Table S6: List of all identified and quantified proteins in both replicates of the quantitative proteome comparision of skin lysates wt and *Ctsl*$^{-/-}$.

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 L1;	P06797	-6,64*	-6,64*	-6,64*	0.00	0.00	36.84
Alpha-actinin-4;	P57780	0.79	1.03	0.91	0.17	0.75	4.80
Myosin-4;	Q5SX39	-4.32	-0.74	-2.53	2.53	11.32	10.78
Myosin-1;	Q5SX40	-5.64	0.23	-2.71	4.15	18.53	24.22
Chymase;	P21844	-3.47	0.77	-1.35	3.00	13.39	22.73
Creatine kinase S-type, mitochondrial;	Q6P8J7	-2.94	-0.84	-1.89	1.49	6.65	14.04
Calsequestrin-1;	O09165	-2.56	-0.84	-1.70	1.22	5.43	13.06
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	-2.47	-0.23	-1.35	1.58	7.07	6.94
Myosin light chain 1/3, skeletal muscle isoform;	P05977	-2.47	0.16	-1.16	1.86	8.32	11.30
Reticulon-2;	O70622	-2.25	-0.89	-1.57	0.96	4.30	11.25
Troponin C, skeletal muscle;	P20801	-2.25	-0.17	-1.21	1.47	6.58	9.62
ADP/ATP translocase 1;	P48962	-2.25	0.18	-1.04	1.72	7.66	5.32
ADP/ATP translocase 2;	P51881	-0.14	1.10	0.48	0.87	3.90	3.65
Cytochrome c oxidase subunit 6B1;	P56391	-2.18	0.08	-1.05	1.60	7.16	4.93
Complement component 7	D3YXF5	-2.12	-2.47	-2.30	0.25	1.12	12.34
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4;	Q62425	-2.12	-0.29	-1.20	1.30	5.79	7.67
Ig heavy chain V region 441;	P01806	-2.00	-2.06	-2.03	0.04	0.19	12.33
Fatty acid-binding protein, liver;	P12710	-1.60	-2.18	-1.89	0.41	1.85	9.71
Mitochondrial 10-formyltetrahydrofolate dehydrogenase;	Q8K009	-2.00	-1.22	-1.61	0.55	2.47	9.07
C-type lectin domain family 11 member A;	O88200	-2.12	-1.56	-1.84	0.40	1.78	13.30
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	-2.00	0.63	-0.68	1.86	8.31	5.45
Myosin-binding protein C, fast-type;	Q5XKE0	-1.94	-0.79	-1.36	0.82	3.65	7.51
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	-1.89	-0.67	-1.28	0.86	3.86	6.55
Uncharacterized protein;	E9Q8T1	-1.89	0.47	-0.71	1.66	7.43	6.15
ATP synthase subunit O, mitochondrial;	Q9DB20	-1.89	-0.07	-0.98	1.28	5.73	3.12
Troponin T, fast skeletal muscle;	Q9QZ47	-1.89	0.55	-0.67	1.72	7.69	8.19
Ig gamma-1 chain C region secreted form;	P01868	-1.84	-1.09	-1.46	0.53	2.36	9.62
Protein-glutamine gamma-glutamyltransferase 2;	P21981	-1.84	-0.34	-1.09	1.06	4.73	7.05
6-phosphofructokinase, muscle type;	P47857	-1.84	-0.40	-1.12	1.02	4.55	7.28
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	-1.84	-0.45	-1.15	0.98	4.37	6.76
Glycine cleavage system H protein, mitochondrial;	Q91WK5	-1.84	-1.03	-1.43	0.57	2.55	5.63
Fructose-1,6-bisphosphatase 1;	Q9QXD6	-1.79	-1.89	-1.84	0.07	0.33	12.31
Decorin;	P28654	-1.74	0.52	-0.61	1.59	7.11	6.10
Ig gamma-2A chain C region, A allele;	P01863	-1.74	-1.15	-1.44	0.41	1.85	8.44
Voltage-dependent anion-selective channel protein 1;	Q60932	-1.74	0.04	-0.85	1.26	5.62	3.80
Mitochondrial inner membrane protein;	Q8CAQ8	-1.74	-0.29	-1.01	1.03	4.58	6.28

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
Sarcalumenin;	Q7TQ48	-2.00	-1.60	-1.80	0.28	1.27	10.20
Myomesin 2; Uncharacterized protein;	Q14BI5	-1.69	0.19	-0.75	1.33	5.93	6.23
Vimentin;	P20152	-1.69	1.06	-0.32	1.94	8.67	5.08
Desmin;	P31001	-1.64	-1.03	-1.34	0.43	1.94	8.51
Neurofilament medium polypeptide;	P08553	-1.40	0.83	-0.28	1.58	7.03	3.25
Collagen alpha-2(VI) chain;	Q02788	-1.64	0.74	-0.45	1.69	7.53	5.38
Synemin;	Q70IV5	-1.64	-0.12	-0.88	1.08	4.81	4.48
ATP synthase subunit delta, mitochondrial;	Q9D3D9	-1.64	-0.17	-0.91	1.04	4.66	5.49
Complement component 6	E9Q6D8	-1.69	-1.84	-1.76	0.10	0.46	10.80
Asporin;	Q99MQ4	-1.60	-0.07	-0.84	1.08	4.81	5.19
Periplakin;	Q9R269	-1.60	0.80	-0.40	1.70	7.57	6.55
ATP synthase subunit beta, mitochondrial;	P56480	-1.52	-0.14	-0.83	0.98	4.35	4.22
Coagulation factor XIII B chain;	Q07968	-1.52	-0.32	-0.92	0.84	3.77	6.03
Fructose-bisphosphate aldolase B;	Q91Y97	-1.52	-2.18	-1.85	0.47	2.11	12.56
Oxidation resistance protein 1;	Q4KMM3	-1.52	-1.74	-1.63	0.16	0.70	7.67
Vitronectin;	P29788	-1.52	-0.92	-1.22	0.42	1.89	7.32
Histone H4;	P62806	-1.47	0.87	-0.30	1.66	7.41	6.33
Complement component 6	Q9WTQ5	-1.47	-1.47	-1.47	0.00	0.00	7.12
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	-1.43	-0.17	-0.80	0.90	4.00	5.29
Plasminogen;	P20918	-1.43	-0.79	-1.11	0.46	2.05	6.21
ES1 protein homolog, mitochondrial;	Q9D172	-1.43	-0.94	-1.19	0.35	1.55	5.07
40S ribosomal protein SA;	P14206	-1.40	0.64	-0.38	1.44	6.43	5.54
Haptoglobin;	Q61646	-1.25	-1.69	-1.47	0.31	1.38	9.12
Voltage-dependent anion-selective channel protein 3;	Q60931	-1.40	0.23	-0.58	1.15	5.12	4.90
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	-1.40	0.31	-0.54	1.21	5.39	4.91
Voltage-dependent L-type calcium channel subunit beta-1;	Q8R3Z5	-1.40	-1.09	-1.24	0.22	0.97	6.48
4-aminobutyrate aminotransferase, mitochondrial;	P61922	-1.40	-1.15	-1.27	0.17	0.77	7.48
Retinal dehydrogenase 1;	P24549	-1.36	-1.43	-1.40	0.05	0.24	6.69
Dynein light chain roadblock-type 1;	P62627	-1.36	-0.67	-1.01	0.49	2.18	5.17
Keratin, type II cytoskeletal 1b;	Q6IFZ6	-1.36	0.50	-0.43	1.31	5.85	3.97
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial;	Q7TSQ8	-1.36	-0.67	-1.01	0.49	2.18	4.28
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	-1.36	-0.74	-1.05	0.44	1.96	4.90
Adenylosuccinate synthetase isozyme 1;	P28650	-1.32	-0.56	-0.94	0.54	2.42	4.28
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	-1.32	-0.23	-0.78	0.77	3.43	3.99
Microfibril-associated glycoprotein 4;	Q9D1H9	-1.32	-0.97	-1.15	0.25	1.11	6.34
Pigment epithelium-derived factor;	P97298	-1.32	-1.43	-1.38	0.08	0.35	7.20
PDZ and LIM domain protein 7;	Q3TJD7	-1.32	-0.81	-1.07	0.36	1.61	5.80
60S ribosomal protein L14;	Q9CR57	-1.29	0.77	-0.26	1.46	6.50	6.10

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
Collagen alpha-1(I) chain;	P11087	-1.29	-1.32	-1.30	0.03	0.11	6.68
Cytochrome c oxidase subunit 2;	P00405	-1.25	0.19	-0.53	1.02	4.55	4.40
Collagen alpha-2(I) chain;	Q01149	-1.40	-1.47	-1.44	0.06	0.25	9.04
Nucleobindin-2;	P81117	-1.25	-1.47	-1.36	0.16	0.70	9.04
Glycogen [starch] synthase, muscle;	Q9Z1E4	-1.25	0.66	-0.30	1.35	6.04	5.39
Transforming growth factor-beta-induced protein ig-h3;	P82198	-1.25	0.62	-0.31	1.33	5.92	5.08
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	-1.22	-0.38	-0.80	0.59	2.65	4.53
Cystatin-C;	P21460	-1.22	-1.09	-1.15	0.09	0.41	7.10
Tetranectin;	P43025	-1.22	-1.43	-1.33	0.15	0.68	6.80
Mitochondrial 2-oxoglutarate/malate carrier protein;	Q9CR62	-1.22	0.37	-0.43	1.12	5.00	4.47
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	-1.22	0.10	-0.56	0.93	4.15	3.62
Glycogen phosphorylase, muscle form;	Q9WUB3	-1.22	0.20	-0.51	1.00	4.48	3.40
Glycogen phosphorylase, brain form;	Q8CI94	0.45	0.54	0.50	0.06	0.26	2.24
Nebulin; Uncharacterized protein;	A2AQA9	-1.22	0.30	-0.46	1.07	4.79	2.64
60S acidic ribosomal protein P2;	P99027	-1.18	0.04	-0.57	0.87	3.87	3.54
Actin, alpha skeletal muscle;	P68134	-1.32	-0.97	-1.15	0.25	1.11	6.15
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	-1.15	-0.23	-0.69	0.65	2.90	3.06
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	-1.15	-0.45	-0.80	0.49	2.20	3.34
Leukemia inhibitory factor receptor;	P42703	-1.12	-2.06	-1.59	0.66	2.96	10.53
ATP synthase subunit gamma, mitochondrial;	Q91VR2	-1.12	0.08	-0.52	0.85	3.80	2.06
Methylmalonyl-CoA mutase, mitochondrial;	P16332	-1.09	0.03	-0.53	0.79	3.53	1.47
Heparin cofactor 2;	P49182	-1.09	-0.79	-0.94	0.21	0.96	4.41
Myomesin-1;	Q62234	-1.09	-0.03	-0.56	0.75	3.35	2.23
Acyl-coenzyme A thioesterase 13;	Q9CQR4	-1.09	-1.29	-1.19	0.14	0.62	7.06
ATP synthase subunit d, mitochondrial;	Q9DCX2	-1.09	0.26	-0.41	0.96	4.27	3.73
Major urinary protein 2;	P11589	-1.09	-1.60	-1.34	0.36	1.61	8.93
40S ribosomal protein S12;	Q6ZWZ6	-1.09	0.72	-0.18	1.28	5.72	4.91
Coproporphyrinogen-III oxidase, mitochondrial;	P36552	-1.06	0.18	-0.44	0.87	3.90	3.43
Myosin light chain kinase, smooth muscle;	Q6PDN3	-1.06	-0.71	-0.89	0.24	1.09	4.13
Adenylate kinase isoenzyme 1;	Q9R0Y5	-1.06	-1.22	-1.14	0.11	0.50	6.38
Carnitine O-acetyltransferase;	P47934	-1.06	-0.47	-0.77	0.41	1.85	3.53
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	-1.06	-0.03	-0.54	0.73	3.25	3.21
Coatomer subunit delta;	Q5XJY5	-1.03	-0.54	-0.78	0.35	1.56	2.73
Arginase-1;	Q61176	-1.03	-2.25	-1.64	0.86	3.86	12.24
Synaptopodin-2;	Q91YE8	-1.03	-0.89	-0.96	0.10	0.44	5.53
Uncharacterized protein;	E9Q2T3	-1.03	0.35	-0.34	0.97	4.34	3.18
Betaine--homocysteine S-methyltransferase 1;	O35490	-1.03	-2.84	-1.93	1.28	5.71	8.40
Phosphoglycerate mutase 2;	O70250	-1.00	-1.03	-1.01	0.02	0.09	5.02

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
Ig mu chain C region secreted form;	P01872	-1.00	-1.00	-1.00	0.00	0.00	5.63
NAD(P)H dehydrogenase [quinone] 1;	Q64669	-1.00	-0.56	-0.78	0.31	1.40	3.97
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	-1.00	-0.18	-0.59	0.58	2.58	3.18
Fructose-bisphosphate aldolase A;	P05064	-1.00	-0.92	-0.96	0.06	0.27	5.03
Fructose-bisphosphate aldolase C;	P05063	0.89	0.65	0.77	0.17	0.75	4.06
Hippocalcin-like protein 1;	P62748	-1.00	-1.43	-1.22	0.31	1.37	6.70
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	-1.00	-0.94	-0.97	0.04	0.18	3.45
Adseverin;	Q60604	-1.00	0.06	-0.47	0.75	3.34	1.84
Serpin B6;	Q60854	-1.00	-0.86	-0.93	0.10	0.44	4.62
Phosphotriesterase-related protein;	Q60866	-1.00	-0.97	-0.99	0.02	0.09	5.30
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	-1.00	-0.22	-0.61	0.55	2.47	1.59
EH domain-binding protein 1-like protein 1;	Q99MS7	-1.00	-1.18	-1.09	0.13	0.58	6.04
40S ribosomal protein S21;	Q9CQR2	-1.00	0.42	-0.29	1.01	4.49	3.65
Transthyretin;	P07309	-0.97	-1.00	-0.99	0.02	0.09	5.21
Carbonic anhydrase 3;	P16015	-0.97	-0.42	-0.69	0.39	1.76	3.38
Fructose-1,6-bisphosphatase isozyme 2;	P70695	-0.97	-0.64	-0.81	0.23	1.03	4.18
Secernin-3;	Q3TMH2	-0.97	-1.25	-1.11	0.20	0.89	6.67
Apolipoprotein A-IV;	P06728	-0.94	-2.84	-1.89	1.34	5.98	11.78
Prothrombin;	P19221	-0.94	-0.71	-0.83	0.16	0.73	3.43
Apolipoprotein A-I;	Q00623	-0.94	-2.25	-1.60	0.93	4.13	12.32
Beta-2-glycoprotein 1;	Q01339	-0.94	-1.64	-1.29	0.50	2.21	8.46
Protein-arginine deiminase type-2;	Q08642	-0.94	-0.69	-0.82	0.18	0.80	4.12
Sulfhydryl oxidase 1;	Q8BND5	-0.94	-0.89	-0.92	0.04	0.17	5.03
Protein Z-dependent protease inhibitor;	Q8R121	-0.94	-0.84	-0.89	0.07	0.33	4.70
Carbohydrate kinase domain-containing protein;	Q9CZ42	-0.94	-0.47	-0.71	0.33	1.48	3.68
Serine protease inhibitor A3K;	P07759	-0.94	-0.76	-0.85	0.13	0.57	3.84
Serine protease inhibitor A3N;	Q91WP6	-0.14	-0.81	-0.47	0.48	2.13	1.87
Uncharacterized protein;	D3Z450	0.53	0.86	0.69	0.23	1.04	3.61
Four and a half LIM domains protein 1;	P97447	-0.94	-0.23	-0.59	0.50	2.24	2.44
Lambda-crystallin homolog;	Q99KP3	-0.94	-0.81	-0.88	0.09	0.42	4.35
Cardiomyopathy-associated protein 5;	Q70KF4	-0.94	-1.40	-1.17	0.32	1.43	6.27
Ig kappa chain V19-17;	P01633	-0.94	-0.52	-0.73	0.30	1.35	3.95
Methionine aminopeptidase 2;	O08663	-0.92	0.99	0.04	1.34	6.00	4.87
Collagen alpha-1(III) chain;	P08121	-0.92	-1.32	-1.12	0.29	1.28	7.00
Lumican;	P51885	-0.92	-0.45	-0.69	0.33	1.46	3.39
Complement component C8 alpha chain;	Q8K182	-0.92	-0.92	-0.92	0.00	0.00	4.74
SH3 and PX domain-containing protein 2B;	A2AAY5	-0.92	-1.09	-1.00	0.12	0.55	4.58
Creatine kinase M-type;	P07310	-0.89	-1.15	-1.02	0.19	0.83	5.88

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
Parvalbumin alpha;	P32848	-0.89	-0.09	-0.49	0.57	2.53	2.60
Calcium-regulated heat stable protein 1;	Q9CR86	-0.89	-0.89	-0.89	0.00	0.00	3.37
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	-0.89	-0.69	-0.79	0.14	0.63	3.50
Creatine kinase U-type, mitochondrial;	P30275	-0.89	0.42	-0.23	0.93	4.14	2.97
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	-0.89	-0.49	-0.69	0.28	1.25	3.10
Ig kappa chain C region;	P01837	-0.86	0.51	-0.18	0.97	4.32	2.97
60S ribosomal protein L12;	P35979	-0.86	0.94	0.04	1.27	5.69	4.51
Cytochrome c, somatic;	P62897	-0.86	-0.27	-0.57	0.42	1.87	2.84
Creatine kinase B-type;	Q04447	-0.86	-1.06	-0.96	0.14	0.62	4.83
Complement factor I;	Q61129	-0.86	-1.03	-0.95	0.12	0.53	4.93
Zinc-alpha-2-glycoprotein;	Q64726	-0.86	-0.74	-0.80	0.09	0.39	3.65
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	-0.86	-0.94	-0.90	0.06	0.26	4.69
Aconitate hydratase, mitochondrial;	Q99KI0	-0.86	-0.58	-0.72	0.20	0.90	3.50
Cell adhesion molecule 3;	Q99N28	-0.86	-0.89	-0.88	0.02	0.09	4.77
Lactoylglutathione lyase;	Q9CPU0	-0.86	-0.56	-0.71	0.22	0.97	3.00
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	-0.86	0.03	-0.42	0.63	2.81	2.23
SPARC;	P07214	-0.86	-1.74	-1.30	0.62	2.76	6.12
Glutamate dehydrogenase 1, mitochondrial;	P26443	-0.86	0.47	-0.20	0.94	4.19	3.39
Plasma protease C1 inhibitor;	P97290	-0.86	-1.03	-0.95	0.12	0.53	4.41
Phosphoglucomutase-1;	Q9D0F9	-0.86	-0.81	-0.84	0.04	0.16	4.39
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	-0.86	-0.71	-0.79	0.11	0.47	3.97
Apolipoprotein A-II;	P09813	-0.86	-1.89	-1.38	0.73	3.24	9.49
Uncharacterized protein;	E9QA15	-0.84	0.48	-0.18	0.93	4.14	2.79
Malate dehydrogenase, mitochondrial;	P08249	-0.81	-0.71	-0.76	0.07	0.31	4.02
Fumarate hydratase, mitochondrial;	P97807	-0.81	-0.27	-0.54	0.38	1.71	1.94
Protein AMBP;	Q07456	-0.81	-1.09	-0.95	0.20	0.88	4.85
L-asparaginase;	Q8C0M9	-0.81	-0.86	-0.84	0.04	0.16	4.26
Phosphoglycolate phosphatase;	Q8CHP8	-0.81	-0.76	-0.79	0.04	0.16	2.97
Hemopexin;	Q91X72	-0.81	-0.45	-0.63	0.25	1.13	2.99
Neurolysin, mitochondrial;	Q91YP2	-0.81	0.10	-0.36	0.64	2.87	1.22
MACRO domain-containing protein 1;	Q922B1	-0.81	-0.76	-0.79	0.04	0.16	3.90
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	-0.81	0.41	-0.20	0.86	3.86	2.79
GMP reductase 1;	Q9DCZ1	-0.81	-0.58	-0.69	0.16	0.74	3.67
Complement factor B;	P04186	-0.81	-0.84	-0.82	0.02	0.08	3.68
Adenylosuccinate lyase;	P54822	-0.81	0.39	-0.21	0.85	3.79	2.94
Voltage-dependent anion-selective channel protein 2;	Q60930	-0.81	0.71	-0.05	1.07	4.79	3.15
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	-0.81	-0.07	-0.44	0.52	2.33	2.20

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
Ig kappa chain V-II region 26-10;	P01631	-0.81	-1.56	-1.18	0.53	2.35	5.29
Complement factor D;	P03953	-0.79	-0.56	-0.67	0.16	0.73	3.05
Alpha-2-HS-glycoprotein;	P29699	-0.79	-0.86	-0.82	0.05	0.24	4.50
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	-0.79	-0.45	-0.62	0.23	1.05	2.68
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	-0.79	-0.42	-0.60	0.26	1.17	2.89
Histidine-rich glycoprotein;	Q9ESB3	-0.79	-0.11	-0.45	0.48	2.15	2.22
Mitogen-activated protein kinase 12;	O08911	-0.79	-0.74	-0.76	0.03	0.15	3.99
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	-0.79	-0.84	-0.81	0.04	0.16	3.54
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	-0.79	-0.43	-0.61	0.25	1.11	3.08
Vesicle-associated membrane protein-associated protein B;	Q9QY76	-0.79	-0.84	-0.81	0.04	0.16	4.34
Integrin beta-4;	A2A863	-0.76	0.71	-0.03	1.04	4.63	3.30
Cell surface glycoprotein MUC18;	Q8R2Y2	-0.76	0.25	-0.26	0.72	3.19	2.19
Plexin domain-containing protein 2;	Q9DC11	-0.76	-0.89	-0.83	0.09	0.40	4.31
Deoxyguanosine kinase, mitochondrial;	Q9QX60	-0.76	-0.49	-0.63	0.19	0.84	3.22
Bisphosphoglycerate mutase;	P15327	-0.76	-0.71	-0.74	0.03	0.15	3.81
Purine nucleoside phosphorylase;	P23492	-0.76	-0.11	-0.43	0.46	2.07	2.03
Prohibitin;	P67778	-0.76	0.93	0.09	1.20	5.35	4.48
Histidine triad nucleotide-binding protein 1;	P70349	-0.76	-0.62	-0.69	0.10	0.44	2.92
Carboxymethylenebutenolidase homolog;	Q8R1G2	-0.76	-0.45	-0.61	0.22	0.97	2.84
Mannose-6-phosphate isomerase;	Q924M7	-0.76	-0.18	-0.47	0.41	1.82	2.34
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	-0.76	-0.40	-0.58	0.26	1.15	2.37
Angiotensinogen;	P11859	-0.74	-0.71	-0.73	0.02	0.08	3.67
Annexin A6;	P14824	-0.74	1.94	0.60	1.89	8.44	8.56
Ceruloplasmin;	Q61147	-0.74	-1.00	-0.87	0.19	0.83	3.60
UPF0586 protein C9orf41 homolog;	Q80UY1	-0.74	-0.89	-0.81	0.11	0.48	3.59
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	-0.74	-0.81	-0.77	0.05	0.23	3.98
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	-0.74	-1.25	-0.99	0.36	1.63	5.16
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	-0.74	-0.30	-0.52	0.31	1.37	2.55
Angiotensin-converting enzyme;	P09470	-0.74	-0.47	-0.61	0.19	0.83	2.87
Triosephosphate isomerase;	P17751	-0.74	-0.71	-0.73	0.02	0.08	3.56
Murinoglobulin-1;	P28665	-0.74	-0.84	-0.79	0.07	0.32	3.11
Adiponectin;	Q60994	-0.74	-0.23	-0.49	0.36	1.59	2.32
Uncharacterized protein;	E9PV38	-0.74	-1.06	-0.90	0.23	1.02	4.35
Uncharacterized protein;	F8VPN4	-0.74	-0.60	-0.67	0.10	0.44	2.55
Acylphosphatase-2;	P56375	-0.71	-0.23	-0.47	0.34	1.51	2.05
Ras suppressor protein 1;	Q01730	-0.71	0.41	-0.15	0.79	3.55	2.76
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	-0.71	-0.81	-0.76	0.07	0.31	3.76

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
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	-0.71	0.06	-0.33	0.54	2.43	1.74
Golgi reassembly-stacking protein 2;	Q99JX3	-0.71	-0.76	-0.74	0.03	0.15	3.66
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	-0.71	-0.76	-0.74	0.03	0.15	2.73
Beta-hexosaminidase subunit alpha;	P29416	-0.71	1.13	0.21	1.30	5.82	4.57
Epidermal growth factor receptor;	Q01279	-0.69	-1.03	-0.86	0.24	1.07	4.75
Mimecan;	Q62000	-0.69	-0.71	-0.70	0.02	0.07	3.34
Sulfite oxidase, mitochondrial;	Q8R086	-0.69	-0.38	-0.53	0.22	0.99	2.11
Prohibitin-2;	O35129	-0.69	0.81	0.06	1.06	4.73	3.59
Aspartate aminotransferase, cytoplasmic;	P05201	-0.69	-0.18	-0.44	0.36	1.60	1.96
Prelamin-A/C;	P48678	-0.69	0.92	0.11	1.14	5.08	2.82
Cytochrome b5;	P56395	-0.69	0.41	-0.14	0.78	3.48	2.73
Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	Q07417	-0.69	0.54	-0.08	0.87	3.87	2.59
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	-0.69	-0.74	-0.71	0.03	0.15	2.88
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	-0.69	-0.52	-0.60	0.12	0.55	2.84
Serotransferrin;	Q921I1	-0.69	-0.71	-0.70	0.02	0.07	3.36
Citrate synthase, mitochondrial;	Q9CZU6	-0.69	-0.49	-0.59	0.14	0.62	2.85
Acylpyruvase FAHD1, mitochondrial;	Q8R0F8	-0.69	-1.00	-0.85	0.22	0.98	4.56
Afamin;	O89020	-0.67	-0.67	-0.67	0.00	0.00	2.84
Interleukin-1 receptor accessory protein;	Q61730	-0.67	-0.94	-0.81	0.20	0.87	4.36
CCA tRNA nucleotidyltransferase 1, mitochondrial;	Q8K1J6	-0.67	0.15	-0.26	0.58	2.58	1.46
Mitochondrial peptide methionine sulfoxide reductase;	Q9D6Y7	-0.67	-0.30	-0.49	0.26	1.15	1.83
Glucose-6-phosphate isomerase;	P06745	-0.67	-0.40	-0.53	0.19	0.86	2.23
Galectin-related protein A;	Q8VED9	-0.67	-0.06	-0.36	0.43	1.92	1.44
ATP synthase subunit g, mitochondrial;	Q9CPQ8	-0.67	0.24	-0.21	0.64	2.86	2.20
Plectin;	Q9QXS1	-0.67	0.54	-0.07	0.85	3.80	2.00
Complement C4-B;	P01029	-0.64	-1.06	-0.85	0.29	1.31	2.58
Serum albumin;	P07724	-0.64	-0.42	-0.53	0.16	0.72	2.08
Cofilin-2;	P45591	-0.64	-1.12	-0.88	0.34	1.50	4.71
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	-0.64	-0.58	-0.61	0.05	0.21	2.70
Retinol-binding protein 4;	Q00724	-0.64	-1.25	-0.95	0.43	1.92	4.16
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	-0.64	-1.15	-0.90	0.36	1.60	4.27
Glycyl-tRNA synthetase;	Q9CZD3	-0.64	-0.40	-0.52	0.18	0.78	2.10
Carboxypeptidase N subunit 2;	Q9DBB9	-0.64	-0.89	-0.77	0.17	0.77	3.88
L-lactate dehydrogenase B chain;	P16125	-0.06	-0.29	-0.17	0.16	0.72	0.73
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	-0.64	-0.40	-0.52	0.18	0.78	2.25
Collagen alpha-1(VI) chain;	Q04857	-0.64	0.59	-0.03	0.87	3.88	2.62
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	-0.64	-0.54	-0.59	0.08	0.34	2.03
UPF0585 protein C16orf13 homolog;	Q9DCS2	-0.64	0.20	-0.22	0.60	2.67	1.60

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
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	-0.64	-0.45	-0.55	0.13	0.60	2.18
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	-0.62	-1.29	-0.95	0.47	2.10	5.61
4-hydroxyphenylpyruvate dioxygenase;	P49429	-0.62	-2.47	-1.55	1.31	5.85	6.52
Pyruvate kinase isozymes M1/M2;	P52480	-0.62	-0.47	-0.55	0.10	0.46	2.32
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	-0.62	-0.49	-0.56	0.09	0.40	2.54
Complement C3;	P01027	-0.60	-0.86	-0.73	0.19	0.83	3.08
Serpin H1;	P19324	-0.60	-1.60	-1.10	0.71	3.16	5.30
Glutathione S-transferase A4;	P24472	-0.60	-0.40	-0.50	0.14	0.64	2.12
Glutathione reductase, mitochondrial;	P47791	-0.60	-0.56	-0.58	0.03	0.14	2.77
Eukaryotic translation initiation factor 5A-1;	P63242	-0.60	0.66	0.03	0.89	3.97	2.61
Coatomer subunit zeta-2;	Q9JHH9	-0.60	-0.52	-0.56	0.06	0.27	2.61
Fetuin-B;	Q9QXC1	-0.60	-0.67	-0.63	0.05	0.21	3.19
Alpha-1-antitrypsin 1-1;	P07758	-0.60	-0.97	-0.79	0.26	1.17	4.38
Alpha-1-antitrypsin 1-2;	P22599	-0.67	-0.89	-0.78	0.16	0.70	4.11
Alpha-1-antitrypsin 1-4;	Q00897	-0.89	-0.58	-0.73	0.22	0.98	3.46
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	-0.60	-0.42	-0.51	0.13	0.58	2.26
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	-0.60	-0.84	-0.72	0.17	0.75	3.59
Uncharacterized protein;	E9PVD2	-0.60	-0.69	-0.64	0.06	0.29	2.54
Nucleoside diphosphate kinase;	E9PZF0	-0.60	-0.22	-0.41	0.27	1.20	1.94
Aspartate aminotransferase, mitochondrial;	P05202	-0.58	-0.47	-0.53	0.07	0.33	2.31
Superoxide dismutase [Mn], mitochondrial;	P09671	-0.58	-0.29	-0.43	0.21	0.92	1.91
Heat shock protein beta-7;	P35385	-0.58	0.69	0.05	0.89	3.99	2.62
182 kDa tankyrase-1-binding protein;	P58871	-0.58	0.35	-0.12	0.65	2.91	1.20
Extended synaptotagmin-1;	Q3U7R1	-0.58	0.98	0.20	1.10	4.91	3.37
Sorbitol dehydrogenase;	Q64442	-0.58	-0.74	-0.66	0.11	0.50	2.68
GDP-fucose protein O-fucosyltransferase 2;	Q8VHI3	-0.58	0.06	-0.26	0.45	2.00	1.48
Isochorismatase domain-containing protein 1;	Q91V64	-0.58	-0.09	-0.33	0.35	1.54	1.40
Glutathione S-transferase Mu 5;	P48774	-0.58	0.53	-0.03	0.78	3.49	2.04
Protein DJ-1;	Q99LX0	-0.58	-1.18	-0.88	0.43	1.91	4.23
Synaptic vesicle membrane protein VAT-1 homolog-like;	Q80TB8	-0.58	-0.47	-0.53	0.07	0.33	2.38
Myc box-dependent-interacting protein 1;	O08539	-0.56	-0.42	-0.49	0.10	0.45	2.05
Heterogeneous nuclear ribonucleoprotein L;	Q8R081	-0.56	0.37	-0.09	0.65	2.91	1.58
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	-0.56	-0.62	-0.59	0.05	0.21	2.82
Ribonuclease 4;	Q9JJH1	-0.56	-0.71	-0.63	0.11	0.50	3.02
Band 4.1-like protein 3;	Q9WV92	-0.56	-0.43	-0.50	0.09	0.39	2.28
Uncharacterized protein;	D3Z0Y2	-0.56	-0.64	-0.60	0.06	0.28	2.55
Delta-aminolevulinic acid dehydratase;	P10518	-0.54	0.07	-0.23	0.43	1.91	1.43
Plasma kallikrein;	P26262	-0.54	-0.74	-0.64	0.14	0.64	3.25

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
Antithrombin-III;	P32261	-0.54	-0.67	-0.60	0.09	0.42	2.49
Transcription elongation factor B polypeptide 2;	P62869	-0.54	0.18	-0.18	0.50	2.24	1.48
Annexin A7;	Q07076	-0.54	-0.32	-0.43	0.15	0.67	1.54
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	-0.54	-0.23	-0.38	0.21	0.95	1.49
Heat shock protein beta-2;	Q99PR8	-0.54	-1.03	-0.78	0.35	1.56	4.05
Selenium-binding protein 1;	P17563	-0.54	-1.03	-0.78	0.35	1.56	3.24
Quinone oxidoreductase;	P47199	-0.54	-0.20	-0.37	0.24	1.05	1.71
Protein transport protein Sec23A;	Q01405	-0.54	-0.92	-0.73	0.27	1.20	3.48
Aldose reductase-related protein 2;	P45377	0.96	0.42	0.69	0.38	1.71	3.32
Alpha-1-syntrophin;	Q61234	-0.54	-1.12	-0.83	0.41	1.85	4.72
Extracellular superoxide dismutase [Cu-Zn];	O09164	-0.52	0.10	-0.21	0.43	1.94	1.42
Gamma-synuclein;	Q9Z0F7	-0.52	-0.29	-0.40	0.16	0.72	1.59
Kininogen-1;	O08677	-0.52	-0.71	-0.61	0.14	0.63	3.07
Annexin A8;	O35640	-0.52	-0.54	-0.53	0.01	0.06	2.23
Rab GDP dissociation inhibitor alpha;	P50396	-0.52	-0.29	-0.40	0.16	0.72	1.52
Alcohol dehydrogenase [NADP+];	Q9JII6	-0.52	-0.32	-0.42	0.14	0.61	1.62
Legumain;	O89017	-0.49	0.55	0.03	0.74	3.28	2.42
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	-0.49	-0.07	-0.28	0.30	1.33	1.20
Spectrin beta chain, brain 1;	Q62261	-0.49	0.49	0.00	0.69	3.09	2.02
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	-0.49	-1.60	-1.05	0.78	3.49	5.12
Beta-lactamase-like protein 2;	Q99KR3	-0.49	-0.67	-0.58	0.12	0.55	2.80
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	-0.49	-1.74	-1.12	0.88	3.92	4.52
Copper homeostasis protein cutC homolog;	Q9D8X1	-0.49	-0.64	-0.57	0.11	0.47	2.67
Hexokinase-2;	O08528	-0.49	-0.54	-0.51	0.03	0.13	1.89
Hexokinase-1;	P17710	0.33	0.19	0.26	0.10	0.45	0.86
Hexokinase-3;	Q3TRM8	-0.17	-0.81	-0.49	0.45	2.03	1.90
Annexin A2;	P07356	-0.49	0.01	-0.24	0.36	1.60	1.22
Annexin A11;	P97384	-0.49	-0.52	-0.50	0.01	0.07	2.30
Xanthine dehydrogenase/oxidase;	Q00519	-0.49	-0.60	-0.55	0.07	0.33	2.11
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	-0.49	0.12	-0.19	0.44	1.95	1.04
3-mercaptopyruvate sulfurtransferase;	Q99J99	-0.49	-0.92	-0.71	0.30	1.33	3.38
Sodium/potassium-transporting ATPase subunit beta-1;	P14094	-0.47	-1.79	-1.13	0.93	4.14	3.75
Biglycan;	P28653	-0.47	0.20	-0.14	0.48	2.13	0.97
Heat shock protein beta-6;	Q5EBG6	-0.47	-0.89	-0.68	0.29	1.31	3.53
Ketosamine-3-kinase;	Q8K274	-0.47	-0.06	-0.27	0.29	1.31	1.11
Arsenite methyltransferase;	Q91WU5	-0.47	-0.86	-0.67	0.27	1.22	3.33
Carboxypeptidase N catalytic chain;	Q9JJN5	-0.47	-1.74	-1.11	0.89	3.99	7.21

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
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	-0.47	-0.94	-0.71	0.33	1.48	3.34
Tetratricopeptide repeat protein 38;	A3KMP2	-0.47	-0.27	-0.37	0.14	0.65	1.58
Myelin protein P0;	P27573	-0.47	0.66	0.09	0.80	3.58	2.43
Aldose reductase;	P45376	-0.47	-0.71	-0.59	0.17	0.75	2.69
Glutathione peroxidase 3;	P46412	-0.47	0.07	-0.20	0.38	1.72	1.26
Proliferation-associated protein 2G4;	P50580	-0.47	0.99	0.26	1.03	4.61	3.65
Thiosulfate sulfurtransferase;	P52196	-0.47	-0.97	-0.72	0.35	1.57	3.87
Serine/threonine-protein phosphatase 2A activator;	P58389	-0.47	-0.18	-0.33	0.21	0.92	1.13
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	-0.47	-0.94	-0.71	0.33	1.48	3.06
Alpha-2-macroglobulin;	Q61838	-0.47	-0.97	-0.72	0.35	1.57	3.38
C-type mannose receptor 2;	Q64449	-0.47	-0.79	-0.63	0.22	0.98	2.72
Interferon-activable protein 205-A;	Q8CGE8	-0.47	0.51	0.02	0.69	3.09	1.89
Inositol (Myo)-1(Or 4)-monophosphatase 1; Inositol (Myo)-1(Or 4)-monophosphatase 1, isoform CRA_a; Myo-inositol monophosphatase 1; Uncharacterized protein;	Q924B0	-0.47	-0.38	-0.43	0.07	0.31	1.60
Protein S100-A6;	P14069	-0.47	-0.92	-0.70	0.31	1.40	3.41
Acylphosphatase-1;	P56376	-0.45	-0.67	-0.56	0.15	0.67	2.62
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	Q91YQ5	-0.45	0.15	-0.15	0.43	1.91	1.16
Uncharacterized protein;	E9Q8E3	-0.45	0.54	0.04	0.70	3.13	1.90
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	-0.45	-1.03	-0.74	0.41	1.82	3.16
Carbonyl reductase [NADPH] 2;	P08074	-0.45	-0.84	-0.65	0.27	1.21	2.99
ATP synthase subunit alpha, mitochondrial;	Q03265	-0.45	-0.30	-0.38	0.11	0.47	1.51
Fumarylacetoacetate hydrolase domain-containing protein 2A;	Q3TC72	-0.45	-0.52	-0.48	0.04	0.19	2.27
Uncharacterized protein;	E9Q0S6	-0.45	-0.07	-0.26	0.27	1.20	1.14
Leukotriene A-4 hydrolase;	P24527	-0.43	-0.34	-0.39	0.07	0.30	1.29
Splicing factor U2AF 65 kDa subunit;	P26369	-0.43	3.25	1.41	2.60	11.62	12.45
Cellular retinoic acid-binding protein 1;	P62965	-0.43	-0.47	-0.45	0.03	0.13	1.78
Tripartite motif-containing protein 72;	Q1XH17	-0.43	-0.76	-0.60	0.23	1.03	2.47
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	-0.43	-0.71	-0.57	0.20	0.88	2.50
Phosphopantothenate--cysteine ligase;	Q8VDG5	-0.43	-0.12	-0.28	0.22	0.99	1.24
Probable proline racemase;	Q9CXA2	-0.43	-0.47	-0.45	0.03	0.13	1.86
Inositol-3-phosphate synthase 1;	Q9JHU9	-0.43	-0.29	-0.36	0.10	0.47	1.52
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	-0.43	-0.71	-0.57	0.20	0.88	2.55
Maleylacetoacetate isomerase;	Q9WVL0	-0.43	-0.18	-0.31	0.18	0.79	1.18
Plasminogen activator inhibitor 2, macrophage;	P12388	-0.43	-0.74	-0.59	0.21	0.96	2.33
Malate dehydrogenase, cytoplasmic;	P14152	-0.43	-0.67	-0.55	0.16	0.74	2.21
Ras-related protein Rab-2A;	P53994	-0.43	-0.81	-0.62	0.27	1.19	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
Myosin light polypeptide 6;	Q60605	-0.43	0.39	-0.02	0.58	2.60	1.61
Valacyclovir hydrolase;	Q8R164	-0.43	-0.45	-0.44	0.01	0.06	2.07
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	-0.43	-0.52	-0.47	0.06	0.26	2.11
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	-0.43	-0.58	-0.51	0.10	0.45	2.22
Caspase-6;	O08738	-0.42	-0.40	-0.41	0.01	0.06	1.25
Ferritin heavy chain;	P09528	-0.42	-0.43	-0.42	0.01	0.06	1.92
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	-0.42	-0.11	-0.26	0.22	0.98	1.05
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	-0.42	-0.84	-0.63	0.30	1.33	2.99
WW domain-binding protein 11;	Q923D5	-0.42	0.99	0.29	0.99	4.42	3.55
Protein canopy homolog 2;	Q9QXT0	-0.42	-0.36	-0.39	0.04	0.18	1.56
Phosphatidylethanolamine-binding protein 1;	P70296	-0.42	-0.47	-0.44	0.04	0.19	2.04
Abhydrolase domain-containing protein 14B;	Q8VCR7	-0.42	-0.92	-0.67	0.35	1.58	3.18
Annexin A3;	O35639	-0.40	-0.64	-0.52	0.18	0.78	2.15
Protein PRRC1;	Q3UPH1	-0.40	-0.54	-0.47	0.10	0.44	2.22
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	-0.40	-0.74	-0.57	0.24	1.08	2.58
Poly(ADP-ribose) glycohydrolase ARH3;	Q8CG72	-0.40	-0.06	-0.23	0.24	1.06	0.82
Metalloreductase STEAP3;	Q8CI59	-0.40	0.43	0.02	0.59	2.62	1.86
Electron transfer flavoprotein subunit beta;	Q9DCW4	-0.40	-0.71	-0.55	0.22	1.00	2.29
Torsin-1B;	Q9ER41	-0.40	-0.32	-0.36	0.05	0.23	1.44
Dysferlin;	Q9ESD7	-0.40	-0.12	-0.26	0.20	0.87	1.09
N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	-0.40	-0.67	-0.53	0.19	0.86	1.91
Procollagen C-endopeptidase enhancer 1;	Q61398	-0.40	-0.84	-0.62	0.31	1.39	2.43
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	-0.40	-0.76	-0.58	0.26	1.15	2.43
NAD-dependent deacetylase sirtuin-2;	Q8VDQ8	-0.40	-0.43	-0.42	0.03	0.12	1.83
Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	-0.40	-0.30	-0.35	0.07	0.29	1.33
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	-0.40	0.21	-0.09	0.43	1.93	1.09
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	-0.40	0.10	-0.15	0.35	1.56	0.90
Actin-related protein 2/3 complex subunit 1A;	Q9R0Q6	-1.22	-0.43	-0.83	0.55	2.47	4.66
Ectonucleoside triphosphate diphosphohydrolase 2;	O55026	-0.38	-0.54	-0.46	0.11	0.50	1.80
COP9 signalosome complex subunit 6;	O88545	-0.38	0.70	0.16	0.76	3.39	2.00
Nucleolin;	P09405	-0.38	1.94	0.78	1.64	7.31	8.25
Ornithine aminotransferase, mitochondrial;	P29758	-0.38	-0.42	-0.40	0.03	0.12	1.68
Indolethylamine N-methyltransferase;	P40936	-0.38	-0.22	-0.30	0.11	0.50	1.09
Annexin A5;	P48036	-0.38	-0.20	-0.29	0.12	0.56	1.20
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	-0.38	-1.09	-0.73	0.50	2.25	2.10
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	-0.38	-0.36	-0.37	0.01	0.06	1.58

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
Omega-amidase NIT2;	Q9JHW2	-0.38	-0.07	-0.23	0.21	0.96	0.88
Glutathione S-transferase P 1;	P19157	-0.38	-0.67	-0.52	0.21	0.92	2.31
Fumarylacetoacetase;	P35505	-0.38	-0.79	-0.58	0.29	1.29	2.86
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	-0.38	-0.79	-0.58	0.29	1.29	2.87
Protein dpy-30 homolog;	Q99LT0	-0.36	0.26	-0.05	0.44	1.96	1.34
Prefoldin subunit 2;	O70591	-0.36	-0.32	-0.34	0.03	0.11	1.45
Echinoderm microtubule-associated protein-like 1;	Q05BC3	-0.36	0.19	-0.08	0.39	1.73	1.14
Proteasome subunit beta type-1;	O09061	-0.34	0.57	0.11	0.64	2.86	1.62
Periaxin;	O55103	-0.34	0.54	0.10	0.62	2.77	1.60
Adenosine kinase;	P55264	-0.34	-0.25	-0.30	0.06	0.28	1.07
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	-0.34	-0.94	-0.64	0.43	1.90	3.14
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	-0.34	0.00	-0.17	0.24	1.07	0.69
Glutathione peroxidase 7;	Q99LJ6	-0.34	-0.92	-0.63	0.41	1.82	3.21
Plasma glutamate carboxypeptidase;	Q9WVJ3	-0.34	-0.67	-0.50	0.23	1.03	2.32
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	-0.34	0.18	-0.08	0.36	1.63	0.89
Glutathione S-transferase Mu 1;	P10649	-0.34	0.07	-0.14	0.29	1.29	0.73
Glutathione S-transferase Mu 2;	P15626	-0.15	-0.03	-0.09	0.09	0.39	0.37
Ras-related protein Rab-5A;	Q9CQD1	0.37	-0.23	0.07	0.42	1.90	1.30
Xaa-Pro dipeptidase;	Q11136	-0.34	-0.45	-0.40	0.08	0.36	1.49
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	-0.34	0.15	-0.09	0.35	1.55	0.89
Dynein light chain 2, cytoplasmic;	Q9D0M5	-0.34	0.68	0.17	0.72	3.21	2.10
3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial;	Q9D404	-0.34	-0.56	-0.45	0.15	0.68	2.11
1,4-alpha-glucan-branching enzyme;	Q9D6Y9	-0.34	-0.40	-0.37	0.04	0.18	1.40
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	-0.34	-0.12	-0.23	0.16	0.69	0.92
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	-0.32	-0.20	-0.26	0.09	0.38	0.95
UPF0556 protein C19orf10 homolog;	Q9CPT4	-0.32	-1.32	-0.82	0.71	3.16	3.81
Galectin-3-binding protein;	Q07797	-0.32	-1.00	-0.66	0.48	2.14	3.13
Peroxiredoxin-2;	Q61171	-0.32	-0.56	-0.44	0.17	0.74	1.82
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	-0.32	0.23	-0.05	0.39	1.73	0.93
PDZ and LIM domain protein 3;	O70209	-0.30	-0.07	-0.19	0.16	0.73	0.77
Carbonic anhydrase 2;	P00920	-0.30	-0.64	-0.47	0.24	1.07	2.15
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	-0.30	-0.43	-0.37	0.09	0.41	1.52
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	-0.30	-0.47	-0.39	0.12	0.54	1.79
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	-0.30	-0.40	-0.35	0.07	0.29	1.28
Galactokinase;	Q9R0N0	-0.30	-0.29	-0.30	0.01	0.06	1.07
Cullin-1;	Q9WTX6	-0.30	0.76	0.23	0.75	3.35	2.66
Probable methylthioribulose-1-phosphate dehydratase;	Q9WVQ5	-0.30	-0.29	-0.30	0.01	0.06	1.15
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	-0.30	-1.25	-0.78	0.67	2.99	2.08

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
UDP-glucose 6-dehydrogenase;	O70475	-0.30	-0.56	-0.43	0.18	0.80	2.01
Keratin, type I cytoskeletal 17;	Q9QWL7	1.00	3.05	2.03	1.45	6.48	17.87
Keratin, type I cytoskeletal 10;	P02535	-1.00	0.38	-0.31	0.98	4.35	3.38
Cytosolic non-specific dipeptidase;	Q9D1A2	-0.30	-0.52	-0.41	0.15	0.67	1.63
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	-0.30	-0.52	-0.41	0.15	0.67	1.71
Uncharacterized protein;	E9PYJ9	-0.30	-0.86	-0.58	0.39	1.76	2.21
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	-0.30	-1.00	-0.65	0.49	2.20	3.50
Uncharacterized protein;	Q3ULW8	-0.30	-0.22	-0.26	0.06	0.27	0.98
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	-0.30	-0.58	-0.44	0.19	0.86	2.11
3-hydroxyanthranilate 3,4-dioxygenase;	Q78JT3	-0.30	-2.00	-1.15	1.20	5.35	8.55
Integrin alpha-5;	P11688	-0.29	-0.18	-0.24	0.07	0.32	1.01
Peptidyl-prolyl cis-trans isomerase C;	P30412	-0.29	-0.67	-0.48	0.27	1.20	2.35
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	-0.29	0.04	-0.12	0.23	1.04	0.65
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	-0.29	-0.94	-0.61	0.46	2.07	2.81
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	-0.29	-0.58	-0.43	0.21	0.92	1.57
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	-0.29	-0.12	-0.20	0.12	0.52	0.85
Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	-0.29	0.59	0.15	0.62	2.75	1.76
Phosphoglycerate kinase 1;	P09411	-0.29	-0.45	-0.37	0.12	0.53	1.62
Lysophosphatidic acid phosphatase type 6;	Q8BP40	-0.29	0.45	0.08	0.52	2.34	1.37
UPF0160 protein MYG1, mitochondrial;	Q9JK81	-0.29	-0.30	-0.30	0.01	0.06	1.07
Spliceosome RNA helicase Ddx39b;	Q9Z1N5	-0.29	1.01	0.36	0.92	4.10	2.64
TOM1-like protein 2;	Q5SRX1	-0.29	-0.06	-0.17	0.16	0.72	0.72
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	-0.27	-0.49	-0.38	0.16	0.71	1.45
Dipeptidyl peptidase 4;	P28843	-0.27	-0.54	-0.40	0.19	0.84	1.43
Laminin subunit alpha-4;	P97927	-0.27	0.72	0.23	0.70	3.13	2.43
Myoferlin;	Q69ZN7	-0.27	0.06	-0.11	0.23	1.03	0.60
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	-0.27	-0.81	-0.54	0.38	1.71	2.60
AP-1 complex subunit beta-1;	O35643	-0.27	0.26	0.00	0.38	1.68	0.89
Adenosylhomocysteinase;	P50247	-0.27	-0.32	-0.30	0.04	0.17	1.23
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	-0.27	0.23	-0.02	0.35	1.57	0.92
Sepiapterin reductase;	Q64105	-0.27	-0.62	-0.45	0.25	1.11	2.10
Coagulation factor XIII A chain;	Q8BH61	-0.27	-0.17	-0.22	0.07	0.32	0.77
Dihydropteridine reductase;	Q8BVI4	-0.27	-0.52	-0.39	0.17	0.78	1.84
Carboxylesterase 3;	Q8VCT4	-0.27	-0.23	-0.25	0.02	0.11	0.86
Liver carboxylesterase N;	P23953	-0.49	-1.18	-0.84	0.49	2.18	4.27
Uncharacterized protein;	D3Z5G7	-1.25	-0.58	-0.92	0.48	2.13	3.19
Calcium/calmodulin-dependent protein kinase type 1;	Q91YS8	-0.27	-0.34	-0.30	0.05	0.22	1.28
Lysosome-associated membrane glycoprotein 1;	P11438	-0.25	-0.27	-0.26	0.01	0.05	1.05

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
Fibulin-2;	P37889	-0.25	0.41	0.08	0.47	2.09	1.37
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	-0.25	-0.34	-0.30	0.06	0.28	1.19
N-acetylglucosamine-6-sulfatase;	Q8BFR4	-0.25	-0.52	-0.38	0.19	0.83	1.69
Presequence protease, mitochondrial;	Q8K411	-0.25	-0.04	-0.15	0.15	0.66	0.61
Apolipoprotein A-I-binding protein;	Q8K4Z3	-0.25	-0.43	-0.34	0.13	0.57	1.54
SPRY domain-containing protein 4;	Q91WK1	-0.25	-0.34	-0.30	0.06	0.28	1.07
Protein NDRG2;	Q9QYG0	-0.25	-0.27	-0.26	0.01	0.05	1.03
S-formylglutathione hydrolase;	Q9R0P3	-0.25	-0.36	-0.31	0.07	0.33	1.21
Glycogen synthase kinase-3 beta;	Q9WV60	-0.25	-0.42	-0.33	0.12	0.51	1.37
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	-0.25	-0.40	-0.32	0.10	0.45	1.29
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	-0.25	-0.47	-0.36	0.16	0.70	1.36
U6 snRNA-associated Sm-like protein LSm2;	O35900	-0.25	0.52	0.13	0.54	2.42	1.67
Spermine synthase;	P97355	-0.25	-0.20	-0.23	0.04	0.16	0.75
Annexin A4;	P97429	-0.25	-0.54	-0.39	0.20	0.89	1.55
Peroxiredoxin-5, mitochondrial;	P99029	-0.25	-0.42	-0.33	0.12	0.51	1.49
Ubiquitin thioesterase OTUB1;	Q7TQI3	-0.25	0.28	0.01	0.37	1.66	0.90
Alpha-mannosidase 2C1;	Q91W89	-0.25	-0.30	-0.28	0.04	0.16	0.97
Flavin reductase (NADPH);	Q923D2	-0.25	-0.84	-0.54	0.41	1.85	2.82
D-dopachrome decarboxylase;	O35215	-0.23	-1.09	-0.66	0.60	2.70	3.89
Vacuolar protein sorting-associated protein 26A;	P40336	-0.23	0.41	0.09	0.46	2.04	1.45
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	-0.23	-0.15	-0.19	0.06	0.26	0.73
Peptidyl-prolyl cis-trans isomerase FKBP3;	Q62446	-0.23	-0.12	-0.18	0.08	0.36	0.74
NADP-dependent malic enzyme;	P06801	-0.23	-0.09	-0.16	0.10	0.46	0.57
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	-0.23	0.08	-0.08	0.22	1.00	0.48
Obg-like ATPase 1;	Q9CZ30	-0.23	-0.09	-0.16	0.10	0.46	0.64
Plasma membrane Ca++ transporting ATPase 4 variant x/e; Uncharacterized protein;	D1FNM8	-0.23	0.52	0.14	0.53	2.37	1.68
Transgelin;	P37804	-0.22	-0.23	-0.23	0.01	0.05	0.87
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	-0.22	-0.60	-0.41	0.27	1.20	1.84
Glutamate--cysteine ligase catalytic subunit;	P97494	-0.22	-0.43	-0.33	0.15	0.68	1.39
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	-0.22	0.66	0.22	0.62	2.77	1.91
Spermidine synthase;	Q64674	-0.22	-0.79	-0.50	0.40	1.79	2.55
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	-0.22	-0.01	-0.12	0.14	0.64	0.45
Catenin alpha-1;	P26231	-0.22	0.77	0.28	0.70	3.13	1.65
Ras-related protein Rab-11B;	P46638	-0.22	-0.25	-0.24	0.02	0.11	0.85
UPF0366 protein C11orf67 homolog;	Q8R0P4	-0.22	-1.18	-0.70	0.68	3.05	3.74
Guanine deaminase;	Q9R111	-0.22	-0.17	-0.19	0.04	0.16	0.73
Septin-5;	Q9Z2Q6	-0.22	0.50	0.14	0.50	2.25	1.54

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	-0.22	0.53	0.15	0.53	2.35	1.68
Ferritin;	Q9CPX4	-0.22	-0.38	-0.30	0.11	0.50	1.14
TIP41-like protein;	Q8BH58	-0.22	-0.17	-0.19	0.04	0.16	0.76
Coatomer subunit alpha;	Q8CIE6	-0.22	-0.22	-0.22	0.00	0.00	0.86
Peroxiredoxin-4;	O08807	-0.20	-0.30	-0.25	0.07	0.33	1.04
Ras-related protein R-Ras;	P10833	-0.20	-0.60	-0.40	0.28	1.26	1.61
78 kDa glucose-regulated protein;	P20029	-0.20	-0.20	-0.20	0.00	0.00	0.52
Heat shock cognate 71 kDa protein;	P63017	-0.17	0.19	0.01	0.25	1.13	0.63
Heat shock 70 kDa protein 1A;	Q61696	0.00	0.45	0.23	0.32	1.43	0.95
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	-0.18	-0.04	-0.11	0.10	0.44	0.42
Prostaglandin reductase 1;	Q91YR9	-0.18	0.10	-0.04	0.20	0.89	0.57
Dual specificity protein phosphatase 3;	Q9D7X3	-0.18	-0.69	-0.44	0.36	1.60	2.05
N-acylglucosamine 2-epimerase;	P82343	-0.18	-0.06	-0.12	0.09	0.39	0.45
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	-0.18	0.24	0.03	0.30	1.34	0.66
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	-0.18	-0.18	-0.18	0.00	0.00	0.54
14 kDa phosphohistidine phosphatase;	Q9DAK9	-0.18	1.06	0.44	0.88	3.92	3.30
Putative ATP-dependent RNA helicase Pl10;	P16381	-0.17	0.97	0.40	0.81	3.60	3.06
Nuclear transport factor 2;	P61971	-0.17	-0.34	-0.25	0.12	0.54	1.09
Eukaryotic translation initiation factor 4E;	P63073	-0.17	-0.60	-0.38	0.30	1.36	1.61
Ribonuclease inhibitor;	Q91VI7	-0.17	-0.18	-0.18	0.01	0.05	0.56
Translationally-controlled tumor protein;	P63028	-0.17	-0.34	-0.25	0.12	0.54	1.11
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	-0.17	0.10	-0.04	0.19	0.84	0.43
Copine-1;	Q8C166	-0.17	-0.18	-0.18	0.01	0.05	0.66
Copine-3;	Q8BT60	-0.47	0.00	-0.24	0.34	1.50	0.66
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	-0.17	-0.09	-0.13	0.06	0.25	0.49
Profilin-2;	Q9JJV2	-0.17	-0.40	-0.28	0.16	0.72	1.08
Prostaglandin reductase 2;	Q8VDQ1	-0.17	-0.25	-0.21	0.06	0.27	0.78
Carbonic anhydrase 1;	P13634	-0.17	-0.56	-0.36	0.27	1.22	1.69
Dihydropyrimidinase-related protein 5;	Q9EQF6	-0.17	-0.29	-0.23	0.08	0.37	0.89
Galectin-3;	P16110	-0.15	-0.23	-0.19	0.06	0.26	0.83
Nicotinamide phosphoribosyltransferase;	Q99KQ4	-0.15	-0.01	-0.08	0.10	0.44	0.31
Filamin-A;	Q8BTM8	-0.15	0.38	0.11	0.38	1.68	0.79
V-type proton ATPase 116 kDa subunit a isoform 1;	Q9Z1G4	-0.15	-0.15	-0.15	0.00	0.00	0.61
Superoxide dismutase [Cu-Zn];	P08228	-0.14	-0.09	-0.11	0.03	0.15	0.43
Galectin-1;	P16045	-0.14	-0.47	-0.31	0.24	1.07	1.42
Calnexin;	P35564	-0.14	0.89	0.38	0.72	3.23	2.66

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
Macrophage mannose receptor 1;	Q61830	-0.14	-0.12	-0.13	0.01	0.05	0.45
BTB/POZ domain-containing protein KCTD12;	Q6WVG3	-0.14	0.38	0.12	0.36	1.63	0.93
Protein phosphatase 1F;	Q8CGA0	-0.14	-1.00	-0.57	0.61	2.73	2.49
Aspartoacylase;	Q8R3P0	-0.14	-0.30	-0.22	0.12	0.53	0.83
Hepatocyte growth factor activator;	Q9R098	-0.14	-0.62	-0.38	0.34	1.53	1.13
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	-0.14	0.39	0.13	0.37	1.66	1.07
Seryl-tRNA synthetase, cytoplasmic;	P26638	-0.14	0.10	-0.02	0.17	0.74	0.38
Disabled homolog 2;	P98078	-0.14	-1.25	-0.69	0.79	3.52	3.33
Adapter molecule crk;	Q64010	-0.14	-0.56	-0.35	0.30	1.33	1.31
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	-0.14	0.08	-0.03	0.16	0.69	0.43
Phosphate carrier protein, mitochondrial;	Q8VEM8	-0.14	0.96	0.41	0.77	3.45	2.41
Ras-related protein Rab-7a;	P51150	-0.12	-0.29	-0.20	0.12	0.52	0.82
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	-0.12	-0.56	-0.34	0.31	1.38	1.50
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	-0.12	0.53	0.20	0.46	2.04	1.36
Magnesium-dependent phosphatase 1;	Q9D967	-0.12	-0.12	-0.12	0.00	0.00	0.46
Glycine N-methyltransferase;	Q9QXF8	-0.12	-1.84	-0.98	1.21	5.42	4.43
Proteasome subunit beta type-2;	Q9R1P3	-0.12	0.00	-0.06	0.08	0.38	0.22
ADP-ribosylation factor-like protein 3;	Q9WUL7	-0.12	-0.43	-0.28	0.22	0.99	1.12
Caveolin-1;	P49817	-0.12	0.72	0.30	0.60	2.66	2.09
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;	P63328	-0.12	-0.36	-0.24	0.17	0.75	0.94
Coronin-1C;	Q9WUM4	-0.12	0.59	0.23	0.50	2.23	1.52
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	-0.12	0.28	0.08	0.28	1.25	0.72
Sorting nexin-2;	Q9CWK8	-0.11	-0.71	-0.41	0.43	1.92	1.93
AP-2 complex subunit beta;	Q9DBG3	-0.11	0.25	0.07	0.25	1.12	0.72
Proteasome subunit beta type-5;	O55234	-0.11	0.19	0.04	0.21	0.93	0.51
Aldehyde dehydrogenase, mitochondrial;	P47738	-0.11	-0.32	-0.21	0.15	0.69	0.81
Glyoxalase domain-containing protein 4;	Q9CPV4	-0.11	-0.32	-0.21	0.15	0.69	0.92
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	-0.09	0.32	0.12	0.29	1.30	0.80
Rho GDP-dissociation inhibitor 1;	Q99PT1	-0.09	-0.40	-0.24	0.22	0.97	1.06
Thioredoxin domain-containing protein 17;	Q9CQM5	-0.09	-0.27	-0.18	0.13	0.57	0.74
Septin-7;	O55131	-0.09	0.28	0.09	0.26	1.15	0.65
Annexin A1;	P10107	-0.09	-0.15	-0.12	0.04	0.20	0.49
Inositol polyphosphate 1-phosphatase;	P49442	-0.09	-0.18	-0.14	0.07	0.30	0.51
Ras-related protein Rab-1A;	P62821	-0.09	-0.42	-0.25	0.23	1.03	1.08
Ras-related protein Rab-14;	Q91V41	0.10	-0.23	-0.07	0.23	1.05	0.70
Ras-related protein Rab-10;	P61027	0.08	-0.23	-0.08	0.22	1.00	0.64
Ras-related protein Rab-8A;	P55258	0.71	0.03	0.37	0.48	2.16	1.67

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Ras-related protein Rab-1B;	Q9D1G1	0.33	-0.03	0.15	0.26	1.14	0.76
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	-0.09	0.39	0.15	0.34	1.51	0.92
Leukocyte elastase inhibitor A;	Q9D154	-0.09	-0.56	-0.32	0.33	1.47	1.29
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	-0.09	0.06	-0.02	0.10	0.46	0.26
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	-0.07	0.99	0.46	0.75	3.35	2.09
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	-0.07	1.16	0.54	0.87	3.89	3.17
Glutamine synthetase;	P15105	-0.07	0.90	0.41	0.69	3.08	2.68
Peptidyl-prolyl cis-trans isomerase FKBP1A;	P26883	-0.07	-0.54	-0.30	0.33	1.46	1.45
Cytoplasmic aconitate hydratase;	P28271	-0.07	-0.30	-0.19	0.16	0.73	0.64
Mitogen-activated protein kinase 14;	P47811	-0.07	0.01	-0.03	0.06	0.28	0.15
Disks large homolog 1;	Q811D0	-0.07	-0.06	-0.07	0.01	0.05	0.23
UPF0587 protein C1orf123 homolog;	Q8BHG2	-0.07	-0.36	-0.22	0.20	0.90	0.93
Serpin B8;	O08800	-0.06	-0.58	-0.32	0.37	1.64	1.38
F-box only protein 7;	Q3U7U3	-0.06	-0.71	-0.39	0.46	2.06	1.93
Fibrinogen beta chain;	Q8K0E8	-0.06	0.61	0.28	0.48	2.12	1.63
Calponin-3;	Q9DAW9	-0.06	0.08	0.01	0.10	0.45	0.26
Cadherin-13;	Q9WTR5	-0.06	0.24	0.09	0.21	0.94	0.62
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	-0.06	-0.58	-0.32	0.37	1.64	1.40
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1;	P47856	-0.06	-0.23	-0.15	0.12	0.55	0.56
Pyruvate carboxylase, mitochondrial;	Q05920	-0.06	0.36	0.15	0.29	1.31	0.91
Corticosteroid-binding globulin;	Q06770	-0.06	-0.01	-0.04	0.03	0.14	0.11
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	-0.06	-0.81	-0.44	0.53	2.37	1.54
Putative transferase CAF17 homolog, mitochondrial;	Q8CAK1	-0.06	0.51	0.22	0.40	1.78	1.32
Nitrilase homolog 1;	Q8VDK1	-0.06	-0.17	-0.11	0.08	0.34	0.45
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	-0.06	0.01	-0.02	0.05	0.23	0.12
Putative hydrolase RBBP9;	O88851	-0.04	-0.89	-0.47	0.60	2.67	2.42
Cytosolic purine 5'-nucleotidase;	Q3V1L4	-0.04	0.40	0.18	0.31	1.40	0.98
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	-0.04	-0.17	-0.11	0.09	0.39	0.41
Selenocysteine lyase;	Q9JLI6	-0.04	0.36	0.16	0.28	1.26	0.70
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	-0.04	-0.56	-0.30	0.36	1.62	1.33
Target of Myb protein 1;	O88746	-0.03	-0.04	-0.04	0.01	0.05	0.14
Alcohol dehydrogenase class-3;	P28474	-0.03	-0.07	-0.05	0.03	0.14	0.18
Tyrosine-protein phosphatase non-receptor type 11;	P35235	-0.03	0.37	0.17	0.28	1.25	0.80
Cysteine and glycine-rich protein 3;	P50462	-0.03	-0.03	-0.03	0.00	0.00	0.10
Rab GDP dissociation inhibitor beta;	Q61598	-0.03	-0.14	-0.08	0.08	0.34	0.26
Protein arginine N-methyltransferase 5;	Q8CIG8	-0.03	0.55	0.26	0.41	1.82	1.37
Thioredoxin domain-containing protein 12;	Q9CQU0	-0.03	-0.12	-0.07	0.06	0.29	0.29

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Vacuolar protein sorting-associated protein 35;	Q9EQH3	-0.03	0.12	0.05	0.11	0.48	0.25
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	-0.03	0.39	0.18	0.30	1.32	0.94
Dihydropyrimidinase-related protein 2;	O08553	-0.03	-0.09	-0.06	0.04	0.19	0.23
Dihydropyrimidinase-related protein 3;	Q62188	0.54	0.25	0.39	0.20	0.90	1.81
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	-0.03	-0.15	-0.09	0.09	0.39	0.31
Actin-related protein 2/3 complex subunit 4;	P59999	-0.03	0.65	0.31	0.48	2.15	1.50
Ubiquitin-fold modifier 1;	P61961	-0.03	-0.36	-0.19	0.23	1.04	0.90
Acyl-protein thioesterase 1;	P97823	-0.03	-0.56	-0.29	0.37	1.66	1.30
Biliverdin reductase A;	Q9CY64	-0.03	-0.09	-0.06	0.04	0.19	0.21
Uncharacterized protein;	E9PWQ3	-0.03	1.29	0.63	0.93	4.17	3.14
Cysteine sulfinic acid decarboxylase;	Q9DBE0	-0.01	-0.45	-0.23	0.31	1.39	0.79
Heme-binding protein 1;	Q9R257	-0.01	-0.86	-0.44	0.60	2.68	1.80
Protein disulfide-isomerase A3;	P27773	-0.01	0.10	0.04	0.08	0.35	0.20
Lupus La protein homolog;	P32067	-0.01	1.55	0.77	1.10	4.92	3.49
Histidine ammonia-lyase;	P35492	-0.01	-0.18	-0.10	0.12	0.54	0.39
DNA damage-binding protein 1;	Q3U1J4	-0.01	0.43	0.21	0.32	1.41	1.02
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	-0.01	-0.27	-0.14	0.18	0.81	0.55
Pyridoxal kinase;	Q8K183	-0.01	-0.34	-0.18	0.23	1.03	0.77
Plastin-3;	Q99K51	-0.01	-0.04	-0.03	0.02	0.09	0.09
von Willebrand factor A domain-containing protein 5A;	Q99KC8	-0.01	0.28	0.13	0.20	0.91	0.52
Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	-0.01	0.47	0.23	0.34	1.51	1.02
Myeloid-associated differentiation marker;	O35682	0.00	0.85	0.42	0.60	2.68	2.13
Myoglobin;	P04247	0.00	-0.47	-0.24	0.34	1.50	1.01
Myotrophin;	P62774	0.00	0.35	0.17	0.24	1.09	0.73
Microtubule-associated protein RP/EB family member 1;	Q61166	0.00	-0.45	-0.23	0.32	1.43	1.08
Osteoclast-stimulating factor 1;	Q62422	0.00	0.28	0.14	0.19	0.87	0.58
Regucalcin;	Q64374	0.00	-1.94	-0.97	1.37	6.13	6.70
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	0.00	0.44	0.22	0.31	1.40	1.00
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	0.00	-0.18	-0.09	0.13	0.58	0.39
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	0.00	0.58	0.29	0.41	1.82	1.37
Phosphoacetylglucosamine mutase;	Q9CYR6	0.00	-0.92	-0.46	0.65	2.89	2.28
Protein DDI1 homolog 2;	A2ADY9	0.01	-0.14	-0.06	0.11	0.47	0.29
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	0.01	0.10	0.06	0.06	0.27	0.21
NAD-dependent malic enzyme, mitochondrial;	Q99KE1	0.01	-0.11	-0.05	0.08	0.38	0.25
Prostaglandin F2 receptor negative regulator;	Q9WV91	0.01	-0.40	-0.19	0.29	1.29	0.74
Fatty acid-binding protein, adipocyte;	P04117	0.01	0.07	0.04	0.04	0.18	0.15
Heat shock protein beta-1;	P14602	0.01	-0.23	-0.11	0.18	0.78	0.47

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Elongation factor 2;	P58252	0.01	0.38	0.20	0.26	1.15	0.72
Heterogeneous nuclear ribonucleoprotein D0;	Q60668	0.01	0.07	0.04	0.04	0.18	0.14
Hypoxia up-regulated protein 1;	Q9JKR6	0.01	0.29	0.15	0.19	0.86	0.59
Sorting nexin-1;	Q9WV80	0.01	-0.54	-0.26	0.39	1.73	1.25
EF hand domain containing 2; Efhd2 protein; Uncharacterized protein;	Q8C845	0.01	-0.92	-0.45	0.66	2.94	2.11
Protein disulfide-isomerase A4;	P08003	0.03	0.36	0.19	0.23	1.03	0.59
Parkinson disease 7 domain-containing protein 1;	Q8BFQ8	0.03	0.40	0.22	0.26	1.17	0.86
Ester hydrolase C11orf54 homolog;	Q91V76	0.03	-0.43	-0.20	0.33	1.46	1.04
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	0.03	-0.01	0.01	0.03	0.14	0.09
Calcineurin-like phosphoesterase domain-containing protein 1;	Q8BFS6	0.03	-0.30	-0.14	0.24	1.05	0.71
Vacuolar protein sorting-associated protein 29;	Q9QZ88	0.03	0.01	0.02	0.01	0.05	0.07
Proteasome subunit alpha type-4;	Q9R1P0	0.03	0.30	0.16	0.19	0.85	0.70
Biotinidase;	Q8CIF4	0.04	1.61	0.83	1.11	4.94	5.90
GDP-mannose 4,6 dehydratase;	Q8K0C9	0.04	0.23	0.14	0.13	0.58	0.48
Ribulose-phosphate 3-epimerase;	Q8VEE0	0.04	-0.29	-0.12	0.23	1.04	0.68
Pyridoxine-5'-phosphate oxidase;	Q91XF0	0.04	-0.23	-0.10	0.20	0.87	0.59
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	0.04	-0.30	-0.13	0.25	1.10	0.46
Protein disulfide-isomerase;	P09103	0.04	0.14	0.09	0.07	0.30	0.26
Alpha-crystallin B chain;	P23927	0.04	-0.32	-0.14	0.26	1.15	0.81
LIM and cysteine-rich domains protein 1;	Q8VEE1	0.04	-0.54	-0.25	0.41	1.82	0.96
TAR DNA-binding protein 43;	Q921F2	0.04	1.65	0.85	1.14	5.08	6.10
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	0.04	-0.07	-0.02	0.08	0.37	0.21
Basal cell adhesion molecule;	Q9R069	0.04	0.15	0.10	0.08	0.34	0.39
Glutathione peroxidase 1;	P11352	0.06	-0.40	-0.17	0.32	1.43	0.88
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	0.06	0.14	0.10	0.06	0.26	0.35
Tripeptidyl-peptidase 2;	Q64514	0.06	1.10	0.58	0.74	3.29	2.32
Signal transducer and activator of transcription 3;	P42227	0.06	-0.76	-0.35	0.58	2.58	2.07
Reticulocalbin-3;	Q8BH97	0.06	-0.14	-0.04	0.14	0.61	0.28
BAG family molecular chaperone regulator 1;	Q60739	0.07	0.77	0.42	0.49	2.20	2.16
CD109 antigen;	Q8R422	0.07	0.72	0.40	0.46	2.06	1.62
Serine/threonine-protein kinase DCLK1;	Q9JLM8	0.07	-0.20	-0.07	0.19	0.86	0.54
S-phase kinase-associated protein 1;	Q9WTX5	0.07	0.49	0.28	0.29	1.31	1.29
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	0.07	-0.56	-0.24	0.44	1.98	1.25
Protein canopy homolog 4;	Q8BQ47	0.07	0.01	0.04	0.04	0.18	0.18
L-xylulose reductase;	Q91X52	0.07	-0.60	-0.26	0.47	2.11	1.59
MAGUK p55 subfamily member 6;	Q9JLB0	0.07	0.23	0.15	0.11	0.50	0.56
Nucleoside diphosphate kinase 3;	Q9WV85	0.07	-0.20	-0.07	0.19	0.86	0.56
Thioredoxin;	P10639	0.08	0.04	0.06	0.03	0.13	0.23

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Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	0.08	-0.38	-0.15	0.33	1.46	0.97
Phosphoglucomutase-2;	Q7TSV4	0.08	-0.23	-0.08	0.22	1.00	0.41
Cytosolic 5'-nucleotidase 3;	Q9D020	0.08	-0.20	-0.06	0.20	0.90	0.53
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	0.08	0.42	0.25	0.24	1.07	1.09
Destrin;	Q9R0P5	0.08	0.58	0.33	0.35	1.55	1.16
Uncharacterized protein;	E9PV24	0.08	0.59	0.33	0.35	1.58	1.20
Beta-galactosidase;	P23780	0.08	0.12	0.10	0.03	0.13	0.39
Peroxiredoxin-1;	P35700	0.08	-0.14	-0.03	0.16	0.69	0.45
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	0.08	0.32	0.20	0.17	0.75	0.76
NSFL1 cofactor p47;	Q9CZ44	0.08	0.18	0.13	0.07	0.29	0.48
Malignant T cell-amplified sequence 1;	Q9DB27	0.08	0.08	0.08	0.00	0.00	0.33
3'(2'),5'-bisphosphate nucleotidase 1;	Q9Z0S1	0.08	-0.20	-0.06	0.20	0.90	0.52
Glucosidase 2 subunit beta;	O08795	0.10	0.49	0.29	0.27	1.22	1.31
Cysteine and glycine-rich protein 1;	P97315	0.10	-0.74	-0.32	0.59	2.64	2.01
Alanine aminotransferase 1;	Q8QZR5	0.10	-0.11	0.00	0.14	0.64	0.39
Lysosomal alpha-glucosidase;	P70699	0.10	0.00	0.05	0.07	0.31	0.20
Uncharacterized protein;	Q3TUE1	0.10	0.92	0.51	0.58	2.59	2.68
COP9 signalosome complex subunit 5;	O35864	0.11	0.76	0.43	0.46	2.04	1.81
Fatty acid-binding protein, heart;	P11404	0.11	-0.56	-0.22	0.47	2.11	1.57
Proteasome subunit beta type-8;	P28063	0.11	0.38	0.25	0.19	0.85	0.88
Crk-like protein;	P47941	0.11	-0.06	0.03	0.12	0.54	0.31
Proteasome subunit beta type-4;	P99026	0.11	0.29	0.20	0.12	0.56	0.78
Proteasome subunit beta type-6;	Q60692	0.11	0.25	0.18	0.10	0.44	0.76
Calcyclin-binding protein;	Q9CXW3	0.11	-0.60	-0.24	0.50	2.24	1.75
Dipeptidyl peptidase 2;	Q9ET22	0.11	-0.03	0.04	0.10	0.44	0.30
Translin-associated protein X;	Q9QZE7	0.11	0.07	0.09	0.03	0.13	0.36
Actin-related protein 3;	Q99JY9	0.11	0.10	0.10	0.01	0.04	0.41
Glia maturation factor beta;	Q9CQI3	0.11	-0.23	-0.06	0.24	1.09	0.71
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	0.12	-0.69	-0.28	0.58	2.57	1.63
Septin-2;	P42208	0.12	0.08	0.10	0.03	0.13	0.36
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	0.12	0.38	0.25	0.18	0.81	1.00
Multifunctional protein ADE2;	Q9DCL9	0.12	0.35	0.23	0.16	0.70	0.77
ATPase Asna1;	O54984	0.14	0.35	0.24	0.15	0.65	1.06
Calreticulin;	P14211	0.14	0.99	0.57	0.60	2.70	3.20
Vitamin D-binding protein;	P21614	0.14	-0.76	-0.31	0.64	2.84	1.92
Mitotic checkpoint protein BUB3;	Q9WVA3	0.14	1.60	0.87	1.03	4.61	5.39
Polymerase I and transcript release factor;	O54724	0.14	0.99	0.56	0.60	2.68	3.03
Diphosphoinositol polyphosphate phosphohydrolase 3-alpha;	P0C027	0.14	-0.18	-0.02	0.23	1.02	0.61

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
Prolyl 3-hydroxylase 1;	Q3V1T4	0.14	-0.27	-0.07	0.29	1.28	0.72
Glutathione S-transferase theta-1;	Q64471	0.14	-0.15	-0.01	0.21	0.92	0.51
Vinculin;	Q64727	0.14	0.35	0.24	0.15	0.65	0.84
Xaa-Pro aminopeptidase 1;	Q6P1B1	0.14	-0.15	-0.01	0.21	0.92	0.57
Major vault protein;	Q9EQK5	0.14	0.71	0.43	0.41	1.82	1.77
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	0.15	-0.58	-0.21	0.52	2.30	1.43
Glutathione S-transferase kappa 1;	Q9DCM2	0.15	0.35	0.25	0.14	0.61	0.82
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	0.15	-0.04	0.05	0.14	0.62	0.33
Guanine nucleotide-binding protein G(k) subunit alpha;	Q9DC51	0.61	0.36	0.49	0.18	0.81	2.24
GDP-L-fucose synthase;	P23591	0.16	0.15	0.16	0.01	0.04	0.62
Actin-related protein 2;	P61161	0.16	0.60	0.38	0.31	1.36	1.66
Acylamino-acid-releasing enzyme;	Q8R146	0.16	-0.29	-0.06	0.32	1.42	0.85
Dipeptidyl peptidase 3;	Q99KK7	0.16	0.16	0.16	0.00	0.00	0.59
Glucosamine-6-phosphate isomerase 1;	O88958	0.16	0.16	0.16	0.00	0.00	0.54
Chromobox protein homolog 3;	P23198	0.16	0.24	0.20	0.05	0.24	0.73
F-actin-capping protein subunit beta;	P47757	0.16	-0.09	0.04	0.18	0.80	0.44
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	0.16	0.15	0.16	0.01	0.04	0.62
Nucleosome assembly protein 1-like 4;	Q78ZA7	0.18	0.37	0.27	0.14	0.60	1.13
Thioredoxin-like protein 1;	Q8CDN6	0.18	0.36	0.27	0.13	0.57	1.07
Perilipin-1;	Q8CGN5	0.18	-0.47	-0.15	0.46	2.05	1.43
Endoplasmic reticulum resident protein 44;	Q9D1Q6	0.18	-0.29	-0.06	0.33	1.46	0.83
Prolargin;	Q9JK53	0.18	1.47	0.82	0.91	4.07	5.37
Integrin beta-1;	P09055	0.18	0.29	0.23	0.08	0.35	0.87
Protein 4.1;	P48193	0.18	-0.06	0.06	0.17	0.74	0.41
Aminopeptidase N;	P97449	0.18	-0.01	0.08	0.13	0.60	0.32
Ubiquitin-like modifier-activating enzyme 1;	Q02053	0.18	-0.06	0.06	0.17	0.74	0.43
Versican core protein;	Q62059	0.18	0.91	0.54	0.52	2.32	2.64
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	0.18	-0.25	-0.04	0.30	1.35	0.90
N-acetyl-D-glucosamine kinase;	Q9QZ08	0.18	0.18	0.18	0.00	0.00	0.75
Platelet glycoprotein 4;	Q08857	0.19	0.25	0.22	0.04	0.20	0.92
N-alpha-acetyltransferase 38, NatC auxiliary subunit;	Q6ZWM4	0.19	0.42	0.31	0.16	0.74	1.31
ATP-dependent RNA helicase DDX42;	Q810A7	0.19	1.14	0.67	0.68	3.01	2.39
Neutral alpha-glucosidase AB;	Q8BHN3	0.19	0.74	0.46	0.39	1.74	2.10
Prolyl endopeptidase;	Q9QUR6	0.19	0.00	0.09	0.13	0.60	0.38
Proteasome subunit beta type-3;	Q9R1P1	0.19	-0.04	0.07	0.16	0.74	0.48
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	0.19	-0.09	0.05	0.20	0.88	0.58
Transketolase;	P40142	0.20	0.20	0.20	0.00	0.00	0.82

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
Peroxisomal multifunctional enzyme type 2;	P51660	0.20	0.16	0.18	0.03	0.12	0.70
Filamin-B;	Q80X90	0.20	0.04	0.12	0.11	0.50	0.35
Ubiquitin-like modifier-activating enzyme 5;	Q8VE47	0.20	-0.84	-0.32	0.73	3.28	2.29
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	0.20	-0.23	-0.02	0.31	1.38	0.90
Band 4.1-like protein 2;	O70318	0.20	-0.14	0.03	0.24	1.07	0.58
Proteasome activator complex subunit 2;	P97372	0.20	-0.29	-0.04	0.35	1.54	0.90
Nischarin;	Q80TM9	0.20	0.03	0.12	0.12	0.55	0.45
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	0.20	-0.20	0.00	0.28	1.27	0.78
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	0.20	0.20	0.20	0.00	0.00	0.72
Toll-interacting protein;	Q9QZ06	0.20	-0.06	0.07	0.18	0.82	0.53
Heat shock protein 4; Heat shock protein 4, isoform CRA_a; Uncharacterized protein;	Q3U2G2	0.20	0.58	0.39	0.26	1.18	1.36
Heat shock 70 kDa protein 4L;	P48722	0.87	0.90	0.89	0.02	0.10	4.38
Trk-fused; Uncharacterized protein;	Q8C2C6	0.20	0.03	0.12	0.12	0.55	0.35
Stress-70 protein, mitochondrial;	P38647	0.21	0.53	0.37	0.22	0.98	1.56
DCC-interacting protein 13-alpha;	Q8K3H0	0.21	-0.30	-0.05	0.37	1.64	1.01
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	0.21	0.89	0.55	0.48	2.13	2.88
Calpain-1 catalytic subunit;	O35350	0.23	0.18	0.20	0.04	0.16	0.73
10 kDa heat shock protein, mitochondrial;	Q64433	0.23	-0.17	0.03	0.28	1.25	0.68
Elongation factor G, mitochondrial;	Q8K0D5	0.23	0.16	0.20	0.05	0.20	0.78
Thioredoxin domain-containing protein 5;	Q91W90	0.23	-0.45	-0.11	0.48	2.15	1.48
UPF0368 protein Cxorf26 homolog;	Q9D0B6	0.23	0.07	0.15	0.11	0.50	0.60
Sorting nexin-5;	Q9D8U8	0.23	-0.32	-0.05	0.39	1.73	0.99
Epididymal secretory protein E1;	Q9Z0J0	0.23	-0.06	0.08	0.20	0.90	0.59
Peptidyl-prolyl cis-trans isomerase A;	P17742	0.23	0.47	0.35	0.17	0.75	1.16
Endoplasmic reticulum resident protein 29;	P57759	0.23	-0.27	-0.02	0.35	1.57	1.05
Profilin-1;	P62962	0.23	0.12	0.18	0.07	0.33	0.71
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	0.23	0.47	0.35	0.17	0.75	1.50
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	0.23	0.38	0.30	0.11	0.48	1.29
WD repeat-containing protein 1;	O88342	0.24	-0.30	-0.03	0.38	1.71	0.90
Thy-1 membrane glycoprotein;	P01831	0.24	0.50	0.37	0.18	0.81	1.58
AP-2 complex subunit alpha-2;	P17427	0.24	0.08	0.16	0.11	0.49	0.55
[Protein ADP-ribosylarginine] hydrolase;	P54923	0.24	-0.69	-0.23	0.66	2.93	2.08
4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	0.24	-0.27	-0.02	0.36	1.60	0.97
Heterogeneous nuclear ribonucleoprotein K;	P61979	0.24	0.55	0.39	0.22	0.97	1.71
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	0.24	0.12	0.18	0.08	0.36	0.60
Proteasome subunit alpha type-7;	Q9Z2U0	0.24	0.29	0.26	0.03	0.15	1.12
Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	0.25	1.88	1.06	1.15	5.13	5.24

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
Gelsolin;	P13020	0.25	-0.47	-0.11	0.51	2.29	1.31
26S proteasome non-ATPase regulatory subunit 4;	O35226	0.26	0.11	0.19	0.11	0.48	0.80
Ig gamma-2B chain C region;	P01867	0.26	0.57	0.41	0.21	0.96	1.74
Basigin;	P18572	0.26	0.12	0.19	0.10	0.44	0.67
Rho GTPase-activating protein 1;	Q5FWK3	0.26	-0.07	0.09	0.24	1.06	0.61
CB1 cannabinoid receptor-interacting protein 1;	Q5M8N0	0.26	-0.34	-0.04	0.43	1.90	1.23
Serine/threonine-protein kinase OSR1;	Q6P9R2	0.26	0.06	0.16	0.15	0.65	0.47
Selenide, water dikinase 1;	Q8BH69	0.26	0.06	0.16	0.15	0.65	0.66
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	0.26	0.93	0.59	0.47	2.09	2.27
Transaldolase;	Q93092	0.26	0.16	0.21	0.07	0.32	0.77
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	0.26	-0.27	0.00	0.38	1.68	0.96
Serine/threonine-protein kinase PAK 2;	Q8CIN4	0.26	-0.15	0.06	0.29	1.31	0.85
Cysteinyl-tRNA synthetase, cytoplasmic;	Q9ER72	0.26	-0.32	-0.03	0.41	1.85	1.13
Aspartyl aminopeptidase;	Q9Z2W0	0.26	-0.40	-0.07	0.47	2.08	1.25
Membrane primary amine oxidase;	O70423	0.28	0.32	0.30	0.03	0.15	1.13
Gamma-butyrobetaine dioxygenase;	Q924Y0	0.28	0.16	0.22	0.08	0.35	0.82
Glutaredoxin-3;	Q9CQM9	0.28	-0.34	-0.03	0.43	1.94	1.26
C-reactive protein;	P14847	0.29	-0.76	-0.24	0.74	3.31	2.54
Microtubule-associated protein 4;	P27546	0.29	-0.18	0.05	0.33	1.49	0.92
Tissue alpha-L-fucosidase;	Q99LJ1	0.29	0.49	0.39	0.14	0.63	1.59
5-hydroxyisourate hydrolase;	Q9CRB3	0.29	0.08	0.19	0.14	0.64	0.71
SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	0.29	-0.30	-0.01	0.42	1.87	1.20
Hemoglobin subunit beta-1;	P02088	0.29	-0.36	-0.04	0.46	2.04	1.44
Hemoglobin subunit beta-2;	P02089	0.61	-0.49	0.06	0.78	3.50	2.49
Prostamide/prostaglandin F synthase;	Q9DB60	0.29	-0.60	-0.16	0.63	2.80	1.91
Proteasome subunit beta type-9;	P28076	0.30	0.38	0.34	0.06	0.25	1.36
Guanylate kinase;	Q64520	0.30	-0.01	0.14	0.22	0.99	0.68
Phytanoyl-CoA dioxygenase domain-containing protein 1;	Q9DB26	0.30	-0.45	-0.08	0.53	2.38	1.65
Guanine nucleotide-binding protein subunit alpha-13;	P27601	0.30	0.23	0.26	0.05	0.23	1.07
Septin-11;	Q8C1B7	0.30	0.93	0.62	0.45	2.00	2.73
Septin-8;	Q8CHH9	0.00	0.18	0.09	0.12	0.56	0.31
Septin-6;	Q9R1T4	0.28	0.43	0.35	0.11	0.50	1.38
Argininosuccinate lyase;	Q91YI0	0.30	-0.30	0.00	0.43	1.90	1.18
Uncharacterized protein;	E9Q616	0.30	0.59	0.44	0.20	0.90	1.53
Uncharacterized protein;	F7CAE1	0.30	-0.42	-0.06	0.50	2.25	1.61
Eukaryotic translation initiation factor 4 gamma 1;	Q6NZJ6	0.30	0.93	0.62	0.45	2.00	2.99
14-3-3 protein gamma;	P61982	0.31	0.54	0.42	0.16	0.71	1.50
Elongation factor Tu, mitochondrial;	Q8BFR5	0.31	-0.17	0.07	0.34	1.51	1.03

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S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	0.31	-0.07	0.12	0.27	1.21	0.81
AP-2 complex subunit alpha-1;	P17426	0.31	0.96	0.63	0.46	2.04	3.32
Serpin B12;	Q9D7P9	0.31	0.31	0.31	0.00	0.00	0.87
Actin-related protein 2/3 complex subunit 3;	Q9JM76	0.31	0.72	0.52	0.29	1.30	2.04
Uncharacterized protein;	E9QK49	0.31	0.12	0.22	0.13	0.59	0.80
Protein S100-A4;	P07091	0.32	0.26	0.29	0.04	0.19	1.25
ADP-ribosylation factor 6;	P62331	0.32	-0.56	-0.12	0.62	2.77	2.01
Chloride intracellular channel protein 1;	Q9Z1Q5	0.32	0.20	0.26	0.08	0.38	1.07
Golgi apparatus protein 1;	Q61543	0.32	0.76	0.54	0.31	1.37	2.46
Heat shock protein 105 kDa;	Q61699	0.32	0.31	0.32	0.01	0.04	1.18
Protein Noxp20;	Q9D281	0.32	-0.94	-0.31	0.89	3.99	2.96
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	0.33	0.31	0.32	0.02	0.07	1.41
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	0.33	0.58	0.45	0.17	0.76	1.73
Dynactin subunit 2;	Q99KJ8	0.33	0.74	0.54	0.29	1.28	2.35
SUMO-activating enzyme subunit 1;	Q9R1T2	0.33	-0.03	0.15	0.26	1.14	0.80
0	A6H630	0.33	0.45	0.39	0.09	0.38	1.36
Small ubiquitin-related modifier 2;	P61957	0.33	0.11	0.22	0.16	0.70	0.97
Integrin beta-5;	O70309	0.35	0.53	0.44	0.13	0.57	2.02
Proteasome subunit alpha type-2;	P49722	0.35	-0.03	0.16	0.26	1.18	0.77
GTPase NRas;	P08556	0.35	0.29	0.32	0.04	0.18	1.37
Sorcin;	Q6P069	0.35	-0.18	0.08	0.37	1.67	1.00
Septin-9;	Q80UG5	0.35	0.87	0.61	0.37	1.66	3.01
Protein disulfide-isomerase A6;	Q922R8	0.35	0.10	0.22	0.17	0.78	0.92
Vacuolar protein-sorting-associated protein 25;	Q9CQ80	0.35	-0.06	0.14	0.29	1.28	0.85
Ubiquitin-conjugating enzyme E2 variant 1;	Q9CZY3	0.35	0.00	0.17	0.24	1.09	0.77
Proteasome subunit alpha type-5;	Q9Z2U1	0.35	0.31	0.33	0.02	0.11	1.31
Junction plakoglobin;	Q02257	0.36	0.39	0.37	0.02	0.11	1.33
Heterogeneous nuclear ribonucleoprotein A1;	P49312	0.37	2.97	1.67	1.84	8.21	8.17
Calcineurin subunit B type 1;	Q63810	0.37	0.77	0.57	0.29	1.28	2.43
NHL repeat-containing protein 3;	Q8CCH2	0.37	0.40	0.38	0.02	0.11	1.51
Eukaryotic translation initiation factor 6;	O55135	0.37	0.45	0.41	0.06	0.27	1.83
Calpain small subunit 1;	O88456	0.37	0.01	0.19	0.25	1.11	0.83
C-terminal-binding protein 1;	O88712	0.37	0.12	0.25	0.17	0.77	1.03
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	0.37	0.01	0.19	0.25	1.11	0.81
Mitogen-activated protein kinase 3;	Q63844	0.37	-0.03	0.17	0.28	1.25	0.87
Mitogen-activated protein kinase 1;	P63085	0.24	1.07	0.65	0.59	2.62	3.04
NADH-cytochrome b5 reductase 3;	Q9DCN2	0.37	0.99	0.68	0.44	1.98	3.16
Proteasome subunit alpha type-6;	Q9QUM9	0.37	0.64	0.50	0.19	0.87	2.04

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Uncharacterized protein;	E9Q9T2	0.37	0.89	0.63	0.37	1.64	2.83
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	-1.29	-0.84	-1.06	0.32	1.42	5.85
Macrophage migration inhibitory factor;	P34884	0.38	0.00	0.19	0.27	1.20	0.77
Serpin B5;	P70124	0.38	0.01	0.20	0.26	1.15	0.88
Proteasome subunit beta type-7;	P70195	0.38	0.90	0.64	0.36	1.63	3.30
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	0.38	0.54	0.46	0.11	0.50	2.18
Alanyl-tRNA synthetase, cytoplasmic;	Q8BGQ7	0.38	-0.14	0.12	0.36	1.63	1.08
Dynamin-1-like protein;	Q8K1M6	0.38	-0.56	-0.09	0.66	2.95	2.12
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	0.38	0.15	0.27	0.16	0.72	0.95
Gamma-glutamylcyclotransferase;	Q9D7X8	0.38	0.35	0.36	0.02	0.11	1.63
Coatomer subunit gamma;	Q9QZE5	0.38	1.09	0.74	0.50	2.25	3.37
Puromycin-sensitive aminopeptidase;	Q11011	0.38	-0.36	0.01	0.52	2.33	1.40
Protein RCC2;	Q8BK67	0.38	1.23	0.81	0.60	2.70	3.37
5-oxoprolinase;	Q8K010	0.38	-0.12	0.13	0.35	1.58	0.87
SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	0.38	0.00	0.19	0.27	1.20	0.82
GTP-binding protein SAR1b;	Q9CQC9	0.43	-0.12	0.16	0.39	1.75	1.20
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	0.39	0.14	0.26	0.18	0.80	1.13
Tubulin-specific chaperone D;	Q8BYA0	0.39	1.22	0.81	0.59	2.62	4.24
MKIAA0079 protein; SEC24 related gene family, member C (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q80U83	0.39	0.56	0.47	0.12	0.52	2.14
Phosphatidylinositol transfer protein alpha isoform;	P53810	0.39	0.04	0.22	0.25	1.10	0.94
Eukaryotic initiation factor 4A-II;	P10630	-0.69	-0.11	-0.40	0.41	1.85	1.90
6-phosphogluconolactonase;	Q9CQ60	0.39	-0.27	0.06	0.47	2.08	1.42
MCG21235; Uncharacterized protein;	Q9D1Q5	0.39	0.52	0.45	0.09	0.40	1.73
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	0.40	-0.25	0.07	0.46	2.06	1.40
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	0.65	0.20	0.43	0.32	1.42	1.69
Cofilin-1;	P18760	0.40	1.12	0.76	0.51	2.28	2.79
Epidermal growth factor receptor substrate 15;	P42567	0.40	0.29	0.34	0.08	0.36	1.35
Ubiquitin-conjugating enzyme E2 K;	P61087	0.40	-0.01	0.19	0.29	1.31	0.89
Vasodilator-stimulated phosphoprotein;	P70460	0.41	0.24	0.33	0.12	0.54	1.38
Costars family protein C6orf115 homolog;	Q4KML4	0.41	0.19	0.30	0.16	0.70	1.28
CD166 antigen;	Q61490	0.41	0.47	0.44	0.04	0.17	1.94
Polyadenylate-binding protein 2;	Q8CCS6	0.41	1.92	1.17	1.07	4.77	8.84
Sorting nexin-6;	Q6P8X1	0.42	-0.56	-0.07	0.69	3.09	2.03
Elongation factor 1-gamma;	Q9D8N0	0.42	0.95	0.69	0.37	1.66	3.49

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
Polyadenylate-binding protein 1;	P29341	0.42	1.02	0.72	0.42	1.89	3.37
Ubiquitin-conjugating enzyme E2 N;	P61089	0.42	-0.01	0.20	0.31	1.38	0.92
Inter-alpha-trypsin inhibitor heavy chain H2;	Q61703	0.42	-0.86	-0.22	0.91	4.05	2.99
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	0.42	-0.27	0.08	0.49	2.18	1.27
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	0.42	1.47	0.94	0.74	3.29	4.59
Heterogeneous nuclear ribonucleoprotein H;	O35737	0.43	1.63	1.03	0.84	3.77	5.93
Nidogen-1;	P10493	0.43	0.83	0.63	0.28	1.26	2.83
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	0.43	-0.17	0.13	0.42	1.90	1.11
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	0.43	0.10	0.27	0.24	1.06	0.96
Bifunctional protein NCOAT;	Q9EQQ9	0.43	0.20	0.32	0.16	0.73	1.28
Ubiquitin-conjugating enzyme E2 L3;	P68037	0.43	0.06	0.25	0.27	1.19	1.07
T-complex protein 1 subunit gamma;	P80318	0.43	0.64	0.54	0.15	0.66	2.33
Protein arginine N-methyltransferase 1;	Q9JIF0	0.43	1.49	0.96	0.74	3.32	5.25
Vigilin;	Q8VDJ3	0.44	0.78	0.61	0.24	1.07	2.44
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	0.44	0.78	0.61	0.24	1.07	2.25
ADP-ribosylation factor 3;	P61205	0.44	-0.09	0.18	0.38	1.68	1.20
ADP-ribosylation factor 5;	P84084	1.17	-0.27	0.45	1.02	4.54	2.59
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	0.44	-0.11	0.17	0.39	1.73	0.97
Pro-interleukin-16;	O54824	0.45	1.66	1.05	0.85	3.79	6.90
Leukocyte surface antigen CD47;	Q61735	0.45	0.08	0.27	0.26	1.17	1.16
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	0.45	0.03	0.24	0.30	1.34	1.01
Ras-related protein Rap-1b;	Q99JI6	0.45	0.28	0.36	0.13	0.57	1.65
Tumor protein D54;	Q9CYZ2	0.45	-0.47	-0.01	0.66	2.93	2.19
GTP-binding nuclear protein Ran;	P62827	0.45	0.04	0.25	0.29	1.30	1.16
55 kDa erythrocyte membrane protein;	P70290	0.45	-0.67	-0.11	0.79	3.54	2.28
Transitional endoplasmic reticulum ATPase;	Q01853	0.47	1.15	0.81	0.49	2.17	3.64
26S proteasome non-ATPase regulatory subunit 3;	P14685	0.47	0.40	0.43	0.05	0.20	1.48
Catalase;	P24270	0.47	0.08	0.27	0.27	1.20	1.13
IgG receptor FcRn large subunit p51;	Q61559	0.48	0.53	0.50	0.04	0.16	2.28
UMP-CMP kinase;	Q9DBP5	0.48	0.10	0.29	0.27	1.19	1.18
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform;	Q6P1F6	0.48	-0.29	0.09	0.54	2.40	1.59
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	0.49	0.10	0.29	0.27	1.22	1.31
Proteasome activator complex subunit 1;	P97371	0.49	0.16	0.32	0.23	1.02	1.35
Regulator of nonsense transcripts 1;	Q9EPU0	0.49	1.72	1.10	0.87	3.91	7.15
Ran-specific GTPase-activating protein;	P34022	0.50	0.60	0.55	0.07	0.31	2.62
Epoxide hydrolase 2;	P34914	0.50	-0.27	0.11	0.54	2.42	1.70
Hormone-sensitive lipase;	P54310	0.50	0.07	0.28	0.30	1.34	1.25

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
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	0.50	-0.01	0.24	0.36	1.61	1.18
Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	0.50	1.90	1.20	0.99	4.42	7.24
Serine/threonine-protein kinase 38;	Q91VJ4	0.50	0.00	0.25	0.35	1.57	1.00
Uncharacterized protein;	F7DBB3	0.50	0.12	0.31	0.26	1.17	1.35
Microtubule-associated protein 1B;	P14873	0.51	0.15	0.33	0.25	1.12	1.35
ELAV-like protein 1;	P70372	0.51	0.72	0.61	0.15	0.68	2.52
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	0.51	0.15	0.33	0.25	1.12	1.23
Twinfilin-1;	Q91YR1	0.51	-0.40	0.06	0.64	2.85	2.03
COP9 signalosome complex subunit 1;	Q99LD4	0.51	-0.32	0.09	0.59	2.61	1.72
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	0.51	0.99	0.75	0.34	1.54	3.38
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	-0.25	-0.32	-0.29	0.05	0.22	1.18
GTP:AMP phosphotransferase, mitochondrial;	Q9WTP7	0.51	0.08	0.30	0.30	1.33	1.32
Nuclear protein localization protein 4 homolog;	P60670	0.52	0.56	0.54	0.03	0.13	2.61
T-complex protein 1 subunit beta;	P80314	0.52	0.43	0.47	0.06	0.26	2.00
COP9 signalosome complex subunit 3;	O88543	0.52	0.52	0.52	0.00	0.00	2.05
Adenylate kinase 2, mitochondrial;	Q9WTP6	0.52	-0.09	0.21	0.43	1.91	1.27
Importin subunit alpha-3;	O35344	0.52	-0.20	0.16	0.51	2.26	1.61
Coactosin-like protein;	Q9CQI6	0.53	0.41	0.47	0.08	0.36	1.96
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	0.53	0.37	0.45	0.11	0.50	1.76
Pleckstrin;	Q9JHK5	0.53	0.87	0.70	0.24	1.09	3.53
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	0.53	-0.04	0.24	0.40	1.80	1.33
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	0.53	0.79	0.66	0.19	0.84	3.12
26S proteasome non-ATPase regulatory subunit 14;	O35593	0.54	0.11	0.32	0.30	1.34	1.34
Transgelin-2;	Q9WVA4	0.54	0.33	0.43	0.14	0.64	1.85
General vesicular transport factor p115;	Q9Z1Z0	0.54	0.20	0.37	0.24	1.05	1.10
Calpain-2 catalytic subunit;	O08529	0.54	-0.03	0.25	0.40	1.78	1.17
N-acetylgalactosamine kinase;	Q68FH4	0.54	-0.36	0.09	0.63	2.82	1.62
Smoothelin-like protein 1;	Q99LM3	0.54	-0.89	-0.18	1.01	4.50	2.76
Band 4.1-like protein 1;	Q9Z2H5	0.54	-0.11	0.22	0.45	2.02	1.28
Long-chain-fatty-acid--CoA ligase 1;	P41216	0.54	0.08	0.31	0.32	1.43	1.35
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;	P31230	0.55	0.44	0.50	0.07	0.32	2.29
Stress-induced-phosphoprotein 1;	Q60864	0.55	0.21	0.38	0.23	1.05	1.62
Thimet oligopeptidase;	Q8C1A5	0.55	0.21	0.38	0.23	1.05	1.57
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase;	Q9D7I5	0.55	0.33	0.44	0.15	0.67	1.93
Phosphoglycerate mutase 1;	Q9DBJ1	0.55	0.11	0.33	0.31	1.37	1.53
Serine/threonine-protein kinase WNK1;	P83741	0.55	0.47	0.51	0.06	0.26	2.29
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	0.55	-1.03	-0.24	1.11	4.97	3.48

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
Coronin-7;	Q9D2V7	0.55	-0.07	0.24	0.44	1.96	1.36
Lysosomal alpha-mannosidase;	O09159	0.56	0.03	0.29	0.37	1.66	1.16
Copper transport protein ATOX1;	O08997	0.57	-0.06	0.25	0.44	1.97	1.11
Cytosol aminopeptidase;	Q9CPY7	0.57	0.28	0.42	0.21	0.92	1.85
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	0.57	0.69	0.63	0.09	0.38	2.77
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	0.57	0.77	0.67	0.15	0.66	2.66
Cyclin-dependent kinase 6;	Q64261	0.57	-0.18	0.19	0.53	2.37	1.64
Dipeptidase 1;	P31428	0.58	-0.49	0.04	0.76	3.37	2.06
UV excision repair protein RAD23 homolog B;	P54728	0.58	0.28	0.43	0.21	0.95	1.85
14-3-3 protein epsilon;	P62259	0.58	1.20	0.89	0.44	1.96	4.20
Anamorsin;	Q8WTY4	0.58	-0.20	0.19	0.55	2.45	1.27
CAP-Gly domain-containing linker protein 1;	Q922J3	0.58	0.18	0.38	0.28	1.26	1.44
Dual specificity protein phosphatase 23;	Q6NT99	0.59	-1.84	-0.63	1.71	7.65	8.60
DAZ-associated protein 1;	Q9JII5	0.59	0.08	0.33	0.35	1.58	1.50
V-type proton ATPase subunit E 1;	P50518	0.59	0.67	0.63	0.06	0.27	3.03
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	0.59	0.77	0.68	0.13	0.57	2.76
Cathepsin B;	P10605	0.60	0.35	0.47	0.18	0.79	2.00
Programmed cell death protein 6;	P12815	0.60	-1.06	-0.23	1.17	5.22	2.94
Farnesyl pyrophosphate synthase;	Q920E5	0.60	0.36	0.48	0.17	0.75	2.04
Synaptobrevin homolog YKT6;	Q9CQW1	0.60	-0.36	0.12	0.67	3.01	1.81
AH receptor-interacting protein;	O08915	0.60	0.67	0.63	0.05	0.23	2.70
Acyl-coenzyme A thioesterase 1;	O55137	0.60	0.12	0.36	0.33	1.49	1.47
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	-0.14	0.36	0.11	0.35	1.55	1.05
Calpastatin;	P51125	0.60	0.16	0.38	0.31	1.39	1.78
Heat shock protein HSP 90-beta;	P11499	0.60	0.19	0.40	0.29	1.31	1.60
Endoplasmin;	P08113	0.08	0.38	0.23	0.21	0.93	0.67
Heat shock protein HSP 90-alpha;	P07901	0.26	0.62	0.44	0.25	1.14	1.86
Inorganic pyrophosphatase;	Q9D819	0.60	0.53	0.57	0.06	0.25	2.27
Far upstream element-binding protein 2;	Q3U0V1	0.61	0.93	0.77	0.22	0.98	3.87
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	0.61	-0.18	0.22	0.56	2.52	1.60
Bleomycin hydrolase;	Q8R016	0.61	0.56	0.59	0.04	0.18	2.41
T-complex protein 1 subunit theta;	P42932	0.62	0.31	0.47	0.22	0.99	1.76
Vitamin K-dependent protein S;	Q08761	0.62	0.35	0.48	0.20	0.88	2.26
Hsp90 co-chaperone Cdc37;	Q61081	0.62	0.30	0.46	0.23	1.02	2.08
COP9 signalosome complex subunit 8;	Q8VBV7	0.62	0.10	0.36	0.37	1.66	1.68
Ubiquitin carboxyl-terminal hydrolase isozyme L5;	Q9WUP7	0.62	0.23	0.43	0.28	1.25	1.59
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	0.62	0.89	0.76	0.19	0.84	3.25
COP9 signalosome complex subunit 2;	P61202	0.62	0.32	0.47	0.21	0.95	1.87

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Tubulin alpha-1A chain;	P68369	0.62	-0.15	0.24	0.55	2.45	1.53
Tubulin alpha-4A chain;	P68368	0.83	-0.14	0.35	0.68	3.06	2.10
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	0.62	-0.23	0.19	0.61	2.71	1.71
Protein MEMO1;	Q91VH6	0.63	0.54	0.58	0.07	0.30	2.57
Alpha-enolase;	P17182	0.63	0.40	0.52	0.16	0.73	2.42
Beta-enolase;	P21550	-0.92	-0.79	-0.85	0.09	0.41	4.55
Gamma-enolase;	P17183	-0.03	-0.11	-0.07	0.05	0.24	0.22
SEC14-like protein 2;	Q99J08	0.64	0.16	0.40	0.34	1.51	1.89
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	0.64	0.10	0.37	0.38	1.72	1.59
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	0.64	0.66	0.65	0.01	0.06	2.98
Complement C1s-A subcomponent;	Q8CG14	0.64	-0.36	0.14	0.71	3.16	2.10
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	0.65	-1.32	-0.34	1.40	6.23	5.80
Epidermal growth factor receptor substrate 15-like 1;	Q60902	0.65	0.33	0.49	0.22	1.00	2.03
Phospholipase B-like 1;	Q8VCI0	0.65	1.30	0.98	0.46	2.05	5.14
Uncharacterized protein;	Q9CX86	0.65	2.03	1.34	0.97	4.34	7.73
Plastin-2;	Q61233	0.65	0.83	0.74	0.13	0.57	3.19
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	0.65	0.24	0.45	0.29	1.30	1.90
Chloride intracellular channel protein 4;	Q9QYB1	0.66	0.20	0.43	0.32	1.45	1.72
Phenylalanyl-tRNA synthetase beta chain;	Q9WUA2	0.67	0.07	0.37	0.42	1.89	1.85
26S protease regulatory subunit 6A;	O88685	0.67	0.03	0.35	0.45	2.02	1.41
Aldehyde dehydrogenase family 1 member A3;	Q9JHW9	0.67	0.06	0.36	0.43	1.93	0.88
V-type proton ATPase catalytic subunit A;	P50516	0.68	0.14	0.41	0.38	1.70	1.73
Serine/threonine-protein phosphatase 6 regulatory subunit 3;	Q922D4	0.69	1.40	1.04	0.50	2.24	5.72
Ribosome-binding protein 1;	Q99PL5	0.69	0.81	0.75	0.08	0.38	3.60
WD repeat-containing protein 61;	Q9ERF3	0.69	1.06	0.88	0.27	1.19	4.87
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	0.69	-0.23	0.23	0.65	2.91	1.70
Retinoid-inducible serine carboxypeptidase;	Q920A5	0.69	0.73	0.71	0.03	0.14	3.24
Phosphomannomutase 2;	Q9Z2M7	0.69	0.95	0.82	0.19	0.83	3.93
Protein prune homolog;	Q8BIW1	0.70	-0.64	0.03	0.95	4.23	3.10
Palmitoyl-protein thioesterase 1;	O88531	0.70	-0.11	0.30	0.57	2.53	1.77
GMP synthase [glutamine-hydrolyzing];	Q3THK7	0.71	0.89	0.80	0.13	0.58	3.82
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	0.71	0.24	0.47	0.33	1.47	2.08
Haloacid dehalogenase-like hydrolase domain-containing protein 3;	Q9CYW4	0.71	0.07	0.39	0.45	2.00	1.41
Tubulin-folding cofactor B;	Q9D1E6	0.71	0.49	0.60	0.16	0.69	2.86
COP9 signalosome complex subunit 7a;	Q9CZ04	0.71	0.18	0.44	0.37	1.67	2.18
14-3-3 protein theta;	P68254	0.71	0.85	0.78	0.09	0.42	3.72
Cold shock domain-containing protein E1;	Q91W50	0.71	0.97	0.84	0.18	0.81	3.78
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	0.71	1.42	1.07	0.50	2.22	5.51

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
ADP-sugar pyrophosphatase;	Q9JKX6	0.71	0.00	0.36	0.50	2.25	1.84
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	0.71	-0.06	0.33	0.55	2.44	1.95
Interleukin-1 receptor antagonist protein;	P25085	0.72	0.77	0.74	0.03	0.14	3.40
Macrophage colony-stimulating factor 1 receptor;	P09581	0.73	-0.54	0.10	0.90	4.00	2.67
Glutamate--cysteine ligase regulatory subunit;	O09172	0.73	0.66	0.70	0.05	0.22	2.93
Clathrin heavy chain 1;	Q68FD5	0.74	0.93	0.84	0.14	0.61	3.12
Nuclease-sensitive element-binding protein 1;	P62960	0.75	2.26	1.50	1.07	4.76	11.53
Nucleophosmin;	Q61937	0.75	2.33	1.54	1.12	4.98	8.98
Uncharacterized protein;	E9Q912	0.75	0.16	0.46	0.41	1.85	2.05
Gbp6 protein; Guanylate binding protein 7; MCG141961, isoform CRA_a; Uncharacterized protein;	Q91Z40	0.76	0.15	0.45	0.43	1.91	1.94
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	0.77	1.82	1.30	0.75	3.34	7.00
Ezrin;	P26040	0.77	0.72	0.74	0.03	0.14	3.45
Moesin;	P26041	-1.43	0.68	-0.38	1.49	6.67	3.79
Radixin;	P26043	-0.94	0.20	-0.37	0.81	3.61	2.97
Protein S100-A11;	P50543	0.77	-0.12	0.32	0.63	2.80	2.21
Coronin-1B;	Q9WUM3	0.77	1.70	1.23	0.66	2.95	7.93
Proteasome subunit beta type-10;	O35955	0.77	-0.03	0.37	0.57	2.53	1.44
Nardilysin;	Q8BHG1	0.77	2.22	1.50	1.02	4.56	11.61
60 kDa heat shock protein, mitochondrial;	P63038	0.78	0.23	0.50	0.39	1.75	2.46
Carbonyl reductase [NADPH] 1;	P48758	0.79	-0.06	0.37	0.60	2.68	2.11
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	0.79	0.57	0.68	0.16	0.71	3.13
Tyrosine-protein kinase CSK;	P41241	0.79	0.39	0.59	0.28	1.27	2.84
Stromal membrane-associated protein 1;	Q91VZ6	0.79	0.15	0.47	0.45	2.02	2.35
Heterogeneous nuclear ribonucleoprotein M;	Q9D0E1	0.80	2.53	1.67	1.23	5.48	13.11
Cytoplasmic dynein 1 intermediate chain 2;	O88487	0.81	0.80	0.80	0.01	0.03	4.12
Polyubiquitin-B;	P0CG49	0.81	0.25	0.53	0.39	1.76	2.61
14-3-3 protein eta;	P68510	0.81	0.73	0.77	0.05	0.24	3.19
Rho-related GTP-binding protein RhoC;	Q62159	0.81	0.12	0.47	0.48	2.16	2.35
Programmed cell death 6-interacting protein;	Q9WU78	0.81	-0.45	0.18	0.89	3.98	2.91
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	0.81	-0.17	0.32	0.69	3.08	2.38
Caspase-1;	P29452	0.82	-0.20	0.31	0.72	3.21	1.88
26S protease regulatory subunit 6B;	P54775	0.82	0.41	0.61	0.29	1.28	2.28
Lon protease homolog, mitochondrial;	Q8CGK3	0.82	-0.79	0.02	1.13	5.06	3.77
NEDD8-conjugating enzyme Ubc12;	P61082	0.82	-0.45	0.18	0.90	4.01	3.04
Transportin-3;	Q6P2B1	0.82	-0.52	0.15	0.94	4.20	2.65
Acetyl-coenzyme A synthetase, cytoplasmic;	Q9QXG4	0.82	0.61	0.72	0.15	0.66	3.54
26S protease regulatory subunit 10B;	P62334	0.83	0.55	0.69	0.20	0.90	2.24

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
Carbamoyl-phosphate synthase [ammonia], mitochondrial;	Q8C196	0.83	-2.25	-0.71	2.18	9.74	6.43
Protein SEC13 homolog;	Q9D1M0	0.83	-0.15	0.34	0.70	3.11	2.32
Cathepsin Z;	Q9WUU7	0.83	0.37	0.60	0.33	1.47	3.09
Clusterin;	Q06890	0.83	-0.84	0.00	1.18	5.27	3.76
Elongation factor 1-beta;	O70251	0.84	1.22	1.03	0.27	1.20	5.03
Glutathione S-transferase omega-1;	O09131	0.84	0.58	0.71	0.19	0.84	3.38
Nuclear migration protein nudC;	O35685	0.85	-0.12	0.36	0.68	3.06	2.39
Alpha-soluble NSF attachment protein;	Q9DB05	0.85	1.30	1.07	0.32	1.42	6.26
COP9 signalosome complex subunit 4;	O88544	0.85	0.66	0.75	0.13	0.59	3.66
Oxysterol-binding protein;	E9QPD4	0.85	-0.69	0.08	1.09	4.86	3.86
Probable E3 ubiquitin-protein ligase HERC4;	Q6PAV2	0.86	0.14	0.50	0.51	2.27	2.20
AP-3 complex subunit beta-1;	Q9Z1T1	0.86	-0.01	0.43	0.62	2.77	1.64
14-3-3 protein beta/alpha;	Q9CQV8	0.86	1.10	0.98	0.17	0.74	4.95
Protein CREG1;	O88668	0.87	1.10	0.99	0.16	0.73	5.60
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	0.87	0.40	0.64	0.33	1.49	3.23
Dihydrofolate reductase;	P00375	0.88	0.60	0.74	0.20	0.87	3.87
Glycolipid transfer protein;	Q9JL62	0.89	0.18	0.53	0.50	2.25	2.74
Protein phosphatase 1B;	P36993	0.90	0.16	0.53	0.52	2.31	2.64
Carnitine O-palmitoyltransferase 2, mitochondrial;	P52825	0.90	-0.92	-0.01	1.28	5.72	4.77
Polypyrimidine tract-binding protein 1;	P17225	0.90	1.17	1.03	0.19	0.87	5.56
Calcium/calmodulin-dependent protein kinase type 1D;	Q8BW96	0.90	-0.18	0.36	0.77	3.43	2.61
Receptor-type tyrosine-protein phosphatase C;	P06800	0.90	1.95	1.43	0.74	3.31	9.84
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	0.90	0.63	0.77	0.19	0.86	2.70
Retinol-binding protein 1;	Q00915	0.91	1.22	1.07	0.22	0.98	6.09
Protein transport protein Sec31A;	Q3UPL0	0.91	-0.06	0.43	0.69	3.06	1.58
Uncharacterized protein;	F6RPJ9	0.91	1.06	0.99	0.11	0.48	5.09
Glutaredoxin-1;	Q9QUH0	0.92	1.08	1.00	0.11	0.50	5.84
Uncharacterized protein;	E9Q1Y3	0.92	0.70	0.81	0.16	0.70	4.19
Inactive tyrosine-protein kinase 7;	Q8BKG3	0.92	0.65	0.78	0.19	0.84	4.08
Cathepsin S;	O70370	0.93	1.16	1.04	0.17	0.75	5.50
Peroxisomal acyl-coenzyme A oxidase 2;	Q9QXD1	0.93	2.34	1.63	1.00	4.45	12.33
Importin subunit alpha-4;	O35343	0.93	1.57	1.25	0.45	2.02	7.55
Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	0.93	0.62	0.78	0.22	0.98	4.17
D-3-phosphoglycerate dehydrogenase;	Q61753	0.93	0.71	0.82	0.16	0.69	3.45
3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	0.94	-0.15	0.39	0.77	3.45	1.88
26S protease regulatory subunit 8;	P62196	0.94	0.00	0.47	0.67	2.97	2.62
Caspase-3;	P70677	0.95	1.01	0.98	0.05	0.21	5.46
Nicotinate phosphoribosyltransferase;	Q8CC86	0.95	-0.76	0.09	1.21	5.40	4.53

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
Sialoadhesin;	Q62230	0.96	0.86	0.91	0.07	0.29	4.82
Epithelial splicing regulatory protein 1;	Q3US41	0.96	2.09	1.53	0.80	3.57	10.09
40S ribosomal protein S3;	P62908	0.97	1.31	1.14	0.24	1.05	6.11
Tripeptidyl-peptidase 1;	O89023	0.98	0.60	0.79	0.27	1.21	3.87
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	0.99	1.28	1.13	0.20	0.91	5.79
Non-specific lipid-transfer protein;	P32020	0.99	0.15	0.57	0.59	2.64	2.44
Protein KIAA1967 homolog;	Q8VDP4	0.99	2.03	1.51	0.73	3.27	7.89
Histone deacetylase 1;	O09106	0.99	1.71	1.35	0.51	2.26	8.62
Inosine triphosphate pyrophosphatase;	Q9D892	1.00	0.38	0.69	0.44	1.96	3.63
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	1.01	0.00	0.50	0.71	3.18	2.92
Fatty acid synthase;	P19096	1.01	0.70	0.86	0.22	1.00	2.76
Talin-1;	P26039	1.01	0.24	0.63	0.55	2.45	1.76
Talin-2;	Q71LX4	-0.14	0.07	-0.03	0.15	0.65	0.35
Ferric-chelate reductase 1;	Q8K385	1.01	1.04	1.03	0.02	0.07	6.01
Tyrosine-protein phosphatase non-receptor type 6;	P29351	1.02	0.60	0.81	0.30	1.34	3.89
Fascin;	Q61553	1.02	0.19	0.61	0.59	2.63	3.35
Sulfotransferase family cytosolic 2B member 1;	O35400	1.02	0.86	0.94	0.12	0.52	4.88
Small ubiquitin-related modifier 1;	P63166	1.03	0.12	0.58	0.64	2.86	2.61
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	1.05	1.13	1.09	0.06	0.26	6.23
Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	1.06	0.76	0.91	0.21	0.95	4.76
Signal transducer and activator of transcription 1;	P42225	1.06	0.49	0.77	0.40	1.81	3.73
Ras-related protein Rab-21;	P35282	1.06	0.06	0.56	0.71	3.18	1.50
Tubulin beta-5 chain;	P99024	1.06	0.24	0.65	0.58	2.60	3.31
Tubulin beta-2A chain;	Q7TMM9	0.98	0.33	0.66	0.46	2.04	3.53
Tubulin beta-4B chain;	P68372	1.08	0.58	0.83	0.36	1.61	4.66
Ubiquitin-associated protein 2-like;	Q80X50	1.06	0.94	1.00	0.09	0.39	5.78
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	1.06	0.18	0.62	0.63	2.80	3.17
SUMO-activating enzyme subunit 2;	Q9Z1F9	1.06	0.73	0.90	0.24	1.05	4.78
CD44 antigen;	P15379	1.06	0.88	0.97	0.13	0.58	5.38
Phosphoserine aminotransferase;	Q99K85	1.07	0.72	0.90	0.25	1.10	4.64
26S proteasome non-ATPase regulatory subunit 7;	P26516	1.08	0.62	0.85	0.32	1.43	4.69
Cytosolic acyl coenzyme A thioester hydrolase;	Q91V12	1.08	0.82	0.95	0.18	0.80	4.68
Dynamin-2;	P39054	1.08	-0.34	0.37	1.01	4.50	3.68
Transportin-1;	Q8BFY9	1.09	0.60	0.84	0.35	1.57	4.31
Transportin-2;	Q99LG2	1.16	-0.11	0.53	0.90	4.00	3.10
Calponin-2;	Q08093	1.10	0.77	0.93	0.23	1.05	5.32
Serine/threonine-protein kinase 24;	Q99KH8	1.10	0.59	0.84	0.37	1.64	3.90
Lysosome-associated membrane glycoprotein 2;	P17047	1.12	0.83	0.98	0.20	0.90	4.24

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
Ganglioside GM2 activator;	Q60648	1.12	0.15	0.63	0.68	3.05	3.66
Poly(rC)-binding protein 1;	P60335	1.12	0.15	0.63	0.68	3.05	3.17
Poly(rC)-binding protein 2;	Q61990	0.86	0.25	0.55	0.43	1.91	2.75
Aldo-keto reductase family 1 member C18;	Q8K023	1.12	0.37	0.74	0.53	2.37	4.06
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	1.12	0.58	0.85	0.38	1.71	3.41
Dipeptidyl peptidase 1;	P97821	1.12	0.95	1.04	0.12	0.55	6.11
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	1.12	0.70	0.91	0.30	1.35	4.34
Amidophosphoribosyltransferase;	Q8CIH9	1.13	0.31	0.72	0.58	2.59	3.53
Uncharacterized protein;	E9Q4K7	1.14	-0.03	0.55	0.83	3.68	3.10
F-actin-capping protein subunit alpha-1;	P47753	1.14	0.01	0.58	0.80	3.57	3.06
Glutaminyl-tRNA synthetase; Uncharacterized protein;	Q8BML9	1.14	0.38	0.76	0.54	2.42	3.17
Sorting nexin-3;	O70492	1.15	-0.71	0.22	1.32	5.88	4.70
Protein FAM49B;	Q921M7	1.17	-0.20	0.48	0.97	4.33	2.76
Coatomer subunit beta';	O55029	1.18	0.47	0.82	0.50	2.24	4.03
N-acetylneuraminate lyase;	Q9DCJ9	1.18	0.86	1.02	0.22	0.98	4.68
Adenylyl cyclase-associated protein 1;	P40124	1.18	0.37	0.78	0.58	2.58	4.22
Protein phosphatase 1A;	P49443	1.19	1.08	1.13	0.08	0.35	6.05
T-complex protein 1 subunit eta;	P80313	1.19	0.39	0.79	0.56	2.52	3.97
Cystatin-B;	Q62426	1.28	1.31	1.29	0.02	0.08	8.35
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	1.21	0.15	0.68	0.75	3.34	2.50
Adenosine deaminase;	P03958	1.21	0.65	0.93	0.40	1.78	4.28
26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	1.21	1.00	1.11	0.15	0.68	4.88
Bcl-2-like protein 13;	P59017	1.21	1.46	1.33	0.18	0.79	8.14
Nucleoside diphosphate-linked moiety X motif 17;	Q9CWD3	1.23	1.14	1.18	0.06	0.28	6.91
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1.23	0.48	0.85	0.53	2.37	3.81
14-3-3 protein sigma;	O70456	1.24	1.53	1.39	0.21	0.92	7.41
T-complex protein 1 subunit delta;	P80315	1.24	0.97	1.11	0.19	0.85	5.06
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1.24	0.76	1.00	0.34	1.52	5.56
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	1.24	-0.29	0.48	1.08	4.81	4.00
Proliferating cell nuclear antigen;	P17918	1.24	1.77	1.50	0.38	1.68	10.47
Periostin;	Q62009	1.21	1.51	1.36	0.21	0.94	8.61
Protein Niban;	Q3UW53	1.25	0.03	0.64	0.86	3.84	2.72
Ras-related C3 botulinum toxin substrate 1;	P63001	1.25	0.55	0.90	0.50	2.23	4.80
Cell division control protein 42 homolog;	P60766	0.71	0.33	0.52	0.27	1.20	2.54
Mevalonate kinase;	Q9R008	1.26	0.47	0.86	0.56	2.50	4.66
Cadherin-1;	P09803	1.26	0.82	1.04	0.31	1.39	5.74
Cellular retinoic acid-binding protein 2;	P22935	1.26	0.71	0.99	0.39	1.73	5.89
SEC14-like protein 4;	Q8R0F9	1.27	0.47	0.87	0.57	2.54	4.39

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Uncharacterized protein;	E9PYU6	1.28	0.82	1.05	0.32	1.42	5.69
Isoleucyl-tRNA synthetase, cytoplasmic;	Q8BU30	1.28	0.48	0.88	0.57	2.53	4.34
Vacuolar protein sorting-associated protein 4B;	P46467	1.28	-0.34	0.47	1.15	5.12	3.54
Chloride channel calcium activated 2; Endothelial chloride channel; MCG120735; Uncharacterized protein;	Q9EQR4	1.24	1.50	1.37	0.19	0.83	8.12
Importin-7;	Q9EPL8	1.28	1.17	1.23	0.08	0.35	6.00
Rho-associated protein kinase 2;	P70336	1.29	0.66	0.97	0.44	1.98	4.02
Diphosphomevalonate decarboxylase;	Q99JF5	1.29	0.91	1.10	0.27	1.19	6.23
Lysosomal protective protein;	P16675	1.29	0.92	1.10	0.26	1.16	6.49
Transcription intermediary factor 1-beta;	Q62318	1.29	1.03	1.16	0.19	0.83	5.76
Pantetheinase;	Q9Z0K8	1.29	1.11	1.20	0.13	0.57	6.20
Large proline-rich protein BAG6;	Q9Z1R2	1.30	1.48	1.39	0.12	0.56	8.93
Uncharacterized protein;	E9Q7G0	1.31	3.58	2.44	1.61	7.19	20.22
Lymphocyte-specific protein 1;	P19973	1.32	0.38	0.85	0.66	2.96	4.74
Fibulin-5;	Q9WVH9	1.32	0.90	1.11	0.30	1.33	6.77
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	1.32	-0.32	0.50	1.16	5.17	4.42
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	1.33	0.72	1.03	0.43	1.91	4.92
Leucyl-cystinyl aminopeptidase;	Q8C129	1.33	1.38	1.35	0.04	0.16	7.65
Latexin;	P70202	1.35	0.93	1.14	0.30	1.34	6.84
Tax1-binding protein 3;	Q9DBG9	1.36	0.56	0.96	0.57	2.53	3.89
PDZ and LIM domain protein 1;	O70400	1.36	0.98	1.17	0.27	1.21	6.30
Perilipin-4;	O88492	1.37	0.33	0.85	0.73	3.26	3.52
Ectonucleoside triphosphate diphosphohydrolase 1;	P55772	1.37	0.99	1.18	0.27	1.20	6.87
Arfip1 protein; Uncharacterized protein;	A2RSX9	1.37	-0.11	0.63	1.04	4.65	4.40
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	1.37	1.04	1.20	0.24	1.06	7.15
Secretory carrier-associated membrane protein 2;	Q9ERN0	1.38	0.60	0.99	0.55	2.46	5.70
T-complex protein 1 subunit epsilon;	P80316	1.38	0.84	1.11	0.38	1.72	6.40
MOB kinase activator 1B;	Q8BPB0	1.40	-0.09	0.65	1.05	4.68	4.81
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	1.41	0.98	1.19	0.30	1.35	6.34
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	1.43	1.52	1.47	0.07	0.29	7.53
Acetyl-CoA acetyltransferase, cytosolic;	Q8CAY6	1.43	0.77	1.10	0.47	2.08	5.68
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	1.44	0.26	0.85	0.83	3.71	4.47
Acid ceramidase;	Q9WV54	1.45	0.89	1.17	0.40	1.77	6.62
Phosphoserine phosphatase;	Q99LS3	1.45	0.70	1.08	0.54	2.39	6.40
Nuclear autoantigenic sperm protein;	Q99MD9	1.46	1.37	1.42	0.06	0.27	7.65
Early endosome antigen 1;	Q8BL66	1.46	0.72	1.09	0.52	2.33	5.75
26S protease regulatory subunit 4;	P62192	1.48	1.06	1.27	0.29	1.31	7.24

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
Ubiquitin-conjugating enzyme E2 D3;	P61079	1.49	-0.18	0.65	1.18	5.27	5.38
Uncharacterized protein;	E9PZ00	1.50	0.70	1.10	0.57	2.53	5.12
V-type proton ATPase subunit H;	Q8BVE3	1.51	-0.17	0.67	1.19	5.30	4.96
6-phosphofructokinase type C;	Q9WUA3	1.52	1.23	1.38	0.20	0.91	6.90
Acetoacetyl-CoA synthetase;	Q9D2R0	1.53	1.01	1.27	0.37	1.64	6.97
Protein diaphanous homolog 1;	O08808	1.54	0.69	1.11	0.60	2.68	5.70
Importin-5;	Q8BKC5	1.54	0.31	0.92	0.87	3.87	3.69
StAR-related lipid transfer protein 5;	Q9EPQ7	1.55	0.89	1.22	0.47	2.09	6.95
Serine hydroxymethyltransferase, cytosolic;	P50431	1.59	1.28	1.43	0.22	0.98	9.03
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	1.58	0.44	1.01	0.80	3.59	6.44
Putative phospholipase B-like 2;	Q3TCN2	1.77	1.45	1.61	0.22	1.00	9.82
Carboxypeptidase E;	Q00493	1.65	1.68	1.66	0.02	0.10	9.09
Heat shock protein 75 kDa, mitochondrial;	Q9CQN1	1.60	0.37	0.98	0.87	3.89	6.22
T-cell specific GTPase; Uncharacterized protein;	Q5SVP4	1.61	-0.38	0.62	1.41	6.29	6.46
Dehydrogenase/reductase SDR family member 1;	Q99L04	1.64	0.93	1.29	0.50	2.24	8.29
Isopentenyl-diphosphate Delta-isomerase 1;	P58044	1.83	1.57	1.70	0.19	0.83	9.68
Uroporphyrinogen decarboxylase;	P70697	1.67	0.61	1.14	0.75	3.35	6.53
Cathepsin D;	P18242	1.93	1.54	1.74	0.28	1.23	12.40
Fatty acid-binding protein, epidermal;	Q05816	1.70	1.16	1.43	0.38	1.68	9.54
Cytoplasmic dynein 1 heavy chain 1;	Q9JHU4	1.71	0.83	1.27	0.62	2.77	7.21
Chitotriosidase-1;	Q9D7Q1	1.72	1.16	1.44	0.40	1.76	9.93
Uncharacterized protein;	E9Q4Z2	1.73	0.53	1.13	0.85	3.80	6.40
Exportin-1;	Q6P5F9	1.75	0.45	1.10	0.91	4.08	6.70
Treacle protein;	O08784	1.69	1.81	1.75	0.08	0.36	12.29
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	1.76	1.77	1.76	0.01	0.03	9.43
SEC23-interacting protein;	Q6NZC7	1.78	-0.42	0.68	1.55	6.92	7.45
Uncharacterized protein;	D3Z4B0	1.78	2.81	2.29	0.73	3.25	18.99
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	1.59	1.98	1.78	0.27	1.22	10.65
Nuclear pore complex-associated intranuclear coiled-coil protein TPR	E9PZZ3	1.57	2.06	1.81	0.34	1.54	12.87
Protein S100-A14;	Q9D2Q8	2.05	1.59	1.82	0.33	1.46	13.33
Importin subunit beta-1;	P70168	1.90	1.03	1.46	0.62	2.75	8.80
Aldehyde dehydrogenase;	E9Q3E1	1.90	0.81	1.35	0.77	3.45	8.02
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	2.00	1.92	1.96	0.06	0.25	13.51
ATP-citrate synthase;	Q91V92	1.80	2.30	2.05	0.35	1.57	15.24
Carboxypeptidase A4;	Q6P8K8	2.35	1.85	2.10	0.35	1.58	16.40
Retroviral-like aspartic protease 1;	Q09PK2	2.05	1.46	1.75	0.42	1.85	12.33
Latent-transforming growth factor beta-binding protein 4;	Q8K4G1	1.86	2.43	2.14	0.40	1.81	12.95
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	2.07	1.39	1.73	0.48	2.15	9.84

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
Gamma-glutamyl hydrolase;	Q9Z0L8	2.09	3.50	2.80	1.00	4.45	22.23
Uridine 5'-monophosphate synthase;	P13439	2.09	0.90	1.50	0.84	3.76	7.98
Exportin-2;	Q9ERK4	2.12	0.03	1.07	1.48	6.59	8.58
Long-chain-fatty-acid--CoA ligase 4;	Q9QUJ7	2.12	3.38	2.75	0.89	3.97	18.59
Glucocorticoid receptor;	P06537	2.17	0.30	1.23	1.32	5.91	9.06
Lymphocyte antigen 6D;	P35459	2.24	2.20	2.22	0.03	0.12	16.41
Short-chain dehydrogenase/reductase family 16C member 6;	Q05A13	2.00	2.57	2.28	0.40	1.80	17.14
Caspase-14;	O89094	2.48	2.36	2.42	0.09	0.38	13.52
Monoglyceride lipase;	O35678	2.57	1.45	2.01	0.79	3.53	13.20
Gasdermin-A;	Q9EST1	2.82	1.15	1.98	1.18	5.26	11.14
Perilipin-2;	P43883	3.46	2.12	2.79	0.95	4.23	15.38
Cornifin-A;	Q62266	4.33	1.46	2.89	2.03	9.06	34.17
Afadin;	Q9QZQ1	4.66	0.97	2.81	2.60	11.63	31.69
CD2-associated protein;	Q9JLQ0	9.30	0.58	4.94	6.17	27.54	19.83