Table S2: Identified and quantified proteins in the second 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 (%)**
Q04446	1,4-alpha-glucan-branching enzyme;	-0.56	-0.17	0.48	4.40
P61604	10 kDa heat shock protein, mitochondrial;	1.05	0.10	0.17	16.70
Q15029	116 kDa U5 small nuclear ribonucleoprotein component;	0.78	0.13	0.34	6.80
P31946	14-3-3 protein beta/alpha;	-0.35	-0.09	0.63	41.50
Q04917	14-3-3 protein eta;	-0.21	-0.07	0.78	26.80
P61981	14-3-3 protein gamma;	-0.35	-0.03	0.60	24.30
P31947	14-3-3 protein sigma;	-0.37	-0.04	0.58	11.70
P27348	14-3-3 protein theta;	-0.37	-0.07	0.60	34.70
P63104	14-3-3 protein zeta/delta;	-0.16	-0.03	0.79	34.70
P62191	26S protease regulatory subunit 4;	-1.18	-1.22	0.47	9.10
Q99460	26S proteasome non-ATPase regulatory subunit 1;	-0.19	-0.02	0.76	2.00
O00231	26S proteasome non-ATPase regulatory subunit 11;	0.38	0.13	0.71	8.50
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13;	-0.16	-0.02	0.78	6.10
Q13200	26S proteasome non-ATPase regulatory subunit 2;	-0.37	-0.20	0.70	7.20
O43242	26S proteasome non-ATPase regulatory subunit 3;	0.78	0.22	0.38	2.10
Q15008	26S proteasome non-ATPase regulatory subunit 6;	0.52	0.03	0.52	2.30
O00233	26S proteasome non-ATPase regulatory subunit 9;	0.69	0.03	0.39	5.40
Q13442	28 kDa heat- and acid-stable phosphoprotein;	0.76	0.53	0.58	16.60
Q9Y2Q9	28S ribosomal protein S28, mitochondrial;	0.45	0.03	0.58	5.30
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial;	0.26	0.04	0.78	3.90
P42765	3-ketoacyl-CoA thiolase, mitochondrial;	1.67	0.21	0.03	5.30
O95861	3'(2'),5'-bisphosphate nucleotidase 1;	-0.33	-0.09	0.65	10.70
Q9BYD6	39S ribosomal protein L1, mitochondrial;	-0.16	-0.02	0.79	3.70
Q9Y3B7	39S ribosomal protein L11, mitochondrial;	7.19	2.33	0.00	6.20
P52815	39S ribosomal protein L12, mitochondrial;	2.43	0.19	0.00	12.60
Q8IXM3	39S ribosomal protein L41, mitochondrial;	4.04	0.62	0.00	8.00
Q13405	39S ribosomal protein L49, mitochondrial;	3.63	1.71	0.00	7.20
P25398	40S ribosomal protein S12;	0.76	0.11	0.35	25.00
P62841	40S ribosomal protein S15;	-0.16	-0.02	0.78	8.30
P62249	40S ribosomal protein S16;	0.27	0.07	0.78	21.20
P08708	40S ribosomal protein S17;	-1.28	-0.06	0.07	7.40
P62269	40S ribosomal protein S18;	-0.24	-0.01	0.70	7.20
P39019	40S ribosomal protein S19;	-0.21	-0.04	0.76	26.20
P15880	40S ribosomal protein S2;	-0.35	-0.24	0.75	26.60
P60866	40S ribosomal protein S20;	-0.49	-0.05	0.48	19.30
P63220	40S ribosomal protein S21;	0.27	0.07	0.78	39.80
P62266	40S ribosomal protein S23;	5.36	6.84	0.01	15.40
P62854	40S ribosomal protein S26;	0.46	0.02	0.57	7.80
Q71UM5	40S ribosomal protein S27-like;	0.76	0.09	0.34	13.10
P42677	40S ribosomal protein S27;	1.08	0.17	0.18	13.10
P62857	40S ribosomal protein S28;	1.12	0.20	0.17	17.40
P23396	40S ribosomal protein S3;	-0.16	-0.05	0.81	39.10
P62861	40S ribosomal protein S30;	0.32	0.01	0.71	16.90
P61247	40S ribosomal protein S3a;	0.51	0.17	0.59	18.60
P62701	40S ribosomal protein S4, X isoform;	-0.14	-0.05	0.83	25.90
P46782	40S ribosomal protein S5;	-0.33	-0.06	0.63	23.00
P62753	40S ribosomal protein S6;	-0.53	-0.05	0.44	14.10
P62241	40S ribosomal protein S8;	-0.33	-0.07	0.64	38.50
P46781	40S ribosomal protein S9;	-0.28	-0.02	0.66	9.80
P08865	40S ribosomal protein SA;	-0.21	-0.12	0.83	21.70
P08195	4F2 cell-surface antigen heavy chain;	1.05	0.79	0.45	12.50
Q01813	6-phosphofructokinase type C;	-0.67	-0.09	0.34	1.50
P08237	6-phosphofructokinase, muscle type;	-0.37	-0.06	0.59	1.50
O95336	6-phosphogluconolactonase;	-0.79	-0.50	0.48	24.40

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P10809	60 kDa heat shock protein, mitochondrial;	1.93	0.91	0.06	28.30
P10155	60 kDa SS-A/Ro ribonucleoprotein;	0.88	0.22	0.31	5.40
P05388	60S acidic ribosomal protein P0;	1.33	0.43	0.14	26.20
P05386	60S acidic ribosomal protein P1;	1.31	0.21	0.10	14.00
P05387	60S acidic ribosomal protein P2;	0.72	0.14	0.39	67.00
P62906	60S ribosomal protein L10a;	0.87	0.06	0.27	22.60
P62913	60S ribosomal protein L11;	0.32	0.03	0.72	12.90
P26373	60S ribosomal protein L13;	-0.56	-0.04	0.41	15.20
P40429	60S ribosomal protein L13a;	0.27	0.01	0.76	7.80
P61313	60S ribosomal protein L15;	-0.51	-0.53	0.74	14.20
P18621	60S ribosomal protein L17;	-0.49	-0.08	0.49	17.40
Q07020	60S ribosomal protein L18;	-0.60	-0.36	0.58	19.70
Q02543	60S ribosomal protein L18a;	-0.72	-0.08	0.30	14.80
P46778	60S ribosomal protein L21;	-0.60	-0.06	0.40	20.60
P35268	60S ribosomal protein L22;	-0.14	-0.01	0.80	10.20
P62829	60S ribosomal protein L23;	-1.18	-0.80	0.33	11.40
P62750	60S ribosomal protein L23a;	0.30	0.02	0.73	8.30
P83731	60S ribosomal protein L24;	-0.51	-0.13	0.50	19.10
P61254	60S ribosomal protein L26;	-0.16	-0.05	0.81	16.60
P61353	60S ribosomal protein L27;	-0.32	-0.09	0.68	36.00
P46776	60S ribosomal protein L27a;	-0.49	-0.04	0.47	14.20
P46779	60S ribosomal protein L28;	-0.35	-0.11	0.65	21.20
P47914	60S ribosomal protein L29;	-0.65	-0.07	0.36	9.40
P39023	60S ribosomal protein L3;	-0.69	-0.26	0.42	9.70
P62888	60S ribosomal protein L30;	-0.14	-0.01	0.80	24.30
P62910	60S ribosomal protein L32;	-0.60	-0.24	0.50	17.00
P18077	60S ribosomal protein L35a;	-0.41	-0.04	0.54	8.20
Q9Y3U8	60S ribosomal protein L36;	-0.49	-0.04	0.47	9.50
P36578	60S ribosomal protein L4;	-0.60	-0.15	0.44	12.90
P18124	60S ribosomal protein L7;	-0.82	-0.30	0.35	14.90
P62424	60S ribosomal protein L7a;	-0.14	-0.01	0.80	7.50
P32969	60S ribosomal protein L9;	-0.21	-0.13	0.83	10.90
P11021	78 kDa glucose-regulated protein;	0.86	0.14	0.29	27.20
Q7L2J0	7SK snRNA methylphosphate capping enzyme;	-1.28	-0.16	0.08	1.50
Q92667	A-kinase anchor protein 1, mitochondrial;	0.30	0.02	0.73	1.40
Q02952	A-kinase anchor protein 12;	-0.67	-0.31	0.48	17.40
O43823	A-kinase anchor protein 8;	2.21	0.58	0.01	2.90
P24752	Acetyl-CoA acetyltransferase, mitochondrial;	0.99	0.12	0.21	2.10
Q13510	Acid ceramidase;	-0.67	-0.23	0.43	14.70
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family men	-0.47	-0.05	0.50	4.50
P61160	Actin-related protein 2;	-1.51	-2.32	0.52	8.90
O15143	Actin-related protein 2/3 complex subunit 1B;	-0.37	-0.17	0.68	9.40
O15144	Actin-related protein 2/3 complex subunit 2;	0.68	0.03	0.39	3.30
P59998	Actin-related protein 2/3 complex subunit 4;	0.19	0.02	0.84	11.30
P62736	Actin, aortic smooth muscle;	1.03	0.04	0.18	25.00
P60709	Actin, cytoplasmic 1;	1.61	0.54	0.08	37.30
P53999	Activated RNA polymerase II transcriptional coactivator p	1.42	0.13	0.06	31.50
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	0.34	0.10	0.73	18.60
P07108	Acyl-CoA-binding protein;	-0.19	-0.04	0.78	9.20
P13798	Acylamino-acid-releasing enzyme;	-0.77	-0.37	0.43	5.70
P07311	Acylphosphatase-1;	0.35	0.17	0.76	22.20
Q6UY14	ADAMTS-like protein 4;	-0.53	-0.14	0.48	1.80
P55263	Adenosine kinase;	-0.45	-0.23	0.65	9.10
P23526	Adenosylhomocysteinase;	-0.84	-0.35	0.35	12.70
P54819	Adenylate kinase 2, mitochondrial;	-0.22	-0.06	0.74	29.70
P00568	Adenylate kinase isoenzyme 1;	-0.16	-0.01	0.78	6.70
P30520	Adenylosuccinate synthetase isozyme 2;	1.30	0.82	0.29	12.70

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q01518	Adenylyl cyclase-associated protein 1;	-0.69	-0.32	0.47	16.60
P35318	ADM;	-2.80	-0.19	0.00	7.00
Q15041	ADP-ribosylation factor-like protein 6-interacting protein	0.92	0.04	0.24	4.90
Q66PJ3	ADP-ribosylation factor-like protein 6-interacting protein	2.38	0.44	0.00	4.40
Q9UKK9	ADP-sugar pyrophosphatase;	-0.22	-0.11	0.80	16.90
P05141	ADP/ATP translocase 2;	2.01	0.30	0.01	7.00
O00468	Agrin;	-0.60	-0.39	0.60	30.30
P14550	Alcohol dehydrogenase [NADP(+)];	0.64	0.46	0.65	12.00
P11766	Alcohol dehydrogenase class-3;	-1.04	-0.34	0.22	11.00
P47895	Aldehyde dehydrogenase family 1 member A3;	-1.18	-0.37	0.17	24.60
Q8IZ83	Aldehyde dehydrogenase family 16 member A1;	-0.12	-0.02	0.82	2.00
P17516	Aldo-keto reductase family 1 member C4;	0.59	0.07	0.46	3.70
P15121	Aldose reductase;	-0.99	-0.23	0.21	18.00
P05187	Alkaline phosphatase, placental type;	-0.67	-0.30	0.47	13.90
P02765	Alpha-2-HS-glycoprotein;	5.57	0.95	0.00	3.30
O43768	Alpha-endosulfine;	-0.53	-0.04	0.43	11.60
P06733	Alpha-enolase;	-0.65	-0.21	0.43	41.70
P06280	Alpha-galactosidase A;	0.38	0.10	0.69	7.90
P35475	Alpha-L-iduronidase;	-1.21	-0.08	0.09	2.00
P54920	Alpha-soluble NSF attachment protein;	-1.04	-2.33	0.75	15.60
P40222	Alpha-taxilin;	-0.32	-0.04	0.64	1.80
Q9BUJ0	Alpha/beta hydrolase domain-containing protein 14A;	2.84	0.53	0.00	3.70
Q06203	Amidophosphoribosyltransferase;	1.27	0.08	0.10	2.30
Q9H4A4	Aminopeptidase B;	1.04	0.97	0.53	3.20
P15514	Amphiregulin;	3.17	4.25	0.14	7.90
P05067	Amyloid beta A4 protein;	-0.60	-0.43	0.62	21.20
Q6FI81	Anamorsin;	-0.47	-0.16	0.57	8.30
P03950	Angiogenin;	2.34	0.15	0.00	6.10
P07355	Annexin A2;	-0.62	-0.14	0.41	52.80
P09525	Annexin A4;	-1.47	-1.14	0.27	6.60
P08758	Annexin A5;	-0.84	-0.39	0.38	25.90
P46013	Antigen KI-67;	0.99	0.36	0.30	6.30
Q10567	AP-1 complex subunit beta-1;	-0.51	-0.35	0.66	3.70
O95782	AP-2 complex subunit alpha-1;	-0.32	-0.08	0.67	3.40
Q96CW1	AP-2 complex subunit mu;	-0.14	-0.02	0.81	3.90
O00203	AP-3 complex subunit beta-1;	0.62	0.02	0.44	0.90
P02656	Apolipoprotein C-III;	0.77	0.13	0.35	16.20
Q9BZZ5	Apoptosis inhibitor 5;	-0.47	-0.21	0.60	4.20
Q07812	Apoptosis regulator BAX;	0.35	0.21	0.78	13.00
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus;	1.02	0.19	0.21	2.10
P54136	Arginine--tRNA ligase, cytoplasmic;	-0.72	-0.25	0.39	5.00
P04424	Argininosuccinate lyase;	-0.56	-0.11	0.44	3.00
P00966	Argininosuccinate synthase;	-0.96	-0.33	0.27	11.40
P17174	Aspartate aminotransferase, cytoplasmic;	-1.90	-3.40	0.48	10.90
P00505	Aspartate aminotransferase, mitochondrial;	0.23	0.04	0.81	20.70
P14868	Aspartate--tRNA ligase, cytoplasmic;	1.02	0.86	0.50	4.00
Q12797	Aspartyl/asparaginyl beta-hydroxylase;	7.98	2.35	0.00	2.40
Q8WWM7	Ataxin-2-like protein;	-1.56	-0.18	0.03	1.10
Q99700	Ataxin-2;	1.86	0.40	0.02	0.80
P25705	ATP synthase subunit alpha, mitochondrial;	3.53	5.01	0.12	14.10
P06576	ATP synthase subunit beta, mitochondrial;	3.70	3.04	0.01	23.60
O75947	ATP synthase subunit d, mitochondrial;	1.89	0.12	0.01	12.40
P30049	ATP synthase subunit delta, mitochondrial;	5.01	4.58	0.00	8.30
P48047	ATP synthase subunit O, mitochondrial;	-1.79	-0.25	0.02	13.10
P18859	ATP synthase-coupling factor 6, mitochondrial;	2.56	0.13	0.00	8.30
Q8NE71	ATP-binding cassette sub-family F member 1;	-0.22	-0.03	0.73	3.70
Q9UG63	ATP-binding cassette sub-family F member 2;	-0.16	-0.01	0.78	1.60

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P53396	ATP-citrate synthase;	-1.14	-0.53	0.24	19.30
Q08211	ATP-dependent RNA helicase A;	2.09	1.75	0.16	7.70
Q92499	ATP-dependent RNA helicase DDX1;	-0.39	-0.06	0.56	2.30
Q9NUU7	ATP-dependent RNA helicase DDX19A;	0.42	0.05	0.62	4.40
Q9GZR7	ATP-dependent RNA helicase DDX24;	5.45	2.80	0.00	1.60
O00148	ATP-dependent RNA helicase DDX39A;	-0.21	-0.02	0.74	15.20
Q86XP3	ATP-dependent RNA helicase DDX42;	0.40	0.05	0.64	3.30
Q9NVI7	ATPase family AAA domain-containing protein 3A;	4.02	1.39	0.00	4.90
O95816	BAG family molecular chaperone regulator 2;	0.65	0.06	0.42	5.20
O95817	BAG family molecular chaperone regulator 3;	-0.21	-0.03	0.75	2.30
Q9H4G0	Band 4.1-like protein 1;	1.23	0.18	0.12	1.20
P50895	Basal cell adhesion molecule;	-0.82	-1.03	0.67	19.40
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1;	-0.69	-0.05	0.31	2.40
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2;	0.28	0.08	0.78	4.50
P35613	Basigin;	1.26	0.11	0.10	3.60
P15291	Beta-1,4-galactosyltransferase 1;	0.25	0.02	0.79	8.00
O60512	Beta-1,4-galactosyltransferase 3;	0.19	0.01	0.84	2.00
O60513	Beta-1,4-galactosyltransferase 4;	-2.14	-2.54	0.25	9.90
P02749	Beta-2-glycoprotein 1;	0.80	0.34	0.43	5.20
P61769	Beta-2-microglobulin;	0.46	0.03	0.57	16.80
P16278	Beta-galactosidase;	-0.41	-0.16	0.62	15.50
P08236	Beta-glucuronidase;	1.70	1.98	0.38	2.80
P07686	Beta-hexosaminidase subunit beta;	0.32	0.07	0.73	24.60
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synth	-1.14	-0.20	0.13	1.90
P53004	Biliverdin reductase A;	-0.24	-0.01	0.70	2.70
Q9H3K6	BolA-like protein 2;	-0.28	-0.04	0.67	18.60
P13497	Bone morphogenetic protein 1;	-0.32	-0.06	0.65	8.40
P22003	Bone morphogenetic protein 5;	3.12	0.54	0.00	2.20
Q9P287	BRCA2 and CDKN1A-interacting protein;	0.90	0.04	0.24	2.90
Q9NQY0	Bridging integrator 3;	3.12	0.20	0.00	3.60
O60885	Bromodomain-containing protein 4;	-1.47	-0.24	0.05	1.80
P11586	C-1-tetrahydrofolate synthase, cytoplasmic;	-0.28	-0.15	0.76	15.40
Q99417	C-Myc-binding protein;	-0.79	-0.11	0.28	19.40
P56545	C-terminal-binding protein 2;	-0.32	-0.21	0.77	4.30
Q9UBG0	C-type mannose receptor 2;	-3.15	-1.95	0.01	1.80
P80162	C-X-C motif chemokine 6;	2.23	0.27	0.00	10.50
Q96EU7	C1GALT1-specific chaperone 1;	4.80	0.71	0.00	2.80
P05937	Calbindin;	1.61	0.10	0.03	4.20
P63098	Calcineurin subunit B type 1;	0.71	0.11	0.38	5.90
Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1;	2.92	1.54	0.01	6.50
Q9Y2V2	Calcium-regulated heat stable protein 1;	-1.04	-0.11	0.14	10.90
Q9HB71	Calcyclin-binding protein;	0.30	0.13	0.80	11.00
Q05682	Caldesmon;	-2.69	-2.60	0.09	7.80
P62158	Calmodulin;	0.38	0.12	0.70	13.40
P27824	Calnexin;	3.91	0.89	0.00	6.60
P17655	Calpain-2 catalytic subunit;	-0.24	-0.18	0.83	2.10
P27797	Calreticulin;	1.11	0.09	0.15	7.90
O43852	Calumenin;	0.81	0.28	0.39	20.00
P10644	cAMP-dependent protein kinase type I-alpha regulatory su	-0.41	-0.33	0.74	9.70
P30622	CAP-Gly domain-containing linker protein 1;	-0.22	-0.10	0.79	0.80
Q14444	Caprin-1;	-0.26	-0.01	0.68	1.60
Q8NCH0	Carbohydrate sulfotransferase 14;	-0.72	-0.34	0.45	18.90
P16152	Carbonyl reductase [NADPH] 1;	-4.01	-7.77	0.17	10.10
Q96DG6	Carboxymethylenebutenolidase homolog;	0.34	0.11	0.73	6.50
P19784	Casein kinase II subunit alpha';	2.13	0.23	0.01	3.70
P67870	Casein kinase II subunit beta;	0.94	0.15	0.24	6.50
P07339	Cathepsin D;	-0.65	-1.03	0.78	29.40

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P07711	Cathepsin L1;	2.32	0.59	0.01	13.50
P11717	Cation-independent mannose-6-phosphate receptor;	0.42	0.11	0.65	5.70
Q03135	Caveolin-1;	-0.65	-0.07	0.36	7.90
Q6YHK3	CD109 antigen;	0.70	0.16	0.41	10.90
Q13740	CD166 antigen;	1.07	0.20	0.19	13.60
Q9Y5K6	CD2-associated protein;	-0.45	-0.03	0.51	1.40
P16070	CD44 antigen;	-1.18	-0.58	0.25	9.80
P13987	CD59 glycoprotein;	2.23	0.19	0.00	9.40
P60033	CD81 antigen;	-0.33	-0.04	0.62	8.50
P60953	Cell division control protein 42 homolog;	0.48	0.07	0.57	8.90
Q99459	Cell division cycle 5-like protein;	3.06	0.34	0.00	3.20
Q99674	Cell growth regulator with EF hand domain protein 1;	-0.22	-0.07	0.76	15.60
Q5SW79	Centrosomal protein of 170 kDa;	10.01	2.83	0.00	0.90
Q53EZ4	Centrosomal protein of 55 kDa;	1.09	0.13	0.16	2.80
O00299	Chloride intracellular channel protein 1;	0.34	0.07	0.71	32.00
Q9Y696	Chloride intracellular channel protein 4;	-0.21	-0.03	0.75	17.40
Q6UVK1	Chondroitin sulfate proteoglycan 4;	-0.65	-0.26	0.47	4.20
Q13185	Chromobox protein homolog 3;	0.46	0.17	0.65	28.40
P45973	Chromobox protein homolog 5;	0.88	0.31	0.36	22.50
O75390	Citrate synthase, mitochondrial;	0.59	0.22	0.55	10.10
Q00610	Clathrin heavy chain 1;	0.77	0.25	0.41	5.30
P09496	Clathrin light chain A;	0.59	0.26	0.58	9.70
Q10570	Cleavage and polyadenylation specificity factor subunit 1;	0.25	0.01	0.79	0.70
O95639	Cleavage and polyadenylation specificity factor subunit 4;	-1.43	-0.12	0.05	3.30
Q16630	Cleavage and polyadenylation specificity factor subunit 6;	-1.96	-0.15	0.01	2.50
P33240	Cleavage stimulation factor subunit 2;	-1.28	-0.22	0.09	3.80
Q7Z460	CLIP-associating protein 1;	-0.41	-0.07	0.55	1.70
P10909	Clusterin;	-1.47	-1.47	0.36	27.40
Q14019	Coactosin-like protein;	-0.87	-0.19	0.25	22.50
P48444	Coatomer subunit delta;	-0.49	-0.04	0.47	2.20
O14579	Coatomer subunit epsilon;	-0.21	-0.04	0.75	3.60
O43405	Cochlin;	3.18	2.48	0.02	11.80
P23528	Cofilin-1;	-0.22	-0.05	0.74	45.20
Q96CT7	Coiled-coil domain-containing protein 124;	-0.22	-0.02	0.72	5.80
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing prot	1.82	0.14	0.02	4.80
O75534	Cold shock domain-containing protein E1;	-0.45	-0.15	0.58	1.50
Q14011	Cold-inducible RNA-binding protein;	0.84	0.31	0.39	20.90
P02462	Collagen alpha-1(IV) chain;	1.55	0.20	0.05	0.80
P12109	Collagen alpha-1(VI) chain;	1.26	0.45	0.18	16.40
Q99715	Collagen alpha-1(XII) chain;	-1.47	-0.81	0.17	8.00
P39060	Collagen alpha-1(XVIII) chain;	1.03	0.24	0.22	2.10
P05997	Collagen alpha-2(V) chain;	4.65	5.70	0.02	4.70
P00736	Complement C1r subcomponent;	0.95	0.71	0.50	12.30
P09871	Complement C1s subcomponent;	1.76	0.09	0.02	1.60
P01024	Complement C3;	2.61	1.53	0.02	33.00
Q07021	Complement component 1 Q subcomponent-binding prote	1.20	0.18	0.13	11.70
P00751	Complement factor B;	-0.26	-0.10	0.74	8.10
P00746	Complement factor D;	1.66	0.22	0.03	8.70
P29279	Connective tissue growth factor;	-1.96	-1.44	0.13	10.00
Q13098	COP9 signalosome complex subunit 1;	0.59	0.24	0.56	4.50
Q9BT78	COP9 signalosome complex subunit 4;	-0.53	-0.20	0.53	6.20
Q92905	COP9 signalosome complex subunit 5;	-0.14	-0.02	0.80	4.50
P36551	Coproporphyrinogen-III oxidase, mitochondrial;	-0.35	-0.03	0.60	3.70
O75367	Core histone macro-H2A.1;	1.60	1.22	0.25	8.90
P31146	Coronin-1A;	-0.37	-0.06	0.59	2.20
Q9BR76	Coronin-1B;	-0.65	-0.20	0.43	5.90
Q9ULV4	Coronin-1C;	0.26	0.01	0.77	2.10

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9P1F3	Costars family protein ABRACL;	-0.32	-0.06	0.65	16.00
P12277	Creatine kinase B-type;	2.38	2.95	0.24	34.60
Q92793	CREB-binding protein;	-2.21	-0.10	0.00	0.40
P46109	Crk-like protein;	-0.62	-0.11	0.39	10.60
Q86VP6	Cullin-associated NEDD8-dissociated protein 1;	-0.82	-0.49	0.46	10.50
O15320	Cutaneous T-cell lymphoma-associated antigen 5;	1.74	4.98	0.70	3.20
P18846	Cyclic AMP-dependent transcription factor ATF-1;	-5.57	0.00	0.00	2.60
P61024	Cyclin-dependent kinases regulatory subunit 1;	-0.33	-0.02	0.61	12.70
P33552	Cyclin-dependent kinases regulatory subunit 2;	-1.85	-0.80	0.05	24.10
P01034	Cystatin-C;	1.86	0.35	0.02	30.10
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1;	-0.69	-0.44	0.53	7.20
P49589	Cysteine--tRNA ligase, cytoplasmic;	0.58	0.78	0.80	2.40
Q9NZV1	Cysteine-rich motor neuron 1 protein;	-0.41	-0.10	0.57	10.40
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial;	3.36	3.63	0.06	16.50
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial;	3.12	0.43	0.00	3.50
Q9UDW1	Cytochrome b-c1 complex subunit 9;	2.81	0.58	0.00	27.00
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial;	3.02	0.31	0.00	5.10
O43169	Cytochrome b5 type B;	-0.41	-0.04	0.54	8.20
P00167	Cytochrome b5;	3.65	2.49	0.00	26.10
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	3.51	0.33	0.00	6.50
P10606	Cytochrome c oxidase subunit 5B, mitochondrial;	3.45	1.50	0.00	17.80
P14854	Cytochrome c oxidase subunit 6B1;	3.96	3.22	0.01	26.70
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial;	0.72	1.54	0.83	27.70
P99999	Cytochrome c;	-0.84	-0.29	0.31	24.80
Q14204	Cytoplasmic dynein 1 heavy chain 1;	0.32	0.17	0.80	1.70
Q13409	Cytoplasmic dynein 1 intermediate chain 2;	-0.22	-0.13	0.81	5.00
Q07065	Cytoskeleton-associated protein 4;	3.02	2.23	0.02	5.60
P28838	Cytosol aminopeptidase;	-0.41	-0.26	0.70	4.60
O00154	Cytosolic acyl coenzyme A thioester hydrolase;	-1.04	-0.50	0.29	12.40
Q96KP4	Cytosolic non-specific dipeptidase;	-0.53	-0.35	0.63	13.30
O43175	D-3-phosphoglycerate dehydrogenase;	0.63	0.08	0.44	6.00
P30046	D-dopachrome decarboxylase;	-0.21	-0.11	0.82	16.10
Q8N163	DBIRD complex subunit KIAA1967;	-1.60	-2.23	0.45	4.00
Q5BKZ1	DBIRD complex subunit ZNF326;	1.22	0.55	0.24	4.30
Q9H773	dCTP pyrophosphatase 1;	-1.14	-0.58	0.27	11.20
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitoch	-0.32	-0.06	0.65	31.00
Q14126	Desmoglein-2;	-0.65	-0.25	0.46	3.40
P60981	Destrin;	-0.84	-0.12	0.24	14.50
Q9Y295	Developmentally-regulated GTP-binding protein 1;	-1.14	-0.08	0.11	8.20
Q9NR28	Diablo homolog, mitochondrial;	0.25	0.02	0.79	4.60
O94907	Dickkopf-related protein 1;	1.65	0.93	0.15	25.90
P09622	Dihydrolipoyl dehydrogenase, mitochondrial;	0.84	0.04	0.28	10.40
P09417	Dihydropteridine reductase;	-0.96	-0.30	0.26	15.60
Q16555	Dihydropyrimidinase-related protein 2;	0.30	0.12	0.78	11.70
P53634	Dipeptidyl peptidase 1;	2.26	0.50	0.01	13.40
Q9UHL4	Dipeptidyl peptidase 2;	0.72	0.29	0.47	15.70
Q9NY33	Dipeptidyl peptidase 3;	0.80	1.70	0.82	3.70
Q13444	Disintegrin and metalloproteinase domain-containing prot	0.34	0.03	0.69	5.30
Q12959	Disks large homolog 1;	1.34	0.42	0.14	2.30
P26358	DNA (cytosine-5)-methyltransferase 1;	-0.26	-0.02	0.68	0.70
O00273	DNA fragmentation factor subunit alpha;	-0.33	-0.04	0.62	5.10
Q9ULG1	DNA helicase INO80;	3.85	0.70	0.00	0.70
P18858	DNA ligase 1;	-2.35	-3.00	0.23	3.00
P43246	DNA mismatch repair protein Msh2;	0.64	0.03	0.42	0.90
Q15054	DNA polymerase delta subunit 3;	-0.90	-0.37	0.32	2.80
P18887	DNA repair protein XRCC1;	-1.74	-0.23	0.02	3.80
P33993	DNA replication licensing factor MCM7;	-0.22	-0.08	0.77	4.60

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Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P11387	DNA topoisomerase 1;	0.78	1.01	0.72	2.90
P27695	DNA-(apurinic or apyrimidinic site) lyase;	0.89	0.12	0.26	9.40
P16989	DNA-binding protein A;	0.42	0.04	0.61	13.70
O15160	DNA-directed RNA polymerases I and III subunit RPAC1	0.66	0.08	0.41	3.80
P52434	DNA-directed RNA polymerases I, II, and III subunit RPA	0.92	0.09	0.24	8.70
Q8WXX5	DnaJ homolog subfamily C member 9;	0.53	0.30	0.66	15.40
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltrans	3.04	2.57	0.04	4.60
O95793	Double-stranded RNA-binding protein Staufen homolog 1	0.27	0.02	0.76	4.50
Q9UJU6	Drebrin-like protein;	-2.90	-0.22	0.00	3.30
Q16643	Drebrin;	1.77	0.36	0.03	4.30
P51452	Dual specificity protein phosphatase 3;	-0.32	-0.10	0.68	12.40
Q13561	Dynactin subunit 2;	0.35	0.22	0.79	12.20
O00429	Dynamin-1-like protein;	-0.90	-0.03	0.19	1.40
Q96FJ2	Dynein light chain 2, cytoplasmic;	0.55	0.32	0.66	32.60
Q8TF09	Dynein light chain roadblock-type 2;	-1.28	-0.16	0.08	12.50
Q14118	Dystroglycan;	0.34	0.09	0.72	9.80
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1;	-0.56	-0.09	0.43	2.00
Q14258	E3 ubiquitin/ISG15 ligase TRIM25;	-1.18	-1.11	0.45	12.90
Q15075	Early endosome antigen 1;	2.22	0.68	0.01	6.20
Q96C19	EF-hand domain-containing protein D2;	0.58	0.15	0.52	8.30
Q9H4M9	EH domain-containing protein 1;	0.55	0.12	0.53	7.30
Q15717	ELAV-like protein 1;	1.81	1.94	0.32	15.60
P68104	Elongation factor 1-alpha 1;	-0.22	-0.09	0.78	14.90
Q05639	Elongation factor 1-alpha 2;	5.03	0.68	0.00	11.00
P29692	Elongation factor 1-delta;	-0.33	-0.09	0.66	17.40
P26641	Elongation factor 1-gamma;	-0.69	-0.68	0.65	13.00
P13639	Elongation factor 2;	-0.53	-0.22	0.54	16.40
P50402	Emerin;	-1.14	-0.70	0.32	9.80
Q99961	Endophilin-A2;	0.60	0.09	0.46	5.40
P30040	Endoplasmic reticulum resident protein 29;	1.48	0.81	0.19	21.80
P14625	Endoplasmin;	1.68	0.68	0.08	10.80
Q9UNN8	Endothelial protein C receptor;	-0.77	-0.08	0.28	20.60
P84090	Enhancer of rudimentary homolog;	0.74	0.06	0.35	26.90
P42126	Enoyl-CoA delta isomerase 1, mitochondrial;	1.04	0.18	0.20	4.30
P30084	Enoyl-CoA hydratase, mitochondrial;	2.69	0.72	0.00	5.90
P20827	Ephrin-A1;	-0.56	-0.02	0.41	8.30
P98172	Ephrin-B1;	-0.24	-0.03	0.70	5.80
P52799	Ephrin-B2;	-0.24	-0.08	0.75	14.10
P00533	Epidermal growth factor receptor;	-1.39	-1.83	0.49	11.20
P61916	Epididymal secretory protein E1;	1.14	0.46	0.25	39.70
Q9Y2E5	Epididymis-specific alpha-mannosidase;	-1.18	-0.80	0.33	5.40
Q96HE7	ERO1-like protein alpha;	-1.39	-2.01	0.53	6.00
Q9H501	ESF1 homolog;	2.43	2.29	0.13	4.90
P60842	Eukaryotic initiation factor 4A-I;	0.82	0.18	0.33	16.00
Q14240	Eukaryotic initiation factor 4A-II;	-0.77	-0.09	0.29	10.10
P38919	Eukaryotic initiation factor 4A-III;	2.84	1.68	0.01	5.40
P15170	Eukaryotic peptide chain release factor GTP-binding subu	-0.19	-0.10	0.83	3.80
P62495	Eukaryotic peptide chain release factor subunit 1;	-0.14	-0.04	0.82	15.30
O14602	Eukaryotic translation initiation factor 1A, Y-chromosoma	-0.99	-0.63	0.39	14.60
P05198	Eukaryotic translation initiation factor 2 subunit 1;	0.30	0.06	0.74	25.70
P20042	Eukaryotic translation initiation factor 2 subunit 2;	4.35	0.63	0.00	3.00
P41091	Eukaryotic translation initiation factor 2 subunit 3;	-0.60	-0.49	0.65	8.90
Q9BY44	Eukaryotic translation initiation factor 2A;	-1.08	-0.20	0.15	9.60
Q14152	Eukaryotic translation initiation factor 3 subunit A;	0.49	0.38	0.75	3.90
Q99613	Eukaryotic translation initiation factor 3 subunit C;	-0.79	-0.72	0.58	6.00
P60228	Eukaryotic translation initiation factor 3 subunit E;	-0.21	-0.05	0.76	8.80
O75821	Eukaryotic translation initiation factor 3 subunit G;	0.42	0.26	0.74	18.80

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q13347	Eukaryotic translation initiation factor 3 subunit I;	0.27	0.07	0.79	12.60
O75822	Eukaryotic translation initiation factor 3 subunit J;	-0.67	-0.29	0.46	11.60
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K;	-2.08	-0.09	0.00	11.50
Q9Y262	Eukaryotic translation initiation factor 3 subunit L;	-0.45	-0.15	0.58	5.30
P55010	Eukaryotic translation initiation factor 5;	4.66	0.24	0.00	2.30
P56537	Eukaryotic translation initiation factor 6;	0.88	0.07	0.26	8.60
Q15024	Exosome complex component RRP42;	0.37	0.03	0.66	4.10
Q16394	Exostosin-1;	-1.08	-0.52	0.28	2.80
O14980	Exportin-1;	-1.04	-0.80	0.42	2.60
P55060	Exportin-2;	0.25	0.04	0.80	3.80
Q9BSJ8	Extended synaptotagmin-1;	0.74	0.08	0.36	1.40
Q16610	Extracellular matrix protein 1;	0.75	0.16	0.38	15.70
P15311	Ezrin;	-0.84	-0.20	0.27	14.00
P52907	F-actin-capping protein subunit alpha-1;	0.19	0.02	0.84	17.80
P47756	F-actin-capping protein subunit beta;	0.26	0.09	0.82	17.70
O60907	F-box-like/WD repeat-containing protein TBL1X;	0.50	0.06	0.55	2.50
Q9Y5B9	FACT complex subunit SPT16;	1.85	0.58	0.04	8.60
Q08945	FACT complex subunit SSRP1;	0.89	0.78	0.57	9.90
Q96AE4	Far upstream element-binding protein 1;	0.60	0.98	0.83	4.80
P14324	Farnesyl pyrophosphate synthase;	0.55	0.06	0.50	14.80
Q9UNN5	FAS-associated factor 1;	-0.47	-0.44	0.75	4.60
Q01469	Fatty acid-binding protein, epidermal;	-0.16	-0.03	0.79	37.00
Q96AC1	Fermitin family homolog 2;	0.88	0.89	0.61	5.10
P02794	Ferritin heavy chain;	-0.62	-0.14	0.41	18.60
Q14512	Fibroblast growth factor-binding protein 1;	-0.69	-0.13	0.34	18.40
P02751	Fibronectin;	-2.28	-1.99	0.11	3.10
P21333	Filamin-A;	0.25	0.10	0.84	26.10
Q14315	Filamin-C;	-0.77	-0.39	0.45	14.70
P30043	Flavin reductase (NADPH);	-0.79	-0.08	0.27	4.90
Q96CP2	FLYWCH family member 2;	0.46	0.08	0.59	8.60
O95633	Follistatin-related protein 3;	-1.51	-3.31	0.64	20.90
Q86VR8	Four-jointed box protein 1;	-1.32	-0.46	0.13	10.50
P04075	Fructose-bisphosphate aldolase A;	-0.22	-0.06	0.74	42.00
P09972	Fructose-bisphosphate aldolase C;	-0.28	-0.11	0.72	21.20
P22466	Galanin peptides;	2.52	0.35	0.00	12.20
P09382	Galectin-1;	-0.24	-0.08	0.74	45.20
Q08380	Galectin-3-binding protein;	0.96	0.20	0.25	28.20
P17931	Galectin-3;	0.21	0.02	0.82	14.80
O75223	Gamma-glutamylcyclotransferase;	0.34	0.03	0.69	11.20
P13284	Gamma-interferon-inducible lysosomal thiol reductase;	0.97	0.04	0.21	8.00
Q16666	Gamma-interferon-inducible protein 16;	0.81	0.32	0.42	3.40
P17900	Ganglioside GM2 activator;	-1.21	-1.14	0.43	17.60
Q13630	GDP-L-fucose synthase;	-0.65	-0.05	0.35	11.50
P06396	Gelsolin;	0.32	0.07	0.74	18.70
P35269	General transcription factor IIF subunit 1;	-0.56	-0.12	0.45	4.40
P13984	General transcription factor IIF subunit 2;	-0.51	-0.06	0.46	6.80
O60763	General vesicular transport factor p115;	0.62	0.03	0.44	0.90
P07093	Glia-derived nexin;	1.00	0.53	0.37	12.60
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase;	-0.28	-0.02	0.66	9.80
P14314	Glucosidase 2 subunit beta;	0.87	0.40	0.41	8.30
P00367	Glutamate dehydrogenase 1, mitochondrial;	1.90	1.23	0.12	14.20
P48507	Glutamate--cysteine ligase regulatory subunit;	-0.69	-0.09	0.33	5.80
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isome	-0.99	-0.45	0.31	4.40
P47897	Glutamine--tRNA ligase;	-0.39	-0.36	0.78	4.40
O76003	Glutaredoxin-3;	0.55	0.39	0.70	17.90
Q86SX6	Glutaredoxin-related protein 5, mitochondrial;	0.76	0.14	0.36	15.90
P78417	Glutathione S-transferase omega-1;	0.45	0.06	0.60	24.50

Table S2

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P09211	Glutathione S-transferase P;	-0.21	-0.10	0.81	45.70
P48637	Glutathione synthetase;	-1.60	-3.00	0.57	3.60
P04406	Glyceraldehyde-3-phosphate dehydrogenase;	-0.45	-0.09	0.54	30.70
P41250	Glycine--tRNA ligase;	-1.14	-0.40	0.20	3.80
P11216	Glycogen phosphorylase, brain form;	-1.39	-1.10	0.31	14.20
P06737	Glycogen phosphorylase, liver form;	0.43	0.19	0.69	14.30
P49915	GMP synthase [glutamine-hydrolyzing];	-0.14	-0.04	0.83	6.60
Q8NBJ4	Golgi membrane protein 1;	-0.84	-0.17	0.26	23.70
P28799	Granulins;	-2.80	-2.33	0.04	11.30
Q8NCC3	Group XV phospholipase A2;	-0.32	-0.07	0.67	9.20
P09341	Growth-regulated alpha protein;	3.82	0.44	0.00	27.10
Q99988	Growth/differentiation factor 15;	-0.41	-0.11	0.58	8.80
P62826	GTP-binding nuclear protein Ran;	-0.35	-0.04	0.60	30.60
Q9Y2T3	Guanine deaminase;	-0.33	-0.11	0.68	24.70
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subun	1.55	0.20	0.05	9.70
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subun	1.70	0.72	0.09	10.00
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;	-0.22	-0.15	0.83	17.70
Q9NX24	H/ACA ribonucleoprotein complex subunit 2;	2.19	0.28	0.00	12.40
O60832	H/ACA ribonucleoprotein complex subunit 4;	1.49	1.24	0.31	9.90
P08107	Heat shock 70 kDa protein 1A/1B;	0.18	0.03	0.86	25.90
P34932	Heat shock 70 kDa protein 4;	-0.60	-0.33	0.56	17.30
P11142	Heat shock cognate 71 kDa protein;	-0.47	-0.27	0.65	41.30
Q92598	Heat shock protein 105 kDa;	-0.32	-0.10	0.69	17.50
P07900	Heat shock protein HSP 90-alpha;	-0.21	-0.04	0.76	34.70
P08238	Heat shock protein HSP 90-beta;	-0.05	-0.01	0.90	21.80
P54652	Heat shock-related 70 kDa protein 2;	2.64	0.19	0.00	14.40
P69905	Hemoglobin subunit alpha;	0.56	0.08	0.50	28.20
P02042	Hemoglobin subunit delta;	-1.01	-0.57	0.34	12.90
Q7Z4V5	Hepatoma-derived growth factor-related protein 2;	0.10	0.04	0.95	6.30
P51858	Hepatoma-derived growth factor;	-0.41	-0.33	0.74	25.80
Q5SSJ5	Heterochromatin protein 1-binding protein 3;	2.56	0.08	0.00	2.70
Q99729	Heterogeneous nuclear ribonucleoprotein A/B;	0.55	0.13	0.54	12.30
Q13151	Heterogeneous nuclear ribonucleoprotein A0;	-2.35	-0.24	0.00	6.60
P09651	Heterogeneous nuclear ribonucleoprotein A1;	1.25	0.81	0.32	14.00
P51991	Heterogeneous nuclear ribonucleoprotein A3;	1.63	0.22	0.04	14.00
O14979	Heterogeneous nuclear ribonucleoprotein D-like;	0.51	0.11	0.56	7.60
Q14103	Heterogeneous nuclear ribonucleoprotein D0;	0.60	0.17	0.51	11.80
P52597	Heterogeneous nuclear ribonucleoprotein F;	-0.47	-0.21	0.60	28.40
P31943	Heterogeneous nuclear ribonucleoprotein H;	0.65	0.27	0.53	25.40
P31942	Heterogeneous nuclear ribonucleoprotein H3;	1.38	0.53	0.15	17.90
P61978	Heterogeneous nuclear ribonucleoprotein K;	0.82	0.32	0.41	29.60
P52272	Heterogeneous nuclear ribonucleoprotein M;	1.56	0.55	0.09	2.70
O60506	Heterogeneous nuclear ribonucleoprotein Q;	1.51	0.80	0.17	27.40
O43390	Heterogeneous nuclear ribonucleoprotein R;	1.24	0.80	0.32	16.70
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2;	-1.96	-0.15	0.01	1.90
Q00839	Heterogeneous nuclear ribonucleoprotein U;	1.63	0.43	0.06	6.10
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1;	1.96	1.27	0.11	35.10
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2;	2.45	0.26	0.00	19.00
P19367	Hexokinase-1;	0.81	1.44	0.78	7.10
P09429	High mobility group protein B1;	0.21	0.02	0.82	17.70
P26583	High mobility group protein B2;	0.21	0.01	0.82	18.20
O15347	High mobility group protein B3;	-0.60	-0.05	0.39	6.50
P17096	High mobility group protein HMG-I/HMG-Y;	2.74	0.21	0.00	22.40
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	1.11	0.17	0.16	9.20
P12081	Histidine--tRNA ligase, cytoplasmic;	0.26	0.05	0.79	10.80
Q13547	Histone deacetylase 1;	-0.16	-0.01	0.78	5.00
P10412	Histone H1.4;	0.58	0.15	0.51	15.00

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P16401	Histone H1.5;	1.28	0.33	0.14	10.20
Q92522	Histone H1x;	1.02	0.17	0.21	7.00
P04908	Histone H2A type 1-B/E;	0.37	0.05	0.67	21.70
P0C0S5	Histone H2A.Z;	2.25	1.00	0.02	25.80
O60814	Histone H2B type 1-K;	-0.19	-0.02	0.76	14.30
P68431	Histone H3.1;	-0.47	-0.23	0.62	5.20
P62805	Histone H4;	-0.96	-0.41	0.31	49.50
P01892	HLA class I histocompatibility antigen, A-2 alpha chain;	0.57	0.04	0.48	23.00
P13747	HLA class I histocompatibility antigen, alpha chain E;	-0.39	-0.17	0.66	10.30
P10321	HLA class I histocompatibility antigen, Cw-7 alpha chain;	1.14	0.66	0.33	23.00
P51610	Host cell factor 1;	0.59	0.21	0.54	1.00
P50502	Hsc70-interacting protein;	-0.24	-0.10	0.76	15.70
Q16543	Hsp90 co-chaperone Cdc37;	-0.19	-0.04	0.77	10.30
Q96S86	Hyaluronan and proteoglycan link protein 3;	-0.99	-0.80	0.47	8.60
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	2.84	0.20	0.00	2.50
Q9Y4L1	Hypoxia up-regulated protein 1;	-1.39	-1.83	0.49	3.70
Q969P0	Immunoglobulin superfamily member 8;	-1.69	-0.16	0.02	2.60
Q13308	Inactive tyrosine-protein kinase 7;	-0.99	-0.51	0.33	6.40
P12268	Inosine-5'-monophosphate dehydrogenase 2;	0.25	0.07	0.82	16.00
P14735	Insulin-degrading enzyme;	-1.39	-0.55	0.13	2.80
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2;	4.88	1.68	0.00	4.50
P01344	Insulin-like growth factor II;	-0.28	-0.06	0.68	18.30
P08833	Insulin-like growth factor-binding protein 1;	-0.77	-0.47	0.49	25.90
P18065	Insulin-like growth factor-binding protein 2;	0.81	0.16	0.33	36.90
P17936	Insulin-like growth factor-binding protein 3;	1.23	1.00	0.40	11.00
P22692	Insulin-like growth factor-binding protein 4;	1.09	0.55	0.32	31.40
P24592	Insulin-like growth factor-binding protein 6;	2.26	0.36	0.00	23.30
P26006	Integrin alpha-3;	0.98	1.19	0.63	2.10
P23229	Integrin alpha-6;	1.59	1.00	0.19	3.10
P05556	Integrin beta-1;	-1.04	-0.99	0.49	4.60
O95965	Integrin beta-like protein 1;	-0.90	-1.34	0.68	18.20
P05362	Intercellular adhesion molecule 1;	-0.72	-0.12	0.31	2.60
P32456	Interferon-induced guanylate-binding protein 2;	-1.39	-0.33	0.08	4.90
P19525	Interferon-induced, double-stranded RNA-activated protei	0.80	0.23	0.37	3.30
Q12905	Interleukin enhancer-binding factor 2;	1.28	0.41	0.16	11.50
Q9NPH3	Interleukin-1 receptor accessory protein;	-0.12	-0.01	0.82	5.10
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog;	-0.35	-0.05	0.61	6.90
Q96CN7	Isochorismatase domain-containing protein 1;	0.75	0.12	0.36	4.70
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic;	-0.35	-0.09	0.64	15.20
P41252	Isoleucine--tRNA ligase, cytoplasmic;	0.27	0.05	0.77	4.00
Q6UW63	KDEL motif-containing protein 1;	1.94	0.29	0.01	2.40
Q8NAB2	Kelch repeat and BTB domain-containing protein 3;	1.09	0.04	0.16	1.20
P13645	Keratin, type I cytoskeletal 10;	0.26	0.02	0.78	4.80
Q04695	Keratin, type I cytoskeletal 17;	-1.01	-0.29	0.21	14.60
P05783	Keratin, type I cytoskeletal 18;	0.82	0.18	0.33	34.40
P08727	Keratin, type I cytoskeletal 19;	2.76	1.52	0.01	16.00
P35527	Keratin, type I cytoskeletal 9;	1.27	0.83	0.31	3.70
P04264	Keratin, type II cytoskeletal 1;	-0.45	-0.26	0.67	14.40
P02538	Keratin, type II cytoskeletal 6A;	-0.12	-0.02	0.83	3.70
Q14CN4	Keratin, type II cytoskeletal 72;	0.75	0.05	0.34	2.30
P05787	Keratin, type II cytoskeletal 8;	0.93	0.30	0.31	40.00
Q07666	KH domain-containing, RNA-binding, signal transduction	0.58	0.06	0.47	3.20
Q86UP2	Kinectin;	-0.16	-0.06	0.82	10.50
Q07866	Kinesin light chain 1;	1.34	1.24	0.41	4.00
P33176	Kinesin-1 heavy chain;	-1.43	-1.77	0.46	8.50
P00338	L-lactate dehydrogenase A chain;	-0.65	-0.19	0.42	21.70
Q6PKG0	La-related protein 1;	1.50	0.20	0.05	1.10

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Q71RC2	La-related protein 4;	0.50	0.05	0.54	1.40
Q04760	Lactoylglutathione lyase;	-0.62	-0.33	0.54	18.50
Q14739	Lamin-B receptor;	-1.43	-0.08	0.05	2.90
P20700	Lamin-B1;	0.89	0.59	0.49	24.70
Q03252	Lamin-B2;	0.45	0.18	0.67	9.50
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;	0.70	0.22	0.45	11.90
P07942	Laminin subunit beta-1;	-0.62	-0.38	0.56	12.00
P55268	Laminin subunit beta-2;	1.95	0.63	0.03	5.50
P11047	Laminin subunit gamma-1;	-0.47	-0.63	0.81	18.50
Q13753	Laminin subunit gamma-2;	0.65	0.29	0.54	5.90
P46379	Large proline-rich protein BAG6;	-0.45	-0.08	0.53	1.10
Q9NS15	Latent-transforming growth factor beta-binding protein 3;	1.62	1.33	0.27	4.80
Q8N2S1	Latent-transforming growth factor beta-binding protein 4;	-0.82	-0.48	0.45	2.00
Q99538	Legumain;	0.99	0.11	0.21	13.40
Q9P2J5	Leucine--tRNA ligase, cytoplasmic;	-0.96	-0.73	0.46	2.40
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	1.51	2.21	0.52	4.40
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1;	-0.19	-0.09	0.83	11.90
Q8N1G4	Leucine-rich repeat-containing protein 47;	-0.26	-0.01	0.68	7.40
Q96AG4	Leucine-rich repeat-containing protein 59;	0.56	0.21	0.58	17.90
Q14847	LIM and SH3 domain protein 1;	-0.53	-0.12	0.47	5.70
Q93052	Lipoma-preferred partner;	1.49	0.19	0.05	2.00
P24666	Low molecular weight phosphotyrosine protein phosphata	-1.51	-0.13	0.03	7.00
P01130	Low-density lipoprotein receptor;	-0.22	-0.11	0.79	3.60
O95232	Luc7-like protein 3;	0.42	0.02	0.61	2.50
P05455	Lupus La protein;	0.35	0.14	0.74	19.60
Q15046	Lysine--tRNA ligase;	0.28	0.06	0.76	9.00
O60341	Lysine-specific histone demethylase 1A;	0.70	0.17	0.43	3.10
P10253	Lysosomal alpha-glucosidase;	-0.32	-0.12	0.70	8.90
O00754	Lysosomal alpha-mannosidase;	0.82	0.47	0.49	3.50
P42785	Lysosomal Pro-X carboxypeptidase;	0.35	0.15	0.75	13.50
P10619	Lysosomal protective protein;	0.35	0.09	0.70	14.00
Q9UMR5	Lysosomal thioesterase PPT2;	0.66	0.06	0.41	3.00
Q9Y4K0	Lysyl oxidase homolog 2;	-0.22	-0.09	0.78	9.90
Q96JB6	Lysyl oxidase homolog 4;	-0.77	-0.18	0.32	15.20
Q96C86	m7GpppX diphosphatase;	-1.24	-1.09	0.39	10.70
P09603	Macrophage colony-stimulating factor 1;	0.62	0.04	0.44	5.20
P40121	Macrophage-capping protein;	0.58	0.12	0.50	16.10
Q14764	Major vault protein;	-1.43	-1.66	0.43	4.60
P40925	Malate dehydrogenase, cytoplasmic;	-0.53	-0.11	0.46	25.70
Q9ULC4	Malignant T-cell-amplified sequence 1;	-0.72	-0.06	0.30	10.50
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA;	-2.60	-0.32	0.00	2.10
P49006	MARCKS-related protein;	0.99	0.07	0.20	7.70
O00339	Matrilin-2;	-0.62	-0.10	0.39	4.50
P43243	Matrin-3;	1.82	0.40	0.03	12.90
Q99542	Matrix metalloproteinase-19;	1.07	0.13	0.17	6.50
Q5JRA6	Melanoma inhibitory activity protein 3;	0.82	0.09	0.30	0.60
O00562	Membrane-associated phosphatidylinositol transfer protei	-4.01	-9.71	0.28	1.90
O00264	Membrane-associated progesterone receptor component 1;	2.71	0.63	0.00	20.00
Q13421	Mesothelin;	0.90	0.25	0.30	32.20
P01033	Metalloproteinase inhibitor 1;	0.98	0.45	0.35	42.00
P16035	Metalloproteinase inhibitor 2;	-0.87	-0.86	0.57	21.40
Q13330	Metastasis-associated protein MTA1;	0.95	0.22	0.26	1.70
O94776	Metastasis-associated protein MTA2;	-1.04	-0.80	0.42	3.60
Q8N6R0	Methyltransferase-like protein 13;	-3.80	-0.53	0.00	1.00
P55081	Microfibrillar-associated protein 1;	3.35	0.44	0.00	3.00
Q13361	Microfibrillar-associated protein 5;	-0.32	-0.04	0.64	6.90
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5;	-1.01	-0.08	0.15	0.30

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P27816	Microtubule-associated protein 4;	-1.08	-0.45	0.24	16.90
Q15691	Microtubule-associated protein RP/EB family member 1;	-0.84	-0.68	0.52	10.10
P10636	Microtubule-associated protein tau;	-1.24	-0.24	0.10	2.00
P21741	Midkine;	-0.49	-0.12	0.51	35.70
Q9Y3D6	Mitochondrial fission 1 protein;	2.10	0.31	0.01	7.20
P62072	Mitochondrial import inner membrane translocase subunit	1.71	0.36	0.04	14.40
Q9Y5L4	Mitochondrial import inner membrane translocase subunit	-0.53	-0.04	0.43	14.70
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit	2.54	2.69	0.15	9.60
Q9Y5J7	Mitochondrial import inner membrane translocase subunit	1.43	0.36	0.09	30.30
Q15388	Mitochondrial import receptor subunit TOM20 homolog;	4.33	0.61	0.00	9.00
O94826	Mitochondrial import receptor subunit TOM70;	1.01	0.72	0.45	3.10
Q16891	Mitochondrial inner membrane protein;	0.99	0.86	0.53	9.90
O43684	Mitotic checkpoint protein BUB3;	0.25	0.02	0.79	10.70
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	2.26	0.92	0.02	10.60
P26038	Moesin;	2.70	3.06	0.15	8.80
P53985	Monocarboxylate transporter 1;	2.22	0.67	0.01	3.40
Q9UKD2	mRNA turnover protein 4 homolog;	1.17	0.16	0.14	7.90
P22234	Multifunctional protein ADE2;	1.28	0.55	0.20	16.90
Q7Z7M0	Multiple epidermal growth factor-like domains protein 8;	5.01	3.50	0.00	0.40
Q9UNW1	Multiple inositol polyphosphate phosphatase 1;	1.12	0.95	0.46	13.80
Q9BQG0	Myb-binding protein 1A;	2.89	0.82	0.00	0.90
Q9NZM1	Myoferlin;	0.75	0.12	0.36	2.30
P60660	Myosin light polypeptide 6;	-0.24	-0.03	0.70	28.50
Q6WCQ1	Myosin phosphatase Rho-interacting protein;	0.69	0.08	0.40	1.20
P35579	Myosin-9;	-0.65	-0.22	0.44	20.70
P58546	Myotrophin;	-0.69	-0.09	0.33	20.30
P29966	Myristoylated alanine-rich C-kinase substrate;	-9.97	-0.01	0.00	11.10
P34059	N-acetylgalactosamine-6-sulfatase;	0.32	0.11	0.76	9.80
Q9UK23	N-acetylglucosamine-1-phosphodiester alpha-N-acetylgluc	-0.60	-0.06	0.40	1.90
P15586	N-acetylglucosamine-6-sulfatase;	-0.37	-0.13	0.64	15.90
Q9H0A0	N-acetyltransferase 10;	1.61	0.15	0.04	1.10
P41227	N-alpha-acetyltransferase 10;	-0.33	-0.11	0.67	16.60
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit;	-1.01	-0.27	0.20	2.70
Q9GZZ1	N-alpha-acetyltransferase 50;	-0.14	-0.02	0.80	5.90
P20933	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	1.75	0.14	0.02	2.30
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	-0.28	-0.02	0.66	12.60
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	-1.74	-4.37	0.64	14.00
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	-0.35	-0.08	0.62	25.10
P15559	NAD(P)H dehydrogenase [quinone] 1;	0.38	0.06	0.66	8.40
Q8NCW5	NAD(P)H-hydrate epimerase;	0.52	0.55	0.78	10.40
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex s	4.26	0.69	0.00	21.20
O95169	NADH dehydrogenase [ubiquinone] 1 beta subcomplex su	3.11	0.13	0.00	4.80
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitocl	4.73	1.61	0.00	9.20
O75306	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2,	1.75	0.40	0.03	4.50
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5;	3.77	0.29	0.00	12.30
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitocl	3.14	2.44	0.02	14.20
O43847	Nardilysin;	0.62	0.13	0.47	2.40
Q13765	Nascent polypeptide-associated complex subunit alpha;	-0.72	-0.25	0.39	25.60
Q13564	NEDD8-activating enzyme E1 regulatory subunit;	-1.14	-0.55	0.26	4.90
Q92859	Neogenin;	-1.28	-1.06	0.35	2.80
Q9UMX5	Neudesin;	0.26	0.08	0.80	12.20
P32004	Neural cell adhesion molecule L1;	2.15	0.84	0.02	10.70
Q9BYT8	Neurolysin, mitochondrial;	1.08	0.14	0.17	1.70
P42857	Neuron-specific protein family member 1;	0.46	0.04	0.58	5.90
O14786	Neuropilin-1;	-3.01	-3.64	0.12	5.40
O60462	Neuropilin-2;	0.46	0.05	0.58	1.30
O15240	Neurosecretory protein VGF;	-1.04	-0.17	0.16	8.90

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q14697	Neutral alpha-glucosidase AB;	0.69	0.21	0.46	2.50
O15226	NF-kappa-B-repressing factor;	1.42	0.09	0.06	1.60
P55769	NHP2-like protein 1;	1.38	0.55	0.16	18.80
P43490	Nicotinamide phosphoribosyltransferase;	-0.53	-0.17	0.51	27.70
Q9Y314	Nitric oxide synthase-interacting protein;	-0.62	-0.24	0.47	13.00
P69849	Nodal modulator 3;	0.38	0.02	0.65	3.30
P05114	Non-histone chromosomal protein HMG-14;	-0.96	-0.07	0.18	11.00
Q9UNZ2	NSFL1 cofactor p47;	-0.60	-0.42	0.61	22.70
P49321	Nuclear autoantigenic sperm protein;	-1.18	-1.19	0.47	6.60
Q14980	Nuclear mitotic apparatus protein 1;	0.26	0.12	0.84	4.80
P57740	Nuclear pore complex protein Nup107;	1.48	0.23	0.06	1.50
Q8N1F7	Nuclear pore complex protein Nup93;	-1.14	-1.88	0.65	3.30
P37198	Nuclear pore glycoprotein p62;	3.41	0.24	0.00	2.70
Q8TAT6	Nuclear protein localization protein 4 homolog;	-1.14	-0.75	0.34	3.50
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase sul	1.74	0.29	0.03	7.80
P67809	Nuclease-sensitive element-binding protein 1;	0.74	0.27	0.45	27.50
P80303	Nucleobindin-2;	0.94	0.11	0.23	3.80
Q14978	Nucleolar and coiled-body phosphoprotein 1;	2.10	0.39	0.01	2.60
Q8WTT2	Nucleolar complex protein 3 homolog;	2.25	0.18	0.00	1.40
O00567	Nucleolar protein 56;	2.47	1.75	0.06	4.90
Q9Y2X3	Nucleolar protein 58;	1.34	0.19	0.09	2.80
Q9NR30	Nucleolar RNA helicase 2;	1.73	2.36	0.44	16.20
P17480	Nucleolar transcription factor 1;	2.08	0.42	0.01	2.10
P19338	Nucleolin;	0.94	0.34	0.32	19.00
P06748	Nucleophosmin;	0.87	0.05	0.26	4.40
P12270	Nucleoprotein TPR;	1.53	0.58	0.11	3.50
P55209	Nucleosome assembly protein 1-like 1;	0.40	0.03	0.63	12.50
Q99733	Nucleosome assembly protein 1-like 4;	-0.24	-0.02	0.70	10.10
Q12830	Nucleosome-remodeling factor subunit BPTF;	3.31	7.26	0.33	0.80
Q9NTK5	Obg-like ATPase 1;	-1.47	-1.79	0.44	16.40
Q5VST9	Obscurin;	-2.35	-1.56	0.05	0.30
Q9NRN5	Olfactomedin-like protein 3;	-1.14	-1.36	0.54	8.60
P04181	Ornithine aminotransferase, mitochondrial;	3.23	0.27	0.00	3.20
Q92882	Osteoclast-stimulating factor 1;	-1.96	-0.61	0.02	8.90
P50897	Palmitoyl-protein thioesterase 1;	-0.33	-0.37	0.84	15.00
Q9BRP8	Partner of Y14 and mago;	-1.04	-0.17	0.16	7.40
O75475	PC4 and SFRS1-interacting protein;	0.82	0.32	0.41	12.10
Q96JY6	PDZ and LIM domain protein 2;	-0.26	-0.05	0.69	2.80
Q96HC4	PDZ and LIM domain protein 5;	0.45	0.16	0.66	10.10
Q9NR12	PDZ and LIM domain protein 7;	-0.32	-0.11	0.70	4.80
P26022	Pentraxin-related protein PTX3;	3.47	1.66	0.00	12.10
P19021	Peptidyl-glycine alpha-amidating monooxygenase;	-0.12	-0.03	0.84	9.70
Q9NYL4	Peptidyl-prolyl cis-trans isomerase FKBP11;	7.63	1.09	0.00	5.00
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A;	-0.16	-0.02	0.78	13.00
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3;	1.11	0.20	0.17	27.70
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;	-0.65	-0.27	0.48	10.00
O43447	Peptidyl-prolyl cis-trans isomerase H;	0.27	0.01	0.76	14.70
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1;	0.78	0.12	0.33	8.40
Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial;	2.73	0.31	0.00	8.40
Q99541	Perilipin-2;	1.42	0.11	0.06	2.50
O60664	Perilipin-3;	0.82	1.37	0.77	7.10
Q06830	Peroxiredoxin-1;	-0.26	-0.03	0.68	45.70
P32119	Peroxiredoxin-2;	-0.51	-0.37	0.67	31.80
P30044	Peroxiredoxin-5, mitochondrial;	0.34	0.06	0.70	17.30
P30041	Peroxiredoxin-6;	1.07	0.35	0.24	23.20
Q8WW12	PEST proteolytic signal-containing nuclear protein;	-1.01	-0.45	0.29	24.70
Q8WWQ0	PH-interacting protein;	2.06	0.37	0.01	1.00

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9Y285	Phenylalanine--tRNA ligase alpha subunit;	1.38	0.15	0.07	2.60
Q9NSD9	Phenylalanine--tRNA ligase beta subunit;	0.26	0.04	0.78	4.80
P30086	Phosphatidylethanolamine-binding protein 1;	-0.51	-0.10	0.48	50.80
P48739	Phosphatidylinositol transfer protein beta isoform;	0.38	0.02	0.65	4.40
P00558	Phosphoglycerate kinase 1;	-0.37	-0.09	0.61	46.00
P18669	Phosphoglycerate mutase 1;	0.26	0.06	0.79	39.80
A6NDG6	Phosphoglycolate phosphatase;	-0.47	-0.05	0.50	7.80
Q9Y263	Phospholipase A-2-activating protein;	-4.61	-1.12	0.00	2.10
Q6P4A8	Phospholipase B-like 1;	0.75	0.05	0.34	7.40
O15067	Phosphoribosylformylglycinamidine synthase;	0.33	0.14	0.77	4.30
Q9Y617	Phosphoserine aminotransferase;	0.84	0.80	0.62	39.70
P36955	Pigment epithelium-derived factor;	3.25	2.33	0.01	12.90
Q96BK5	PIN2/TERF1-interacting telomerase inhibitor 1;	2.82	0.27	0.00	2.70
Q9H307	Pinin;	1.85	1.23	0.14	3.50
Q9BTY2	Plasma alpha-L-fucosidase;	0.99	0.15	0.21	4.30
P23634	Plasma membrane calcium-transporting ATPase 4;	-0.72	-1.16	0.76	3.50
P05155	Plasma protease C1 inhibitor;	-1.08	-0.43	0.23	9.40
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein;	-0.28	-0.07	0.69	15.20
P13797	Plastin-3;	-1.51	-0.30	0.05	7.80
P68402	Platelet-activating factor acetylhydrolase IB subunit beta;	-1.39	-0.22	0.06	8.30
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamm	-0.77	-0.35	0.42	11.30
Q9NRA1	Platelet-derived growth factor C;	-1.04	-0.24	0.17	5.20
Q8WV24	Pleckstrin homology-like domain family A member 1;	0.38	0.08	0.67	2.20
Q15149	Plectin;	-0.45	-0.25	0.66	19.60
O43660	Pleiotropic regulator 1;	0.80	0.08	0.31	2.50
O15031	Plexin-B2;	-0.77	-0.42	0.46	1.30
Q92692	Poliovirus receptor-related protein 2;	0.40	0.07	0.65	3.30
P11940	Polyadenylate-binding protein 1;	1.16	0.35	0.20	17.00
Q13310	Polyadenylate-binding protein 4;	-0.62	-0.48	0.63	12.40
Q6NZI2	Polymerase I and transcript release factor;	-0.65	-0.29	0.49	19.00
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;	-0.35	-0.14	0.68	16.60
P26599	Polypyrimidine tract-binding protein 1;	0.88	0.09	0.26	9.00
P0CG47	Polyubiquitin-B;	-0.32	-0.04	0.64	56.30
Q9Y3B4	Pre-mRNA branch site protein p14;	0.96	0.23	0.26	20.80
Q9UMS4	Pre-mRNA-processing factor 19;	0.82	0.15	0.32	7.50
Q9NW64	Pre-mRNA-splicing factor RBM22;	2.00	0.15	0.01	2.40
O60925	Prefoldin subunit 1;	-2.60	-0.16	0.00	8.20
Q9UHV9	Prefoldin subunit 2;	-0.65	-0.20	0.43	16.90
Q99471	Prefoldin subunit 5;	-0.41	-0.22	0.67	24.70
O15212	Prefoldin subunit 6;	-0.90	-0.07	0.20	9.30
P02545	Prelamin-A/C;	0.32	0.07	0.74	39.20
Q96IZ0	PRKC apoptosis WT1 regulator protein;	-2.35	-1.92	0.10	8.50
Q92841	Probable ATP-dependent RNA helicase DDX17;	-0.14	-0.01	0.80	10.50
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23;	-0.24	-0.03	0.70	2.80
P17844	Probable ATP-dependent RNA helicase DDX5;	0.65	0.29	0.54	11.10
Q9HD20	Probable cation-transporting ATPase 13A1;	5.99	1.13	0.00	1.80
Q9UKZ9	Procollagen C-endopeptidase enhancer 2;	-1.24	-0.15	0.09	6.00
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	0.52	0.18	0.59	22.00
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3;	0.35	0.08	0.70	16.10
P07737	Profilin-1;	-0.21	-0.05	0.76	62.10
Q8WUM4	Programmed cell death 6-interacting protein;	-0.84	-1.38	0.73	12.20
O75340	Programmed cell death protein 6;	1.23	0.49	0.21	14.70
P12004	Proliferating cell nuclear antigen;	-0.47	-0.16	0.56	33.00
Q9UQ80	Proliferation-associated protein 2G4;	-0.47	-0.14	0.55	28.20
Q8IZL8	Proline-, glutamic acid- and leucine-rich protein 1;	1.23	0.94	0.38	4.00
Q32P28	Prolyl 3-hydroxylase 1;	0.40	0.09	0.66	1.40
Q8NBP7	Proprotein convertase subtilisin/kexin type 9;	-0.53	-0.10	0.46	25.60

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
Q9P2B2	Prostaglandin F2 receptor negative regulator;	-0.37	-0.02	0.57	1.10
P41222	Prostaglandin-H2 D-isomerase;	3.73	0.29	0.00	17.40
Q06323	Proteasome activator complex subunit 1;	0.56	0.25	0.60	25.70
P61289	Proteasome activator complex subunit 3;	-1.56	-1.05	0.20	6.70
Q9BT73	Proteasome assembly chaperone 3;	-0.22	-0.02	0.72	12.30
P25786	Proteasome subunit alpha type-1;	-0.56	-0.52	0.70	17.10
P25787	Proteasome subunit alpha type-2;	-0.19	-0.04	0.78	27.80
P25789	Proteasome subunit alpha type-4;	-0.51	-0.11	0.49	10.00
P28066	Proteasome subunit alpha type-5;	0.28	0.09	0.78	15.40
P28072	Proteasome subunit beta type-6;	-0.37	-0.03	0.57	12.60
P28062	Proteasome subunit beta type-8;	-0.77	-0.04	0.28	4.30
Q8IVF2	Protein AHNAK2;	0.81	1.01	0.70	3.60
Q99873	Protein arginine N-methyltransferase 1;	-1.24	-0.47	0.17	6.90
Q8WUW1	Protein BRICK1;	-1.04	-0.07	0.14	12.00
Q9Y2B0	Protein canopy homolog 2;	0.25	0.03	0.79	8.80
O60888	Protein CutA;	-0.26	-0.02	0.68	7.80
O00622	Protein CYR61;	-0.82	-0.13	0.26	9.40
P35659	Protein DEK;	1.05	0.96	0.51	10.10
P30101	Protein disulfide-isomerase A3;	0.30	0.12	0.78	28.30
P13667	Protein disulfide-isomerase A4;	-0.22	-0.08	0.77	15.80
Q15084	Protein disulfide-isomerase A6;	0.48	0.07	0.57	16.80
Q99497	Protein DJ-1;	-0.19	-0.05	0.78	41.80
Q8N8S7	Protein enabled homolog;	0.87	0.11	0.28	2.00
Q92520	Protein FAM3C;	-1.01	-0.25	0.19	33.90
Q9NUQ9	Protein FAM49B;	-1.60	-0.24	0.03	4.00
Q9UNF0	Protein kinase C and casein kinase substrate in neurons pr	-0.77	-0.43	0.47	6.80
Q96EK9	Protein KTI12 homolog;	-4.01	-0.65	0.00	3.70
Q9BRT6	Protein LLP homolog;	2.02	0.15	0.01	10.90
Q9BXY0	Protein MAK16 homolog;	2.35	0.44	0.00	5.30
Q9BZQ8	Protein Niban;	0.53	0.06	0.51	2.30
O14974	Protein phosphatase 1 regulatory subunit 12A;	-0.45	-0.09	0.54	2.00
Q9Y520	Protein PRRC2C;	-0.22	-0.12	0.81	1.00
Q96PU8	Protein quaking;	3.63	0.45	0.00	5.00
Q13123	Protein Red;	0.49	0.04	0.55	2.00
P60903	Protein S100-A10;	2.52	1.74	0.05	17.50
Q96FQ6	Protein S100-A16;	0.37	0.04	0.67	34.00
P26447	Protein S100-A4;	-0.41	-0.13	0.59	35.60
P25815	Protein S100-P;	-2.60	-0.32	0.00	13.70
P53992	Protein transport protein Sec24C;	0.48	0.35	0.74	2.70
O94979	Protein transport protein Sec31A;	1.93	0.13	0.01	1.60
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	0.30	0.03	0.73	12.30
P06454	Prothymosin alpha;	-0.16	-0.01	0.78	9.00
P61457	Pterin-4-alpha-carbinolamine dehydratase;	-1.21	-0.70	0.26	17.30
P55786	Puromycin-sensitive aminopeptidase;	-0.62	-0.26	0.49	11.60
Q5T1J5	Putative coiled-coil-helix-coiled-coil-helix domain-contai	-0.33	-0.22	0.76	27.20
Q6P1N9	Putative deoxyribonuclease TATDN1;	0.65	0.04	0.41	3.70
Q49A26	Putative oxidoreductase GLYR1;	2.55	1.56	0.03	5.10
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1;	-0.87	-0.19	0.25	8.60
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA	0.60	0.18	0.51	5.70
O60231	Putative pre-mRNA-splicing factor ATP-dependent RNA	1.18	0.20	0.15	1.20
Q9NQ29	Putative RNA-binding protein Luc7-like 1;	0.23	0.05	0.82	6.70
A6NL28	Putative tropomyosin alpha-3 chain-like protein;	-0.49	-0.05	0.48	10.30
O00764	Pyridoxal kinase;	-1.04	-0.09	0.14	3.20
P14618	Pyruvate kinase isozymes M1/M2;	-0.60	-0.32	0.56	44.30
Q08257	Quinone oxidoreductase;	-0.14	-0.02	0.81	5.20
P50395	Rab GDP dissociation inhibitor beta;	-1.32	-1.44	0.45	26.50
Q9UHA4	Ragulator complex protein LAMTOR3;	1.71	0.15	0.02	8.10

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
O43504	Ragulator complex protein LAMTOR5;	0.41	0.05	0.63	22.00
Q9HD47	Ran guanine nucleotide release factor;	-0.87	-0.11	0.22	7.00
Q9H6Z4	Ran-binding protein 3;	2.13	0.27	0.01	2.10
P43487	Ran-specific GTPase-activating protein;	-0.19	-0.01	0.76	10.90
P46940	Ras GTPase-activating-like protein IQGAP1;	-0.47	-0.35	0.70	7.40
P61106	Ras-related protein Rab-14;	0.65	0.06	0.42	11.60
P62820	Ras-related protein Rab-1A;	0.86	0.24	0.33	18.90
P61019	Ras-related protein Rab-2A;	-0.28	-0.03	0.66	5.70
P51148	Ras-related protein Rab-5C;	1.42	0.63	0.16	11.60
P61224	Ras-related protein Rap-1b;	-3.43	-0.37	0.00	6.00
P10586	Receptor-type tyrosine-protein phosphatase F;	0.23	0.08	0.84	11.70
P23470	Receptor-type tyrosine-protein phosphatase gamma;	-0.69	-0.21	0.39	2.70
Q15262	Receptor-type tyrosine-protein phosphatase kappa;	0.33	0.05	0.71	1.60
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing prote	-0.24	-0.04	0.71	9.50
P18754	Regulator of chromosome condensation;	0.30	0.08	0.76	8.10
Q9BZR6	Reticulon-4 receptor;	0.32	0.02	0.71	2.50
Q9NQC3	Reticulon-4;	1.09	0.04	0.16	1.10
O75116	Rho-associated protein kinase 2;	-0.33	-0.08	0.64	2.40
P08134	Rho-related GTP-binding protein RhoC;	2.35	2.00	0.11	16.10
P13489	Ribonuclease inhibitor;	-1.08	-1.23	0.54	10.00
O00584	Ribonuclease T2;	0.80	0.18	0.35	30.50
Q99575	Ribonucleases P/MRP protein subunit POP1;	0.37	0.08	0.69	1.70
P11908	Ribose-phosphate pyrophosphokinase 2;	-0.56	-0.06	0.42	5.30
O76021	Ribosomal L1 domain-containing protein 1;	1.70	1.06	0.16	9.40
Q14684	Ribosomal RNA processing protein 1 homolog B;	-0.62	-0.35	0.55	5.30
Q9GZL7	Ribosome biogenesis protein WDR12;	2.22	0.73	0.01	6.40
Q9H7B2	Ribosome production factor 2 homolog;	0.58	0.49	0.71	7.50
Q9P2E9	Ribosome-binding protein 1;	-0.67	-0.87	0.73	6.00
P38159	RNA-binding motif protein, X chromosome;	2.54	0.98	0.01	15.10
Q9NTZ6	RNA-binding protein 12;	1.37	0.15	0.08	1.90
P49756	RNA-binding protein 25;	0.66	0.06	0.41	1.20
Q9NW13	RNA-binding protein 28;	3.90	0.96	0.00	3.20
Q14498	RNA-binding protein 39;	1.01	0.11	0.20	4.90
Q9Y5S9	RNA-binding protein 8A;	1.70	0.16	0.03	10.90
Q01844	RNA-binding protein EWS;	0.21	0.01	0.82	2.10
P35637	RNA-binding protein FUS;	0.63	0.19	0.50	8.20
Q9UKM9	RNA-binding protein Raly;	1.88	0.25	0.02	9.80
Q9Y6N7	Roundabout homolog 1;	-1.43	-3.66	0.70	1.10
Q9Y230	RuvB-like 2;	-1.18	-1.14	0.46	6.90
P31153	S-adenosylmethionine synthase isoform type-2;	-0.53	-0.10	0.46	15.70
P10768	S-formylglutathione hydrolase;	0.88	0.34	0.36	8.50
Q13126	S-methyl-5'-thioadenosine phosphorylase;	-1.56	-0.69	0.11	16.30
P82979	SAP domain-containing ribonucleoprotein;	-0.35	-0.05	0.60	9.00
Q8WVN6	Secreted and transmembrane protein 1;	0.26	0.07	0.80	7.70
P49903	Selenide, water dikinase 1;	0.42	0.03	0.61	3.80
Q14563	Semaphorin-3A;	1.49	0.52	0.11	10.20
Q99985	Semaphorin-3C;	-0.28	-0.06	0.68	17.70
Q9H3T2	Semaphorin-6C;	-2.90	-1.08	0.00	1.20
O75326	Semaphorin-7A;	-1.96	-1.06	0.07	3.60
Q9NVA2	Septin-11;	0.45	0.15	0.65	15.40
Q15019	Septin-2;	0.70	0.36	0.53	12.70
Q9UHD8	Septin-9;	-0.24	-0.03	0.70	11.90
O95084	Serine protease 23;	-1.32	-0.49	0.14	27.90
Q92743	Serine protease HTRA1;	-0.67	-0.06	0.34	10.40
P49591	Serine--tRNA ligase, cytoplasmic;	-0.39	-0.19	0.67	5.30
Q9Y3F4	Serine-threonine kinase receptor-associated protein;	-0.60	-0.54	0.67	28.00
Q07955	Serine/arginine-rich splicing factor 1;	0.50	0.17	0.61	35.90

Table S2

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Q05519	Serine/arginine-rich splicing factor 11;	0.95	0.11	0.23	5.20
P84103	Serine/arginine-rich splicing factor 3;	0.98	0.19	0.24	10.40
Q13243	Serine/arginine-rich splicing factor 5;	1.07	0.11	0.17	4.40
Q13247	Serine/arginine-rich splicing factor 6;	-0.53	-0.73	0.79	6.10
Q16629	Serine/arginine-rich splicing factor 7;	0.40	0.06	0.64	3.80
Q13242	Serine/arginine-rich splicing factor 9;	1.35	0.53	0.16	17.60
Q16513	Serine/threonine-protein kinase N2;	-0.60	-0.05	0.39	0.90
O95747	Serine/threonine-protein kinase OSR1;	-0.32	-0.10	0.68	8.20
Q13177	Serine/threonine-protein kinase PAK 2;	0.89	1.52	0.75	9.50
P62714	Serine/threonine-protein phosphatase 2A catalytic subunit	-1.43	-1.04	0.26	6.10
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic s	-0.32	-0.09	0.68	9.40
P50453	Serpin B9;	1.30	0.12	0.09	3.20
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3;	-0.28	-0.02	0.66	16.10
O75368	SH3 domain-binding glutamic acid-rich-like protein;	-1.85	-0.13	0.01	8.80
P29353	SHC-transforming protein 1;	0.40	0.10	0.67	2.10
Q9HAT2	Sialate O-acetylesterase;	0.43	0.08	0.62	11.70
Q9NR45	Sialic acid synthase;	-1.56	-0.18	0.03	3.60
Q99519	Sialidase-1;	-0.69	-0.06	0.32	11.10
Q9UHB9	Signal recognition particle 68 kDa protein;	3.31	0.43	0.00	1.60
P49458	Signal recognition particle 9 kDa protein;	1.28	0.08	0.09	12.80
P08240	Signal recognition particle receptor subunit alpha;	6.44	1.51	0.00	2.70
Q9Y5M8	Signal recognition particle receptor subunit beta;	2.81	2.91	0.10	14.80
Q29RF7	Sister chromatid cohesion protein PDS5 homolog A;	-0.96	-0.20	0.21	1.00
O75093	Slit homolog 1 protein;	-0.77	-0.48	0.50	0.60
O43765	Small glutamine-rich tetratricopeptide repeat-containing p	-0.26	-0.02	0.68	4.20
P62304	Small nuclear ribonucleoprotein E;	0.96	0.08	0.22	13.00
P62306	Small nuclear ribonucleoprotein F;	4.56	0.92	0.00	9.30
A8MWD9	Small nuclear ribonucleoprotein G-like protein;	0.90	0.03	0.24	15.80
P62314	Small nuclear ribonucleoprotein Sm D1;	1.42	0.19	0.07	9.20
P62316	Small nuclear ribonucleoprotein Sm D2;	1.21	0.27	0.14	31.40
P62318	Small nuclear ribonucleoprotein Sm D3;	1.50	0.55	0.11	23.80
P14678	Small nuclear ribonucleoprotein-associated proteins B and	0.88	0.03	0.26	12.50
P63165	Small ubiquitin-related modifier 1;	0.35	0.01	0.67	15.80
P55854	Small ubiquitin-related modifier 3;	0.58	0.05	0.47	12.60
Q13573	SNW domain-containing protein 1;	1.56	0.45	0.07	2.60
P05023	Sodium/potassium-transporting ATPase subunit alpha-1;	0.48	0.24	0.68	4.20
O15244	Solute carrier family 22 member 2;	-0.77	-0.04	0.28	3.10
Q00796	Sorbitol dehydrogenase;	-0.77	-0.04	0.28	2.50
Q99523	Sortilin;	-0.53	-0.62	0.76	4.60
Q96L92	Sorting nexin-27;	0.28	0.03	0.75	2.80
Q9Y5X3	Sorting nexin-5;	-0.72	-0.04	0.29	4.70
P09486	SPARC;	-0.56	-0.19	0.50	35.30
Q9NUQ6	SPATS2-like protein;	2.69	2.96	0.14	6.10
P19623	Spermidine synthase;	-0.60	-0.21	0.48	12.90
P52788	Spermine synthase;	-1.24	-0.68	0.24	5.20
Q13838	Spliceosome RNA helicase DDX39B;	0.34	0.10	0.73	17.30
Q15637	Splicing factor 1;	-0.24	-0.16	0.81	8.10
Q15459	Splicing factor 3A subunit 1;	0.43	0.17	0.68	7.60
Q15428	Splicing factor 3A subunit 2;	2.54	0.27	0.00	3.90
Q12874	Splicing factor 3A subunit 3;	2.24	4.69	0.49	4.20
O75533	Splicing factor 3B subunit 1;	0.68	0.52	0.65	5.20
Q15393	Splicing factor 3B subunit 3;	0.82	0.37	0.44	11.10
Q15427	Splicing factor 3B subunit 4;	1.05	0.11	0.18	3.30
P23246	Splicing factor, proline- and glutamine-rich;	0.43	0.07	0.61	11.00
P37268	Squalene synthase;	3.80	0.93	0.00	3.10
Q14247	Src substrate cortactin;	-1.47	-1.22	0.30	10.90
P52823	Stanniocalcin-1;	0.78	0.08	0.33	5.70

Table S2

Uniprot accession	**Name**	**Fold-change ($\log_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q7KZF4	Staphylococcal nuclease domain-containing protein 1;	-0.49	-0.10	0.50	9.20
Q9NZ72	Stathmin-3;	-0.77	-0.08	0.28	9.40
P38646	Stress-70 protein, mitochondrial;	1.17	0.45	0.23	14.70
Q14683	Structural maintenance of chromosomes protein 1A;	0.68	0.07	0.40	0.80
Q9UQE7	Structural maintenance of chromosomes protein 3;	1.02	0.07	0.19	1.70
Q8NBJ7	Sulfatase-modifying factor 2;	0.56	0.43	0.71	26.90
Q6ZRP7	Sulfhydryl oxidase 2;	-0.90	-0.77	0.52	13.20
P63279	SUMO-conjugating enzyme UBC9;	-0.32	-0.11	0.69	19.60
P42285	Superkiller viralicidic activity 2-like 2;	-0.22	-0.16	0.83	4.50
P00441	Superoxide dismutase [Cu-Zn];	-0.21	-0.05	0.76	23.40
P04179	Superoxide dismutase [Mn], mitochondrial;	0.62	0.06	0.44	6.30
P78539	Sushi repeat-containing protein SRPX;	-1.47	-0.29	0.06	2.80
O60687	Sushi repeat-containing protein SRPX2;	-0.60	-0.24	0.50	9.20
Q92922	SWI/SNF complex subunit SMARCC1;	1.27	0.33	0.14	2.10
O60264	SWI/SNF-related matrix-associated actin-dependent regul	2.09	0.28	0.01	1.10
Q99536	Synaptic vesicle membrane protein VAT-1 homolog;	1.67	3.67	0.63	9.40
P57105	Synaptojanin-2-binding protein;	4.11	1.01	0.00	8.30
P18827	Syndecan-1;	-1.79	-0.25	0.02	5.50
P31431	Syndecan-4;	1.26	0.13	0.10	7.10
O00560	Syntenin-1;	-0.56	-0.15	0.46	7.00
P17987	T-complex protein 1 subunit alpha;	-0.28	-0.11	0.72	22.10
P78371	T-complex protein 1 subunit beta;	-0.77	-0.42	0.46	25.80
P50991	T-complex protein 1 subunit delta;	-0.24	-0.09	0.76	26.30
Q99832	T-complex protein 1 subunit eta;	-0.37	-0.09	0.61	10.10
P49368	T-complex protein 1 subunit gamma;	-0.22	-0.09	0.78	17.60
P50990	T-complex protein 1 subunit theta;	-0.87	-0.43	0.37	34.90
P40227	T-complex protein 1 subunit zeta;	-1.18	-0.42	0.19	20.70
Q9Y490	Talin-1;	-0.16	-0.07	0.83	5.20
Q7Z7G0	Target of Nesh-SH3;	3.10	2.21	0.02	6.10
Q92804	TATA-binding protein-associated factor 2N;	0.96	0.04	0.21	5.20
O14907	Tax1-binding protein 3;	-0.84	-0.09	0.23	13.70
Q08629	Testican-1;	1.60	0.75	0.13	15.50
P05452	Tetranectin;	-1.51	-0.17	0.04	5.90
O43657	Tetraspanin-6;	-0.87	-0.14	0.23	4.50
P52888	Thimet oligopeptidase;	-0.79	-0.56	0.52	7.70
Q9P2K2	Thioredoxin domain-containing protein 16;	-1.74	-0.35	0.02	3.00
Q9BRA2	Thioredoxin domain-containing protein 17;	-0.22	-0.09	0.77	15.40
Q8NBS9	Thioredoxin domain-containing protein 5;	-0.56	-0.64	0.75	15.30
Q16881	Thioredoxin reductase 1, cytoplasmic;	0.90	0.14	0.26	4.80
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	1.89	0.26	0.02	17.60
Q86V81	THO complex subunit 4;	0.51	0.11	0.56	11.30
P07996	Thrombospondin-1;	-1.56	-0.37	0.05	17.50
P49746	Thrombospondin-3;	1.58	1.13	0.24	6.50
Q9Y2W1	Thyroid hormone receptor-associated protein 3;	-0.33	-0.16	0.72	3.00
Q15654	Thyroid receptor-interacting protein 6;	-0.62	-0.08	0.38	3.80
Q9UKU6	Thyrotropin-releasing hormone-degrading ectoenzyme;	-0.56	-0.25	0.54	3.20
Q9UDY2	Tight junction protein ZO-2;	-1.79	-0.87	0.07	5.60
O75663	TIP41-like protein;	0.53	0.12	0.54	12.10
P04066	Tissue alpha-L-fucosidase;	-0.82	-0.32	0.36	6.20
P10646	Tissue factor pathway inhibitor;	1.95	0.42	0.02	7.60
P00750	Tissue-type plasminogen activator;	2.89	1.24	0.00	20.10
Q8WZ42	Titin;	-2.28	-7.74	0.65	0.10
O14657	Torsin-1B;	-0.47	-0.14	0.55	9.50
O43493	Trans-Golgi network integral membrane protein 2;	-0.82	-0.17	0.28	2.90
Q96EM0	Trans-L-3-hydroxyproline dehydratase;	-0.35	-0.05	0.60	8.80
P23193	Transcription elongation factor A protein 1;	0.35	0.03	0.67	7.30
Q5H9L2	Transcription elongation factor A protein-like 5;	-0.45	-0.02	0.51	4.50

Table S2

Uniprot accession	**Name**	**Fold-change ($\log_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q15370	Transcription elongation factor B polypeptide 2;	-0.26	-0.01	0.68	7.60
O00267	Transcription elongation factor SPT5;	-0.56	-0.11	0.44	2.90
Q7KZ85	Transcription elongation factor SPT6;	0.63	0.07	0.44	0.70
O14776	Transcription elongation regulator 1;	0.72	0.03	0.35	1.10
Q00059	Transcription factor A, mitochondrial;	1.97	1.14	0.09	8.50
P20290	Transcription factor BTF3;	0.48	0.06	0.57	12.60
P35713	Transcription factor SOX-18;	0.69	0.07	0.39	2.30
Q13263	Transcription intermediary factor 1-beta;	-0.45	-0.32	0.70	5.90
Q8WXI9	Transcriptional repressor p66-beta;	-0.87	-0.10	0.22	2.40
Q12788	Transducin beta-like protein 3;	2.90	0.89	0.00	1.60
P02786	Transferrin receptor protein 1;	1.89	1.10	0.10	11.20
Q03167	Transforming growth factor beta receptor type 3;	0.58	0.12	0.50	3.40
P01137	Transforming growth factor beta-1;	1.01	0.22	0.23	15.90
Q15582	Transforming growth factor-beta-induced protein ig-h3;	-2.08	-2.19	0.21	3.50
P55072	Transitional endoplasmic reticulum ATPase;	-0.39	-0.13	0.62	31.30
P29401	Transketolase;	-1.47	-0.81	0.17	25.40
Q9UI10	Translation initiation factor eIF-2B subunit delta;	-1.32	-0.23	0.08	2.70
Q99598	Translin-associated protein X;	0.25	0.04	0.80	4.50
P49755	Transmembrane emp24 domain-containing protein 10;	2.85	0.15	0.00	4.10
Q9UHN6	Transmembrane protein 2;	-0.79	-0.08	0.27	2.50
Q13428	Treacle protein;	0.32	0.10	0.76	1.40
P40939	Trifunctional enzyme subunit alpha, mitochondrial;	4.93	0.86	0.00	1.20
P55084	Trifunctional enzyme subunit beta, mitochondrial;	2.08	5.42	0.61	4.90
P22102	Trifunctional purine biosynthetic protein adenosine-3;	1.90	0.35	0.02	2.70
P60174	Triosephosphate isomerase;	-0.51	-0.13	0.50	50.00
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase;	-2.14	-0.19	0.00	2.50
Q9Y3I0	tRNA-splicing ligase RtcB homolog;	-0.41	-0.17	0.63	12.30
P06753	Tropomyosin alpha-3 chain;	-0.37	-0.15	0.66	14.80
P07951	Tropomyosin beta chain;	0.10	0.14	0.98	10.90
P23381	Tryptophan--tRNA ligase, cytoplasmic;	0.40	0.32	0.80	17.40
P68363	Tubulin alpha-1B chain;	-0.22	-0.05	0.74	32.60
P68366	Tubulin alpha-4A chain;	-2.43	-0.26	0.00	23.00
P07437	Tubulin beta chain;	-0.60	-0.24	0.50	28.80
P68371	Tubulin beta-4B chain;	-0.45	-0.08	0.53	31.50
Q14166	Tubulin--tyrosine ligase-like protein 12;	-0.53	-0.05	0.43	1.60
Q99426	Tubulin-folding cofactor B;	-1.32	-1.11	0.35	7.80
O75347	Tubulin-specific chaperone A;	-0.49	-0.13	0.51	49.10
Q9GZM7	Tubulointerstitial nephritis antigen-like;	0.49	0.05	0.55	2.80
O00300	Tumor necrosis factor receptor superfamily member 11B;	-4.61	-5.62	0.02	9.00
Q9NP84	Tumor necrosis factor receptor superfamily member 12A;	-1.69	-0.06	0.02	7.80
P19438	Tumor necrosis factor receptor superfamily member 1A;	-1.01	-0.98	0.51	6.40
O95407	Tumor necrosis factor receptor superfamily member 6B;	1.11	0.20	0.17	14.30
O43399	Tumor protein D54;	-1.43	-2.16	0.53	16.00
Q6IBS0	Twinfilin-2;	-0.28	-0.04	0.66	9.70
Q9UIG0	Tyrosine-protein kinase BAZ1B;	5.26	1.63	0.00	1.10
P30530	Tyrosine-protein kinase receptor UFO;	-1.90	-0.99	0.07	2.10
Q06124	Tyrosine-protein phosphatase non-receptor type 11;	0.28	0.02	0.74	2.80
P08621	U1 small nuclear ribonucleoprotein 70 kDa;	0.33	0.05	0.71	7.10
P09234	U1 small nuclear ribonucleoprotein C;	-1.14	-0.13	0.12	7.50
O15042	U2 snRNP-associated SURP motif-containing protein;	1.15	0.07	0.13	1.20
O00566	U3 small nucleolar ribonucleoprotein protein MPP10;	2.32	0.26	0.00	1.90
O43818	U3 small nucleolar RNA-interacting protein 2;	3.80	0.19	0.00	2.30
O43290	U4/U6.U5 tri-snRNP-associated protein 1;	0.74	0.16	0.39	5.80
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase;	-0.24	-0.13	0.79	4.50
Q9Y333	U6 snRNA-associated Sm-like protein LSm2;	0.88	0.28	0.33	27.40
P45974	Ubiquitin carboxyl-terminal hydrolase 5;	-0.82	-0.33	0.37	3.50
Q93009	Ubiquitin carboxyl-terminal hydrolase 7;	0.41	0.32	0.79	3.00

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3;	-0.33	-0.06	0.63	8.70
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5;	0.88	0.08	0.26	6.70
O14562	Ubiquitin domain-containing protein UBFD1;	-0.19	-0.02	0.76	3.60
Q96FW1	Ubiquitin thioesterase OTUB1;	-0.22	-0.02	0.72	7.40
P61086	Ubiquitin-conjugating enzyme E2 K;	-0.79	-0.30	0.37	13.50
Q9C0C9	Ubiquitin-conjugating enzyme E2 O;	0.96	0.05	0.21	0.90
Q13404	Ubiquitin-conjugating enzyme E2 variant 1;	-0.21	-0.05	0.77	32.00
P61960	Ubiquitin-fold modifier 1;	-0.45	-0.06	0.52	17.60
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1;	6.70	0.89	0.00	10.20
P22314	Ubiquitin-like modifier-activating enzyme 1;	-0.79	-0.51	0.49	12.60
Q05086	Ubiquitin-protein ligase E3A;	1.74	0.17	0.02	1.00
Q14376	UDP-glucose 4-epimerase;	-0.69	-0.09	0.33	5.70
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1;	0.41	0.35	0.80	1.70
Q8NBZ7	UDP-glucuronic acid decarboxylase 1;	0.75	0.11	0.36	4.00
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;	-0.62	-0.14	0.41	7.50
Q92614	Unconventional myosin-XVIIIa;	-0.14	-0.01	0.80	0.50
Q9H741	UPF0454 protein C12orf49;	-0.82	-0.10	0.25	6.30
Q9BY42	UPF0549 protein C20orf43;	-3.15	-1.39	0.00	7.20
Q9Y224	UPF0568 protein C14orf166;	-0.45	-0.17	0.60	17.20
P00749	Urokinase-type plasminogen activator;	-0.35	-0.16	0.70	11.40
P06132	Uroporphyrinogen decarboxylase;	-0.26	-0.11	0.75	4.60
P54727	UV excision repair protein RAD23 homolog B;	0.25	0.05	0.80	4.20
P38606	V-type proton ATPase catalytic subunit A;	-1.43	-3.16	0.66	9.20
P21281	V-type proton ATPase subunit B, brain isoform;	1.80	1.42	0.21	7.20
Q9UBQ0	Vacuolar protein sorting-associated protein 29;	-0.39	-0.06	0.56	12.60
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolo	-0.49	-0.07	0.48	6.50
P26640	Valine--tRNA ligase;	-0.62	-0.12	0.40	4.40
P50552	Vasodilator-stimulated phosphoprotein;	0.21	0.02	0.82	3.20
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein]	2.35	0.21	0.00	3.00
Q9NZ01	Very-long-chain enoyl-CoA reductase;	3.34	0.24	0.00	6.20
P63027	Vesicle-associated membrane protein 2;	3.08	0.50	0.00	17.00
P51809	Vesicle-associated membrane protein 7;	-2.90	-0.22	0.00	4.10
P46459	Vesicle-fusing ATPase;	3.86	0.64	0.00	3.20
O75396	Vesicle-trafficking protein SEC22b;	0.94	0.10	0.23	4.70
P18206	Vinculin;	0.77	0.38	0.49	14.60
P07225	Vitamin K-dependent protein S;	-1.51	-1.38	0.31	4.30
P04004	Vitronectin;	-0.16	-0.03	0.79	3.10
O75083	WD repeat-containing protein 1;	-1.04	-0.43	0.25	9.10
Q9BV38	WD repeat-containing protein 18;	2.00	0.15	0.01	1.90
Q15061	WD repeat-containing protein 43;	1.34	0.23	0.09	2.80
P61964	WD repeat-containing protein 5;	0.52	0.04	0.52	4.80
Q8IWA0	WD repeat-containing protein 75;	3.32	0.34	0.00	2.30
Q96FK6	WD repeat-containing protein 89;	1.70	0.45	0.05	4.70
Q2TAY7	WD40 repeat-containing protein SMU1;	1.76	0.68	0.07	6.40
P13010	X-ray repair cross-complementing protein 5;	0.25	0.07	0.81	15.00
P12956	X-ray repair cross-complementing protein 6;	0.30	0.07	0.75	25.00
Q9H1B5	Xylosyltransferase 2;	-0.53	-0.15	0.49	2.70
P49750	YLP motif-containing protein 1;	1.16	0.17	0.15	1.10
Q7Z739	YTH domain family protein 3;	0.52	0.03	0.52	1.60
O75152	Zinc finger CCCH domain-containing protein 11A;	1.90	0.14	0.01	1.60
Q8WU90	Zinc finger CCCH domain-containing protein 15;	-2.60	-0.95	0.00	7.30
O43670	Zinc finger protein 207;	-0.60	-0.24	0.50	8.80
Q8TAW3	Zinc finger protein 671;	4.95	0.89	0.00	1.50
Q96KR1	Zinc finger RNA-binding protein;	5.81	2.02	0.00	2.00
P25311	Zinc-alpha-2-glycoprotein;	-1.90	-0.14	0.01	4.00
P51688		-0.22	-0.16	0.84	9.20
Q9BRK5		0.19	0.02	0.84	20.70

Table S2

Uniprot accession	Name	Fold-change (log$_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P54577		0.19	0.02	0.84	4.70
Q13283		-0.12	-0.03	0.84	30.90
Q8NHP8		0.26	0.13	0.84	13.60
Q9BS26		0.32	0.24	0.84	7.60
P00492		0.21	0.06	0.84	37.60
Q9UBT2		0.52	0.79	0.84	4.80
P20618		-0.11	-0.01	0.84	38.60
Q9H0C8		-0.11	-0.01	0.84	3.10
P30566		0.19	0.03	0.84	4.10
P23284		-0.19	-0.11	0.84	34.70
Q92820		-0.11	-0.01	0.84	24.20
P61970		-0.11	-0.01	0.84	16.50
P36952		-0.11	-0.02	0.85	16.30
Q9GZP4		-0.11	-0.02	0.85	15.20
Q96GQ7		-0.22	-0.18	0.85	2.80
Q16531		0.19	0.04	0.85	4.60
P07858		-0.12	-0.04	0.85	26.00
P49327		0.27	0.17	0.85	9.60
O95881		-0.16	-0.09	0.85	17.40
Q96IU4		0.18	0.01	0.85	11.40
P62081		0.23	0.10	0.85	19.10
Q9HAV7		-0.11	-0.02	0.85	5.10
P20062		-0.22	-0.19	0.85	4.20
P04040		0.18	0.02	0.85	10.20
P62280		0.23	0.11	0.85	27.80
P51149		0.18	0.02	0.85	6.30
O14672		0.21	0.08	0.86	8.40
P29218		-0.11	-0.03	0.86	8.30
Q9Y265		-0.12	-0.05	0.86	18.90
P50914		0.59	1.18	0.86	9.80
P52565		-0.09	-0.01	0.86	7.40
P17050		-0.09	-0.01	0.86	5.10
Q9Y287		0.18	0.03	0.86	6.80
Q15417		-0.12	-0.05	0.86	13.70
Q9P258		-0.12	-0.05	0.86	10.50
Q9UBP4		-0.09	-0.01	0.86	6.30
O75718		-0.09	-0.01	0.86	2.70
P63208		-0.11	-0.03	0.86	20.20
O75509		-0.09	-0.01	0.86	4.60
P49736		-0.14	-0.08	0.86	2.80
Q14155		0.18	0.04	0.86	1.20
P50454		-0.21	-0.18	0.86	11.70
P37802		0.19	0.07	0.86	35.20
P62891		-0.09	-0.02	0.87	19.60
O00505		-0.09	-0.02	0.87	2.50
P55884		0.23	0.13	0.87	12.20
Q6EMK4		-0.11	-0.04	0.87	8.00
Q9UGV2		0.17	0.01	0.87	4.00
Q09666		-0.22	-0.22	0.87	11.20
P46783		-0.09	-0.02	0.87	14.50
P12429		0.40	0.54	0.87	22.60
P04844		0.52	1.00	0.87	4.90
Q9HC38		0.17	0.02	0.87	10.50
Q9HB07		0.17	0.02	0.87	3.70
O14950		-0.09	-0.02	0.87	23.40
P61204		0.19	0.08	0.87	26.00
P31948		-0.12	-0.06	0.88	9.80

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P48643		-0.11	-0.05	0.88	15.50
P62333		-0.08	0.00	0.88	5.70
P62899		-0.08	0.00	0.88	21.60
P31150		-0.08	0.00	0.88	4.90
P51665		-0.08	0.00	0.88	3.10
P98175		-0.08	-0.01	0.88	1.40
Q04637		-0.12	-0.07	0.88	5.40
P16144		-0.14	-0.10	0.88	9.30
Q9NWV4		-0.12	-0.07	0.88	15.00
Q14566		0.17	0.04	0.88	9.10
Q15365		0.17	0.04	0.88	25.60
Q15366		-0.12	-0.01	0.82	14.20
P04792		-0.11	-0.05	0.88	24.40
P61158		-0.08	-0.01	0.88	18.90
P53041		0.15	0.01	0.88	1.40
Q92688		0.15	0.01	0.89	19.90
P49720		0.15	0.01	0.89	7.80
Q96I99		-0.08	-0.02	0.89	2.30
Q9BXP5		-0.14	-0.10	0.89	2.40
P33991		0.15	0.01	0.89	5.70
Q9GZX9		0.15	0.01	0.89	6.70
Q02818		0.18	0.08	0.89	27.50
Q9P0S2		0.15	0.02	0.89	13.20
Q6DKI1		0.34	0.46	0.89	10.60
Q96PK2		-0.08	-0.02	0.89	0.50
Q9UQ35		-0.28	-0.42	0.89	2.60
Q9HB40		-0.21	-0.23	0.89	4.60
P07237		0.15	0.03	0.89	29.70
Q09028		0.15	0.04	0.89	11.30
P62277		-0.08	-0.02	0.90	24.50
P08670		-0.08	-0.02	0.90	42.50
P06744		0.15	0.04	0.90	24.90
P40926		-0.11	-0.07	0.90	42.30
Q14008		0.17	0.07	0.90	2.00
P30085		-0.05	0.00	0.90	16.80
O15371		-0.05	0.00	0.90	3.10
P24534		-0.08	-0.03	0.90	23.60
Q9NYL9		-0.08	-0.03	0.90	2.60
Q15233		0.15	0.04	0.90	9.30
P02768		-0.16	-0.16	0.90	4.60
P07954		0.15	0.05	0.90	10.00
P09960		0.17	0.07	0.90	25.70
Q15185		0.14	0.01	0.90	13.10
Q15257		-0.08	-0.03	0.90	9.50
P98179		0.14	0.02	0.90	21.00
O75369		0.18	0.11	0.90	22.50
O43707		0.14	0.02	0.90	43.40
P12814		0.23	0.09	0.84	37.80
Q14157		-0.05	-0.01	0.90	2.90
O75787		-0.11	-0.07	0.91	12.90
P78330		-0.05	-0.01	0.91	17.30
Q9H0D6		0.21	0.17	0.91	3.80
P39687		0.14	0.02	0.91	23.70
Q9NYF8		-0.08	-0.03	0.91	4.60
P47755		-0.05	-0.01	0.91	10.80
Q9BVM2		0.17	0.09	0.91	10.30
P48745		-0.05	-0.01	0.91	7.60

Table S2

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
Q96I24		0.26	0.31	0.91	6.10
P98088		0.15	0.07	0.91	1.60
Q13435		-0.08	-0.04	0.91	6.70
P52292		0.14	0.04	0.91	6.40
P08729		-0.09	-0.06	0.92	16.80
P62263		-0.08	-0.04	0.92	15.20
Q9UHG2		-0.03	0.00	0.92	31.20
P13693		-0.05	-0.02	0.92	23.80
Q8WVQ1		-0.05	-0.02	0.92	20.00
P68036		-0.03	0.00	0.92	33.10
Q9NQW7		-0.03	0.00	0.92	5.00
P62937		-0.03	0.00	0.92	36.40
Q02878		-0.03	-0.01	0.92	16.30
Q8NC56		-0.19	-0.29	0.92	4.80
Q15904		-0.03	-0.01	0.92	18.10
P52209		0.11	0.02	0.92	19.50
O00592		0.32	0.58	0.92	4.10
Q12904		-0.03	-0.01	0.92	11.50
Q13813		0.14	0.06	0.92	10.50
P63010		0.11	0.02	0.92	6.50
Q01105		-0.03	-0.01	0.93	30.00
P61088		-0.03	-0.01	0.93	23.70
O00139		-0.05	-0.02	0.93	2.50
O94985		0.11	0.03	0.93	15.80
P54802		-0.05	-0.02	0.93	5.20
P62258		0.11	0.04	0.93	47.50
Q9NPR2		-0.11	-0.12	0.93	5.40
O15230		0.14	0.08	0.93	17.90
Q8NFZ8		-0.03	-0.01	0.94	13.90
Q14974		0.11	0.04	0.94	10.70
P31939		-0.05	-0.03	0.94	14.90
Q8N114		-0.01	0.00	0.94	2.90
P83916		-0.01	0.00	0.94	14.60
P60983		0.10	0.01	0.94	14.10
O60749		0.10	0.01	0.94	1.90
Q86UD1		-0.01	0.00	0.94	3.30
Q12792		-0.01	0.00	0.94	6.30
Q9NQP4		-0.01	0.00	0.94	9.00
Q9BZM5		0.10	0.01	0.94	8.50
Q9UNS2		-0.01	0.00	0.94	3.50
P61221		0.10	0.01	0.94	3.30
Q99650		-0.01	0.00	0.94	1.00
O95810		-0.01	0.00	0.94	10.40
Q13423		0.19	0.24	0.94	4.00
Q16181		-0.01	0.00	0.94	5.30
P04083		-0.12	-0.17	0.94	57.20
Q99436		-0.01	0.00	0.94	7.60
P98160		0.14	0.09	0.94	14.40
P48147		-0.05	-0.03	0.94	5.50
Q15907		-0.01	0.00	0.94	39.40
O14737		0.10	0.02	0.94	19.20
Q13451		-0.01	0.00	0.94	3.50
P62993		0.10	0.02	0.94	24.90
O00391		-0.01	0.00	0.94	21.70
Q8IWU5		0.10	0.02	0.94	8.60
P30153		-0.01	0.00	0.94	20.00
Q9BXJ9		-0.08	-0.07	0.94	2.10

Table S2

Uniprot accession	Name	Fold-change ($\log_2$) of ASAPratio	Fold-change standard deviation	ASPAratio p-value	Sequence coverage (%)
P31040		-0.39	-1.62	0.94	4.80
O95777		-0.01	0.00	0.95	27.10
P30626		0.10	0.03	0.95	38.40
P09012		0.10	0.04	0.95	8.90
P04080		-0.01	-0.01	0.95	19.40
Q9UBR2		-0.01	-0.01	0.95	15.80
P02753		-0.11	-0.18	0.95	10.90
C9JH25		-0.37	-1.76	0.95	2.20
Q9NPH2		0.11	0.08	0.95	4.80
P52655		0.09	0.00	0.95	2.90
Q08431		0.09	0.00	0.95	2.60
Q13867		-0.01	-0.01	0.95	7.90
Q12765		0.00	0.00	0.96	7.70
P01009		0.09	0.01	0.96	14.10
Q9UL46		0.00	0.00	0.96	3.80
Q15847		0.00	0.00	0.96	18.40
P46777		0.09	0.01	0.96	15.80
Q16851		0.00	0.00	0.96	1.80
Q5SRI9		-0.03	-0.03	0.96	4.30
P35080		0.09	0.02	0.96	10.00
P35052		-0.01	-0.01	0.96	14.70
P23588		0.00	0.00	0.96	6.10
P04062		0.09	0.02	0.96	17.00
O00410		0.00	0.00	0.96	6.70
Q12906		-0.08	-0.11	0.96	13.00
P63241		0.09	0.03	0.96	19.00
P26639		-0.01	-0.01	0.97	11.60
Q01082		0.00	0.00	0.97	6.20
Q9NRN7		-0.03	-0.04	0.97	5.50
P48723		0.11	0.13	0.97	21.00
Q92945		-0.01	-0.01	0.97	12.00
Q15181		0.09	0.05	0.97	19.00
P00491		-0.01	-0.01	0.97	13.50
P48681		0.00	0.00	0.97	2.00
Q6P5R6		0.07	0.01	0.97	9.80
Q5VY43		0.07	0.01	0.97	1.10
O14818		0.07	0.01	0.97	18.50
Q13554		0.07	0.01	0.97	2.50
O14773		0.07	0.01	0.97	8.20
Q9Y383		0.07	0.01	0.97	6.40
Q9UHX1		0.09	0.06	0.97	14.50
O00115		0.01	0.00	0.97	13.10
P28074		0.01	0.00	0.97	4.60
P62244		0.01	0.00	0.97	13.80
Q641Q3		0.01	0.00	0.97	7.70
Q14703		0.01	0.00	0.97	0.80
P34897		0.01	0.00	0.97	3.20
P09601		0.01	0.00	0.97	5.60
P60900		0.07	0.02	0.97	13.00
P09497		0.01	0.00	0.98	12.70
Q9BWS9		0.01	0.00	0.98	3.60
Q06481		0.07	0.02	0.98	7.90
O15355		0.01	0.00	0.98	11.50
P25205		0.01	0.00	0.98	3.70
O75937		0.07	0.02	0.98	9.90
P37837		0.07	0.02	0.98	22.60
P37235		0.07	0.03	0.98	22.30

Table S2

Uniprot accession	**Name**	**Fold-change (log$_2$) of ASAPratio**	**Fold-change standard deviation**	**ASPAratio p-value**	**Sequence coverage (%)**
P55058		-0.01	-0.02	0.98	24.50
P25788		0.11	0.20	0.98	12.90
Q96PZ0		0.07	0.03	0.98	3.60
P06865		0.09	0.08	0.98	21.40
P07602		0.00	0.00	0.98	12.80
P07814		0.07	0.05	0.98	7.40
O43505		0.01	0.01	0.98	18.80
Q13620		0.09	0.13	0.99	2.20
P09874		0.01	0.01	0.99	15.40
P43034		0.06	0.00	0.99	6.80
Q9UNE7		0.06	0.00	0.99	10.20
O75882		0.06	0.01	0.99	2.40
Q13685		0.06	0.01	0.99	3.00
P15531		0.06	0.01	0.99	57.20
P22392		0.25	0.03	0.79	47.40
P26368		0.06	0.01	0.99	15.40
P78347		0.06	0.02	0.99	2.40
Q9Y266		0.06	0.02	0.99	10.30
P43686		0.04	0.00	0.99	6.50
Q9Y3A5		0.04	0.00	0.99	7.20
P49721		0.04	0.01	0.99	10.00
P46926		0.04	0.01	0.99	11.40
P36957		0.01	0.03	0.99	7.90
P43251		0.04	0.02	0.99	5.70
P49588		0.04	0.02	1.00	4.60