Table S1: Identified and quantified proteins in the first 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 (%)**
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesteras	-0.84	-0.63	0.55	3.30
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase;	0.75	0.08	0.41	7.30
Q04446	1,4-alpha-glucan-branching enzyme;	-0.12	-0.03	0.89	8.70
P61604	10 kDa heat shock protein, mitochondrial;	0.60	0.10	0.51	30.40
Q15029	116 kDa U5 small nuclear ribonucleoprotein component;	-0.18	-0.11	0.88	13.30
Q9NRX4	14 kDa phosphohistidine phosphatase;	-0.36	-0.02	0.69	8.80
P31946	14-3-3 protein beta/alpha;	-0.84	-0.16	0.37	41.50
P62258	14-3-3 protein epsilon;	-1.00	-0.34	0.32	44.70
Q04917	14-3-3 protein eta;	-0.56	-0.38	0.68	34.60
P61981	14-3-3 protein gamma;	-0.60	-0.07	0.50	24.70
P31947	14-3-3 protein sigma;	-0.58	-0.31	0.62	19.40
P27348	14-3-3 protein theta;	-0.34	-0.16	0.77	38.40
P63104	14-3-3 protein zeta/delta;	-0.54	-0.29	0.65	38.40
Q8N543	2-oxoglutarate and iron-dependent oxygenase domain-con	0.15	0.01	0.86	1.80
P62333	26S protease regulatory subunit 10B;	0.45	0.05	0.61	9.00
P17980	26S protease regulatory subunit 6A;	-0.38	-0.51	0.86	19.10
P43686	26S protease regulatory subunit 6B;	1.25	0.06	0.16	3.30
O00231	26S proteasome non-ATPase regulatory subunit 11;	1.04	0.12	0.25	11.10
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13;	-0.03	-0.01	0.97	13.00
O00487	26S proteasome non-ATPase regulatory subunit 14;	1.72	0.23	0.06	4.20
Q13200	26S proteasome non-ATPase regulatory subunit 2;	0.71	0.34	0.53	10.00
O43242	26S proteasome non-ATPase regulatory subunit 3;	1.45	0.30	0.12	9.90
P55036	26S proteasome non-ATPase regulatory subunit 4;	0.00	0.00	1.00	4.00
Q16401	26S proteasome non-ATPase regulatory subunit 5;	-0.40	-0.20	0.73	12.50
Q15008	26S proteasome non-ATPase regulatory subunit 6;	1.17	0.33	0.23	11.60
P51665	26S proteasome non-ATPase regulatory subunit 7;	0.69	0.03	0.44	9.90
P48556	26S proteasome non-ATPase regulatory subunit 8;	0.78	0.21	0.42	5.40
O00233	26S proteasome non-ATPase regulatory subunit 9;	0.28	0.03	0.76	5.40
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial;	-0.79	-0.26	0.44	8.00
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	-0.69	-0.10	0.45	3.10
P42765	3-ketoacyl-CoA thiolase, mitochondrial;	0.51	0.07	0.58	3.30
O95861	3'(2'),5'-bisphosphate nucleotidase 1;	-1.06	-0.46	0.34	9.10
P49189	4-trimethylaminobutyraldehyde dehydrogenase;	0.07	0.01	0.94	2.40
P46783	40S ribosomal protein S10;	0.64	0.07	0.48	14.50
P62280	40S ribosomal protein S11;	1.50	1.12	0.28	20.90
P25398	40S ribosomal protein S12;	-0.04	-0.02	0.96	46.20
P62277	40S ribosomal protein S13;	0.98	0.11	0.28	24.50
P62263	40S ribosomal protein S14;	0.94	0.15	0.31	15.20
P62841	40S ribosomal protein S15;	0.63	0.12	0.50	8.30
P62244	40S ribosomal protein S15a;	0.25	0.04	0.79	13.80
P62249	40S ribosomal protein S16;	1.71	0.36	0.07	28.10
P62269	40S ribosomal protein S18;	0.71	0.34	0.53	27.00
P39019	40S ribosomal protein S19;	0.03	0.01	0.98	24.10
P15880	40S ribosomal protein S2;	0.28	0.11	0.79	22.90
P63220	40S ribosomal protein S21;	-0.40	-0.04	0.65	28.90
P62266	40S ribosomal protein S23;	3.89	3.85	0.02	7.70
P62847	40S ribosomal protein S24;	0.64	0.05	0.48	8.30
P62851	40S ribosomal protein S25;	0.73	0.03	0.41	7.20
Q71UM5	40S ribosomal protein S27-like;	0.79	0.16	0.40	28.60
P42677	40S ribosomal protein S27;	1.07	0.26	0.26	28.60
P62857	40S ribosomal protein S28;	0.20	0.02	0.82	17.40
P23396	40S ribosomal protein S3;	0.68	0.22	0.50	45.70
P61247	40S ribosomal protein S3a;	0.70	0.40	0.57	24.60
P62701	40S ribosomal protein S4, X isoform;	0.88	0.16	0.34	22.40

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P46782	40S ribosomal protein S5;	-0.43	-0.10	0.65	23.00
P62753	40S ribosomal protein S6;	0.15	0.08	0.89	15.70
P62081	40S ribosomal protein S7;	0.50	0.25	0.67	14.90
P62241	40S ribosomal protein S8;	0.75	0.16	0.43	29.30
P46781	40S ribosomal protein S9;	0.48	0.08	0.61	9.80
P08865	40S ribosomal protein SA;	-0.15	-0.06	0.89	20.00
Q9BRK5	45 kDa calcium-binding protein;	0.58	0.14	0.55	24.30
P08195	4F2 cell-surface antigen heavy chain;	0.95	0.38	0.37	4.90
O14841	5-oxoprolinase;	-0.54	-0.23	0.63	2.70
Q9H0D6	5'-3' exoribonuclease 2;	-0.60	-0.25	0.57	6.10
Q5TFE4	5'-nucleotidase domain-containing protein 1;	-1.22	-0.14	0.18	7.90
P21589	5'-nucleotidase;	-0.32	-0.10	0.75	2.10
Q01813	6-phosphofructokinase type C;	-0.92	-1.16	0.65	8.20
P08237	6-phosphofructokinase, muscle type;	0.90	0.11	0.32	1.50
P52209	6-phosphogluconate dehydrogenase, decarboxylating;	0.03	0.02	0.99	24.60
O95336	6-phosphogluconolactonase;	-1.22	-0.85	0.37	41.50
P10809	60 kDa heat shock protein, mitochondrial;	-0.11	-0.05	0.92	30.20
P05388	60S acidic ribosomal protein P0;	0.97	0.20	0.30	35.60
P05386	60S acidic ribosomal protein P1;	0.91	0.12	0.32	14.00
P05387	60S acidic ribosomal protein P2;	0.48	0.12	0.63	55.70
P62906	60S ribosomal protein L10a;	0.25	0.07	0.80	34.60
P62913	60S ribosomal protein L11;	0.37	0.08	0.70	12.90
P30050	60S ribosomal protein L12;	0.33	0.12	0.75	54.50
P26373	60S ribosomal protein L13;	0.49	0.28	0.69	14.70
P50914	60S ribosomal protein L14;	1.04	0.45	0.34	20.90
P61313	60S ribosomal protein L15;	0.88	0.24	0.36	5.90
P18621	60S ribosomal protein L17;	0.63	0.14	0.51	26.10
Q07020	60S ribosomal protein L18;	0.20	0.07	0.84	18.60
Q02543	60S ribosomal protein L18a;	1.29	0.55	0.24	17.00
P46778	60S ribosomal protein L21;	0.77	0.56	0.58	16.20
Q6P5R6	60S ribosomal protein L22-like 1;	0.92	0.15	0.32	9.80
P35268	60S ribosomal protein L22;	0.60	0.04	0.50	10.20
P62829	60S ribosomal protein L23;	-0.43	-0.61	0.85	36.40
P62750	60S ribosomal protein L23a;	0.60	0.12	0.52	13.50
P83731	60S ribosomal protein L24;	0.56	0.05	0.54	19.10
P61353	60S ribosomal protein L27;	0.43	0.21	0.70	14.70
P47914	60S ribosomal protein L29;	0.82	0.09	0.36	9.40
P39023	60S ribosomal protein L3;	0.15	0.10	0.91	13.60
P62888	60S ribosomal protein L30;	0.19	0.01	0.83	24.30
P62899	60S ribosomal protein L31;	0.24	0.04	0.80	24.80
P62910	60S ribosomal protein L32;	-0.09	-0.01	0.92	17.00
P18077	60S ribosomal protein L35a;	1.78	0.15	0.05	16.40
Q9Y3U8	60S ribosomal protein L36;	-0.20	-0.10	0.86	20.00
P61513	60S ribosomal protein L37a;	-0.43	-0.03	0.63	13.00
P63173	60S ribosomal protein L38;	-2.06	-0.09	0.02	10.00
P36578	60S ribosomal protein L4;	1.32	0.81	0.29	12.40
P46777	60S ribosomal protein L5;	-0.94	-0.40	0.39	33.30
Q02878	60S ribosomal protein L6;	0.71	0.45	0.58	27.40
P18124	60S ribosomal protein L7;	0.51	0.10	0.59	14.90
P62424	60S ribosomal protein L7a;	0.82	0.07	0.36	3.40
P62917	60S ribosomal protein L8;	-1.06	-1.02	0.52	10.50
P32969	60S ribosomal protein L9;	-0.56	-0.43	0.70	10.90
Q9Y221	60S ribosome subunit biogenesis protein NIP7 homolog;	1.01	0.15	0.27	7.80
P11021	78 kDa glucose-regulated protein;	0.25	0.10	0.81	31.80
Q7L2J0	7SK snRNA methylphosphate capping enzyme;	-2.40	-0.13	0.01	1.50
Q02952	A-kinase anchor protein 12;	-0.38	-0.36	0.82	18.90
Q9ULX6	A-kinase anchor protein 8-like;	-1.32	-0.20	0.15	2.30

Table S1

Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic;	0.48	0.27	0.70	19.10
P24752	Acetyl-CoA acetyltransferase, mitochondrial;	-0.54	-0.10	0.57	2.10
Q13085	Acetyl-CoA carboxylase 1;	3.24	0.52	0.00	0.50
P50553	Achaete-scute homolog 1;	-2.25	-0.11	0.01	4.20
Q13510	Acid ceramidase;	0.59	0.37	0.65	21.00
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family men	-0.69	-0.46	0.60	23.70
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family men	-0.69	-0.22	0.49	24.30
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family men	0.71	0.06	0.43	4.50
Q99798	Aconitate hydratase, mitochondrial;	-0.54	-0.19	0.60	4.50
P61160	Actin-related protein 2;	-1.06	-1.26	0.59	16.20
Q92747	Actin-related protein 2/3 complex subunit 1A;	0.12	0.02	0.89	7.00
O15143	Actin-related protein 2/3 complex subunit 1B;	0.21	0.10	0.85	21.50
O15144	Actin-related protein 2/3 complex subunit 2;	-0.58	-0.35	0.64	13.70
P59998	Actin-related protein 2/3 complex subunit 4;	0.91	0.79	0.55	11.30
O15511	Actin-related protein 2/3 complex subunit 5;	-0.92	-0.09	0.31	29.10
P61158	Actin-related protein 3;	-0.92	-0.29	0.37	34.40
P62736	Actin, aortic smooth muscle;	0.00	0.00	1.00	27.70
P60709	Actin, cytoplasmic 1;	-0.58	-0.40	0.66	43.50
P53999	Activated RNA polymerase II transcriptional coactivator p	0.91	0.44	0.42	37.00
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	0.39	0.08	0.68	23.40
P07108	Acyl-CoA-binding protein;	0.40	0.07	0.66	32.20
O75608	Acyl-protein thioesterase 1;	1.13	0.06	0.21	4.80
O95372	Acyl-protein thioesterase 2;	-2.56	-2.86	0.16	15.60
P13798	Acylamino-acid-releasing enzyme;	-1.06	-0.49	0.35	9.30
P07311	Acylphosphatase-1;	-1.43	-0.16	0.11	13.10
Q6UY14	ADAMTS-like protein 4;	-0.27	-0.13	0.81	5.80
P46108	Adapter molecule crk;	0.58	0.56	0.73	10.50
P00813	Adenosine deaminase;	3.70	0.46	0.00	2.80
P55263	Adenosine kinase;	0.07	0.02	0.94	15.50
P23526	Adenosylhomocysteinase;	-0.60	-0.24	0.57	30.60
P54819	Adenylate kinase 2, mitochondrial;	-2.00	-1.52	0.15	33.10
P00568	Adenylate kinase isoenzyme 1;	0.07	0.01	0.94	11.30
P30566	Adenylosuccinate lyase;	0.03	0.01	0.98	10.30
P30520	Adenylosuccinate synthetase isozyme 2;	0.08	0.08	0.96	9.60
Q01518	Adenylyl cyclase-associated protein 1;	-1.12	-0.58	0.33	20.20
P61204	ADP-ribosylation factor 3;	-0.12	-0.01	0.89	27.60
P62330	ADP-ribosylation factor 6;	0.21	0.09	0.84	14.30
Q9NZ52	ADP-ribosylation factor-binding protein GGA3;	0.08	0.01	0.92	1.70
Q9UKK9	ADP-sugar pyrophosphatase;	-0.64	-0.16	0.51	32.90
P55196	Afadin;	-0.23	-0.03	0.80	2.00
O43488	Aflatoxin B1 aldehyde reductase member 2;	-1.22	-0.11	0.18	8.40
O00468	Agrin;	0.68	0.48	0.62	24.00
O00170	AH receptor-interacting protein;	-0.60	-0.12	0.52	12.10
P49588	Alanine--tRNA ligase, cytoplasmic;	0.71	0.36	0.54	9.60
P14550	Alcohol dehydrogenase [NADP(+)];	0.63	0.49	0.66	18.80
P11766	Alcohol dehydrogenase class-3;	-1.22	-0.79	0.35	17.10
P47895	Aldehyde dehydrogenase family 1 member A3;	-0.89	-0.48	0.45	21.30
Q8IZ83	Aldehyde dehydrogenase family 16 member A1;	-0.84	-0.15	0.36	2.00
P15121	Aldose reductase;	-1.47	-0.82	0.22	28.20
P05187	Alkaline phosphatase, placental type;	-0.69	-0.09	0.45	21.10
P10696	Alkaline phosphatase, placental-like;	1.20	0.20	0.19	21.20
Q9BYC5	Alpha-(1,6)-fucosyltransferase;	1.86	0.14	0.04	2.10
P01011	Alpha-1-antichymotrypsin;	2.03	1.42	0.13	12.30
P01009	Alpha-1-antitrypsin;	2.74	0.29	0.00	15.30
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosai	0.65	0.15	0.49	5.40
Q09328	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosan	-0.94	-1.02	0.60	5.80
P02765	Alpha-2-HS-glycoprotein;	-0.04	0.00	0.96	5.20

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P30533	Alpha-2-macroglobulin receptor-associated protein;	-1.74	-0.23	0.05	3.60
P01023	Alpha-2-macroglobulin;	1.05	0.23	0.27	1.40
P12814	Alpha-actinin-1;	0.28	0.21	0.84	46.70
Q08043	Alpha-actinin-3;	-6.64	0.00	0.00	9.90
O43707	Alpha-actinin-4;	-0.23	-0.11	0.84	51.00
P06733	Alpha-enolase;	-1.32	-0.66	0.24	43.50
P06280	Alpha-galactosidase A;	1.02	0.72	0.45	13.10
Q9C0B1	Alpha-ketoglutarate-dependent dioxygenase FTO;	-0.49	-0.07	0.58	3.80
P35475	Alpha-L-iduronidase;	0.12	0.05	0.91	8.00
Q16706	Alpha-mannosidase 2;	-0.58	-0.46	0.69	4.30
P54802	Alpha-N-acetylglucosaminidase;	0.26	0.30	0.89	9.20
P54920	Alpha-soluble NSF attachment protein;	-2.06	-2.66	0.32	9.80
Q9BUJ0	Alpha/beta hydrolase domain-containing protein 14A;	7.96	1.24	0.00	5.90
Q96IU4	Alpha/beta hydrolase domain-containing protein 14B;	0.79	0.06	0.38	17.60
Q06203	Amidophosphoribosyltransferase;	0.51	0.26	0.66	4.40
Q12904	Aminoacyl tRNA synthase complex-interacting multifunct	-0.60	-0.61	0.72	13.10
Q03154	Aminoacylase-1;	-1.52	-0.61	0.15	9.80
Q9H4A4	Aminopeptidase B;	0.19	0.12	0.89	22.50
Q01433	AMP deaminase 2;	-0.25	-0.01	0.78	1.10
P05067	Amyloid beta A4 protein;	0.24	0.12	0.84	21.20
Q06481	Amyloid-like protein 2;	0.90	0.15	0.33	3.00
Q6FI81	Anamorsin;	0.81	0.09	0.38	4.80
Q13685	Angio-associated migratory cell protein;	1.02	0.14	0.26	3.00
P04083	Annexin A1;	-0.84	-0.43	0.47	52.00
P50995	Annexin A11;	-0.84	-0.40	0.46	9.10
P07355	Annexin A2;	-1.00	-0.28	0.30	49.90
P12429	Annexin A3;	1.77	1.65	0.27	26.30
P08758	Annexin A5;	-1.25	-0.57	0.26	33.10
P46013	Antigen KI-67;	3.12	0.65	0.00	0.30
P01008	Antithrombin-III;	0.91	0.04	0.31	3.90
Q10567	AP-1 complex subunit beta-1;	-1.25	-0.89	0.36	7.30
Q9BXS5	AP-1 complex subunit mu-1;	-0.15	-0.10	0.91	12.50
O95782	AP-2 complex subunit alpha-1;	-0.36	-0.06	0.70	9.70
O94973	AP-2 complex subunit alpha-2;	-1.74	-0.41	0.07	6.30
P63010	AP-2 complex subunit beta;	0.11	0.06	0.93	14.80
Q96CW1	AP-2 complex subunit mu;	-0.12	-0.03	0.90	13.60
O00203	AP-3 complex subunit beta-1;	-0.32	-0.02	0.73	0.90
O14617	AP-3 complex subunit delta-1;	1.36	0.21	0.14	1.60
Q9Y2T2	AP-3 complex subunit mu-1;	-1.74	-0.17	0.05	2.90
P04114	Apolipoprotein B-100;	3.23	0.18	0.00	0.30
P02656	Apolipoprotein C-III;	1.01	0.21	0.29	16.20
Q9BZZ5	Apoptosis inhibitor 5;	-0.40	-0.05	0.66	11.30
O95831	Apoptosis-inducing factor 1, mitochondrial;	-0.97	-0.69	0.47	9.30
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus;	0.18	0.02	0.85	2.40
P54136	Arginine--tRNA ligase, cytoplasmic;	-0.43	-0.22	0.71	14.10
P04424	Argininosuccinate lyase;	-1.15	-0.28	0.23	8.00
Q8N5I2	Arrestin domain-containing protein 1;	0.90	0.05	0.31	2.80
P15289	Arylsulfatase A;	1.26	0.10	0.16	2.80
O43776	Asparagine--tRNA ligase, cytoplasmic;	-0.23	-0.04	0.81	8.00
P17174	Aspartate aminotransferase, cytoplasmic;	0.18	0.08	0.88	22.00
P00505	Aspartate aminotransferase, mitochondrial;	-1.09	-0.81	0.43	25.30
P14868	Aspartate--tRNA ligase, cytoplasmic;	-0.94	-0.91	0.57	13.00
Q9ULA0	Aspartyl aminopeptidase;	-1.22	-0.11	0.18	3.20
Q15121	Astrocytic phosphoprotein PEA-15;	4.08	0.61	0.00	9.20
Q8WWM7	Ataxin-2-like protein;	-0.67	-0.06	0.46	1.10
P06576	ATP synthase subunit beta, mitochondrial;	0.25	0.07	0.80	5.50
P61221	ATP-binding cassette sub-family E member 1;	-0.97	-1.31	0.65	8.70

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q8NE71	ATP-binding cassette sub-family F member 1;	-0.76	-0.06	0.40	2.50
P53396	ATP-citrate synthase;	-0.29	-0.31	0.87	22.30
P46063	ATP-dependent DNA helicase Q1;	0.48	0.04	0.60	2.50
Q08211	ATP-dependent RNA helicase A;	0.53	0.14	0.59	11.80
Q92499	ATP-dependent RNA helicase DDX1;	-0.45	-0.14	0.65	8.80
Q9NUU7	ATP-dependent RNA helicase DDX19A;	1.33	0.32	0.16	4.40
O00571	ATP-dependent RNA helicase DDX3X;	1.01	0.44	0.35	1.50
Q86XP3	ATP-dependent RNA helicase DDX42;	-0.43	-0.12	0.66	7.40
O75882	Attractin;	-0.01	-0.01	0.99	0.70
O75531	Barrier-to-autointegration factor;	1.84	0.37	0.05	13.50
P50895	Basal cell adhesion molecule;	0.20	0.07	0.84	15.00
P98160	Basement membrane-specific heparan sulfate proteoglycan	1.06	0.85	0.46	15.20
P35613	Basigin;	-0.27	-0.12	0.81	8.80
P15291	Beta-1,4-galactosyltransferase 1;	-0.32	-0.08	0.74	8.30
O60513	Beta-1,4-galactosyltransferase 4;	-0.12	-0.03	0.90	9.90
P02749	Beta-2-glycoprotein 1;	0.37	0.02	0.68	2.60
P13929	Beta-enolase;	0.20	0.16	0.89	13.10
P16278	Beta-galactosidase;	-0.36	-0.33	0.82	19.90
P08236	Beta-glucuronidase;	2.95	2.19	0.03	4.60
P06865	Beta-hexosaminidase subunit alpha;	0.19	0.29	0.94	17.60
P07686	Beta-hexosaminidase subunit beta;	1.08	0.49	0.33	23.40
O00462	Beta-mannosidase;	-0.03	-0.02	0.98	9.20
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synth	-0.49	-0.07	0.58	7.10
P07814	Bifunctional glutamate/proline--tRNA ligase;	-0.03	-0.01	0.98	8.10
P31939	Bifunctional purine biosynthesis protein PURH;	-0.03	-0.01	0.98	24.80
Q9Y223	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-ac	0.73	0.11	0.43	1.90
P43251	Biotinidase;	-0.12	-0.07	0.92	4.10
Q13867	Bleomycin hydrolase;	-0.84	-0.16	0.37	6.80
Q9H3K6	BolA-like protein 2;	-1.47	-1.11	0.30	51.20
P13497	Bone morphogenetic protein 1;	-0.03	-0.02	0.98	7.10
P22003	Bone morphogenetic protein 5;	5.63	1.02	0.00	2.20
Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein	-0.40	-0.13	0.69	8.00
Q9P287	BRCA2 and CDKN1A-interacting protein;	0.00	0.00	1.00	15.90
P11586	C-1-tetrahydrofolate synthase, cytoplasmic;	-0.09	-0.04	0.94	22.60
P13500	C-C motif chemokine 2;	1.38	0.17	0.13	11.10
O60271	C-Jun-amino-terminal kinase-interacting protein 4;	-0.20	-0.07	0.84	3.10
P56545	C-terminal-binding protein 2;	0.31	0.05	0.74	11.00
Q9UBG0	C-type mannose receptor 2;	-3.06	-2.80	0.06	4.40
P80162	C-X-C motif chemokine 6;	1.54	0.14	0.09	10.50
Q96EU7	C1GALT1-specific chaperone 1;	0.69	0.08	0.45	4.10
P27708	CAD protein;	1.19	0.31	0.22	2.60
P55290	Cadherin-13;	-0.94	-0.18	0.31	3.80
P63098	Calcineurin subunit B type 1;	3.29	0.55	0.00	5.90
Q9Y376	Calcium-binding protein 39;	-0.60	-0.43	0.66	15.50
Q9Y2V2	Calcium-regulated heat stable protein 1;	0.25	0.02	0.78	10.90
Q13554	Calcium/calmodulin-dependent protein kinase type II subu	0.12	0.02	0.89	2.50
Q9HB71	Calcyclin-binding protein;	-0.29	-0.20	0.83	32.90
P62158	Calmodulin;	0.55	0.24	0.62	14.10
P04632	Calpain small subunit 1;	-0.29	-0.06	0.76	8.60
P17655	Calpain-2 catalytic subunit;	-0.04	-0.01	0.96	7.30
Q99439	Calponin-2;	-1.94	-0.22	0.03	3.60
Q15417	Calponin-3;	0.25	0.02	0.78	6.40
P27797	Calreticulin;	0.63	0.31	0.58	15.60
P22676	Calretinin;	0.86	0.92	0.63	16.20
O94985	Calsyntenin-1;	0.66	0.25	0.53	14.80
O43852	Calumenin;	1.38	0.47	0.17	20.60
Q8NCH0	Carbohydrate sulfotransferase 14;	0.77	0.09	0.40	15.70

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q96DG6	Carboxymethylenebutenolidase homolog;	0.08	0.06	0.95	11.00
Q9UI42	Carboxypeptidase A4;	-1.15	-0.64	0.33	13.10
O75718	Cartilage-associated protein;	1.20	0.08	0.18	2.70
P68400	Casein kinase II subunit alpha;	4.03	0.42	0.00	3.30
P19784	Casein kinase II subunit alpha';	2.62	0.35	0.00	3.70
P04040	Catalase;	-0.29	-0.23	0.84	9.10
P07858	Cathepsin B;	-0.60	-0.22	0.56	17.70
P07339	Cathepsin D;	0.74	0.30	0.49	21.60
P07711	Cathepsin L1;	2.01	1.09	0.09	15.60
Q9UBR2	Cathepsin Z;	0.30	0.15	0.80	10.20
P20645	Cation-dependent mannose-6-phosphate receptor;	-1.60	-0.19	0.08	5.10
P11717	Cation-independent mannose-6-phosphate receptor;	0.60	0.16	0.54	4.50
Q03135	Caveolin-1;	0.21	0.02	0.81	7.90
A5YKK6	CCR4-NOT transcription complex subunit 1;	1.73	0.98	0.15	1.30
Q6YHK3	CD109 antigen;	0.54	0.36	0.68	17.00
Q13740	CD166 antigen;	0.98	0.66	0.46	19.00
Q9Y5K6	CD2-associated protein;	-0.97	-0.11	0.28	3.10
P16070	CD44 antigen;	-1.40	-0.70	0.22	7.70
P13987	CD59 glycoprotein;	1.22	0.09	0.18	9.40
P21926	CD9 antigen;	0.69	0.28	0.52	7.00
Q15642	Cdc42-interacting protein 4;	-1.06	-0.11	0.25	3.30
Q8NFZ8	Cell adhesion molecule 4;	0.37	0.60	0.89	14.90
P60953	Cell division control protein 42 homolog;	-1.40	-0.33	0.15	14.70
Q99459	Cell division cycle 5-like protein;	-0.43	-0.07	0.64	2.20
Q99674	Cell growth regulator with EF hand domain protein 1;	0.55	0.37	0.68	12.30
Q9NX58	Cell growth-regulating nucleolar protein;	-0.60	-0.07	0.50	2.60
P43121	Cell surface glycoprotein MUC18;	1.40	0.14	0.12	1.90
P62633	Cellular nucleic acid-binding protein;	-2.18	-1.39	0.08	22.00
O00299	Chloride intracellular channel protein 1;	0.19	0.05	0.85	32.00
Q9Y696	Chloride intracellular channel protein 4;	-0.67	-0.35	0.57	22.10
Q6UVK1	Chondroitin sulfate proteoglycan 4;	0.48	0.31	0.72	5.30
P83916	Chromobox protein homolog 1;	-0.29	-0.02	0.75	14.60
Q13185	Chromobox protein homolog 3;	0.18	0.09	0.88	28.40
P45973	Chromobox protein homolog 5;	-0.04	-0.02	0.96	12.60
O75390	Citrate synthase, mitochondrial;	-0.01	-0.01	0.99	6.70
Q00610	Clathrin heavy chain 1;	0.07	0.04	0.95	17.30
P09497	Clathrin light chain B;	0.03	0.02	0.99	15.30
Q10570	Cleavage and polyadenylation specificity factor subunit 1;	-0.12	-0.04	0.90	3.70
Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3;	-0.40	-0.35	0.80	3.90
O43809	Cleavage and polyadenylation specificity factor subunit 5;	0.55	0.35	0.67	6.60
Q16630	Cleavage and polyadenylation specificity factor subunit 6;	-0.43	-0.24	0.72	4.90
O75153	Clustered mitochondria protein homolog;	0.20	0.08	0.85	2.50
P10909	Clusterin;	0.24	0.16	0.86	25.80
Q14019	Coactosin-like protein;	-0.27	-0.06	0.78	31.00
P00742	Coagulation factor X;	6.53	1.31	0.00	3.90
P53621	Coatomer subunit alpha;	0.44	0.13	0.65	2.20
P53618	Coatomer subunit beta;	-0.76	-0.45	0.54	2.40
P35606	Coatomer subunit beta';	0.26	0.04	0.77	1.40
P48444	Coatomer subunit delta;	-0.29	-0.15	0.80	15.90
O14579	Coatomer subunit epsilon;	-0.84	-0.06	0.35	3.60
Q9Y678	Coatomer subunit gamma-1;	-0.36	-0.08	0.71	2.40
O43405	Cochlin;	3.05	1.81	0.01	18.20
P23528	Cofilin-1;	-0.12	-0.03	0.90	45.20
Q9Y281	Cofilin-2;	-1.12	-1.53	0.61	18.70
Q8WVM7	Cohesin subunit SA-1;	1.41	0.11	0.12	0.70
Q86WR0	Coiled-coil domain-containing protein 25;	-2.18	-0.10	0.02	6.20
O75534	Cold shock domain-containing protein E1;	0.31	0.10	0.76	1.50

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Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q14011	Cold-inducible RNA-binding protein;	-1.43	-1.74	0.46	19.80
P12109	Collagen alpha-1(VI) chain;	1.94	0.50	0.04	16.10
Q99715	Collagen alpha-1(XII) chain;	-0.01	0.00	0.99	4.80
P39060	Collagen alpha-1(XVIII) chain;	2.13	1.05	0.06	5.60
P08123	Collagen alpha-2(I) chain;	2.99	3.26	0.10	1.30
P05997	Collagen alpha-2(V) chain;	5.55	7.62	0.01	2.70
P29400	Collagen alpha-5(IV) chain;	1.87	1.17	0.14	1.90
A8TX70	Collagen alpha-5(VI) chain;	1.66	0.23	0.07	0.40
Q6UXH8	Collagen and calcium-binding EGF domain-containing pr	0.61	0.33	0.60	7.10
P00736	Complement C1r subcomponent;	0.69	0.55	0.64	7.70
P01024	Complement C3;	1.61	0.77	0.16	39.40
Q07021	Complement component 1 Q subcomponent-binding prote	0.03	0.01	0.98	7.10
P00751	Complement factor B;	0.55	0.31	0.65	11.30
P00746	Complement factor D;	0.61	0.43	0.65	33.20
P29279	Connective tissue growth factor;	0.24	0.36	0.92	10.00
Q13098	COP9 signalosome complex subunit 1;	-0.34	-0.16	0.76	4.50
P61201	COP9 signalosome complex subunit 2;	-1.22	-0.77	0.34	14.20
Q9UNS2	COP9 signalosome complex subunit 3;	-1.00	-0.22	0.29	10.20
Q9BT78	COP9 signalosome complex subunit 4;	-0.79	-0.29	0.45	13.80
Q92905	COP9 signalosome complex subunit 5;	-1.06	-0.18	0.25	8.70
Q7L5N1	COP9 signalosome complex subunit 6;	-0.92	-0.10	0.32	11.30
Q99627	COP9 signalosome complex subunit 8;	-0.76	-0.05	0.40	6.20
Q99829	Copine-1;	1.02	1.17	0.59	6.70
O75131	Copine-3;	-1.15	-0.49	0.28	6.30
Q9NTM9	Copper homeostasis protein cutC homolog;	0.63	0.09	0.49	12.10
P36551	Coproporphyrinogen-III oxidase, mitochondrial;	-3.47	-7.72	0.30	10.60
O75367	Core histone macro-H2A.1;	-0.89	-0.15	0.34	5.40
P31146	Coronin-1A;	0.06	0.01	0.95	3.70
Q9ULV4	Coronin-1C;	0.15	0.04	0.87	11.40
Q9P1F3	Costars family protein ABRACL;	-2.18	-0.50	0.02	16.00
P12277	Creatine kinase B-type;	3.22	6.74	0.31	36.70
P46109	Crk-like protein;	0.04	0.01	0.97	11.90
Q13616	Cullin-1;	-1.64	-0.46	0.09	2.30
Q13617	Cullin-2;	-0.58	-0.04	0.52	1.70
Q13619	Cullin-4A;	-0.36	-0.10	0.71	7.60
Q13620	Cullin-4B;	1.32	0.26	0.16	6.60
Q86VP6	Cullin-associated NEDD8-dissociated protein 1;	-0.40	-0.13	0.69	23.70
P24941	Cyclin-dependent kinase 2;	6.59	1.50	0.00	8.70
Q00534	Cyclin-dependent kinase 6;	0.08	0.06	0.95	7.40
P61024	Cyclin-dependent kinases regulatory subunit 1;	0.60	0.03	0.51	12.70
P33552	Cyclin-dependent kinases regulatory subunit 2;	-0.07	-0.01	0.94	12.70
Q8ND76	Cyclin-Y;	2.65	0.72	0.01	4.40
P04080	Cystatin-B;	0.83	0.09	0.36	40.80
P01034	Cystatin-C;	2.14	0.18	0.02	18.50
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1;	-0.92	-0.54	0.46	11.70
P49589	Cysteine--tRNA ligase, cytoplasmic;	-0.15	-0.03	0.88	8.40
Q9NZV1	Cysteine-rich motor neuron 1 protein;	-0.20	-0.06	0.83	4.40
Q9P0S2	Cytochrome c oxidase assembly protein COX16 homolog,	0.61	0.06	0.49	13.20
P14854	Cytochrome c oxidase subunit 6B1;	-1.94	-0.22	0.03	12.80
P21399	Cytoplasmic aconitate hydratase;	-1.52	-0.30	0.11	5.10
Q14204	Cytoplasmic dynein 1 heavy chain 1;	0.11	0.11	0.95	4.30
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1;	0.08	0.01	0.92	2.30
O43237	Cytoplasmic dynein 1 light intermediate chain 2;	0.42	0.04	0.64	3.00
Q7L576	Cytoplasmic FMR1-interacting protein 1;	-0.84	-0.49	0.50	3.60
Q14008	Cytoskeleton-associated protein 5;	-0.71	-0.22	0.47	3.90
P28838	Cytosol aminopeptidase;	-3.18	-2.90	0.04	10.20
O00154	Cytosolic acyl coenzyme A thioester hydrolase;	-0.64	-0.43	0.63	13.20

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Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q96KP4	Cytosolic non-specific dipeptidase;	-0.09	-0.06	0.95	21.30
P49902	Cytosolic purine 5'-nucleotidase;	-0.01	0.00	0.99	1.60
O43175	D-3-phosphoglycerate dehydrogenase;	-0.71	-0.09	0.43	5.10
P30046	D-dopachrome decarboxylase;	0.74	0.44	0.55	28.80
Q8N163	DBIRD complex subunit KIAA1967;	-2.06	-0.34	0.02	1.60
Q9UKG1	DCC-interacting protein 13-alpha;	-0.67	-0.12	0.48	2.40
Q9H773	dCTP pyrophosphatase 1;	-1.12	-0.73	0.38	11.20
P13716	Delta-aminolevulinic acid dehydratase;	0.21	0.02	0.81	5.80
O00115	Deoxyribonuclease-2-alpha;	0.71	0.15	0.45	12.20
O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidase;	-0.47	-0.05	0.60	9.80
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitoch	-0.27	-0.11	0.80	27.80
Q02487	Desmocollin-2;	-0.23	-0.01	0.80	2.20
Q14126	Desmoglein-2;	0.33	0.06	0.72	4.90
P60981	Destrin;	-0.97	-1.12	0.61	19.40
Q9Y295	Developmentally-regulated GTP-binding protein 1;	-0.60	-0.26	0.58	10.60
Q01459	Di-N-acetylchitobiase;	-1.25	-0.89	0.36	8.60
Q9NR28	Diablo homolog, mitochondrial;	-1.84	-0.79	0.10	10.00
O94907	Dickkopf-related protein 1;	2.06	0.92	0.06	34.60
Q9UBP4	Dickkopf-related protein 3;	2.06	0.16	0.02	6.30
P09622	Dihydrolipoyl dehydrogenase, mitochondrial;	-1.84	-4.33	0.60	9.60
P09417	Dihydropteridine reductase;	-1.69	-0.76	0.12	23.40
Q16555	Dihydropyrimidinase-related protein 2;	-1.32	-1.42	0.46	28.30
Q12882	Dihydropyrimidine dehydrogenase [NADP(+)];	0.20	0.04	0.83	2.10
P53634	Dipeptidyl peptidase 1;	1.85	0.49	0.06	17.30
Q9UHL4	Dipeptidyl peptidase 2;	1.73	0.33	0.06	15.70
Q9NY33	Dipeptidyl peptidase 3;	-0.81	-0.30	0.44	11.70
Q86TI2	Dipeptidyl peptidase 9;	0.79	0.24	0.42	2.50
O14672	Disintegrin and metalloproteinase domain-containing prot	0.86	0.29	0.40	7.90
Q13444	Disintegrin and metalloproteinase domain-containing prot	0.88	0.62	0.51	11.80
P78536	Disintegrin and metalloproteinase domain-containing prot	0.82	0.49	0.51	4.10
Q13443	Disintegrin and metalloproteinase domain-containing prot	0.12	0.08	0.92	3.10
Q16531	DNA damage-binding protein 1;	-0.92	-0.54	0.46	13.60
Q92466	DNA damage-binding protein 2;	-0.03	-0.01	0.97	4.40
O00273	DNA fragmentation factor subunit alpha;	-0.40	-0.32	0.78	16.30
P18858	DNA ligase 1;	-1.00	-2.72	0.80	3.00
P06746	DNA polymerase beta;	-0.49	-0.06	0.58	3.30
P18887	DNA repair protein XRCC1;	-1.09	-0.23	0.25	2.20
Q9BRT9	DNA replication complex GINS protein SLD5;	-0.47	-0.05	0.60	6.30
P49736	DNA replication licensing factor MCM2;	0.55	0.33	0.66	4.20
P25205	DNA replication licensing factor MCM3;	1.29	1.23	0.43	6.20
P33992	DNA replication licensing factor MCM5;	1.60	1.21	0.26	5.60
Q14566	DNA replication licensing factor MCM6;	0.84	0.53	0.50	10.50
P33993	DNA replication licensing factor MCM7;	1.45	0.23	0.11	1.40
P11387	DNA topoisomerase 1;	0.65	1.00	0.79	2.90
P27695	DNA-(apurinic or apyrimidinic site) lyase;	0.55	0.30	0.65	22.00
P78527	DNA-dependent protein kinase catalytic subunit;	1.44	1.28	0.36	1.30
P30876	DNA-directed RNA polymerase II subunit RPB2;	-0.12	-0.01	0.89	1.10
O15160	DNA-directed RNA polymerases I and III subunit RPAC1	0.64	0.12	0.49	3.80
P52434	DNA-directed RNA polymerases I, II, and III subunit RPA	0.24	0.03	0.80	10.70
P31689	DnaJ homolog subfamily A member 1;	0.51	0.05	0.57	3.30
O75937	DnaJ homolog subfamily C member 8;	0.00	0.00	1.00	9.90
O95793	Double-stranded RNA-binding protein Staufen homolog 1	-0.40	-0.30	0.78	4.70
P55265	Double-stranded RNA-specific adenosine deaminase;	-0.76	-0.67	0.63	7.10
Q16643	Drebrin;	3.15	0.54	0.00	3.10
P51452	Dual specificity protein phosphatase 3;	-0.43	-0.05	0.64	12.40
Q14203	Dynactin subunit 1;	0.69	0.05	0.44	0.90
Q13561	Dynactin subunit 2;	0.60	0.20	0.56	10.70

Table S1

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Q96FJ2	Dynein light chain 2, cytoplasmic;	-1.43	-1.55	0.42	57.30
Q9NP97	Dynein light chain roadblock-type 1;	-1.47	-1.52	0.40	51.00
Q8IZA0	Dyslexia-associated protein KIAA0319-like protein;	0.97	0.15	0.29	1.60
Q14118	Dystroglycan;	1.12	0.55	0.33	20.60
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1;	-0.76	-0.27	0.47	2.00
Q9UNE7	E3 ubiquitin-protein ligase CHIP;	-0.17	-0.08	0.88	8.90
Q99496	E3 ubiquitin-protein ligase RING2;	0.36	0.05	0.70	3.60
Q5T4S7	E3 ubiquitin-protein ligase UBR4;	-2.18	-3.57	0.38	0.70
Q14258	E3 ubiquitin/ISG15 ligase TRIM25;	-1.09	-1.30	0.57	15.60
Q15075	Early endosome antigen 1;	1.26	1.22	0.44	2.80
O95834	Echinoderm microtubule-associated protein-like 2;	-0.45	-0.12	0.64	7.20
Q9HC35	Echinoderm microtubule-associated protein-like 4;	-0.43	-0.36	0.77	3.40
Q96C19	EF-hand domain-containing protein D2;	1.04	0.41	0.33	15.40
O95967	EGF-containing fibulin-like extracellular matrix protein 2;	-1.84	-1.71	0.26	8.80
Q9H4M9	EH domain-containing protein 1;	-0.84	-0.81	0.61	12.40
Q9NZN4	EH domain-containing protein 2;	-0.12	-0.01	0.89	3.90
Q15717	ELAV-like protein 1;	-0.36	-0.10	0.71	23.60
P68104	Elongation factor 1-alpha 1;	-0.23	-0.06	0.81	20.10
Q05639	Elongation factor 1-alpha 2;	2.58	0.52	0.01	12.50
P24534	Elongation factor 1-beta;	0.15	0.03	0.87	24.40
P29692	Elongation factor 1-delta;	-0.76	-0.13	0.42	22.10
P26641	Elongation factor 1-gamma;	-0.40	-0.17	0.71	18.10
P13639	Elongation factor 2;	-0.45	-0.18	0.67	23.20
P50402	Emerin;	-0.67	-0.04	0.46	5.10
Q99961	Endophilin-A2;	0.42	0.04	0.64	2.30
Q9UKM7	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alph	1.62	0.42	0.09	4.70
P30040	Endoplasmic reticulum resident protein 29;	0.77	0.17	0.42	18.00
Q9BS26	Endoplasmic reticulum resident protein 44;	0.06	0.04	0.97	7.90
P14625	Endoplasmin;	1.52	0.84	0.20	16.40
Q9UNN8	Endothelial protein C receptor;	0.75	0.21	0.44	20.60
P84090	Enhancer of rudimentary homolog;	-1.29	-1.44	0.48	26.90
Q9UHY7	Enolase-phosphatase E1;	-0.56	-0.03	0.54	4.60
P42126	Enoyl-CoA delta isomerase 1, mitochondrial;	-1.12	-0.37	0.26	4.30
P30084	Enoyl-CoA hydratase, mitochondrial;	0.87	0.71	0.55	11.70
P20827	Ephrin-A1;	0.82	0.18	0.38	8.30
P52799	Ephrin-B2;	-0.64	-0.06	0.48	4.80
P42566	Epidermal growth factor receptor substrate 15;	0.55	0.23	0.61	1.50
P00533	Epidermal growth factor receptor;	-0.17	-0.08	0.88	7.40
Q9UHF1	Epidermal growth factor-like protein 7;	1.09	0.37	0.28	16.80
P61916	Epididymal secretory protein E1;	0.00	0.00	1.00	43.00
Q9Y2E5	Epididymis-specific alpha-mannosidase;	-0.29	-0.07	0.76	2.50
Q96HE7	ERO1-like protein alpha;	0.32	0.08	0.74	3.00
P60842	Eukaryotic initiation factor 4A-I;	1.26	0.34	0.20	24.40
Q14240	Eukaryotic initiation factor 4A-II;	0.07	0.03	0.95	22.10
P38919	Eukaryotic initiation factor 4A-III;	-0.45	-0.12	0.64	10.50
P15170	Eukaryotic peptide chain release factor GTP-binding subu	-0.47	-0.24	0.68	9.40
P62495	Eukaryotic peptide chain release factor subunit 1;	-0.69	-0.27	0.51	13.00
O14602	Eukaryotic translation initiation factor 1A, Y-chromosoma	-0.04	0.00	0.96	6.90
O60739	Eukaryotic translation initiation factor 1b;	0.21	0.01	0.81	14.20
P05198	Eukaryotic translation initiation factor 2 subunit 1;	-0.03	-0.02	0.98	20.30
P20042	Eukaryotic translation initiation factor 2 subunit 2;	-0.32	-1.59	0.97	5.70
P41091	Eukaryotic translation initiation factor 2 subunit 3;	-0.04	-0.02	0.96	17.40
Q9BY44	Eukaryotic translation initiation factor 2A;	-2.00	-2.24	0.29	7.00
Q14152	Eukaryotic translation initiation factor 3 subunit A;	-0.32	-0.10	0.75	5.40
P55884	Eukaryotic translation initiation factor 3 subunit B;	0.63	0.28	0.57	12.00
Q99613	Eukaryotic translation initiation factor 3 subunit C;	-1.06	-0.71	0.42	8.80
O15371	Eukaryotic translation initiation factor 3 subunit D;	-0.56	-0.30	0.64	4.20

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P60228	Eukaryotic translation initiation factor 3 subunit E;	-0.60	-0.27	0.58	8.80
O00303	Eukaryotic translation initiation factor 3 subunit F;	-0.97	-0.50	0.40	18.80
O75821	Eukaryotic translation initiation factor 3 subunit G;	0.37	0.03	0.69	2.80
O15372	Eukaryotic translation initiation factor 3 subunit H;	-0.34	-0.07	0.72	6.00
Q13347	Eukaryotic translation initiation factor 3 subunit I;	-0.17	-0.03	0.86	16.00
O75822	Eukaryotic translation initiation factor 3 subunit J;	0.04	0.00	0.97	3.10
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K;	-0.11	-0.01	0.91	11.50
Q9Y262	Eukaryotic translation initiation factor 3 subunit L;	-0.94	-0.69	0.50	9.60
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M;	-0.01	-0.01	0.99	16.00
Q04637	Eukaryotic translation initiation factor 4 gamma 1;	0.24	0.13	0.84	5.10
P23588	Eukaryotic translation initiation factor 4B;	-0.67	-0.53	0.65	7.40
P06730	Eukaryotic translation initiation factor 4E;	-0.64	-0.26	0.55	11.50
P63241	Eukaryotic translation initiation factor 5A-1;	-0.01	-0.01	0.99	19.00
O60841	Eukaryotic translation initiation factor 5B;	-0.81	-0.47	0.51	6.70
O00471	Exocyst complex component 5;	3.07	4.85	0.21	4.70
Q15024	Exosome complex component RRP42;	-0.01	0.00	0.99	7.90
Q9UBQ6	Exostosin-like 2;	0.59	0.47	0.69	11.80
P55060	Exportin-2;	-0.34	-0.27	0.82	9.50
O43592	Exportin-T;	-0.76	-0.68	0.63	3.70
Q16610	Extracellular matrix protein 1;	1.18	0.62	0.31	17.20
Q86XX4	Extracellular matrix protein FRAS1;	2.93	1.88	0.02	2.10
Q8IWU5	Extracellular sulfatase Sulf-2;	0.51	0.20	0.63	8.40
P08294	Extracellular superoxide dismutase [Cu-Zn];	-1.22	-0.11	0.18	5.40
P15311	Ezrin;	-1.00	-0.48	0.37	21.20
P52907	F-actin-capping protein subunit alpha-1;	-0.79	-0.45	0.52	40.90
P47755	F-actin-capping protein subunit alpha-2;	-0.97	-0.40	0.36	22.00
P47756	F-actin-capping protein subunit beta;	-0.60	-0.24	0.57	17.00
Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1;	-0.45	-0.12	0.64	7.40
Q9Y5B9	FACT complex subunit SPT16;	0.72	0.11	0.43	4.10
Q08945	FACT complex subunit SSRP1;	0.00	0.00	1.00	5.60
Q96AE4	Far upstream element-binding protein 1;	-1.12	-1.22	0.53	16.00
Q92945	Far upstream element-binding protein 2;	-1.06	-0.60	0.38	12.10
P14324	Farnesyl pyrophosphate synthase;	-0.29	-0.32	0.88	16.90
Q9UNN5	FAS-associated factor 1;	-0.01	0.00	0.99	1.70
Q16658	Fascin;	1.14	0.11	0.21	5.70
P49327	Fatty acid synthase;	0.48	0.21	0.67	22.50
Q01469	Fatty acid-binding protein, epidermal;	-1.25	-1.13	0.43	57.80
P05413	Fatty acid-binding protein, heart;	-1.00	-0.16	0.27	10.50
Q96AC1	Fermitin family homolog 2;	-0.07	-0.07	0.97	9.90
P02794	Ferritin heavy chain;	-1.52	-0.95	0.24	18.60
P02792	Ferritin light chain;	-0.38	-0.05	0.68	17.10
Q8N441	Fibroblast growth factor receptor-like 1;	1.16	0.33	0.24	5.00
Q14512	Fibroblast growth factor-binding protein 1;	0.18	0.07	0.87	28.20
P02751	Fibronectin;	0.28	0.17	0.82	1.50
Q9UBX5	Fibulin-5;	-0.27	-0.01	0.76	7.40
P21333	Filamin-A;	0.37	0.21	0.76	23.30
O75369	Filamin-B;	0.24	0.15	0.85	28.20
Q14315	Filamin-C;	0.26	0.12	0.81	15.80
P30043	Flavin reductase (NADPH);	0.48	0.06	0.60	4.90
O95633	Follistatin-related protein 3;	-0.18	-0.16	0.90	8.70
Q86VR8	Four-jointed box protein 1;	1.29	0.16	0.16	5.30
P51114	Fragile X mental retardation syndrome-related protein 1;	-0.04	-0.03	0.97	3.40
Q16595	Frataxin, mitochondrial;	0.40	0.07	0.66	8.10
P04075	Fructose-bisphosphate aldolase A;	-0.97	-0.59	0.44	45.30
P09972	Fructose-bisphosphate aldolase C;	-1.29	-2.01	0.60	33.20
P07954	Fumarate hydratase, mitochondrial;	0.90	0.45	0.43	9.40
P16930	Fumarylacetoacetase;	-0.58	-0.36	0.65	7.60

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein	-0.54	-0.33	0.67	14.00
P09382	Galectin-1;	-0.94	-0.38	0.38	51.10
Q08380	Galectin-3-binding protein;	1.80	0.90	0.12	30.60
P17931	Galectin-3;	-0.04	0.00	0.96	22.80
P09104	Gamma-enolase;	-1.25	-0.66	0.29	6.50
Q92820	Gamma-glutamyl hydrolase;	0.69	0.17	0.48	24.20
O75223	Gamma-glutamylcyclotransferase;	0.18	0.04	0.86	16.50
P13284	Gamma-interferon-inducible lysosomal thiol reductase;	-0.81	-1.48	0.77	5.20
P17900	Ganglioside GM2 activator;	-0.54	-0.61	0.78	14.00
Q9H488	GDP-fucose protein O-fucosyltransferase 1;	0.82	0.08	0.36	4.10
O60547	GDP-mannose 4,6 dehydratase;	-1.69	-0.27	0.07	5.40
P06396	Gelsolin;	0.56	0.21	0.59	13.90
Q8TEQ6	Gem-associated protein 5;	0.55	0.57	0.75	2.50
P78347	General transcription factor II-I;	0.60	0.37	0.63	3.60
P35269	General transcription factor IIF subunit 1;	-0.56	-0.07	0.54	2.30
P13984	General transcription factor IIF subunit 2;	-0.23	-0.02	0.80	11.20
Q9NQX3	Gephyrin;	3.04	0.18	0.00	1.40
P60983	Glia maturation factor beta;	-0.09	-0.04	0.94	13.40
P07093	Glia-derived nexin;	0.91	0.35	0.39	15.80
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase;	-0.92	-0.54	0.46	17.90
P46926	Glucosamine-6-phosphate isomerase 1;	-0.69	-0.46	0.60	24.60
P11413	Glucose-6-phosphate 1-dehydrogenase;	-0.97	-0.51	0.41	10.50
P06744	Glucose-6-phosphate isomerase;	-0.07	-0.03	0.95	24.90
P14314	Glucosidase 2 subunit beta;	-5.64	0.00	0.00	2.30
P04062	Glucosylceramidase;	0.75	0.27	0.47	14.00
P00367	Glutamate dehydrogenase 1, mitochondrial;	0.65	0.07	0.47	7.20
P48506	Glutamate--cysteine ligase catalytic subunit;	-0.92	-0.07	0.31	1.30
P48507	Glutamate--cysteine ligase regulatory subunit;	-0.81	-0.36	0.46	10.90
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isome	-0.34	-0.19	0.78	4.60
P47897	Glutamine--tRNA ligase;	-1.12	-1.05	0.49	12.60
O76003	Glutaredoxin-3;	0.14	0.08	0.91	14.60
Q86SX6	Glutaredoxin-related protein 5, mitochondrial;	0.53	0.05	0.56	7.00
P00390	Glutathione reductase, mitochondrial;	0.77	0.16	0.41	2.90
Q9Y2Q3	Glutathione S-transferase kappa 1;	-0.04	-0.01	0.96	4.90
P78417	Glutathione S-transferase omega-1;	0.37	0.09	0.70	26.60
P09211	Glutathione S-transferase P;	-1.15	-1.36	0.55	45.70
P48637	Glutathione synthetase;	-1.15	-1.33	0.54	14.30
P04406	Glyceraldehyde-3-phosphate dehydrogenase;	-0.92	-0.50	0.44	34.00
P41250	Glycine--tRNA ligase;	-0.15	-0.11	0.91	11.00
P11216	Glycogen phosphorylase, brain form;	-2.18	-1.99	0.17	28.40
P06737	Glycogen phosphorylase, liver form;	-0.20	-0.09	0.85	29.20
P46976	Glycogenin-1;	-0.56	-0.24	0.61	12.90
P30419	Glycylpeptide N-tetradecanoyltransferase 1;	-0.43	-0.02	0.63	2.20
Q9HC38	Glyoxalase domain-containing protein 4;	-0.32	-0.04	0.73	17.30
P35052	Glypican-1;	1.22	1.00	0.41	30.30
P49915	GMP synthase [glutamine-hydrolyzing];	0.30	0.08	0.76	11.10
Q8NBJ4	Golgi membrane protein 1;	0.31	0.08	0.75	9.50
O95249	Golgi SNAP receptor complex member 1;	1.30	0.16	0.15	4.80
P28799	Granulins;	0.61	0.29	0.58	16.90
Q8NCC3	Group XV phospholipase A2;	0.82	0.19	0.39	13.60
P62993	Growth factor receptor-bound protein 2;	-0.76	-0.59	0.60	20.70
P09341	Growth-regulated alpha protein;	0.75	0.25	0.46	37.40
Q99988	Growth/differentiation factor 15;	1.55	1.03	0.24	9.10
Q9HAV7	GrpE protein homolog 1, mitochondrial;	-2.25	-0.54	0.02	5.10
P62826	GTP-binding nuclear protein Ran;	-0.12	-0.02	0.89	31.00
Q9Y2T3	Guanine deaminase;	-0.71	-0.28	0.49	38.30
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subun	0.11	0.06	0.93	10.00

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P38405	Guanine nucleotide-binding protein G(olf) subunit alpha;	1.59	0.20	0.08	3.10
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;	0.04	0.01	0.97	27.80
O60832	H/ACA ribonucleoprotein complex subunit 4;	-1.15	-1.05	0.47	7.80
Q9H0R4	Haloacid dehalogenase-like hydrolase domain-containing	-1.32	-0.20	0.15	8.10
P48723	Heat shock 70 kDa protein 13;	2.07	0.81	0.05	10.40
P08107	Heat shock 70 kDa protein 1A/1B;	-0.45	-0.17	0.66	27.30
P34932	Heat shock 70 kDa protein 4;	-1.00	-0.90	0.52	22.90
P11142	Heat shock cognate 71 kDa protein;	-0.71	-0.26	0.49	41.30
Q92598	Heat shock protein 105 kDa;	0.40	0.16	0.70	10.30
Q12931	Heat shock protein 75 kDa, mitochondrial;	0.48	0.05	0.60	1.30
P04792	Heat shock protein beta-1;	0.45	0.11	0.63	20.00
P07900	Heat shock protein HSP 90-alpha;	-0.54	-0.20	0.61	40.60
P08238	Heat shock protein HSP 90-beta;	0.07	0.03	0.94	32.90
P54652	Heat shock-related 70 kDa protein 2;	2.98	0.34	0.00	14.70
Q9NRV9	Heme-binding protein 1;	0.25	0.07	0.80	8.50
P69905	Hemoglobin subunit alpha;	0.31	0.03	0.73	21.80
P02042	Hemoglobin subunit delta;	0.25	0.07	0.80	12.90
P08581	Hepatocyte growth factor receptor;	2.71	0.32	0.00	0.90
O14964	Hepatocyte growth factor-regulated tyrosine kinase substr	-0.45	-0.18	0.67	3.00
Q7Z4V5	Hepatoma-derived growth factor-related protein 2;	-0.12	-0.05	0.91	5.40
P51858	Hepatoma-derived growth factor;	-0.34	-0.18	0.77	17.90
Q99729	Heterogeneous nuclear ribonucleoprotein A/B;	-0.18	-0.04	0.85	11.70
Q13151	Heterogeneous nuclear ribonucleoprotein A0;	0.28	0.05	0.77	11.50
P09651	Heterogeneous nuclear ribonucleoprotein A1;	-0.11	-0.01	0.91	13.20
O60812	Heterogeneous nuclear ribonucleoprotein C-like 1;	0.81	0.04	0.37	12.60
O14979	Heterogeneous nuclear ribonucleoprotein D-like;	0.14	0.03	0.88	10.00
Q14103	Heterogeneous nuclear ribonucleoprotein D0;	-0.38	-0.08	0.69	19.20
P52597	Heterogeneous nuclear ribonucleoprotein F;	-0.45	-0.35	0.75	22.20
P31943	Heterogeneous nuclear ribonucleoprotein H;	0.37	0.23	0.78	20.30
P31942	Heterogeneous nuclear ribonucleoprotein H3;	0.77	0.09	0.40	8.40
P61978	Heterogeneous nuclear ribonucleoprotein K;	0.49	0.31	0.71	29.20
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like;	1.12	0.13	0.22	3.00
P52272	Heterogeneous nuclear ribonucleoprotein M;	0.61	0.25	0.56	9.00
O60506	Heterogeneous nuclear ribonucleoprotein Q;	0.18	0.14	0.90	28.30
O43390	Heterogeneous nuclear ribonucleoprotein R;	-0.64	-0.36	0.60	21.20
Q00839	Heterogeneous nuclear ribonucleoprotein U;	0.14	0.04	0.89	4.50
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1;	0.38	0.08	0.69	17.00
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2;	0.37	0.03	0.69	15.70
P09429	High mobility group protein B1;	-1.15	-0.38	0.25	17.70
P26583	High mobility group protein B2;	-0.97	-0.11	0.28	23.40
P37235	Hippocalcin-like protein 1;	-0.67	-0.28	0.54	19.70
P49773	Histidine triad nucleotide-binding protein 1;	-0.36	-0.19	0.76	29.40
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	-0.03	-0.01	0.97	21.50
P12081	Histidine--tRNA ligase, cytoplasmic;	0.20	0.03	0.83	13.00
Q92769	Histone deacetylase 2;	0.25	0.10	0.81	6.40
P10412	Histone H1.4;	-0.29	-0.13	0.80	15.00
Q92522	Histone H1x;	-2.00	-0.40	0.03	7.00
P04908	Histone H2A type 1-B/E;	-1.60	-0.24	0.08	21.70
P0C0S5	Histone H2A.Z;	-0.64	-0.03	0.48	14.80
O60814	Histone H2B type 1-K;	-1.84	-1.31	0.18	26.20
P68431	Histone H3.1;	-0.54	-0.20	0.61	11.90
P62805	Histone H4;	-2.18	-0.70	0.03	33.00
Q86X55	Histone-arginine methyltransferase CARM1;	0.11	0.06	0.93	4.40
Q09028	Histone-binding protein RBBP4;	-0.69	-0.36	0.55	17.40
P01892	HLA class I histocompatibility antigen, A-2 alpha chain;	0.87	0.57	0.50	26.60
P10314	HLA class I histocompatibility antigen, A-32 alpha chain;	0.19	0.01	0.83	20.00
P10321	HLA class I histocompatibility antigen, Cw-7 alpha chain;	1.70	0.12	0.06	29.50

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P51610	Host cell factor 1;	0.42	0.07	0.65	2.10
P50502	Hsc70-interacting protein;	-0.29	-0.10	0.78	20.90
Q16543	Hsp90 co-chaperone Cdc37;	-0.84	-0.43	0.47	13.50
Q96S86	Hyaluronan and proteoglycan link protein 3;	2.94	0.15	0.00	2.80
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial;	-1.32	-0.20	0.15	13.30
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	4.32	0.32	0.00	4.20
P00492	Hypoxanthine-guanine phosphoribosyltransferase;	-0.03	-0.01	0.98	45.00
Q9Y4L1	Hypoxia up-regulated protein 1;	0.37	0.18	0.75	2.50
Q8WZA9	Immunity-related GTPase family Q protein;	0.14	0.03	0.88	2.20
Q969P0	Immunoglobulin superfamily member 8;	-0.89	-0.36	0.41	5.70
O00505	Importin subunit alpha-3;	-0.12	-0.02	0.89	2.50
O00629	Importin subunit alpha-4;	-0.47	-0.07	0.60	5.20
Q14974	Importin subunit beta-1;	-0.18	-0.13	0.89	20.80
O00410	Importin-5;	-0.49	-0.38	0.72	23.30
O95373	Importin-7;	-0.49	-0.18	0.63	8.20
Q96P70	Importin-9;	-0.40	-0.32	0.78	3.70
Q13308	Inactive tyrosine-protein kinase 7;	-0.23	-0.03	0.80	8.40
Q15181	Inorganic pyrophosphatase;	-0.18	-0.18	0.91	32.90
Q9BY32	Inosine triphosphate pyrophosphatase;	-1.32	-0.13	0.14	8.80
P12268	Inosine-5'-monophosphate dehydrogenase 2;	0.98	0.46	0.38	10.70
P29218	Inositol monophosphatase 1;	-0.27	-0.03	0.77	3.60
Q9NPH2	Inositol-3-phosphate synthase 1;	0.32	0.09	0.74	7.90
P14735	Insulin-degrading enzyme;	-0.40	-0.04	0.65	4.70
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2;	-0.32	-0.04	0.73	2.00
P01344	Insulin-like growth factor II;	1.04	0.06	0.25	5.00
P18065	Insulin-like growth factor-binding protein 2;	1.54	0.51	0.13	26.20
P17936	Insulin-like growth factor-binding protein 3;	3.73	1.11	0.00	23.40
P24592	Insulin-like growth factor-binding protein 6;	2.71	2.21	0.07	11.70
P26006	Integrin alpha-3;	1.15	3.00	0.77	2.10
P23229	Integrin alpha-6;	0.99	0.20	0.30	1.00
P05556	Integrin beta-1;	-0.60	-0.44	0.66	4.60
P16144	Integrin beta-4;	-0.12	-0.07	0.92	9.00
O95965	Integrin beta-like protein 1;	-1.22	-1.33	0.50	14.00
Q9H0C8	Integrin-linked kinase-associated serine/threonine phospha	0.28	0.03	0.76	3.10
P05362	Intercellular adhesion molecule 1;	-0.54	-0.08	0.56	5.30
P80217	Interferon-induced 35 kDa protein;	-0.60	-0.34	0.62	7.30
Q12905	Interleukin enhancer-binding factor 2;	-0.29	-0.06	0.76	25.40
Q12906	Interleukin enhancer-binding factor 3;	-0.64	-0.51	0.66	18.80
P03956	Interstitial collagenase;	-0.76	-1.08	0.73	11.90
Q96CN7	Isochorismatase domain-containing protein 1;	0.53	0.22	0.63	4.70
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic;	-0.94	-0.85	0.55	33.80
P41252	Isoleucine--tRNA ligase, cytoplasmic;	-0.17	-0.10	0.90	8.30
P05783	Keratin, type I cytoskeletal 18;	0.24	0.09	0.82	28.60
P08727	Keratin, type I cytoskeletal 19;	3.77	3.78	0.03	15.80
P04264	Keratin, type II cytoskeletal 1;	1.64	0.14	0.07	1.40
P19013	Keratin, type II cytoskeletal 4;	-2.74	-4.38	0.26	3.90
P05787	Keratin, type II cytoskeletal 8;	0.50	0.47	0.76	38.70
Q07666	KH domain-containing, RNA-binding, signal transduction	-0.17	-0.10	0.89	6.10
Q86UP2	Kinectin;	-0.17	-0.09	0.89	5.30
Q07866	Kinesin light chain 1;	1.54	1.46	0.34	4.70
P33176	Kinesin-1 heavy chain;	-0.04	-0.03	0.97	5.70
Q6YP21	Kynurenine--oxoglutarate transaminase 3;	-1.64	-1.03	0.19	10.80
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopar	-0.11	-0.01	0.91	2.90
P00338	L-lactate dehydrogenase A chain;	-1.00	-0.32	0.32	23.80
Q71RC2	La-related protein 4;	2.28	0.36	0.01	1.40
Q9NPC4	Lactosylceramide 4-alpha-galactosyltransferase;	0.66	0.15	0.49	6.80
P20700	Lamin-B1;	-0.11	-0.06	0.93	11.10

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q03252	Lamin-B2;	-0.54	-0.12	0.58	5.70
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;	-0.29	-0.16	0.81	11.90
O15230	Laminin subunit alpha-5;	1.50	1.55	0.39	17.20
P07942	Laminin subunit beta-1;	2.32	1.78	0.10	9.80
P55268	Laminin subunit beta-2;	2.53	1.87	0.07	6.80
P11047	Laminin subunit gamma-1;	1.16	1.92	0.65	18.10
Q13753	Laminin subunit gamma-2;	1.84	0.78	0.09	4.40
O43813	LanC-like protein 1;	-1.94	-0.22	0.03	3.30
Q9NS86	LanC-like protein 2;	-1.32	-0.53	0.21	9.60
Q9NS15	Latent-transforming growth factor beta-binding protein 3;	1.61	0.82	0.16	6.00
Q8N2S1	Latent-transforming growth factor beta-binding protein 4;	-0.15	-0.11	0.91	7.60
Q14696	LDLR chaperone MESD;	-0.29	-0.01	0.75	4.30
Q99538	Legumain;	1.21	0.59	0.28	15.20
Q9UIC8	Leucine carboxyl methyltransferase 1;	-0.20	-0.03	0.82	2.40
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	0.14	0.05	0.89	2.40
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1;	-0.17	-0.08	0.88	2.50
Q8N6Y2	Leucine-rich repeat-containing protein 17;	-0.43	-0.36	0.77	6.30
Q8N1G4	Leucine-rich repeat-containing protein 47;	-0.40	-0.17	0.71	12.50
Q96AG4	Leucine-rich repeat-containing protein 59;	-0.58	-0.23	0.59	19.90
P30740	Leukocyte elastase inhibitor;	-0.54	-0.05	0.56	3.20
P09960	Leukotriene A-4 hydrolase;	-0.01	-0.01	0.99	37.80
Q9UPQ0	LIM and calponin homology domains-containing protein 1	0.75	0.08	0.41	1.60
P24666	Low molecular weight phosphotyrosine protein phosphata	-0.36	-0.03	0.69	7.00
P01130	Low-density lipoprotein receptor;	-0.58	-0.21	0.57	4.70
P05455	Lupus La protein;	0.03	0.01	0.98	16.40
P46736	Lys-63-specific deubiquitinase BRCC36;	-1.69	-1.53	0.29	7.60
Q15046	Lysine--tRNA ligase;	-0.04	-0.01	0.96	6.40
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase;	2.43	0.29	0.01	6.30
P11117	Lysosomal acid phosphatase;	-2.40	-0.38	0.01	3.30
P10253	Lysosomal alpha-glucosidase;	0.73	0.13	0.43	10.00
O00754	Lysosomal alpha-mannosidase;	1.32	0.75	0.27	5.50
P42785	Lysosomal Pro-X carboxypeptidase;	0.90	0.57	0.49	14.50
P10619	Lysosomal protective protein;	0.45	0.32	0.73	16.70
Q9UMR5	Lysosomal thioesterase PPT2;	1.60	0.17	0.08	13.60
P11279	Lysosome-associated membrane glycoprotein 1;	4.04	0.27	0.00	2.20
Q9Y4K0	Lysyl oxidase homolog 2;	0.31	0.15	0.79	9.20
Q96JB6	Lysyl oxidase homolog 4;	-0.49	-0.15	0.62	14.60
Q96C86	m7GpppX diphosphatase;	-0.69	-0.17	0.47	14.50
P09603	Macrophage colony-stimulating factor 1;	0.99	0.12	0.27	2.90
P40121	Macrophage-capping protein;	0.28	0.06	0.77	11.80
Q14764	Major vault protein;	-1.06	-0.79	0.45	2.70
P40925	Malate dehydrogenase, cytoplasmic;	-0.69	-0.37	0.56	20.70
P40926	Malate dehydrogenase, mitochondrial;	-0.69	-0.35	0.55	37.60
Q9ULC4	Malignant T-cell-amplified sequence 1;	-1.32	-0.40	0.18	25.40
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA;	-2.64	-0.50	0.00	2.10
O60476	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB;	0.26	0.17	0.84	4.70
P43243	Matrin-3;	-0.03	-0.02	0.98	8.50
Q99542	Matrix metalloproteinase-19;	2.02	0.63	0.04	4.50
Q5JRA6	Melanoma inhibitory activity protein 3;	1.92	0.41	0.04	0.60
P08582	Melanotransferrin;	1.32	0.29	0.16	1.60
P15529	Membrane cofactor protein;	0.37	0.24	0.78	3.80
Q13421	Mesothelin;	1.43	0.46	0.15	33.20
P01033	Metalloproteinase inhibitor 1;	1.07	0.87	0.47	36.70
P16035	Metalloproteinase inhibitor 2;	0.86	0.29	0.40	17.30
Q13330	Metastasis-associated protein MTA1;	0.50	0.11	0.60	3.50
O94776	Metastasis-associated protein MTA2;	-0.81	-0.17	0.39	5.80
Q9UJH8	Meteorin;	0.82	0.12	0.37	4.80

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9NZL9	Methionine adenosyltransferase 2 subunit beta;	-0.49	-0.23	0.65	10.50
P16455	Methylated-DNA--protein-cysteine methyltransferase;	-1.00	-0.52	0.39	15.50
Q13361	Microfibrillar-associated protein 5;	-1.47	-0.16	0.10	6.90
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5;	-0.49	-0.22	0.65	0.90
Q96PK2	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5;	0.18	0.03	0.85	1.00
P27816	Microtubule-associated protein 4;	-0.49	-0.36	0.71	7.50
Q15691	Microtubule-associated protein RP/EB family member 1;	-0.03	-0.01	0.98	14.20
P21741	Midkine;	0.26	0.12	0.81	21.70
Q7Z434	Mitochondrial antiviral-signaling protein;	-0.27	-0.07	0.78	2.20
Q16891	Mitochondrial inner membrane protein;	0.53	0.54	0.76	7.00
Q9UJ68	Mitochondrial peptide methionine sulfoxide reductase;	0.81	0.11	0.38	6.40
Q10713	Mitochondrial-processing peptidase subunit alpha;	-1.74	-0.17	0.05	2.10
P28482	Mitogen-activated protein kinase 1;	-0.71	-0.48	0.59	18.90
Q16539	Mitogen-activated protein kinase 14;	0.55	0.23	0.61	7.80
P45983	Mitogen-activated protein kinase 8;	-0.79	-0.16	0.41	2.40
O43684	Mitotic checkpoint protein BUB3;	-0.36	-0.03	0.69	8.20
Q7L9L4	MOB kinase activator 1B;	-0.47	-0.15	0.63	16.20
Q9Y3A3	MOB-like protein phocein;	-0.84	-0.08	0.35	6.20
P26038	Moesin;	2.37	1.79	0.09	16.80
P53985	Monocarboxylate transporter 1;	0.72	0.06	0.42	2.40
Q9H7C9	Mth938 domain-containing protein;	-3.06	-0.77	0.00	13.10
P98088	Mucin-5AC;	-3.18	-7.53	0.36	1.20
P22234	Multifunctional protein ADE2;	0.86	0.50	0.49	22.80
Q9UNW1	Multiple inositol polyphosphate phosphatase 1;	2.36	1.52	0.07	12.10
Q9NZM1	Myoferlin;	-0.47	-0.09	0.61	1.80
P12829	Myosin light chain 4;	7.42	1.01	0.00	6.60
P60660	Myosin light polypeptide 6;	-0.23	-0.05	0.81	37.70
Q6WCQ1	Myosin phosphatase Rho-interacting protein;	-1.47	-0.70	0.19	2.20
O14950	Myosin regulatory light chain 12B;	0.06	0.01	0.95	23.40
P35579	Myosin-9;	-0.43	-0.33	0.76	12.20
P58546	Myotrophin;	-0.18	-0.02	0.84	20.30
P29966	Myristoylated alanine-rich C-kinase substrate;	-6.64	0.00	0.00	5.70
P34059	N-acetylgalactosamine-6-sulfatase;	0.92	0.93	0.59	8.80
Q86SF2	N-acetylgalactosaminyltransferase 7;	3.79	0.22	0.00	1.70
Q9UJJ9	N-acetylglucosamine-1-phosphotransferase subunit gamm	1.54	0.38	0.11	17.70
P15586	N-acetylglucosamine-6-sulfatase;	0.25	0.12	0.83	13.80
O43505	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltrans	0.50	0.29	0.68	14.70
P41227	N-alpha-acetyltransferase 10;	0.31	0.08	0.75	19.60
P61599	N-alpha-acetyltransferase 20;	0.53	0.04	0.56	8.40
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit;	0.49	0.39	0.74	7.20
O95777	N-alpha-acetyltransferase 38, NatC auxiliary subunit;	-0.54	-0.16	0.60	36.50
Q9GZZ1	N-alpha-acetyltransferase 50;	0.64	0.10	0.48	12.40
Q13287	N-myc-interactor;	-0.92	-0.43	0.42	9.80
P20933	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	1.13	0.58	0.33	6.40
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	-0.04	-0.01	0.96	14.00
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	1.43	0.15	0.11	10.50
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	-0.29	-0.07	0.76	21.20
P15559	NAD(P)H dehydrogenase [quinone] 1;	-0.17	-0.05	0.86	8.40
Q8NCW5	NAD(P)H-hydrate epimerase;	-0.69	-0.05	0.44	14.20
O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4,	-1.15	-0.15	0.20	8.60
P48163	NADP-dependent malic enzyme;	-0.71	-0.25	0.48	9.80
O43847	Nardilysin;	0.03	0.02	0.99	4.60
Q13765	Nascent polypeptide-associated complex subunit alpha;	-0.49	-0.29	0.68	25.60
Q9Y2A7	Nck-associated protein 1;	-0.84	-0.45	0.47	2.70
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit;	-0.17	-0.05	0.87	3.90
Q13564	NEDD8-activating enzyme E1 regulatory subunit;	-0.84	-0.12	0.36	6.40
P61081	NEDD8-conjugating enzyme Ubc12;	-2.06	-1.03	0.07	31.10

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q8WX92	Negative elongation factor B;	-1.06	-0.18	0.25	2.10
Q92859	Neogenin;	-2.74	-3.83	0.22	2.10
Q9UMX5	Neudesin;	0.88	0.50	0.47	37.20
P32004	Neural cell adhesion molecule L1;	2.18	1.04	0.05	7.00
Q09666	Neuroblast differentiation-associated protein AHNAK;	1.13	0.83	0.41	8.40
Q9BYT8	Neurolysin, mitochondrial;	-0.34	-0.13	0.75	5.30
O14786	Neuropilin-1;	-0.56	-0.05	0.54	1.40
O15240	Neurosecretory protein VGF;	0.04	0.01	0.97	9.30
Q14697	Neutral alpha-glucosidase AB;	0.71	0.22	0.48	2.40
Q15758	Neutral amino acid transporter B(0);	0.86	0.18	0.37	3.90
P55769	NHP2-like protein 1;	0.06	0.00	0.95	8.60
Q96TA1	Niban-like protein 1;	-0.60	-0.26	0.58	5.60
P43490	Nicotinamide phosphoribosyltransferase;	-0.69	-0.21	0.49	26.30
Q6XQN6	Nicotinate phosphoribosyltransferase;	0.32	0.05	0.73	3.30
Q9GZT8	NIF3-like protein 1;	-0.47	-0.05	0.60	2.70
Q9Y2I1	Nischarin;	-0.81	-0.13	0.38	0.80
Q9Y314	Nitric oxide synthase-interacting protein;	1.43	0.16	0.12	3.70
Q86X76	Nitrilase homolog 1;	-0.17	-0.01	0.85	4.60
Q9BZM5	NKG2D ligand 2;	0.74	0.10	0.42	14.20
Q9UNZ2	NSFL1 cofactor p47;	-1.09	-1.44	0.60	20.30
P49321	Nuclear autoantigenic sperm protein;	-0.09	-0.02	0.93	6.50
Q09161	Nuclear cap-binding protein subunit 1;	-1.06	-0.95	0.50	5.10
Q00653	Nuclear factor NF-kappa-B p100 subunit;	1.95	0.44	0.04	1.30
Q9Y266	Nuclear migration protein nudC;	-0.79	-0.39	0.49	13.90
Q14980	Nuclear mitotic apparatus protein 1;	-0.76	-0.65	0.62	4.30
Q9UKX7	Nuclear pore complex protein Nup50;	-1.64	-0.15	0.07	3.20
Q9UHY1	Nuclear receptor-binding protein;	0.92	0.11	0.31	2.60
P61970	Nuclear transport factor 2;	-1.25	-0.89	0.36	29.10
P67809	Nuclease-sensitive element-binding protein 1;	0.43	0.07	0.64	17.00
Q02818	Nucleobindin-1;	1.33	0.26	0.16	31.70
Q14978	Nucleolar and coiled-body phosphoprotein 1;	-2.40	-1.39	0.05	2.40
O00567	Nucleolar protein 56;	0.11	0.04	0.92	3.90
Q9NR30	Nucleolar RNA helicase 2;	1.50	0.85	0.22	12.10
P19338	Nucleolin;	0.14	0.06	0.90	21.40
Q01085	Nucleolysin TIAR;	-0.64	-0.10	0.49	4.80
P06748	Nucleophosmin;	-0.32	-0.06	0.74	23.50
P12270	Nucleoprotein TPR;	-0.09	-0.03	0.93	1.40
P15531	Nucleoside diphosphate kinase A;	0.64	0.13	0.50	57.20
P0C025	Nucleoside diphosphate-linked moiety X motif 17;	-2.00	-0.72	0.05	7.60
P55209	Nucleosome assembly protein 1-like 1;	0.43	0.24	0.72	14.30
Q99733	Nucleosome assembly protein 1-like 4;	-0.40	-0.12	0.68	7.20
Q9NTK5	Obg-like ATPase 1;	-0.38	-0.26	0.77	18.70
Q8NH19	Olfactory receptor 10AG1;	-0.17	-0.03	0.86	3.00
Q9NQR4	Omega-amidase NIT2;	-0.18	-0.01	0.84	4.00
Q99650	Oncostatin-M-specific receptor subunit beta;	2.13	0.66	0.03	2.10
Q92882	Osteoclast-stimulating factor 1;	-2.74	-0.18	0.00	18.20
Q86UD1	Out at first protein homolog;	1.04	0.64	0.41	8.40
Q9BXW6	Oxysterol-binding protein-related protein 1;	-1.06	-0.18	0.25	1.40
Q9NWT1	p21-activated protein kinase-interacting protein 1;	-1.74	-0.17	0.05	2.80
P50897	Palmitoyl-protein thioesterase 1;	0.77	0.47	0.54	29.70
P20962	Parathymosin;	-0.38	-0.04	0.67	10.80
P49023	Paxillin;	-1.69	-1.42	0.26	3.90
O75475	PC4 and SFRS1-interacting protein;	-0.79	-0.87	0.67	7.40
Q5JVF3	PCI domain-containing protein 2;	1.91	0.24	0.04	4.00
Q96JY6	PDZ and LIM domain protein 2;	1.07	0.15	0.24	2.80
Q96HC4	PDZ and LIM domain protein 5;	-0.56	-0.82	0.81	8.10
Q9NR12	PDZ and LIM domain protein 7;	-0.92	-0.62	0.49	4.80

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P26022	Pentraxin-related protein PTX3;	3.52	2.42	0.01	21.00
Q8IYS1	Peptidase M20 domain-containing protein 2;	3.00	0.32	0.00	3.00
P19021	Peptidyl-glycine alpha-amidating monooxygenase;	-0.04	-0.02	0.96	13.40
P62937	Peptidyl-prolyl cis-trans isomerase A;	-1.32	-1.42	0.46	46.70
P23284	Peptidyl-prolyl cis-trans isomerase B;	-0.17	-0.09	0.89	31.50
Q08752	Peptidyl-prolyl cis-trans isomerase D;	0.08	0.01	0.92	2.40
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A;	-0.49	-0.04	0.58	27.80
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3;	1.04	0.26	0.28	14.70
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;	-0.60	-0.63	0.73	27.50
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1;	-0.01	0.00	0.99	15.10
Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containir	-0.12	-0.04	0.90	1.50
O60664	Perilipin-3;	-0.79	-0.61	0.58	12.20
O14936	Peripheral plasma membrane protein CASK;	-1.64	-0.31	0.08	2.80
Q06830	Peroxiredoxin-1;	-0.29	-0.07	0.76	41.20
P32119	Peroxiredoxin-2;	-1.47	-0.21	0.11	31.80
Q13162	Peroxiredoxin-4;	0.37	0.09	0.70	15.50
P30044	Peroxiredoxin-5, mitochondrial;	-0.09	-0.01	0.92	23.80
P30041	Peroxiredoxin-6;	-0.18	-0.19	0.92	34.80
Q8WW12	PEST proteolytic signal-containing nuclear protein;	0.78	0.16	0.41	22.50
Q9Y285	Phenylalanine--tRNA ligase alpha subunit;	0.08	0.01	0.92	2.60
Q9NSD9	Phenylalanine--tRNA ligase beta subunit;	0.07	0.02	0.94	16.00
P30086	Phosphatidylethanolamine-binding protein 1;	-0.60	-0.15	0.53	51.90
Q00169	Phosphatidylinositol transfer protein alpha isoform;	0.38	0.05	0.68	7.80
P48739	Phosphatidylinositol transfer protein beta isoform;	-0.07	-0.01	0.94	13.70
Q13492	Phosphatidylinositol-binding clathrin assembly protein;	-0.45	-0.05	0.62	2.30
P36871	Phosphoglucomutase-1;	-3.32	-2.33	0.02	8.90
Q96G03	Phosphoglucomutase-2;	-2.25	-2.25	0.19	6.00
P00558	Phosphoglycerate kinase 1;	-1.12	-0.73	0.38	55.40
P18669	Phosphoglycerate mutase 1;	-0.20	-0.06	0.84	35.40
A6NDG6	Phosphoglycolate phosphatase;	-0.84	-0.61	0.54	16.20
Q6P4A8	Phospholipase B-like 1;	1.44	0.11	0.11	6.10
P55058	Phospholipid transfer protein;	2.13	0.54	0.03	30.80
O15305	Phosphomannomutase 2;	-0.54	-0.44	0.72	14.20
O60256	Phosphoribosyl pyrophosphate synthase-associated proteir	-0.54	-0.57	0.77	11.40
O15067	Phosphoribosylformylglycinamidine synthase;	0.84	0.59	0.53	3.20
Q9Y617	Phosphoserine aminotransferase;	1.41	0.76	0.23	39.70
P78330	Phosphoserine phosphatase;	-0.69	-0.59	0.65	24.90
P36955	Pigment epithelium-derived factor;	3.83	3.05	0.01	23.20
Q9H307	Pinin;	-0.03	-0.01	0.97	2.40
Q9GZP4	PITH domain-containing protein 1;	0.33	0.16	0.76	19.00
Q9BTY2	Plasma alpha-L-fucosidase;	1.96	0.29	0.03	12.00
P05155	Plasma protease C1 inhibitor;	0.28	0.08	0.78	16.20
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein;	-0.25	-0.07	0.80	10.80
P05121	Plasminogen activator inhibitor 1;	0.60	0.21	0.55	12.70
Q14651	Plastin-1;	-2.56	-2.11	0.08	6.40
P13797	Plastin-3;	-1.29	-0.47	0.21	11.40
Q5VY43	Platelet endothelial aggregation receptor 1;	-0.36	-0.04	0.69	1.10
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha:	-0.49	-0.31	0.69	9.00
P68402	Platelet-activating factor acetylhydrolase IB subunit beta;	0.25	0.04	0.79	8.30
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamn	0.24	0.02	0.79	3.90
Q15198	Platelet-derived growth factor receptor-like protein;	-0.17	-0.02	0.85	3.20
Q15149	Plectin;	-0.60	-0.37	0.63	16.50
O43660	Pleiotropic regulator 1;	-1.12	-0.10	0.21	2.50
O15031	Plexin-B2;	2.64	0.46	0.00	0.70
Q92692	Poliovirus receptor-related protein 2;	0.48	0.19	0.66	7.40
P15151	Poliovirus receptor;	-5.64	0.00	0.00	2.90
P09874	Poly [ADP-ribose] polymerase 1;	-1.22	-1.53	0.55	16.60

Table S1

Uniprot accession	**Name**	**Fold-change ($\log_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
P51003	Poly(A) polymerase alpha;	2.01	0.20	0.03	1.90
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3;	-2.06	-4.46	0.53	10.70
Q15365	Poly(rC)-binding protein 1;	-0.18	-0.07	0.86	32.00
Q15366	Poly(rC)-binding protein 2;	-0.38	-0.18	0.74	24.90
Q9UHX1	Poly(U)-binding-splicing factor PUF60;	0.03	0.01	0.98	15.00
P11940	Polyadenylate-binding protein 1;	0.72	0.31	0.51	19.80
Q13310	Polyadenylate-binding protein 4;	0.77	0.13	0.40	7.30
Q96DU9	Polyadenylate-binding protein 5;	3.75	0.21	0.00	5.00
Q6NZI2	Polymerase I and transcript release factor;	-0.18	-0.07	0.86	20.30
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;	0.44	0.22	0.70	19.40
P26599	Polypyrimidine tract-binding protein 1;	-1.15	-0.82	0.40	23.20
Q9Y3B4	Pre-mRNA branch site protein p14;	-2.56	-0.45	0.01	11.20
Q9UMS4	Pre-mRNA-processing factor 19;	2.78	0.39	0.00	2.20
O75400	Pre-mRNA-processing factor 40 homolog A;	0.07	0.01	0.94	1.50
Q6P2Q9	Pre-mRNA-processing-splicing factor 8;	0.77	0.49	0.55	2.50
Q9UHV9	Prefoldin subunit 2;	-0.40	-0.09	0.67	24.00
P61758	Prefoldin subunit 3;	-1.43	-0.12	0.11	5.10
Q9NQP4	Prefoldin subunit 4;	-1.25	-1.25	0.46	20.10
Q99471	Prefoldin subunit 5;	-1.84	-2.03	0.32	14.90
P20742	Pregnancy zone protein;	0.69	0.04	0.44	2.40
P02545	Prelamin-A/C;	-0.27	-0.19	0.84	44.70
P07602	Proactivator polypeptide;	2.13	1.64	0.13	31.90
Q9NV35	Probable 8-oxo-dGTP diphosphatase NUDT15;	2.08	0.25	0.02	7.30
Q92841	Probable ATP-dependent RNA helicase DDX17;	-0.27	-0.14	0.82	10.30
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23;	-1.64	-0.87	0.17	7.20
P26196	Probable ATP-dependent RNA helicase DDX6;	0.59	0.26	0.59	10.40
Q96GX9	Probable methylthioribulose-1-phosphate dehydratase;	-0.89	-0.71	0.55	12.00
Q9UKZ9	Procollagen C-endopeptidase enhancer 2;	-1.00	-0.42	0.35	9.40
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	0.94	0.29	0.35	20.50
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3;	0.11	0.06	0.93	17.60
P07737	Profilin-1;	-1.09	-0.70	0.39	62.10
P35080	Profilin-2;	-0.25	-0.20	0.86	15.70
Q8WUM4	Programmed cell death 6-interacting protein;	-0.79	-0.94	0.69	18.00
Q53EL6	Programmed cell death protein 4;	0.73	0.06	0.42	3.40
O14737	Programmed cell death protein 5;	-0.58	-0.16	0.55	17.60
O75340	Programmed cell death protein 6;	0.18	0.02	0.85	9.90
P12004	Proliferating cell nuclear antigen;	-0.56	-0.29	0.63	36.00
Q9UQ80	Proliferation-associated protein 2G4;	-0.69	-0.41	0.58	38.30
Q8IZL8	Proline-, glutamic acid- and leucine-rich protein 1;	-1.15	-0.44	0.27	1.90
P48147	Prolyl endopeptidase;	-0.47	-0.24	0.68	10.40
P29122	Proprotein convertase subtilisin/kexin type 6;	0.64	0.10	0.49	2.50
Q8NBP7	Proprotein convertase subtilisin/kexin type 9;	0.53	0.19	0.61	21.20
Q9UHG2	ProSAAS;	-0.71	-0.05	0.42	3.80
Q15185	Prostaglandin E synthase 3;	-0.40	-0.24	0.75	17.50
Q9P2B2	Prostaglandin F2 receptor negative regulator;	-0.94	-0.45	0.40	9.60
Q14914	Prostaglandin reductase 1;	-0.81	-0.11	0.37	4.30
P41222	Prostaglandin-H2 D-isomerase;	3.55	1.12	0.00	17.40
Q06323	Proteasome activator complex subunit 1;	-0.15	-0.10	0.91	25.30
Q9UL46	Proteasome activator complex subunit 2;	-1.84	-1.84	0.29	10.50
P61289	Proteasome activator complex subunit 3;	-1.84	-1.77	0.27	6.70
Q9BT73	Proteasome assembly chaperone 3;	0.03	0.00	0.98	12.30
P25786	Proteasome subunit alpha type-1;	0.32	0.60	0.91	17.90
P25787	Proteasome subunit alpha type-2;	-0.54	-0.11	0.57	20.90
P25788	Proteasome subunit alpha type-3;	5.42	20.05	0.32	8.20
P28066	Proteasome subunit alpha type-5;	-0.36	-0.18	0.76	45.60
P60900	Proteasome subunit alpha type-6;	-1.22	-1.05	0.43	26.40
O14818	Proteasome subunit alpha type-7;	0.12	0.03	0.90	28.60

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P20618	Proteasome subunit beta type-1;	-0.15	-0.05	0.89	38.60
P49720	Proteasome subunit beta type-3;	0.04	0.00	0.97	22.00
P28070	Proteasome subunit beta type-4;	-0.76	-0.04	0.40	3.40
P28072	Proteasome subunit beta type-6;	-0.36	-0.30	0.81	13.00
Q99436	Proteasome subunit beta type-7;	-0.25	-0.06	0.80	11.20
P28062	Proteasome subunit beta type-8;	-1.29	-0.60	0.24	18.50
Q8IVF2	Protein AHNAK2;	2.57	0.58	0.01	3.90
Q99873	Protein arginine N-methyltransferase 1;	-0.43	-0.19	0.69	30.50
O14744	Protein arginine N-methyltransferase 5;	0.51	0.23	0.65	4.60
Q9UKV8	Protein argonaute-2;	-2.25	-1.50	0.08	3.50
Q9Y2B0	Protein canopy homolog 2;	-0.58	-0.08	0.52	13.70
O75629	Protein CREG1;	1.79	0.11	0.05	5.50
O60888	Protein CutA;	0.44	0.04	0.62	7.80
O00622	Protein CYR61;	-0.45	-0.06	0.62	11.80
O60610	Protein diaphanous homolog 1;	-1.40	-0.18	0.13	0.90
P30101	Protein disulfide-isomerase A3;	-0.12	-0.10	0.93	25.70
P13667	Protein disulfide-isomerase A4;	-0.71	-0.23	0.48	19.80
Q15084	Protein disulfide-isomerase A6;	0.71	0.58	0.63	17.50
P07237	Protein disulfide-isomerase;	-0.09	-0.03	0.93	31.90
Q99497	Protein DJ-1;	-0.54	-0.23	0.63	37.00
Q01658	Protein Dr1;	0.31	0.05	0.74	7.40
Q92520	Protein FAM3C;	-1.32	-0.53	0.21	39.60
Q9NUQ9	Protein FAM49B;	-1.00	-0.50	0.38	21.30
Q14320	Protein FAM50A;	0.32	0.05	0.73	4.10
Q8NCA5	Protein FAM98A;	0.32	0.03	0.72	2.30
P49354	Protein farnesyltransferase/geranylgeranyltransferase type-	-0.32	-0.02	0.73	3.40
Q13045	Protein flightless-1 homolog;	0.14	0.05	0.89	1.30
O94992	Protein HEXIM1;	0.26	0.06	0.78	7.00
Q9UNF0	Protein kinase C and casein kinase substrate in neurons pr	-1.32	-1.26	0.42	11.70
Q9UKS6	Protein kinase C and casein kinase substrate in neurons pr	0.20	0.04	0.83	6.60
Q96EK9	Protein KTI12 homolog;	-6.64	0.00	0.00	3.70
Q9BRT6	Protein LLP homolog;	-0.71	-0.07	0.43	10.90
P61326	Protein mago nashi homolog;	2.15	5.36	0.56	14.40
Q9UGV2	Protein NDRG3;	-0.47	-0.07	0.60	4.00
O14974	Protein phosphatase 1 regulatory subunit 12A;	-0.58	-0.07	0.52	1.90
Q15435	Protein phosphatase 1 regulatory subunit 7;	5.04	0.84	0.00	3.10
P35813	Protein phosphatase 1A;	-0.49	-0.05	0.58	2.90
O75688	Protein phosphatase 1B;	-1.89	-0.28	0.04	2.30
P49593	Protein phosphatase 1F;	-0.17	-0.02	0.85	3.50
O15355	Protein phosphatase 1G;	-0.32	-0.08	0.74	8.40
P41236	Protein phosphatase inhibitor 2;	0.40	0.02	0.65	4.90
Q9P258	Protein RCC2;	-0.43	-0.18	0.69	14.90
P31949	Protein S100-A11;	-0.49	-0.02	0.57	30.50
Q99584	Protein S100-A13;	-1.03	-0.19	0.28	40.80
Q96FQ6	Protein S100-A16;	-0.38	-0.04	0.67	23.30
P26447	Protein S100-A4;	-0.89	-0.28	0.38	26.70
P25815	Protein S100-P;	-3.18	-0.58	0.00	13.70
Q01105	Protein SET;	0.00	0.00	1.00	17.90
P18583	Protein SON;	2.61	3.76	0.25	1.70
Q15437	Protein transport protein Sec23B;	-1.52	-0.61	0.15	4.40
P53992	Protein transport protein Sec24C;	0.25	0.03	0.79	6.40
O94979	Protein transport protein Sec31A;	1.22	0.33	0.21	3.70
Q12974	Protein tyrosine phosphatase type IVA 2;	-0.29	-0.03	0.75	8.40
P28300	Protein-lysine 6-oxidase;	1.93	0.13	0.03	3.10
P06454	Prothymosin alpha;	0.11	0.01	0.91	9.00
P00491	Purine nucleoside phosphorylase;	0.40	0.23	0.74	22.10
P55786	Puromycin-sensitive aminopeptidase;	-1.29	-0.63	0.26	19.40

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
O43865	Putative adenosylhomocysteinase 2;	0.14	0.02	0.88	2.30
Q96GX2	Putative ataxin-7-like protein 3B;	-0.20	-0.05	0.83	10.30
Q6P158	Putative ATP-dependent RNA helicase DHX57;	-0.45	-0.03	0.61	2.20
O75884	Putative hydrolase RBBP9;	-0.76	-0.06	0.40	8.10
O60361	Putative nucleoside diphosphate kinase;	0.21	0.05	0.82	54.00
Q49A26	Putative oxidoreductase GLYR1;	-0.23	-0.14	0.86	4.90
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1;	-1.89	-0.21	0.04	8.60
Q8NHP8	Putative phospholipase B-like 2;	1.32	0.28	0.16	12.10
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA h	-0.38	-0.09	0.69	7.50
P98179	Putative RNA-binding protein 3;	-0.64	-0.22	0.53	27.40
Q9Y383	Putative RNA-binding protein Luc7-like 2;	-0.34	-0.06	0.72	8.70
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10	0.77	0.42	0.52	3.30
A6NL28	Putative tropomyosin alpha-3 chain-like protein;	-0.49	-0.09	0.59	6.30
Q9NVS9	Pyridoxine-5'-phosphate oxidase;	-0.64	-0.11	0.49	11.50
P14618	Pyruvate kinase isozymes M1/M2;	-0.94	-0.47	0.41	51.60
Q53FA7	Quinone oxidoreductase PIG3;	-0.15	-0.12	0.92	10.80
P31150	Rab GDP dissociation inhibitor alpha;	-1.43	-0.81	0.24	11.40
Q6IAA8	Ragulator complex protein LAMTOR1;	3.47	0.23	0.00	7.50
Q9UHA4	Ragulator complex protein LAMTOR3;	-0.09	-0.01	0.92	8.10
O43504	Ragulator complex protein LAMTOR5;	-0.11	-0.01	0.91	22.00
Q9HD47	Ran guanine nucleotide release factor;	0.03	0.00	0.98	7.00
Q9H6Z4	Ran-binding protein 3;	2.00	0.29	0.03	2.10
P43487	Ran-specific GTPase-activating protein;	0.45	0.06	0.62	10.90
A6NKT7	RanBP2-like and GRIP domain-containing protein 3;	0.44	0.05	0.62	0.70
P52306	Rap1 GTPase-GDP dissociation stimulator 1;	0.61	0.14	0.51	1.60
Q13283	Ras GTPase-activating protein-binding protein 1;	-0.76	-0.52	0.57	28.80
P46940	Ras GTPase-activating-like protein IQGAP1;	-0.20	-0.09	0.85	12.80
Q15404	Ras suppressor protein 1;	-0.15	-0.04	0.88	9.40
P63000	Ras-related C3 botulinum toxin substrate 1;	-0.27	-0.09	0.79	17.70
Q15907	Ras-related protein Rab-11B;	-0.36	-0.07	0.70	39.40
P61106	Ras-related protein Rab-14;	-0.32	-0.03	0.73	11.60
P62820	Ras-related protein Rab-1A;	0.15	0.02	0.86	22.90
Q9UL25	Ras-related protein Rab-21;	0.32	0.14	0.77	9.80
P61019	Ras-related protein Rab-2A;	0.28	0.04	0.76	6.60
P51149	Ras-related protein Rab-7a;	-1.06	-1.37	0.61	15.90
P61224	Ras-related protein Rap-1b;	-0.43	-0.06	0.64	6.00
P10586	Receptor-type tyrosine-protein phosphatase F;	0.86	0.59	0.52	13.80
P23470	Receptor-type tyrosine-protein phosphatase gamma;	-0.07	-0.01	0.94	3.40
Q15262	Receptor-type tyrosine-protein phosphatase kappa;	1.06	0.77	0.45	3.30
Q06330	Recombining binding protein suppressor of hairless;	-0.54	-0.11	0.57	3.20
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing prote	-0.67	-0.12	0.48	4.60
P18754	Regulator of chromosome condensation;	-0.97	-0.17	0.29	8.10
O75787	Renin receptor;	0.14	0.15	0.94	13.70
P35244	Replication protein A 14 kDa subunit;	-0.25	-0.03	0.78	13.20
Q9UKL0	REST corepressor 1;	0.51	0.11	0.59	3.90
Q15293	Reticulocalbin-1;	0.94	0.18	0.31	4.50
Q9BZR6	Reticulon-4 receptor;	1.47	0.09	0.10	2.50
Q99969	Retinoic acid receptor responder protein 2;	0.60	0.05	0.50	14.10
Q9HB40	Retinoid-inducible serine carboxypeptidase;	0.43	0.42	0.79	18.10
P52565	Rho GDP-dissociation inhibitor 1;	-0.38	-0.02	0.67	7.40
Q92888	Rho guanine nucleotide exchange factor 1;	2.04	0.13	0.02	1.10
O75116	Rho-associated protein kinase 2;	-1.47	-0.21	0.11	2.50
P08134	Rho-related GTP-binding protein RhoC;	-0.18	-0.01	0.84	11.40
P13489	Ribonuclease inhibitor;	-1.29	-0.53	0.23	19.50
O00584	Ribonuclease T2;	1.09	0.20	0.24	20.30
P52758	Ribonuclease UK114;	0.08	0.01	0.92	7.30
P60891	Ribose-phosphate pyrophosphokinase 1;	-0.27	-0.03	0.77	13.50

Table S1

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P11908	Ribose-phosphate pyrophosphokinase 2;	0.50	0.08	0.59	13.50
Q9Y3A5	Ribosome maturation protein SBDS;	0.03	0.00	0.98	18.00
Q9P2E9	Ribosome-binding protein 1;	-1.89	-0.35	0.04	1.00
Q9Y508	RING finger protein 114;	0.15	0.01	0.86	5.30
Q9H6T3	RNA polymerase II-associated protein 3;	-1.29	-0.25	0.17	2.00
P38159	RNA-binding motif protein, X chromosome;	-0.17	-0.04	0.86	14.30
Q9NTZ6	RNA-binding protein 12;	-0.49	-0.33	0.70	5.40
P49756	RNA-binding protein 25;	-0.29	-0.18	0.82	5.10
Q14498	RNA-binding protein 39;	0.07	0.03	0.94	5.30
Q9Y5S9	RNA-binding protein 8A;	-0.18	-0.02	0.84	6.30
Q01844	RNA-binding protein EWS;	-0.71	-0.42	0.56	4.00
P35637	RNA-binding protein FUS;	0.82	0.05	0.36	4.40
Q9Y6N7	Roundabout homolog 1;	-0.94	-1.25	0.66	1.90
P22087	rRNA 2'-O-methyltransferase fibrillarin;	0.24	0.02	0.79	9.30
Q9Y265	RuvB-like 1;	0.21	0.07	0.83	20.40
Q9Y230	RuvB-like 2;	-0.69	-0.56	0.64	19.00
P31153	S-adenosylmethionine synthase isoform type-2;	-0.29	-0.17	0.81	20.50
P10768	S-formylglutathione hydrolase;	-0.25	-0.11	0.82	11.30
Q13126	S-methyl-5'-thioadenosine phosphorylase;	-2.18	-2.68	0.27	24.00
Q15424	Scaffold attachment factor B1;	-0.20	-0.12	0.87	4.70
Q8WVM8	Sec1 family domain-containing protein 1;	-0.01	0.00	0.99	1.60
Q9Y6Y8	SEC23-interacting protein;	1.34	0.16	0.14	1.40
Q12765	Secernin-1;	1.32	0.13	0.14	5.10
Q8WVN6	Secreted and transmembrane protein 1;	2.32	0.32	0.01	7.70
Q6UXD5	Seizure 6-like protein 2;	0.95	0.12	0.30	1.00
P49903	Selenide, water dikinase 1;	-0.25	-0.08	0.81	3.80
Q96I15	Selenocysteine lyase;	-1.00	-0.44	0.36	7.20
Q14563	Semaphorin-3A;	1.58	0.61	0.13	14.70
Q99985	Semaphorin-3C;	-0.27	-0.16	0.83	27.70
Q9NPR2	Semaphorin-4B;	0.15	0.01	0.86	3.40
Q92854	Semaphorin-4D;	0.99	0.18	0.28	3.50
Q9H3T2	Semaphorin-6C;	-0.69	-0.22	0.49	1.20
O75326	Semaphorin-7A;	1.23	0.81	0.34	3.60
Q9P0V9	Septin-10;	-0.03	-0.01	0.97	4.00
Q9NVA2	Septin-11;	0.24	0.10	0.83	18.40
Q15019	Septin-2;	-0.49	-0.32	0.70	28.00
Q9UHD8	Septin-9;	-0.23	-0.06	0.81	10.90
P34896	Serine hydroxymethyltransferase, cytosolic;	-0.89	-0.10	0.33	2.10
P34897	Serine hydroxymethyltransferase, mitochondrial;	0.61	0.04	0.49	2.20
O95084	Serine protease 23;	-0.71	-0.47	0.58	25.10
Q92743	Serine protease HTRA1;	0.64	0.37	0.60	12.50
P49591	Serine--tRNA ligase, cytoplasmic;	-0.54	-0.05	0.56	2.90
Q9Y3F4	Serine-threonine kinase receptor-associated protein;	-0.34	-0.04	0.71	24.60
Q9UQ35	Serine/arginine repetitive matrix protein 2;	-0.81	-3.54	0.90	1.60
Q07955	Serine/arginine-rich splicing factor 1;	0.31	0.16	0.79	15.70
Q05519	Serine/arginine-rich splicing factor 11;	0.31	0.09	0.75	5.20
P84103	Serine/arginine-rich splicing factor 3;	-0.03	0.00	0.97	10.40
Q13243	Serine/arginine-rich splicing factor 5;	1.78	0.20	0.05	4.40
Q13247	Serine/arginine-rich splicing factor 6;	-0.32	-0.45	0.89	9.60
Q16629	Serine/arginine-rich splicing factor 7;	1.06	0.07	0.24	3.80
Q13242	Serine/arginine-rich splicing factor 9;	1.53	0.48	0.13	7.70
Q9Y6E0	Serine/threonine-protein kinase 24;	0.08	0.01	0.92	4.50
O95747	Serine/threonine-protein kinase OSR1;	0.45	0.23	0.69	7.00
Q13177	Serine/threonine-protein kinase PAK 2;	0.64	0.45	0.64	6.90
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulator	-0.11	-0.01	0.91	2.50
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulator	-1.12	-0.54	0.32	21.60
Q15257	Serine/threonine-protein phosphatase 2A activator;	0.58	0.05	0.53	6.40

Table S1

Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P62714	Serine/threonine-protein phosphatase 2A catalytic subunit	-1.09	-0.46	0.31	6.10
P60510	Serine/threonine-protein phosphatase 4 catalytic subunit;	-0.58	-0.49	0.70	15.60
Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit	0.61	0.12	0.51	3.60
P53041	Serine/threonine-protein phosphatase 5;	0.18	0.02	0.85	1.40
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit;	0.50	0.04	0.58	3.90
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic s	-0.38	-0.05	0.68	16.70
P02787	Serotransferrin;	-0.89	-0.03	0.33	2.00
P36952	Serpin B5;	-0.32	-0.08	0.74	28.50
P35237	Serpin B6;	-0.97	-1.12	0.61	23.40
P50453	Serpin B9;	1.23	0.93	0.38	8.80
P50454	Serpin H1;	0.30	0.18	0.81	13.90
Q9BXP5	Serrate RNA effector molecule homolog;	1.03	0.10	0.25	2.40
P02768	Serum albumin;	-0.18	-0.11	0.88	4.60
O95810	Serum deprivation-response protein;	0.87	0.10	0.34	3.30
Q6GMV2	SET and MYND domain-containing protein 5;	0.15	0.02	0.86	2.60
P29353	SHC-transforming protein 1;	0.11	0.01	0.91	2.10
Q9HAT2	Sialate O-acetylesterase;	1.48	0.47	0.14	13.80
Q9NR45	Sialic acid synthase;	-1.25	-0.12	0.17	8.60
Q99519	Sialidase-1;	0.28	0.24	0.86	18.80
P37108	Signal recognition particle 14 kDa protein;	-0.67	-0.09	0.47	8.80
O76094	Signal recognition particle 72 kDa protein;	0.26	0.02	0.77	1.60
P49458	Signal recognition particle 9 kDa protein;	0.65	0.58	0.67	22.10
Q92783	Signal transducing adapter molecule 1;	-0.58	-0.07	0.52	2.20
O75093	Slit homolog 1 protein;	-0.36	-0.10	0.71	0.60
O43765	Small glutamine-rich tetratricopeptide repeat-containing pı	-0.47	-0.20	0.66	15.30
P62304	Small nuclear ribonucleoprotein E;	0.03	0.00	0.98	12.00
P62306	Small nuclear ribonucleoprotein F;	-1.43	-0.23	0.12	9.30
A8MWD9	Small nuclear ribonucleoprotein G-like protein;	1.41	0.10	0.12	15.80
P62314	Small nuclear ribonucleoprotein Sm D1;	0.87	0.52	0.48	9.20
P62316	Small nuclear ribonucleoprotein Sm D2;	-0.97	-1.03	0.58	55.10
P62318	Small nuclear ribonucleoprotein Sm D3;	0.08	0.02	0.92	7.10
P14678	Small nuclear ribonucleoprotein-associated proteins B and	-0.71	-0.28	0.49	23.80
P63165	Small ubiquitin-related modifier 1;	-0.45	-0.03	0.61	11.90
P55854	Small ubiquitin-related modifier 3;	0.15	0.05	0.88	12.60
P05023	Sodium/potassium-transporting ATPase subunit alpha-1;	0.32	0.10	0.75	3.30
Q8WVQ1	Soluble calcium-activated nucleotidase 1;	0.49	0.19	0.65	18.00
P11166	Solute carrier family 2, facilitated glucose transporter men	1.47	0.24	0.11	2.60
Q00796	Sorbitol dehydrogenase;	-0.89	-0.59	0.50	11.80
P30626	Sorcin;	-0.89	-0.36	0.41	22.70
Q13596	Sorting nexin-1;	-1.47	-0.12	0.10	2.70
Q9Y5X3	Sorting nexin-5;	-0.89	-0.54	0.49	2.70
Q9UNH7	Sorting nexin-6;	0.60	0.13	0.53	7.60
Q9Y5X1	Sorting nexin-9;	-1.32	-0.20	0.15	2.40
P09486	SPARC;	0.56	0.26	0.62	26.40
Q13813	Spectrin alpha chain, non-erythrocytic 1;	0.38	0.21	0.75	12.00
P11277	Spectrin beta chain, erythrocytic;	9.96	0.36	0.00	1.60
Q01082	Spectrin beta chain, non-erythrocytic 1;	-0.38	-0.32	0.80	9.60
P19623	Spermidine synthase;	0.28	0.02	0.76	3.30
P52788	Spermine synthase;	-0.60	-0.24	0.57	10.40
Q13838	Spliceosome RNA helicase DDX39B;	0.18	0.12	0.90	26.60
Q15637	Splicing factor 1;	-0.89	-0.97	0.63	7.80
Q15459	Splicing factor 3A subunit 1;	-0.45	-0.29	0.73	14.20
Q15428	Splicing factor 3A subunit 2;	2.18	0.32	0.02	3.90
Q12874	Splicing factor 3A subunit 3;	0.00	0.00	1.00	7.00
O75533	Splicing factor 3B subunit 1;	-0.04	-0.02	0.96	6.60
Q13435	Splicing factor 3B subunit 2;	-0.58	-0.35	0.64	10.20
Q15393	Splicing factor 3B subunit 3;	-0.25	-0.10	0.82	9.40

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9BWJ5	Splicing factor 3B subunit 5;	0.19	0.01	0.83	10.50
P26368	Splicing factor U2AF 65 kDa subunit;	-0.47	-0.19	0.65	15.40
P23246	Splicing factor, proline- and glutamine-rich;	0.28	0.04	0.76	8.90
Q15020	Squamous cell carcinoma antigen recognized by T-cells 3;	-0.32	-0.26	0.83	3.60
Q14247	Src substrate cortactin;	-3.84	0.00	0.00	2.00
P52823	Stanniocalcin-1;	0.31	0.09	0.75	13.40
Q7KZF4	Staphylococcal nuclease domain-containing protein 1;	0.04	0.04	0.98	14.90
P16949	Stathmin;	-0.20	-0.07	0.84	29.50
Q9H2G2	STE20-like serine/threonine-protein kinase;	0.45	0.17	0.66	3.60
P38646	Stress-70 protein, mitochondrial;	-0.12	-0.03	0.90	7.80
P31948	Stress-induced-phosphoprotein 1;	-1.06	-0.79	0.45	15.70
Q14683	Structural maintenance of chromosomes protein 1A;	1.28	0.26	0.17	0.80
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subun	0.26	0.10	0.80	4.80
Q8NBJ7	Sulfatase-modifying factor 2;	-0.38	-0.06	0.68	22.60
O00391	Sulfhydryl oxidase 1;	1.88	0.73	0.07	22.20
Q6ZRP7	Sulfhydryl oxidase 2;	-0.17	-0.09	0.89	10.50
Q9UBE0	SUMO-activating enzyme subunit 1;	-0.56	-0.08	0.55	4.00
Q9UBT2	SUMO-activating enzyme subunit 2;	0.21	0.04	0.82	10.80
P63279	SUMO-conjugating enzyme UBC9;	-0.49	-0.06	0.58	19.60
P42285	Superkiller viralicidic activity 2-like 2;	0.59	0.37	0.65	2.00
P00441	Superoxide dismutase [Cu-Zn];	-0.20	-0.02	0.82	9.10
P04179	Superoxide dismutase [Mn], mitochondrial;	0.59	0.07	0.52	6.30
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog;	2.75	0.35	0.00	4.10
P78539	Sushi repeat-containing protein SRPX;	0.19	0.05	0.85	2.80
O60687	Sushi repeat-containing protein SRPX2;	0.06	0.04	0.97	5.60
Q92922	SWI/SNF complex subunit SMARCC1;	-1.22	-1.13	0.45	3.10
Q9UH65	Switch-associated protein 70;	-0.34	-0.03	0.71	1.90
Q99536	Synaptic vesicle membrane protein VAT-1 homolog;	-1.09	-1.11	0.53	7.10
P31431	Syndecan-4;	1.77	0.18	0.05	13.60
O00560	Syntenin-1;	-0.40	-0.26	0.76	7.00
P17987	T-complex protein 1 subunit alpha;	-0.32	-0.12	0.76	35.30
P78371	T-complex protein 1 subunit beta;	-0.45	-0.31	0.73	38.30
P50991	T-complex protein 1 subunit delta;	-0.81	-0.64	0.57	30.80
P48643	T-complex protein 1 subunit epsilon;	-0.58	-0.41	0.67	17.70
Q99832	T-complex protein 1 subunit eta;	-0.56	-0.14	0.57	24.90
P49368	T-complex protein 1 subunit gamma;	-0.40	-0.19	0.72	25.70
P50990	T-complex protein 1 subunit theta;	-0.49	-0.15	0.62	50.00
P40227	T-complex protein 1 subunit zeta;	-0.76	-0.18	0.43	25.00
Q9Y490	Talin-1;	-0.67	-0.37	0.58	17.80
Q7Z7G0	Target of Nesh-SH3;	5.04	4.41	0.00	4.10
O14907	Tax1-binding protein 3;	0.91	0.19	0.33	13.70
Q08629	Testican-1;	2.54	0.53	0.01	6.40
Q9BRA2	Thioredoxin domain-containing protein 17;	-0.11	-0.02	0.91	18.70
Q8NBS9	Thioredoxin domain-containing protein 5;	-1.12	-1.22	0.53	23.40
Q16881	Thioredoxin reductase 1, cytoplasmic;	0.25	0.06	0.80	14.60
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	1.01	0.25	0.29	17.60
P10599	Thioredoxin;	-0.12	-0.06	0.91	21.00
Q86V81	THO complex subunit 4;	-0.94	-0.04	0.29	4.30
P26639	Threonine--tRNA ligase, cytoplasmic;	0.07	0.05	0.96	13.70
P07996	Thrombospondin-1;	-1.60	-1.70	0.36	21.60
P49746	Thrombospondin-3;	3.36	1.63	0.00	8.40
Q9P016	Thymocyte nuclear protein 1;	-1.47	-0.16	0.10	4.90
Q9Y2W1	Thyroid hormone receptor-associated protein 3;	-0.04	-0.02	0.97	4.40
Q9UKU6	Thyrotropin-releasing hormone-degrading ectoenzyme;	0.91	0.13	0.32	4.50
Q07157	Tight junction protein ZO-1;	0.48	0.06	0.61	0.70
Q9UDY2	Tight junction protein ZO-2;	-1.12	-0.85	0.42	5.90
O75663	TIP41-like protein;	0.97	0.18	0.30	11.00

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
P10646	Tissue factor pathway inhibitor;	2.21	1.09	0.05	12.80
Q8WZ42	Titin;	4.20	3.64	0.01	0.30
O14657	Torsin-1B;	1.36	0.14	0.13	4.20
Q96EM0	Trans-L-3-hydroxyproline dehydratase;	-0.58	-0.08	0.52	8.80
P37837	Transaldolase;	-0.38	-0.12	0.70	16.60
P20062	Transcobalamin-2;	1.25	0.12	0.17	8.40
P23193	Transcription elongation factor A protein 1;	0.82	0.07	0.37	3.00
Q5H9L2	Transcription elongation factor A protein-like 5;	0.07	0.00	0.94	4.50
Q15370	Transcription elongation factor B polypeptide 2;	-0.45	-0.05	0.62	35.60
O00267	Transcription elongation factor SPT5;	-1.06	-0.84	0.47	5.60
Q7KZ85	Transcription elongation factor SPT6;	-0.40	-0.07	0.66	1.30
O14776	Transcription elongation regulator 1;	0.28	0.06	0.77	2.10
P20290	Transcription factor BTF3;	0.51	0.05	0.57	9.20
Q13263	Transcription intermediary factor 1-beta;	0.11	0.04	0.92	7.80
Q04724	Transducin-like enhancer protein 1;	-0.12	-0.08	0.92	2.60
P02786	Transferrin receptor protein 1;	1.71	0.78	0.12	17.50
P01137	Transforming growth factor beta-1;	1.89	0.71	0.07	14.90
Q15582	Transforming growth factor-beta-induced protein ig-h3;	-1.12	-0.46	0.29	10.80
P37802	Transgelin-2;	-0.23	-0.09	0.83	35.20
P55072	Transitional endoplasmic reticulum ATPase;	-1.00	-0.44	0.36	33.70
P29401	Transketolase;	-2.32	-1.63	0.08	30.00
Q92616	Translational activator GCN1;	2.12	0.20	0.02	0.40
P13693	Translationally-controlled tumor protein;	-0.20	-0.07	0.84	27.30
Q99598	Translin-associated protein X;	-0.69	-0.21	0.49	7.90
Q15631	Translin;	-0.18	-0.02	0.84	8.80
Q99805	Transmembrane 9 superfamily member 2;	1.57	0.21	0.08	2.10
P49755	Transmembrane emp24 domain-containing protein 10;	1.01	0.15	0.27	5.50
Q24JP5	Transmembrane protein 132A;	1.73	0.21	0.06	1.40
Q9UHN6	Transmembrane protein 2;	-1.52	-0.74	0.18	4.30
Q92973	Transportin-1;	0.65	0.69	0.71	6.70
Q9Y5L0	Transportin-3;	-0.18	-0.02	0.84	2.60
Q13428	Treacle protein;	0.78	0.05	0.38	0.80
P22102	Trifunctional purine biosynthetic protein adenosine-3;	2.03	0.58	0.04	6.30
P60174	Triosephosphate isomerase;	-1.22	-0.60	0.29	57.00
O14773	Tripeptidyl-peptidase 1;	1.41	0.20	0.12	14.20
P29144	Tripeptidyl-peptidase 2;	0.61	0.29	0.58	4.60
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase;	-1.43	-0.19	0.12	1.30
Q9Y3I0	tRNA-splicing ligase RtcB homolog;	-0.69	-0.35	0.55	17.20
Q9NYL9	Tropomodulin-3;	0.92	0.51	0.44	5.70
Q8IWU9	Tryptophan 5-hydroxylase 2;	-4.64	-8.13	0.12	2.90
P23381	Tryptophan--tRNA ligase, cytoplasmic;	0.36	0.16	0.75	17.20
P68363	Tubulin alpha-1B chain;	0.55	0.20	0.60	35.50
P07437	Tubulin beta chain;	-0.56	-0.16	0.57	34.20
P68371	Tubulin beta-4B chain;	-0.18	-0.02	0.84	30.30
Q14166	Tubulin--tyrosine ligase-like protein 12;	-0.36	-0.07	0.70	10.10
Q9GZM7	Tubulointerstitial nephritis antigen-like;	-0.29	-0.03	0.75	2.80
O00300	Tumor necrosis factor receptor superfamily member 11B;	-4.64	-6.97	0.06	8.00
Q9NP84	Tumor necrosis factor receptor superfamily member 12A;	-0.84	-0.03	0.35	7.80
P19438	Tumor necrosis factor receptor superfamily member 1A;	0.21	0.03	0.81	3.30
O75509	Tumor necrosis factor receptor superfamily member 21;	-1.74	-0.23	0.05	2.70
O95407	Tumor necrosis factor receptor superfamily member 6B;	1.95	0.44	0.04	21.70
O43399	Tumor protein D54;	1.74	2.64	0.46	11.20
Q12888	Tumor suppressor p53-binding protein 1;	0.86	0.44	0.45	1.70
Q99816	Tumor susceptibility gene 101 protein;	-2.18	-0.89	0.04	6.90
Q12792	Twinfilin-1;	-0.76	-0.13	0.42	8.60
Q6IBS0	Twinfilin-2;	-0.43	-0.21	0.71	17.50
Q9GZX9	Twisted gastrulation protein homolog 1;	0.50	0.02	0.58	6.70

Table S1

Uniprot accession	Name	Fold-change (log_2) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P54577	Tyrosine--tRNA ligase, cytoplasmic;	0.04	0.02	0.97	8.50
P06241	Tyrosine-protein kinase Fyn;	-2.18	-4.77	0.51	3.00
P30530	Tyrosine-protein kinase receptor UFO;	0.44	0.07	0.63	3.40
Q06124	Tyrosine-protein phosphatase non-receptor type 11;	0.43	0.15	0.68	6.40
P08621	U1 small nuclear ribonucleoprotein 70 kDa;	-0.09	-0.02	0.93	10.80
P09012	U1 small nuclear ribonucleoprotein A;	-0.71	-0.02	0.42	13.50
P09234	U1 small nuclear ribonucleoprotein C;	-1.69	-0.38	0.08	11.30
P08579	U2 small nuclear ribonucleoprotein B'';	-0.23	-0.04	0.81	14.70
O43818	U3 small nucleolar RNA-interacting protein 2;	0.58	1.20	0.86	9.10
O43395	U4/U6 small nuclear ribonucleoprotein Prp3;	-0.67	-0.50	0.64	8.30
O43172	U4/U6 small nuclear ribonucleoprotein Prp4;	-0.25	-0.07	0.80	2.30
Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2;	-0.79	-0.07	0.39	5.30
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase;	-0.89	-0.51	0.47	11.00
Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein;	-1.15	-0.13	0.20	7.30
O15116	U6 snRNA-associated Sm-like protein LSm1;	-0.47	-0.11	0.62	12.00
Q9Y333	U6 snRNA-associated Sm-like protein LSm2;	0.38	0.15	0.72	27.40
Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4;	-0.69	-0.03	0.44	14.40
Q9UMX0	Ubiquilin-1;	-0.60	-0.09	0.51	2.50
Q9NRR5	Ubiquilin-4;	-0.64	-0.26	0.55	1.80
P54578	Ubiquitin carboxyl-terminal hydrolase 14;	-0.25	-0.04	0.79	4.00
P45974	Ubiquitin carboxyl-terminal hydrolase 5;	-0.27	-0.22	0.86	3.50
Q93009	Ubiquitin carboxyl-terminal hydrolase 7;	-0.47	-0.05	0.60	5.10
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3;	-2.25	-0.32	0.01	8.70
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5;	1.35	0.19	0.14	6.70
O14562	Ubiquitin domain-containing protein UBFD1;	-0.25	-0.03	0.79	3.60
Q92890	Ubiquitin fusion degradation protein 1 homolog;	-0.81	-0.16	0.39	9.10
Q96FW1	Ubiquitin thioesterase OTUB1;	-0.79	-0.15	0.40	15.90
P62979	Ubiquitin-40S ribosomal protein S27a;	-1.00	-1.24	0.61	42.30
Q14157	Ubiquitin-associated protein 2-like;	-0.67	-0.29	0.54	5.40
P61077	Ubiquitin-conjugating enzyme E2 D3;	0.24	0.03	0.80	7.50
P62253	Ubiquitin-conjugating enzyme E2 G1;	-0.94	-0.05	0.29	7.10
P62256	Ubiquitin-conjugating enzyme E2 H;	-0.01	0.00	0.99	8.20
P61086	Ubiquitin-conjugating enzyme E2 K;	-1.09	-0.77	0.42	15.00
P68036	Ubiquitin-conjugating enzyme E2 L3;	-0.58	-0.10	0.53	47.40
P61088	Ubiquitin-conjugating enzyme E2 N;	-0.20	-0.10	0.86	28.30
P49427	Ubiquitin-conjugating enzyme E2 R1;	0.55	0.04	0.54	3.40
Q13404	Ubiquitin-conjugating enzyme E2 variant 1;	-0.12	-0.01	0.89	13.80
Q9H832	Ubiquitin-conjugating enzyme E2 Z;	-0.89	-0.17	0.35	5.10
P61960	Ubiquitin-fold modifier 1;	-0.67	-0.22	0.51	27.10
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1;	0.20	0.08	0.85	5.40
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1;	0.07	0.01	0.94	7.50
P22314	Ubiquitin-like modifier-activating enzyme 1;	-0.97	-0.57	0.43	19.70
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3;	1.84	0.49	0.06	4.10
Q05086	Ubiquitin-protein ligase E3A;	0.11	0.01	0.91	1.60
Q14376	UDP-glucose 4-epimerase;	0.07	0.01	0.94	2.90
O60701	UDP-glucose 6-dehydrogenase;	-0.47	-0.41	0.76	6.30
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1;	0.87	0.31	0.40	3.40
Q8NBZ7	UDP-glucuronic acid decarboxylase 1;	1.40	0.20	0.13	4.00
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;	1.05	0.43	0.33	19.00
P30085	UMP-CMP kinase;	0.77	0.28	0.46	25.00
Q9BXV9	Uncharacterized protein C14orf142;	-0.71	-0.23	0.48	18.00
Q92614	Unconventional myosin-XVIIIa;	-0.25	-0.02	0.78	0.50
Q9HB07	UPF0160 protein MYG1, mitochondrial;	-1.06	-0.42	0.32	11.70
Q9BVG4	UPF0368 protein Cxorf26;	-0.07	-0.01	0.94	4.30
Q9H741	UPF0454 protein C12orf49;	0.33	0.05	0.71	6.30
Q5T6V5	UPF0553 protein C9orf64;	0.44	0.03	0.62	3.50
Q969H8	UPF0556 protein C19orf10;	1.36	0.69	0.24	12.10

Table S1

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9Y224	UPF0568 protein C14orf166;	-0.23	-0.06	0.81	13.90
Q96S19	UPF0585 protein C16orf13;	-0.29	-0.05	0.75	11.80
Q8N4J0	UPF0586 protein C9orf41;	-2.00	-2.48	0.32	10.80
Q9NWV4	UPF0587 protein C1orf123;	-0.71	-0.20	0.46	15.00
Q9GZN8	UPF0687 protein C20orf27;	-0.40	-0.17	0.71	13.80
Q9H3H3	UPF0696 protein C11orf68;	-0.38	-0.04	0.67	16.70
P00749	Urokinase-type plasminogen activator;	0.08	0.04	0.94	19.50
P06132	Uroporphyrinogen decarboxylase;	-0.34	-0.07	0.72	9.30
Q16851	UTP--glucose-1-phosphate uridylyltransferase;	-0.17	-0.05	0.87	8.70
P54727	UV excision repair protein RAD23 homolog B;	0.32	0.09	0.74	16.60
Q96N03	V-set and transmembrane domain-containing protein 2-lik	2.49	0.37	0.01	5.90
P38606	V-type proton ATPase catalytic subunit A;	-2.74	-0.18	0.00	1.90
P21281	V-type proton ATPase subunit B, brain isoform;	-1.47	-2.09	0.51	7.20
Q15904	V-type proton ATPase subunit S1;	1.09	0.55	0.34	16.20
Q709C8	Vacuolar protein sorting-associated protein 13C;	-6.64	0.00	0.00	0.50
O75436	Vacuolar protein sorting-associated protein 26A;	-0.34	-0.25	0.81	13.50
Q9UBQ0	Vacuolar protein sorting-associated protein 29;	-0.23	-0.04	0.81	12.60
Q96QK1	Vacuolar protein sorting-associated protein 35;	-0.11	-0.04	0.92	2.90
P26640	Valine--tRNA ligase;	-0.20	-0.06	0.83	6.60
P50552	Vasodilator-stimulated phosphoprotein;	0.36	0.24	0.79	5.80
Q6EMK4	Vasorin;	0.82	0.05	0.36	8.00
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitoch	-2.56	-0.15	0.00	1.50
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein]	0.75	0.06	0.40	3.00
Q9P0L0	Vesicle-associated membrane protein-associated protein A	-0.71	-0.09	0.43	10.00
O75396	Vesicle-trafficking protein SEC22b;	-0.07	-0.01	0.94	4.70
Q12907	Vesicular integral-membrane protein VIP36;	-0.18	-0.12	0.89	6.50
Q00341	Vigilin;	-0.84	-1.27	0.72	4.60
P08670	Vimentin;	0.00	0.00	1.00	37.30
P18206	Vinculin;	1.28	1.04	0.39	21.60
P04004	Vitronectin;	0.45	0.06	0.62	3.10
Q6PCB0	von Willebrand factor A domain-containing protein 1;	2.32	0.23	0.01	3.60
Q5VU97	VWFA and cache domain-containing protein 1;	-0.76	-0.46	0.55	2.00
O75083	WD repeat-containing protein 1;	-2.25	-1.61	0.10	17.30
Q8NI36	WD repeat-containing protein 36;	0.38	0.02	0.67	2.60
Q15061	WD repeat-containing protein 43;	-0.43	-0.05	0.64	1.60
Q6UXN9	WD repeat-containing protein 82;	-2.64	-0.50	0.00	4.50
Q96FK6	WD repeat-containing protein 89;	-0.27	-0.06	0.78	7.80
Q2TAY7	WD40 repeat-containing protein SMU1;	0.37	0.03	0.69	3.90
P13010	X-ray repair cross-complementing protein 5;	0.12	0.06	0.91	21.30
P12956	X-ray repair cross-complementing protein 6;	0.20	0.04	0.83	23.20
Q9NQW7	Xaa-Pro aminopeptidase 1;	0.07	0.04	0.95	9.50
P12955	Xaa-Pro dipeptidase;	-0.89	-0.58	0.49	8.90
Q9H1B5	Xylosyltransferase 2;	0.15	0.01	0.86	1.70
Q7Z739	YTH domain family protein 3;	0.43	0.03	0.63	1.60
Q6PJT7	Zinc finger CCCH domain-containing protein 14;	0.06	0.01	0.95	1.50
Q7Z2W4	Zinc finger CCCH-type antiviral protein 1;	0.03	0.00	0.98	1.30
O43670	Zinc finger protein 207;	-0.89	-0.23	0.36	7.70
O75312	Zinc finger protein ZPR1;	0.26	0.02	0.77	2.80
O95218	Zinc finger Ran-binding domain-containing protein 2;	-1.60	-0.15	0.08	2.40
Q96KR1	Zinc finger RNA-binding protein;	-0.17	-0.02	0.85	1.30
Q9ULF5	Zinc transporter ZIP10;	1.66	1.74	0.34	3.00
Q13433	Zinc transporter ZIP6;	5.55	2.78	0.00	1.30
P25311	Zinc-alpha-2-glycoprotein;	0.15	0.07	0.89	13.10
Q15942	Zyxin;	-2.18	-2.38	0.22	3.80
O14980		-0.56	-0.21	0.60	12.20