Table S4

Table S4: Proteins that are identified and quantified in all three replicates of global proteome comparison

Averaged ratios are normalized to hK expression / control.

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q04446	1,4-alpha-glucan-branching enzyme;	-0.48	0.80
P61604	10 kDa heat shock protein, mitochondrial;	0.49	0.54
Q15029	116 kDa U5 small nuclear ribonucleoprotein component;	0.02	0.79
P31946	14-3-3 protein beta/alpha;	-0.72	0.58
P62258	14-3-3 protein epsilon;	0.12	0.73
Q04917	14-3-3 protein eta;	-0.35	0.95
P61981	14-3-3 protein gamma;	-0.40	0.84
P31947	14-3-3 protein sigma;	-0.43	0.87
P27348	14-3-3 protein theta;	-0.30	0.94
P63104	14-3-3 protein zeta/delta;	-0.32	0.95
P62333	26S protease regulatory subunit 10B;	0.43	0.78
P43686	26S protease regulatory subunit 6B;	0.62	0.58
O00231	26S proteasome non-ATPase regulatory subunit 11;	0.54	0.71
Q13200	26S proteasome non-ATPase regulatory subunit 2;	0.39	0.77
O43242	26S proteasome non-ATPase regulatory subunit 3;	0.76	0.40
Q15008	26S proteasome non-ATPase regulatory subunit 6;	0.45	0.59
O00233	26S proteasome non-ATPase regulatory subunit 9;	0.15	0.78
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial;	-0.14	0.88
O95861	3'(2'),5'-bisphosphate nucleotidase 1;	-0.37	0.75
P46783	40S ribosomal protein S10;	0.03	0.87
P62280	40S ribosomal protein S11;	0.60	0.81
P25398	40S ribosomal protein S12;	0.23	0.90
P62277	40S ribosomal protein S13;	0.30	0.83
P62263	40S ribosomal protein S14;	0.30	0.85
P62841	40S ribosomal protein S15;	0.09	0.91
P62244	40S ribosomal protein S15a;	0.02	0.99
P62249	40S ribosomal protein S16;	0.57	0.40
P62269	40S ribosomal protein S18;	0.17	0.91
P39019	40S ribosomal protein S19;	0.03	0.98
P15880	40S ribosomal protein S2;	0.04	0.97
P63220	40S ribosomal protein S21;	-0.03	0.96
P62266	40S ribosomal protein S23;	1.75	0.00
Q71UM5	40S ribosomal protein S27-like;	0.63	0.59
P42677	40S ribosomal protein S27;	0.75	0.39
P62857	40S ribosomal protein S28;	0.29	0.59
P23396	40S ribosomal protein S3;	0.25	0.90
P61247	40S ribosomal protein S3a;	0.38	0.90
P62701	40S ribosomal protein S4, X isoform;	0.20	0.85
P46782	40S ribosomal protein S5;	-0.17	0.90
P62753	40S ribosomal protein S6;	-0.03	0.88
P62081	40S ribosomal protein S7;	0.15	0.96
P62241	40S ribosomal protein S8;	0.26	0.78
P46781	40S ribosomal protein S9;	0.46	0.69
P08865	40S ribosomal protein SA;	-0.16	0.99

Table S4

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q9BRK5	45 kDa calcium-binding protein;	0.46	0.85
P08195	4F2 cell-surface antigen heavy chain;	0.78	0.68
Q9H0D6	5'-3' exoribonuclease 2;	-0.06	0.95
Q01813	6-phosphofructokinase type C;	-0.86	0.56
P08237	6-phosphofructokinase, muscle type;	-0.03	0.63
P52209	6-phosphogluconate dehydrogenase, decarboxylating;	-0.03	1.00
O95336	6-phosphogluconolactonase;	-1.00	0.53
P10809	60 kDa heat shock protein, mitochondrial;	0.91	0.28
P05388	60S acidic ribosomal protein P0;	1.00	0.29
P05386	60S acidic ribosomal protein P1;	0.97	0.22
P05387	60S acidic ribosomal protein P2;	0.49	0.76
P62906	60S ribosomal protein L10a;	0.61	0.61
P62913	60S ribosomal protein L11;	0.33	0.92
P26373	60S ribosomal protein L13;	0.05	0.82
P50914	60S ribosomal protein L14;	0.43	0.83
P61313	60S ribosomal protein L15;	0.15	0.83
P18621	60S ribosomal protein L17;	0.03	0.83
Q07020	60S ribosomal protein L18;	-0.05	0.93
Q02543	60S ribosomal protein L18a;	0.23	0.48
P46778	60S ribosomal protein L21;	-0.05	0.76
P62829	60S ribosomal protein L23;	-0.20	0.76
P62750	60S ribosomal protein L23a;	0.12	0.83
P83731	60S ribosomal protein L24;	0.03	0.84
P61353	60S ribosomal protein L27;	0.04	0.96
P47914	60S ribosomal protein L29;	-0.01	0.63
P39023	60S ribosomal protein L3;	0.01	0.81
P62888	60S ribosomal protein L30;	-0.48	0.92
P62899	60S ribosomal protein L31;	0.19	0.97
P62910	60S ribosomal protein L32;	-0.34	0.92
P18077	60S ribosomal protein L35a;	0.63	0.22
P36578	60S ribosomal protein L4;	0.16	0.62
P46777	60S ribosomal protein L5;	-0.82	0.54
Q02878	60S ribosomal protein L6;	0.20	0.97
P18124	60S ribosomal protein L7;	0.12	0.68
P62424	60S ribosomal protein L7a;	0.17	0.85
P32969	60S ribosomal protein L9;	-0.19	0.97
P11021	78 kDa glucose-regulated protein;	0.58	0.67
Q02952	A-kinase anchor protein 12;	-0.34	0.93
Q13510	Acid ceramidase;	0.04	0.81
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family	-0.10	0.94
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family	-0.25	0.93
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family	0.18	0.72
P61160	Actin-related protein 2;	-0.38	0.74
O15143	Actin-related protein 2/3 complex subunit 1B;	-0.20	0.94
O15144	Actin-related protein 2/3 complex subunit 2;	-0.06	0.80

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
P59998	Actin-related protein 2/3 complex subunit 4;	0.14	0.84
P61158	Actin-related protein 3;	-0.24	0.87
P62736	Actin, aortic smooth muscle;	0.01	0.53
P60709	Actin, cytoplasmic 1;	0.12	0.31
P53999	Activated RNA polymerase II transcriptional coactivator	0.82	0.28
O95433	Activator of 90 kDa heat shock protein ATPase homolog	0.38	0.91
P07108	Acyl-CoA-binding protein;	-0.01	0.95
P13798	Acylamino-acid-releasing enzyme;	-0.57	0.68
P07311	Acylphosphatase-1;	-0.26	0.49
Q6UY14	ADAMTS-like protein 4;	0.20	0.69
P23526	Adenosylhomocysteinase;	-0.76	0.59
P54819	Adenylate kinase 2, mitochondrial;	-1.01	0.47
P30566	Adenylosuccinate lyase;	0.16	0.99
P30520	Adenylosuccinate synthetase isozyme 2;	0.51	0.83
Q01518	Adenylyl cyclase-associated protein 1;	-0.86	0.53
P61204	ADP-ribosylation factor 3;	-0.22	0.94
Q9UKK9	ADP-sugar pyrophosphatase;	-0.24	0.92
O00468	Agrin;	0.41	0.66
P49588	Alanine--tRNA ligase, cytoplasmic;	0.26	0.97
P14550	Alcohol dehydrogenase [NADP(+)];	0.53	0.89
P11766	Alcohol dehydrogenase class-3;	-0.98	0.39
P47895	Aldehyde dehydrogenase family 1 member A3;	-0.71	0.52
Q8IZ83	Aldehyde dehydrogenase family 16 member A1;	-0.55	0.73
P15121	Aldose reductase;	-1.10	0.27
P05187	Alkaline phosphatase, placental type;	-0.48	0.78
P01009	Alpha-1-antitrypsin;	1.41	0.02
P12814	Alpha-actinin-1;	0.34	0.97
O43707	Alpha-actinin-4;	-0.01	0.99
P06733	Alpha-enolase;	-1.25	0.23
P06280	Alpha-galactosidase A;	0.84	0.57
P35475	Alpha-L-iduronidase;	-0.38	0.54
P54802	Alpha-N-acetylglucosaminidase;	0.52	0.81
Q96IU4	Alpha/beta hydrolase domain-containing protein 14B;	0.34	0.88
Q12904	Aminoacyl tRNA synthase complex-interacting	-0.35	0.97
Q9H4A4	Aminopeptidase B;	0.31	0.93
P05067	Amyloid beta A4 protein;	0.11	0.85
Q06481	Amyloid-like protein 2;	0.58	0.71
Q13685	Angio-associated migratory cell protein;	0.42	0.80
P04083	Annexin A1;	-0.49	0.88
P07355	Annexin A2;	-0.94	0.36
P12429	Annexin A3;	1.14	0.53
P08758	Annexin A5;	-1.13	0.29
P46013	Antigen KI-67;	1.86	0.00
O95782	AP-2 complex subunit alpha-1;	-0.38	0.90
P63010	AP-2 complex subunit beta;	0.21	0.99
Q96CW1	AP-2 complex subunit mu;	-0.34	0.93

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
P02656	Apolipoprotein C-III;	0.57	0.59
Q9BZZ5	Apoptosis inhibitor 5;	-0.44	0.87
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus;	0.29	0.71
P54136	Arginine--tRNA ligase, cytoplasmic;	-0.46	0.83
P04424	Argininosuccinate lyase;	-0.63	0.57
P17174	Aspartate aminotransferase, cytoplasmic;	-0.93	0.76
P00505	Aspartate aminotransferase, mitochondrial;	-0.21	0.87
P14868	Aspartate--tRNA ligase, cytoplasmic;	0.52	0.61
Q8WWM7	Ataxin-2-like protein;	-0.85	0.19
P61221	ATP-binding cassette sub-family E member 1;	-0.43	0.95
Q8NE71	ATP-binding cassette sub-family F member 1;	-0.74	0.54
P53396	ATP-citrate synthase;	-0.67	0.69
Q08211	ATP-dependent RNA helicase A;	1.04	0.46
Q92499	ATP-dependent RNA helicase DDX1;	-0.55	0.76
Q9NUU7	ATP-dependent RNA helicase DDX19A;	0.59	0.58
O75882	Attractin;	0.73	0.44
P50895	Basal cell adhesion molecule;	0.24	0.87
P98160	Basement membrane-specific heparan sulfate	1.02	0.48
P35613	Basigin;	0.72	0.27
P15291	Beta-1,4-galactosyltransferase 1;	0.05	0.96
O60513	Beta-1,4-galactosyltransferase 4;	-1.02	0.62
P02749	Beta-2-glycoprotein 1;	0.68	0.65
P16278	Beta-galactosidase;	0.04	0.85
P08236	Beta-glucuronidase;	2.33	0.07
P06865	Beta-hexosaminidase subunit alpha;	0.61	0.78
P07686	Beta-hexosaminidase subunit beta;	1.03	0.50
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate	-0.90	0.31
P07814	Bifunctional glutamate/proline--tRNA ligase;	0.08	1.00
P31939	Bifunctional purine biosynthesis protein PURH;	-0.17	0.99
P43251	Biotinidase;	-0.07	1.00
Q9H3K6	BolA-like protein 2;	-0.55	0.75
P13497	Bone morphogenetic protein 1;	0.22	0.85
Q9P287	BRCA2 and CDKN1A-interacting protein;	0.29	0.83
P11586	C-1-tetrahydrofolate synthase, cytoplasmic;	-0.17	0.99
P56545	C-terminal-binding protein 2;	-0.02	0.98
Q9UBG0	C-type mannose receptor 2;	-2.60	0.00
Q96EU7	C1GALT1-specific chaperone 1;	2.07	0.02
P63098	Calcineurin subunit B type 1;	1.55	0.01
Q9Y2V2	Calcium-regulated heat stable protein 1;	-0.03	0.48
Q13554	Calcium/calmodulin-dependent protein kinase type II	-0.03	1.00
Q9HB71	Calcyclin-binding protein;	0.14	0.95
P62158	Calmodulin;	0.21	0.91
P17655	Calpain-2 catalytic subunit;	0.15	0.96
Q15417	Calponin-3;	0.00	0.99
P27797	Calreticulin;	0.84	0.42
O94985	Calsyntenin-1;	0.61	0.74
O43852	Calumenin;	1.31	0.27

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
Q8NCH0	Carbohydrate sulfotransferase 14;	0.13	0.68
P19784	Casein kinase II subunit alpha';	1.41	0.00
P04040	Catalase;	-0.46	0.85
P07858	Cathepsin B;	0.04	0.83
P07339	Cathepsin D;	0.25	0.79
P07711	Cathepsin L1;	2.16	0.00
Q9UBR2	Cathepsin Z;	0.39	0.91
P11717	Cation-independent mannose-6-phosphate receptor;	0.39	0.88
Q03135	Caveolin-1;	-0.09	0.83
Q6YHK3	CD109 antigen;	0.72	0.64
Q13740	CD166 antigen;	0.98	0.35
Q9Y5K6	CD2-associated protein;	-0.56	0.64
P16070	CD44 antigen;	-1.09	0.33
P13987	CD59 glycoprotein;	1.65	0.01
Q8NFZ8	Cell adhesion molecule 4;	0.78	0.47
Q99459	Cell division cycle 5-like protein;	0.77	0.02
Q99674	Cell growth regulator with EF hand domain protein 1;	0.36	0.85
O00299	Chloride intracellular channel protein 1;	0.19	0.98
Q9Y696	Chloride intracellular channel protein 4;	-0.53	0.82
Q6UVK1	Chondroitin sulfate proteoglycan 4;	0.20	0.73
P83916	Chromobox protein homolog 1;	-0.46	0.83
Q13185	Chromobox protein homolog 3;	-0.05	0.87
P45973	Chromobox protein homolog 5;	-0.08	0.82
O75390	Citrate synthase, mitochondrial;	0.37	0.90
Q00610	Clathrin heavy chain 1;	0.38	0.88
Q10570	Cleavage and polyadenylation specificity factor subunit 1;	-0.18	0.94
P10909	Clusterin;	-0.35	0.85
Q14019	Coactosin-like protein;	-0.55	0.67
P48444	Coatomer subunit delta;	-0.30	0.91
O14579	Coatomer subunit epsilon;	-0.09	0.64
O43405	Cochlin;	3.75	0.00
P23528	Cofilin-1;	-0.26	0.96
O75534	Cold shock domain-containing protein E1;	-0.04	0.94
Q14011	Cold-inducible RNA-binding protein;	-0.39	0.63
P12109	Collagen alpha-1(VI) chain;	1.88	0.01
Q99715	Collagen alpha-1(XII) chain;	-0.68	0.62
P39060	Collagen alpha-1(XVIII) chain;	1.67	0.06
P05997	Collagen alpha-2(V) chain;	4.93	0.00
P00736	Complement C1r subcomponent;	1.02	0.46
P01024	Complement C3;	2.24	0.01
Q07021	Complement component 1 Q subcomponent-binding	0.61	0.52
P00751	Complement factor B;	0.66	0.60
P00746	Complement factor D;	1.26	0.08
P29279	Connective tissue growth factor;	-0.70	0.59
Q13098	COP9 signalosome complex subunit 1;	0.06	0.94
Q9UNS2	COP9 signalosome complex subunit 3;	-0.33	0.84

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Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q9BT78	COP9 signalosome complex subunit 4;	-0.44	0.82
Q92905	COP9 signalosome complex subunit 5;	-0.51	0.72
P36551	Coproporphyrinogen-III oxidase, mitochondrial;	-1.50	0.62
O75367	Core histone macro-H2A.1;	-0.03	0.40
P31146	Coronin-1A;	-0.41	0.86
Q9ULV4	Coronin-1C;	0.12	0.99
P12277	Creatine kinase B-type;	3.29	0.11
P46109	Crk-like protein;	-0.07	0.85
Q13620	Cullin-4B;	0.53	0.67
Q86VP6	Cullin-associated NEDD8-dissociated protein 1;	-0.59	0.80
P04080	Cystatin-B;	0.41	0.82
P01034	Cystatin-C;	1.90	0.00
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1;	0.00	0.53
P49589	Cysteine--tRNA ligase, cytoplasmic;	-0.22	0.89
Q9NZV1	Cysteine-rich motor neuron 1 protein;	0.04	0.84
Q9P0S2	Cytochrome c oxidase assembly protein COX16	0.63	0.69
P14854	Cytochrome c oxidase subunit 6B1;	0.56	0.01
Q14204	Cytoplasmic dynein 1 heavy chain 1;	0.41	0.93
Q14008	Cytoskeleton-associated protein 5;	-0.54	0.72
P28838	Cytosol aminopeptidase;	-1.91	0.05
O00154	Cytosolic acyl coenzyme A thioester hydrolase;	-0.56	0.75
Q96KP4	Cytosolic non-specific dipeptidase;	-0.60	0.86
O43175	D-3-phosphoglycerate dehydrogenase;	-0.17	0.70
P30046	D-dopachrome decarboxylase;	0.31	0.88
Q8N163	DBIRD complex subunit KIAA1967;	0.20	0.00
Q9H773	dCTP pyrophosphatase 1;	-1.03	0.42
O00115	Deoxyribonuclease-2-alpha;	0.61	0.67
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase,	-0.17	0.96
Q14126	Desmoglein-2;	0.16	0.70
P60981	Destrin;	-0.71	0.64
Q9NR28	Diablo homolog, mitochondrial;	-0.82	0.35
O94907	Dickkopf-related protein 1;	2.13	0.01
Q9UBP4	Dickkopf-related protein 3;	1.39	0.07
P09622	Dihydrolipoyl dehydrogenase, mitochondrial;	-0.23	0.65
P09417	Dihydropteridine reductase;	-1.36	0.13
Q16555	Dihydropyrimidinase-related protein 2;	-0.51	0.83
P53634	Dipeptidyl peptidase 1;	2.16	0.00
Q9UHL4	Dipeptidyl peptidase 2;	1.23	0.14
Q9NY33	Dipeptidyl peptidase 3;	-0.01	0.91
O14672	Disintegrin and metalloproteinase domain-containing	0.61	0.73
Q13444	Disintegrin and metalloproteinase domain-containing	0.97	0.46
Q16531	DNA damage-binding protein 1;	-0.32	0.91
P18887	DNA repair protein XRCC1;	-0.79	0.07
P49736	DNA replication licensing factor MCM2;	0.23	0.95
P25205	DNA replication licensing factor MCM3;	0.48	0.92
Q14566	DNA replication licensing factor MCM6;	0.51	0.87

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
P27695	DNA-(apurinic or apyrimidinic site) lyase;	0.59	0.65
O75937	DnaJ homolog subfamily C member 8;	-0.18	0.98
Q16643	Drebrin;	2.07	0.00
P51452	Dual specificity protein phosphatase 3;	-0.18	0.92
Q13561	Dynactin subunit 2;	0.36	0.93
Q96FJ2	Dynein light chain 2, cytoplasmic;	-0.48	0.77
Q14118	Dystroglycan;	0.93	0.44
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1;	-0.73	0.57
Q9UNE7	E3 ubiquitin-protein ligase CHIP;	0.29	0.96
Q14258	E3 ubiquitin/ISG15 ligase TRIM25;	-0.50	0.73
Q15075	Early endosome antigen 1;	1.85	0.04
Q96C19	EF-hand domain-containing protein D2;	0.84	0.51
Q9H4M9	EH domain-containing protein 1;	-0.07	0.88
Q15717	ELAV-like protein 1;	0.27	0.69
P68104	Elongation factor 1-alpha 1;	-0.36	0.93
Q05639	Elongation factor 1-alpha 2;	2.83	0.00
P24534	Elongation factor 1-beta;	-0.05	0.99
P29692	Elongation factor 1-delta;	-0.72	0.66
P26641	Elongation factor 1-gamma;	-0.50	0.91
P13639	Elongation factor 2;	-0.40	0.89
P50402	Emerin;	-1.51	0.06
Q99961	Endophilin-A2;	0.64	0.72
P30040	Endoplasmic reticulum resident protein 29;	1.13	0.28
Q9BS26	Endoplasmic reticulum resident protein 44;	0.28	0.97
P14625	Endoplasmin;	1.49	0.10
Q9UNN8	Endothelial protein C receptor;	0.21	0.50
P84090	Enhancer of rudimentary homolog;	-0.61	0.56
P42126	Enoyl-CoA delta isomerase 1, mitochondrial;	0.87	0.03
P30084	Enoyl-CoA hydratase, mitochondrial;	1.17	0.03
P20827	Ephrin-A1;	0.20	0.63
P00533	Epidermal growth factor receptor;	-0.41	0.90
P61916	Epididymal secretory protein E1;	1.14	0.22
Q9Y2E5	Epididymis-specific alpha-mannosidase;	0.30	0.47
Q96HE7	ERO1-like protein alpha;	0.00	0.65
P60842	Eukaryotic initiation factor 4A-I;	0.86	0.38
Q14240	Eukaryotic initiation factor 4A-II;	-0.63	0.54
P38919	Eukaryotic initiation factor 4A-III;	0.83	0.14
P15170	Eukaryotic peptide chain release factor GTP-binding	-0.41	0.92
P62495	Eukaryotic peptide chain release factor subunit 1;	-0.02	0.84
O14602	Eukaryotic translation initiation factor 1A, Y-	-0.45	0.88
P05198	Eukaryotic translation initiation factor 2 subunit 1;	0.34	0.96
P20042	Eukaryotic translation initiation factor 2 subunit 2;	1.07	0.02
P41091	Eukaryotic translation initiation factor 2 subunit 3;	-0.10	0.96
Q9BY44	Eukaryotic translation initiation factor 2A;	-1.05	0.39
Q14152	Eukaryotic translation initiation factor 3 subunit A;	0.18	0.95
P55884	Eukaryotic translation initiation factor 3 subunit B;	0.25	0.96
Q99613	Eukaryotic translation initiation factor 3 subunit C;	-0.29	0.63

Table S4

Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
O15371	Eukaryotic translation initiation factor 3 subunit D;	-0.24	0.98
P60228	Eukaryotic translation initiation factor 3 subunit E;	0.05	0.86
O75821	Eukaryotic translation initiation factor 3 subunit G;	0.41	0.91
Q13347	Eukaryotic translation initiation factor 3 subunit I;	0.13	0.97
O75822	Eukaryotic translation initiation factor 3 subunit J;	-0.29	0.93
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K;	-0.85	0.07
Q9Y262	Eukaryotic translation initiation factor 3 subunit L;	-0.44	0.85
Q04637	Eukaryotic translation initiation factor 4 gamma 1;	0.13	0.98
P23588	Eukaryotic translation initiation factor 4B;	0.30	0.79
P63241	Eukaryotic translation initiation factor 5A-1;	-0.08	1.00
Q15024	Exosome complex component RRP42;	0.25	0.96
O14980	Exportin-1	-0.74	0.72
P55060	Exportin-2;	-0.19	0.96
Q16610	Extracellular matrix protein 1;	1.21	0.23
Q8IWU5	Extracellular sulfatase Sulf-2;	0.35	0.93
P15311	Ezrin;	-0.87	0.43
P52907	F-actin-capping protein subunit alpha-1;	-0.29	0.92
P47755	F-actin-capping protein subunit alpha-2;	-0.36	0.90
P47756	F-actin-capping protein subunit beta;	-0.11	0.95
Q9Y5B9	FACT complex subunit SPT16;	1.11	0.15
Q08945	FACT complex subunit SSRP1;	0.60	0.81
Q96AE4	Far upstream element-binding protein 1;	-0.22	0.94
Q92945	Far upstream element-binding protein 2;	-0.42	0.91
P14324	Farnesyl pyrophosphate synthase;	0.24	0.88
P49327	Fatty acid synthase;	0.48	0.89
Q01469	Fatty acid-binding protein, epidermal;	-0.66	0.83
Q96AC1	Fermitin family homolog 2;	0.68	0.68
P02794	Ferritin heavy chain;	-0.96	0.44
Q14512	Fibroblast growth factor-binding protein 1;	-0.31	0.82
P02751	Fibronectin;	-0.71	0.57
P21333	Filamin-A;	0.38	0.94
O75369	Filamin-B;	0.41	0.92
Q14315	Filamin-C;	-0.33	0.85
P30043	Flavin reductase (NADPH);	0.55	0.19
O95633	Follistatin-related protein 3;	-0.31	0.87
P04075	Fructose-bisphosphate aldolase A;	-0.66	0.73
P09972	Fructose-bisphosphate aldolase C;	-0.32	0.91
P07954	Fumarate hydratase, mitochondrial;	0.65	0.73
P09382	Galectin-1;	-0.73	0.64
Q08380	Galectin-3-binding protein;	1.59	0.06
P17931	Galectin-3;	-0.14	0.97
Q92820	Gamma-glutamyl hydrolase;	0.52	0.71
O75223	Gamma-glutamylcyclotransferase;	0.14	0.98

Table S4

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
P13284	Gamma-interferon-inducible lysosomal thiol reductase;	0.70	0.28
P17900	Ganglioside GM2 activator;	-0.42	0.80
P06396	Gelsolin;	0.57	0.78
P78347	General transcription factor II-I;	0.66	0.68
P35269	General transcription factor IIF subunit 1;	-0.66	0.62
P60983	Glia maturation factor beta;	-0.05	1.00
P07093	Glia-derived nexin;	1.14	0.40
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase;	-0.59	0.76
P06744	Glucose-6-phosphate isomerase;	-0.11	0.99
P14314	Glucosidase 2 subunit beta;	-1.18	0.01
P04062	Glucosylceramidase;	0.41	0.88
P00367	Glutamate dehydrogenase 1, mitochondrial;	1.34	0.20
P48507	Glutamate--cysteine ligase regulatory subunit;	-0.45	0.66
P47897	Glutamine--tRNA ligase;	-0.33	0.88
O76003	Glutaredoxin-3;	0.61	0.79
Q86SX6	Glutaredoxin-related protein 5, mitochondrial;	0.44	0.77
P78417	Glutathione S-transferase omega-1;	0.35	0.91
P09211	Glutathione S-transferase P;	-0.67	0.88
P04406	Glyceraldehyde-3-phosphate dehydrogenase;	-0.72	0.66
P11216	Glycogen phosphorylase, brain form;	-1.68	0.24
P06737	Glycogen phosphorylase, liver form;	0.07	0.98
Q9HC38	Glyoxalase domain-containing protein 4;	0.21	0.92
P35052	Glypican-1;	0.84	0.64
P49915	GMP synthase [glutamine-hydrolyzing];	-0.12	0.94
Q8NBJ4	Golgi membrane protein 1;	0.08	0.59
P28799	Granulins;	-0.28	0.11
Q8NCC3	Group XV phospholipase A2;	0.32	0.74
P62993	Growth factor receptor-bound protein 2;	-0.21	0.97
P09341	Growth-regulated alpha protein;	2.45	0.00
Q99988	Growth/differentiation factor 15;	0.64	0.48
Q9HAV7	GrpE protein homolog 1, mitochondrial;	-0.31	0.12
P62826	GTP-binding nuclear protein Ran;	-0.43	0.84
Q9Y2T3	Guanine deaminase;	-0.48	0.84
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T)	0.61	0.53
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;	-0.21	0.98
O60832	H/ACA ribonucleoprotein complex subunit 4;	-0.04	0.60
P48723	Heat shock 70 kDa protein 13;	1.00	0.27
P08107	Heat shock 70 kDa protein 1A/1B;	-0.19	0.96
P34932	Heat shock 70 kDa protein 4;	-0.58	0.86
P11142	Heat shock cognate 71 kDa protein;	-0.30	0.86
Q92598	Heat shock protein 105 kDa;	0.27	0.91
P04792	Heat shock protein beta-1;	0.31	0.91
P07900	Heat shock protein HSP 90-alpha;	-0.46	0.86

Table S4

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
P08238	Heat shock protein HSP 90-beta;	-0.07	1.00
P69905	Hemoglobin subunit alpha;	0.41	0.85
P02042	Hemoglobin subunit delta;	0.04	0.66
Q7Z4V5	Hepatoma-derived growth factor-related protein 2;	-0.34	0.90
P51858	Hepatoma-derived growth factor;	-0.38	0.95
Q99729	Heterogeneous nuclear ribonucleoprotein A/B;	0.03	0.93
Q13151	Heterogeneous nuclear ribonucleoprotein A0;	-0.39	0.02
P09651	Heterogeneous nuclear ribonucleoprotein A1;	0.43	0.84
Q14103	Heterogeneous nuclear ribonucleoprotein D0;	-0.14	0.80
P52597	Heterogeneous nuclear ribonucleoprotein F;	-0.31	0.95
P31943	Heterogeneous nuclear ribonucleoprotein H;	0.36	0.93
P31942	Heterogeneous nuclear ribonucleoprotein H3;	0.70	0.46
P61978	Heterogeneous nuclear ribonucleoprotein K;	0.61	0.77
P52272	Heterogeneous nuclear ribonucleoprotein M;	0.89	0.36
O60506	Heterogeneous nuclear ribonucleoprotein Q;	0.78	0.56
O43390	Heterogeneous nuclear ribonucleoprotein R;	0.26	0.73
Q00839	Heterogeneous nuclear ribonucleoprotein U;	0.83	0.29
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1;	0.86	0.48
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2;	0.88	0.03
P09429	High mobility group protein B1;	-0.57	0.62
P26583	High mobility group protein B2;	-0.44	0.70
P37235	Hippocalcin-like protein 1;	-0.38	0.95
Q9BX68	Histidine triad nucleotide-binding protein 2,	0.59	0.55
P12081	Histidine--tRNA ligase, cytoplasmic;	-0.07	0.93
P10412	Histone H1.4;	-0.04	0.88
Q92522	Histone H1x;	-0.78	0.04
P04908	Histone H2A type 1-B/E;	-0.85	0.21
P0C0S5	Histone H2A.Z;	0.51	0.18
O60814	Histone H2B type 1-K;	-1.06	0.40
P68431	Histone H3.1;	-0.64	0.72
P62805	Histone H4;	-1.20	0.13
Q09028	Histone-binding protein RBBP4;	-0.39	0.89
P01892	HLA class I histocompatibility antigen, A-2 alpha chain;	0.65	0.71
P10321	HLA class I histocompatibility antigen, Cw-7 alpha chain;	1.73	0.08
P51610	Host cell factor 1;	0.06	0.73
P50502	Hsc70-interacting protein;	-0.27	0.96
Q16543	Hsp90 co-chaperone Cdc37;	-0.37	0.91
P60953	http://www.extend-partition.com/free-partition-	-0.77	0.26
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	1.75	0.00
P00492	Hypoxanthine-guanine phosphoribosyltransferase;	-0.14	0.98
Q9Y4L1	Hypoxia up-regulated protein 1;	-0.09	0.80
Q969P0	Immunoglobulin superfamily member 8;	-1.60	0.08
O00505	Importin subunit alpha-3;	0.36	0.75
Q14974	Importin subunit beta-1;	-0.13	0.99
O00410	Importin-5;	-0.23	0.99
Q13308	Inactive tyrosine-protein kinase 7;	-0.57	0.76
Q15181	Inorganic pyrophosphatase;	0.06	0.99

Table S4

Uniprot accession	**Name**	**Averaged fold-change (log_2) of ASAPratio**	**Combined ASPAratio p-value**
P12268	Inosine-5'-monophosphate dehydrogenase 2;	0.63	0.78
P29218	Inositol monophosphatase 1;	-0.16	0.99
Q9NPH2	Inositol-3-phosphate synthase 1;	0.41	0.89
P14735	Insulin-degrading enzyme;	-0.53	0.51
P01344	Insulin-like growth factor II;	0.57	0.50
P18065	Insulin-like growth factor-binding protein 2;	1.35	0.10
P17936	Insulin-like growth factor-binding protein 3;	2.70	0.00
P24592	Insulin-like growth factor-binding protein 6;	3.08	0.00
P23229	Integrin alpha-6;	1.26	0.23
P05556	Integrin beta-1;	-0.43	0.83
P16144	Integrin beta-4;	-0.08	1.00
O95965	Integrin beta-like protein 1;	-0.56	0.81
Q9H0C8	Integrin-linked kinase-associated serine/threonine	0.10	0.98
Q12905	Interleukin enhancer-binding factor 2;	0.18	0.55
Q12906	Interleukin enhancer-binding factor 3;	0.02	0.96
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic;	-0.47	0.90
P41252	Isoleucine--tRNA ligase, cytoplasmic;	0.41	0.88
P05783	Keratin, type I cytoskeletal 18;	0.26	0.82
P08727	Keratin, type I cytoskeletal 19;	3.14	0.00
P05787	Keratin, type II cytoskeletal 8;	0.42	0.80
Q07666	KH domain-containing, RNA-binding, signal	-0.12	0.80
Q86UP2	Kinectin;	0.00	0.98
Q07866	Kinesin light chain 1;	1.18	0.59
P33176	Kinesin-1 heavy chain;	-0.36	0.88
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-	-0.28	0.97
P00338	L-lactate dehydrogenase A chain;	-1.06	0.35
P20700	Lamin-B1;	0.13	0.91
Q03252	Lamin-B2;	-0.06	0.92
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;	0.46	0.78
O15230	Laminin subunit alpha-5;	1.11	0.43
P07942	Laminin subunit beta-1;	1.13	0.17
P55268	Laminin subunit beta-2;	2.70	0.00
P11047	Laminin subunit gamma-1;	0.88	0.47
Q13753	Laminin subunit gamma-2;	1.19	0.25
Q9NS15	Latent-transforming growth factor beta-binding protein 3;	1.75	0.10
Q8N2S1	Latent-transforming growth factor beta-binding protein 4;	-0.01	0.77
Q99538	Legumain;	1.30	0.13
Q8N1G4	Leucine-rich repeat-containing protein 47;	-0.44	0.87
Q96AG4	Leucine-rich repeat-containing protein 59;	-0.07	0.88
P09960	Leukotriene A-4 hydrolase;	0.08	1.00
P24666	Low molecular weight phosphotyrosine protein	-0.68	0.27
P01130	Low-density lipoprotein receptor;	-0.17	0.91

Table S4

Uniprot accession	**Name**	**Averaged fold-change (log$_2$) of ASAPratio**	**Combined ASPAratio p-value**
P05455	Lupus La protein;	0.02	0.98
Q15046	Lysine--tRNA ligase;	-0.11	0.96
P10253	Lysosomal alpha-glucosidase;	0.50	0.59
O00754	Lysosomal alpha-mannosidase;	1.23	0.26
P42785	Lysosomal Pro-X carboxypeptidase;	0.71	0.75
P10619	Lysosomal protective protein;	0.71	0.63
Q9UMR5	Lysosomal thioesterase PPT2;	1.21	0.12
Q9Y4K0	Lysyl oxidase homolog 2;	0.39	0.78
Q96JB6	Lysyl oxidase homolog 4;	-0.57	0.70
Q96C86	m7GpppX diphosphatase;	-0.90	0.60
P09603	Macrophage colony-stimulating factor 1;	1.59	0.03
P40121	Macrophage-capping protein;	0.41	0.86
Q14764	Major vault protein;	-0.47	0.60
P40925	Malate dehydrogenase, cytoplasmic;	-0.71	0.62
P40926	Malate dehydrogenase, mitochondrial;	-0.20	0.94
Q9ULC4	Malignant T-cell-amplified sequence 1;	-0.86	0.35
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA;	-2.37	0.00
P43243	Matrin-3;	0.69	0.25
Q99542	Matrix metalloproteinase-19;	1.65	0.02
Q5JRA6	Melanoma inhibitory activity protein 3;	1.45	0.05
Q13421	Mesothelin;	1.27	0.15
P01033	Metalloproteinase inhibitor 1;	1.25	0.25
P16035	Metalloproteinase inhibitor 2;	0.43	0.42
Q13330	Metastasis-associated protein MTA1;	0.37	0.66
O94776	Metastasis-associated protein MTA2;	-0.35	0.66
Q96PK2	Microtubule-actin cross-linking factor 1, isoforms	-0.19	0.95
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms	0.28	0.07
P27816	Microtubule-associated protein 4;	-0.49	0.72
Q15691	Microtubule-associated protein RP/EB family member 1;	-0.44	0.93
P21741	Midkine;	0.41	0.50
Q16891	Mitochondrial inner membrane protein;	0.49	0.93
O43684	Mitotic checkpoint protein BUB3;	-0.24	0.91
P26038	Moesin;	2.83	0.04
P53985	Monocarboxylate transporter 1;	1.79	0.01
P98088	Mucin-5AC;	-0.95	0.87
P22234	Multifunctional protein ADE2;	0.98	0.40
Q9UNW1	Multiple inositol polyphosphate phosphatase 1;	1.79	0.08
Q9NZM1	Myoferlin;	0.20	0.77
P60660	Myosin light polypeptide 6;	-0.29	0.95
Q6WCQ1	Myosin phosphatase Rho-interacting protein;	0.04	0.37
O14950	Myosin regulatory light chain 12B;	-0.09	1.00
P35579	Myosin-9;	-0.37	0.90
P58546	Myotrophin;	-0.45	0.77
P29966	Myristoylated alanine-rich C-kinase substrate;	-6.49	0.00

Table S4

Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
P34059	N-acetylgalactosamine-6-sulfatase;	0.96	0.51
P15586	N-acetylglucosamine-6-sulfatase;	0.18	0.87
O43505	N-acetyllactosaminide beta-1,3-N-	0.75	0.59
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit;	-0.82	0.19
O95777	N-alpha-acetyltransferase 38, NatC auxiliary subunit;	-0.82	0.43
Q9GZZ1	N-alpha-acetyltransferase 50;	0.27	0.87
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	0.51	0.36
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	-0.33	0.92
P15559	NAD(P)H dehydrogenase [quinone] 1;	0.01	0.97
Q8NCW5	NAD(P)H-hydrate epimerase;	-0.40	0.74
O43847	Nardilysin;	0.42	0.91
Q13765	Nascent polypeptide-associated complex subunit alpha;	-0.24	0.76
Q92859	Neogenin;	-2.00	0.15
Q9UMX5	Neudesin;	0.68	0.74
P32004	Neural cell adhesion molecule L1;	2.01	0.01
Q09666	Neuroblast differentiation-associated protein AHNAK;	0.60	0.80
Q9BYT8	Neurolysin, mitochondrial;	0.09	0.57
O14786	Neuropilin-1;	-1.80	0.17
O15240	Neurosecretory protein VGF;	-0.39	0.68
Q14697	Neutral alpha-glucosidase AB;	0.74	0.69
P55769	NHP2-like protein 1;	0.47	0.70
P43490	Nicotinamide phosphoribosyltransferase;	-0.53	0.77
Q9Y314	Nitric oxide synthase-interacting protein;	0.49	0.31
Q9UNZ2	NSFL1 cofactor p47;	-0.93	0.66
P49321	Nuclear autoantigenic sperm protein;	-0.45	0.94
Q9Y266	Nuclear migration protein nudC;	-0.22	0.95
Q14980	Nuclear mitotic apparatus protein 1;	-0.27	0.95
P61970	Nuclear transport factor 2;	-0.21	0.79
P67809	Nuclease-sensitive element-binding protein 1;	0.45	0.83
Q02818	Nucleobindin-1;	0.86	0.40
Q14978	Nucleolar and coiled-body phosphoprotein 1;	-0.06	0.02
Q9NR30	Nucleolar RNA helicase 2;	1.49	0.32
P19338	Nucleolin;	0.53	0.79
P06748	Nucleophosmin;	0.32	0.69
P12270	Nucleoprotein TPR;	0.89	0.35
P15531	Nucleoside diphosphate kinase A;	0.29	0.94
P55209	Nucleosome assembly protein 1-like 1;	0.54	0.84
Q99733	Nucleosome assembly protein 1-like 4;	-0.43	0.86
Q9NTK5	Obg-like ATPase 1;	-0.62	0.90
Q92882	Osteoclast-stimulating factor 1;	-2.36	0.00
Q86UD1	Out at first protein homolog;	0.83	0.48
P50897	Palmitoyl-protein thioesterase 1;	0.50	0.71
O75475	PC4 and SFRS1-interacting protein;	-0.08	0.81
Q96HC4	PDZ and LIM domain protein 5;	0.17	0.88
Q9NR12	PDZ and LIM domain protein 7;	-0.19	0.81

Table S4

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
P26022	Pentraxin-related protein PTX3;	3.38	0.00
P19021	Peptidyl-glycine alpha-amidating monooxygenase;	0.17	0.95
P62937	Peptidyl-prolyl cis-trans isomerase A;	-0.73	0.78
P23284	Peptidyl-prolyl cis-trans isomerase B;	0.14	0.92
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A;	0.14	0.80
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3;	1.16	0.22
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;	-0.39	0.89
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1;	-0.09	0.68
O60664	Perilipin-3;	0.20	0.88
Q06830	Peroxiredoxin-1;	-0.45	0.86
P32119	Peroxiredoxin-2;	-1.32	0.14
P30044	Peroxiredoxin-5, mitochondrial;	0.05	0.99
P30041	Peroxiredoxin-6;	0.52	0.65
Q8WW12	PEST proteolytic signal-containing nuclear protein;	-0.37	0.44
Q9NSD9	Phenylalanine--tRNA ligase beta subunit;	0.03	0.99
P30086	Phosphatidylethanolamine-binding protein 1;	-0.63	0.68
P48739	Phosphatidylinositol transfer protein beta isoform;	0.01	0.97
P00558	Phosphoglycerate kinase 1;	-0.79	0.62
P18669	Phosphoglycerate mutase 1;	-0.05	0.98
A6NDG6	Phosphoglycolate phosphatase;	-0.25	0.74
Q6P4A8	Phospholipase B-like 1;	1.36	0.08
P55058	Phospholipid transfer protein;	1.27	0.11
O15067	Phosphoribosylformylglycinamidine synthase;	0.30	0.91
Q9Y617	Phosphoserine aminotransferase;	1.27	0.30
P78330	Phosphoserine phosphatase;	-0.44	0.93
P36955	Pigment epithelium-derived factor;	3.56	0.00
Q9H307	Pinin;	0.40	0.55
Q9GZP4	PITH domain-containing protein 1;	-0.07	0.96
Q9BTY2	Plasma alpha-L-fucosidase;	1.47	0.04
P05155	Plasma protease C1 inhibitor;	-0.23	0.72
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein;	-0.06	0.95
P43034	Platelet-activating factor acetylhydrolase IB subunit	0.37	0.72
P68402	Platelet-activating factor acetylhydrolase IB subunit beta;	-0.59	0.32
Q15102	Platelet-activating factor acetylhydrolase IB subunit	-0.19	0.90
Q15149	Plectin;	-0.61	0.84
O15031	Plexin-B2;	0.88	0.03
Q92692	Poliovirus receptor-related protein 2;	0.55	0.86
P09874	Poly [ADP-ribose] polymerase 1;	-0.06	0.92
Q15365	Poly(rC)-binding protein 1;	-0.03	1.00
Q15366	Poly(rC)-binding protein 2;	-0.27	0.96
Q9UHX1	Poly(U)-binding-splicing factor PUF60;	-0.08	1.00
P11940	Polyadenylate-binding protein 1;	0.86	0.44
Q6NZI2	Polymerase I and transcript release factor;	-0.18	0.91
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;	0.29	0.81
P26599	Polypyrimidine tract-binding protein 1;	0.05	0.54

Table S4

Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q9Y3B4	Pre-mRNA branch site protein p14;	-0.62	0.04
Q9UMS4	Pre-mRNA-processing factor 19;	0.67	0.01
Q9UHV9	Prefoldin subunit 2;	-0.51	0.78
Q9NQP4	Prefoldin subunit 4;	-0.38	0.93
Q99471	Prefoldin subunit 5;	-1.13	0.53
P02545	Prelamin-A/C;	-0.11	0.96
P07602	Proactivator polypeptide;	1.61	0.23
Q92841	Probable ATP-dependent RNA helicase DDX17;	-0.45	0.89
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23;	-1.25	0.20
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	0.88	0.47
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3;	0.67	0.80
P07737	Profilin-1;	-0.66	0.75
P35080	Profilin-2;	0.15	0.97
Q8WUM4	Programmed cell death 6-interacting protein;	-0.53	0.96
O14737	Programmed cell death protein 5;	-0.37	0.89
O75340	Programmed cell death protein 6;	0.50	0.72
P12004	Proliferating cell nuclear antigen;	-0.53	0.85
Q9UQ80	Proliferation-associated protein 2G4;	-0.34	0.87
P48147	Prolyl endopeptidase;	-0.18	0.99
Q8NBP7	Proprotein convertase subtilisin/kexin type 9;	0.08	0.81
Q9UHG2	ProSAAS;	0.29	0.44
Q15185	Prostaglandin E synthase 3;	0.12	0.93
Q9P2B2	Prostaglandin F2 receptor negative regulator;	-0.64	0.69
P41222	Prostaglandin-H2 D-isomerase;	4.10	0.00
Q06323	Proteasome activator complex subunit 1;	0.38	0.90
Q9BT73	Proteasome assembly chaperone 3;	-0.31	0.92
P25786	Proteasome subunit alpha type-1;	-0.18	0.97
P25787	Proteasome subunit alpha type-2;	-0.21	0.93
P28066	Proteasome subunit alpha type-5;	-0.06	0.98
P60900	Proteasome subunit alpha type-6;	-0.31	0.91
O14818	Proteasome subunit alpha type-7;	0.05	1.00
P20618	Proteasome subunit beta type-1;	-0.21	0.98
P49720	Proteasome subunit beta type-3;	0.11	1.00
P28072	Proteasome subunit beta type-6;	0.21	0.70
Q99436	Proteasome subunit beta type-7;	0.05	0.97
P28062	Proteasome subunit beta type-8;	-0.35	0.27
Q8IVF2	Protein AHNAK2;	1.76	0.05
Q99873	Protein arginine N-methyltransferase 1;	-0.61	0.61
Q9Y2B0	Protein canopy homolog 2;	0.08	0.84
O60888	Protein CutA;	0.02	0.93
P30101	Protein disulfide-isomerase A3;	0.24	0.97
P13667	Protein disulfide-isomerase A4;	-0.41	0.88
Q15084	Protein disulfide-isomerase A6;	0.26	0.87
P07237	Protein disulfide-isomerase;	0.13	0.99
Q99497	Protein DJ-1;	-0.60	0.74

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Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q92520	Protein FAM3C;	-1.27	0.15
Q9NUQ9	Protein FAM49B;	-1.66	0.02
Q9UNF0	Protein kinase C and casein kinase substrate in neurons	-0.46	0.66
Q9BRT6	Protein LLP homolog;	0.41	0.07
O14974	Protein phosphatase 1 regulatory subunit 12A;	-0.27	0.81
O15355	Protein phosphatase 1G;	-0.07	0.99
Q9P258	Protein RCC2;	-0.21	0.98
Q96FQ6	Protein S100-A16;	-0.18	0.87
P26447	Protein S100-A4;	-0.93	0.57
P25815	Protein S100-P;	-2.36	0.00
Q01105	Protein SET;	-0.09	1.00
P53992	Protein transport protein Sec24C;	0.50	0.94
O94979	Protein transport protein Sec31A;	1.16	0.05
P06454	Prothymosin alpha;	0.34	0.80
P00491	Purine nucleoside phosphorylase;	0.62	0.69
P55786	Puromycin-sensitive aminopeptidase;	-0.54	0.61
Q49A26	Putative oxidoreductase GLYR1;	1.01	0.19
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1;	-1.49	0.04
Q8NHP8	Putative phospholipase B-like 2;	0.97	0.33
Q9Y383	Putative RNA-binding protein Luc7-like 2;	-0.27	0.96
A6NL28	Putative tropomyosin alpha-3 chain-like protein;	-0.59	0.69
P14618	Pyruvate kinase isozymes M1/M2;	-0.89	0.57
P31150	Rab GDP dissociation inhibitor alpha;	-0.19	0.53
O43504	Ragulator complex protein LAMTOR5;	-0.18	0.85
P43487	Ran-specific GTPase-activating protein;	-0.09	0.88
Q13283	Ras GTPase-activating protein-binding protein 1;	-0.52	0.85
P46940	Ras GTPase-activating-like protein IQGAP1;	-0.39	0.94
Q15907	Ras-related protein Rab-11B;	-0.30	0.96
P61106	Ras-related protein Rab-14;	-0.31	0.54
P62820	Ras-related protein Rab-1A;	0.16	0.77
P51149	Ras-related protein Rab-7a;	-0.41	0.94
P10586	Receptor-type tyrosine-protein phosphatase F;	0.75	0.70
P23470	Receptor-type tyrosine-protein phosphatase gamma;	-0.39	0.86
Q15262	Receptor-type tyrosine-protein phosphatase kappa;	0.72	0.77
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing	-0.50	0.79
P18754	Regulator of chromosome condensation;	-0.37	0.73
O75787	Renin receptor;	0.14	0.99
Q9BZR6	Reticulon-4 receptor;	0.68	0.45
Q9HB40	Retinoid-inducible serine carboxypeptidase;	0.58	0.63
P52565	Rho GDP-dissociation inhibitor 1;	-0.49	0.81
O75116	Rho-associated protein kinase 2;	-0.95	0.29
P08134	Rho-related GTP-binding protein RhoC;	0.66	0.55
P13489	Ribonuclease inhibitor;	-0.74	0.63
O00584	Ribonuclease T2;	1.28	0.15
P11908	Ribose-phosphate pyrophosphokinase 2;	-0.38	0.56
Q9Y3A5	Ribosome maturation protein SBDS;	0.31	0.97

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Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
Q9P2E9	Ribosome-binding protein 1;	-1.04	0.25
P38159	RNA-binding motif protein, X chromosome;	0.56	0.08
Q9NTZ6	RNA-binding protein 12;	0.25	0.43
P49756	RNA-binding protein 25;	0.29	0.81
Q14498	RNA-binding protein 39;	0.40	0.73
Q01844	RNA-binding protein EWS;	-0.10	0.93
P35637	RNA-binding protein FUS;	0.42	0.73
Q9Y265	RuvB-like 1;	0.17	0.96
Q9Y230	RuvB-like 2;	-0.41	0.76
P31153	S-adenosylmethionine synthase isoform type-2;	-0.27	0.92
P10768	S-formylglutathione hydrolase;	0.13	0.85
Q13126	S-methyl-5'-thioadenosine phosphorylase;	-1.75	0.14
Q12765	Secernin-1;	0.49	0.64
Q8WVN6	Secreted and transmembrane protein 1;	1.36	0.04
P49903	Selenide, water dikinase 1;	-0.32	0.77
Q14563	Semaphorin-3A;	1.67	0.04
Q99985	Semaphorin-3C;	-0.11	0.96
Q9NPR2	Semaphorin-4B;	0.19	0.97
Q9H3T2	Semaphorin-6C;	-1.40	0.01
Q9NVA2	Septin-11;	0.44	0.88
Q15019	Septin-2;	0.01	0.90
Q9UHD8	Septin-9;	-0.40	0.92
O95084	Serine protease 23;	-0.87	0.43
Q92743	Serine protease HTRA1;	0.21	0.62
P49591	Serine--tRNA ligase, cytoplasmic;	-0.35	0.91
Q9Y3F4	Serine-threonine kinase receptor-associated protein;	-0.32	0.96
Q9UQ35	Serine/arginine repetitive matrix protein 2;	-0.50	0.99
Q07955	Serine/arginine-rich splicing factor 1;	0.77	0.67
Q05519	Serine/arginine-rich splicing factor 11;	0.21	0.61
Q13247	Serine/arginine-rich splicing factor 6;	0.81	0.54
Q16629	Serine/arginine-rich splicing factor 7;	0.44	0.69
Q13242	Serine/arginine-rich splicing factor 9;	0.88	0.23
O95747	Serine/threonine-protein kinase OSR1;	0.41	0.84
Q13177	Serine/threonine-protein kinase PAK 2;	0.87	0.72
P30153	Serine/threonine-protein phosphatase 2A 65 kDa	-0.60	0.81
Q15257	Serine/threonine-protein phosphatase 2A activator;	-0.25	0.71
P62714	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform;	-0.78	0.50
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic	-0.25	0.95
P36952	Serpin B5;	-0.03	0.97
P50454	Serpin H1;	0.52	0.82
Q9BXP5	Serrate RNA effector molecule homolog;	0.05	0.64
P02768	Serum albumin;	-0.09	1.00
O95810	Serum deprivation-response protein;	0.50	0.76
P29353	SHC-transforming protein 1;	0.17	0.98
Q9HAT2	Sialate O-acetylesterase;	1.13	0.23

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
Q9NR45	Sialic acid synthase;	-1.20	0.07
Q99519	Sialidase-1;	0.03	0.75
P49458	Signal recognition particle 9 kDa protein;	0.40	0.37
P62304	Small nuclear ribonucleoprotein E;	0.22	0.74
P62306	Small nuclear ribonucleoprotein F;	0.97	0.01
P62316	Small nuclear ribonucleoprotein Sm D2;	0.07	0.55
P62318	Small nuclear ribonucleoprotein Sm D3;	0.37	0.51
P14678	Small nuclear ribonucleoprotein-associated proteins B	0.00	0.63
P63165	Small ubiquitin-related modifier 1;	-0.14	0.90
P55854	Small ubiquitin-related modifier 3;	0.10	0.88
P05023	Sodium/potassium-transporting ATPase subunit alpha-1;	0.60	0.78
Q8WVQ1	Soluble calcium-activated nucleotidase 1;	0.28	0.94
Q00796	Sorbitol dehydrogenase;	-0.81	0.51
P30626	Sorcin;	-0.49	0.82
Q9Y5X3	Sorting nexin-5;	-0.59	0.66
P09486	SPARC;	0.30	0.67
Q13813	Spectrin alpha chain, non-erythrocytic 1;	0.37	0.95
Q01082	Spectrin beta chain, non-erythrocytic 1;	0.08	0.99
P52788	Spermine synthase;	-0.50	0.60
Q13838	Spliceosome RNA helicase DDX39B;	-0.02	0.94
Q15637	Splicing factor 1;	-0.44	0.96
Q15459	Splicing factor 3A subunit 1;	0.00	0.96
Q15428	Splicing factor 3A subunit 2;	1.41	0.00
O75533	Splicing factor 3B subunit 1;	0.30	0.98
Q15393	Splicing factor 3B subunit 3;	0.26	0.87
P26368	Splicing factor U2AF 65 kDa subunit;	-0.11	0.98
P23246	Splicing factor, proline- and glutamine-rich;	0.45	0.92
Q14247	Src substrate cortactin;	0.09	0.00
Q7KZF4	Staphylococcal nuclease domain-containing protein 1;	-0.04	0.93
P38646	Stress-70 protein, mitochondrial;	0.64	0.61
P31948	Stress-induced-phosphoprotein 1;	-0.39	0.93
Q14683	Structural maintenance of chromosomes protein 1A;	0.97	0.41
Q8NBJ7	Sulfatase-modifying factor 2;	0.19	0.91
O00391	Sulfhydryl oxidase 1;	1.17	0.23
Q6ZRP7	Sulfhydryl oxidase 2;	-0.33	0.94
Q9UBT2	SUMO-activating enzyme subunit 2;	0.12	0.98
P63279	SUMO-conjugating enzyme UBC9;	-0.27	0.93
P42285	Superkiller viralicidic activity 2-like 2;	-0.01	0.94
P00441	Superoxide dismutase [Cu-Zn];	-0.14	0.99
P04179	Superoxide dismutase [Mn], mitochondrial;	0.44	0.79
P78539	Sushi repeat-containing protein SRPX;	-0.53	0.37
O60687	Sushi repeat-containing protein SRPX2;	-0.02	0.90
Q99536	Synaptic vesicle membrane protein VAT-1 homolog;	0.30	0.83
O00560	Syntenin-1;	-0.18	0.84
P17987	T-complex protein 1 subunit alpha;	-0.28	0.96
P78371	T-complex protein 1 subunit beta;	-0.61	0.78

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Uniprot accession	Name	Averaged fold-change ($\log_2$) of ASAPratio	Combined ASPAratio p-value
P50991	T-complex protein 1 subunit delta;	-0.53	0.88
P48643	T-complex protein 1 subunit epsilon;	-0.37	0.95
Q99832	T-complex protein 1 subunit eta;	-0.39	0.89
P49368	T-complex protein 1 subunit gamma;	-0.41	0.91
P50990	T-complex protein 1 subunit theta;	-0.59	0.75
P40227	T-complex protein 1 subunit zeta;	-0.96	0.36
Q9Y490	Talin-1;	-0.35	0.94
Q7Z7G0	Target of Nesh-SH3;	4.38	0.00
Q08629	Testican-1;	2.12	0.00
Q9BRA2	Thioredoxin domain-containing protein 17;	-0.20	0.98
Q8NBS9	Thioredoxin domain-containing protein 5;	-0.56	0.93
Q16881	Thioredoxin reductase 1, cytoplasmic;	0.41	0.77
P30048	Thioredoxin-dependent peroxide reductase,	1.30	0.05
Q86V81	THO complex subunit 4;	-0.47	0.49
P26639	Threonine--tRNA ligase, cytoplasmic;	0.38	0.96
P07996	Thrombospondin-1;	-1.59	0.07
P49746	Thrombospondin-3;	2.43	0.00
Q9Y2W1	Thyroid hormone receptor-associated protein 3;	-0.18	0.99
Q9UKU6	Thyrotropin-releasing hormone-degrading ectoenzyme;	0.03	0.69
Q9UDY2	Tight junction protein ZO-2;	-1.32	0.22
O75663	TIP41-like protein;	0.64	0.63
P10646	Tissue factor pathway inhibitor;	2.10	0.00
Q8WZ42	Titin;	1.03	0.06
O14657	Torsin-1B;	0.71	0.24
Q96EM0	Trans-L-3-hydroxyproline dehydratase;	-0.60	0.69
P37837	Transaldolase;	-0.26	0.97
P20062	Transcobalamin-2;	0.98	0.34
P23193	Transcription elongation factor A protein 1;	-0.05	0.61
Q15370	Transcription elongation factor B polypeptide 2;	0.05	0.79
O00267	Transcription elongation factor SPT5;	-0.64	0.73
Q7KZ85	Transcription elongation factor SPT6;	0.29	0.76
O14776	Transcription elongation regulator 1;	0.40	0.82
P20290	Transcription factor BTF3;	0.41	0.85
Q13263	Transcription intermediary factor 1-beta;	-0.28	0.96
P02786	Transferrin receptor protein 1;	1.85	0.04
P01137	Transforming growth factor beta-1;	1.60	0.04
Q15582	Transforming growth factor-beta-induced protein ig-h3;	-1.22	0.40
P37802	Transgelin-2;	-0.14	0.98
P55072	Transitional endoplasmic reticulum ATPase;	-0.59	0.75
P29401	Transketolase;	-1.50	0.17
P13693	Translationally-controlled tumor protein;	-0.08	1.00
Q99598	Translin-associated protein X;	-0.40	0.78
P49755	Transmembrane emp24 domain-containing protein 10;	1.61	0.01
P22102	Trifunctional purine biosynthetic protein adenosine-3;	1.80	0.01
P60174	Triosephosphate isomerase;	-0.97	0.41

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Uniprot accession	**Name**	**Averaged fold-change ($\log_2$) of ASAPratio**	**Combined ASPAratio p-value**
O14773	Tripeptidyl-peptidase 1;	1.08	0.20
Q9Y3I0	tRNA-splicing ligase RtcB homolog;	-0.61	0.78
Q9NYL9	Tropomodulin-3;	0.19	0.90
P23381	Tryptophan--tRNA ligase, cytoplasmic;	0.55	0.91
P07437	Tubulin beta chain;	-0.03	0.57
P68371	Tubulin beta-4B chain;	-0.49	0.79
Q14166	Tubulin--tyrosine ligase-like protein 12;	-0.13	0.84
Q9GZM7	Tubulointerstitial nephritis antigen-like;	0.13	0.91
O00300	Tumor necrosis factor receptor superfamily member 11B;	-3.63	0.01
Q9NP84	Tumor necrosis factor receptor superfamily member 12A;	-0.47	0.06
P19438	Tumor necrosis factor receptor superfamily member 1A;	0.24	0.48
O75509	Tumor necrosis factor receptor superfamily member 21;	-0.45	0.32
O95407	Tumor necrosis factor receptor superfamily member 6B;	1.52	0.03
O43399	Tumor protein D54;	0.25	0.74
Q12792	Twinfilin-1;	-0.68	0.86
Q6IBS0	Twinfilin-2;	-0.38	0.91
Q9GZX9	Twisted gastrulation protein homolog 1;	0.35	0.91
P30530	Tyrosine-protein kinase receptor UFO;	-0.34	0.31
P08621	U1 small nuclear ribonucleoprotein 70 kDa;	-0.09	0.98
P09012	U1 small nuclear ribonucleoprotein A;	-0.42	0.82
P09234	U1 small nuclear ribonucleoprotein C;	-1.15	0.11
O43818	U3 small nucleolar RNA-interacting protein 2;	1.63	0.02
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase;	-0.37	0.91
Q9Y333	U6 snRNA-associated Sm-like protein LSm2;	-0.15	0.35
P45974	Ubiquitin carboxyl-terminal hydrolase 5;	-0.69	0.66
Q93009	Ubiquitin carboxyl-terminal hydrolase 7;	0.24	0.84
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3;	-0.78	0.13
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5;	1.01	0.24
O14562	Ubiquitin domain-containing protein UBFD1;	-0.28	0.95
Q96FW1	Ubiquitin thioesterase OTUB1;	-0.27	0.83
Q14157	Ubiquitin-associated protein 2-like;	-0.38	0.92
P61086	Ubiquitin-conjugating enzyme E2 K;	-1.13	0.32
P68036	Ubiquitin-conjugating enzyme E2 L3;	-0.34	0.91
P61088	Ubiquitin-conjugating enzyme E2 N;	-0.16	0.99
Q13404	Ubiquitin-conjugating enzyme E2 variant 1;	-0.38	0.90
P61960	Ubiquitin-fold modifier 1;	-0.76	0.55
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1;	2.19	0.02
P22314	Ubiquitin-like modifier-activating enzyme 1;	-0.90	0.60
Q14376	UDP-glucose 4-epimerase;	-0.33	0.82

Table S4

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Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1;	0.77	0.64
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;	0.01	0.60
P30085	UMP-CMP kinase;	0.45	0.83
Q92614	Unconventional myosin-XVIIIa;	-0.37	0.90
Q9HB07	UPF0160 protein MYG1, mitochondrial;	-0.66	0.58
Q9H741	UPF0454 protein C12orf49;	-0.09	0.70
Q9Y224	UPF0568 protein C14orf166;	-0.35	0.93
Q9NWV4	UPF0587 protein C1orf123;	-0.51	0.85
P00749	Urokinase-type plasminogen activator;	0.01	0.97
P06132	Uroporphyrinogen decarboxylase;	-0.26	0.96
Q16851	UTP--glucose-1-phosphate uridylyltransferase;	-0.40	0.88
P54727	UV excision repair protein RAD23 homolog B;	0.12	0.98
P38606	V-type proton ATPase catalytic subunit A;	-0.72	0.01
Q15904	V-type proton ATPase subunit S1;	0.53	0.77
Q9UBQ0	Vacuolar protein sorting-associated protein 29;	-0.27	0.94
P26640	Valine--tRNA ligase;	-0.58	0.69
P50552	Vasodilator-stimulated phosphoprotein;	0.20	0.99
Q6EMK4	Vasorin;	0.54	0.67
O75396	Vesicle-trafficking protein SEC22b;	0.07	0.68
P08670	Vimentin;	-0.14	1.00
P18206	Vinculin;	0.91	0.63
P04004	Vitronectin;	0.27	0.88
O75083	WD repeat-containing protein 1;	-1.24	0.26
Q96FK6	WD repeat-containing protein 89;	0.33	0.29
Q2TAY7	WD40 repeat-containing protein SMU1;	0.37	0.22
P13010	X-ray repair cross-complementing protein 5;	0.37	0.95
P12956	X-ray repair cross-complementing protein 6;	0.03	0.95
Q9NQW7	Xaa-Pro aminopeptidase 1;	0.05	1.00
Q9H1B5	Xylosyltransferase 2;	0.32	0.56
Q7Z739	YTH domain family protein 3;	0.66	0.62
O43670	Zinc finger protein 207;	-0.61	0.70
P25311	Zinc-alpha-2-glycoprotein;	-0.26	0.08