES	
Q9UBQ5;K7ERF1;	Eukaryotic translation	EIF3K	25.059	46.8	15	15	53.473	0	67341	59159	76551	67907	76548	64300	87608	64155	87790	72711	Enriched	Enriched	Enriched	Moderate	YES	
Q9UBQ7;U3KQ56;	Glyoxylate reductase	GRHPR	35.668	40.9	25	25	121.6	0	103290	73382	73559	105470	100180	93741	112430	161820	63707	102140	Enriched	Enriched	Enriched	Moderate	YES	
Q9UBR2	Cathepsin Z	CTSZ	33.868	14.5	4	4	8.2513	0	23559	15061	16599	23615	20626	13138	6997.8	11029	3644.1	10246	Moderate	Low	Moderate	Moderate	YES	
Q9UBS0	Ribosomal protein S6	RPS6KB2	53.455	2.5	1	1	2.0876	0.0069	4311.3	5667.1	5714.6	3686.5	7337.8	3989.3	5643.7	3216.8	3462.9	4260.7	Moderate	Low	Moderate	Moderate		
Q9UBS3	DnaJ homolog subfar	DNAJB9	25.518	6.3	1	1	8.0794	0	2353.5	2559.8	3413.9	3717.1	3543	3258.5	4869.8	2040.4	1864.7	3558.9	Enriched	Enriched	Enriched	Enriched	YES	
Q9UBS4	DnaJ homolog subfar	DNAJB11	40.513	34.6	23	22	323.31	0	225330	156200	165310	222950	194110	244110	194840	190430	78154	180870	Enriched	Enriched	Enriched	No expres	YES	
Q9UBS8-2;Q9UBS	E3 ubiquitin-protein	RNF14	39.633	5.5	2	2	3.7844	0.0006	7581.2	6324.1	8255.5	5354	10484	5431.9	10151	7460.5	5384.4	6836.8	Low	Moderate	Enriched	Moderate	YES	
Q9UBT2;Q9UBT2-	SUMO-activating enz	UBA2	71.223	24.7	18	18	72.721	0	82179	60908	73843	85305	77058	72180	101780	112300	68578	96507	Moderate	Enriched	Enriched	Enriched	YES	
Q9UBU3-4;Q9UBU	Appetite-regulating h	GHRL	11.656	51	7	7	59.802	0	77392	46438	52436	47952	38596	27260	19977	22491	18733	24024	Enriched	Moderate	Enriched	No expression		
Q9UBU6	Protein FAM8A1	FAM8A1	44.123	11.1	3	3	11.195	0	12178	10917	10854	11478	15897	9410.9	9766	9726.7	6285	10879	Enriched	Enriched	Enriched	Enriched	YES	
Q9UBV2	Protein sel-1 homolo	SEL1L	88.754	23.2	20	20	44.374	0	83321	72043	74848	79073	96258	81593	72760	71595	47077	76739	Moderate	Enriched	Enriched	Moderate	YES	
Q9UBV8	Peflin	PEF1	30.381	10.6	5	5	7.9821	0	23336	15933	23305	31145	22310	22347	51040	34893	24208	28654	Low	Enriched	Enriched	No expres	YES	
Q9UBW8;F5H7C6;	COP9 signalosome co	COPS7A	30.276	21.5	5	5	28.377	0	12278	8899.5	10646	9429.2	13005	9980.9	10024	11324	5593.7	10210	Low	Enriched	Enriched	Moderate	YES	
Q9UD71;J3KSJ8;J3	Protein phosphatase 1	PPP1R1B	22.963	35.3	7	7	47.66	0	25853	27702	37311	29988	30843	35616	35270	27530	24316	36648	Enriched	Enriched	Enriched	No expres	YES	
Q9UDR5;F8WE53;	Alpha-aminoadipic se	AASS	102.13	13.3	10	10	47.035	0	57713	44179	58075	42675	62554	41044	47519	50030	28728	54428	No expres	Low	Low	No expres	YES	
Q9UDT6-2;Q9UDT	CAP-Gly domain-cor	CLIP2	111.78	9.3	9	9	41.339	0	25354	23606	25243	23040	31571	20040	23433	21512	15793	22461	Moderate	Moderate	Moderate	Enriched	YES	
Q9UDW1;Q9UDW	Cytochrome b-c1 cor	UQCR10	7.3084	27	4	4	36.39	0	18978	17711	23597	20561	20289	12758	35473	42664	16896	41652					YES	
Q9UDY2-3;Q9UDY	Tight junction protein	TJP2	131.37	21.2	22	20	130.08	0	55397	50450	66522	52019	78853	50811	146980	120570	93686	76474	Enriched	Enriched	Enriched	Moderate	YES	
Q9UDY4	DnaJ homolog subfar	DNAJB4	37.806	27.6	9	8	17.565	0	26724	18525	20037	32675	22847	46765	22163	33681	10489	36830	Low	Enriched	Enriched	No expression		
Q9UEE9;Q9UEE9-	Craniofacial developr	CFDP1	33.592	17.7	5	5	11.041	0	16871	20563	18330	18779	21979	12306	14749	13492	7754	13667	Low	Enriched	Enriched	Enriched	YES	
Q9UEU0;Q9UEU0-	Vesicle transport thro	VTI1B	26.688	25.9	5	5	12.013	0	6174.9	5658.1	5479.5	4533.1	7195.9	4534.8	4530.9	4170.7	2795.3	4145.2	Enriched	Enriched	Enriched	Moderate	YES	
Q9UEW8-2;Q9UEV	STE20/SPS1-related	STK39	57.937	16.2	9	8	35.361	0	31336	25680	28919	31918	34100	30001	31937	36121	17558	26743	Enriched	Enriched	Enriched	Moderate	YES	
Q9UEY8-2;A0A08	Gamma-adducin	ADD3	75.67	29.2	25	25	97.093	0	170700	117620	134180	173610	148550	161630	196460	170260	98823	167130	Enriched	Enriched	Enriched	Enriched	YES	
Q9UFC0	Leucine-rich repeat a	LRWD1	70.86	4.8	4	3	5.2588	0.00022	2187.4	1122.6	1361.7	1531.8	1867.7	1843.2	1581.4	1216.9	755.99	1807.3	Moderate	Enriched	Moderate	No expression		
Q9UFN0	Protein NipSnap hom	NIPSNAP3A	28.466	22.7	6	6	26.781	0	26836	16798	21544	27294	31057	19675	18835	20143	10059	18970	Low	Moderate	Enriched	No expres	YES	
Q9UFW8;C9JUJ0	CGG triplet repeat-bi	CGGBP1	18.82	15.6	3	3	11.713	0	10050	9401.8	7406.4	6910	12491	6900.8	8667.1	12811	5271.3	8802.4	Enriched	Enriched	Enriched	Low	YES	
Q9UG63;Q9UG63-	ATP-binding cassette	ABCF2	71.289	12.8	9	9	13.762	0	11463	10120	9939.2	12789	12879	13892	40046	49825	12669	13090	Moderate	Enriched	Enriched	Moderate	YES	
Q9UGI8	Testin	TES	47.996	39.7	23	1	2.4983	0.00378	3175.4	2939.6	2867.7	1853.1	3705.6	1421	3707	2350.1	2650.3	3161.7	Enriched	Enriched	Enriched	Moderate	YES	
Q9UGI8-2	Testin	TES	46.91	40.3	23	1	57.56	0	110500	85041	91660	70648	116740	95916	116030	121690	61681	109520	Enriched	Enriched	Enriched	Moderate	YES	
Q9UGM6	Tryptophan--tRNA li	WARS2	40.146	16.9	6	6	15.287	0	19371	11841	17337	25839	16482	23670	25977	36657	9534.3	26951	Low	Enriched	Enriched	No expres	YES	
Q9UGP8	Translocation protein	SEC63	87.996	32.4	26	26	76.546	0	173920	120520	112800	132160	161920	194770	150170	117990	54079	138370	Enriched	Enriched	Enriched	Enriched	YES	
Q9UGR2-2;Q9UGF	Zinc finger CCCH do	ZC3H7B	109.86	1	1	1	2.6281	0.00273	3026.6	2556.9	2332.2	3726.1	2757.1	1984.1	1675.6	2661.7	675.11	2822.7	Enriched	Low	Moderate	Low		
Q9UGT4	Sushi domain-contair	SUSD2	90.207	4.4	4	4	10.615	0	10411	13148	16537	9712.1	20320	10607	21596	21567	9367	16275	Low	Moderate	Moderate	No expres	YES	
Q9UGV2;Q5TH30	Protein NDRG3	NDRG3	41.408	11.7	4	1	4.654	0.00043	24635	21179	21482	23989	28066	20543	22676	20432	15701	22135	Enriched	Enriched	Enriched	No expres	YES	
Q9UH62	Armadillo repeat-con	ARMCX3	42.5	9.8	3	3	9.574	0	16452	14410	16004	15062	20462	12965	14908	12294	11719	13182	Enriched	Enriched	Enriched	No expres	YES	
Q9UH65;E7EMB1	Switch-associated pro	SWAP70	68.997	19.7	12	12	18.697	0	54157	45681	57894	57111	54502	46231	100090	92612	51296	52689	Low	Low	Enriched	Low	YES	
Q9UH99;Q9UH99-	SUN domain-contain	SUN2	80.31	30.3	26	18	67.498	0	75287	55398	61645	82552	66947	73458	82304	83528	41559	82525					YES	
Q9UHB6;Q9UHB6	LIM domain and acti	LIMA1;TRMT1	85.225	34.3	31	31	136.88	0	112800	107110	111580	109590	126920	100720	123470	148720	82189	134330	Enriched	Enriched	Enriched	No expres	YES	
Q9UHB9;Q9UHB9	Signal recognition pa	SRP68	70.729	43.7	43	43	177.93	0	196540	158570	168410	176790	182540	214960	242100	217350	132970	215360	Enriched	Enriched	Enriched	Enriched	YES	
Q9UHD2	Serine/threonine-prot	TBK1	83.641	7.1	4	4	9.4569	0	15740	12911	15204	14316	18679	12712	14731	13416	8746.4	13698	Enriched	Moderate	Enriched	No expres	YES	
Q9UHD8-7;Q9UHI	Septin-9	SEPT9	63.502	34	22	21	135.31	0	113990	100700	109300	109910	126530	111630	148840	147030	87992	128120	Enriched	Enriched	Enriched	Enriched	YES	
Q9UHD9	Ubiquilin-2	UBQLN2	65.695	14.7	8	4	37.721	0	23532	19379	22439	19560	34277	19169	24244	22346	9184.2	21788	Moderate	Moderate	Enriched	Moderate	YES	
Q9UHG0;H0Y784	Doublecortin domain	DCDC2	52.833	11.3	4	4	16.51	0	9355.4	7911.9	10847	8925.1	11246	6426.4	9227	9833.9	4681.9	10266	No expres	Enriched	Enriched	No expres	YES	
Q9UHG2	ProSAAS;KEP;Big S	PCSK1N	27.372	21.5	10	10	48.657	0	14121	11387	16131	10861	17225	17177	21995	11072	28912	19174	Enriched	Low	Enriched	No expres	YES	
Q9UHG3	Prenylcysteine oxidas	PCYOX1	56.639	35.8	24	2	110.28	0	164920	99160	128870	125080	111670	137780	191690	153190	90975	187190	No expres	No expres	Moderate	No expres	YES	
Q9UHG3-2	Prenylcysteine oxidas	PCYOX1	48.506	39	23	1	8.7128	0	6552.1	4584.8	3656.4	3162.2	6116.5	6479.9	5891.6	2721.1	4209.5	7059.6	No expres	No expres	Moderate	No expres	YES	
Q9UHI6;Q9UHI6-2	Probable ATP-depen	DDX20	92.239	2.9	2	2	4.2458	0.00063	4333.5	1985	2012.6	5369.9	2044.9	3001.3	2069.7	3026.9	1631.6	3225.2	Moderate	Enriched	Enriched	No expression		
Q9UHJ6	Sedoheptulokinase	SHPK	51.49	16.9	6	6	10.724	0	18483	16028	15571	16621	19450	12891	12878	14559	8248.4	16179	Enriched	Moderate	Moderate	No expres	YES	
Q9UHL4	Dipeptidyl peptidase	DPP7	54.341	29.5	21	21	95.049	0	110690	66757	80089	92853	70911	105760	77787	93077	31002	80498	Enriched	Enriched	Enriched	No expres	YES	
Q9UHQ4;B7Z2L0;(	B-cell receptor-assoc	BCAP29	28.32	13.7	6	6	18.389	0	8091.1	8314.9	11450	11397	14244	8412.4	12245	9682.9	7792	10305	Moderate	Enriched	Enriched	Moderate	YES	
Q9UHQ9;H7C0R7	NADH-cytochrome b	CYB5R1	34.094	18	8	7	35.9	0	49949	43237	43910	55535	51328	52802	50131	57079	30408	58139	Moderate	Enriched	Enriched	Enriched	YES	
Q9UHR4	Brain-specific angiog	BAIAP2L1	56.882	6.7	3	3	12.77	0	7091.9	7545.3	8105.1	6849.2	10870	8342.5	14811	7771.8	14828	8411	Enriched	Enriched	Enriched	No expres	YES	
Q9UHV9	Prefoldin subunit 2	PFDN2	16.648	50	11	11	34.314	0	47308	42373	46875	47214	64520	31318	41733	37525	29674	38884	Enriched	Enriched	Enriched	No expres	YES	
Q9UHX1-4;Q9UH)	Poly(U)-binding-splic	PUF60	54.024	23.2	13	8	73.134	0	74845	68294	71634	72841	71594	81540	143110	120140	75816	107490	Enriched	Enriched	Enriched	Enriched	YES	
Q9UHY1;F8W6G1	Nuclear receptor-bin	NRBP1	59.844	15.9	8	8	85.899	0	67937	45110	49724	75936	52387	42703	53870	63543	39387	67207	Moderate	Moderate	Enriched	No expres	YES	
Q9UHY7;D6RA00;	Enolase-phosphatase	ENOPH1	28.932	36.4	8	8	33.414	0	61770	38140	52679	62052	51615	55662	64886	65405	30234	61507	Moderate	Enriched	Enriched	No expres	YES	
Q9UI08-3;Q9UI08;	Ena/VASP-like prote	EVL	41.577	14.9	4	4	10.357	0	6049.9	5492.1	5234.2	4308.7	7923.1	2693	4163.8	4608.7	2838	4397.3	No expres	Moderate	Enriched	No expres	YES	
Q9UI09	NADH dehydrogenas	NDUFA12	17.114	53.1	11	11	68.501	0	62126	49715	57818	66200	68104	55033	49422	64880	28186	61596	Enriched	Enriched	Enriched	No expres	YES	
Q9UI10-3;Q9UI10-	Translation initiation	EIF2B4	57.457	20.9	11	11	70.352	0	37590	31165	36273	32645	44288	27134	33538	27175	22637	30532	Moderate	Enriched	Enriched	Enriched	YES	
Q9UID3;Q9UID3-2	Vacuolar protein sort	VPS51	86.041	5.5	4	4	8.728	0	27167	24698	23064	18906	23932	21037	32765	23861	18637	24468					YES	
Q9UIG0-2;Q9UIG0	Tyrosine-protein kina	BAZ1B	170.45	3.4	6	6	10.901	0	42922	36333	39603	35453	41003	47387	43724	61555	23413	53068	No expres	Moderate	Enriched	Low	YES	
Q9UIJ7;Q9UIJ7-3;(	GTP:AMP phosphotr	AK3	25.565	54.2	21	21	214.2	0	134440	95800	100810	97742	115240	129490	128320	164860	71055	160450	Low	Enriched	Enriched	No expres	YES	
Q9UIS9-4;Q9UIS9-	Methyl-CpG-binding	MBD1	55.166	13.7	5	5	20.669	0	27695	13487	20484	20165	18740	12659	43823	23721	14973	24011	Enriched	Enriched	Enriched	Enriched	YES	
Q9UIV1	CCR4-NOT transcrip	CNOT7	32.745	9.8	2	1	2.6962	0.00238	17518	14145	15986	18301	17765	13417	14194	16392	8351.1	15392	Enriched	Enriched	Enriched	No expres	YES	
Q9UJ04	Testis-specific Y-enco	TSPYL4	45.125	2.2	1	1	2.3658	0.00428	7808.6	4780.7	7512.5	987.91	10750	2308.4	2890.3	1924.7	2865.7	5532.4	Enriched	Enriched	Enriched	Enriched		
Q9UJ14;Q9UJ14-4;	Gamma-glutamyltran	GGT7	70.466	5.7	3	3	3.8335	0.00061	21373	22683	27498	15008	26681	12035	21025	17882	17977	18874	Low	Enriched	Moderate	No expres	YES	
Q9UJ68-2;Q9UJ68-	Mitochondrial peptid	MSRA	18.963	23.1	3	3	6.003	0	12049	8457.8	8497.5	10115	9513.9	10239	12814	10630	11180	11058	Enriched	Enriched	Enriched	No expres	YES	
Q9UJ70;Q9UJ70-2;	N-acetyl-D-glucosam	NAGK	37.375	38.1	17	17	72.673	0	54849	39187	47581	63241	53815	56768	58273	64413	30781	42391	Low	Enriched	Enriched	No expres	YES	
Q9UJA5-4;Q9UJA5	tRNA (adenine(58)-N	TRMT6	36.439	8	2	2	5.0696	0.00044	12234	8694.3	11568	11001	13269	11810	13351	11861	7964.2	12188	Moderate	Moderate	Moderate	No expres	YES	
Q9UJC3-2;Q9UJC3	Protein Hook homolo	HOOK1	80.021	11.2	8	8	16.614	0	14259	11919	9898	18620	11682	15510	14074	14532	19035	13478	No expres	Enriched	Enriched	No expres	YES	
Q9UJC5	SH3 domain-binding	SH3BGRL2	12.326	39.3	6	6	28.132	0	65800	46482	59267	95463	52499	51881	50606	44794	26941	56486	Moderate	Enriched	Enriched	No expres	YES	
Q9UJS0;Q9UJS0-2	Calcium-binding mito	SLC25A13	74.175	35.1	33	28	143.23	0	153840	91265	117540	124010	146830	110980	129790	107840	75394	131820	Moderate	Moderate	Moderate	Moderate	YES	
Q9UJU6-2;Q9UJU6	Drebrin-like protein	DBNL	48.294	39.7	24	24	240.95	0	67777	60850	66710	84593	71568	75416	89064	97988	60026	95309	Enriched	Enriched	Enriched	No expres	YES	
Q9UJW0;Q9UJW0-	Dynactin subunit 4	DCTN4	52.337	13.7	6	6	32.743	0	14539	15866	17472	11896	19621	17347	26947	32056	8960	17416	Enriched	Enriched	Enriched	No expres	YES	
Q9UJW2	Tubulointerstitial ner	TINAG	54.604	2.3	2	2	2.0955	0.00674	983.7	699.15	1024.3	489.96	822.19	3861.1	5385.7	5758.2	2607.5	2738.8	Moderate	Low	Moderate	No expres	YES	
Q9UJX3-2;Q9UJX3	Anaphase-promoting	ANAPC7	60.002	10.2	4	4	7.5003	0	5122.2	3850.2	3958.1	2534.2	4942.9	3031.8	3996.6	4039.9	4774.3	5656	Enriched	Enriched	Enriched	No expres	YES	
Q9UJX6-2;Q9UJX6	Anaphase-promoting	ANAPC2	93.468	3.2	2	2	3.0912	0.00095	9967.4	12806	12495	14137	16492	6918.7	7340.4	6778.4	3400.7	8088.8	Moderate	Enriched	Moderate	No expres	YES	
Q9UJY5-4;Q9UJY5	ADP-ribosylation fac	GGA1	61.378	3.4	2	2	4.7236	0.00043	26736	26669	25999	22011	27270	26082	21702	27375	11080	19302	Enriched	Enriched	Enriched	No expres	YES	
Q9UJZ1;A0A087W	Stomatin-like protein	STOML2	38.534	38.5	23	23	223.08	0	92144	63124	70999	88894	89816	99905	105580	123010	50866	102400	Low	Enriched	Enriched	Enriched	YES	
Q9UK22	F-box only protein 2	FBXO2	33.327	41.9	18	18	144.11	0	50224	39765	40151	46130	43548	41703	23332	30206	14102	36111	Enriched	Enriched	Enriched	No expres	YES	
Q9UK45	U6 snRNA-associated	LSM7	11.602	22.3	2	2	10.362	0	27475	10747	16994	55867	12717	26483	24525	48519	18498	38891	Moderate	Moderate	Enriched	No expression		
Q9UK59;F8WAY1	Lariat debranching er	DBR1	61.554	6.1	2	2	7.9727	0	13676	12071	10179	9143.6	11732	4855.2	10407	7013.4	8073.2	9609.7	Low	Moderate	Moderate	No expres	YES	
Q9UK61-3;Q9UK6	Protein FAM208A	FAM208A	170.81	2.3	4	4	6.5114	0	15556	9055.6	17156	23495	12274	19648	24625	37375	10435	24810					YES	
Q9UKA4	A-kinase anchor prot	AKAP11	210.51	1.1	2	2	2.3072	0.00479	9711.8	14603	13097	5195	12250	9580.1	41327	23222	11041	11271	Low	Enriched	Enriched	Enriched	YES	
Q9UKD2	mRNA turnover prot	MRTO4	27.56	14.2	3	3	6.8107	0	10358	8088.7	12768	6223.3	13414	6930.7	14660	11322	9204.3	14232	Low	Moderate	Enriched	No expres	YES	
Q9UKG1	DCC-interacting prot	APPL1	79.663	31.6	29	29	153.34	0	116420	89271	112010	103650	123360	96180	129770	113110	82018	107670	Low	Moderate	Enriched	No expres	YES	
Q9UKJ3-2;Q9UKJ3	G patch domain-cont	GPATCH8	155.19	0.8	1	1	2.168	0.00594	2545.8	1713.4	2889.6	1957.2	3363.8	1265.1	2791.3	1690.1	2541.3	2830.6	Moderate	Moderate	Enriched	Moderate	YES	
Q9UKK3	Poly [ADP-ribose] po	PARP4	192.59	4.8	6	6	10.376	0	12206	15468	15538	9981.1	18026	8605.1	9772.3	9718.5	7690.7	9297.5	Enriched	Enriched	Enriched	Moderate	YES	
Q9UKM9;Q5QPL9	RNA-binding protein	RALY	32.463	31.7	13	13	19.358	0	27875	16945	20182	21481	22845	30690	40270	39705	24799	35728	Moderate	Moderate	Enriched	No expres	YES	
Q9UKR5	Probable ergosterol b	C14orf1	15.864	15.7	3	3	3.2965	0.00078	11270	7333.4	7975	9134.4	5634	3788.3	4859.1	4940.8	2392.9	4225.1	Enriched	Enriched	Enriched	Moderate		
Q9UKS6;E9PIY1;E	Protein kinase C and	PACSIN3	48.486	22.4	12	12	36.13	0	62785	43309	57131	51875	53650	58394	75920	54771	50530	72471	Moderate	Low	Low	No expres	YES	
Q9UKU7-2;Q9UKU	Isobutyryl-CoA dehy	ACAD8	31.023	24.3	8	7	10.109	0	40701	43890	44637	29495	54125	30080	39424	36353	25734	34397	No expres	Enriched	Enriched	No expres	YES	
Q9UKV8;Q9UKV8	Protein argonaute-2	AGO2	97.207	18.6	15	8	12.252	0	26322	20969	24097	23712	27797	24164	25243	24843	13155	23362					YES	
Q9UKX7-2;Q9UKX	Nuclear pore comple	NUP50	46.862	22.5	8	8	37.245	0	34288	25106	32568	33362	34994	22961	30140	24749	17899	38652	Enriched	Enriched	Enriched	Moderate	YES	
Q9UKY7;Q9UKY7	Protein CDV3 homol	CDV3	27.335	27.1	15	15	94.249	0	84522	72577	74426	57700	96445	84254	65741	60909	34387	67471	Enriched	Enriched	Enriched	Enriched	YES	
Q9UL03-3;Q9UL03	Integrator complex su	INTS6	98.986	6.4	5	5	7.3657	0	9248.8	9220.6	9498.7	8965.3	10705	9046.6	9187.6	9963.7	5123	9385.1	Enriched	Moderate	Enriched	No expres	YES	
Q9UL12;Q9UL12-2	Sarcosine dehydroger	SARDH	101.04	38.7	49	18	240.14	0	356400	180240	231380	258810	341380	194520	165240	239240	105220	258770	Moderate	Moderate	Low	No expres	YES	
Q9UL15;Q9UL15-2	BAG family molecula	BAG5	51.199	15	5	5	39.161	0	10045	5981.2	8331.1	9546.8	11463	11602	11928	10458	4915.4	10376	Enriched	Enriched	Enriched	Enriched	YES	
Q9UL18;Q5TA58	Protein argonaute-1;I	AGO1	97.213	25.7	22	12	50.508	0	127590	104910	117600	110100	136070	95056	113220	120460	70933	113590						
Q9UL25	Ras-related protein R	RAB21	24.347	32.9	10	9	40.246	0	18614	14515	19974	15230	27467	25775	24375	33616	17444	26689	Moderate	Moderate	Enriched	Moderate	YES	
Q9UL26	Ras-related protein R	RAB22A	21.855	20.6	3	3	9.9087	0	17930	10882	12310	14150	17665	12261	15209	13673	6866.1	17799	No expres	Moderate	Enriched	Enriched	YES	
Q9ULC3	Ras-related protein R	RAB23	26.659	11.4	2	2	3.9608	0.00061	12515	9491.4	13992	11287	11738	7089.8	10346	9377.6	5200	10851	Moderate	Moderate	Enriched	No expres	YES	
Q9ULC4;Q9ULC4-	Malignant T-cell-amp	MCTS1	20.555	64.6	18	18	158.79	0	146660	68916	95061	141960	99375	163450	139670	198730	57165	154060	Low	Enriched	Enriched	No expres	YES	
Q9ULD0;Q9ULD0-	2-oxoglutarate dehyd	OGDHL	114.48	8	10	3	3.4206	0.00079	3030.5	1273.6	2285.9	5104	1436.6	3039.7	3321.9	5026.9	1694.1	4833.1	No expres	No expres	Moderate	No expres	YES	
Q9ULD2-2;Q9ULD	Microtubule-associat	MTUS1	135.66	8.1	10	10	25.296	0	57864	34351	43980	43896	59970	28913	35377	40677	31050	46005	Moderate	Enriched	Enriched	Enriched	YES	
Q9ULG6-2;Q9ULG	Cell cycle progressio	CCPG1	71.853	7.7	6	6	20.768	0	35236	15838	21302	42579	19710	58972	28730	37513	11527	28445	Moderate	Enriched	Enriched	Moderate		
Q9ULP9-2;Q9ULP9	TBC1 domain family	TBC1D24	62.317	11.6	8	8	17.066	0	32689	25471	27961	25681	37580	30318	43913	41495	20829	32995	Low	Enriched	Enriched	No expres	YES	
Q9ULR5	Polyadenylate-bindin	PAIP2B	14.237	42.3	8	8	32.07	0	26480	22289	25048	24019	28045	39133	53889	45128	18594	33024	Low	Enriched	Enriched	Moderate		
Q9ULV0;A0A0A0M	Unconventional myo	MYO5B	213.67	2.9	7	3	5.1921	0.00044	4495.8	3387.5	3470.4	5265.7	4356.6	3800.4	3106.5	3735.6	1598.3	3461.3	Enriched	Enriched	Enriched	No expres	YES	
Q9ULZ3-3;Q9ULZ	Apoptosis-associated	PYCARD	15.03	27.4	7	7	18.052	0	17587	17981	17741	25989	18352	21948	37296	60974	16630	24101	Moderate	Low	Moderate	No expres	YES	
Q9UM82	Spermatogenesis-asso	SPATA2	58.427	3.3	1	1	3.4111	0.00079	3697.1	2876.4	3658	2167.1	4183	1645.3	2747.5	2086.9	2257.2	2533	Moderate	Moderate	Moderate	Moderate		
Q9UMS4;F5GY56	Pre-mRNA-processin	PRPF19	55.18	26	13	13	48.246	0	57990	51149	52225	54312	64197	46467	52547	55633	29891	55244	Moderate	Enriched	Enriched	Low	YES	
Q9UMX0;Q9UMX0	Ubiquilin-1	UBQLN1	62.518	23.4	14	8	79.453	0	82795	60100	70147	78899	69860	69244	65664	67169	39177	75739	Enriched	Enriched	Enriched	No expres	YES	
Q9UMX5	Neudesin	NENF	18.856	55.8	10	10	33.811	0	64548	45946	54094	105030	61724	74499	54163	57149	24791	69314	Moderate	Enriched	Enriched	Moderate	YES	
Q9UMY1;H7C2B1	Nucleolar protein 7	NOL7	29.426	8.2	2	2	3.6536	0.0008	12716	10022	10004	13711	11034	13973	10779	11456	5551.7	10085	Enriched	Enriched	Enriched	No expres	YES	
Q9UMZ2-6;Q9UM	Synergin gamma	SYNRG	119.51	6.9	6	6	13.16	0	19638	16504	17713	14880	23414	11687	12829	15658	7514.2	16254					YES	
Q9UN37	Vacuolar protein sort	VPS4A	48.897	19.7	12	2	3.0083	0.00151	32185	31277	35618	32742	35341	25646	26238	25704	18778	28207	Enriched	Enriched	Enriched	No expres	YES	
Q9UN86-2;Q9UN8	Ras GTPase-activatin	G3BP2	50.817	18.9	10	8	21.062	0	22959	25265	28825	18655	39131	29436	37524	31409	17055	26406	Enriched	Enriched	Enriched	Enriched	YES	
Q9UNE2-2;Q9UNE	Rab effector Noc2	RPH3AL	31.19	10.1	2	2	4.6958	0.00043	7219.2	4966.3	8377.3	4022.5	6434.2	6451.7	4829.1	5035.4	4871.7	8373.9	Moderate	Enriched	Enriched	No expres	YES	YES
Q9UNF0-2;Q9UNF	Protein kinase C and	PACSIN2	51.353	35.5	35	35	215.6	0	195140	152070	187080	172390	188040	179540	346610	182290	201940	204650	Enriched	Enriched	Enriched	No expres	YES	
Q9UNF1;Q5H907;(	Melanoma-associated	MAGED2	64.953	5.8	5	5	20.239	0	14097	17727	28376	9718.2	31218	12364	14366	9012	8356.3	11325	No expres	Moderate	Enriched	Enriched	YES	
Q9UNK0;K7EQB1	Syntaxin-8	STX8	26.906	29.7	6	6	22.892	0	10242	7894.8	7297.1	12651	7850.3	10561	9196.2	14179	5168.6	9988.5	Enriched	Enriched	Enriched	Enriched	YES	
Q9UNM6;A0A087'	26S proteasome non-	PSMD13	42.945	41	26	26	43.394	0	81426	70301	81689	83580	91710	86806	121150	105370	73410	81706	Enriched	Enriched	Enriched	Enriched	YES	
Q9UNQ2;D6RCL3	Probable dimethylade	DIMT1	35.236	15	4	4	5.8802	0	24676	11045	17228	18242	16479	23027	20323	25536	9980.4	21345						
Q9UNW1;Q9UNW	Multiple inositol poly	MINPP1	55.051	10.1	6	6	25.239	0	9635.2	7208.9	6877	10527	8328.5	8918.3	6713.2	11603	6021.1	10059	Low	Moderate	Enriched	Low	YES	
Q9UNX4	WD repeat-containing	WDR3	106.1	6.4	5	5	13.043	0	31775	38108	26446	22003	40029	29237	20695	15570	11202	21031	Enriched	Moderate	Enriched	No expres	YES	
Q9UNZ2;Q9UNZ2-	NSFL1 cofactor p47	NSFL1C	40.572	60.5	32	32	301.15	0	137140	92253	113120	109340	157750	118300	207830	150260	121930	154750	Enriched	Enriched	Enriched	Moderate	YES	
Q9UP83;Q9UP83-2	Conserved oligomeric	COG5	92.742	6.3	6	6	7.5724	0	13579	13155	12617	12438	17756	13668	14442	9035.8	7919.3	12539	Enriched	Enriched	Enriched	Moderate	YES	
Q9UPN7	Serine/threonine-prot	PPP6R1	96.723	3.4	2	2	6.3456	0	11911	8726.5	9613	9112.3	8753	9487.4	12864	12623	8036.5	12373					YES	
Q9UPU5	Ubiquitin carboxyl-te	USP24	294.36	1.8	5	5	8.0848	0	10795	8657.5	11468	11025	11111	8834	8733.9	9411.5	5373.4	11306	Low	Moderate	Enriched	Enriched	YES	
Q9UPY3-2;Q9UPY	Endoribonuclease Di	DICER1	208.45	1.2	2	2	3.5669	0.00079	10215	9527.7	9471.7	8192.4	12030	7487.5	10155	10092	7332.8	11655	Enriched	Enriched	Enriched	Enriched	YES	
Q9UPY6-2;Q9UPY	Wiskott-Aldrich synd	WASF3	55.006	10.8	6	3	5.934	0	9451.5	7346.9	8007.5	9293.4	9516.2	5939	8152.6	9137.3	4513.3	10691	No expres	Moderate	Enriched	Moderate		
Q9UPY8-2;Q9UPY	Microtubule-associat	MAPRE3	30.38	18.8	6	3	4.5379	0.00043	14556	12387	17806	16948	18260	11625	11794	9417.6	6675.7	13559	No expres	No expres	Moderate	Enriched	YES	
Q9UPZ3-2;Q9UPZ	Hermansky-Pudlak sy	HPS5	114.82	1.9	2	2	2.6462	0.00274	2055	1810.4	1977.6	1183.5	2429.2	3660.5	3931.7	2772.9	2434.8	3547.2	Low	Low	Moderate	Low		
Q9UQ35;Q9UQ35-	Serine/arginine repeti	SRRM2	299.61	11.3	30	30	142.81	0	112550	86265	111110	98911	143980	94198	95618	96486	57213	118170	Enriched	Moderate	Enriched	Enriched	YES	
Q9UQ80;Q9UQ80-	Proliferation-associat	PA2G4	43.786	52	44	44	235.86	0	306780	246230	287070	211180	288550	299510	544050	381920	247650	346240	Enriched	Enriched	Enriched	Enriched	YES	
Q9UQ90	Paraplegin	SPG7	88.234	4.4	3	3	4.716	0.00043	14356	12454	11531	10244	14096	6512.2	9656.3	6816.1	4967.9	10950	Enriched	Enriched	Enriched	Enriched	YES	
Q9UQB3-2;Q9UQB	Catenin delta-2	CTNND2	126.53	6.3	6	6	14.33	0	24038	26210	28671	29873	31822	21456	22367	22155	15929	28162	Moderate	Moderate	Moderate	Moderate	YES	
Q9UQE7	Structural maintenan	SMC3	141.54	34.7	43	43	154.09	0	199240	155730	195980	176320	199260	199630	247110	258220	141600	250890	Low	Enriched	Enriched	Moderate	YES	
Q9UQN3;C9J0A7;(	Charged multivesicul	CHMP2B	23.906	21.6	5	5	17.861	0	11058	8455.6	11220	10659	12029	14958	25757	18265	15535	18321	Moderate	Enriched	Enriched	Moderate	YES	
Q9Y224;G3V4C6;I	UPF0568 protein C14	C14orf166	28.068	48	18	18	78.052	0	80693	54468	69482	86179	79311	126120	150520	159730	67444	109700	Enriched	Enriched	Enriched	No expres	YES	
Q9Y230;Q9Y230-2	RuvB-like 2	RUVBL2	51.156	37.4	23	23	114.05	0	131560	79209	99004	116300	113350	116130	136990	172270	69437	121240	Enriched	Enriched	Enriched	Enriched	YES	
Q9Y235	Probable C->U-editir	APOBEC2	25.703	24.6	6	6	90.966	0	73188	35871	52310	50826	46650	48844	65937	50110	38410	54754	Moderate	Moderate	Enriched	No expres	YES	
Q9Y259	Choline/ethanolamin	CHKB	45.271	6.1	3	3	9.1951	0	3149.7	3195.8	4213.5	2207.3	5543.6	2434.8	5989.6	2684	4344.2	3095.2	Enriched	Enriched	Enriched	Moderate		
Q9Y263;E5RIM3	Phospholipase A-2-ac	PLAA	87.156	19.2	15	15	39.163	0	47525	46460	55590	42653	63306	53641	50576	45392	30461	42769	Moderate	Moderate	Enriched	No expres	YES	
Q9Y265;Q9Y265-2	RuvB-like 1	RUVBL1	50.227	37.1	20	20	69.932	0	81907	60829	72901	67191	76025	76607	80516	76000	43451	76537	Enriched	Moderate	Moderate	Enriched	YES	
Q9Y266;A0A0A0M	Nuclear migration pro	NUDC	38.242	29.6	13	13	30.373	0	64785	67488	66932	62168	78555	49220	76739	63007	56477	69223	Enriched	Enriched	Enriched	Enriched	YES	
Q9Y276;C9J1S9;H	Mitochondrial chaper	BCS1L	47.534	22	10	9	39.202	0	53154	41009	39541	59182	43474	46688	46170	58842	22067	53594	Enriched	Enriched	Enriched	Enriched	YES	
Q9Y277;Q9Y277-2	Voltage-dependent ar	VDAC3	30.658	32.5	15	12	179.08	0	68662	52585	67272	69061	65273	75423	124890	142900	36657	79824	Enriched	Enriched	Enriched	Enriched	YES	

Q9Y279-3;Q9Y279	V-set and immunoglo	VSIG4	33.857	5.2	1	1	1.8827	0.00846	1937.4	1216.6	1490.1	6169.9	1610	2887.4	1956.4	3215.2	1504.7	3270.7	Enriched	Moderate	Moderate	Moderate	YES
Q9Y281-3;Q9Y281	Cofilin-2	CFL2	16.916	53.7	14	6	39.203	0	15865	15358	16610	15238	18669	33311	35116	29245	11642	15212	Low	Enriched	Enriched	No expres	YES
Q9Y294	Histone chaperone A	ASF1A	22.968	4.9	1	1	2.1072	0.00676	14428	10283	13702	12093	15570	9906.2	8550.1	9645.9	4058.4	11328	No expres	Moderate	Enriched	No expres	YES
Q9Y295	Developmentally-reg	DRG1	40.542	34.1	17	17	54.688	0	90567	84495	84806	81045	104200	68744	107790	116050	56326	81756	Enriched	Enriched	Enriched	Enriched	YES
Q9Y2A7;Q9Y2A7-	Nck-associated protei	NCKAP1	128.79	21.2	33	33	65.807	0	136240	107970	116690	101250	152110	83531	98465	101230	50349	104200	Low	Enriched	Enriched	Enriched	YES
Q9Y2B0	Protein canopy homo	CNPY2	20.652	66.5	24	1	2.103	0.00675	1076.2	984.21	1118.9	1123.7	2029.3	2520.4	1093.1	956.5	695.29	1614.1	Enriched	Enriched	Enriched	Enriched	YES
Q9Y2D9	Zinc finger protein 65	ZNF652	69.743	3.6	2	1	13.254	0	5835.7	6307.1	6610.8	4733.1	9285	3596.3	7288	6055.6	4279.1	6609.2	Enriched	Enriched	Enriched	No expression	
Q9Y2G2-2;Q9Y2G	Caspase recruitment	CARD8	32.368	10.1	2	2	4.1795	0.00062	1988.3	1940.8	2294.7	1546.9	4107.2	3854.6	79439	57873	5921	4304.3	Moderate	Low	Moderate	Moderate	
Q9Y2H0-3;Q9Y2H	Disks large-associatec	DLGAP4	49.478	10.6	6	5	19.901	0	21047	18105	23968	14617	21696	26600	25234	27316	14263	22338	Enriched	Enriched	Enriched	Enriched	YES
Q9Y2H1-2;Q9Y2H	Serine/threonine-prot	STK38L	43.17	5.7	2	2	3.0851	0.00114	6183.4	4040.8	5145.5	3339.1	5806.7	5476.1	4895.6	7319.6	2024	6440.5	Moderate	Enriched	Enriched	Moderate	YES
Q9Y2H6-2;Q9Y2H	Fibronectin type-III d	FNDC3A	125.82	11.8	14	14	117.37	0	76420	63080	65640	46761	95055	48891	46006	41164	26524	49984	Moderate	Enriched	Enriched	Enriched	YES
Q9Y2I9;F8VZ81;Q	TBC1 domain family	TBC1D30	102.74	6.8	5	5	41.878	0	26188	19134	19291	21180	32618	20957	21392	22107	13205	21052	Low	Moderate	Moderate	Low	YES
Q9Y2J2-2;A0A0A	Band 4.1-like protein	EPB41L3	96.513	15.7	13	12	42.783	0	28895	29727	35501	29109	42033	31120	34106	26516	24848	32371	No expres	No expres	Moderate	Enriched	YES
Q9Y2L1;F2Z2C0;	Exosome complex ex	DIS3	109	9.5	8	8	23.365	0	13562	12320	15768	9990.4	15915	7604.5	11573	8921.3	8655.5	11558	Moderate	Enriched	Enriched	No expres	YES
Q9Y2Q3;Q9Y2Q3-	Glutathione S-transfe	GSTK1	25.497	44.7	16	16	99.78	0	91025	64149	68454	114060	78047	128710	138990	232210	76625	167200	Enriched	Enriched	Enriched	No expres	YES
Q9Y2Q5;Q9Y2Q5-	Ragulator complex pr	LAMTOR2	13.507	25.6	4	4	6.6801	0	6318.1	6339.7	7487.9	7977.4	5326.7	4687.1	4434.6	6173.3	5801.8	6171.6					YES
Q9Y2Q9;H0YAT2;	28S ribosomal protei	MRPS28	20.843	16.6	3	2	3.1391	0.00095	5033.7	4664.7	4764.5	4893.2	6582.3	6477.7	3702.5	2424.3	1008.8	2730.1	Moderate	Enriched	Enriched	No expres	YES
Q9Y2R0;K7EPV0	Cytochrome c oxidas	COA3	11.731	26.4	4	4	8.9371	0	17025	11994	13828	14141	16607	16251	15569	25985	7584.9	14507					YES
Q9Y2S2-2;Q9Y2S2	Lambda-crystallin ho	CRYL1	33.358	19.9	11	11	31.488	0	50530	29852	35665	43202	36855	52320	49255	51434	26249	55248	Enriched	Enriched	Enriched	No expres	YES
Q9Y2S6	Translation machiner	TMA7	7.0662	39.1	5	5	8.7575	0	25438	10299	23553	41963	17898	22243	26013	10006	25200	39718					YES
Q9Y2S7;B4DEM9	Polymerase delta-inte	POLDIP2	42.033	11.1	4	4	9.5999	0	3520.1	2917.6	4008.6	3306.9	4596	2845.7	3563.2	2873.2	2053.9	2666.6	Enriched	Enriched	Enriched	No expres	YES
Q9Y2T2	AP-3 complex subun	AP3M1	46.939	21.1	9	7	54.139	0	146930	84679	96934	92923	127980	107170	79393	81050	38704	96463	Enriched	Enriched	Enriched	No expres	YES
Q9Y2U8	Inner nuclear membra	LEMD3	99.996	6	4	4	13.697	0	13624	15399	16829	13882	21277	8731.1	12254	15951	6732	13841	Moderate	Moderate	Enriched	No expres	YES
Q9Y2V2	Calcium-regulated he	CARHSP1	15.892	16.3	4	4	46.855	0	4340.7	6905.5	8455.1	3759.5	9123.2	3822.3	8095.7	4887.2	6478.7	5463.1	Enriched	Enriched	Enriched	No expres	YES
Q9Y2W1	Thyroid hormone rec	THRAP3	108.66	17.6	19	18	190.66	0	112790	80630	97766	95373	123690	113630	140270	128520	79794	136620	Enriched	Enriched	Enriched	No expres	YES
Q9Y2W2;F5H5G4	WW domain-binding	WBP11	69.997	10.8	6	6	20.292	0	13071	9568.5	10860	14217	10701	14697	14715	14645	8598.4	15400	Enriched	Enriched	Enriched	No expres	YES
Q9Y2X3	Nucleolar protein 58	NOP58	59.578	44.8	29	29	121.8	0	235820	159970	201680	147470	239440	162930	184290	159180	107270	177600	Enriched	Enriched	Enriched	No expres	YES
Q9Y2Y0-2;Q9Y2Y	ADP-ribosylation fac	ARL2BP	17.711	26.3	3	3	13.627	0	1295.4	1274.1	1731.5	840.93	2210.8	1424.9	3089.5	1735.4	1704.5	2055.5	Enriched	Enriched	Enriched	Enriched	
Q9Y2Z0-2;Q9Y2Z	Suppressor of G2 alle	SUGT1	37.804	32.4	13	13	64.474	0	61852	51445	53000	72010	62233	49821	63184	71034	32873	70382	Enriched	Enriched	Enriched	No expres	YES
Q9Y2Z4;H0YHS6	Tyrosine--tRNA ligas	YARS2	53.198	12.4	8	8	31.129	0	77379	56754	71072	95236	71442	73021	80280	83157	43634	86351	Enriched	Moderate	Moderate	No expres	YES
Q9Y303;Q9Y303-2	Putative N-acetylgluc	AMDHD2	43.747	13	4	4	5.1917	0.00044	9256.2	9306.4	14482	12907	13805	9020	9797.3	13050	6270.9	10292	No expres	Enriched	Low	No expression	
Q9Y305;Q9Y305-2	Acyl-coenzyme A thi	ACOT9	49.901	36.9	23	23	51.381	0	66699	47197	56707	59038	70853	46848	55980	53230	30947	63344	Moderate	Enriched	Enriched	No expres	YES
Q9Y315;E9PPM8;	Putative deoxyribose-	DERA	35.23	25.2	12	12	22.322	0	45770	37672	43169	36868	53656	32196	38704	33843	22353	37950	Enriched	Enriched	Enriched	No expres	YES
Q9Y316-2;Q9Y316	Protein MEMO1	MEMO1	31.307	4.7	1	1	1.9964	0.00787	4500.7	5194	5452.2	4965.1	7412.3	4173.7	8078.7	6456.4	4275.6	4974.8	Enriched	Enriched	Enriched	No expres	YES
Q9Y320-2;Q9Y320	Thioredoxin-related t	TMX2	29.642	24.4	7	7	18.809	0	45169	22251	26770	36468	35184	68001	43691	56662	18877	50678	Moderate	Enriched	Enriched	No expres	YES
Q9Y333	U6 snRNA-associatec	LSM2	10.834	37.9	7	7	19.552	0	12426	11008	14274	29649	13985	12955	13776	20156	8605	15554	Low	Moderate	Enriched	Enriched	YES
Q9Y371-3	Endophilin-B1	SH3GLB1	29.318	25.7	8	1	3.0482	0.00132	3667.6	3782.4	3870.8	3492.7	4942.6	2690.2	2709.7	3059.4	2354	2740.2	Moderate	Enriched	Enriched	Enriched	YES
Q9Y376;A0A087X	Calcium-binding prot	CAB39	39.869	21.7	11	11	31.603	0	54379	37453	37699	49824	42099	52101	46879	66241	22001	50030	Moderate	Enriched	Enriched	No expres	YES
Q9Y383;Q9Y383-3	Putative RNA-bindin	LUC7L2;C7orf55	46.513	27.6	14	6	75.595	0	43003	35301	36104	37335	51655	43490	80883	76737	33443	47086	Enriched	Enriched	Enriched	No expres	YES
Q9Y385	Ubiquitin-conjugatin	UBE2J1	35.198	8.8	3	3	7.4736	0	20913	16179	18663	15902	25370	12824	14135	14147	8380.6	17372	Enriched	Enriched	Enriched	Enriched	YES
Q9Y399	28S ribosomal protei	MRPS2	33.249	6.1	1	1	3.305	0.00078	3940.7	4253.7	3461.5	2987.5	8459.9	2369.8	2417.5	1689.4	1595.6	3540.5	Low	Enriched	Enriched	No expres	YES
Q9Y3A2	Probable U3 small nu	UTP11L	30.446	7.1	2	2	2.9125	0.00187	2208	1555.3	1980.3	1832.6	2659.7	1735.9	2767.2	1864.5	1880.8	2226.7	Moderate	Enriched	Enriched	No expression	
Q9Y3A5;A0A087X	Ribosome maturation	SBDS	28.763	39.2	16	16	57.526	0	87546	63677	81062	76266	84110	112900	148610	132670	78555	110380	Moderate	Enriched	Enriched	No expres	YES
Q9Y3A6	Transmembrane emp	TMED5	26.005	14	7	7	70.37	0	49606	13574	21942	61800	21983	25898	18031	21838	9460.5	32944	Moderate	Enriched	Enriched	Enriched	YES
Q9Y3B4	Splicing factor 3B sul	SF3B6	14.585	40	7	7	24.159	0	24862	17160	22401	18729	24908	36739	76974	45744	41327	31932					YES
Q9Y3B9	RRP15-like protein	RRP15	31.484	12.1	3	3	5.7603	0	2837.8	2043	2651.6	2216.8	3324.3	2948.6	2807.8	2234.3	1204	2331	Moderate	Low	Moderate	No expres	YES
Q9Y3C1;D6RIC3;	Nucleolar protein 16	NOP16	21.188	30.3	6	6	27.183	0	42448	25139	33242	35576	45993	41137	36971	49791	16276	44345	Moderate	Moderate	Enriched	Moderate	YES
Q9Y3C4-2;Q9Y3C	EKC/KEOPS comple	TPRKB	16.093	39.4	6	6	12.663	0	12602	7333.4	8339.6	15457	9744.1	11958	11142	11857	4541.3	12687	Moderate	Enriched	Enriched	No expres	YES
Q9Y3C6	Peptidyl-prolyl cis-tra	PPIL1	18.237	30.7	6	6	29.844	0	24269	16954	24388	33015	24495	21601	30803	23127	20474	29164	No expres	Moderate	Enriched	No expres	YES
Q9Y3C8	Ubiquitin-fold modifi	UFC1	19.458	25.7	8	8	16.187	0	54391	39459	40164	41009	69792	98574	77093	59238	44526	54407	Enriched	Enriched	Enriched	No expres	YES
Q9Y3D0;J3QLT9;J	Mitotic spindle-assoc	FAM96B	17.663	16	2	2	3.2298	0.00077	12818	8817.9	5900.4	10863	7116.3	11019	7460.3	5141.6	3360.1	11389	Enriched	Enriched	Enriched	No expres	YES
Q9Y3D3;A6ND22;	28S ribosomal protei	MRPS16	15.345	22.6	2	2	11.526	0	3636.5	2775.3	3207.4	2765.8	4875.9	2327.9	3072.2	2777.3	2027.4	3781.9	Low	Enriched	Enriched	No expres	YES
Q9Y3D6	Mitochondrial fission	FIS1	16.937	22.4	7	7	87.837	0	32995	29155	31135	28246	41019	23714	50154	54481	21271	34334	Enriched	Enriched	Enriched	No expres	YES
Q9Y3E1;H3BTV7;	Hepatoma-derived gr	HDGFRP3	22.619	27.1	6	5	9.2318	0	8960.3	8016.4	11400	7734.4	13484	6175	5406.9	5233.5	2554.4	7103.6	Low	Low	Enriched	No expres	YES
Q9Y3E2	BolA-like protein 1	BOLA1	14.289	10.2	2	2	2.243	0.00511	5017.7	4986.9	4393.9	4453.5	5540	4049.3	3585.1	2734.3	3355.9	4591.4	Enriched	Moderate	Moderate	No expres	YES
Q9Y3E7-4;Q9Y3E	Charged multivesicul	CHMP3	20.77	5.5	1	1	2.7413	0.00239	833.01	674.95	842.56	470.52	1224.2	1097.7	21741	5467.8	6718.8	2085.5					YES
Q9Y3F4;Q9Y3F4-2	Serine-threonine kina	STRAP	38.438	39.1	18	18	88.932	0	71181	48317	55981	70194	71507	80905	56288	59492	31796	64506	Enriched	Enriched	Enriched	Enriched	YES
Q9Y3I0	tRNA-splicing ligase	RTCB	55.21	40.8	36	36	208.36	0	269150	175640	232940	240750	254470	333420	322250	305830	137270	272830					YES
Q9Y3I1-3;Q9Y3I1-	F-box only protein 7	FBXO7	45.78	2.5	1	1	2.7799	0.0024	4189.1	2248.6	2630.3	3290	3426.6	1668.2	2641.7	2832.8	1722.6	2575.5	Enriched	Enriched	Enriched	Enriched	
Q9Y3L5;A0A087X	Ras-related protein R	RAP2C	20.745	20.2	4	2	11.685	0	2297	1630.8	2034.6	1933.2	2116.8	1728	2059.5	2538.3	1494.8	2513.9	Moderate	Low	Enriched	No expres	YES
Q9Y3P9;Q9Y3P9-3	Rab GTPase-activatin	RABGAP1	121.74	5.6	6	6	25.789	0	35594	34433	35288	33241	42074	26276	31493	27442	23223	31915	Enriched	Enriched	Enriched	Enriched	YES
Q9Y3Q3;G3V1J9;F	Transmembrane emp	TMED3	24.777	15.2	5	5	12.963	0	6208.7	3276.1	4203.1	6636.7	5439.7	10298	3268.8	2989.4	1918.8	4186	Enriched	Enriched	Enriched	Enriched	YES
Q9Y3Q8;H7BZ77;	TSC22 domain family	TSC22D4	41.026	12.7	4	3	83.611	0	24141	12248	15174	31661	17682	27715	16683	17750	7861.5	24228	Enriched	Low	Moderate	Enriched	YES
Q9Y3R5-2;Q9Y3R	Protein dopey-2	DOPEY2	257.39	1.1	2	2	3.8891	0.00061	4346.8	3543.2	3834.1	6825.2	3341.5	4024	3401.2	6796.6	1846.4	5294.9	Low	Low	Moderate	Moderate	YES
Q9Y3T6	R3H and coiled-coil	R3HCC1	53.259	6.7	3	3	6.1728	0	11001	10663	9531	6156.2	13354	5015.6	6612.1	6018.5	3815.7	7198.8	Enriched	Enriched	Enriched	Enriched	
Q9Y3T9	Nucleolar complex pr	NOC2L	84.918	4	4	4	8.5482	0	16176	11450	14446	13153	19271	13012	23257	17256	11753	20007	No expres	Moderate	Moderate	Low	YES
Q9Y3U8	60S ribosomal protei	RPL36	12.254	32.4	12	12	23.293	0	41845	20436	36719	36819	34469	55495	57803	65013	23721	62840	Enriched	Enriched	Enriched	No expres	YES
Q9Y3X0;M0QYB4	Coiled-coil domain-c	CCDC9	59.702	21.1	18	18	58.646	0	49113	36479	52640	51910	62431	45748	140340	81024	81214	85881	Enriched	Enriched	Moderate	Enriched	YES
X6R700;Q9Y3Y2-	Chromatin target of	CHTOP	23.661	28.7	9	9	17.59	0	43577	42614	46094	35217	55100	38495	55293	42486	30270	45431					YES
Q9Y3Z3;Q9Y3Z3-2	Deoxynucleoside trip	SAMHD1	72.2	53.7	47	47	159.26	0	242050	220830	213650	222150	247780	283580	227770	204880	138440	229140	Enriched	Enriched	Enriched	Moderate	YES
Q9Y446;Q9Y446-2	Plakophilin-3	PKP3	87.081	25.7	20	20	69.433	0	84772	45977	65972	48432	72344	63718	81849	60385	39810	73561	Moderate	Enriched	Enriched	Low	YES
Q9Y450-4;Q9Y450	HBS1-like protein	HBS1L	70.624	19.5	14	14	58.617	0	56218	40178	43710	45162	56257	59502	52535	40283	20074	47876	Moderate	Enriched	Enriched	Low	YES
Q9Y478;F5H4Y8	5-AMP-activated pro	PRKAB1	30.382	10	3	2	5.1454	0.00044	33626	31185	34475	32407	39444	47497	29270	32211	15039	28492	Moderate	Moderate	Enriched	Low	
Q9Y490	Talin-1	TLN1	269.76	44.7	163	145	323.31	0	485460	403680	428120	503560	488510	482330	613750	690510	366480	620340	Moderate	Low	Moderate	Enriched	YES
Q9Y4B6-2;Q9Y4B	Protein VPRBP	VPRBP	168.93	2.3	3	3	5.1399	0.00044	13381	8001.4	9847.9	16474	10516	12618	15917	13284	8262.4	11888	Enriched	Enriched	Enriched	Moderate	YES
Q9Y4D1-2;Q9Y4D	Disheveled-associatec	DAAM1	122.3	2.4	2	2	6.8265	0	10216	6593.4	8778.8	6835.3	6853.9	7572.7	9047.4	5780.4	2989.2	9635.8	Moderate	Enriched	Enriched	Enriched	YES
Q9Y4D7-2;Q9Y4D	Plexin-D1	PLXND1	195.56	1.9	2	2	14.369	0	5511.2	4301.9	6126.5	6096.3	6564.9	6427.7	6056.2	7636.2	2911.6	6631	Moderate	Enriched	Enriched	Enriched	YES
Q9Y4E8-2;Q9Y4E	Ubiquitin carboxyl-te	USP15	109.3	11	12	11	20.74	0	31671	30245	33062	32173	42040	30030	38021	32222	17239	38533	Moderate	Moderate	Enriched	Moderate	YES
Q9Y4F1;C9JME2;	FERM, RhoGEF and	FARP1	118.63	14.1	16	13	193.58	0	99287	76593	88015	88210	98874	78919	100370	100780	59681	99885	Enriched	Enriched	Enriched	Enriched	YES
Q9Y4F5-3;Q9Y4F5	Centrosomal protein	CEP170B	163.63	3.9	5	5	7.4494	0	20531	14709	16656	18875	20633	16732	19537	20005	10351	21244					YES
Q9Y4G6;H0YMT1	Talin-2	TLN2	271.61	23.1	64	46	155.17	0	206750	167600	197280	189720	221170	170310	234230	219080	141320	221320	Enriched	Moderate	Moderate	Moderate	YES
Q9Y4G8	Rap guanine nucleoti	RAPGEF2	167.41	2.3	3	3	6.3731	0	6722.3	4235.2	4405.3	8896.5	5554.9	5602.7	6112.1	5775	12382	7639.5	Moderate	Enriched	Enriched	Enriched	
Q9Y4J8-13;Q9Y4J8	Dystrobrevin alpha	DTNA	77.25	20.8	17	8	93.351	0	59632	37853	45252	61760	53545	76642	47015	48475	22635	53583	Low	Enriched	Enriched	Low	YES
Q9Y4K3	TNF receptor-associa	TRAF6	59.573	11.3	5	5	9.1599	0	11284	8742.2	9545.9	10277	10667	11170	21688	26353	13107	15548	Enriched	Low	Moderate	Moderate	
Q9Y4L1;A0A087X	Hypoxia up-regulatec	HYOU1	111.33	48.4	108	96	323.31	0	802670	654340	560600	679690	842330	843810	698620	932670	381740	728370	Moderate	Enriched	Enriched	Moderate	YES
Q9Y4P8-3;Q9Y4P8	WD repeat domain pl	WIPI2	42.077	9.1	2	2	5.9213	0	18995	15612	16970	23182	17334	25988	21192	23063	11996	21751	Enriched	Enriched	Enriched	Enriched	YES
Q9Y4W6	AFG3-like protein 2	AFG3L2	88.583	21.2	21	21	84.878	0	108180	78610	79777	103630	101860	70770	79253	76294	49155	103380	Enriched	Enriched	Enriched	Enriched	YES
Q9Y4X5	E3 ubiquitin-protein	ARIH1	64.117	5.4	3	3	6.2936	0	4124.6	2815.9	2917.7	2248.2	2827.4	4120.4	4326.7	4044.4	2135.9	3385.9	Moderate	Moderate	Enriched	Enriched	
Q9Y4Y9-2;Q9Y4Y	U6 snRNA-associatec	LSM5	6.8498	37.1	4	4	19.948	0	14196	9717.1	12001	15582	11831	15384	15579	18254	7098.8	14732	Moderate	Enriched	Enriched	No expression	
U3KQS7;V9GZ56;	U6 snRNA-associatec	LSM4	12.455	23.9	3	3	14.611	0	31875	3727.1	12587	22467	5411.3	30898	20121	36832	8657.9	51446	Moderate	Enriched	Enriched	Moderate	YES
Q9Y512	Sorting and assembly	SAMM50	51.976	18.6	8	8	40.416	0	45722	27709	32556	65505	38569	58664	34141	40036	17310	58373	Enriched	Enriched	Enriched	Enriched	YES
Q9Y570;Q9Y570-4	Protein phosphatase	PPME1	42.315	10.4	4	4	9.6672	0	15788	13620	15909	10095	19497	16599	22908	22913	11358	18772	Enriched	Enriched	Enriched	No expres	YES
Q9Y5B0;A0A0A0	RNA polymerase II s	CTDP1	104.4	3.9	4	4	23.307	0	21019	17138	20873	15577	30876	17230	27628	17503	23194	25260	Moderate	Moderate	Moderate	Low	YES
Q9Y5B9	FACT complex subu	SUPT16H	119.91	15.3	18	18	34.872	0	68701	78286	90084	49275	102300	41974	102680	71458	83939	75821	Enriched	Enriched	Enriched	No expres	YES
Q9Y5J1	U3 small nucleolar R	UTP18	62.003	9.4	4	4	5.5287	0	4114.3	3561.5	3943.6	3242.2	6652.8	3700.3	8277.2	5187	5307.3	6161.6	Enriched	Enriched	Enriched	Enriched	YES
Q9Y5J6;F2Z2B0	Mitochondrial impor	TIMM10B	11.586	24.3	2	2	4.1101	0.00062	7677.3	7253.9	8327.8	5070.4	9397.5	4054.5	6293.2	6297.6	4252.4	7058.7					YES
Q9Y5J7;G3V502	Mitochondrial impor	TIMM9	10.378	53.9	7	7	25.511	0	31566	20793	24315	44047	25271	29318	27282	44609	20715	47548	Enriched	Enriched	Enriched	No expres	YES
Q9Y5K6	CD2-associated prote	CD2AP	71.45	29.6	21	21	51.992	0	93797	63724	71418	71705	79533	69787	84797	75929	44110	81637	Low	Moderate	Enriched	Enriched	YES
Q9Y5L4;K7EIT2	Mitochondrial impor	TIMM13	10.5	40	7	7	26.623	0	40624	31803	35527	31011	54124	24291	41168	32598	23334	37352	Enriched	Enriched	Enriched	No expres	YES
Q9Y5M8;H7C4H2	Signal recognition pa	SRPRB	29.702	62.7	46	46	307.8	0	279140	179190	210570	309010	211690	308070	283750	315580	119950	249020	Enriched	Enriched	Enriched	Moderate	YES
Q9Y5P4-2;Q9Y5P4	Collagen type IV alpl	COL4A3BP	68.006	7.4	4	4	6.7138	0	6710.1	5293.6	5164.8	4118.7	6812.3	3571.5	3507.1	3397.6	2180.3	4927.4	Moderate	Enriched	Enriched	No expres	YES
Q9Y5P6;Q9Y5P6-2	Mannose-1-phosphat	GMPPB	39.834	35	22	22	116.28	0	115180	59942	64278	98142	99704	91417	65241	69535	30664	84291	Moderate	Enriched	Enriched	No expres	YES
Q9Y5Q8-2;Q9Y5Q	General transcription	GTF3C5	58.266	12.2	5	5	7.1982	0	9477	7758	11239	8929.4	10494	7420.8	13680	11022	10010	14337	Low	Enriched	Enriched	No expres	YES
Q9Y5Q9	General transcription	GTF3C3	101.27	3.7	3	3	15.508	0	11834	8468.4	10767	11871	12739	10056	12425	9233.6	7529.5	13677	Low	Moderate	Enriched	No expres	YES
Q9Y5S2;H0YLY0	Serine/threonine-prot	CDC42BPB	194.31	4.5	9	8	19.407	0	5658.4	4398.1	5172.6	5588.4	5851.4	4971.2	4434.8	4487.2	2474.3	5469.6	No expres	Moderate	Moderate	No expres	YES
Q9Y5S9;Q9Y5S9-2	RNA-binding protein	RBM8A	19.889	40.8	14	14	135.98	0	52004	46087	58789	35464	60758	45780	104550	82407	63829	62301	Moderate	Enriched	Enriched	Enriched	YES
Q9Y5T5-5;Q9Y5T5	Ubiquitin carboxyl-te	USP16	46.599	6.9	3	3	14.303	0	14109	7776.9	12109	11631	11903	10831	4336.5	5319.9	2985.5	9074.6	Enriched	Enriched	Enriched	No expres	YES
Q9Y5U9	Immediate early resp	IER3IP1	8.9687	24.4	2	2	79.16	0	31052	28296	25552	36633	28200	14508	21666	25730	6261.6	24107	Enriched	Enriched	Enriched	No expres	YES
Q9Y5V0;H0YC70	Zinc finger protein 70	ZNF706	8.4977	28.9	3	3	4.1036	0.00062	13726	11062	12234	12509	13841	12984	14003	10885	8926.5	12307	Enriched	Enriched	Enriched	No expres	YES
Q9Y5X2	Sorting nexin-8	SNX8	52.569	4.3	2	2	3.1211	0.00095	11336	8975	12136	10747	13423	9500.7	10923	11572	5266.8	11477	Moderate	Low	Low	No expres	YES
Q9Y5X3;Q5QPE4;	Sorting nexin-5	SNX5	46.816	36.9	23	22	66.057	0	107010	82116	88182	114970	106190	122780	102480	128090	40847	102190	Enriched	Enriched	Enriched	No expres	YES
Q9Y5Y2;H3BNF0;	Cytosolic Fe-S cluste	NUBP2	28.825	20.7	5	5	23.494	0	14858	10863	10745	12815	15459	10463	7732	11900	4627.2	12745	Enriched	Moderate	Moderate	No expres	YES
Q9Y5Y6	Suppressor of tumori	ST14	94.769	10.4	9	9	36.274	0	52144	43018	42483	39247	61960	39172	45201	50363	26752	39301	Enriched	Enriched	Enriched	Enriched	YES
Q9Y5Z4;Q9Y5Z4-2	Heme-binding protei	HEBP2	22.875	39	10	10	23.878	0	22971	21550	19597	20475	22301	22704	28673	28959	14927	28084	Enriched	Enriched	Enriched	Enriched	YES
Q9Y608-2;Q9Y608	Leucine-rich repeat fl	LRRFIP2	45.413	14.5	6	5	9.0237	0	41882	41370	43869	30057	49116	34202	28957	23553	18086	33823	Enriched	Moderate	Enriched	No expres	YES
Q9Y617;Q9Y617-2	Phosphoserine amino	PSAT1	40.422	53.8	36	36	157.21	0	136770	94982	109000	130430	122580	162980	174270	182590	67000	115540	Low	Enriched	Enriched	No expres	YES
Q9Y619	Mitochondrial ornith	SLC25A15	32.736	6.6	2	2	2.6666	0.00256	26445	19802	25075	17880	29965	19511	24754	23530	13608	19520	No expres	Enriched	Moderate	No expres	YES
Q9Y624;A0A087W	Junctional adhesion	F11R	32.583	29.1	10	10	20.37	0	68180	54969	63102	76769	90731	77559	81488	61679	43202	75501	Enriched	Enriched	Enriched	No expres	YES
Q9Y639-1;Q9Y639	Neuroplastin	NPTN;DKFZp566H1924	31.291	27	9	9	23.872	0	35744	31244	39205	34681	45117	30006	56118	45477	24122	46713	Enriched	Enriched	Enriched	Enriched	YES
Q9Y646;A0A087W	Carboxypeptidase Q	CPQ	51.887	17.2	8	8	26.18	0	28179	25730	31994	11415	27731	65309	50128	21869	12157	26879					YES
Q9Y666;H0YB78	Solute carrier family	SLC12A7	119.1	5.3	4	4	12.992	0	11684	7468.9	8647	17954	17954	9968.9	5109.5	6909.6	2771.5	11829	Enriched	Enriched	Enriched	No expres	YES
Q9Y673;Q9Y673-2	Dolichyl-phosphate b	ALG5	36.946	36.4	26	26	199.92	0	235680	126090	143680	203130	184930	190870	165670	139470	70178	166380	Enriched	Enriched	Enriched	No expres	YES
Q9Y676	28S ribosomal protei	MRPS18B	29.395	12.8	3	3	8.3367	0	11074	7729.4	11743	8296.2	11963	7293.5	9115.9	9124.7	6580.1	12322	Moderate	Enriched	Enriched	Enriched	YES
Q9Y678	Coatomer subunit ga	COPG1	97.717	53.3	89	72	323.31	0	504920	292000	343180	648830	439310	476140	411850	577730	224270	481670					YES
Q9Y679-3;Q9Y679	Ancient ubiquitous p	AUP1	41.385	9.7	3	3	8.3985	0	21984	15196	16749	25196	16766	17734	17387	20373	9510.3	19481	Moderate	Enriched	Enriched	No expres	YES
Q9Y696	Chloride intracellular	CLIC4	28.772	49.4	18	17	146.8	0	170000	123920	140170	139350	194080	139910	126490	162750	58822	140920	No expres	Moderate	Enriched	Moderate	YES
Q9Y697;Q9Y697-2	Cysteine desulfurase,	NFS1	50.195	16.2	8	8	38.514	0	45294	40108	39396	33756	51127	38429	39078	37310	19806	38962	Enriched	Enriched	Enriched	No expres	YES
Q9Y6A4	Cilia- and flagella-ass	CFAP20	22.774	13	3	3	3.7911	0.00061	10993	8225.9	8561.1	7258.9	11938	13608	9585.4	8899.6	4897.9	9165.2					YES
Q9Y6A9;C9JBL1;	Signal peptidase com	SPCS1	11.805	30.4	5	5	51.222	0	64576	46728	44574	41367	65608	49365	38386	27180	22404	37387	Enriched	Enriched	Enriched	No expres	YES
Q9Y6B6;D6RD69	GTP-binding protein	SAR1B	22.41	54.5	17	0	157.77	0	91611	48410	58570	115140	66157	102380	112820	143770	92735	113680	Enriched	Enriched	Enriched	No expression	
Q9Y6C2	EMILIN-1	EMILIN1	106.67	27.6	33	33	228.21	0	106050	97456	109910	128420	139050	108480	145750	175360	76449	125780	Low	No expres	Low	Low	YES
Q9Y6D5	Brefeldin A-inhibited	ARFGEF2	202.04	15.2	30	21	78.365	0	92985	58251	66148	63048	80552	82142	55286	51608	22830	64117	Low	Enriched	Enriched	Low	YES
Q9Y6D6;E5RIF2	Brefeldin A-inhibited	ARFGEF1	208.76	7.1	15	6	18.614	0	27638	17012	24679	30192	32433	23291	40218	21969	19027	29707	Enriched	Enriched	Enriched	Enriched	YES
Q9Y6D9;Q9Y6D9-	Mitotic spindle asser	MAD1L1	83.066	4	3	3	2.6461	0.00274	4888.5	2850.2	3369.8	6694.2	7082.7	2635.8	1876.7	4221.6	1366.1	5747	No expres	No expres	Low	No expres	YES
Q9Y6G9;E9PHI6	Cytoplasmic dynein 1	DYNC1LI1	56.578	23.5	12	10	68.51	0	68078	49987	60637	58345	55083	66233	60022	67938	33590	70118	Enriched	Enriched	Enriched	No expres	YES
Q9Y6H1;Q5T1J5	Coiled-coil-helix-coil	CHCHD2;CHCHD2P9	15.512	27.2	3	3	8.3671	0	8052.5	8401.3	8813.8	8856.4	9942	8226.2	13942	9837.1	9617	11375	Enriched	Enriched	Enriched	No expres	YES
Q9Y6I3;Q9Y6I3-3;	Epsin-1	EPN1	60.293	16.8	11	8	43.849	0	56657	45889	69884	45496	69519	46387	68602	42275	32726	58986	Enriched	Enriched	Moderate	No expres	YES
Q9Y6I9;C9JXQ7;C	Testis-expressed sequ	TEX264	34.188	6.7	2	2	3.6661	0.0008	1495.6	1813.4	1557.1	1521.9	2495.1	1281.3	1695.1	2097.7	1078.9	2081.2	Moderate	Enriched	Moderate	No expres	YES
Q9Y6K0	Choline/ethanolamin	CEPT1	46.553	7.9	5	5	11.231	0	12333	11180	14402	8911.4	15708	14582	20328	22270	8787.2	13509	Enriched	Moderate	Enriched	No expres	YES
Q9Y6N5	Sulfide:quinone oxid	SQRDL	49.96	38.2	25	12	157.4	0	141630	123380	124920	147880	169260	142080	195130	190140	105830	198210	Enriched	Enriched	Enriched	No expres	YES
Q9Y6Q5-2;Q9Y6Q	AP-1 complex subun	AP1M2	48.209	26.4	12	10	103.41	0	48381	39053	41980	39690	61379	39925	70901	44193	38721	45399	Low	Enriched	Enriched	No expres	YES
Q9Y6R1;Q9Y6R1-	Electrogenic sodium	SLC4A4	121.46	19.8	25	25	130.56	0	131750	113120	127040	170440	142360	151600	130110	161390	80438	164990	Enriched	Enriched	Enriched	Enriched	YES
Q9Y6U3;Q9Y6U3-	Adseverin	SCIN	80.488	3.2	2	2	3.1935	0.00077	6930.8	4710.9	6719	5758.5	7684.2	7839.3	4581.2	3836.4	2337.1	4753.7	Low	Moderate	Moderate	No expres	YES
Q9Y6W3	Calpain-7	CAPN7	92.651	4.1	3	3	4.8293	0.00043	5891.9	2882.1	4289.6	9410	3185.9	6691.1	5558.4	7283	4211.9	6981.5	Low	Moderate	Enriched	No expres	YES
Q9Y6W5-2;Q9Y6	Wiskott-Aldrich synd	WASF2	31.979	32.4	17	14	62.207	0	78140	39964	65168	109520	49587	77613	107560	99637	51251	124260	Enriched	Enriched	Enriched	Moderate	YES
Q9Y6X5	Bis(5-adenosyl)-triph	ENPP4	51.641	7.7	4	4	3.9946	0.00062	14269	9800.3	11531	11187	19768	12906	13343	13697	5961.1	13139	Low	Moderate	Enriched	Enriched	
Q9Y6Y8;Q9Y6Y8-	SEC23-interacting pr	SEC23IP	111.08	27	31	31	185.29	0	244390	164680	204070	192210	228190	190190	221530	195860	109250	219870	Low	Moderate	Enriched	No expres	YES
R4GNB2;R4GN35;	DENN domain-conta	DENND4C	212.71	4.4	8	8	20.67	0	55547	45101	59351	40690	74470	44093	69382	52727	33101	52477	Moderate	Enriched	Enriched	No expres	YES
R4GN98;P06703	Protein S100;Protein	S100A6	9.681	48.2	18	18	49.803	0	109450	118200	135770	118540	147930	96754	193370	167860	111130	150780	Enriched	Enriched	Enriched	No expres	YES
R4GNF9		TSTD1	7.0579	40.3	3	2	4.6678	0.00043	5410.3	2964.3	3611.4	18173	3247.6	6227	5059.5	8750.7	3475	11912					YES
R4GNG3		GIT2	71.504	6.2	3	1	17.389	0	16748	10256	11802	12317	13939	25170	11230	20579	6390.2	21526	Enriched	Enriched	Enriched	No expres	YES
S4R359		HNRNPK	10.6	84	18	3	69.487	0	6062.7	6524.9	7057.4	4783.6	8934.6	13874	45573	40123	33205	17728	Enriched	Enriched	Enriched	Enriched	YES
S4R456		RPS15	8.0266	50	17	1	3.8208	0.00061	24727	7116.9	9217.8	12621	11336	7231.6	10818	11635	6418.1	12632	Enriched	Enriched	Enriched	Enriched	YES
U3KPZ5		PHB2	11.134	26.2	7	3	4.9841	0.00044	3207.1	2617	2277.2	3808.7	3339.1	4065.8	4996.9	4207.8	1948.2	3939.6	Enriched	Enriched	Enriched	Enriched	YES
U3KQ84	Dolichyl-diphosphoo	DDOST	17.162	29.7	16	4	4.9455	0.00044	9466.4	9148.1	7771	8175.2	10140	6267.5	10763	7711.2	5013.7	8072.4	Moderate	Enriched	Enriched	Enriched	YES
V9GYL0		PEPD	4.2779	40.5	2	2	37.163	0	20554	14803	19844	7429.6	15151	27082	24253	11937	5453.4	19078	Enriched	Enriched	Enriched	Moderate	YES
X6R8S9		PITHD1	11.389	35.7	5	3	23.304	0	16782	17578	20419	3779.1	35472	7734.6	17004	5178	5620.8	7128.1					YES

[a] Pancreas enriched proteins indicate the at least five-fold higher gene expressions in the pancreatic tissue as compared to all other tissues analyzed in their study.

Table S2. Gene Ontology funcational annotation enrichment analysis of significantly changed proteins using DAVID bioinformatic database. The 5357 proteins identified in pancreatic tissue are used as "background" for enrichment calculation.

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini	Fisher Exact	Genes
GOTERM_BP_FAT	GO:0008630~DNA damage response, signal transduction resulting in induction of apoptosis	4	2.94	0.0019	107	10	3986	14.90	8.46E-01	9.10E-05	O95881, P31947, P29590
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	5	3.68	0.0024	107	22	3986	8.47	6.88E-01	2.30E-04	O95881, P31947, Q13619, P29590
GOTERM_BP_FAT	GO:0042770~DNA damage response, signal transduction	5	3.68	0.0067	107	29	3986	6.42	8.88E-01	9.00E-04	O95881, Q06124, P31947, P29590
GOTERM_BP_FAT	GO:0045765~regulation of angiogenesis	4	2.94	0.0112	107	18	3986	8.28	9.35E-01	1.10E-03	Q9NY15, Q9BUP3, Q9UBU3, P29590
GOTERM_BP_FAT	GO:0016525~negative regulation of angiogenesis	3	2.21	0.0177	107	8	3986	13.97	9.69E-01	9.50E-04	Q9NY15, Q9UBU3, P29590
GOTERM_BP_FAT	GO:0006921~cell structure disassembly during apoptosis	3	2.21	0.0177	107	8	3986	13.97	9.69E-01	9.50E-04	O95881, Q12983
GOTERM_BP_FAT	GO:0006309~DNA fragmentation involved in apoptosis	3	2.21	0.0177	107	8	3986	13.97	9.69E-01	9.50E-04	O95881, Q12983
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	9	6.62	0.0180	107	126	3986	2.66	9.48E-01	6.20E-03	P46100, O95881, Q06124, P31947, Q13619, P15927, P29590, P48730
GOTERM_BP_FAT	GO:0006997~nucleus organization	4	2.94	0.0220	107	23	3986	6.48	9.55E-01	2.90E-03	O95881, Q12983, P29590
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	10	7.35	0.0244	107	159	3986	2.34	9.51E-01	9.60E-03	P62937, Q12857, P46100, O95881, Q13619, Q12983, P15927, P29590, P48730
GOTERM_BP_FAT	GO:0006308~DNA catabolic process	4	2.94	0.0247	107	24	3986	6.21	9.33E-01	3.40E-03	O95881, Q12983, P15927
GOTERM_BP_FAT	GO:0030262~apoptotic nuclear changes	3	2.21	0.0274	107	10	3986	11.18	9.34E-01	2.00E-03	O95881, Q12983
GOTERM_BP_FAT	GO:0000737~DNA catabolic process, endonucleolytic	3	2.21	0.0329	107	11	3986	10.16	9.49E-01	2.70E-03	O95881, Q12983
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	8	5.88	0.0364	107	118	3986	2.53	9.51E-01	1.30E-02	Q96BZ9, P09493, Q8IYB5, P07951, Q5H9R7, P31947, O75190, P29590
GOTERM_BP_FAT	GO:0033554~cellular response to stress	11	8.09	0.0419	107	203	3986	2.02	9.60E-01	1.90E-02	P09493, P46100, O95881, Q06124, Q9NR50, P31947, Q13619, P15927, P29590, P4873
GOTERM_BP_FAT	GO:0051462~regulation of cortisol secretion	2	1.47	0.0525	107	2	3986	37.25	9.77E-01	7.10E-04	Q06124, Q9UBU3
GOTERM_BP_FAT	GO:0040013~negative regulation of locomotion	3	2.21	0.0735	107	17	3986	6.57	9.93E-01	9.70E-03	P09493, P18206, Q9UBU3
GOTERM_BP_FAT	GO:0045069~regulation of viral genome replication	2	1.47	0.0777	107	3	3986	24.83	9.93E-01	2.10E-03	P62937, Q15025
GOTERM_BP_FAT	GO:0060123~regulation of growth hormone secretion	2	1.47	0.0777	107	3	3986	24.83	9.93E-01	2.10E-03	Q06124, Q9UBU3
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	7	5.15	0.0926	107	118	3986	2.21	9.96E-01	3.80E-02	O95881, P31947, Q9BUP3, Q13619, Q12983, P29590
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	7	5.15	0.0926	107	118	3986	2.21	9.96E-01	3.80E-02	O95881, P31947, Q9BUP3, Q13619, Q12983, P29590
GOTERM_MF_FAT	GO:0019153~protein-disulfide reductase (glutathione) activity	2	1.47	0.0548	108	2	3848	35.63	1.00E+00	7.80E-04	O95881
GOTERM_MF_FAT	GO:0005484~SNAP receptor activity	3	2.21	0.0561	108	14	3848	7.63	1.00E+00	6.20E-03	Q86Y82, P56962, Q9NYM9
GOTERM_MF_FAT	GO:0019788~NEDD8 ligase activity	2	1.47	0.0811	108	3	3848	23.75	9.99E-01	2.30E-03	P61081, Q969M7
GOTERM_MF_FAT	GO:0031625~ubiquitin protein ligase binding	3	2.21	0.0878	108	18	3848	5.94	9.98E-01	1.30E-02	Q9UJX6, Q13619, P29590
GOTERM_CC_FAT	GO:0005865~striated muscle thin filament	3	2.21	0.0047	111	4	3858	26.07	6.30E-01	9.10E-05	P09493, P06753, P07951
GOTERM_CC_FAT	GO:0005862~muscle thin filament tropomyosin	3	2.21	0.0047	111	4	3858	26.07	6.30E-01	9.10E-05	P09493, P06753, P07951
GOTERM_CC_FAT	GO:0030530~heterogeneous nuclear ribonucleoprotein complex	3	2.21	0.0830	111	17	3858	6.13	1.00E+00	1.20E-02	Q13151, P52597, Q9UKM9
GOTERM_CC_FAT	GO:0016604~nuclear body	6	4.41	0.0901	111	84	3858	2.48	9.99E-01	3.30E-02	Q8WTT2, Q86XP3, P09234, P61326, O43809, P29590

0

Table S3. The list of significantly changed proteins identified by Benjamini-Hochberg based two-samples *t*-test between T1D and healthy controls.

Accession	Protein names	Gene nam	Unique pe	Sequence	Mol. weig	Fold chang	(-Log t-test	Test statistic
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADS	17	32.5	44.3	1.53	4.337	6.312
Q96CM8	Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	2	4.4	63.7	1.54	3.343	4.814
P63261	Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed;Actin, cyto	ACTG1;A	14	62.9	41.8	1.52	3.385	4.856
Q8NHP1	Aflatoxin B1 aldehyde reductase member 4	AKR7L	0	35.3	37.0	3.19	3.506	5.627
P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	26	37.7	57.2	1.47	4.146	5.880
P05186	Alkaline phosphatase, tissue-nonspecific isozyme	ALPL	2	3.1	48.9	1.85	3.198	4.828
Q9UJX6	Anaphase-promoting complex subunit 2	ANAPC2	2	3.2	93.5	0.48	3.844	-5.991
P36404	ADP-ribosylation factor-like protein 2	ARL2;AR	5	19	20.9	2.27	3.590	5.618
P46100	Transcriptional regulator ATRX	ATRX	4	2.6	278.2	2.67	4.280	7.024
O75934	Pre-mRNA-splicing factor SPF27	BCAS2	7	25.3	26.1	1.94	4.411	6.951
C9K0G7	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	BDH1	1	7.2	18.4	0.67	4.016	-5.730
Q9NYM9	BET1-like protein	BET1L	4	45	12.4	1.99	4.136	6.471
Q12983	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	BNIP3	1	6.7	19.9	6.23	4.262	7.323
Q9UKR5	Probable ergosterol biosynthetic protein 28	C14orf1	3	15.7	15.9	0.49	3.251	-4.985
Q6P1N0	Coiled-coil and C2 domain-containing protein 1A	CC2D1A	11	12.5	103.9	0.74	6.469	-8.999
Q16204	Coiled-coil domain-containing protein 6	CCDC6	9	16.9	53.3	1.47	3.698	5.233
P40227	T-complex protein 1 subunit zeta	CCT6A	33	42.2	58.0	0.66	4.649	-6.789
P41208	Centrin-2	CETN2	9	43	19.7	0.63	4.000	-5.876
Q9UEE9	Craniofacial development protein 1	CFDP1	5	17.7	33.6	0.63	3.758	-5.477
Q8IWX8	Calcium homeostasis endoplasmic reticulum protein	CHERP	10	11.5	104.9	0.65	3.709	-5.351
Q9UQN3	Charged multivesicular body protein 2b	CHMP2B	5	21.6	23.9	1.73	3.440	5.130
O15551	Claudin-3	CLDN3	4	15.9	23.3	4.99	6.060	12.089
Q9P003	Protein cornichon homolog 4	CNIH4	1	13.9	15.8	2.16	3.343	5.172
Q7Z7A1	Centriolin	CNTRL	1	6.9	16.9	5.94	3.350	5.471
P02462	Collagen alpha-1(IV) chain;Arresten	COL4A1	11	5.9	128.0	1.72	3.464	5.163
Q9Y6G5	COMM domain-containing protein 10	COMMD1	2	15.8	15.9	0.47	3.257	-5.022
H0Y8G2	Coatomer subunit gamma-1	COPG1	2	63.2	8.4	0.26	3.306	-5.319
Q5RI15	Cytochrome c oxidase protein 20 homolog	COX20	2	19.5	13.3	0.44	3.358	-5.229
P48730	Casein kinase I isoform delta	CSNK1D	2	7.7	49.1	0.68	3.594	-5.085
Q13619	Cullin-4A	CUL4A	3	9.2	87.7	3.54	4.092	6.792
P20711	Aromatic-L-amino-acid decarboxylase	DDC	2	7.9	24.8	4.12	5.640	10.655
Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	23	22.5	90.1	0.67	3.371	-4.815
O75190	DnaJ homolog subfamily B member 6	DNAJB6	1	17.8	35.7	2.24	3.335	5.180
P50570	Dynamin-2	DNM2	2	20.8	98.0	1.57	3.788	5.517
O60941	Dystrobrevin;Dystrobrevin beta	DTNB	7	25.6	70.5	0.72	3.944	-5.400
Q9NR50	Translation initiation factor eIF-2B subunit gamma	EIF2B3	20	31	50.2	0.77	4.050	-5.226
Q13542	Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	1	10.8	12.9	0.33	3.552	-5.693
Q15056	Eukaryotic translation initiation factor 4H	EIF4H	24	43.9	25.2	1.68	3.908	5.827
Q9Y282	Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3	4	11.7	36.9	0.41	4.230	-6.855
Q16595	Frataxin, mitochondrial;Frataxin intermediate form;Frataxin(56-210);Frataxin(	FXN	6	38.5	14.9	0.64	3.348	-4.858
Q14376	UDP-glucose 4-epimerase	GALE	8	23.3	38.3	1.81	3.366	5.068
Q14697	Neutral alpha-glucosidase AB	GANAB	1	41.8	109.4	0.27	3.320	-5.338
P0CAP1	DNA-directed RNA polymerase II subunit GRINL1A	GCOM1;P	1	1.8	64.0	4.32	3.148	5.064
Q96RP9	Elongation factor G, mitochondrial	GFM1	21	22.5	83.5	0.71	3.888	-5.380
Q9UBU3	Appetite-regulating hormone;Ghrelin-27;Ghrelin-28;Obestatin	GHRL	7	51	11.7	0.44	3.200	-4.967
P51610	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-ter	HCFC1	15	6.4	213.5	1.45	3.594	5.045
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA	21	43	30.8	1.61	3.433	5.025
P52597	Heterogeneous nuclear ribonucleoprotein F	HNRNPF	18	29.9	45.7	1.97	4.050	6.307
S4R359	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	3	84	10.6	4.19	3.108	4.991
M0QZM1	Heterogeneous nuclear ribonucleoprotein M	HNRNPM	1	47	39.9	2.59	3.395	5.353
Q9BUP3	Oxidoreductase HTATIP2	HTATIP2	3	14.3	22.0	5.93	3.397	5.558
Q96MX6	Calcineurin subunit B type 1;WD repeat-containing protein 92	HZGJ;PPP	4	5.6	84.7	0.67	3.488	-4.953
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	2	5	43.1	0.66	4.225	-6.096
P49441	Inositol polyphosphate 1-phosphatase	INPP1	3	17	44.0	1.81	4.127	6.329
Q9NWZ3	Interleukin-1 receptor-associated kinase 4	IRAK4	2	18.3	24.3	0.67	3.829	-5.468
Q9P2H0	Uncharacterized protein KIAA1377	KIAA1377	2	1.6	125.9	0.54	3.730	-5.674
O00139	Kinesin-like protein KIF2A	KIF2A	2	9.9	32.7	0.49	3.554	-5.482
O00629	Importin subunit alpha-3	KPNA4	0	12.1	57.9	0.61	3.568	-5.263
Q92615	La-related protein 4B	LARP4B	4	7.2	80.6	0.75	3.778	-4.994
Q03252	Lamin-B2	LMNB2	48	50	69.9	1.69	3.563	5.295
Q6P1A2	Lysophospholipid acyltransferase 5	LPCAT3	3	7.4	46.8	0.67	4.706	-6.824
Q9BS40	Latexin	LXN	3	11.7	25.8	0.44	3.340	-5.195
P61326	Protein mago nashi homolog;Protein mago nashi homolog 2	MAGOH;	7	39	17.2	2.18	3.542	5.509
Q8N4V1	Membrane magnesium transporter 1	MMGT1	1	16.8	14.7	0.58	3.523	-5.256
Q9H8L6	Multimerin-2	MMRN2	2	2.6	104.4	2.52	3.132	4.901
O96033	Molybdopterin synthase sulfur carrier subunit	MOCS2	1	13.3	9.2	2.42	3.311	5.179
Q9H2W6	39S ribosomal protein L46, mitochondrial	MRPL46	4	14.7	31.7	0.62	3.483	-5.110
Q5VZE5	N-alpha-acetyltransferase 35, NatC auxiliary subunit	NAA35	1	1.4	83.6	2.75	3.291	5.198
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	7	44.2	15.2	0.73	3.912	-5.307
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NDUFS5	9	54.7	12.5	1.74	3.353	5.002
Q12857	Nuclear factor 1;Nuclear factor 1 A-type;Nuclear factor 1 X-type	NFIA;NFI	5	13.5	51.5	0.48	3.950	-6.187
Q8WTT2	Nucleolar complex protein 3 homolog	NOC3L	4	2.8	92.5	0.59	3.255	-4.835
O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	8	30	26.2	1.47	3.986	5.650

Q8N138	ORM1-like protein 3;ORM1-like protein 1;ORM1-like protein 2	ORMDL3;	1	11.8	11.8	0.48	3.269	-5.032
I3L0S0	Protein disulfide-isomerase	P4HB	13	70.3	16.2	0.45	3.393	-5.278
H0YBN4	Polyadenylate-binding protein 1	PABPC1	1	56.6	19.7	4.50	3.367	5.459
F8VPF3	Myosin light polypeptide 6	PDE6H	2	76.2	14.4	0.43	3.803	-6.013
Q8NEN9	PDZ domain-containing protein 8	PDZD8	1	1.2	128.6	0.61	3.922	-5.821
O15212	Prefoldin subunit 6	PFDN6	4	25.6	14.6	0.55	3.925	-5.970
Q8IWS0	PHD finger protein 6	PHF6	2	6.9	37.6	0.55	4.876	-7.721
P78356	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	PIP4K2B	4	15.1	47.4	0.72	3.804	-5.191
P29590	Protein PML	PML	9	15.2	62.0	0.72	4.775	-6.617
P62937	Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase A, N-	PPIA	11	66.1	18.0	1.91	3.344	5.082
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta iso	PPP2R1B	3	18.1	66.2	1.75	4.320	6.610
Q5H9R7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	9	11.7	92.4	0.72	3.525	-4.827
Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1	25	29.5	105.8	0.75	4.240	-5.627
Q06124	Tyrosine-protein phosphatase non-receptor type 11	PTPN11	8	12.5	68.0	0.75	4.603	-6.107
P62820	Ras-related protein Rab-1A	RAB1A	20	65.9	22.7	1.88	3.525	5.358
Q3YEC7	Rab-like protein 6	RABL6	17	20.4	79.5	0.59	5.071	-7.902
Q9UKM9	RNA-binding protein Raly	RALY	13	31.7	32.5	1.57	4.199	6.164
Q96S59	Ran-binding protein 9	RANBP9	2	4	77.8	0.64	3.458	-5.022
Q9H477	Ribokinase	RBKS	2	7.3	30.4	0.34	4.374	-7.278
Q8ND24	RING finger protein 214	RNF214	4	7.5	61.3	0.51	3.746	-5.773
P15927	Replication protein A 32 kDa subunit	RPA2	5	10.7	29.2	0.54	3.956	-6.054
P39019	40S ribosomal protein S19	RPS19	12	64.8	16.1	1.86	3.283	4.964
P62081	40S ribosomal protein S7	RPS7	37	51	22.1	2.22	3.482	5.420
Q96T51	RUN and FYVE domain-containing protein 1	RUFY1	8	12.9	79.8	1.73	4.030	6.082
Q9Y3A5	Ribosome maturation protein SBDS	SBDS	16	39.2	28.8	1.47	4.395	6.270
Q86TU7	Histone-lysine N-methyltransferase setd3	SETD3	2	6.8	33.3	5.36	3.369	5.492
Q8WTS6	Histone-lysine N-methyltransferase SETD7	SETD7	4	9.4	40.1	2.39	3.144	4.899
P31947	14-3-3 protein sigma	SFN	2	16.2	24.3	5.85	3.756	6.245
Q8IYB5	Stromal membrane-associated protein 1	SMAP1	2	4.6	49.2	0.59	3.943	-5.896
Q92925	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub	SMARCD	5	16.9	26.7	1.60	3.888	5.705
A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing prote	SMCHD1	9	5.3	215.7	0.66	3.607	-5.177
P09661	U2 small nuclear ribonucleoprotein A	SNRPA1	16	40	28.4	0.68	4.311	-6.123
P09234	U1 small nuclear ribonucleoprotein C	SNRPC	2	11.7	19.7	3.45	3.421	5.497
Q14515	SPARC-like protein 1	SPARCL1	4	11.9	61.8	0.25	3.231	-5.199
Q9NY15	Stabilin-1	STAB1	7	3.2	275.5	0.51	3.844	-5.925
Q13033	Striatin-3	STRN3	4	6	77.7	0.66	4.733	-6.939
Q86Y82	Syntaxin-12	STX12	4	17	31.6	1.98	4.598	7.343
P56962	Syntaxin-17	STX17	3	41.5	5.0	3.09	3.798	6.156
Q8NFX7	Syntaxin-binding protein 6	STXBP6	4	10	23.6	2.06	3.728	5.782
Q96BZ9	TBC1 domain family member 20	TBC1D20	2	5.2	45.9	2.71	3.963	6.407
P16035	Metalloproteinase inhibitor 2	TIMP2	3	20	24.4	0.67	3.588	-5.099
Q9UJW2	Tubulointerstitial nephritis antigen	TINAG	2	2.3	54.6	5.00	4.704	8.283
Q9HC07	Transmembrane protein 165	TMEM165	4	16.4	34.9	0.33	3.629	-5.834
Q9NV96	Cell cycle control protein 50A	TMEM30A	5	12.2	40.7	0.45	3.771	-5.923
Q6PI78	Transmembrane protein 65	TMEM65	3	14.2	25.5	0.65	4.116	-5.964
Q96MH6	Transmembrane protein 68	TMEM68	4	14.2	37.4	0.56	3.313	-4.975
Q9H1E5	Thioredoxin-related transmembrane protein 4	TMX4	6	13.5	39.0	0.54	3.320	-5.008
Q15025	TNFAIP3-interacting protein 1	TNIP1	2	3.7	55.7	0.56	3.457	-5.196
P60174	Triosephosphate isomerase	TPI1	74	81.5	26.7	1.41	3.467	4.806
P09493	Tropomyosin alpha-1 chain	TPM1	0	68.4	37.5	1.90	3.828	5.875
P09493	Tropomyosin alpha-1 chain	TPM1	0	68.3	32.8	0.17	3.967	-6.675
P07951	Tropomyosin beta chain	TPM2	0	58.5	33.0	2.28	3.850	6.083
P06753	Tropomyosin alpha-3 chain	TPM3	0	64.5	29.0	1.62	3.797	5.585
Q5T0D9	Tumor protein p63-regulated gene 1-like protein	TPRG1L	2	13.1	23.3	0.50	3.448	-5.288
P19075	Tetraspanin-8	TSPAN8	6	14.3	26.0	3.07	3.429	5.477
Q99614	Tetratricopeptide repeat protein 1	TTC1	7	23.6	33.5	0.34	5.107	-8.952
Q6NXR4	TELO2-interacting protein 2	TTI2	1	4.4	53.3	2.25	3.438	5.353
Q9BQE3	Tubulin alpha-1C chain	TUBA1C;	3	55.1	57.7	0.59	3.820	-5.705
M0QY37	Tubulin beta-4A chain	TUBB4A	1	57.8	12.0	0.17	3.809	-6.352
O95881	Thioredoxin domain-containing protein 12	TXNDC12	11	37.8	19.2	0.65	3.548	-5.115
Q969M7	NEDD8-conjugating enzyme UBE2F	UBE2F	3	25.2	15.7	0.43	3.444	-5.389
P61081	NEDD8-conjugating enzyme Ubc12	UBE2M	4	19.1	20.9	0.71	3.720	-5.148
Q712K3	Ubiquitin-conjugating enzyme E2 R2	UBE2R2	2	10.5	27.2	0.39	3.364	-5.298
Q9NWZ5	Uridine-cytidine kinase-like 1	UCKL1	5	13.2	44.6	0.72	3.787	-5.169
Q9H1J1	Regulator of nonsense transcripts 3A	UPF3A	1	9.3	17.1	3.57	3.293	5.278
Q9BRT	Ubiquinol-cytochrome-c reductase complex assembly factor 2	UQCC2	1	9.9	11.9	0.66	3.455	-4.959
O95399	Urotensin-2	UTS2	1	5.8	16.3	14.71	4.762	8.679
P18206	Vinculin	VCL	120	60	116.7	1.57	3.316	4.814
Q5JSD2	Voltage-dependent anion-selective channel protein 2	VDAC2	1	45.1	22.2	0.14	3.602	-5.969
Q8TBZ3	WD repeat-containing protein 20	WDR20;A	3	4.4	67.5	11.73	3.847	6.520
Q15061	WD repeat-containing protein 43	WDR43	5	5.9	74.9	4.70	5.035	9.085
Q14202	Zinc finger MYM-type protein 3	ZMYM3	2	2	141.8	0.60	4.750	-7.282