

## **Supplementary Methods**

### **Immunohistochemistry:**

Standard histological approaches described previously were used.<sup>1</sup> The proteins EMILIN1, CILP1, LTBP3, and FBLN5 were evaluated by immunohistochemistry using routine heat induced epitope retrieval (HIER) with 10 mM sodium citrate, pH 6.0, 0.05% Tween 20 followed by overnight incubation. EMILIN1 (Protein Tech) was incubated at a 1:50 ratio, CILP1 (Novus Biologicals) at a 1:25 ratio, LTBP3 (Santa Cruz at a 1:25 ratio, and Fbln5 (abcam) at a 1:500 ratio. Secondary antibodies were applied in ratios of 1:300 Fluor-conjugated secondary antibodies were purchased from Jackson ImmunoResearch (West Grove, PA). Imaging was performed on the Leica TCS SP5 AOBS Confocal Microscope System (Leica Microsystems Inc., Exton, PA).

### **Staining:**

Hearts were isolated and processed as described previously.<sup>2</sup> Movat's Pentachrome stain (Polyscientific R&D) was used to assess ECM organization as previously described.<sup>3</sup>

**Proteomic Analysis:** Aortic valve cusps were dissected as previously described,<sup>4</sup> with attention to eliminating cellular contamination from the aortic wall. Quantification using bicinchoninic acid assay showed an average of  $111 \pm 14$   $\mu\text{g}$  protein from 10 sets of AV (3 cusps per set). A total of 60  $\mu\text{g}$  of protein extracted from microdissected AV was loaded onto a 12% Bis-Tris minigel (Invitrogen, Carlsbad, CA). Electrophoresis was performed for 15 minutes at 150 volts using MOPS-SDS running buffer, until the 250 kDa protein molecular weight marker was observed at approximately 0.4 cm below the well. Gels were washed in ice-cold water for 10 minutes and briefly stained (SimplyBlue SafeStain,

Invitrogen, Grand Island NY) to visualize the protein bands. Each lane (length ~1.8 cm) was minced into 1 mm cubes. Gel cubes were treated by in-gel digestion, followed by peptide extraction using established protocols.<sup>5 6</sup>

Peptides were analyzed in triplicate via Multidimensional Protein Information Technology (MudPIT). Peptides were pressure cell loaded onto a biphasic pre-column fritted using an Upchurch M-520 filter union. The 150- $\mu\text{m}$  fused silica microcapillary column was packed with 4 cm of 5- $\mu\text{m}$  C18 reverse-phase resin (Jupiter, Phenomenex) followed by 4 cm of strong cation-exchange resin (Luna SCX, Phenomenex). Once loaded, it was placed in-line with a 100  $\mu\text{m}$   $\times$  20 cm, C18 packed emitter tip column (Jupiter C18, 3  $\mu\text{m}$ , 300  $\text{\AA}$ , Phenomenex) an Eksigent NanoLC-1D plus HPLC pump. Multidimensional separation was accomplished using 5  $\mu\text{l}$  pulses of ammonium acetate in 0.1% formic acid (25, 50, 75, 100, 150, 200, 250, 300, 500, 750, 1000 mM) each followed by a 115 min reversed phase gradient from water 0.1% formic acid to 40% ACN 0.1% formic acid. Peptides eluted directly from the analytical column into the LTQ ion trap (Thermo Scientific, Inc., San Jose, CA). Each full MS scan ( $m/z$  range 350 – 1800) was followed by nine MS/MS events on the most abundant peaks. Dynamic exclusion was enabled with an exclusion list size of 150 and a duration of 60 s.

**Proteomic processing and data analysis.** MS/MS data were searched using both Sequest and Mascot against a concatenated Uniprot mouse database (downloaded 08/2013) with a fixed modification of carbamidomethylation, due to chemical reduction of the cysteine bonds required for tryptic access, and variable modifications of deamidation (N, Q) and oxidation (M), common chemical modifications that may occur during gel running and peptide extraction and are indistinguishable from biological

occurrence.<sup>6,7</sup> Peptides were clustered using ProteoIQ (version 2.5.0.1) at a protein level false discovery rate of  $\leq 1\%$ , a peptide probability of 0.95, and unique peptide count per protein in at least one group  $\geq 2$ . Significantly altered proteins were determined based on evaluation of comparative populations using 1) total spectral counts in one or more groups greater than 5; 2) t-test with  $p$ -value cutoffs of  $\leq 0.05$ ; 3) ratios of  $\geq 2$ -fold between one or more groups. These species were included in analysis of regulated networks.

**Bioinformatic analysis.** Pathways were calculated using WebGestalt enriching against KEGG and Wikipathways using a threshold of two fold enrichment,  $p$ -value  $\leq 1.0E-3$  as a cutoff point.<sup>8</sup> Reference set was the mouse genome using the hypergeometric statistical method and allowing for multiple testing using the Bonferroni-Hochberg correction.<sup>9</sup> Expression levels with gene symbols were input into Ingenuity Pathways Analysis (IPA, QIAGEN Redwood City, [www.qiagen.com/ingenuity](http://www.qiagen.com/ingenuity)) v24390178 build 346717 to evaluate enrichment of biological functions and processes. A Comparison Analysis was used to calculate functions for each total proteome, filtered using a negative log  $p$ -value cutoff  $\leq 3$  as a threshold. ToppCluster was used to calculate functions and processes of subsets with hypergeometric testing and allowing for Bonferroni adjustment of  $p$ -value.<sup>10</sup> Data were visualized using IPA or the TM4 Microarray Software Suite.<sup>11</sup>

**Target Networks.** The target network for EMILIN1-TGFB1 interaction was built in Ingenuity. ECM proteins that had a significant alteration in any proteomic group comparison were used. Molecules were added manually to Ingenuity and the Build function “Connect” was used to connect interactions between proteins using settings of

all species, all diseases, all biofluids, and discluding any chemical or microRNA interactions (under Nodes). MicroRNA interactions were discluded under data sources. An additional search was done using STRING<sup>12</sup> for each protein, using mouse as the species, with up to 20 interactions, and using confidence levels of 0.8 to allow predicted interactions based on gene neighborhood, gene fusion, and gene co-occurrence and well as using text mining, co-expression studies and protein homology to find relationships between molecules from curated databases.

## References

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The [Figure\\_6\\_ECM\\_Proteomics\\_Summarized](#) summarizes quantitative aspects and trends in ECM proteins involved in the EMILIN1-TGFB1 network.

The [Table\\_MASTER\\_PROTEOMICS\\_QUALITATIVE](#) reports descriptive proteomic data such as protein length, isoelectric point, sequence coverage for each proteome and each replicate, probabilities associated with each protein group number of peptides overall (referred to as "Peptides", Total number of non-redundant peptides matched, counting multiple matches to peptides with the same primary sequence (despite different charge states or modifications) as "Nonredundant". Protein group probabilities and protein probabilities are reported for each replicate, along with number of peptides.

The [Table\\_MASTER\\_PROTEOMICS\\_QUANTITATIVE](#) reports total spectral counts per proteome, spectral counts per replicate, fold change ratios. Results of t-test less than the cutoff p-value of 0.05 are highlighted in pink.

**Supplement Table 1A. Functions. Full details are available as excel files of each function from authors.**

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*Functions represented in Figure 3A, calculated as described in text.*

*ns= not significant, <-log p-value 3.0*

*Functions are represented by negative Log p-value*

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Diseases and Bio Functions

	<b>AdWT</b>	<b>AgWT</b>	<b>AdEM</b>	<b>AgEM</b>
fibrogenesis	ns	22.76	26.89	25.77
angiogenesis	21.24	25.54	25.45	23.26
binding of cells	19.16	22.81	22.59	21.26
cell movement of phagocytes	11.59	12.94	12.02	14.31
quantity of carbohydrate	9.69	11.57	14.01	14.11
formation of myofibrils	10.01	9.96	11.26	12.30
quantity of focal adhesions	10.15	12.97	12.90	11.95
adhesion of endothelial cells	8.19	8.61	10.49	10.70
metabolism of carbohydrate	8.70	9.40	11.71	10.56
inflammatory response	8.01	10.16	9.87	10.34
adhesion of immune cells	ns	ns	8.84	10.33
cell movement of neutrophils	ns	ns	8.78	9.87
quantity of connective tissue	ns	ns	9.61	9.17
morphology of cardiovascular tissue	ns	ns	ns	8.32

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**Supplement Table 1B. Pathways. Full details are available as excel files from authors.**


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*Pathways calculation represented in Figure 3B . Pathways were calculated as described in text.*

*Pathways were selected from total output based on relevance to heart valve biology*

*KEGG and Wikipathways are reported for each proteome.*

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Pathways are represented by negative Log p-value

Pathways	WtY	WtA	EmY	EmA
KEGG Focal Adhesion	65.20	66.60	63.50	62.88
KEGG ECM-receptor Interaction	43.20	38.87	40.79	38.29
Wiki EGFR1 Signaling	14.79	16.73	22.54	22.54
KEGG PPAR Signaling	16.03	17.93	18.86	20.23
KEGG Insulin Signaling	12.80	11.14	15.73	15.96
KEGG Calcium Signaling	12.94	14.68	13.15	13.40
KEGG MAPK Signaling	6.20	6.33	8.61	8.61
KEGG TGF Beta Signaling	7.87	7.53	6.81	7.71
KEGG Wnt Signaling	10.76	7.84	8.91	7.70
KEGG N-Glycan Biosynthesis	6.63	6.99	8.32	7.44
Wiki Inflammatory Response	6.96	7.28	6.80	5.84
KEGG Apoptosis	0.00	4.00	4.60	4.03
KEGG VEGF Signaling	3.39	5.02	0.00	4.00
KEGG mTOR Signaling	0.00	0.00	0.00	3.10





























Source	Sequence ID	Gene	Accession #	Protein	Accession #	AA1	AA2	AA3	AA4	AA5	AA6	AA7	AA8	AA9	AA10	AA11	AA12	AA13	AA14	AA15	AA16	AA17	AA18	AA19	AA20	AA21	AA22	AA23	AA24	AA25	AA26	AA27	AA28	AA29	AA30	AA31	AA32	AA33	AA34	AA35	AA36	AA37	AA38	AA39	AA40	AA41	AA42	AA43	AA44	AA45	AA46	AA47	AA48	AA49	AA50	AA51	AA52	AA53	AA54	AA55	AA56	AA57	AA58	AA59	AA60	AA61	AA62	AA63	AA64	AA65	AA66	AA67	AA68	AA69	AA70	AA71	AA72	AA73	AA74	AA75	AA76	AA77	AA78	AA79	AA80	AA81	AA82	AA83	AA84	AA85	AA86	AA87	AA88	AA89	AA90	AA91	AA92	AA93	AA94	AA95	AA96	AA97	AA98	AA99	AA100
Source	Sequence ID	Gene	Accession #	Protein	Accession #	AA1	AA2	AA3	AA4	AA5	AA6	AA7	AA8	AA9	AA10	AA11	AA12	AA13	AA14	AA15	AA16	AA17	AA18	AA19	AA20	AA21	AA22	AA23	AA24	AA25	AA26	AA27	AA28	AA29	AA30	AA31	AA32	AA33	AA34	AA35	AA36	AA37	AA38	AA39	AA40	AA41	AA42	AA43	AA44	AA45	AA46	AA47	AA48	AA49	AA50	AA51	AA52	AA53	AA54	AA55	AA56	AA57	AA58	AA59	AA60	AA61	AA62	AA63	AA64	AA65	AA66	AA67	AA68	AA69	AA70	AA71	AA72	AA73	AA74	AA75	AA76	AA77	AA78	AA79	AA80	AA81	AA82	AA83	AA84	AA85	AA86	AA87	AA88	AA89	AA90	AA91	AA92	AA93	AA94	AA95	AA96	AA97	AA98	AA99	AA100
Source	Sequence ID	Gene	Accession #	Protein	Accession #	AA1	AA2	AA3	AA4	AA5	AA6	AA7	AA8	AA9	AA10	AA11	AA12	AA13	AA14	AA15	AA16	AA17	AA18	AA19	AA20	AA21	AA22	AA23	AA24	AA25	AA26	AA27	AA28	AA29	AA30	AA31	AA32	AA33	AA34	AA35	AA36	AA37	AA38	AA39	AA40	AA41	AA42	AA43	AA44	AA45	AA46	AA47	AA48	AA49	AA50	AA51	AA52	AA53	AA54	AA55	AA56	AA57	AA58	AA59	AA60	AA61	AA62	AA63	AA64	AA65	AA66	AA67	AA68	AA69	AA70	AA71	AA72	AA73	AA74	AA75	AA76	AA77	AA78	AA79	AA80	AA81	AA82	AA83	AA84	AA85	AA86	AA87	AA88	AA89	AA90	AA91	AA92	AA93	AA94	AA95	AA96	AA97	AA98	AA99	AA100

# MASTER PROTEOMICS QUANTITATIVE

Source	Sequence ID	Protein Name	Gene Symbol	Ratio				Log Ratio				p-value				AdEM Total Spectral Count	AgEM Total Spectral Count	AdWT Total Spectral Count	AgWT Total Spectral Count	AdEMrp1 Normalized SC	AdEMrp2 Normalized SC	AdEMrp3 Normalized SC	AgEMrp1 Normalized SC	AgEMrp2 Normalized SC	AgEMrp3 Normalized SC	AdWTrp1 Normalized SC	AdWTrp2 Normalized SC	AdWTrp3 Normalized SC	AgWTrp1 Normalized SC	AgWTrp2 Normalized SC	AgWTrp3 Normalized SC
				AdEM/AdWT	Ratio AgEM/AgWT	Ratio AgEM/AdWT	Ratio AgWT/AdWT	Log Ratio AdEM/AdWT	Log Ratio AgEM/AgWT	Log Ratio AgEM/AdWT	Log Ratio AgWT/AdWT	p-value AdEM/AdWT	p-value AgEM/AgWT	p-value AgEM/AdWT	p-value AgWT/AdWT																
TOP PROTEIN	sp Q66048 CLPL_MOUSE	Centriole-lumenal protein	Cplp	0.06	0.10	1.33	0.78	-1.26	-1.02	0.12	0.11	-0.11	0.003	0.000	0.643	0.238	0.28	0.4	54	42	0	1	17	23	14	16	12	14	14		
TOP PROTEIN	sp Q42011 TNSH3D_MOUSE	Tensin-3	Tns3	0.01	0.01	7.00	0.00	-0.88	-0.88	0.00	0.00	0.00	0.00	0.00	0.368	0.11	218	30	119	77	0	0	159	10	73	37	30	17	30		
TOP PROTEIN	sp Q99411 EMILIN_MOUSE	Emilin-1	Emil1	0.00	0.00	NA	0.66	NA	NA	NA	-0.18	0.00	0.000	0.000	NA	0.153	0	0	152	100	0	0	49	68	35	33	37	30			
TOP PROTEIN	sp F48036 ANKRD_MOUSE	Ankrd15	Ankrd15	1.41	0.70	1.23	2.48	0.15	0.16	0.09	0.39	0.06	0.046	0.012	0.016	0.002	79	97	36	139	27	25	27	31	31	35	47	41			
TOP PROTEIN	sp Q9D921 ANKRD_MOUSE	Ankrd14	Ankrd14	0.17	0.17	1.44	0.00	-0.11	-0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50	60	0	0	0	0	15	17	14	23	10	15			
TOP PROTEIN	sp Q77048 SRCA_MOUSE	Sarcoplasmic reticulum calcium ATPase	Sarcalum	0.47	0.93	1.59	0.80	-0.33	-0.03	0.20	0.00	0.00	0.002	0.028	0.161	0.045	87	188	185	148	30	40	49	34	54	63	50	51			
TOP PROTEIN	sp P56480 ATP_MOUSE	ATP synthase subunit alpha	Atp5a1	0.52	0.79	1.31	0.87	-0.28	-0.10	0.12	0.06	0.005	0.005	0.122	0.195	0.069	124	161	264	2063	360	468	433	685	504	34	67	688			
TOP PROTEIN	sp Q9R233 ANKRD_MOUSE	Ankrd13	Ankrd13	4.50	1.64	1.00	2.75	0.14	0.21	0.44	0.00	0.00	0.00	0.00	0.00	0.00	17	18	11	11	5	9	1	1	2	1	2	7			
TOP PROTEIN	sp Q99711 AGRI_MOUSE	Rho GTPase-activating protein 1	Arhgap1	4.25	1.25	0.59	2.00	0.63	0.10	-0.23	0.30	0.04	0.010	0.519	0.135	0.047	17	10	4	8	4	7	6	2	3	5	1	2			
TOP PROTEIN	sp Q9R442 AGRI_MOUSE	Rho GTPase-activating protein 2	Arhgap2	3.50	NA	1.00	0.60	NA	0.04	0.00	NA	0.024	0.124	1.000	0.116	0	7	2	0	0	2	2	3	0	4	3	1	0			
TOP PROTEIN	sp Q9C499 AGRI_MOUSE	Rho GTPase-activating protein 3	Arhgap3	4.12	1.64	0.80	2.00	0.65	0.30	0.22	0.05	0.010	0.182	1.000	0.116	0	1	0	0	0	2	2	2	0	4	3	1	0			
TOP PROTEIN	sp Q8U212 B2K_MOUSE	B2K protein	B2k1	3.25	1.13	0.69	2.00	0.80	0.05	-0.16	0.30	0.033	0.643	0.205	0.148	13	9	4	8	3	4	6	3	3	3	1	2	1			
TOP PROTEIN	sp Q93589 ANKRD_MOUSE	Ankrd5	Ankrd5	3.00	0.25	0.43	12.00	0.85	-0.60	-0.37	1.08	0.30	0.033	0.007	0.116	0.000	13	3	1	12	3	2	2	2	0	1	0	1	0		
TOP PROTEIN	sp F18819 BMPR_MOUSE	Bone morphogenetic protein receptor type 1A	Bmpr1a	0.18	0.18	0.29	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4	4	0	0	2	2	1	1	1	1	1	1	1		
TOP PROTEIN	sp Q9D815 ILMN2_MOUSE	Vesicular integrin-like protein 2	Ilmn2	3.40	3.00	0.53	0.60	0.53	-0.48	-0.28	0.22	0.033	0.116	0.116	0.492	17	9	5	3	4	7	6	4	1	4	1	4	2			
TOP PROTEIN	sp Q93115 SMO2_MOUSE	Small nuclear ribonucleoprotein A2	Smo2	0.40	0.40	1.00	0.90	0.40	-0.35	0.00	-0.05	0.033	0.132	1.000	0.643	0	1	0	2	0	2	3	4	1	2	3	2	3			
TOP PROTEIN	sp Q34781 SMO2_MOUSE	Small nuclear ribonucleoprotein A1	Smo1	0.17	0.17	0.83	0.83	0.17	-0.17	0.00	0.00	0.00	0.14	0.00	0.00	0.00	12	12	0	0	2	2	3	4	1	2	3	2			
TOP PROTEIN	sp Q35710 DYH1_MOUSE	Dynein heavy chain 1	Dyh1	0.38	0.71	1.88	1.00	-0.42	-0.15	0.27	0.00	0.015	0.335	0.091	1.000	8	15	21	21	3	3	3	2	7	4	4	5	8			
TOP PROTEIN	sp P51116 CADM_MOUSE	Cell adhesion molecule 1	Cadher1	0.38	0.71	1.88	1.00	-0.42	-0.15	0.27	0.00	0.015	0.335	0.091	1.000	8	15	21	21	3	3	2	7	4	4	5	8	8			
TOP PROTEIN	sp Q92417 B2K_MOUSE	B2K protein	B2k1	0.43	0.43	0.83	0.83	0.43	-0.15	0.46	0.18	0.010	0.335	0.091	1.000	31	44	49	49	6	6	6	11	18	11	18	11	12			
TOP PROTEIN	sp Q80701 MGME_MOUSE	Multiple epidermal growth factor receptor 1	Mgfr1	1.00	0.54	0.70	13.00	1.00	-0.27	-0.15	1.11	0.003	0.251	0.468	0.013	10	7	1	13	3	0	0	1	0	0	0	3	4			
TOP PROTEIN	sp Q8K461 L1TRP_MOUSE	L1-type 1 transmembrane protein	L1trp1	1.45	0.73	0.54	1.07	0.16	-0.44	-0.27	0.03	0.036	0.140	0.009	0.690	149	80	109	110	51	44	34	29	32	19	29	42	32			
TOP PROTEIN	sp Q93144 B2K_MOUSE	B2K protein	B2k1	0.87	0.88	0.92	0.92	0.22	0.20	0.30	0.12	0.006	0.140	0.009	0.690	10	5	6	6	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp E9Q031 HQQO3_MOUSE	Protein Gm2035	Gm2035	1.29	0.97	1.79	1.05	-0.11	-0.02	0.10	0.02	0.026	0.672	0.053	0.402	142	112	110	116	45	52	45	35	43	34	40	33	37			
TOP PROTEIN	sp Q99411 EMILIN_MOUSE	Emilin-1	Emil1	0.60	2.00	3.33	4.00	0.78	0.30	1.62	0.40	0.007	0.140	0.009	0.690	6	8	1	4	2	2	2	3	4	3	4	3	4			
TOP PROTEIN	sp Q94475 SRA1_MOUSE	Scavenger receptor class B type 1	Sra1	4.40	1.60	2.00	6.00	0.85	-0.40	0.30	0.12	0.031	0.251	0.468	0.013	10	7	1	13	3	0	0	1	0	0	0	1	2			
TOP PROTEIN	sp Q37277 DYH1_MOUSE	Dynein light chain 1	Dyl1	1.75	0.95	0.66	2.12	0.82	-0.02	-0.18	0.08	0.02	0.002	0.603	0.278	0.116	93	61	53	64	17	28	28	17	18	18	26	16			
TOP PROTEIN	sp Q93115 SMO2_MOUSE	Small nuclear ribonucleoprotein A2	Smo2	0.40	0.40	1.00	0.90	0.40	-0.35	0.00	-0.05	0.033	0.132	1.000	0.643	0	1	0	2	0	0	0	2	3	4	1	2	3			
TOP PROTEIN	sp Q34781 SMO2_MOUSE	Small nuclear ribonucleoprotein A1	Smo1	0.17	0.17	0.83	0.83	0.17	-0.17	0.00	0.00	0.00	0.14	0.00	0.00	0.00	12	12	0	0	2	2	3	4	1	2	3	2			
TOP PROTEIN	sp Q35710 DYH1_MOUSE	Dynein heavy chain 1	Dyh1	0.38	0.71	1.88	1.00	-0.42	-0.15	0.27	0.00	0.015	0.335	0.091	1.000	8	15	21	21	3	3	3	2	7	4	4	5	8			
TOP PROTEIN	sp P51116 CADM_MOUSE	Cell adhesion molecule 1	Cadher1	0.38	0.71	1.88	1.00	-0.42	-0.15	0.27	0.00	0.015	0.335	0.091	1.000	8	15	21	21	3	3	2	7	4	4	5	8	8			
TOP PROTEIN	sp Q92417 B2K_MOUSE	B2K protein	B2k1	0.43	0.43	0.83	0.83	0.43	-0.15	0.46	0.18	0.010	0.335	0.091	1.000	31	44	49	49	6	6	6	11	18	11	18	11	12			
TOP PROTEIN	sp Q80701 MGME_MOUSE	Multiple epidermal growth factor receptor 1	Mgfr1	1.00	0.54	0.70	13.00	1.00	-0.27	-0.15	1.11	0.003	0.251	0.468	0.013	10	7	1	13	3	0	0	1	0	0	0	0	3			
TOP PROTEIN	sp Q8K461 L1TRP_MOUSE	L1-type 1 transmembrane protein	L1trp1	1.45	0.73	0.54	1.07	0.16	-0.44	-0.27	0.03	0.036	0.140	0.009	0.690	149	80	109	110	51	44	34	29	32	19	29	42	32			
TOP PROTEIN	sp Q93144 B2K_MOUSE	B2K protein	B2k1	0.87	0.88	0.92	0.92	0.22	0.20	0.30	0.12	0.006	0.140	0.009	0.690	10	5	6	6	1	1	1	1	1	1	1	1	1			
TOP PROTEIN	sp E9Q031 HQQO3_MOUSE	Protein Gm2035	Gm2035	1.29	0.97	1.79	1.05	-0.11	-0.02	0.10	0.02	0.026	0.672	0.053	0.402	142	112	110	116	45	52	45	35	43	34	40	33	37			
TOP PROTEIN	sp Q99411 EMILIN_MOUSE	Emilin-1	Emil1	0.60	2.00	3.33	4.00	0.78	0.30	1.62	0.40	0.007	0.140	0.009	0.690	6	8	1	4	2	2	2	3	4	3	4	3	4			
TOP PROTEIN	sp Q94475 SRA1_MOUSE	Scavenger receptor class B type 1	Sra1	4.40	1.60	2.00	6.00	0.85	-0.40	0.30	0.12	0.031	0.251	0.468	0.013	10	7	1	13	3	0	0	1	0	0	0	1	2			
TOP PROTEIN	sp Q37277 DYH1_MOUSE	Dynein light chain 1	Dyl1	1.75	0.95	0.66	2.12	0.82	-0.02	-0.18	0.08	0.02	0.002	0.603	0.278	0.116	93	61	53	64	17	28	28	17	18	18	26	16			
TOP PROTEIN	sp Q93115 SMO2_MOUSE	Small nuclear ribonucleoprotein A2	Smo2	0.40	0.40	1.00	0.90	0.40	-0.35	0.00	-0.05	0.033	0.132	1.000	0.643	0	1	0	2	0	0	0	2	3	4	1	2	3			
TOP PROTEIN	sp Q34781 SMO2_MOUSE	Small nuclear ribonucleoprotein A1	Smo1	0.17	0.17	0.83	0.83	0.17	-0.17	0.00	0.00	0.00	0.14	0.00	0.00	0.00	12	12	0	0	2	2	3	4	1	2	3				
TOP PROTEIN	sp Q35710 DYH1_MOUSE	Dynein heavy chain 1	Dyh1	0.38	0.71	1.88	1.00	-0.42	-0.15	0.27	0.00	0.015	0.335	0.091	1.000	8	15	21	21	3	3	3	2	7	4	4	5	8			
TOP PROTEIN	sp P51116 CADM_MOUSE	Cell adhesion molecule 1	Cadher1	0.38	0.71	1.88	1																								

Source	Sequence ID	Ratio AEM/AGWT	Ratio AGEM/AGWT	Ratio AGEM/AGWT	Ratio AGWT/AGWT	Log Ratio AEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGWT/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	p-value AGEM/AGWT	p-value AGWT/AGWT	AgEM Total Spectral Count	AgEM Total Spectral Count	AgWT Total Spectral Count	AgWT Total Spectral Count	AgEMrpt1 Normalized SC	AgEMrpt2 Normalized SC	AgEMrpt3 Normalized SC	AgEMrpt1 Normalized SC	AgEMrpt2 Normalized SC	AgEMrpt3 Normalized SC	AgWTrpt1 Normalized SC	AgWTrpt2 Normalized SC	AgWTrpt3 Normalized SC	AgWTrpt1 Normalized SC	AgWTrpt2 Normalized SC	AgWTrpt3 Normalized SC	
TOP PROTEIN	sp Q5D100 MYO1D_MOUSE	1.24	1.97	0.97	0.61	0.10	0.29	-0.01	0.21	0.349	0.038	0.874	0.099	31	59	30	30	16	21	24	20	25	14	15	22	10	10	10	10	
TOP PROTEIN	sp P08277 HSP70_MOUSE	0.91	0.40	0.60	1.18	0.07	0.52	0.39	0.27	0.04	0.004	0.005	0.004	11	4	11	11	2	2	2	2	2	2	2	2	2	2	2	2	
TOP PROTEIN	sp A0X935 ZTNH_MOUSE	0.90	0.11	0.59	1.60	0.05	0.25	-0.26	0.20	0.643	0.042	0.116	0.184	9	5	10	16	4	3	2	2	1	2	4	3	7	3	6	6	
TOP PROTEIN	sp Q9P9V0 HRR_MOUSE	0.82	1.79	1.19	0.55	-0.09	0.25	-0.08	0.26	0.242	0.049	0.330	0.058	36	43	44	24	11	12	13	11	12	16	17	11	9	9	6	6	
TOP PROTEIN	sp P17333 NUPA_MOUSE	1.36	0.61	0.79	0.55	0.13	0.26	0.12	0.34	0.13	0.009	0.011	0.016	11	13	16	16	6	6	6	6	6	6	6	6	6	6	6	6	
TOP PROTEIN	sp P82350 SGCA_MOUSE	0.88	0.40	1.33	1.23	-0.07	0.33	0.12	0.08	0.116	0.003	0.069	0.251	6	8	14	17	0	2	4	3	3	2	4	4	6	6	5	6	
TOP PROTEIN	sp Q60724 SZT2_MOUSE	0.43	2.07	1.33	0.21	-0.06	0.45	0.12	0.38	0.696	0.003	0.399	0.002	21	28	24	10	3	7	11	9	8	11	7	9	8	3	4	3	
TOP PROTEIN	sp Q5D686 FAM73A_MOUSE	0.75	2.67	0.43	0.41	-0.12	0.45	0.12	0.44	0.12	0.017	0.017	0.017	3	8	4	1	1	2	3	2	2	3	2	3	2	3	2	3	
TOP PROTEIN	sp Q9C2V7 Q9C2V7_MOUSE	0.69	2.60	1.44	0.38	-0.11	0.41	0.16	0.41	0.275	0.023	0.329	0.005	9	13	13	5	5	2	2	2	5	3	5	4	4	2	1	2	
TOP PROTEIN	sp Q00519 HSH_MOUSE	1.39	1.00	0.95	0.67	0.12	0.28	-0.02	0.18	0.279	0.003	0.742	0.189	19	15	10	10	5	8	7	6	6	7	6	3	6	3	4	3	
TOP PROTEIN	sp Q5D163 FKBP_MOUSE	1.21	0.67	0.82	0.67	0.11	0.46	0.22	0.18	0.08	0.001	0.001	0.001	120	120	120	120	11	10	10	9	9	9	9	9	9	9	9	9	
TOP PROTEIN	sp F7CK47 F7CK47_MOUSE	0.81	1.68	1.08	0.52	-0.09	0.23	0.03	0.28	0.357	0.022	0.678	0.033	39	42	48	25	11	17	11	12	15	15	17	19	12	9	10	10	
TOP PROTEIN	sp Q3R0U9 F3C1A_MOUSE	0.96	2.67	1.48	0.54	-0.02	0.43	0.17	0.27	0.904	0.013	0.187	0.070	27	40	28	15	5	11	11	11	11	17	17	12	11	6	11	4	
TOP PROTEIN	sp Q9H633 HSP_MOUSE	1.76	0.64	0.87	0.68	0.12	0.27	0.08	0.28	0.12	0.006	0.017	0.008	60	60	60	60	20	20	20	20	20	20	20	20	20	20	20	20	20
TOP PROTEIN	sp Q9E84A HSP_MOUSE	1.03	0.44	1.33	0.31	0.01	0.65	0.12	0.51	0.936	0.003	0.387	0.067	30	40	29	9	4	14	12	14	15	5	11	13	1	1	5	3	
TOP PROTEIN	sp Q8V044 HSP_MOUSE	0.75	0.38	0.83	1.63	-0.12	0.41	-0.08	0.21	0.692	0.005	0.643	0.326	6	5	8	13	2	3	1	2	1	2	1	2	1	3	5	4	
TOP PROTEIN	sp Q8V044 HSP_MOUSE	0.75	0.38	0.83	1.63	-0.12	0.41	-0.08	0.21	0.692	0.005	0.643	0.326	6	5	8	13	2	3	1	2	1	2	1	2	1	3	5	4	
TOP PROTEIN	sp F18V07 F18V07_MOUSE	0.86	3.56	1.78	0.30	-0.22	0.55	0.25	0.52	0.238	0.012	0.108	0.050	18	32	30	9	3	5	10	12	11	9	6	12	12	6	1	2	
TOP PROTEIN	sp P12154 UBA1_MOUSE	1.88	2.07	1.07	0.75	0.27	0.43	0.03	0.12	0.210	0.019	0.851	0.374	15	16	8	6	3	8	4	5	4	6	6	3	1	3	2	3	
TOP PROTEIN	sp Q9P9W1 HSP_MOUSE	1.18	7.50	0.91	0.74	0.01	0.61	0.29	0.31	0.275	0.019	0.889	0.380	20	20	15	17	10	11	12	11	12	11	12	11	11	11	11	11	
TOP PROTEIN	sp P48787 TNFR_MOUSE	1.17	0.52	0.51	1.17	-0.07	0.28	-0.29	0.06	0.646	0.002	0.142	0.374	49	25	42	48	25	11	13	8	9	8	11	14	17	18	15	15	
TOP PROTEIN	sp Q3R0U9 HRR_MOUSE	1.62	2.00	0.95	0.74	0.21	0.30	-0.02	0.11	0.205	0.024	0.899	0.349	19	20	13	10	5	6	10	8	7	5	3	6	4	3	4		
TOP PROTEIN	sp F7CK47 F3C1A_MOUSE	1.31	0.68	0.82	0.52	0.12	0.27	-0.09	0.19	0.322	0.047	0.116	0.207	21	17	16	25	8	6	7	5	6	6	7	5	6	10	8		
TOP PROTEIN	sp Q9P9K7 DPP3_MOUSE	1.56	6.50	2.60	0.22	-0.16	0.81	0.41	0.65	0.561	0.018	0.007	0.330	5	13	9	2	1	2	2	4	6	3	0	2	7	1	1	0	
TOP PROTEIN	sp Q9C2V7 HSP_MOUSE	1.33	0.64	0.82	0.52	0.12	0.27	-0.09	0.19	0.322	0.047	0.116	0.207	21	17	16	25	12	9	7	5	6	6	7	5	6	10	8		
TOP PROTEIN	sp Q3S451 F3C1A_MOUSE	0.86	NA	0.67	1.19	0.02	0.49	0.18	0.64	0.768	0.016	0.561	0.021	6	4	7	7	6	3	0	2	1	6	6	7	1	0	0	0	
TOP PROTEIN	sp P29533 VCAM1_MOUSE	1.27	0.63	1.05	2.13	0.10	0.20	0.32	0.33	0.492	0.022	0.845	0.013	19	20	15	32	6	9	4	6	6	8	4	7	4	11	9	12	
TOP PROTEIN	sp Q3R0U9 HRR_MOUSE	1.80	2.40	1.50	0.50	0.38	0.18	0.30	0.80	0.422	0.025	0.116	0.300	3	9	2	3	6	9	2	3	5	4	4	4	2	2	1	2	
TOP PROTEIN	sp Q9E114 HSP_MOUSE	1.40	1.50	1.40	0.80	0.10	0.28	0.10	0.42	0.80	0.012	0.089	0.300	8	12	10	5	4	4	4	2	4	4	2	4	2	4	2	4	
TOP PROTEIN	sp P36371 TAP2_MOUSE	1.01	2.43	0.81	0.64	0.28	0.39	0.09	0.20	0.279	0.011	0.651	0.047	21	17	11	7	3	6	12	5	5	7	3	4	4	2	2	3	
TOP PROTEIN	sp P22473 HSP_MOUSE	1.97	2.90	1.81	0.67	0.07	0.69	0.26	0.18	0.028	0.001	0.253	0.088	16	29	15	10	3	5	11	9	9	9	9	9	9	9	9	9	
TOP PROTEIN	sp P36371 TAP2_MOUSE	1.01	2.43	0.81	0.64	0.28	0.39	0.09	0.20	0.279	0.011	0.651	0.047	21	17	11	7	3	6	12	5	5	7	3	4	4	2	2	3	
TOP PROTEIN	sp P48787 TNFR_MOUSE	1.17	0.52	0.51	1.17	-0.07	0.28	-0.29	0.06	0.646	0.002	0.142	0.374	49	25	42	48	25	11	13	8	9	8	11	14	17	18	15	15	
TOP PROTEIN	sp Q3R0U9 HRR_MOUSE	1.62	2.00	0.95	0.74	0.21	0.30	-0.02	0.11	0.205	0.024	0.899	0.349	19	20	13	10	5	6	10	8	7	5	3	6	4	3	4		
TOP PROTEIN	sp F7CK47 F3C1A_MOUSE	1.31	0.68	0.82	0.52	0.12	0.27	-0.09	0.19	0.322	0.047	0.116	0.207	21	17	16	25	8	6	7	5	6	6	7	5	6	10	8		
TOP PROTEIN	sp Q9P9K7 DPP3_MOUSE	1.56	6.50	2.60	0.22	-0.16	0.81	0.41	0.65	0.561	0.018	0.007	0.330	5	13	9	2	1	2	2	4	6	3	0	2	7	1	1	0	
TOP PROTEIN	sp Q9C2V7 HSP_MOUSE	1.33	0.64	0.82	0.52	0.12	0.27	-0.09	0.19	0.322	0.047	0.116	0.207	21	17	16	25	12	9	7	5	6	6	7	5	6	10	8		
TOP PROTEIN	sp Q3S451 F3C1A_MOUSE	0.86	NA	0.67	1.19	0.02	0.49	0.18	0.64	0.768	0.016	0.561	0.021	6	4	7	7	6	3	0	2	1	6	6	7	1	0	0	0	
TOP PROTEIN	sp P29533 VCAM1_MOUSE	1.27	0.63	1.05	2.13	0.10	0.20	0.32	0.33	0.492	0.022	0.845	0.013	19	20	15	32	6	9	4	6	6	8	4	7	4	11	9	12	
TOP PROTEIN	sp Q3R0U9 HRR_MOUSE	1.80	2.40	1.50	0.50	0.38	0.18	0.30	0.80	0.422	0.025	0.116	0.300	3	9	2	3	6	9	2	3	5	4	4	4	2	2	1	2	
TOP PROTEIN	sp Q9E114 HSP_MOUSE	1.40	1.50	1.40	0.80	0.10	0.28	0.10	0.42	0.80	0.012	0.089	0.300	8	12	10	5	4	4	4	2	4	4	2	4	2	4	2	4	
TOP PROTEIN	sp P36371 TAP2_MOUSE	1.01	2.43	0.81	0.64	0.28	0.39	0.09	0.20	0.279	0.011	0.651	0.047	21	17	11	7	3	6	12	5	5	7	3	4	4	2	2	3	
TOP PROTEIN	sp P22473 HSP_MOUSE	1.97	2.90	1.81	0.67	0.07	0.69	0.26	0.18	0.028	0.001	0.253	0.088	16	29	15	10	3	5	11	9	9	9	9	9	9	9	9	9	
TOP PROTEIN	sp P36371 TAP2_MOUSE	1.01	2.43	0.81	0																									









Source	Sequence ID	Sequence Name	Gene Symbol	Ratio AEM/AGWT	Ratio AGEM/AGWT	Ratio AGEM/AGWT	Ratio AGWT/AGWT	Log Ratio AEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGWT/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	AgEM Total Spectral Count	AgEM Total Spectral Count	AgWT Total Spectral Count	AgWT Total Spectral Count	AgEMrp1 Normalized	AgEMrp2 Normalized	AgEMrp3 Normalized	AgEMrp1 Normalized	AgEMrp2 Normalized	AgEMrp3 Normalized	AgWTrp1 Normalized	AgWTrp2 Normalized	AgWTrp3 Normalized	AgWTrp1 Normalized	AgWTrp2 Normalized	AgWTrp3 Normalized	
TOP PROTEIN	sp1P24431(DHE3_MOUSE)	Glutamate dehydrogenase	Gdh1	1.24	1.01	0.75	0.92	0.09	0.01	-0.12	0.04	0.270	0.938	0.165	0.609	109	82	88	81	44	37	28	32	27	25	23	24	34	25	33		
TOP PROTEIN	sp1P24432(GN27_MOUSE)	60S ribosomal protein	Rpl17	1.17	1.20	1.02	0.63	0.12	0.04	-0.21	0.349	0.811	0.949	0.121	0.349	12	11	11	10	2	7	3	5	1	3	4	2	1	3	2		
TOP PROTEIN	sp1Q9C164(L1L7_MOUSE)	60S ribosomal protein	Rpl17	1.50	2.20	0.92	0.63	0.18	0.34	-0.04	-0.20	0.492	0.955	0.561	0.349	12	11	11	8	5	2	7	3	5	1	3	4	2	1	3		
TOP PROTEIN	sp1Q60770(STBL8_MOUSE)	Syntenin-binding protein	Stbip3	1.09	2.00	1.17	0.64	0.10	0.30	0.07	-0.20	0.815	1.002	0.561	0.387	12	14	11	7	3	4	5	5	6	3	6	2	1	3	3		
TOP PROTEIN	sp1Q60770(STBL8_MOUSE)	60S ribosomal protein	Rpl17	1.09	2.13	1.17	0.64	0.10	0.30	0.07	-0.20	0.815	1.002	0.561	0.387	12	14	11	7	3	4	5	5	6	3	6	2	1	3	3		
CO-TO PROTEIN	sp1D29W155(DGWF5_MOUSE)	Epidemiol growth fact	Egfr	0.80	1.00	0.75	0.60	-0.10	0.00	-0.12	0.22	0.230	1.000	0.374	0.116	8	6	10	6	3	2	3	2	3	1	4	3	3	3	2	1	
TOP PROTEIN	sp1Q21279(LGFR_MOUSE)	Epidermal growth fact	Egfr	0.80	1.00	0.75	0.60	-0.10	0.00	-0.12	0.22	0.230	1.000	0.374	0.116	8	6	10	6	3	2	3	2	3	1	4	3	3	3	2	1	
TOP PROTEIN	sp1Q20875(LY8C_MOUSE)	Meth	Meth	0.80	1.00	0.75	0.60	-0.10	0.00	-0.12	0.22	0.230	1.000	0.374	0.116	8	6	10	6	3	2	3	2	3	1	4	3	3	3	2	1	
TOP PROTEIN	sp1P82349(SGCR_MOUSE)	Beta-sarcoglycan	Sgcr	0.94	1.11	0.63	0.53	-0.03	0.05	-0.20	-0.28	0.742	0.872	0.184	0.205	16	10	17	9	5	6	5	5	4	1	6	7	4	1	6	2	
TOP PROTEIN	sp1Q60933(PHML_MOUSE)	Protein PHM	Phm1	1.33	1.40	0.88	0.83	0.12	0.15	-0.06	-0.08	0.670	0.422	0.834	0.643	8	7	6	5	4	4	4	0	1	3	3	2	2	1	6	2	
TOP PROTEIN	sp1Q60933(PHML_MOUSE)	Protein PHM	Phm1	1.33	1.40	0.88	0.83	0.12	0.15	-0.06	-0.08	0.670	0.422	0.834	0.643	8	7	6	5	4	4	4	0	1	3	3	2	2	1	6	2	
TOP PROTEIN	sp1P97315(SGPP_MOUSE)	Cytosine and glycine r	Crp1	0.84	0.45	0.53	1.11	-0.02	-0.35	-0.28	0.05	0.899	0.065	0.140	0.801	17	9	18	20	6	4	7	3	1	5	10	6	2	7	5	4	
TOP PROTEIN	sp1P61522(SGBT_MOUSE)	4-aminobutyrate amin	Abat	0.83	2.27	0.67	1.01	-0.08	0.36	0.22	0.21	0.629	0.185	0.298	0.184	15	25	18	11	3	4	8	12	9	4	6	8	4	2	5	4	
TOP PROTEIN	sp1Q20249(LM_MOUSE)	Palmitolein-1	Paln1	1.88	1.00	0.84	0.84	0.18	0.00	0.00	0.13	0.870	0.131	0.238	0.116	17	17	10	11	9	4	5	3	2	5	3	2	3	3	3	3	
TOP PROTEIN	sp1E193282(SRQ32_MOUSE)	Synaptotagmin	Syp150	1.94	1.54	0.61	0.76	0.29	0.19	-0.22	0.12	0.052	0.485	0.217	0.552	33	20	17	13	10	11	12	12	2	6	7	4	2	4	3	6	
TOP PROTEIN	sp1Q29988(NUC1_MOUSE)	Nucleoporin core complex	Nup55	1.29	0.90	0.50	0.71	-0.11	-0.05	-0.30	-0.15	0.492	0.795	0.176	0.294	18	9	14	10	3	7	8	2	5	2	3	6	5	4	4	4	
TOP PROTEIN	sp1P11432(LAFAL_MOUSE)	Adaptor 8 of class C con	Adap8	1.27	1.33	0.83	0.79	0.15	0.00	0.00	0.14	0.361	0.900	0.224	0.441	14	14	10	9	9	10	9	10	7	8	10	12	10	12	21	25	
TOP PROTEIN	sp1Q60604(ADSV_MOUSE)	Adenovirus	Gln3	1.58	1.27	1.00	1.25	0.20	0.10	0.00	0.10	0.091	0.469	1.000	0.519	19	19	12	15	6	7	9	5	5	2	5	5	4	4	7	7	
TOP PROTEIN	sp1Q2C269(SLUG3_MOUSE)	Gliadin alpha-3	Gli3	1.00	0.75	0.75	1.00	0.00	-0.12	-0.12	0.00	1.000	0.374	0.725	1.000	3	3	4	4	0	3	1	1	1	1	2	0	2	1	1	4	7
TOP PROTEIN	sp1Q2C269(SLUG3_MOUSE)	Gliadin alpha-3	Gli3	1.00	0.75	0.75	1.00	0.00	-0.12	-0.12	0.00	1.000	0.374	0.725	1.000	3	3	4	4	0	3	1	1	1	1	2	0	2	1	1	4	7
TOP PROTEIN	sp1Q2C269(SLUG3_MOUSE)	Gliadin alpha-3	Gli3	1.00	0.75	0.75	1.00	0.00	-0.12	-0.12	0.00	1.000	0.374	0.725	1.000	3	3	4	4	0	3	1	1	1	1	2	0	2	1	1	4	7
TOP PROTEIN	sp1P26431(HAD1_MOUSE)	Radiatin	Rads1	1.03	0.96	0.73	0.81	0.01	0.02	-0.12	-0.09	0.893	0.749	0.174	0.308	69	52	67	64	22	18	29	19	18	29	20	18	29	20	17	16	
TOP PROTEIN	sp1Q31263(APTA_MOUSE)	ATP synthase subunit	Atp5a1	0.77	1.09	1.05	0.73	-0.11	0.04	0.01	-0.14	0.184	0.633	0.901	0.092	686	706	886	649	205	308	173	291	226	189	291	284	311	205	265	179	
TOP PROTEIN	sp1Q31263(APTA_MOUSE)	Glutathione synthetase	Gsh1	0.17	1.00	0.60	0.80	0.00	0.00	0.00	0.189	1.000	0.101	0.643	1	4	6	4	1	0	0	1	2	0	1	2	0	3	0	3	1	
TOP PROTEIN	sp1P51853(SGR_MOUSE)	Glutathione synthetase	Gsh1	0.17	1.00	0.60	0.80	0.00	0.00	0.00	0.189	1.000	0.101	0.643	1	4	6	4	1	0	0	1	2	0	1	2	0	3	0	3	1	
TOP PROTEIN	sp1Q24548(DIC1L_MOUSE)	DnaI homolog subunit	Dnaq1L1	0.91	1.63	1.40	0.74	-0.04	0.21	0.11	-0.14	0.874	0.152	0.869	0.349	10	13	11	8	4	4	6	3	2	2	2	3	3	3	3	1	
TOP PROTEIN	sp1Q24548(DIC1L_MOUSE)	DnaI homolog subunit	Dnaq1L1	0.91	1.63	1.40	0.74	-0.04	0.21	0.11	-0.14	0.874	0.152	0.869	0.349	10	13	11	8	4	4	6	3	2	2	2	3	3	3	3	1	
TOP PROTEIN	sp1Q24548(DIC1L_MOUSE)	DnaI homolog subunit	Dnaq1L1	0.91	1.63	1.40	0.74	-0.04	0.21	0.11	-0.14	0.874	0.152	0.869	0.349	10	13	11	8	4	4	6	3	2	2	2	3	3	3	3	1	
TOP PROTEIN	sp1Q24548(DIC1L_MOUSE)	DnaI homolog subunit	Dnaq1L1	0.91	1.63	1.40	0.74	-0.04	0.21	0.11	-0.14	0.874	0.152	0.869	0.349	10	13	11	8	4	4	6	3	2	2	2	3	3	3	3	1	
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4	3	3	2	3	3		
TOP PROTEIN	sp1Q36344(MKO1_MOUSE)	NADPH-activated pyr	Makp3	1.43	1.88	1.50	1.14	0.15	0.27	0.18	0.06	0.247	0.210	0.938	0.678	10	15	7	8	2	5	3	3	8	4</							



Source	Sequence ID	Sequence Name	Gene Symbol	Ratio AEM/AGWT	Ratio AGM/AGWT	Ratio AGM/AGWT	Ratio AGM/AGWT	Log Ratio AEM/AGWT	Log Ratio AGM/AGWT	Log Ratio AGM/AGWT	Log Ratio AEM/AGWT	p-value AEM/AGWT	p-value AGM/AGWT	p-value AEM/AGWT	p-value AGM/AGWT	AdEM Total Spectral Count	AgEM Total Spectral Count	AdWT Total Spectral Count	AgWT Total Spectral Count	AdEMrp1 Normalized SC	AdEMrp2 Normalized SC	AdEMrp3 Normalized SC	AgEMrp1 Normalized SC	AgEMrp2 Normalized SC	AgEMrp3 Normalized SC	AdWTrp1 Normalized SC	AdWTrp2 Normalized SC	AdWTrp3 Normalized SC	AgWTrp1 Normalized SC	AgWTrp2 Normalized SC	AgWTrp3 Normalized SC
TOP PROTEIN	sp P13291 HA81A_MOUSE	Ras-related protein Ras	Rasb1	1.50	0.45	0.56	1.83	0.18	0.34	-0.26	0.26	0.482	0.145	0.374	0.189	5	3	6	11	5	1	3	1	3	1	2	2	2	5	4	
TOP PROTEIN	sp P13292 HA81B_MOUSE	Ras-related protein Ras	Rasb1	0.147	1.25	0.15	0.41	0.18	0.37	-0.12	0.15	0.288	0.118	0.318	0.122	6	9	9	4	1	2	3	2	4	2	4	2	2	0	0	
TOP PROTEIN	sp P13293 T3YVC_MOUSE	Manose 6-phosphatase	Mps1	0.90	2.25	1.00	0.44	-0.18	0.35	-0.18	0.35	0.288	0.132	0.288	0.132	6	9	9	4	1	2	3	2	4	2	2	2	0	0		
TOP PROTEIN	sp Q92M47 HAM_MOUSE	Manose 6-phosphatase	Mps1	0.90	2.25	1.00	0.44	-0.18	0.35	-0.18	0.35	0.288	0.132	0.288	0.132	6	9	9	4	1	2	3	2	4	2	2	2	0	0		
TOP PROTEIN	sp P13294 T3YVC_MOUSE	Manose 6-phosphatase	Mps1	0.90	2.25	1.00	0.44	-0.18	0.35	-0.18	0.35	0.288	0.132	0.288	0.132	6	9	9	4	1	2	3	2	4	2	2	2	0	0		
TOP PROTEIN	sp Q92M47 HAM_MOUSE	Manose 6-phosphatase	Mps1	0.90	2.25	1.00	0.44	-0.18	0.35	-0.18	0.35	0.288	0.132	0.288	0.132	6	9	9	4	1	2	3	2	4	2	2	2	0	0		
TOP PROTEIN	sp P13295 CNAL_MOUSE	Catenin alpha1	Cttna1	0.87	1.09	0.50	0.71	-0.06	0.04	-0.05	0.15	0.558	0.649	0.565	0.231	78	70	100	64	22	31	25	30	22	41	27	22	25	17		
TOP PROTEIN	sp Q5295 PHE_MOUSE	Transcriptional activator	Hnra1	0.57	3.00	1.50	0.29	-0.24	0.48	0.18	0.54	0.101	0.205	0.374	0.089	4	6	7	2	2	1	1	3	2	3	2	2	0	2		
TOP PROTEIN	sp Q5296 PHE_MOUSE	Transcriptional activator	Hnra1	0.57	3.00	1.50	0.29	-0.24	0.48	0.18	0.54	0.101	0.205	0.374	0.089	4	6	7	2	2	1	1	3	2	3	2	2	0	2		
TOP PROTEIN	sp P13342 MYHE_MOUSE	Myosin 8	Myh8	1.13	1.47	1.21	0.86	-0.19	0.04	0.08	-0.07	0.209	0.709	0.491	0.578	307	372	473	407	105	84	118	171	123	78	123	121	229	157	134	
TOP PROTEIN	sp Q4737 TOPR_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5297 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5298 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5299 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5300 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5301 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5302 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5303 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5304 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5305 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5306 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5307 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5308 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5309 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5310 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5311 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5312 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5313 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5314 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5315 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5316 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5317 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5318 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5319 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5320 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5321 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5322 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5323 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5324 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5325 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5326 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5327 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22	0.86	-0.05	0.20	0.09	0.06	0.725	0.148	0.492	0.678	3	3	4	8	7	3	4	2	3	5	2	2	4	2	3	
TOP PROTEIN	sp Q5328 PHE_MOUSE	Transferrin receptor	Tfrc	0.65	1.57	1.22																									





Source	Sequence ID	Sequence Name	Gene Symbol	Ratio AEM/AGWT	Ratio AGEM/AGWT	Ratio AEM/AGM	Ratio AGM/AGWT	Log Ratio AEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AEM/AGM	Log Ratio AGM/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	p-value AEM/AGM	p-value AGM/AGWT	AdEM Total Spectral Count	AgEM Total Spectral Count	AdWT Total Spectral Count	AgWT Total Spectral Count	AdEMrp1 Normalized SC	AdEMrp2 Normalized SC	AdEMrp3 Normalized SC	AgEMrp1 Normalized SC	AgEMrp2 Normalized SC	AgEMrp3 Normalized SC	AdWTrp1 Normalized SC	AdWTrp2 Normalized SC	AdWTrp3 Normalized SC	AgWTrp1 Normalized SC	AgWTrp2 Normalized SC	AgWTrp3 Normalized SC	
TOP PROTEIN	sp1474562 GPT1_MOUSE	Sequence 2 of Glutaminyl-peptide transferase	Gpt1	3.00	3.00	1.00	1.00	0.00	0.48	0.48	0.00	0.00	0.374	0.116	1.000	1.000	1.000	1.000	1	2	3	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp1209165 GRIK1_MOUSE	Gamma-aminobutyric acid receptor ionotropic subunit 1	Grik1	3.00	3.00	1.00	1.00	0.00	0.48	0.48	0.00	0.00	0.374	0.116	1.000	1.000	1.000	1.000	1	2	3	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp1099707 HNF1_MOUSE	Nuclear Nrx export factor	Hnf1	0.67	0.67	0.00	0.00	-0.18	-0.07	-0.00	0.00	0.00	0.725	0.643	1.000	1.000	1.000	1.000	2	2	3	3	0	0	1	1	0	2	1	0	2	1
TOP PROTEIN	sp1622593 H3H3_MOUSE	H4.3 protein epsilon	HnfE	1.12	0.82	0.79	1.05	0.05	0.05	-0.17	-0.10	0.02	0.566	0.387	0.398	0.374	0.48	18	43	45	20	17	11	9	12	17	15	14	14	14	16	15
TOP PROTEIN	sp1143119 H4H4_MOUSE	H4.3 protein epsilon	HnfE	1.16	0.85	0.85	1.05	0.02	0.02	-0.10	-0.10	0.02	0.566	0.387	0.398	0.374	0.48	18	43	45	20	17	11	9	12	17	15	14	14	14	16	15
TOP PROTEIN	sp1061247 HA2P_MOUSE	Alpha-2-Haptoglobin	Hapt2	1.17	1.67	1.43	1.00	0.07	0.22	0.15	0.00	0.00	0.830	0.205	0.468	0.100	6	7	10	6	1	4	2	3	5	2	0	2	4	2	2	
TOP PROTEIN	sp1090405 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	0.79	0.50	1.23	0.64	-0.10	-0.18	0.09	0.19	0.05	0.305	0.447	0.669	1.000	1.000	1.000	1.000	22	27	28	18	4	9	9	3	5	2	4	2	9
TOP PROTEIN	sp1090405 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.25	0.80	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.374	0.116	1.000	1.000	1.000	1.000	1	2	3	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp1090405 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.07	0.64	1.22	1.00	0.05	0.09	0.09	0.02	0.759	0.435	0.201	0.894	0.62	272	331	254	266	86	110	76	95	114	122	77	114	63	57	135	74
TOP PROTEIN	sp133405 HMGCoA_MOUSE	Methylcrotonyl-CoA carboxylase	HmgCoA	1.91	1.65	0.80	1.12	-0.04	-0.19	-0.10	0.05	0.807	0.203	0.527	0.743	0.30	24	33	33	37	6	13	11	12	6	17	10	6	9	16	12	12
TOP PROTEIN	sp1143242 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	2.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.374	0.116	1.000	1.000	1.000	1.000	1.000	1	2	3	1	1	1	1	1	1	1	1	1	1	1
CO-TO PROTEIN	tr1039707 HNF1_MOUSE	Sodium/potassium-transporting ATPase	Atpa2	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135	142	104	31	51	64	55	53	27	42	61	39	42	33	29	29
TOP PROTEIN	sp1028194 HNF1_MOUSE	Nuclear Nrx export factor	HnfE	1.03	1.30	0.92	0.73	0.01	0.11	-0.03	-0.14	0.916	0.351	0.794	0.184	146	135															

Source	Sequence ID	Sequence Name	Gene Symbol	Ratio	Ratio	Ratio	Ratio	Log Ratio	Log Ratio	Log Ratio	Log Ratio	p-value	p-value	p-value	p-value	AdEM Total	AgEM Total	AdWT Total	AgWT Total	AdEMrp1	AdEMrp2	AdEMrp3	AgEMrp1	AgEMrp2	AgEMrp3	AdWTrp1	AdWTrp2	AdWTrp3	AgWTrp1	AgWTrp2	AgWTrp3			
				AdEM/AdWT	AgEM/AgWT	Spectral Count	Spectral Count	Spectral Count	Spectral Count	Normalized																								
TOP PROTEIN	sp1P262821F57_MOUSE	45 ribosomal protein	Rps7	0.73	1.14	0.73	0.47	-0.13	0.06	-0.14	-0.33	0.087	0.778	0.588	0.224	1	4	6	1	4	6	1	4	3	8	3	3	1	3	1				
TOP PROTEIN	sp1P21511_MOUSE	Centromere-associated protein 1	Cenpf1	0.82	0.97	0.81	0.97	-0.01	-0.04	-0.01	-0.04	0.084	0.624	0.577	0.676	597	678	597	781	218	218	218	218	218	218	218	218	218	218	218	218			
TOP PROTEIN	sp1O548621_MOUSE	Centromere-associated protein 2	Cenpf2	0.75	2.00	0.67	2.03	-0.12	0.30	-0.18	0.60	0.374	0.519	0.374	0.101	3	2	4	1	1	1	1	1	1	2	1	0	1	0	1	0			
TOP PROTEIN	sp1P12113_MOUSE	Programmed cell death 1	Pdcd1	0.60	0.75	NA	2.00	NA	0.12	NA	0.30	0.136	0.643	0.158	0.230	2	2	4	0	0	0	0	0	1	1	1	0	2	1	0	1			
TOP PROTEIN	sp1O532491_MOUSE	Hand domain protein 2	Hndc2	0.82	0.82	0.82	0.82	0.00	0.00	0.00	0.00	0.23	0.768	0.23	1	12	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp1O2C614_MOUSE	Biliverdin reductase A	Bilr1a	0.40	1.00	1.00	0.40	0.00	0.00	0.00	0.40	0.251	1.000	0.251	2	2	5	2	1	1	0	0	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp1O2B621_MOUSE	Tubulin tyrosine ligase	Ttly	0.40	1.00	1.00	0.40	0.00	0.00	0.00	0.40	0.374	0.158	0.158	0.374	0	3	1	0	0	0	0	0	0	2	1	0	1	0	0	0	0		
TOP PROTEIN	sp1O2C614_MOUSE	Novel 26-nucleotide RNA	Nov26	0.40	1.00	1.00	0.40	0.00	0.00	0.00	0.40	0.251	1.000	0.251	2	2	5	2	1	1	0	0	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp1O2B810_MOUSE	Citrate lyase subunit 1	Cfl1	0.67	0.25	0.50	1.33	-0.18	-0.60	0.30	0.12	0.374	0.101	0.519	0.374	1	1	3	4	1	0	0	1	0	1	0	1	1	1	1	1	1		
TOP PROTEIN	sp1O2B919_MOUSE	Four and a half LIM domain 1	Fhl4	1.25	0.50	0.60	1.50	-0.10	-0.30	0.22	0.18	0.778	0.288	0.561	0.492	2	1	4	6	0	2	3	0	2	2	0	2	2	2	3	2	1	1	
TOP PROTEIN	sp1O2C817_MOUSE	Arachidonate 5-lipoxygenase 1	Alo5	1.18	1.18	1.18	1.18	0.00	0.00	0.00	0.00	0.12	0.752	0.18	1	4	1	1	0	1	0	0	1	0	1	0	0	0	0	0	0	0		
TOP PROTEIN	sp1P39651_MOUSE	Arachidonate 12-lipoxygenase 2	Alo2	1.33	2.00	1.50	0.67	0.32	0.48	0.18	0.18	0.752	0.275	0.609	0.643	4	6	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
TOP PROTEIN	sp1P6749_MOUSE	SRF GTPase-activating protein 2	Gis2	1.00	2.50	0.83	0.67	0.30	0.40	-0.08	0.18	0.158	0.251	0.374	0.725	2	5	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2		
TOP PROTEIN	sp1O2C614_MOUSE	Novel 26-nucleotide RNA	Nov26	0.40	1.00	1.00	0.40	0.00	0.00	0.00	0.40	0.251	1.000	0.251	2	2	5	2	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1P62900_MOUSE	60S ribosomal protein L31	L31	1.20	0.75	0.50	0.80	0.08	-0.12	0.30	-0.10	0.768	0.275	0.288	0.778	6	3	5	4	3	1	2	1	2	1	2	3	0	2	0	2	0	2	
TOP PROTEIN	sp1P29610_MOUSE	Aryl GTP synthetase 1	Ags1	1.00	1.46	1.46	1.00	0.00	0.16	0.16	0.00	1.000	0.368	0.468	1.000	13	19	13	13	1	8	4	4	6	9	5	4	4	3	3	3	3		
TOP PROTEIN	sp1P32241_MOUSE	Arabinoside 3-epimerase	Ara3	0.96	1.00	1.00	0.96	0.00	0.00	0.00	0.00	0.961	0.029	0.969	0.969	49	53	51	51	1	8	4	4	6	9	5	4	4	3	3	3	3		
TOP PROTEIN	sp1O8890_MOUSE	Actin alpha-1	Acta1	0.99	1.68	0.93	0.55	0.00	0.23	0.03	0.26	0.990	0.993	0.917	0.016	141	131	142	78	25	21	55	78	37	16	42	56	32	22	24	24	24		
TOP PROTEIN	sp1O8M425_MOUSE	Soliking factor 3A subunit	Sf3a1	1.13	0.40	0.44	0.11	0.05	0.60	-0.35	-0.90	0.842	0.349	0.279	0.135	9	4	8	1	2	2	5	0	1	3	5	0	1	1	0	1	0	1	
TOP PROTEIN	sp1O2C002_MOUSE	Arachidonate 5-lipoxygenase 1	Alo5	0.88	1.00	1.00	0.88	0.00	0.00	0.00	0.00	0.742	0.174	0.174	0.61	1	4	3	1	4	1	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1O2C56_MOUSE	26S proteasome non-ATP subunit	Psmc3	0.83	1.50	0.60	0.33	-0.08	0.18	-0.22	0.48	0.795	0.374	0.374	0.275	5	3	6	2	1	3	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1O7740_MOUSE	Protein Fc gamma 1C	Fcgc1	1.00	4.00	0.50	0.50	0.00	0.60	0.30	-0.30	1.000	0.349	0.519	0.878	2	4	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1P5044_MOUSE	MEV-related integral envelope protein	Mev1	2.00	2.00	2.00	2.00	0.00	0.00	0.00	0.00	0.759	0.519	0.519	2	2	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp1O8X71_MOUSE	Sphingosine 1-phosphate receptor 1	S1pr1	1.11	0.83	1.13	0.88	0.05	-0.08	0.05	0.25	0.815	0.492	0.815	0.492	12	10	8	9	4	3	5	4	2	4	2	4	2	3	1	5	4		
TOP PROTEIN	sp1O1X322_MOUSE	MGC15360	Dgk1	1.27	1.22	1.00	1.00	0.00	0.00	0.00	0.00	0.205	0.560	1.000	0.879	28	28	28	28	9	8	13	9	8	9	5	6	5	6	5	6	5		
TOP PROTEIN	sp1O6133_MOUSE	Striatin 2	Str2	0.96	0.73	1.14	0.99	0.02	0.02	0.14	0.63	0.986	0.467	0.986	0.467	34	11	78	42	34	11	78	42	34	11	78	42	34	11	78	42	34	11	
TOP PROTEIN	sp1O81M1_MOUSE	Equilibrative nucleoside transporter 1	Slc29a1	1.08	0.75	0.75	0.77	0.03	0.02	0.12	-0.11	0.840	0.768	0.497	0.101	28	21	26	20	5	8	15	9	6	6	9	7	10	7	6	6	6		
TOP PROTEIN	sp1O81M1_MOUSE	Equilibrative nucleoside transporter 1	Slc29a1	1.08	1.05	0.77	0.77	0.03	0.02	0.12	-0.11	0.840	0.768	0.497	0.101	28	21	26	20	5	8	15	9	6	6	9	7	10	7	6	6	6		
TOP PROTEIN	sp1O81M1_MOUSE	Equilibrative nucleoside transporter 1	Slc29a1	1.08	1.10	0.75	0.75	0.03	0.02	0.12	-0.11	0.840	0.768	0.497	0.101	28	21	26	20	5	8	15	9	6	6	9	7	10	7	6	6	6		
TOP PROTEIN	sp1P5044_MOUSE	Cytidine and glycine-uracil nucleoside transporter	Crcp	0.96	0.94	0.88	0.69	-0.02	-0.02	0.17	0.19	0.815	0.405	0.205	0.25	17	26	18	12	10	3	4	4	7	6	9	11	7	4	1	0	1		
TOP PROTEIN	sp1O2B013_MOUSE	Rac-related GTP-binding protein 2	Rrg2	0.75	2.00	0.33	0.60	-0.12	0.374	0.101	0.30	0.374	0.101	0.374	0.230	3	4	4	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1O8B184_MOUSE	Mediator of RNA polymerase II transcription subunit 1	Medc1	1.33	1.00	1.00	1.00	0.00	0.00	0.00	0.00	1.33	0.374	0.374	0.374	4	4	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp1O8B184_MOUSE	Mediator of RNA polymerase II transcription subunit 1	Medc1	1.33	1.00	1.00	1.00	0.00	0.00	0.00	0.00	1.33	0.374	0.374	0.374	4	4	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp1O8B184_MOUSE	Mediator of RNA polymerase II transcription subunit 1	Medc1	1.33	1.00	1.00	1.00	0.00	0.00	0.00	0.00	1.33	0.374	0.374	0.374	4	4	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp1O81M1_MOUSE	NADH dehydrogenase subunit 11	Nd11	1.33	1.00	0.50	0.70	0.00	-0.23	0.10	-0.23	0.768	0.400	0.400	0.400	12	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
TOP PROTEIN	sp1O81M1_MOUSE	NADH dehydrogenase subunit 11	Nd11	1.33	1.00	0.50	0.70	0.00	-0.23	0.10	-0.23	0.768	0.400	0.400	0.400	12	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
TOP PROTEIN	sp1O81M1_MOUSE	NADH dehydrogenase subunit 11	Nd11	1.33	1.00	0.50	0.70	0.00	-0.23	0.10	-0.23	0.768	0.400	0.400	0.400	12	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
TOP PROTEIN	sp1O6128_MOUSE	Aggrecan core protein 1	Acan	1.17	0.95	0.71	0.84	0.07	-0.02	0.15	0.06	0.956	0.905	0.489	0.547	16	16	23	17	16	2	12	17	16	2	12	17	16	2	12	17	16	2	
TOP PROTEIN	sp1O2123_MOUSE	Protein Fc gamma 1C	Fcgc1	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	1.000	0.349	0.519	0.878	6	6	7	6	6	7	6	7	6	6									

Source	Sequence ID	4-Sequence Name	Gene Symbol	Ratio		Ratio		Log Ratio		Log Ratio		Log Ratio		p-value		p-value		p-value		p-value		AdEM Total		AdGT Total		AdWT Total		AdEMrpt1		AdEMrpt2		AdEMrpt3		AdGTm.rpt2		AdGTm.rpt3		AdWTm.rpt1		AdWTm.rpt2		AdWTm.rpt3		AdWTm.rpt1		AdWTm.rpt2		AdWTm.rpt3			
				AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT	AdEM/AdWT	AdGT/AdWT																
TOP PROTEIN	tr D3Z7R1 D3Z7R_MOUSE	Reticulon-4 interaction	Rtn4ip1	1.00	0.80	1.33	1.67	0.00	0.00	0.10	0.12	0.22	0.22	1.000	0.802	0.768	0.561	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5		
TOP PROTEIN	tr Q20400 H10_MOUSE	Rtn4ip2	Rtn4ip2	1.00	1.00	1.00	1.00	0.00	0.00	0.12	0.12	0.12	0.12	1.000	0.802	0.802	0.768	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5	1	2	3	5		
TOP PROTEIN	tr P72708 HMGAT_MOUSE	Alpha-1,3-mannosyl-glycanase	Mgp11	1.00	4.00	1.33	0.50	-0.18	0.60	0.12	-0.30	-0.30	-0.30	0.735	1.001	0.643	0.678	3	4	2	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0				
TOP PROTEIN	tr G6G2T9 HNDM1_MOUSE	Nomod1 modulator 1	Nomod1	0.86	1.00	1.21	1.05	-0.06	0.00	0.08	0.02	0.00	0.00	0.629	1.000	0.566	0.778	3	7	9	6	10	7	6	9	10	7	6	9	10	7	6	9	10	7	6	9	10	7	6	9	10	7	6	9	10	7	6	9		
TOP PROTEIN	tr F98871 HNDM1_MOUSE	Cav1	Cav1	1.15	1.05	0.82	0.59	-0.15	0.02	0.00	0.00	0.00	0.00	0.497	0.775	0.402	0.775	4	5	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4			
TOP PROTEIN	tr Q9R112 HSDH_MOUSE	Sulfidopyruvate oxidase	Sdpo1	0.96	0.85	1.05	1.17	0.02	-0.07	0.02	-0.02	0.07	0.08	0.484	0.442	0.802	0.492	22	23	23	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	
TOP PROTEIN	tr P28544 HSDH_MOUSE	Deconin	Deconin	1.56	1.03	0.75	0.56	-0.19	0.01	-0.11	-0.07	-0.07	-0.07	0.393	0.902	0.567	0.580	1170	898	750	872	665	226	279	375	305	105	218	185	340	343	222	316	198	358	111	81	116	114	114	114	114	114	114	114	114	114	114	114	114	114
TOP PROTEIN	tr F11539 HSDH_MOUSE	Thio1	Thio1	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.000	1.000	1.000	1.000	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	tr P58242 ASPM5_MOUSE	Actinophonylin	Smpd3b	1.33	0.75	0.75	1.33	0.12	-0.12	-0.12	-0.12	-0.12	-0.12	0.643	0.374	0.374	0.643	4	3	3	4	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	tr F78923 HNDM1_MOUSE	Up-regulated during aging	Umag5	0.69	0.85	1.22	1.00	-0.16	-0.07	0.09	0.00	0.00	0.00	0.442	0.653	0.759	1.000	9	11	13	13	0	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5		
TOP PROTEIN	tr Q28932 HNDM1_MOUSE	Adiponectin-1	Adipo1	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.000	1.000	1.000	1.000	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	tr Q35379 HMPL_MOUSE	Multidrug resistance-1	Abcg1	1.10	1.09	1.09	1.10	-0.04	0.04	0.04	0.04	0.04	0.04	0.862	0.815	0.815	0.862	11	12	10	11	3	0	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6		
TOP PROTEIN	tr F59023 HNDM1_MOUSE	Striated muscle-specific 1	Spec1	0.16	1.20	4.00	0.50	-0.80	0.04	0.04	0.04	0.04	0.04	0.184	0.839	0.404	0.272	3	12	19	10	0	3	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6	4	2	5	6		
TOP PROTEIN	tr Q28933 HNDM1_MOUSE	Phf1	Phf1	1.10	1.49	1.49	1.10	-0.16	0.00	0.00	0.00	0.00	0.00	0.783	0.658	0.658	0.783	14	13	12	17	6	2	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4	3	4		
TOP PROTEIN	tr Q55949 LCU_MOUSE	Clustered mitochondrion	Cluh	0.33	2.00	4.00	0.67	-0.48	0.30	0.60	0.60	0.60	0.60	0.374	0.519	0.349	0.643	1	4	3	2	0	1	0	0	3	1	1	0	0	3	1	1	0	2	0	1	0	2	0	1	0	2	0	1	0	2	0			
TOP PROTEIN	tr Q55949 LCU_MOUSE	Clustered mitochondrion 2	Cluh2	0.33	2.00	4.00	0.67	-0.48	0.30	0.60	0.60	0.60	0.60	0.374	0.519	0.349	0.643	1	4	3	2	0	1	0	0	3	1	1	0	0	3	1	1	0	2	0	1	0	2	0	1	0	2	0	1	0	2	0			
TOP PROTEIN	tr P20219 HNDM1_MOUSE	Hemoglobin subunit beta	Hbb-2	1.15	1.00	0.82	0.59	-0.16	0.00	0.00	0.00	0.00	0.00	0.782	0.653	0.653	0.782	10	11	10	11	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5	4	5			
TOP PROTEIN	tr Q3U109 HMMD_MOUSE	Regulator of microtubule	Rmp3	1.17	1.00	0.71	0.17	-0.07	0.70	-0.15	-0.78	-0.81	-0.78	0.815	0.230	0.621	0.189	7	5	6	1	2	4	3	2	1	2	4	3	2	1	2	4	3	2	1	2	4	3	2	1	2	4	3	2	1	2	4			
TOP PROTEIN	tr Q51033 LAP2B_MOUSE	Lamina-associated pol	Ltap2	1.21	1.26	1.00	0.96	0.08	0.10	-0.00	0.00	0.00	0.00	0.633	0.305	1.000	0.917	29	29	24	23	12	10	7	12	7	10	3	13	8	6	9	10	7	6	9	10	7	6	9	10	7	6	9	10	7	6	9			
TOP PROTEIN	tr P19163 HMMD_MOUSE	Actin-related protein 2	Arp2	0.93	1.20	1.20	0.93	-0.06	0.00	0.00	0.00	0.00	0.00	0.859	1.000	0.859	1.000	14	18	15	15	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6	5	6			
TOP PROTEIN	tr Q9D204 CCDC4_MOUSE	Coiled coil domain-co	Cch47	0.58	1.67	1.36	0.47	-0.24	0.22	0.13	-0.32	-0.40	-0.40	0.405	0.407	0.609	0.279	11	15	19	9	2	6	3	2	9	4	6	11	2	3	4	6	11	2	3	4	6	11	2	3	4	6	11	2	3	4				
TOP PROTEIN	tr Q2K863 F10T_MOUSE	Highly conserved F10	Hcf10	0.80	1.00	1.50	0.40	-0.20	0.48	0.18	-0.40	-0.40	-0.40	0.802	0.275	0.561	0.468	4	6	5	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				
TOP PROTEIN	tr Q20207 F10T_MOUSE	Tropoblast glycoprotein	Tgfbp4	1.75	1.00	0.40	0.40	-0.24	0.40	0.40	0.40	0.40	0.40	0.247	0.701	0.512	0.247	2	3	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				
TOP PROTEIN	tr F1K0V91 HNDM1_MOUSE	Lamina subunit beta-1	Lamb1	0.72	1.04	1.04	0.72	-0.14	0.02	0.02	-0.14	-0.28	-0.28	0.956	0.950	0.950	0.956	26	27	26	26	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6			
TOP PROTEIN	tr F1K0V91 HNDM1_MOUSE	Lamina subunit beta-2	Lamb2	0.72	1.04	1.04	0.72	-0.14	0.02	0.02	-0.14	-0.28	-0.28	0.956	0.950	0.950	0.956	26	27	26	26	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6	13	18	2	7	6			
TOP PROTEIN	tr P02489 TNLM_MOUSE	Tnfr1	Tnfr1	1.15	1.06	0.90	0.86	-0.06	0.06	0.04	0.00	0.00	0.00	0.308	0.762	0.655	0.755	478	431	415	405	170	127	181	120	195	116	141	168	126	137	121	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117		
TOP PROTEIN	tr Q2AMM0 HMDC_MOUSE	Mucin-related coiled	Mucrc	0.91	1.43	1.20	0.43	-0.15	-0.48	-0.70	-0.37	-0.37	-0.37	0.519	0.374	0.148	0.205	5	1	7	3	1	2	3	1	1	0																								



Source	Sequence ID	Sequence Name	Gene Symbol	Ratio AEM/AGWT	Ratio AGEM/AGWT	Ratio AGEM/AGWT	Ratio AGWT/AGWT	Log Ratio AEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AGWT/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	p-value AGEM/AGWT	p-value AGWT/AGWT	AgEM Total Spectral Count	AgEM Total Spectral Count	AgWT Total Spectral Count	AgWT Total Spectral Count	AgEMrnp1 Normalized SC	AgEMrnp2 Normalized SC	AgEMrnp3 Normalized SC	AgM1rnp1 Normalized SC	AgM1rnp2 Normalized SC	AgM1rnp3 Normalized SC	AdWT1rnp1 Normalized SC	AdWT2rnp1 Normalized SC	AdWT3rnp1 Normalized SC	AgWT1rnp1 Normalized SC	AgWT2rnp1 Normalized SC	AgWT3rnp1 Normalized SC
TOP PROTEIN	sp Q8R044 GIL1_MOUSE	Protein GIL1	Gil1	1.67	0.00	0.00	1.00	0.22	NA	NA	NA	0.643	0.158	0.218	10.00	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q8B877 TUBB1_MOUSE	Tubulin beta class III	Tubb1	1.18	1.10	1.10	2.00	0.00	0.00	0.00	0.00	0.725	0.40	0.725	10.00	4	4	4	0	0	0	0	0	0	0	0	0	0	0	0	
TOP PROTEIN	sp Q91WV5 ASMT_MOUSE	Arsonic methyltransferase	Asmt1	1.25	0.40	0.40	1.25	0.10	-0.40	-0.40	0.10	0.519	0.349	0.251	0.678	5	2	4	5	2	2	1	0	0	2	2	1	1	1	1	
TOP PROTEIN	sp D8FQ22 D8FQ22_MOUSE	Peroneal membrane protein	Pfam13b	0.75	0.50	0.67	1.00	-0.12	0.30	-0.18	0.00	0.768	0.422	0.725	1.000	2	2	4	4	1	2	0	2	0	1	3	0	2	1	1	
CO-TO PROTEIN	sp J2AAB9 TUBB1_MOUSE	Tubulin beta class III	Tubb1	0.12	0.75	0.75	1.00	-0.12	0.45	0.45	0.00	0.725	0.443	0.725	1.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q8C011 TBMXA_MOUSE	Thioredoxin-related T	Tmxa3	0.75	0.83	1.67	1.50	-0.15	-0.08	0.22	0.18	0.725	0.643	0.374	0.492	3	5	4	6	0	1	2	2	1	0	2	1	0	2	1	2
TOP PROTEIN	sp Q85C11 CTNNA3_MOUSE	Catenin alpha 3	Cttna3	0.75	1.13	1.87	1.54	-0.12	0.05	0.26	0.06	0.653	0.877	0.547	0.820	5	9	7	8	2	2	1	7	1	1	1	1	5	3	3	
TOP PROTEIN	sp F15639 C12orf43_MOUSE	LOC100289254	C12orf43	0.94	1.10	1.10	1.00	0.00	0.00	0.00	0.00	0.618	0.255	0.618	1.000	7	7	7	7	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q92171 TSP4_MOUSE	Thrombospondin-4	Tsp4	1.06	1.18	1.94	1.85	0.03	0.07	-0.03	0.07	0.705	0.740	0.892	0.422	69	65	65	55	24	20	25	34	27	4	1	27	17	22	14	19
TOP PROTEIN	sp F14371 CDB3_MOUSE	CDB3 antigen	Cdb3	1.00	0.71	1.00	1.00	0.00	0.15	0.00	0.15	1.000	0.422	1.000	0.422	10	5	5	7	2	1	2	2	1	1	1	2	2	1	3	3
TOP PROTEIN	sp F12C94 C9orf2_MOUSE	C9orf2	C9orf2	0.86	1.11	1.11	1.00	0.00	0.48	0.48	0.00	0.62	0.786	0.786	1.000	7	7	7	7	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp F40240 C9orf2_MOUSE	C9orf2	C9orf2	1.05	1.15	1.15	1.00	0.02	0.06	0.06	0.02	0.746	0.774	0.798	0.943	41	47	39	41	1	17	23	21	16	10	26	8	5	9	25	7
TOP PROTEIN	sp F46638 R1B1_MOUSE	Ras-related protein R1B1	Rab11b	1.18	1.38	0.85	0.75	0.07	0.14	0.07	0.14	0.795	0.417	0.693	0.577	26	22	22	16	10	12	4	7	4	11	1	11	10	4	7	5
TOP PROTEIN	sp F86833 H3_MOUSE	Histone H3	H3	1.12	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.709	0.651	0.709	1.000	9	9	9	9	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q8R64 ANGAS1_MOUSE	Activator of 90 kDa histone H1	Aha1	0.88	5.00	1.43	0.25	-0.06	0.70	0.15	-0.06	0.854	0.073	0.588	0.145	7	10	8	2	0	5	2	3	1	0	5	3	3	4	0	0
TOP PROTEIN	sp Q82159 RHOC_MOUSE	Rho-related GTP-binding protein 2	Rhoc	1.15	1.30	0.87	0.75	0.06	0.11	-0.06	0.11	0.768	0.539	0.725	0.624	15	13	13	10	3	5	7	7	3	3	1	5	7	2	4	2
TOP PROTEIN	sp Q86847 C12orf43_MOUSE	LOC100289254	C12orf43	1.04	1.10	1.10	1.00	0.00	0.00	0.00	0.00	0.883	0.612	0.883	1.000	277	280	297	277	101	66	117	101	66	117	101	66	117	89	122	
TOP PROTEIN	sp Q8R171 NINL_MOUSE	Niban like protein 1	Fam129b	1.57	3.25	1.18	0.57	0.20	0.51	0.07	0.24	0.499	0.284	0.811	0.251	11	13	7	4	1	7	3	2	2	2	2	2	2	2	2	2
TOP PROTEIN	sp F56179 HBMF_MOUSE	6 kDa mitochondrial protein	Mpfb	1.00	1.00	0.89	0.89	0.00	0.00	-0.05	0.00	1.000	1.000	1.000	0.643	9	8	9	8	2	4	3	3	3	3	3	3	3	3	3	3
TOP PROTEIN	sp F8Y901 C12orf43_MOUSE	LOC100289254	C12orf43	1.30	1.30	1.00	1.00	0.00	0.00	0.00	0.00	0.766	0.622	0.766	1.000	4	4	4	4	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q91W47 D91W47_MOUSE	Isocitrate dehydrogenase	Ihd3b	1.16	1.02	1.01	0.81	0.01	0.06	-0.01	-0.04	0.703	0.815	0.307	0.807	52	42	45	41	12	20	16	13	13	19	5	21	14	15	12	
CO-TO PROTEIN	sp Q03173 ENAM_MOUSE	Enamulin 2 of Protease	Enah	1.00	1.00	0.60	0.20	0.00	0.48	-0.22	-0.70	1.000	0.329	0.682	0.230	10	6	10	2	1	0	9	3	0	6	4	0	0	0	0	0
CO-TO PROTEIN	sp Q03173 ENAM_MOUSE	Enamulin 2 of Protease	Enah	1.00	1.00	0.60	0.20	0.00	0.48	-0.22	-0.70	1.000	0.329	0.682	0.230	10	6	10	2	1	0	9	3	0	6	4	0	0	0	0	0
TOP PROTEIN	sp Q03173 ENAM_MOUSE	Enamulin 2 of Protease	Enah	1.00	1.00	0.60	0.20	0.00	0.48	-0.22	-0.70	1.000	0.329	0.682	0.230	10	6	10	2	1	0	9	3	0	6	4	0	0	0	0	0
TOP PROTEIN	sp F86833 H3_MOUSE	Histone H3	H3	0.90	4.00	1.00	0.50	0.00	0.48	-0.22	-0.70	1.000	0.329	0.682	0.230	10	6	10	2	1	0	9	3	0	6	4	0	0	0	0	0
TOP PROTEIN	sp Q78R4 APOO1_MOUSE	Apolipoprotein O-like	Apo1	1.00	2.00	1.28	0.89	0.00	0.16	0.11	0.05	1.000	0.424	0.604	0.783	8	18	23	18	16	2	8	5	6	12	6	3	9	3	8	5
TOP PROTEIN	sp Q82159 RHOC_MOUSE	Rho-related GTP-binding protein 2	Rhoc	4.00	2.00	1.44	0.50	0.00	0.30	-0.30	0.00	0.349	0.678	0.579	1.000	4	2	1	1	3	0	1	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q82159 RHOC_MOUSE	Rho-related GTP-binding protein 2	Rhoc	1.25	1.00	1.11	0.80	0.00	0.50	0.75	0.00	0.795	0.519	0.422	1.000	5	9	10	10	1	0	5	3	0	5	3	0	4	2	4	2
TOP PROTEIN	sp Q82159 RHOC_MOUSE	Rho-related GTP-binding protein 2	Rhoc	0.82	1.00	1.11	0.80	0.00	0.10	0.05	0.10	0.795	0.579	0.830	0.422	9	10	10	8	1	3	5	2	5	3	4	3	3	2	4	2
TOP PROTEIN	sp Q82159 RHOC_MOUSE	Rho-related GTP-binding protein 2	Rhoc	0.97	1.10	1.10	0.87	0.00	0.07	0.00	0.00	0.740	0.607	0.607	0.607	52	58	58	52	18	16	11	10	17	8	16	8	16	21	5	
TOP PROTEIN	sp Q8R161 TREN1_MOUSE	TREN1	Tren1	1.49	1.11	1.11	0.81	0.11	0.16	0.11	0.11	0.942	0.539	0.942	0.539	13	13	10	2	1	3	10	2	4	7	4	7	4	7	4	
TOP PROTEIN	sp Q8R161 TREN1_MOUSE	TREN1	Tren1	0.69	1.30	1.44	0.77	-0.16	0.11	0.16	0.11	0.442	0.539	0.442	0.539	9	13	13	10	2	4	3	2	4	7	2	4	7	4	3	4
TOP PROTEIN	sp Q92060 D92060_MOUSE	Carbonyl oligomeric n	Comp1	1.99	0.89	0.94	0.99	-0.03	0.79	-0.03	0.79	0.682	0.862	0.862	0.862	115	170	147	148	46	59	54	68	68	68	68	68	68	64	34	42
TOP PROTEIN	sp Q07113 NPM1_MOUSE	Nucleolin	Npm1	1.38	1.09	1.09	1.00	0.18	0.18	0.00	0.18	0.624	0.492	0.872	1.000	12	11	12	11	2	1	0	3	1	0	5	3	3	3	3	3
TOP PROTEIN	sp Q99272 ACAT1_MOUSE	Acetyl coenzyme A:1	Slc33a1	1.67	2.00	0.40	0.33	0.22	0.30	-0.40	0.48	0.492	0.678	0.349	0.374	5	2	3	1	1	3	2	0	1	2	0	0	0	0	1	0
TOP PROTEIN	sp F23991 SRRP_MOUSE	SRRP alpha-1 related	Srrp1b	1.13	1.17	1.17	1.00	0.00	0.00	0.00	0.00	0.811	0.627	0.811	1.000	13	14	13	13	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q91930 GP1BA_MOUSE	GP1BA	GP1ba	1.67	1.25	2.00	2.67	0.22	0.10	0.30	0.43	0.643	0.519	0.232	0.189	5	10	3	8	0	3	2	2	5	3	0	2	3	2	3	3
TOP PROTEIN	sp F62W60 HFOK_MOUSE	Nucleosome sensitive factor	Hfo1	0.88	1.17	1.00	0.75	-0.06	0.07	0.00	0.12	0.678	0.788	1.000	0.374	7	7	8	6	3	3	1	2	4	3	3	3	2	3	2	3
TOP PROTEIN	sp Q92059 NMG2_MOUSE	NMG2	Nmg2	1.00	1.10	1.10	1.00	0.00	0.48	0.48	0.00	0.62	0.859	0.859	1.000	12	11	11	11	0	0	0	0	0	0	0	0	0	0	0	0
TOP PROTEIN	sp Q92059 NMG2_MOUSE	NMG2	Nmg2	0.92	1.18	0.92	0.62	0.03	0.14	-0.04	-0.21	0.859	0.684	0.890	0.406	12	11	13	8	5	4	3	8	2	1	6	2	1	6	2	4
CO-TO PROTEIN	sp Q8R161 TREN1_MOUSE	TREN1	Tren1	1.22	1.25	0.91	0.89	0.09	0.10	-0.04	-0.05																				



Source	Sequence ID	Sequence Name	Gene Symbol	Ratio AEM/AGWT	Ratio AGEM/AGWT	Ratio AEM/AGM	Ratio AGM/AGWT	Log Ratio AEM/AGWT	Log Ratio AGEM/AGWT	Log Ratio AEM/AGM	Log Ratio AGM/AGWT	p-value AEM/AGWT	p-value AGEM/AGWT	p-value AEM/AGM	p-value AGM/AGWT	AdEM Total Spectral Count	AgEM Total Spectral Count	AdWT Total Spectral Count	AgWT Total Spectral Count	AdEMrp1 Normalized SC	AdEMrp2 Normalized SC	AdEMrp3 Normalized SC	AgEMrp1 Normalized SC	AgEMrp2 Normalized SC	AgEMrp3 Normalized SC	AdWTrp1 Normalized SC	AdWTrp2 Normalized SC	AdWTrp3 Normalized SC	AgWTrp1 Normalized SC	AgWTrp2 Normalized SC	AgWTrp3 Normalized SC	
TOP PROTEIN	sp I18PV12 HPV22_MOUSE	Cullin-5	Cul5	1.33	1.00	1.13	1.50	0.12	0.00	0.05	0.18	0.643	1.000	0.795	0.482	2	4	2	9	2	4	2	2	5	0	2	4	3	2			
TOP PROTEIN	sp I18PV12 HPV22_MOUSE	Cullin-5	Cul5	1.33	1.00	1.13	1.50	0.12	0.00	0.05	0.18	0.643	1.000	0.795	0.482	2	4	2	9	2	4	2	2	5	0	2	4	3	2			
TOP PROTEIN	sp Q9DVA5 CUL5_MOUSE	Cullin-5	Cul5	1.33	1.00	1.13	1.50	0.12	0.00	0.05	0.18	0.643	1.000	0.795	0.482	8	9	6	9	2	4	2	2	5	0	2	4	3	2			
TOP PROTEIN	sp Q9DVA5 CUL5_MOUSE	Cullin-5	Cul5	1.33	1.00	1.13	1.50	0.12	0.00	0.05	0.18	0.643	1.000	0.795	0.482	13	14	14	13	3	5	5	2	8	4	4	6	3	5	5		
TOP PROTEIN	sp I18Q601 CTC_MOUSE	C1-1 centromere protein	Mifn1	0.67	2.33	1.25	0.50	-0.18	0.37	0.24	-0.07	0.288	0.175	0.288	4	7	6	3	4	1	1	1	2	2	2	1	2	1	2			
TOP PROTEIN	sp P16460 ASSY_MOUSE	Argininosuccinate synthetase	Ass1	0.67	2.33	1.75	0.50	-0.18	0.37	0.24	-0.07	0.30	0.561	0.411	0.566	0.288	4	7	6	3	1	3	0	1	5	1	1	3	1	2		
TOP PROTEIN	sp P14152 LCT_MOUSE	Lactalbumin dehydrogenase	Msd1	0.67	1.26	1.16	0.89	-0.01	0.10	0.07	0.05	0.938	0.529	0.675	0.753	74	86	76	68	28	26	20	12	34	40	14	22	40	24	19	25	
TOP PROTEIN	sp Q24761 GPII_MOUSE	Glycophorin II	Ves1	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	1.000	1.000	1.000	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
TOP PROTEIN	sp P16120 SGLT_MOUSE	Glucose transporter pro	Sglt3a1	1.00	0.60	1.00	1.67	0.00	-0.22	0.00	0.22	1.000	0.374	1.000	0.374	3	3	3	5	2	0	1	2	1	0	0	2	1	2	1	2	
TOP PROTEIN	sp Q08795 PLG_MOUSE	Plasminogen 2 subunit	Pkcin3	1.00	0.62	0.85	0.92	0.00	0.04	-0.07	0.03	1.000	0.872	1.000	0.874	13	11	13	12	2	6	5	6	3	2	1	7	5	6	1	2	
TOP PROTEIN	sp Q08795 PLG_MOUSE	Plasminogen 2 subunit	Pkcin3	1.00	0.62	0.85	0.92	0.00	0.04	-0.07	0.03	1.000	0.872	1.000	0.874	13	11	13	12	2	6	5	6	3	2	1	7	5	6	1	2	
TOP PROTEIN	sp Q9DQZ2 PLK_MOUSE	Plk1	Pkic1	1.00	1.33	1.00	1.00	0.00	0.12	0.12	0.00	1.000	0.643	0.643	1.000	3	4	3	3	0	1	2	1	2	1	0	2	1	0	2	1	
TOP PROTEIN	sp Q07797 LGBR_MOUSE	Glycocalyx-binding pro	Lgpb3ap	0.75	1.67	1.67	0.75	-0.12	0.22	0.22	-0.12	0.643	0.492	0.492	0.643	3	5	4	3	0	1	2	1	3	1	1	1	2	0	2	1	
TOP PROTEIN	sp P34668 HBM_MOUSE	Hypoxanthine phosphorib	Hbpl1	0.85	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.872	0.851	0.872	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2		
TOP PROTEIN	sp Q6P949 RAB5_MOUSE	Ras-related protein R5	Rab35	1.25	1.00	1.00	1.50	0.10	0.00	0.08	0.18	0.542	1.000	0.643	0.561	5	6	4	6	2	3	1	3	2	4	6	2	3	1	2	2	
TOP PROTEIN	sp Q29233 LCHL_MOUSE	Cytoskeleton b-1-com	Lgacr3	1.41	1.10	0.89	1.15	0.15	0.04	-0.05	0.06	0.721	0.786	0.822	0.585	387	344	274	314	33	218	136	143	62	139	91	86	97	92	148	74	
TOP PROTEIN	sp P16460 ASSY_MOUSE	Argininosuccinate synthetase	Ass1	1.25	1.75	1.00	1.75	0.00	0.12	0.12	0.00	1.000	0.468	0.468	1.000	4	7	7	7	2	1	3	2	3	2	3	0	3	0	3	2	
TOP PROTEIN	sp Q61738 H1AT_MOUSE	Isomorph Alpha 21B1 o	Hgat7	0.63	0.78	1.40	1.13	-0.20	-0.11	0.15	0.05	0.588	0.643	0.653	0.851	5	7	8	9	4	1	0	3	3	1	1	2	5	5	1	3	
TOP PROTEIN	sp Q61738 H1AT_MOUSE	Isomorph Alpha 21B1 o	Hgat7	0.63	0.78	1.40	1.13	-0.20	-0.11	0.15	0.05	0.588	0.643	0.653	0.851	5	7	8	9	4	1	0	3	3	1	1	2	5	5	1	3	
TOP PROTEIN	sp Q88919 H2A_MOUSE	alpha-mannosidase 2	Man2a1	0.89	0.82	1.13	1.22	0.09	0.09	0.09	0.09	0.788	0.92	0.788	0.92	8	9	9	11	3	2	2	3	2	2	3	5	4	6	4	6	
TOP PROTEIN	sp Q88919 H2A_MOUSE	alpha-mannosidase 2	Man2a1	0.89	0.82	1.13	1.22	0.09	0.09	0.09	0.09	0.788	0.92	0.788	0.92	8	9	9	11	3	2	2	3	2	3	2	4	4	1	4	6	
TOP PROTEIN	sp P12018 PLAM_MOUSE	Plasminogen	Plg	1.08	1.03	1.13	0.89	-0.03	0.01	-0.07	0.05	0.863	0.629	0.693	0.778	41	35	38	34	6	19	16	12	7	19	6	13	12	7	15	16	
TOP PROTEIN	sp Q27468 SVR_MOUSE	Glybosamine aminogly	Svra3	0.88	0.95	0.00	0.00	0.00	0.00	0.04	0.06	0.906	0.768	1.000	0.768	21	21	24	22	5	9	7	6	8	7	9	4	7	9	6		
TOP PROTEIN	sp Q55126 NIP2_MOUSE	Protein Nip2p hom	Gbas	0.88	0.95	1.00	0.92	-0.06	0.02	0.00	0.04	0.696	0.768	1.000	0.768	21	21	24	22	5	9	7	6	8	7	9	4	7	9	6		
TOP PROTEIN	sp Q9W77 NIP2_MOUSE	Protein Nip2p hom	Hmyc1	0.87	1.04	1.00	0.94	-0.01	0.02	0.00	-0.03	0.873	0.805	1.000	0.790	147	147	147	147	52	49	52	56	3	39	56	39	56	51	40	41	
TOP PROTEIN	sp P44279 HLS_MOUSE	Hesionein 1	Hes1a1	1.09	1.09	1.00	1.00	0.04	0.04	0.04	0.04	0.742	0.842	0.859	0.519	12	12	10	10	4	4	3	3	3	3	3	3	3	3	3	3	
TOP PROTEIN	sp Q92206 MECP2_MOUSE	Methyl-CpG-binding p	MeCP2	0.75	1.25	1.11	0.67	-0.12	0.10	0.05	-0.18	0.687	0.742	0.882	0.561	9	10	12	8	4	4	4	1	2	7	1	8	1	3	3	2	
TOP PROTEIN	sp Q92206 MECP2_MOUSE	Methyl-CpG-binding p	MeCP2	0.75	1.25	1.11	0.67	-0.12	0.10	0.05	-0.18	0.687	0.742	0.882	0.561	9	10	12	8	4	4	4	1	2	7	1	8	1	3	3	2	
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16	11	8	1	1	1	1	1	1	1	1	1	1	1	1	1
TOP PROTEIN	sp Q88910 MYC_MOUSE	Myb-like protein 1	Mybl2	1.13	0.97	1.00	1.00	0.00	0.00	0.00	0.00	0.851	0.931	0.866	0.931	31	16															



Figure\_6\_ECM\_Proteomics\_Summarized

Source	Sequence Id	Sequence Name	Gene Symbol	AdEM	AgEM	AdWT	AgWT	Trend	Log Ratio AdEM/AdWT	Log Ratio AgEM/AgWT	Log Ratio AgEM/AdEM	Log Ratio AgWT/AdWT	p-value AdEM/AdWT	p-value AgEM/AgWT	p-value AgEM/AdEM	p-value AgWT/AdWT	AdEM	AdEM	AdEM	AgEM	AgEM	AgEM	AdWT	AdWT	AdWT	AgWT	AgWT	AgWT	AgWT
				Total Spectral Count	Total Spectral Count	Total Spectral Count	Total Spectral Count										rep1 Normalized SC	rep2 Normalized SC	rep3 Normalized SC	rep1 Normalized SC	rep2 Normalized SC	rep3 Normalized SC	rep1 Normalized SC	rep2 Normalized SC	rep3 Normalized SC	rep1 Normalized SC	rep2 Normalized SC	rep3 Normalized SC	
TOP PROTEIN	sp Q99K41 EMILN1_MOUSE	EMILN-1	Emiln1	0	0	152	100		NA	NA	NA	-0.18	0.006	0.000	NA	0.151	0	0	0	0	0	0	49	68	35	33	37	30	
TOP PROTEIN	sp Q66080 CLP1_MOUSE	Cartilage intermediate layer protein 1	Clp1	3	4	54	42		-1.26	-1.02	0.12	-0.11	0.003	0.000	0.663	0.238	0	2	1	1	2	1	17	23	14	16	12	14	
TOP PROTEIN	sp Q021W4 GGF1_MOUSE	Growth/differentiation factor 11	Gdf11	30	37	77	57		-0.41	-0.19	0.09	-0.13	0.044	0.362	0.550	0.432	9	6	15	17	11	9	22	20	35	31	14	12	
TOP PROTEIN	sp Q08879-2 FBLN1_MOUSE	Isoform C of Fibulin-1	Fbln1	13	9	11	35		0.07	-0.59	-0.16	0.50	0.678	0.011	0.442	0.013	4	4	5	2	6	1	4	6	1	14	11	10	
TOP PROTEIN	sp Q9VWH9 FBLN5_MOUSE	Fibulin-5	Fbln5	212	85	133	219		0.20	-0.41	-0.40	0.22	0.507	0.027	0.260	0.244	131	29	52	27	45	13	81	34	18	91	61	67	
TOP PROTEIN	sp P55021 MFAP2_MOUSE	Microfibrillar-associated protein 2	Mfap2	23	12	13	15		0.25	-0.10	-0.28	0.06	0.069	0.519	0.038	0.710	9	7	7	6	3	3	3	7	3	3	6	6	
TOP PROTEIN	sp Q61810-2 LTBP3_MOUSE	Isoform 2 of Latent-transforming growth factor beta-binding protein 3	Ltbp3	12	4	6	4		0.30	0.00	-0.48	-0.18	0.158	1.000	0.039	0.561	4	3	5	2	2	0	3	3	0	1	1	2	
TOP PROTEIN	sp Q35468 WNT9B_MOUSE	Protein Wnt-9b	Wnt9b	12	20	12	4		0.00	0.70	0.22	-0.48	1.000	0.035	0.402	0.016	0	4	8	10	5	5	4	5	3	1	2	1	
TOP PROTEIN	sp AGH584 COL6A5_MOUSE	Collagen alpha-3(VI) chain	Col6a5	42	74	41	28		0.01	0.42	0.25	-0.17	0.851	0.004	0.019	0.034	11	15	16	29	24	21	13	13	15	11	10	7	
TOP PROTEIN	sp Q9Q250 COL4A3_MOUSE	Collagen alpha-3(VI) chain	Col4a3	6	13	7	9		-0.07	0.16	0.34	0.11	0.725	0.116	0.062	0.561	2	2	2	5	4	4	4	1	2	4	3	2	
TOP PROTEIN	sp Q9R045 ANG1_MOUSE	Angiopoietin-related protein 2	Angptl2	12	16	2	10		0.78	0.20	0.12	0.70	0.132	0.279	0.575	0.047	1	4	7	8	4	4	1	1	0	5	2	3	
TOP PROTEIN	sp P29788 VTNC_MOUSE	Vitronectin	Vtn	58	56	88	85		0.18	-0.18	-0.02	0.35	0.152	0.020	0.868	0.004	16	16	26	16	22	18	12	16	10	32	26	27	
TOP PROTEIN	sp P21956-2 MFGM_MOUSE	Isoform 2 of Lactadherin	Mfge8	344	282	220	413		0.19	-0.17	-0.09	0.27	0.230	0.185	0.587	0.029	156	64	124	123	109	50	78	90	52	163	109	141	
TOP PROTEIN	v I3327H8 D327H8_MOUSE	Protein Clp2	Clp2	48	51	24	21		0.15	0.39	0.03	-0.21	0.155	0.150	0.877	0.041	13	14	21	27	16	8	10	13	11	7	9	5	
TOP PROTEIN	sp QBC1E6 COPA_MOUSE	Coatomer subunit alpha	Copa	69	60	69	33		0.00	0.26	-0.06	-0.32	1.000	0.011	0.511	0.004	17	22	30	20	23	17	20	23	26	13	10	10	