

SUPPLEMENTARY DATA

First insight into the proteome landscape of the porcine short posterior ciliary arteries:

Key signalling pathways maintaining physiologic functions

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Supplementary Table S1:
Complete list of the proteins identified from the porcine sPCA employing discovery proteomics strategy.

No.	Protein ID	Protein Name	Gene Name	Intensity	Intensity R1	Intensity R2	Intensity R3	iBAQ	iBAQ R1	iBAQ R2	iBAQ R3
1	F1RII7	Hemoglobin subunit beta	HBB	4.50E+10	1.79E+10	1.02E+10	1.68E+10	4.09E+09	1.63E+09	9.30E+08	1.53E+09
2	P01965	Hemoglobin subunit alpha	HBA	2.70E+10	9.95E+09	6.73E+09	1.04E+10	3.00E+09	1.11E+09	7.48E+08	1.15E+09
3	P00761	Uncharacterized protein	LOC100302368	3.18E+10	1.59E+10	6.85E+09	8.99E+09	2.65E+09	1.33E+09	5.71E+08	7.49E+08
4	B6VNT8	Cardiac muscle alpha actin 1	ACTC1	5.14E+10	1.73E+10	1.05E+10	2.36E+10	2.23E+09	7.54E+08	4.56E+08	1.02E+09
5	F1RUN2	Serum albumin	ALB	8.80E+10	2.30E+10	2.55E+10	3.95E+10	1.96E+09	5.10E+08	5.67E+08	8.79E+08
6	P01846	Ig lambda chain C region		3.46E+09	1.31E+09	9.25E+08	1.23E+09	5.77E+08	2.18E+08	1.54E+08	2.05E+08
7	F1SQ09	Uncharacterized protein	LUM	8.77E+09	2.47E+09	2.48E+09	3.82E+09	5.16E+08	1.45E+08	1.46E+08	2.25E+08
8	F1SJS8	Transgelin	TAGLN	8.13E+09	3.10E+09	1.74E+09	3.29E+09	4.78E+08	1.82E+08	1.03E+08	1.94E+08
9	F1STC5	Uncharacterized protein (Fragment)		2.03E+09	6.57E+08	5.21E+08	8.55E+08	4.06E+08	1.31E+08	1.04E+08	1.71E+08
10	Q86W17	Protease serine 1 (Fragment)	PRSS1	2.24E+09	1.13E+09	6.49E+08	4.69E+08	3.74E+08	1.88E+08	1.08E+08	7.82E+07
11	I3LVD5	Actin, cytoplasmic 2	ACTG1	8.34E+09	1.92E+09	1.51E+09	3.92E+09	3.63E+08	1.27E+08	6.55E+07	7.02E+07
12	Q9XSD9	Desmin	DCN	6.53E+09	1.92E+09	1.68E+09	2.93E+09	3.11E+08	9.12E+07	8.02E+07	1.39E+08
13	L8B0W0	IgG heavy chain	IGHG	5.85E+09	1.88E+09	1.15E+09	2.82E+09	2.66E+08	8.56E+07	5.24E+07	1.28E+08
14	L8B173	IgG heavy chain	IGHG	5.83E+09	1.61E+09	1.67E+09	2.55E+09	2.33E+08	6.43E+07	6.69E+07	1.02E+08
15	F1SKM9	Galectin	LGALS1	2.17E+09	7.39E+08	8.03E+08	6.31E+08	2.17E+08	7.39E+07	8.03E+07	6.31E+07
16	P09571	Serotransferrin	TF	9.91E+09	3.48E+09	2.79E+09	3.64E+09	2.16E+08	7.57E+07	6.06E+07	7.92E+07
17	Q6ZM40	Tropomyosin 1 (Alpha), isoform CRA	TPM1	5.47E+09	2.51E+09	1.30E+09	1.66E+09	2.03E+08	9.28E+07	4.80E+07	6.17E+07
18	AOA0H5ANC0	Osteoglycin/mimcan	OGN	3.72E+09	1.47E+09	8.54E+08	1.39E+09	1.86E+08	7.35E+07	4.27E+07	6.96E+07
19	P02543	Vimentin	VIM	6.20E+09	2.11E+09	1.50E+09	2.59E+09	1.77E+08	6.04E+07	4.29E+07	7.40E+07
20	P79260	S-arrestin	SAG	3.85E+09	1.02E+09	9.12E+08	1.92E+09	1.67E+08	4.42E+07	3.97E+07	8.36E+07
21	AOA0S2Z4H2	Protein S100-A1	S100A1	4.89E+09	1.53E+09	1.80E+08	1.56E+08	1.63E+08	5.09E+07	6.01E+07	5.20E+07
22	F1RXC2	Uncharacterized protein	CA2	2.71E+09	1.15E+09	7.75E+08	7.87E+08	1.59E+08	6.74E+07	4.56E+07	4.63E+07
23	I3LPP5	Creatine kinase B-type	CKB	2.10E+09	9.48E+08	3.65E+08	7.86E+08	1.50E+08	6.77E+07	2.61E+07	5.62E+07
24	P00355	Glyceroldehyde-3-phosphate dehydrogenase	GAPDH	3.99E+09	1.31E+09	8.15E+08	9.70E+08	1.47E+08	6.23E+07	3.88E+07	4.62E+07
25	I3LSR6	Protein S100	S100B	5.65E+08	9.11E+08	1.48E+08	2.26E+08	1.41E+08	4.78E+07	3.69E+07	5.65E+07
26	DOG7F6	Triosephosphate isomerase	TPPI	2.20E+09	7.84E+08	6.40E+08	7.73E+08	1.29E+08	4.61E+07	3.77E+07	4.55E+07
27	D2YH4	Actin alpha 2	ACTA2	2.92E+09	1.23E+09	6.02E+08	1.08E+09	1.27E+08	5.37E+07	2.62E+07	4.70E+07
28	F1RKG8	Phosphatidylethanolamine-binding protein 1	PEBP1	1.77E+09	6.66E+08	4.04E+08	7.00E+08	1.26E+08	4.76E+07	2.88E+07	5.00E+07
29	I3LL97	Cysteine and glycine-rich protein 1	CSRP1	1.86E+09	7.49E+08	5.03E+08	6.04E+08	1.24E+08	4.99E+07	3.35E+07	4.02E+07
30	B4DGK4	Synaptotagmin-7	SYT7	4.93E+08	3.15E+08	2.65E+07	1.51E+08	1.23E+08	7.88E+07	6.63E+06	3.78E+07
31	P19620	Annexin A2	ANXA2	3.07E+09	1.36E+09	8.41E+08	8.70E+08	1.18E+08	5.24E+07	3.23E+07	3.35E+07
32	F1SG00	Uncharacterized protein	TPM2	2.66E+09	9.69E+08	5.88E+08	1.10E+09	1.16E+08	4.21E+07	2.55E+07	4.80E+07
33	Q5XLD3	Creatine kinase M-type	CKM	2.79E+09	1.14E+09	5.76E+08	1.08E+09	1.12E+08	4.54E+07	2.30E+07	4.31E+07
34	I3LK59	Uncharacterized protein	ENO1	2.63E+09	7.50E+08	7.24E+08	1.15E+09	1.09E+08	3.13E+07	3.02E+07	4.80E+07
35	A1XQ76	Myosin light chain 1/3, skeletal muscle isoform	MYL1	1.29E+09	3.01E+08	3.39E+08	6.48E+08	1.07E+08	2.51E+07	2.82E+07	5.40E+07
36	P2Z5C1	Annexin	ANXA5	2.44E+09	7.32E+08	6.52E+08	1.05E+09	1.06E+08	3.18E+07	2.83E+07	4.57E+07
37	P80031	Glutathione S-transferase P	GSTP1	1.24E+09	4.09E+08	3.01E+08	5.31E+08	1.03E+08	3.41E+07	2.51E+07	4.43E+07
38	Q5HYS4	Filamin A	FLNA	1.56E+09	6.67E+08	4.17E+08	4.71E+08	1.03E+08	4.22E+07	2.76E+07	3.12E+07
39	F1R1B9	Alpha-actinin-4	ACTN4	6.17E+09	2.46E+09	1.50E+09	2.21E+09	1.01E+08	4.04E+07	2.46E+07	3.62E+07
40	Q29568	Phosphopyruvate hydratase	PFKP	9.87E+08	2.46E+08	2.62E+08	4.79E+08	9.87E+07	2.46E+07	2.62E+07	4.79E+07
41	K7GP55	Biglycan	BGN	1.86E+09	7.64E+08	4.58E+08	6.36E+08	9.78E+07	4.02E+07	2.41E+07	3.35E+07
42	L8ECP2	Alternative protein PTPDC1	PTPDC1	3.61E+08	1.95E+08	1.00E+08	6.61E+07	9.03E+07	4.87E+07	2.51E+07	1.65E+07
43	Q08092	Calponin-1	CNN1	1.59E+09	7.71E+08	3.27E+08	4.95E+08	8.85E+07	4.28E+07	1.82E+07	2.75E+07
44	V9HWH2	Creatine kinase brain isoform 1	HEL_S_29	2.00E+09	7.56E+08	4.22E+08	8.25E+08	8.71E+07	3.29E+07	1.84E+07	3.59E+07
45	FSW1R7	Myosin light polypeptide 6	MYL6	9.57E+08	3.24E+08	2.06E+08	4.27E+08	8.70E+07	2.94E+07	1.88E+07	3.88E+07
46	Q5XLD2	Myosin regulatory light chain 2	HUMMLC2B	1.04E+09	3.07E+08	2.71E+08	4.65E+08	8.70E+07	2.56E+07	2.26E+07	3.87E+07
47	AOA0C3S001	Apolipoprotein A-I	APOA1	1.66E+09	5.77E+08	4.04E+08	6.83E+08	8.32E+07	2.88E+07	2.02E+07	3.41E+07
48	F1SFT7	Alpha-2-HS-glycoprotein	AHSG	1.34E+09	3.40E+08	3.40E+08	6.55E+08	7.85E+07	2.00E+07	2.00E+07	3.85E+07
49	Q3SX09	Hemoglobin subunit beta		8.58E+08	4.85E+08	1.68E+08	2.04E+08	7.80E+07	4.41E+07	1.53E+07	1.86E+07
50	L8B0U3	IgG heavy chain	IGHG	1.58E+09	5.08E+08	3.92E+08	6.83E+08	7.54E+07	2.42E+07	1.87E+07	3.25E+07
51	F1STC2	Uncharacterized protein (Fragment)		3.74E+08	1.20E+08	1.11E+08	1.42E+08	7.47E+07	2.41E+07	2.22E+07	2.84E+07
52	V9HW98	Epididymis luminal protein 2	HEL2	1.31E+09	5.07E+08	3.19E+08	4.88E+08	7.30E+07	2.82E+07	1.77E+07	2.71E+07
53	F1SHL9	Pyruvate kinase	PKM	2.83E+09	1.09E+09	8.09E+08	9.30E+08	7.25E+07	2.79E+07	2.07E+07	2.88E+07
54	P62936	Peptidyl-prolyl cis-trans isomerase A	PIPA	1.01E+09	4.97E+08	1.86E+08	3.30E+08	7.23E+07	3.55E+07	1.33E+07	2.36E+07
55	DOG6X5	Glutamine synthetase	GLUL	1.33E+09	4.92E+08	2.86E+08	5.48E+08	6.98E+07	2.59E+07	1.51E+07	2.88E+07
56	F1SDX9	Peroxiredoxin 2	PRDX2	9.71E+08	2.92E+08	2.31E+08	4.49E+08	6.93E+07	2.08E+07	1.65E+07	3.20E+07
57	F1SCD0	Uncharacterized protein	LOC396685	1.71E+09	5.04E+08	4.87E+08	7.22E+08	6.59E+07	1.94E+07	1.87E+07	2.78E+07
58	Q8SPS7	Haptoglobin	HP	1.51E+09	6.08E+08	3.61E+08	5.43E+08	6.58E+07	2.65E+07	1.57E+07	2.36E+07
59	Q1KYT0	Beta-enolase	ENO3	2.04E+09	6.07E+08	5.54E+08	8.76E+08	6.57E+07	1.96E+07	1.79E+07	2.83E+07
60	F1RFY1	Profilin	PFN1	5.80E+08	2.66E+08	2.12E+08	1.02E+08	6.44E+07	2.95E+07	2.36E+07	1.13E+07
61	F6KPG5	Albumin (Fragment)	ALB	2.69E+09	7.20E+08	9.33E+08	1.04E+09	6.41E+07	1.71E+07	2.22E+07	2.47E+07
62	P50828	Hemopexin	HPX	1.63E+09	4.88E+08	4.81E+08	6.62E+08	6.27E+07	1.88E+07	1.85E+07	2.55E+07
63	AOA075B7H9	Uncharacterized protein (Fragment)		2.49E+08	7.52E+07	6.26E+07	1.11E+08	6.21E+07	1.88E+07	1.57E+07	2.77E+07
64	L0K5C7	Alternative protein SCP2	SCP2	2.45E+08	7.98E+07	6.69E+07	9.79E+07	6.12E+07	2.00E+07	1.67E+07	2.45E+07
65	L8B0R9	IgG heavy chain	IGHG	1.22E+09	2.97E+08	3.37E+08	6.09E+08	6.09E+07	1.48E+07	1.07E+07	2.84E+07
66	I3Q839	Polychaetinin-B (Fragment)	UBB	5.29E+08	8.02E+08	1.25E+08	5.38E+08	5.88E+07	2.00E+07	3.99E+07	2.48E+07
67	F1S4B4	Uncharacterized protein	PRELP	1.44E+09	5.26E+08	3.28E+08	5.87E+08	5.76E+07	2.10E+07	1.31E+07	2.35E+07
68	V9HW7	Fructose-bisphosphate aldolase	HEL_S_87p	1.35E+09	5.80E+08	2.41E+08	5.28E+08	5.62E+07	2.42E+07	1.01E+07	2.20E+07
69	P10668	Cofilin-1	CFL1	6.46E+08	2.48E+08	1.52E+08	2.45E+08	5.38E+07	2.07E+07	1.27E+07	2.04E+07
70	P20305	Gelsolin (Fragment)	GSN	2.19E+09	7.52E+08	5.07E+08	9.32E+08	5.34E+07	1.83E+07	1.24E+07	2.27E+07
71	F1SM43	S-arrestin	SAG	4.56E+08	1.26E+08	1.06E+08	2.25E+08	5.07E+07	1.40E+07	1.18E+07	2.50E+07
72	K7GL43	Uncharacterized protein (Fragment)	THY1	3.95E+08	1.55E+08	1.08E+08	1.32E+08	4.94E+07	1.93E+07	1.52E+07	1.66E+07
73	F1SLA0	ATP synthase subunit beta	ATP5B	1.47E+09	3.70E+08	3.61E+08	7.41E+08	4.91E+07	1.23E+07	1.20E+07	2.47E+07
74	Q6FHU2	Epididymis secretory protein Li 35 (Fragment)	PGAM1	7.36E+08	3.06E+08	2.52E+08	1.78E+08	4.91E+07	2.04E+07	1.68E+07	1.19E+07
75	D0PN11	Epididymis luminal protein 4	YWHAZ	9.30E+08	3.80E+08	2.52E+08	2.98E+08	4.90E+07	2.00E+07	1.33E+07	1.57E+07
76	F1S1G8	Amine oxidase	AOC3	1.55E+09	6.15E+08	4.00E+08	5.39E+08	4.86E+07	1.92E+07	1.25E+07	1.69E+07
77	P2Z5B6	Tropomyosin alpha-1 chain	TPM1	1.03E+09	5.27E+08	2.51E+08	2.51E+08	4.47E+07	2.29E+07	1.09E+07	1.09E+07
78	Q5S1U1	Heat shock protein beta-1	HSPB1	5.77E+08	2.04E+08	1.47E+08	2.26E+08	4.44E+07	1.57E+07	1.13E+07	1.74E+07
79	Q2S3B7	Phosphoglycerate kinase 1	PGK1	1.40E+09	4.58E+08	2.80E+08	6.60E+08	4.37E+07	1.43E+07	1.07E+07	2.02E+07
80	Q5Z3R1	Beta-actin-like protein 2	ACTB2	1.02E+09	1.65E+08	1.72E+08	4.84E+08	3.25E+07	1.72E+07	1.17E+07	2.02E+07
81	AOA024R694	Actinin, alpha 1, isoform CRA	ACTN1	2.44E+09	1.01E+09	5.87E+08	8.43E+08	4.21E+07	1.74E+07	1.01E+07	1.45E+07
82	F1R1J5	Fructose-bisphosphate aldolase	ALDOC	1.00E+09	3.36E+08	2.05E+08	4.62E+08	4.18E+07	1.40E+07	8.54E+06	1.92E+07
83	P00346	Malate dehydrogenase, mitochondrial	MDH2	9.83E+08	4.55E+08	1.88E+08	3.40E+08	4.10E+07	1.90E+07	7.83E+06	1.42E+07
84	Q0VAS5	Histone H4	HIST1H4H	2.35E+08	1.47E+08	5.73E+07	3.05E+07	3.91E+07	2.45E+07	9.55E+06	5.09E+06
85	Q9GMA6	Alpha-1-antichymotrypsin 2	SERPINA3-2								

Supplementary Table S1: (continued)

145	A0A024R5W6	Tropomyosin 1 (Alpha, isoform CRA	TPM1	3.28E+08	1.65E+08	7.65E+07	8.66E+07	1.43E+07	7.18E+06	3.33E+06	3.77E+06
146	F1RF07	GTP-binding nuclear protein Ran	RAN	1.68E+08	6.68E+07	5.11E+07	5.04E+07	1.40E+07	5.57E+06	4.26E+06	4.20E+06
147	Q6IP79	Elongation factor 1-alpha	EELF1A1	3.51E+08	1.20E+08	8.31E+07	1.48E+08	1.40E+07	4.79E+06	3.32E+06	5.91E+06
148	B1PSB6	Adiponectin (Fragment)	ADIPOQ	2.09E+08	8.33E+07	5.44E+07	7.15E+07	1.40E+07	5.56E+06	3.63E+06	4.77E+06
149	I3LN42	Uncharacterized protein	GC	4.02E+08	1.25E+08	1.31E+08	1.46E+08	1.39E+07	4.29E+06	4.52E+06	5.05E+06
150	F1S177	Uncharacterized protein	LOC100519994	3.67E+08	1.76E+08	8.06E+07	1.10E+08	1.36E+07	6.52E+06	2.98E+06	4.08E+06
151	F1S184	Uncharacterized protein	PGM1	5.13E+08	1.63E+08	1.46E+08	2.04E+08	1.35E+07	4.29E+06	3.85E+06	5.36E+06
152	Q9F6X8	Protein disulfide-isomerase	I3QRU4	4.78E+08	1.49E+08	1.60E+08	1.68E+08	1.33E+07	4.14E+06	4.44E+06	4.68E+06
153	I3QRU4	Vesicle-associated membrane protein 2	VAMP2	6.62E+07	3.20E+07	1.10E+07	2.32E+07	1.32E+07	6.41E+06	2.19E+06	4.64E+06
154	P13645	Keratin, type I cytoskeletal 10	KRT10	3.69E+08	1.35E+08	7.66E+07	1.57E+08	1.32E+07	4.82E+06	2.73E+06	4.96E+06
155	F1S3E7	Uncharacterized protein	CALB2	2.50E+08	8.74E+07	7.53E+07	8.73E+07	1.32E+07	4.60E+06	3.96E+06	4.59E+06
156	E1CA35	Protein disulfide-isomerase	IPP-S8	4.68E+08	1.74E+08	1.47E+08	1.47E+08	1.30E+07	4.82E+06	4.09E+06	4.08E+06
157	Q3ZD69	Prelamin-A/C	LMNA	5.61E+08	1.74E+08	1.27E+08	2.60E+08	1.27E+07	3.96E+06	2.89E+06	5.90E+06
158	Q8IZ29	Tubulin, beta 2C	TUBB2C	2.80E+08	1.21E+08	6.02E+07	9.95E+07	1.27E+07	5.48E+06	2.74E+06	4.52E+06
159	F2Z4Z1	Uncharacterized protein	YWHAQ	2.29E+08	9.51E+07	7.50E+07	5.86E+07	1.27E+07	5.28E+06	4.17E+06	3.26E+06
160	P00339	L-lactate dehydrogenase A chain	LDHA	3.02E+08	1.35E+08	5.22E+07	1.15E+08	1.26E+07	5.61E+06	2.17E+06	4.79E+06
161	Q9T5X9	Peroxisomal protein	PRDX6	2.01E+08	1.01E+08	3.34E+07	6.63E+07	1.26E+07	6.33E+06	2.90E+06	4.14E+06
162	F1SC20	Alpha-1B-glycoprotein	A1BG	3.48E+08	7.69E+07	9.79E+07	1.73E+08	1.24E+07	2.75E+06	3.50E+06	6.17E+06
163	Q6S4N2	Heat shock 70 kDa protein 1B	HSPA1B	4.43E+08	1.18E+08	1.33E+08	1.91E+08	1.23E+07	3.28E+06	3.70E+06	5.31E+06
164	F1S1V3	Uncharacterized protein	ANP32A	1.35E+08	5.62E+07	3.24E+07	4.63E+07	1.23E+07	5.11E+06	2.94E+06	4.21E+06
165	F1S1B60	Superoxide dismutase	SOD2	1.34E+08	4.55E+07	3.37E+07	5.51E+07	1.22E+07	4.13E+06	3.07E+06	5.01E+06
166	P00503	Aspartate aminotransferase, cytoplasmic	GOT1	3.26E+08	1.25E+08	7.52E+07	1.26E+08	1.21E+07	4.64E+06	2.78E+06	4.67E+06
167	Q29290	Cystatin-B	CS1B	9.63E+07	2.01E+07	3.69E+07	3.93E+07	1.20E+07	2.51E+06	4.21E+06	4.91E+06
168	F1SCC7	Uncharacterized protein	LOC100156325	2.76E+08	8.17E+07	8.06E+07	1.14E+08	1.20E+07	3.55E+06	3.51E+06	4.96E+06
169	V9HAC6	Penicillin-prolyl cis-trans isomerase	HEI-S-39	1.92E+08	8.51E+07	4.85E+07	9.06E+07	1.20E+07	3.45E+06	2.91E+06	5.67E+06
170	F1SA98	Uncharacterized protein	YWHAQ	2.28E+08	9.14E+07	6.76E+07	6.92E+07	1.20E+07	4.81E+06	3.56E+06	3.64E+06
171	A0A140TAK8	Uncharacterized protein	APHO	2.64E+08	7.31E+07	7.64E+07	1.14E+08	1.20E+07	3.32E+06	3.47E+06	5.19E+06
172	F1SCC6	Uncharacterized protein	LOC100153899	3.06E+08	9.71E+07	9.13E+07	1.18E+08	1.18E+07	3.73E+06	3.51E+06	4.52E+06
173	F1SKJ8	Uncharacterized protein	PVALB	1.05E+08	3.52E+07	3.90E+07	3.12E+07	1.17E+07	3.92E+06	4.33E+06	3.47E+06
174	V9HWE0	Annexin	HEL-S-7	3.03E+08	9.13E+07	7.66E+07	1.35E+08	1.16E+07	3.51E+06	2.94E+06	5.19E+06
175	Q5MJE5	Cathepsin D protein (Fragment)	HEI-S-7	2.20E+08	8.46E+07	7.11E+07	6.43E+07	1.16E+07	4.45E+06	3.74E+06	3.38E+06
176	F1S1F5	Uncharacterized protein	HRG	3.57E+08	2.34E+08	1.10E+08	1.26E+07	1.15E+07	7.54E+06	3.56E+06	4.08E+05
177	K7EK07	Histone H3 (Fragment)	HEF3B	6.81E+07	4.73E+07	1.39E+07	6.90E+06	1.14E+07	7.89E+06	2.32E+06	1.15E+06
178	F1R1W7	Calnexin	CASQ1	1.81E+08	5.76E+07	6.20E+07	6.18E+07	1.13E+07	3.60E+06	3.88E+06	3.86E+06
179	F1RLH7	Uncharacterized protein	COX6B	7.65E+07	4.10E+07	1.63E+07	1.92E+07	1.09E+07	5.85E+06	2.33E+06	2.75E+06
180	P00506	Aspartate aminotransferase, mitochondrial	GOT2	3.38E+08	1.76E+08	6.32E+07	9.88E+07	1.09E+07	5.66E+06	2.04E+06	3.19E+06
181	J9JL5	Protein S100	LOC100620367	5.36E+07	2.20E+07	1.71E+07	1.07E+07	1.45E+06	3.42E+06	3.42E+06	2.90E+06
182	P50447	Alpha-1-antitrypsin	SERPINA1	2.68E+08	5.11E+07	1.06E+08	1.11E+08	1.07E+07	2.04E+06	4.24E+06	4.43E+06
183	Q5S1S4	Carbonic anhydrase 3	CAS3	1.70E+08	8.49E+07	4.16E+07	4.35E+07	1.06E+07	5.30E+06	2.68E+06	2.72E+06
184	F1SCC9	Uncharacterized protein	CA3	6.30E+07	2.36E+07	2.56E+07	1.38E+07	1.05E+07	3.93E+06	4.26E+06	2.31E+06
185	F1SEN2	Glutamate dehydrogenase 1, mitochondrial	GLUD1	3.84E+08	1.03E+08	1.31E+08	1.49E+08	1.04E+07	2.79E+06	3.53E+06	4.04E+06
186	L8B0S2	IgG heavy chain	IGHG	2.38E+08	7.28E+07	6.21E+07	1.03E+08	1.04E+07	3.16E+06	2.70E+06	4.49E+06
187	K7EQW8	Tropomyosin alpha-4 chain (Fragment)	TPM4	3.10E+07	3.10E+07	0.00E+00	0.00E+00	1.03E+07	1.03E+07	0.00E+00	0.00E+00
188	L8B0V2	IgG heavy chain	IGHG	1.53E+08	3.50E+07	4.44E+07	7.34E+07	1.02E+07	2.33E+06	2.96E+06	4.89E+06
189	P08132	Annexin A4	ANXA4	2.32E+08	7.42E+07	5.73E+07	1.01E+08	1.01E+07	3.23E+06	2.49E+06	4.38E+06
190	P80276	Aldose reductase	AKR1B1	2.09E+08	9.87E+07	5.71E+07	5.34E+07	9.96E+06	4.70E+06	2.72E+06	2.54E+06
191	F1RUK8	Rab GDP dissociation inhibitor beta	GDI2	2.97E+08	8.47E+07	8.14E+07	1.31E+08	9.89E+06	2.82E+06	2.71E+06	4.36E+06
192	Q6IBG1	MYL9 protein	MYL9	1.08E+08	4.53E+07	2.42E+07	3.87E+07	9.83E+06	4.11E+06	2.20E+06	3.52E+06
193	Q29092	Endoplasmic	HSP90B1	4.69E+08	2.08E+08	1.08E+08	1.52E+08	9.76E+06	4.34E+06	2.26E+06	3.17E+06
194	F1SRC8	Uncharacterized protein	CLEC3B	1.16E+08	4.20E+07	2.44E+07	5.00E+07	9.70E+06	3.50E+06	2.03E+06	4.17E+06
195	Q3ZQ10	RSU1 protein (Fragment)	RSU1	1.44E+08	7.41E+07	3.22E+07	3.80E+07	9.61E+06	4.94E+06	2.14E+06	2.53E+06
196	F1S418	Uncharacterized protein	PRDX3	1.42E+08	4.43E+07	3.66E+07	6.14E+07	9.49E+06	2.95E+06	2.44E+06	4.09E+06
197	P02189	Myoglobin	MB	1.13E+08	3.60E+07	2.73E+07	4.93E+07	9.37E+06	3.30E+06	2.28E+06	4.10E+06
198	F1S566	Uncharacterized protein	MYH13	1.17E+09	8.14E+08	2.83E+08	7.69E+07	9.31E+06	6.46E+06	2.24E+06	6.11E+05
199	F1RTJ3	Uncharacterized protein	LOC100525453	2.32E+08	9.45E+07	5.86E+07	7.85E+07	9.26E+06	3.78E+06	2.35E+06	3.14E+06
200	P45846	Dermatopontin	DPT	7.30E+07	3.92E+07	1.25E+07	2.13E+07	9.13E+06	4.90E+06	1.56E+06	2.67E+06
201	A0A0C4DFV9	Protein SET	SET	9.12E+07	4.90E+07	2.02E+07	2.20E+07	9.12E+06	4.90E+06	2.02E+06	2.20E+06
202	Q2EN76	Nucleoside diphosphate kinase B	NME2	1.27E+08	5.65E+07	1.93E+07	5.14E+07	9.09E+06	4.04E+06	1.38E+06	3.67E+06
203	Q7M2W6	Alpha-crystallin B chain	CRYAB	1.18E+08	2.71E+07	2.75E+07	6.35E+07	9.09E+06	2.09E+06	2.11E+06	4.89E+06
204	Q45FV6	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	1.17E+08	4.08E+07	2.74E+07	4.87E+07	8.99E+06	3.14E+06	2.11E+06	3.74E+06
205	F2Z5Y9	Uncharacterized protein	RAB11B	1.43E+08	4.90E+07	3.38E+07	6.00E+07	8.93E+06	3.06E+06	2.11E+06	3.75E+06
206	F2Z5E2	Uncharacterized protein	SERPINC1	2.72E+08	7.08E+07	9.65E+07	1.05E+08	8.77E+06	2.28E+06	3.11E+06	5.37E+06
207	F1SMC0	Adenylyl cyclase-associated protein	CP	2.27E+08	6.73E+07	5.90E+07	1.00E+08	8.72E+06	2.59E+06	2.27E+06	3.86E+06
208	I3VKE6	Ceruloplasmin	RAP1A	5.27E+08	2.40E+08	1.18E+08	1.69E+08	8.50E+06	3.88E+06	1.90E+06	2.73E+06
209	A8K4H9	RAP1A, member of RAS oncogene family	RAP1A	8.42E+07	2.36E+07	2.30E+07	3.77E+07	8.42E+06	2.36E+06	2.30E+06	3.77E+06
210	F1S8C5	Aconitate hydratase, mitochondrial	ACO2	3.60E+08	1.39E+08	6.80E+07	1.54E+08	8.38E+06	2.35E+06	1.58E+06	3.72E+06
211	Q29014	Alpha-1 acid glycoprotein (Fragment)	ORM1	1.17E+08	9.93E+07	3.11E+07	5.65E+07	6.35E+06	2.09E+06	1.45E+06	4.03E+06
212	L8B165	IgG heavy chain	IGHG	1.90E+08	5.72E+07	4.67E+07	8.58E+07	8.25E+06	2.49E+06	2.03E+06	3.73E+06
213	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3BGR13	3.26E+07	1.12E+07	4.60E+06	1.68E+07	8.14E+06	2.80E+06	1.15E+06	4.20E+06
214	F1SUE3	Uncharacterized protein	PPA1	1.46E+08	8.30E+07	2.00E+07	4.34E+07	8.13E+06	4.61E+06	1.11E+06	2.41E+06
215	Q5G6V9	Cofilin-2	CFL2	1.05E+08	3.87E+07	2.48E+07	4.11E+07	8.05E+06	2.98E+06	1.91E+06	3.17E+06
216	F1RTN3	Moesin	MSN	3.04E+08	6.85E+07	9.32E+07	1.42E+08	1.80E+06	2.45E+06	1.38E+06	3.74E+06
217	F1S1E6	Uncharacterized protein	PGM5	2.23E+08	6.99E+07	7.56E+07	7.71E+07	7.95E+06	2.50E+06	2.70E+06	2.75E+06
218	Q00716	Superoxide dismutase [Cu-Zn]	SM	7.88E+07	2.50E+07	2.61E+07	2.77E+07	7.88E+06	2.50E+06	2.61E+06	2.77E+06
219	F2Z5G3	Uncharacterized protein	CALM3	7.09E+07	1.33E+07	7.16E+06	5.04E+07	7.88E+06	1.48E+06	7.06E+05	5.60E+06
220	F2Z5U4	Ras-related protein Rab-1B	RAB1B	1.40E+08	4.10E+07	3.74E+07	6.20E+07	7.80E+06	2.28E+06	2.08E+06	3.44E+06
221	I3LQH7	Uncharacterized protein	BLVRB	1.01E+08	2.86E+07	2.61E+07	4.62E+07	7.76E+06	2.20E+06	2.01E+06	3.55E+06
222	Q06AS6	GBI2	GNAI2	1.55E+08	7.39E+07	3.54E+07	4.53E+07	7.73E+06	3.69E+06	1.77E+06	2.27E+06
223	F8W617	Heterogeneous nuclear ribonucleoprotein A1	HNRNP1	1.38E+08	5.09E+07	2.87E+07	5.79E+07	7.64E+06	2.83E+06	1.59E+06	3.22E+06
224	K7CKS0	Peroxisomal protein	PRDX1	1.15E+08	3.71E+07	2.98E+07	4.77E+07	7.64E+06	2.47E+06	1.99E+06	2.85E+06
225	A7XZEA	Beta tropomyosin isoform	TPM2b	7.70E+07	2.45E+07	2.61E+07	5.93E+07	7.39E+06	3.67E+06	1.45E+06	2.58E+06
226	Q29443	Serotransferrin	RAB6A	3.53E+08	1.11E+08	9.27E+07	1.50E+08	7.35E+06	2.30E+06	1.93E+06	3.12E+06
227	F1R193	Transferrin	TAGLN2	1.02E+08	4.38E+07	2.13E+07	3.65E+07	7.26E+06	3.13E+06	1.52E+06	2.60E+06
228	Q2EN74	Epidermal fatty acid-binding protein	FABP5	7.89E+07	3.44E+07	1.12E+07	3.33E+07	7.17E+06	3.13E+06	1.02E+06	3.02E+06
229	G6UIZ1	Glutathione peroxidase									

Supplementary Table S1: (continued)

293	G9F6Y0	Phosducin (Fragment)	PDC	6.85E+07	3.32E+07	1.88E+07	1.65E+07	4.89E+06	2.37E+06	1.34E+06	1.18E+06
294	F1RK3	Uncharacterized protein	HINT1	3.38E+07	1.80E+07	8.79E+06	7.00E+06	4.83E+06	2.57E+06	1.26E+06	1.00E+06
295	H7BZ3	Protein disulfide-isomerase A3 (Fragment)	PDIA3	4.32E+07	1.59E+07	2.05E+07	6.74E+06	4.80E+06	1.77E+06	2.28E+06	7.49E+05
296	F1S6Q7	ATP synthase subunit delta, mitochondrial	ATP5D	2.87E+07	9.68E+06	3.06E+06	1.59E+07	4.78E+06	1.61E+06	5.10E+05	2.65E+06
297	F1RM62	Uncharacterized protein	HSPB6	3.34E+07	8.79E+06	1.12E+07	1.34E+07	4.77E+06	1.26E+06	1.60E+06	1.91E+06
298	F1T0F7	Cellular retinoic acid binding protein 1	CRABP1	5.71E+07	2.73E+07	9.90E+06	1.98E+07	4.76E+06	2.28E+06	8.25E+05	1.65E+06
299	P80310	Protein S100-A12	S100A12	2.83E+07	1.01E+07	1.09E+07	7.40E+06	4.72E+06	1.68E+06	1.81E+06	1.23E+06
300	E1CA6	Protein disulfide isomerase P5	pdi-p5	1.18E+08	4.79E+07	3.13E+07	3.85E+07	4.71E+06	1.92E+06	1.25E+06	1.54E+06
301	L0R4Z3	Alternative protein KCTD3	KCTD3	2.35E+07	3.67E+06	7.43E+06	1.24E+07	4.70E+06	7.34E+05	1.49E+06	2.48E+06
302	B0LY42	CD147		7.99E+07	4.28E+07	1.79E+07	1.93E+07	4.70E+06	2.52E+06	1.05E+06	1.13E+06
303	P59768	Guanine nucleotide-binding protein G(i)(G(S)/G(O) subunit gamma-2	GNG2	2.80E+07	1.08E+07	7.00E+06	1.02E+07	4.67E+06	1.80E+06	1.17E+06	1.71E+06
304	Q3YL6	Serine/arginine-rich splicing factor 1	SRSF1	6.99E+07	2.98E+07	1.79E+07	2.22E+07	4.66E+06	1.99E+06	1.19E+06	1.48E+06
305	F1SLF0	Uncharacterized protein	SPR	7.91E+07	3.23E+07	2.56E+07	2.13E+07	4.65E+06	1.90E+06	1.50E+06	1.25E+06
306	B4DX77	Nicotin-1	NICN1	6.04E+07	4.23E+07	1.81E+07	0.00E+00	4.64E+06	3.25E+06	1.39E+06	0.00E+00
307	Q9MZ16	Voltage-dependent anion-selective channel protein 1	VDAC1	8.29E+07	3.85E+07	1.28E+07	3.16E+07	4.61E+06	2.14E+06	7.12E+05	1.75E+06
308	F1SH8	Transitional endoplasmic reticulum ATPase	VCP	2.21E+08	8.90E+07	5.83E+07	7.35E+07	4.60E+06	1.85E+06	1.21E+06	1.53E+06
309	F1SD87	Uncharacterized protein	FBLN5	1.01E+08	3.39E+07	2.55E+07	4.16E+07	4.59E+06	1.54E+06	1.16E+06	1.89E+06
310	C9J7L5	Acetyl-coenzyme A synthetase, cytoplasmic (Fragment)	ACSS2	3.66E+07	3.42E+07	2.33E+06	0.00E+00	4.57E+06	4.28E+06	2.92E+05	0.00E+00
311	Q7Z612	Acidic ribosomal phosphoprotein P1	RPLP1	1.83E+07	1.02E+07	7.01E+06	1.07E+06	4.57E+06	2.54E+06	1.75E+06	2.68E+05
312	F1S285	Uncharacterized protein	COL14A1	4.10E+08	1.96E+08	1.11E+08	1.02E+08	4.55E+06	2.18E+06	1.24E+06	1.13E+06
313	F1S0M2	Uncharacterized protein	HRSPI2	4.43E+07	1.74E+07	1.43E+07	1.27E+07	4.43E+06	1.74E+06	1.43E+06	1.27E+06
314	F1S2K3	Uncharacterized protein	NUTF2	3.54E+07	1.33E+07	1.30E+07	9.11E+06	4.42E+06	1.66E+06	1.62E+06	1.14E+06
315	F1RYZ0	60S acidic ribosomal protein P2	RPLP2	2.20E+07	7.31E+06	7.62E+06	7.05E+06	4.40E+06	1.46E+06	1.52E+06	1.41E+06
316	Q00773	Tetraspanin	CD81	3.95E+07	3.12E+07	4.08E+06	4.27E+06	4.39E+06	3.46E+06	4.54E+05	4.75E+05
317	A0A158RFU6	RAB7, member RAS oncogene family, isoform CRA	RAB7A	7.45E+07	2.71E+07	2.05E+07	2.69E+07	4.38E+06	1.59E+06	1.21E+06	1.58E+06
318	L8B0X5	IgG heavy chain	IgHG	8.76E+07	1.06E+07	2.10E+07	2.60E+07	4.38E+06	2.03E+06	1.05E+06	1.30E+06
319	A0A087X2J4	Vacuolar protein sorting-associated protein 11 homolog (Fragment)	VPS11	5.68E+07	2.57E+07	1.04E+07	2.07E+07	4.37E+06	1.97E+06	8.03E+05	1.59E+06
320	Q6QAT1	40S ribosomal protein S28	RPS28	1.30E+07	6.04E+06	3.07E+06	3.88E+06	4.33E+06	2.01E+06	1.02E+06	1.29E+06
321	Q53Y06	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1	ATP6V1E1	6.86E+07	2.84E+07	1.84E+07	4.29E+07	4.29E+06	1.78E+06	1.21E+06	1.36E+06
322	Q9GJT2	S-fornylglutathione hydrolase	ESD	6.79E+07	3.53E+07	1.12E+07	2.13E+07	4.24E+06	2.21E+06	7.01E+05	1.33E+06
323	L8B0W9	IgG heavy chain	IgHG	7.62E+07	2.57E+07	2.21E+07	2.85E+07	4.23E+06	1.43E+06	1.23E+06	1.58E+06
324	F1S1R4	SH3 domain-binding glutamic acid-rich-like protein	SH3BGR1	3.79E+07	1.32E+07	1.28E+07	1.20E+07	4.22E+06	1.47E+06	1.42E+06	1.33E+06
325	P10523	S-arrestin	SAG	1.10E+08	1.37E+07	2.02E+07	7.57E+07	4.21E+06	5.27E+05	7.77E+05	2.91E+06
326	L3LD72	Uncharacterized protein	EHD2	1.47E+08	6.21E+07	3.86E+07	4.59E+07	4.19E+06	1.78E+06	1.10E+06	1.31E+06
327	B9TSR8	Complement factor B	CFB	1.84E+08	7.34E+07	4.88E+07	6.15E+07	4.17E+06	1.67E+06	1.11E+06	1.40E+06
328	Q6FIC5	Chloride intracellular channel protein	CLIC4	7.07E+07	3.58E+07	1.89E+07	1.59E+07	4.16E+06	2.11E+06	1.11E+06	9.38E+05
329	Q00772	Cell division control protein 42 homolog	CDC42	3.73E+07	1.12E+07	9.83E+06	1.62E+07	4.14E+06	1.24E+06	1.09E+06	1.80E+06
330	F1RQ99	Uncharacterized protein	PRDX5	4.12E+07	2.07E+07	6.32E+06	1.42E+07	4.12E+06	2.07E+06	6.32E+05	1.42E+06
331	F1S4K6	Uncharacterized protein	ATP5L	2.88E+07	9.03E+06	8.11E+06	1.17E+07	4.12E+06	1.17E+06	1.16E+06	1.66E+06
332	F1S5R9	Guanylate kinase	GUK1	5.73E+07	1.43E+07	1.97E+07	2.32E+07	4.09E+06	1.02E+06	1.41E+06	1.66E+06
333	F1SHD6	Uncharacterized protein	FEF1B2	6.13E+07	2.27E+07	2.12E+07	1.74E+07	4.09E+06	1.52E+06	1.41E+06	1.16E+06
334	F2Z560	Uncharacterized protein	RAB3C	5.72E+07	2.26E+07	1.24E+07	2.22E+07	4.08E+06	1.61E+06	8.84E+05	1.58E+06
335	F1RHL9	Uncharacterized protein	ACTN2	2.52E+08	8.73E+07	7.64E+07	8.86E+07	4.07E+06	1.41E+06	1.23E+06	1.43E+06
336	Q5U0A0	Proteasome subunit alpha type	PSMA5	4.85E+07	2.28E+07	8.30E+06	1.74E+07	4.04E+06	1.90E+06	6.92E+05	1.45E+06
337	F1RY6	Transaldolase	TALDO1	8.35E+07	4.50E+07	1.58E+07	2.27E+07	3.98E+06	2.14E+06	7.53E+05	1.08E+06
338	P09623	Dihydrolipoyl dehydrogenase, mitochondrial	DLI	1.06E+08	3.23E+07	3.05E+07	4.35E+07	3.94E+06	1.20E+06	1.13E+06	1.61E+06
339	L3LDW9	Small nuclear ribonucleoprotein E	SNRPE	1.57E+07	4.05E+06	5.44E+06	6.22E+06	3.93E+06	1.01E+06	1.36E+06	1.56E+06
340	F1SMZ7	Uncharacterized protein	HSPD1	1.37E+08	5.91E+07	4.03E+07	3.80E+07	3.93E+06	1.69E+06	1.15E+06	1.09E+06
341	L3LKF3	Fascin	LOC100625519	1.17E+08	3.98E+07	3.97E+07	3.76E+07	3.90E+06	1.33E+06	1.32E+06	1.25E+06
342	E7EQG2	Eukaryotic initiation factor 4A-II	EIF4A2	8.58E+07	2.63E+07	1.94E+07	4.01E+07	3.90E+06	1.20E+06	8.80E+05	1.82E+06
343	Q8MJ30	Dihydropteridine reductase	QDPR	6.60E+07	2.50E+07	2.17E+07	1.93E+07	3.88E+06	1.47E+06	1.28E+06	1.14E+06
344	Q1W230	14-3-3 sigma protein	Sm	6.97E+07	2.08E+07	2.46E+07	2.42E+07	3.87E+06	1.16E+06	1.37E+06	1.34E+06
345	A0A024R7V6	RAB2, member RAS oncogene family, isoform CRA	RAB2	8.80E+07	1.68E+07	1.15E+07	2.98E+07	3.87E+06	1.12E+06	7.65E+05	1.98E+06
346	Q52N34	ADP-ribosylation factor-like protein 3	ARL3	4.19E+07	1.28E+07	1.13E+07	1.78E+07	3.81E+06	1.16E+06	1.03E+06	1.62E+06
347	Q6IAV3	Eukaryotic translation initiation factor 1, isoform CRA	SUI1	1.88E+07	8.52E+06	5.67E+06	4.65E+06	3.77E+06	1.70E+06	1.13E+06	9.31E+05
348	Q95250	Membrane-associated progesterone receptor component 1	PGRMC1	3.77E+07	1.71E+07	9.03E+06	1.16E+07	3.77E+06	1.71E+06	9.03E+05	1.16E+06
349	A0A024R216	Hepatoma-derived growth factor, related protein 3, isoform CRA	HDFGRFP3	3.76E+07	1.53E+07	1.06E+07	1.17E+07	3.76E+06	1.53E+06	1.06E+06	1.17E+06
350	F1RHW4	Uncharacterized protein	RFB	5.63E+07	2.42E+07	1.42E+07	1.78E+07	3.75E+06	1.61E+06	9.48E+05	1.19E+06
351	F1RX37	Fibrinogen beta chain	FGB	1.27E+08	5.90E+07	2.89E+07	3.86E+07	3.72E+06	1.74E+06	8.50E+05	1.14E+06
352	A0A075B7I7	Uncharacterized protein (Fragment)		2.60E+07	1.12E+07	5.02E+06	9.71E+06	3.71E+06	1.60E+06	7.17E+05	1.39E+06
353	C9J0J7	Profilin	PFN2	2.22E+07	1.26E+07	4.22E+06	5.42E+06	3.71E+06	2.10E+06	7.03E+05	9.04E+05
354	F1S1W8	Uncharacterized protein	SERPING1	9.22E+07	2.41E+07	1.88E+07	4.94E+07	3.69E+06	9.63E+05	7.50E+05	1.98E+06
355	P35527	Keratin, type I cytoskeletal 9	KRT9	1.11E+08	3.67E+07	3.78E+07	3.62E+07	3.69E+06	1.22E+06	1.26E+06	1.21E+06
356	Q6FHM2	GNB2 protein	GNB2	4.76E+07	2.53E+07	9.58E+06	1.12E+07	3.66E+06	1.95E+06	7.37E+05	9.76E+05
357	Q00772	Fatty acid-binding protein, heart	FABP3	4.74E+07	2.06E+07	1.54E+07	1.47E+07	3.65E+06	1.19E+06	1.19E+06	8.76E+05
358	F2Z5D2	Uncharacterized protein	ACTR3	7.94E+07	2.94E+07	1.70E+07	3.37E+07	3.61E+06	1.36E+06	7.72E+05	1.04E+06
359	L3LAA0	Uncharacterized protein (Fragment)		2.16E+07	5.51E+06	6.32E+06	8.73E+06	3.16E+06	1.05E+06	4.53E+05	1.42E+06
360	P63246	Receptor of activated protein C kinase 1	RACK1	7.85E+07	4.52E+07	1.04E+07	2.29E+07	3.57E+06	2.05E+06	4.73E+05	1.04E+06
361	K7GQD4	Protein S100 (Fragment)	S100A16	1.78E+07	4.42E+06	5.82E+06	7.58E+06	3.56E+06	8.85E+05	1.16E+06	1.52E+06
362	B4DKJ4	cDNA FLJ57738, highly similar to Translationally-controlled tumor protein	TPT1	2.13E+07	5.99E+06	3.68E+06	1.16E+07	3.55E+06	9.98E+05	6.14E+05	1.94E+06
363	Q6FHG6	PRELP protein (Fragment)	PRELP	8.86E+07	3.76E+07	2.14E+07	2.96E+07	3.54E+06	1.50E+06	8.58E+05	1.18E+06
364	F1S3W0	Cytochrome b-c1 complex subunit 6	LOC100524873	2.82E+07	6.50E+06	1.10E+07	1.08E+07	3.53E+06	8.12E+05	1.37E+06	1.35E+06
365	H0YMA1	Proteasome subunit alpha type (Fragment)	PSMA4	3.88E+07	1.53E+07	1.33E+07	1.02E+07	3.53E+06	1.39E+06	1.21E+06	9.29E+05
366	F1RPC8	Uncharacterized protein	CRYM	4.91E+07	1.94E+07	9.58E+06	2.01E+07	3.51E+06	1.39E+06	6.85E+05	1.43E+06
367	L3LFW6	Uncharacterized protein	UBE2V1	4.20E+07	1.55E+07	3.30E+06	2.32E+07	3.50E+06	1.29E+06	2.75E+05	1.93E+06
368	H8BPD9	Nucleoside diphosphate kinase 3 (Fragment)	NME3	1.39E+07	4.26E+06	2.77E+06	6.90E+06	3.48E+06	1.07E+06	6.92E+05	1.72E+06
369	K7GM19	Tetraspanin (Fragment)	CD9	2.08E+07	6.00E+06	1.50E+06	1.33E+07	3.47E+06	1.00E+06	2.50E+05	2.22E+06
370	K7GRY0	Uncharacterized protein (Fragment)	UBA1	1.90E+08	7.59E+07	4.27E+07	7.10E+07	3.45E+06	1.38E+06	7.77E+05	1.29E+06
371	L3LS04	Uncharacterized protein	ACTN1	9.85E+07	3.93E+07	2.69E+07	3.23E+07	3.40E+06	1.36E+06	9.27E+05	1.11E+06
372	L3LHC8	Uncharacterized protein	LOC100522692	5.06E+07	2.94E+07	1.15E+07	1.87E+07	3.37E+06	1.36E+06	7.91E+05	1.34E+06
373	L3LRX0	Uncharacterized protein	C14H10orf116	1.35E+07	1.62E+06	3.19E+06	5.67E+06	3.16E+06	1.08E+06	1.98E+05	1.42E+06
374	V9HW56	Epididymis secretory protein Li 108	HEL_S-108	7.03E+07	2.77E+07	2.04E+07	2.22E+07	3.35E+06	1.32E+06	9.72E+05	1.06E+06
375	L8AXK3	IgG heavy chain	IgHG	6.98E+07	2.11E+07	2.06E+07	2.81E+07	3.32E+06	1.01E+06	9.80E+05	1.34E+06
376	P00348	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	6.31E+07	3.03E+07	9.82E+06					

Supplementary Table S1: (continued)

441	F1RX35	Uncharacterized protein	LOC100627396	7.50E+07	5.57E+07	1.83E+07	2.10E+07	2.50E+06	1.19E+06	6.10E+05	7.00E+05
442	F1RLG5	Receptor expression-enhancing protein	REEP5	1.99E+07	9.39E+06	4.32E+06	6.22E+06	2.49E+06	1.17E+06	5.41E+05	7.77E+05
443	P24540	Acylphosphatase-1	ACYP1	1.74E+07	4.52E+06	6.17E+06	6.73E+06	2.49E+06	6.45E+05	8.81E+05	9.61E+05
444	I3L7T8	Uncharacterized protein	ATP5H	1.99E+07	7.69E+06	7.12E+06	5.08E+06	2.49E+06	9.61E+05	8.90E+05	6.35E+05
445	Q00P29	Beta actin (Fragment)	ACTB	4.97E+06	4.97E+06	0.00E+00	0.00E+00	2.48E+06	2.48E+06	0.00E+00	0.00E+00
446	P02769	Bovine serum albumin precursor		1.12E+08	5.62E+07	5.18E+07	3.65E+06	2.48E+06	1.25E+06	1.15E+06	8.12E+04
447	Q6B7T8	Serine/threonine-protein phosphatase	PPP2CA	4.47E+07	2.73E+07	9.76E+06	7.65E+06	2.48E+06	1.51E+06	5.42E+05	4.25E+05
448	F1SKM0	Uncharacterized protein	UQCRC1	5.93E+07	1.81E+07	1.92E+07	2.20E+07	2.47E+06	7.55E+05	8.00E+05	9.17E+05
449	Q53R19	Actin related protein 2/3 complex, subunit 2, 34kDa, isoform CRA	ARPC2	5.56E+07	1.90E+07	1.19E+07	2.47E+07	2.42E+06	8.25E+05	5.17E+05	1.07E+06
450	Q07717	Beta-2-microglobulin	B2M	1.69E+07	3.29E+06	5.30E+06	8.32E+06	2.42E+06	4.70E+05	7.58E+05	1.19E+06
451	K7CP49	Uncharacterized protein	MCAM	7.90E+07	3.67E+07	1.67E+07	2.56E+07	2.39E+06	1.11E+06	5.05E+05	7.77E+05
452	B4E2P9	cDNA FLJ57038, highly similar to Filamin-A		1.10E+08	4.41E+07	2.84E+07	3.70E+07	2.38E+06	9.58E+05	6.18E+05	8.04E+05
453	Q000H8	Glutathione S-transferase mu 2 (Fragment)		3.32E+07	1.37E+07	8.47E+06	1.10E+07	2.37E+06	9.81E+05	6.05E+05	7.89E+05
454	Q5P53	Tubulin beta chain	TUBB	4.95E+07	2.51E+07	1.46E+07	9.78E+06	2.36E+06	1.20E+06	6.96E+05	4.66E+05
455	F1SR80	Uncharacterized protein	LOC100158003	5.35E+07	1.18E+07	1.39E+07	2.78E+07	2.32E+06	5.13E+05	6.05E+05	1.21E+06
456	F2Z5N0	Proteasome subunit alpha type	PSMA6	3.94E+07	1.60E+07	9.59E+06	1.38E+07	2.32E+06	9.41E+05	5.64E+05	8.14E+05
457	F1SSG6	Uncharacterized protein	ANP32B	2.78E+07	1.16E+07	5.94E+06	1.02E+07	2.32E+06	9.70E+05	4.95E+05	8.53E+05
458	B3KY04	cDNA FLJ46506 fis, clone THYMU3030752, highly similar to BTB/POZ domain-containing protein KCTD12	KC	3.94E+07	1.86E+07	1.29E+07	7.81E+06	2.32E+06	1.10E+06	7.61E+05	4.59E+05
459	F1SK35	Uncharacterized protein	RLBP1	4.16E+07	2.26E+07	5.40E+06	1.37E+07	2.31E+06	1.25E+06	3.00E+05	7.59E+05
460	I3LUC8	Peptidyl-prolyl cis-trans isomerase		3.45E+07	9.14E+06	9.35E+06	1.60E+07	2.30E+06	6.09E+05	6.23E+05	1.07E+06
461	F1SKY2	Uncharacterized protein	NTF2	5.52E+07	1.82E+07	1.68E+07	2.02E+07	2.30E+06	7.57E+05	7.00E+05	8.41E+05
462	F1S1A9	Uncharacterized protein	APOA2	1.38E+07	5.88E+06	3.11E+06	4.79E+06	2.30E+06	9.80E+05	5.19E+05	7.98E+05
463	Q9N1F5	Glutathione S-transferase omega-1	GSTO1	3.61E+07	1.44E+07	1.16E+07	1.01E+07	2.26E+06	9.01E+05	7.25E+05	6.30E+05
464	I3LRH2	Uncharacterized protein	LOC100519984	1.04E+08	2.44E+07	3.69E+07	4.23E+07	2.25E+06	5.31E+05	8.03E+05	9.20E+05
465	K7CR9V	Uncharacterized protein	RS1	2.92E+07	1.47E+07	6.59E+06	7.98E+06	2.25E+06	1.13E+06	5.07E+05	6.14E+05
466	F1RH33	Catechol O-methyltransferase	COMT	3.34E+07	1.48E+07	7.84E+06	1.08E+07	2.23E+06	9.87E+05	5.23E+05	7.18E+05
467	F1SQX9	Uncharacterized protein	APOD	2.21E+07	8.54E+06	7.18E+06	6.37E+06	2.21E+06	8.54E+05	7.18E+05	6.37E+05
468	F2Z5G9	Uncharacterized protein	SNRPP1	1.10E+07	4.59E+06	3.37E+06	3.07E+06	2.21E+06	9.19E+05	6.74E+05	6.13E+05
469	I3L9V2	Uncharacterized protein	VATI	4.63E+07	2.19E+07	6.50E+06	1.79E+07	2.20E+06	1.04E+06	3.10E+05	8.52E+05
470	Q00P25	Hypoxanthine phosphoribosyltransferase 1 (Fragment)	HPRT1	6.60E+06	6.60E+06	0.00E+00	0.00E+00	2.20E+06	2.20E+06	0.00E+00	0.00E+00
471	A0A024R5Z9	Pyruvate kinase	PKM2	8.57E+07	2.85E+07	3.25E+07	2.47E+07	2.20E+06	7.30E+05	8.34E+05	6.33E+05
472	F1ST02	Proteasome subunit beta type	PSMB4	2.39E+07	5.99E+06	5.15E+06	1.28E+07	2.17E+06	5.45E+05	4.68E+05	1.16E+06
473	I3LER5	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	2.61E+07	1.72E+07	1.25E+06	7.65E+06	2.17E+06	1.43E+06	1.04E+05	6.38E+05
474	Q49AN9	SNRPG protein	SNRPG	4.33E+06	1.13E+06	9.82E+05	2.23E+06	2.17E+06	5.63E+05	4.91E+05	1.11E+06
475	P80229	Leukocyte elastase inhibitor	SERP1NB1	5.76E+07	3.12E+07	1.46E+07	1.18E+07	2.13E+06	1.16E+06	5.39E+05	4.38E+05
476	I3LR51	Uncharacterized protein	FKBP3	1.92E+07	8.03E+06	6.51E+06	4.63E+06	2.13E+06	8.92E+05	7.24E+05	5.15E+05
477	P68137	Actin, alpha skeletal muscle	ACTA1	4.85E+07	6.24E+06	8.87E+06	3.34E+07	2.11E+06	2.71E+05	3.86E+05	1.45E+06
478	Q2LE71	Actin-related protein 2/3 complex subunit 3	ARPC3	2.52E+07	8.31E+06	6.95E+06	9.97E+06	2.10E+06	6.92E+05	5.79E+05	8.31E+05
479	A0A024R883	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1, isoform CRA	ATP6V1G1	1.47E+07	5.79E+06	1.55E+06	7.37E+06	1.10E+06	8.27E+05	2.27E+05	1.05E+06
480	I3LQ50	Uncharacterized protein	HNRNPK	5.42E+07	1.47E+07	1.70E+07	2.25E+07	2.08E+06	5.64E+05	6.84E+05	8.66E+05
481	Q86TY5	Galectin	HCG	2.29E+07	1.23E+07	4.54E+06	6.05E+06	2.08E+06	1.12E+06	4.13E+05	5.50E+05
482	I3LY4	Uncharacterized protein	NQO2	1.04E+07	2.65E+06	3.25E+06	4.51E+06	2.08E+06	5.29E+05	6.15E+05	9.02E+05
483	F1S232	4-trimethylaminobutylaldehyde dehydrogenase	ALDH1A1	7.26E+07	1.77E+07	2.41E+07	3.09E+07	2.08E+06	5.05E+05	6.87E+05	8.83E+05
484	Q2NLD4	PURA protein (Fragment)	PURA	3.11E+07	9.28E+06	5.80E+06	1.60E+07	2.07E+06	6.19E+05	3.87E+05	1.07E+06
485	F1RLU1	Uncharacterized protein	HSD17B10	3.31E+07	1.74E+07	9.02E+06	6.64E+06	2.07E+06	1.09E+06	5.64E+05	4.15E+05
486	I3LQ51	Proteasome subunit beta type	PSMB1	2.88E+07	9.75E+06	4.94E+06	1.41E+07	2.06E+06	6.97E+05	3.53E+05	1.01E+06
487	I3LAQ6	Uncharacterized protein	ABHD14B	2.25E+07	7.56E+06	6.28E+06	8.67E+06	2.05E+06	6.87E+05	5.71E+05	7.88E+05
488	C3S7K6	Calcium-binding protein A9	S100A9	1.22E+07	3.11E+06	2.35E+06	6.74E+06	2.03E+06	5.18E+05	3.92E+05	1.12E+06
489	F1S8H5	DNA-(apurinic or apyrimidinic site) lyase	APEX1	3.85E+07	2.91E+07	2.71E+06	6.69E+06	2.03E+06	1.53E+06	1.42E+05	3.52E+05
490	D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	2.83E+07	1.32E+07	6.31E+06	8.79E+06	2.02E+06	9.41E+05	4.50E+05	6.28E+05
491	P37111	Aminoacylase-1	ACY1	4.82E+07	1.36E+07	1.29E+07	2.16E+07	2.01E+06	5.68E+05	5.36E+05	9.02E+05
492	Q94875	Sorbin and SH3 domain-containing protein 2	SORBS2	1.26E+08	5.08E+07	2.85E+07	4.67E+07	2.00E+06	8.06E+05	4.53E+05	7.41E+05
493	Q028R0	Cystatin	CST3	1.59E+07	5.59E+06	6.52E+06	3.78E+06	1.99E+06	6.99E+05	8.15E+05	4.93E+05
494	K7CQW5	Ectonucleoside triphosphate diphosphohydrolase 1 (Fragment)	ENTPD1	1.74E+07	5.90E+06	4.41E+06	7.13E+06	1.94E+06	6.56E+05	4.89E+05	7.92E+05
495	F1RH2	Uncharacterized protein	HDGF	3.46E+07	1.15E+07	1.16E+07	1.15E+07	1.92E+06	6.38E+05	6.45E+05	6.37E+05
496	F1ST88	Uncharacterized protein	GLPFR2	1.89E+07	6.58E+06	4.47E+06	7.82E+06	1.89E+06	6.58E+05	4.47E+05	7.82E+05
497	P86412	Myelin P2 protein	PMP2	2.26E+07	1.27E+07	3.69E+06	6.24E+06	1.88E+06	1.06E+06	3.07E+05	5.20E+05
498	P51525	Prophenin-2	PPP2R1	3.20E+07	1.39E+07	8.71E+06	9.43E+06	1.88E+06	8.18E+05	5.12E+05	5.54E+05
499	Q53GF5	Proteasome subunit alpha type (Fragment)	PS1	3.00E+07	1.11E+07	8.40E+06	1.05E+07	1.88E+06	6.95E+05	5.25E+05	6.57E+05
500	F1RL38	Uncharacterized protein	DDT	1.47E+07	3.40E+06	5.95E+06	5.40E+06	1.84E+06	4.24E+05	7.44E+05	6.75E+05
501	F1RYJ8	Uncharacterized protein	CSRP2	2.56E+07	1.18E+07	6.52E+06	7.34E+06	1.83E+06	8.41E+05	4.66E+05	5.24E+05
502	I3L916	Uncharacterized protein	BCAM	6.76E+07	1.38E+07	2.12E+07	3.26E+07	1.83E+06	3.72E+05	5.74E+05	8.80E+05
503	M3UZ63	UPF056 protein C19orf10	C19orf10	2.18E+07	1.17E+07	1.37E+06	8.73E+06	1.82E+06	9.74E+05	1.14E+05	7.27E+05
504	Q710C4	Adenosylhomocysteinase	AHCY	4.30E+07	1.74E+07	1.04E+07	1.53E+07	1.79E+06	7.24E+05	4.32E+05	6.37E+05
505	F1KPW9	Elongation factor 1-gamma	EEF1G	4.47E+07	1.82E+07	9.79E+06	1.66E+07	1.79E+06	7.30E+05	3.99E+05	6.65E+05
506	F2Z5P9	Uncharacterized protein	LOC100739296	1.24E+07	1.54E+06	4.66E+06	6.23E+06	1.78E+06	2.20E+05	8.33E+05	8.81E+05
507	Q6RAY0	Ubiquitin-conjugating enzyme E2 D3 (Fragment)	UBE2D3	5.31E+06	1.04E+06	0.00E+00	1.28E+06	1.77E+06	1.33E+06	6.09E+05	4.26E+05
508	F1SAC1	Uncharacterized protein	ECHS1	3.18E+07	1.43E+07	9.53E+06	7.94E+06	1.77E+06	7.96E+05	5.29E+05	4.41E+05
509	Q6LAQ8	Electron transfer flavoprotein subunit beta	ETFb	2.47E+07	1.22E+07	8.90E+06	3.56E+06	1.76E+06	8.73E+05	6.66E+05	2.54E+05
510	F1SFF3	Uncharacterized protein	S100A14	1.41E+07	6.08E+06	3.72E+06	4.25E+06	1.76E+06	7.60E+05	4.66E+05	5.32E+05
511	Q9UEH5	24-kDa subunit of complex I (Fragment)	NDUFV2	2.45E+07	8.78E+06	6.48E+06	9.20E+06	1.75E+06	6.27E+05	4.63E+05	6.57E+05
512	F1RZR6	Uncharacterized protein	CUTA	1.22E+07	4.71E+06	4.00E+06	3.50E+06	1.74E+06	6.73E+05	5.71E+05	5.00E+05
513	P35908	Keratin, type II cytoskeletal 2 epidermal	KRT2	7.45E+07	2.92E+07	1.52E+07	3.01E+07	1.73E+06	6.79E+05	3.54E+05	7.01E+05
514	I3LC07	Uncharacterized protein	RAB18	2.43E+07	8.78E+06	6.92E+06	8.56E+06	1.73E+06	6.27E+05	4.94E+05	6.11E+05
515	F1STY7	Uncharacterized protein	AAMD	8.60E+06	4.59E+06	1.99E+06	2.02E+06	1.72E+06	9.19E+05	3.98E+05	4.04E+05
516	L8AXL9	IgG heavy chain	IGHG	3.08E+07	1.36E+07	1.15E+07	5.73E+06	1.71E+06	7.56E+05	6.38E+05	3.18E+05
517	F1S134	Uncharacterized protein	COX5A	2.05E+07	2.96E+06	9.37E+06	8.20E+06	1.71E+06	2.46E+05	7.81E+05	6.83E+05
518	A6YNL5	Calpain 2	Capn2	6.33E+07	2.08E+07	1.68E+07	2.58E+07	1.71E+06	5.61E+05	4.53E+05	6.96E+05
519	F1S956	Uncharacterized protein	PGLS	2.04E+07	8.94E+06	6.45E+06	5.04E+06	1.70E+06	7.45E+05	3.37E+05	4.20E+05
520	A0A024R4X0	NADH-cytochrome b5 reductase	CYB5B3	2.72E+07	1.30E+07	5.81E+06	1.70E+06	1.80E+06	8.13E+05	5.99E+05	5.21E+05
521	F1RGI3	Succinate dehydrogenase, mitochondrial	HSDPA9	7.22E+07	1.62E+07	1.72E+07	2.88E+07	1.68E+06	6.09E+05	3.98E+05	1.00E+06
522	F1SAD9	Protein disulfide-isomerase	PDI4A	7.53E+07	2.73E+07	2.40E+07	2.40E+07	1.67E+06	6.07E+05	5.34E+05	5.33E+05
523	Q8SP19	Cytochrome c oxidase subunit 7A1, mitochondrial	COX7A1	8.25E+06	3.45E+06	1.71E+06	3.09E+06	1.65E+06	6.90E+05	3.42E+05	6.19E+05
524	K9J6J2	Erythrocyte band 7 integral membrane protein isoform a	STOM_tvl	2.79E+0							

Supplementary Table S1: (continued)

589	Q53F20	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant (Fragment)	ANP32E	1.25E+07	4.71E+06	2.72E+06	5.10E+06	1.25E+06	4.71E+05	2.72E+05	5.10E+05
590	K7EM02	Katanin p60 ATPase-containing subunit A-like 2 (Fragment)	KATNAL2	1.13E+07	1.72E+06	4.25E+06	5.30E+06	1.25E+06	1.91E+05	4.72E+05	5.89E+05
591	F1S9Q3	Heat shock 70 kDa protein 1B	HSPA1B	4.76E+07	1.39E+07	1.50E+07	1.87E+07	1.25E+06	3.66E+05	3.95E+05	4.91E+05
592	A1XQ53	Mitochondrial NDUF4	NDUF4	7.50E+06	4.26E+06	2.21E+06	1.03E+06	1.25E+06	7.11E+05	3.68E+05	1.72E+05
593	F1S3B3	Uncharacterized protein	SYPL1	1.24E+07	5.38E+06	3.83E+06	3.23E+06	1.24E+06	5.38E+05	3.83E+05	3.23E+05
594	F1RM51	Glucosamine-6-phosphate isomerase	GNPDA1	2.11E+07	7.66E+06	5.92E+06	7.51E+06	1.24E+06	4.50E+05	3.48E+05	4.42E+05
595	F1S9H9	Uncharacterized protein		1.24E+07	4.84E+06	3.79E+06	3.75E+06	1.24E+06	4.84E+05	3.79E+05	3.75E+05
596	I3LDC7	Isocitrate dehydrogenase [NADP]	IDH1	3.83E+07	1.66E+07	7.16E+06	1.46E+07	1.24E+06	5.34E+05	2.31E+05	4.71E+05
597	P46405	40S ribosomal protein S12	RPS12	8.59E+06	1.45E+06	5.82E+06	1.32E+06	1.23E+06	2.07E+05	8.32E+05	1.88E+05
598	Q5TUC3	Tropomyosin beta chain	TPM2	2.81E+07	1.35E+07	5.12E+06	9.44E+06	1.22E+06	5.88E+05	2.23E+05	4.10E+05
599	K7ENX8	Cold-inducible RNA-binding protein (Fragment)	CIRBP	6.09E+06	1.71E+06	2.82E+06	1.55E+06	1.22E+06	3.41E+05	5.65E+05	3.11E+05
600	F1SL37	Leukocyte surface antigen CD47	CD47	1.34E+07	2.21E+06	3.16E+06	6.01E+06	1.22E+06	3.82E+05	2.87E+05	5.46E+05
601	F1RKY2	Uncharacterized protein	SERPND1	3.26E+07	1.53E+07	1.04E+07	6.98E+06	1.21E+06	5.67E+05	3.84E+05	2.59E+05
602	F1SMF6	Uncharacterized protein	ITGA1	7.20E+07	3.11E+07	1.81E+07	2.27E+07	1.20E+06	5.19E+05	3.02E+05	3.79E+05
603	A2A2D0	Stathmin (Fragment)	STMN1	7.19E+06	1.89E+06	1.64E+06	3.66E+06	1.20E+06	3.16E+05	2.73E+05	6.10E+05
604	K9WF9	Ras GTPase-activating-like protein IQGAP1	IQGAP1	1.12E+08	5.54E+07	2.01E+07	3.70E+07	1.20E+06	5.89E+05	2.14E+05	3.93E+05
605	F1RIA7	Uncharacterized protein	TMEM109	1.20E+07	5.80E+06	2.78E+06	3.38E+06	1.20E+06	5.80E+05	2.78E+05	3.38E+05
606	F1SK45	GTP-AMP phosphotransferase AK3, mitochondrial	AK3	2.27E+07	1.30E+07	4.34E+06	5.37E+06	1.19E+06	6.84E+05	2.28E+05	2.83E+05
607	H6VRG2	Keratin 1	KRT1	4.17E+07	1.26E+07	1.08E+07	1.84E+07	1.19E+06	3.59E+05	3.08E+05	5.26E+05
608	Q29052	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	5.95E+07	2.11E+07	1.95E+07	1.89E+07	1.19E+06	4.22E+05	3.90E+05	3.78E+05
609	AA024RB09	RAB5B, member RAS oncogene family, isoform CRA	RAB5B	1.66E+07	7.00E+06	3.55E+06	6.10E+06	1.19E+06	5.00E+05	2.53E+05	4.36E+05
610	C9MW4	Protein IQCJ-SCHIP1 (Fragment)	IQCJ-SCHIP1	7.12E+06	1.96E+06	3.17E+06	2.00E+06	1.19E+06	3.26E+05	5.29E+05	3.33E+05
611	F1SM07	Uncharacterized protein	COP58	1.07E+07	1.34E+06	4.24E+06	5.08E+06	1.18E+06	1.49E+05	3.71E+05	5.65E+05
612	F1RU33	Uncharacterized protein	BANF1	9.43E+06	3.29E+06	2.40E+06	3.74E+06	1.18E+06	4.11E+05	3.00E+05	4.68E+05
613	F1RY55	Uncharacterized protein	SEPT11	3.90E+07	2.91E+06	8.28E+06	1.53E+07	1.18E+06	3.20E+05	3.19E+05	5.87E+05
614	AKK683	cDNA FLJ77570		4.58E+07	1.95E+07	1.19E+07	1.44E+07	1.18E+06	5.00E+05	3.06E+05	3.70E+05
615	P02662	Alpha-S1-casain		1.29E+07	0.00E+00	0.00E+00	1.29E+07	1.17E+06	0.00E+00	0.00E+00	1.17E+06
616	C1PIG4	cAMP-dependent protein kinase regulatory subunit type II alpha	PRKAR2A	2.58E+07	1.12E+07	5.40E+06	9.26E+06	1.17E+06	5.08E+05	2.45E+05	4.21E+05
617	F1S2Q3	Uncharacterized protein	TMED10	1.39E+07	2.26E+06	5.72E+06	5.94E+06	1.16E+06	1.88E+05	4.77E+05	4.95E+05
618	G8FUN5	Y box binding protein 1 (Fragment)	YBX1	1.15E+07	7.54E+06	3.66E+06	3.21E+05	1.15E+06	7.54E+05	3.66E+05	3.21E+04
619	Q6IB24	PDE6D protein	PDE6D	5.73E+06	5.39E+06	3.40E+05	0.00E+00	1.15E+06	1.08E+06	6.81E+04	0.00E+00
620	AA023T787	RNA-binding protein 8A	RBM8	9.16E+06	2.97E+06	1.11E+06	5.08E+06	1.15E+06	3.71E+05	1.38E+05	6.35E+05
621	F8V5A6	NEDD8	NEDD8	3.42E+06	1.70E+06	6.08E+05	1.11E+06	1.14E+06	5.66E+05	2.03E+05	3.71E+05
622	F1RGE3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	9.08E+06	2.94E+06	2.70E+06	3.43E+06	1.14E+06	3.68E+05	3.38E+05	4.29E+05
623	F1RPD4	Uncharacterized protein	LOC100620271	5.67E+06	1.93E+06	1.02E+06	2.72E+06	1.13E+06	3.86E+05	2.04E+05	5.45E+05
624	Q53GD8	Peptidyl-prolyl cis-trans isomerase (Fragment)	FKBP3	1.59E+07	6.62E+06	5.72E+06	3.54E+06	1.13E+06	4.73E+05	4.09E+05	2.53E+05
625	P27917	Apolipoprotein C-III	APOC3	8.98E+06	4.76E+06	1.24E+06	2.97E+06	1.12E+06	5.95E+05	1.55E+05	3.72E+05
626	Q8MHY0	MYL2	MLC-2V	1.23E+07	3.44E+06	2.91E+06	5.97E+06	1.12E+06	3.13E+05	2.65E+05	5.43E+05
627	F1RL64	Uncharacterized protein	VPS29	8.88E+06	2.63E+06	2.91E+06	3.35E+06	1.11E+06	3.20E+05	3.19E+05	4.82E+05
628	F1SQW8	Uncharacterized protein	ARGHD2	1.53E+07	2.93E+06	4.94E+06	5.44E+06	1.09E+06	3.52E+05	3.53E+05	3.88E+05
629	I3LG67	Uncharacterized protein	MARCKS	1.09E+07	8.41E+06	2.50E+06	0.00E+00	1.09E+06	8.41E+05	2.50E+05	0.00E+00
630	V9HW65	Annexin	HEL-S-270	2.72E+07	1.23E+07	5.94E+06	9.05E+06	1.09E+06	4.90E+05	2.38E+05	3.62E+05
631	K7ZMG1	Putative cysteine-rich protein 2	CRP2	1.41E+07	1.26E+07	5.97E+05	9.05E+05	1.08E+06	9.68E+05	4.59E+04	6.96E+04
632	F8SP2	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	2.82E+07	8.53E+06	1.07E+07	8.94E+06	1.08E+06	3.28E+05	4.11E+05	3.44E+05
633	V9HW15	Cofilin 1 (Non-muscle), isoform CRA	HEL-S-15	1.30E+07	3.38E+06	2.76E+06	6.83E+06	1.08E+06	2.82E+05	3.30E+05	5.69E+05
634	F1RQ06	Peptidyl-prolyl cis-trans isomerase	FKBP2	8.62E+06	4.11E+06	2.87E+06	1.64E+06	1.08E+06	5.13E+05	2.58E+05	2.05E+05
635	AA068F143	Glutathione peroxidase	GPX1	1.62E+07	6.43E+06	2.52E+06	7.21E+06	1.08E+06	4.29E+05	1.68E+05	4.80E+05
636	I3LAJ6	Uncharacterized protein	RALA	1.07E+07	6.73E+06	2.59E+06	1.42E+06	1.07E+06	6.73E+05	2.59E+05	1.42E+05
637	F8V502	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH1A1	2.47E+07	1.01E+07	5.64E+06	8.87E+06	1.07E+06	4.41E+05	2.45E+05	3.85E+05
638	AKK8B9	cDNA FLJ77368		2.02E+07	4.36E+06	7.18E+06	8.69E+06	1.06E+06	2.29E+05	3.78E+05	4.58E+05
639	A91M01	Progesterone receptor membrane component 2	PGRMC2	1.28E+07	4.28E+06	2.33E+06	6.14E+06	1.06E+06	3.57E+05	1.94E+05	5.12E+05
640	Q2EN81	ATP synthase subunit O, mitochondrial	ATPSO	1.36E+07	4.21E+06	3.47E+06	5.96E+06	1.05E+06	3.24E+05	2.67E+05	4.59E+05
641	F1RN90	Vacuolar protein sorting-associated protein 29	VPS29	1.15E+07	2.34E+06	2.54E+06	4.65E+06	1.05E+06	3.95E+05	2.31E+05	4.22E+05
642	Q29024	Spliceosome RNA helicase DDX39B	DDX39B	2.51E+07	1.09E+07	6.99E+06	7.22E+06	1.04E+06	4.53E+05	2.91E+05	3.01E+05
643	F1SEL7	Retinol-binding protein 3	RBP3	6.16E+07	4.39E+07	7.51E+06	1.02E+07	1.04E+06	7.43E+05	1.27E+05	1.73E+05
644	I3LQ84	Uncharacterized protein	COL6A2	5.84E+07	2.99E+07	1.38E+07	1.48E+07	1.04E+06	5.33E+05	2.46E+05	2.64E+05
645	I3LR69	Ferritin	FTH1	1.25E+07	5.56E+06	2.43E+06	4.54E+06	1.04E+06	4.63E+05	2.02E+05	3.78E+05
646	B5APU3	Actin-related protein 2-like protein	ACTR2	2.19E+07	1.60E+07	0.00E+00	5.91E+06	1.04E+06	7.61E+05	0.00E+00	2.81E+05
647	B7Z361	Reticulon	RTN3	7.26E+06	5.29E+06	0.00E+00	1.97E+06	1.04E+06	7.56E+05	0.00E+00	2.81E+05
648	Q863Z0	Proteasome activator complex subunit 2	PSME2	1.86E+07	9.61E+06	4.64E+06	4.35E+06	1.03E+06	5.34E+05	2.58E+05	2.42E+05
649	K9IWG6	Spectrin beta chain, brain 1 (Fragment)	SPTBN1	1.65E+08	8.44E+07	4.62E+07	3.46E+07	1.03E+06	5.28E+05	2.89E+05	2.16E+05
650	G3DRF8	Proteasome subunit beta type	PSMB6	1.13E+07	3.12E+06	4.48E+06	3.74E+06	1.03E+06	2.84E+05	4.07E+05	5.40E+05
651	I3LS94	Uncharacterized protein	EIF4H	1.64E+07	6.35E+06	6.46E+06	3.63E+06	1.03E+06	3.97E+05	4.04E+05	2.27E+05
652	AA087X0T8	Cell adhesion molecule 1	CADMI1	2.47E+07	8.10E+06	7.42E+06	9.16E+06	1.03E+06	3.36E+05	3.09E+05	3.82E+05
653	F1SIP0	Uncharacterized protein	SEPT2	2.25E+07	1.07E+07	5.75E+06	5.41E+06	1.02E+06	3.25E+05	2.53E+05	2.46E+05
654	ASV1V6	Fatty acid synthase	FASN	1.39E+08	4.73E+07	4.51E+07	4.85E+07	1.02E+06	3.48E+05	3.32E+05	3.73E+05
655	Q29582	Pyruvate kinase M2 (Fragment)	PKM2	5.09E+06	5.09E+06	0.00E+00	0.00E+00	1.02E+06	1.02E+06	0.00E+00	0.00E+00
656	J3K505	Chromobox protein homolog 1 (Fragment)	CBX1	1.01E+07	4.93E+06	1.42E+06	3.79E+06	1.01E+06	4.93E+05	1.42E+05	3.79E+05
657	F1RKL0	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3A	2.33E+07	1.20E+07	5.73E+06	5.57E+06	1.01E+06	5.20E+05	2.49E+05	2.42E+05
658	M3UZ42	Ubiquitin-fold modifier 1	UFM1	5.05E+06	1.45E+06	1.38E+06	2.22E+06	1.01E+06	2.89E+05	2.77E+05	4.44E+05
659	AA024R7R3	Beta-synuclein (Fragment)	SNCB	8.05E+06	4.35E+06	7.86E+05	2.92E+06	1.01E+06	5.43E+05	9.82E+04	3.65E+05
660	P04574	Calpain small subunit 1	CAPNS1	1.40E+07	6.64E+06	2.87E+06	4.54E+06	1.00E+06	4.74E+05	2.05E+05	3.24E+05
661	A4D110	Putative uncharacterized protein	LOC401309	5.01E+06	9.61E+05	1.68E+06	2.37E+06	1.00E+06	1.92E+05	3.36E+05	4.75E+05
662	Q53J08	Cellular retinol binding protein 1	CRBP1	1.19E+07	8.35E+06	6.21E+05	2.94E+06	9.93E+05	6.96E+05	5.17E+04	2.45E+05
663	COMHR2	Clathrin heavy chain	CLTC	9.71E+07	4.82E+07	2.56E+07	2.33E+07	9.91E+05	4.92E+05	2.61E+05	2.37E+05
664	O02668	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	5.34E+07	1.04E+07	2.05E+07	2.25E+07	9.90E+05	1.93E+05	3.79E+05	4.17E+05
665	O77773	Uncharacterized protein									

Supplementary Table S1: (continued)

737	D0G7F1	Sterol carrier protein 2	SCP2	2.48E+07	2.05E+06	0.00E+00	2.27E+07	7.50E+05	6.22E+04	0.00E+00	6.88E+05
738	V9HW83	Aldehyde dehydrogenase 1 family, member A1, isoform CRA	HEL_S-53c	1.87E+07	4.70E+06	6.96E+06	7.01E+06	7.47E+05	1.88E+05	2.78E+05	2.80E+05
739	I3LUR7	Uncharacterized protein	COL6A3	1.42E+08	7.11E+07	3.21E+07	3.92E+07	7.41E+05	3.70E+05	1.67E+05	2.04E+05
740	Q9N0F1	Dihydrodipolyslysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	1.93E+07	6.83E+06	5.13E+06	7.31E+06	7.41E+05	2.63E+05	1.97E+05	2.81E+05
741	B5APU6	Actin related protein 2/3 complex subunit 1B	ARPC1B	1.48E+07	1.05E+07	2.91E+06	1.36E+06	7.41E+05	5.27E+05	1.46E+05	6.78E+04
742	B4D38	Adenylyl cyclase-associated protein	CAP1	2.44E+07	1.17E+07	3.67E+06	9.02E+06	7.40E+05	3.55E+05	1.11E+05	2.73E+05
743	K7GMM2	Uncharacterized protein (Fragment)	NCALD	1.04E+07	5.00E+06	1.44E+06	3.92E+06	7.39E+05	3.57E+05	1.03E+05	2.80E+05
744	F1RKJ9	Uncharacterized protein	ISOC1	1.18E+07	3.69E+06	3.60E+06	4.54E+06	7.39E+05	2.30E+05	2.25E+05	2.84E+05
745	B6DX83	V-cr1 sarcoma virus CT10 oncogene-like protein isoform b	CRK	1.11E+07	6.15E+06	1.81E+06	3.12E+06	7.38E+05	4.10E+05	1.21E+05	2.08E+05
746	F1RL15	Uncharacterized protein	LOC100523824	5.45E+07	2.96E+07	1.29E+07	1.20E+07	7.37E+05	4.00E+05	1.75E+05	1.62E+05
747	Q6CNC0	GRB2 protein (Fragment)	GRB2	1.40E+07	5.38E+06	2.18E+06	6.40E+06	7.35E+05	2.83E+05	1.15E+05	3.37E+05
748	I3LDY2	Uncharacterized protein	LOC100739304	1.02E+07	3.40E+06	2.83E+06	4.02E+06	7.32E+05	2.43E+05	1.02E+05	2.87E+05
749	E5RK64	Vesicle-associated membrane protein-associated protein B/C	VAPP	2.92E+06	1.19E+06	6.82E+05	1.05E+06	7.29E+05	2.97E+05	1.71E+05	2.62E+05
750	B7Z5Q2	cDNA FLJ58075, highly similar to Ceruloplasmin (EC 1.16.3.1)	VAPP	3.64E+07	2.23E+07	6.62E+06	7.55E+06	7.29E+05	4.45E+05	1.32E+05	1.51E+05
751	M0QXHO	Thioredoxin, mitochondrial	TXN2	2.18E+06	0.00E+00	8.30E+05	1.35E+06	7.28E+05	0.00E+00	2.77E+05	4.51E+05
752	F1SEN8	Uncharacterized protein	LDB3	2.31E+07	9.52E+06	5.66E+06	7.97E+06	7.23E+05	2.97E+05	1.02E+05	2.49E+05
753	A2IP6	HRV Fab 027-VL (Fragment)		4.33E+06	4.33E+06	0.00E+00	0.00E+00	7.21E+05	7.21E+05	0.00E+00	0.00E+00
754	F5H7R9	Parathyroid hormone (Fragment)	PTMS	2.16E+06	0.00E+00	0.00E+00	2.16E+06	7.20E+05	0.00E+00	0.00E+00	7.20E+05
755	P62760	Visinin-like protein 1	VSNL1	1.08E+07	2.98E+06	2.68E+06	5.14E+06	7.20E+05	1.98E+05	1.79E+05	3.43E+05
756	I3LH71	Uncharacterized protein	LOC100511115	1.43E+07	9.54E+06	4.77E+06	0.00E+00	7.16E+05	4.77E+05	2.39E+05	0.00E+00
757	F1S0C1	S-(hydroxymethyl)glutathione dehydrogenase	ADHS	1.57E+07	1.24E+07	1.23E+06	2.10E+06	7.13E+05	5.61E+05	5.09E+04	9.54E+04
758	F1RP34	NAD(P)H-hydrate epimerase	APOA1BP	1.06E+07	9.49E+06	0.00E+00	1.08E+06	7.05E+05	6.32E+05	0.00E+00	7.23E+04
759	F1SME6	Uncharacterized protein		2.11E+07	3.56E+06	7.97E+06	9.56E+06	7.03E+05	1.19E+05	2.66E+05	3.19E+05
760	F1RL11	Uncharacterized protein	HSD17B14	1.12E+07	4.76E+06	5.49E+06	9.80E+05	7.02E+05	2.97E+05	3.43E+05	6.13E+04
761	F1SME5	Alpha-actinin-1	ACTN1	3.78E+07	2.64E+07	2.24E+06	9.17E+06	7.00E+05	4.89E+05	4.14E+04	1.70E+05
762	F2Z2F3	Uncharacterized protein	MTAP-ANRIL fusion	7.69E+06	1.14E+06	1.95E+06	2.60E+06	6.99E+05	2.85E+05	1.78E+05	2.36E+05
763	P50897	Palmitoyl-protein thioesterase 1	PPT1	8.97E+06	4.46E+06	1.43E+06	3.09E+06	6.90E+05	3.43E+05	1.10E+05	2.37E+05
764	F2Z584	Histone H2B	HIST1H2BD	7.52E+06	3.51E+06	2.11E+06	1.90E+06	6.84E+05	3.19E+05	1.92E+05	1.73E+05
765	H0YB39	Heterogenous nuclear ribonucleoprotein H (Fragment)	HNRNP11	1.23E+07	5.26E+06	4.90E+06	2.13E+06	6.83E+05	2.92E+05	2.72E+05	1.19E+05
766	F1SV23	Uncharacterized protein	NDUFS5	4.77E+06	2.59E+06	1.67E+06	5.06E+05	6.82E+05	3.70E+05	2.69E+05	7.23E+04
767	C9J8R8	Glycogenin-1 (Fragment)	GYGI	2.71E+06	4.92E+05	2.70E+05	1.95E+06	6.78E+05	1.23E+05	6.76E+04	4.87E+05
768	F1RWJ6	Uncharacterized protein	NPEPPS	3.85E+07	2.04E+07	7.36E+06	1.07E+07	6.75E+05	3.58E+05	1.29E+05	1.88E+05
769	P48819	Vitronectin	VTN	1.88E+07	4.73E+06	6.60E+06	7.44E+06	6.70E+05	1.69E+05	2.36E+05	2.66E+05
770	Q28936	Fibrinogen A-alpha-chain (Fragment)		1.67E+07	4.55E+06	5.54E+06	6.62E+06	6.68E+05	1.82E+05	2.22E+05	2.65E+05
771	H3BQQ9	SUMO-conjugating enzyme (Fragment)	UBE2I	5.34E+06	3.71E+06	8.47E+05	7.80E+05	6.67E+05	4.64E+05	1.06E+05	9.75E+04
772	F1S530	60S ribosomal protein L5	RPL5	1.13E+07	5.11E+06	2.87E+06	3.33E+06	6.65E+05	3.01E+05	1.69E+05	1.96E+05
773	F1S5H5	Uncharacterized protein	PDBH	1.40E+07	8.88E+06	3.51E+06	1.57E+06	6.65E+05	4.23E+05	1.67E+05	7.47E+04
774	Q29583	Glutathione transferase mu (Fragment)		5.95E+06	8.23E+05	1.75E+06	3.38E+06	6.61E+05	9.14E+04	1.94E+05	3.75E+05
775	F1SME6	V-type proton ATPase subunit F	ATP6V1F	5.28E+06	5.63E+05	2.95E+06	2.67E+06	6.61E+05	9.70E+04	1.94E+05	3.33E+05
776	L8AXM5	IgC heavy chain	IGHG	1.32E+07	2.39E+06	3.25E+06	6.51E+06	6.58E+05	1.70E+05	1.62E+05	3.26E+05
777	F1RPW8	Uncharacterized protein	ASRGL1	9.19E+06	4.06E+06	2.46E+06	2.67E+06	6.56E+05	2.90E+05	1.75E+05	1.91E+05
778	Q29561	UMP-CMP kinase	CMPK1	7.87E+06	4.04E+06	1.74E+06	2.09E+06	6.56E+05	3.37E+05	1.45E+05	1.74E+05
779	F2Z522	Uncharacterized protein	LOC100623805	5.90E+06	2.23E+06	1.73E+06	1.94E+06	6.55E+05	2.47E+05	1.93E+05	2.15E+05
780	B3KX15	cDNA FLJ44468 fis	SRSF2	6.55E+06	5.28E+06	0.00E+00	1.27E+06	6.55E+05	5.28E+05	0.00E+00	1.27E+05
781	F1RNZ1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRCF1	1.05E+07	5.17E+06	3.20E+06	2.10E+06	6.54E+05	3.23E+05	2.00E+05	1.31E+05
782	K7GNZ6	Uncharacterized protein (Fragment)	SSR4	5.22E+06	2.54E+06	4.24E+05	2.25E+06	6.52E+05	3.18E+05	5.30E+04	2.81E+05
783	F1RVM1	Uncharacterized protein	APOBEC2	8.48E+06	4.66E+06	1.14E+06	2.68E+06	6.52E+05	3.58E+05	8.77E+04	2.06E+05
784	P10775	Ribonuclease inhibitor	RNIH	1.69E+07	1.07E+07	5.06E+06	1.18E+06	6.51E+05	4.11E+05	1.95E+05	4.53E+04
785	F1S5D0	Uncharacterized protein	BST1	1.04E+07	4.19E+06	1.91E+06	4.31E+06	6.51E+05	2.62E+05	1.20E+05	2.70E+05
786	A0A024R7G2	RAB3D, member RAS oncogene family, isoform CRA	RAB3D	1.04E+07	4.15E+06	2.89E+06	3.32E+06	6.48E+05	2.59E+05	1.81E+05	2.07E+05
787	A8KA83	cDNA FLJ78586		1.03E+07	4.36E+06	2.79E+06	3.14E+06	6.43E+05	2.72E+05	1.75E+05	1.96E+05
788	K9J4R8	Protein S100-A13	S100A13	5.13E+06	4.51E+05	2.14E+06	2.54E+06	6.41E+05	5.64E+04	2.68E+05	3.17E+05
789	V9HW51	Epididymis secretory protein Li 114	HEL_S-114	9.57E+06	6.73E+06	1.10E+06	1.73E+06	6.38E+05	4.49E+05	1.76E+04	1.65E+05
790	F1STC3	Uncharacterized protein		3.19E+06	2.22E+06	0.00E+00	9.67E+05	6.38E+05	4.44E+05	0.00E+00	1.93E+05
791	P36968	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	9.52E+06	3.10E+06	2.16E+06	4.27E+06	6.35E+05	2.06E+05	1.44E+05	2.84E+05
792	Q8SPA2	MHC class II antigen	SLA-DRB	1.07E+07	4.72E+06	3.03E+06	3.00E+06	6.32E+05	2.78E+05	1.78E+05	1.76E+05
793	H7C547	Sodium/potassium-transporting ATPase subunit beta-3 (Fragment)	ATP1B3	1.89E+06	1.40E+06	4.90E+05	0.00E+00	6.29E+05	4.66E+05	1.63E+05	0.00E+00
794	F1S5S1	Uncharacterized protein	LOC100153701	1.26E+07	6.21E+06	2.36E+06	4.01E+06	6.29E+05	3.11E+05	1.18E+05	2.00E+05
795	F1SEY8	Uncharacterized protein	LOC100738775	2.77E+07	2.42E+06	0.00E+00	2.52E+07	6.29E+05	5.49E+04	0.00E+00	5.74E+05
796	D3DTX7	Collagen, type I, alpha 1, isoform CRA	COL1A1	3.33E+07	1.82E+07	8.25E+06	6.84E+06	6.28E+05	3.43E+05	1.56E+05	1.29E+05
797	F1S8H8	Purine nucleoside phosphorylase	PNP	1.44E+07	3.71E+06	4.50E+06	6.23E+06	6.28E+05	1.62E+05	1.96E+05	2.71E+05
798	F1SUP1	Uncharacterized protein	AKR7A2	1.00E+07	6.26E+06	1.31E+06	2.44E+06	6.25E+05	3.91E+05	8.17E+04	1.52E+05
799	Z4YP82	SPARC	SPARC	9.37E+06	2.06E+06	4.33E+06	2.98E+06	6.25E+05	1.37E+05	2.89E+05	1.99E+05
800	I3LS13	Adenylate kinase 2, mitochondrial	AK2	1.06E+07	5.94E+06	2.33E+06	2.35E+06	6.25E+05	3.49E+05	1.37E+05	1.38E+05
801	Q3HUX1	Fatty acid translocase/CD36	CD36	1.06E+07	2.41E+06	6.48E+06	1.72E+06	6.24E+05	1.42E+05	3.81E+05	1.01E+05
802	F1S5K7	Uncharacterized protein (Fragment)	ALDH3A2	1.18E+07	6.48E+06	2.94E+06	2.33E+06	6.21E+05	2.94E+05	1.55E+05	1.25E+05
803	Q0AS88	GBA3	GBA3	1.05E+07	1.84E+06	1.35E+06	2.91E+06	6.18E+05	2.85E+05	1.91E+05	6.13E+05
804	I3LH27	Uncharacterized protein	CRIC3	1.17E+07	1.17E+07	0.00E+00	0.00E+00	6.14E+05	6.14E+05	0.00E+00	0.00E+00
805	F1S766	Uncharacterized protein	MACOH	8.60E+06	4.71E+06	7.83E+05	3.11E+06	6.14E+05	3.36E+05	5.59E+04	2.22E+05
806	F2Z5C5	Uncharacterized protein	LSMG	3.06E+06	1.62E+06	5.53E+05	8.94E+05	6.12E+05	3.23E+05	1.11E+05	1.79E+05
807	A0A087WQW5	Arrestin-C	ARR3	1.10E+07	4.77E+06	2.01E+06	4.24E+06	6.12E+05	2.65E+05	1.12E+05	2.35E+05
808	I3LS72	Uncharacterized protein	COL6A1	1.83E+07	7.76E+06	4.39E+06	6.13E+06	6.10E+05	2.59E+05	1.46E+05	2.04E+05
809	I3LJ03	Uncharacterized protein		1.83E+06	1.06E+06	0.00E+00	7.70E+05	6.10E+05	3.53E+05	0.00E+00	2.57E+05
810	F1SKQ7	Uncharacterized protein	GOLGA1	3.41E+07	2.75E+07	0.00E+00	6.61E+06	6.09E+05	4.91E+05	0.00E+00	1.18E+05
811	M9TGS8	Mitochondrial delta,delta2-dienoyl-CoA isomerase	Eci1	1.03E+07	4.07E+06	3.65E+06	2.60E+06	6.07E+05	2.39E+05	2.15E+05	1.53E+05
812	F1S133	Uncharacterized protein	CFI	2.35E+07	1.38E+07	5.41E+06	4.35E+06	6.03E+05	3.53E+05	1.39E+05	1.12E+05
813	Q0IN1	Keratin 77	Krt77 Keratin, type II	2.34E+07	4.98E+06	8.37E+06	1.01E+07	6.00E+05	1.28E+05	2.15E+05	2.58E+05
814	F1RKM0	Uncharacterized protein	LNMB1	2.28E+07	7.29E+06	7.94E+06	7.53E+06	5.99E+05	1.92E+05	2.09E+05	1.98E+05
815	F1S1H25	Uncharacterized protein	RAB21	8.97E+06	3.33E+06	1.43E+06	4.21E+06	5.98E+05	2.22E+05	9.55E+04	2.81E+05
816	F1RGS1	Uncharacterized protein (Fragment)	LAMTOR2	1.20E+06	0.00E+00	3.17E+05	0.00E+00	5.98E+05	0.00E+00	0.00E+00	1.58E+05
817	A2NXY3	Light chain Fab (Fragment)		2.38E+06	2.38E+06	0.00E+00	0.00E+00	5.94E+05	0.00E+00	0.00E+00	0.00E+00
818	F1S0V3	Annexin	ANXA6	2.25E+07	7.23E+06	8.22E+06	7.06E+06	5.92E+05	1.90E+05	2.16E+05	1.86E+05
819	I3LVJ7	Uncharacterized protein	PSMA7	8.88E+06	5.33E+06	3.55E+06	0.00E+00	5.92E+05	3.56E+05	2.36E+05	0.00E+00
820	I3LN22	Uncharacterized protein	LOC100510904	4.14E+06	0.00E+00	1.59E+06	2.54E+				

Supplementary Table S1: (continued)									
ID	Gene	Description	Gene	Value 1	Value 2	Value 3	Value 4	Value 5	Value 6
885	H3BQW8	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)	HAGH	5.3E+06	2.4E+06	1.4E+06	1.6E+06	4.6E+05	2.04E+05
886	I3LDC3	Uncharacterized protein	NDUFB10	5.9E+06	2.7E+06	1.2E+06	1.9E+06	4.6E+05	2.12E+05
887	I3LUP5	Synaposomal-associated protein	LOC100627770	4.5E+06	3.3E+06	3.7E+05	9.0E+05	4.5E+05	3.3E+05
888	F1RKM1	Uncharacterized protein	ALDH7A1	1.0E+07	6.2E+06	1.6E+06	2.2E+06	4.5E+05	2.8E+05
889	F2Z576	Histone H3	HIST1H3E	2.7E+06	2.2E+06	4.8E+05	0.0E+00	4.5E+05	3.7E+05
890	K7GS78	Signal transducer and activator of transcription 1 (Fragment)	STAT1	7.3E+06	3.1E+05	2.5E+05	6.7E+06	4.5E+05	1.9E+04
891	AOA024R280	Phosphoserine aminotransferase 1, isoform CRA	PSAT1	1.0E+07	5.3E+06	2.7E+06	2.7E+06	4.5E+05	2.3E+05
892	B1AL9	Ribose-phosphate pyrophosphokinase 1	PRPS1	7.2E+06	4.4E+06	2.0E+06	7.7E+05	4.5E+05	2.7E+05
893	F1SEQ7	Uncharacterized protein	FAM213A	6.3E+06	3.5E+06	1.1E+06	1.6E+06	4.5E+05	2.5E+05
894	K7GQ9	Uncharacterized protein (Fragment)	GSTZ1	6.3E+06	1.6E+06	1.6E+06	3.0E+06	4.5E+05	1.1E+05
895	I3L7B0	Uncharacterized protein	RPS7	3.6E+06	1.8E+06	1.2E+06	6.5E+05	4.5E+05	2.1E+05
896	I3LZ28	Uncharacterized protein	LOC100516656	4.0E+06	2.5E+06	0.0E+00	1.5E+06	4.4E+05	2.7E+05
897	A0P01	Serine protease inhibitor 9	PI9	9.8E+06	4.5E+06	1.7E+06	3.5E+06	4.4E+05	2.0E+05
898	F1SQR8	Leukotriene A(4) hydrolase	LTA4H	1.7E+07	6.2E+06	5.8E+06	5.4E+06	4.4E+05	1.6E+05
899	F1SB63	Uncharacterized protein	TCP1	1.5E+07	4.4E+06	6.0E+06	5.1E+06	4.4E+05	1.7E+05
900	I3LEV7	Uncharacterized protein	SH3BGR	4.0E+06	1.0E+06	1.0E+06	1.9E+06	4.4E+05	1.1E+05
901	AKK6Y1	cDNA FLJ75526	PA2G4	1.0E+07	4.1E+06	2.2E+06	3.8E+06	4.4E+05	1.7E+05
902	P19619	Annexin A1	ANXA1	9.6E+06	5.0E+06	8.5E+05	3.7E+06	4.4E+05	2.3E+05
903	D0G0C8	Chaperonin containing TCP1, subunit 2 (Beta)	CC22	1.5E+07	4.5E+06	7.4E+06	3.8E+06	4.3E+05	1.2E+05
904	AOA087WZ50	Ly-6/neurotoxin-like protein 1 (Fragment)	LYNX1	1.3E+06	4.2E+05	4.7E+05	4.1E+05	4.3E+05	1.4E+05
905	Q69DK8	Complement C1s subcomponent		1.0E+07	2.5E+06	3.4E+06	4.4E+06	4.3E+05	1.0E+05
906	AOA052Z377	Annexin (Fragment)	ANXA6	2.1E+07	6.7E+06	6.3E+06	8.6E+06	4.3E+05	1.3E+05
907	Q7Z517	Transgelin	TAGLN3	7.8E+06	3.2E+06	1.5E+06	2.6E+06	4.3E+05	1.8E+05
908	V9HW91	Epididymis secretory sperm binding protein Li 8a	HEL_S-8a	9.1E+06	3.1E+06	2.0E+06	3.9E+06	4.3E+05	1.5E+05
909	F1SSW4	Uncharacterized protein	TMM9	2.9E+06	3.9E+05	9.9E+05	1.2E+06	4.3E+05	6.8E+04
910	C9TK8	Obsc-like ATPase 1 (Fragment)	OLA1	3.8E+06	3.6E+06	1.4E+06	1.0E+06	4.3E+05	1.5E+05
911	F1S393	Uncharacterized protein	CYB5B	4.3E+06	1.6E+06	1.1E+06	1.4E+06	4.3E+05	1.6E+05
912	Q9LPN1	Serine/threonine-protein phosphatase (Fragment)	PPP1CC	7.3E+06	2.8E+06	1.6E+06	2.8E+06	4.3E+05	1.6E+05
913	Q1HB0	ATP synthase protein 8	ATP8	1.7E+06	6.7E+05	4.2E+05	6.1E+05	4.2E+05	1.6E+05
914	F1RBE0	Uncharacterized protein	MESDC2	6.8E+06	2.0E+06	2.4E+06	2.3E+06	4.2E+05	1.2E+05
915	P23687	Prolyl endopeptidase	PREP	2.1E+07	7.1E+06	6.1E+06	8.1E+06	4.2E+05	1.3E+05
916	F1STB2	Uncharacterized protein	HINT2	5.1E+06	1.5E+06	3.0E+06	5.4E+05	4.2E+05	2.1E+05
917	V9HVX8	Epididymis luminal protein 109	HEL_109	1.4E+07	9.2E+06	4.8E+06	0.0E+00	4.2E+05	2.8E+05
918	Q0QF01	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	1.5E+07	4.7E+06	5.8E+06	4.7E+06	4.2E+05	1.3E+05
919	F1S0M9	Peptidyl-prolyl cis-trans isomerase	FKBP10	8.4E+06	1.9E+06	2.3E+06	4.1E+06	4.2E+05	9.9E+04
920	Q53F48	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant (Fragment)	HNRP33	8.4E+06	3.0E+06	1.4E+06	3.9E+06	4.2E+05	1.5E+05
921	D6RDM7	Ubiquitin-conjugating enzyme E2 K (Fragment)	UBE2K	4.2E+06	2.6E+06	6.9E+05	8.8E+05	4.2E+05	2.6E+05
922	F1RZM4	Uncharacterized protein	LAMA4	3.6E+07	1.4E+07	1.0E+07	1.1E+07	4.1E+05	1.6E+05
923	F1RLC5	Ferritin	FTMT	7.4E+06	7.4E+06	4.9E+06	0.0E+00	4.1E+05	4.1E+05
924	F1S543	Calponin	CNP3	7.8E+06	3.7E+06	8.0E+05	3.3E+06	4.1E+05	1.9E+05
925	I3LE8	1,2-dihydroxy-3-keto-5-methylthiopentane dioxxygenase	ADH1	5.3E+06	1.3E+06	2.3E+06	1.6E+06	4.1E+05	1.0E+05
926	F1S596	Uncharacterized protein	PRKCSH	8.6E+06	1.2E+06	3.1E+06	4.4E+06	4.1E+05	5.3E+04
927	P01762	Ig heavy chain V-III region TRO		2.4E+06	2.4E+06	0.0E+00	0.0E+00	4.0E+05	4.0E+05
928	H7BXF3	Transformer-2 protein homolog beta (Fragment)	TRA2B	2.8E+06	2.0E+06	7.8E+05	0.0E+00	4.0E+05	2.9E+05
929	J3QL22	COP9 signalosome complex subunit 3	COPS3	8.1E+05	0.0E+00	4.7E+05	3.3E+05	4.0E+05	0.0E+00
930	R4GN98	Protein S100 (Fragment)	S100A6	2.0E+06	2.0E+06	0.0E+00	0.0E+00	4.0E+05	4.0E+05
931	Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	GNB4	5.7E+06	4.2E+06	5.8E+05	8.8E+05	4.0E+05	3.0E+05
932	F1SEX0	Uncharacterized protein	DDAH1	4.8E+06	3.7E+06	0.0E+00	1.1E+06	4.0E+05	3.1E+05
933	F1RU0	Adenylyl cyclase-associated protein	CAP2	1.1E+07	3.3E+06	3.9E+06	3.9E+06	4.0E+05	1.2E+05
934	H0YB22	40S ribosomal protein S14 (Fragment)	RPS14	2.3E+06	1.0E+06	5.2E+05	7.8E+05	3.9E+05	1.7E+05
935	Q7YS28	Pyruvate carboxylase	PC	2.6E+07	1.4E+07	4.0E+06	7.6E+06	3.9E+05	2.2E+05
936	I3LRH3	Uncharacterized protein	LOC100625256	6.7E+06	1.4E+06	2.3E+06	2.9E+06	3.9E+05	8.2E+04
937	I3LL4	Uncharacterized protein	MYO1C	2.8E+07	1.3E+07	9.9E+06	0.0E+00	3.9E+05	2.4E+05
938	H0YHM7	Peptidyl-prolyl cis-trans isomerase FKBP11 (Fragment)	FKBP11	1.5E+06	1.1E+06	4.2E+05	0.0E+00	3.9E+05	2.8E+05
939	D3GGC9	Actinin-associated LIM protein 3	PDLIM3	7.0E+06	3.9E+06	1.4E+06	1.6E+06	3.9E+05	2.1E+05
940	D3DR14	HCG2011315, isoform CRA	hCG_2011315	2.7E+06	2.3E+06	0.0E+00	4.0E+05	3.9E+05	3.5E+05
941	F1SBE5	Uncharacterized protein	PTGS1	1.1E+07	6.4E+06	4.1E+06	7.2E+05	3.9E+05	2.3E+05
942	Q2YGT9	60S ribosomal protein L6	RPL6	6.6E+06	3.9E+06	2.3E+06	2.8E+06	3.8E+05	2.3E+05
943	AKK304	cDNA FLJ75636, highly similar to Homo sapiens FYVE, RhoGEF and PH domain containing 2, mRNA	FGD2	1.8E+07	5.5E+06	4.6E+06	8.0E+06	3.8E+05	1.8E+05
944	F1RIF3	Uncharacterized protein	FAH	9.2E+06	2.8E+06	2.8E+06	3.5E+06	3.8E+05	1.8E+05
945	AOA087WW18	Protein archease (Fragment)	ZBTB80S	7.6E+05	3.9E+05	3.7E+05	0.0E+00	3.8E+05	1.9E+05
946	F1SLR1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUF8	4.5E+06	2.1E+06	7.4E+05	1.7E+06	3.8E+05	1.7E+05
947	F1S0P3	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	1.1E+07	4.6E+06	1.7E+06	5.4E+06	3.8E+05	1.4E+05
948	I3LH91	Uncharacterized protein	PALLD	5.6E+06	9.1E+05	2.0E+06	2.6E+06	3.7E+05	6.1E+04
949	I3LR0	Inosine 5-monophosphate dehydrogenase	IMPDH1	9.9E+06	4.9E+06	3.9E+06	1.4E+06	6.9E+05	1.3E+05
950	F1SS26	Uncharacterized protein	TBRSS1	2.4E+07	1.4E+07	4.9E+06	5.7E+06	6.5E+05	2.8E+05
951	I3GFB	Uncharacterized protein	PCDH15	8.3E+06	9.0E+05	2.6E+06	2.6E+06	6.4E+05	1.0E+05
952	AOA01H3W508	Beta-crystallin B2 (Fragment)	CRYBB2	4.7E+06	2.0E+06	8.4E+05	1.8E+06	3.6E+05	1.6E+05
953	F1SK0	Myosin-11	MYH11	1.5E+07	1.0E+07	3.3E+06	1.8E+06	6.3E+05	2.9E+05
954	P59083	14 kDa phosphohistidine phosphatase (Fragments)	PHPT1	1.4E+06	8.7E+05	0.0E+00	5.7E+05	3.6E+05	2.1E+05
955	V9HWF0	Epididymis secretory protein Li 28	HEL_S-28	1.0E+07	6.7E+06	1.3E+06	2.0E+06	3.6E+05	2.4E+05
956	Q7YQ92	MHC class II antigen (Fragment)	SLA-DRA1	4.6E+06	2.0E+06	1.0E+06	1.6E+06	3.6E+05	1.5E+05
957	Q6P53	Uncharacterized protein		3.6E+06	3.6E+06	0.0E+00	0.0E+00	3.6E+05	3.6E+05
958	F1SU03	Uncharacterized protein		2.7E+07	1.1E+07	1.1E+07	4.4E+06	3.6E+05	1.5E+05
959	Q0PM28	Pigment epithelium-derived factor	SERPINF1	8.2E+06	5.8E+06	1.4E+06	1.0E+06	3.6E+05	2.5E+05
960	Q9BUA6	Myosin regulatory light chain 10	MYL10	5.0E+06	0.0E+00	1.4E+06	3.6E+06	3.6E+05	0.0E+00
961	I3LCA2	Uncharacterized protein	CCT8	1.4E+07	3.4E+06	8.1E+06	2.7E+06	3.6E+05	8.6E+04
962	P02535	Isoform 1 of Keratin, type I cytoskeletal 10		1.0E+07	0.0E+00	0.0E+00	1.0E+07	3.5E+05	0.0E+00
963	F1S196	Inter-alpha-trypsin inhibitor heavy chain HI	ITIH1	1.6E+07	5.7E+06	6.0E+06	4.9E+06	3.5E+05	1.2E+05
964	I3L3D6	Sodium/potassium-translocating ATPase subunit alpha (Fragment)	atp1a1	1.8E+07	1.0E+07	4.9E+06	3.1E+06	3.4E+05	1.9E+05
965	F1SES5	Uncharacterized protein	NDFU9B	2.5E+06	9.0E+05	0.0E+00	2.6E+06	3.5E+05	0.0E+00
966	P0819	Acylphosphatase-2	ACY2P2	2.8E+06	1.5E+06	5.7E+05	7.0E+05	3.5E+05	1.9E+05
967	I3LK24	Uncharacterized protein	HNRNPR	1.3E+07	6.1E+06	3.3E+06	4.2E+06	3.5E+05	1.5E+05
968	F1S4D5	Uncharacterized protein	CCBL2	7.0E+06	1.8E+06	2.0E+06	3.1E+06	3.5E+05	9.2E+04
969	Q684M6	CDC37 cell division cycle 37 protein	CDC37	6.6E+06	2.7E+06	1.9E+06	2.0E+06	3.4E+05	1.4E+05
970	Q6LBM3	Fibroblast growth factor	fgf gene	1.7E+06	0.0E+00	4.7E+05	1.2E+06	3.4E+05	0.0E+00
971	C9J6B1	Ras-related protein Ral-B (Fragment)	RALB	3.1E+06	1.9E+06	1.1E+06	0.0E+00	3.4E+05	2.2E+05
972	Q9BV28	TUBB3 protein (Fragment)	TUBB3	6.9E+06	4.4E+05	3.3E+06	3.2E+06	3.4E+05	2.3E+04
973	M0QZ2	40S ribosomal protein S5	RPS5	2.0E+06	1.9E+06	0.0E+00	9.9E+04	3.4E+05	3.0E+05
974	L8AXL3	IgG heavy chain	IGHG	6.2E+06	4.1E+06	1.4E+06	6.3E+05	3.4E+05	2.3E+05
975	P06753	Tropomyosin alpha-3 chain	TPM3	8.2E+06	7.0E+06	5.6E+05	7.1E+05	3.4E+05	2.9E+05
976	F1RX84	Uncharacterized protein	PROSC	5.8E+06	2.4E+06	1.7E+06	1.6E+06	3.4E+05	1.4E+05
977	K7GR19	Tetraspanin	CD151	4.4E+06	3.6E+06	0.0E+00	7.7E+05	3.1E+05	2.8E+05
978	I3B7B8	Protocadherin-15	PCDH15	1.8E+07	1.0E+07	6.8E+06	8.4E+06	3.4E+05	1.9E+05
979	F1S1S	Uncharacterized protein	INMT	3.0E+06	6.3E+06	7.1E+05	0.0E+00	3.4E+05	2.6E+05
980	C9J3L8	Translocin-associated protein subunit alpha	SSR1	3.7E+06	1.9E+0				

Supplementary Table S1: (continued)

1033	I3L8S3	Uncharacterized protein	CMBL	3.25E+06	1.48E+06	1.16E+06	6.11E+05	2.95E+05	1.34E+05	1.05E+05	5.56E+04
1034	B7Z39	Delta-aminolevulinic acid dehydratase		5.31E+06	2.47E+06	0.00E+00	2.84E+06	2.95E+05	1.37E+05	0.00E+00	1.58E+05
1035	F1SA70	Uncharacterized protein	HSPA2	1.18E+07	3.34E+06	3.84E+06	4.62E+06	2.95E+05	8.35E+04	9.59E+04	1.16E+05
1036	F5GYN4	Ubiquitin thioesterase OTUB1	OTUB1	4.42E+06	1.70E+06	1.30E+06	1.42E+06	2.95E+05	1.14E+05	8.68E+04	9.44E+04
1037	I4AY87	Macrophage migration inhibitory factor (Fragment)	MIF	1.47E+06	0.00E+00	7.84E+05	6.85E+05	2.94E+05	0.00E+00	1.57E+05	1.37E+05
1038	B7Z722	Tropomyosin I (Alpha), isoform CRA	TPM1	6.14E+06	1.40E+06	2.40E+06	2.34E+06	2.92E+05	6.68E+04	1.14E+05	1.11E+05
1039	AA0A087WYV2	IQ and AAA domain-containing protein 1-like	IQCA1L	1.46E+07	0.00E+00	1.17E+07	2.88E+06	2.92E+05	0.00E+00	2.34E+05	5.76E+04
1040	Q6DUB5	Peripheral benzodiazepine receptor transcript variant	TSPO	8.75E+05	8.75E+05	0.00E+00	0.00E+00	2.92E+05	2.92E+05	0.00E+00	0.00E+00
1041	F1RUM1	Uncharacterized protein	AFM	1.08E+07	2.96E+06	3.37E+06	4.43E+06	2.91E+05	8.00E+04	9.09E+04	1.20E+05
1042	F1SFR6	Succinyl-CoA ligase subunit beta	SUCLG2	8.14E+06	8.14E+06	0.00E+00	0.00E+00	2.91E+05	2.91E+05	0.00E+00	0.00E+00
1043	Q5T8U5	Surfeit 4	SURF4	2.61E+06	2.61E+06	0.00E+00	0.00E+00	2.90E+05	2.90E+05	0.00E+00	0.00E+00
1044	Q6AAL7	Ras-related protein Rab-1B	RAB1B	5.22E+06	1.73E+05	2.00E+06	3.05E+06	2.90E+05	2.99E+03	1.11E+05	1.70E+05
1045	X5FAU3	CDGSH iron sulfur domain 1	C10orf70	1.74E+06	0.00E+00	9.44E+05	7.94E+05	2.90E+05	0.00E+00	1.57E+05	1.32E+05
1046	I3Q728	Mitotic checkpoint protein BUB3 (Fragment)	BUB3	4.33E+06	2.04E+06	8.11E+05	1.48E+06	2.89E+05	1.36E+05	5.41E+04	9.89E+04
1047	M0R3H0	40S ribosomal protein S16	RPS16	2.29E+06	7.81E+05	1.27E+05	1.38E+06	2.86E+05	9.76E+04	1.58E+04	1.73E+05
1048	F1RUK4	Uncharacterized protein	WDR61	4.57E+06	3.42E+06	0.00E+00	1.15E+06	2.86E+05	2.14E+05	0.00E+00	7.21E+04
1049	F1SHD7	Uncharacterized protein	NDUFS1	1.28E+07	4.42E+06	4.41E+06	4.00E+06	2.85E+05	9.83E+04	9.80E+04	8.88E+04
1050	F1SK70	Uncharacterized protein	PROS	1.70E+06	2.78E+05	5.18E+05	9.08E+05	2.84E+05	4.63E+04	8.64E+04	1.51E+05
1051	F1SPT5	Uncharacterized protein	LAMB2	2.88E+07	8.46E+06	1.01E+07	1.02E+07	2.82E+05	8.29E+04	9.00E+04	1.00E+05
1052	Q9S287	Sucrase-isomaltase, intestinal (Fragment)		1.40E+06	0.00E+00	0.00E+00	1.40E+06	2.81E+05	0.00E+00	0.00E+00	2.81E+05
1053	I3LEZ3	Uncharacterized protein	LSAMP	2.51E+06	2.51E+06	0.00E+00	0.00E+00	2.79E+05	2.79E+05	0.00E+00	0.00E+00
1054	Q2JFN3	Calcium/calmodulin-dependent protein kinase II isoform gamma-C protein kinase II	CAMK2G	7.80E+06	4.56E+06	1.36E+06	1.89E+06	2.79E+05	1.63E+05	4.86E+04	6.73E+04
1055	D2XN65	Glycerol-3-phosphate dehydrogenase [NAD(+)]	gPD	6.65E+06	5.15E+06	1.01E+06	4.98E+05	2.77E+05	2.14E+05	4.20E+04	2.08E+04
1056	F6J1T9	Callicreinin subunit B type 1	PPP3R1	2.77E+06	0.00E+00	5.06E+05	2.26E+06	2.77E+05	0.00E+00	5.06E+04	2.26E+05
1057	S4R435	Peroxisomal acyl coenzyme A hydratase 1 (Fragment)	RPS19-NUDT3	5.84E+06	2.03E+06	1.46E+06	2.05E+06	2.77E+05	1.01E+05	7.31E+04	1.02E+05
1058	AA0A05Z2473	Protein phosphatase 1 regulatory subunit 12B isoform 1 (Fragment)	PPP1R12B	5.25E+06	2.25E+06	0.00E+00	0.00E+00	2.76E+05	2.76E+05	0.00E+00	0.00E+00
1059	B2R8A2	cDNA FLJ93804, highly similar to Homo sapiens gp25L2 protein (HSGP25L2G), mRNA	TM	4.10E+06	2.59E+06	0.00E+00	1.51E+06	2.74E+05	1.73E+05	0.00E+00	1.01E+05
1060	P12309	Glutaredoxin-1	GLRX	2.18E+06	0.00E+00	6.19E+05	1.56E+06	2.72E+05	0.00E+00	7.73E+04	1.95E+05
1061	F1RX93	Uncharacterized protein	MIEN1	2.18E+06	0.00E+00	5.47E+05	1.63E+06	2.72E+05	0.00E+00	6.83E+04	2.04E+05
1062	Q96I80	Mammalian ependymin related protein 1	MERP1	5.43E+06	1.94E+06	1.52E+06	1.97E+06	2.71E+05	9.71E+04	7.58E+04	9.86E+04
1063	F1SEN4	Uncharacterized protein	LOC100517243	1.08E+06	0.00E+00	3.40E+05	7.45E+05	2.71E+05	0.00E+00	8.00E+04	1.86E+05
1064	K7GPE2	Eukaryotic translation initiation factor 1b	EIF1B	1.35E+06	4.99E+05	5.47E+05	3.08E+05	2.71E+05	9.97E+04	1.09E+05	6.16E+04
1065	F1S6R7	Polypyrimidine tract-binding factor 1	PBTBP1	5.67E+06	1.79E+06	1.19E+06	2.69E+06	2.70E+05	8.54E+04	5.67E+04	1.28E+05
1066	B2CNZ7	Cathepsin B	CTSB	4.59E+06	3.06E+06	4.04E+05	1.13E+06	2.70E+05	1.80E+05	2.38E+04	6.63E+04
1067	F1SE55	Uncharacterized protein	ASAH1	6.45E+06	2.05E+06	1.79E+06	2.62E+06	2.69E+05	8.53E+04	7.86E+04	1.09E+05
1068	E9KL42	Epididymal secretory sperm binding protein L1 188a		6.98E+06	2.19E+06	1.32E+06	3.48E+06	2.69E+05	8.43E+04	5.06E+04	1.34E+05
1069	Q6PN0	Reticulon	RTN4	2.95E+06	2.95E+06	0.00E+00	0.00E+00	2.68E+05	2.68E+05	0.00E+00	0.00E+00
1070	F1SB42	Uncharacterized protein	EZR	5.36E+06	1.00E+06	1.80E+06	2.56E+06	2.68E+05	5.01E+04	8.29E+04	1.28E+05
1071	A7B326	Hydroxysteroid dehydrogenase 10 isoform 1 (Fragment)	SNRPF	1.72E+07	1.94E+06	2.18E+06	0.00E+00	2.57E+05	1.21E+05	1.36E+05	0.00E+00
1072	F1S031	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	2.40E+06	6.63E+05	1.16E+06	5.83E+05	2.67E+05	7.37E+04	1.28E+05	6.48E+04
1073	K7ESJ4	Programmed cell death protein 5	PDCD5	1.06E+06	2.34E+05	5.51E+05	2.77E+05	2.65E+05	5.84E+04	1.38E+05	6.92E+04
1074	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA	CC17	6.61E+06	5.85E+05	2.76E+06	3.27E+06	2.65E+05	2.34E+04	1.10E+05	1.31E+05
1075	F1S3H7	Uncharacterized protein	PTGR2	3.96E+06	3.03E+06	9.25E+05	0.00E+00	2.64E+05	2.02E+05	6.17E+04	0.00E+00
1076	Q5T8U3	60S ribosomal protein L7a (Fragment)	RPL7A	2.63E+06	4.63E+05	1.39E+06	7.78E+05	2.63E+05	4.63E+04	1.39E+05	7.78E+04
1077	C9JFR7	Cytochrome c (Fragment)	CYCS	2.10E+06	0.00E+00	0.00E+00	2.10E+06	2.63E+05	0.00E+00	0.00E+00	2.63E+05
1078	B5APU7	Actin related protein 2/3 complex subunit 2		6.03E+06	4.03E+06	0.00E+00	2.00E+06	2.62E+05	1.75E+05	0.00E+00	8.72E+04
1079	F1SR76	Uncharacterized protein	DNPEP	5.76E+06	2.11E+06	2.36E+06	1.30E+06	2.62E+05	9.57E+04	1.07E+05	5.90E+04
1080	F2ZF52	Uncharacterized protein	RAB10	4.44E+06	1.90E+06	4.21E+05	2.12E+06	2.61E+05	1.12E+05	2.48E+04	1.25E+05
1081	P10114	Ras-related protein Rap-2a	RAP2A	3.13E+06	1.27E+06	4.84E+05	1.37E+06	2.60E+05	1.06E+05	4.03E+04	1.14E+05
1082	B7Z871	cDNA FLJ50930, highly similar to Lipoma-preferred partner		5.46E+06	3.64E+06	0.00E+00	1.82E+06	2.60E+05	1.73E+05	0.00E+00	8.66E+04
1083	I3LDQ9	Phosphotransferase		2.06E+06	1.93E+06	0.00E+00	1.31E+05	2.57E+05	2.41E+05	0.00E+00	1.64E+04
1084	AA0A05Z2410	Hydroxysteroid dehydrogenase 10 isoform 1 (Fragment)	HSD17B10	4.11E+06	1.94E+06	2.18E+06	0.00E+00	2.57E+05	1.21E+05	1.36E+05	0.00E+00
1085	F1S0R4	Uncharacterized protein	SNRPF	1.29E+06	8.50E+05	3.06E+05	4.29E+05	2.57E+05	1.10E+05	6.12E+04	8.59E+04
1086	F1RJJ3	Uncharacterized protein	SBDS	4.37E+06	3.36E+06	0.00E+00	1.01E+06	2.57E+05	1.98E+05	0.00E+00	5.92E+04
1087	M3VK17	CD276 molecule tvl	CD276	6.42E+06	1.27E+06	1.59E+06	3.56E+06	2.57E+05	5.06E+04	6.37E+04	1.42E+05
1088	I3LF44	Uncharacterized protein	CPPEP1	3.58E+06	1.55E+06	6.72E+05	1.36E+06	2.56E+05	1.11E+05	4.80E+04	9.72E+04
1089	F1RVH5	Peptidyl-prolyl cis-trans isomerase	LOC100524880	3.06E+06	4.50E+05	9.96E+05	1.62E+06	2.55E+05	3.75E+04	8.30E+04	1.35E+05
1090	H0YJ99	26S protease regulatory subunit 10B	PSMCG	1.02E+06	4.71E+05	2.74E+05	2.74E+05	2.55E+05	1.18E+05	6.66E+04	6.84E+04
1091	I3LC25	Uncharacterized protein	LMNB2	1.07E+07	4.30E+06	1.93E+06	4.43E+06	2.54E+05	1.02E+05	4.60E+04	1.06E+05
1092	H0YJN9	Legumain (Fragment)	LGMN	1.27E+06	4.09E+05	3.22E+05	5.36E+05	2.54E+05	8.18E+04	6.45E+04	1.07E+05
1093	Q53FH6	Mitogen-activated protein kinase kinase 1 interacting protein 1 variant (Fragment)		2.28E+06	8.74E+05	9.10E+05	4.91E+05	2.53E+05	9.72E+04	1.01E+05	5.46E+04
1094	J3KS22	L-xylulose reductase (Fragment)	DCXR	3.79E+06	2.09E+06	8.98E+05	8.09E+05	2.53E+05	1.39E+05	5.99E+04	5.39E+04
1095	L8AXM9	IgG heavy chain	IgH5	5.05E+06	1.05E+06	1.60E+06	2.39E+06	2.52E+05	5.26E+04	8.01E+04	1.20E+05
1096	Q6B9V5	SLC25A6 protein	SLC25A6	4.57E+06	3.43E+06	2.05E+06	0.00E+00	2.49E+05	1.56E+05	9.31E+04	0.00E+00
1097	O11780	Transforming growth factor-beta-induced protein ig-h3	TGFB1	1.02E+07	3.29E+06	2.80E+06	4.08E+06	2.48E+05	8.03E+04	6.83E+04	9.96E+04
1098	K7GK9V	Uncharacterized protein	CD109	1.76E+07	7.26E+06	5.61E+06	2.33E+06	2.48E+05	7.90E+04	6.96E+04	6.96E+04
1099	F1SK08	Uncharacterized protein	NRP1	3.96E+06	1.30E+06	3.67E+06	2.30E+06	2.48E+05	1.02E+05	2.30E+04	1.43E+05
1100	F1RNR7	Uncharacterized protein	PSMD9	2.97E+06	1.80E+06	5.78E+05	5.86E+05	2.47E+05	1.50E+05	4.82E+04	4.89E+04
1101	K7GRD9	Uncharacterized protein (Fragment)	LAMP2	2.47E+06	1.47E+06	4.44E+05	5.54E+05	2.47E+05	1.47E+05	4.44E+04	5.54E+04
1102	F1SAB6	Acyl carrier protein	NDUFAB1	2.22E+06	7.02E+05	6.68E+05	8.51E+05	2.47E+05	7.80E+04	7.42E+04	9.46E+04
1103	G9M4N3	Toll interacting protein	Tollip	3.45E+06	1.44E+06	1.04E+06	9.65E+05	2.46E+05	1.03E+05	7.44E+04	6.89E+04
1104	F1SVA0	Uncharacterized protein	PEP1	1.97E+06	1.24E+06	2.19E+05	5.04E+05	2.46E+05	1.55E+05	2.73E+04	6.30E+04
1105	F1SL34	Uncharacterized protein (Fragment)	ALCAM	8.09E+06	5.82E+06	1.12E+06	1.16E+06	2.45E+05	1.76E+05	3.38E+04	3.51E+04
1106	Q1KLJ4	Proliferating cell nuclear antigen (Fragment)	PCNA	2.70E+06	8.24E+05	7.54E+05	1.12E+06	2.45E+05	7.49E+04	6.86E+04	1.02E+05
1107	F1SR53	Uncharacterized protein	ITGAS	1.17E+07	5.20E+06	2.54E+06	3.95E+06	2.44E+05	1.08E+05	5.30E+04	8.24E+04
1108	I3LCR9	Uncharacterized protein	MYOM1	2.42E+07	1.54E+07	3.83E+06	4.97E+06	2.42E+05	1.54E+05	3.83E+04	4.97E+04
1109	AA0A024R4T4	Ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast), isoform CRA	UBE2M	2.90E+06	1.86E+06	3.43E+05	7.01E+05	2.42E+05	1.55E+05	2.86E+04	5.84E+04
1110	B4DIC4	cDNA FLJ52195, highly similar to LIM and SH3 domain protein 1	LASP1	2.42E+06	2.42E+06	0.00E+00	0.00E+00	2.42E+05	2.42E+05	0.00E+00	0.00E+00
1111	Q5TD07	Ribosyl(dihydro)nicotinamide dehydrogenase [quinone]	NQO2	3.37E+06	5.53E+05	4.78E+05	2.34E+06	2.41E+05	3.95E+04	3.42E+04	1.67E+05
1112	O8K030	Protease serine 1 (Fragment)	PRSS1	1.68E+06	1.45E+06	0.00E+00	2.40E+06	2.07E+05	0.00E+00	0.00E+00	0.00E+00
1113	AA0A09YYJ0	Protein canyon homolog 4 (Fragment)	CNY14	1.67E+06	6.74E+05	2.22E+05	7.70E+05	2.38E+05	9.63E+04	3.17E+04	1.10E+05
1114	K7ENT6	Tropomyosin alpha-4 chain (Fragment)	TPM4	4.04E+06	2.93E+06	1.11E+06	0.00E+00	2.38E+05	1.72E+05	6.55E+04	0.00E+00
1115	F1SK12	Sulfurtransferase	IST1	4.50E+06	4.50E+06	0					

Supplementary Table S1: (continued)

1181	F1S788	Uncharacterized protein	CSA	6.06E+06	0.00E+00	2.41E+06	3.64E+06	1.95E+05	0.00E+00	7.79E+04	1.17E+05
1182	I3L6T2	Uncharacterized protein	UBE2V2	2.15E+06	1.65E+06	0.00E+00	5.01E+05	1.95E+05	1.50E+05	0.00E+00	4.56E+04
1183	I6XPV3	Voltage-dependent anion channel 3 (Fragment)	VDAC3	2.92E+06	1.13E+06	6.64E+05	1.12E+06	1.95E+05	7.56E+04	4.43E+04	7.47E+04
1184	F1S5Z8	Uncharacterized protein	SYPL2	2.14E+06	1.44E+06	7.03E+05	0.00E+00	1.95E+05	1.31E+05	6.39E+04	0.00E+00
1185	B1PK17	Aspartoacylase	ASPA	4.27E+06	3.28E+06	0.00E+00	9.87E+05	1.94E+05	1.49E+05	0.00E+00	4.48E+04
1186	A0A0A0MS07	Ig gamma-1 chain C region (Fragment)	IGHG1	2.51E+06	2.51E+06	0.00E+00	0.00E+00	1.93E+05	1.93E+05	0.00E+00	0.00E+00
1187	Q6JLA8	Four and a half LIM domains 3 (Fragment)	FHL3	2.31E+06	1.28E+06	7.57E+05	2.71E+05	1.93E+05	1.07E+05	6.31E+04	2.26E+04
1188	C9JDZ2	Fas apoptotic inhibitory molecule 1 (Fragment)	FAIM	1.35E+06	3.25E+05	1.44E+05	8.78E+05	1.92E+05	4.64E+04	2.06E+04	1.25E+05
1189	I3LNB4	Uncharacterized protein	ALDHHA1	5.95E+06	1.56E+06	2.92E+06	1.48E+06	1.92E+05	5.03E+04	9.41E+04	4.76E+04
1190	F1RWL7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	NDFUF8	2.30E+06	2.11E+06	1.96E+05	0.00E+00	1.92E+05	1.75E+05	1.64E+04	0.00E+00
1191	Q8MZ3	m7GpppX diphosphatase	DCPS	3.83E+06	1.52E+06	1.53E+06	7.84E+05	1.91E+05	7.60E+04	7.63E+04	3.92E+04
1192	Q9BS10	Similar to ribosomal protein S8 (Fragment)	RPS8	1.14E+06	1.31E+05	3.03E+05	5.06E+05	1.90E+05	5.52E+04	5.05E+04	8.44E+04
1193	FSVXH9	Poly(C)-binding protein 2 (Fragment)	PCBP2	2.27E+06	1.49E+06	7.83E+05	0.00E+00	1.89E+05	1.24E+05	6.53E+04	0.00E+00
1194	Q8SQ26	Lambda-crystallin homolog	CRYL1	3.60E+06	2.79E+06	0.00E+00	8.04E+05	1.89E+05	1.47E+05	0.00E+00	4.23E+04
1195	F1SAE9	Uncharacterized protein	LAMB1	1.77E+07	4.37E+06	6.25E+06	7.07E+06	1.88E+05	4.65E+04	6.65E+04	7.52E+04
1196	F1SEC0	Uncharacterized protein	DCTN3	2.43E+06	7.25E+05	3.51E+05	1.36E+06	1.87E+05	5.58E+04	2.70E+04	1.04E+05
1197	F1RZD0	Uncharacterized protein	FKBP7	3.37E+06	1.60E+06	6.48E+05	1.12E+06	1.87E+05	8.88E+04	3.60E+04	6.24E+04
1198	F1S109	Uncharacterized protein	PPP1R7	4.10E+06	2.27E+06	8.86E+05	9.43E+05	1.86E+05	1.03E+05	4.03E+04	4.29E+04
1199	V9HW80	Epididymus luminal protein 220	HEL_S-70	8.93E+06	2.74E+06	2.03E+06	4.16E+06	1.86E+05	5.71E+04	4.23E+04	8.67E+04
1200	I3LMU6	Uncharacterized protein	RGN3	2.60E+06	1.55E+06	0.00E+00	1.05E+06	1.85E+05	1.10E+05	0.00E+00	7.50E+04
1201	F1SK86	Uncharacterized protein	FKBP4	6.62E+06	5.97E+05	3.36E+06	2.66E+06	1.84E+05	1.66E+04	9.35E+04	7.39E+04
1202	P63096	Guanine nucleotide-binding protein (G) subunit alpha-1	GNAH1	3.12E+06	2.19E+06	9.35E+05	0.00E+00	1.84E+05	1.29E+05	5.50E+04	0.00E+00
1203	F1RIE2	Uncharacterized protein	DDB1	1.06E+07	2.55E+06	1.44E+06	6.59E+06	1.82E+05	4.39E+04	2.48E+04	1.14E+05
1204	Q19PV1	Alpha-1,4 glucan phosphorylase (Fragment)	PYGM	9.11E+06	4.03E+06	2.18E+06	2.90E+06	1.82E+05	8.06E+04	4.35E+04	5.80E+04
1205	Q6Q210	Transcription and mRNA export factor ENY2	ENY2	1.26E+06	3.36E+05	4.91E+05	4.37E+05	1.81E+05	4.80E+04	7.02E+04	6.25E+04
1206	I3LJW4	Aconitate hydratase	ACO1	8.84E+06	4.45E+06	2.09E+06	2.30E+06	1.80E+05	9.08E+04	4.27E+04	4.69E+04
1207	F1RLQ2	Prelamin-A/C	LMNA	7.91E+06	5.03E+06	2.19E+06	6.89E+05	1.80E+05	1.14E+05	4.98E+04	1.57E+04
1208	K91VR9	Importin subunit beta-1	KPNB1	7.89E+06	3.74E+06	2.48E+06	1.67E+06	1.79E+05	8.51E+04	5.63E+04	3.79E+04
1209	F1RPY1	Uncharacterized protein	ATL3	5.36E+06	2.60E+06	1.78E+06	9.78E+05	1.79E+05	8.67E+04	4.98E+04	3.26E+04
1210	A0A087WXS7	ATPase ASNA1	ASNA1	2.83E+06	1.71E+06	1.12E+06	0.00E+00	1.77E+05	1.07E+05	6.88E+04	0.00E+00
1211	I3LBB2	Vacuolar protein sorting-associated protein 35	VPS35	6.66E+06	1.60E+06	1.59E+06	3.46E+06	1.75E+05	4.22E+04	4.20E+04	9.12E+04
1212	B7Z230	cDNA FLJ53833, highly similar to FK506-binding protein 9 (EC 5.2.1.8)	FKBP9	3.85E+06	1.55E+06	1.53E+06	7.57E+05	1.75E+05	7.06E+04	6.97E+04	3.44E+04
1213	A0A0E3KLW5	Nucleoside diphosphate linked moiety X-type motif 3	NUDT3	1.92E+06	7.52E+05	4.35E+05	7.34E+05	1.75E+05	6.84E+04	3.95E+04	6.67E+04
1214	E5R90	Uncharacterized protein C1orf198 (Fragment)	C1orf198	1.90E+06	1.90E+06	0.00E+00	0.00E+00	1.72E+05	1.72E+05	0.00E+00	0.00E+00
1215	G3V5X4	Nesprin-2	SYNE2	7.73E+07	3.30E+07	0.00E+00	4.43E+07	1.72E+05	7.35E+04	0.00E+00	9.87E+04
1216	O97580	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial (Fragment)	SUCLA2	4.41E+06	3.55E+06	8.62E+05	0.00E+00	1.70E+05	1.36E+05	3.32E+04	0.00E+00
1217	F8VU6	60S ribosomal protein L18 (Fragment)	RPL18	1.01E+06	0.00E+00	1.01E+06	0.00E+00	1.69E+05	0.00E+00	1.69E+05	0.00E+00
1218	F1RT62	Uncharacterized protein	ITGA3	7.41E+06	1.80E+06	1.29E+06	4.32E+06	1.68E+05	4.10E+04	2.94E+04	9.81E+04
1219	Q6Q210	Amine oxidase [flavin-containing] A	MAOA	4.54E+06	1.45E+06	7.33E+05	2.36E+06	1.68E+05	5.36E+04	7.21E+04	8.72E+04
1220	I3LH26	Uncharacterized protein	DHX9	1.24E+07	7.18E+06	2.28E+06	2.96E+06	1.68E+05	9.71E+04	3.08E+04	4.00E+04
1221	I3LJY8	Uncharacterized protein	HSD17B12	1.98E+06	0.00E+00	6.13E+05	1.37E+06	1.65E+05	0.00E+00	5.11E+04	1.14E+05
1222	Q9NZ48	Uncharacterized hematopoietic stem/progenitor cells protein MDS026	PPP	1.32E+06	2.71E+05	2.90E+05	7.55E+05	1.64E+05	3.39E+04	3.63E+04	9.43E+04
1223	H3BNG3	40S ribosomal protein S2 (Fragment)	RPS2	3.28E+05	0.00E+00	3.28E+05	0.00E+00	1.64E+05	0.00E+00	1.64E+05	0.00E+00
1224	B5KN59	NADH-ubiquinone oxidoreductase chain 1	ND1	1.15E+06	2.36E+05	2.81E+05	6.28E+05	1.64E+05	3.38E+04	4.02E+04	8.97E+04
1225	B3KNZ3	cDNA FLJ30801 fis, clone FBRA2001217, highly similar to Homo sapiens LIM and senescent cell antigen-like domains 2 (LIMS2), mRNA		3.59E+06	3.29E+06	2.97E+05	0.00E+00	1.63E+05	1.50E+05	1.35E+04	0.00E+00
1226	P02584	Profilin-1		1.47E+06	5.34E+05	7.09E+05	2.25E+05	1.63E+05	5.93E+04	7.88E+04	2.50E+04
1227	A6NJH9	Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AY	1.30E+06	1.30E+06	0.00E+00	0.00E+00	1.62E+05	1.62E+05	0.00E+00	0.00E+00
1228	F1SEN1	Annexin	ANXA8	3.86E+06	2.23E+06	1.63E+06	0.00E+00	1.61E+05	9.29E+04	6.79E+04	0.00E+00
1229	Q0VGA5	SARS protein	SARS	4.98E+06	8.57E+05	2.29E+06	1.74E+06	1.61E+05	2.77E+04	7.70E+04	5.61E+04
1230	D0G0B3	Acetyl-Coenzyme A acyltransferase 2	ACA2	3.53E+06	1.48E+06	8.37E+05	1.22E+06	1.61E+05	6.72E+04	3.80E+04	5.54E+04
1231	M3V839	Mitogen-activated protein kinase	MAPK3	3.69E+06	3.69E+06	0.00E+00	0.00E+00	1.60E+05	1.60E+05	0.00E+00	0.00E+00
1232	F1S6K5	Uncharacterized protein	APRT	2.23E+06	1.23E+06	5.59E+05	4.60E+05	1.59E+05	8.80E+04	3.85E+04	3.29E+04
1233	M0R129	40S ribosomal protein S19 (Fragment)	RPS19	9.51E+05	7.83E+05	0.00E+00	1.68E+05	1.58E+05	1.30E+05	0.00E+00	2.80E+04
1234	Q9T136	Fibrillin-1	FBN1	2.57E+07	1.38E+07	1.19E+07	0.00E+00	1.58E+05	8.49E+04	7.28E+04	0.00E+00
1235	BSZ277	Peptidyl-prolyl cis-trans isomerase	PPP13	2.19E+06	9.44E+05	4.89E+05	7.60E+05	1.57E+05	6.74E+04	3.49E+04	5.43E+04
1236	Q06AB3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	2.03E+06	1.09E+06	9.39E+05	0.00E+00	1.56E+05	8.38E+04	7.22E+04	0.00E+00
1237	A8KAQ5	cDNA FLJ77404, highly similar to Homo sapiens small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen) (SNRP70), transcript variant 1, mRNA		2.96E+06	2.25E+06	7.17E+05	0.00E+00	1.56E+05	1.18E+04	3.77E+04	0.00E+00
1238	A0A140VJZ1	Testicular tissue protein Li 218		7.00E+06	3.29E+06	1.75E+06	1.96E+06	1.56E+05	7.31E+04	3.89E+04	4.35E+04
1239	F1RFE2	Uncharacterized protein		4.32E+06	0.00E+00	0.00E+00	4.32E+06	1.54E+05	0.00E+00	0.00E+00	1.54E+05
1240	F1SP18	Uncharacterized protein	TARS	6.16E+06	1.20E+06	1.21E+06	3.75E+06	1.54E+05	3.01E+04	3.02E+04	9.37E+04
1241	B1AK87	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA	CAPZB	2.76E+06	1.21E+06	3.53E+05	1.20E+06	1.54E+05	6.75E+04	1.96E+04	6.64E+04
1242	F1SPG9	Uncharacterized protein	ESYT1	8.89E+06	3.48E+06	2.74E+06	2.67E+06	1.53E+05	6.00E+04	4.73E+04	4.60E+04
1243	Q29529	Carbonyl reductase [NADPH] 2	CBR2	2.29E+06	1.34E+06	9.59E+05	0.00E+00	1.53E+05	8.90E+04	6.40E+04	0.00E+00
1244	A0A0K0K1J6	Epididymus secretory protein Li 96 (Fragment)	HEL_S-96	1.37E+06	0.00E+00	1.37E+06	0.00E+00	1.53E+05	0.00E+00	1.53E+05	0.00E+00
1245	P12271	Retinaldehyde-binding protein 1	RLBP1	2.74E+06	2.35E+06	0.00E+00	3.83E+06	1.52E+05	1.31E+05	0.00E+00	2.13E+04
1246	I3LH57	Uncharacterized protein	COX9	2.73E+06	2.03E+06	5.59E+05	1.44E+06	1.52E+05	1.13E+05	3.10E+04	8.22E+03
1247	B3RZ73	Alpha v integrin subunit	ITGAV	3.13E+06	1.83E+06	3.00E+06	1.50E+06	1.50E+05	2.71E+04	2.83E+04	2.42E+04
1248	F1S193	Uncharacterized protein	NTT1	2.69E+06	1.60E+06	6.59E+05	4.33E+05	1.50E+05	8.90E+04	3.66E+04	2.41E+04
1249	Q29554	Trifunctional enzyme subunit alpha, mitochondrial	HADHA	6.70E+06	2.38E+06	1.84E+06	2.47E+06	1.49E+05	5.30E+04	4.10E+04	5.49E+04
1250	Q6HY5	MHC class II antigen (Fragment)	SLA-DOB1	2.68E+06	2.68E+06	0.00E+00	0.00E+00	1.49E+05	1.49E+05	0.00E+00	0.00E+00
1251	Q05CR9	SYNCRIP protein (Fragment)	SYNCRIP	4.12E+06	1.65E+06	2.46E+06	0.00E+00	1.47E+05	5.91E+04	8.80E+04	0.00E+00
1252	F1S3U9	Uncharacterized protein	PRDX1	2.05E+06	2.05E+06	0.00E+00	0.00E+00	1.47E+05	1.47E+05	0.00E+00	0.00E+00
1253	I3LRH0	Uncharacterized protein	PRX	1.06E+07	6.32E+06	1.95E+06	2.36E+06	1.46E+05	8.66E+04	2.67E+04	3.23E+04
1254	Q29558	NADP-dependent malic enzyme (Fragment)	ME1	4.63E+06	0.00E+00	3.58E+06	1.05E+06	1.45E+05	0.00E+00	1.12E+05	3.27E+04
1255	V9HWF5	Peptidyl-prolyl cis-trans isomerase	HEL_S-69p	2.02E+06	1.34E+06	6.78E+05	0.00E+00	1.44E+05	9.57E+04	4.85E+04	0.00E+00
1256	K7GLU6	Uncharacterized protein (Fragment)	ERAP1	6.77E+06	2.28E+06	1.98E+06	2.51E+06	1.44E+05	4.86E+04	4.20E+04	5.34E+04
1257	K7GLP2	Uncharacterized protein	LOC100737768	1.01E+06	0.00E+00	0.00E+00	1.01E+06	1.44E+05	0.00E+00	0.00E+00	1.44E+05
1258	F1RY18	Uncharacterized protein	CSL3A1	1.18E+07	3.05E+06	3.64E+06	5.07E+06	1.43E+05	3.72E+04	4.44E+04	6.18E+04
1259	Q4ZG77	Putative uncharacterized protein PSM14 (Fragment)	PSM14	5.70E+05	5.70E+05	0.00E+00	0.00E+00	1.43E+05	1.43E+05	0.00E+00	0.00E+00
1260	F1S8K3	UTP-glucose-1-phosphate uridylyltransferase	UGP2	3.56E+06	2.65E+06	6.63E+05	2.42E+06	1.42E+05	1.06E+05	2.68E+04	6.32E+03
1261	Q13885	Tubulin beta-2A chain	TUBB2A	2.10E+06	1.65E+06	3.65E+05	9.49E+04	1.41E+05	2.20E+05	6.83E+04	4.31E+03
1262	I3L8K0	Uncharacterized protein		7.01E+05	7.01E+05	0.00E+00	0.00E+00	1.40E+05	1.40E+05	0.00E+00	0.00E+00
1263	I3L7K2	Phosphoinositide phospholipase C	PLCD								

Supplementary Table S1: (continued)

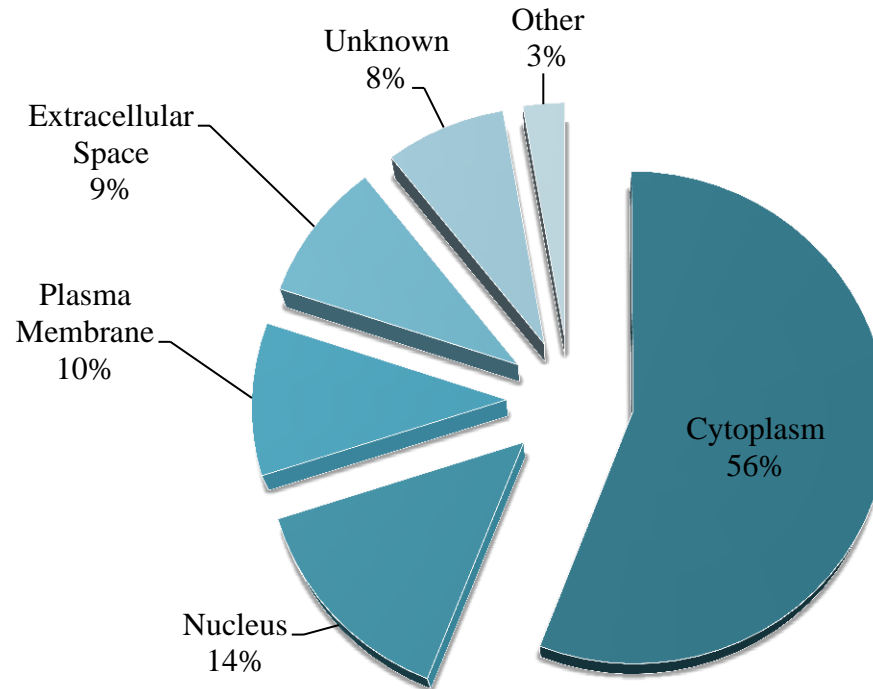
1329	H9LB34	Protein phosphatase 1B magnesium-dependent beta isoform (Fragment)	PPM1B	1.47E+06	0.00E+00	7.01E+05	7.68E+05	1.13E+05	0.00E+00	5.39E+04	5.91E+04
1330	I3LKP0	Uncharacterized protein	SYNM	9.13E+06	3.79E+06	2.77E+06	2.56E+06	1.13E+05	4.68E+04	3.42E+04	3.16E+04
1331	A7UIU7	ATP-citrate synthase	ACL	7.29E+06	4.79E+06	1.51E+06	9.91E+05	1.12E+05	7.38E+04	2.32E+04	1.52E+04
1332	G8ENM3	Ribokinase	RBKS	1.90E+06	6.52E+05	2.91E+05	9.56E+05	1.12E+05	3.84E+04	1.71E+04	5.62E+04
1333	Q76N53	Ribosomal protein L31 (Fragment)	RPL31	3.35E+05	0.00E+00	3.35E+05	0.00E+00	1.12E+05	0.00E+00	1.12E+05	0.00E+00
1334	K9VL7	Prolow-density lipoprotein receptor-related protein 1	LRP1	2.84E+07	9.51E+06	8.16E+06	1.07E+07	1.11E+05	3.71E+04	3.19E+04	4.20E+04
1335	P63267	Actin, gamma-enteric smooth muscle	ACTG2	2.55E+06	2.55E+06	0.00E+00	0.00E+00	1.11E+05	1.11E+05	0.00E+00	0.00E+00
1336	V9HW72	Epididymis secretory sperm binding protein Li 94n	HEL_S-94n	4.64E+06	5.53E+05	8.75E+05	3.21E+06	1.10E+05	1.32E+04	2.08E+04	7.65E+04
1337	K7GRN9	Uncharacterized protein	FAMI29A	3.74E+06	2.28E+06	9.01E+05	5.61E+05	1.10E+05	6.71E+04	2.65E+04	1.65E+04
1338	F1RR45	Uncharacterized protein	CRAT	3.85E+06	9.69E+05	1.10E+06	1.78E+06	1.10E+05	2.77E+04	3.15E+04	5.09E+04
1339	F1S605	Uncharacterized protein	CSFM3	2.17E+06	1.27E+06	2.70E+05	6.34E+05	1.09E+05	6.35E+04	1.35E+04	3.17E+04
1340	D3DQ64	Adenylate kinase 4, mitochondrial	AK4	1.30E+06	6.39E+05	0.00E+00	6.44E+05	1.09E+05	5.32E+04	0.00E+00	5.54E+04
1341	B4DTY8	cDNA FLJ61587, highly similar to Integrin alpha-1 (Fragment)	ITGAI	6.71E+06	2.18E+06	1.78E+06	2.75E+06	1.08E+05	3.52E+04	2.87E+04	4.44E+04
1342	A0A024RAB6	Heparan sulfate proteoglycan 2 (Perlecan), isoform CRA	HSPG2	2.03E+07	1.31E+07	5.27E+06	1.87E+06	1.08E+05	6.98E+04	2.80E+04	9.97E+03
1343	F1S150	Uncharacterized protein	NDUFB3	5.36E+05	0.00E+00	2.85E+05	2.51E+05	1.07E+05	0.00E+00	5.70E+04	5.02E+04
1344	F1RY03	Uncharacterized protein	FHL5	2.35E+06	2.35E+06	0.00E+00	0.00E+00	1.07E+05	1.07E+05	0.00E+00	0.00E+00
1345	E9PKR8	Sulfotransferase (Fragment)	SULT1A2	1.69E+06	1.16E+06	5.35E+05	0.00E+00	1.06E+05	7.23E+04	3.35E+04	0.00E+00
1346	F1RK01	Uncharacterized protein	CPB2	2.54E+06	0.00E+00	1.31E+06	1.23E+06	1.06E+05	0.00E+00	5.46E+04	5.11E+04
1347	B2R5U3	EH-domain containing 1, isoform CRA	EHD1	3.48E+06	3.29E+05	1.89E+06	1.26E+06	1.06E+05	9.97E+03	5.74E+04	3.81E+04
1348	I3L812	Uncharacterized protein	TPP1	2.63E+06	8.60E+05	8.16E+05	9.58E+05	1.05E+05	3.44E+04	3.26E+04	3.83E+04
1349	I3LTR9	Uncharacterized protein		1.05E+06	1.05E+06	0.00E+00	0.00E+00	1.05E+05	1.05E+05	0.00E+00	0.00E+00
1350	F1SU59	Annexin	ANXA7	2.73E+06	1.49E+06	1.08E+06	1.60E+05	1.05E+05	5.74E+04	4.14E+04	6.15E+03
1351	P11216	Glycogen phosphorylase, brain form	PYGB	5.77E+06	4.27E+06	8.67E+05	6.37E+05	1.05E+05	7.76E+04	1.58E+04	1.16E+04
1352	F1SK65	Uncharacterized protein		1.68E+06	5.61E+05	0.00E+00	1.12E+06	1.05E+05	3.51E+04	0.00E+00	6.97E+04
1353	I3LND3	Adenylate cyclase-associated protein	ACAP2	3.25E+06	3.17E+05	6.91E+05	2.24E+06	1.05E+05	1.02E+04	2.23E+04	7.22E+04
1354	F1SLI4	Uncharacterized protein	DHX30	8.90E+06	6.39E+06	0.00E+00	5.51E+06	1.05E+05	6.34E+04	0.00E+00	4.13E+04
1355	F1SUF2	Uncharacterized protein	HK1	4.59E+06	2.15E+06	1.40E+06	1.04E+06	1.04E+05	4.88E+04	3.19E+04	2.36E+04
1356	F1SU06	Uncharacterized protein	HP1BP3	3.02E+06	9.20E+05	1.24E+06	8.63E+05	1.04E+05	3.17E+04	4.27E+04	2.98E+04
1357	P56537	Eukaryotic translation initiation factor 6	EIF6	1.04E+06	1.04E+06	0.00E+00	0.00E+00	1.04E+05	1.04E+05	0.00E+00	0.00E+00
1358	O59F58	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa isoform b variant (Fragment)	EIF3	1.13E+06	0.00E+00	0.00E+00	1.13E+06	1.03E+05	0.00E+00	6.00E+00	1.03E+05
1359	I3LFZ2	Uncharacterized protein	RPA3	8.11E+05	0.00E+00	6.15E+05	1.96E+05	1.01E+05	0.00E+00	7.99E+04	2.45E+04
1360	Q6PIX2	SFPQ protein (Fragment)	SFPQ	2.63E+06	1.48E+06	5.06E+05	6.47E+05	1.01E+05	5.69E+04	1.95E+04	2.49E+04
1361	B4DEX8	Methionine adenosyltransferase II, alpha, isoform CRA	MAT2A	1.81E+06	1.81E+06	0.00E+00	0.00E+00	1.01E+05	1.01E+05	0.00E+00	0.00E+00
1362	F1SQ05	Uncharacterized protein	PHEX	4.53E+06	1.12E+06	1.23E+06	2.17E+06	1.01E+05	2.49E+04	2.73E+04	4.83E+04
1363	F2Z518	Uncharacterized protein	RAB8A	1.70E+06	5.67E+05	3.89E+05	7.43E+05	9.99E+04	3.34E+04	2.29E+04	4.37E+04
1364	Q8IWR8	Ribosomal protein L19 (Fragment)	RPL19	7.96E+05	0.00E+00	7.96E+05	0.00E+00	9.95E+04	0.00E+00	9.95E+04	0.00E+00
1365	Q2TJA5	Aldo-keto reductase	akr	2.38E+06	1.63E+06	7.50E+05	0.00E+00	9.95E+04	6.80E+04	3.13E+04	0.00E+00
1366	M3TY11	Phosphoglucosaminase 2	PGM2	3.92E+06	7.60E+05	6.93E+05	2.47E+06	8.40E+04	1.90E+04	1.73E+04	6.17E+04
1367	I3LND2	Uncharacterized protein	FMNL2	6.36E+06	0.00E+00	0.00E+00	6.36E+06	9.79E+04	0.00E+00	0.00E+00	9.79E+04
1368	A5A759	Keratin 2A	KRT2A	4.11E+06	0.00E+00	0.00E+00	4.11E+06	9.78E+04	0.00E+00	0.00E+00	9.78E+04
1369	I3LRH5	Uncharacterized protein	EPDR1	5.83E+05	5.83E+05	0.00E+00	0.00E+00	9.71E+04	9.71E+04	0.00E+00	0.00E+00
1370	F1SFF8	Alpha-1,4-glucan phosphorylase	PYGL	5.53E+06	3.92E+06	1.02E+06	5.86E+05	9.70E+04	6.89E+04	1.79E+04	1.03E+04
1371	F1RXD4	Uncharacterized protein	RMDN1	2.13E+06	2.13E+06	0.00E+00	0.00E+00	9.69E+04	9.69E+04	0.00E+00	0.00E+00
1372	Q6NVY0	Calycylin binding protein	CACYBP	1.55E+06	5.34E+05	1.02E+06	0.00E+00	9.69E+04	3.34E+04	6.35E+04	0.00E+00
1373	F1SS12	Uncharacterized protein	DHR57	2.03E+06	1.53E+06	5.00E+05	0.00E+00	9.68E+04	7.30E+04	2.38E+04	0.00E+00
1374	P18650	Apolipoprotein E	APOE	2.42E+06	1.02E+06	4.85E+05	9.18E+05	9.68E+04	4.07E+04	1.94E+04	3.67E+04
1375	Q53FX5	Lin-7 homolog C variant (Fragment)	LINC7	1.55E+06	8.10E+05	0.00E+00	7.38E+05	9.68E+04	5.06E+04	0.00E+00	4.62E+04
1376	A0ZYT4	Elongation initiation factor 4E (Fragment)	EIF4E	1.06E+06	1.06E+06	0.00E+00	0.00E+00	9.66E+04	9.66E+04	0.00E+00	0.00E+00
1377	F1SSN5	Uncharacterized protein	KTN1	8.84E+06	2.88E+06	2.47E+06	3.49E+06	9.61E+04	3.13E+04	2.68E+04	3.79E+04
1378	V9GYF8	Rab GDP dissociation inhibitor beta (Fragment)	GDI2	9.59E+05	9.59E+05	0.00E+00	0.00E+00	9.59E+04	9.59E+04	0.00E+00	0.00E+00
1379	F1RIU3	Uncharacterized protein	LOC102163415	2.68E+06	7.61E+05	7.79E+05	1.14E+06	9.58E+04	2.72E+04	2.78E+04	4.08E+04
1380	A0A0F7G8J1	Plasminogen	PLG	4.73E+06	1.06E+06	8.44E+05	2.83E+06	9.47E+04	2.12E+04	1.69E+04	5.66E+04
1381	A8K8U3	Calcium transporting ATPase	ATP2B4	5.95E+06	4.66E+06	1.06E+06	2.24E+05	9.44E+04	7.00E+04	1.85E+04	3.56E+03
1382	V9HVZ4	Glyceraldehyde-3-phosphate dehydrogenase	HEL_S-162p	1.79E+06	1.79E+06	0.00E+00	0.00E+00	9.41E+04	9.41E+04	0.00E+00	0.00E+00
1383	I3LPN0	Tryptase	MCT7	1.41E+06	4.53E+05	4.64E+05	4.93E+05	9.40E+04	3.02E+04	3.09E+04	3.29E+04
1384	I3LDP5	Uncharacterized protein	SUSD2	3.19E+06	1.51E+06	1.68E+06	0.00E+00	9.37E+04	4.43E+04	4.94E+04	0.00E+00
1385	B8YQC1	Galectin (Fragment)	LGALS1	8.34E+05	8.34E+05	0.00E+00	0.00E+00	9.27E+04	9.27E+04	0.00E+00	0.00E+00
1386	Q8HXW0	L-gulonolactone oxidase	GULO	2.04E+06	0.00E+00	1.10E+06	9.40E+05	9.25E+04	0.00E+00	4.98E+04	4.27E+04
1387	Q9BWJ5	Splicing factor 3B subunit 5	SF3B5	5.52E+05	0.00E+00	1.93E+05	3.59E+05	9.19E+04	0.00E+00	3.21E+04	5.98E+04
1388	G3V5E4	Glucosamine 6-phosphate N-acetyltransferase	GPNPAT	6.38E+05	3.65E+05	0.00E+00	2.73E+05	9.12E+04	5.22E+04	0.00E+00	3.90E+04
1389	V9HWJ7	Epididymis secretory protein Li 37	HEL_S-37	3.72E+06	1.96E+06	1.10E+06	6.61E+05	9.07E+04	4.79E+04	2.67E+04	1.61E+04
1390	L7X0X2	Fas-associated death domain protein (Fragment)	FADD	3.61E+05	3.61E+05	0.00E+00	0.00E+00	9.02E+04	9.02E+04	0.00E+00	0.00E+00
1391	F1S4D7	Uncharacterized protein	GBP1	2.97E+06	2.49E+06	4.86E+05	0.00E+00	9.01E+04	7.54E+04	1.47E+04	0.00E+00
1392	Q8XW6	Dihydropyrimidinase-like 3	DPYSL3	2.97E+06	0.00E+00	0.00E+00	2.97E+06	9.00E+04	0.00E+00	0.00E+00	9.00E+04
1393	F1RWX8	Uncharacterized protein	UBAI	5.29E+06	5.32E+05	3.51E+06	8.97E+04	9.02E+03	5.94E+04	2.12E+04	0.00E+00
1394	A5GFK7	Cathepsin Z	CTSZ	1.16E+06	1.61E+06	0.00E+00	0.00E+00	8.94E+04	8.94E+04	0.00E+00	0.00E+00
1395	K01K41	Tapasin	TAPBP	1.07E+06	0.00E+00	0.00E+00	0.00E+00	8.94E+04	8.94E+04	0.00E+00	0.00E+00
1396	I3L0P9	Centrobilin (Fragment)	CNTROB	1.16E+06	0.00E+00	0.00E+00	1.16E+06	8.92E+04	0.00E+00	0.00E+00	8.92E+04
1397	G3V325	Protein ATP5I2-PTCD1	ATP5I2-PTCD1	3.83E+06	2.38E+06	1.46E+06	0.00E+00	8.91E+04	5.52E+04	3.39E+04	0.00E+00
1398	O59FM5	Guanine nucleotide-binding protein G, alpha subunit variant (Fragment)	GNAI1	2.04E+06	1.26E+06	0.00E+00	7.86E+05	8.87E+04	5.46E+04	0.00E+00	3.42E+04
1399	E2QR11	Prolyl 3-hydroxylase 1 (Fragment)	P3H1	7.09E+05	7.09E+05	0.00E+00	0.00E+00	8.87E+04	8.87E+04	0.00E+00	0.00E+00
1400	F1RMN7	Hemopexin	HPX	2.31E+06	0.00E+00	1.04E+06	1.26E+06	8.87E+04	0.00E+00	4.01E+04	4.85E+04
1401	I3LN38	Uncharacterized protein		2.92E+06	0.00E+00	1.19E+06	1.73E+06	8.86E+04	0.00E+00	3.62E+04	5.25E+04
1402	F1S8M9	Uncharacterized protein	LRPAP1	2.12E+06	1.02E+06	6.80E+05	4.19E+05	8.84E+04	4.27E+04	2.83E+04	1.75E+04
1403	F1RGY5	Uncharacterized protein		1.59E+06	1.23E+06	0.00E+00	3.61E+05	8.83E+04	6.82E+04	0.00E+00	2.01E+04
1404	F1RLE5	Uncharacterized protein	TMED7	1.23E+06	3.44E+05	0.00E+00	8.90E+05	8.81E+04	2.45E+04	0.00E+00	6.36E+04
1405	Q5T6H7	Xaa-Pro aminopeptidase 1	XPNPPE1	3.08E+06	9.32E+05	1.01E+06	1.14E+06	8.80E+04	2.66E+04	2.89E+04	3.25E+04
1406	M0R0Y3	RuvB-like helicase	RUVB1	1.67E+06	1.05E+06	6.18E+05	0.00E+00	8.76E+04	5.51E+04	3.25E+04	0.00E+00
1407	Q53Q16	Putative uncharacterized protein FRZB (Fragment)	FRZB	6.99E+05	6.99E+05	0.00E+00	0.00E+00	8.74E+04	8.74E+04	0.00E+00	0.00E+00
1408	I3R819	Uncharacterized protein	TMEM38A	8.65E+05	8.65E+05	0.00E+00	0.00E+00	8.65E+04	8.65E+04	0.00E+00	0.00E+00
1409	F1S7C4	Methionine S-sulfide reductase B3 (Fragment)	MSRB3	2.07E+05	5.29E+05	0.00E+00	2.47E+05	8.62E+04	5.88E+04	0.00E+00	2.74E+04
1410	A0A142CHG9	GO2-q chimeric G-protein		1.89E+06	1.89E+06	0.00E+00	0.00E+00	8.60E+04	8.60E+04	0.00E+00	0.00E+00
1411	Q6DKJ4	Nucleoredoxin	NXN	1.97E+06	0.00E+00	1.45E+06	5.24E+05	8.58E+04	0.00E+00	6.30E+04	2.28E+04
1412	F1S6C3	Uncharacterized protein	ACAD8	1.03E+06	6.66E+05	3.64E+05</					

Supplementary Table S1: (continued)

1477	F1SI9	Uncharacterized protein	PSAT1	1.89E+06	1.43E+06	4.61E+05	0.00E+00	6.75E+04	5.10E+04	1.65E+04	0.00E+00
1478	I3L1T5	Deoxyribonuclease-1-like 1	DNASE1L1	1.14E+06	5.14E+05	6.25E+05	0.00E+00	6.70E+04	3.02E+04	3.68E+04	0.00E+00
1479	F1S4Y9	Uncharacterized protein	RALY	1.34E+06	4.69E+05	8.67E+05	0.00E+00	6.68E+04	2.34E+04	4.34E+04	0.00E+00
1480	F1RY7	Uncharacterized protein	PDDC1	8.01E+05	2.98E+05	5.03E+05	0.00E+00	6.67E+04	2.48E+04	4.19E+04	0.00E+00
1481	I3L725	Uncharacterized protein	RHOE	3.34E+05	3.34E+05	0.00E+00	0.00E+00	6.67E+04	6.67E+04	0.00E+00	0.00E+00
1482	B5BU72	Phosphatidylinositol-binding clathrin assembly protein isoform 2	PICALM	1.73E+06	6.83E+05	5.80E+05	4.65E+05	6.64E+04	2.63E+04	2.23E+04	1.79E+04
1483	F1SK12	Uncharacterized protein	MAP1B	7.70E+06	6.56E+05	4.58E+06	2.47E+06	6.64E+04	5.66E+03	3.94E+04	2.13E+04
1484	E9PNR9	Protein arginine N-methyltransferase 1 (Fragment)	PRMT1	5.91E+05	5.91E+05	0.00E+00	0.00E+00	6.56E+04	6.56E+04	0.00E+00	0.00E+00
1485	C9JG1	Biglycan (Fragment)	BGN	7.19E+05	0.00E+00	7.19E+05	0.00E+00	6.54E+04	0.00E+00	6.54E+04	0.00E+00
1486	Q49AG2	TMED5 protein	TMED5	6.53E+05	3.46E+05	3.07E+05	0.00E+00	6.53E+04	3.46E+04	3.07E+04	0.00E+00
1487	P23229	Incirgin alpha-6	ITGA6	4.48E+06	1.46E+06	1.57E+06	1.45E+06	6.49E+04	2.11E+04	2.28E+04	2.10E+04
1488	F1RUV5	Uncharacterized protein	PC	2.43E+06	1.00E+06	6.77E+05	7.51E+05	6.39E+04	2.63E+04	1.28E+04	1.98E+04
1489	I3LQ57	Uncharacterized protein	PTER	1.40E+06	1.31E+05	4.56E+05	8.09E+05	6.35E+04	5.96E+03	2.07E+04	3.68E+04
1490	P81693	Low molecular weight phosphotyrosine protein phosphatase	ACP1	5.70E+05	5.70E+05	0.00E+00	0.00E+00	6.33E+04	6.33E+04	0.00E+00	0.00E+00
1491	F1RF28	Uncharacterized protein		2.71E+06	2.07E+06	4.50E+05	1.92E+05	6.30E+04	4.80E+04	1.05E+04	4.47E+03
1492	F1SRV4	Glutathione S-transferase kappa 1	GSTK1	1.06E+06	8.63E+05	0.00E+00	1.98E+05	6.24E+04	5.08E+04	0.00E+00	1.17E+04
1493	B3KY79	cDNA FLJ46620 fis, clone TLUNG2000654, highly similar to Keratin, type II cytoskeletal 7		2.00E+06	1.68E+06	3.19E+05	0.00E+00	6.24E+04	5.24E+04	9.97E+03	0.00E+00
1494	I3L138	Uncharacterized protein	ATF7IP2	2.55E+06	4.30E+05	0.00E+00	0.00E+00	6.23E+04	1.05E+04	0.00E+00	5.18E+04
1495	F1RZC6	Uncharacterized protein	CCDC141	5.42E+06	0.00E+00	0.00E+00	5.42E+06	6.16E+04	0.00E+00	0.00E+00	6.16E+04
1496	Q9H6N6	Putative uncharacterized protein MYH16	MYH16	5.04E+06	3.47E+06	1.29E+06	2.73E+05	6.14E+04	4.24E+04	1.57E+04	3.33E+03
1497	H7C400	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (Fragment)	HHCH	2.45E+05	2.45E+05	0.00E+00	0.00E+00	6.12E+04	6.12E+04	0.00E+00	0.00E+00
1498	AOA024R972	Laminin, gamma 1 (Formerly LAMB2), isoform CRA	LAMC1	5.08E+06	2.49E+06	0.00E+00	2.58E+06	6.12E+04	3.00E+04	0.00E+00	3.11E+04
1499	F1S1I4	Uncharacterized protein	GARS	3.16E+06	1.85E+06	7.52E+05	5.64E+05	6.08E+04	3.55E+04	1.45E+04	1.08E+04
1500	Q87B16	Putative uncharacterized protein (Fragment)		1.03E+06	1.03E+06	0.00E+00	0.00E+00	6.05E+04	6.05E+04	0.00E+00	0.00E+00
1501	B7ZAS0	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	7.24E+05	7.24E+05	0.00E+00	0.00E+00	6.04E+04	6.04E+04	0.00E+00	0.00E+00
1502	Q5L091	Neuroblastoma RAS viral (V-ras) oncogene homolog	NRAS	6.64E+05	6.64E+05	0.00E+00	0.00E+00	6.04E+04	6.04E+04	0.00E+00	0.00E+00
1503	A2ACR1	Proteasome subunit beta type	PSMB9	6.00E+05	1.42E+05	2.67E+05	1.90E+05	6.00E+04	1.42E+04	2.67E+04	1.90E+04
1504	F1S186	Uncharacterized protein	CSPG4	5.86E+06	1.96E+05	2.37E+06	3.30E+06	5.98E+04	2.00E+03	2.42E+04	3.37E+04
1505	I3LBG8	Uncharacterized protein	PON3	8.25E+05	3.58E+05	4.68E+05	0.00E+00	5.90E+04	2.56E+04	3.34E+04	0.00E+00
1506	F2ZK55	Uncharacterized protein	TUBB4A	1.30E+06	1.30E+06	0.00E+00	0.00E+00	5.89E+04	5.89E+04	0.00E+00	0.00E+00
1507	AOA0U5BLD0	Inactive dehydrogenase/reductase isoform	spDHR11	9.42E+05	9.42E+05	0.00E+00	0.00E+00	5.89E+04	5.89E+04	0.00E+00	0.00E+00
1508	Q5TFK1	Eukaryotic translation initiation factor 3 subunit I (Fragment)	EIF3	6.48E+05	6.48E+05	0.00E+00	0.00E+00	5.89E+04	5.89E+04	0.00E+00	0.00E+00
1509	AOA024QZE7	Transforming growth factor beta 1 induced transcript 1, isoform CRA	TGFB11	1.47E+06	1.25E+06	2.22E+05	0.00E+00	5.88E+04	4.99E+04	8.00E+03	0.00E+00
1510	Q5J808	Rho-related GTP-binding protein RhoC (Fragment)	RHOC	6.46E+05	0.00E+00	0.00E+00	6.46E+05	5.87E+04	0.00E+00	0.00E+00	5.87E+04
1511	F2Z5R6	Uncharacterized protein	CAND1	3.88E+06	2.08E+06	1.06E+06	7.46E+05	5.79E+04	3.10E+04	0.00E+00	1.11E+04
1512	F1R1U2	Uncharacterized protein	LACTB2	9.27E+05	5.33E+05	3.93E+05	0.00E+00	5.79E+04	3.33E+04	2.46E+04	0.00E+00
1513	K94F3	UDP-glucose glycoprotein glucosyltransferase 1	UGT1	4.95E+06	9.20E+05	2.87E+06	1.17E+06	5.76E+04	1.07E+04	3.33E+04	1.36E+04
1514	I3LBF1	Inhibitor of carbonic anhydrase	ICA	2.22E+06	5.26E+05	3.86E+05	1.31E+06	5.69E+04	1.35E+04	9.90E+03	3.55E+04
1515	B7ZAS0	cDNA FLJ39088, highly similar to UV excision repair protein RAD23 homolog B		6.83E+05	0.00E+00	6.83E+05	0.00E+00	5.68E+04	0.00E+00	5.68E+04	0.00E+00
1516	F1S7K2	Uncharacterized protein	LRG1	1.25E+06	0.27E+05	1.02E+06	0.00E+00	5.67E+04	1.03E+04	4.64E+04	0.00E+00
1517	F1S188	Beta-hexosaminidase	HEXA	1.47E+06	7.26E+05	4.41E+05	3.00E+05	5.64E+04	2.79E+04	1.69E+04	1.15E+04
1518	F1SK02	Uncharacterized protein	ARPN	7.90E+05	7.90E+05	0.00E+00	0.00E+00	5.64E+04	5.64E+04	0.00E+00	0.00E+00
1519	K9IV06	Plectin (Fragment)	PLEC	1.50E+07	8.07E+06	2.67E+06	4.30E+06	5.59E+04	3.00E+04	9.92E+03	1.60E+04
1520	P14543	Nidogen-1	NID1	3.02E+06	2.05E+06	4.78E+05	4.88E+05	5.49E+04	3.73E+04	8.69E+03	8.88E+03
1521	F1RPO5	Uncharacterized protein	DNAJA2	1.37E+06	1.37E+06	0.00E+00	0.00E+00	5.48E+04	5.48E+04	0.00E+00	0.00E+00
1522	F1SP54	Uncharacterized protein	NIPSNAP3B	9.31E+05	9.31E+05	0.00E+00	0.00E+00	5.48E+04	5.48E+04	0.00E+00	0.00E+00
1523	F5XVC2	von Willebrand factor	VWF	7.57E+06	2.71E+06	2.27E+06	2.59E+06	5.45E+04	1.95E+04	1.64E+04	1.86E+04
1524	Q5Q444	Putative uncharacterized protein DKFZp547A0616 (Fragment)	DKFZp547A0616	5.96E+05	3.54E+05	2.42E+05	0.00E+00	5.42E+04	3.22E+04	2.20E+04	0.00E+00
1525	H0YF18	Tubby-related protein 3 (Fragment)	TULP3	4.33E+05	0.00E+00	0.00E+00	4.33E+05	5.41E+04	0.00E+00	0.00E+00	5.41E+04
1526	I3LX8	Sulfotransferase		1.24E+06	1.24E+06	0.00E+00	0.00E+00	5.39E+04	5.39E+04	0.00E+00	0.00E+00
1527	B7Z1M6	cDNA FLJ57716, highly similar to 40S ribosomal protein S4, X isoform	Rps4	5.90E+05	5.90E+05	0.00E+00	0.00E+00	5.36E+04	5.36E+04	0.00E+00	0.00E+00
1528	V9JW42	Epithelium secretory protein LI 105	HEL15-105	1.98E+06	6.03E+05	0.00E+00	1.37E+06	5.34E+04	1.63E+04	0.00E+00	3.71E+04
1529	I3LR8	Uncharacterized protein	PCBP3	9.08E+05	9.08E+05	0.00E+00	0.00E+00	5.34E+04	5.34E+04	0.00E+00	0.00E+00
1530	F1RL80	Branched chain-amino-acid aminotransferase	BCAT2	1.27E+06	1.08E+06	1.96E+05	0.00E+00	5.30E+04	4.49E+04	8.19E+03	0.00E+00
1531	Q8HX66	MHC class I antigen (Fragment)	SLA-1	1.11E+06	1.11E+06	0.00E+00	0.00E+00	5.29E+04	5.29E+04	0.00E+00	0.00E+00
1532	D6RGE0	40S ribosomal protein S3a (Fragment)	RPS3A	2.10E+05	0.00E+00	2.10E+05	0.00E+00	5.26E+04	0.00E+00	5.26E+04	0.00E+00
1533	F1S3P5	Uncharacterized protein	ENPP1	2.41E+06	4.77E+05	4.54E+05	1.48E+06	5.13E+04	1.02E+04	9.65E+03	3.15E+04
1534	F1SL03	Uncharacterized protein		2.82E+06	1.41E+06	1.41E+06	0.00E+00	5.12E+04	2.56E+04	2.56E+04	0.00E+00
1535	B4DGN8	cDNA FLJ53377, highly similar to Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 (EC 1.14.11.4)		2.35E+06	0.00E+00	5.43E+05	1.81E+06	5.11E+04	0.00E+00	1.18E+04	3.93E+04
1536	I3LC92	Uncharacterized protein	ENOSF1	1.37E+06	0.00E+00	4.62E+05	9.09E+05	5.08E+04	0.00E+00	1.71E+04	3.37E+04
1537	F1RNT9	Uncharacterized protein	LNPEP	2.87E+06	1.15E+06	6.47E+05	1.07E+06	5.03E+04	2.02E+04	1.14E+04	1.88E+04
1538	F1S1F4	Uncharacterized protein	KNG1	1.43E+06	0.00E+00	1.43E+06	0.00E+00	4.92E+04	0.00E+00	4.92E+04	0.00E+00
1539	K7GN08	Uncharacterized protein	LICAM	3.14E+06	2.63E+06	1.70E+05	3.38E+05	4.90E+04	4.11E+04	2.65E+03	5.28E+03
1540	E9PMR5	Myelin basic protein	MBP	3.92E+05	0.00E+00	3.92E+05	0.00E+00	4.90E+04	0.00E+00	4.90E+04	0.00E+00
1541	Q0VGS4	TNS1 protein	TNS1	4.31E+06	2.03E+06	4.51E+05	1.82E+06	4.90E+04	2.31E+04	5.12E+03	2.07E+04
1542	E7EP33	60S ribosomal protein L14	RPL14	4.87E+05	0.00E+00	4.87E+05	0.00E+00	4.87E+04	0.00E+00	4.87E+04	0.00E+00
1543	F1SN05	Eukaryotic translation initiation factor 3 subunit J	EIF3J	7.70E+05	6.49E+05	1.21E+05	0.00E+00	4.81E+04	4.06E+04	2.87E+03	0.00E+00
1544	K7GQL2	Coagulation factor XIII, A1 polypeptide	F13A1	2.20E+06	7.20E+05	1.09E+06	3.97E+05	4.79E+04	1.57E+04	3.66E+04	8.63E+03
1545	P09497	Clathrin light chain B	CLTB	4.74E+05	0.00E+00	4.74E+05	0.00E+00	4.74E+04	0.00E+00	4.74E+04	0.00E+00
1546	I3L7Z6	Protein S100	S100A6	2.84E+05	0.00E+00	0.00E+00	2.84E+05	4.73E+04	0.00E+00	0.00E+00	4.73E+04
1547	F1S2E3	Peptidyl-prolyl cis-trans isomerase	PPF	7.92E+05	7.92E+05	0.00E+00	0.00E+00	4.66E+04	4.66E+04	0.00E+00	0.00E+00
1548	F1SAR5	Uncharacterized protein	LIPEX5	4.19E+05	0.00E+00	4.19E+05	0.00E+00	4.66E+04	0.00E+00	4.66E+04	0.00E+00
1549	I3LFQ5	6-phosphofruktokinase	PFKL	2.00E+06	1.06E+06	4.24E+05	5.18E+05	4.65E+04	2.46E+04	9.87E+03	1.21E+04
1550	F1SKG6	Sodium/potassium-transporting ATPase subunit beta	ATP1B3	6.48E+05	0.00E+00	0.00E+00	6.48E+05	4.63E+04	0.00E+00	0.00E+00	4.63E+04
1551	F2Z5W2	Cell division control protein 42 homolog	CDC42	4.14E+05	4.14E+05	0.00E+00	0.00E+00	4.60E+04	4.60E+04	0.00E+00	0.00E+00
1552	Q9TUQ3	Complement component C7	C7	2.33E+06	6.26E+05	5.02E+05	1.21E+06	4.57E+04	1.23E+04	9.85E+03	2.36E+04
1553	I3LVG4	GripE protein homolog	GRPEL1	8.11E+05	2.97E+05	2.45E+05	2.68E+05	4.50E+04	1.65E+04	1.36E+04	1.49E+04
1554	Q9HBM8	cDNA FLJ7849, highly similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase alpha (EC 2.3.1.51)		5.35E+05	5.35E+05	0.00E+00	0.00E+00	4.46E+04	4.46E+04	0.00E+00	0.00E+00
1555	B4E3D0	cDNA FLJ55017, highly similar to Caldesmon	CALDI	9.76E+05	9.76E+05	0.00E+00	0.00E+00	4.44E+04	4.44E+04	0.00E+00	0.00E+00
1556	F1SN05	cDNA FLJ36593 fis, clone TRACH2014077, highly similar to Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA		6.06E+05	0.00E+00	6.06E+05	0.00E+00	4.43E+04	0.00E+00	4.43E+04	0.00E+00
1557	K7GQ88	Uncharacterized protein	CP	2.51E+06	6.62E+05	4.49E+05	1.40E+06	4.41E+04	1.16E+04	7.87E+03	2.46E+04
1558	B4DUT1	cDNA FLJ52688, highly similar to SET and MYND domain-containing protein 5	SMYD5	5.27E+05	5.27E+05	0.00E+00	0.00E+00	4.39E+04	4.39E+04	0.00E+00	0.00E+00
1559	I3L677	Glucose									

Supplementary Table S1: (continued)

1619	F1SL07	Uncharacterized protein	NDUF9	7.99E+05	0.00E+00	7.99E+05	0.00E+00	2.96E+04	0.00E+00	2.96E+04	0.00E+00
1620	Q6EEI7	Mannose receptor C1 (Fragment)	MRC1	2.28E+06	9.73E+05	4.49E+05	8.62E+05	2.93E+04	1.25E+04	5.75E+03	1.11E+04
1621	F1SHR2	Uncharacterized protein	BCL2L13	6.13E+05	3.16E+05	2.96E+05	0.00E+00	2.92E+04	1.51E+04	1.41E+04	0.00E+00
1622	I3LLT4	Uncharacterized protein	CYP20A1	2.61E+05	2.61E+05	0.00E+00	0.00E+00	2.90E+04	2.90E+04	0.00E+00	0.00E+00
1623	F1S1A8	Uncharacterized protein	NDUF52	8.59E+05	0.00E+00	8.59E+05	0.00E+00	2.86E+04	0.00E+00	2.86E+04	0.00E+00
1624	Q8DXJ3	Small nuclear ribonucleoprotein component	SNRP116	1.50E+06	7.87E+05	7.11E+05	0.00E+00	2.83E+04	1.48E+04	1.34E+04	0.00E+00
1625	P11607	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	1.49E+06	1.49E+06	0.00E+00	0.00E+00	2.81E+04	2.81E+04	0.00E+00	0.00E+00
1626	B4DEX5	Prion protein interacting protein, isoform CRA	PRNPIP	2.81E+05	2.81E+05	0.00E+00	0.00E+00	2.81E+04	2.81E+04	0.00E+00	0.00E+00
1627	A0A024R115	Pyridoxal (Pyridoxine, vitamin B6) phosphatase, isoform CRA	PDXP	5.05E+05	0.00E+00	0.00E+00	5.05E+05	2.80E+04	0.00E+00	0.00E+00	2.80E+04
1628	I3L1F2	Uncharacterized protein	RPN2	7.25E+05	0.00E+00	7.25E+05	0.00E+00	2.79E+04	0.00E+00	2.79E+04	0.00E+00
1629	A0A087X0P0	Centromere-associated protein E	CENPE	5.60E+06	1.70E+06	0.00E+00	3.90E+06	2.79E+04	8.45E+03	0.00E+00	1.94E+04
1630	F1RKY8	Uncharacterized protein	PSMD11	8.03E+05	8.03E+05	0.00E+00	0.00E+00	2.77E+04	2.77E+04	0.00E+00	0.00E+00
1631	F1S091	Uncharacterized protein	RAB8B	4.07E+05	1.37E+05	2.70E+05	0.00E+00	2.71E+04	9.16E+03	1.80E+04	0.00E+00
1632	Q8VED5	Keratin 79	Krt79 Keratin 79	8.69E+05	0.00E+00	0.00E+00	8.69E+05	2.71E+04	0.00E+00	0.00E+00	2.71E+04
1633	Q8SPR7	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-4	PLCD4	8.03E+05	0.00E+00	2.50E+05	5.52E+05	2.68E+04	0.00E+00	8.35E+03	1.84E+04
1634	E5RGJ2	ER membrane protein complex subunit 2 (Fragment)	EMC2	1.87E+05	1.87E+05	0.00E+00	0.00E+00	2.66E+04	2.66E+04	0.00E+00	0.00E+00
1635	Q9GLP2	Vitamin K-dependent protein C	PROC	7.63E+05	2.87E+05	4.75E+05	0.00E+00	2.54E+04	9.58E+03	1.58E+04	0.00E+00
1636	P02666	Beta-casein		2.03E+05	0.00E+00	0.00E+00	2.03E+05	2.53E+04	0.00E+00	0.00E+00	2.53E+04
1637	F1SIX7	Uncharacterized protein	LOC106504190	5.52E+05	5.52E+05	0.00E+00	0.00E+00	2.51E+04	2.51E+04	0.00E+00	0.00E+00
1638	Q05BX4	PSMD1 protein (Fragment)	PSMD1	1.08E+06	0.00E+00	1.19E+05	9.57E+05	2.50E+04	0.00E+00	2.76E+03	2.23E+04
1639	B4DJ25	cDNA FLJ52302, highly similar to Nuclear receptor corepressor 1		1.54E+06	0.00E+00	0.00E+00	1.54E+06	2.49E+04	0.00E+00	0.00E+00	2.49E+04
1640	A0A024R319	Laminin, beta 2 (Laminin 5), isoform CRA	LAMB2	2.64E+06	0.00E+00	1.17E+06	1.47E+06	2.42E+04	0.00E+00	1.07E+04	1.35E+04
1641	F1SDX6	Uncharacterized protein	TGM2	1.03E+06	5.98E+05	2.46E+05	1.86E+05	2.39E+04	1.39E+04	5.72E+03	4.32E+03
1642	B4DIL5	cDNA FLJ54516, highly similar to Adapter-related protein complex 2 beta-1 subunit		4.77E+05	0.00E+00	0.00E+00	4.77E+05	2.38E+04	0.00E+00	0.00E+00	2.38E+04
1643	K7CP98	Uncharacterized protein	TRM23	7.39E+05	4.49E+05	1.77E+05	1.13E+05	2.38E+04	1.45E+04	5.70E+03	3.66E+03
1644	F1RU52	Uncharacterized protein	LOC100626654	1.05E+06	2.08E+05	5.55E+05	2.86E+05	2.38E+04	4.73E+03	1.26E+04	6.49E+03
1645	Q4GI88	CAMK2D protein (Fragment)	CAMK2D	4.52E+05	4.52E+05	0.00E+00	0.00E+00	2.38E+04	2.38E+04	0.00E+00	0.00E+00
1646	P22612	cAMP-dependent protein kinase catalytic subunit gamma	PRKACG	4.74E+05	0.00E+00	4.74E+05	0.00E+00	2.37E+04	0.00E+00	2.37E+04	0.00E+00
1647	F1SIG7	Uncharacterized protein	SCRN1	4.47E+05	0.00E+00	4.47E+05	0.00E+00	2.35E+04	0.00E+00	2.35E+04	0.00E+00
1648	F1RLR8	Uncharacterized protein	GGT5	6.81E+05	5.14E+05	0.00E+00	1.67E+05	2.35E+04	1.77E+04	0.00E+00	5.77E+03
1649	O14980	Exportin-1	XPO1	1.36E+06	1.02E+06	0.00E+00	3.39E+05	2.34E+04	1.76E+04	0.00E+00	5.84E+03
1650	J3KNV4	Integrin alpha-7	ITGA7	1.26E+06	1.26E+06	0.00E+00	0.00E+00	2.34E+04	2.34E+04	0.00E+00	0.00E+00
1651	I3LGD9	Uncharacterized protein	AGRN	2.47E+06	7.60E+05	1.71E+06	0.00E+00	2.33E+04	7.17E+03	1.62E+04	0.00E+00
1652	A0A052Z3A5	Acyl-CoA dehydrogenase C-4 to C-12 straight chain isoform 4 (Fragment)	ACADM	3.29E+05	3.29E+05	0.00E+00	0.00E+00	2.19E+04	2.19E+04	0.00E+00	0.00E+00
1653	F1SUN0	Uncharacterized protein	ARRB1	4.94E+05	2.93E+05	2.01E+05	0.00E+00	2.15E+04	1.27E+04	8.74E+03	0.00E+00
1654	I3L3J8	Sodium/potassium-transporting ATPase subunit beta (Fragment)	ATP1B2	1.93E+05	0.00E+00	1.93E+05	0.00E+00	2.14E+04	0.00E+00	2.14E+04	0.00E+00
1655	F1S8R4	Uncharacterized protein	IVD	4.85E+05	0.00E+00	0.00E+00	4.85E+05	2.11E+04	0.00E+00	0.00E+00	2.11E+04
1656	Q138L4	Beta-1-synuclein	SNB1	7.38E+05	0.00E+00	7.38E+05	0.00E+00	2.11E+04	0.00E+00	2.11E+04	0.00E+00
1657	K7CKK3	Myosin-13	MYH13	2.60E+06	2.60E+06	0.00E+00	0.00E+00	2.08E+04	2.08E+04	0.00E+00	0.00E+00
1658	J9J19	4-aminobutyrate aminotransferase, mitochondrial	ABAT	6.74E+05	0.00E+00	4.29E+05	2.45E+05	2.04E+04	0.00E+00	1.30E+04	7.41E+03
1659	F1RVH7	Uncharacterized protein	IGFBP7	3.24E+05	3.24E+05	0.00E+00	0.00E+00	2.02E+04	2.02E+04	0.00E+00	0.00E+00
1660	D6RD63	COP9 signalosome complex subunit 4 (Fragment)	COP9	3.96E+05	0.00E+00	3.96E+05	0.00E+00	1.98E+04	0.00E+00	1.98E+04	0.00E+00
1661	Q5T1S7	Serine/threonine-protein phosphatase (Fragment)	PPP6C	1.18E+05	1.18E+05	0.00E+00	0.00E+00	1.97E+04	1.97E+04	0.00E+00	0.00E+00
1662	I3LKD2	Uncharacterized protein	FAM162A	2.16E+05	2.16E+05	0.00E+00	0.00E+00	1.96E+04	1.96E+04	0.00E+00	0.00E+00
1663	Q4W4Y1	Dopamine receptor interacting protein 4	DRIP4	1.09E+06	0.00E+00	4.69E+05	6.21E+05	1.95E+04	0.00E+00	8.38E+03	1.11E+04
1664	B2RD36	cDNA, FLJ96437		3.28E+05	0.00E+00	3.28E+05	0.00E+00	1.93E+04	0.00E+00	1.93E+04	0.00E+00
1665	F1S3Q8	Uncharacterized protein	VNN3	4.38E+05	0.00E+00	2.09E+05	2.29E+05	1.90E+04	0.00E+00	9.07E+03	9.96E+03
1666	B0IIS4	DNHD1 variant protein (Fragment)	DNHD1	3.73E+06	3.64E+06	0.00E+00	9.09E+04	1.85E+04	0.00E+00	4.62E+02	0.00E+00
1667	F1RQQ7	Alpha-1,4 glucan phosphorylase	PYGB	9.01E+05	0.00E+00	3.77E+05	5.23E+05	1.88E+04	0.00E+00	7.86E+03	1.09E+04
1668	F1RWZ4	Uncharacterized protein	ECT2	4.68E+05	4.68E+05	0.00E+00	0.00E+00	1.87E+04	1.87E+04	0.00E+00	0.00E+00
1669	F1S8G5	Thimet oligopeptidase	THOP1	7.56E+05	7.56E+05	0.00E+00	0.00E+00	1.85E+04	1.85E+04	0.00E+00	0.00E+00
1670	F1S5S1	Uncharacterized protein	IBA57	3.63E+05	2.27E+05	1.36E+05	0.00E+00	1.82E+04	1.14E+04	6.81E+03	0.00E+00
1671	K7CQZ6	Uncharacterized protein	ATP6AP2	3.27E+05	3.27E+05	0.00E+00	0.00E+00	1.81E+04	1.81E+04	0.00E+00	0.00E+00
1672	A0A0U4BW16	Non-muscle myosin heavy chain 9	MYH9	2.20E+06	1.98E+06	2.23E+05	0.00E+00	1.76E+04	1.58E+04	1.78E+03	0.00E+00
1673	F1SFM2	Uncharacterized protein	CHL1	9.15E+05	9.15E+05	0.00E+00	0.00E+00	1.76E+04	1.76E+04	0.00E+00	0.00E+00
1674	Q9LQ85	Putative uncharacterized protein DKFZp564O1822 (Fragment)	DKFZp564O1822	4.22E+05	0.00E+00	0.00E+00	4.22E+05	1.76E+04	0.00E+00	0.00E+00	1.76E+04
1675	K9VC5	Protein-arginine deiminase type-2	PADI2	6.50E+05	1.93E+05	0.00E+00	4.57E+05	1.76E+04	5.23E+03	0.00E+00	1.23E+04
1676	F1SH60	Uncharacterized protein	CPSF6	1.91E+05	0.00E+00	1.91E+05	0.00E+00	1.74E+04	0.00E+00	1.74E+04	0.00E+00
1677	Q1T7A9	Type VI collagen alpha-1 chain (Fragment)	COL6A1	1.21E+05	0.00E+00	0.00E+00	1.21E+05	1.72E+04	0.00E+00	0.00E+00	1.72E+04
1678	V9HW49	Epididymis secretory sperm binding protein Li 62p	HEL_S_62p	1.85E+06	0.00E+00	0.00E+00	1.85E+06	1.72E+04	0.00E+00	0.00E+00	1.72E+04
1679	I3LMP2	Uncharacterized protein	ABHD10	3.59E+05	3.59E+05	0.00E+00	0.00E+00	1.71E+04	1.71E+04	0.00E+00	0.00E+00
1680	M3TYW5	Glutanyl-prolyl-tRNA synthetase	QARS	7.56E+05	2.57E+05	2.02E+05	2.97E+05	1.68E+04	5.72E+03	4.49E+03	6.59E+03
1681	F1RZR9	Chloride intracellular channel protein	CLIC2	2.64E+05	0.00E+00	2.64E+05	0.00E+00	1.65E+04	0.00E+00	1.65E+04	0.00E+00
1682	F1S4X9	Glutathione synthetase	GSS	4.85E+05	4.85E+05	0.00E+00	0.00E+00	1.62E+04	1.62E+04	0.00E+00	0.00E+00
1683	A0A087X0A8	Collagen alpha-1(XII) chain	COL12A1	1.71E+06	1.41E+06	0.00E+00	3.01E+05	1.62E+04	1.33E+04	0.00E+00	2.84E+03
1684	Q3YM45	cGMP-dependent protein kinase	PKA1	6.56E+05	4.26E+05	9.21E+04	1.60E+05	1.60E+04	1.04E+04	2.25E+03	3.25E+03
1685	O44409	Apolipoprotein A-IV	APOA4	4.67E+05	0.00E+00	4.67E+05	0.00E+00	1.56E+04	0.00E+00	1.56E+04	0.00E+00
1686	F1RRY6	Uncharacterized protein	PTGES2	3.75E+05	3.75E+05	0.00E+00	0.00E+00	1.44E+04	1.44E+04	0.00E+00	0.00E+00
1687	F1SAY0	Uncharacterized protein (Fragment)	PTGFRN	7.50E+05	0.00E+00	0.00E+00	7.50E+05	1.44E+04	0.00E+00	0.00E+00	1.44E+04
1688	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	4.04E+06	1.55E+06	2.49E+06	0.00E+00	1.42E+04	5.42E+03	8.74E+03	0.00E+00
1689	D9YZV5	Tropomyosin 1 (Alpha) isoform 4	TPM1	3.17E+05	3.17E+05	0.00E+00	0.00E+00	1.38E+04	1.38E+04	0.00E+00	0.00E+00
1690	F1S168	Alpha-mannosidase	MAN2C1	7.01E+05	4.53E+05	0.00E+00	2.48E+05	1.37E+04	8.88E+03	0.00E+00	4.87E+03
1691	F1SKJ1	Uncharacterized protein	MYH9	1.69E+06	1.41E+06	0.00E+00	2.79E+05	1.37E+04	1.14E+04	0.00E+00	2.25E+03
1692	X6RJS7	Lys-63-specific deubiquitinase BRCC36 (Fragment)	BRCC3	1.62E+05	0.00E+00	0.00E+00	1.62E+05	1.35E+04	0.00E+00	0.00E+00	1.35E+04
1693	I3LW7	Uncharacterized protein		6.00E+05	2.88E+05	0.00E+00	3.12E+05	1.30E+04	6.25E+03	0.00E+00	6.78E+03
1694	F1RYL9	Uncharacterized protein	USO1	6.64E+05	6.64E+05	0.00E+00	0.00E+00	1.30E+04	1.30E+04	0.00E+00	0.00E+00
1695	B3KZM6	cDNA FLJ13058 fs, clone NT2RP3001587, highly similar to Ubiquitin-like 1-activating enzyme E1B		4.56E+05	0.00E+00	4.56E+05	0.00E+00	1.30E+04	0.00E+00	1.30E+04	0.00E+00
1696	E7ENL6	Collagen alpha-3(VI) chain	COL6A3	2.16E+06	2.85E+05	6.55E+05	1.22E+06	1.30E+04	1.71E+03	3.94E+03	7.34E+03
1697	Q860V2	MHC class I antigen	SLA-I	2.33E+05	0.00E+00	2.33E+05	0.00E+00	1.29E+04	0.00E+00	1.29E+04	0.00E+00
1698	I3LR46	Uncharacterized protein	TRPM3	1.56E+06	0.00E+00	0.00E+00	1.56E+06	1.25E+04	0.00E+00	0.00E+00	1.25E+04
1699	J9T9K7	CD163 protein	CD163	4.67E+05	6.09E+05	1.54E+05	0.00E+00	1.25E+04	9.99E+03	2.52E+03	0.00E+00
1700	F1SG42	10-formyltetrahydrofolate dehydrogenase	ALDH1L2	8.36E+05	6.48E+05	0.00E+00	1.88E+05	1.25E+04	9.67E+03	0.00E+00	2.81E+03
1701	Q6YSS6	FYVE and coiled-coil domain containing 1 (Fragment)	FYCO1	6.44E+05	0.00						



Supplementary Figure S1

The major Gene Ontology Cellular Component terms (GOCCs) of the proteins identified from the porcine sPCA. A large majority of the identified proteins are from the cytoplasm, while 14 % and 10 % are nuclear and plasma membrane proteins. Only a small percentage of the sPCA proteins are localized in the extracellular space, while the remaining 11 % corresponded to other unknown cellular compartments.

Supplementary Table S2:
Complete list of the GOBP of proteins identified from the porcine sPCA analysed employing DAVID functional analysis tool.

No.	Term	Count	%	P-Value	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
1	GO:000691-generation of precursor metabolites and energy	112	0.4105722	1.43E-40	1185	313	13528	4.0849705	5.19E-37	5.19E-37	2.63E-37
2	GO:0015980-energy derivation by oxidation of organic compounds	58	0.2126178	4.55E-24	1185	144	13528	4.5981247	1.65E-20	8.25E-21	8.36E-21
3	GO:0045333-cellular respiration	46	0.1686279	1.15E-22	1185	97	13528	5.4137892	4.18E-19	1.39E-19	1.21E-19
4	GO:005114-oxidation reduction	133	0.4875545	8.33E-22	1185	639	13528	2.3761072	3.03E-18	7.56E-19	1.53E-18
5	GO:0006414-translational elongation	44	0.1612962	6.24E-20	1185	101	13528	4.9733216	2.26E-16	4.53E-17	1.15E-16
6	GO:0006007-glucose catabolic process	30	0.1099747	3.43E-16	1185	58	13528	5.904845	1.21E-12	2.02E-13	6.11E-13
7	GO:0006119-oxidative phosphorylation	30	0.1099747	3.43E-16	1185	58	13528	5.904845	1.21E-12	2.02E-13	6.11E-13
8	GO:0022900-electron transport chain	41	0.1502988	4.12E-15	1185	114	13528	4.1057665	1.49E-11	1.86E-12	7.55E-12
9	GO:0046365-monosaccharide catabolic process	32	0.1173064	4.52E-15	1185	71	13528	5.1452547	1.65E-11	1.84E-12	8.37E-12
10	GO:0044275-cellular carbohydrate catabolic process	35	0.1283038	5.18E-15	1185	85	13528	4.7007198	1.89E-11	1.89E-12	9.59E-12
11	GO:0006006-glucose metabolic process	48	0.1759595	5.90E-15	1185	153	13528	3.5815008	2.14E-11	1.94E-12	1.08E-11
12	GO:0046164-alcohol catabolic process	34	0.124638	6.92E-15	1185	81	13528	4.7919154	2.50E-11	2.08E-12	1.27E-11
13	GO:0006096-glycolysis	25	0.0916456	7.35E-14	1185	47	13528	6.0723584	2.67E-10	2.05E-11	1.35E-10
14	GO:0022904-respiratory electron transport chain	29	0.1063089	8.96E-14	1185	64	13528	5.1728903	3.25E-10	2.32E-11	1.65E-10
15	GO:0019320-hexose catabolic process	30	0.1099747	1.15E-13	1185	69	13528	4.9634929	4.18E-10	2.79E-11	2.12E-10
16	GO:0005996-monosaccharide metabolic process	57	0.2089519	1.85E-13	1185	222	13528	2.9311438	6.72E-10	4.20E-11	3.41E-10
17	GO:0007010-cytoskeleton organization	87	0.3189266	3.47E-13	1185	436	13528	2.27797	1.26E-09	7.41E-11	6.38E-10
18	GO:0006457-protein folding	49	0.1796254	5.70E-13	1185	177	13528	3.1603709	2.07E-09	1.15E-10	1.05E-09
19	GO:0003029-actin filament-based process	59	0.2162836	5.95E-13	1185	241	13528	2.7947966	2.16E-09	1.14E-10	1.09E-09
20	GO:0016052-carbohydrate catabolic process	37	0.1356355	7.09E-13	1185	109	13528	3.8751674	2.90E-09	1.45E-10	1.47E-09
21	GO:0042775-mitochondrial ATP synthesis coupled electron transport	26	0.0953114	1.10E-12	1185	56	13528	5.3003014	3.98E-09	1.89E-10	2.01E-09
22	GO:0042773-ATP synthesis coupled electron transport	26	0.0953114	1.10E-12	1185	56	13528	5.3003014	3.98E-09	1.89E-10	2.01E-09
23	GO:0031400-negative regulation of protein modification process	38	0.1393013	3.06E-12	1185	119	13528	3.6454562	1.11E-08	5.05E-10	5.63E-09
24	GO:0019318-hexose metabolic process	50	0.1832912	3.84E-12	1185	192	13528	2.9729255	1.39E-08	6.06E-10	7.06E-09
25	GO:0006120-mitochondrial electron transport, NADH to ubiquinone	22	0.0806481	4.46E-12	1185	42	13528	5.9798272	1.67E-08	6.97E-10	8.47E-09
26	GO:0030036-actin cytoskeleton organization	55	0.2016203	5.12E-12	1185	226	13528	2.7782383	1.86E-08	7.44E-10	9.42E-09
27	GO:0065003-macromolecular complex assembly	113	0.4142381	5.37E-12	1185	665	13528	1.9398674	1.95E-08	7.50E-10	9.88E-09
28	GO:0051187-cofactor catabolic process	19	0.0696506	5.50E-12	1185	31	13528	6.9969239	1.99E-08	7.39E-10	1.01E-08
29	GO:0009060-aerobic respiration	20	0.0733165	7.21E-12	1185	35	13528	6.5234479	2.62E-08	9.35E-10	1.33E-08
30	GO:0051443-positive regulation of ubiquitin-protein ligase activity	28	0.1026431	9.34E-12	1185	70	13528	4.5664135	3.39E-08	1.17E-09	1.72E-08
31	GO:0006732-coenzyme metabolic process	43	0.1576304	1.05E-11	1185	153	13528	3.2084278	3.80E-08	1.27E-09	1.93E-08
32	GO:0009109-coenzyme catabolic process	17	0.062319	2.46E-11	1185	26	13528	7.4643298	8.92E-08	2.88E-09	4.52E-08
33	GO:0051186-cofactor metabolic process	49	0.1796254	2.56E-11	1185	195	13528	2.8686444	9.31E-08	2.91E-09	4.72E-08
34	GO:0051438-regulation of ubiquitin-protein ligase activity	29	0.1063089	2.93E-11	1185	78	13528	4.2444228	1.06E-07	3.22E-09	5.39E-08
35	GO:0051351-positive regulation of ligase activity	28	0.1026431	2.96E-11	1185	73	13528	4.3787527	1.07E-07	3.16E-09	5.44E-08
36	GO:0046366-acetyl-CoA catabolic process	16	0.0586532	3.11E-11	1185	23	13528	7.9415887	1.13E-07	3.23E-09	5.73E-08
37	GO:0006099-tricarboxylic acid cycle	16	0.0586532	3.11E-11	1185	23	13528	7.9415887	1.13E-07	3.23E-09	5.73E-08
38	GO:0043933-macromolecular complex subunit organization	116	0.4252355	3.58E-11	1185	710	13528	1.8651548	1.30E-07	3.61E-09	6.58E-08
39	GO:0031398-positive regulation of protein ubiquitination	30	0.1099747	3.93E-11	1185	84	13528	4.0771549	1.43E-07	3.86E-09	7.23E-08
40	GO:0010035-response to inorganic substance	50	0.1832912	4.93E-11	1185	205	13528	2.7843985	1.79E-07	4.71E-09	9.06E-08
41	GO:0031145-anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	26	0.0953114	5.91E-11	1185	65	13528	4.5664135	2.15E-07	5.50E-09	1.09E-07
42	GO:0051436-negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	26	0.0953114	5.91E-11	1185	65	13528	4.5664135	2.15E-07	5.50E-09	1.09E-07
43	GO:0032369-negative regulation of cellular protein metabolic process	46	0.1686279	6.17E-11	1185	180	13528	2.9174308	2.24E-07	5.60E-09	1.13E-07
44	GO:0051248-negative regulation of protein metabolic process	47	0.1722937	6.84E-11	1185	187	13528	2.8692705	2.48E-07	6.05E-09	1.26E-07
45	GO:0006084-acetyl-CoA metabolic process	18	0.0659848	7.54E-11	1185	31	13528	6.6286648	2.74E-07	6.51E-09	1.39E-07
46	GO:0051340-regulation of ligase activity	29	0.1063089	8.24E-11	1185	81	13528	4.087222	2.99E-07	6.96E-09	1.52E-07
47	GO:0051439-regulation of ubiquitin-protein ligase activity during mitotic cell cycle	27	0.0989772	8.90E-11	1185	71	13528	4.3413086	3.23E-07	7.35E-09	1.64E-07
48	GO:0051444-negative regulation of ubiquitin-protein ligase activity	26	0.0953114	1.28E-10	1185	67	13528	4.4301027	4.64E-07	1.03E-08	2.35E-07
49	GO:0051352-negative regulation of ligase activity	26	0.0953114	1.28E-10	1185	67	13528	4.4301027	4.64E-07	1.03E-08	2.35E-07
50	GO:0051437-positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	26	0.0953114	1.28E-10	1185	68	13528	4.3649541	6.74E-07	1.46E-08	3.41E-07
51	GO:0031396-regulation of protein ubiquitination	32	0.1173064	1.92E-10	1185	100	13528	3.6531308	6.99E-07	1.49E-08	3.54E-07
52	GO:0009259-ribonucleotide metabolic process	39	0.1429671	6.78E-10	1185	147	13528	3.0287436	2.46E-06	5.13E-08	1.25E-06
53	GO:0006412-translation	65	0.2382785	9.38E-10	1185	331	13528	2.2418193	3.40E-06	6.95E-08	1.72E-06
54	GO:0009150-purine ribonucleotide metabolic process	37	0.1356355	1.45E-09	1185	138	13528	3.0608206	5.28E-06	1.06E-07	2.68E-06
55	GO:0031397-negative regulation of protein ubiquitination	26	0.0953114	1.47E-09	1185	74	13528	4.0110389	5.33E-06	1.05E-07	2.70E-06
56	GO:0010498-proteasomal protein catabolic process	31	0.1136405	1.56E-09	1185	102	13528	3.4695789	5.65E-06	1.09E-07	2.86E-06
57	GO:0043161-proteasomal ubiquitin-dependent protein catabolic process	31	0.1136405	1.56E-09	1185	102	13528	3.4695789	5.65E-06	1.09E-07	2.86E-06
58	GO:0006936-muscle contraction	38	0.1393013	8.20E-09	1185	153	13528	2.8355548	2.98E-05	5.62E-07	1.51E-05
59	GO:002526-acute inflammatory response	29	0.1063089	1.11E-08	1185	98	13528	3.3782141	4.03E-05	7.46E-07	2.04E-05
60	GO:0003012-muscle system process	40	0.1466529	1.11E-08	1185	168	13528	2.7181033	4.05E-05	7.36E-07	2.05E-05
61	GO:0010033-response to organic substance	109	0.3995748	1.35E-08	1185	721	13528	1.7258636	4.92E-05	8.78E-07	2.49E-05
62	GO:0007021-protein complex biogenesis	83	0.3042634	2.43E-08	1185	505	13528	1.8762986	8.82E-05	1.55E-06	4.47E-05
63	GO:0006461-protein complex assembly	83	0.3042634	2.43E-08	1185	505	13528	1.8762986	8.82E-05	1.55E-06	4.47E-05
64	GO:0032368-regulation of cellular protein metabolic process	49	0.2386901	3.02E-08	1185	474	13528	1.9026723	1.10E-04	1.89E-06	5.56E-05
65	GO:0051259-protein oligomerization	40	0.1466529	3.12E-08	1185	174	13528	2.6243756	1.13E-04	1.92E-06	5.74E-05
66	GO:0045454-cell redox homeostasis	22	0.0806481	3.94E-08	1185	63	13528	3.9865515	1.43E-04	2.38E-06	7.24E-05
67	GO:0009152-purine ribonucleotide biosynthetic process	31	0.1136405	5.14E-08	1185	117	13528	3.0247611	1.86E-04	3.06E-06	9.45E-05
68	GO:0034622-cellular macromolecular complex assembly	59	0.2162836	5.16E-08	1185	318	13528	2.1180692	1.87E-04	3.02E-06	9.49E-05
69	GO:0009260-ribonucleotide biosynthetic process	32	0.1173064	5.82E-08	1185	124	13528	2.9460732	2.11E-04	3.35E-06	1.07E-04
70	GO:0051260-protein homooligomerization	27	0.0989772	9.64E-08	1185	95	13528	3.244557	3.50E-04	5.47E-06	1.77E-04
71	GO:0044271-nitrogen compound biosynthetic process	59	0.2162836	1.13E-07	1185	325	13528	2.0724492	4.11E-04	6.32E-06	2.08E-04
72	GO:0009144-purine nucleoside triphosphate metabolic process	31	0.1136405	1.41E-07	1185	122	13528	2.9007955	5.11E-04	7.75E-06	2.59E-04
73	GO:0051493-regulation of cytoskeleton organization	33	0.1209722	1.64E-07	1185	136	13528	2.770067	5.95E-04	8.88E-06	3.01E-04
74	GO:0007264-small GTPase mediated signal transduction	56	0.2052861	1.69E-07	1185	305	13528	2.0960587	6.14E-04	9.03E-06	3.11E-04
75	GO:0006081-cellular aldehyde metabolic process	14	0.0513215	1.78E-07	1185	28	13528	5.7080169	6.45E-04	9.35E-06	3.27E-04
76	GO:0006979-response to oxidative stress	37	0.1356355	1.83E-07	1185	164	13528	2.5755686	6.65E-04	9.50E-06	3.37E-

Supplementary Table S2: (continued)

154	GO:003100-regulation of endocytosis	17	0.062319	4.93E-05	1185	61	13528	3.1815176	1.64E-01	1.29E-03	9.07E-02
155	GO:0034599-cellular response to oxidative stress	14	0.0513215	5.00E-05	1185	43	13528	3.7168482	1.66E-01	1.30E-03	9.19E-02
156	GO:0007596-blood coagulation	23	0.0843139	5.75E-05	1185	102	13528	2.5742037	1.88E-01	1.48E-03	1.06E-01
157	GO:0050817-coagulation	23	0.0843139	5.75E-05	1185	102	13528	2.5742037	1.88E-01	1.48E-03	1.06E-01
158	GO:0043603-cellular amide metabolic process	16	0.0586532	6.48E-05	1185	56	13528	3.2617239	2.10E-01	1.66E-03	1.19E-01
159	GO:0070301-cellular response to hydrogen peroxide	9	0.0329924	6.62E-05	1185	18	13528	5.7080169	2.14E-01	1.68E-03	1.22E-01
160	GO:0060627-regulation of vesicle-mediated transport	22	0.0806481	6.77E-05	1185	96	13528	2.6161744	2.18E-01	1.70E-03	1.24E-01
161	GO:0043062-extracellular structure organization	31	0.1136405	7.12E-05	1185	163	13528	2.1711475	2.28E-01	1.78E-03	1.31E-01
162	GO:0010941-regulation of cell death	104	0.3812456	7.51E-05	1185	815	13528	1.45677	2.39E-01	1.86E-03	1.38E-01
163	GO:0030195-negative regulation of blood coagulation	10	0.0366582	7.71E-05	1185	23	13528	4.9634929	2.44E-01	1.90E-03	1.42E-01
164	GO:0051262-protein tetramerization	13	0.0476557	8.01E-05	1185	39	13528	3.8053446	2.52E-01	1.96E-03	1.47E-01
165	GO:0034655-nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	16	0.0586532	1.00E-04	1185	58	13528	3.1492507	3.05E-01	2.44E-03	1.85E-01
166	GO:0034656-nucleobase, nucleoside and nucleotide catabolic process	16	0.0586532	1.00E-04	1185	58	13528	3.1492507	3.05E-01	2.44E-03	1.85E-01
167	GO:0015985-energy coupled proton transport, down electrochemical gradient	13	0.0476557	1.05E-04	1185	40	13528	3.710211	3.18E-01	2.55E-03	1.94E-01
168	GO:0015986-ATP synthesis coupled proton transport	13	0.0476557	1.05E-04	1185	40	13528	3.710211	3.18E-01	2.55E-03	1.94E-01
169	GO:0060548-negative regulation of cell death	54	0.1979545	1.16E-04	1185	360	13528	1.7124051	3.44E-01	2.79E-03	2.13E-01
170	GO:0051789-response to protein stimulus	23	0.0843139	1.22E-04	1185	107	13528	2.4539138	3.58E-01	2.91E-03	2.24E-01
171	GO:0006959-humoral immune response	19	0.0696506	1.27E-04	1185	79	13528	2.7456284	3.69E-01	3.00E-03	2.33E-01
172	GO:0042274-ribosomal small subunit biogenesis	7	0.0256608	1.39E-04	1185	11	13528	7.2647488	3.97E-01	3.28E-03	2.56E-01
173	GO:0043066-negative regulation of apoptosis	53	0.1942886	1.40E-04	1185	354	13528	1.7091802	3.99E-01	3.28E-03	2.58E-01
174	GO:0009261-ribonucleoside catabolic process	10	0.0366582	1.64E-04	1185	25	13528	4.5664135	4.49E-01	3.81E-03	3.01E-01
175	GO:0043067-regulation of programmed cell death	102	0.373914	1.64E-04	1185	812	13528	1.4340338	4.49E-01	3.79E-03	3.01E-01
176	GO:0006800-oxygen and reactive oxygen species metabolic process	17	0.062319	1.66E-04	1185	67	13528	2.8966056	4.52E-01	3.80E-03	3.04E-01
177	GO:0042981-regulation of apoptosis	101	0.3702482	1.76E-04	1185	804	13528	1.4341037	4.71E-01	4.00E-03	3.22E-01
178	GO:0032535-regulation of cellular component size	43	0.1576304	1.87E-04	1185	271	13528	1.8114002	4.92E-01	4.23E-03	3.43E-01
179	GO:0043069-negative regulation of programmed cell death	53	0.1942886	2.02E-04	1185	359	13528	1.6853755	5.19E-01	4.54E-03	3.70E-01
180	GO:0050878-regulation of body fluid levels	27	0.0989772	2.04E-04	1185	141	13528	2.186049	5.24E-01	4.57E-03	3.75E-01
181	GO:0034220-ion transmembrane transport	14	0.0513215	2.19E-04	1185	49	13528	3.2617239	5.48E-01	4.86E-03	4.01E-01
182	GO:0046364-monosaccharide biosynthetic process	12	0.0439899	2.23E-04	1185	37	13528	3.7024974	5.55E-01	4.92E-03	4.09E-01
183	GO:0042592-homeostatic process	95	0.3482532	2.25E-04	1185	751	13528	1.4441055	5.58E-01	4.94E-03	4.13E-01
184	GO:0007265-Ras protein signal transduction	22	0.0806481	2.58E-04	1185	105	13528	2.3919309	6.09E-01	5.63E-03	4.74E-01
185	GO:006014-D-ribose metabolic process	5	0.0183291	2.72E-04	1185	5	13528	11.416034	6.27E-01	5.89E-03	4.98E-01
186	GO:006818-hydrogen transport	16	0.0586532	2.72E-04	1185	63	13528	2.8993102	6.28E-01	5.86E-03	4.99E-01
187	GO:0002449-lymphocyte mediated immunity	17	0.062319	2.85E-04	1185	70	13528	2.7724653	6.44E-01	6.09E-03	5.22E-01
188	GO:0046165-alcohol biosynthetic process	13	0.0476557	2.87E-04	1185	44	13528	3.3729191	6.47E-01	6.11E-03	5.26E-01
189	GO:0046700-heterocycle catabolic process	18	0.0659848	2.89E-04	1185	77	13528	2.6686832	6.50E-01	6.12E-03	5.31E-01
190	GO:0010038-response to metal ion	25	0.0916456	3.08E-04	1185	129	13528	2.2124096	6.73E-01	6.47E-03	5.64E-01
191	GO:0030155-regulation of cell adhesion	26	0.0953114	3.17E-04	1185	137	13528	2.1665466	6.84E-01	6.63E-03	5.81E-01
192	GO:0030834-regulation of actin filament depolymerization	10	0.0366582	3.21E-04	1185	27	13528	4.2281607	6.88E-01	6.67E-03	5.88E-01
193	GO:0051235-maintenance of location	16	0.0586532	3.27E-04	1185	64	13528	2.8540084	6.95E-01	6.76E-03	6.00E-01
194	GO:0000398-nuclear mRNA splicing, via spliceosome	28	0.1026431	3.27E-04	1185	153	13528	2.0892088	6.95E-01	6.72E-03	6.00E-01
195	GO:0000375-RNA splicing, via transesterification reactions	28	0.1026431	3.27E-04	1185	153	13528	2.0892088	6.95E-01	6.72E-03	6.00E-01
196	GO:0000377-RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	28	0.1026431	3.27E-04	1185	153	13528	2.0892088	6.95E-01	6.72E-03	6.00E-01
197	GO:0051604-protein maturation	24	0.0879798	3.34E-04	1185	122	13528	2.2457771	7.02E-01	6.82E-03	6.12E-01
198	GO:0043244-regulation of protein complex disassembly	14	0.0513215	3.36E-04	1185	51	13528	3.1338132	7.05E-01	6.84E-03	6.17E-01
199	GO:0009310-amine catabolic process	18	0.0659848	3.40E-04	1185	78	13528	2.6344693	7.09E-01	6.88E-03	6.24E-01
200	GO:0007517-muscle organ development	35	0.1283038	3.58E-04	1185	211	13528	1.8936549	7.27E-01	7.19E-03	6.56E-01
201	GO:0002443-leukocyte mediated immunity	19	0.0696506	3.90E-04	1185	86	13528	2.522147	7.58E-01	7.80E-03	7.15E-01
202	GO:0051605-protein maturation by peptide bond cleavage	19	0.0696506	3.90E-04	1185	86	13528	2.522147	7.58E-01	7.80E-03	7.15E-01
203	GO:0006937-regulation of muscle contraction	17	0.062319	4.00E-04	1185	72	13528	2.6954524	7.66E-01	7.94E-03	7.33E-01
204	GO:0008104-protein localization	107	0.3922431	4.15E-04	1185	882	13528	1.3849383	7.78E-01	8.20E-03	7.60E-01
205	GO:0002253-activation of immune response	20	0.0733165	4.34E-04	1185	94	13528	2.4289434	7.93E-01	8.53E-03	7.95E-01
206	GO:0031032-actomyosin structure organization	10	0.0366582	4.36E-04	1185	28	13528	4.0771549	7.95E-01	8.52E-03	7.99E-01
207	GO:0051241-negative regulation of multicellular organismal process	29	0.1063089	4.48E-04	1185	164	13528	2.0186889	8.03E-01	8.70E-03	8.20E-01
208	GO:0031333-negative regulation of protein complex assembly	11	0.0403241	4.72E-04	1185	34	13528	3.6934227	8.20E-01	9.12E-03	8.64E-01
209	GO:0006998-pentose-phosphate shunt	6	0.0219949	4.75E-04	1185	9	13528	7.6106892	8.22E-01	9.14E-03	8.71E-01
210	GO:0009154-purine ribonucleotide catabolic process	9	0.0329924	4.99E-04	1185	23	13528	4.4671436	8.36E-01	9.53E-03	9.13E-01
211	GO:0007044-cell-substrate junction assembly	9	0.0329924	4.99E-04	1185	23	13528	4.4671436	8.36E-01	9.53E-03	9.13E-01
212	GO:0030199-collagen fibril organization	10	0.0366582	5.84E-04	1185	29	13528	3.9365634	8.80E-01	1.11E-02	1.07E+00
213	GO:0015992-proton transport	15	0.0549874	6.42E-04	1185	61	13528	2.8072214	9.03E-01	1.21E-02	1.17E+00
214	GO:0009063-cellular amino acid catabolic process	16	0.0586532	6.53E-04	1185	68	13528	2.6861256	9.07E-01	1.23E-02	1.19E+00
215	GO:0009719-response to endogenous stimulus	56	0.2052861	6.68E-04	1185	405	13528	1.5785133	9.12E-01	1.25E-02	1.22E+00
216	GO:0051651-maintenance of location in cell	13	0.0476557	6.83E-04	1185	48	13528	3.0918425	9.16E-01	1.27E-02	1.25E+00
217	GO:0009143-nucleoside triphosphate catabolic process	9	0.0329924	6.91E-04	1185	24	13528	4.2810127	9.19E-01	1.28E-02	1.26E+00
218	GO:0010608-posttranscriptional regulation of gene expression	34	0.124638	7.45E-04	1185	211	13528	1.8395505	9.33E-01	1.37E-02	1.36E+00
219	GO:0034637-cellular carboxylate biosynthetic process	16	0.0586532	7.68E-04	1185	69	13528	2.6471962	9.38E-01	1.41E-02	1.40E+00
220	GO:0010927-cellular component assembly involved in morphogenesis	11	0.0403241	7.79E-04	1185	36	13528	3.4883235	9.41E-01	1.42E-02	1.42E+00
221	GO:0050572-iron ion homeostasis	11	0.0403241	7.79E-04	1185	36	13528	3.4883235	9.41E-01	1.42E-02	1.42E+00
222	GO:0045184-establishment of protein localization	94	0.3445874	7.92E-04	1185	769	13528	1.395458	9.44E-01	1.43E-02	1.45E+00
223	GO:0051258-protein polymerization	13	0.0476557	8.33E-04	1185	49	13528	3.0287436	9.52E-01	1.50E-02	1.52E+00
224	GO:0006107-oxaloacetate metabolic process	6	0.0219949	8.82E-04	1185	10	13528	6.8496203	9.59E-01	1.58E-02	1.61E+00
225	GO:0009185-ribonucleoside diphosphate metabolic process	6	0.0219949	8.82E-04	1185	10	13528	6.8496203	9.59E-01	1.58E-02	1.61E+00
226	GO:0030194-positive regulation of blood coagulation	6	0.0219949	8.82E-04	1185	10	13528	6.8496203	9.59E-01	1.58E-02	1.61E+00
227	GO:0006916-anti-apoptosis	33	0.1209722	9.99E-04	1185	206	13528	1.8287821	9.73E-01	1.78E-02	1.82E+00
228	GO:0006879-cellular iron ion homeostasis	8	0.0293266	1.00E-03	1185	31	13528	3.6825915	9.74E-01	1.78E-02	1.83E+00
229	GO:0009065-glutamine family amino acid catabolic process	8	0.0293266	1.00E-03	1185	20	13528	4.5664135	9.80E-01	1.91E-02	1.97E+00
230	GO:0009725-response to hormone stimulus	51	0.186957	1.10E-03	1185	367	13528	1.5864243	9.81E-01	1.93E-02	2.00E+00
231	GO:0042060-wound healing	31	0.1136405	1.18E-03	1185	191	13528	1.8528641	9.86E-01	2.06E-02	2.15E+00
232	GO:0009166-nucleotide catabolic process	13	0.0476557	1.22E-03	1185	51	13528	2.9099694	9.88E-01	2.11E-02	2.22E+00
233	GO:0007266-Rho protein signal transduction	11	0.0403241	1.23E-03	1185	38	13528	3.3046414	9.89E-01	2.13E-02	2.24E+00
234	GO:0007568-aging	21	0.0769823	1.27E-03	1185	110	13528	2.1794246	9.90E-01	2.18E-02	2.31E+00
235	GO:0015031-protein transport	92	0.3372558	1.29E-03	1185	762	13528	1.3783138	9.91E-01	2.21E-02	2.35E+00
236	GO:0002252-immune effector process	24	0.0879798	1.29E-03	1185	134	13528	2.0446628	9.91E-01	2.20E-02	2.35E+00
237	GO:0032101-regulation of response to external stimulus	27	0.0989772	1.35E-03	1185	159	13528	1.9385718	9.93E-01	2.29E-02	

Supplementary Table S2: (continued)

308	GO:0009126-purine nucleoside monophosphate metabolic process	7	0.0256608	5.88E-03	1185	20	13528	3.9956118	1.00E+00	7.77E-02	1.03E+01
309	GO:016071-mRNA metabolic process	48	0.1759595	6.05E-03	1185	370	13528	1.480999	1.00E+00	7.94E-02	1.06E+01
310	GO:055082-cellular chemical homeostasis	49	0.1796254	6.15E-03	1185	380	13528	1.4720675	1.00E+00	8.04E-02	1.07E+01
311	GO:008015-blood circulation	28	0.1026431	6.15E-03	1185	186	13528	1.7185427	1.00E+00	8.02E-02	1.07E+01
312	GO:003013-circulatory system process	28	0.1026431	6.15E-03	1185	186	13528	1.7185427	1.00E+00	8.02E-02	1.07E+01
313	GO:001666-response to hypoxia	22	0.0806481	6.21E-03	1185	134	13528	1.8742742	1.00E+00	8.06E-02	1.08E+01
314	GO:0034728-nucleosome organization	17	0.062319	6.50E-03	1185	93	13528	2.0868019	1.00E+00	8.40E-02	1.13E+01
315	GO:0006953-acute-phase response	10	0.0366582	6.65E-03	1185	40	13528	2.8540084	1.00E+00	8.55E-02	1.15E+01
316	GO:0009067-aspartate family amino acid biosynthetic process	6	0.0219949	7.26E-03	1185	15	13528	4.5664135	1.00E+00	9.26E-02	1.25E+01
317	GO:0051017-actin filament bundle formation	7	0.0256608	7.64E-03	1185	21	13528	3.8053446	1.00E+00	9.69E-02	1.32E+01
318	GO:0034242-negative regulation of protein complex disassembly	10	0.0366582	7.87E-03	1185	41	13528	2.7843985	1.00E+00	9.94E-02	1.35E+01
319	GO:0044057-regulation of system process	41	0.1502988	7.92E-03	1185	309	13528	1.5147488	1.00E+00	9.96E-02	1.36E+01
320	GO:0006103-2-oxoglutarate metabolic process	5	0.0183291	7.97E-03	1185	10	13528	5.7080169	1.00E+00	9.99E-02	1.37E+01
321	GO:0042273-ribosomal large subunit biogenesis	5	0.0183291	7.97E-03	1185	10	13528	5.7080169	1.00E+00	9.99E-02	1.37E+01
322	GO:0033700-phospholipid efflux	5	0.0183291	7.97E-03	1185	10	13528	5.7080169	1.00E+00	9.99E-02	1.37E+01
323	GO:0006417-regulation of translation	22	0.0806481	7.99E-03	1185	137	13528	1.8332317	1.00E+00	9.98E-02	1.37E+01
324	GO:0009408-response to heat	12	0.0439899	8.36E-03	1185	56	13528	2.4462929	1.00E+00	1.04E-01	1.43E+01
325	GO:0016042-lipid catabolic process	26	0.0955114	8.65E-03	1185	173	13528	1.7157045	1.00E+00	1.07E-01	1.48E+01
326	GO:0030837-negative regulation of actin filament polymerization	8	0.0293266	8.89E-03	1185	28	13528	3.2617239	1.00E+00	1.09E-01	1.51E+01
327	GO:0003297-microtubule cytoskeleton organization	23	0.0843139	8.90E-03	1185	147	13528	1.7861822	1.00E+00	1.09E-01	1.53E+01
328	GO:0070525-regulation of microtubule cytoskeleton organization	10	0.0366582	9.26E-03	1185	42	13528	2.7181033	1.00E+00	1.13E-01	1.57E+01
329	GO:0048738-cardiac muscle tissue development	12	0.0439899	9.56E-03	1185	57	13528	2.4033755	1.00E+00	1.16E-01	1.62E+01
330	GO:0006897-endocytosis	31	0.1136405	9.80E-03	1185	220	13528	1.6086229	1.00E+00	1.18E-01	1.66E+01
331	GO:0010324-membrane invagination	31	0.1136405	9.80E-03	1185	220	13528	1.6086229	1.00E+00	1.18E-01	1.66E+01
332	GO:001959-regulation of cytokine-mediated signaling pathway	6	0.0219949	9.81E-03	1185	16	13528	4.2810127	1.00E+00	1.18E-01	1.66E+01
333	GO:0043691-reverse cholesterol transport	6	0.0219949	9.81E-03	1185	16	13528	4.2810127	1.00E+00	1.18E-01	1.66E+01
334	GO:0022604-regulation of cell morphogenesis	21	0.0769823	9.91E-03	1185	131	13528	1.8300512	1.00E+00	1.19E-01	1.67E+01
335	GO:003018-vascular process in circulatory system	12	0.0439899	1.09E-02	1185	58	13528	2.361938	1.00E+00	1.29E-01	1.82E+01
336	GO:0042159-lipoprotein catabolic process	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
337	GO:0046031-ADP metabolic process	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
338	GO:0014866-skeletal myofibril assembly	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
339	GO:0070613-regulation of protein processing	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
340	GO:0010953-regulation of protein maturation by peptide bond cleavage	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
341	GO:0043277-apoptotic cell clearance	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
342	GO:0009068-aspartate family amino acid catabolic process	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
343	GO:0006729-tetrahydrobiopterin biosynthetic process	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
344	GO:0051918-negative regulation of fibrinolysis	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
345	GO:0006085-acetyl-CoA biosynthetic process	4	0.0146633	1.09E-02	1185	6	13528	7.6106892	1.00E+00	1.29E-01	1.83E+01
346	GO:0009062-fatty acid catabolic process	9	0.0329924	1.11E-02	1185	36	13528	2.8540084	1.00E+00	1.31E-01	1.86E+01
347	GO:0019218-regulation of steroid metabolic process	9	0.0329924	1.11E-02	1185	36	13528	2.8540084	1.00E+00	1.31E-01	1.86E+01
348	GO:0032870-cellular response to hormone stimulus	21	0.0769823	1.16E-02	1185	133	13528	1.8025316	1.00E+00	1.36E-01	1.94E+01
349	GO:0043324-negative regulation of neuron apoptosis	11	0.0403241	1.18E-02	1185	51	13528	2.4622818	1.00E+00	1.38E-01	1.96E+01
350	GO:0009112-nucleobase metabolic process	7	0.0256608	1.22E-02	1185	23	13528	3.4744451	1.00E+00	1.42E-01	2.02E+01
351	GO:003015-heart process	7	0.0256608	1.22E-02	1185	23	13528	3.4744451	1.00E+00	1.42E-01	2.02E+01
352	GO:0030048-actin filament-based movement	7	0.0256608	1.22E-02	1185	23	13528	3.4744451	1.00E+00	1.42E-01	2.02E+01
353	GO:0042364-water-soluble vitamin biosynthetic process	7	0.0256608	1.22E-02	1185	23	13528	3.4744451	1.00E+00	1.42E-01	2.02E+01
354	GO:0060047-heart contraction	7	0.0256608	1.22E-02	1185	23	13528	3.4744451	1.00E+00	1.42E-01	2.02E+01
355	GO:0009266-response to temperature stimulus	15	0.0549874	1.25E-02	1185	83	13528	2.0631386	1.00E+00	1.44E-01	2.06E+01
356	GO:0010638-positive regulation of organelle organization	15	0.0549874	1.25E-02	1185	83	13528	2.0631386	1.00E+00	1.44E-01	2.06E+01
357	GO:0006323-DNA packaging	19	0.0696506	1.29E-02	1185	117	13528	1.8538858	1.00E+00	1.48E-01	2.13E+01
358	GO:0030301-cholesterol transport	9	0.0329924	1.31E-02	1185	37	13528	2.7768731	1.00E+00	1.50E-01	2.15E+01
359	GO:0015918-sterol transport	9	0.0329924	1.31E-02	1185	37	13528	2.7768731	1.00E+00	1.50E-01	2.15E+01
360	GO:0042493-response to drug	30	0.1099747	1.34E-02	1185	216	13528	1.5855602	1.00E+00	1.53E-01	2.20E+01
361	GO:0016050-vesicle organization	11	0.0403241	1.35E-02	1185	52	13528	2.4149302	1.00E+00	1.53E-01	2.21E+01
362	GO:0051291-protein heterooligomerization	11	0.0403241	1.35E-02	1185	52	13528	2.4149302	1.00E+00	1.53E-01	2.21E+01
363	GO:0030705-cytoskeleton-dependent intracellular transport	11	0.0403241	1.35E-02	1185	52	13528	2.4149302	1.00E+00	1.53E-01	2.21E+01
364	GO:0050727-regulation of inflammatory response	14	0.0513215	1.40E-02	1185	76	13528	2.1029536	1.00E+00	1.58E-01	2.29E+01
365	GO:0001568-blood vessel development	33	0.1209722	1.43E-02	1185	245	13528	1.5376699	1.00E+00	1.60E-01	2.33E+01
366	GO:0006397-mRNA processing	41	0.1502988	1.45E-02	1185	321	13528	1.4581227	1.00E+00	1.62E-01	2.35E+01
367	GO:0050873-brown fat cell differentiation	7	0.0256608	1.51E-02	1185	24	13528	3.3296765	1.00E+00	1.68E-01	2.44E+01
368	GO:0001906-cell killing	7	0.0256608	1.51E-02	1185	24	13528	3.3296765	1.00E+00	1.68E-01	2.44E+01
369	GO:0014706-striated muscle tissue development	19	0.0696506	1.52E-02	1185	119	13528	1.8227281	1.00E+00	1.69E-01	2.46E+01
370	GO:0002460-adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	14	0.0513215	1.56E-02	1185	77	13528	2.0756425	1.00E+00	1.71E-01	2.51E+01
371	GO:0002350-adaptive immune response	14	0.0513215	1.56E-02	1185	77	13528	2.0756425	1.00E+00	1.71E-01	2.51E+01
372	GO:0019139-hexose biosynthetic process	8	0.0293266	1.57E-02	1185	31	13528	2.9460732	1.00E+00	1.72E-01	2.52E+01
373	GO:0014823-response to activin	5	0.0183291	1.63E-02	1185	12	13528	4.7566807	1.00E+00	1.78E-01	2.61E+01
374	GO:0019216-regulation of lipid metabolic process	18	0.0659848	1.75E-02	1185	112	13528	1.8347197	1.00E+00	1.89E-01	2.77E+01
375	GO:0014070-response to organic cyclic substance	19	0.0696506	1.79E-02	1185	121	13528	1.7926003	1.00E+00	1.92E-01	2.82E+01
376	GO:0046148-pigment biosynthetic process	9	0.0329924	1.79E-02	1185	39	13528	2.6344693	1.00E+00	1.92E-01	2.82E+01
377	GO:0034440-lipid oxidation	9	0.0329924	1.79E-02	1185	39	13528	2.6344693	1.00E+00	1.92E-01	2.82E+01
378	GO:0019395-fatty acid oxidation	9	0.0329924	1.79E-02	1185	39	13528	2.6344693	1.00E+00	1.92E-01	2.82E+01
379	GO:0033627-cell adhesion mediated by integrin	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
380	GO:0045599-negative regulation of fat cell differentiation	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
381	GO:0051131-chaperone-mediated protein complex assembly	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
382	GO:0043206-fibril organization	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
383	GO:0046033-AMP metabolic process	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
384	GO:0019430-removal of superoxide radicals	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
385	GO:0051238-sequestering of metal ion	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
386	GO:0046146-tetrahydrobiopterin metabolic process	4	0.0146633	1.79E-02	1185	7	13528	6.5234479	1.00E+00	1.91E-01	2.82E+01
387	GO:0009161-ribonucleoside monophosphate metabolic process	7	0.0256608	1.85E-02	1185	25	13528	3.1964895	1.00E+00	1.96E-01	2.90E+01
388	GO:0001936-regulation of endothelial cell proliferation	8	0.0293266	1.86E-02	1185	32	13528	2.8540084	1.00E+00	1.97E-01	2.92E+01
389	GO:0022402-cell cycle process	65	0.2382785	1.92E-02	1185	565	13528	1.313349	1.00E+00	2.02E-01	3.00E+01
390	GO:0051494-negative regulation of cytoskeleton organization	11	0.0403241	1.97E-02	1185	55	13528	2.2832068	1.00E+00	2.06E-01	3.06E+01
391	GO:0001944-vasculature development	33	0.1209722	1.97E-02	1185	251	13528	1.5009128	1.00E+00	2.06E-01	3.07E+01
392	GO:0051146-striated muscle cell differentiation	15	0.0549874	2.02E-02	1185	88	13528</				

Supplementary Table S2: (continued)

462	GO:0009743-response to carbohydrate stimulus	11	0.0403241	3.42E-02	1185	60	13528	2.0929395	1.00E+00	3.04E-01	4.73E-01
463	GO:0010769-regulation of cell morphogenesis involved in differentiation	13	0.0476557	3.47E-02	1185	77	13528	1.9273823	1.00E+00	3.07E-01	4.78E-01
464	GO:0009057-macromolecule catabolic process	84	0.3079292	3.47E-02	1185	781	13528	1.2278449	1.00E+00	3.06E-01	4.78E-01
465	GO:0048878-chemical homeostasis	58	0.2126178	3.48E-02	1185	512	13528	1.2932226	1.00E+00	3.06E-01	4.79E-01
466	GO:0055002-striated muscle cell development	10	0.0366582	3.50E-02	1185	52	13528	2.1953911	1.00E+00	3.07E-01	4.80E-01
467	GO:0009064-glutamine family amino acid metabolic process	10	0.0366582	3.50E-02	1185	52	13528	2.1953911	1.00E+00	3.07E-01	4.80E-01
468	GO:0034613-cellular protein localization	48	0.1759595	3.51E-02	1185	411	13528	1.3332594	1.00E+00	3.06E-01	4.81E-01
469	GO:0052547-regulation of peptidase activity	14	0.0513215	3.58E-02	1185	86	13528	1.8584241	1.00E+00	3.11E-01	4.88E-01
470	GO:0007584-response to nutrient	20	0.0733165	3.62E-02	1185	140	13528	1.630862	1.00E+00	3.13E-01	4.92E-01
471	GO:0006901-vesicle coating	5	0.0183291	3.64E-02	1185	15	13528	3.8053446	1.00E+00	3.14E-01	4.95E-01
472	GO:0043489-RNA stabilization	5	0.0183291	3.64E-02	1185	15	13528	3.8053446	1.00E+00	3.14E-01	4.95E-01
473	GO:0045806-negative regulation of endocytosis	5	0.0183291	3.64E-02	1185	15	13528	3.8053446	1.00E+00	3.14E-01	4.95E-01
474	GO:0048255-mRNA stabilization	5	0.0183291	3.64E-02	1185	15	13528	3.8053446	1.00E+00	3.14E-01	4.95E-01
475	GO:0032369-negative regulation of lipid transport	5	0.0183291	3.64E-02	1185	15	13528	3.8053446	1.00E+00	3.14E-01	4.95E-01
476	GO:0030003-cellular cation homeostasis	32	0.1173064	3.65E-02	1185	254	13528	1.4382405	1.00E+00	3.14E-01	4.95E-01
477	GO:0042278-purine nucleoside metabolic process	7	0.0256608	3.67E-02	1185	29	13528	2.7555944	1.00E+00	3.15E-01	4.98E-01
478	GO:0046128-purine ribonucleoside metabolic process	7	0.0256608	3.67E-02	1185	29	13528	2.7555944	1.00E+00	3.15E-01	4.98E-01
479	GO:0045807-positive regulation of endocytosis	7	0.0256608	3.67E-02	1185	29	13528	2.7555944	1.00E+00	3.15E-01	4.98E-01
480	GO:0042254-ribosome biogenesis	18	0.0659848	3.68E-02	1185	122	13528	1.6843328	1.00E+00	3.15E-01	4.99E-01
481	GO:0006599-phosphagen metabolic process	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
482	GO:0006600-creatine metabolic process	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
483	GO:0033275-actin-myosin filament sliding	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
484	GO:0030049-muscle filament sliding	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
485	GO:0070252-actin-mediated cell contraction	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
486	GO:0030212-hyaluronan metabolic process	4	0.0146633	3.76E-02	1185	9	13528	5.0737928	1.00E+00	3.20E-01	5.06E-01
487	GO:0040013-negative regulation of locomotion	11	0.0403241	3.79E-02	1185	61	13528	2.058629	1.00E+00	3.21E-01	5.08E-01
488	GO:0006942-regulation of striated muscle contraction	6	0.0219949	3.82E-02	1185	22	13528	3.1134638	1.00E+00	3.22E-01	5.11E-01
489	GO:0006282-regulation of DNA repair	6	0.0219949	3.82E-02	1185	22	13528	3.1134638	1.00E+00	3.22E-01	5.11E-01
490	GO:0045103-intermediate filament-based process	6	0.0219949	3.82E-02	1185	22	13528	3.1134638	1.00E+00	3.22E-01	5.11E-01
491	GO:0043488-regulation of mRNA stability	6	0.0219949	3.82E-02	1185	22	13528	3.1134638	1.00E+00	3.22E-01	5.11E-01
492	GO:0048584-positive regulation of response to stimulus	30	0.1099747	3.89E-02	1185	236	13528	1.4511907	1.00E+00	3.27E-01	5.18E-01
493	GO:0070727-cellular macromolecule localization	48	0.1759595	3.90E-02	1185	414	13528	1.3235981	1.00E+00	3.27E-01	5.19E-01
494	GO:0006631-fatty acid metabolic process	26	0.0953114	3.98E-02	1185	198	13528	1.4990751	1.00E+00	3.32E-01	5.26E-01
495	GO:0010975-regulation of neuron projection development	12	0.0439899	3.99E-02	1185	70	13528	1.9570344	1.00E+00	3.31E-01	5.27E-01
496	GO:0007229-integrin-mediated signaling pathway	12	0.0439899	3.99E-02	1185	70	13528	1.9570344	1.00E+00	3.31E-01	5.27E-01
497	GO:0006533-aspartate catabolic process	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
498	GO:0033631-cell-cell adhesion mediated by integrin	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
499	GO:0060334-regulation of interferon-gamma-mediated signaling pathway	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
500	GO:0032488-Cdc42 protein signal transduction	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
501	GO:0006531-aspartate metabolic process	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
502	GO:0006152-purine nucleoside catabolic process	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
503	GO:0006104-succinyl-CoA metabolic process	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
504	GO:0006007-pinoxylation	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
505	GO:0010955-negative regulation of protein maturation by peptide bond cleavage	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
506	GO:0046130-purine ribonucleoside catabolic process	3	0.0109975	4.07E-02	1185	4	13528	8.5620253	1.00E+00	3.37E-01	5.35E-01
507	GO:0022613-ribonucleoprotein complex biogenesis	24	0.0879798	4.21E-02	1185	180	13528	1.5221378	1.00E+00	3.45E-01	5.46E-01
508	GO:0045834-positive regulation of lipid metabolic process	9	0.0329924	4.43E-02	1185	46	13528	2.2335718	1.00E+00	3.59E-01	5.65E-01
509	GO:0009119-ribonucleoside metabolic process	9	0.0329924	4.43E-02	1185	46	13528	2.2335718	1.00E+00	3.59E-01	5.65E-01
510	GO:0006458-de novo protein folding	5	0.0183291	4.53E-02	1185	16	13528	3.5675105	1.00E+00	3.65E-01	5.74E-01
511	GO:0050764-regulation of phagocytosis	5	0.0183291	4.53E-02	1185	16	13528	3.5675105	1.00E+00	3.65E-01	5.74E-01
512	GO:0030032-lamellipodium assembly	5	0.0183291	4.53E-02	1185	16	13528	3.5675105	1.00E+00	3.65E-01	5.74E-01
513	GO:0006900-membrane budding	5	0.0183291	4.53E-02	1185	16	13528	3.5675105	1.00E+00	3.65E-01	5.74E-01
514	GO:0048545-response to steroid hormone stimulus	25	0.0916456	4.78E-02	1185	192	13528	1.4864627	1.00E+00	3.80E-01	5.94E-01
515	GO:0009309-amine biosynthetic process	13	0.0476557	4.86E-02	1185	81	13528	1.8322029	1.00E+00	3.84E-01	6.00E-01
516	GO:0031346-positive regulation of cell projection organization	9	0.0329924	4.94E-02	1185	47	13528	2.186049	1.00E+00	3.89E-01	6.06E-01
517	GO:0003033-response to superoxide	4	0.0146633	5.03E-02	1185	10	13528	4.5664135	1.00E+00	3.93E-01	6.13E-01
518	GO:0018279-protein amino acid N-linked glycosylation via asparagine	4	0.0146633	5.03E-02	1185	10	13528	4.5664135	1.00E+00	3.93E-01	6.13E-01
519	GO:0001909-leukocyte mediated cytotoxicity	4	0.0146633	5.03E-02	1185	10	13528	4.5664135	1.00E+00	3.93E-01	6.13E-01
520	GO:0018196-peptidyl-asparagine modification	4	0.0146633	5.03E-02	1185	10	13528	4.5664135	1.00E+00	3.93E-01	6.13E-01
521	GO:0048585-negative regulation of response to stimulus	15	0.0549874	5.28E-02	1185	100	13528	1.7124051	1.00E+00	4.08E-01	6.31E-01
522	GO:0055001-muscle cell development	10	0.0366582	5.28E-02	1185	56	13528	2.0385775	1.00E+00	4.07E-01	6.32E-01
523	GO:0043487-regulation of RNA stability	6	0.0219949	5.33E-02	1185	24	13528	2.8540084	1.00E+00	4.09E-01	6.35E-01
524	GO:0006596-RNA processing	60	0.2199494	5.42E-02	1185	547	13528	1.2522158	1.00E+00	4.14E-01	6.41E-01
525	GO:0051004-regulation of lipoprotein lipase activity	5	0.0183291	5.53E-02	1185	17	13528	3.357657	1.00E+00	4.19E-01	6.49E-01
526	GO:0042310-vasoconstriction	5	0.0183291	5.53E-02	1185	17	13528	3.357657	1.00E+00	4.19E-01	6.49E-01
527	GO:0034199-activation of protein kinase A activity	5	0.0183291	5.53E-02	1185	17	13528	3.357657	1.00E+00	4.19E-01	6.49E-01
528	GO:0044265-cellular macromolecule catabolic process	77	0.2822684	5.53E-02	1185	725	13528	1.2124615	1.00E+00	4.19E-01	6.49E-01
529	GO:001933-negative regulation of protein amino acid phosphorylation	7	0.0256608	5.62E-02	1185	32	13528	2.4972574	1.00E+00	4.23E-01	6.55E-01
530	GO:0030168-platelet activation	7	0.0256608	5.62E-02	1185	32	13528	2.4972574	1.00E+00	4.23E-01	6.55E-01
531	GO:0010876-lipid localization	21	0.0769823	5.66E-02	1185	157	13528	1.5269854	1.00E+00	4.24E-01	6.57E-01
532	GO:0030031-cell projection assembly	13	0.0476557	5.68E-02	1185	83	13528	1.7880535	1.00E+00	4.25E-01	6.59E-01
533	GO:0030163-protein catabolic process	67	0.2456102	5.77E-02	1185	622	13528	1.2297014	1.00E+00	4.29E-01	6.65E-01
534	GO:0050770-regulation of axonogenesis	10	0.0366582	5.81E-02	1185	57	13528	2.0028129	1.00E+00	4.30E-01	6.67E-01
535	GO:0005976-polysaccharide metabolic process	16	0.0586532	5.97E-02	1185	111	13528	1.6455544	1.00E+00	4.39E-01	6.78E-01
536	GO:0006766-vitamin metabolic process	12	0.0439899	6.10E-02	1185	75	13528	1.8265654	1.00E+00	4.45E-01	6.85E-01
537	GO:0031667-response to nutrient levels	25	0.0916456	6.10E-02	1185	197	13528	1.4487352	1.00E+00	4.44E-01	6.85E-01
538	GO:0010743-regulation of foam cell differentiation	6	0.0219949	6.21E-02	1185	25	13528	2.7398481	1.00E+00	4.49E-01	6.92E-01
539											

Supplementary Table S3:

Relationship types between proteins identified in the significant (p<0.05) vasoactive pathways in the porcine sPCA_IPA analysis

From Molecule(s)	Relationship Type	To Molecule(s)	Catalyst(s)
4.1R	protein-protein interactions	FODRIN	
4.1R	protein-protein interactions	ZO2	
AFADIN	protein-protein interactions	F-ACTIN	
AFADIN	protein-protein interactions	JAM	
AFADIN	protein-protein interactions	NECTIN	
AKT	causation	Cell proliferation	
CASK	protein-protein interactions	JAM	
CDC42	protein-protein interactions	PAR6	
CDK4-ZONAB	causation	G1/S phase transition	
CDK4-ZONAB	membership	CDK4	
CDK4-ZONAB	membership	ZONAB	
CEBP	protein-protein interactions	AP-1	
CEBP-AP-1	causation	Epithelial celldifferentiation	
CEBP-AP-1	causation	Epithelial cellproliferation	
CEBP-AP-1	membership	AP-1	
CEBP-AP-1	membership	CEBP	
CGN	inhibition	GEFH1	
CGN	protein-protein interactions	F-ACTIN	
CGN	protein-protein interactions	GEFH1	
CGN	protein-protein interactions	JAM	
CGN	protein-protein interactions	MYOSIN	
CGN	protein-protein interactions	ZO1	
CGN	protein-protein interactions	ZO2	
CGN	protein-protein interactions	ZO3	
CLDN	protein-protein interactions	CLDN	
CRB3	protein-protein interactions	PALS1	
CRB3	protein-protein interactions	PAR6	
CRB3	protein-protein interactions	PATJ	
CSTF-CPSF-SYMPK	causation	mRNApolyadenylation	
CSTF-CPSF-SYMPK	membership	CPSF	
CSTF-CPSF-SYMPK	membership	CSTF	
CSTF-CPSF-SYMPK	membership	SYMPK	
CTNNB1	protein-protein interactions	MAGI-2	
CTNNB1	reaction	MAGI-2	VCL
F-ACTIN	causation	Actinnucleation	
GEFH1	activation	RHOA	
JAM	protein-protein interactions	JAM	
JAM	protein-protein interactions	ZO1	
MAGI-1	protein-protein interactions	JAM	
MAGI-2	activation	PTEN	
MAGI-2	protein-protein interactions	PTEN	
MLCK	causation	Tight junctionpermeability	
MUPP1	protein-protein interactions	CLDN	
NECTIN	protein-protein interactions	AFADIN	
NECTIN	protein-protein interactions	CLDN	
NECTIN	protein-protein interactions	OCLN	
NF-κB	expression	MLCK	
OCLN	protein-protein interactions	CGN	
OCLN	protein-protein interactions	F-ACTIN	
OCLN	protein-protein interactions	OCLN	
OCLN	protein-protein interactions	ZO1	
OCLN	protein-protein interactions	ZO2	

Supplementary Table S3: (continued)

OCLN	protein-protein interactions	ZO3	
PAR3	protein-protein interactions	JAM	
PAR3	protein-protein interactions	PAR6	
PAR3	protein-protein interactions	TIAM1	
PAR6	activation	SMURF1	
PAR6	protein-protein interactions	PALS1	
PAR6	protein-protein interactions	SMURF1	
PAR6	protein-protein interactions	aPKC	
PAR6	protein-protein interactions	mLGL	
PATJ	protein-protein interactions	PALS1	
PATJ	protein-protein interactions	ZO3	
PKA	activation	VASP	
PKA	phosphorylation	VASP	
PP2A	inhibition	aPKC	
PTEN	inhibition	AKT	
RAB13	inhibition	PKA	
RAB13	protein-protein interactions	PKA	
RHOA	causation	Actinorganization	
RHOA	causation	Epithelial to mesenchymal transition(EMT)	
SMURF1	inhibition	RHOA	
SNARE	causation	Vesicletrafficking	
STX4	causation	Vesicletransport	
STX4	protein-protein interactions	SNARE	
STX4	protein-protein interactions	mLGL	
SYMPK	activation	HSF1	
SYMPK	protein-protein interactions	CPSF	
SYMPK	protein-protein interactions	CSTF	
SYMPK	protein-protein interactions	HSF1	
TGF-β	activation	TGFBR	
TGF-β	protein-protein interactions	TGFBR	
TGFBR	phosphorylation	PAR6	
TIAM1	activation	RAC1	
TIAM1	protein-protein interactions	PAR3	
TNF-α	activation	TNFR	
TNF-α	protein-protein interactions	TNFR	
VAP33	protein-protein interactions	OCLN	
VASP	protein-protein interactions	F-ACTIN	
VCL	protein-protein interactions	CTNNA1	
ZO1	protein-protein interactions	CASK	
ZO1	protein-protein interactions	CGN	
ZO1	protein-protein interactions	CLDN	
ZO1	protein-protein interactions	CTNNA1	
ZO1	protein-protein interactions	F-ACTIN	
ZO1	protein-protein interactions	FODRIN	
ZO1	protein-protein interactions	RAB13	
ZO1	protein-protein interactions	ZO2	
ZO1	protein-protein interactions	ZO3	
ZO1	protein-protein interactions	ZONAB	
ZO2	inhibition	CEBP-AP-1	
ZO2	protein-protein interactions	4.1R	
ZO2	protein-protein interactions	CLDN	
ZO2	protein-protein interactions	F-ACTIN	
ZO2	protein-protein interactions	SAFB	
ZO3	protein-protein interactions	CLDN	
ZO3	protein-protein interactions	F-ACTIN	
ZONAB	protein-protein interactions	CDK4	
ZONAB	reaction	ZONAB	ZO1
ZONAB	translocation	ZONAB	
aPKC	inhibition	MARK2	
aPKC	inhibition	mLGL	
aPKC	phosphorylation	MARK2	
aPKC	phosphorylation	mLGL	
aPKC	protein-protein interactions	PAR3	
aPKC	protein-protein interactions	PAR6	

Supplementary Table S4:
PANTHER analysis of Parkinson's and Huntington' disease pathways

Parkinson disease	
Gene Name	Protein names
HSPA1B	Heat shock 70 kDa protein 1B
HSPA1L	Heat shock 70 kDa protein 1-like
HSPA2	Heat shock-related 70 kDa protein 2
HSPA5	78 kDa glucose-regulated protein
HSPA6	Heat shock 70 kDa protein 6
HSPA8	Heat shock cognate 71 kDa protein
HSPA9	Stress-70 protein, mitochondrial
MAPK1	Mitogen-activated protein kinase 1
MAPK3	Mitogen-activated protein kinase 3
NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial
PSMA1	Proteasome subunit alpha type-1
PSMA2	Proteasome subunit alpha type-2
PSMA3	Proteasome subunit alpha type-3
PSMA4	Proteasome subunit alpha type-4
PSMA5	Proteasome subunit alpha type-5
PSMA6	Proteasome subunit alpha type-6
PSMA7	Proteasome subunit alpha type-7
PSMB1	Proteasome subunit beta type-1
PSMB10	Proteasome subunit beta type-10
PSMB3	Proteasome subunit beta type-3
PSMB4	Proteasome subunit beta type-4
SEPT2	Septin-2
SFN	14-3-3 protein sigma
SNCB	Beta-synuclein
SNCG	Gamma-synuclein
UBE2L3	Ubiquitin-conjugating enzyme E2 L3
YWHAB	14-3-3 protein beta/alpha
YWHAE	14-3-3 protein epsilon
YWHAG	14-3-3 protein gamma
YWHAH	14-3-3 protein eta
YWHAQ	14-3-3 protein theta
YWHAZ	14-3-3 protein zeta/delta

Huntington disease	
Gene Name	Protein names
ACTR1A	Alpha-centractin
ACTR1B	Beta-centractin
ACTR2	Actin-related protein 2
ACTR3	Actin-related protein 3
AKT2	RAC-beta serine/threonine-protein kinase
ARF1	ADP-ribosylation factor 1
ARF4	ADP-ribosylation factor 4
ARL8B	ADP-ribosylation factor-like protein 8B
ARPC1A	Actin-related protein 2/3 complex subunit 1A
ARPC1B	Actin-related protein 2/3 complex subunit 1B
ARPC5	Actin-related protein 2/3 complex subunit 5
ARPC5L	Actin-related protein 2/3 complex subunit 5-like protein
CAPN1	Calpain-1 catalytic subunit
CAPN2	Calpain-2 catalytic subunit
CAPNS1	Calpain small subunit 1
CDC42	Cell division control protein 42 homolog
CLTA	Clathrin light chain A
CLTB	Clathrin light chain B
CRYZ	Quinone oxidoreductase
CYC1	Cytochrome c1, heme protein, mitochondrial
CYFIP1	Cytoplasmic FMR1-interacting protein 1
DNAH12	Dynein heavy chain 12, axonemal
DYNC1H1	Cytoplasmic dynein 1 heavy chain 1
NCOR1	Nuclear receptor corepressor 1
PACSIN1	Protein kinase C and casein kinase substrate in neurons protein 1
PACSIN2	Protein kinase C and casein kinase substrate in neurons protein 2
RAB11B	Ras-related protein Rab-11
RAC1	Ras-related C3 botulinum toxin substrate 1
RHOG	Rho-related GTP-binding protein RhoG
TRIM23	E3 ubiquitin-protein ligase TRIM23
TUBB	Tubulin beta chain
TUBB2A	Tubulin beta-2A chain
TUBB2C	Tubulin beta-4B chain
TUBB3	Tubulin beta-3 chain
VAT1	Synaptic vesicle membrane protein VAT-1 homolog
VAT1L	Synaptic vesicle membrane protein VAT-1 homolog-like