Table S3. TMT-MS data from WT, D3 PCKO and D5 PCKO mice.

List of significantly (fold change [FC]>1.25, false discovery rate [FDR]<0.1) altered proteins in D5 PCKO vs. WT, or D3 PCKO vs. WT muscles.

Accession	Description	WT-Avg	D5-Avg	logFC	fold change	up in	PValue	FDR
sp|Q8BWA5|KLH31_MOUSE	Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=1	147511.6667	54469.33333	-1.451082	2.73	WT-Avg	6.21E-50	1.70E-46
sp|Q8BUZ1|ABRA_MOUSE	Actin-binding Rho-activating protein OS=Mus musculus GN=Abra PE=1 SV=1	218693	589951	1.4210827	2.68	D5-Avg	1.11E-41	1.53E-38
sp|Q9JKB3|YBOX3_MOUSE	Y-box-binding protein 3 OS=Mus musculus GN=Ybx3 PE=1 SV=2	298423.3333	142376.6667	-1.080007	2.11	WT-Avg	4.28E-39	3.18E-36
sp|Q8CI12|SMTL2_MOUSE	Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1	563046.6667	241191	-1.237611	2.36	WT-Avg	4.64E-39	3.18E-36
sp|Q60949|TBCD1_MOUSE	TBC1 domain family member 1 OS=Mus musculus GN=Tbc1d1 PE=1 SV=3	343528	176383	-0.975055	1.97	WT-Avg	2.11E-36	1.16E-33
sp|Q8VBT1|TXLNB_MOUSE	Beta-taxilin OS=Mus musculus GN=Txlnb PE=1 SV=2	142490	61181	-1.23188	2.35	WT-Avg	2.09E-33	9.58E-31
sp|Q8C0L9|GPCP1_MOUSE	Glycerophosphocholine phosphodiesterase GPCPD1 OS=Mus musculus GN=Gpcpd1 PE=1 SV=1	167436	80403.66667	-1.072572	2.10	WT-Avg	3.24E-32	1.27E-29
sp|Q6ZPU9|KBP_MOUSE	KIF1-binding protein OS=Mus musculus GN=Kif1bp PE=1 SV=2	31380	66266.66667	1.066438	2.09	D5-Avg	4.19E-30	1.44E-27
sp|Q9CYG7|TOM34_MOUSE	Mitochondrial import receptor subunit TOM34 OS=Mus musculus GN=Tomm34 PE=1 SV=1	109162	192046.6667	0.8029507	1.74	D5-Avg	3.95E-29	1.20E-26
sp|Q7TPW1|NEXN_MOUSE	Nexilin OS=Mus musculus GN=Nexn PE=1 SV=3	205358.6667	83236.33333	-1.316178	2.49	WT-Avg	1.09E-28	2.99E-26
sp|P14142|GTR4_MOUSE	Solute carrier family 2, facilitated glucose transporter member 4 OS=Mus musculus GN=Slc2a4 PE=1 S	176710	82299	-1.11223	2.16	WT-Avg	2.05E-27	5.12E-25
sp|Q921U8|SMTN_MOUSE	Smoothelin OS=Mus musculus GN=Smtn PE=1 SV=2	161383.6667	79332.66667	-1.03699	2.05	WT-Avg	5.93E-26	1.36E-23
sp|Q9JMH9|MY18A_MOUSE	Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2	254435.3333	141656.3333	-0.856334	1.81	WT-Avg	5.24E-25	1.11E-22
sp|Q7M729|SCN4B_MOUSE	Sodium channel subunit beta-4 OS=Mus musculus GN=Scn4b PE=1 SV=1	372933.3333	144260	-1.384274	2.61	WT-Avg	8.80E-23	1.73E-20
sp|Q9JJG0|TACC2_MOUSE	Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2	57067.33333	29182.66667	-0.981361	1.97	WT-Avg	1.04E-22	1.90E-20
sp|O89114|DNJB5_MOUSE	DnaJ homolog subfamily B member 5 OS=Mus musculus GN=Dnajb5 PE=2 SV=1	146768	82173	-0.849682	1.80	WT-Avg	1.72E-22	2.94E-20
sp|P15105|GLNA_MOUSE	Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	220566.3333	114845.6667	-0.952015	1.93	WT-Avg	2.85E-19	4.60E-17
sp|P70699|LYAG_MOUSE	Lysosomal alpha-glucosidase OS=Mus musculus GN=Gaa PE=1 SV=2	148302	226301.3333	0.596955	1.51	D5-Avg	2.88E-18	4.39E-16
sp|Q9Z2P8|VAMP5_MOUSE	Vesicle-associated membrane protein 5 OS=Mus musculus GN=Vamp5 PE=1 SV=1	91580	54513.33333	-0.761609	1.70	WT-Avg	3.90E-18	5.63E-16
sp|P60824|CIRBP_MOUSE	Cold-inducible RNA-binding protein OS=Mus musculus GN=Cirbp PE=1 SV=1	44570.66667	92143.33333	1.0372867	2.05	D5-Avg	5.17E-18	7.09E-16
sp|E9QA62|LMOD3_MOUSE	Leiomodin-3 OS=Mus musculus GN=Lmod3 PE=1 SV=1	75453.33333	34812	-1.126776	2.18	WT-Avg	1.20E-17	1.57E-15
sp|P47856|GFPT1_MOUSE	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 PE=1	6058.666667	15452.33333	1.3392667	2.53	D5-Avg	2.15E-17	2.68E-15
sp|Q61584|FXR1_MOUSE	Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 PE=1 SV=2	569958.6667	375145.3333	-0.616006	1.53	WT-Avg	1.30E-16	1.55E-14
sp|P51150|RAB7A_MOUSE	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	645346	430145	-0.598384	1.51	WT-Avg	1.17E-15	1.33E-13
sp|Q64152|BTF3_MOUSE	Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=1 SV=3	77968	50199.66667	-0.648149	1.57	WT-Avg	5.74E-15	5.91E-13
sp|Q8R5A0|SMYD2_MOUSE	N-lysine methyltransferase SMYD2 OS=Mus musculus GN=Smyd2 PE=1 SV=1	337649.3333	218318	-0.643358	1.56	WT-Avg	5.75E-15	5.91E-13
sp|Q99MS7|EH1L1_MOUSE	EH domain-binding protein 1-like protein 1 OS=Mus musculus GN=Ehbp1l1 PE=1 SV=1	314706.6667	208972.3333	-0.603656	1.52	WT-Avg	5.82E-15	5.91E-13
sp|Q9D1K2|VATF_MOUSE	V-type proton ATPase subunit F OS=Mus musculus GN=Atp6v1f PE=1 SV=2	42824.66667	73546.66667	0.7687711	1.70	D5-Avg	6.90E-15	6.77E-13
sp|Q6PEE3|RIR2B_MOUSE	Ribonucleoside-diphosphate reductase subunit M2 B OS=Mus musculus GN=Rrm2b PE=1 SV=1	11960.33333	23344	0.9520701	1.93	D5-Avg	1.42E-14	1.35E-12
sp|P07934|PHKG1_MOUSE	Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform OS=Mus musculus GN=P	3054298	1840874	-0.744669	1.68	WT-Avg	2.04E-14	1.87E-12
sp|P62932|FBX40_MOUSE	F-box only protein 40 OS=Mus musculus GN=Fbxo40 PE=1 SV=1	114422.6667	50830.33333	-1.183749	2.27	WT-Avg	2.25E-14	2.00E-12
sp|O35127|C10_MOUSE	Protein C10 OS=Mus musculus GN=Grcc10 PE=1 SV=1	33423	57225.66667	0.7639526	1.70	D5-Avg	3.48E-14	2.99E-12
sp|Q5DTJ9|MYPN_MOUSE	Myopalladin OS=Mus musculus GN=Mypn PE=1 SV=2	668699.6667	461513.6667	-0.546937	1.46	WT-Avg	7.38E-14	6.14E-12
sp|P28658|ATX10_MOUSE	Ataxin-10 OS=Mus musculus GN=Atxn10 PE=1 SV=2	52509	80502.33333	0.6044307	1.52	D5-Avg	8.99E-14	7.25E-12
sp|Q38HM4|TRI63_MOUSE	E3 ubiquitin-protein ligase TRIM63 OS=Mus musculus GN=Trim63 PE=1 SV=1	25554.33333	67795	1.3956871	2.63	D5-Avg	1.01E-13	7.88E-12
sp|P17047|LAMP2_MOUSE	Lysosome-associated membrane glycoprotein 2 OS=Mus musculus GN=Lamp2 PE=1 SV=2	139975.3333	208600	0.5618903	1.48	D5-Avg	1.05E-13	7.99E-12
sp|Q8R010|AIMP2_MOUSE	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Mus musculus GN=Aimp2	133585	87423	-0.624953	1.54	WT-Avg	5.23E-13	3.78E-11
tr|E9PWZ3|E9PWZ3_MOUSE	Ribosomal protein L3-like OS=Mus musculus GN=Rpl3l PE=1 SV=1	437923.3333	313323.3333	-0.496082	1.41	WT-Avg	7.60E-13	5.35E-11
sp|Q922J3|CLIP1_MOUSE	CAP-Gly domain-containing linker protein 1 OS=Mus musculus GN=Clip1 PE=1 SV=1	934660.6667	651001.3333	-0.53522	1.45	WT-Avg	1.22E-12	8.39E-11
sp|Q9CR57|RL14_MOUSE	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 SV=3	252610	182847.3333	-0.478667	1.39	WT-Avg	1.26E-12	8.46E-11
sp|A3KFX0|5NT1A_MOUSE	Cytosolic 5'-nucleotidase 1A OS=Mus musculus GN=Nt5c1a PE=1 SV=1	194399	131212	-0.580745	1.50	WT-Avg	1.46E-12	9.54E-11
sp|O09012|PEX5_MOUSE	Peroxisomal targeting signal 1 receptor OS=Mus musculus GN=Pex5 PE=1 SV=2	7827.666667	14445.66667	0.8707712	1.83	D5-Avg	1.54E-12	9.80E-11
sp|Q80Y55|BSDC1_MOUSE	BSD domain-containing protein 1 OS=Mus musculus GN=Bsdc1 PE=1 SV=1	8429.333333	15267.33333	0.8463134	1.80	D5-Avg	1.57E-12	9.80E-11
sp|Q91YI0|ARLY_MOUSE	Argininosuccinate lyase OS=Mus musculus GN=Asl PE=1 SV=1	81110.66667	123289.6667	0.5905612	1.51	D5-Avg	1.98E-12	1.20E-10
sp|Q9QYG0|NDRG2_MOUSE	Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1	1934231.667	1313727	-0.570237	1.48	WT-Avg	2.74E-12	1.63E-10
sp|Q8BJF9|CHM2B_MOUSE	Charged multivesicular body protein 2b OS=Mus musculus GN=Chmp2b PE=1 SV=1	56751.66667	84484.33333	0.5627829	1.48	D5-Avg	4.56E-12	2.66E-10
sp|Q8VE91|RETR1_MOUSE	Reticulophagy regulator 1 OS=Mus musculus GN=Retreg1d PE=1 SV=2	41030.66667	23524	-0.813575	1.76	WT-Avg	5.10E-12	2.92E-10
sp|P53996|CNBP_MOUSE	Cellular nucleic acid-binding protein OS=Mus musculus GN=Cnbp PE=1 SV=2	256807	176105	-0.557223	1.47	WT-Avg	1.20E-11	6.73E-10
sp|Q7TSH2|KPBB_MOUSE	Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1	3091699.333	1957538.667	-0.673803	1.60	WT-Avg	1.44E-11	7.89E-10
sp|P67984|RL22_MOUSE	60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=1 SV=2	323440	222480	-0.553246	1.47	WT-Avg	1.65E-11	8.88E-10
sp|Q8K268|ABCF3_MOUSE	ATP-binding cassette sub-family F member 3 OS=Mus musculus GN=Abcf3 PE=1 SV=1	77729	112353.3333	0.5200069	1.43	D5-Avg	1.83E-11	9.63E-10
sp|Q80U95|UBE3C_MOUSE	Ubiquitin-protein ligase E3C OS=Mus musculus GN=Ube3c PE=1 SV=2	25666	40755.66667	0.6562772	1.58	D5-Avg	2.14E-11	1.11E-09
sp|Q62418|DBNL_MOUSE	Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2	37574.33333	67801.66667	0.8415097	1.79	D5-Avg	2.32E-11	1.18E-09
sp|Q3UZA1|CPZIP_MOUSE	CapZ-interacting protein OS=Mus musculus GN=Rcsd1 PE=1 SV=1	94126.66667	62297.33333	-0.605538	1.52	WT-Avg	2.37E-11	1.18E-09
sp|Q8K0C4|CP51A_MOUSE	Lanosterol 14-alpha demethylase OS=Mus musculus GN=Cyp51a1 PE=1 SV=1	9500.333333	18517.66667	0.9544823	1.94	D5-Avg	7.35E-11	3.54E-09
sp|P42232|STA5B_MOUSE	Signal transducer and activator of transcription 5B OS=Mus musculus GN=Stat5b PE=1 SV=1	134346.6667	93686.66667	-0.533214	1.45	WT-Avg	9.70E-11	4.59E-09
sp|P84099|RL19_MOUSE	60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	181266.6667	126073.3333	-0.535812	1.45	WT-Avg	1.07E-10	4.97E-09
sp|P62717|RL18A_MOUSE	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	306896.6667	219530	-0.496382	1.41	WT-Avg	1.25E-10	5.70E-09
sp|Q9DAR7|DCPS_MOUSE	m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=1	25140.66667	39135.33333	0.6258072	1.54	D5-Avg	1.76E-10	7.93E-09
sp|P60843|IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1	451366.6667	640212	0.4934519	1.41	D5-Avg	2.00E-10	8.69E-09
sp|P62911|RL32_MOUSE	60S ribosomal protein L32 OS=Mus musculus GN=Rpl32 PE=1 SV=2	106630.6667	73666.33333	-0.545929	1.46	WT-Avg	2.98E-10	1.28E-08
sp|Q8BXZ1|TMX3_MOUSE	Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3 PE=1 SV=2	181109.3333	243188.3333	0.4131016	1.33	D5-Avg	4.05E-10	1.71E-08
sp|Q9JHQ5|LZTL1_MOUSE	Leucine zipper transcription factor-like protein 1 OS=Mus musculus GN=Lztfl1 PE=1 SV=1	31699.66667	50065.33333	0.6486357	1.57	D5-Avg	5.30E-10	2.21E-08
sp|Q8BG95|MYPT2_MOUSE	Protein phosphatase 1 regulatory subunit 12B OS=Mus musculus GN=Ppp1r12b PE=1 SV=2	474219.6667	279248.3333	-0.77855	1.72	WT-Avg	6.77E-10	2.77E-08
sp|Q8N7N5|DCAF8_MOUSE	DDB1- and CUL4-associated factor 8 OS=Mus musculus GN=Dcaf8 PE=1 SV=1	101561.3333	144311	0.4945039	1.41	D5-Avg	7.19E-10	2.90E-08
sp|O88569|ROA2_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	757536	1036891.667	0.4413906	1.36	D5-Avg	1.45E-09	5.78E-08
sp|P61027|RAB10_MOUSE	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	864533.3333	634322.6667	-0.460337	1.38	WT-Avg	1.73E-09	6.73E-08
sp|P47962|RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	748510	545846.3333	-0.467292	1.38	WT-Avg	1.75E-09	6.73E-08
sp|Q62351|TFR1_MOUSE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	68507	49161.33333	-0.490884	1.41	WT-Avg	1.76E-09	6.73E-08
sp|O08915|AIP_MOUSE	AH receptor-interacting protein OS=Mus musculus GN=Aip PE=1 SV=1	87842.66667	127976.3333	0.5285332	1.44	D5-Avg	1.82E-09	6.83E-08
sp|P62918|RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2	127491.6667	91424.33333	-0.493093	1.41	WT-Avg	2.43E-09	8.90E-08
sp|P14115|RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=1 SV=5	760550	571680.3333	-0.424293	1.34	WT-Avg	2.63E-09	9.51E-08
sp|P47740|AL3A2_MOUSE	Fatty aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2 PE=1 SV=2	83646.66667	115060	0.4473672	1.36	D5-Avg	2.76E-09	9.84E-08
sp|Q9ER60|SCN4A_MOUSE	Sodium channel protein type 4 subunit alpha OS=Mus musculus GN=Scn4a PE=2 SV=1	342527	236511	-0.548964	1.46	WT-Avg	2.80E-09	9.85E-08
sp|P0C5K1|SBK2_MOUSE	Serine/threonine-protein kinase SBK2 OS=Mus musculus GN=Sbk2 PE=3 SV=2	378886.6667	263996.6667	-0.532721	1.45	WT-Avg	3.11E-09	1.08E-07
sp|O70493|SNX12_MOUSE	Sorting nexin-12 OS=Mus musculus GN=Snx12 PE=1 SV=1	71480.33333	105025	0.5447911	1.46	D5-Avg	3.46E-09	1.19E-07
sp|Q8VCI5|PEX19_MOUSE	Peroxisomal biogenesis factor 19 OS=Mus musculus GN=Pex19 PE=1 SV=1	43549.66667	69254.66667	0.6589424	1.58	D5-Avg	3.60E-09	1.22E-07
sp|P62242|RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	514566.6667	383236.6667	-0.437262	1.35	WT-Avg	4.10E-09	1.37E-07
sp|Q8CGC7|SYEP_MOUSE	Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4	2430532	1722597	-0.510786	1.42	WT-Avg	4.41E-09	1.46E-07
sp|Q9D1R9|RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=1 SV=2	766560	543103.3333	-0.507589	1.42	WT-Avg	4.85E-09	1.59E-07
sp|P53026|RL10A_MOUSE	60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	910606.3333	669566.6667	-0.456136	1.37	WT-Avg	5.18E-09	1.67E-07
sp|Q99MR9|PPR3A_MOUSE	Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=2	2918748	2087442.667	-0.495763	1.41	WT-Avg	5.30E-09	1.69E-07
sp|P62245|RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=1 SV=2	447595	345643.6667	-0.385487	1.31	WT-Avg	8.30E-09	2.59E-07
sp|Q8BP67|RL24_MOUSE	60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=1 SV=2	327900.6667	220309.6667	-0.584258	1.50	WT-Avg	1.60E-08	4.95E-07
tr|A2A9K7|A2A9K7_MOUSE	Connector enhancer of kinase suppressor of Ras 1 OS=Mus musculus GN=Cnksr1 PE=1 SV=1	54150	36986	-0.562622	1.48	WT-Avg	1.67E-08	5.08E-07
sp|P41105|RL28_MOUSE	60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	470180	352766.6667	-0.426345	1.34	WT-Avg	3.20E-08	9.66E-07
sp|P84091|AP2M1_MOUSE	AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	134670	189180	0.476695	1.39	D5-Avg	3.83E-08	1.14E-06
sp|P56501|UCP3_MOUSE	Mitochondrial uncoupling protein 3 OS=Mus musculus GN=Ucp3 PE=1 SV=1	156759	112570	-0.490569	1.40	WT-Avg	4.67E-08	1.36E-06
sp|Q9CPV4|GLOD4_MOUSE	Glyoxalase domain-containing protein 4 OS=Mus musculus GN=Glod4 PE=1 SV=1	818085.6667	1072847.333	0.3786808	1.30	D5-Avg	4.67E-08	1.36E-06
sp|P35979|RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	226326	176276	-0.373158	1.30	WT-Avg	6.49E-08	1.87E-06
sp|Q61160|FADD_MOUSE	FAS-associated death domain protein OS=Mus musculus GN=Fadd PE=1 SV=1	43103	62651.66667	0.5291111	1.44	D5-Avg	6.88E-08	1.97E-06
sp|Q9JM14|NT5C_MOUSE	5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus GN=Nt5c PE=1 SV=1	61635.66667	89514	0.5264332	1.44	D5-Avg	7.56E-08	2.14E-06
sp|Q920M5|CORO6_MOUSE	Coronin-6 OS=Mus musculus GN=Coro6 PE=1 SV=1	396253.3333	297900	-0.422194	1.34	WT-Avg	8.37E-08	2.34E-06
sp|P47963|RL13_MOUSE	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=1 SV=3	468772	350504.6667	-0.431975	1.35	WT-Avg	8.80E-08	2.44E-06

sp|Q9D2N9|VP33A_MOUSE	Vacuolar protein sorting-associated protein 33A OS=Mus musculus GN=Vps33a PE=1 SV=2	24501.33333	35299	0.5141591	1.43	D5-Avg	9.06E-08	2.49E-06
sp|P14206|RSSA_MOUSE	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	616898.3333	480558.3333	-0.372458	1.29	WT-Avg	1.05E-07	2.85E-06
sp|Q9ESL4|M3K20_MOUSE	Mitogen-activated protein kinase kinase kinase 20 OS=Mus musculus GN=Map3k20 PE=1 SV=1	148126	107791	-0.471595	1.39	WT-Avg	1.36E-07	3.66E-06
sp|Q9QYI3|DNJC7_MOUSE	DnaJ homolog subfamily C member 7 OS=Mus musculus GN=Dnajc7 PE=1 SV=2	39518.33333	54959.66667	0.4624666	1.38	D5-Avg	1.39E-07	3.70E-06
sp|Q60598|SRC8_MOUSE	Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2	82687	113526.6667	0.443717	1.36	D5-Avg	1.45E-07	3.82E-06
sp|Q8BH97|RCN3_MOUSE	Reticulocalbin-3 OS=Mus musculus GN=Rcn3 PE=1 SV=1	28048	18796.66667	-0.590546	1.51	WT-Avg	1.56E-07	4.08E-06
sp|Q8BLY2|SYTC2_MOUSE	Probable threonine--tRNA ligase 2, cytoplasmic OS=Mus musculus GN=Tarsl2 PE=1 SV=1	252348.3333	187553.3333	-0.44221	1.36	WT-Avg	1.72E-07	4.46E-06
sp|Q9QZF2|GPC1_MOUSE	Glypican-1 OS=Mus musculus GN=Gpc1 PE=1 SV=1	100788.3333	76802.66667	-0.404634	1.32	WT-Avg	2.18E-07	5.58E-06
sp|O09167|RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=1 SV=3	396600.6667	298079.3333	-0.425068	1.34	WT-Avg	2.23E-07	5.66E-06
sp|Q8VCH8|UBXN4_MOUSE	UBX domain-containing protein 4 OS=Mus musculus GN=Ubxn4 PE=1 SV=1	18622	26653.33333	0.5052118	1.42	D5-Avg	2.48E-07	6.25E-06
sp|P62281|RS11_MOUSE	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3	765940	557606.6667	-0.469781	1.38	WT-Avg	2.58E-07	6.43E-06
sp|P60867|RS20_MOUSE	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	723820	516216.6667	-0.499276	1.41	WT-Avg	2.98E-07	7.36E-06
sp|Q921F2|TADBP_MOUSE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	185617.3333	243312.6667	0.378007	1.30	D5-Avg	3.26E-07	7.98E-06
sp|P62900|RL31_MOUSE	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=1 SV=1	307503.3333	222460	-0.478414	1.39	WT-Avg	4.06E-07	9.87E-06
sp|P14148|RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2	1299696.667	1014780	-0.36944	1.29	WT-Avg	4.17E-07	9.98E-06
sp|P55096|ABCD3_MOUSE	ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2	121576.6667	167963.3333	0.4548058	1.37	D5-Avg	4.18E-07	9.98E-06
sp|Q99NB8|UBQL4_MOUSE	Ubiquilin-4 OS=Mus musculus GN=Ubqln4 PE=1 SV=1	73616.33333	99021	0.4158932	1.33	D5-Avg	4.36E-07	1.03E-05
sp|Q9CQ02|COMD4_MOUSE	COMM domain-containing protein 4 OS=Mus musculus GN=Commd4 PE=1 SV=1	11843.33333	17725.66667	0.5681587	1.48	D5-Avg	4.76E-07	1.11E-05
sp|Q61166|MARE1_MOUSE	Microtubule-associated protein RP/EB family member 1 OS=Mus musculus GN=Mapre1 PE=1 SV=3	133693.3333	173626.6667	0.3642736	1.29	D5-Avg	4.79E-07	1.11E-05
sp|P51667|MLRV_MOUSE	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Mus musculus GN=Myl2 PE=1	388054.6667	913547.3333	1.2273985	2.34	D5-Avg	4.92E-07	1.14E-05
sp|Q99PL6|UBXN6_MOUSE	UBX domain-containing protein 6 OS=Mus musculus GN=Ubxn6 PE=1 SV=1	48660.66667	66384	0.4357651	1.35	D5-Avg	5.05E-07	1.15E-05
sp|P14869|RLA0_MOUSE	60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3	1030782.333	800067.3333	-0.377454	1.30	WT-Avg	5.53E-07	1.26E-05
sp|Q80XB4|NRAP_MOUSE	Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=3	1569441.333	910189.6667	-0.796427	1.74	WT-Avg	5.68E-07	1.28E-05
sp|P62962|PROF1_MOUSE	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	1216062	1649681.333	0.4285924	1.35	D5-Avg	5.77E-07	1.29E-05
sp|P35279|RAB6A_MOUSE	Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4	43351.33333	59380	0.4430825	1.36	D5-Avg	6.34E-07	1.40E-05
sp|P18826|KPB1_MOUSE	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Mus musculus GN=Phka	4753646.667	3183166.667	-0.593013	1.51	WT-Avg	6.60E-07	1.45E-05
sp|P63147|UBE2B_MOUSE	Ubiquitin-conjugating enzyme E2 B OS=Mus musculus GN=Ube2b PE=1 SV=1	104563.3333	77473.33333	-0.44585	1.36	WT-Avg	6.90E-07	1.50E-05
sp|Q7TNG5|EMAL2_MOUSE	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus GN=Eml2 PE=1 SV=1	247036	320420	0.3622614	1.29	D5-Avg	8.02E-07	1.73E-05
sp|P35980|RL18_MOUSE	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=1 SV=3	647076.6667	460770	-0.50189	1.42	WT-Avg	8.54E-07	1.83E-05
sp|A3KG59|P20D2_MOUSE	Peptidase M20 domain-containing protein 2 OS=Mus musculus GN=Pm20d2 PE=1 SV=1	148293.3333	110853.3333	-0.430132	1.35	WT-Avg	8.82E-07	1.88E-05
sp|Q9ER00|STX12_MOUSE	Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1	74083.33333	96716.66667	0.3723318	1.29	D5-Avg	9.06E-07	1.91E-05
sp|Q9D8B4|NDUAB_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Mus musculus GN=Ndufa11 P	325466.6667	258045.6667	-0.345953	1.27	WT-Avg	9.75E-07	2.04E-05
sp|O70571|PDK4_MOUSE	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 4, mitochondrial OS=Mus musculus GN	525719.3333	847484.3333	0.676758	1.60	D5-Avg	1.03E-06	2.14E-05
sp|P24549|AL1A1_MOUSE	Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5	644996.6667	479322	-0.440867	1.36	WT-Avg	1.20E-06	2.48E-05
sp|Q8BLU2|MT21C_MOUSE	Protein-lysine methyltransferase METTL21C OS=Mus musculus GN=Mettl21c PE=2 SV=1	50893.33333	25869	-0.99572	1.99	WT-Avg	1.22E-06	2.49E-05
sp|Q6ZWN5|RS9_MOUSE	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=1 SV=3	892105.6667	699021.6667	-0.363905	1.29	WT-Avg	1.39E-06	2.78E-05
sp|Q9R059|FHL3_MOUSE	Four and a half LIM domains protein 3 OS=Mus musculus GN=Fhl3 PE=1 SV=2	1227954.667	951960.3333	-0.37995	1.30	WT-Avg	1.42E-06	2.82E-05
sp|Q8BJU0|SGTA_MOUSE	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Mus musculus GN=Sgta PE	400313.3333	504536.6667	0.3216103	1.25	D5-Avg	1.43E-06	2.82E-05
sp|Q9JK92|HSPB8_MOUSE	Heat shock protein beta-8 OS=Mus musculus GN=Hspb8 PE=1 SV=1	268893.3333	198516.6667	-0.45057	1.37	WT-Avg	1.44E-06	2.82E-05
sp|Q8VIB3|SIA10_MOUSE	Type 2 lactosamine alpha-2,3-sialyltransferase OS=Mus musculus GN=St3gal6 PE=2 SV=3	17507.33333	11536.66667	-0.615459	1.53	WT-Avg	1.46E-06	2.84E-05
sp|Q9R0H0|ACOX1_MOUSE	Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=Acox1 PE=1 SV=5	154282.3333	221620.6667	0.5124935	1.43	D5-Avg	1.48E-06	2.87E-05
sp|Q3TW96|UAP1L_MOUSE	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap1l1 PE=1 SV=1	11262.66667	16567.33333	0.5453614	1.46	D5-Avg	1.54E-06	2.95E-05
sp|P47941|CRKL_MOUSE	Crk-like protein OS=Mus musculus GN=Crkl PE=1 SV=2	202436.6667	257210	0.3333935	1.26	D5-Avg	1.71E-06	3.24E-05
sp|P48722|HS74L_MOUSE	Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2	73579	102616	0.4680213	1.38	D5-Avg	1.73E-06	3.26E-05
sp|P12970|RL7A_MOUSE	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=1 SV=2	178246.6667	133926.6667	-0.425293	1.34	WT-Avg	1.79E-06	3.35E-05
sp|P62702|RS4X_MOUSE	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=1 SV=2	203643.3333	159376.6667	-0.365432	1.29	WT-Avg	1.92E-06	3.55E-05
sp|Q9CY58|PAIRB_MOUSE	Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2	712841	559524	-0.362552	1.29	WT-Avg	1.96E-06	3.61E-05
sp|A2AWA9|RBGP1_MOUSE	Rab GTPase-activating protein 1 OS=Mus musculus GN=Rabgap1 PE=1 SV=1	8179	14596.33333	0.8249852	1.77	D5-Avg	1.98E-06	3.61E-05
sp|Q5SW19|CLU_MOUSE	Clustered mitochondria protein homolog OS=Mus musculus GN=Cluh PE=1 SV=2	125805.6667	95757	-0.406886	1.33	WT-Avg	2.09E-06	3.81E-05
sp|P62889|RL30_MOUSE	60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=1 SV=2	195570	146800	-0.42855	1.35	WT-Avg	2.21E-06	3.96E-05
sp|Q9Z2Y3|HOME1_MOUSE	Homer protein homolog 1 OS=Mus musculus GN=Homer1 PE=1 SV=2	112615.3333	87243.66667	-0.381756	1.30	WT-Avg	2.23E-06	3.97E-05
sp|P47955|RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	305317.6667	239058.3333	-0.365869	1.29	WT-Avg	2.35E-06	4.13E-05
sp|Q8R0N6|HOT_MOUSE	Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Mus musculus GN=Adhfe1 PE=1 SV=2	33650.33333	23353.66667	-0.537046	1.45	WT-Avg	2.41E-06	4.22E-05
sp|Q9Z0P5|TWF2_MOUSE	Twinfilin-2 OS=Mus musculus GN=Twf2 PE=1 SV=1	231577	178872.6667	-0.384919	1.31	WT-Avg	2.63E-06	4.56E-05
sp|P97461|RS5_MOUSE	40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=3	393265.3333	305299.6667	-0.377479	1.30	WT-Avg	2.71E-06	4.67E-05
sp|P63276|RS17_MOUSE	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	1090452	837129	-0.392983	1.31	WT-Avg	2.78E-06	4.77E-05
sp|Q64347|CLCN1_MOUSE	Chloride channel protein 1 OS=Mus musculus GN=Clcn1 PE=1 SV=3	21754	14907	-0.558139	1.47	WT-Avg	2.84E-06	4.84E-05
sp|P70280|VAMP7_MOUSE	Vesicle-associated membrane protein 7 OS=Mus musculus GN=Vamp7 PE=1 SV=1	31710.33333	44553.66667	0.4771959	1.39	D5-Avg	3.01E-06	5.08E-05
sp|Q9ERP3|TRI54_MOUSE	Tripartite motif-containing protein 54 OS=Mus musculus GN=Trim54 PE=1 SV=1	65903	48811	-0.445228	1.36	WT-Avg	3.09E-06	5.17E-05
sp|P62754|RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	395981	304205	-0.391758	1.31	WT-Avg	3.15E-06	5.24E-05
sp|Q60575|KIF1B_MOUSE	Kinesin-like protein KIF1B OS=Mus musculus GN=Kif1b PE=1 SV=2	38748.66667	27869	-0.486701	1.40	WT-Avg	3.21E-06	5.31E-05
sp|Q8BGM7|AAKG3_MOUSE	5'-AMP-activated protein kinase subunit gamma-3 OS=Mus musculus GN=Prkag3 PE=1 SV=1	26417	17578	-0.602749	1.52	WT-Avg	3.26E-06	5.36E-05
sp|Q9R062|GLYG_MOUSE	Glycogenin-1 OS=Mus musculus GN=Gyg1 PE=1 SV=3	1500601.667	1193770.333	-0.342707	1.27	WT-Avg	3.28E-06	5.36E-05
sp|P61211|ARL1_MOUSE	ADP-ribosylation factor-like protein 1 OS=Mus musculus GN=Arl1 PE=1 SV=1	88612	118948.3333	0.4141888	1.33	D5-Avg	3.45E-06	5.56E-05
sp|Q9D783|KLH40_MOUSE	Kelch-like protein 40 OS=Mus musculus GN=Klhl40 PE=1 SV=1	1092173.333	743752.6667	-0.564491	1.48	WT-Avg	3.68E-06	5.88E-05
sp|Q8K3R3|PLCD4_MOUSE	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-4 OS=Mus musculus GN=Plcd4 PE=1	36546.66667	26748	-0.464424	1.38	WT-Avg	3.90E-06	6.18E-05
sp|Q62348|TSN_MOUSE	Translin OS=Mus musculus GN=Tsn PE=1 SV=1	261260	333030	0.3391564	1.27	D5-Avg	4.05E-06	6.39E-05
tr|J3QN89|J3QN89_MOUSE	Angio-associated migratory protein OS=Mus musculus GN=Aamp PE=1 SV=1	14449	20474.33333	0.4919298	1.41	D5-Avg	4.37E-06	6.86E-05
sp|P61759|PFD3_MOUSE	Prefoldin subunit 3 OS=Mus musculus GN=Vbp1 PE=1 SV=2	191834.6667	245656	0.3439233	1.27	D5-Avg	4.51E-06	7.00E-05
sp|Q8CGY6|UN45B_MOUSE	Protein unc-45 homolog B OS=Mus musculus GN=Unc45b PE=1 SV=1	1434853	1089232.667	-0.41134	1.33	WT-Avg	4.85E-06	7.47E-05
sp|Q9EPL9|ACOX3_MOUSE	Peroxisomal acyl-coenzyme A oxidase 3 OS=Mus musculus GN=Acox3 PE=1 SV=2	26979	37189	0.4519218	1.37	D5-Avg	5.16E-06	7.89E-05
sp|P61924|COPZ1_MOUSE	Coatomer subunit zeta-1 OS=Mus musculus GN=Copz1 PE=1 SV=1	29857	41395.33333	0.4601467	1.38	D5-Avg	5.18E-06	7.89E-05
sp|O70209|PDLI3_MOUSE	PDZ and LIM domain protein 3 OS=Mus musculus GN=Pdlim3 PE=1 SV=1	2427618	1718913.667	-0.508374	1.42	WT-Avg	5.96E-06	8.99E-05
sp|Q99L04|DHRS1_MOUSE	Dehydrogenase/reductase SDR family member 1 OS=Mus musculus GN=Dhrs1 PE=1 SV=1	29263.33333	41180	0.4816864	1.40	D5-Avg	6.18E-06	9.21E-05
sp|P62320|SMD3_MOUSE	Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	171583.3333	223290	0.3687882	1.29	D5-Avg	6.35E-06	9.42E-05
sp|Q7TQI3|OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	355744	453976	0.3404683	1.27	D5-Avg	6.52E-06	9.62E-05
sp|Q9WV85|NDK3_MOUSE	Nucleoside diphosphate kinase 3 OS=Mus musculus GN=Nme3 PE=1 SV=3	19515	27730	0.4951177	1.41	D5-Avg	6.57E-06	9.64E-05
sp|P02798|MT2_MOUSE	Metallothionein-2 OS=Mus musculus GN=Mt2 PE=1 SV=2	5170.666667	15098.66667	1.5435967	2.92	D5-Avg	6.84E-06	9.98E-05
sp|Q9EQU5|SET_MOUSE	Protein SET OS=Mus musculus GN=Set PE=1 SV=1	72790	95063.33333	0.3733671	1.30	D5-Avg	6.92E-06	1.00E-04
sp|P62908|RS3_MOUSE	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	1296033.333	1029876.667	-0.343747	1.27	WT-Avg	6.99E-06	1.01E-04
sp|Q9CQR2|RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=1 SV=1	242833.3333	184216.6667	-0.411991	1.33	WT-Avg	8.11E-06	1.17E-04
sp|P62301|RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	600390	467163.3333	-0.374983	1.30	WT-Avg	9.00E-06	1.29E-04
sp|Q61586|GPAT1_MOUSE	Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Mus musculus GN=Gpam PE=1 SV=2	19696.33333	13398.33333	-0.568438	1.48	WT-Avg	9.43E-06	1.34E-04
sp|P63325|RS10_MOUSE	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	506051.3333	402772.3333	-0.341368	1.27	WT-Avg	1.09E-05	1.54E-04
sp|Q8CJ53|CIP4_MOUSE	Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 PE=1 SV=2	548896.6667	441193.6667	-0.328318	1.26	WT-Avg	1.17E-05	1.64E-04
sp|P14131|RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=1 SV=4	562567	435426.6667	-0.382093	1.30	WT-Avg	1.18E-05	1.65E-04
sp|Q91Z38|TTC1_MOUSE	Tetratricopeptide repeat protein 1 OS=Mus musculus GN=Ttc1 PE=1 SV=1	12365.66667	17869.66667	0.5188769	1.43	D5-Avg	1.19E-05	1.66E-04
sp|P21460|CYTC_MOUSE	Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2	223060	174270	-0.369834	1.29	WT-Avg	1.27E-05	1.76E-04
sp|P47911|RL6_MOUSE	60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	2081430	1612963.667	-0.379703	1.30	WT-Avg	1.35E-05	1.86E-04
sp|Q9WUL7|ARL3_MOUSE	ADP-ribosylation factor-like protein 3 OS=Mus musculus GN=Arl3 PE=1 SV=1	53847	72330.66667	0.413219	1.33	D5-Avg	1.36E-05	1.87E-04
sp|P63323|RS12_MOUSE	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	555626.6667	443963.3333	-0.336672	1.26	WT-Avg	1.40E-05	1.91E-04
sp|O70133|DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	99392.33333	125434.3333	0.3233443	1.25	D5-Avg	1.40E-05	1.91E-04
sp|Q99LI8|HGS_MOUSE	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Mus musculus GN=Hgs PE=1 SV=2	56143.33333	72158	0.3503345	1.27	D5-Avg	1.47E-05	1.98E-04
sp|P59325|IF5_MOUSE	Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Eif5 PE=1 SV=1	444200	575273.3333	0.3617492	1.28	D5-Avg	1.48E-05	1.99E-04
sp|Q3UFY7|5NT3B_MOUSE	7-methylguanosine phosphate-specific 5'-nucleotidase OS=Mus musculus GN=Nt5c3b PE=1 SV=3	19974	27236.66667	0.436061	1.35	D5-Avg	1.56E-05	2.08E-04
sp|Q9D8E6|RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	1328289.333	1020847.333	-0.391299	1.31	WT-Avg	1.57E-05	2.09E-04
sp|P99027|RLA2_MOUSE	60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3	914863.3333	739269.3333	-0.320017	1.25	WT-Avg	1.69E-05	2.23E-04
sp|P62141|PP1B_MOUSE	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Mus musculus GN=Ppp1cb PE=1	106359	79345.66667	-0.435983	1.35	WT-Avg	1.80E-05	2.36E-04

sp|P31230|AIMP1_MOUSE	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1	438273.3333	331633.6667	-0.417333	1.34	WT-Avg	1.90E-05	2.48E-04
sp|Q99KK2|NEUA_MOUSE	N-acylneuraminate cytidylyltransferase OS=Mus musculus GN=Cmas PE=1 SV=2	29968	40875.66667	0.4359236	1.35	D5-Avg	2.02E-05	2.63E-04
sp|P00493|HPRT_MOUSE	Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus GN=Hprt1 PE=1 SV=3	36813.33333	48780	0.3936997	1.31	D5-Avg	2.17E-05	2.82E-04
sp|P70170|ABCC9_MOUSE	ATP-binding cassette sub-family C member 9 OS=Mus musculus GN=Abcc9 PE=1 SV=2	356530	272900.3333	-0.399913	1.32	WT-Avg	2.30E-05	2.97E-04
sp|Q9CQC9|SAR1B_MOUSE	GTP-binding protein SAR1b OS=Mus musculus GN=Sar1b PE=1 SV=1	903230	718123.3333	-0.34405	1.27	WT-Avg	2.59E-05	3.31E-04
sp|P63168|DYL1_MOUSE	Dynein light chain 1, cytoplasmic OS=Mus musculus GN=Dynll1 PE=1 SV=1	270113.3333	341280	0.3261092	1.25	D5-Avg	2.81E-05	3.58E-04
sp|Q60936|COQ8A_MOUSE	Atypical kinase COQ8A, mitochondrial OS=Mus musculus GN=Coq8a PE=1 SV=2	2303829.333	1627979.333	-0.509243	1.42	WT-Avg	2.86E-05	3.61E-04
sp|Q9CXW3|CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	131456.6667	168296.6667	0.3425641	1.27	D5-Avg	2.87E-05	3.61E-04
sp|P60605|UB2G2_MOUSE	Ubiquitin-conjugating enzyme E2 G2 OS=Mus musculus GN=Ube2g2 PE=1 SV=1	19032.66667	26194	0.4466229	1.36	D5-Avg	3.18E-05	3.99E-04
sp|P62267|RS23_MOUSE	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=1 SV=3	463060.6667	367465.6667	-0.346184	1.27	WT-Avg	3.22E-05	4.02E-04
sp|P10126|EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	1820329	1455194.667	-0.33432	1.26	WT-Avg	3.30E-05	4.10E-04
sp|P55302|AMRP_MOUSE	Alpha-2-macroglobulin receptor-associated protein OS=Mus musculus GN=Lrpap1 PE=1 SV=1	210741.6667	266634.3333	0.3254091	1.25	D5-Avg	3.31E-05	4.10E-04
sp|Q5SSW2|PSME4_MOUSE	Proteasome activator complex subunit 4 OS=Mus musculus GN=Psme4 PE=1 SV=1	81999.66667	65724.66667	-0.332003	1.26	WT-Avg	3.35E-05	4.13E-04
sp|Q8K4L3|SVIL_MOUSE	Supervillin OS=Mus musculus GN=Svil PE=1 SV=1	153879.3333	122458.3333	-0.342002	1.27	WT-Avg	3.64E-05	4.44E-04
sp|O54988|SLK_MOUSE	STE20-like serine/threonine-protein kinase OS=Mus musculus GN=Slk PE=1 SV=2	73085.66667	97840	0.4089408	1.33	D5-Avg	3.66E-05	4.45E-04
sp|Q9CPR4|RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=3	825840	655471.6667	-0.346092	1.27	WT-Avg	3.83E-05	4.62E-04
sp|Q9QZM0|UBQL2_MOUSE	Ubiquilin-2 OS=Mus musculus GN=Ubqln2 PE=1 SV=2	34090.66667	47524	0.4695958	1.38	D5-Avg	4.00E-05	4.79E-04
sp|P70670|NACAM_MOUSE	Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=N	4716680.667	3435555	-0.46923	1.38	WT-Avg	4.35E-05	5.20E-04
sp|Q91WK2|EIF3H_MOUSE	Eukaryotic translation initiation factor 3 subunit H OS=Mus musculus GN=Eif3h PE=1 SV=1	137240	110989	-0.318056	1.25	WT-Avg	4.53E-05	5.36E-04
sp|Q99KK7|DPP3_MOUSE	Dipeptidyl peptidase 3 OS=Mus musculus GN=Dpp3 PE=1 SV=2	577105.3333	726143.6667	0.3179054	1.25	D5-Avg	4.66E-05	5.49E-04
tr|G3X972|G3X972_MOUSE	SEC24 related gene family, member C (S. cerevisiae), isoform CRA_a OS=Mus musculus GN=Sec24c PE	91548.33333	115345.6667	0.3208734	1.25	D5-Avg	4.68E-05	5.49E-04
sp|Q9DBE8|ALG2_MOUSE	Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Mus musculus GN=Alg2 PE=1 SV=2	39014.66667	49983	0.3450598	1.27	D5-Avg	5.19E-05	6.04E-04
sp|Q80ZK0|RT10_MOUSE	28S ribosomal protein S10, mitochondrial OS=Mus musculus GN=Mrps10 PE=1 SV=1	39506.66667	52751.66667	0.4027408	1.32	D5-Avg	5.41E-05	6.26E-04
sp|P59481|LMA2L_MOUSE	VIP36-like protein OS=Mus musculus GN=Lman2l PE=1 SV=1	52121.66667	66556.66667	0.339891	1.27	D5-Avg	5.90E-05	6.80E-04
sp|P97822|AN32E_MOUSE	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Mus musculus GN=Anp32e PE=1	52703.33333	70174.33333	0.4031477	1.32	D5-Avg	5.94E-05	6.83E-04
sp|Q8BFQ4|WDR82_MOUSE	WD repeat-containing protein 82 OS=Mus musculus GN=Wdr82 PE=1 SV=1	9145	13114.33333	0.5097121	1.42	D5-Avg	6.04E-05	6.91E-04
sp|Q149B8|PERM1_MOUSE	PGC-1 and ERR-induced regulator in muscle protein 1 OS=Mus musculus GN=Perm1 PE=1 SV=2	253324	195456	-0.385136	1.31	WT-Avg	6.35E-05	7.21E-04
sp|P62264|RS14_MOUSE	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=1 SV=3	178190	137576.6667	-0.384248	1.31	WT-Avg	6.50E-05	7.34E-04
sp|Q3U1J4|DDB1_MOUSE	DNA damage-binding protein 1 OS=Mus musculus GN=Ddb1 PE=1 SV=2	1958343.667	2489374	0.3339196	1.26	D5-Avg	6.56E-05	7.38E-04
sp|P61358|RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 SV=2	290416.6667	227456.6667	-0.366006	1.29	WT-Avg	6.67E-05	7.47E-04
sp|Q6PA06|ATLA2_MOUSE	Atlastin-2 OS=Mus musculus GN=Atl2 PE=1 SV=1	667127.3333	528320.3333	-0.350638	1.28	WT-Avg	7.70E-05	8.58E-04
sp|Q60715|P4HA1_MOUSE	Prolyl 4-hydroxylase subunit alpha-1 OS=Mus musculus GN=P4ha1 PE=1 SV=2	32257.66667	23686.66667	-0.457525	1.37	WT-Avg	7.81E-05	8.64E-04
sp|Q8K3H0|DP13A_MOUSE	DCC-interacting protein 13-alpha OS=Mus musculus GN=Appl1 PE=1 SV=1	56380	71083.33333	0.3218278	1.25	D5-Avg	8.37E-05	9.19E-04
sp|P32020|NLTP_MOUSE	Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3	401814.6667	537093.3333	0.4097894	1.33	D5-Avg	8.79E-05	9.57E-04
sp|P62746|RHOB_MOUSE	Rho-related GTP-binding protein RhoB OS=Mus musculus GN=Rhob PE=1 SV=1	10581.66667	15373	0.5292808	1.44	D5-Avg	9.26E-05	1.00E-03
sp|Q8BHN0|PPM1L_MOUSE	Protein phosphatase 1L OS=Mus musculus GN=Ppm1l PE=1 SV=1	14429	10000	-0.538668	1.45	WT-Avg	1.01E-04	1.07E-03
sp|Q9Z247|FKBP9_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Mus musculus GN=Fkbp9 PE=1 SV=1	53342.33333	70172.33333	0.3834684	1.30	D5-Avg	1.01E-04	1.07E-03
sp|Q8BMK4|CKAP4_MOUSE	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=1 SV=2	71411.33333	52338.66667	-0.458577	1.37	WT-Avg	1.02E-04	1.08E-03
sp|Q3U0V1|FUBP2_MOUSE	Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=2	33402.33333	44922.66667	0.4156474	1.33	D5-Avg	1.06E-04	1.12E-03
sp|O08579|EMD_MOUSE	Emerin OS=Mus musculus GN=Emd PE=1 SV=1	66473.66667	86928.33333	0.376565	1.30	D5-Avg	1.14E-04	1.19E-03
sp|Q69ZQ1|MYORG_MOUSE	Myogenesis-regulating glycosidase OS=Mus musculus GN=Myorg PE=1 SV=2	78672.66667	61271.33333	-0.373243	1.30	WT-Avg	1.18E-04	1.23E-03
sp|Q5SRX1|TM1L2_MOUSE	TOM1-like protein 2 OS=Mus musculus GN=Tom1l2 PE=1 SV=1	93105.33333	121565	0.3721001	1.29	D5-Avg	1.22E-04	1.27E-03
sp|Q9DBG1|CP27A_MOUSE	Sterol 26-hydroxylase, mitochondrial OS=Mus musculus GN=Cyp27a1 PE=1 SV=1	129572.6667	102307.6667	-0.35153	1.28	WT-Avg	1.26E-04	1.30E-03
sp|Q68FH4|GALK2_MOUSE	N-acetylgalactosamine kinase OS=Mus musculus GN=Galk2 PE=1 SV=1	15331.33333	20909	0.4341077	1.35	D5-Avg	1.26E-04	1.30E-03
sp|P97351|RS3A_MOUSE	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	2157374.333	1725148	-0.335047	1.26	WT-Avg	1.45E-04	1.47E-03
sp|Q64520|KGUA_MOUSE	Guanylate kinase OS=Mus musculus GN=Guk1 PE=1 SV=2	45076.66667	57803.33333	0.3466145	1.27	D5-Avg	1.46E-04	1.47E-03
sp|Q91YX5|LGAT1_MOUSE	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1 OS=Mus musculus GN=Lpgat1 PE=1 SV=1	30572.66667	42140	0.4538915	1.37	D5-Avg	1.51E-04	1.52E-03
sp|Q17ST2|KCNA7_MOUSE	Potassium voltage-gated channel subfamily A member 7 OS=Mus musculus GN=Kcna7 PE=2 SV=2	45186.66667	35937.66667	-0.342951	1.27	WT-Avg	1.74E-04	1.74E-03
sp|Q80UU9|PGRC2_MOUSE	Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2	14026.33333	19040	0.4276152	1.35	D5-Avg	1.81E-04	1.81E-03
sp|Q99JX4|EIF3M_MOUSE	Eukaryotic translation initiation factor 3 subunit M OS=Mus musculus GN=Eif3m PE=1 SV=1	74099.33333	59299.33333	-0.335737	1.26	WT-Avg	2.11E-04	2.07E-03
sp|P29699|FETUA_MOUSE	Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1	897512.6667	643788.6667	-0.492169	1.41	WT-Avg	2.18E-04	2.14E-03
sp|Q6PDM2|SRSF1_MOUSE	Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3	226990	291053.3333	0.3486211	1.27	D5-Avg	2.55E-04	2.46E-03
sp|B9EJR8|DAAF5_MOUSE	Dynein assembly factor 5, axonemal OS=Mus musculus GN=Dnaaf5 PE=1 SV=1	35282.66667	47806	0.4224872	1.34	D5-Avg	2.58E-04	2.48E-03
sp|Q9CYT6|CAP2_MOUSE	Adenylyl cyclase-associated protein 2 OS=Mus musculus GN=Cap2 PE=1 SV=1	640515.3333	500854.6667	-0.368935	1.29	WT-Avg	2.64E-04	2.53E-03
sp|B2RVY9|TM182_MOUSE	Transmembrane protein 182 OS=Mus musculus GN=Tmem182 PE=1 SV=1	58628	43590.66667	-0.440513	1.36	WT-Avg	2.66E-04	2.54E-03
sp|Q8R570|SNP47_MOUSE	Synaptosomal-associated protein 47 OS=Mus musculus GN=Snap47 PE=1 SV=1	9029	14108.33333	0.6275505	1.54	D5-Avg	2.67E-04	2.54E-03
sp|Q8VEH5|EPMIP_MOUSE	EPM2A-interacting protein 1 OS=Mus musculus GN=Epm2aip1 PE=1 SV=1	29419	37925	0.3544021	1.28	D5-Avg	2.83E-04	2.66E-03
sp|Q60648|SAP3_MOUSE	Ganglioside GM2 activator OS=Mus musculus GN=Gm2a PE=1 SV=2	10157.33333	13765.33333	0.4242944	1.34	D5-Avg	2.84E-04	2.66E-03
sp|Q8C129|LCAP_MOUSE	Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep PE=1 SV=1	44932.66667	34534.33333	-0.389686	1.31	WT-Avg	2.84E-04	2.66E-03
sp|Q9Z1R2|BAG6_MOUSE	Large proline-rich protein BAG6 OS=Mus musculus GN=Bag6 PE=1 SV=1	32493.33333	43214	0.4015864	1.32	D5-Avg	2.85E-04	2.66E-03
sp|Q8CI94|PYGB_MOUSE	Glycogen phosphorylase, brain form OS=Mus musculus GN=Pygb PE=1 SV=3	48781.66667	61955	0.3336131	1.26	D5-Avg	2.89E-04	2.69E-03
sp|Q8BQM4|HEAT3_MOUSE	HEAT repeat-containing protein 3 OS=Mus musculus GN=Heatr3 PE=1 SV=1	6812.666667	9640.666667	0.4888024	1.40	D5-Avg	2.94E-04	2.72E-03
sp|O55142|RL35A_MOUSE	60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=1 SV=2	149033.3333	102713.3333	-0.553042	1.47	WT-Avg	2.96E-04	2.73E-03
sp|P20029|GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	4192302.333	5618011	0.4096901	1.33	D5-Avg	3.55E-04	3.20E-03
sp|Q6ZWV3|RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=1 SV=3	138538.3333	99907.66667	-0.480956	1.40	WT-Avg	3.58E-04	3.22E-03
sp|Q8BRF7|SCFD1_MOUSE	Sec1 family domain-containing protein 1 OS=Mus musculus GN=Scfd1 PE=1 SV=1	88592.33333	113443.3333	0.3428585	1.27	D5-Avg	3.62E-04	3.25E-03
sp|Q9JMG1|EDF1_MOUSE	Endothelial differentiation-related factor 1 OS=Mus musculus GN=Edf1 PE=1 SV=1	174170	139293.3333	-0.335987	1.26	WT-Avg	3.71E-04	3.30E-03
sp|Q60692|PSB6_MOUSE	Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3	200220.3333	161097.3333	-0.327894	1.26	WT-Avg	3.72E-04	3.31E-03
sp|Q9D1E6|TBCB_MOUSE	Tubulin-folding cofactor B OS=Mus musculus GN=Tbcb PE=1 SV=2	34880.33333	46052.66667	0.3904655	1.31	D5-Avg	3.81E-04	3.38E-03
sp|Q61543|GSLG1_MOUSE	Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	42726.33333	53776.66667	0.3183321	1.25	D5-Avg	4.00E-04	3.52E-03
sp|Q8BHG1|NRDC_MOUSE	Nardilysin OS=Mus musculus GN=Nrdc PE=1 SV=1	64805.33333	83481	0.3503933	1.27	D5-Avg	4.01E-04	3.52E-03
sp|Q8QZZ7|TPRKB_MOUSE	EKC/KEOPS complex subunit Tprkb OS=Mus musculus GN=Tprkb PE=1 SV=1	13905.33333	19714	0.4926853	1.41	D5-Avg	4.21E-04	3.66E-03
sp|Q99NB9|SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	29344	37005.33333	0.3226344	1.25	D5-Avg	4.33E-04	3.72E-03
sp|Q9CZP5|BCS1_MOUSE	Mitochondrial chaperone BCS1 OS=Mus musculus GN=Bcs1l PE=1 SV=1	57505.66667	44481.66667	-0.380282	1.30	WT-Avg	4.46E-04	3.82E-03
sp|Q99JT9|MTND_MOUSE	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Mus musculus GN=Adi1 PE=1 SV=1	28982.33333	42353.33333	0.5336487	1.45	D5-Avg	4.89E-04	4.15E-03
sp|P62852|RS25_MOUSE	40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 SV=1	1269040.333	945548	-0.434067	1.35	WT-Avg	5.00E-04	4.22E-03
sp|O35465|FKBP8_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Mus musculus GN=Fkbp8 PE=1 SV=2	93338.33333	125840.6667	0.4199233	1.34	D5-Avg	5.24E-04	4.40E-03
sp|Q61189|ICLN_MOUSE	Methylosome subunit pICln OS=Mus musculus GN=Clns1a PE=1 SV=1	23700	29786.66667	0.3178609	1.25	D5-Avg	5.25E-04	4.40E-03
sp|Q9JJ28|FLII_MOUSE	Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1 SV=1	43882	33391.33333	-0.405325	1.32	WT-Avg	5.35E-04	4.45E-03
sp|P98192|GNPAT_MOUSE	Dihydroxyacetone phosphate acyltransferase OS=Mus musculus GN=Gnpat PE=1 SV=1	61907.33333	77735.66667	0.3168093	1.25	D5-Avg	5.71E-04	4.72E-03
sp|P62849|RS24_MOUSE	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	208880	167036.6667	-0.332719	1.26	WT-Avg	5.74E-04	4.73E-03
sp|Q61735|CD47_MOUSE	Leukocyte surface antigen CD47 OS=Mus musculus GN=Cd47 PE=1 SV=2	35873.33333	45920	0.3428484	1.27	D5-Avg	6.05E-04	4.96E-03
sp|Q8K3K8|OPTN_MOUSE	Optineurin OS=Mus musculus GN=Optn PE=1 SV=1	50830	41105.33333	-0.31953	1.25	WT-Avg	6.12E-04	5.00E-03
sp|Q9Z1E4|GYS1_MOUSE	Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2	4566615	3543616	-0.377409	1.30	WT-Avg	6.35E-04	5.14E-03
sp|Q6PDQ2|CHD4_MOUSE	Chromodomain-helicase-DNA-binding protein 4 OS=Mus musculus GN=Chd4 PE=1 SV=1	13841	18626.33333	0.4139641	1.33	D5-Avg	6.46E-04	5.18E-03
sp|Q8C5Q4|GRSF1_MOUSE	G-rich sequence factor 1 OS=Mus musculus GN=Grsf1 PE=1 SV=2	34027.66667	44933	0.3904922	1.31	D5-Avg	6.46E-04	5.18E-03
sp|P62743|AP2S1_MOUSE	AP-2 complex subunit sigma OS=Mus musculus GN=Ap2s1 PE=1 SV=1	58209.66667	74017.66667	0.3327771	1.26	D5-Avg	6.48E-04	5.18E-03
sp|P34884|MIF_MOUSE	Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2	128719	169607.6667	0.3832712	1.30	D5-Avg	6.70E-04	5.30E-03
sp|P70257|NFIX_MOUSE	Nuclear factor 1 X-type OS=Mus musculus GN=Nfix PE=1 SV=2	27893	21253	-0.403826	1.32	WT-Avg	6.73E-04	5.31E-03
sp|Q8BTY8|SCFD2_MOUSE	Sec1 family domain-containing protein 2 OS=Mus musculus GN=Scfd2 PE=1 SV=1	13513	17528.66667	0.3620257	1.29	D5-Avg	6.81E-04	5.36E-03
sp|Q9JJI8|RL38_MOUSE	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=1 SV=3	96743.33333	76890	-0.34363	1.27	WT-Avg	7.04E-04	5.49E-03
tr|Q3ULW8|Q3ULW8_MOUSE	Poly [ADP-ribose] polymerase OS=Mus musculus GN=Parp3 PE=1 SV=1	55105	44443	-0.321419	1.25	WT-Avg	7.24E-04	5.61E-03
sp|Q9CQ71|RFA3_MOUSE	Replication protein A 14 kDa subunit OS=Mus musculus GN=Rpa3 PE=1 SV=1	14740.33333	18765.66667	0.335797	1.26	D5-Avg	9.01E-04	6.84E-03
sp|Q91Z83|MYH7_MOUSE	Myosin-7 OS=Mus musculus GN=Myh7 PE=2 SV=1	412234.3333	1288826.333	1.6386243	3.11	D5-Avg	9.93E-04	7.36E-03
sp|Q3UBX0|TM109_MOUSE	Transmembrane protein 109 OS=Mus musculus GN=Tmem109 PE=1 SV=2	417866.6667	337666.6667	-0.32109	1.25	WT-Avg	1.02E-03	7.55E-03
sp|Q61249|IGBP1_MOUSE	Immunoglobulin-binding protein 1 OS=Mus musculus GN=Igbp1 PE=1 SV=1	17824.66667	24121.66667	0.4209526	1.34	D5-Avg	1.12E-03	8.13E-03
sp|P70695|F16P2_MOUSE	Fructose-1,6-bisphosphatase isozyme 2 OS=Mus musculus GN=Fbp2 PE=1 SV=2	1203422	869646	-0.483876	1.40	WT-Avg	1.17E-03	8.42E-03
sp|P52760|RIDA_MOUSE	2-iminobutanoate/2-iminopropanoate deaminase OS=Mus musculus GN=Rida PE=1 SV=3	67393	94884	0.4775046	1.39	D5-Avg	1.25E-03	8.97E-03

sp|Q9CRB8|MTFP1_MOUSE	Mitochondrial fission process protein 1 OS=Mus musculus GN=Mtfp1 PE=1 SV=1	261657	209971.3333	-0.326871	1.25	WT-Avg	1.44E-03	1.00E-02
sp|Q9CY16|RT28_MOUSE	28S ribosomal protein S28, mitochondrial OS=Mus musculus GN=Mrps28 PE=1 SV=1	247823.3333	161126.6667	-0.638614	1.56	WT-Avg	1.45E-03	1.01E-02
sp|Q9Z2G6|SE1L1_MOUSE	Protein sel-1 homolog 1 OS=Mus musculus GN=Sel1l PE=1 SV=2	6308	9731	0.6171297	1.53	D5-Avg	1.57E-03	1.08E-02
tr|F8VPN4|F8VPN4_MOUSE	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase OS=Mus musculus GN=Agl PE=1 SV=1	14288293.33	10915158.33	-0.401807	1.32	WT-Avg	1.77E-03	1.19E-02
sp|Q8CCS6|PABP2_MOUSE	Polyadenylate-binding protein 2 OS=Mus musculus GN=Pabpn1 PE=1 SV=3	19668.66667	25939.66667	0.3895218	1.31	D5-Avg	1.85E-03	1.23E-02
sp|P21614|VTDB_MOUSE	Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2	581802	471024	-0.318687	1.25	WT-Avg	1.89E-03	1.25E-02
sp|P68040|RACK1_MOUSE	Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3	1600745.333	1283156.333	-0.331138	1.26	WT-Avg	1.93E-03	1.26E-02
sp|P55012|S12A2_MOUSE	Solute carrier family 12 member 2 OS=Mus musculus GN=Slc12a2 PE=1 SV=2	91366.66667	69953.33333	-0.40021	1.32	WT-Avg	1.95E-03	1.28E-02
sp|P70333|HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnph2 PE=1 SV=1	21355.33333	27232	0.3392623	1.27	D5-Avg	1.96E-03	1.28E-02
sp|Q3TC93|H1BP3_MOUSE	HCLS1-binding protein 3 OS=Mus musculus GN=Hs1bp3 PE=1 SV=2	4890	6948.666667	0.4976214	1.41	D5-Avg	2.12E-03	1.37E-02
sp|Q99LM3|SMTL1_MOUSE	Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1	102630	69782.33333	-0.563155	1.48	WT-Avg	2.20E-03	1.40E-02
sp|Q99PU8|DHX30_MOUSE	Putative ATP-dependent RNA helicase DHX30 OS=Mus musculus GN=Dhx30 PE=1 SV=1	5218.333333	7142.666667	0.4378663	1.35	D5-Avg	2.20E-03	1.40E-02
sp|Q62422|OSTF1_MOUSE	Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2	56473	72463.66667	0.3472319	1.27	D5-Avg	2.29E-03	1.45E-02
sp|Q99LN9|DOHH_MOUSE	Deoxyhypusine hydroxylase OS=Mus musculus GN=Dohh PE=1 SV=2	11733	15140.33333	0.3559332	1.28	D5-Avg	2.34E-03	1.47E-02
sp|P47964|RL36_MOUSE	60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=3 SV=2	159853.3333	124863.3333	-0.368805	1.29	WT-Avg	2.43E-03	1.53E-02
sp|Q5SVR0|TBC9B_MOUSE	TBC1 domain family member 9B OS=Mus musculus GN=Tbc1d9b PE=1 SV=1	24474.33333	31638.33333	0.3615825	1.28	D5-Avg	2.80E-03	1.72E-02
sp|Q9D1C8|VPS28_MOUSE	Vacuolar protein sorting-associated protein 28 homolog OS=Mus musculus GN=Vps28 PE=1 SV=1	26871.33333	34090.33333	0.3294801	1.26	D5-Avg	2.83E-03	1.74E-02
sp|O55226|CHAD_MOUSE	Chondroadherin OS=Mus musculus GN=Chad PE=2 SV=1	20165	14980.33333	-0.443695	1.36	WT-Avg	2.84E-03	1.74E-02
sp|O88531|PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=1 SV=2	30496.66667	38516.66667	0.3239923	1.25	D5-Avg	2.90E-03	1.76E-02
sp|Q8R0H9|GGA1_MOUSE	ADP-ribosylation factor-binding protein GGA1 OS=Mus musculus GN=Gga1 PE=1 SV=1	18620.33333	23638.66667	0.3312486	1.26	D5-Avg	2.91E-03	1.77E-02
sp|P26645|MARCS_MOUSE	Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	97385.66667	73947	-0.411904	1.33	WT-Avg	2.93E-03	1.78E-02
sp|Q9WVJ3|CBPQ_MOUSE	Carboxypeptidase Q OS=Mus musculus GN=Cpq PE=1 SV=1	15726	20212.33333	0.3511354	1.28	D5-Avg	2.95E-03	1.78E-02
tr|B1ART2|B1ART2_MOUSE	Vacuolar protein sorting 13D OS=Mus musculus GN=Vps13d PE=1 SV=2	9697.666667	12459.33333	0.3497323	1.27	D5-Avg	3.15E-03	1.89E-02
sp|P97449|AMPN_MOUSE	Aminopeptidase N OS=Mus musculus GN=Anpep PE=1 SV=4	84316	63458.33333	-0.42225	1.34	WT-Avg	3.16E-03	1.90E-02
sp|Q3UVK0|ERMP1_MOUSE	Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus GN=Ermp1 PE=1 SV=2	21204.33333	27493	0.3611848	1.28	D5-Avg	3.18E-03	1.90E-02
sp|Q9DC29|ABCB6_MOUSE	ATP-binding cassette sub-family B member 6, mitochondrial OS=Mus musculus GN=Abcb6 PE=1 SV=1	19977	16129.33333	-0.320254	1.25	WT-Avg	3.27E-03	1.95E-02
sp|Q6P5H2|NEST_MOUSE	Nestin OS=Mus musculus GN=Nes PE=1 SV=1	29525.33333	21249.66667	-0.484513	1.40	WT-Avg	3.40E-03	2.01E-02
sp|Q9WTK7|STK11_MOUSE	Serine/threonine-protein kinase STK11 OS=Mus musculus GN=Stk11 PE=1 SV=1	4144.333333	6097.666667	0.5425624	1.46	D5-Avg	3.58E-03	2.10E-02
sp|Q91YN9|BAG2_MOUSE	BAG family molecular chaperone regulator 2 OS=Mus musculus GN=Bag2 PE=1 SV=1	54520	69200	0.3298261	1.26	D5-Avg	3.66E-03	2.13E-02
sp|P70336|ROCK2_MOUSE	Rho-associated protein kinase 2 OS=Mus musculus GN=Rock2 PE=1 SV=1	13207	16729.66667	0.3277271	1.26	D5-Avg	4.19E-03	2.38E-02
sp|Q3UPH1|PRRC1_MOUSE	Protein PRRC1 OS=Mus musculus GN=Prrc1 PE=1 SV=1	25523.33333	20594.33333	-0.319409	1.25	WT-Avg	4.58E-03	2.54E-02
sp|O55143|AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	109482.3333	153081	0.4748467	1.39	D5-Avg	4.71E-03	2.60E-02
sp|P08121|CO3A1_MOUSE	Collagen alpha-1(III) chain OS=Mus musculus GN=Col3a1 PE=1 SV=4	115917.6667	170279	0.5385906	1.45	D5-Avg	4.72E-03	2.60E-02
sp|P60840|ENSA_MOUSE	Alpha-endosulfine OS=Mus musculus GN=Ensa PE=1 SV=1	46306.66667	58680	0.3257226	1.25	D5-Avg	4.85E-03	2.65E-02
sp|Q9JJA4|WDR12_MOUSE	Ribosome biogenesis protein WDR12 OS=Mus musculus GN=Wdr12 PE=1 SV=1	11469.66667	14420	0.3179024	1.25	D5-Avg	4.93E-03	2.68E-02
sp|Q9Z2L6|MINP1_MOUSE	Multiple inositol polyphosphate phosphatase 1 OS=Mus musculus GN=Minpp1 PE=1 SV=3	22416	28579.33333	0.339156	1.27	D5-Avg	4.94E-03	2.69E-02
sp|P21107|TPM3_MOUSE	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=3	59144.33333	92864.66667	0.6411332	1.56	D5-Avg	5.05E-03	2.73E-02
sp|Q9Z1T2|TSP4_MOUSE	Thrombospondin-4 OS=Mus musculus GN=Thbs4 PE=1 SV=1	1041015.667	836996	-0.324218	1.25	WT-Avg	5.59E-03	2.97E-02
sp|O70373|XIRP1_MOUSE	Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2	660671.6667	432500.3333	-0.618743	1.54	WT-Avg	5.99E-03	3.13E-02
sp|A6H584|CO6A5_MOUSE	Collagen alpha-5(VI) chain OS=Mus musculus GN=Col6a5 PE=1 SV=4	13140.33333	63708.33333	2.272001	4.83	D5-Avg	6.10E-03	3.17E-02
sp|Q01063|PDE4D_MOUSE	cAMP-specific 3',5'-cyclic phosphodiesterase 4D OS=Mus musculus GN=Pde4d PE=1 SV=2	13520.66667	10624.66667	-0.359871	1.28	WT-Avg	6.41E-03	3.32E-02
sp|Q8VBZ3|CLPT1_MOUSE	Cleft lip and palate transmembrane protein 1 homolog OS=Mus musculus GN=Clptm1 PE=1 SV=1	62976.66667	82476	0.3748568	1.30	D5-Avg	6.42E-03	3.32E-02
sp|Q80UJ7|RB3GP_MOUSE	Rab3 GTPase-activating protein catalytic subunit OS=Mus musculus GN=Rab3gap1 PE=1 SV=4	9459.333333	12230.66667	0.360488	1.28	D5-Avg	6.57E-03	3.39E-02
sp|P11930|NUD19_MOUSE	Nucleoside diphosphate-linked moiety X motif 19 OS=Mus musculus GN=Nudt19 PE=1 SV=2	13617.66667	18043	0.3981424	1.32	D5-Avg	6.77E-03	3.48E-02
sp|Q80UY1|CARME_MOUSE	Carnosine N-methyltransferase OS=Mus musculus GN=Carnmt1 PE=1 SV=1	694334.3333	546161	-0.360038	1.28	WT-Avg	6.87E-03	3.52E-02
sp|Q8VCR8|MYLK2_MOUSE	Myosin light chain kinase 2, skeletal/cardiac muscle OS=Mus musculus GN=Mylk2 PE=1 SV=2	6195590.333	4419238	-0.505256	1.42	WT-Avg	6.96E-03	3.55E-02
sp|Q91Z31|PTBP2_MOUSE	Polypyrimidine tract-binding protein 2 OS=Mus musculus GN=Ptbp2 PE=1 SV=2	10078.66667	12694.33333	0.3220616	1.25	D5-Avg	7.65E-03	3.80E-02
sp|Q7TN98|CPEB4_MOUSE	Cytoplasmic polyadenylation element-binding protein 4 OS=Mus musculus GN=Cpeb4 PE=1 SV=1	16985	13628	-0.328733	1.26	WT-Avg	7.99E-03	3.95E-02
sp|A2AUC9|KLH41_MOUSE	Kelch-like protein 41 OS=Mus musculus GN=Klhl41 PE=1 SV=1	4959219.333	3890353	-0.361406	1.28	WT-Avg	8.25E-03	4.03E-02
sp|Q9CR41|HYPK_MOUSE	Huntingtin-interacting protein K OS=Mus musculus GN=Hypk PE=1 SV=2	60435	77048.66667	0.3393027	1.27	D5-Avg	8.29E-03	4.04E-02
sp|Q9D0B6|PBDC1_MOUSE	Protein PBDC1 OS=Mus musculus GN=Pbdc1 PE=1 SV=1	14700	18606.66667	0.3271743	1.25	D5-Avg	1.01E-02	4.76E-02
sp|Q9QZZ6|DERM_MOUSE	Dermatopontin OS=Mus musculus GN=Dpt PE=1 SV=1	134853	183585.6667	0.4295064	1.35	D5-Avg	1.16E-02	5.33E-02
sp|P40936|INMT_MOUSE	Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1	120796.6667	155976.6667	0.3532688	1.28	D5-Avg	1.28E-02	5.83E-02
sp|Q9Z2D0|MTMR9_MOUSE	Myotubularin-related protein 9 OS=Mus musculus GN=Mtmr9 PE=1 SV=2	12452.66667	22904.66667	0.8618082	1.82	D5-Avg	1.42E-02	6.33E-02
sp|P62897|CYC_MOUSE	Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2	5462693	4356900.333	-0.336359	1.26	WT-Avg	1.49E-02	6.56E-02
sp|Q8BYM8|SYCM_MOUSE	Probable cysteine--tRNA ligase, mitochondrial OS=Mus musculus GN=Cars2 PE=1 SV=2	10860.66667	13792.33333	0.3322948	1.26	D5-Avg	1.50E-02	6.57E-02
sp|Q5U3K5|RABL6_MOUSE	Rab-like protein 6 OS=Mus musculus GN=Rabl6 PE=1 SV=2	10589.66667	13775	0.3700837	1.29	D5-Avg	1.57E-02	6.86E-02
sp|Q9D1G5|LRC57_MOUSE	Leucine-rich repeat-containing protein 57 OS=Mus musculus GN=Lrrc57 PE=1 SV=1	32676.66667	56076	0.7619983	1.70	D5-Avg	2.01E-02	8.30E-02
tr|E9Q7P1|E9Q7P1_MOUSE	Collagen, type XXII, alpha 1 OS=Mus musculus GN=Col22a1 PE=1 SV=1	17814.33333	22516.33333	0.3221452	1.25	D5-Avg	2.36E-02	9.33E-02
sp|A6H8H2|DEN4C_MOUSE	DENN domain-containing protein 4C OS=Mus musculus GN=Dennd4c PE=1 SV=1	11289.66667	14648	0.3642585	1.29	D5-Avg	2.44E-02	9.60E-02
sp|P70290|EM55_MOUSE	55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1	45213	56825	0.3184825	1.25	D5-Avg	2.45E-02	9.60E-02

Accession	Description	WT-Avg	D3-Avg	logFC	fold change	up in	PValue	FDR
sp|Q7TPW1|NEXN_MOUSE	Nexilin OS=Mus musculus GN=Nexn PE=1 SV=3	205358.6667	104132	-9.58E-01	1.94	WT-Avg	4.25E-24	1.17E-20
sp|Q8BUZ1|ABRA_MOUSE	Actin-binding Rho-activating protein OS=Mus musculus GN=Abra PE=1 SV=1	218693	407583.3333	9.24E-01	1.90	D5-Avg	8.36E-22	1.15E-18
sp|P62932|FBX40_MOUSE	F-box only protein 40 OS=Mus musculus GN=Fbxo40 PE=1 SV=1	114422.6667	67450.33333	-7.39E-01	1.67	WT-Avg	8.66E-21	7.93E-18
sp|Q60949|TBCD1_MOUSE	TBC1 domain family member 1 OS=Mus musculus GN=Tbc1d1 PE=1 SV=3	343528	206361.3333	-7.15E-01	1.64	WT-Avg	1.09E-19	7.50E-17
sp|Q6ZPU9|KBP_MOUSE	KIF1-binding protein OS=Mus musculus GN=Kif1bp PE=1 SV=2	31380	52283.33333	7.60E-01	1.69	D5-Avg	3.37E-17	1.85E-14
sp|Q9JJG0|TACC2_MOUSE	Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2	57067.33333	32917.33333	-7.75E-01	1.71	WT-Avg	4.12E-17	1.89E-14
sp|P15105|GLNA_MOUSE	Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	220566.3333	130040	-7.38E-01	1.67	WT-Avg	6.21E-14	2.43E-11
sp|E9QA62|LMOD3_MOUSE	Leiomodin-3 OS=Mus musculus GN=Lmod3 PE=1 SV=1	75453.33333	45463.33333	-7.07E-01	1.63	WT-Avg	6.13E-12	2.10E-09
sp|Q99JI1|MSTN1_MOUSE	Musculoskeletal embryonic nuclear protein 1 OS=Mus musculus GN=Mustn1 PE=1 SV=1	276840	98241.66667	-1.46E+00	2.75	WT-Avg	3.69E-11	1.13E-08
sp|Q9CXW3|CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	131456.6667	187476.6667	5.33E-01	1.45	D5-Avg	2.63E-10	7.21E-08
sp|P35385|HSPB7_MOUSE	Heat shock protein beta-7 OS=Mus musculus GN=Hspb7 PE=1 SV=3	1141940	610485	-8.77E-01	1.84	WT-Avg	1.17E-09	2.92E-07
sp|Q7M729|SCN4B_MOUSE	Sodium channel subunit beta-4 OS=Mus musculus GN=Scn4b PE=1 SV=1	372933.3333	247156.6667	-5.74E-01	1.49	WT-Avg	1.81E-09	4.14E-07
sp|Q9JKB3|YBOX3_MOUSE	Y-box-binding protein 3 OS=Mus musculus GN=Ybx3 PE=1 SV=2	298423.3333	188363.3333	-6.45E-01	1.56	WT-Avg	2.11E-09	4.45E-07
sp|Q8VE91|RETR1_MOUSE	Reticulophagy regulator 1 OS=Mus musculus GN=Retreg1d PE=1 SV=2	41030.66667	27225.66667	-5.68E-01	1.48	WT-Avg	2.66E-09	4.87E-07
sp|O70209|PDLI3_MOUSE	PDZ and LIM domain protein 3 OS=Mus musculus GN=Pdlim3 PE=1 SV=1	2427618	1691527.333	-4.97E-01	1.41	WT-Avg	2.62E-09	4.87E-07
sp|P0C5K1|SBK2_MOUSE	Serine/threonine-protein kinase SBK2 OS=Mus musculus GN=Sbk2 PE=3 SV=2	378886.6667	266720	-4.82E-01	1.40	WT-Avg	3.26E-09	5.59E-07
sp|Q9D783|KLH40_MOUSE	Kelch-like protein 40 OS=Mus musculus GN=Klhl40 PE=1 SV=1	1092173.333	681602.3333	-6.55E-01	1.57	WT-Avg	4.95E-09	7.99E-07
sp|Q80XB4|NRAP_MOUSE	Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=3	1569441.333	846637	-8.66E-01	1.82	WT-Avg	1.35E-08	2.06E-06
sp|P50462|CSRP3_MOUSE	Cysteine and glycine-rich protein 3 OS=Mus musculus GN=Csrp3 PE=1 SV=1	429137	218917.3333	-9.44E-01	1.92	WT-Avg	2.01E-08	2.91E-06
sp|Q8BWA5|KLH31_MOUSE	Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=1	147511.6667	98411.66667	-5.65E-01	1.48	WT-Avg	2.14E-08	2.94E-06
sp|Q921U8|SMTN_MOUSE	Smoothelin OS=Mus musculus GN=Smtn PE=1 SV=2	161383.6667	116170.3333	-4.53E-01	1.37	WT-Avg	2.28E-08	2.97E-06
sp|O89114|DNJB5_MOUSE	DnaJ homolog subfamily B member 5 OS=Mus musculus GN=Dnajb5 PE=2 SV=1	146768	104603.3333	-4.67E-01	1.38	WT-Avg	3.03E-08	3.78E-06
sp|Q9JMH9|MY18A_MOUSE	Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2	254435.3333	185050.6667	-4.36E-01	1.35	WT-Avg	8.23E-08	9.41E-06
sp|Q8VBT1|TXLNB_MOUSE	Beta-taxilin OS=Mus musculus GN=Txlnb PE=1 SV=2	142490	105773.6667	-4.08E-01	1.33	WT-Avg	1.00E-07	1.10E-05
tr|A2A9K7|A2A9K7_MOUSE	Connector enhancer of kinase suppressor of Ras 1 OS=Mus musculus GN=Cnksr1 PE=1 SV=1	54150	39248.66667	-4.43E-01	1.36	WT-Avg	1.30E-07	1.37E-05
sp|Q99LM3|SMTL1_MOUSE	Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1	102630	57846.66667	-7.99E-01	1.74	WT-Avg	2.28E-07	2.24E-05
sp|P42232|STA5B_MOUSE	Signal transducer and activator of transcription 5B OS=Mus musculus GN=Stat5b PE=1 SV=1	134346.6667	97503.66667	-4.40E-01	1.36	WT-Avg	2.28E-07	2.24E-05
sp|Q8R1Q3|ANGL7_MOUSE	Angiopoietin-related protein 7 OS=Mus musculus GN=Angptl7 PE=2 SV=1	18160.33333	11799	-6.01E-01	1.52	WT-Avg	2.74E-07	2.59E-05
tr|Q3ULW8|Q3ULW8_MOUSE	Poly [ADP-ribose] polymerase OS=Mus musculus GN=Parp3 PE=1 SV=1	55105	40185.33333	-4.33E-01	1.35	WT-Avg	3.51E-07	3.21E-05
sp|Q8C5Q4|GRSF1_MOUSE	G-rich sequence factor 1 OS=Mus musculus GN=Grsf1 PE=1 SV=2	34027.66667	46542	4.76E-01	1.39	D5-Avg	4.73E-07	4.19E-05
sp|Q8C0L9|GPCP1_MOUSE	Glycerophosphocholine phosphodiesterase GPCPD1 OS=Mus musculus GN=Gpcpd1 PE=1 SV=1	167436	124624	-4.06E-01	1.33	WT-Avg	5.53E-07	4.75E-05
sp|P47856|GFPT1_MOUSE	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 PE=1	6058.666667	11255.66667	9.16E-01	1.89	D5-Avg	7.52E-07	6.26E-05
sp|Q9Z0P5|TWF2_MOUSE	Twinfilin-2 OS=Mus musculus GN=Twf2 PE=1 SV=1	231577	178344.6667	-3.56E-01	1.28	WT-Avg	8.55E-07	6.90E-05
sp|Q91Z38|TTC1_MOUSE	Tetratricopeptide repeat protein 1 OS=Mus musculus GN=Ttc1 PE=1 SV=1	12365.66667	17361.33333	5.12E-01	1.43	D5-Avg	9.41E-07	7.38E-05

sp|P51150|RAB7A_MOUSE	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	645346	491568.6667	-3.72E-01	1.29	WT-Avg	1.02E-06	7.78E-05
sp|P97447|FHL1_MOUSE	Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=3	21126859	13744655	-5.95E-01	1.51	WT-Avg	1.88E-06	1.40E-04
sp|Q61702|ITIH1_MOUSE	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Mus musculus GN=Itih1 PE=1 SV=2	151372.6667	113215.3333	-3.96E-01	1.32	WT-Avg	2.20E-06	1.59E-04
sp|Q9D1K2|VATF_MOUSE	V-type proton ATPase subunit F OS=Mus musculus GN=Atp6v1f PE=1 SV=2	42824.66667	57326.66667	4.46E-01	1.36	D5-Avg	2.55E-06	1.79E-04
sp|Q9WV06|ANKR2_MOUSE	Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=1 SV=3	1356584.667	734699.3333	-8.56E-01	1.81	WT-Avg	2.81E-06	1.93E-04
sp|Q8BK84|DUPD1_MOUSE	Dual specificity phosphatase DUPD1 OS=Mus musculus GN=Dupd1 PE=2 SV=1	69460	98900	5.33E-01	1.45	D5-Avg	2.99E-06	2.00E-04
tr|E9PYF4|E9PYF4_MOUSE	LIM domain only 7 OS=Mus musculus GN=Lmo7 PE=1 SV=1	59878	45316	-3.79E-01	1.30	WT-Avg	5.47E-06	3.57E-04
tr|E0CYV9|E0CYV9_MOUSE	RIKEN cDNA 1110002E22 gene OS=Mus musculus GN=1110002E22Rik PE=1 SV=1	20162.33333	13487.66667	-5.62E-01	1.48	WT-Avg	7.11E-06	4.54E-04
sp|Q8CI12|SMTL2_MOUSE	Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1	563046.6667	399249	-4.74E-01	1.39	WT-Avg	7.50E-06	4.68E-04
sp|P14602|HSPB1_MOUSE	Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	2869981	1856156	-6.02E-01	1.52	WT-Avg	1.10E-05	6.54E-04
sp|Q8BQM4|HEAT3_MOUSE	HEAT repeat-containing protein 3 OS=Mus musculus GN=Heatr3 PE=1 SV=1	6812.666667	10036.66667	5.84E-01	1.50	D5-Avg	1.44E-05	8.43E-04
sp|Q6PEE3|RIR2B_MOUSE	Ribonucleoside-diphosphate reductase subunit M2 B OS=Mus musculus GN=Rrm2b PE=1 SV=1	11960.33333	16216.33333	4.61E-01	1.38	D5-Avg	2.82E-05	1.58E-03
sp|Q8K268|ABCF3_MOUSE	ATP-binding cassette sub-family F member 3 OS=Mus musculus GN=Abcf3 PE=1 SV=1	77729	95272	3.17E-01	1.25	D5-Avg	4.04E-05	2.18E-03
sp|A6X935|ITIH4_MOUSE	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=2	323517	211947.3333	-5.82E-01	1.50	WT-Avg	4.56E-05	2.39E-03
sp|Q9D2R6|COA3_MOUSE	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial OS=Mus musculus GN=Coa3 PE=1 SV	107444	136140	3.62E-01	1.29	D5-Avg	5.16E-05	2.63E-03
sp|Q8VDB8|LRRC2_MOUSE	Leucine-rich repeat-containing protein 2 OS=Mus musculus GN=Lrrc2 PE=2 SV=1	57700.66667	44840	-3.40E-01	1.27	WT-Avg	5.37E-05	2.68E-03
sp|A2AWA9|RBGP1_MOUSE	Rab GTPase-activating protein 1 OS=Mus musculus GN=Rabgap1 PE=1 SV=1	8179	12373.66667	6.20E-01	1.54	D5-Avg	8.14E-05	3.72E-03
sp|Q7TQH0|ATX2L_MOUSE	Ataxin-2-like protein OS=Mus musculus GN=Atxn2l PE=1 SV=1	17557	23028	4.10E-01	1.33	D5-Avg	8.98E-05	3.98E-03
sp|Q61543|GSLG1_MOUSE	Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	42726.33333	52877.66667	3.29E-01	1.26	D5-Avg	8.89E-05	3.98E-03
sp|O70373|XIRP1_MOUSE	Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2	660671.6667	355698.6667	-8.69E-01	1.83	WT-Avg	1.06E-04	4.62E-03
sp|Q3UZA1|CPZIP_MOUSE	CapZ-interacting protein OS=Mus musculus GN=Rcsd1 PE=1 SV=1	94126.66667	72826	-3.47E-01	1.27	WT-Avg	1.11E-04	4.70E-03
sp|P0CW02|LY6C1_MOUSE	Lymphocyte antigen 6C1 OS=Mus musculus GN=Ly6c1 PE=2 SV=1	128569.3333	99602.66667	-3.45E-01	1.27	WT-Avg	1.10E-04	4.70E-03
sp|Q8BG95|MYPT2_MOUSE	Protein phosphatase 1 regulatory subunit 12B OS=Mus musculus GN=Ppp1r12b PE=1 SV=2	474219.6667	335806.6667	-4.82E-01	1.40	WT-Avg	1.24E-04	5.18E-03
sp|O09012|PEX5_MOUSE	Peroxisomal targeting signal 1 receptor OS=Mus musculus GN=Pex5 PE=1 SV=2	7827.666667	11088.33333	5.21E-01	1.44	D5-Avg	1.32E-04	5.32E-03
sp|Q07456|AMBP_MOUSE	Protein AMBP OS=Mus musculus GN=Ambp PE=1 SV=2	94463.33333	72937.66667	-3.50E-01	1.27	WT-Avg	1.32E-04	5.32E-03
sp|P08207|S10AA_MOUSE	Protein S100-A10 OS=Mus musculus GN=S100a10 PE=1 SV=2	197980	154573.3333	-3.38E-01	1.26	WT-Avg	1.39E-04	5.51E-03
sp|Q6NZB0|DNJC8_MOUSE	DnaJ homolog subfamily C member 8 OS=Mus musculus GN=Dnajc8 PE=1 SV=2	75983.33333	94326.66667	3.36E-01	1.26	D5-Avg	1.50E-04	5.86E-03
sp|Q60648|SAP3_MOUSE	Ganglioside GM2 activator OS=Mus musculus GN=Gm2a PE=1 SV=2	10157.33333	13716.33333	4.52E-01	1.37	D5-Avg	1.78E-04	6.79E-03
sp|O54988|SLK_MOUSE	STE20-like serine/threonine-protein kinase OS=Mus musculus GN=Slk PE=1 SV=2	73085.66667	94291	3.88E-01	1.31	D5-Avg	2.29E-04	8.61E-03
sp|Q8BYL4|SYYM_MOUSE	Tyrosine--tRNA ligase, mitochondrial OS=Mus musculus GN=Yars2 PE=1 SV=2	31888.66667	40306.66667	3.62E-01	1.29	D5-Avg	2.33E-04	8.66E-03
sp|P01872|IGHM_MOUSE	Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2	51788.33333	37478	-4.42E-01	1.36	WT-Avg	2.46E-04	8.87E-03
sp|Q9D832|DNJB4_MOUSE	DnaJ homolog subfamily B member 4 OS=Mus musculus GN=Dnajb4 PE=1 SV=1	1010974.333	774075.3333	-3.59E-01	1.28	WT-Avg	2.59E-04	9.23E-03
sp|Q69ZN7|MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	21325.33333	16286.33333	-3.69E-01	1.29	WT-Avg	3.06E-04	1.06E-02
sp|Q9CQG1|CHAC2_MOUSE	Putative glutathione-specific gamma-glutamylcyclotransferase 2 OS=Mus musculus GN=Chac2 PE=1 SV	35087.33333	27010	-3.57E-01	1.28	WT-Avg	3.39E-04	1.16E-02
sp|P01027|CO3_MOUSE	Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	3330627	2434722	-4.29E-01	1.35	WT-Avg	4.23E-04	1.40E-02
sp|Q80XI3|IF4G3_MOUSE	Eukaryotic translation initiation factor 4 gamma 3 OS=Mus musculus GN=Eif4g3 PE=1 SV=2	41523.33333	31656.66667	-3.68E-01	1.29	WT-Avg	4.60E-04	1.47E-02
sp|Q9JHQ5|LZTL1_MOUSE	Leucine zipper transcription factor-like protein 1 OS=Mus musculus GN=Lztfl1 PE=1 SV=1	31699.66667	39229.66667	3.32E-01	1.26	D5-Avg	6.21E-04	1.85E-02
sp|P23927|CRYAB_MOUSE	Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	10846422.67	6989370	-6.06E-01	1.52	WT-Avg	6.88E-04	1.99E-02
sp|Q60973|RBBP7_MOUSE	Histone-binding protein RBBP7 OS=Mus musculus GN=Rbbp7 PE=1 SV=1	62783.33333	78843.33333	3.48E-01	1.27	D5-Avg	7.00E-04	2.00E-02
sp|Q8VCH8|UBXN4_MOUSE	UBX domain-containing protein 4 OS=Mus musculus GN=Ubxn4 PE=1 SV=1	18622	22999	3.27E-01	1.25	D5-Avg	7.38E-04	2.07E-02
sp|Q80UU9|PGRC2_MOUSE	Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2	14026.33333	17646	3.52E-01	1.28	D5-Avg	7.55E-04	2.09E-02
sp|Q8VIB3|SIA10_MOUSE	Type 2 lactosamine alpha-2,3-sialyltransferase OS=Mus musculus GN=St3gal6 PE=2 SV=3	17507.33333	12206.66667	-4.97E-01	1.41	WT-Avg	9.23E-04	2.48E-02
sp|Q9Z2D0|MTMR9_MOUSE	Myotubularin-related protein 9 OS=Mus musculus GN=Mtmr9 PE=1 SV=2	12452.66667	21051	7.74E-01	1.71	D5-Avg	9.34E-04	2.49E-02
sp|Q3TC93|H1BP3_MOUSE	HCLS1-binding protein 3 OS=Mus musculus GN=Hs1bp3 PE=1 SV=2	4890	6930.333333	5.26E-01	1.44	D5-Avg	9.86E-04	2.60E-02
sp|Q920M5|CORO6_MOUSE	Coronin-6 OS=Mus musculus GN=Coro6 PE=1 SV=1	396253.3333	312350	-3.17E-01	1.25	WT-Avg	1.07E-03	2.77E-02
sp|Q62417|SRBS1_MOUSE	Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2	99699.33333	77310	-3.45E-01	1.27	WT-Avg	1.20E-03	3.06E-02
sp|Q8VEE1|LMCD1_MOUSE	LIM and cysteine-rich domains protein 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=1	2495010.667	1808197	-4.37E-01	1.35	WT-Avg	1.25E-03	3.15E-02
sp|P61290|PSME3_MOUSE	Proteasome activator complex subunit 3 OS=Mus musculus GN=Psme3 PE=1 SV=1	56463.66667	69610.66667	3.22E-01	1.25	D5-Avg	1.28E-03	3.18E-02
sp|Q06770|CBG_MOUSE	Corticosteroid-binding globulin OS=Mus musculus GN=Serpina6 PE=1 SV=1	41094	30891.66667	-3.88E-01	1.31	WT-Avg	1.52E-03	3.65E-02
sp|P49222|EPB42_MOUSE	Erythrocyte membrane protein band 4.2 OS=Mus musculus GN=Epb42 PE=1 SV=3	64103.33333	47757	-3.99E-01	1.32	WT-Avg	2.03E-03	4.63E-02
sp|Q80Y55|BSDC1_MOUSE	BSD domain-containing protein 1 OS=Mus musculus GN=Bsdc1 PE=1 SV=1	8429.333333	10884.66667	3.94E-01	1.31	D5-Avg	2.07E-03	4.66E-02
sp|Q61646|HPT_MOUSE	Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1	112587.6667	208106.6667	9.08E-01	1.88	D5-Avg	2.32E-03	4.94E-02
sp|Q99K01|PDXD1_MOUSE	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 PE=1	5989.666667	8074	4.51E-01	1.37	D5-Avg	2.44E-03	5.12E-02
sp|Q02844|TRYB1_MOUSE	Tryptase OS=Mus musculus GN=Tpsab1 PE=2 SV=1	26716.66667	20417	-3.70E-01	1.29	WT-Avg	2.85E-03	5.76E-02
sp|Q8BLR9|HIF1N_MOUSE	Hypoxia-inducible factor 1-alpha inhibitor OS=Mus musculus GN=Hif1an PE=1 SV=2	22385.33333	28721	3.84E-01	1.30	D5-Avg	3.37E-03	6.74E-02
sp|Q80X19|COEA1_MOUSE	Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1 PE=1 SV=2	103958.6667	80917.66667	-3.44E-01	1.27	WT-Avg	3.46E-03	6.88E-02
sp|A2ABU4|MYOM3_MOUSE	Myomesin-3 OS=Mus musculus GN=Myom3 PE=1 SV=1	2925400	2160929.333	-4.16E-01	1.33	WT-Avg	3.80E-03	7.40E-02
sp|Q8BFQ4|WDR82_MOUSE	WD repeat-containing protein 82 OS=Mus musculus GN=Wdr82 PE=1 SV=1	9145	11660	3.76E-01	1.30	D5-Avg	3.79E-03	7.40E-02
sp|Q8R2G4|NAR3_MOUSE	Ecto-ADP-ribosyltransferase 3 OS=Mus musculus GN=Art3 PE=1 SV=2	471362.6667	360970.3333	-3.57E-01	1.28	WT-Avg	4.16E-03	7.74E-02
sp|Q61586|GPAT1_MOUSE	Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Mus musculus GN=Gpam PE=1 SV=2	19696.33333	15551.33333	-3.18E-01	1.25	WT-Avg	4.45E-03	8.11E-02
sp|Q9EPJ9|ARFG1_MOUSE	ADP-ribosylation factor GTPase-activating protein 1 OS=Mus musculus GN=Arfgap1 PE=1 SV=2	26870.33333	33648	3.42E-01	1.27	D5-Avg	5.78E-03	9.79E-02