Table S5: List of all identified and quantified proteins in both replicates of the quantitative proteome comparision of skin lysates wt and *Ctsb*$^{-/-}$.

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Cathepsin B;	P10605	-6,64*	-6,64*	-6,64*	0.00	0.00	36.84
Betaine--homocysteine S-methyltransferase 1;	O35490	-6.64	-2.94	-4.79	2.62	11.68	30.45
Fructose-bisphosphate aldolase B;	Q91Y97	-4.64	-3.47	-4.06	0.83	3.69	39.65
Glycine N-methyltransferase;	Q9QXF8	-4.64	2.04	-1.30	4.72	21.09	24.84
Fatty acid-binding protein, liver;	P12710	-3.84	-2.12	-2.98	1.21	5.42	24.67
Fatty acid-binding protein, heart;	P11404	-1.56	-1.47	-1.52	0.06	0.26	8.56
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	-1.40	-1.40	-1.40	0.00	0.00	7.79
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	-1.29	-0.17	-0.73	0.79	3.53	13.09
N-acetylmuramoyl-L-alanine amidase;	Q8VCS0	-1.25	-0.20	-0.73	0.74	3.32	3.99
Uncharacterized protein;	D3YYM6	-1.25	3.14	0.94	3.11	13.87	20.53
Serpin H1;	P19324	-1.18	-0.62	-0.90	0.40	1.78	6.92
60S ribosomal protein L12;	P35979	-1.18	-0.34	-0.76	0.60	2.66	3.79
Mitochondrial carrier homolog 2;	Q791V5	-1.18	-2.12	-1.65	0.66	2.95	6.86
Carboxypeptidase B2;	Q9JHH6	-1.15	-0.40	-0.77	0.53	2.39	11.19
60S acidic ribosomal protein P2;	P99027	-1.12	0.26	-0.43	0.98	4.37	9.33
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	-1.06	-1.22	-1.14	0.11	0.50	9.44
Uncharacterized protein;	E9Q6D8	-1.06	-0.40	-0.73	0.47	2.09	5.32
Angiotensin-converting enzyme;	P09470	-1.06	-0.89	-0.97	0.12	0.54	7.64
Collagen alpha-1(I) chain;	P11087	-1.06	-1.89	-1.47	0.59	2.62	7.62
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	-1.03	-0.69	-0.86	0.24	1.07	8.24
Ig mu chain C region secreted form;	P01872	-1.03	-0.40	-0.71	0.45	2.00	8.99
Oxidation resistance protein 1;	Q4KMM3	-1.03	-0.86	-0.95	0.12	0.53	7.66
A-kinase anchor protein 12;	Q9WTQ5	-1.03	-1.25	-1.14	0.16	0.70	5.08
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	-0.97	-2.00	-1.49	0.73	3.25	13.33
Major urinary protein 2;	P11589	-0.47	-0.89	-0.68	0.29	1.31	4.68
Myosin-binding protein H;	P70402	-0.94	-3.32	-2.13	1.68	7.51	16.45
Cysteine-rich with EGF-like domain protein 2;	Q9CYA0	-0.94	-0.27	-0.61	0.48	2.13	4.61
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	-0.94	0.96	0.01	1.34	5.99	5.36
Complement component C9;	P06683	-0.92	-0.04	-0.48	0.62	2.75	5.44
Myosin-binding protein C, fast-type;	Q5XKE0	-0.92	-1.18	-1.05	0.19	0.85	8.45
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	-0.92	-1.25	-1.08	0.24	1.06	5.18
Carbonyl reductase [NADPH] 2;	P08074	-0.92	-0.58	-0.75	0.24	1.07	5.23
Dipeptidase 1;	P31428	-0.89	0.38	-0.26	0.90	4.00	6.84
Leukemia inhibitory factor receptor;	P42703	-0.86	-0.03	-0.45	0.59	2.63	5.29
Protein canopy homolog 2;	Q9QXT0	-0.86	0.08	-0.39	0.67	2.99	7.07

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Complement component 6	D3YXF5	-0.86	-1.47	-1.17	0.43	1.93	5.77
COP9 signalosome complex subunit 1;	Q99LD4	-0.86	0.10	-0.38	0.68	3.03	5.69
Equilibrative nucleoside transporter 1;	Q9JIM1	-0.86	0.53	-0.17	0.98	4.38	8.19
Macrophage colony-stimulating factor 1 receptor;	P09581	-0.86	-1.12	-0.99	0.18	0.81	9.73
Niemann-Pick C1 protein;	O35604	-0.81	-0.06	-0.44	0.53	2.37	6.19
SPARC;	P07214	-0.81	-1.79	-1.30	0.69	3.08	10.37
Murinoglobulin-1;	P28665	-0.81	-0.29	-0.55	0.37	1.66	3.58
Complement component C8 alpha chain;	Q8K182	-0.81	0.07	-0.37	0.62	2.78	3.71
Hypoxia up-regulated protein 1;	Q9JKR6	-0.81	0.04	-0.38	0.60	2.70	2.04
Complement component 6	Q9CQF9	-0.81	-0.64	-0.73	0.12	0.53	6.97
Complement component C8 beta chain;	Q8BH35	-0.79	-0.18	-0.49	0.43	1.90	5.37
Protein phosphatase 1F;	Q8CGA0	-0.79	-0.32	-0.55	0.33	1.46	2.40
Aminopeptidase B;	Q8VCT3	-0.79	0.36	-0.22	0.81	3.61	2.97
Mitochondrial-processing peptidase subunit alpha;	Q9DC61	-0.79	-0.18	-0.49	0.43	1.90	2.95
S-formylglutathione hydrolase;	Q9R0P3	-0.79	-1.64	-1.22	0.61	2.71	10.44
UDP-glucose 6-dehydrogenase;	O70475	-0.79	-0.74	-0.76	0.03	0.15	5.98
Adenylosuccinate lyase;	P54822	-0.79	-0.45	-0.62	0.23	1.05	2.46
Afamin;	O89020	-0.76	-0.42	-0.59	0.24	1.09	3.06
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	-0.76	-0.18	-0.47	0.41	1.82	1.91
Thioredoxin domain-containing protein 5;	Q91W90	-0.76	-0.11	-0.43	0.46	2.07	5.21
Collagen triple helix repeat-containing protein 1;	Q9D1D6	-0.76	-2.32	-1.54	1.10	4.93	13.30
Histidine-rich glycoprotein;	Q9ESB3	-0.76	-1.09	-0.93	0.23	1.04	4.80
Nucleobindin-1;	Q02819	-0.76	-1.84	-1.30	0.76	3.40	7.20
Clathrin light polypeptide (Lca); Uncharacterized protein;	B1AWE0	-0.76	0.12	-0.32	0.63	2.79	5.68
Uncharacterized protein;	E9PV38	-0.76	-0.23	-0.50	0.37	1.66	2.73
Uncharacterized protein;	Q9DBD0	-0.76	-0.14	-0.45	0.44	1.97	2.48
Collagen alpha-1(III) chain;	P08121	-0.74	-1.03	-0.88	0.21	0.92	7.47
Glutathione peroxidase 7;	Q99LJ6	-0.74	-0.17	-0.45	0.40	1.80	5.67
Prolyl 4-hydroxylase subunit alpha-1;	Q60715	-0.74	0.39	-0.17	0.80	3.56	5.38
Myeloid-associated differentiation marker;	O35682	-0.71	0.45	-0.13	0.83	3.68	5.68
Collagen alpha-2(I) chain;	Q01149	-0.71	-2.12	-1.42	0.99	4.44	9.38
Sulfated glycoprotein 1;	Q61207	-0.71	-1.00	-0.86	0.20	0.91	6.14
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	-0.71	0.72	0.00	1.01	4.53	4.25
Epidermal growth factor receptor;	Q01279	-0.71	-0.30	-0.51	0.29	1.29	3.66
4F2 cell-surface antigen heavy chain;	P10852	-0.69	2.22	0.77	2.06	9.20	9.79
Hemopexin;	Q91X72	-0.69	-0.81	-0.75	0.09	0.38	6.64
Vacuolar protein sorting-associated protein 29;	Q9QZ88	-0.69	-1.09	-0.89	0.28	1.26	7.44
Cytosolic non-specific dipeptidase;	Q9D1A2	-0.69	-0.52	-0.60	0.12	0.55	5.61

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	-0.69	-0.52	-0.60	0.12	0.55	5.53
Uncharacterized protein;	F8VPN4	-0.69	-0.42	-0.55	0.19	0.87	3.44
SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	-0.69	1.08	0.19	1.25	5.58	6.01
Secretory carrier-associated membrane protein 4;	Q9JKV5	-0.69	-3.84	-2.26	2.23	9.93	24.62
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	-0.69	0.19	-0.25	0.62	2.77	1.95
Beta-glucuronidase;	P12265	-0.67	-0.42	-0.54	0.18	0.80	2.75
Splicing factor U2AF 65 kDa subunit;	P26369	-0.64	-1.89	-1.27	0.88	3.93	10.12
Biglycan;	P28653	-0.64	-3.32	-1.98	1.89	8.45	17.87
Coatomer subunit delta;	Q5XJY5	-0.64	-1.00	-0.82	0.25	1.12	4.07
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	-0.64	-1.74	-1.19	0.77	3.45	7.50
Carboxypeptidase N subunit 2;	Q9DBB9	-0.64	0.03	-0.31	0.48	2.12	1.63
Sorting nexin-1;	Q9WV80	-0.64	0.49	-0.08	0.80	3.56	3.66
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	-0.64	0.80	0.08	1.02	4.56	3.01
40S ribosomal protein SA;	P14206	-0.62	-0.81	-0.72	0.13	0.60	4.81
Macrophage mannose receptor 1;	Q61830	-0.62	-0.76	-0.69	0.10	0.44	4.52
SEC23-interacting protein;	Q6NZC7	-0.62	1.09	0.24	1.21	5.40	7.19
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	-0.62	-1.09	-0.86	0.33	1.48	6.55
Cell cycle control protein 50A;	Q8VEK0	-0.62	-1.36	-0.99	0.52	2.33	3.57
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	-0.62	0.76	0.07	0.97	4.35	6.10
Protein disulfide-isomerase A3;	P27773	-0.62	-0.18	-0.40	0.31	1.38	2.37
N-acylglucosamine 2-epimerase;	P82343	-0.62	0.24	-0.19	0.61	2.71	2.23
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	-0.62	-0.20	-0.41	0.30	1.33	2.07
UPF0587 protein C1orf123 homolog;	Q8BHG2	-0.62	-0.20	-0.41	0.30	1.33	1.43
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	-0.62	-0.17	-0.39	0.32	1.43	4.01
Paralemmin-1;	Q9Z0P4	-0.62	-0.47	-0.55	0.10	0.46	4.56
Histone deacetylase 2;	P70288	-0.62	0.24	-0.19	0.61	2.71	3.73
Plasma kallikrein;	P26262	-0.60	-0.12	-0.36	0.34	1.51	2.80
Ceruloplasmin;	Q61147	-0.60	-0.60	-0.60	0.00	0.00	4.84
Lon protease homolog, mitochondrial;	Q8CGK3	-0.60	1.10	0.25	1.20	5.38	4.57
Complement component C8 gamma chain;	Q8VCG4	-0.60	0.12	-0.24	0.51	2.28	4.02
Disabled homolog 2;	P98078	-0.60	-0.45	-0.53	0.10	0.46	4.68
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	-0.60	0.35	-0.13	0.67	2.98	2.48
Frizzled-7;	Q61090	-0.60	1.11	0.26	1.21	5.40	6.91
Coagulation factor XII;	Q80YC5	-0.60	-1.40	-1.00	0.56	2.52	7.64
Uncharacterized protein;	F7DBB3	-0.60	-0.76	-0.68	0.11	0.51	2.44
Phosphoenolpyruvate carboxykinase, cytosolic [GTP];	Q9Z2V4	-0.60	-0.34	-0.47	0.18	0.82	1.78

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Receptor-type tyrosine-protein phosphatase C;	P06800	-0.58	-0.23	-0.41	0.24	1.09	1.97
Peptidyl-prolyl cis-trans isomerase C;	P30412	-0.58	-0.58	-0.58	0.00	0.00	4.85
Peroxiredoxin-4;	O08807	-0.58	-0.43	-0.51	0.10	0.45	4.38
Adseverin;	Q60604	-0.58	-0.86	-0.72	0.20	0.90	3.36
Ubiquitin-associated protein 2-like;	Q80X50	-0.58	0.31	-0.13	0.63	2.80	1.88
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	-0.58	-1.03	-0.80	0.32	1.42	5.51
STE20-like serine/threonine-protein kinase;	O54988	-0.56	1.41	0.43	1.39	6.19	7.39
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	-0.56	-0.40	-0.48	0.11	0.51	3.86
Nicotinamide phosphoribosyltransferase;	Q99KQ4	-0.56	-0.74	-0.65	0.13	0.57	3.25
Palmitoyl-protein thioesterase 1;	O88531	-0.56	0.60	0.02	0.81	3.63	2.87
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	-0.56	-0.11	-0.33	0.32	1.42	2.22
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;	P63094	-0.11	0.33	0.11	0.31	1.38	1.08
AP-1 complex subunit beta-1;	O35643	-0.52	0.64	0.06	0.82	3.65	2.64
Antithrombin-III;	P32261	-0.52	-0.03	-0.27	0.34	1.53	1.47
Ran-specific GTPase-activating protein;	P34022	-0.52	1.21	0.35	1.22	5.46	4.50
Tetranectin;	P43025	-0.52	-2.00	-1.26	1.05	4.69	9.76
40S ribosomal protein S20;	P60867	-0.52	1.78	0.63	1.62	7.24	7.97
Nucleobindin-2;	P81117	-0.52	-1.09	-0.80	0.41	1.81	4.81
Complement factor I;	Q61129	-0.52	-0.52	-0.52	0.00	0.00	3.53
Sorbitol dehydrogenase;	Q64442	-0.52	-0.71	-0.61	0.14	0.63	3.33
Oligoribonuclease, mitochondrial;	Q9D8S4	-0.52	1.50	0.49	1.43	6.36	6.87
Inositol-3-phosphate synthase 1;	Q9JHU9	-0.52	0.23	-0.14	0.52	2.34	3.63
Uncharacterized protein;	F8VQL5	-0.52	-0.09	-0.30	0.30	1.34	3.32
Dynamin-2;	P39054	-0.52	0.83	0.16	0.95	4.25	3.37
CUGBP Elav-like family member 2;	Q9Z0H4	-0.52	0.33	-0.09	0.60	2.68	3.73
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	-0.49	0.35	-0.07	0.59	2.65	2.37
Dipeptidyl peptidase 2;	Q9ET22	-0.49	-0.64	-0.57	0.11	0.47	3.55
Plasma glutamate carboxypeptidase;	Q9WVJ3	-0.49	-0.52	-0.50	0.01	0.07	3.18
ATP synthase subunit alpha, mitochondrial;	Q03265	-0.49	-1.47	-0.98	0.69	3.09	4.97
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	-0.49	-0.06	-0.28	0.31	1.37	2.80
Myoferlin;	Q69ZN7	-0.49	-0.17	-0.33	0.23	1.03	2.24
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	-0.49	1.03	0.27	1.08	4.81	3.79
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	-0.64	0.08	-0.28	0.51	2.30	1.64
Complement factor H;	P06909	-0.49	-0.94	-0.72	0.32	1.42	3.24
Reversion-inducing cysteine-rich protein with Kazal motifs;	Q9Z0J1	-0.49	1.68	0.59	1.54	6.87	8.60
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	-0.49	0.01	-0.24	0.36	1.60	2.90
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	-0.47	-1.47	-0.97	0.71	3.16	5.60
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	-0.47	-0.42	-0.44	0.04	0.19	3.73

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Cell adhesion molecule 3;	Q99N28	-0.47	-0.67	-0.57	0.14	0.61	4.27
S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	-0.47	0.45	-0.01	0.66	2.93	2.64
40S ribosomal protein S21;	Q9CQR2	-0.47	0.74	0.13	0.86	3.83	3.92
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	-0.47	0.08	-0.20	0.39	1.76	1.47
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	-0.47	0.38	-0.05	0.60	2.69	3.69
Protein S100-A13;	P97352	-0.45	-1.00	-0.73	0.39	1.72	4.04
Probable proline racemase;	Q9CXA2	-0.45	-0.30	-0.38	0.11	0.47	2.50
Glycyl-tRNA synthetase;	Q9CZD3	-0.45	0.16	-0.15	0.44	1.95	1.33
ADP-ribosylation factor-like protein 3;	Q9WUL7	-0.45	0.12	-0.17	0.41	1.82	2.89
Gelsolin;	P13020	-0.45	-0.47	-0.46	0.01	0.06	1.73
SAM domain and HD domain-containing protein 1;	Q60710	-0.45	-1.40	-0.93	0.67	2.97	4.90
Alpha-2-macroglobulin;	Q61838	-0.45	0.37	-0.04	0.58	2.59	3.25
Argininosuccinate lyase;	Q91YI0	-0.45	-0.14	-0.30	0.22	1.00	3.03
Argininosuccinate synthase;	P16460	-0.45	2.38	0.96	2.00	8.95	8.64
Tripartite motif-containing protein 72;	Q1XH17	-0.43	-0.67	-0.55	0.16	0.74	2.46
Spermidine synthase;	Q64674	-0.43	-0.67	-0.55	0.16	0.74	3.32
Zinc-alpha-2-glycoprotein;	Q64726	-0.43	-0.23	-0.33	0.14	0.63	2.90
Ribulose-phosphate 3-epimerase;	Q8VEE0	-0.43	0.48	0.02	0.64	2.87	2.48
Phosphoacetylglucosamine mutase;	Q9CYR6	-0.43	-0.18	-0.31	0.18	0.79	2.42
Epidermal growth factor receptor substrate 15;	P42567	-0.43	-0.22	-0.33	0.15	0.68	1.82
UPF0160 protein MYG1, mitochondrial;	Q9JK81	-0.43	-0.04	-0.24	0.28	1.23	1.88
Cathepsin E;	P70269	-0.43	1.44	0.51	1.33	5.93	6.70
Leukotriene A-4 hydrolase;	P24527	-0.42	-0.58	-0.50	0.12	0.51	2.12
Ras-related protein Rab-23;	P35288	-0.42	-0.12	-0.27	0.21	0.93	2.21
14 kDa phosphohistidine phosphatase;	Q9DAK9	-0.42	0.35	-0.04	0.54	2.40	2.85
Carboxypeptidase N catalytic chain;	Q9JJN5	-0.42	0.14	-0.14	0.39	1.75	2.28
Catalase;	P24270	-0.42	-1.22	-0.82	0.57	2.53	3.17
Xanthine dehydrogenase/oxidase;	Q00519	-0.42	-0.81	-0.61	0.28	1.25	3.73
0	Q8R164	-0.42	-0.89	-0.65	0.34	1.50	2.81
NEDD9-interacting protein with calponin homology and LIM domains;	Q8VDP3	-0.42	0.12	-0.15	0.38	1.70	2.16
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	-0.42	-1.79	-1.10	0.97	4.33	7.12
Flavin reductase (NADPH);	Q923D2	-0.42	-0.56	-0.49	0.10	0.45	2.25
Vitamin D-binding protein;	P21614	-0.38	-0.30	-0.34	0.05	0.23	2.57
Alpha-2-HS-glycoprotein;	P29699	-0.38	-0.47	-0.43	0.07	0.31	3.14
Protein AMBP;	Q07456	-0.38	0.53	0.07	0.64	2.85	2.59
Prostaglandin reductase 1;	Q91YR9	-0.38	-0.14	-0.26	0.17	0.76	0.90
Serine protease inhibitor A3K;	P07759	-0.38	-0.43	-0.41	0.04	0.18	3.10
Uncharacterized protein;	D3Z450	0.71	-0.49	0.11	0.85	3.79	3.94

Protein	Uniprot	Fold change (log$_2$) of ASAPRatio replicate 1	Fold change (log$_2$) of ASAPRatio replicate 2	Average fold change (log$_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Serine protease inhibitor A3N;	Q91WP6	-0.49	-0.34	-0.42	0.11	0.49	3.62
Septin-2;	P42208	-0.38	-1.52	-0.95	0.80	3.59	4.35
Thiosulfate sulfurtransferase;	P52196	-0.38	-0.58	-0.48	0.14	0.63	3.40
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	-0.38	-0.74	-0.56	0.25	1.14	3.64
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	-0.38	0.65	0.14	0.73	3.25	3.25
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	-0.38	-1.94	-1.16	1.11	4.94	6.35
Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	-0.38	-0.42	-0.40	0.03	0.12	1.83
Golgi reassembly-stacking protein 2;	Q99JX3	-0.38	0.23	-0.08	0.43	1.91	2.59
Nucleoside diphosphate kinase;	E9PZF0	-0.38	-0.54	-0.46	0.11	0.50	2.11
Serum albumin;	P07724	-0.36	-0.67	-0.51	0.22	0.98	2.58
Prothrombin;	P19221	-0.36	0.26	-0.05	0.44	1.96	1.93
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	-0.36	-0.94	-0.65	0.41	1.85	3.41
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	-0.36	-1.60	-0.98	0.88	3.92	6.16
Sorting nexin-5;	Q9D8U8	-0.36	0.06	-0.15	0.29	1.31	1.64
Glutamate dehydrogenase 1, mitochondrial;	P26443	-0.36	-3.18	-1.77	2.00	8.92	16.93
F-actin-capping protein subunit alpha-1;	P47753	-0.36	0.31	-0.02	0.47	2.11	2.11
F-actin-capping protein subunit alpha-2;	P47754	-0.52	-0.56	-0.54	0.03	0.13	3.98
Ras-related protein Rab-1A;	P62821	-0.36	0.57	0.10	0.65	2.92	2.90
Ras-related protein Rab-14;	Q91V41	-0.09	0.26	0.09	0.25	1.11	0.85
Ras-related protein Rab-1B;	Q9D1G1	0.35	0.78	0.56	0.31	1.38	3.68
Ras-related protein Rab-10;	P61027	0.18	0.93	0.56	0.54	2.39	3.04
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	-0.36	0.23	-0.07	0.41	1.85	2.20
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;	P62880	-0.36	-0.54	-0.45	0.13	0.56	1.84
Aminopeptidase N;	P97449	-0.36	-0.27	-0.31	0.06	0.28	2.05
Leukocyte elastase inhibitor A;	Q9D154	-0.36	-0.64	-0.50	0.20	0.90	2.93
Fetuin-B;	Q9QXC1	-0.36	-0.56	-0.46	0.14	0.63	3.20
Guanine deaminase;	Q9R111	-0.36	-1.64	-1.00	0.91	4.06	5.97
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	-0.36	0.19	-0.08	0.39	1.73	2.40
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	-0.36	-0.01	-0.19	0.24	1.09	2.06
Myc box-dependent-interacting protein 1;	O08539	-0.34	-0.94	-0.64	0.43	1.90	2.44
Complement C4-B;	P01029	-0.34	-0.71	-0.53	0.26	1.18	2.64
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	-0.34	-0.81	-0.58	0.33	1.49	2.87
Sulfhydryl oxidase 1;	Q8BND5	-0.34	-0.29	-0.31	0.04	0.17	2.26
Dihydropyrimidinase-related protein 2;	O08553	-0.34	-1.12	-0.73	0.55	2.46	3.61
Uncharacterized protein;	E9PWE8	-0.12	-0.43	-0.28	0.22	0.99	1.38
Vacuolar protein sorting-associated protein 26A;	P40336	-0.34	-0.58	-0.46	0.17	0.75	2.26
Ras-related protein Rab-2A;	P53994	-0.34	0.18	-0.08	0.36	1.63	1.90
Endoplasmic reticulum resident protein 29;	P57759	-0.34	-0.54	-0.44	0.14	0.62	2.65

Protein	Uniprot	Fold change (log_2) of ASAPRatio replicate 1	Fold change (log_2) of ASAPRatio replicate 2	Average fold change (log_2) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Histidine triad nucleotide-binding protein 1;	P70349	-0.34	0.03	-0.16	0.26	1.16	0.85
Lysosomal alpha-glucosidase;	P70699	-0.34	-0.17	-0.25	0.12	0.54	1.38
Keratin, type II cytoskeletal 1b;	Q6IFZ6	-0.34	0.06	-0.14	0.28	1.25	1.20
Clathrin light chain B;	Q6IRU5	-0.34	-0.52	-0.43	0.12	0.55	2.87
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	-0.34	-0.03	-0.18	0.22	0.98	0.96
Protein DJ-1;	Q99LX0	-0.34	-0.67	-0.50	0.23	1.03	2.02
Extracellular matrix protein 1;	Q61508	-0.34	-1.15	-0.75	0.57	2.56	3.70
Beta-hexosaminidase subunit beta;	P20060	-0.34	-1.89	-1.11	1.10	4.89	8.44
Adenosine kinase;	P55264	-0.32	-0.23	-0.28	0.06	0.28	1.47
Fibulin-1;	Q08879	-0.32	-0.45	-0.39	0.09	0.42	2.29
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	-0.32	0.04	-0.14	0.26	1.15	1.12
Alpha-1-antitrypsin 1-1;	P07758	-0.32	0.00	-0.16	0.23	1.02	1.64
Alpha-1-antitrypsin 1-2;	P22599	-0.25	-0.20	-0.23	0.04	0.16	1.67
Alpha-1-antitrypsin 1-4;	Q00897	-0.62	-0.23	-0.43	0.27	1.22	4.80
Elongation factor 1-alpha 1;	P10126	-0.32	0.12	-0.10	0.32	1.41	1.62
Elongation factor 1-alpha 2;	P62631	0.20	-1.00	-0.40	0.85	3.79	3.22
Selenium-binding protein 1;	P17563	-0.32	0.08	-0.12	0.29	1.28	1.51
Dipeptidyl peptidase 1;	P97821	-0.32	0.75	0.21	0.76	3.38	2.98
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	-0.32	0.50	0.09	0.58	2.58	1.65
Arachidonate 5-lipoxygenase;	P48999	-0.32	-0.38	-0.35	0.04	0.17	2.35
Cartilage-associated protein;	Q9CYD3	-0.32	2.14	0.91	1.74	7.78	9.42
D-dopachrome decarboxylase;	O35215	-0.30	-0.89	-0.60	0.41	1.85	2.54
Annexin A3;	O35639	-0.30	-0.60	-0.45	0.21	0.93	2.47
Proteasome subunit alpha type-3;	O70435	-0.30	0.01	-0.15	0.22	1.00	0.59
BAG family molecular chaperone regulator 3;	Q9JLV1	-0.30	-0.30	-0.30	0.00	0.00	2.10
Galactokinase;	Q9R0N0	-0.30	0.31	0.00	0.43	1.94	2.08
Protein disulfide-isomerase;	P09103	-0.30	-0.06	-0.18	0.17	0.77	1.61
V-type proton ATPase catalytic subunit A;	P50516	-0.30	-0.12	-0.21	0.13	0.58	1.56
Elongation factor 2;	P58252	-0.30	0.36	0.03	0.47	2.08	1.57
Retinoid-inducible serine carboxypeptidase;	Q920A5	-0.30	-0.36	-0.33	0.04	0.17	1.65
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	-0.30	0.42	0.06	0.51	2.29	2.20
Obg-like ATPase 1;	Q9CZ30	-0.30	0.89	0.29	0.84	3.76	2.75
Aspartyl aminopeptidase;	Q9Z2W0	-0.30	-0.34	-0.32	0.03	0.11	2.15
Creatine kinase M-type;	P07310	-0.29	-0.62	-0.45	0.24	1.06	2.65
Creatine kinase B-type;	Q04447	-0.29	-0.56	-0.42	0.19	0.85	2.36
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	-0.29	-0.64	-0.47	0.25	1.13	2.45
Neutral alpha-glucosidase AB;	Q8BHN3	-0.29	-0.11	-0.20	0.13	0.57	1.33
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	-0.29	-1.18	-0.74	0.63	2.83	3.18

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Aldose 1-epimerase;	Q8K157	-0.29	-1.00	-0.64	0.50	2.25	3.88
ATP-dependent RNA helicase DDX1;	Q91VR5	-0.29	-0.14	-0.21	0.11	0.47	1.72
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	-0.29	0.19	-0.05	0.34	1.50	1.24
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	-0.29	0.51	0.11	0.56	2.50	1.80
Epididymal secretory protein E1;	Q9Z0J0	-0.29	-0.52	-0.40	0.16	0.72	2.50
Inositol monophosphatase 1;	O55023	-0.29	-0.12	-0.20	0.12	0.52	1.24
Glutathione S-transferase Mu 2;	P15626	-0.29	-0.56	-0.42	0.19	0.85	2.57
Glutathione S-transferase Mu 1;	P10649	-0.11	-0.86	-0.48	0.54	2.39	2.49
Fumarylacetoacetase;	P35505	-0.29	-0.54	-0.41	0.18	0.79	2.23
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	-0.29	-0.76	-0.52	0.34	1.50	2.64
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	-0.29	0.01	-0.14	0.21	0.95	0.74
Bleomycin hydrolase;	Q8R016	-0.29	0.37	0.04	0.46	2.06	1.81
Saccharopine dehydrogenase-like oxidoreductase;	Q8R127	-0.29	-0.64	-0.47	0.25	1.13	2.66
Mannose-6-phosphate isomerase;	Q924M7	-0.29	-0.32	-0.30	0.03	0.11	1.68
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	-0.29	1.44	0.58	1.22	5.46	4.92
Xin actin-binding repeat-containing protein 1;	O70373	-0.29	-2.06	-1.17	1.25	5.60	8.84
Proteasome subunit beta type-10;	O35955	-0.29	-0.38	-0.33	0.06	0.29	1.46
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	-0.27	0.26	0.00	0.38	1.68	1.69
Steroid receptor RNA activator 1;	Q80VJ2	-0.27	0.77	0.25	0.73	3.27	3.21
Reticulocalbin-3;	Q8BH97	-0.27	-0.60	-0.43	0.23	1.04	2.44
Serpin B8;	O08800	-0.25	-0.76	-0.51	0.36	1.61	2.82
Epididymis-specific alpha-mannosidase;	O54782	-0.25	-0.12	-0.19	0.09	0.42	1.53
Dystrophin;	P11531	-0.25	0.00	-0.13	0.18	0.80	1.11
Indolethylamine N-methyltransferase;	P40936	-0.25	-1.52	-0.88	0.89	3.99	4.46
Heparin cofactor 2;	P49182	-0.25	-0.58	-0.42	0.23	1.03	2.32
Apolipoprotein A-I;	Q00623	-0.25	1.29	0.52	1.09	4.86	4.86
Ganglioside GM2 activator;	Q60648	-0.25	0.62	0.19	0.62	2.76	2.43
Eukaryotic translation initiation factor 3 subunit H;	Q91WK2	-0.25	2.07	0.91	1.64	7.34	8.08
Torsin-1B;	Q9ER41	-0.25	-0.20	-0.23	0.04	0.16	1.58
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	-0.25	-0.18	-0.22	0.05	0.21	1.54
Phosphatidylinositol transfer protein alpha isoform;	P53810	-0.25	0.60	0.18	0.61	2.70	2.67
Plasma protease C1 inhibitor;	P97290	-0.25	-0.92	-0.58	0.47	2.10	3.27
Periostin;	Q62009	-0.25	0.61	0.18	0.61	2.73	2.23
Zyxin;	Q62523	-0.25	1.00	0.37	0.89	3.95	3.54
Major vault protein;	Q9EQK5	-0.25	-0.97	-0.61	0.51	2.27	3.28
Uncharacterized protein;	Q3TUE1	-0.25	0.21	-0.02	0.33	1.47	1.20
Synaptophysin-like protein 1;	O09117	-0.25	0.28	0.01	0.37	1.66	1.82
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial;	O88696	-0.23	0.43	0.10	0.47	2.11	1.68

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T-complex protein 1 subunit theta;	P42932	-0.23	1.45	0.61	1.19	5.31	3.61
Ras-related protein Rab-7a;	P51150	-0.23	0.44	0.11	0.48	2.14	2.09
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	-0.23	-1.06	-0.65	0.58	2.60	2.54
Acyl-CoA synthetase short-chain family member 3, mitochondrial;	Q14DH7	-0.23	-1.40	-0.82	0.82	3.67	3.83
Calcium-regulated heat stable protein 1;	Q9CR86	-0.23	-0.47	-0.35	0.17	0.76	2.15
Sorting nexin-2;	Q9CWK8	-0.23	0.64	0.20	0.62	2.77	2.39
Endoplasmic reticulum resident protein 44;	Q9D1Q6	-0.23	-0.30	-0.27	0.05	0.22	1.45
Phosphoglycerate mutase 1;	Q9DBJ1	-0.23	-0.42	-0.32	0.13	0.57	1.87
Ribonuclease 4;	Q9JJH1	-0.23	-0.42	-0.32	0.13	0.57	1.37
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	-0.23	-0.04	-0.14	0.13	0.60	1.12
N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	-0.23	-0.36	-0.30	0.09	0.39	1.77
Myosin light chain 1/3, skeletal muscle isoform;	P05977	-0.23	-2.00	-1.12	1.25	5.58	7.55
Lysosomal protective protein;	P16675	-0.23	-0.27	-0.25	0.02	0.11	1.45
Purine nucleoside phosphorylase;	P23492	-0.23	-0.47	-0.35	0.17	0.76	1.93
Cytochrome b5;	P56395	-0.23	-0.47	-0.35	0.17	0.76	2.12
Heat shock protein 105 kDa;	Q61699	-0.23	0.24	0.00	0.33	1.49	0.85
Inorganic pyrophosphatase;	Q9D819	-0.23	0.12	-0.06	0.25	1.13	1.38
Voltage-dependent calcium channel subunit alpha-2/delta-1;	O08532	-0.22	-0.62	-0.42	0.28	1.27	2.47
Ornithine aminotransferase, mitochondrial;	P29758	-0.22	0.14	-0.04	0.25	1.12	0.85
182 kDa tankyrase-1-binding protein;	P58871	-0.22	-0.04	-0.13	0.12	0.55	0.84
Far upstream element-binding protein 2;	Q3U0V1	-0.22	-0.06	-0.14	0.11	0.50	0.86
Arginase-1;	Q61176	-0.22	-2.00	-1.11	1.26	5.63	6.44
Phosphoglucomutase-2;	Q7TSV4	-0.22	0.12	-0.05	0.24	1.08	0.99
Phostensin;	Q8BQ30	-0.22	0.19	-0.01	0.29	1.28	1.42
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	-0.22	0.35	0.06	0.40	1.78	1.33
ES1 protein homolog, mitochondrial;	Q9D172	-0.22	-0.92	-0.57	0.49	2.20	2.61
4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	-0.22	-0.47	-0.35	0.18	0.81	1.91
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	-0.22	-0.03	-0.12	0.13	0.60	0.61
Glucosamine-6-phosphate isomerase 1;	O88958	-0.22	0.19	-0.01	0.29	1.28	0.88
Adenosylhomocysteinase;	P50247	-0.22	0.37	0.07	0.41	1.85	1.74
Pyruvate kinase isozymes M1/M2;	P52480	-0.22	-0.52	-0.37	0.21	0.94	1.65
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	-0.22	-0.67	-0.44	0.32	1.42	2.33
Serotransferrin;	Q921I1	-0.22	-0.49	-0.36	0.20	0.87	2.06
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	-0.22	-0.42	-0.32	0.14	0.62	1.53
Phosphoglucomutase-1;	Q9D0F9	-0.22	-0.52	-0.37	0.21	0.94	2.01
Cysteine sulfinic acid decarboxylase;	Q9DBE0	-0.22	-0.20	-0.21	0.01	0.05	1.11
Choline transporter-like protein 2;	Q8BY89	-0.22	-0.11	-0.16	0.08	0.36	1.21
Complement C3;	P01027	-0.20	-0.29	-0.24	0.06	0.27	1.20

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Plasminogen;	P20918	-0.20	-0.47	-0.34	0.19	0.86	1.75
Ras-related protein Rab-21;	P35282	-0.20	0.90	0.35	0.77	3.46	2.91
Dynein light chain roadblock-type 1;	P62627	-0.20	-0.15	-0.18	0.03	0.15	1.13
Stress-induced-phosphoprotein 1;	Q60864	-0.20	0.48	0.14	0.48	2.13	1.62
Gephyrin;	Q8BUV3	-0.20	0.19	-0.01	0.28	1.23	0.72
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	-0.20	-0.04	-0.12	0.11	0.50	0.97
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	-0.20	0.15	-0.03	0.25	1.11	0.80
Neudesin;	Q9CQ45	-0.20	-0.03	-0.12	0.12	0.54	0.98
Tetratricopeptide repeat protein 38;	A3KMP2	-0.20	-0.40	-0.30	0.14	0.62	1.17
COP9 signalosome complex subunit 3;	O88543	-0.20	1.34	0.57	1.09	4.86	3.98
0	P35492	-0.20	-0.76	-0.48	0.40	1.77	2.48
Myosin regulatory light chain 2, skeletal muscle isoform;	P97457	-0.20	-1.43	-0.82	0.87	3.89	3.00
Junction plakoglobin;	Q02257	-0.20	1.31	0.55	1.06	4.75	3.32
Catenin beta-1;	Q02248	0.48	0.20	0.34	0.19	0.86	1.19
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	-0.20	-0.89	-0.55	0.49	2.17	2.16
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	-0.20	-1.79	-0.99	1.12	5.00	6.09
Uncharacterized protein;	F8WIT2	-0.20	-0.56	-0.38	0.25	1.12	1.57
PDZ and LIM domain protein 1;	O70400	-0.20	1.31	0.55	1.07	4.77	4.61
Ig heavy chain V region 441;	P01806	-0.18	-2.32	-1.25	1.51	6.75	9.36
ATP synthase subunit beta, mitochondrial;	P56480	-0.18	-1.69	-0.94	1.06	4.75	6.00
Cellular retinoic acid-binding protein 1;	P62965	-0.18	-0.06	-0.12	0.09	0.39	0.77
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	-0.18	1.02	0.42	0.85	3.80	3.51
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	-0.18	-2.74	-1.46	1.81	8.06	9.23
Protein SEC13 homolog;	Q9D1M0	-0.18	-0.12	-0.15	0.05	0.20	0.84
Protein NDRG2;	Q9QYG0	-0.18	-0.49	-0.34	0.22	0.98	1.67
Ahnak protein; MCG17833, isoform CRA_b; Uncharacterized protein;	Q8R2L7	-0.18	-0.92	-0.55	0.52	2.31	2.97
Integrin beta-1;	P09055	-0.18	-0.03	-0.11	0.11	0.49	0.60
Chromobox protein homolog 3;	P23198	-0.18	0.44	0.13	0.44	1.98	1.43
Microtubule-associated protein 4;	P27546	-0.18	-0.32	-0.25	0.10	0.44	1.29
Protein transport protein Sec23A;	Q01405	-0.18	-0.22	-0.20	0.02	0.11	1.22
Pyridoxal kinase;	Q8K183	-0.18	-0.45	-0.32	0.19	0.85	1.56
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	-0.18	-0.20	-0.19	0.01	0.05	0.99
Uncharacterized protein;	D3Z0Y2	-0.18	-1.00	-0.59	0.58	2.58	3.33
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	-0.18	0.29	0.05	0.33	1.49	1.45
Histamine N-methyltransferase;	Q91VF2	-0.18	-0.34	-0.26	0.11	0.49	1.34
Dynactin subunit 2;	Q99KJ8	-0.17	0.32	0.08	0.35	1.55	1.21
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	-0.17	-0.62	-0.39	0.32	1.43	1.64
Phosphoglycerate mutase 2;	O70250	-0.15	-0.64	-0.40	0.35	1.55	2.12

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Cytoplasmic dynein 1 intermediate chain 2;	O88487	-0.15	0.36	0.10	0.36	1.60	1.10
Basigin;	P18572	-0.15	-0.25	-0.20	0.07	0.32	1.20
Myristoylated alanine-rich C-kinase substrate;	P26645	-0.15	0.59	0.22	0.52	2.33	1.98
Cytoplasmic aconitate hydratase;	P28271	-0.15	-0.62	-0.39	0.33	1.48	1.80
Protein phosphatase 1A;	P49443	-0.15	0.29	0.07	0.31	1.39	1.14
Neural cell adhesion molecule L1-like protein;	P70232	-0.15	-1.29	-0.72	0.80	3.58	4.36
Fructose-1,6-bisphosphatase isozyme 2;	P70695	-0.15	-0.84	-0.49	0.48	2.16	1.83
Hsp90 co-chaperone Cdc37;	Q61081	-0.15	1.60	0.73	1.24	5.54	5.40
Myomesin-1;	Q62234	-0.15	-1.40	-0.77	0.88	3.93	3.21
Hematopoietic progenitor cell antigen CD34;	Q64314	-0.15	-0.62	-0.39	0.33	1.48	1.97
Ribonuclease inhibitor;	Q91VI7	-0.15	-0.43	-0.29	0.20	0.89	1.56
Electron transfer flavoprotein subunit beta;	Q9DCW4	-0.15	-0.03	-0.09	0.09	0.39	0.51
Profilin-2;	Q9JJV2	-0.15	0.79	0.32	0.67	2.98	2.59
Kininogen-1;	O08677	-0.15	-0.20	-0.18	0.03	0.15	1.10
Sorting nexin-3;	O70492	-0.15	1.72	0.78	1.32	5.90	5.64
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	-0.15	-0.12	-0.14	0.02	0.10	0.93
Beta-galactosidase;	P23780	-0.15	-1.03	-0.59	0.62	2.77	3.19
Aldose reductase;	P45376	-0.15	-0.60	-0.38	0.32	1.41	2.07
Profilin-1;	P62962	-0.15	-0.03	-0.09	0.09	0.39	0.81
Clusterin;	Q06890	-0.15	1.31	0.58	1.03	4.60	4.13
Serpin B6;	Q60854	-0.15	-1.09	-0.62	0.66	2.96	3.57
Uncharacterized protein;	E9Q9T2	0.26	-1.69	-0.71	1.38	6.17	5.45
Plastin-2;	Q61233	-0.15	-1.09	-0.62	0.66	2.96	3.06
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	-0.15	0.04	-0.05	0.14	0.62	0.60
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	-0.15	-0.30	-0.23	0.11	0.48	1.16
Protein disulfide-isomerase A4;	P08003	-0.14	0.11	-0.01	0.17	0.78	0.65
Lysosome-associated membrane glycoprotein 1;	P11438	-0.14	-1.18	-0.66	0.74	3.31	3.63
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	-0.14	0.07	-0.03	0.15	0.65	0.66
Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	-0.14	-0.32	-0.23	0.13	0.59	1.32
EH domain-containing protein 4;	Q9EQP2	-0.14	0.11	-0.01	0.17	0.78	0.67
Hepatoma-derived growth factor;	P51859	-0.14	0.71	0.28	0.59	2.65	1.76
Actin, alpha cardiac muscle 1;	P68033	-0.14	-0.81	-0.47	0.48	2.13	2.63
Heat shock 70 kDa protein 4L;	P48722	-0.45	0.45	0.00	0.64	2.87	2.03
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	-0.14	-0.52	-0.33	0.27	1.20	1.18
Dynein light chain 2, cytoplasmic;	Q9D0M5	-0.14	-0.62	-0.38	0.34	1.53	1.68
StAR-related lipid transfer protein 5;	Q9EPQ7	-0.14	1.18	0.52	0.93	4.14	3.82
Transgelin-2;	Q9WVA4	-0.14	0.44	0.15	0.41	1.83	1.34
Opioid growth factor receptor;	Q99PG2	-0.14	0.71	0.29	0.60	2.68	2.31

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Alpha-adducin;	Q9QYC0	-0.14	-0.58	-0.36	0.31	1.40	1.66
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	-0.14	1.87	0.87	1.42	6.34	6.56
Heterogeneous nuclear ribonucleoprotein H;	O35737	-0.12	0.24	0.06	0.25	1.13	0.97
Protein S100-A1;	P56565	-0.12	0.82	0.35	0.66	2.95	2.41
Serrate RNA effector molecule homolog;	Q99MR6	-0.12	-0.56	-0.34	0.31	1.38	1.14
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	-0.12	0.14	0.01	0.18	0.81	0.75
Iron-sulfur cluster assembly 2 homolog, mitochondrial;	Q9DCB8	-0.12	-0.23	-0.18	0.08	0.36	0.98
Prolyl endopeptidase;	Q9QUR6	-0.12	0.64	0.26	0.54	2.41	1.77
Myomesin 2; Uncharacterized protein;	Q14BI5	-0.12	-1.52	-0.82	0.99	4.40	3.04
H-2 class I histocompatibility antigen, L-D alpha chain;	P01897	-0.12	0.03	-0.05	0.11	0.47	0.50
H-2 class I histocompatibility antigen, K-B alpha chain;	P01901	-0.01	0.18	0.08	0.13	0.60	0.38
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	-0.89	0.70	-0.10	1.12	5.00	4.75
Phosphoglycerate kinase 1;	P09411	-0.12	-0.30	-0.21	0.13	0.58	1.18
GTP-binding nuclear protein Ran;	P62827	-0.12	0.88	0.38	0.71	3.16	2.37
T-complex protein 1 subunit epsilon;	P80316	-0.12	1.43	0.65	1.09	4.89	4.51
UPF0366 protein C11orf67 homolog;	Q8R0P4	-0.12	-0.42	-0.27	0.21	0.93	1.30
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	-0.11	-1.25	-0.68	0.81	3.62	2.53
Transforming growth factor-beta-induced protein ig-h3;	P82198	-0.11	-1.64	-0.87	1.09	4.86	5.53
Xaa-Pro dipeptidase;	Q11136	-0.11	-0.43	-0.27	0.23	1.04	1.24
Hydroxysteroid dehydrogenase-like protein 2;	Q2TPA8	-0.11	0.19	0.04	0.21	0.93	0.77
Leukocyte surface antigen CD47;	Q61735	-0.11	-0.29	-0.20	0.13	0.57	0.93
UPF0586 protein C9orf41 homolog;	Q80UY1	-0.11	-0.15	-0.13	0.03	0.15	0.72
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	-0.11	0.06	-0.02	0.11	0.51	0.58
Beta-lactamase-like protein 2;	Q99KR3	-0.11	-0.56	-0.33	0.32	1.42	1.53
Thioredoxin domain-containing protein 17;	Q9CQM5	-0.11	0.37	0.13	0.33	1.49	1.21
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	-0.11	-1.00	-0.55	0.63	2.83	2.78
AP-2 complex subunit beta;	Q9DBG3	-0.11	0.19	0.04	0.21	0.93	0.75
Glutathione S-transferase kappa 1;	Q9DCM2	-0.11	1.00	0.45	0.78	3.49	2.46
Glycogen synthase kinase-3 beta;	Q9WV60	-0.11	0.35	0.12	0.32	1.42	1.12
Mitotic checkpoint protein BUB3;	Q9WVA3	-0.11	-0.76	-0.43	0.46	2.07	2.14
C-terminal-binding protein 1;	O88712	-0.11	-0.49	-0.30	0.28	1.23	1.49
C-terminal-binding protein 2;	P56546	-0.04	0.14	0.05	0.13	0.57	0.47
Heat shock cognate 71 kDa protein;	P63017	-0.11	0.26	0.08	0.26	1.16	0.92
Heat shock 70 kDa protein 1A;	Q61696	0.25	0.18	0.21	0.05	0.24	1.57
78 kDa glucose-regulated protein;	P20029	-0.79	-0.25	-0.52	0.38	1.69	3.17
Secernin-3;	Q3TMH2	-0.11	-0.45	-0.28	0.25	1.10	1.34
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	-0.11	-0.27	-0.19	0.12	0.52	0.87
Copine-3;	Q8BT60	-0.11	-0.32	-0.21	0.15	0.69	1.01

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Copine-1;	Q8C166	-0.25	-0.47	-0.36	0.16	0.70	2.18
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	-0.11	-0.45	-0.28	0.25	1.10	1.05
Mitogen-activated protein kinase 9;	Q9WTU6	-0.11	0.59	0.24	0.49	2.18	1.71
Lysosomal alpha-mannosidase;	O09159	-0.09	-0.47	-0.28	0.27	1.22	1.12
Cathepsin S;	O70370	-0.09	-1.60	-0.84	1.07	4.77	4.78
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2;	O88428	-0.09	-0.07	-0.08	0.01	0.05	0.44
Calreticulin;	P14211	-0.09	0.21	0.06	0.21	0.96	0.70
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	-0.09	0.26	0.09	0.25	1.11	0.89
Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	P70441	-0.09	1.28	0.60	0.97	4.32	2.79
T-complex protein 1 subunit delta;	P80315	-0.09	2.29	1.10	1.68	7.51	9.02
Vitamin K-dependent protein S;	Q08761	-0.09	0.28	0.09	0.26	1.15	0.88
Zinc finger CCCH domain-containing protein 15;	Q3TIV5	-0.09	0.16	0.04	0.18	0.80	0.66
Suprabasin;	Q8CIT9	-0.09	-1.40	-0.74	0.92	4.13	2.99
Pyridoxine-5'-phosphate oxidase;	Q91XF0	-0.09	-0.11	-0.10	0.01	0.05	0.55
von Willebrand factor A domain-containing protein 5A;	Q99KC8	-0.09	-0.64	-0.37	0.39	1.75	1.49
Ribosome-binding protein 1;	Q99PL5	-0.09	-1.47	-0.78	0.98	4.37	4.11
Thioredoxin domain-containing protein 12;	Q9CQU0	-0.09	0.23	0.07	0.22	1.00	0.82
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	-0.09	0.63	0.27	0.51	2.28	1.71
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	-0.09	-0.34	-0.21	0.18	0.79	1.07
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	-0.09	-0.18	-0.14	0.07	0.30	0.59
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	-0.09	-0.23	-0.16	0.10	0.46	0.68
Glutathione S-transferase P 1;	P19157	-0.09	-0.32	-0.21	0.16	0.74	1.00
Aldehyde dehydrogenase, mitochondrial;	P47738	-0.09	-0.64	-0.37	0.39	1.75	1.46
Retinal dehydrogenase 1;	P24549	-0.22	-1.69	-0.95	1.04	4.65	5.27
Aldehyde dehydrogenase, cytosolic 1;	O35945	0.35	0.21	0.28	0.09	0.41	2.27
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	-0.09	-0.64	-0.37	0.39	1.75	1.53
Myosin light polypeptide 6;	Q60605	-0.09	-0.54	-0.31	0.32	1.41	1.49
Nischarin;	Q80TM9	-0.09	1.03	0.47	0.79	3.53	2.53
Nitrilase homolog 1;	Q8VDK1	-0.09	-0.29	-0.19	0.14	0.62	0.91
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	-0.09	0.23	0.07	0.22	1.00	0.75
MCG142264, isoform CRA_a; Uncharacterized protein;	D3Z494	-0.09	-0.34	-0.21	0.18	0.79	1.02
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	-0.09	-0.40	-0.24	0.22	0.97	1.13
Rho GTPase-activating protein 1;	Q5FWK3	-0.09	1.71	0.81	1.27	5.68	4.14
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	-0.09	1.73	0.82	1.29	5.75	5.72
WD repeat-containing protein 1;	O88342	-0.07	-0.06	-0.07	0.01	0.05	0.36
Vitronectin;	P29788	-0.07	-0.15	-0.11	0.06	0.25	0.56
Fascin;	Q61553	-0.07	0.99	0.46	0.75	3.37	2.37

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Transaldolase;	Q93092	-0.07	0.04	-0.02	0.08	0.37	0.33
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	-0.07	-0.15	-0.11	0.06	0.25	0.55
Prostamide/prostaglandin F synthase;	Q9DB60	-0.07	0.19	0.06	0.19	0.83	0.62
Omega-amidase NIT2;	Q9JHW2	-0.07	-0.20	-0.14	0.09	0.40	0.64
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	-0.07	0.37	0.15	0.31	1.39	0.93
Sepiapterin reductase;	Q64105	-0.07	-0.29	-0.18	0.15	0.67	0.84
ATP synthase subunit gamma, mitochondrial;	Q91VR2	-0.07	-1.52	-0.79	1.02	4.55	4.43
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	-0.07	-0.47	-0.27	0.28	1.26	1.18
Proteolipid protein 2;	Q9R1Q7	-0.07	0.15	0.04	0.16	0.71	0.57
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	-0.06	1.89	0.92	1.38	6.16	6.66
Protein DDI1 homolog 2;	A2ADY9	-0.04	0.77	0.36	0.57	2.56	1.97
Glucosidase 2 subunit beta;	O08795	-0.04	0.97	0.46	0.72	3.20	2.51
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	-0.04	0.49	0.22	0.37	1.67	1.03
NADP-dependent malic enzyme;	P06801	-0.04	-0.22	-0.13	0.12	0.55	0.54
Epoxide hydrolase 2;	P34914	-0.04	0.14	0.05	0.13	0.57	0.46
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	-0.04	0.14	0.05	0.13	0.57	0.32
Ras suppressor protein 1;	Q01730	-0.04	-0.60	-0.32	0.39	1.75	1.51
Calcium-binding protein 39;	Q06138	-0.04	1.06	0.51	0.78	3.50	2.63
Aldehyde dehydrogenase family 16 member A1;	Q571I9	-0.04	0.86	0.41	0.64	2.84	2.17
Guanylate kinase;	Q64520	-0.04	0.47	0.21	0.36	1.61	1.21
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	-0.04	0.82	0.39	0.61	2.71	1.70
Putative hydroxypyruvate isomerase;	Q8R1F5	-0.04	-0.32	-0.18	0.20	0.88	0.84
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	-0.04	-0.43	-0.24	0.28	1.23	1.03
Protein S100-A14;	Q9D2Q8	-0.04	1.10	0.53	0.81	3.62	3.11
ATP synthase subunit delta, mitochondrial;	Q9D3D9	-0.04	-1.47	-0.76	1.01	4.51	4.47
Apoptosis-inducing factor 1, mitochondrial;	Q9Z0X1	-0.04	-1.64	-0.84	1.13	5.05	3.87
L-lactate dehydrogenase A chain;	P06151	-0.04	-0.74	-0.39	0.49	2.19	1.87
L-lactate dehydrogenase B chain;	P16125	0.15	-0.42	-0.13	0.40	1.79	1.57
Cathepsin D;	P18242	-0.04	-0.25	-0.15	0.15	0.66	0.69
Phospholipase A-2-activating protein;	P27612	-0.04	1.65	0.80	1.20	5.34	4.01
Creatine kinase U-type, mitochondrial;	P30275	-0.04	-1.84	-0.94	1.27	5.66	6.38
Peroxiredoxin-1;	P35700	-0.04	-0.32	-0.18	0.20	0.88	0.86
S-adenosylmethionine synthase isoform type-2;	Q3THS6	-0.04	0.52	0.24	0.40	1.77	1.22
Rho GDP-dissociation inhibitor 2;	Q61599	-0.04	0.03	-0.01	0.05	0.23	0.22
D-3-phosphoglycerate dehydrogenase;	Q61753	-0.04	1.47	0.71	1.07	4.76	4.39
Ubiquitin thioesterase OTUB1;	Q7TQI3	-0.04	0.71	0.34	0.54	2.39	1.76
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	-0.04	0.04	0.00	0.06	0.27	0.26
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	-0.04	-0.60	-0.32	0.39	1.75	1.19

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Uncharacterized protein;	E9Q616	-0.04	-0.23	-0.14	0.13	0.60	0.53
Oxysterol-binding protein;	E9QPD4	-0.04	0.99	0.47	0.73	3.25	2.77
GMP synthase [glutamine-hydrolyzing];	Q3THK7	-0.04	0.86	0.41	0.64	2.84	2.34
Oxysterol-binding protein-related protein 9;	A2A8Z1	-0.04	0.65	0.30	0.49	2.19	1.66
Protein unc-119 homolog B;	Q8C4B4	-0.04	0.60	0.28	0.46	2.05	1.54
Proteasome subunit beta type-5;	O55234	-0.03	0.55	0.26	0.41	1.82	1.14
Prefoldin subunit 2;	O70591	-0.03	1.28	0.63	0.93	4.14	3.80
SUMO-conjugating enzyme UBC9;	P63280	-0.03	-0.14	-0.08	0.08	0.34	0.40
T-complex protein 1 subunit beta;	P80314	-0.03	1.82	0.89	1.30	5.82	4.61
Osteoclast-stimulating factor 1;	Q62422	-0.03	-0.03	-0.03	0.00	0.00	0.17
Lactoylglutathione lyase;	Q9CPU0	-0.03	-0.20	-0.12	0.12	0.54	0.53
Adenylate kinase isoenzyme 1;	Q9R0Y5	-0.03	-0.42	-0.22	0.27	1.22	1.00
Uncharacterized protein;	E9PVD2	-0.03	0.29	0.13	0.22	1.00	0.62
Septin-7;	O55131	-0.03	-0.89	-0.46	0.61	2.71	1.94
Adenylyl cyclase-associated protein 1;	P40124	-0.03	0.54	0.25	0.40	1.78	1.03
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;	P62137	-0.03	0.03	0.00	0.04	0.18	0.15
Acyl-protein thioesterase 1;	P97823	-0.03	-0.03	-0.03	0.00	0.00	0.15
Ubiquitin-like modifier-activating enzyme 1;	Q02053	-0.03	0.67	0.32	0.49	2.20	1.62
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	-0.03	1.64	0.81	1.18	5.28	4.40
Alcohol dehydrogenase [NADP+];	Q9JII6	-0.03	-0.22	-0.12	0.13	0.60	0.55
Glutathione reductase, mitochondrial;	P47791	-0.01	-0.29	-0.15	0.19	0.86	0.60
Annexin A5;	P48036	-0.01	-0.54	-0.27	0.37	1.64	1.23
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	-0.01	-0.38	-0.20	0.26	1.15	0.79
Vacuolar protein sorting-associated protein 45;	P97390	-0.01	-0.20	-0.11	0.13	0.59	0.43
Beta-2-glycoprotein 1;	Q01339	-0.01	-0.38	-0.20	0.26	1.15	0.64
Rab GDP dissociation inhibitor beta;	Q61598	-0.01	0.25	0.12	0.19	0.84	0.54
Transcription factor BTF3;	Q64152	-0.01	2.00	0.99	1.42	6.35	7.11
L-asparaginase;	Q8C0M9	-0.01	-0.36	-0.19	0.24	1.09	0.76
Protein Z-dependent protease inhibitor;	Q8R121	-0.01	0.30	0.14	0.22	0.99	0.53
Oxysterol-binding protein-related protein 1;	Q91XL9	-0.01	-0.52	-0.26	0.35	1.58	1.13
Dipeptidyl peptidase 3;	Q99KK7	-0.01	0.03	0.01	0.03	0.14	0.08
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	-0.01	-0.79	-0.40	0.55	2.44	1.99
Uncharacterized protein;	E9PV24	-0.01	0.19	0.09	0.14	0.64	0.36
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	-0.01	1.14	0.56	0.81	3.64	2.36
Glutathione peroxidase 3;	P46412	-0.01	-1.15	-0.58	0.80	3.59	3.23
Xaa-Pro aminopeptidase 1;	Q6P1B1	-0.01	-0.03	-0.02	0.01	0.05	0.07
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	-0.01	-0.14	-0.08	0.09	0.39	0.29

Protein	Uniprot	Fold change (log$_2$) of ASAPRatio replicate 1	Fold change (log$_2$) of ASAPRatio replicate 2	Average fold change (log$_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	-0.01	0.24	0.11	0.18	0.80	0.50
Protein disulfide-isomerase A6;	Q922R8	-0.01	1.28	0.63	0.91	4.07	3.32
3-mercaptopyruvate sulfurtransferase;	Q99J99	-0.01	-0.23	-0.12	0.16	0.69	0.47
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	-0.01	0.01	0.00	0.02	0.09	0.08
Transketolase;	P40142	0.00	-0.12	-0.06	0.08	0.38	0.22
60S acidic ribosomal protein P1;	P47955	0.00	0.56	0.28	0.39	1.76	1.19
Proteasome subunit beta type-4;	P99026	0.00	0.26	0.13	0.19	0.83	0.43
Mitogen-activated protein kinase 3;	Q63844	0.00	0.10	0.05	0.07	0.31	0.18
10 kDa heat shock protein, mitochondrial;	Q64433	0.00	0.28	0.14	0.19	0.87	0.55
Phosphoglycolate phosphatase;	Q8CHP8	0.00	-0.30	-0.15	0.21	0.96	0.58
Apolipoprotein A-I-binding protein;	Q8K4Z3	0.00	-0.20	-0.10	0.14	0.63	0.39
Anamorsin;	Q8WTY4	0.00	1.49	0.75	1.05	4.71	4.41
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	0.00	-1.56	-0.78	1.10	4.91	4.94
Acid ceramidase;	Q9WV54	0.00	0.48	0.24	0.34	1.50	0.97
Chloride intracellular channel protein 1;	Q9Z1Q5	0.00	0.15	0.08	0.11	0.48	0.28
Complement factor B;	P04186	0.00	-0.14	-0.07	0.10	0.43	0.25
Glucose-6-phosphate isomerase;	P06745	0.00	-0.60	-0.30	0.42	1.89	1.32
Bisphosphoglycerate mutase;	P15327	0.00	0.31	0.16	0.22	0.98	0.54
Quinone oxidoreductase;	P47199	0.00	-0.60	-0.30	0.42	1.89	1.31
Phosphatidylethanolamine-binding protein 1;	P70296	0.00	-0.32	-0.16	0.23	1.02	0.67
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	0.00	-0.97	-0.49	0.69	3.07	1.82
Peroxiredoxin-2;	Q61171	0.00	0.37	0.18	0.26	1.16	0.76
Abhydrolase domain-containing protein 14B;	Q8VCR7	0.00	-0.56	-0.28	0.39	1.76	1.25
NADH-cytochrome b5 reductase 3;	Q9DCN2	0.00	-0.38	-0.19	0.27	1.19	0.69
DAZ-associated protein 1;	Q9JII5	0.00	0.15	0.08	0.11	0.48	0.29
Complement factor D;	P03953	0.01	-1.09	-0.54	0.78	3.48	2.98
Tyrosine-protein kinase CSK;	P41241	0.01	0.11	0.06	0.07	0.31	0.24
Fumarate hydratase, mitochondrial;	P97807	0.01	-0.47	-0.23	0.35	1.54	0.89
Retinol-binding protein 4;	Q00724	0.01	0.31	0.16	0.21	0.93	0.68
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	0.01	0.60	0.30	0.41	1.83	1.36
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	0.01	-0.20	-0.09	0.15	0.68	0.45
Interleukin-1 receptor accessory protein;	Q61730	0.01	-0.03	-0.01	0.03	0.14	0.10
Selenide, water dikinase 1;	Q8BH69	0.01	0.12	0.07	0.08	0.35	0.32
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	0.01	1.82	0.92	1.28	5.71	4.37
Sulfite oxidase, mitochondrial;	Q8R086	0.01	-0.69	-0.34	0.50	2.22	1.68
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	0.01	-0.12	-0.05	0.09	0.42	0.29
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	0.01	-1.79	-0.89	1.27	5.68	6.04
Peptidyl-prolyl cis-trans isomerase A;	P17742	0.01	0.44	0.23	0.30	1.36	0.87

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Ras-related protein Rab-11B;	P46638	0.01	0.50	0.26	0.34	1.52	1.13
Rab GDP dissociation inhibitor alpha;	P50396	0.01	0.28	0.14	0.18	0.82	0.63
60 kDa heat shock protein, mitochondrial;	P63038	0.01	1.14	0.58	0.79	3.55	3.16
PEST proteolytic signal-containing nuclear protein;	Q6P8I4	0.01	0.00	0.01	0.01	0.04	0.08
6-phosphogluconolactonase;	Q9CQ60	0.01	0.14	0.08	0.09	0.39	0.34
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	0.01	-2.47	-1.23	1.76	7.85	8.28
AMP deaminase 1;	Q3V1D3	0.01	0.11	0.06	0.07	0.31	0.26
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	0.01	-0.58	-0.28	0.42	1.87	1.35
Lipoma-preferred partner homolog;	Q8BFW7	0.01	0.70	0.36	0.48	2.15	1.67
Serine/threonine-protein phosphatase;	F7BX26	0.03	0.47	0.25	0.31	1.38	1.00
N-acetyl-D-glucosamine kinase;	Q9QZ08	0.03	0.71	0.37	0.48	2.16	1.71
Proteasome subunit beta type-1;	O09061	0.04	0.21	0.13	0.12	0.54	0.41
Thioredoxin;	P10639	0.04	0.15	0.10	0.08	0.34	0.42
Glutathione S-transferase A4;	P24472	0.04	-0.07	-0.02	0.08	0.37	0.22
Serine hydroxymethyltransferase, cytosolic;	P50431	0.04	1.69	0.87	1.16	5.19	4.51
Transcription elongation factor B polypeptide 2;	P62869	0.04	0.30	0.17	0.18	0.81	0.68
Eukaryotic translation initiation factor 4E;	P63073	0.04	0.41	0.23	0.26	1.16	0.96
Protein FAM63A;	Q76LS9	0.04	0.73	0.39	0.49	2.17	1.83
Isochorismatase domain-containing protein 1;	Q91V64	0.04	0.10	0.07	0.04	0.17	0.32
Cytosol aminopeptidase;	Q9CPY7	0.04	1.76	0.90	1.21	5.41	5.78
Coactosin-like protein;	Q9CQI6	0.04	-0.64	-0.30	0.49	2.17	1.46
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	0.04	-0.18	-0.07	0.16	0.72	0.46
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial;	O88986	0.04	0.62	0.33	0.41	1.83	1.48
Ubiquitin-conjugating enzyme E2 L3;	P68037	0.04	0.55	0.29	0.36	1.59	0.96
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	0.04	0.73	0.39	0.49	2.17	1.68
Puromycin-sensitive aminopeptidase;	Q11011	0.04	-0.20	-0.08	0.17	0.77	0.45
Peptidyl-prolyl cis-trans isomerase;	A2BGI8	0.04	-0.67	-0.31	0.50	2.24	1.61
Nuclear migration protein nudC;	O35685	0.04	2.06	1.05	1.43	6.38	6.98
WW domain-binding protein 11;	Q923D5	0.04	0.50	0.27	0.32	1.43	0.95
Extracellular superoxide dismutase [Cu-Zn];	O09164	0.06	-2.00	-0.97	1.45	6.49	4.25
Heterogeneous nuclear ribonucleoprotein A1;	P49312	0.06	0.08	0.07	0.02	0.09	0.32
CD166 antigen;	Q61490	0.06	0.60	0.33	0.38	1.70	1.55
Protein canopy homolog 4;	Q8BQ47	0.06	0.72	0.39	0.47	2.10	1.86
Presequence protease, mitochondrial;	Q8K411	0.06	0.55	0.30	0.35	1.54	1.16
Galectin-related protein A;	Q8VED9	0.06	0.33	0.20	0.20	0.87	0.86
MACRO domain-containing protein 1;	Q922B1	0.06	-0.79	-0.36	0.60	2.66	2.12
Ran-binding protein 3;	Q9CT10	0.06	0.86	0.46	0.56	2.52	2.18
Perilipin-3;	Q9DBG5	0.06	0.45	0.26	0.28	1.25	0.96

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E3 SUMO-protein ligase RanBP2;	Q9ERU9	0.06	1.02	0.54	0.68	3.04	2.82
CD2-associated protein;	Q9JLQ0	0.06	1.03	0.54	0.69	3.07	2.66
Cadherin-13;	Q9WTR5	0.06	-0.89	-0.42	0.67	2.99	2.42
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	0.06	-0.34	-0.14	0.28	1.25	0.85
Apolipoprotein A-II;	P09813	0.06	1.27	0.66	0.86	3.83	3.80
Triosephosphate isomerase;	P17751	0.06	-0.45	-0.20	0.36	1.61	1.17
Proliferating cell nuclear antigen;	P17918	0.06	1.28	0.67	0.86	3.85	3.75
Protein S100-A11;	P50543	0.06	-0.17	-0.06	0.16	0.71	0.50
Poly(rC)-binding protein 1;	P60335	0.06	1.41	0.73	0.96	4.27	4.26
Poly(rC)-binding protein 2;	Q61990	-0.11	1.41	0.65	1.07	4.77	4.35
Serine/threonine-protein kinase PAK 2;	Q8CIN4	0.06	0.92	0.49	0.61	2.72	2.40
Aldo-keto reductase family 1 member C18;	Q8K023	0.06	-0.30	-0.12	0.26	1.14	0.84
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	0.06	-0.42	-0.18	0.33	1.49	1.08
Uncharacterized protein;	F6ZFU0	0.06	0.51	0.28	0.32	1.42	1.31
Protein FAM114A2;	Q8VE88	0.06	1.23	0.64	0.83	3.69	2.71
C-type lectin domain family 11 member A;	O88200	0.07	-0.25	-0.09	0.23	1.02	0.78
Delta-aminolevulinic acid dehydratase;	P10518	0.07	0.40	0.24	0.23	1.04	1.03
Apolipoprotein C-III;	P33622	0.07	2.35	1.21	1.61	7.20	9.16
ADP-ribosylation factor 6;	P62331	0.07	0.78	0.43	0.50	2.25	2.13
Latexin;	P70202	0.07	0.63	0.35	0.40	1.77	1.69
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	0.07	0.55	0.31	0.34	1.50	1.02
Synemin;	Q70IV5	0.07	-0.38	-0.15	0.32	1.41	1.00
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	0.07	-2.64	-1.29	1.92	8.57	9.04
Thimet oligopeptidase;	Q8C1A5	0.07	0.04	0.06	0.02	0.09	0.34
Rho GDP-dissociation inhibitor 1;	Q99PT1	0.07	0.18	0.12	0.07	0.33	0.62
SUMO-activating enzyme subunit 1;	Q9R1T2	0.07	0.64	0.36	0.40	1.81	1.72
Ig gamma-2A chain C region, A allele;	P01863	0.07	-1.32	-0.63	0.98	4.39	4.16
Peroxiredoxin-5, mitochondrial;	P99029	0.07	-0.20	-0.07	0.19	0.86	0.69
Corticosteroid-binding globulin;	Q06770	0.07	-0.14	-0.03	0.15	0.65	0.55
Protein transport protein Sec31A;	Q3UPL0	0.07	0.50	0.28	0.30	1.34	1.11
Eukaryotic translation initiation factor 2A;	Q8BJW6	0.07	0.11	0.09	0.03	0.13	0.45
Actin-related protein 2/3 complex subunit 3;	Q9JM76	0.07	-0.58	-0.25	0.46	2.05	1.53
Troponin T, fast skeletal muscle;	Q9QZ47	0.07	-0.71	-0.32	0.55	2.47	1.75
Band 4.1-like protein 3;	Q9WV92	0.07	-0.56	-0.24	0.44	1.98	1.45
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	0.07	-0.84	-0.38	0.64	2.86	2.27
Glycogen synthase kinase-3 alpha;	Q2NL51	0.07	0.96	0.51	0.63	2.80	2.66

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Superoxide dismutase [Cu-Zn];	P08228	0.08	-0.74	-0.33	0.58	2.59	1.77
Stress-70 protein, mitochondrial;	P38647	0.08	0.23	0.16	0.10	0.45	0.79
V-type proton ATPase subunit B, brain isoform;	P62814	0.08	0.50	0.29	0.29	1.30	1.19
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	0.08	-0.42	-0.17	0.35	1.58	1.21
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	0.08	-0.36	-0.14	0.31	1.40	1.03
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	0.08	0.37	0.23	0.20	0.89	1.09
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	0.08	0.19	0.14	0.07	0.33	0.70
Elongation factor 1-gamma;	Q9D8N0	0.08	0.78	0.43	0.49	2.20	2.13
Valyl-tRNA synthetase;	Q9Z1Q9	0.08	0.96	0.52	0.62	2.77	2.75
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	0.08	-0.79	-0.35	0.62	2.75	2.29
Annexin A2;	P07356	0.08	-1.32	-0.62	0.99	4.44	3.61
Cofilin-1;	P18760	0.08	0.57	0.33	0.34	1.52	1.59
Beta-enolase;	P21550	0.08	-0.47	-0.20	0.39	1.76	1.36
Alpha-enolase;	P17182	-0.23	-0.03	-0.13	0.14	0.65	0.83
Enolase;	B0QZL1	-0.22	-1.09	-0.65	0.62	2.75	3.93
Procollagen C-endopeptidase enhancer 1;	Q61398	0.08	-0.76	-0.34	0.60	2.67	1.55
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	0.08	1.15	0.62	0.75	3.37	3.12
Septin-11;	Q8C1B7	0.08	-0.45	-0.19	0.38	1.70	1.30
Secernin-1;	Q9CZC8	0.08	-0.42	-0.17	0.35	1.58	1.21
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	0.08	0.44	0.26	0.25	1.14	1.26
RuvB-like 1;	P60122	0.08	1.01	0.55	0.66	2.94	2.33
Coronin-1B;	Q9WUM3	0.08	-0.23	-0.08	0.22	1.00	0.73
Glutathione peroxidase 1;	P11352	0.10	-0.25	-0.08	0.25	1.10	0.70
Alcohol dehydrogenase class-3;	P28474	0.10	-0.32	-0.11	0.30	1.33	1.08
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	0.10	0.24	0.17	0.10	0.45	0.89
N-acetylneuraminate lyase;	Q9DCJ9	0.10	-0.67	-0.28	0.54	2.42	1.91
Protein ETHE1, mitochondrial;	Q9DCM0	0.10	-0.03	0.03	0.09	0.40	0.45
Eukaryotic translation initiation factor 3 subunit G;	Q9Z1D1	0.10	1.33	0.71	0.87	3.88	4.27
Polyadenylate-binding protein 1;	P29341	0.10	0.55	0.32	0.32	1.41	1.56
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	0.10	0.59	0.34	0.34	1.54	1.53
Annexin A11;	P97384	0.10	-0.29	-0.09	0.27	1.21	0.79
Adiponectin;	Q60994	0.10	-0.92	-0.41	0.72	3.20	2.80
Sorcin;	Q6P069	0.10	0.35	0.22	0.17	0.78	0.98
Sulfatase-modifying factor 2;	Q8BPG6	0.10	0.07	0.08	0.02	0.09	0.58
Fermitin family homolog 2;	Q8CIB5	0.10	0.28	0.19	0.13	0.56	0.95
CAP-Gly domain-containing linker protein 1;	Q922J3	0.10	-0.76	-0.33	0.61	2.71	2.11
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	0.10	0.28	0.19	0.13	0.56	0.88

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Uncharacterized protein;	E9Q2P1	0.10	-1.09	-0.50	0.84	3.75	2.93
NK13; Serine (Or cysteine) peptidase inhibitor, clade B, member 6b; Serine (Or cysteine) peptidase inhibitor, clade B, member 6b, isoform CRA_a; Uncharacterized protein;	O08804	0.10	-1.00	-0.45	0.78	3.47	2.93
GDP-D-glucose phosphorylase C15orf58 homolog;	Q3TLS3	0.10	0.19	0.14	0.06	0.29	0.77
Copper transport protein ATOX1;	O08997	0.11	1.30	0.71	0.84	3.75	3.84
Malate dehydrogenase, mitochondrial;	P08249	0.11	-0.29	-0.09	0.28	1.25	0.99
Microtubule-associated protein 1B;	P14873	0.11	-0.42	-0.15	0.37	1.66	1.36
Serine/threonine-protein kinase WNK1;	P83741	0.11	0.11	0.11	0.00	0.00	0.67
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	0.11	1.25	0.68	0.81	3.60	3.90
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	0.11	-0.30	-0.10	0.29	1.31	1.12
GMP reductase 1;	Q9DCZ1	0.11	-0.12	0.00	0.16	0.73	0.76
Hexokinase-2;	O08528	0.11	-0.84	-0.36	0.67	2.99	1.77
Hexokinase-1;	P17710	0.33	0.24	0.29	0.07	0.30	1.96
Seryl-tRNA synthetase, cytoplasmic;	P26638	0.11	0.83	0.47	0.51	2.28	2.41
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	0.11	0.35	0.23	0.17	0.74	1.13
Exportin-2;	Q9ERK4	0.11	2.69	1.40	1.82	8.14	11.79
Serine/threonine-protein phosphatase 6 catalytic subunit;	Q9CQR6	0.11	0.36	0.23	0.17	0.77	1.24
Eukaryotic translation initiation factor 3 subunit E;	P60229	0.11	2.68	1.39	1.81	8.10	10.92
Methylosome protein 50;	Q99J09	0.11	0.67	0.39	0.39	1.76	1.92
Laminin subunit gamma-1;	P02468	0.14	-0.07	0.03	0.15	0.67	0.69
Lumican;	P51885	0.14	-0.64	-0.25	0.55	2.47	2.02
Microtubule-associated protein RP/EB family member 1;	Q61166	0.14	0.53	0.33	0.27	1.22	1.70
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	0.14	0.04	0.09	0.07	0.30	0.46
Cytochrome b-c1 complex subunit 7;	Q9D855	0.14	-1.84	-0.85	1.40	6.23	6.41
Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	0.14	-1.25	-0.56	0.98	4.39	3.68
Destrin;	Q9R0P5	0.14	-0.20	-0.03	0.24	1.07	0.90
Malate dehydrogenase, cytoplasmic;	P14152	0.14	-0.20	-0.03	0.24	1.07	0.97
Radixin;	P26043	0.14	0.04	0.09	0.07	0.30	0.64
Moesin;	P26041	0.20	-0.84	-0.32	0.73	3.28	2.76
Ezrin;	P26040	0.62	0.12	0.37	0.35	1.58	4.33
Caveolin-1;	P49817	0.14	-0.36	-0.11	0.35	1.57	1.23
Mitogen-activated protein kinase 1;	P63085	0.14	0.44	0.29	0.22	0.97	1.35
Galactose-1-phosphate uridylyltransferase;	Q03249	0.14	0.51	0.32	0.26	1.16	1.46
Collagen alpha-1(VI) chain;	Q04857	0.14	-0.92	-0.39	0.75	3.33	2.14
Vinculin;	Q64727	0.14	0.61	0.38	0.34	1.50	1.70
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	0.14	0.77	0.45	0.44	1.98	2.02
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	0.14	-0.36	-0.11	0.35	1.57	1.11

Protein	Uniprot	Fold change (log$_2$) of ASAPRatio replicate 1	Fold change (log$_2$) of ASAPRatio replicate 2	Average fold change (log$_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Glyoxalase domain-containing protein 4;	Q9CPV4	0.14	0.06	0.10	0.06	0.26	0.65
Biotinidase;	Q8CIF4	0.14	-0.30	-0.08	0.31	1.40	1.20
Dehydrogenase/reductase SDR family member 7;	Q9CXR1	0.14	-0.30	-0.08	0.31	1.40	1.14
Aspartate aminotransferase, mitochondrial;	P05202	0.15	-0.45	-0.15	0.43	1.91	1.50
Adenylosuccinate synthetase isozyme 1;	P28650	0.15	-0.76	-0.31	0.64	2.88	2.30
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	0.15	1.02	0.59	0.62	2.75	3.37
Phospholipase B-like 1;	Q8VCI0	0.15	-1.06	-0.45	0.86	3.82	3.43
Ester hydrolase C11orf54 homolog;	Q91V76	0.15	-0.20	-0.03	0.25	1.11	0.73
Aconitate hydratase, mitochondrial;	Q99KI0	0.15	-0.52	-0.18	0.47	2.10	1.76
Serine/threonine-protein phosphatase 2A activator;	P58389	0.15	-0.29	-0.07	0.31	1.38	1.08
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	0.15	0.11	0.13	0.03	0.13	0.86
Coronin-7;	Q9D2V7	0.15	0.33	0.24	0.13	0.57	1.14
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial;	P53395	0.15	0.08	0.12	0.05	0.21	0.84
AH receptor-interacting protein;	O08915	0.16	1.40	0.78	0.87	3.89	4.81
Ferritin heavy chain;	P09528	0.16	-1.25	-0.54	1.00	4.47	4.26
Galectin-3;	P16110	0.16	0.45	0.31	0.21	0.92	1.53
Cofilin-2;	P45591	0.16	-0.12	0.02	0.20	0.89	0.92
Adenylosuccinate synthetase isozyme 2;	P46664	0.16	0.29	0.23	0.09	0.39	1.25
Carbonyl reductase [NADPH] 1;	P48758	0.16	0.39	0.28	0.16	0.72	1.51
Myotrophin;	P62774	0.16	0.21	0.19	0.04	0.16	1.19
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	0.16	0.49	0.32	0.23	1.02	1.56
Acyl-coenzyme A thioesterase 1;	O55137	0.16	0.48	0.32	0.22	0.98	1.59
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	-0.25	-0.52	-0.38	0.19	0.83	1.88
Myelin protein P0;	P27573	0.16	-0.52	-0.18	0.48	2.14	1.65
Cell division control protein 42 homolog;	P60766	0.16	0.59	0.37	0.30	1.33	1.74
Ras-related C3 botulinum toxin substrate 1;	P63001	-0.81	0.28	-0.27	0.77	3.43	5.02
Septin-9;	Q80UG5	0.16	-1.36	-0.60	1.08	4.80	3.91
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	0.16	-0.03	0.07	0.14	0.61	0.70
Actin-related protein 3;	Q99JY9	0.16	-0.52	-0.18	0.48	2.14	1.71
Proteasome subunit alpha type-5;	Q9Z2U1	0.16	0.58	0.37	0.29	1.30	1.84
Uncharacterized protein;	F6RPJ9	0.16	0.51	0.33	0.24	1.08	1.56
Histone-binding protein RBBP4;	Q60972	0.16	1.28	0.72	0.79	3.51	3.87
Ig alpha chain C region;	P01878	0.18	-0.20	-0.01	0.27	1.19	1.16
Transthyretin;	P07309	0.18	0.12	0.15	0.04	0.16	1.08
Uroporphyrinogen decarboxylase;	P70697	0.18	0.50	0.34	0.23	1.01	1.88
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	0.18	1.26	0.72	0.77	3.43	4.04

Protein	Uniprot	Fold change (log$_2$) of ASAPRatio replicate 1	Fold change (log$_2$) of ASAPRatio replicate 2	Average fold change (log$_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	0.18	-0.15	0.01	0.23	1.04	1.01
Calcium/calmodulin-dependent protein kinase type II subunit alpha;	P11798	0.18	-0.89	-0.36	0.75	3.36	3.07
ADP-ribosylation factor 3;	P61205	0.18	0.30	0.24	0.09	0.39	1.30
ADP-ribosylation factor 5;	P84084	0.06	2.36	1.21	1.63	7.26	9.42
Translationally-controlled tumor protein;	P63028	0.18	0.21	0.20	0.03	0.12	1.22
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	0.18	0.86	0.52	0.48	2.15	2.77
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	0.18	-0.43	-0.13	0.43	1.93	1.52
Epoxide hydrolase 1;	Q9D379	0.18	-0.62	-0.22	0.56	2.52	2.23
Apolipoprotein A-IV;	P06728	0.19	1.01	0.60	0.58	2.58	3.09
Galectin-1;	P16045	0.19	-0.04	0.07	0.16	0.74	0.91
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	0.19	-0.22	-0.01	0.29	1.28	1.28
28S ribosomal protein S36, mitochondrial;	Q9CQX8	0.19	1.15	0.67	0.68	3.04	4.02
Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform;	P07934	0.19	1.33	0.76	0.81	3.60	4.66
Fatty acid-binding protein, epidermal;	Q05816	0.19	1.52	0.86	0.94	4.20	5.21
Adapter molecule crk;	Q64010	0.19	0.19	0.19	0.00	0.00	1.30
Carboxylesterase 3;	Q8VCT4	0.19	-1.18	-0.50	0.97	4.33	3.36
Liver carboxylesterase N;	P23953	-0.07	-0.32	-0.20	0.18	0.78	0.94
Uncharacterized protein;	D3Z5G7	-0.15	-0.42	-0.28	0.19	0.83	1.58
Enoyl-CoA hydratase domain-containing protein 1;	Q9D9V3	0.19	0.61	0.40	0.30	1.34	1.19
ATP synthase subunit O, mitochondrial;	Q9DB20	0.19	-1.89	-0.85	1.47	6.56	6.65
TIP41-like protein;	Q8BH58	0.19	0.11	0.15	0.06	0.25	1.05
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	0.19	1.52	0.86	0.94	4.20	5.70
S-phase kinase-associated protein 1;	Q9WTX5	0.19	-0.76	-0.29	0.67	3.00	1.96
Crk-like protein;	P47941	0.20	0.10	0.15	0.07	0.33	1.19
40S ribosomal protein S14;	P62264	0.20	3.61	1.91	2.41	10.75	19.70
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	0.20	0.38	0.29	0.13	0.56	1.76
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	0.20	0.19	0.20	0.01	0.04	1.30
UMP-CMP kinase;	Q9DBP5	0.20	0.26	0.23	0.04	0.19	1.15
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	0.20	0.56	0.38	0.25	1.12	2.25
Heat shock protein HSP 90-beta;	P11499	0.20	1.32	0.76	0.79	3.54	3.41
Heat shock protein HSP 90-alpha;	P07901	0.23	1.52	0.87	0.91	4.07	4.69
Endoplasmin;	P08113	0.10	0.81	0.45	0.50	2.24	1.29
BTB/POZ domain-containing protein KCTD12;	Q6WVG3	0.20	0.08	0.14	0.08	0.37	0.64
Uncharacterized protein;	E9PYJ9	0.20	-0.34	-0.07	0.38	1.71	1.21
Uncharacterized protein;	E9Q0S6	0.20	-0.49	-0.15	0.49	2.20	1.70
40S ribosomal protein S12;	Q6ZWZ6	0.20	0.11	0.16	0.06	0.29	0.91

Protein	Uniprot	Fold change (log$_2$) of ASAPRatio replicate 1	Fold change (log$_2$) of ASAPRatio replicate 2	Average fold change (log$_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Complement component 1, q subcomponent binding protein; Complement component 1, q subcomponent binding protein, isoform CRA_b; Uncharacterized protein; p32-RACK;	Q8R5L1	0.20	0.47	0.33	0.19	0.83	1.92
Annexin A4;	P97429	0.21	-0.23	-0.01	0.32	1.41	1.39
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	0.23	-0.36	-0.07	0.41	1.85	1.51
Haptoglobin;	Q61646	0.23	0.82	0.52	0.42	1.86	3.01
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	0.23	-2.84	-1.31	2.17	9.67	6.13
Phosphotriesterase-related protein;	Q60866	0.23	-0.12	0.05	0.25	1.10	0.85
Programmed cell death 6-interacting protein;	Q9WU78	0.23	1.18	0.71	0.68	3.02	3.07
Calpain-1 catalytic subunit;	O35350	0.24	0.29	0.26	0.03	0.15	1.67
Proteasome subunit beta type-8;	P28063	0.24	-0.52	-0.14	0.53	2.38	2.09
Lysophosphatidic acid phosphatase type 6;	Q8BP40	0.24	0.07	0.15	0.12	0.53	1.21
Asporin;	Q99MQ4	0.24	-1.00	-0.38	0.88	3.91	3.24
ADP/ATP translocase 1;	P48962	0.24	-2.64	-1.20	2.04	9.10	11.62
ADP/ATP translocase 2;	P51881	0.20	-0.97	-0.38	0.83	3.70	3.54
Heterogeneous nuclear ribonucleoprotein K;	P61979	0.24	0.75	0.49	0.36	1.61	2.75
Carboxymethylenebutenolidase homolog;	Q8R1G2	0.24	-0.94	-0.35	0.84	3.73	3.56
TAR DNA-binding protein 43;	Q921F2	0.24	0.48	0.36	0.17	0.75	1.32
Calumenin;	O35887	0.24	0.10	0.17	0.10	0.45	1.37
Cytochrome c oxidase subunit 2;	P00405	0.25	-2.06	-0.90	1.63	7.29	8.63
Programmed cell death protein 6;	P12815	0.25	1.82	1.04	1.11	4.95	5.18
Protein-glutamine gamma-glutamyltransferase 2;	P21981	0.25	-0.25	0.00	0.36	1.59	1.18
Costars family protein C6orf115 homolog;	Q4KML4	0.25	0.54	0.39	0.20	0.90	2.09
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	0.25	-0.27	-0.01	0.37	1.64	1.36
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	0.25	-0.07	0.09	0.23	1.03	0.94
Elongation factor Tu, mitochondrial;	Q8BFR5	0.25	0.11	0.18	0.10	0.44	1.45
Alanine aminotransferase 1;	Q8QZR5	0.25	-0.42	-0.08	0.47	2.10	1.88
Microfibril-associated glycoprotein 4;	Q9D1H9	0.25	-1.29	-0.52	1.09	4.85	4.38
Ribosome-recycling factor, mitochondrial;	Q9D6S7	0.25	-0.42	-0.08	0.47	2.10	2.06
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	0.25	0.86	0.55	0.43	1.91	3.38
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	0.25	0.33	0.29	0.06	0.26	1.88
Cathepsin L1;	P06797	0.25	0.85	0.55	0.42	1.88	3.03
14-3-3 protein zeta/delta;	P63101	0.25	1.01	0.63	0.53	2.39	3.50
Spermine synthase;	P97355	0.25	-0.84	-0.29	0.77	3.43	3.08
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	0.25	-0.15	0.05	0.28	1.27	1.22
ATP synthase subunit g, mitochondrial;	Q9CPQ8	0.25	-2.00	-0.87	1.59	7.11	8.62
Proteasome subunit alpha type-6;	Q9QUM9	0.25	0.60	0.42	0.24	1.09	2.47

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Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	0.25	0.23	0.24	0.02	0.08	1.73
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	0.25	2.28	1.26	1.43	6.40	9.85
Arylsulfatase B;	P50429	0.26	-0.11	0.08	0.26	1.16	0.64
Acylphosphatase-1;	P56376	0.26	-0.52	-0.13	0.55	2.46	1.81
Synaptobrevin homolog YKT6;	Q9CQW1	0.26	2.02	1.14	1.24	5.54	7.43
Chloride intracellular channel protein 4;	Q9QYB1	0.26	0.84	0.55	0.41	1.82	3.24
Calpain-2 catalytic subunit;	O08529	0.26	1.33	0.80	0.75	3.36	4.92
Talin-1;	P26039	0.26	1.14	0.70	0.62	2.78	3.78
Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	0.26	0.82	0.54	0.39	1.75	3.21
Early endosome antigen 1;	Q8BL66	0.26	0.12	0.19	0.10	0.44	1.03
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	0.26	-0.43	-0.09	0.49	2.20	1.40
26S proteasome non-ATPase regulatory subunit 4;	O35226	0.28	0.95	0.61	0.48	2.13	3.82
Sorting nexin-6;	Q6P8X1	0.28	0.52	0.40	0.17	0.76	1.68
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	0.28	0.44	0.36	0.12	0.53	2.00
Fibrinogen beta chain;	Q8K0E8	0.28	-0.22	0.03	0.35	1.56	1.88
Reticulon-4;	Q99P72	0.28	0.55	0.41	0.19	0.86	2.34
SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	0.28	-0.12	0.08	0.28	1.25	1.56
Band 4.1-like protein 2;	O70318	0.28	0.04	0.16	0.16	0.73	1.32
Glia maturation factor gamma;	Q9ERL7	-0.01	-1.06	-0.54	0.74	3.30	2.32
SPRY domain-containing protein 4;	Q91WK1	0.28	-0.32	-0.02	0.42	1.88	2.09
Uridine diphosphate glucose pyrophosphatase;	Q9D142	0.28	0.33	0.30	0.04	0.18	2.06
Uncharacterized protein;	E9Q8T1	0.29	-0.20	0.04	0.35	1.54	1.44
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform;	P62715	0.30	0.75	0.52	0.32	1.42	3.16
Cytochrome c, somatic;	P62897	0.30	-0.14	0.08	0.31	1.37	1.73
Eukaryotic translation initiation factor 5A-1;	P63242	0.30	-0.22	0.04	0.37	1.63	1.82
Annexin A7;	Q07076	0.30	0.60	0.45	0.21	0.93	2.59
Myosin light chain kinase, smooth muscle;	Q6PDN3	0.30	0.08	0.19	0.15	0.68	0.83
Fibrinogen gamma chain;	Q8VCM7	0.30	-0.52	-0.11	0.58	2.57	2.35
Copper homeostasis protein cutC homolog;	Q9D8X1	0.30	-0.84	-0.27	0.80	3.59	3.27
Voltage-dependent anion-selective channel protein 2;	Q60930	0.30	-1.15	-0.43	1.03	4.58	4.37
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	0.30	1.29	0.79	0.70	3.12	3.64
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	0.30	1.38	0.84	0.77	3.43	4.03
Plastin-3;	Q99K51	0.30	0.11	0.21	0.13	0.59	1.36
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	0.30	0.68	0.49	0.27	1.20	2.49
Toll-interacting protein;	Q9QZ06	0.30	0.03	0.16	0.19	0.85	1.55
NEDD8-conjugating enzyme Ubc12;	P61082	0.30	1.80	1.05	1.06	4.74	6.95
Large proline-rich protein BAG6;	Q9Z1R2	0.30	0.93	0.61	0.44	1.98	3.74

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Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	0.31	1.12	0.71	0.57	2.55	3.96
Ubiquitin-fold modifier 1;	P61961	0.31	0.59	0.45	0.19	0.87	2.87
Sarcalumenin;	Q7TQ48	0.31	0.50	0.40	0.13	0.59	2.38
Cold shock domain-containing protein E1;	Q91W50	0.31	1.52	0.92	0.86	3.82	6.29
Ribonuclease T2;	Q9CQ01	0.31	1.85	1.08	1.09	4.86	7.64
Glutaredoxin-3;	Q9CQM9	0.31	1.87	1.09	1.10	4.93	7.71
ATP synthase subunit d, mitochondrial;	Q9DCX2	0.31	-0.97	-0.33	0.91	4.04	3.72
Glutathione S-transferase omega-1;	O09131	0.31	0.32	0.32	0.01	0.04	1.60
Eukaryotic initiation factor 4A-II;	P10630	0.31	0.39	0.35	0.06	0.25	2.22
Eukaryotic initiation factor 4A-I;	P60843	0.39	1.70	1.04	0.92	4.12	6.76
Voltage-dependent anion-selective channel protein 1;	Q60932	0.31	-1.69	-0.69	1.41	6.31	5.06
Transportin-3;	Q6P2B1	0.31	1.75	1.03	1.02	4.56	6.65
Adenylate kinase 2, mitochondrial;	Q9WTP6	0.31	0.76	0.53	0.32	1.41	2.83
Ras GTPase-activating protein-binding protein 1;	P97855	0.31	0.41	0.36	0.07	0.32	2.40
RING finger protein 114;	Q9ET26	0.31	2.93	1.62	1.86	8.28	14.77
T-complex protein 1 subunit zeta;	P80317	0.31	1.98	1.15	1.18	5.28	5.79
Small ubiquitin-related modifier 2;	P61957	0.31	1.99	1.15	1.19	5.31	8.74
Cystatin-B;	Q62426	0.31	1.36	0.83	0.74	3.30	5.46
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	0.32	-1.74	-0.71	1.46	6.50	6.30
Creatine kinase S-type, mitochondrial;	Q6P8J7	0.32	-2.84	-1.26	2.23	9.97	6.23
Troponin C, skeletal muscle;	P20801	0.32	-3.32	-1.50	2.58	11.50	12.50
Elongation factor G, mitochondrial;	Q8K0D5	0.32	0.56	0.44	0.17	0.74	2.01
Gamma-butyrobetaine dioxygenase;	Q924Y0	0.32	-1.32	-0.50	1.16	5.19	5.11
COP9 signalosome complex subunit 4;	O88544	0.32	1.46	0.89	0.80	3.59	4.95
PDZ and LIM domain protein 3;	O70209	0.33	0.16	0.25	0.12	0.54	1.67
Caspase-14;	O89094	0.33	2.21	1.27	1.32	5.91	8.42
Superoxide dismutase [Mn], mitochondrial;	P09671	0.33	-0.03	0.15	0.26	1.14	1.33
GDP-L-fucose synthase;	P23591	0.33	0.19	0.26	0.10	0.45	1.73
Cysteine and glycine-rich protein 1;	P97315	0.33	-0.45	-0.06	0.56	2.48	2.20
N-acetylglucosamine-6-sulfatase;	Q8BFR4	0.33	0.30	0.32	0.02	0.11	1.89
Thioredoxin-like protein 1;	Q8CDN6	0.33	0.78	0.56	0.32	1.42	3.62
Acylamino-acid-releasing enzyme;	Q8R146	0.33	1.04	0.69	0.50	2.24	3.75
5-hydroxyisourate hydrolase;	Q9CRB3	0.33	0.30	0.32	0.02	0.11	2.36
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	0.33	-0.07	0.13	0.29	1.28	1.25
ADP-sugar pyrophosphatase;	Q9JKX6	0.33	0.26	0.30	0.05	0.22	1.86
General vesicular transport factor p115;	Q9Z1Z0	0.33	2.47	1.40	1.51	6.75	10.72
Plasminogen activator inhibitor 2, macrophage;	P12388	0.33	-0.64	-0.16	0.69	3.08	2.86
Mitogen-activated protein kinase 14;	P47811	0.33	0.62	0.48	0.21	0.92	2.96

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Protein Niban;	Q3UW53	0.33	1.23	0.78	0.64	2.84	4.36
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	0.33	-0.40	-0.03	0.52	2.30	2.25
Aldehyde dehydrogenase;	E9Q3E1	0.33	0.63	0.48	0.21	0.94	2.73
Coatomer subunit beta;	Q9JIF7	0.33	1.86	1.10	1.08	4.82	7.10
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	0.33	0.61	0.47	0.20	0.89	2.81
COP9 signalosome complex subunit 5;	O35864	0.35	0.44	0.39	0.07	0.31	1.51
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	0.35	0.44	0.39	0.07	0.31	2.81
V-type proton ATPase subunit H;	Q8BVE3	0.35	1.06	0.70	0.51	2.27	4.37
Uncharacterized protein;	E9Q8E3	0.35	-1.89	-0.77	1.58	7.05	6.01
Annexin A8;	O35640	0.35	-0.34	0.00	0.48	2.16	2.52
Apolipoprotein E;	P08226	0.35	1.82	1.08	1.04	4.66	6.82
Ras-related protein Rab-5C;	P35278	0.35	1.19	0.77	0.60	2.66	4.59
UV excision repair protein RAD23 homolog B;	P54728	0.35	0.70	0.52	0.25	1.11	2.67
Tubulin beta-5 chain;	P99024	0.35	2.90	1.62	1.81	8.06	14.83
Tubulin beta-2A chain;	Q7TMM9	0.16	1.92	1.04	1.24	5.55	5.69
Uncharacterized protein;	E9PWQ3	0.35	-0.32	0.01	0.47	2.11	1.08
Target of Myb protein 1;	O88746	0.36	0.16	0.26	0.14	0.61	0.89
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	0.36	0.69	0.52	0.23	1.04	3.23
Serpin B5;	P70124	0.36	0.71	0.54	0.25	1.13	3.42
Mimecan;	Q62000	0.36	0.45	0.41	0.07	0.31	2.13
Versican core protein;	Q62059	0.36	0.20	0.28	0.11	0.49	2.22
Protein arginine N-methyltransferase 5;	Q8CIG8	0.36	1.30	0.83	0.67	2.98	4.95
Acyl-coenzyme A thioesterase 13;	Q9CQR4	0.36	0.14	0.25	0.15	0.69	2.32
Proliferation-associated protein 2G4;	P50580	0.36	-0.62	-0.13	0.69	3.08	2.83
ATP-binding cassette sub-family E member 1;	P61222	0.36	0.60	0.48	0.17	0.75	2.84
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	0.38	1.37	0.87	0.70	3.12	4.75
Ly6/PLAUR domain-containing protein 5;	Q9D7Z7	0.38	0.90	0.64	0.36	1.63	3.83
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	0.38	-0.12	0.13	0.35	1.58	2.05
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	0.38	0.15	0.27	0.16	0.72	1.93
Transitional endoplasmic reticulum ATPase;	Q01853	0.39	1.66	1.03	0.90	4.02	6.57
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	0.39	0.97	0.68	0.41	1.83	3.75
3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	0.39	0.39	0.39	0.00	0.00	2.98
Carbonic anhydrase 13;	Q9D6N1	0.39	-0.15	0.12	0.38	1.71	2.03
Proteasomal ubiquitin receptor ADRM1;	Q9JKV1	0.39	1.78	1.08	0.98	4.38	5.39
Annexin A1;	P10107	0.39	0.00	0.20	0.28	1.23	2.17
Protein RCC2;	Q8BK67	0.39	-1.00	-0.31	0.98	4.39	3.25
Phosphoserine aminotransferase;	Q99K85	0.39	-0.01	0.19	0.29	1.28	1.96

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1;	Q62077	0.39	1.29	0.84	0.63	2.83	5.89
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	0.40	-1.79	-0.69	1.55	6.90	7.67
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	0.40	1.50	0.95	0.78	3.47	6.06
NSFL1 cofactor p47;	Q9CZ44	0.40	0.71	0.55	0.21	0.96	3.70
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	0.40	-0.07	0.16	0.34	1.50	2.05
Inactive tyrosine-protein kinase 7;	Q8BKG3	0.40	1.64	1.02	0.87	3.90	6.97
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial;	P50136	0.41	0.45	0.43	0.03	0.14	2.97
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	0.41	0.25	0.33	0.11	0.51	2.75
Echinoderm microtubule-associated protein-like 1;	Q05BC3	0.41	-1.03	-0.31	1.02	4.55	3.37
Retroviral-like aspartic protease 1;	Q09PK2	0.41	1.10	0.76	0.49	2.19	4.94
Drebrin-like protein;	Q62418	0.41	0.33	0.37	0.06	0.25	2.28
Farnesyl pyrophosphate synthase;	Q920E5	0.41	0.92	0.66	0.36	1.60	4.46
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	0.41	1.25	0.83	0.59	2.63	5.81
Integrin beta-4;	A2A863	0.41	-0.84	-0.21	0.88	3.94	3.89
Glutamine synthetase;	P15105	0.41	-1.84	-0.71	1.59	7.10	6.09
Transgelin;	P37804	0.42	0.24	0.33	0.13	0.58	2.75
Acylphosphatase-2;	P56375	0.42	-0.20	0.11	0.44	1.97	2.53
14-3-3 protein theta;	P68254	0.42	1.12	0.77	0.49	2.20	5.23
Platelet glycoprotein 4;	Q08857	0.42	-0.62	-0.10	0.74	3.29	3.60
Zinc transporter SLC39A7;	Q31125	0.42	-0.64	-0.11	0.75	3.37	3.89
Perilipin-1;	Q8CGN5	0.42	0.75	0.59	0.23	1.03	2.49
Acetoacetyl-CoA synthetase;	Q9D2R0	0.42	0.90	0.66	0.34	1.52	3.59
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	0.42	0.16	0.29	0.18	0.82	2.51
Protein diaphanous homolog 1;	O08808	0.42	1.48	0.95	0.74	3.32	5.10
Lambda-crystallin homolog;	Q99KP3	0.42	-0.56	-0.07	0.69	3.09	2.89
Alpha-galactosidase A;	P51569	0.44	1.01	0.73	0.40	1.78	5.00
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	0.44	0.04	0.24	0.28	1.27	2.51
CD109 antigen;	Q8R422	0.44	-0.01	0.22	0.32	1.45	2.59
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	0.44	-1.06	-0.31	1.06	4.74	5.03
SUMO-activating enzyme subunit 2;	Q9Z1F9	0.44	1.99	1.22	1.09	4.87	8.22
Protein S100-A4;	P07091	0.44	-0.67	-0.11	0.79	3.51	3.89
Actin-related protein 2/3 complex subunit 4;	P59999	0.44	-0.32	0.06	0.54	2.42	2.86
Proteasome subunit alpha type-4;	Q9R1P0	0.44	0.32	0.38	0.09	0.39	2.31
Uncharacterized protein;	E9QJY4	0.44	0.15	0.30	0.21	0.92	2.74
E3 ubiquitin-protein ligase NEDD4;	P46935	0.44	1.35	0.89	0.64	2.84	4.04
Ig heavy chain V region MOPC 104E;	P01756	0.45	-0.97	-0.26	1.01	4.50	5.25
Coatomer subunit gamma;	Q9QZE5	0.45	1.60	1.03	0.81	3.61	6.63

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
Secernin-2;	Q8VCA8	0.45	-0.92	-0.23	0.97	4.32	3.04
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	0.45	-0.92	-0.23	0.97	4.32	3.95
Protein arginine N-methyltransferase 1;	Q9JIF0	0.45	0.55	0.50	0.07	0.29	3.82
Proteasome subunit alpha type-7;	Q9Z2U0	0.45	0.86	0.66	0.28	1.27	4.86
Proteasome subunit beta type-7;	P70195	0.47	0.43	0.45	0.02	0.10	3.26
Vasodilator-stimulated phosphoprotein;	P70460	0.47	0.23	0.35	0.17	0.75	2.79
Voltage-dependent anion-selective channel protein 3;	Q60931	0.47	-2.00	-0.77	1.74	7.78	9.13
Calponin-3;	Q9DAW9	0.47	1.85	1.16	0.98	4.37	7.28
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	0.47	1.08	0.77	0.44	1.95	3.75
Acyl-CoA dehydrogenase family member 9, mitochondrial;	Q8JZN5	0.47	0.54	0.50	0.05	0.22	3.27
Uncharacterized protein;	E9Q7G0	0.47	1.27	0.87	0.57	2.54	3.70
Carbohydrate kinase domain-containing protein;	Q9CZ42	0.47	-0.27	0.10	0.52	2.32	1.78
Ig kappa chain C region;	P01837	0.48	-0.97	-0.25	1.02	4.56	5.04
Methylmalonyl-CoA mutase, mitochondrial;	P16332	0.48	0.74	0.61	0.19	0.84	2.95
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	0.48	0.61	0.54	0.10	0.44	3.10
Calmodulin-4;	Q9JM83	0.48	0.33	0.40	0.10	0.45	3.55
Cathepsin Z;	Q9WUU7	0.48	0.29	0.38	0.13	0.59	3.33
Gamma-synuclein;	Q9Z0F7	0.48	0.59	0.53	0.08	0.35	4.23
Uncharacterized protein;	Q9CX86	0.48	0.39	0.43	0.06	0.27	3.73
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	0.48	1.89	1.18	1.00	4.47	8.90
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	0.48	0.79	0.63	0.22	1.00	4.80
Dual specificity protein phosphatase 3;	Q9D7X3	0.49	0.60	0.54	0.08	0.35	4.16
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	0.49	-0.42	0.04	0.64	2.84	3.54
Maleylacetoacetate isomerase;	Q9WVL0	0.49	-0.09	0.20	0.41	1.81	2.47
Glycogen phosphorylase, muscle form;	Q9WUB3	0.49	-0.32	0.08	0.57	2.55	3.04
Glycogen phosphorylase, brain form;	Q8CI94	0.07	0.11	0.09	0.03	0.13	0.46
Glycogen phosphorylase, liver form;	Q9ET01	-0.15	-0.64	-0.40	0.35	1.55	2.18
T-complex protein 1 subunit eta;	P80313	0.50	2.18	1.34	1.19	5.30	8.01
DCC-interacting protein 13-alpha;	Q8K3H0	0.50	1.51	1.00	0.71	3.19	7.76
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	0.50	-0.07	0.21	0.40	1.80	2.30
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	0.50	0.60	0.55	0.07	0.31	2.90
Titin;	A2ASS6	0.50	-1.22	-0.36	1.21	5.41	3.47
Monoglyceride lipase;	O35678	0.50	0.49	0.49	0.01	0.03	3.17
Tubulin alpha-4A chain;	P68368	0.55	2.03	1.29	1.05	4.69	7.84
Acyl-CoA-binding protein;	P31786	0.50	1.18	0.84	0.48	2.15	6.25
Coronin-1C;	Q9WUM4	0.50	-0.89	-0.20	0.98	4.37	5.33
Proteasome subunit alpha type-2;	P49722	0.52	0.68	0.60	0.11	0.51	4.25
5'-nucleotidase;	Q61503	0.52	0.00	0.26	0.36	1.63	0.85

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Filamin-B;	Q80X90	0.52	0.82	0.67	0.22	0.97	4.12
Heme-binding protein 1;	Q9R257	0.52	0.12	0.32	0.28	1.24	3.31
Coagulation factor XIII A chain;	Q8BH61	0.52	-0.27	0.12	0.56	2.48	3.29
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	0.53	0.45	0.49	0.05	0.23	3.99
Perilipin-2;	P43883	0.53	-0.22	0.15	0.53	2.35	1.59
26S proteasome non-ATPase regulatory subunit 7;	P26516	0.54	1.60	1.07	0.76	3.37	6.28
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial;	Q9CXZ1	0.54	-1.52	-0.49	1.45	6.47	5.29
Cytosolic 5'-nucleotidase 3;	Q9D020	0.54	0.43	0.48	0.07	0.33	3.62
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	0.54	1.00	0.77	0.33	1.46	4.92
Proteasome subunit alpha type-1;	Q9R1P4	0.54	0.99	0.76	0.32	1.42	3.32
Twinfilin-2;	Q9Z0P5	0.54	-0.06	0.24	0.42	1.88	3.40
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	0.54	0.12	0.33	0.29	1.30	1.21
Lupus La protein homolog;	P32067	0.54	0.76	0.65	0.16	0.70	3.23
5-oxoprolinase;	Q8K010	0.54	1.67	1.10	0.80	3.58	7.25
14-3-3 protein beta/alpha;	Q9CQV8	0.54	1.01	0.77	0.33	1.49	5.77
14-3-3 protein eta;	P68510	0.60	1.02	0.81	0.29	1.32	6.56
Dysferlin;	Q9ESD7	0.55	0.48	0.51	0.05	0.22	4.59
26S protease regulatory subunit 6A;	O88685	0.55	1.09	0.82	0.39	1.72	4.12
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	0.55	0.54	0.54	0.01	0.03	2.64
Proteasome subunit beta type-3;	Q9R1P1	0.55	0.50	0.52	0.04	0.16	3.97
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	0.55	-0.69	-0.07	0.87	3.90	4.76
Carbonic anhydrase 2;	P00920	0.56	0.84	0.70	0.20	0.90	3.35
6-phosphofructokinase, liver type;	P12382	0.56	1.47	1.01	0.64	2.87	5.12
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	0.56	1.10	0.83	0.39	1.73	5.91
COP9 signalosome complex subunit 8;	Q8VBV7	0.56	1.02	0.79	0.33	1.47	3.69
2-aminoethanethiol dioxygenase;	Q6PDY2	0.56	0.20	0.38	0.25	1.12	3.68
U6 snRNA-associated Sm-like protein LSm2;	O35900	0.57	0.07	0.32	0.35	1.57	2.95
Niban-like protein 1;	Q8R1F1	0.57	0.74	0.65	0.12	0.55	4.35
Ig kappa chain V-V region L6;	P01638	0.57	-1.09	-0.26	1.17	5.22	6.32
Galectin-3-binding protein;	Q07797	0.57	-0.11	0.23	0.47	2.12	1.50
Ig gamma-2B chain C region;	P01867	0.59	-0.42	0.09	0.71	3.16	4.39
Thiamin pyrophosphokinase 1;	Q9R0M5	0.59	0.15	0.37	0.31	1.37	3.71
14-3-3 protein gamma;	P61982	0.60	0.77	0.68	0.13	0.57	5.71
Importin subunit beta-1;	P70168	0.60	2.34	1.47	1.23	5.51	8.92
V-type proton ATPase subunit E 1;	P50518	0.60	-0.45	0.07	0.74	3.31	4.68
Cytochrome P450 2F2;	P33267	0.60	-1.36	-0.38	1.38	6.17	7.43
Ig gamma-1 chain C region secreted form;	P01868	0.60	-0.71	-0.05	0.93	4.16	5.89
Peroxisomal multifunctional enzyme type 2;	P51660	0.60	-0.07	0.27	0.48	2.14	4.01

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MAP kinase-activated protein kinase 3;	Q3UMW7	0.60	0.47	0.53	0.10	0.44	4.90
Membrane primary amine oxidase;	O70423	0.60	-0.86	-0.13	1.04	4.63	4.84
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	0.60	0.90	0.75	0.21	0.92	5.64
Multifunctional protein ADE2;	Q9DCL9	0.60	1.26	0.93	0.46	2.06	5.25
Mitogen-activated protein kinase 12;	O08911	0.61	0.12	0.37	0.35	1.55	3.73
Sulfotransferase family cytosolic 2B member 1;	O35400	0.61	1.80	1.21	0.84	3.75	7.55
Pyruvate carboxylase, mitochondrial;	Q05920	0.61	0.15	0.38	0.33	1.46	3.41
Tumor protein D54;	Q9CYZ2	0.61	0.40	0.51	0.15	0.67	4.64
Diphosphomevalonate decarboxylase;	Q99JF5	0.62	0.61	0.62	0.01	0.03	5.53
Coronin-1A;	O89053	0.62	-0.76	-0.07	0.98	4.37	5.89
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	0.62	-0.84	-0.11	1.03	4.61	5.97
ATP-citrate synthase;	Q91V92	0.62	1.25	0.94	0.44	1.98	6.60
T-complex protein 1 subunit alpha;	P11983	0.62	2.97	1.80	1.66	7.42	17.08
Non-specific lipid-transfer protein;	P32020	0.64	0.81	0.72	0.12	0.52	5.48
Tripeptidyl-peptidase 1;	O89023	0.65	0.82	0.74	0.12	0.55	4.19
Decorin;	P28654	0.65	-1.09	-0.22	1.23	5.49	7.02
Hormone-sensitive lipase;	P54310	0.65	1.18	0.92	0.38	1.68	6.88
Gamma-glutamylcyclotransferase;	Q9D7X8	0.65	0.55	0.60	0.07	0.33	4.27
Keratin, type I cytoskeletal 17;	Q9QWL7	0.65	0.21	0.43	0.31	1.38	3.26
Acyl-coenzyme A thioesterase 9, mitochondrial;	Q9R0X4	0.65	0.45	0.55	0.14	0.62	4.19
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	0.66	2.00	1.33	0.94	4.22	7.64
Epidermal growth factor receptor kinase substrate 8-like protein 1;	Q8R5F8	0.67	-0.01	0.33	0.48	2.16	4.60
Heat shock protein beta-2;	Q99PR8	0.67	0.50	0.58	0.12	0.55	3.77
Mevalonate kinase;	Q9R008	0.68	0.67	0.67	0.01	0.03	5.45
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	0.69	1.29	0.99	0.43	1.91	6.60
Sorting nexin-27;	Q3UHD6	0.69	0.61	0.65	0.05	0.23	2.73
Fatty acid-binding protein, adipocyte;	P04117	0.71	-0.25	0.23	0.68	3.02	5.75
6-phosphofructokinase type C;	Q9WUA3	0.71	1.90	1.30	0.84	3.76	11.03
Ubiquitin-protein ligase E3A;	O08759	0.71	1.95	1.33	0.88	3.91	10.80
Gasdermin-A;	Q9EST1	0.71	2.90	1.81	1.54	6.89	14.24
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	0.72	0.94	0.83	0.15	0.69	3.48
14-3-3 protein epsilon;	P62259	0.72	1.41	1.06	0.48	2.16	8.14
PDZ and LIM domain protein 5;	Q8CI51	0.72	0.80	0.76	0.05	0.24	6.31
Citrate synthase, mitochondrial;	Q9CZU6	0.72	0.36	0.54	0.26	1.16	4.48
Four and a half LIM domains 3; Uncharacterized protein;	A6H6N4	0.72	1.19	0.96	0.33	1.47	5.11
Protein kinase, cAMP dependent regulatory, type II alpha; Protein kinase, cAMP dependent regulatory, type II alpha, isoform CRA_b; Uncharacterized protein; cAMP-dependent protein kinase type II-alpha regulatory chain;	Q8K1M3	0.72	-0.09	0.32	0.57	2.56	5.64

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
MCG21235; Uncharacterized protein;	Q9D1Q5	0.73	-0.92	-0.09	1.16	5.20	6.05
Fatty acid synthase;	P19096	0.74	1.06	0.90	0.23	1.02	4.53
Prolargin;	Q9JK53	0.74	0.12	0.43	0.44	1.94	4.63
26S proteasome non-ATPase regulatory subunit 14;	O35593	0.74	1.19	0.96	0.32	1.42	8.75
Parvalbumin alpha;	P32848	0.76	-3.64	-1.44	3.11	13.89	23.29
26S protease regulatory subunit 7;	P46471	0.76	1.25	1.00	0.35	1.54	6.10
26S proteasome non-ATPase regulatory subunit 11;	Q8BG32	0.76	1.82	1.29	0.75	3.36	11.88
ATP-dependent RNA helicase DDX19A;	Q61655	0.76	2.32	1.54	1.11	4.94	14.65
Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	0.77	2.60	1.68	1.30	5.80	10.08
Cadherin-1;	P09803	0.77	1.92	1.35	0.81	3.61	12.07
Clathrin heavy chain 1;	Q68FD5	0.77	2.27	1.52	1.06	4.71	10.80
Cell surface glycoprotein MUC18;	Q8R2Y2	0.77	-0.01	0.38	0.56	2.49	2.39
Heat shock protein beta-1;	P14602	0.78	1.05	0.92	0.19	0.85	8.87
Spectrin alpha chain, brain;	P16546	0.78	-0.32	0.23	0.78	3.49	3.80
Nidogen-1;	P10493	0.79	0.57	0.68	0.16	0.71	7.09
Long-chain-fatty-acid--CoA ligase 1;	P41216	0.79	0.41	0.60	0.27	1.20	5.73
Carnitine O-acetyltransferase;	P47934	0.79	-0.71	0.04	1.06	4.75	7.32
Proteasome activator complex subunit 1;	P97371	0.79	-0.47	0.16	0.89	3.99	5.81
Vacuolar protein sorting-associated protein 35;	Q9EQH3	0.79	0.47	0.63	0.23	1.03	4.40
Filamin-A;	Q8BTM8	0.79	-0.09	0.35	0.62	2.78	3.25
Suppressor of G2 allele of SKP1 homolog;	Q9CX34	0.79	1.53	1.16	0.52	2.34	6.91
26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	0.80	1.19	0.99	0.28	1.23	8.47
Proteasome activator complex subunit 2;	P97372	0.80	0.14	0.47	0.47	2.09	3.11
14-3-3 protein sigma;	O70456	0.83	1.38	1.11	0.39	1.73	10.60
SEC14-like protein 4;	Q8R0F9	0.83	0.74	0.79	0.07	0.29	8.14
Alpha-crystallin B chain;	P23927	0.83	0.28	0.55	0.39	1.76	7.31
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	0.86	0.82	0.84	0.02	0.10	4.08
Uncharacterized protein;	F7CAE1	0.87	1.37	1.12	0.35	1.56	9.70
Chondroitin sulfate proteoglycan 4;	Q8VHY0	0.87	2.17	1.52	0.92	4.11	12.84
Hemoglobin subunit beta-1;	P02088	0.89	1.57	1.23	0.48	2.15	11.73
Hemoglobin subunit beta-2;	P02089	0.82	1.80	1.31	0.69	3.09	11.82
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	0.90	1.28	1.09	0.27	1.20	7.99
Laminin subunit alpha-4;	P97927	0.90	-0.22	0.34	0.79	3.54	7.70
Ig gamma-3 chain C region;	P03987	0.91	-1.40	-0.24	1.63	7.28	11.16
26S protease regulatory subunit 6B;	P54775	0.92	2.16	1.54	0.88	3.91	13.87
40S ribosomal protein S3;	P62908	0.93	3.41	2.17	1.75	7.83	16.78
Angio-associated migratory protein; Uncharacterized protein;	Q3TJ22	0.93	1.95	1.44	0.72	3.23	13.11
Perilipin-4;	O88492	0.95	0.72	0.84	0.16	0.72	4.36

Protein	Uniprot	Fold change ($\log_2$) of ASAPRatio replicate 1	Fold change ($\log_2$) of ASAPRatio replicate 2	Average fold change ($\log_2$) of ASAPRatio	Standard deviation	90 % confidence interval (t-test)	Fisher's exact test
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	0.96	2.04	1.50	0.76	3.41	11.88
Periplakin;	Q9R269	0.97	-1.18	-0.11	1.52	6.80	9.59
tRNA (cytosine(34)-C(5))-methyltransferase;	Q1HFZ0	0.98	1.35	1.16	0.26	1.17	7.32
Myosin-4;	Q5SX39	0.98	-1.52	-0.27	1.76	7.87	11.82
Myosin-1;	Q5SX40	3.40	-3.06	0.17	4.57	20.39	35.28
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	0.98	-0.18	0.40	0.82	3.67	9.01
Calsequestrin-1;	O09165	0.99	1.74	1.36	0.53	2.35	12.57
Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	1.00	1.65	1.32	0.46	2.04	8.03
Polymerase I and transcript release factor	O54724	1.04	0.87	0.96	0.12	0.54	10.03
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1.06	1.18	1.12	0.08	0.38	5.08
Fibulin-5;	Q9WVH9	1.07	1.18	1.13	0.08	0.36	11.20
Nebulin; Uncharacterized protein;	A2AQA9	1.07	-0.54	0.27	1.13	5.07	3.57
26S protease regulatory subunit 4;	P62192	1.08	1.95	1.51	0.61	2.74	10.86
Spectrin beta chain, brain 1;	Q62261	1.08	0.67	0.88	0.29	1.31	6.66
Alpha-actinin-4;	P57780	1.09	1.43	1.26	0.24	1.08	8.53
Heat shock protein beta-6;	Q5EBG6	1.11	0.23	0.67	0.63	2.79	8.37
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1.15	0.73	0.94	0.30	1.33	10.09
Carbonic anhydrase 1;	P13634	1.16	0.88	1.02	0.20	0.89	10.22
26S protease regulatory subunit 8;	P62196	1.17	1.50	1.33	0.23	1.03	6.29
Myoglobin;	P04247	1.18	-0.12	0.53	0.92	4.11	9.97
RelA-associated inhibitor;	Q5I1X5	1.20	1.25	1.22	0.04	0.16	14.33
Monofunctional C1-tetrahydrofolate synthase, mitochondrial;	Q3V3R1	1.20	1.40	1.30	0.14	0.63	14.00
26S protease regulatory subunit 10B;	P62334	1.21	2.21	1.71	0.70	3.15	16.01
Tripartite motif-containing protein 29;	Q8R2Q0	1.21	1.74	1.48	0.37	1.65	18.46
Kinesin-1 heavy chain;	Q61768	1.28	2.26	1.77	0.69	3.10	18.67
Plectin;	Q9QXS1	1.30	0.04	0.67	0.89	3.97	3.71
Heat shock protein beta-7;	P35385	1.32	-0.86	0.23	1.54	6.89	12.72
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	1.36	-2.32	-0.48	2.60	11.63	15.05
Filamin-C;	Q8VHX6	1.38	-0.52	0.43	1.34	5.98	7.35
6-phosphofructokinase, muscle type;	P47857	1.41	-0.01	0.70	1.01	4.50	11.25
Vimentin;	P20152	1.49	-0.71	0.39	1.55	6.94	6.91
Protein CREG1;	O88668	1.67	0.51	1.09	0.83	3.69	20.57
Rho-associated protein kinase 2;	P70336	1.79	0.93	1.36	0.61	2.71	23.41
Histone H2A type 1;	P22752	1.94	1.52	1.73	0.29	1.31	32.12
Protein-arginine deiminase type-2;	Q08642	2.06	0.92	1.49	0.81	3.60	15.47
Histone H4;	P62806	2.38	-0.40	0.99	1.97	8.78	27.39
Microtubule-actin cross-linking factor 1;	Q9QXZ0	9.96	1.75	5.86	5.81	25.92	23.18