Table S3: Identified and quantified proteins in the third replicate of global proteome comparison.
All proteins have a ProteinProphet probability score > 0.90, equivalent to an FDR < 0.01.
Ratios are normalized to hK expression / control.

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase;	0.28	0.01	0.77	7.30
Q04446	1,4-alpha-glucan-branching enzyme;	-0.78	-0.25	0.51	3.70
P61604	10 kDa heat shock protein, mitochondrial;	-0.19	-0.10	0.91	38.20
Q15029	116 kDa U5 small nuclear ribonucleoprotein component;	-0.54	-0.52	0.70	10.20
Q9NRX4	14 kDa phosphohistidine phosphatase;	0.53	0.16	0.69	25.60
P31946	14-3-3 protein beta/alpha;	-0.99	-0.90	0.41	33.70
P62258	14-3-3 protein epsilon;	1.24	0.28	0.56	56.50
Q04917	14-3-3 protein eta;	-0.30	-0.12	0.83	27.60
P61981	14-3-3 protein gamma;	-0.26	-0.08	0.85	20.60
P31947	14-3-3 protein sigma;	-0.33	-0.06	0.80	19.40
P27348	14-3-3 protein theta;	-0.18	-0.03	0.90	38.40
P63104	14-3-3 protein zeta/delta;	-0.26	-0.10	0.86	46.10
P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase;	-2.30	-2.72	0.04	2.60
P62333	26S protease regulatory subunit 10B;	0.93	0.03	0.38	3.30
P17980	26S protease regulatory subunit 6A;	1.69	0.16	0.35	11.60
P43686	26S protease regulatory subunit 6B;	0.56	0.03	0.59	3.30
P35998	26S protease regulatory subunit 7;	0.26	0.01	0.78	2.50
Q99460	26S proteasome non-ATPase regulatory subunit 1;	0.47	0.11	0.68	3.30
O00231	26S proteasome non-ATPase regulatory subunit 11;	0.21	0.09	0.85	11.10
Q13200	26S proteasome non-ATPase regulatory subunit 2;	0.84	0.16	0.53	9.90
O43242	26S proteasome non-ATPase regulatory subunit 3;	0.03	0.01	0.96	9.90
Q16401	26S proteasome non-ATPase regulatory subunit 5;	0.82	0.20	0.58	5.60
Q15008	26S proteasome non-ATPase regulatory subunit 6;	-0.35	-0.36	0.83	6.20
O00233	26S proteasome non-ATPase regulatory subunit 9;	-0.51	-0.10	0.68	5.40
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial;	0.11	0.01	0.89	8.00
O95861	3'(2'),5'-bisphosphate nucleotidase 1;	0.28	0.11	0.82	15.90
P49189	4-trimethylaminobutyraldehyde dehydrogenase;	2.02	0.11	0.23	5.70
P46783	40S ribosomal protein S10;	-0.46	-0.14	0.71	14.50
P62280	40S ribosomal protein S11;	0.08	0.02	0.92	20.90
P25398	40S ribosomal protein S12;	-0.03	0.00	0.99	37.90
P62277	40S ribosomal protein S13;	0.00	0.00	0.97	19.20
P62263	40S ribosomal protein S14;	0.03	0.00	0.95	15.20
P62841	40S ribosomal protein S15;	-0.21	-0.03	0.88	8.30
P62244	40S ribosomal protein S15a;	-0.19	-0.03	0.89	13.80
P62249	40S ribosomal protein S16;	-0.27	-0.02	0.83	24.70
P08708	40S ribosomal protein S17;	0.08	0.00	0.91	7.40
P62269	40S ribosomal protein S18;	0.06	0.02	0.93	19.10
P39019	40S ribosomal protein S19;	0.28	0.07	0.79	17.20
P15880	40S ribosomal protein S2;	0.21	0.05	0.84	21.20
P60866	40S ribosomal protein S20;	0.03	0.01	0.94	25.20
P63220	40S ribosomal protein S21;	0.03	0.00	0.95	39.80
P62266	40S ribosomal protein S23;	-4.01	-131.42	0.00	7.70
P62847	40S ribosomal protein S24;	0.74	0.02	0.48	8.30
P62851	40S ribosomal protein S25;	-0.09	-0.01	0.97	15.20
P62854	40S ribosomal protein S26;	2.80	0.14	0.45	27.00
Q71UM5	40S ribosomal protein S27-like;	0.33	0.03	0.73	28.60
P42677	40S ribosomal protein S27;	0.09	0.01	0.91	28.60
P62857	40S ribosomal protein S28;	-0.45	-0.10	0.72	30.40
P23396	40S ribosomal protein S3;	0.24	0.05	0.81	28.80
P61247	40S ribosomal protein S3a;	-0.07	-0.02	0.98	13.60
P62701	40S ribosomal protein S4, X isoform;	-0.13	-0.02	0.94	20.20

Table S3

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P46782	40S ribosomal protein S5;	0.26	0.04	0.79	12.30
P62753	40S ribosomal protein S6;	0.30	0.05	0.76	9.60
P62081	40S ribosomal protein S7;	-0.27	-0.03	0.83	14.40
P62241	40S ribosomal protein S8;	0.37	0.08	0.74	32.70
P46781	40S ribosomal protein S9;	1.18	0.12	0.36	22.20
P08865	40S ribosomal protein SA;	-0.13	-0.07	0.95	16.60
Q9BRK5	45 kDa calcium-binding protein;	0.60	0.04	0.57	24.30
P08195	4F2 cell-surface antigen heavy chain;	0.35	0.19	0.82	11.70
O14841	5-oxoprolinase;	0.84	0.04	0.43	1.00
Q9H0D6	5'-3' exoribonuclease 2;	0.21	0.12	0.87	6.40
Q5TFE4	5'-nucleotidase domain-containing protein 1;	-2.31	-6.21	0.04	4.60
P21589	5'-nucleotidase;	-0.10	-0.03	0.96	5.10
Q01813	6-phosphofructokinase type C;	-1.01	-0.55	0.39	2.60
P08237	6-phosphofructokinase, muscle type;	-0.62	-0.18	0.61	1.50
P52209	6-phosphogluconate dehydrogenase, decarboxylating;	-0.23	-0.06	0.87	24.60
O95336	6-phosphogluconolactonase;	-0.98	-1.40	0.45	41.50
P10809	60 kDa heat shock protein, mitochondrial;	0.90	0.08	0.42	27.60
P10155	60 kDa SS-A/Ro ribonucleoprotein;	0.21	0.05	0.83	8.40
P05388	60S acidic ribosomal protein P0;	0.69	0.12	0.57	24.00
P05386	60S acidic ribosomal protein P1;	0.69	0.05	0.51	14.00
P05387	60S acidic ribosomal protein P2;	0.28	0.02	0.77	67.00
P62906	60S ribosomal protein L10a;	0.72	0.04	0.50	15.20
P62913	60S ribosomal protein L11;	0.30	0.02	0.75	12.90
P30050	60S ribosomal protein L12;	0.28	0.02	0.77	54.50
P26373	60S ribosomal protein L13;	0.21	0.02	0.82	19.90
P50914	60S ribosomal protein L14;	-0.34	-0.29	0.82	10.20
P61313	60S ribosomal protein L15;	0.08	0.01	0.91	10.30
P18621	60S ribosomal protein L17;	-0.06	-0.01	1.00	17.40
Q07020	60S ribosomal protein L18;	0.26	0.05	0.80	12.80
Q02543	60S ribosomal protein L18a;	0.12	0.01	0.88	9.70
P46778	60S ribosomal protein L21;	-0.31	-0.03	0.81	20.60
P62829	60S ribosomal protein L23;	1.01	0.35	0.66	36.40
P62750	60S ribosomal protein L23a;	-0.55	-0.23	0.66	13.50
P83731	60S ribosomal protein L24;	0.05	0.01	0.93	19.10
P61254	60S ribosomal protein L26;	1.28	0.01	0.22	6.20
P61353	60S ribosomal protein L27;	0.01	0.00	0.96	30.10
P46776	60S ribosomal protein L27a;	-1.69	-1.30	0.13	7.40
P47914	60S ribosomal protein L29;	-0.22	-0.03	0.87	9.40
P39023	60S ribosomal protein L3;	0.56	0.05	0.59	5.70
P62888	60S ribosomal protein L30;	-1.48	-16.65	0.55	24.30
P62899	60S ribosomal protein L31;	0.41	0.12	0.73	18.40
P62910	60S ribosomal protein L32;	-0.34	-0.07	0.79	14.80
P18077	60S ribosomal protein L35a;	0.51	0.03	0.61	8.20
P62891	60S ribosomal protein L39;	0.11	0.01	0.88	19.60
P36578	60S ribosomal protein L4;	-0.26	-0.14	0.86	11.90
P46777	60S ribosomal protein L5;	-1.61	-6.83	0.22	15.50
Q02878	60S ribosomal protein L6;	-0.07	-0.02	0.98	21.50
P18124	60S ribosomal protein L7;	0.67	0.22	0.67	15.30
P62424	60S ribosomal protein L7a;	-0.18	-0.07	0.91	16.20
P62917	60S ribosomal protein L8;	1.08	0.11	0.38	10.50
P32969	60S ribosomal protein L9;	0.19	0.11	0.88	19.30

Table S3

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P36639	7,8-dihydro-8-oxoguanine triphosphatase;	0.93	0.04	0.38	7.60
P11021	78 kDa glucose-regulated protein;	0.62	0.05	0.56	28.90
Q02952	A-kinase anchor protein 12;	0.01	0.01	0.97	21.40
O43823	A-kinase anchor protein 8;	1.47	0.04	0.18	2.90
Q8IZP0	Abl interactor 1;	-0.19	-0.08	0.90	3.10
Q9NYB9	Abl interactor 2;	-0.14	-0.01	0.93	3.10
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic;	0.65	0.22	0.68	18.90
Q13085	Acetyl-CoA carboxylase 1;	3.61	0.00	0.00	1.60
Q13510	Acid ceramidase;	0.21	0.02	0.82	16.20
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family	0.26	0.01	0.78	12.00
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family	-0.22	-0.04	0.87	12.70
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E;	0.32	0.02	0.74	4.50
Q99798	Aconitate hydratase, mitochondrial;	3.61	0.04	0.21	2.70
P61160	Actin-related protein 2;	1.43	0.31	0.57	18.50
Q92747	Actin-related protein 2/3 complex subunit 1A;	-0.67	-0.21	0.58	5.90
O15143	Actin-related protein 2/3 complex subunit 1B;	-0.46	-0.06	0.71	9.40
O15144	Actin-related protein 2/3 complex subunit 2;	-0.27	-0.08	0.84	11.30
P59998	Actin-related protein 2/3 complex subunit 4;	-0.69	-0.14	0.56	16.10
O15511	Actin-related protein 2/3 complex subunit 5;	1.01	0.03	0.34	12.60
P61158	Actin-related protein 3;	0.26	0.20	0.88	24.20
P62736	Actin, aortic smooth muscle;	-1.01	-1.72	0.44	32.40
P60709	Actin, cytoplasmic 1;	-0.69	-0.40	0.57	37.90
P53999	Activated RNA polymerase II transcriptional coactivator	0.14	0.05	0.88	26.00
O95433	Activator of 90 kDa heat shock protein ATPase homolog	0.41	0.10	0.71	25.70
P07108	Acyl-CoA-binding protein;	-0.23	-0.12	0.88	50.60
P49753	Acyl-coenzyme A thioesterase 2, mitochondrial;	1.51	0.22	0.44	10.70
O95372	Acyl-protein thioesterase 2;	-1.32	-1.12	0.25	7.80
P13798	Acylamino-acid-releasing enzyme;	0.12	0.10	0.92	8.70
P07311	Acylphosphatase-1;	0.30	0.06	0.77	23.20
Q6UY14	ADAMTS-like protein 4;	1.39	0.15	0.36	7.40
P46108	Adapter molecule crk;	-0.47	-0.14	0.70	13.20
P00813	Adenosine deaminase;	-2.13	-4.20	0.06	2.80
P23526	Adenosylhomocysteinase;	-0.84	-0.56	0.48	23.10
P54819	Adenylate kinase 2, mitochondrial;	-0.79	-0.89	0.54	29.30
P30566	Adenylosuccinate lyase;	0.24	0.01	0.79	14.00
P30520	Adenylosuccinate synthetase isozyme 2;	0.14	0.03	0.87	9.60
Q01518	Adenylyl cyclase-associated protein 1;	-0.77	-0.17	0.51	14.30
Q15847	Adipose most abundant gene transcript 2 protein;	-0.57	-0.24	0.64	40.80
P35318	ADM;	-1.26	-2.17	0.30	32.40
P61204	ADP-ribosylation factor 3;	-0.74	-0.20	0.53	16.00
Q9UKK9	ADP-sugar pyrophosphatase;	0.16	0.08	0.89	13.20
P55196	Afadin;	-0.19	-0.05	0.89	1.20
O00468	Agrin;	1.14	0.10	0.35	32.10
O00170	AH receptor-interacting protein;	-0.95	-0.69	0.43	8.80
P49588	Alanine--tRNA ligase, cytoplasmic;	0.03	0.01	0.96	10.50
P14550	Alcohol dehydrogenase [NADP(+)];	0.33	0.04	0.74	22.20
P11766	Alcohol dehydrogenase class-3;	-0.68	-0.09	0.57	17.10
P47895	Aldehyde dehydrogenase family 1 member A3;	-0.06	-0.05	1.00	17.20
Q8IZ83	Aldehyde dehydrogenase family 16 member A1;	-0.70	-0.32	0.56	2.00

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P42330	Aldo-keto reductase family 1 member C3;	-0.48	-0.19	0.70	17.30
P15121	Aldose reductase;	-0.85	-1.00	0.51	31.60
P05187	Alkaline phosphatase, placental type;	-0.09	-0.01	0.97	21.10
P10696	Alkaline phosphatase, placental-like;	0.53	0.03	0.60	21.20
P01011	Alpha-1-antichymotrypsin;	1.79	0.02	0.09	13.20
P01009	Alpha-1-antitrypsin;	1.39	0.07	0.24	25.60
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-	1.47	0.02	0.17	3.60
P30533	Alpha-2-macroglobulin receptor-associated protein;	1.08	0.04	0.31	3.60
P12814	Alpha-actinin-1;	0.51	0.16	0.70	43.90
O43707	Alpha-actinin-4;	0.06	0.01	0.92	51.90
P61163	Alpha-centractin;	-3.08	-32.36	0.01	5.90
P06733	Alpha-enolase;	-1.77	-7.58	0.16	48.60
P06280	Alpha-galactosidase A;	1.11	0.02	0.29	5.40
P35475	Alpha-L-iduronidase;	-0.04	-0.05	1.00	3.10
Q16706	Alpha-mannosidase 2;	0.22	0.01	0.80	5.90
P54802	Alpha-N-acetylglucosaminidase;	1.35	0.09	0.27	5.50
P40222	Alpha-taxilin;	-0.87	-0.57	0.47	1.80
Q96IU4	Alpha/beta hydrolase domain-containing protein 14B;	0.05	0.02	0.94	28.10
Q12904	Aminoacyl tRNA synthase complex-interacting	-0.41	-0.12	0.74	21.80
Q03154	Aminoacylase-1;	-1.21	-9.17	0.63	5.90
Q9H4A4	Aminopeptidase B;	-0.31	-0.09	0.82	15.40
P15514	Amphiregulin;	2.52	0.01	0.02	7.90
P05067	Amyloid beta A4 protein;	0.69	0.06	0.52	22.50
Q06481	Amyloid-like protein 2;	0.77	0.03	0.47	6.80
Q13685	Angio-associated migratory cell protein;	0.17	0.01	0.85	3.00
P03950	Angiogenin;	4.01	0.01	0.00	13.60
Q9BY76	Angiopoietin-related protein 4;	-0.47	-0.29	0.72	6.90
P04083	Annexin A1;	-0.52	-0.34	0.69	45.40
P50995	Annexin A11;	-0.32	-0.19	0.83	11.10
P07355	Annexin A2;	-1.20	-1.22	0.31	50.40
P12429	Annexin A3;	1.24	0.12	0.33	26.30
P08758	Annexin A5;	-1.28	-1.44	0.27	24.70
P46013	Antigen KI-67;	1.47	0.05	0.19	2.10
P01008	Antithrombin-III;	0.05	0.00	0.93	2.40
Q9BXS5	AP-1 complex subunit mu-1;	0.47	0.06	0.66	5.90
O95782	AP-2 complex subunit alpha-1;	-0.46	-0.25	0.72	5.30
P63010	AP-2 complex subunit beta;	0.41	0.18	0.78	10.50
Q96CW1	AP-2 complex subunit mu;	-0.77	-0.46	0.53	10.10
P02656	Apolipoprotein C-III;	-0.06	-0.01	0.99	16.20
Q9BZZ5	Apoptosis inhibitor 5;	-0.47	-0.29	0.72	12.80
Q07812	Apoptosis regulator BAX;	4.27	0.00	0.00	10.40
O95831	Apoptosis-inducing factor 1, mitochondrial;	0.21	0.16	0.89	7.20
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus;	-0.33	-0.38	0.85	2.60
P54136	Arginine--tRNA ligase, cytoplasmic;	-0.23	-0.08	0.87	14.50
P04424	Argininosuccinate lyase;	-0.19	-0.20	0.93	5.40
P15289	Arylsulfatase A;	1.18	0.02	0.27	2.80
P08243	Asparagine synthetase [glutamine-hydrolyzing];	1.47	0.02	0.17	5.30
O43776	Asparagine--tRNA ligase, cytoplasmic;	0.17	0.08	0.88	5.70
P17174	Aspartate aminotransferase, cytoplasmic;	-1.07	-2.37	0.44	17.70
P00505	Aspartate aminotransferase, mitochondrial;	0.22	0.06	0.82	15.10

Table S3

Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P14868	Aspartate--tRNA ligase, cytoplasmic;	1.47	0.17	0.38	4.00
O14497	AT-rich interactive domain-containing protein 1A;	0.19	0.01	0.83	0.50
Q8WWM7	Ataxin-2-like protein;	-0.32	-0.42	0.87	3.30
Q99700	Ataxin-2;	2.02	0.02	0.06	0.80
P61221	ATP-binding cassette sub-family E member 1;	-0.42	-0.06	0.73	7.00
Q8NE71	ATP-binding cassette sub-family F member 1;	-1.25	-1.06	0.28	3.40
Q9UG63	ATP-binding cassette sub-family F member 2;	-0.06	-0.05	0.99	4.50
P53396	ATP-citrate synthase;	-0.59	-0.54	0.66	23.50
Q08211	ATP-dependent RNA helicase A;	0.51	0.06	0.62	11.00
Q92499	ATP-dependent RNA helicase DDX1;	-0.81	-0.61	0.51	12.80
Q9NUU7	ATP-dependent RNA helicase DDX19A;	0.03	0.01	0.95	4.40
O00148	ATP-dependent RNA helicase DDX39A;	0.65	0.03	0.53	21.30
O75882	Attractin;	2.14	0.02	0.06	2.40
O95816	BAG family molecular chaperone regulator 2;	-0.71	-0.18	0.54	5.20
O95817	BAG family molecular chaperone regulator 3;	-0.89	-1.54	0.52	9.40
O43491	Band 4.1-like protein 2;	3.15	0.01	0.01	2.50
O75531	Barrier-to-autointegration factor;	1.28	0.16	0.39	34.80
P50895	Basal cell adhesion molecule;	1.35	0.26	0.52	25.60
P98160	Basement membrane-specific heparan sulfate	1.85	0.07	0.15	18.00
P35613	Basigin;	1.18	0.04	0.28	12.50
Q9NYF8	Bcl-2-associated transcription factor 1;	-0.39	-0.11	0.76	2.60
Q00973	Beta-1,4 N-acetylgalactosaminyltransferase 1;	-0.27	-0.08	0.85	5.10
P15291	Beta-1,4-galactosyltransferase 1;	0.22	0.05	0.82	9.30
O60513	Beta-1,4-galactosyltransferase 4;	-0.81	-0.30	0.49	5.20
O43286	Beta-1,4-galactosyltransferase 5;	2.28	0.01	0.04	2.60
P02749	Beta-2-glycoprotein 1;	0.87	0.02	0.41	2.60
P61769	Beta-2-microglobulin;	0.74	0.05	0.49	35.30
P13929	Beta-enolase;	-0.26	-0.04	0.85	9.90
P16278	Beta-galactosidase;	0.87	0.16	0.52	15.20
P08236	Beta-glucuronidase;	2.35	0.10	0.22	6.30
P06865	Beta-hexosaminidase subunit alpha;	1.56	0.09	0.22	19.10
P07686	Beta-hexosaminidase subunit beta;	1.69	0.13	0.29	23.00
O00462	Beta-mannosidase;	1.39	0.05	0.22	5.70
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate	-1.06	-0.60	0.36	5.10
P07814	Bifunctional glutamate/proline--tRNA ligase;	0.21	0.03	0.82	10.30
P31939	Bifunctional purine biosynthesis protein PURH;	-0.45	-0.16	0.73	25.50
P53004	Biliverdin reductase A;	-0.13	-0.01	0.94	8.10
P43251	Biotinidase;	-0.13	-0.08	0.95	5.70
Q9H3K6	BolA-like protein 2;	0.11	0.03	0.89	51.20
P13497	Bone morphogenetic protein 1;	1.01	0.12	0.42	8.10
Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein	-0.74	-0.78	0.57	7.40
Q9P287	BRCA2 and CDKN1A-interacting protein;	-0.03	-0.01	0.99	12.70
P11586	C-1-tetrahydrofolate synthase, cytoplasmic;	-0.15	-0.10	0.93	19.50
O60271	C-Jun-amino-terminal kinase-interacting protein 4;	-0.51	-0.35	0.70	4.50
Q99417	C-Myc-binding protein;	1.24	0.03	0.24	10.70
Q13363	C-terminal-binding protein 1;	-1.90	-3.12	0.09	6.80
P56545	C-terminal-binding protein 2;	-0.06	-0.01	0.99	13.00
Q9UBG0	C-type mannose receptor 2;	-1.61	-2.49	0.16	2.60
Q96EU7	C1GALT1-specific chaperone 1;	0.74	0.78	0.86	7.20
P55290	Cadherin-13;	-1.17	-0.89	0.31	5.00
P63098	Calcineurin subunit B type 1;	0.65	0.03	0.53	5.90
Q9Y376	Calcium-binding protein 39;	-1.71	-4.60	0.15	6.50
Q9Y2V2	Calcium-regulated heat stable protein 1;	0.69	0.14	0.58	18.40
Q13554	Calcium/calmodulin-dependent protein kinase type II	-0.28	-0.06	0.83	2.50

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9HB71	Calcyclin-binding protein;	0.41	0.06	0.69	29.80
P62158	Calmodulin;	-0.28	-0.07	0.83	28.20
P27824	Calnexin;	-0.33	-0.03	0.80	1.70
P04632	Calpain small subunit 1;	-0.42	-0.10	0.73	11.90
P07384	Calpain-1 catalytic subunit;	0.03	0.02	0.96	3.20
P17655	Calpain-2 catalytic subunit;	0.74	0.17	0.59	8.30
Q99439	Calponin-2;	-1.34	-1.29	0.24	3.60
Q15417	Calponin-3;	-0.11	-0.10	0.97	6.40
P27797	Calreticulin;	0.77	0.15	0.56	9.60
P22676	Calretinin;	1.04	0.13	0.43	20.30
O94985	Calsyntenin-1;	1.04	0.06	0.35	16.60
O43852	Calumenin;	1.74	0.16	0.33	17.50
P10644	cAMP-dependent protein kinase type I-alpha regulatory	-1.28	-1.37	0.27	8.70
P13861	cAMP-dependent protein kinase type II-alpha regulatory	0.03	0.00	0.94	3.70
Q14444	Caprin-1;	-0.68	-0.18	0.56	1.60
Q8NCH0	Carbohydrate sulfotransferase 14;	0.35	0.08	0.75	12.00
P00918	Carbonic anhydrase 2;	-1.42	-1.40	0.22	4.60
P16152	Carbonyl reductase [NADPH] 1;	-2.58	-40.86	0.05	24.50
Q9UI42	Carboxypeptidase A4;	0.24	0.03	0.80	7.80
P68400	Casein kinase II subunit alpha;	2.52	0.01	0.02	3.80
P19784	Casein kinase II subunit alpha';	-0.52	-0.10	0.67	3.70
P04040	Catalase;	-1.28	-4.21	0.36	4.70
P07858	Cathepsin B;	0.84	0.14	0.51	36.60
P07339	Cathepsin D;	0.65	0.06	0.54	34.20
P07711	Cathepsin L1;	2.14	0.03	0.06	16.50
O60911	Cathepsin L2;	-1.38	-1.75	0.24	6.30
Q9UBR2	Cathepsin Z;	0.87	0.10	0.46	23.40
Q8WUX2	Cation transport regulator-like protein 2;	-0.54	-0.17	0.66	8.70
P20645	Cation-dependent mannose-6-phosphate receptor;	0.77	0.02	0.46	5.10
P11717	Cation-independent mannose-6-phosphate receptor;	0.16	0.04	0.87	5.40
Q03135	Caveolin-1;	0.17	0.02	0.85	7.90
Q6YHK3	CD109 antigen;	0.93	0.10	0.43	14.30
Q13740	CD166 antigen;	0.90	0.06	0.40	21.40
Q9Y5K6	CD2-associated protein;	-0.27	-0.02	0.83	1.40
P16070	CD44 antigen;	-0.70	-0.71	0.59	8.80
P13987	CD59 glycoprotein;	1.51	0.05	0.18	15.60
P60033	CD81 antigen;	0.77	0.13	0.54	16.50
P21926	CD9 antigen;	0.24	0.02	0.79	3.90
Q8NFZ8	Cell adhesion molecule 4;	2.02	0.04	0.07	21.60
Q4KMG0	Cell adhesion molecule-related/down-regulated by	-0.03	0.00	0.99	1.30
P60953	Cell division control protein 42 homolog;	-1.39	-2.62	0.25	14.70
Q99459	Cell division cycle 5-like protein;	-0.31	-0.06	0.81	4.10
Q8IX12	Cell division cycle and apoptosis regulator protein 1;	1.24	0.03	0.25	0.90
Q99674	Cell growth regulator with EF hand domain protein 1;	0.77	0.10	0.50	12.30
Q9NX58	Cell growth-regulating nucleolar protein;	-1.78	-4.56	0.13	7.40
P43121	Cell surface glycoprotein MUC18;	0.60	0.03	0.56	1.90
P62633	Cellular nucleic acid-binding protein;	0.05	0.02	0.95	22.00
Q5SW79	Centrosomal protein of 170 kDa;	-0.11	-0.14	0.97	2.00
Q53EZ4	Centrosomal protein of 55 kDa;	2.08	0.01	0.05	2.80
O75503	Ceroid-lipofuscinosis neuronal protein 5;	0.67	0.08	0.55	10.10
O00299	Chloride intracellular channel protein 1;	0.03	0.01	0.95	61.40
Q9Y696	Chloride intracellular channel protein 4;	-0.72	-0.44	0.55	24.90
P49585	Choline-phosphate cytidylyltransferase A;	0.06	0.01	0.92	4.10
Q6UVK1	Chondroitin sulfate proteoglycan 4;	0.77	0.07	0.49	10.50
P83916	Chromobox protein homolog 1;	-1.07	-0.41	0.35	14.60

Table S3

Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q13185	Chromobox protein homolog 3;	-0.79	-0.29	0.50	28.40
P45973	Chromobox protein homolog 5;	-1.07	-7.03	0.68	14.70
Q14839	Chromodomain-helicase-DNA-binding protein 4;	-1.39	-15.28	0.60	2.00
O75390	Citrate synthase, mitochondrial;	0.53	0.03	0.60	4.30
Q00610	Clathrin heavy chain 1;	0.30	0.04	0.77	16.50
P09496	Clathrin light chain A;	0.21	0.01	0.81	3.20
Q10570	Cleavage and polyadenylation specificity factor subunit 1;	-0.66	-0.45	0.60	1.90
O95639	Cleavage and polyadenylation specificity factor subunit 4;	0.32	0.03	0.74	7.80
O43809	Cleavage and polyadenylation specificity factor subunit 5;	-0.21	-0.16	0.90	8.40
Q7Z460	CLIP-associating protein 1;	-0.88	-0.65	0.46	2.10
P10909	Clusterin;	0.19	0.02	0.84	30.70
Q11201	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-	2.52	0.01	0.02	4.70
Q14019	Coactosin-like protein;	-0.51	-0.33	0.70	25.40
P00742	Coagulation factor X;	1.79	0.02	0.10	3.90
P48444	Coatomer subunit delta;	-0.13	-0.03	0.94	6.50
O14579	Coatomer subunit epsilon;	0.77	0.01	0.45	3.60
Q9UBF2	Coatomer subunit gamma-2;	-1.47	-0.94	0.19	1.40
O43405	Cochlin;	5.01	0.01	0.00	7.10
P23528	Cofilin-1;	-0.43	-0.20	0.74	39.20
Q9Y281	Cofilin-2;	0.87	0.06	0.43	23.50
Q76M96	Coiled-coil domain-containing protein 80;	1.96	0.06	0.12	8.50
O75534	Cold shock domain-containing protein E1;	0.03	0.01	0.96	1.50
Q14011	Cold-inducible RNA-binding protein;	-0.57	-0.12	0.64	6.40
P12109	Collagen alpha-1(VI) chain;	2.43	0.04	0.05	15.90
Q99715	Collagen alpha-1(XII) chain;	-0.55	-0.28	0.66	3.80
P39060	Collagen alpha-1(XVIII) chain;	1.85	0.09	0.18	6.70
P05997	Collagen alpha-2(V) chain;	4.61	0.01	0.05	8.00
P29400	Collagen alpha-5(IV) chain;	1.90	0.02	0.08	2.40
Q6UXH8	Collagen and calcium-binding EGF domain-containing	0.58	0.02	0.57	7.10
P00736	Complement C1r subcomponent;	1.43	0.03	0.19	11.50
P09871	Complement C1s subcomponent;	2.43	0.06	0.10	7.30
P01024	Complement C3;	2.52	0.04	0.06	46.00
Q07021	Complement component 1 Q subcomponent-binding	0.60	0.05	0.57	7.10
P00751	Complement factor B;	1.69	0.09	0.21	15.20
P00746	Complement factor D;	1.51	0.02	0.15	37.90
P29279	Connective tissue growth factor;	-0.39	-0.56	0.84	6.30
Q9NX05	Constitutive coactivator of PPAR-gamma-like protein 2;	4.61	0.00	0.00	2.60
Q13098	COP9 signalosome complex subunit 1;	-0.06	-0.04	0.99	8.40
P61201	COP9 signalosome complex subunit 2;	0.51	0.32	0.80	13.50
Q9UNS2	COP9 signalosome complex subunit 3;	0.03	0.01	0.94	3.50
Q9BT78	COP9 signalosome complex subunit 4;	0.00	0.00	0.97	6.90
Q92905	COP9 signalosome complex subunit 5;	-0.33	-0.05	0.79	4.50
Q99829	Copine-1;	-0.62	-0.46	0.63	4.70
Q9NTM9	Copper homeostasis protein cutC homolog;	1.28	0.03	0.23	12.10
O00244	Copper transport protein ATOX1;	-0.80	-0.18	0.49	25.00
P36551	Coproporphyrinogen-III oxidase, mitochondrial;	-0.67	-0.61	0.61	6.20
O75367	Core histone macro-H2A.1;	-0.79	-0.63	0.52	8.30
P31146	Coronin-1A;	-0.91	-1.36	0.50	3.70
Q9BR76	Coronin-1B;	-0.28	-0.36	0.89	5.90
Q9ULV4	Coronin-1C;	-0.06	-0.01	0.99	7.60
P12277	Creatine kinase B-type;	4.27	0.02	0.08	34.40
Q92793	CREB-binding protein;	2.02	0.01	0.06	0.40
P46109	Crk-like protein;	0.37	0.02	0.71	6.90
Q13616	Cullin-1;	-0.18	-0.25	0.95	4.00

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q13617	Cullin-2;	-0.13	-0.09	0.95	3.90
Q13620	Cullin-4B;	0.17	0.02	0.85	3.70
Q86VP6	Cullin-associated NEDD8-dissociated protein 1;	-0.55	-0.57	0.70	16.90
Q00536	Cyclin-dependent kinase 16;	-0.61	-1.96	0.81	4.40
P42773	Cyclin-dependent kinase 4 inhibitor C;	-0.68	-0.23	0.57	11.30
Q00534	Cyclin-dependent kinase 6;	-0.84	-1.61	0.58	4.90
O75909	Cyclin-K;	-1.23	-1.29	0.29	3.30
P04080	Cystatin-B;	0.41	0.03	0.69	40.80
P01034	Cystatin-C;	1.69	0.03	0.13	30.10
P21291	Cysteine and glycine-rich protein 1;	-0.06	-0.01	1.00	8.80
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1;	1.60	0.14	0.32	9.30
P49589	Cysteine--tRNA ligase, cytoplasmic;	-1.09	-2.63	0.44	5.50
Q9NZV1	Cysteine-rich motor neuron 1 protein;	0.74	0.12	0.54	9.50
P00167	Cytochrome b5;	0.21	0.01	0.82	20.10
Q9P0S2	Cytochrome c oxidase assembly protein COX16	1.11	0.07	0.32	13.20
P14854	Cytochrome c oxidase subunit 6B1;	-0.34	-0.07	0.78	12.80
P99999	Cytochrome c;	-0.40	-0.08	0.74	17.10
P21399	Cytoplasmic aconitate hydratase;	-0.15	-0.21	0.95	3.90
Q14204	Cytoplasmic dynein 1 heavy chain 1;	0.79	0.13	0.52	3.20
Q13409	Cytoplasmic dynein 1 intermediate chain 2;	-0.70	-0.78	0.60	3.60
O43237	Cytoplasmic dynein 1 light intermediate chain 2;	0.00	0.00	0.97	3.00
Q7L576	Cytoplasmic FMR1-interacting protein 1;	1.21	0.28	0.56	2.60
P16333	Cytoplasmic protein NCK1;	-0.34	-0.10	0.79	3.70
Q14008	Cytoskeleton-associated protein 5;	-1.07	-1.20	0.37	2.40
P28838	Cytosol aminopeptidase;	-2.13	-8.28	0.07	11.00
O00154	Cytosolic acyl coenzyme A thioester hydrolase;	0.00	0.00	0.97	22.40
Q96KP4	Cytosolic non-specific dipeptidase;	-1.18	-4.66	0.47	17.30
P49902	Cytosolic purine 5'-nucleotidase;	1.47	0.03	0.17	1.60
O43175	D-3-phosphoglycerate dehydrogenase;	-0.42	-0.39	0.78	6.60
P30046	D-dopachrome decarboxylase;	0.41	0.02	0.67	22.00
Q8N163	DBIRD complex subunit KIAA1967;	4.27	0.00	0.00	1.60
Q9UKG1	DCC-interacting protein 13-alpha;	-1.11	-0.60	0.33	2.40
Q9H773	dCTP pyrophosphatase 1;	-0.83	-0.18	0.47	5.30
P13716	Delta-aminolevulinic acid dehydratase;	0.51	0.04	0.61	8.50
O00115	Deoxyribonuclease-2-alpha;	1.11	0.04	0.30	19.70
O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidase;	-1.18	-0.48	0.30	9.80
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase,	0.08	0.05	0.94	27.80
Q02487	Desmocollin-2;	0.56	0.26	0.74	1.10
Q14126	Desmoglein-2;	0.79	0.05	0.46	6.40
P15924	Desmoplakin;	-0.09	-0.03	0.97	0.90
P60981	Destrin;	-0.32	-0.03	0.80	11.50
Q01459	Di-N-acetylchitobiase;	-0.11	-0.01	0.95	5.50
Q9NR28	Diablo homolog, mitochondrial;	-0.86	-0.47	0.47	10.00
O94907	Dickkopf-related protein 1;	2.69	0.02	0.02	45.50
Q9UBP4	Dickkopf-related protein 3;	2.21	0.08	0.15	17.70
P09622	Dihydrolipoyl dehydrogenase, mitochondrial;	0.32	0.02	0.74	5.90
P36957	Dihydrolipoyllysine-residue succinyltransferase	1.43	0.04	0.20	4.60
P09417	Dihydropteridine reductase;	-1.42	-2.90	0.24	18.40
Q16555	Dihydropyrimidinase-related protein 2;	-0.51	-0.21	0.68	23.60
Q12882	Dihydropyrimidine dehydrogenase [NADP(+)];	0.21	0.02	0.83	2.10
P53634	Dipeptidyl peptidase 1;	2.35	0.06	0.10	22.90
Q9UHL4	Dipeptidyl peptidase 2;	1.24	0.07	0.28	19.30
Q9NY33	Dipeptidyl peptidase 3;	-0.03	-0.03	0.99	5.60
Q86TI2	Dipeptidyl peptidase 9;	0.14	0.07	0.90	3.40

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Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9BQC3	Diphthamide biosynthesis protein 2;	6.64	0.00	0.00	4.10
Q8IYB7	DIS3-like exonuclease 2;	-0.99	-1.01	0.41	2.70
O14672	Disintegrin and metalloproteinase domain-containing	0.77	0.08	0.48	8.40
Q13444	Disintegrin and metalloproteinase domain-containing	1.69	0.06	0.16	7.90
P78536	Disintegrin and metalloproteinase domain-containing	0.17	0.01	0.85	3.00
Q13443	Disintegrin and metalloproteinase domain-containing	1.60	0.03	0.15	1.70
Q12959	Disks large homolog 1;	-0.10	-0.01	0.96	2.40
Q16531	DNA damage-binding protein 1;	-0.25	-0.16	0.88	8.80
Q92466	DNA damage-binding protein 2;	-0.83	-0.34	0.48	4.40
P18887	DNA repair protein XRCC1;	0.47	0.05	0.65	3.80
P49736	DNA replication licensing factor MCM2;	0.30	0.02	0.76	2.40
P25205	DNA replication licensing factor MCM3;	0.12	0.03	0.88	2.60
P33991	DNA replication licensing factor MCM4;	0.32	0.03	0.74	4.20
Q14566	DNA replication licensing factor MCM6;	0.53	0.12	0.65	8.30
P27695	DNA-(apurinic or apyrimidinic site) lyase;	0.33	0.03	0.73	21.10
P16989	DNA-binding protein A;	1.04	0.03	0.33	9.10
P78527	DNA-dependent protein kinase catalytic subunit;	0.49	0.20	0.74	1.30
P31689	DnaJ homolog subfamily A member 1;	1.79	0.14	0.29	3.30
O75937	DnaJ homolog subfamily C member 8;	-0.62	-0.32	0.61	9.50
Q16643	Drebrin;	1.28	0.04	0.23	4.30
P36507	Dual specificity mitogen-activated protein kinase kinase	0.82	0.02	0.43	3.10
P51452	Dual specificity protein phosphatase 3;	0.21	0.03	0.83	13.50
Q13561	Dynactin subunit 2;	0.12	0.04	0.89	15.70
O00429	Dynamin-1-like protein;	-0.38	-0.33	0.80	7.50
O60313	Dynamin-like 120 kDa protein, mitochondrial;	0.37	0.03	0.71	1.50
P63167	Dynein light chain 1, cytoplasmic;	-0.33	-0.07	0.79	37.10
Q96FJ2	Dynein light chain 2, cytoplasmic;	-0.57	-0.54	0.68	44.90
Q9NP97	Dynein light chain roadblock-type 1;	-0.84	-0.25	0.47	16.70
Q8IZA0	Dyslexia-associated protein KIAA0319-like protein;	0.22	0.02	0.81	2.40
Q14118	Dystroglycan;	1.32	0.05	0.23	19.20
P49792	E3 SUMO-protein ligase RanBP2;	-0.33	-0.22	0.82	1.30
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1;	-0.87	-0.30	0.46	2.00
Q9UNE7	E3 ubiquitin-protein ligase CHIP;	0.99	0.22	0.54	10.60
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1;	0.72	0.03	0.49	1.00
Q14258	E3 ubiquitin/ISG15 ligase TRIM25;	0.77	0.26	0.65	17.50
Q15075	Early endosome antigen 1;	2.08	0.12	0.25	6.90
O95834	Echinoderm microtubule-associated protein-like 2;	-0.43	-0.65	0.81	8.80
Q9HC35	Echinoderm microtubule-associated protein-like 4;	0.28	0.08	0.80	4.90
Q96C19	EF-hand domain-containing protein D2;	0.90	0.07	0.43	16.70
O95967	EGF-containing fibulin-like extracellular matrix protein	0.65	0.21	0.66	11.70
Q9H4M9	EH domain-containing protein 1;	0.08	0.02	0.92	10.30
Q15717	ELAV-like protein 1;	-0.64	-0.60	0.63	16.90
P68104	Elongation factor 1-alpha 1;	-0.62	-0.23	0.61	29.40
Q05639	Elongation factor 1-alpha 2;	0.87	0.02	0.41	20.70
P24534	Elongation factor 1-beta;	-0.22	-0.08	0.88	24.40
P29692	Elongation factor 1-delta;	-1.07	-2.80	0.46	38.10
P26641	Elongation factor 1-gamma;	-0.40	-0.13	0.76	16.50
P13639	Elongation factor 2;	-0.22	-0.12	0.89	19.00
P49411	Elongation factor Tu, mitochondrial;	0.72	0.18	0.61	9.70
P50402	Emerin;	-2.72	-8.40	0.01	6.70
Q99961	Endophilin-A2;	0.90	0.19	0.55	5.40
Q9NR46	Endophilin-B2;	2.52	0.02	0.03	3.80
P30040	Endoplasmic reticulum resident protein 29;	1.14	0.05	0.29	20.70
Q9BS26	Endoplasmic reticulum resident protein 44;	0.47	0.04	0.65	7.10

Table S3

Uniprot accession	**Name**	**Fold-change (log_2) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
P14625	Endoplasmin;	1.28	0.07	0.27	15.90
Q9UNN8	Endothelial protein C receptor;	0.65	0.08	0.56	20.60
Q6P2E9	Enhancer of mRNA-decapping protein 4;	0.21	0.01	0.81	1.10
P84090	Enhancer of rudimentary homolog;	-1.30	-8.26	0.51	23.10
Q9NPA8	Enhancer of yellow 2 transcription factor homolog;	-1.21	-0.89	0.30	16.80
P42126	Enoyl-CoA delta isomerase 1, mitochondrial;	2.69	0.01	0.02	4.30
P30084	Enoyl-CoA hydratase, mitochondrial;	-0.04	0.00	1.00	4.50
P54764	Ephrin type-A receptor 4;	0.82	0.12	0.50	4.00
P54760	Ephrin type-B receptor 4;	-0.84	-0.27	0.47	2.30
P20827	Ephrin-A1;	0.33	0.02	0.73	3.90
Q9UBC2	Epidermal growth factor receptor substrate 15-like 1;	-1.77	-5.35	0.14	3.40
P00533	Epidermal growth factor receptor;	0.33	0.10	0.77	10.80
Q9UHF1	Epidermal growth factor-like protein 7;	2.90	0.05	0.10	21.60
P61916	Epididymal secretory protein E1;	2.28	0.04	0.06	38.40
Q9Y2E5	Epididymis-specific alpha-mannosidase;	2.35	0.11	0.24	8.00
P58107	Epiplakin;	0.99	0.03	0.35	3.60
Q96HE7	ERO1-like protein alpha;	1.08	0.05	0.31	5.10
P60842	Eukaryotic initiation factor 4A-I;	0.51	0.05	0.62	24.60
Q14240	Eukaryotic initiation factor 4A-II;	-1.20	-0.47	0.29	19.70
P38919	Eukaryotic initiation factor 4A-III;	0.11	0.02	0.90	9.00
P15170	Eukaryotic peptide chain release factor GTP-binding	-0.57	-0.36	0.65	6.20
P62495	Eukaryotic peptide chain release factor subunit 1;	0.77	0.20	0.61	12.60
O14602	Eukaryotic translation initiation factor 1A, Y-	-0.32	-0.11	0.81	6.90
P05198	Eukaryotic translation initiation factor 2 subunit 1;	0.74	0.26	0.67	21.30
P20042	Eukaryotic translation initiation factor 2 subunit 2;	-0.81	-2.83	0.70	6.60
P41091	Eukaryotic translation initiation factor 2 subunit 3;	0.33	0.08	0.76	22.50
Q9BY44	Eukaryotic translation initiation factor 2A;	-0.07	-0.02	0.98	10.10
Q14152	Eukaryotic translation initiation factor 3 subunit A;	0.37	0.13	0.77	9.30
P55884	Eukaryotic translation initiation factor 3 subunit B;	-0.13	-0.05	0.94	6.50
Q99613	Eukaryotic translation initiation factor 3 subunit C;	0.99	0.15	0.47	8.00
O15371	Eukaryotic translation initiation factor 3 subunit D;	-0.11	-0.03	0.95	5.70
P60228	Eukaryotic translation initiation factor 3 subunit E;	0.96	0.29	0.62	11.00
O75821	Eukaryotic translation initiation factor 3 subunit G;	0.43	0.07	0.69	10.00
O15372	Eukaryotic translation initiation factor 3 subunit H;	-0.61	-0.13	0.61	3.40
Q13347	Eukaryotic translation initiation factor 3 subunit I;	0.28	0.07	0.80	9.20
O75822	Eukaryotic translation initiation factor 3 subunit J;	-0.23	-0.04	0.86	14.30
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K;	-0.37	-0.07	0.77	6.40
Q9Y262	Eukaryotic translation initiation factor 3 subunit L;	0.08	0.01	0.91	4.40
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M;	0.67	0.10	0.56	14.40
Q04637	Eukaryotic translation initiation factor 4 gamma 1;	0.28	0.08	0.80	5.30
P23588	Eukaryotic translation initiation factor 4B;	1.56	0.15	0.34	3.90
P06730	Eukaryotic translation initiation factor 4E;	-0.64	-0.26	0.59	18.00
Q15056	Eukaryotic translation initiation factor 4H;	0.41	0.02	0.67	9.30
P55010	Eukaryotic translation initiation factor 5;	-0.42	-0.05	0.73	7.00
P63241	Eukaryotic translation initiation factor 5A-1;	-0.31	-0.07	0.81	19.00
O60841	Eukaryotic translation initiation factor 5B;	0.41	0.14	0.74	5.10
P56537	Eukaryotic translation initiation factor 6;	-0.22	-0.05	0.87	31.40
Q9Y3B2	Exosome complex component CSL4;	0.21	0.04	0.83	7.20
Q9NPD3	Exosome complex component RRP41;	3.28	0.00	0.00	5.70
Q15024	Exosome complex component RRP42;	0.39	0.06	0.71	7.90
O14980	Exportin-1;	-0.62	-0.51	0.63	5.20
P55060	Exportin-2;	-0.48	-0.33	0.72	6.40
Q16610	Extracellular matrix protein 1;	1.69	0.05	0.14	29.30
Q86XX4	Extracellular matrix protein FRAS1;	2.43	0.05	0.07	4.10
Q8IWU5	Extracellular sulfatase Sulf-2;	0.43	0.03	0.67	10.80

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P08294	Extracellular superoxide dismutase [Cu-Zn];	-1.23	-1.22	0.29	12.10
P15311	Ezrin;	-0.78	-0.53	0.52	20.10
P52907	F-actin-capping protein subunit alpha-1;	-0.28	-0.18	0.85	45.80
P47755	F-actin-capping protein subunit alpha-2;	-0.06	-0.06	1.00	21.70
P47756	F-actin-capping protein subunit beta;	0.01	0.01	0.97	11.90
Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1;	-0.65	-0.20	0.59	4.90
Q9Y5B9	FACT complex subunit SPT16;	0.77	0.18	0.58	6.10
Q08945	FACT complex subunit SSRP1;	0.90	0.02	0.39	4.10
Q96AE4	Far upstream element-binding protein 1;	-0.14	-0.07	0.93	12.30
Q92945	Far upstream element-binding protein 2;	-0.18	-0.16	0.93	21.00
P14324	Farnesyl pyrophosphate synthase;	0.47	0.12	0.70	16.90
Q16658	Fascin;	1.24	0.06	0.26	10.10
P49327	Fatty acid synthase;	0.69	0.11	0.56	22.30
Q01469	Fatty acid-binding protein, epidermal;	-0.57	-0.75	0.71	57.80
P05413	Fatty acid-binding protein, heart;	0.47	0.20	0.75	17.30
Q96AC1	Fermitin family homolog 2;	1.24	0.01	0.23	1.50
P02794	Ferritin heavy chain;	-0.74	-0.67	0.56	13.10
P02792	Ferritin light chain;	1.85	0.01	0.08	8.60
Q8N441	Fibroblast growth factor receptor-like 1;	2.69	0.16	0.47	4.40
Q14512	Fibroblast growth factor-binding protein 1;	-0.40	-0.34	0.79	28.20
P02751	Fibronectin;	-0.11	-0.10	0.97	2.20
P21333	Filamin-A;	0.51	0.08	0.63	26.60
O75369	Filamin-B;	0.82	0.11	0.49	34.10
Q14315	Filamin-C;	-0.49	-0.36	0.72	10.70
P30043	Flavin reductase (NADPH);	1.96	0.02	0.08	9.20
O95633	Follistatin-related protein 3;	0.77	0.10	0.51	16.30
Q06787	Fragile X mental retardation protein 1;	0.12	0.02	0.88	2.10
P04075	Fructose-bisphosphate aldolase A;	-0.78	-0.45	0.51	51.10
P09972	Fructose-bisphosphate aldolase C;	0.60	0.44	0.82	36.50
P07954	Fumarate hydratase, mitochondrial;	0.90	0.07	0.42	4.10
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein	0.96	0.10	0.41	10.80
P09382	Galectin-1;	-1.00	-1.30	0.42	31.90
Q08380	Galectin-3-binding protein;	2.02	0.04	0.08	35.40
P17931	Galectin-3;	-0.57	-0.23	0.64	28.40
Q92820	Gamma-glutamyl hydrolase;	0.99	0.07	0.38	25.20
O75223	Gamma-glutamylcyclotransferase;	-0.10	-0.03	0.96	11.20
P13284	Gamma-interferon-inducible lysosomal thiol reductase;	1.96	0.07	0.15	12.40
Q16666	Gamma-interferon-inducible protein 16;	0.11	0.04	0.91	3.40
O76070	Gamma-synuclein;	2.02	0.08	0.16	22.80
P17900	Ganglioside GM2 activator;	0.47	0.05	0.65	15.00
P01350	Gastrin;	2.52	0.00	0.02	16.80
Q9H488	GDP-fucose protein O-fucosyltransferase 1;	-0.22	-0.03	0.87	4.10
Q13630	GDP-L-fucose synthase;	-1.63	-8.11	0.24	15.30
P06396	Gelsolin;	0.84	0.09	0.46	21.10
P78347	General transcription factor II-I;	1.32	0.03	0.22	2.20
P35269	General transcription factor IIF subunit 1;	-0.87	-0.27	0.45	2.30
P60983	Glia maturation factor beta;	-0.17	-0.02	0.91	11.30
P07093	Glia-derived nexin;	1.51	0.13	0.31	22.10
Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein;	0.79	0.06	0.46	2.30
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase;	-0.59	-0.19	0.62	17.90
P11413	Glucose-6-phosphate 1-dehydrogenase;	-0.37	-0.14	0.78	7.00
P06744	Glucose-6-phosphate isomerase;	-0.41	-0.24	0.76	23.50
P14314	Glucosidase 2 subunit beta;	1.24	0.04	0.26	7.40

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Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q4G148	Glucoside xylosyltransferase 1;	3.80	0.02	0.05	6.40
P04062	Glucosylceramidase;	0.41	0.02	0.67	9.10
P00367	Glutamate dehydrogenase 1, mitochondrial;	1.47	0.09	0.24	19.90
P48507	Glutamate--cysteine ligase regulatory subunit;	0.16	0.04	0.87	10.90
O94925	Glutaminase kidney isoform, mitochondrial;	0.62	0.38	0.78	4.20
O94808	Glutamine--fructose-6-phosphate aminotransferase	-0.17	-0.03	0.91	2.90
P47897	Glutamine--tRNA ligase;	0.51	0.28	0.78	13.90
O76003	Glutaredoxin-3;	1.14	0.09	0.33	23.60
Q86SX6	Glutaredoxin-related protein 5, mitochondrial;	0.05	0.01	0.93	8.90
P00390	Glutathione reductase, mitochondrial;	-0.11	-0.02	0.95	4.00
P78417	Glutathione S-transferase omega-1;	0.22	0.06	0.83	23.70
P09211	Glutathione S-transferase P;	-0.66	-1.18	0.69	41.00
P30711	Glutathione S-transferase theta-1;	-0.31	-0.15	0.83	6.20
P04406	Glyceraldehyde-3-phosphate dehydrogenase;	-0.78	-0.64	0.52	34.00
P35573	Glycogen debranching enzyme;	-2.77	-24.65	0.02	0.80
P11216	Glycogen phosphorylase, brain form;	-1.47	-9.02	0.38	24.90
P06737	Glycogen phosphorylase, liver form;	-0.03	-0.02	0.99	29.60
Q9HC38	Glyoxalase domain-containing protein 4;	0.79	0.19	0.58	19.80
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase;	-1.18	-2.46	0.36	12.50
P35052	Glypican-1;	1.32	0.11	0.30	26.20
P49915	GMP synthase [glutamine-hydrolyzing];	-0.53	-0.13	0.66	3.00
Q92896	Golgi apparatus protein 1;	2.02	0.10	0.19	1.80
Q8NBJ4	Golgi membrane protein 1;	0.77	0.09	0.51	12.50
O95249	Golgi SNAP receptor complex member 1;	-0.57	-0.12	0.64	4.80
P28799	Granulins;	1.35	0.05	0.23	24.80
Q9NZ20	Group 3 secretory phospholipase A2;	1.39	0.03	0.20	2.20
Q8NCC3	Group XV phospholipase A2;	0.47	0.07	0.66	16.70
P62993	Growth factor receptor-bound protein 2;	0.03	0.00	0.94	8.80
P09341	Growth-regulated alpha protein;	2.80	0.03	0.03	44.90
Q99988	Growth/differentiation factor 15;	0.77	0.05	0.46	18.80
Q9HAV7	GrpE protein homolog 1, mitochondrial;	1.43	0.19	0.42	12.90
P62826	GTP-binding nuclear protein Ran;	-0.82	-0.38	0.49	39.40
Q9Y2T3	Guanine deaminase;	-0.39	-0.21	0.77	30.20
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2;	0.35	0.02	0.72	3.70
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T)	1.60	0.02	0.14	9.10
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T)	0.03	0.00	0.94	9.10
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;	-0.46	-0.36	0.75	40.70
Q8N4P3	Guanosine-3',5'-bis(diphosphate) 3'-	-3.52	-76.73	0.00	7.80
Q9NY12	H/ACA ribonucleoprotein complex subunit 1;	0.11	0.02	0.90	8.30
Q9NX24	H/ACA ribonucleoprotein complex subunit 2;	0.01	0.00	0.96	12.40
O60832	H/ACA ribonucleoprotein complex subunit 4;	-0.47	-0.12	0.70	6.20
Q9H0R4	Haloacid dehalogenase-like hydrolase domain-containing	-1.90	-3.85	0.09	5.00
P48723	Heat shock 70 kDa protein 13;	0.82	0.07	0.46	8.70
P08107	Heat shock 70 kDa protein 1A/1B;	-0.28	-0.11	0.83	23.70
P34932	Heat shock 70 kDa protein 4;	-0.13	-0.06	0.94	15.20
P11142	Heat shock cognate 71 kDa protein;	0.30	0.20	0.85	37.80
Q92598	Heat shock protein 105 kDa;	0.72	0.32	0.72	15.70
P04792	Heat shock protein beta-1;	0.58	0.12	0.63	24.40
P07900	Heat shock protein HSP 90-alpha;	-0.64	-0.33	0.60	35.90
P08238	Heat shock protein HSP 90-beta;	-0.25	-0.11	0.87	32.00
Q9H910	Hematological and neurological expressed 1-like protein;	-0.04	-0.01	1.00	15.30
P30519	Heme oxygenase 2;	1.51	0.13	0.31	8.90

Table S3

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P69905	Hemoglobin subunit alpha;	0.37	0.04	0.72	28.20
P02042	Hemoglobin subunit delta;	0.87	0.11	0.47	12.90
O14964	Hepatocyte growth factor-regulated tyrosine kinase	1.64	0.02	0.13	1.30
Q7Z4V5	Hepatoma-derived growth factor-related protein 2;	-0.99	-0.57	0.40	2.20
P51858	Hepatoma-derived growth factor;	-0.38	-0.03	0.76	17.90
Q5SSJ5	Heterochromatin protein 1-binding protein 3;	0.41	0.01	0.67	2.70
Q99729	Heterogeneous nuclear ribonucleoprotein A/B;	-0.27	-0.05	0.84	2.40
Q13151	Heterogeneous nuclear ribonucleoprotein A0;	0.90	0.07	0.43	11.50
P09651	Heterogeneous nuclear ribonucleoprotein A1;	0.16	0.04	0.87	13.40
P51991	Heterogeneous nuclear ribonucleoprotein A3;	0.39	0.03	0.70	6.60
O60812	Heterogeneous nuclear ribonucleoprotein C-like 1;	-0.11	-0.01	0.95	12.60
Q14103	Heterogeneous nuclear ribonucleoprotein D0;	-0.65	-0.68	0.63	13.80
P52597	Heterogeneous nuclear ribonucleoprotein F;	-0.01	-0.01	0.98	23.10
P31943	Heterogeneous nuclear ribonucleoprotein H;	0.08	0.04	0.93	23.40
P31942	Heterogeneous nuclear ribonucleoprotein H3;	-0.06	-0.01	1.00	8.40
P61978	Heterogeneous nuclear ribonucleoprotein K;	0.51	0.13	0.67	32.00
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like;	-2.75	-9.75	0.01	3.00
P14866	Heterogeneous nuclear ribonucleoprotein L;	-0.33	-0.17	0.81	19.70
P52272	Heterogeneous nuclear ribonucleoprotein M;	0.49	0.14	0.70	7.90
O60506	Heterogeneous nuclear ribonucleoprotein Q;	0.65	0.10	0.57	25.70
O43390	Heterogeneous nuclear ribonucleoprotein R;	0.19	0.06	0.85	14.70
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein	1.11	0.03	0.29	3.00
Q00839	Heterogeneous nuclear ribonucleoprotein U;	0.72	0.07	0.51	9.80
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1;	0.22	0.02	0.81	23.20
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2;	-0.17	-0.02	0.91	15.70
P19367	Hexokinase-1;	2.35	0.24	0.57	5.30
P09429	High mobility group protein B1;	-0.78	-0.77	0.54	25.10
P26583	High mobility group protein B2;	-0.56	-0.25	0.65	17.20
P37235	Hippocalcin-like protein 1;	-0.55	-2.17	0.86	9.30
P49773	Histidine triad nucleotide-binding protein 1;	-0.86	-0.34	0.46	27.00
Q9BX68	Histidine triad nucleotide-binding protein 2,	0.69	0.09	0.54	21.50
P12081	Histidine--tRNA ligase, cytoplasmic;	-0.66	-0.40	0.60	10.40
Q9NVP2	Histone chaperone ASF1B;	-0.14	-0.01	0.93	4.00
Q92769	Histone deacetylase 2;	0.06	0.01	0.92	9.80
P10412	Histone H1.4;	-0.41	-0.20	0.75	9.40
P16401	Histone H1.5;	-1.11	-0.24	0.33	9.30
Q92522	Histone H1x;	-1.36	-1.08	0.23	7.00
P04908	Histone H2A type 1-B/E;	-1.33	-1.56	0.26	27.10
P0C0S5	Histone H2A.Z;	-0.07	-0.01	0.98	20.30
O60814	Histone H2B type 1-K;	-1.15	-1.20	0.33	14.30
P68431	Histone H3.1;	-0.92	-0.17	0.42	5.20
P62805	Histone H4;	-0.46	-0.15	0.72	40.80
Q09028	Histone-binding protein RBBP4;	-0.62	-0.50	0.64	14.60
Q16576	Histone-binding protein RBBP7;	-0.41	-0.07	0.74	11.80
P01892	HLA class I histocompatibility antigen, A-2 alpha chain;	0.51	0.10	0.65	26.80
P10314	HLA class I histocompatibility antigen, A-32 alpha chain;	1.28	0.14	0.36	23.80
P10321	HLA class I histocompatibility antigen, Cw-7 alpha chain;	2.35	0.08	0.17	23.00
P51610	Host cell factor 1;	-0.83	-0.25	0.48	1.50
P50502	Hsc70-interacting protein;	-0.28	-0.11	0.84	23.00
Q16543	Hsp90 co-chaperone Cdc37;	-0.07	-0.02	0.98	15.90
Q9NX55	Huntingtin-interacting protein K;	-0.26	-0.07	0.85	11.60
Q12794	Hyaluronidase-1;	1.39	0.02	0.19	1.80
Q9UJM8	Hydroxyacid oxidase 1;	-2.10	-56.91	0.40	3.80

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	-0.09	-0.01	0.97	3.20
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial;	-1.85	-8.15	0.13	9.40
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	-1.90	-2.05	0.09	2.50
P00492	Hypoxanthine-guanine phosphoribosyltransferase;	-0.60	-0.60	0.66	34.90
Q9Y4L1	Hypoxia up-regulated protein 1;	0.74	0.17	0.59	2.50
P55899	IgG receptor FcRn large subunit p51;	1.79	0.03	0.10	3.30
Q969P0	Immunoglobulin superfamily member 8;	-2.21	-71.59	0.39	4.20
P52292	Importin subunit alpha-2;	0.90	0.02	0.39	3.80
O00505	Importin subunit alpha-3;	1.28	0.02	0.23	5.20
O00629	Importin subunit alpha-4;	1.32	0.02	0.22	5.20
O15131	Importin subunit alpha-6;	0.01	0.00	0.96	2.10
Q14974	Importin subunit beta-1;	-0.33	-0.26	0.83	11.00
Q8TEX9	Importin-4;	1.74	0.01	0.10	3.00
O00410	Importin-5;	-0.19	-0.06	0.89	18.40
O95373	Importin-7;	1.01	0.14	0.44	6.30
Q13308	Inactive tyrosine-protein kinase 7;	-0.49	-0.08	0.69	3.80
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial;	0.21	0.01	0.81	11.70
Q15181	Inorganic pyrophosphatase;	0.28	0.06	0.79	13.80
Q9BY32	Inosine triphosphate pyrophosphatase;	0.32	0.02	0.74	8.80
P12268	Inosine-5'-monophosphate dehydrogenase 2;	0.67	0.19	0.64	12.30
P29218	Inositol monophosphatase 1;	-0.11	-0.08	0.96	7.60
Q9NPH2	Inositol-3-phosphate synthase 1;	0.79	0.05	0.45	3.00
P14735	Insulin-degrading enzyme;	0.21	0.05	0.83	2.80
P01344	Insulin-like growth factor II;	0.96	0.10	0.41	18.30
P08833	Insulin-like growth factor-binding protein 1;	-0.96	-1.12	0.44	20.80
P18065	Insulin-like growth factor-binding protein 2;	1.69	0.03	0.12	38.20
P17936	Insulin-like growth factor-binding protein 3;	3.15	0.03	0.04	34.70
P22692	Insulin-like growth factor-binding protein 4;	0.87	0.10	0.46	34.50
P24592	Insulin-like growth factor-binding protein 6;	4.27	0.01	0.03	39.60
P23229	Integrin alpha-6;	1.21	0.07	0.29	1.80
P06756	Integrin alpha-V;	-0.43	-0.06	0.72	1.00
P05556	Integrin beta-1;	0.35	0.09	0.75	6.60
P16144	Integrin beta-4;	0.03	0.01	0.95	6.70
O95965	Integrin beta-like protein 1;	0.45	0.05	0.66	24.30
Q9H0C8	Integrin-linked kinase-associated serine/threonine	0.12	0.01	0.87	3.10
P32456	Interferon-induced guanylate-binding protein 2;	-1.93	-17.16	0.18	4.90
Q12905	Interleukin enhancer-binding factor 2;	-0.46	-0.15	0.71	22.60
Q12906	Interleukin enhancer-binding factor 3;	0.77	0.43	0.76	19.00
Q9NPH3	Interleukin-1 receptor accessory protein;	0.39	0.01	0.70	1.80
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog;	-1.41	-2.59	0.24	6.90
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic;	-0.11	-0.06	0.96	26.80
P41252	Isoleucine--tRNA ligase, cytoplasmic;	1.14	0.17	0.43	6.00
P53990	IST1 homolog;	0.72	0.07	0.51	7.10
P14923	Junction plakoglobin;	-1.13	-0.76	0.33	2.70
Q6UW63	KDEL motif-containing protein 1;	1.96	0.02	0.07	2.40
Q04695	Keratin, type I cytoskeletal 17;	-0.06	-0.05	0.99	6.70
P05783	Keratin, type I cytoskeletal 18;	-0.28	-0.26	0.87	33.70
P08727	Keratin, type I cytoskeletal 19;	2.90	0.04	0.05	18.20
P02538	Keratin, type II cytoskeletal 6A;	-0.42	-0.10	0.73	3.70
P08729	Keratin, type II cytoskeletal 7;	-1.99	-42.59	0.40	17.30
Q14CN4	Keratin, type II cytoskeletal 72;	-4.71	-278.39	0.00	2.30
P05787	Keratin, type II cytoskeletal 8;	-0.15	-0.07	0.93	38.70
Q07666	KH domain-containing, RNA-binding, signal	-0.78	-0.21	0.50	3.20

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q86UP2	Kinectin;	0.33	0.09	0.76	12.20
Q07866	Kinesin light chain 1;	0.65	0.24	0.69	8.40
P33176	Kinesin-1 heavy chain;	0.41	0.06	0.70	6.30
Q6YP21	Kynurenine--oxoglutarate transaminase 3;	-0.32	-0.66	0.90	8.10
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-	-0.70	-0.81	0.60	9.10
P00338	L-lactate dehydrogenase A chain;	-1.52	-6.58	0.27	27.40
Q08431	Lactadherin;	1.35	0.02	0.20	2.60
Q04760	Lactoylglutathione lyase;	-0.33	-0.68	0.90	31.00
P20700	Lamin-B1;	-0.39	-0.21	0.77	11.30
Q03252	Lamin-B2;	-0.10	-0.03	0.96	15.50
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;	0.96	0.23	0.56	18.50
O15230	Laminin subunit alpha-5;	1.69	0.05	0.15	26.40
P07942	Laminin subunit beta-1;	1.69	0.08	0.18	17.90
P55268	Laminin subunit beta-2;	3.61	0.02	0.04	16.20
P11047	Laminin subunit gamma-1;	1.96	0.06	0.12	23.20
Q13753	Laminin subunit gamma-2;	1.08	0.13	0.41	3.80
O43813	LanC-like protein 1;	-0.83	-0.23	0.48	4.00
Q9NS86	LanC-like protein 2;	-2.06	-17.67	0.13	9.10
P46379	Large proline-rich protein BAG6;	-1.01	-0.73	0.39	1.10
Q14767	Latent-transforming growth factor beta-binding protein 2;	1.24	0.04	0.26	3.60
Q9NS15	Latent-transforming growth factor beta-binding protein 3;	2.02	0.06	0.10	8.70
Q8N2S1	Latent-transforming growth factor beta-binding protein 4;	0.93	0.14	0.47	18.60
Q99538	Legumain;	1.69	0.04	0.13	15.20
Q9UIC8	Leucine carboxyl methyltransferase 1;	-1.25	-0.89	0.28	2.40
Q9P2J5	Leucine--tRNA ligase, cytoplasmic;	-0.68	-1.13	0.67	3.80
Q8N6Y2	Leucine-rich repeat-containing protein 17;	1.69	0.02	0.12	5.70
Q8N1G4	Leucine-rich repeat-containing protein 47;	-0.68	-0.67	0.61	9.10
Q96AG4	Leucine-rich repeat-containing protein 59;	-0.19	-0.10	0.91	22.10
P09960	Leukotriene A-4 hydrolase;	0.08	0.02	0.92	28.30
P24666	Low molecular weight phosphotyrosine protein	-0.17	-0.08	0.92	12.70
Q14114	Low-density lipoprotein receptor-related protein 8;	-0.09	-0.01	0.97	1.50
P01130	Low-density lipoprotein receptor;	0.30	0.07	0.78	3.10
P05455	Lupus La protein;	-0.33	-0.16	0.81	9.60
P46736	Lys-63-specific deubiquitinase BRCC36;	-1.11	-0.57	0.33	4.70
Q15046	Lysine--tRNA ligase;	-0.57	-0.50	0.67	7.20
O60341	Lysine-specific histone demethylase 1A;	-0.03	0.00	0.99	2.80
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase;	2.21	0.08	0.16	11.50
P10253	Lysosomal alpha-glucosidase;	1.08	0.06	0.32	11.80
O00754	Lysosomal alpha-mannosidase;	1.56	0.04	0.16	4.90
P42785	Lysosomal Pro-X carboxypeptidase;	0.87	0.12	0.49	9.70
P10619	Lysosomal protective protein;	1.32	0.03	0.22	22.50
Q9UMR5	Lysosomal thioesterase PPT2;	1.39	0.05	0.21	16.20
P11279	Lysosome-associated membrane glycoprotein 1;	-1.16	-5.81	0.55	4.80
Q9Y4K0	Lysyl oxidase homolog 2;	1.08	0.05	0.33	12.50
Q96JB6	Lysyl oxidase homolog 4;	-0.46	-0.31	0.73	17.70
Q96C86	m7GpppX diphosphatase;	-0.76	-0.69	0.55	10.70
P09603	Macrophage colony-stimulating factor 1;	3.15	0.01	0.01	7.60
P40121	Macrophage-capping protein;	0.37	0.03	0.71	22.70
Q14764	Major vault protein;	1.08	0.23	0.53	8.00
P40925	Malate dehydrogenase, cytoplasmic;	-0.91	-0.38	0.43	28.70
P40926	Malate dehydrogenase, mitochondrial;	0.21	0.05	0.83	32.80
Q9ULC4	Malignant T-cell-amplified sequence 1;	-0.55	-0.11	0.65	10.50
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA;	-1.86	-2.43	0.10	2.10
O60476	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB;	0.17	0.06	0.87	4.70
P49137	MAP kinase-activated protein kinase 2;	-0.68	-0.34	0.57	3.10
P49006	MARCKS-related protein;	-0.92	-0.29	0.43	7.70

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P43243	Matrin-3;	0.28	0.06	0.79	9.20
Q99542	Matrix metalloproteinase-19;	1.85	0.03	0.10	14.00
Q86YW9	Mediator of RNA polymerase II transcription subunit 12-	-0.27	-0.13	0.85	1.50
Q5JRA6	Melanoma inhibitory activity protein 3;	1.60	0.02	0.14	0.60
P08582	Melanotransferrin;	1.08	0.15	0.43	3.10
P15529	Membrane cofactor protein;	0.67	0.03	0.51	3.80
Q13421	Mesothelin;	1.47	0.05	0.19	37.30
P01033	Metalloproteinase inhibitor 1;	1.69	0.04	0.12	45.40
P16035	Metalloproteinase inhibitor 2;	1.32	0.02	0.22	13.60
Q13330	Metastasis-associated protein MTA1;	-0.32	-0.11	0.81	5.60
O94776	Metastasis-associated protein MTA2;	0.79	0.47	0.77	7.60
Q641Q3	Meteorin-like protein;	1.24	0.02	0.25	4.80
Q9NZL9	Methionine adenosyltransferase 2 subunit beta;	-0.32	-0.07	0.81	8.10
P50579	Methionine aminopeptidase 2;	0.03	0.01	0.96	9.00
P56192	Methionine--tRNA ligase, cytoplasmic;	-0.66	-0.91	0.66	7.30
P16455	Methylated-DNA--protein-cysteine methyltransferase;	1.96	0.02	0.07	8.70
Q9BQA1	Methylosome protein 50;	1.90	0.03	0.09	4.40
Q9BV20	Methylthioribose-1-phosphate isomerase;	-1.73	-1.21	0.12	9.20
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms	2.35	0.01	0.03	1.90
Q96PK2	Microtubule-actin cross-linking factor 1, isoforms	-0.67	-0.30	0.58	2.20
P27816	Microtubule-associated protein 4;	0.09	0.07	0.94	12.80
Q15691	Microtubule-associated protein RP/EB family member 1;	-0.46	-0.41	0.76	11.20
P21741	Midkine;	1.47	0.02	0.17	14.00
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit	-0.67	-0.16	0.57	4.80
Q9Y5J7	Mitochondrial import inner membrane translocase subunit	-0.40	-0.07	0.74	47.20
Q16891	Mitochondrial inner membrane protein;	-0.03	-0.01	0.99	11.10
P28482	Mitogen-activated protein kinase 1;	-0.34	-0.44	0.85	14.70
Q16539	Mitogen-activated protein kinase 14;	0.24	0.03	0.80	4.20
O43684	Mitotic checkpoint protein BUB3;	-0.61	-0.38	0.63	16.50
Q7L9L4	MOB kinase activator 1B;	-0.87	-0.27	0.45	10.60
P26038	Moesin;	3.43	0.04	0.11	19.40
P53985	Monocarboxylate transporter 1;	2.43	0.02	0.03	5.80
O43148	mRNA cap guanine-N7 methyltransferase;	-2.41	-9.91	0.03	2.30
P78406	mRNA export factor;	1.14	0.02	0.28	4.10
Q9NPI6	mRNA-decapping enzyme 1A;	-1.18	-1.01	0.31	2.10
Q9H7C9	Mth938 domain-containing protein;	-3.55	-106.05	0.00	13.10
P98088	Mucin-5AC;	0.17	0.07	0.87	4.50
P22234	Multifunctional protein ADE2;	0.82	0.06	0.45	11.80
Q9UNW1	Multiple inositol polyphosphate phosphatase 1;	1.90	0.05	0.12	17.90
O00499	Myc box-dependent-interacting protein 1;	-0.99	-1.05	0.42	6.20
O95297	Myelin protein zero-like protein 1;	0.96	0.05	0.37	5.60
Q9NZM1	Myoferlin;	0.32	0.25	0.86	4.80
P60660	Myosin light polypeptide 6;	-0.40	-0.14	0.76	37.70
Q6WCQ1	Myosin phosphatase Rho-interacting protein;	0.90	0.16	0.51	5.90
O14950	Myosin regulatory light chain 12B;	-0.23	-0.13	0.88	12.30
P35580	Myosin-10;	-1.70	-4.01	0.15	4.00
P35579	Myosin-9;	-0.03	-0.02	0.99	18.50
P58546	Myotrophin;	-0.48	-0.07	0.69	14.40
P29966	Myristoylated alanine-rich C-kinase substrate;	-2.86	-15.32	0.01	5.70
Q9UJ70	N-acetyl-D-glucosamine kinase;	-2.56	-21.97	0.03	10.50
P34059	N-acetylgalactosamine-6-sulfatase;	1.64	0.05	0.16	12.30
Q9UK23	N-acetylglucosamine-1-phosphodiester alpha-N-	1.60	0.06	0.18	1.90
Q9UJJ9	N-acetylglucosamine-1-phosphotransferase subunit	1.85	0.05	0.12	21.00
P15586	N-acetylglucosamine-6-sulfatase;	0.67	0.08	0.55	12.30
O43505	N-acetyllactosaminide beta-1,3-N-	1.74	0.06	0.15	13.30
Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit;	2.80	0.00	0.01	2.80

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P61599	N-alpha-acetyltransferase 20;	0.08	0.01	0.91	8.40
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit;	-1.94	-3.20	0.09	1.30
O95777	N-alpha-acetyltransferase 38, NatC auxiliary subunit;	-1.91	-2.86	0.09	16.70
Q9GZZ1	N-alpha-acetyltransferase 50;	0.30	0.02	0.75	12.40
P51688	N-sulphoglucosamine sulphohydrolase;	1.39	0.11	0.29	9.20
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	1.85	0.26	0.51	24.20
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	-0.37	-0.20	0.79	21.50
P15559	NAD(P)H dehydrogenase [quinone] 1;	-0.17	-0.04	0.91	11.30
Q8NCW5	NAD(P)H-hydrate epimerase;	-1.03	-2.71	0.49	14.20
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex	0.72	0.03	0.49	4.10
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2,	0.84	0.06	0.44	4.00
P00387	NADH-cytochrome b5 reductase 3;	-4.35	-202.24	0.00	4.00
P16435	NADPH--cytochrome P450 reductase;	-3.42	-59.32	0.00	3.40
O43847	Nardilysin;	0.60	0.29	0.75	3.20
Q13765	Nascent polypeptide-associated complex subunit alpha;	0.49	0.13	0.69	25.60
P61081	NEDD8-conjugating enzyme Ubc12;	-0.69	-1.08	0.65	16.90
Q92859	Neogenin;	-1.98	-11.58	0.11	2.30
O95631	Netrin-1;	-1.01	-4.64	0.63	5.30
Q9UMX5	Neudesin;	0.90	0.12	0.46	31.40
P32004	Neural cell adhesion molecule L1;	1.69	0.07	0.18	13.30
Q09666	Neuroblast differentiation-associated protein AHNAK;	0.90	0.24	0.59	22.00
P46531	Neurogenic locus notch homolog protein 1;	3.43	0.01	0.00	1.10
Q9BYT8	Neurolysin, mitochondrial;	-0.48	-0.14	0.70	1.70
O14786	Neuropilin-1;	-1.84	-9.93	0.15	4.00
O15240	Neurosecretory protein VGF;	-0.17	-0.03	0.91	7.60
Q14697	Neutral alpha-glucosidase AB;	0.82	0.27	0.64	7.20
Q15758	Neutral amino acid transporter B(0);	1.28	0.04	0.24	3.70
Q5JS37	NHL repeat-containing protein 3;	0.08	0.01	0.91	4.00
P55769	NHP2-like protein 1;	-0.01	0.00	0.98	18.00
Q96TA1	Niban-like protein 1;	-1.50	-0.80	0.18	7.00
P43490	Nicotinamide phosphoribosyltransferase;	-0.37	-0.16	0.78	26.10
Q6XQN6	Nicotinate phosphoribosyltransferase;	-0.10	-0.02	0.96	3.50
Q9GZT8	NIF3-like protein 1;	-0.84	-0.24	0.47	9.30
Q9Y2I1	Nischarin;	-1.35	-1.79	0.25	0.80
Q9Y314	Nitric oxide synthase-interacting protein;	0.67	0.03	0.52	3.70
Q86X76	Nitrilase homolog 1;	-0.99	-0.18	0.39	6.70
Q15233	Non-POU domain-containing octamer-binding protein;	0.17	0.01	0.85	4.00
Q9UNZ2	NSFL1 cofactor p47;	-1.11	-1.21	0.35	13.80
P49321	Nuclear autoantigenic sperm protein;	-0.09	-0.03	0.97	7.40
Q9Y266	Nuclear migration protein nudC;	0.08	0.05	0.93	22.70
Q14980	Nuclear mitotic apparatus protein 1;	-0.31	-0.31	0.86	9.10
P35658	Nuclear pore complex protein Nup214;	-0.50	-0.13	0.68	1.70
Q9UKX7	Nuclear pore complex protein Nup50;	0.28	0.01	0.77	8.30
Q8TAT6	Nuclear protein localization protein 4 homolog;	-0.37	-0.03	0.77	2.00
Q9HCD5	Nuclear receptor coactivator 5;	-0.14	-0.01	0.93	2.90
P61970	Nuclear transport factor 2;	0.72	0.29	0.70	26.80
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase	-0.10	-0.02	0.96	7.80
P67809	Nuclease-sensitive element-binding protein 1;	0.19	0.02	0.84	21.00
Q02818	Nucleobindin-1;	1.08	0.05	0.33	31.70
P80303	Nucleobindin-2;	1.43	0.10	0.26	12.60
Q14978	Nucleolar and coiled-body phosphoprotein 1;	0.11	0.01	0.90	3.60
Q9Y3C1	Nucleolar protein 16;	1.28	0.12	0.32	10.10
Q9NR30	Nucleolar RNA helicase 2;	1.24	0.10	0.32	13.40
P19338	Nucleolin;	0.51	0.19	0.72	20.10
P06748	Nucleophosmin;	0.41	0.11	0.73	21.10

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P12270	Nucleoprotein TPR;	1.24	0.12	0.34	1.40
P15531	Nucleoside diphosphate kinase A;	0.17	0.03	0.85	57.20
P22392	Nucleoside diphosphate kinase B;	0.21	0.04	0.82	57.20
P55209	Nucleosome assembly protein 1-like 1;	0.79	0.17	0.57	11.50
Q99733	Nucleosome assembly protein 1-like 4;	-0.64	-0.13	0.59	7.20
Q9NTK5	Obg-like ATPase 1;	-0.01	-0.02	0.99	24.00
Q92882	Osteoclast-stimulating factor 1;	-2.39	-17.40	0.04	7.00
Q86UD1	Out at first protein homolog;	1.47	0.02	0.16	3.30
Q9BZF2	Oxysterol-binding protein-related protein 7;	9.97	0.00	0.00	2.40
Q96ST3	Paired amphipathic helix protein Sin3a;	-1.28	-1.56	0.28	0.90
P50897	Palmitoyl-protein thioesterase 1;	1.04	0.05	0.34	19.90
Q8WXF1	Paraspeckle component 1;	1.08	0.13	0.41	3.60
P20962	Parathymosin;	-1.07	-0.60	0.36	10.80
Q8TEW0	Partitioning defective 3 homolog;	1.24	0.04	0.25	1.00
P49023	Paxillin;	-0.37	-0.23	0.79	6.80
O75475	PC4 and SFRS1-interacting protein;	-0.27	-0.03	0.83	2.10
Q5JVF3	PCI domain-containing protein 2;	-0.77	-0.24	0.51	3.00
Q96HC4	PDZ and LIM domain protein 5;	0.62	0.08	0.57	16.80
Q9NR12	PDZ and LIM domain protein 7;	0.67	0.20	0.64	4.80
O14908	PDZ domain-containing protein GIPC1;	0.12	0.02	0.88	3.90
P26022	Pentraxin-related protein PTX3;	3.15	0.04	0.08	14.40
P19021	Peptidyl-glycine alpha-amidating monooxygenase;	0.67	0.09	0.55	6.90
P62937	Peptidyl-prolyl cis-trans isomerase A;	-0.84	-0.42	0.48	41.20
P23284	Peptidyl-prolyl cis-trans isomerase B;	0.79	0.09	0.48	36.60
Q9UNP9	Peptidyl-prolyl cis-trans isomerase E;	-1.32	-0.95	0.25	5.00
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A;	1.08	0.19	0.49	27.80
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3;	1.32	0.14	0.35	27.70
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;	0.08	0.02	0.92	19.80
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5;	-0.34	-0.10	0.79	7.90
O43447	Peptidyl-prolyl cis-trans isomerase H;	0.00	0.00	0.97	4.50
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1;	-1.04	-1.58	0.41	25.30
Q99541	Perilipin-2;	-1.03	-0.71	0.38	3.00
O60664	Perilipin-3;	0.56	0.16	0.68	17.70
Q06830	Peroxiredoxin-1;	-0.79	-0.73	0.53	49.70
P32119	Peroxiredoxin-2;	-1.99	-11.87	0.11	31.80
Q13162	Peroxiredoxin-4;	0.72	0.06	0.51	20.70
P30044	Peroxiredoxin-5, mitochondrial;	-0.10	-0.09	0.97	23.80
P30041	Peroxiredoxin-6;	0.67	0.09	0.55	37.50
Q8WW12	PEST proteolytic signal-containing nuclear protein;	-0.87	-0.55	0.47	29.80
Q9NSD9	Phenylalanine--tRNA ligase beta subunit;	-0.23	-0.07	0.87	10.70
P30086	Phosphatidylethanolamine-binding protein 1;	-0.78	-0.62	0.53	56.10
O00459	Phosphatidylinositol 3-kinase regulatory subunit beta;	1.32	0.02	0.21	1.90
Q00169	Phosphatidylinositol transfer protein alpha isoform;	0.22	0.30	0.93	7.80
P48739	Phosphatidylinositol transfer protein beta isoform;	-0.27	-0.09	0.84	9.20
Q13492	Phosphatidylinositol-binding clathrin assembly protein;	-0.01	0.00	0.98	2.30
P36871	Phosphoglucomutase-1;	0.77	0.31	0.69	11.60
Q96G03	Phosphoglucomutase-2;	-2.73	-58.33	0.04	4.10
P00558	Phosphoglycerate kinase 1;	-0.89	-0.89	0.47	40.80
P18669	Phosphoglycerate mutase 1;	-0.19	-0.07	0.89	46.90
A6NDG6	Phosphoglycolate phosphatase;	0.56	0.11	0.63	8.70
Q6P4A8	Phospholipase B-like 1;	1.90	0.04	0.10	8.30
P55058	Phospholipid transfer protein;	1.69	0.09	0.21	18.30
Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate	-0.53	-0.11	0.66	4.80

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O15305	Phosphomannomutase 2;	-1.25	-0.30	0.27	2.80
O60256	Phosphoribosyl pyrophosphate synthase-associated	0.51	0.02	0.62	3.90
O15067	Phosphoribosylformylglycinamidine synthase;	-0.26	-0.08	0.85	5.60
Q9Y617	Phosphoserine aminotransferase;	1.56	0.06	0.19	39.70
P78330	Phosphoserine phosphatase;	-0.59	-0.60	0.67	26.70
P36955	Pigment epithelium-derived factor;	3.61	0.02	0.03	18.20
Q9H307	Pinin;	-0.61	-0.18	0.61	3.50
Q9GZP4	PITH domain-containing protein 1;	-0.42	-0.09	0.73	9.50
Q9BTY2	Plasma alpha-L-fucosidase;	1.47	0.03	0.18	14.80
P20020	Plasma membrane calcium-transporting ATPase 1;	3.28	0.02	0.02	1.40
P05155	Plasma protease C1 inhibitor;	0.12	0.02	0.88	16.20
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein;	0.35	0.17	0.80	8.80
P05121	Plasminogen activator inhibitor 1;	0.69	0.06	0.52	6.00
Q14651	Plastin-1;	-1.66	-2.16	0.15	5.60
P43034	Platelet-activating factor acetylhydrolase IB subunit	1.56	0.10	0.23	13.70
P68402	Platelet-activating factor acetylhydrolase IB subunit beta;	-0.64	-0.29	0.60	8.30
Q15102	Platelet-activating factor acetylhydrolase IB subunit	-0.03	-0.02	0.99	7.80
Q9NRA1	Platelet-derived growth factor C;	-0.49	-0.11	0.69	7.20
Q8WV24	Pleckstrin homology-like domain family A member 1;	3.61	0.00	0.00	2.20
Q15149	Plectin;	-0.77	-1.26	0.60	16.40
O15031	Plexin-B2;	0.77	0.07	0.49	3.00
Q92692	Poliovirus receptor-related protein 2;	0.77	0.24	0.64	9.10
Q9NQS3	Poliovirus receptor-related protein 3;	0.82	0.04	0.44	4.20
P15151	Poliovirus receptor;	0.69	0.02	0.50	7.00
P09874	Poly [ADP-ribose] polymerase 1;	1.01	0.41	0.69	16.90
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3;	-0.96	-0.48	0.41	11.30
Q15365	Poly(rC)-binding protein 1;	-0.07	-0.02	0.98	32.90
Q15366	Poly(rC)-binding protein 2;	-0.32	-0.12	0.81	22.70
Q9UHX1	Poly(U)-binding-splicing factor PUF60;	-0.37	-0.08	0.77	7.50
P11940	Polyadenylate-binding protein 1;	0.69	0.09	0.54	23.00
Q6NZI2	Polymerase I and transcript release factor;	0.28	0.13	0.83	19.00
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;	0.77	0.04	0.47	14.50
P26599	Polypyrimidine tract-binding protein 1;	0.41	0.22	0.80	16.90
Q9Y3B4	Pre-mRNA branch site protein p14;	-0.27	-0.04	0.84	11.20
Q9UMS4	Pre-mRNA-processing factor 19;	-1.58	-2.74	0.17	7.50
Q6P2Q9	Pre-mRNA-processing-splicing factor 8;	-0.13	-0.02	0.94	0.90
O75934	Pre-mRNA-splicing factor SPF27;	-0.53	-0.10	0.66	6.70
Q8IY81	pre-rRNA processing protein FTSJ3;	0.74	0.21	0.63	4.80
O60925	Prefoldin subunit 1;	-0.68	-0.12	0.57	9.00
Q9UHV9	Prefoldin subunit 2;	-0.50	-0.23	0.69	14.90
P61758	Prefoldin subunit 3;	-0.15	-0.09	0.93	9.60
Q9NQP4	Prefoldin subunit 4;	0.12	0.10	0.92	20.10
Q99471	Prefoldin subunit 5;	-1.15	-2.16	0.37	16.90
O15212	Prefoldin subunit 6;	-0.99	-0.36	0.39	15.50
P20742	Pregnancy zone protein;	0.11	0.02	0.90	3.50
P02545	Prelamin-A/C;	-0.39	-0.20	0.77	46.70
Q96IZ0	PRKC apoptosis WT1 regulator protein;	-2.64	-25.09	0.02	4.70
P07602	Proactivator polypeptide;	2.69	0.06	0.13	37.40
Q92841	Probable ATP-dependent RNA helicase DDX17;	-0.94	-1.66	0.49	17.80
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23;	-1.87	-7.13	0.12	5.50
P17844	Probable ATP-dependent RNA helicase DDX5;	0.24	0.02	0.80	8.10
P26196	Probable ATP-dependent RNA helicase DDX6;	-0.01	-0.01	0.98	10.40
Q96GX9	Probable methylthioribulose-1-phosphate dehydratase;	-0.76	-0.50	0.53	7.00
Q99848	Probable rRNA-processing protein EBP2;	0.65	0.03	0.53	7.20
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	1.18	0.06	0.30	25.60

Table S3

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3;	1.56	0.15	0.34	16.80
P07737	Profilin-1;	-0.68	-0.52	0.60	62.10
P35080	Profilin-2;	0.60	0.12	0.62	25.00
Q8WUM4	Programmed cell death 6-interacting protein;	0.05	0.04	0.96	13.90
Q53EL6	Programmed cell death protein 4;	1.18	0.05	0.28	7.20
O14737	Programmed cell death protein 5;	-0.62	-0.19	0.61	19.20
O75340	Programmed cell death protein 6;	0.11	0.05	0.91	15.20
P12004	Proliferating cell nuclear antigen;	-0.56	-0.98	0.75	44.10
Q9UQ80	Proliferation-associated protein 2G4;	0.14	0.12	0.92	40.40
O94903	Proline synthase co-transcribed bacterial homolog	-0.19	-0.12	0.91	8.70
Q07954	Prolow-density lipoprotein receptor-related protein 1;	1.18	0.07	0.30	1.80
Q32P28	Prolyl 3-hydroxylase 1;	1.79	0.16	0.33	5.70
P48147	Prolyl endopeptidase;	-0.03	-0.02	0.99	5.90
Q8NBP7	Proprotein convertase subtilisin/kexin type 9;	0.24	0.04	0.80	23.60
Q9UHG2	ProSAAS;	1.60	0.02	0.14	30.40
Q15185	Prostaglandin E synthase 3;	0.62	0.08	0.57	28.10
Q9P2B2	Prostaglandin F2 receptor negative regulator;	-0.61	-0.31	0.62	5.00
P41222	Prostaglandin-H2 D-isomerase;	5.01	0.00	0.00	17.40
Q06323	Proteasome activator complex subunit 1;	0.72	0.17	0.60	26.10
Q9BT73	Proteasome assembly chaperone 3;	-0.72	-0.14	0.53	12.30
Q5JS54	Proteasome assembly chaperone 4;	-1.87	-4.98	0.11	20.30
P25786	Proteasome subunit alpha type-1;	-0.31	-0.07	0.81	14.80
P25787	Proteasome subunit alpha type-2;	0.11	0.02	0.89	14.10
P28066	Proteasome subunit alpha type-5;	-0.10	-0.02	0.96	22.80
P60900	Proteasome subunit alpha type-6;	0.21	0.03	0.82	23.20
O14818	Proteasome subunit alpha type-7;	-0.04	-0.02	1.00	31.90
P20618	Proteasome subunit beta type-1;	-0.37	-0.13	0.78	35.70
P49720	Proteasome subunit beta type-3;	0.12	0.09	0.92	18.50
P28074	Proteasome subunit beta type-5;	0.79	0.25	0.64	14.80
P28072	Proteasome subunit beta type-6;	1.35	0.12	0.32	13.00
Q99436	Proteasome subunit beta type-7;	0.41	0.07	0.70	7.60
P28062	Proteasome subunit beta type-8;	1.01	0.02	0.34	9.10
Q8IVF2	Protein AHNAK2;	1.90	0.17	0.37	5.40
Q99873	Protein arginine N-methyltransferase 1;	-0.15	-0.06	0.92	17.20
O14744	Protein arginine N-methyltransferase 5;	-0.35	-0.04	0.78	2.70
Q9Y2B0	Protein canopy homolog 2;	0.58	0.10	0.62	20.30
Q9BT09	Protein canopy homolog 3;	0.11	0.01	0.90	6.50
O75629	Protein CREG1;	0.84	0.03	0.42	5.50
O60888	Protein CutA;	-0.13	-0.01	0.94	7.80
P30101	Protein disulfide-isomerase A3;	0.53	0.19	0.71	33.30
P13667	Protein disulfide-isomerase A4;	-0.28	-0.05	0.83	15.30
Q15084	Protein disulfide-isomerase A6;	-0.41	-0.43	0.79	12.70
P07237	Protein disulfide-isomerase;	0.32	0.04	0.75	31.50
Q99497	Protein DJ-1;	-1.08	-0.52	0.35	43.90
Q92520	Protein FAM3C;	-1.48	-3.00	0.22	33.90
Q9NUQ9	Protein FAM49B;	-2.37	-5.00	0.03	5.90
Q8NCA5	Protein FAM98A;	-0.60	-0.14	0.61	2.30
Q52LJ0	Protein FAM98B;	0.08	0.02	0.92	12.70
Q13045	Protein flightless-1 homolog;	0.49	0.02	0.63	0.60
O94992	Protein HEXIM1;	0.00	0.00	0.97	3.90
Q9UNF0	Protein kinase C and casein kinase substrate in neurons	0.72	0.23	0.66	12.60
Q9UKS6	Protein kinase C and casein kinase substrate in neurons	-0.47	-0.15	0.70	3.80
Q9BRT6	Protein LLP homolog;	-0.09	-0.01	0.97	10.90
Q9Y316	Protein MEMO1;	-0.46	-0.08	0.71	4.70
Q92597	Protein NDRG1;	-0.14	-0.01	0.93	4.10

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Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9BZQ8	Protein Niban;	-0.40	-0.67	0.85	3.60
P48745	Protein NOV homolog;	1.64	0.15	0.32	13.40
O14974	Protein phosphatase 1 regulatory subunit 12A;	0.21	0.01	0.81	2.70
P49593	Protein phosphatase 1F;	-0.04	0.00	1.00	7.90
O15355	Protein phosphatase 1G;	0.11	0.03	0.89	8.40
Q9Y570	Protein phosphatase methylesterase 1;	-1.71	-3.31	0.14	6.00
Q9P258	Protein RCC2;	-0.06	-0.02	0.99	23.20
Q96FQ6	Protein S100-A16;	-0.54	-0.14	0.65	23.30
P33764	Protein S100-A3;	-0.45	-0.04	0.72	10.90
P26447	Protein S100-A4;	-1.49	-10.43	0.40	18.80
P25815	Protein S100-P;	-1.28	-0.41	0.26	24.20
Q01105	Protein SET;	-0.23	-0.18	0.89	22.80
Q8N114	Protein shisa-5;	1.28	0.02	0.22	2.90
Q6PL24	Protein TMED8;	0.32	0.03	0.74	5.50
Q15436	Protein transport protein Sec23A;	0.35	0.03	0.72	7.30
Q15437	Protein transport protein Sec23B;	-1.63	-4.36	0.17	5.20
P53992	Protein transport protein Sec24C;	0.77	0.32	0.70	6.80
O94979	Protein transport protein Sec31A;	0.33	0.17	0.82	5.10
Q12974	Protein tyrosine phosphatase type IVA 2;	-0.50	-0.08	0.68	8.40
Q9H3U1	Protein unc-45 homolog A;	0.37	0.01	0.71	4.40
Q69YN4	Protein virilizer homolog;	0.37	0.06	0.72	1.30
Q9GZM5	Protein YIPF3;	-0.43	-0.04	0.72	2.90
O60507	Protein-tyrosine sulfotransferase 1;	0.56	0.04	0.59	4.30
P06454	Prothymosin alpha;	1.08	0.02	0.30	9.00
P00491	Purine nucleoside phosphorylase;	1.47	0.06	0.20	22.50
P55786	Puromycin-sensitive aminopeptidase;	0.30	0.17	0.85	17.20
Q5T1J5	Putative coiled-coil-helix-coiled-coil-helix domain-	-1.29	-2.14	0.29	27.20
O60361	Putative nucleoside diphosphate kinase;	1.43	0.01	0.18	45.30
Q49A26	Putative oxidoreductase GLYR1;	0.72	0.03	0.49	2.00
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1;	-1.72	-2.32	0.13	8.60
Q8NHP8	Putative phospholipase B-like 2;	1.32	0.06	0.24	18.30
O60231	Putative pre-mRNA-splicing factor ATP-dependent RNA	-0.46	-0.14	0.72	1.20
Q9Y383	Putative RNA-binding protein Luc7-like 2;	-0.53	-0.09	0.66	8.70
Q9HBR0	Putative sodium-coupled neutral amino acid transporter	0.03	0.01	0.96	3.30
A6NL28	Putative tropomyosin alpha-3 chain-like protein;	-0.78	-0.21	0.50	10.30
Q53H96	Pyrroline-5-carboxylate reductase 3;	-1.39	-1.76	0.23	8.40
P14618	Pyruvate kinase isozymes M1/M2;	-1.11	-2.22	0.40	45.80
Q53FA7	Quinone oxidoreductase PIG3;	1.96	0.18	0.39	10.80
O95825	Quinone oxidoreductase-like protein 1;	-0.38	-0.04	0.76	4.30
Q08257	Quinone oxidoreductase;	-0.34	-0.11	0.79	5.20
P31150	Rab GDP dissociation inhibitor alpha;	0.93	0.02	0.37	8.90
P50395	Rab GDP dissociation inhibitor beta;	0.14	0.15	0.93	34.20
Q9Y3P9	Rab GTPase-activating protein 1;	-0.13	-0.02	0.94	1.50
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit;	-3.28	-27.27	0.00	1.10
Q9H0H5	Rac GTPase-activating protein 1;	1.08	0.04	0.32	2.50
P35241	Radixin;	-0.32	-0.04	0.80	12.20
Q6IAA8	Ragulator complex protein LAMTOR1;	-5.45	-8673.19	0.00	7.50
O43504	Ragulator complex protein LAMTOR5;	-0.86	-0.31	0.46	22.00
Q96D71	RalBP1-associated Eps domain-containing protein 1;	-0.57	-0.29	0.65	1.60
P43487	Ran-specific GTPase-activating protein;	-0.53	-0.08	0.66	10.00
P52306	Rap1 GTPase-GDP dissociation stimulator 1;	-0.03	0.00	0.99	2.80
Q13283	Ras GTPase-activating protein-binding protein 1;	-0.68	-0.18	0.56	23.80
Q9UN86	Ras GTPase-activating protein-binding protein 2;	0.58	0.04	0.58	7.10
P46940	Ras GTPase-activating-like protein IQGAP1;	-0.49	-0.33	0.71	10.30

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Q15404	Ras suppressor protein 1;	-0.15	-0.03	0.92	9.40
P63000	Ras-related C3 botulinum toxin substrate 1;	-1.34	-1.99	0.26	22.90
Q15907	Ras-related protein Rab-11B;	-0.52	-0.59	0.73	30.30
P61106	Ras-related protein Rab-14;	-1.25	-0.45	0.27	11.60
P62820	Ras-related protein Rab-1A;	-0.52	-0.17	0.67	22.90
P51149	Ras-related protein Rab-7a;	-0.35	-0.07	0.78	6.30
P61006	Ras-related protein Rab-8A;	-1.06	-0.88	0.37	16.40
O14827	Ras-specific guanine nucleotide-releasing factor 2;	-0.07	-0.03	0.98	2.00
P10586	Receptor-type tyrosine-protein phosphatase F;	1.14	0.09	0.34	12.70
P23470	Receptor-type tyrosine-protein phosphatase gamma;	-0.40	-0.22	0.76	2.80
Q15262	Receptor-type tyrosine-protein phosphatase kappa;	0.77	0.20	0.61	6.50
Q06330	Recombining binding protein suppressor of hairless;	-0.67	-0.33	0.58	3.20
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing	-0.60	-0.21	0.62	13.20
P18754	Regulator of chromosome condensation;	-0.42	-0.23	0.75	14.70
Q92900	Regulator of nonsense transcripts 1;	0.03	0.00	0.95	1.50
Q9HAU5	Regulator of nonsense transcripts 2;	0.19	0.02	0.84	1.30
Q8WUF5	RelA-associated inhibitor;	-1.50	-0.98	0.18	1.00
Q96T23	Remodeling and spacing factor 1;	2.80	0.01	0.01	1.00
O75787	Renin receptor;	0.39	0.09	0.73	14.90
P35244	Replication protein A 14 kDa subunit;	0.65	0.12	0.59	21.50
P15927	Replication protein A 32 kDa subunit;	2.21	0.14	0.33	13.30
Q9P2K3	REST corepressor 3;	0.19	0.01	0.83	1.50
Q14257	Reticulocalbin-2;	0.58	0.12	0.63	8.50
Q9BZR6	Reticulon-4 receptor;	0.26	0.01	0.78	2.50
Q9NQC3	Reticulon-4;	0.26	0.03	0.79	2.30
Q99969	Retinoic acid receptor responder protein 2;	-0.45	-0.05	0.72	7.40
Q9HB40	Retinoid-inducible serine carboxypeptidase;	1.51	0.03	0.16	6.00
P52565	Rho GDP-dissociation inhibitor 1;	-0.99	-0.36	0.39	7.40
O75116	Rho-associated protein kinase 2;	-1.03	-0.55	0.37	5.60
P08134	Rho-related GTP-binding protein RhoC;	-0.18	-0.05	0.91	17.10
P34096	Ribonuclease 4;	3.61	0.01	0.01	27.90
P13489	Ribonuclease inhibitor;	0.16	0.12	0.91	10.00
O00584	Ribonuclease T2;	1.96	0.05	0.11	22.70
P52758	Ribonuclease UK114;	-0.99	-0.47	0.39	7.30
Q99575	Ribonucleases P/MRP protein subunit POP1;	0.00	0.00	0.97	3.10
P60891	Ribose-phosphate pyrophosphokinase 1;	0.11	0.01	0.90	9.70
P11908	Ribose-phosphate pyrophosphokinase 2;	-1.08	-0.75	0.35	9.70
Q14684	Ribosomal RNA processing protein 1 homolog B;	-0.17	-0.02	0.91	2.00
Q9GZL7	Ribosome biogenesis protein WDR12;	0.56	0.14	0.66	6.40
Q9Y3A5	Ribosome maturation protein SBDS;	0.84	0.14	0.51	13.60
Q9P2E9	Ribosome-binding protein 1;	-0.57	-0.28	0.64	8.30
P16083	Ribosyldihydronicotinamide dehydrogenase [quinone];	1.43	0.01	0.18	4.80
Q9C0B0	RING finger protein unkempt homolog;	1.24	0.02	0.24	1.40
P38159	RNA-binding motif protein, X chromosome;	-0.70	-0.11	0.55	14.30
P98175	RNA-binding protein 10;	-0.49	-0.28	0.71	3.10
Q9NTZ6	RNA-binding protein 12;	-0.11	-0.03	0.95	6.80
Q8IXT5	RNA-binding protein 12B;	-2.00	-8.24	0.09	1.10
P49756	RNA-binding protein 25;	0.51	0.12	0.66	3.90
Q14498	RNA-binding protein 39;	0.11	0.02	0.90	5.30
Q01844	RNA-binding protein EWS;	0.19	0.01	0.84	2.10
P35637	RNA-binding protein FUS;	-0.18	-0.08	0.91	7.20
Q15287	RNA-binding protein with serine-rich domain 1;	0.30	0.02	0.75	3.90
P22087	rRNA 2'-O-methyltransferase fibrillarin;	2.69	0.00	0.01	12.50
Q9Y265	RuvB-like 1;	0.41	0.04	0.68	20.40

Table S3

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q9Y230	RuvB-like 2;	0.65	0.17	0.63	12.30
P31153	S-adenosylmethionine synthase isoform type-2;	0.00	0.00	0.97	13.70
P10768	S-formylglutathione hydrolase;	-0.25	-0.13	0.87	16.30
Q13126	S-methyl-5'-thioadenosine phosphorylase;	-1.50	-6.73	0.29	20.10
P82979	SAP domain-containing ribonucleoprotein;	-0.49	-0.10	0.69	13.80
Q15424	Scaffold attachment factor B1;	-0.14	-0.05	0.93	2.20
Q8WVM8	Sec1 family domain-containing protein 1;	2.35	0.01	0.03	1.60
O76054	SEC14-like protein 2;	-0.84	-0.16	0.47	2.70
Q12765	Secernin-1;	0.16	0.01	0.86	3.10
Q8WVN6	Secreted and transmembrane protein 1;	1.51	0.02	0.16	7.70
Q9UHJ6	Sedoheptulokinase;	-1.52	-1.80	0.18	4.40
P49903	Selenide, water dikinase 1;	-1.12	-2.29	0.39	7.70
Q96I15	Selenocysteine lyase;	-1.21	-0.73	0.29	4.50
Q14563	Semaphorin-3A;	1.96	0.05	0.10	12.10
Q99985	Semaphorin-3C;	0.21	0.05	0.83	27.00
Q9NPR2	Semaphorin-4B;	0.51	0.02	0.62	4.60
Q9H3T2	Semaphorin-6C;	-0.60	-0.29	0.62	3.50
Q9NVA2	Septin-11;	0.65	0.07	0.56	22.10
Q15019	Septin-2;	-0.17	-0.05	0.91	20.80
Q16181	Septin-7;	-0.23	-0.03	0.86	5.50
Q92599	Septin-8;	-1.21	-1.14	0.30	6.80
Q9UHD8	Septin-9;	-0.73	-1.29	0.63	16.70
Q13501	Sequestosome-1;	0.06	0.04	0.94	14.10
O95084	Serine protease 23;	-0.57	-0.34	0.65	18.00
Q92743	Serine protease HTRA1;	0.65	0.07	0.55	9.60
P49591	Serine--tRNA ligase, cytoplasmic;	-0.13	-0.02	0.94	6.80
Q9Y3F4	Serine-threonine kinase receptor-associated protein;	-0.03	-0.01	0.99	29.70
Q9UQ35	Serine/arginine repetitive matrix protein 2;	-0.40	-0.28	0.77	3.30
Q07955	Serine/arginine-rich splicing factor 1;	1.51	0.12	0.28	12.10
Q05519	Serine/arginine-rich splicing factor 11;	-0.63	-0.42	0.61	9.50
Q13247	Serine/arginine-rich splicing factor 6;	3.28	0.04	0.12	11.60
Q16629	Serine/arginine-rich splicing factor 7;	-0.14	-0.02	0.93	9.70
Q13242	Serine/arginine-rich splicing factor 9;	-0.23	-0.04	0.86	3.60
O95747	Serine/threonine-protein kinase OSR1;	1.08	0.24	0.55	4.90
Q13177	Serine/threonine-protein kinase PAK 2;	1.08	0.05	0.33	11.30
Q99986	Serine/threonine-protein kinase VRK1;	0.33	0.02	0.73	2.00
P63151	Serine/threonine-protein phosphatase 2A 55 kDa	-0.53	-0.92	0.77	4.30
P30153	Serine/threonine-protein phosphatase 2A 65 kDa	-0.66	-1.62	0.74	19.70
Q15257	Serine/threonine-protein phosphatase 2A activator;	-1.25	-2.57	0.33	3.60
P62714	Serine/threonine-protein phosphatase 2A catalytic subunit	0.19	0.05	0.85	8.70
P60510	Serine/threonine-protein phosphatase 4 catalytic subunit;	-0.70	-0.37	0.57	6.80
Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit	0.24	0.03	0.80	3.60
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic	-0.04	-0.01	1.00	9.40
P36952	Serpin B5;	0.33	0.14	0.80	37.30
P35237	Serpin B6;	-1.21	-4.73	0.45	11.70
P50454	Serpin H1;	1.47	0.14	0.34	11.20
Q9BXP5	Serrate RNA effector molecule homolog;	-0.75	-0.44	0.53	7.20
P02768	Serum albumin;	0.08	0.01	0.91	4.60
O95810	Serum deprivation-response protein;	0.65	0.10	0.58	13.60
P29353	SHC-transforming protein 1;	0.00	0.00	0.97	2.10
Q9HAT2	Sialate O-acetylesterase;	1.47	0.06	0.21	11.70
Q9NR45	Sialic acid synthase;	-0.78	-1.19	0.58	5.00
Q99519	Sialidase-1;	0.51	0.11	0.65	13.70
P49458	Signal recognition particle 9 kDa protein;	-0.72	-1.08	0.62	22.10
Q92783	Signal transducing adapter molecule 1;	-0.55	-0.13	0.65	2.20
P62304	Small nuclear ribonucleoprotein E;	-0.32	-0.09	0.81	12.00
P62306	Small nuclear ribonucleoprotein F;	-0.22	-0.02	0.87	9.30

Table S3

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P62316	Small nuclear ribonucleoprotein Sm D2;	-0.03	-0.01	0.99	33.10
P62318	Small nuclear ribonucleoprotein Sm D3;	-0.48	-0.19	0.70	23.80
P14678	Small nuclear ribonucleoprotein-associated proteins B	-0.17	-0.02	0.91	21.20
P63165	Small ubiquitin-related modifier 1;	-0.33	-0.12	0.80	20.80
P55854	Small ubiquitin-related modifier 3;	-0.45	-0.10	0.72	12.60
P05023	Sodium/potassium-transporting ATPase subunit alpha-1;	1.01	0.10	0.39	4.20
Q8WVQ1	Soluble calcium-activated nucleotidase 1;	0.39	0.05	0.71	17.00
A1L4H1	Soluble scavenger receptor cysteine-rich domain-	1.04	0.06	0.35	0.80
Q00796	Sorbitol dehydrogenase;	-0.77	-0.42	0.52	11.20
P30626	Sorcin;	-0.67	-0.43	0.59	22.70
Q9Y5X3	Sorting nexin-5;	-0.17	-0.02	0.91	5.00
Q9UNH7	Sorting nexin-6;	0.58	0.02	0.57	2.50
Q9Y5X1	Sorting nexin-9;	-0.67	-0.17	0.57	2.40
P09486	SPARC;	0.90	0.08	0.43	37.30
Q13813	Spectrin alpha chain, non-erythrocytic 1;	0.58	0.11	0.62	10.50
Q01082	Spectrin beta chain, non-erythrocytic 1;	0.62	0.38	0.78	7.80
P52788	Spermine synthase;	0.35	0.07	0.74	10.10
Q13838	Spliceosome RNA helicase DDX39B;	-0.59	-0.15	0.62	25.90
Q15637	Splicing factor 1;	-0.18	-0.07	0.91	7.80
Q15459	Splicing factor 3A subunit 1;	0.03	0.03	0.96	9.20
Q15428	Splicing factor 3A subunit 2;	-0.48	-0.77	0.79	8.00
O75533	Splicing factor 3B subunit 1;	0.26	0.20	0.88	8.30
Q15393	Splicing factor 3B subunit 3;	0.22	0.07	0.83	4.80
Q15427	Splicing factor 3B subunit 4;	-0.03	0.00	0.99	3.30
P26368	Splicing factor U2AF 65 kDa subunit;	0.08	0.03	0.92	15.40
O95104	Splicing factor, arginine/serine-rich 15;	-1.67	-2.45	0.14	1.40
P23246	Splicing factor, proline- and glutamine-rich;	0.65	0.44	0.80	10.50
Q9GZT3	SRA stem-loop-interacting RNA-binding protein,	0.26	0.02	0.78	12.80
Q14247	Src substrate cortactin;	5.57	0.00	0.00	2.00
Q7KZF4	Staphylococcal nuclease domain-containing protein 1;	0.33	0.16	0.81	16.50
P16949	Stathmin;	-0.95	-0.38	0.41	29.50
Q9H2G2	STE20-like serine/threonine-protein kinase;	0.99	0.10	0.40	3.30
P38646	Stress-70 protein, mitochondrial;	0.87	0.15	0.51	6.00
P31948	Stress-induced-phosphoprotein 1;	0.00	0.00	0.98	15.70
Q13033	Striatin-3;	1.39	0.02	0.19	2.60
O43815	Striatin;	-0.40	-0.06	0.74	2.20
Q14683	Structural maintenance of chromosomes protein 1A;	0.96	0.36	0.67	3.30
Q8NBJ7	Sulfatase-modifying factor 2;	0.39	0.08	0.72	21.60
O00391	Sulfhydryl oxidase 1;	1.64	0.11	0.25	29.90
Q6ZRP7	Sulfhydryl oxidase 2;	0.08	0.02	0.92	3.70
Q9UBE0	SUMO-activating enzyme subunit 1;	0.08	0.02	0.92	6.10
Q9UBT2	SUMO-activating enzyme subunit 2;	-0.37	-0.25	0.80	10.80
P63279	SUMO-conjugating enzyme UBC9;	-0.01	0.00	0.98	13.90
P42285	Superkiller viralicidic activity 2-like 2;	-0.38	-0.24	0.79	6.10
P00441	Superoxide dismutase [Cu-Zn];	-0.01	0.00	0.98	9.10
P04179	Superoxide dismutase [Mn], mitochondrial;	0.11	0.01	0.90	6.30
P78539	Sushi repeat-containing protein SRPX;	-0.30	-0.08	0.82	2.80
O60687	Sushi repeat-containing protein SRPX2;	0.49	0.11	0.68	9.90
Q8TAQ2	SWI/SNF complex subunit SMARCC2;	0.90	0.12	0.46	2.10
Q9UH65	Switch-associated protein 70;	-0.93	-0.20	0.42	2.70
Q92797	Symplekin;	-1.49	-12.26	0.44	2.20
Q96A49	Synapse-associated protein 1;	0.62	0.01	0.55	3.70
Q99536	Synaptic vesicle membrane protein VAT-1 homolog;	0.32	0.02	0.74	9.70
Q86Y82	Syntaxin-12;	-0.91	-1.58	0.51	11.60
O00560	Syntenin-1;	0.41	0.12	0.74	7.00
P17987	T-complex protein 1 subunit alpha;	-0.25	-0.17	0.88	33.80
P78371	T-complex protein 1 subunit beta;	-0.62	-0.17	0.61	34.00

Table S3

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
P50991	T-complex protein 1 subunit delta;	-0.53	-0.44	0.70	38.20
P48643	T-complex protein 1 subunit epsilon;	-0.41	-0.35	0.78	15.50
Q99832	T-complex protein 1 subunit eta;	-0.25	-0.28	0.90	20.30
P49368	T-complex protein 1 subunit gamma;	-0.62	-0.30	0.61	20.40
P50990	T-complex protein 1 subunit theta;	-0.40	-0.25	0.77	35.40
P40227	T-complex protein 1 subunit zeta;	-0.95	-1.28	0.46	22.20
Q9Y490	Talin-1;	-0.23	-0.16	0.89	15.80
Q7Z7G0	Target of Nesh-SH3;	5.01	0.01	0.00	8.60
Q08629	Testican-1;	2.21	0.04	0.08	20.00
O43657	Tetraspanin-6;	0.87	0.04	0.42	4.50
P52888	Thimet oligopeptidase;	-0.94	-1.75	0.50	8.60
O95881	Thioredoxin domain-containing protein 12;	-0.77	-0.24	0.51	8.70
Q9BRA2	Thioredoxin domain-containing protein 17;	-0.26	-0.03	0.85	26.80
Q8NBS9	Thioredoxin domain-containing protein 5;	-0.01	0.00	0.98	14.60
Q16881	Thioredoxin reductase 1, cytoplasmic;	0.09	0.02	0.91	13.30
P30048	Thioredoxin-dependent peroxide reductase,	0.99	0.05	0.36	17.60
P10599	Thioredoxin;	-0.57	-0.14	0.63	21.00
Q86V81	THO complex subunit 4;	-0.96	-0.19	0.40	4.30
P26639	Threonine--tRNA ligase, cytoplasmic;	1.08	0.20	0.50	21.20
P07996	Thrombospondin-1;	-1.62	-4.18	0.18	17.40
P49746	Thrombospondin-3;	2.35	0.07	0.11	12.10
Q9Y2W1	Thyroid hormone receptor-associated protein 3;	-0.17	-0.03	0.91	6.20
Q15643	Thyroid receptor-interacting protein 11;	0.03	0.01	0.95	1.20
Q15654	Thyroid receptor-interacting protein 6;	-0.13	-0.02	0.94	3.80
Q9UKU6	Thyrotropin-releasing hormone-degrading ectoenzyme;	-0.27	-0.10	0.84	3.10
Q07157	Tight junction protein ZO-1;	-0.45	-0.13	0.72	2.10
Q9UDY2	Tight junction protein ZO-2;	-1.05	-3.18	0.51	8.70
O75663	TIP41-like protein;	0.43	0.10	0.70	7.40
P04066	Tissue alpha-L-fucosidase;	1.79	0.07	0.15	6.20
P10646	Tissue factor pathway inhibitor;	2.14	0.02	0.05	21.70
P00750	Tissue-type plasminogen activator;	2.14	0.03	0.06	21.90
Q8WZ42	Titin;	1.18	0.35	0.63	0.30
O14657	Torsin-1B;	1.24	0.03	0.25	6.20
Q9NXH8	Torsin-4A;	0.90	0.02	0.39	2.10
Q96EM0	Trans-L-3-hydroxyproline dehydratase;	-0.88	-0.40	0.45	4.00
P37837	Transaldolase;	-0.49	-0.45	0.73	19.00
P20062	Transcobalamin-2;	1.90	0.11	0.24	8.00
P23193	Transcription elongation factor A protein 1;	-1.33	-6.70	0.42	7.30
Q96EI5	Transcription elongation factor A protein-like 4;	0.41	0.03	0.69	9.80
Q15369	Transcription elongation factor B polypeptide 1;	-1.21	-1.07	0.30	10.70
Q15370	Transcription elongation factor B polypeptide 2;	0.87	0.13	0.49	28.00
O00267	Transcription elongation factor SPT5;	-0.32	-0.07	0.81	1.50
Q7KZ85	Transcription elongation factor SPT6;	0.65	0.17	0.64	1.40
O14776	Transcription elongation regulator 1;	0.21	0.10	0.87	5.60
P20290	Transcription factor BTF3;	0.24	0.02	0.79	9.20
Q13263	Transcription intermediary factor 1-beta;	-0.50	-0.49	0.73	7.70
P02786	Transferrin receptor protein 1;	1.96	0.06	0.12	10.30
Q03167	Transforming growth factor beta receptor type 3;	0.72	0.03	0.49	3.20
P01137	Transforming growth factor beta-1;	1.90	0.03	0.09	9.20
Q15582	Transforming growth factor-beta-induced protein ig-h3;	-0.46	-0.06	0.71	6.70
P37802	Transgelin-2;	-0.38	-0.04	0.76	36.70

Table S3

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P55072	Transitional endoplasmic reticulum ATPase;	-0.37	-0.26	0.80	33.40
P29401	Transketolase;	-0.72	-3.55	0.81	27.90
Q14232	Translation initiation factor eIF-2B subunit alpha;	-0.66	-0.69	0.63	9.80
Q96EY4	Translation machinery-associated protein 16;	-0.77	-0.26	0.52	7.40
P13693	Translationally-controlled tumor protein;	0.00	0.00	0.98	27.30
Q99598	Translin-associated protein X;	-0.75	-0.24	0.52	4.50
Q99805	Transmembrane 9 superfamily member 2;	1.85	0.02	0.09	2.10
P49755	Transmembrane emp24 domain-containing protein 10;	0.96	0.03	0.36	5.50
Q9Y5L0	Transportin-3;	-0.73	-0.23	0.53	2.70
P22102	Trifunctional purine biosynthetic protein adenosine-3;	1.47	0.06	0.21	5.90
P60174	Triosephosphate isomerase;	-1.18	-1.55	0.32	57.00
O14773	Tripeptidyl-peptidase 1;	1.74	0.04	0.12	14.20
P29144	Tripeptidyl-peptidase 2;	0.72	0.27	0.68	4.10
Q9UJA5	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic	-0.47	-0.22	0.71	3.40
Q9Y3I0	tRNA-splicing ligase RtcB homolog;	-0.74	-0.93	0.59	10.50
Q9NYL9	Tropomodulin-3;	-0.27	-0.11	0.84	5.70
P06753	Tropomyosin alpha-3 chain;	-1.08	-3.67	0.51	14.80
P23381	Tryptophan--tRNA ligase, cytoplasmic;	0.90	0.22	0.57	23.40
Q71U36	Tubulin alpha-1A chain;	-0.49	-0.13	0.69	28.50
P68366	Tubulin alpha-4A chain;	-4.78	-709.03	0.00	15.80
P07437	Tubulin beta chain;	1.08	0.03	0.32	28.40
Q13509	Tubulin beta-3 chain;	-1.21	-0.76	0.29	22.90
P68371	Tubulin beta-4B chain;	-0.84	-0.19	0.47	27.20
P23258	Tubulin gamma-1 chain;	0.41	0.02	0.69	2.40
Q14166	Tubulin--tyrosine ligase-like protein 12;	0.51	0.43	0.84	12.10
O75347	Tubulin-specific chaperone A;	0.90	0.17	0.53	23.10
Q9GZM7	Tubulointerstitial nephritis antigen-like;	0.19	0.01	0.83	2.80
O00300	Tumor necrosis factor receptor superfamily member 11B;	-1.63	-2.74	0.16	10.70
Q9NP84	Tumor necrosis factor receptor superfamily member 12A;	1.11	0.10	0.36	7.80
P19438	Tumor necrosis factor receptor superfamily member 1A;	1.51	0.02	0.15	3.30
O75509	Tumor necrosis factor receptor superfamily member 21;	0.47	0.03	0.64	2.70
O95407	Tumor necrosis factor receptor superfamily member 6B;	1.51	0.02	0.16	23.70
O43399	Tumor protein D54;	0.43	0.09	0.70	14.10
Q99816	Tumor susceptibility gene 101 protein;	-0.50	-0.65	0.76	6.90
Q12792	Twinfilin-1;	-1.28	-14.95	0.70	9.10
Q6IBS0	Twinfilin-2;	-0.42	-0.16	0.74	20.10
Q9GZX9	Twisted gastrulation protein homolog 1;	0.41	0.01	0.67	6.70
P30530	Tyrosine-protein kinase receptor UFO;	0.43	0.01	0.66	2.10
P08621	U1 small nuclear ribonucleoprotein 70 kDa;	-0.52	-1.51	0.84	12.40
P09012	U1 small nuclear ribonucleoprotein A;	-0.64	-0.09	0.59	7.40
P09234	U1 small nuclear ribonucleoprotein C;	-0.62	-0.27	0.61	11.30
P09661	U2 small nuclear ribonucleoprotein A';	2.52	0.13	0.35	15.70
O00566	U3 small nucleolar ribonucleoprotein protein MPP10;	-0.11	-0.02	0.95	2.10
O43818	U3 small nucleolar RNA-interacting protein 2;	0.51	0.03	0.62	9.10
O43395	U4/U6 small nuclear ribonucleoprotein Prp3;	-0.53	-0.25	0.67	7.80
O43172	U4/U6 small nuclear ribonucleoprotein Prp4;	-1.94	-31.15	0.33	7.70
O43290	U4/U6.U5 tri-snRNP-associated protein 1;	0.39	0.03	0.70	1.90
Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2;	0.49	0.03	0.63	2.10
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase;	0.03	0.02	0.95	8.00
O15116	U6 snRNA-associated Sm-like protein LSm1;	0.41	0.04	0.68	17.30
Q9Y333	U6 snRNA-associated Sm-like protein LSm2;	-1.70	-3.81	0.15	35.80
P62310	U6 snRNA-associated Sm-like protein LSm3;	1.43	0.02	0.18	11.80
Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4;	-1.07	-0.79	0.36	14.40
Q9UK45	U6 snRNA-associated Sm-like protein LSm7;	-0.28	-0.02	0.83	15.50

Table S3

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q9UMX0	Ubiquilin-1;	-0.61	-0.10	0.61	5.10
P45974	Ubiquitin carboxyl-terminal hydrolase 5;	-0.98	-0.62	0.40	3.50
Q93009	Ubiquitin carboxyl-terminal hydrolase 7;	0.79	0.15	0.54	7.40
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3;	0.24	0.08	0.83	17.40
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5;	0.79	0.11	0.50	6.70
O14562	Ubiquitin domain-containing protein UBFD1;	-0.40	-0.19	0.76	13.30
Q96FW1	Ubiquitin thioesterase OTUB1;	0.21	0.06	0.83	16.60
P62979	Ubiquitin-40S ribosomal protein S27a;	1.43	0.13	0.32	42.30
Q14157	Ubiquitin-associated protein 2-like;	-0.43	-0.24	0.74	2.90
Q969T4	Ubiquitin-conjugating enzyme E2 E3;	4.61	0.00	0.00	9.00
P62256	Ubiquitin-conjugating enzyme E2 H;	-2.19	-21.41	0.10	8.20
P61086	Ubiquitin-conjugating enzyme E2 K;	-1.50	-1.61	0.19	16.50
P68036	Ubiquitin-conjugating enzyme E2 L3;	-0.42	-0.07	0.73	27.30
P61088	Ubiquitin-conjugating enzyme E2 N;	-0.23	-0.04	0.87	46.70
Q13404	Ubiquitin-conjugating enzyme E2 variant 1;	-0.81	-0.19	0.49	19.30
P61960	Ubiquitin-fold modifier 1;	-1.16	-0.64	0.31	17.60
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1;	-0.33	-0.06	0.80	5.40
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1;	-1.47	-3.39	0.23	7.50
P22314	Ubiquitin-like modifier-activating enzyme 1;	-0.94	-1.46	0.48	20.30
Q9NY97	UDP-GlcNAc:betaGal beta-1,3-N-	0.65	0.03	0.53	3.80
Q14376	UDP-glucose 4-epimerase;	-0.37	-0.07	0.77	2.90
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1;	1.01	0.08	0.38	1.40
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;	-0.40	-0.18	0.76	8.80
P30085	UMP-CMP kinase;	0.62	0.10	0.59	29.10
Q8N715	Uncharacterized protein C1orf65;	1.14	0.02	0.28	1.30
Q92614	Unconventional myosin-XVIIIa;	-0.72	-0.14	0.54	0.50
Q9HB07	UPF0160 protein MYG1, mitochondrial;	-1.09	-0.63	0.34	3.70
Q9H741	UPF0454 protein C12orf49;	0.22	0.02	0.80	6.30
Q9BY42	UPF0549 protein C20orf43;	-0.47	-0.25	0.72	6.20
Q969H8	UPF0556 protein C19orf10;	0.39	0.02	0.70	5.20
Q9Y224	UPF0568 protein C14orf166;	-0.35	-0.15	0.79	18.00
Q6UXG2	UPF0577 protein KIAA1324;	-2.12	-5.04	0.06	2.70
Q8N4J0	UPF0586 protein C9orf41;	-3.34	-57.04	0.00	2.70
Q9NWV4	UPF0587 protein C1orf123;	-0.70	-1.15	0.65	34.40
Q9GZN8	UPF0687 protein C20orf27;	-0.52	-0.10	0.66	13.80
Q9H3H3	UPF0696 protein C11orf68;	-0.41	-0.15	0.75	9.60
Q03405	Urokinase plasminogen activator surface receptor;	-2.79	-10.61	0.01	4.80
P00749	Urokinase-type plasminogen activator;	0.30	0.02	0.76	21.80
P06132	Uroporphyrinogen decarboxylase;	-0.19	-0.04	0.90	11.20
Q16851	UTP--glucose-1-phosphate uridylyltransferase;	-1.04	-0.58	0.37	12.20
P46939	Utrophin;	-0.19	-0.04	0.89	0.40
P54727	UV excision repair protein RAD23 homolog B;	-0.21	-0.24	0.92	8.10
P38606	V-type proton ATPase catalytic subunit A;	2.02	0.01	0.06	1.90
Q16864	V-type proton ATPase subunit F;	-0.58	-0.28	0.64	10.10
Q15904	V-type proton ATPase subunit S1;	0.53	0.06	0.61	18.10
O75436	Vacuolar protein sorting-associated protein 26A;	0.93	0.19	0.53	16.50
Q9UBQ0	Vacuolar protein sorting-associated protein 29;	-0.19	-0.02	0.89	17.00
Q96QK1	Vacuolar protein sorting-associated protein 35;	0.69	0.18	0.61	3.30
P26640	Valine--tRNA ligase;	-0.92	-0.36	0.43	4.40
P50552	Vasodilator-stimulated phosphoprotein;	0.03	0.01	0.95	13.20
Q6EMK4	Vasorin;	0.90	0.09	0.43	9.50
Q9P0L0	Vesicle-associated membrane protein-associated protein	-0.53	-0.08	0.66	5.60

Table S3

Uniprot accession	**Name**	**Fold-change ($\log_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
O95292	Vesicle-associated membrane protein-associated protein	0.11	0.01	0.89	7.80
O75396	Vesicle-trafficking protein SEC22b;	-0.67	-0.79	0.63	13.50
Q00341	Vigilin;	0.53	0.02	0.59	1.20
P08670	Vimentin;	-0.33	-0.29	0.83	38.00
P18206	Vinculin;	0.69	0.18	0.61	13.00
P07225	Vitamin K-dependent protein S;	-0.80	-0.49	0.50	2.70
P04004	Vitronectin;	0.51	0.04	0.62	3.10
Q6PCB0	von Willebrand factor A domain-containing protein 1;	0.84	0.11	0.48	6.70
Q5VU97	VWFA and cache domain-containing protein 1;	-0.81	-0.28	0.49	0.90
Q5SNT6	WASH complex subunit FAM21B;	0.22	0.03	0.81	1.30
O75083	WD repeat-containing protein 1;	-0.43	-0.86	0.84	19.00
P61964	WD repeat-containing protein 5;	-0.23	-0.10	0.87	9.30
Q96FK6	WD repeat-containing protein 89;	-0.46	-0.07	0.71	7.80
Q96MX6	WD repeat-containing protein 92;	-0.97	-0.23	0.40	4.50
Q2TAY7	WD40 repeat-containing protein SMU1;	-1.02	-0.27	0.37	1.90
P13010	X-ray repair cross-complementing protein 5;	0.74	0.16	0.58	17.80
P12956	X-ray repair cross-complementing protein 6;	-0.41	-0.08	0.74	22.80
Q9NQW7	Xaa-Pro aminopeptidase 1;	0.11	0.02	0.90	3.90
P12955	Xaa-Pro dipeptidase;	1.24	0.29	0.56	10.50
Q9H1B5	Xylosyltransferase 2;	1.35	0.02	0.20	3.10
Q7Z739	YTH domain family protein 3;	1.01	0.02	0.34	1.20
O75152	Zinc finger CCCH domain-containing protein 11A;	0.84	0.05	0.43	1.60
O43670	Zinc finger protein 207;	-0.33	-0.23	0.82	8.80
Q14966	Zinc finger protein 638;	-0.63	-0.23	0.60	0.90
Q9ULF5	Zinc transporter ZIP10;	2.90	0.01	0.01	3.90
P25311	Zinc-alpha-2-glycoprotein;	0.96	0.15	0.47	12.40
Q15942	Zyxin;	-0.66	-0.77	0.64	4.70