

Supplementary Data for “Quantitative Proteomics of Dorsolateral Prefrontal Cortex Reveals an Early Pattern of Synaptic Dysmaturation in Children with Idiopathic Autism”

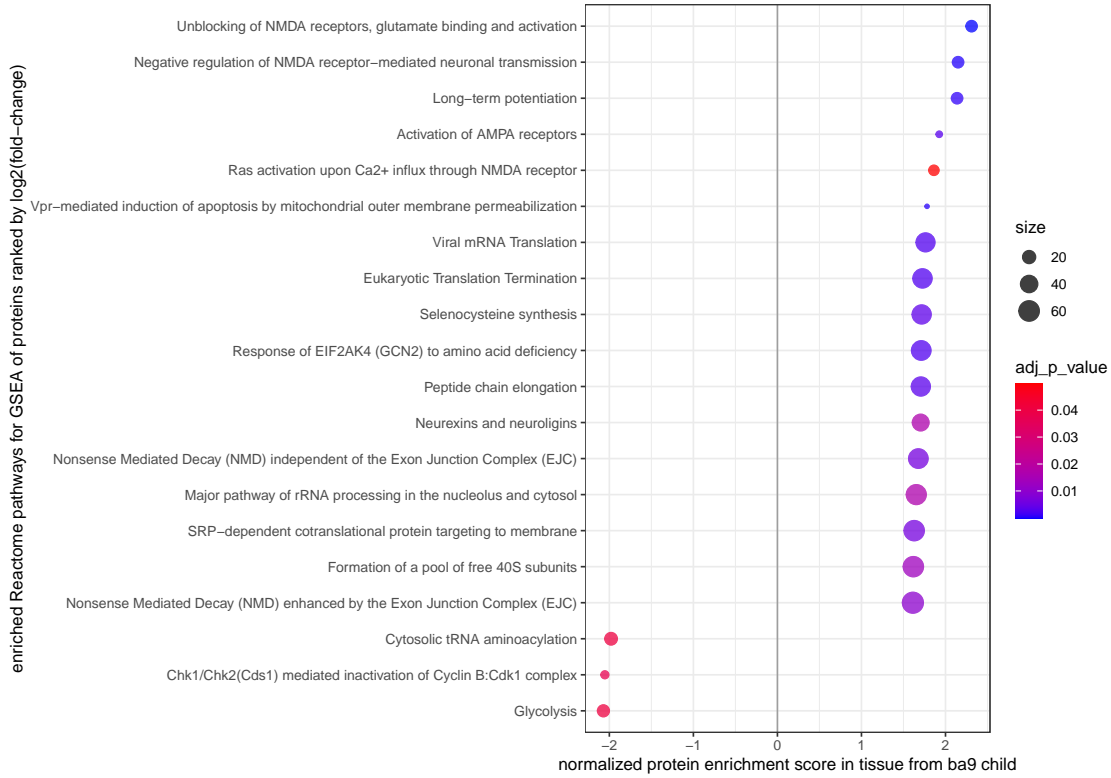
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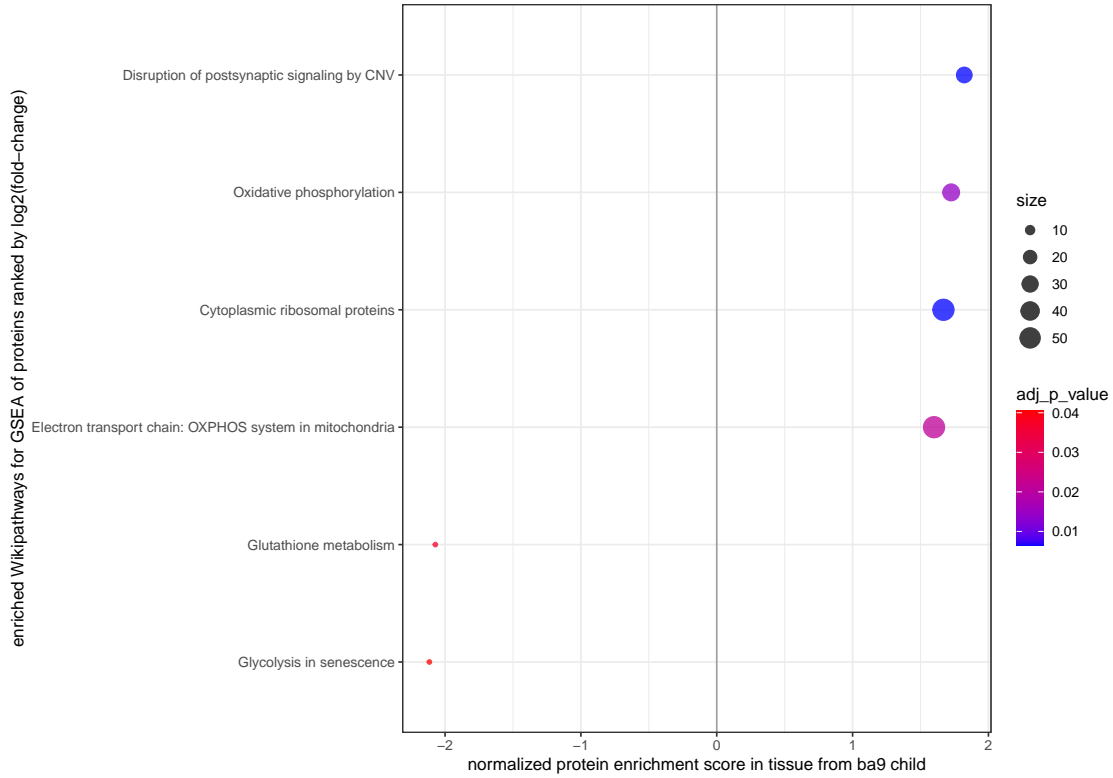


(a) Child Reactome

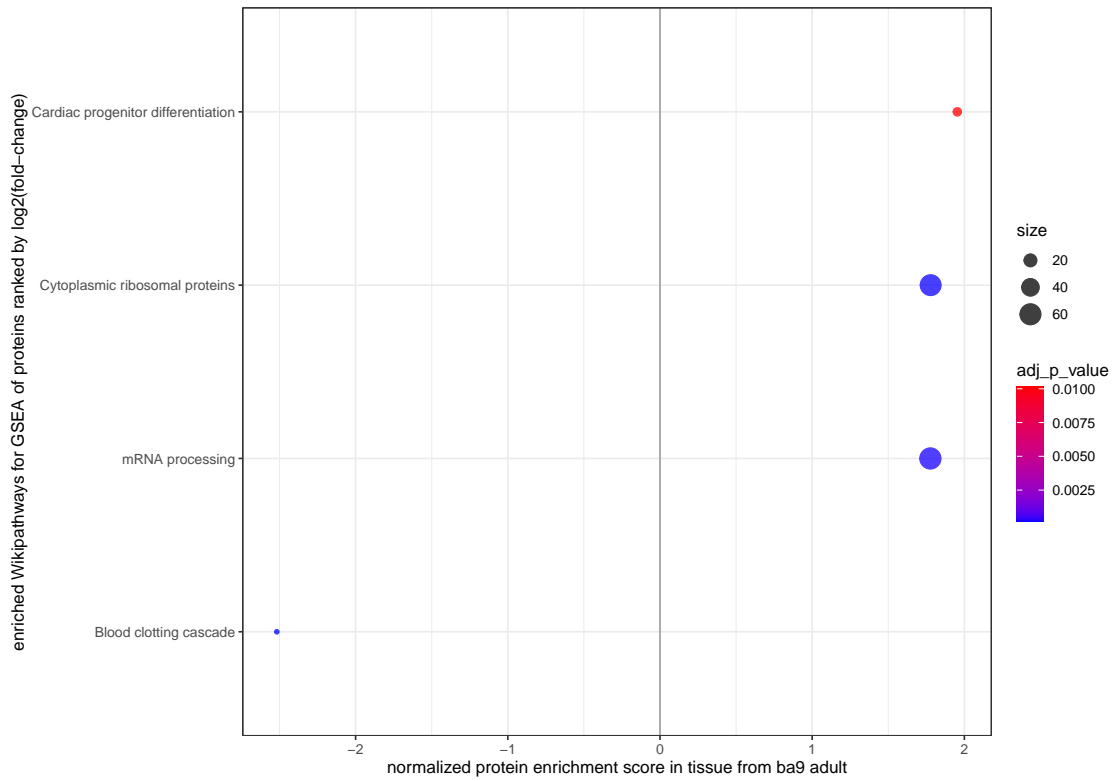


(b) Adult Reactome

Figure S1: GSEA enrichment of Reactome pathways for proteins ranked by $\log_2(\text{fold-change})$

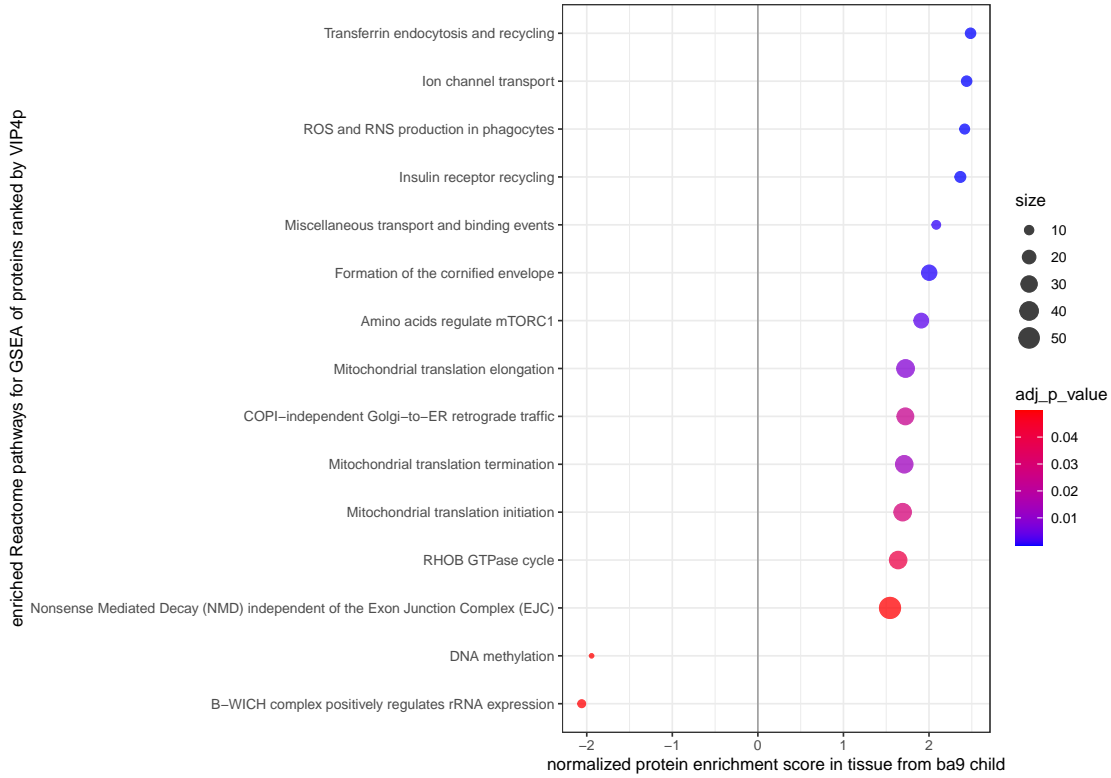


(a) Child WikiPathways

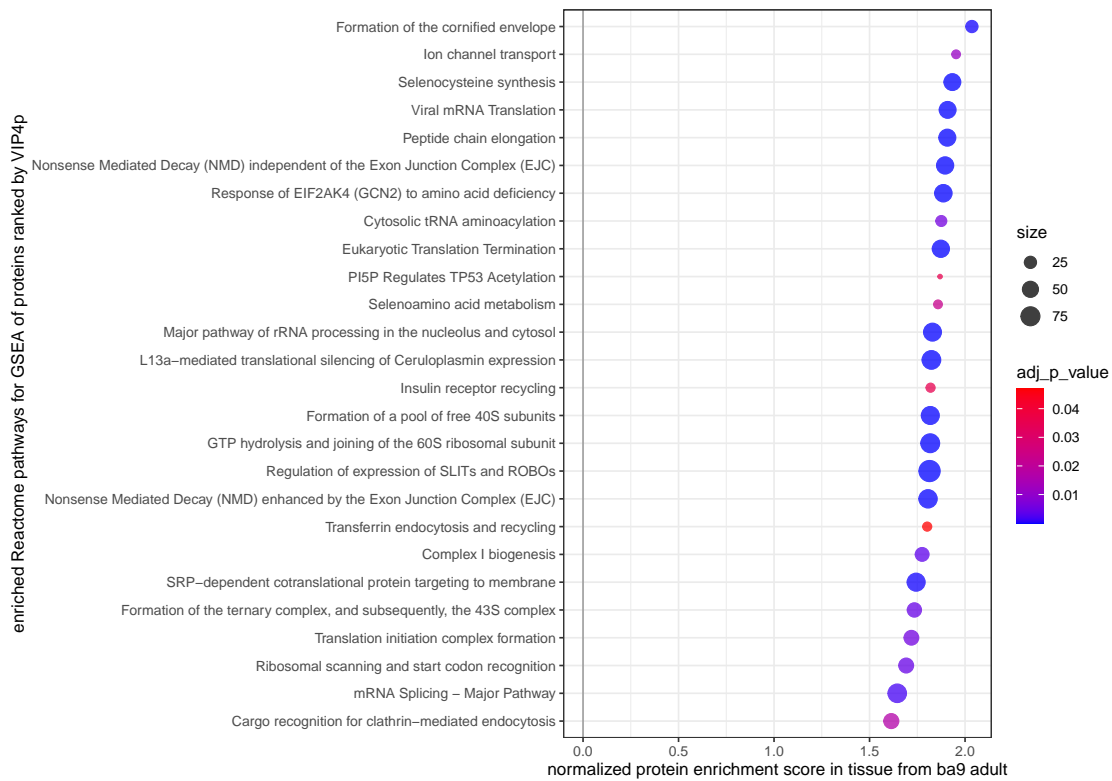


(b) Adult WikiPathways

Figure S2: GSEA enrichment of WikiPathways for proteins ranked by $\log_2(\text{fold-change})$



(a) Child Reactome



(b) Adult Reactome

Figure S3: GSEA enrichment of Reactome pathways for proteins ranked by VIP4p

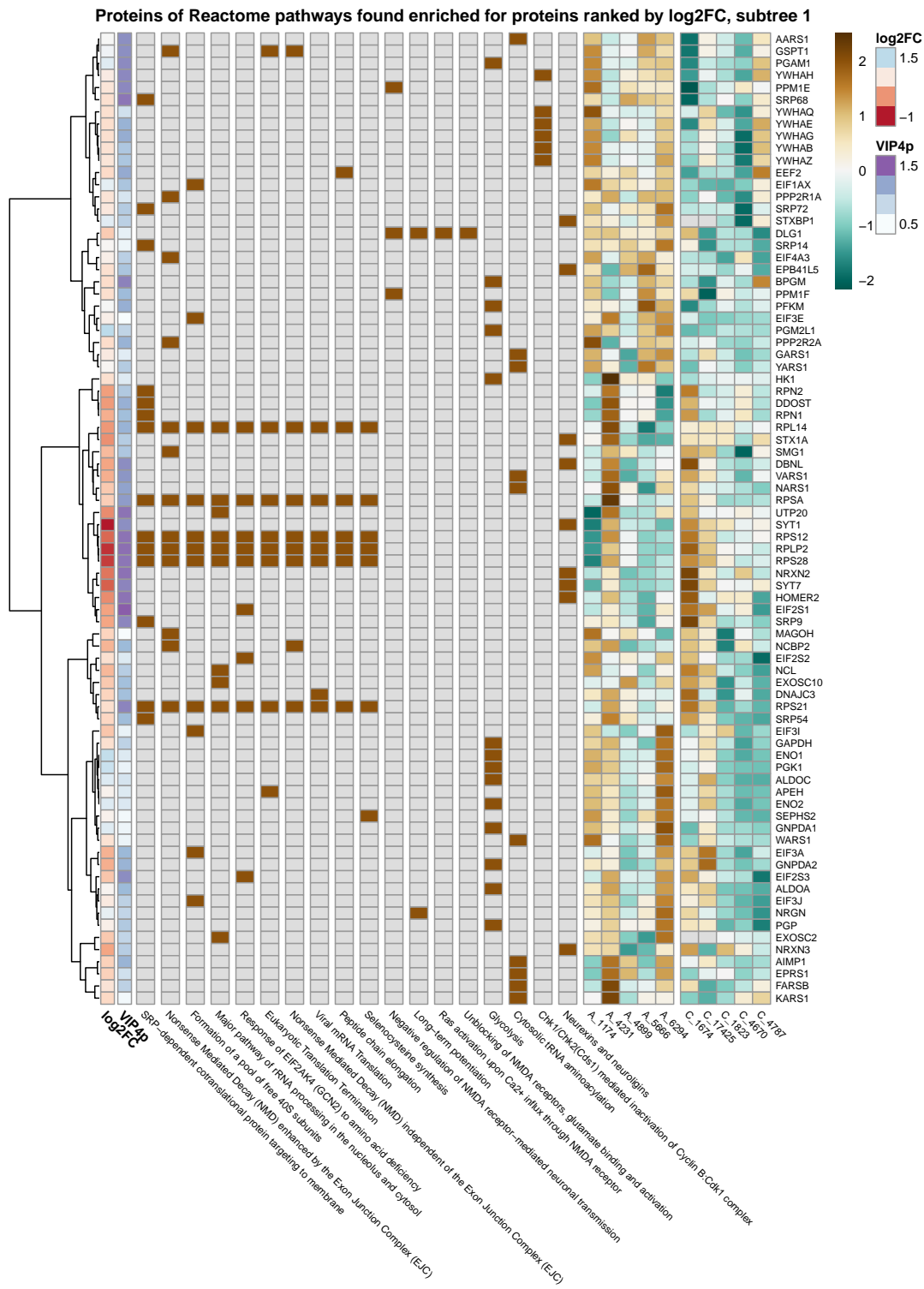


Figure S4: Heatmap 1 of Reactome pathways for children, log₂(FC)-ranked proteins

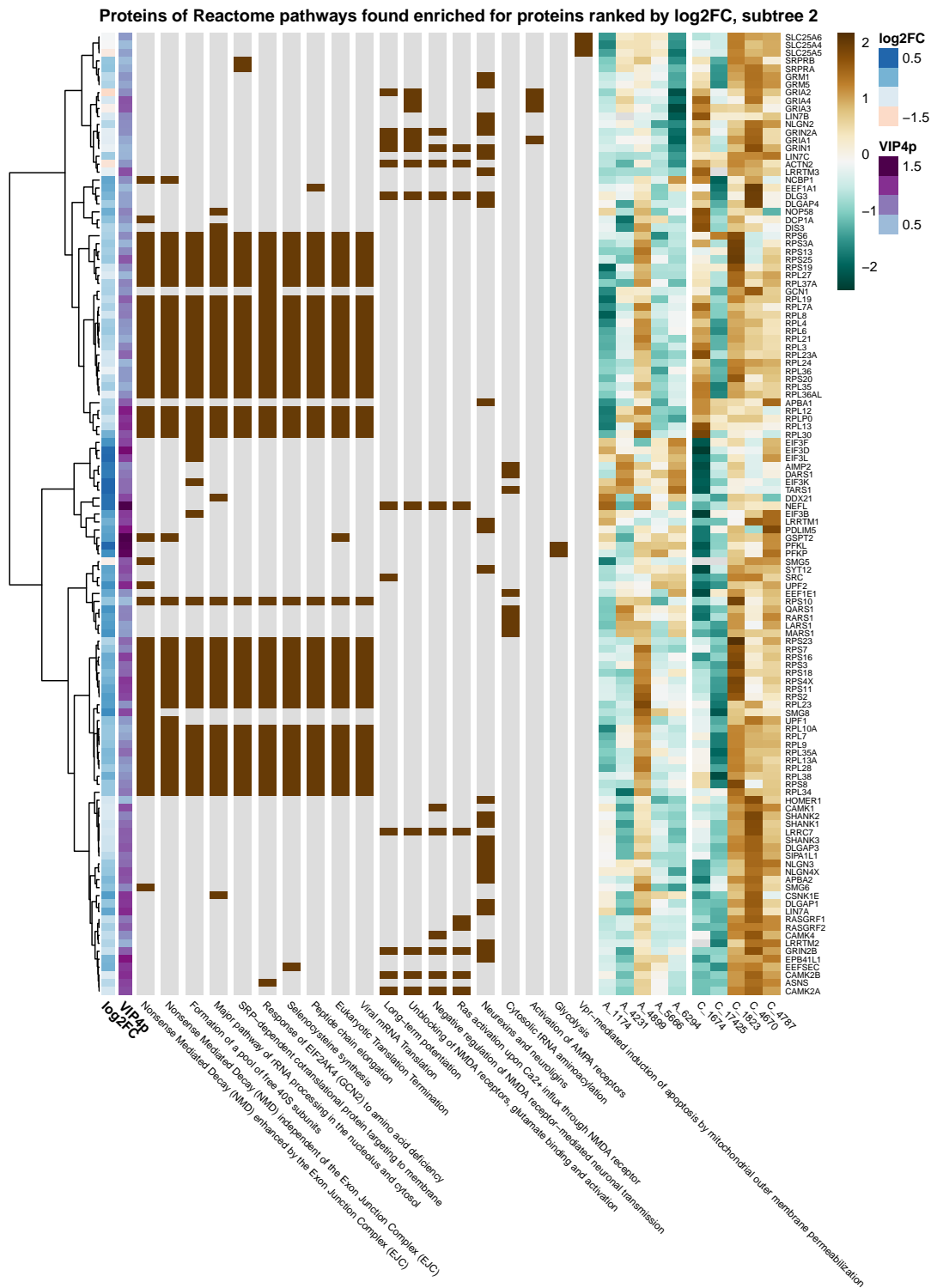


Figure S5: Heatmap 2 of Reactome pathways for children, log₂(FC)-ranked proteins

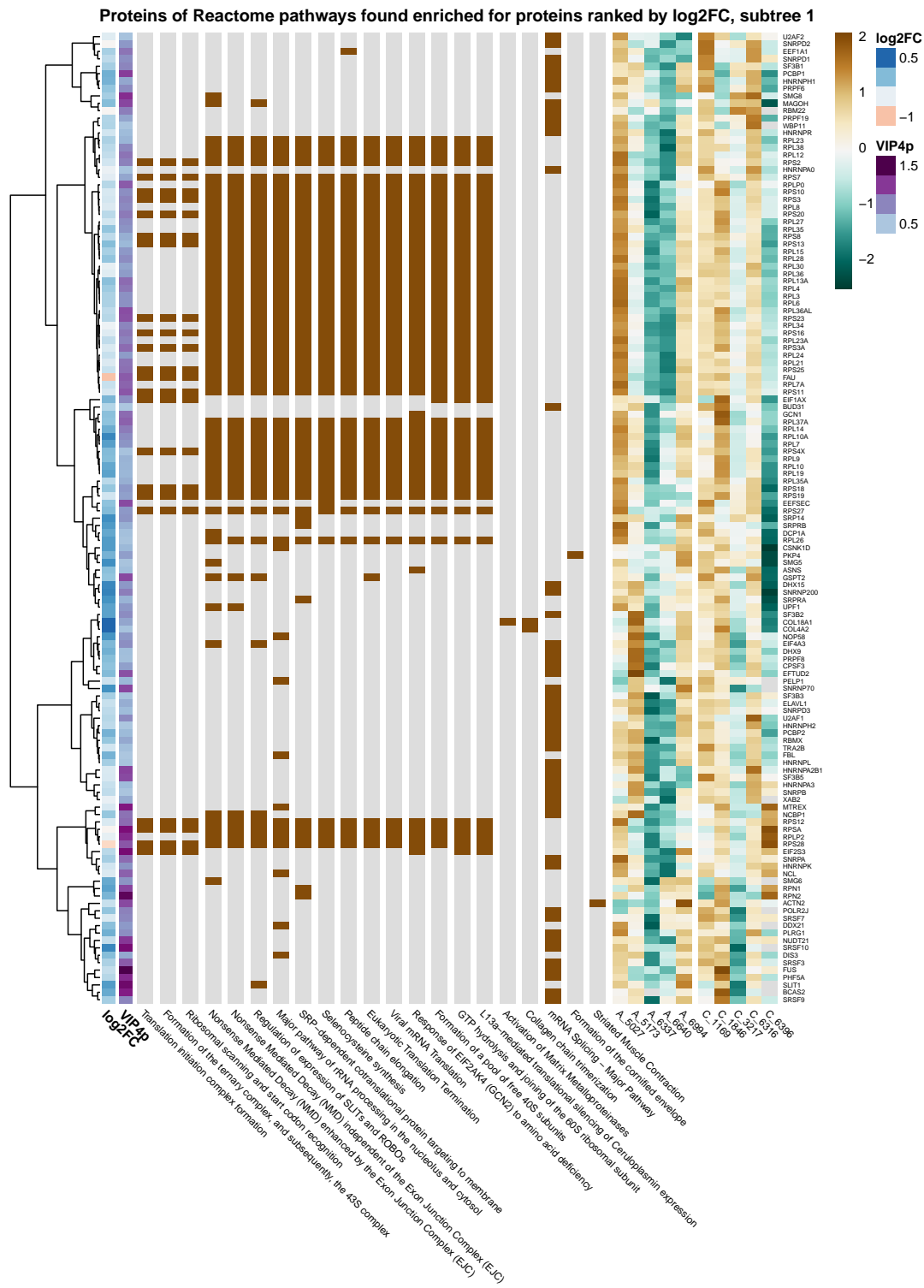


Figure S6: Heatmap 1 of Reactome pathways for adults, log₂(FC)-ranked proteins

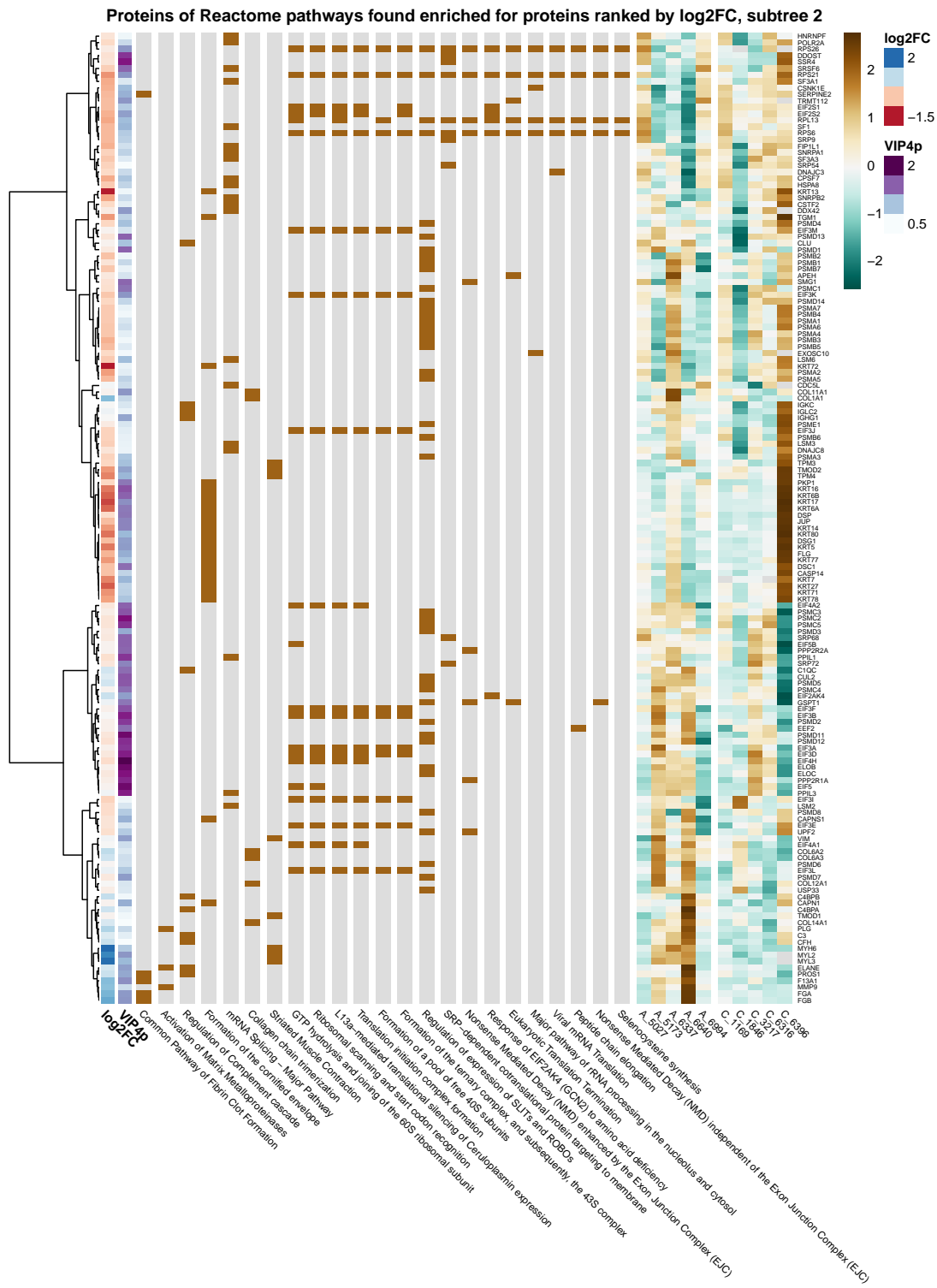


Figure S7: Heatmap 2 of Reactome pathways for adults, log₂(FC)-ranked proteins

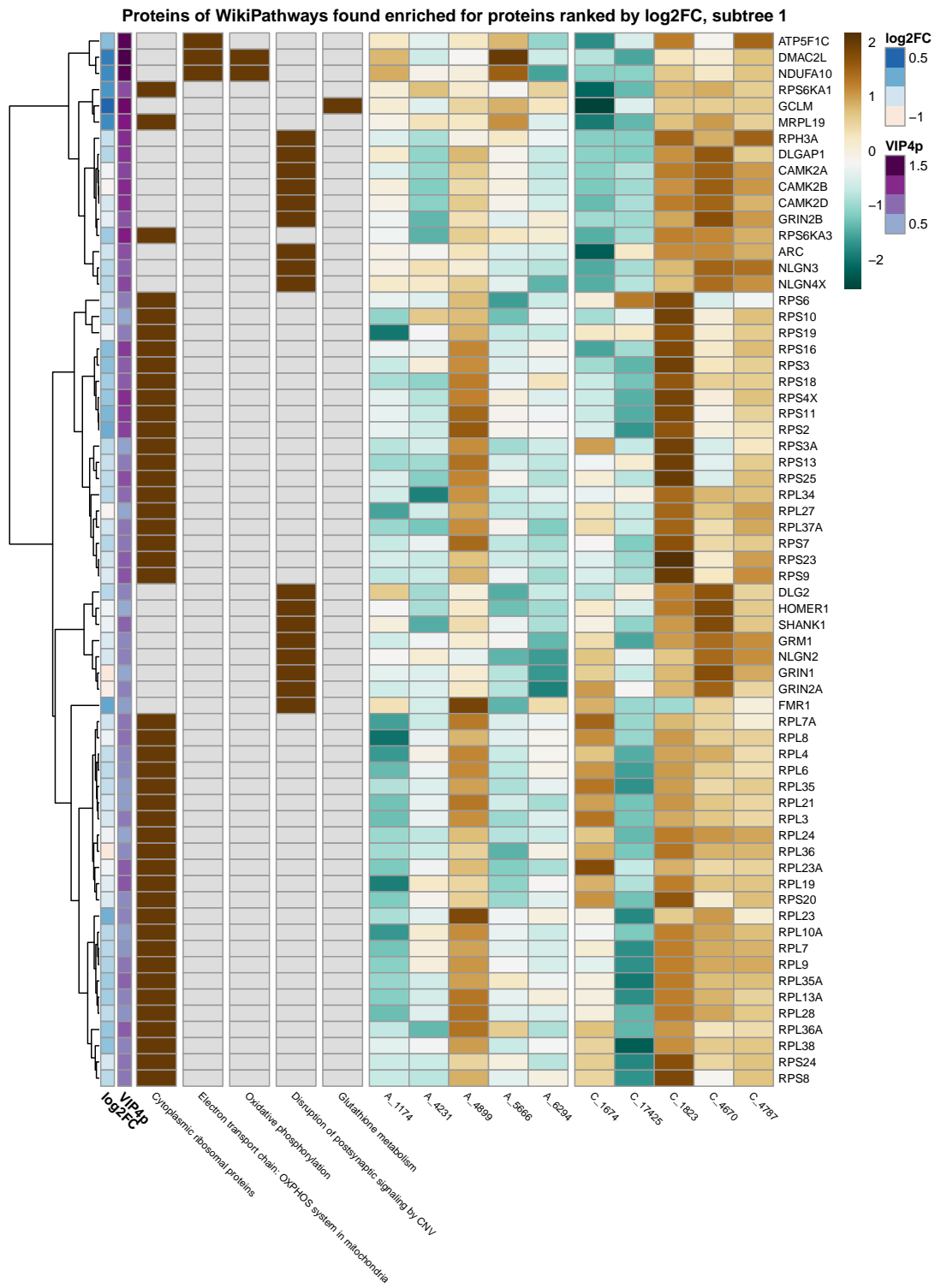


Figure S8: Heatmap 1 of WikiPathways for children, log₂(FC)-ranked proteins

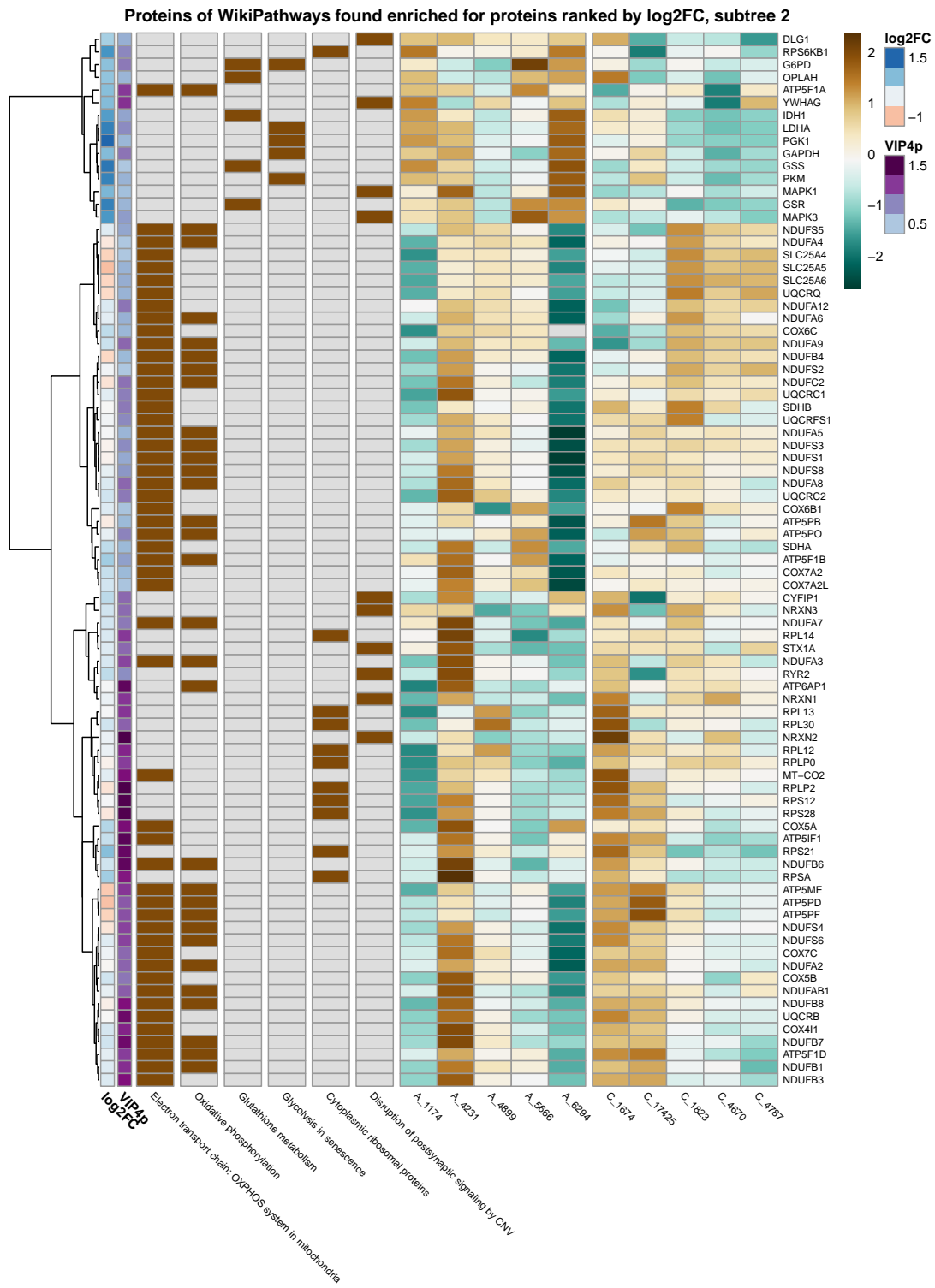


Figure S9: Heatmap 2 of WikiPathways for children, log₂(FC)-ranked proteins

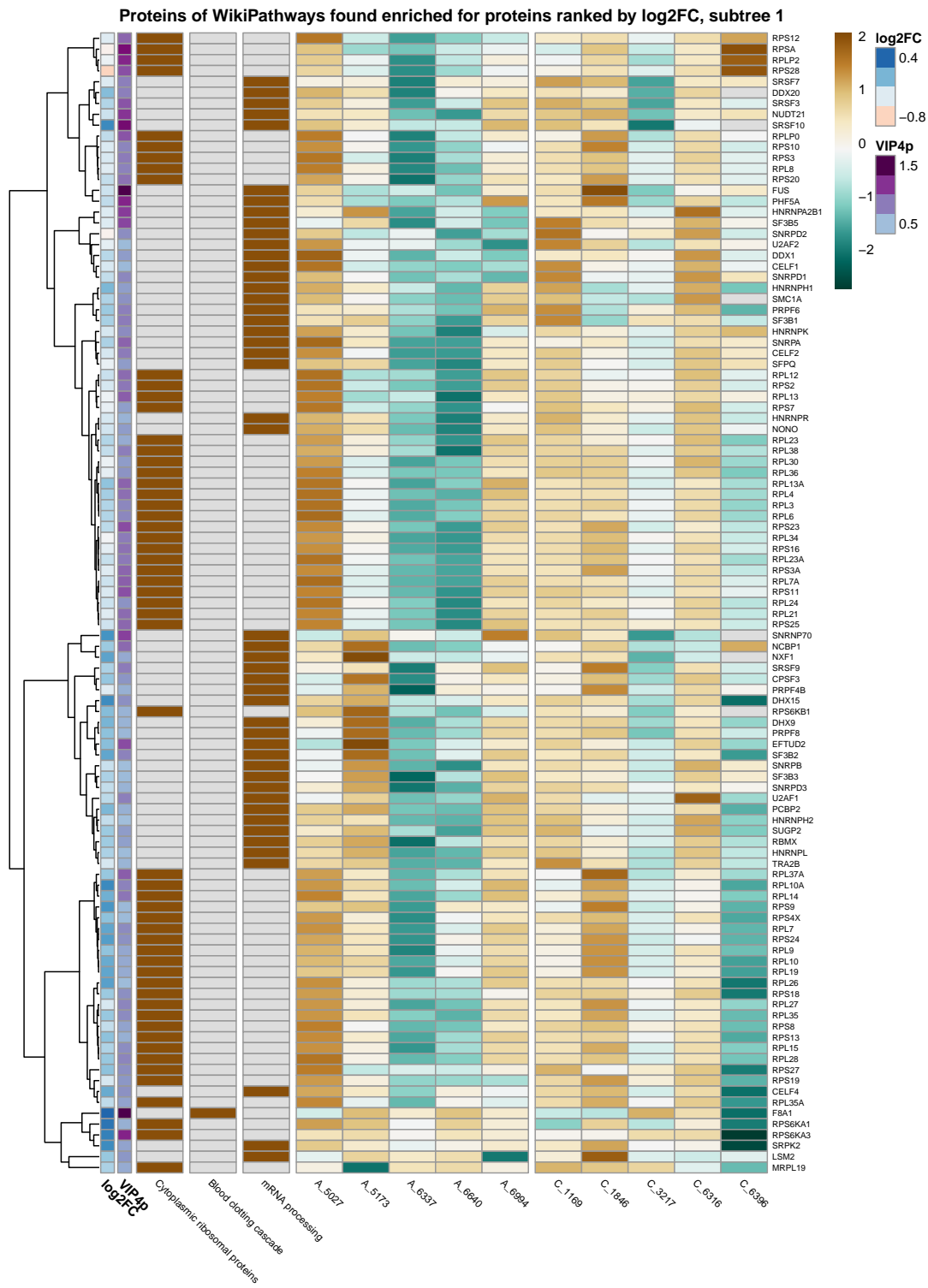


Figure S10: Heatmap 1 of WikiPathways for adults, log₂(FC)-ranked proteins

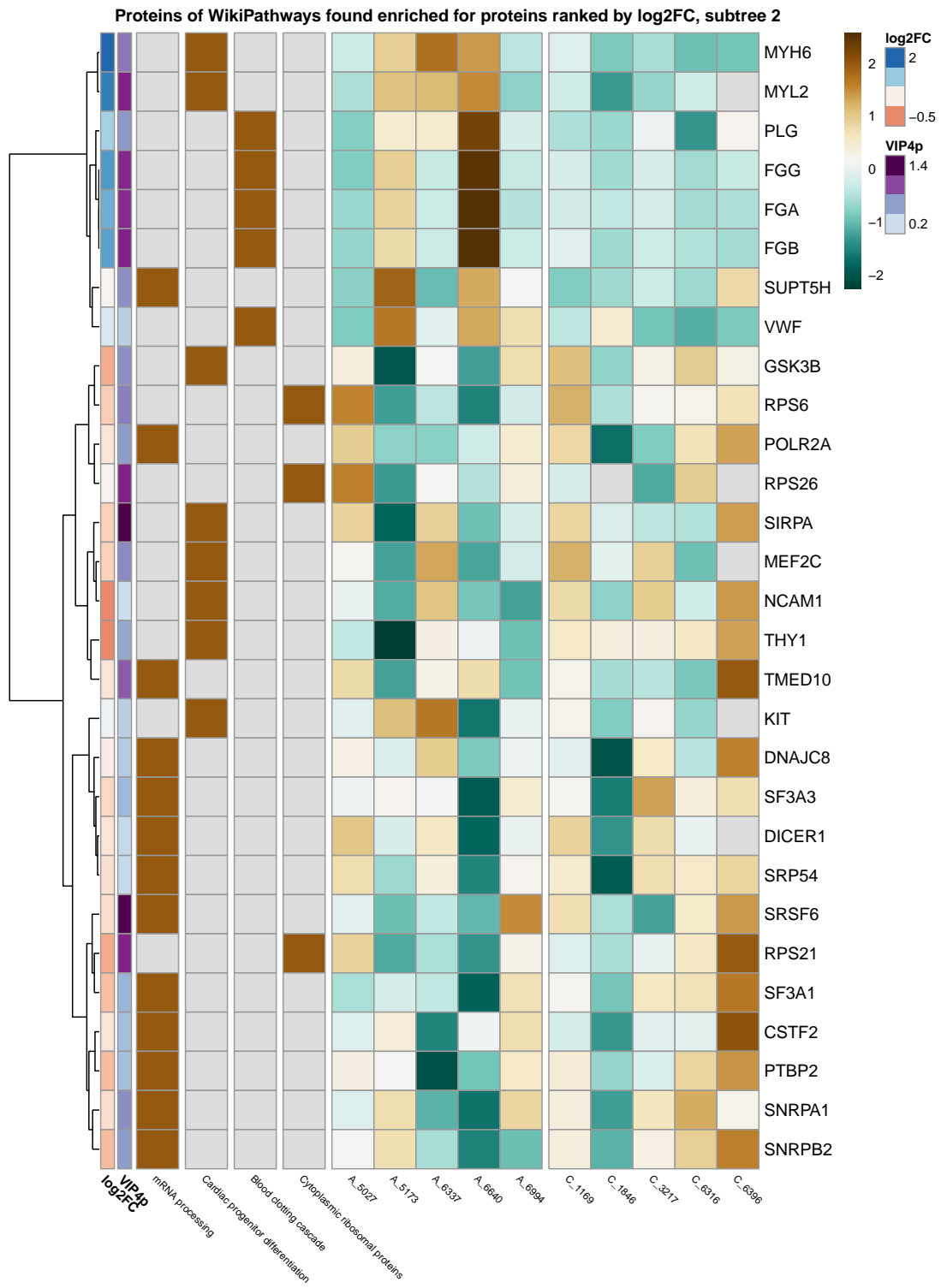


Figure S11: Heatmap 2 of WikiPathways for adults, log2(FC)-ranked proteins

Table S1: Significant differentially expressed proteins from children

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
A0A3B3ISV5	A0A3B3ISV5	Uncharacterized protein	3.6e-07	0.7549
A0A3B3ITX4	A0A3B3ITX4	Uncharacterized protein	0.0294	-1.0600
P04217	A1BG	Alpha-1B-glycoprotein	0.0109	1.1167
P01023	A2M	Alpha-2-macroglobulin	3.4e-13	0.9091
Q2M2I8	AAK1	AP2-associated protein kinase 1	0.0111	0.4786
H3BNQ7	ABAT	4-aminobutyrate aminotransferase, mitochondrial	6.9e-06	0.9499
Q9UBJ2	ABCD2	ATP-binding cassette sub-family D member 2	0.0013	-0.7740
Q9NUQ8	ABCF3	ATP-binding cassette sub-family F member 3	0.0434	-0.7234
Q9NUJ1	ABHD10	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	0.0215	0.5975
Q8IZP0	ABI1	Abl interactor 1	0.0162	-0.5218
A0A3B3IS55	ABLIM1	Actin-binding LIM protein 1	8.1e-04	-0.6125
Q6H8Q1	ABLIM2	Actin-binding LIM protein 2	0.0075	-0.6284
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1.1e-04	0.8222
Q5T4U5	ACADM	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain, isoform CRA_a	0.0104	0.5507
P49748	ACADVL	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	3.5e-11	-0.7976
Q15057	ACAP2	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	0.044	0.6320
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	0.0186	0.9934
P53396	ACLY	ATP-citrate synthase	8.4e-09	0.7133
P21399	ACO1	Cytoplasmic aconitate hydratase	5.0e-05	1.2813
A2A274	ACO2	Aconitate hydratase, mitochondrial	2.2e-16	1.1651
O00154	ACOT7	Cytosolic acyl coenzyme A thioester hydrolase	2.1e-08	1.2013
P12814	ACTN1	Alpha-actinin-1	2.2e-16	-1.3296
P35609	ACTN2	Alpha-actinin-2	2.2e-16	-1.4944
O43707	ACTN4	Alpha-actinin-4	3.7e-08	-0.5344
P61160	ACTR2	Actin-related protein 2	0.0115	0.3502
P61158	ACTR3	Actin-related protein 3	0.0232	0.3419
Q9P1U1	ACTR3B	Actin-related protein 3B	0.0049	0.4726
E7EWD3	ADAM23	Disintegrin and metalloproteinase domain-containing protein 23	3.5e-04	-1.0677
P11766	ADH5	Alcohol dehydrogenase class-3	3.8e-13	1.6052
P35573	AGL	Glycogen debranching enzyme	0.0017	0.8783
P23526	AHCY	Adenosylhomocysteinase	2.5e-09	1.1531
O43865	AHCYL1	S-adenosylhomocysteine hydrolase-like protein 1	2.5e-16	0.8926
Q96HN2	AHCYL2	Adenosylhomocysteinase 3	0.0483	0.6036
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	8.6e-04	-0.3111
O95433	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	0.0027	1.0705
Q13155	AIMP2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	0.0011	0.8005
C9J069	AJM1	Apical junction component 1 homolog	0.0335	-0.6300
P00568	AK1	Adenylate kinase isoenzyme 1	5.6e-06	1.2882
Q9UIJ7	AK3	GTP:AMP phosphotransferase AK3, mitochondrial	7.7e-07	1.7728

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
O43687	AKAP7	A-kinase anchor protein 7 isoforms alpha and beta	0.0218	0.5524
P14550	AKR1A1	Aldo-keto reductase family 1 member A1	6.3e-05	1.3495
P15121	AKR1B1	Aldo-keto reductase family 1 member B1	1.2e-06	1.8426
P00352	ALDH1A1	Retinal dehydrogenase 1	0.0074	0.9100
O75891	ALDH1L1	Cytosolic 10-formyltetrahydrofolate dehydrogenase	0.002	0.6887
P05091	ALDH2	Aldehyde dehydrogenase, mitochondrial	6.1e-06	0.7464
P30038	ALDH4A1	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	0.0242	0.9306
P51649	ALDH5A1	Succinate-semialdehyde dehydrogenase, mitochondrial	4.5e-06	0.8238
Q02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	1.3e-05	0.8694
A0A1B0GTG2	ALDH7A1	Alpha-aminoadipic semialdehyde dehydrogenase	4.1e-11	1.2887
P49189	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	1.3e-07	1.3497
P04075	ALDOA	Fructose-bisphosphate aldolase A	4.4e-12	0.8925
P09972	ALDOC	Fructose-bisphosphate aldolase C	9.5e-15	1.2409
Q01433	AMPD2	AMP deaminase 2	0.0433	0.5424
P49418	AMPH	Amphiphysin	4.4e-05	0.4832
P16157	ANK1	Ankyrin-1	4.3e-04	-0.6421
Q01484	ANK2	Ankyrin-2	1.3e-14	-0.2813
Q8IV38	ANKMY2	Ankyrin repeat and MYND domain-containing protein 2	0.009	0.4438
P08133	ANXA6	Annexin A6	2.2e-16	1.3436
O43747	AP1G1	AP-1 complex subunit gamma-1	0.0026	0.5231
K7EJL1	AP1M1	AP-1 complex subunit mu-1	0.0061	0.7477
O94973	AP2A2	AP-2 complex subunit alpha-2	9.2e-05	0.3651
Q96CW1	AP2M1	AP-2 complex subunit mu	3.0e-05	0.5457
Q13367	AP3B2	AP-3 complex subunit beta-2	3.5e-10	0.5009
P25054	APC	Adenomatous polyposis coli protein	0.0206	-0.5777
P13798	APEH	Acylamino-acid-releasing enzyme	5.0e-05	0.8401
P02647	APOA1	Apolipoprotein A-I	0.0399	0.6076
P02649	APOE	Apolipoprotein E	0.0049	0.6816
P61204	ARF3	ADP-ribosylation factor 3	0.0283	0.9699
Q5TH69	ARFGEF3	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	0.0385	0.3820
A7KAX9	ARHGAP32	Rho GTPase-activating protein 32	0.0141	-0.5838
P52565	ARHGDI1	Rho GDP-dissociation inhibitor 1	6.6e-09	1.6342
Q9NVT9	ARMC1	Armadillo repeat-containing protein 1	0.0027	1.1637
Q92747	ARPC1A	Actin-related protein 2/3 complex subunit 1A	2.1e-10	0.5181
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	0.0394	0.8836
O15511	ARPC5	Actin-related protein 2/3 complex subunit 5	0.0201	0.4906
O43150	ASAP2	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	0.023	0.4253
Q7L266	ASRGL1	Isoaspartyl peptidase/L-asparaginase	7.4e-05	1.0240
P00966	ASS1	Argininosuccinate synthase	1.7e-04	1.0369
Q86WG3	ATCAY	Caytaxin	0.0237	0.9732
Q9NT62	ATG3	Ubiquitin-like-conjugating enzyme ATG3	0.0341	1.0214

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
O95352	ATG7	Ubiquitin-like modifier-activating enzyme ATG7	0.0015	0.9280
P31939	ATIC	Bifunctional purine biosynthesis protein PURH	1.5e-04	1.0027
B1AKY9	ATP1A2	Sodium/potassium-transporting ATPase subunit alpha	0.0015	0.3370
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	9.8e-07	0.6566
P20020	ATP2B1	Plasma membrane calcium-transporting ATPase 1	7.4e-08	0.6248
A0A2U3TZI3	ATP2B2	Calcium-transporting ATPase	6.5e-07	0.5848
Q16720	ATP2B3	Plasma membrane calcium-transporting ATPase 3	0.0053	1.1061
P25705	ATP5F1A	ATP synthase subunit alpha, mitochondrial	7.3e-09	0.5138
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	0.0095	-1.1395
P24539	ATP5PB	ATP synthase F(0) complex subunit B1, mitochondrial	0.0219	-0.7479
O75947	ATP5PD	ATP synthase subunit d, mitochondrial	1.1e-07	-1.2763
P18859	ATP5PF	ATP synthase-coupling factor 6, mitochondrial	3.7e-04	-1.0296
Q93050	ATP6V0A1	V-type proton ATPase 116 kDa subunit a isoform 1	1.8e-06	-0.5801
P27449	ATP6V0C	V-type proton ATPase 16 kDa proteolipid subunit	0.0101	-0.9300
F5GYQ1	ATP6V0D1	V-type proton ATPase subunit	0.0109	-0.5046
P38606	ATP6V1A	V-type proton ATPase catalytic subunit A	5.8e-04	-0.3160
Q9Y5K8	ATP6V1D	V-type proton ATPase subunit D	0.0039	0.4153
P36543	ATP6V1E1	V-type proton ATPase subunit E 1	0.0039	-0.3527
Q9UBB4	ATXN10	Ataxin-10	3.8e-04	0.8789
Q13825	AUH	Methylglutaconyl-CoA hydratase, mitochondrial	1.7e-04	-0.6691
Q9UQB8	BAIAP2	Brain-specific angiogenesis inhibitor 1-associated protein 2	3.2e-15	-0.5550
P80723	BASP1	Brain acid soluble protein 1	2.2e-16	0.9408
H0Y542	BCAS1	Breast carcinoma-amplified sequence 1 (Fragment)	0.0496	0.5900
O00499	BIN1	Myc box-dependent-interacting protein 1	1.6e-10	0.8263
P53004	BLVRA	Biliverdin reductase A	0.013	1.0643
P30043	BLVRB	Flavin reductase (NADPH)	0.0176	0.9777
Q9UPA5	BSN	Protein bassoon	1.8e-07	-0.4282
A0A1B0GUL6	BTBD8	BTB/POZ domain-containing protein 8	0.0478	0.3305
Q07021	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	0.0304	-0.7569
Q9GZN8	C20orf27	UPF0687 protein C20orf27	0.0115	1.1108
P01024	C3	Complement C3	1.2e-08	0.9933
F5GXS0	C4B	Complement C4-B	1.0e-04	0.9575
E5RHP7	CA1	Carbonic anhydrase 1 (Fragment)	1.3e-07	2.1918
P54289	CACNA2D1	Voltage-dependent calcium channel subunit alpha-2/delta-1	5.6e-07	-0.4571
C9JVC9	CACNA2D2	Voltage-dependent calcium channel subunit alpha-2/delta-2	9.6e-06	-0.7742
Q8IZS8	CACNA2D3	Voltage-dependent calcium channel subunit alpha-2/delta-3	0.0031	-0.6158
F1T0E5	CADPS	Calcium-dependent secretion activator 1	1.4e-04	0.4625
P05937	CALB1	Calbindin	7.9e-04	1.6951

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
H3BN14	CALB2	Calretinin (Fragment)	4.8e-04	1.5471
Q9P1Z2	CALCOCO1	Calcium-binding and coiled-coil domain-containing protein 1	0.0139	0.5801
P27797	CALR	Calreticulin	3.3e-04	0.9691
Q96NX5	CAMK1G	Calcium/calmodulin-dependent protein kinase type 1G	0.0377	-0.7699
Q9UQM7	CAMK2A	Calcium/calmodulin-dependent protein kinase type II subunit alpha	1.0e-03	-0.6622
Q16566	CAMK4	Calcium/calmodulin-dependent protein kinase type IV	0.0097	-0.4156
Q96RR4	CAMKK2	Calcium/calmodulin-dependent protein kinase kinase 2	0.0396	-0.4038
Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	2.2e-16	0.6481
P27824	CANX	Calnexin	0.0059	0.5501
Q01518	CAP1	Adenylyl cyclase-associated protein 1	1.0e-07	0.4746
P40123	CAP2	Adenylyl cyclase-associated protein 2	4.4e-05	0.5823
P07384	CAPN1	Calpain-1 catalytic subunit	0.0109	0.3150
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	0.0075	-0.5752
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	5.0e-12	-0.8425
B1AK88	CAPZB	F-actin-capping protein subunit beta	1.1e-09	-0.5832
Q5VZK9	CARMIL1	F-actin-uncapping protein LRRC16A	0.0268	0.3739
Q8WXD9	CASKIN1	Caskin-1	0.0148	-0.3394
P16152	CBR1	Carbonyl reductase [NADPH] 1	2.1e-06	1.8062
P0DN79	CBSL	Cystathionine beta-synthase-like protein	0.0195	1.5153
O60826	CCDC22	Coiled-coil domain-containing protein 22	0.0447	0.4600
F8W9X7	CCDC93	Coiled-coil domain-containing protein 93	0.0173	0.8759
P78371	CCT2	T-complex protein 1 subunit beta	0.0016	0.3272
P50991	CCT4	T-complex protein 1 subunit delta	0.0056	0.4052
P50990	CCT8	T-complex protein 1 subunit theta	0.0046	0.2658
P60953	CDC42	Cell division control protein 42 homolog	6.8e-07	1.3075
Q13634	CDH18	Cadherin-18	0.0018	-0.9339
Q9ULB4	CDH9	Cadherin-9	0.0072	-1.0221
Q9HCU4	CELSR2	Cadherin EGF LAG seven-pass G-type receptor 2	0.0309	-0.9130
P41208	CETN2	Centrin-2	0.0127	-0.4936
E9PK25	CFL1	Cofilin-1	1.3e-05	0.7404
Q9H444	CHMP4B	Charged multivesicular body protein 4b	4.4e-05	-0.5902
A0A2R8YEI5	CHN2	Beta-chimaerin	0.0483	-0.6861
Q14011	CIRBP	Cold-inducible RNA-binding protein	0.0384	0.9205
Q8N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	0.0101	-0.7281
H7BYJ3	CIT	Citron Rho-interacting kinase (Fragment)	0.0305	-0.4070
P12277	CKB	Creatine kinase B-type	2.2e-04	0.7598
E7EW49	CLASP2	CLIP-associating protein 2	0.0041	0.3090
Q14677	CLINT1	Clathrin interactor 1	1.8e-04	1.1079
O94985	CLSTN1	Calsyntenin-1	3.0e-04	0.6173
P09496	CLTA	Clathrin light chain A	0.0233	0.6238
P09497	CLTB	Clathrin light chain B	9.6e-04	0.9839

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
A0A087WVQ6	CLTC	Clathrin heavy chain	2.2e-16	0.8630
Q8NFW8	CMAS	N-acylneuraminate cytidyltransferase	5.2e-05	0.6204
Q96KP4	CNDP2	Cytosolic non-specific dipeptidase	5.8e-05	1.2636
Q9BT09	CNPY3	Protein canopy homolog 3	0.0148	0.8178
Q96F85	CNRIP1	CB1 cannabinoid receptor-interacting protein 1	4.1e-11	1.7360
Q12860	CNTN1	Contactin-1	6.5e-10	-0.3771
Q8IWW2	CNTN4	Contactin-4	0.0074	-0.3841
Q9Y678	COPG1	Coatomer subunit gamma-1	0.0277	0.4233
P61201	COPS2	COP9 signalosome complex subunit 2	4.5e-04	0.7581
Q9BT78	COPS4	COP9 signalosome complex subunit 4	2.6e-05	0.6431
Q92905	COPS5	COP9 signalosome complex subunit 5	0.0057	0.5428
Q9UBW8	COPS7A	COP9 signalosome complex subunit 7a	0.0066	0.8825
P31146	CORO1A	Coronin-1A	6.1e-15	0.9036
Q9BR76	CORO1B	Coronin-1B	0.0309	0.4728
Q9UQ03	CORO2B	Coronin-2B	0.0025	-0.4885
Q14019	COTL1	Coactosin-like protein	0.008	1.1038
Q86YQ8	CPNE8	Copine-8	0.0326	0.5364
Q14194	CRMP1	Dihydropyrimidinase-related protein 1	6.7e-15	0.9760
Q14894	CRYM	Ketimine reductase mu-crystallin	3.1e-13	1.8293
P35221	CTNNA1	Catenin alpha-1	0.0011	-0.4775
P26232	CTNNA2	Catenin alpha-2	1.1e-05	-0.5336
A0A1B0GVD5	CTSD	Cathepsin D	3.9e-05	0.6045
Q13618	CUL3	Cullin-3	0.0343	0.5042
Q9UHQ9	CYB5R1	NADH-cytochrome b5 reductase 1	2.4e-04	-0.7344
Q16643	DBN1	Drebrin	8.7e-08	-0.6273
P11182	DBT	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	3.7e-04	-0.4372
O15075	DCLK1	Serine/threonine-protein kinase DCLK1	0.0489	0.3126
Q13561	DCTN2	Dynactin subunit 2	0.0205	-0.3051
O94760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	6.6e-09	1.3470
Q5SRR8	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment)	7.9e-04	1.2228
P30046	DDT	D-dopachrome decarboxylase	0.0018	1.6003
Q92499	DDX1	ATP-dependent RNA helicase DDX1	1.9e-06	0.3527
A0A1W2PQ51	DDX17	Probable ATP-dependent RNA helicase DDX17	5.5e-07	0.7776
Q13838	DDX39B	Spliceosome RNA helicase DDX39B	2.2e-04	0.8751
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	1.6e-04	-0.7002
Q08211	DHX9	ATP-dependent RNA helicase A	0.0184	0.7503
Q9NR28	DIABLO	Diablo homolog, mitochondrial	0.0198	0.6028
P10515	DLAT	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	9.3e-08	0.9651
E9PEX6	DLD	Dihydrolipoyl dehydrogenase	1.9e-09	0.8082
B9EGL1	DLG4	DLG4 protein	0.0032	-0.7379

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
Q9Y2H0	DLGAP4	Disks large-associated protein 4	0.0026	-0.6134
Q08495	DMTN	Dematin	1.8e-06	-0.6264
F5H269	DMXL1	DmX-like protein 1	0.0194	-0.2459
Q8TDJ6	DMXL2	DmX-like protein 2	2.1e-12	-0.3617
P25685	DNAJB1	DnaJ homolog subfamily B member 1	1.2e-04	-0.4779
Q9UDY4	DNAJB4	DnaJ homolog subfamily B member 4	0.002	-0.4502
O75953	DNAJB5	DnaJ homolog subfamily B member 5	0.026	-0.7001
Q96DA6	DNAJC19	Mitochondrial import inner membrane translocase subunit TIM14	0.0022	-0.6073
O75061	DNAJC6	Putative tyrosine-protein phosphatase auxilin	0.0012	0.5527
A0A0D9SFB1	DNM1	Dynamin-1	2.1e-04	0.2054
A0A0U1RQP1	DNM1	Dynamin-1	2.1e-04	0.2054
G8JLD5	DNM1L	Dynamin-1-like protein	2.2e-16	1.2614
O00429	DNM1L	Dynamin-1-like protein	2.2e-16	1.2614
Q9UQ16	DNM3	Dynamin-3	0.0152	0.2580
Q9BZ29	DOCK9	Dedicator of cytokinesis protein 9	0.034	-0.4379
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	2.2e-16	1.0527
Q14195	DPYSL3	Dihydropyrimidinase-related protein 3	3.0e-12	1.2664
O14531	DPYSL4	Dihydropyrimidinase-related protein 4	1.4e-09	1.0767
Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	2.2e-16	1.2326
F6RFD5	DSTN	Destrin	0.0071	0.7247
O60941	DTNB	Dystrobrevin beta	0.0201	-0.4004
P51452	DUSP3	Dual specificity protein phosphatase 3	0.0036	1.8049
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	5.4e-06	-0.1532
Q9Y6G9	DYNC1LI1	Cytoplasmic dynein 1 light intermediate chain 1	1.0e-04	-0.4037
O43237	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	0.0451	-0.3517
Q8NCM8	DYNC2H1	Cytoplasmic dynein 2 heavy chain 1	0.044	-0.4989
P30084	ECHS1	Enoyl-CoA hydratase, mitochondrial	7.7e-11	1.1881
P26641	EEF1G	Elongation factor 1-gamma	0.004	0.3600
P13639	EEF2	Elongation factor 2	8.7e-07	0.5210
Q9NZN3	EHD3	EH domain-containing protein 3	0.006	0.4261
P47813	EIF1AX	Eukaryotic translation initiation factor 1A, X-chromosomal	3.5e-05	1.1599
P20042	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	0.0091	0.6469
P41091	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	0.0207	0.4048
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E	8.9e-05	0.8006
A0A087WZK9	EIF3H	Eukaryotic translation initiation factor 3 subunit H	0.0235	0.4532
O75822	EIF3J	Eukaryotic translation initiation factor 3 subunit J	0.0016	0.6424
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II	0.0105	0.7773
P38919	EIF4A3	Eukaryotic initiation factor 4A-III	0.0078	0.7500
E7EX17	EIF4B	Eukaryotic translation initiation factor 4B	0.0059	1.1343
E7EX73	EIF4G1	Eukaryotic translation initiation factor 4 gamma 1	1.5e-04	0.4765
O43432	EIF4G3	Eukaryotic translation initiation factor 4 gamma 3	0.0093	0.3525
P55010	EIF5	Eukaryotic translation initiation factor 5	0.0361	0.5743
I3L397	EIF5A	Eukaryotic translation initiation factor 5A (Fragment)	8.3e-06	0.7658

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
Q5R3F8	ELFN2	Protein phosphatase 1 regulatory subunit 29	0.0168	-0.8109
A0A0U1RRM6	ENAH	Protein enabled homolog	0.0091	-0.6187
P06733	ENO1	Alpha-enolase	2.2e-16	1.5125
P09104	ENO2	Gamma-enolase	1.2e-04	1.5396
E9PHY5	EPB41L2	Band 4.1-like protein 2	2.1e-04	0.5038
A0A0A0MRA8	EPB41L3	Band 4.1-like protein 3	6.2e-04	0.2181
P54764	EPHA4	Ephrin type-A receptor 4	0.0185	-0.4933
Q9Y6I3	EPN1	Epsin-1	6.9e-04	0.6581
Q96J88	EPSTI1	Epithelial-stromal interaction protein 1	0.0196	-0.5027
X6RLX0	ERC1	ELKS/Rab6-interacting/CAST family member 1	5.6e-05	-0.7277
O15083	ERC2	ERC protein 2	1.9e-05	-0.7354
O43414	ERI3	ERI1 exoribonuclease 3	2.1e-04	0.8615
P10768	ESD	S-formylglutathione hydrolase	2.1e-04	1.1951
B7Z7P8	ETF1	Eukaryotic peptide chain release factor subunit 1	6.2e-05	0.8224
P13804	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	2.6e-06	0.9831
P38117	ETFB	Electron transfer flavoprotein subunit beta	6.0e-05	1.3079
Q9UI08	EVL	Ena/VASP-like protein	0.0406	-0.3448
P15311	EZR	Ezrin	0.013	0.5365
O15540	FABP7	Fatty acid-binding protein, brain	0.0069	1.6254
Q9NRY5	FAM114A2	Protein FAM114A2	0.0246	0.7264
Q8IXS8	FAM126B	Protein FAM126B	0.0354	-0.3581
Q52LJ0	FAM98B	Protein FAM98B	2.2e-04	0.6135
K7ER00	FARSA	Phenylalanine-tRNA ligase alpha subunit	0.0081	0.4556
Q9NSD9	FARSB	Phenylalanine-tRNA ligase beta subunit	8.1e-06	0.6149
P49327	FASN	Fatty acid synthase	2.0e-12	0.7258
Q8TF61	FBXO41	F-box only protein 41	0.0219	-0.3909
P14324	FDPS	Farnesyl pyrophosphate synthase	0.0196	0.8493
P02671	FGA	Fibrinogen alpha chain	0.0049	0.4792
C9JEU5	FGG	Fibrinogen gamma chain	0.0213	0.4764
P07954	FH	Fumarate hydratase, mitochondrial	8.9e-07	0.8864
Q5JXI8	FHL1	Four and a half LIM domains protein 1 (Fragment)	0.0473	0.9171
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	0.0029	0.7755
P21333	FLNA	Filamin-A	0.0099	0.2432
O75955	FLOT1	Flotillin-1	3.5e-04	-0.4089
Q14254	FLOT2	Flotillin-2	5.3e-05	-0.5270
O43155	FLRT2	Leucine-rich repeat transmembrane protein FLRT2	0.05	-0.6095
Q9H479	FN3K	Fructosamine-3-kinase	5.5e-14	0.9813
Q9HA64	FN3KRP	Ketosamine-3-kinase	0.0082	0.9219
Q16658	FSCN1	Fascin	0.0236	0.5373
Q9BTV5	FSD1	Fibronectin type III and SPRY domain-containing protein 1	3.4e-04	0.5561
A0A0C4DG97	FSD1L	FSD1-like protein	0.0037	0.3671
P02794	FTH1	Ferritin heavy chain	3.8e-04	0.9982
P02792	FTL	Ferritin light chain	5.6e-05	0.9558
P35637	FUS	RNA-binding protein FUS	0.002	0.6518

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	0.0278	0.5722
P60520	GABARAPL2	Gamma-aminobutyric acid receptor-associated protein-like 2	7.6e-07	-0.6391
Q9UBS5	GABBR1	Gamma-aminobutyric acid type B receptor subunit 1	6.4e-05	-0.5831
P14867	GABRA1	Gamma-aminobutyric acid receptor subunit alpha-1	0.0109	-0.4685
P28472	GABRB3	Gamma-aminobutyric acid receptor subunit beta-3	0.0407	-0.7577
Q14697	GANAB	Neutral alpha-glucosidase AB	0.0228	0.7523
P17677	GAP43	Neuromodulin	0.0351	0.3829
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	2.2e-16	0.7086
P22102	GART	Trifunctional purine biosynthetic protein adenosine-3	0.0296	0.6360
Q9Y2T3	GDA	Guanine deaminase	3.4e-14	1.3378
P31150	GDI1	Rab GDP dissociation inhibitor alpha	2.2e-16	1.2155
P50395	GDI2	Rab GDP dissociation inhibitor beta	1.0e-06	1.1792
K7EMP8	GFAP	Glial fibrillary acidic protein	9.3e-08	0.8679
Q9NZ52	GGA3	ADP-ribosylation factor-binding protein GGA3	0.0127	1.3875
Q6Y7W6	GIGYF2	GRB10-interacting GYF protein 2	0.0451	-0.6345
P17302	GJA1	Gap junction alpha-1 protein	0.0359	-0.5931
Q04760	GLO1	Lactoylglutathione lyase	1.4e-06	1.0381
F6TLX2	GLOD4	Glyoxalase domain-containing protein 4	5.5e-04	1.9466
A0A2R8YDT1	GLUL	Glutamine synthetase	9.3e-16	1.0722
P36915	GNL1	Guanine nucleotide-binding protein-like 1	0.0059	0.9834
P46926	GNPDA1	Glucosamine-6-phosphate isomerase 1	0.0046	1.3757
P17174	GOT1	Aspartate aminotransferase, cytoplasmic	1.3e-13	1.8316
P00505	GOT2	Aspartate aminotransferase, mitochondrial	1.7e-10	0.9369
Q8N335	GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	7.9e-08	1.5523
Q5T848	GPR158	Probable G-protein coupled receptor 158	0.0016	0.5989
Q7Z2K8	GPRIN1	G protein-regulated inducer of neurite outgrowth 1	3.1e-04	0.3917
P62993	GRB2	Growth factor receptor-bound protein 2	4.4e-06	1.3421
Q9UBQ7	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	0.0205	1.5461
P42261	GRIA1	Glutamate receptor 1	3.0e-07	-1.0619
H0Y972	GRIA2	Glutamate receptor 2 (Fragment)	2.2e-16	-1.0809
P42262	GRIA2	Glutamate receptor 2	2.2e-16	-1.0809
P42263	GRIA3	Glutamate receptor 3	1.8e-08	-1.0398
P48058	GRIA4	Glutamate receptor 4	3.6e-05	-0.7505
Q05586	GRIN1	Glutamate receptor ionotropic, NMDA 1	9.4e-12	-0.9982
Q12879	GRIN2A	Glutamate receptor ionotropic, NMDA 2A	1.9e-08	-0.9411
Q13224	GRIN2B	Glutamate receptor ionotropic, NMDA 2B	0.004	-0.6589
A0A0A0MT01	GSN	Gelsolin	0.0306	0.3735
P15170	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0.0091	0.4736
P48637	GSS	Glutathione synthetase	0.0281	1.0849
E7EWW9	GSTM1	Glutathione S-transferase Mu 1	7.0e-04	1.3128
E9PHN7	GSTM2	Glutathione S-transferase Mu 2	0.0036	1.4926
P78417	GSTO1	Glutathione S-transferase omega-1	0.0041	1.3453
P46976	GYG1	Glycogenin-1	0.0268	0.7498
H0YFD6	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	6.9e-04	0.2946

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
Q16775	HAGH	Hydroxyacylglutathione hydrolase, mitochondrial	0.0478	0.4151
P10915	HAPLN1	Hyaluronan and proteoglycan link protein 1	0.0323	-0.2592
P02042	HBD	Hemoglobin subunit delta	2.2e-16	1.6296
P51858	HDGF	Hepatoma-derived growth factor	0.0466	1.2052
A0A3B3IRV5	HEBP1	Heme-binding protein 1 (Fragment)	0.0194	0.7685
J3KPF0	HECTD4	Probable E3 ubiquitin-protein ligase HECTD4	1.4e-05	-0.4247
O14964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	2.1e-04	0.6676
Q6NVY1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	2.4e-04	1.3400
D6RE99	HINT1	Histidine triad nucleotide-binding protein 1	0.0063	1.7528
O00291	HIP1	Huntingtin-interacting protein 1	4.8e-05	1.2090
P19367	HK1	Hexokinase-1	8.5e-07	0.5746
F8W6I7	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	2.0e-04	0.5125
P22626	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	1.5e-06	0.7282
B4DY08	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	0.001	0.4409
P31942	HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	0.0475	0.7922
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	2.1e-06	0.5579
P14866	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	1.1e-05	0.5927
Q8WVV9	HNRNPLL	Heterogeneous nuclear ribonucleoprotein L-like	0.0317	1.1729
Q86YM7	HOMER1	Homer protein homolog 1	5.5e-06	-0.6333
P84074	HPCA	Neuron-specific calcium-binding protein hippocalcin	0.0179	1.0503
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	1.0e-06	1.4829
O75506	HSBP1	Heat shock factor-binding protein 1	0.0161	-1.0979
Q99714	HSD17B10	3-hydroxyacyl-CoA dehydrogenase type-2	0.0359	0.6958
Q8NBQ5	HSD17B11	Estradiol 17-beta-dehydrogenase 11	0.0359	-0.4976
P51659	HSD17B4	Peroxisomal multifunctional enzyme type 2	8.9e-11	-0.8031
Q6YN16	HSDL2	Hydroxysteroid dehydrogenase-like protein 2	9.2e-06	0.8780
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	2.2e-16	0.7803
P08238	HSP90AB1	Heat shock protein HSP 90-beta	2.1e-06	0.7504
P14625	HSP90B1	Endoplasmic	2.1e-10	0.8587
Q0VDF9	HSPA14	Heat shock 70 kDa protein 14	0.0387	-1.5659
A0A0G2JIW1	HSPA1B	Heat shock 70 kDa protein 1B	8.4e-05	0.3263
P54652	HSPA2	Heat shock-related 70 kDa protein 2	5.7e-07	0.4869
P34932	HSPA4	Heat shock 70 kDa protein 4	1.3e-14	0.8323
O95757	HSPA4L	Heat shock 70 kDa protein 4L	3.7e-05	0.4617
P11142	HSPA8	Heat shock cognate 71 kDa protein	0.0174	0.1779
P38646	HSPA9	Stress-70 protein, mitochondrial	2.7e-08	0.5411
P10809	HSPD1	60 kDa heat shock protein, mitochondrial	0.0052	0.3368
P61604	HSPE1	10 kDa heat shock protein, mitochondrial	1.4e-06	1.0908
Q92598	HSPH1	Heat shock protein 105 kDa	4.8e-05	0.6149
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	0.0116	0.3522
Q9Y4L1	HYOU1	Hypoxia up-regulated protein 1	0.0248	0.2789
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	2.4e-05	0.8860
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	1.6e-06	0.8465
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	2.7e-06	1.1450

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	0.0023	0.5502
P78318	IGBP1	Immunoglobulin-binding protein 1	0.0099	-0.6495
Q96ID5	IGSF21	Immunoglobulin superfamily member 21	0.0131	-0.4717
Q969P0	IGSF8	Immunoglobulin superfamily member 8	0.0023	-0.7464
Q71H61	ILDR2	Immunoglobulin-like domain-containing receptor 2	0.0213	-1.1644
Q16352	INA	Alpha-internexin	0.0205	0.5948
H0Y8C6	IPO5	Importin-5 (Fragment)	0.0134	0.5367
P46940	IQGAP1	Ras GTPase-activating-like protein IQGAP1	0.0103	0.5884
Q8WZA9	IRGQ	Immunity-related GTPase family Q protein	5.4e-11	1.1299
H3BMU1	IST1	IST1 homolog (Fragment)	6.9e-04	-0.5664
Q8WXH2	JPH3	Junctophilin-3	0.0182	-0.6562
H7BXZ5	KALRN	Kalirin (Fragment)	0.0098	-0.5375
O60268	KIAA0513	Uncharacterized protein KIAA0513	0.001	0.6974
Q9HCM3	KIAA1549	UPF0606 protein KIAA1549	3.3e-04	-0.7482
Q6ZVL6	KIAA1549L	UPF0606 protein KIAA1549L	9.6e-06	-0.5539
P33176	KIF5B	Kinesin-1 heavy chain	1.7e-04	0.5303
O60282	KIF5C	Kinesin heavy chain isoform 5C	1.2e-05	0.4668
G3V3H3	KLC1	Kinesin light chain 1	6.0e-12	0.7456
Q76NI1	KNDC1	Kinase non-catalytic C-lobe domain-containing protein 1	1.6e-04	-0.6440
Q14974	KPNB1	Importin subunit beta-1	2.1e-04	0.6586
P01116	KRAS	GTPase KRas	7.1e-04	0.7627
Q04695	KRT17	Keratin, type I cytoskeletal 17	0.0165	0.8326
P04259	KRT6B	Keratin, type II cytoskeletal 6B	0.0017	0.6159
Q86UP2	KTN1	Kinectin	0.0077	0.3334
P28838	LAP3	Cytosol aminopeptidase	1.3e-04	0.6763
P00338	LDHA	L-lactate dehydrogenase A chain	2.2e-16	1.3462
P07195	LDHB	L-lactate dehydrogenase B chain	2.2e-16	1.4732
P09382	LGALS1	Galectin-1	1.2e-04	0.8178
Q3ZCW2	LGALSL	Galectin-related protein	0.006	1.8083
O95970	LGI1	Leucine-rich glioma-inactivated protein 1	1.2e-08	-0.6458
Q03252	LMNB2	Lamin-B2	0.0026	0.5375
Q5VUJ6	LRCH2	Leucine-rich repeat and calponin homology domain-containing protein 2	0.0308	-1.3853
P30533	LRPAP1	Alpha-2-macroglobulin receptor-associated protein	0.0411	0.5627
Q8N1G4	LRRC47	Leucine-rich repeat-containing protein 47	0.0058	0.5006
Q8IUZ0	LRRC49	Leucine-rich repeat-containing protein 49	0.0449	-1.0630
Q96NW7	LRRC7	Leucine-rich repeat-containing protein 7	0.0415	-0.6716
Q9Y608	LRRFIP2	Leucine-rich repeat flightless-interacting protein 2	0.0294	-0.5733
Q9NQ48	LZTFL1	Leucine zipper transcription factor-like protein 1	8.1e-06	0.7072
E9PGC8	MAP1A	Microtubule-associated protein 1A	2.9e-04	0.2225
Q02750	MAP2K1	Dual specificity mitogen-activated protein kinase 1	5.6e-04	0.9659
Q96T17	MAP7D2	MAP7 domain-containing protein 2	0.0059	0.6273
P28482	MAPK1	Mitogen-activated protein kinase 1	3.7e-13	0.8053

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
P27361	MAPK3	Mitogen-activated protein kinase 3	0.0029	0.6272
Q9UPY8	MAPRE3	Microtubule-associated protein RP/EB family member 3	4.3e-05	0.7721
A0A0G2JQJ7	MAPT	Microtubule-associated protein	3.7e-04	0.3749
P29966	MARCKS	Myristoylated alanine-rich C-kinase substrate	1.2e-06	1.3507
P49006	MARCKSL1	MARCKS-related protein	7.3e-04	1.4762
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	0.0229	0.6730
Q68D91	MBLAC2	Metallo-beta-lactamase domain-containing protein 2	0.0436	0.6348
P02686	MBP	Myelin basic protein	0.0354	0.4434
J3QKL5	MBP	Myelin basic protein (Fragment)	0.0354	0.4434
H7BYR8	MBP	Myelin basic protein	0.0354	0.4434
Q8IVS2	MCAT	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	0.0283	-0.6718
P40925	MDH1	Malate dehydrogenase, cytoplasmic	2.2e-16	1.3951
P48163	ME1	NADP-dependent malic enzyme	0.0014	1.0747
E9PD12	MIB2	E3 ubiquitin-protein ligase MIB2	0.0378	-0.8084
Q8TDZ2	MICAL1	[F-actin]-monooxygenase MICAL1	0.01	-0.5245
Q5R3B4	MPC2	Mitochondrial pyruvate carrier (Fragment)	0.0067	-0.8922
A0A494BZV2	MPRIIP	Myosin phosphatase Rho-interacting protein	0.023	-0.2988
P82650	MRPS22	28S ribosomal protein S22, mitochondrial	0.0469	-0.7190
P26038	MSN	Moesin	3.4e-04	0.7077
P58546	MTPN	Myotrophin	2.2e-04	1.9371
Q14764	MVP	Major vault protein	0.0213	0.7537
P35580	MYH10	Myosin-10	4.3e-16	-0.5951
P35579	MYH9	Myosin-9	1.1e-12	-0.5082
O14950	MYL12B	Myosin regulatory light chain 12B	3.8e-04	-1.0113
B7Z6Z4	MYL6	Myosin light polypeptide 6	1.2e-07	-0.7508
P14649	MYL6B	Myosin light chain 6B	7.6e-10	-1.2849
P24844	MYL9	Myosin regulatory light polypeptide 9	4.8e-05	-0.8652
E9PDF6	MYO1B	Unconventional myosin-Ib	0.0319	-0.3927
Q9Y4I1	MYO5A	Unconventional myosin-Va	7.1e-05	-0.2635
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	0.014	0.5643
Q99747	NAPG	Gamma-soluble NSF attachment protein	0.006	0.3627
P61601	NCALD	Neurocalcin-delta	1.6e-05	1.6642
Q9UBB6	NCDN	Neurochondrin	9.7e-05	1.1409
Q9Y2A7	NCKAP1	Nck-associated protein 1	0.0017	-0.1779
Q9GZM8	NDEL1	Nuclear distribution protein nudE-like 1	0.011	-0.4689
P28331	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.0065	-0.5312
O43181	NDUFS4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	0.0278	-0.9967
P07196	NEFL	Neurofilament light polypeptide	0.0119	0.5945
E7ESP9	NEFM	Neurofilament medium polypeptide	0.0016	0.4659
Q7Z3B1	NEGR1	Neuronal growth regulator 1	4.4e-08	-0.7633
P21359	NF1	Neurofibromin	0.0014	-0.4288
P51513	NOVA1	RNA-binding protein Nova-1	0.0251	0.3899

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
Q9UNW9	NOVA2	RNA-binding protein Nova-2	0.0392	0.5188
E9PLK3	NPEPPS	Aminopeptidase	1.1e-15	1.2965
Q8TAT6	NPLOC4	Nuclear protein localization protein 4 homolog	0.0014	0.6183
Q92686	NRGN	Neurogranin	0.013	1.3373
A0A1D5RMU6	NRXN1	Neurexin-1-beta	0.0013	-0.5882
P46459	NSF	Vesicle-fusing ATPase	0.0164	-0.2263
Q9UNZ2	NSFL1C	NSFL1 cofactor p47	0.0067	0.7284
Q9Y266	NUDC	Nuclear migration protein nudC	0.0015	0.5723
Q8WVJ2	NUDCD2	NudC domain-containing protein 2	0.0487	1.2863
A0A024RBG1	NUDT4B	Diphosphoinositol polyphosphate phosphohydrolase NUDT4B	0.0223	-0.9628
O15294	OGT	UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase 110 kDa subunit	2.5e-06	-0.7883
Q9NTK5	OLA1	Obg-like ATPase 1	2.9e-11	1.2373
Q99784	OLFM1	Noelin	2.2e-04	-0.5602
O95897	OLFM2	Noelin-2	2.6e-08	-0.7902
Q96PB7	OLFM3	Noelin-3	1.7e-07	-0.7895
O60313	OPA1	Dynamin-like 120 kDa protein, mitochondrial	0.0227	0.4303
P22059	OSBP	Oxysterol-binding protein 1	0.0278	0.5000
Q9BXW6	OSBPL1A	Oxysterol-binding protein-related protein 1	0.0305	2.0563
J3KR44	OTUB1	Ubiquitin thioesterase	0.0249	1.1216
P55809	OXCT1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	5.4e-10	0.9385
Q8N573	OXR1	Oxidation resistance protein 1	1.0e-12	0.6514
P07237	P4HB	Protein disulfide-isomerase	0.0082	0.3245
Q9Y2J8	PADI2	Protein-arginine deiminase type-2	4.2e-04	1.2187
P43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha	5.9e-06	0.8309
D6REB4	PAIP1	Polyadenylate-binding protein-interacting protein 1	0.0087	0.6909
Q13153	PAK1	Serine/threonine-protein kinase PAK 1	1.2e-04	0.6223
Q13177	PAK2	Serine/threonine-protein kinase PAK 2	3.6e-06	1.1189
O75914	PAK3	Serine/threonine-protein kinase PAK 3	7.1e-14	0.8833
O96013	PAK4	Serine/threonine-protein kinase PAK 4	0.0118	0.6463
K7ELW0	PARK7	Protein/nucleic acid deglycase DJ-1	0.0401	1.2756
P09874	PARP1	Poly [ADP-ribose] polymerase 1	5.7e-04	0.4669
E9PFP8	PCBP3	Poly(rC)-binding protein 3	5.1e-05	0.5823
P05165	PCCA	Propionyl-CoA carboxylase alpha chain, mitochondrial	0.0439	0.5643
Q9Y6V0	PCLO	Protein piccolo	1.0e-04	-0.2757
I3L1R7	PCYT2	Ethanolamine-phosphate cytidyltransferase	0.0119	0.8360
Q8WUM4	PDCD6IP	Programmed cell death 6-interacting protein	2.2e-16	1.0846
Q14123	PDE1C	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C	0.0351	0.8568
O00408	PDE2A	cGMP-dependent 3',5'-cyclic phosphodiesterase	0.0036	0.3824
Q07343	PDE4B	cAMP-specific 3',5'-cyclic phosphodiesterase 4B	0.03	1.1814

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P08559	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	5.0e-05	0.5964
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	8.2e-10	0.9769
O00330	PDHX	Pyruvate dehydrogenase protein X component, mitochondrial	1.1e-05	0.8427
P30101	PDIA3	Protein disulfide-isomerase A3	4.7e-08	0.8709
Q96GD0	PDXP	Pyridoxal phosphate phosphatase	0.0084	2.4754
Q15121	PEA15	Astrocytic phosphoprotein PEA-15	3.4e-05	1.5788
P30086	PEBP1	Phosphatidylethanolamine-binding protein 1	1.7e-07	1.5887
P17858	PFKL	ATP-dependent 6-phosphofructokinase, liver type	0.0037	0.6427
P08237	PFKM	ATP-dependent 6-phosphofructokinase, muscle type	4.2e-12	0.9579
P07737	PFN1	Profilin-1	1.1e-08	1.4517
C9J0J7	PFN2	Profilin	0.0022	0.4865
P35080	PFN2	Profilin-2	0.0022	0.4865
P18669	PGAM1	Phosphoglycerate mutase 1	9.8e-08	1.0096
Q96HS1	PGAM5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	0.004	-0.6462
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	6.6e-09	1.2192
P00558	PGK1	Phosphoglycerate kinase 1	2.2e-16	1.4977
O95336	PGLS	6-phosphogluconolactonase	0.0067	1.1396
A0A3B3ITK7	PGM1	Phosphoglucomutase-1	2.6e-04	1.8161
Q6PCE3	PGM2L1	Glucose 1,6-bisphosphate synthase	3.7e-06	1.4777
O43175	PHGDH	D-3-phosphoglycerate dehydrogenase	1.7e-11	1.1826
Q9NRX4	PHPT1	14 kDa phosphohistidine phosphatase	0.0043	1.3934
Q96FC7	PHYHIPL	Phytanoyl-CoA hydroxylase-interacting protein-like	2.2e-07	0.8832
P42356	PI4KA	Phosphatidylinositol 4-kinase alpha	7.9e-04	-0.3180
Q13492	PICALM	Phosphatidylinositol-binding clathrin assembly protein	0.013	0.3726
Q8TBX8	PIP4K2C	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	0.0174	-0.5791
Q9GZP4	PITHD1	PITH domain-containing protein 1	0.0068	0.8400
H3BR70	PKM	Pyruvate kinase	2.2e-16	1.4135
P14618	PKM	Pyruvate kinase PKM	2.2e-16	1.4135
Q9NQ66	PLCB1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1	2.2e-16	0.6577
H3BUD4	PLCL1	Phosphoinositide phospholipase C (Fragment)	0.0027	1.0297
A0A0A0MSQ0	PLS3	Plastin-3	7.2e-04	0.7657
Q9H2U2	PPA2	Inorganic pyrophosphatase 2, mitochondrial	0.0434	0.9289
Q08752	PPID	Peptidyl-prolyl cis-trans isomerase D	0.0359	0.5620
Q9Y3C6	PPIL1	Peptidyl-prolyl cis-trans isomerase-like 1	0.0109	0.9798
O75688	PPM1B	Protein phosphatase 1B	0.0061	0.9997
Q9Y570	PPME1	Protein phosphatase methylesterase 1	2.5e-04	1.1420
A0A3B3ISJ2	PPP1R13B	Apoptosis-stimulating of p53 protein 1 (Fragment)	0.0413	-0.4739
Q6ZMI0	PPP1R21	Protein phosphatase 1 regulatory subunit 21	0.0055	0.3583
Q15435	PPP1R7	Protein phosphatase 1 regulatory subunit 7	3.5e-06	0.7001

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
Q9ULJ8	PPP1R9A	Neurabin-1	0.0044	-0.5881
Q96SB3	PPP1R9B	Neurabin-2	1.1e-05	-0.7123
P30153	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	6.8e-11	0.5774
P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0.0246	0.6618
Q08209	PPP3CA	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	6.3e-10	0.9513
P16298	PPP3CB	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	1.7e-05	0.6529
F6U1T9	PPP3R1	Calcineurin subunit B type 1	0.0415	0.7660
H0YDU8	PPP5C	Serine/threonine-protein phosphatase (Fragment)	1.2e-04	0.5729
P32119	PRDX2	Peroxiredoxin-2	2.0e-05	0.6484
P30044	PRDX5	Peroxiredoxin-5, mitochondrial	1.9e-04	1.1255
P30041	PRDX6	Peroxiredoxin-6	9.2e-10	1.5580
P48147	PREP	Prolyl endopeptidase	1.8e-05	1.2246
P13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory subunit	0.0143	0.3222
P78527	PRKDC	DNA-dependent protein kinase catalytic subunit	0.0012	-0.2147
O14744	PRMT5	Protein arginine N-methyltransferase 5	0.0139	0.5118
P11908	PRPS2	Ribose-phosphate pyrophosphokinase 2	0.0077	0.7856
Q9Y617	PSAT1	Phosphoserine aminotransferase	1.6e-07	1.6974
B4DKF8	PSD3	PH and SEC7 domain-containing protein 3	0.0295	-0.1659
E5RJ29	PSD3	PH and SEC7 domain-containing protein 3	0.0295	-0.1659
P25786	PSMA1	Proteasome subunit alpha type-1	1.1e-04	0.7963
P25787	PSMA2	Proteasome subunit alpha type-2	0.0434	0.9824
P25788	PSMA3	Proteasome subunit alpha type-3	3.3e-04	0.6898
P25789	PSMA4	Proteasome subunit alpha type-4	0.0071	0.7406
P28066	PSMA5	Proteasome subunit alpha type-5	6.1e-04	0.9630
P60900	PSMA6	Proteasome subunit alpha type-6	0.0271	0.5458
O14818	PSMA7	Proteasome subunit alpha type-7	2.4e-04	0.6850
P28074	PSMB5	Proteasome subunit beta type-5	1.2e-05	1.0689
P28072	PSMB6	Proteasome subunit beta type-6	0.0393	0.9785
P62191	PSMC1	26S proteasome regulatory subunit 4	0.0159	0.3634
P35998	PSMC2	26S proteasome regulatory subunit 7	7.7e-05	0.5075
P62195	PSMC5	26S proteasome regulatory subunit 8	4.1e-05	0.5752
Q06323	PSME1	Proteasome activator complex subunit 1	0.0087	0.8923
H0YM70	PSME2	Proteasome activator complex subunit 2	0.0261	0.7410
A6NLN1	PTBP1	Polypyrimidine tract binding protein 1, isoform CRA_b	0.0049	0.4299
Q14914	PTGR1	Prostaglandin reductase 1	1.2e-05	1.2818
Q15257	PTPA	Serine/threonine-protein phosphatase 2A activator	9.4e-04	1.3407
Q06124	PTPN11	Tyrosine-protein phosphatase non-receptor type 11	0.0015	1.2156
Q9H3S7	PTPN23	Tyrosine-protein phosphatase non-receptor type 23	0.006	0.5115
Q15262	PTPRK	Receptor-type tyrosine-protein phosphatase kappa	0.0084	-0.7636
P11216	PYGB	Glycogen phosphorylase, brain form	3.0e-04	0.5311

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P11217	PYGM	Glycogen phosphorylase, muscle form	4.8e-05	0.7657
Q15907	RAB11B	Ras-related protein Rab-11B	3.0e-09	1.3314
X6RFL8	RAB14	Ras-related protein Rab-14 (Fragment)	1.3e-06	0.7031
P62820	RAB1A	Ras-related protein Rab-1A	6.4e-04	0.8045
P61019	RAB2A	Ras-related protein Rab-2A	4.5e-05	0.6631
Q15286	RAB35	Ras-related protein Rab-35	0.0445	0.4481
P20336	RAB3A	Ras-related protein Rab-3A	9.5e-06	1.4240
Q96E17	RAB3C	Ras-related protein Rab-3C	0.018	0.9340
P61020	RAB5B	Ras-related protein Rab-5B	0.0125	0.8557
P51148	RAB5C	Ras-related protein Rab-5C	8.2e-04	1.2839
Q9NRW1	RAB6B	Ras-related protein Rab-6B	0.0096	0.6586
P51149	RAB7A	Ras-related protein Rab-7a	2.4e-05	0.9885
Q15276	RABEP1	Rab GTPase-binding effector protein 1	0.0351	0.2753
Q3YEC7	RABL6	Rab-like protein 6	0.013	0.5374
P54727	RAD23B	UV excision repair protein RAD23 homolog B	6.9e-04	0.9441
P11233	RALA	Ras-related protein Ral-A	8.5e-09	0.7430
B5MDF5	RAN	GTP-binding nuclear protein Ran	2.0e-06	1.0514
P46060	RANGAP1	Ran GTPase-activating protein 1	0.0049	0.5267
P62834	RAP1A	Ras-related protein Rap-1A	2.0e-04	1.4620
P52306	RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1	9.5e-08	0.7938
A0A2R8YGD3	RAPGEF2	Rap guanine nucleotide exchange factor 2	0.0424	0.3837
Q8WZA2	RAPGEF4	Rap guanine nucleotide exchange factor 4	0.0022	-0.6817
Q9UJF2	RASAL2	Ras GTPase-activating protein nGAP	0.0265	-0.5217
Q8TDY2	RB1CC1	RB1-inducible coiled-coil protein 1	0.0169	-0.4971
Q15293	RCN1	Reticulocalbin-1	0.0496	0.5883
Q9HBH5	RDH14	Retinol dehydrogenase 14	0.0213	0.5756
A0A2R8Y5S7	RDX	Radixin	1.1e-04	0.3469
Q00765	REEP5	Receptor expression-enhancing protein 5	0.004	0.9097
Q8NFB8	REPS2	RalBP1-associated Eps domain-containing protein 2	0.0237	0.3497
P49758	RGS6	Regulator of G-protein signaling 6	0.0036	1.0011
P52758	RIDA	2-iminobutanoate/2-iminopropanoate deaminase	0.0094	1.5022
Q9UJD0	RIMS3	Regulating synaptic membrane exocytosis protein 3	0.0366	0.6499
P13489	RNH1	Ribonuclease inhibitor	0.0021	1.2510
O75116	ROCK2	Rho-associated protein kinase 2	2.0e-09	0.6575
P84098	RPL19	60S ribosomal protein L19	0.034	-0.6746
P62750	RPL23A	60S ribosomal protein L23a	2.1e-04	-0.6117
P61353	RPL27	60S ribosomal protein L27	0.0279	-0.8298
E9PLL6	RPL27A	60S ribosomal protein L27a	0.0229	-0.8620
P39023	RPL3	60S ribosomal protein L3	0.0159	-0.3648
H7C2W9	RPL31	60S ribosomal protein L31 (Fragment)	9.3e-04	-0.9350
Q9Y3U8	RPL36	60S ribosomal protein L36	0.0336	-0.9574
P36578	RPL4	60S ribosomal protein L4	0.0194	-0.4762
Q02878	RPL6	60S ribosomal protein L6	0.0256	-0.3917
P18124	RPL7	60S ribosomal protein L7	0.0153	-0.4298
P62424	RPL7A	60S ribosomal protein L7a	0.0305	-0.4556
P05388	RPLP0	60S acidic ribosomal protein P0	5.8e-05	-0.6536

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P05387	RPLP2	60S acidic ribosomal protein P2	9.3e-04	-0.9447
P39019	RPS19	40S ribosomal protein S19	2.3e-04	-0.5096
P60866	RPS20	40S ribosomal protein S20	0.0457	-0.5597
P61247	RPS3A	40S ribosomal protein S3a	0.0127	-0.3852
Q8N122	RPTOR	Regulatory-associated protein of mTOR	0.0109	0.5457
Q9Y3I0	RTCB	tRNA-splicing ligase RtcB homolog	0.0055	0.2872
Q16799	RTN1	Reticulon-1	0.0197	0.6256
O95197	RTN3	Reticulon-3	0.005	0.3759
Q9NQC3	RTN4	Reticulon-4	1.4e-06	0.4792
Q59EK9	RUNDC3A	RUN domain-containing protein 3A	0.0209	0.9482
Q99584	S100A13	Protein S100-A13	0.0025	0.9231
Q9NZJ4	SACS	Sacsin	5.4e-08	-0.6349
Q9Y3A5	SBDS	Ribosome maturation protein SBDS	0.0021	0.5310
Q8NBX0	SCCPDH	Saccharopine dehydrogenase-like oxidoreductase	2.5e-04	-0.9698
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	4.9e-04	0.6164
Q12765	SCRN1	Secernin-1	2.2e-04	1.1851
Q96GA7	SDSL	Serine dehydratase-like	0.0309	0.8458
O75396	SEC22B	Vesicle-trafficking protein SEC22b	0.0265	0.4947
F5H365	SEC23A	Protein transport protein SEC23	0.0434	0.7227
Q13228	SELENBP1	Methanethiol oxidase	2.1e-06	1.6758
A0A2R8Y4H2	SEPTIN3	Septin 3	1.8e-06	-0.5856
G3XAH0	SEPTIN5	HCG2002594, isoform CRA_c	0.003	-0.3591
Q99719	SEPTIN5	Septin-5	0.003	-0.3591
Q14141	SEPTIN6	Septin-6	2.9e-07	-0.6284
Q16181	SEPTIN7	Septin-7	1.5e-04	-0.3240
Q92599	SEPTIN8	Septin-8	2.1e-08	-0.5467
Q9UHD8	SEPTIN9	Septin-9	6.9e-04	-0.4038
A0A024R6I7	SERPINA1	Alpha-1-antitrypsin	0.0399	0.8116
P30740	SERPINB1	Leukocyte elastase inhibitor	0.0401	0.7949
P36955	SERPINF1	Pigment epithelium-derived factor	0.0063	0.8041
P23246	SFPQ	Splicing factor, proline- and glutamine-rich	0.0456	-0.3701
O43765	SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	0.001	0.7574
Q96EQ0	SGTB	Small glutamine-rich tetratricopeptide repeat-containing protein beta	0.0384	0.6582
Q9UJC5	SH3BGRL2	SH3 domain-binding glutamic acid-rich-like protein 2	0.0029	-0.9433
Q99961	SH3GL1	Endophilin-A2	2.2e-16	1.0444
Q99962	SH3GL2	Endophilin-A1	7.7e-11	0.8321
Q99963	SH3GL3	Endophilin-A3	6.3e-12	1.0671
Q96B97	SH3KBP1	SH3 domain-containing kinase-binding protein 1	1.9e-04	-0.4669
Q5TCZ1	SH3PXD2A	SH3 and PX domain-containing protein 2A	0.0035	-0.5390
Q9Y566	SHANK1	SH3 and multiple ankyrin repeat domains protein 1	0.0029	-0.6396
Q9UPX8	SHANK2	SH3 and multiple ankyrin repeat domains protein 2	1.1e-04	-0.6733
Q9BYB0	SHANK3	SH3 and multiple ankyrin repeat domains protein 3	5.9e-05	-0.7989
A0MZ66	SHTN1	Shootin-1	0.0107	0.5143
A0A087WYM3	SIRT2	NAD-dependent protein deacetylase	0.0213	0.9633

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
E5RJR5	SKP1	S-phase kinase-associated protein 1	0.0279	-0.3440
P55011	SLC12A2	Solute carrier family 12 member 2	0.0036	0.4765
Q02978	SLC25A11	Mitochondrial 2-oxoglutarate/malate carrier protein	4.1e-04	-0.9781
O75746	SLC25A12	Calcium-binding mitochondrial carrier protein Aralar1	0.0237	-0.5925
E9PJH7	SLC25A22	Mitochondrial glutamate carrier 1 (Fragment)	5.2e-04	-1.0657
Q00325	SLC25A3	Phosphate carrier protein, mitochondrial	4.0e-07	-1.1105
P12235	SLC25A4	ADP/ATP translocase 1	0.0095	-1.3297
Q96AG3	SLC25A46	Solute carrier family 25 member 46	0.0243	-0.6210
P12236	SLC25A6	ADP/ATP translocase 3	8.9e-06	-0.9785
Q9H2G2	SLK	STE20-like serine/threonine-protein kinase	0.0182	0.2757
Q8IYB5	SMAP1	Stromal membrane-associated protein 1	0.0447	0.5079
O60641	SNAP91	Clathrin coat assembly protein AP180	7.6e-07	0.6429
E7EPV7	SNCA	Alpha-synuclein	5.6e-13	1.6297
Q16143	SNCB	Beta-synuclein	7.7e-11	1.5759
O76070	SNCG	Gamma-synuclein	1.1e-04	1.1300
P08621	SNRNP70	U1 small nuclear ribonucleoprotein 70 kDa	0.0095	1.3711
P09012	SNRPA	U1 small nuclear ribonucleoprotein A	0.0345	0.7952
Q13596	SNX1	Sorting nexin-1	2.1e-05	0.7093
Q15036	SNX17	Sorting nexin-17	0.0273	-0.5856
Q96RF0	SNX18	Sorting nexin-18	9.8e-04	-0.6815
O60749	SNX2	Sorting nexin-2	0.0024	0.5892
Q9UNH7	SNX6	Sorting nexin-6	7.9e-04	0.7295
P04179	SOD2	Superoxide dismutase [Mn], mitochondrial	1.1e-04	1.0118
E9PJP2	SOGA3	Protein SOGA3	4.0e-07	0.6744
Q9BX66	SORBS1	Sorbin and SH3 domain-containing protein 1	1.3e-04	-0.6790
P02549	SPTA1	Spectrin alpha chain, erythrocytic 1	1.8e-10	-0.8842
A0A0D9SGF6	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	2.2e-16	-0.7423
P11277	SPTB	Spectrin beta chain, erythrocytic	1.0e-08	-0.6246
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	2.2e-16	-0.4225
O15020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	5.3e-05	-0.2257
Q9C0H9	SRCIN1	SRC kinase signaling inhibitor 1	2.0e-04	-0.4440
O43295	SRGAP3	SLIT-ROBO Rho GTPase-activating protein 3	0.0207	0.3612
P30626	SRI	Sorcin	9.1e-06	1.1702
P37108	SRP14	Signal recognition particle 14 kDa protein	0.038	0.9461
P61011	SRP54	Signal recognition particle 54 kDa protein	8.5e-05	0.6234
Q9UHB9	SRP68	Signal recognition particle subunit SRP68	0.0341	0.7819
O76094	SRP72	Signal recognition particle subunit SRP72	0.0028	0.6622
P50502	ST13	Hsc70-interacting protein	0.001	0.6447
Q92783	STAM	Signal transducing adapter molecule 1	0.0096	0.4769
P31948	STIP1	Stress-induced-phosphoprotein 1	0.0015	0.4117
P16949	STMN1	Stathmin	9.2e-04	1.2763
E5RGX5	STMN2	Stathmin	1.5e-07	1.8456
Q86Y82	STX12	Syntaxin-12	2.2e-04	0.5358
P61764	STXBP1	Syntaxin-binding protein 1	8.1e-16	0.6849
A0A1B0GTP9	STXBP1	Syntaxin-binding protein 1	8.1e-16	0.6849

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
A0A2R8Y6Y7	SUCLA2	Succinate-CoA ligase [ADP-forming] subunit beta, mitochondrial	0.0015	0.8319
Q9Y2Z0	SUGT1	Protein SGT1 homolog	0.0475	0.6373
Q9Y5B9	SUPT16H	FACT complex subunit SPT16	0.0094	0.9033
P17600	SYN1	Synapsin-1	0.0028	-0.3779
Q8NF91	SYNE1	Nesprin-1	2.5e-04	-0.3229
C9JFZ1	SYNJ1	Synaptojanin-1	4.4e-11	0.5674
O15061	SYNM	Synemin	0.0048	0.4973
Q8N3V7	SYNPO	Synaptopodin	2.2e-16	-1.4218
H0Y9Y3	SYNPO2	Synaptopodin-2 (Fragment)	0.0193	-0.8938
P21579	SYT1	Synaptotagmin-1	1.8e-10	-1.0908
O00445	SYT5	Synaptotagmin-5	0.0116	-0.5687
Q9UI15	TAGLN3	Transgelin-3	0.0082	0.5313
P37837	TALDO1	Transaldolase	5.4e-10	1.4577
J3KTM5	TANC2	Protein TANC2 (Fragment)	0.0219	-0.4501
Q9HCD6	TANC2	Protein TANC2	0.0219	-0.4501
A0A494C0X0	TBCB	Tubulin-folding cofactor B	0.001	1.1874
A0A2R8Y5Q8	TBCE	Tubulin-specific chaperone E	0.0021	1.4547
Q00059	TFAM	Transcription factor A, mitochondrial	2.3e-08	-1.0428
P29401	TKT	Transketolase	2.2e-16	1.4825
Q9Y490	TLN1	Talin-1	1.1e-08	0.4769
Q9Y4G6	TLN2	Talin-2	2.2e-16	0.5190
P28289	TMOD1	Tropomodulin-1	5.4e-06	-0.8035
Q9NZR1	TMOD2	Tropomodulin-2	3.0e-12	-0.8838
P62328	TMSB4X	Thymosin beta-4	0.0274	1.8072
Q96JJ7	TMX3	Protein disulfide-isomerase TMX3	0.0305	0.9532
Q92752	TNR	Tenascin-R	0.0032	-0.2628
Q9H0E2	TOLLIP	Toll-interacting protein	6.7e-04	0.8015
O60784	TOM1	Target of Myb protein 1	0.0189	0.9272
Q15785	TOMM34	Mitochondrial import receptor subunit TOM34	0.0036	-0.4776
O94826	TOMM70	Mitochondrial import receptor subunit TOM70	0.0046	0.4257
Q16890	TPD52L1	Tumor protein D53	0.0233	-0.5979
P60174	TPI1	Triosephosphate isomerase	2.2e-16	1.4523
A0A087WWU8	TPM3	Tropomyosin alpha-3 chain	0.0109	-0.3881
P06753	TPM3	Tropomyosin alpha-3 chain	0.0109	-0.3881
A0A494C1B8	TPP2	Tripeptidyl-peptidase 2	0.0124	0.4996
Q9BW30	TPPP3	Tubulin polymerization-promoting protein family member 3	0.0035	0.8277
Q5W0H4	TPT1	Translationally-controlled tumor protein	8.3e-08	1.2758
Q12931	TRAP1	Heat shock protein 75 kDa, mitochondrial	0.0162	0.7083
H3BP13	TRAPPC2L	Trafficking protein particle complex subunit 2-like protein	0.0038	-0.5716
O43617	TRAPPC3	Trafficking protein particle complex subunit 3	0.0073	-0.5065
Q9Y296	TRAPPC4	Trafficking protein particle complex subunit 4	0.0109	-0.5712
Q9C040	TRIM2	Tripartite motif-containing protein 2	0.0192	0.3257
Q96Q11	TRNT1	CCA tRNA nucleotidyltransferase 1, mitochondrial	0.0213	0.8691

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P43897	TSFM	Elongation factor Ts, mitochondrial	0.0294	-0.8669
Q7Z4L5	TTC21B	Tetratricopeptide repeat protein 21B	0.0269	-0.7990
Q13509	TUBB3	Tubulin beta-3 chain	5.8e-04	0.5857
P49411	TUFM	Elongation factor Tu, mitochondrial	0.0147	-0.5705
Q6IBS0	TWF2	Twinfilin-2	0.0489	0.4215
P40222	TXLNA	Alpha-taxilin	7.1e-05	-0.5656
Q9BRA2	TXNDC17	Thioredoxin domain-containing protein 17	0.0392	1.2653
Q8NBS9	TXNDC5	Thioredoxin domain-containing protein 5	0.0051	0.8365
Q43396	TXNL1	Thioredoxin-like protein 1	0.0135	0.5699
F8W809	TXNRD1	Thioredoxin reductase 1, cytoplasmic	6.5e-05	1.2041
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	3.3e-15	1.4128
P68036	UBE2L3	Ubiquitin-conjugating enzyme E2 L3	5.0e-04	0.7797
P61081	UBE2M	NEDD8-conjugating enzyme Ubc12	8.6e-06	0.8960
P61088	UBE2N	Ubiquitin-conjugating enzyme E2 N	6.8e-12	1.2739
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	1.9e-06	0.8669
Q15819	UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2	0.0025	1.6999
Q05086	UBE3A	Ubiquitin-protein ligase E3A	0.0284	0.8519
O14562	UBFD1	Ubiquitin domain-containing protein UBFD1	0.0216	0.5898
P09936	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	9.7e-10	1.6288
O94874	UFL1	E3 UFM1-protein ligase 1	0.0175	0.6009
H0Y614	UFM1	Ubiquitin-fold modifier 1 (Fragment)	0.0278	0.7961
Q9NYU2	UGGT1	UDP-glucose:glycoprotein glucosyltransferase 1	0.0118	0.6524
E7EUC7	UGP2	UTP-glucose-1-phosphate uridylyltransferase	6.4e-11	1.0628
O60763	USO1	General vesicular transport factor p115	1.2e-06	0.7034
P54578	USP14	Ubiquitin carboxyl-terminal hydrolase 14	3.5e-05	0.7077
Q8NFA0	USP32	Ubiquitin carboxyl-terminal hydrolase 32	0.0213	1.1277
Q93009	USP7	Ubiquitin carboxyl-terminal hydrolase 7	0.0051	0.5556
P40818	USP8	Ubiquitin carboxyl-terminal hydrolase 8	0.0102	-0.4310
Q93008	USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	0.0239	0.4187
O95292	VAPB	Vesicle-associated membrane protein-associated protein B/C	0.0092	0.3971
Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	0.0065	0.9272
Q9HCJ6	VAT1L	Synaptic vesicle membrane protein VAT-1 homolog-like	0.0489	0.7047
P55072	VCP	Transitional endoplasmic reticulum ATPase	1.6e-05	0.5037
F2Z3A6	VEZT	Vezatin	0.0272	-0.8457
P08670	VIM	Vimentin	0.0022	0.4879
Q96RL7	VPS13A	Vacuolar protein sorting-associated protein 13A	5.6e-07	0.7634
Q9UBQ0	VPS29	Vacuolar protein sorting-associated protein 29	0.0126	0.7748
Q96QK1	VPS35	Vacuolar protein sorting-associated protein 35	0.0036	0.6484
Q9NRW7	VPS45	Vacuolar protein sorting-associated protein 45	0.0058	0.4025
Q9Y2B5	VPS9D1	VPS9 domain-containing protein 1	0.0443	0.8722
P62760	VSNL1	Visinin-like protein 1	9.2e-05	0.7112
A0A087WY55	VTA1	Chromosome 6 open reading frame 55, isoform CRA_b	2.7e-04	0.5833

Table S1: Significant differentially expressed proteins from children (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
O75083	WDR1	WD repeat-containing protein 1	2.2e-16	1.0150
E7ESC9	WDR17	WD repeat-containing protein 17	0.0161	0.4442
Q9NQW7	XPNPEP1	Xaa-Pro aminopeptidase 1	0.007	1.4331
O14980	XPO1	Exportin-1	0.0489	0.7697
E7ESC6	XPO7	Exportin-7	2.0e-06	1.1659
P13010	XRCC5	X-ray repair cross-complementing protein 5	4.3e-09	0.5722
P12956	XRCC6	X-ray repair cross-complementing protein 6	4.3e-08	0.5716
O15498	YKT6	Synaptobrevin homolog YKT6	0.0015	0.5613
P31946	YWHAB	14-3-3 protein beta/alpha	0.0015	0.5866
P62258	YWHAE	14-3-3 protein epsilon	3.8e-04	0.4311
P61981	YWHAG	14-3-3 protein gamma	0.0361	0.5078
Q04917	YWHAH	14-3-3 protein eta	2.6e-06	0.7080
P27348	YWHAQ	14-3-3 protein theta	0.0075	0.6862
P63104	YWHAZ	14-3-3 protein zeta/delta	5.6e-09	0.6579
Q96GY0	ZC2HC1A	Zinc finger C2HC domain-containing protein 1A	1.0e-04	0.6627
H3BRB6	ZNRF1	E3 ubiquitin-protein ligase ZNRF1	0.03	-1.0801

812 proteins, 574 up-regulated, 238 down-regulated

Table S2: Significant differentially expressed proteins from adults

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
P01023	A2M	Alpha-2-macroglobulin	9.7e-04	0.7428
Q6H8Q1	ABLIM2	Actin-binding LIM protein 2	0.0263	-0.3344
P53396	ACLY	ATP-citrate synthase	0.0049	0.3086
H9KV75	ACTN1	Alpha-actinin-1	2.9e-10	-0.5718
P12814	ACTN1	Alpha-actinin-1	2.9e-10	-0.5718
P35609	ACTN2	Alpha-actinin-2	0.0259	-0.2705
O43707	ACTN4	Alpha-actinin-4	1.5e-05	-0.5032
Q9P0K1	ADAM22	Disintegrin and metalloproteinase domain-containing protein 22	0.0108	-0.5594
P35611	ADD1	Alpha-adducin	0.0322	-0.2796
P35612	ADD2	Beta-adducin	7.9e-04	-0.3572
Q8IVF2	AHNAK2	Protein AHNAK2	4.7e-08	-0.6383
Q02952	AKAP12	A-kinase anchor protein 12	7.8e-10	-0.6510
Q02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	2.3e-04	0.6756
P49418	AMPH	Amphiphysin	4.3e-06	-0.4652
P16157	ANK1	Ankyrin-1	2.2e-16	1.1527
Q01484	ANK2	Ankyrin-2	2.2e-16	-0.4209
P08133	ANXA6	Annexin A6	0.0055	0.4388
O95782	AP2A1	AP-2 complex subunit alpha-1	2.1e-07	-0.3258
A0A087X253	AP2B1	AP complex subunit beta	6.8e-10	-0.3468
Q17R89	ARHGAP44	Rho GTPase-activating protein 44	0.0356	-0.5033
V9GYM8	ARHGEF2	Rho guanine nucleotide exchange factor 2	0.0477	-0.3234
Q92747	ARPC1A	Actin-related protein 2/3 complex subunit 1A	0.0289	-0.2216
O15144	ARPC2	Actin-related protein 2/3 complex subunit 2	8.5e-05	-0.4081
P25705	ATP5F1A	ATP synthase subunit alpha, mitochondrial	0.0473	0.2448
Q93050	ATP6V0A1	V-type proton ATPase 116 kDa subunit a isoform 1	0.0022	-0.4285
F5GYQ1	ATP6V0D1	V-type proton ATPase subunit	0.0227	-0.5312
P38606	ATP6V1A	V-type proton ATPase catalytic subunit A	0.0044	-0.2852
Q9Y2Q0	ATP8A1	Phospholipid-transporting ATPase IA	0.0012	0.4262
Q13825	AUH	Methylglutaconyl-CoA hydratase, mitochondrial	0.0391	-0.3307
P80723	BASP1	Brain acid soluble protein 1	1.6e-08	-0.7159
O00499	BIN1	Myc box-dependent-interacting protein 1	0.0228	-0.4134
Q9UPA5	BSN	Protein bassoon	2.0e-14	-0.5702
A0A1B0GUL6	BTBD8	BTB/POZ domain-containing protein 8	5.4e-04	-0.9376
P01024	C3	Complement C3	3.3e-04	0.8051
P22748	CA4	Carbonic anhydrase 4	0.0053	-0.6880
P54289	CACNA2D1	Voltage-dependent calcium channel subunit alpha-2/delta-1	2.0e-04	-0.4247
Q16566	CAMK4	Calcium/calmodulin-dependent protein kinase type IV	0.0404	-0.3555
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	0.0199	-0.6545
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	0.034	-0.6189
B1AK88	CAPZB	F-actin-capping protein subunit beta	0.0139	-0.3013
P47756	CAPZB	F-actin-capping protein subunit beta	0.0139	-0.3013
Q8WXD9	CASKIN1	Caskin-1	4.9e-04	-0.5270

Table S2: Significant differentially expressed proteins from adults (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
Q5SW79	CEP170	Centrosomal protein of 170 kDa	0.0036	-0.3472
Q9Y4F5	CEP170B	Centrosomal protein of 170 kDa protein B	0.0332	-0.3300
Q14008	CKAP5	Cytoskeleton-associated protein 5	7.8e-04	-0.2398
P12277	CKB	Creatine kinase B-type	0.0261	0.5775
P30622	CLIP1	CAP-Gly domain-containing linker protein 1	0.0204	-0.3180
Q9UDT6	CLIP2	CAP-Gly domain-containing linker protein 2	2.6e-04	-0.3796
P09543	CNP	2',3'-cyclic-nucleotide 3'-phosphodiesterase	7.5e-04	0.3815
Q12860	CNTN1	Contactin-1	1.9e-06	-0.4092
Q05707	COL14A1	Collagen alpha-1(XIV) chain	1.8e-05	0.7599
P02452	COL1A1	Collagen alpha-1(I) chain	0.0108	1.1134
Q9ULV4	CORO1C	Coronin-1C	0.0058	-0.3321
P29762	CRABP1	Cellular retinoic acid-binding protein 1	0.0088	1.6025
P02511	CRYAB	Alpha-crystallin B chain	0.001	0.6200
Q14247	CTTN	Src substrate cortactin	1.1e-06	-0.7194
Q96F07	CYFIP2	Cytoplasmic FMR1-interacting protein 2	0.0228	-0.1842
Q16643	DBN1	Drebrin	1.9e-04	-0.5681
P81605	DCD	Dermcidin	0.0015	-0.7000
Q13561	DCTN2	Dynactin subunit 2	0.0304	-0.3251
O00571	DDX3X	ATP-dependent RNA helicase DDX3X	0.0475	-0.3185
Q8TDJ6	DMXL2	DmX-like protein 2	1.4e-07	-0.3172
O14576	DYNC1H1	Cytoplasmic dynein 1 intermediate chain 1	0.001	-0.7617
Q9Y6G9	DYNC1LI1	Cytoplasmic dynein 1 light intermediate chain 1	1.5e-05	-0.4682
O43237	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	1.8e-04	-0.4315
O60869	EDF1	Endothelial differentiation-related factor 1	0.0092	-0.8558
Q96C19	EFHD2	EF-hand domain-containing protein D2	0.0119	-0.8062
Q9H4M9	EHD1	EH domain-containing protein 1	7.8e-04	0.6610
Q9NZN4	EHD2	EH domain-containing protein 2	0.0139	0.4941
A8MUM1	EIPR1	EARP and GARP complex-interacting protein 1	0.0325	-0.5040
A0A2R8YD30	EPB41	Erythrocyte membrane protein band 4.1 (Elliptocytosis 1, RH-linked), isoform CRA_e	6.3e-12	1.1333
A8K968	EPB41L3	Band 4.1-like protein 3	0.0445	-0.2408
Q9Y2J2	EPB41L3	Band 4.1-like protein 3	0.0445	-0.2408
P16452	EPB42	Erythrocyte membrane protein band 4.2	0.0013	1.2109
Q9UBC2	EPS15L1	Epidermal growth factor receptor substrate 15-like 1	3.8e-04	-0.5144
Q9BSJ8	ESYT1	Extended synaptotagmin-1	0.0139	0.3806
A0A499FIX8	ESYT2	Extended synaptotagmin-2	0.0287	0.3802
Q9UI08	EVL	Ena/VASP-like protein	0.0027	-0.5963
P00488	F13A1	Coagulation factor XIII A chain	0.0323	1.3253
Q9NSD9	FARSB	Phenylalanine-tRNA ligase beta subunit	0.0344	-0.2818
P49327	FASN	Fatty acid synthase	0.0335	0.3050
Q8TF61	FBXO41	F-box only protein 41	0.0119	-0.4374
P02671	FGA	Fibrinogen alpha chain	2.8e-05	1.2400
P02675	FGB	Fibrinogen beta chain	0.0097	1.0210
C9JEU5	FGG	Fibrinogen gamma chain	6.0e-05	1.2511
Q00688	FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	9.7e-04	-0.7519
Q9NZ56	FMN2	Formin-2	0.0333	-0.4679

Table S2: Significant differentially expressed proteins from adults (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	0.0449	0.4339
P17677	GAP43	Neuromodulin	2.5e-04	-1.1782
Q8TB36	GDAP1	Ganglioside-induced differentiation-associated protein 1	0.0046	0.5644
K7EMP8	GFAP	Glial fibrillary acidic protein	8.3e-05	0.4318
A0A2R8YDT1	GLUL	Glutamine synthetase	5.5e-04	-0.6963
Q7Z2K8	GPRIN1	G protein-regulated inducer of neurite outgrowth 1	2.9e-05	-0.4745
H0Y972	GRIA2	Glutamate receptor 2 (Fragment)	1.1e-04	-0.3377
P42262	GRIA2	Glutamate receptor 2	1.1e-04	-0.3377
P42263	GRIA3	Glutamate receptor 3	0.0183	-0.3875
P48058	GRIA4	Glutamate receptor 4	0.0203	-0.3301
Q14832	GRM3	Metabotropic glutamate receptor 3	0.0244	-0.3372
A0A3B3ITW1	GSK3B	Glycogen synthase kinase-3 beta	0.0316	-0.8194
P15170	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0.0364	0.3503
E9PHN7	GSTM2	Glutathione S-transferase Mu 2	0.0341	0.8401
H0YFD6	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	1.2e-06	0.3657
P02042	HBD	Hemoglobin subunit delta	2.9e-10	1.6059
P19367	HK1	Hexokinase-1	4.9e-05	0.3367
F8W6I7	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	0.0123	-0.4814
B4DY08	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	0.0021	-0.6128
H0Y8G5	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.0057	-0.4471
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	3.2e-04	-0.4930
O43390	HNRNPR	Heterogeneous nuclear ribonucleoprotein R	0.0382	-0.4611
P00738	HP	Haptoglobin	0.0228	1.1207
P51659	HSD17B4	Peroxisomal multifunctional enzyme type 2	0.0108	-0.2603
Q3SXM5	HSDL1	Inactive hydroxysteroid dehydrogenase-like protein 1	0.0203	0.7759
P11142	HSPA8	Heat shock cognate 71 kDa protein	0.0263	-0.2189
P10809	HSPD1	60 kDa heat shock protein, mitochondrial	0.0053	0.2885
P42858	HTT	Huntingtin	0.0215	0.2960
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	0.0014	0.5057
Q96ID5	IGSF21	Immunoglobulin superfamily member 21	0.0274	-0.5569
A0A0A0MTH3	ILK	Integrin-linked protein kinase	0.0108	0.4199
B9A067	IMMT	MICOS complex subunit MIC60	0.02	0.2241
A0A3F2YNW8	ITPR1	Inositol 1,4,5-trisphosphate receptor type 1	0.0236	0.3216
Q15811	ITSN1	Intersectin-1	0.01	-0.2580
Q6ZVL6	KIAA1549L	UPF0606 protein KIAA1549L	3.9e-04	-0.5817
P13646	KRT13	Keratin, type I cytoskeletal 13	0.0059	-1.4276
P02533	KRT14	Keratin, type I cytoskeletal 14	4.9e-05	-0.9068
Q04695	KRT17	Keratin, type I cytoskeletal 17	0.0228	-1.2949
P13647	KRT5	Keratin, type II cytoskeletal 5	5.4e-04	-0.8061
P04259	KRT6B	Keratin, type II cytoskeletal 6B	1.6e-04	-0.9768
Q14847	LASP1	LIM and SH3 domain protein 1	0.0023	-0.5872
O95970	LGI1	Leucine-rich glioma-inactivated protein 1	6.6e-04	-0.4280
P02545	LMNA	Prelamin-A/C	2.8e-05	-0.6551

Table S2: Significant differentially expressed proteins from adults (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P20700	LMNB1	Lamin-B1	0.01	-0.4531
Q13449	LSAMP	Limbic system-associated membrane protein	0.0479	-0.4633
E7EQB2	LTF	Lactotransferrin (Fragment)	8.9e-06	1.1882
E9PGC8	MAP1A	Microtubule-associated protein 1A	2.2e-16	-0.6578
P46821	MAP1B	Microtubule-associated protein 1B	2.2e-16	-0.6519
P11137	MAP2	Microtubule-associated protein 2	2.2e-16	-0.7282
F8W9U4	MAP4	Microtubule-associated protein	1.6e-08	-0.5757
P27816	MAP4	Microtubule-associated protein 4	1.6e-08	-0.5757
Q96JE9	MAP6	Microtubule-associated protein 6	2.2e-16	-0.9282
A0A0G2JQJ7	MAPT	Microtubule-associated protein	1.5e-08	-0.5721
Q9P0L2	MARK1	Serine/threonine-protein kinase MARK1	0.0301	-0.3550
Q86UE4	MTDH	Protein LYRIC	0.0297	-0.9413
P43490	NAMPT	Nicotinamide phosphoribosyltransferase	1.7e-04	0.5761
A0A0D9SF30	NCAM1	Neural cell adhesion molecule 1 (Fragment)	0.0073	-0.3008
P13591	NCAM1	Neural cell adhesion molecule 1	0.0073	-0.3008
Q9Y2A7	NCKAP1	Nck-associated protein 1	1.0e-05	-0.2638
P19338	NCL	Nucleolin	0.0092	-0.4099
Q16795	NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.0445	0.5646
P12036	NEFH	Neurofilament heavy polypeptide	0.0087	-0.7125
P07196	NEFL	Neurofilament light polypeptide	0.0014	-0.6389
P07197	NEFM	Neurofilament medium polypeptide	1.2e-06	-0.6722
O94856	NFASC	Neurofascin	5.5e-04	-0.5325
P06748	NPM1	Nucleophosmin	0.0378	-0.5093
O95897	OLFM2	Noelin-2	2.9e-04	-0.6660
O60313	OPA1	Dynamin-like 120 kDa protein, mitochondrial	0.0015	0.2875
Q14982	OPCML	Opioid-binding protein/cell adhesion molecule	0.0074	-0.5459
P55809	OXCT1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	6.3e-04	0.7805
Q9UQ80	PA2G4	Proliferation-associated protein 2G4	0.0028	-0.5457
A0A087WTT1	PABPC1	Polyadenylate-binding protein	0.0015	-0.4240
Q13310	PABPC4	Polyadenylate-binding protein 4	0.0264	-0.3896
Q9BY11	PACSIN1	Protein kinase C and casein kinase substrate in neurons protein 1	6.5e-07	-0.6005
Q9Y2J8	PADI2	Protein-arginine deiminase type-2	9.8e-04	0.8023
O75781	PALM	Paralemmin-1	8.9e-06	-0.6310
Q96AQ6	PBXIP1	Pre-B-cell leukemia transcription factor-interacting protein 1	0.0063	0.5467
P11498	PC	Pyruvate carboxylase, mitochondrial	4.5e-05	0.4919
Q9Y6V0	PCLO	Protein piccolo	2.2e-16	-0.5516
P17858	PFKL	ATP-dependent 6-phosphofructokinase, liver type	0.0061	0.3717
Q6PCE3	PGM2L1	Glucose 1,6-bisphosphate synthase	0.0101	0.6420
Q9NQ66	PLCB1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1	6.0e-05	-0.4088
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	1.5e-04	-0.4708
Q9ULJ8	PPP1R9A	Neurabin-1	6.6e-04	-0.6727

Table S2: Significant differentially expressed proteins from adults (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log2(A/C)
Q96SB3	PPP1R9B	Neurabin-2	0.0178	-0.4797
P32119	PRDX2	Peroxiredoxin-2	0.0132	0.3970
O14744	PRMT5	Protein arginine N-methyltransferase 5	6.5e-06	0.6228
Q9Y617	PSAT1	Phosphoserine aminotransferase	0.0099	0.7084
E5RJ29	PSD3	PH and SEC7 domain-containing protein 3	0.0203	-0.2275
B4DKF8	PSD3	PH and SEC7 domain-containing protein 3	0.0203	-0.2275
Q8WXF1	PSPC1	Paraspeckle component 1	0.0013	-0.6474
A0A494C0U4	PTPRZ1	Receptor-type tyrosine-protein phosphatase zeta	1.6e-04	-0.4718
P11216	PYGB	Glycogen phosphorylase, brain form	3.6e-08	0.4505
Q96TC7	RMDN3	Regulator of microtubule dynamics protein 3	0.016	0.5359
Q9Y2J0	RPH3A	Rabphilin-3A	3.8e-04	-0.5045
P26373	RPL13	60S ribosomal protein L13	0.0113	-0.7806
O95248	SBF1	Myotubularin-related protein 5	0.0247	0.3128
Q8NBX0	SCCPDH	Saccharopine dehydrogenase-like oxidoreductase	0.0297	0.4766
D6RER5	SEPTIN11	Septin 11	0.0149	-0.5042
A0A2R8Y4H2	SEPTIN3	Septin 3	7.7e-07	-0.5529
G3XAH0	SEPTIN5	HCG2002594, isoform CRA_c	2.8e-07	-0.5091
Q99719	SEPTIN5	Septin-5	2.8e-07	-0.5091
Q14141	SEPTIN6	Septin-6	6.5e-07	-0.6028
Q16181	SEPTIN7	Septin-7	3.0e-10	-0.5180
Q92599	SEPTIN8	Septin-8	9.7e-04	-0.3968
Q9UHD8	SEPTIN9	Septin-9	5.1e-11	-0.6365
A0A024R6I7	SERPINA1	Alpha-1-antitrypsin	0.0049	1.0232
P23246	SFPQ	Splicing factor, proline- and glutamine-rich	0.0074	-0.5707
Q9BQI5	SGIP1	SH3-containing GRB2-like protein 3-interacting protein 1	3.7e-08	-0.7409
Q96B97	SH3KBP1	SH3 domain-containing kinase-binding protein 1	0.0379	-0.3615
Q9H2X9	SLC12A5	Solute carrier family 12 member 5	0.0068	-0.3207
Q00325	SLC25A3	Phosphate carrier protein, mitochondrial	0.0137	0.4015
P02730	SLC4A1	Band 3 anion transport protein	1.2e-05	1.2039
Q9BX66	SORBS1	Sorbin and SH3 domain-containing protein 1	0.0044	-0.4296
P02549	SPTA1	Spectrin alpha chain, erythrocytic 1	2.2e-16	1.3582
A0A0D9SGF6	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	2.2e-16	-0.3053
P11277	SPTB	Spectrin beta chain, erythrocytic	2.2e-16	1.2303
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	1.9e-12	-0.2467
O15020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	0.0287	-0.1381
P27105	STOM	Erythrocyte band 7 integral membrane protein	0.0122	1.0906
P61764	STXBP1	Syntaxin-binding protein 1	5.4e-04	0.4252
A0A1B0GTP9	STXBP1	Syntaxin-binding protein 1	5.4e-04	0.4252
P53999	SUB1	Activated RNA polymerase II transcriptional coactivator p15	0.0098	-0.6136
P17600	SYN1	Synapsin-1	2.8e-11	-0.5887
C9JFZ1	SYNJ1	Synaptojanin-1	3.8e-04	-0.3585
Q8N3V7	SYNPO	Synaptopodin	1.4e-08	-0.7932
P21579	SYT1	Synaptotagmin-1	1.6e-04	-0.4968
Q9UI15	TAGLN3	Transgelin-3	3.5e-04	-0.8186

Table S2: Significant differentially expressed proteins from adults (*continued*)

UniProtID	Gene Name	Description	Adjusted p-value	log ₂ (A/C)
P21980	TGM2	Protein-glutamine gamma-glutamyltransferase 2	0.0128	1.0116
J3QRJ3	THY1	Thy-1 membrane glycoprotein	0.0418	-0.6389
Q9UDY2	TJP2	Tight junction protein ZO-2	0.0297	0.3998
P29401	TKT	Transketolase	8.1e-05	0.5434
Q9NZR1	TMOD2	Tropomodulin-2	1.9e-06	-0.7184
P67936	TPM4	Tropomyosin alpha-4 chain	0.0023	-0.7267
Q13885	TUBB2A	Tubulin beta-2A chain	8.3e-05	0.4569
Q13509	TUBB3	Tubulin beta-3 chain	0.0481	0.4298
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	4.9e-05	0.8526
Q14157	UBAP2L	Ubiquitin-associated protein 2-like	0.0215	-0.5814
P09936	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.0203	0.9351

226 proteins, 73 up-regulated, 153 down-regulated

Table S3: Significantly enriched Reactome pathways for proteins ranked by log2(fold-change) in children

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Unblocking of NMDA receptors, glutamate binding and activation	0.0000	2.3105	14	ACTN2, CAMK2A, CAMK2B, DLG1, DLG3, GRIA1, GRIA2, GRIA3, GRIA4, GRIN1, GRIN2A, GRIN2B, LRRC7, NEFL
Negative regulation of NMDA receptor-mediated neuronal transmission	0.0006	2.1498	14	ACTN2, CAMK1, CAMK2A, CAMK2B, CAMK4, DLG1, DLG3, GRIN1, GRIN2A, GRIN2B, LRRC7, NEFL, PPM1E, PPM1F
Long-term potentiation	0.0011	2.1379	14	ACTN2, CAMK2A, CAMK2B, DLG1, DLG3, GRIA1, GRIA2, GRIN1, GRIN2A, GRIN2B, LRRC7, NEFL, NRGN, SRC
Activation of AMPA receptors	0.0035	1.9252	4	GRIA1, GRIA2, GRIA3, GRIA4
Ras activation upon Ca ²⁺ influx through NMDA receptor	0.0499	1.8620	11	ACTN2, CAMK2A, CAMK2B, DLG1, DLG3, GRIN1, GRIN2B, LRRC7, NEFL, RASGRF1, RASGRF2
Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	0.0007	1.7803	3	SLC25A4, SLC25A5, SLC25A6
Viral mRNA Translation	0.0030	1.7624	50	DNAJC3, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Eukaryotic Translation Termination	0.0030	1.7263	52	APEH, GSPT1, GSPT2, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Selenocysteine synthesis	0.0041	1.7164	51	EEFSEC, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SEPHS2

Table S3: Significantly enriched Reactome pathways for proteins ranked by log2(fold-change) in children (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Response of EIF2AK4 (GCN2) to amino acid deficiency	0.0030	1.7114	54	ASNS, EIF2S1, EIF2S2, EIF2S3, GCN1, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Peptide chain elongation	0.0037	1.7067	51	EEF1A1, EEF2, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Neurexins and neuroligins	0.0170	1.7048	37	APBA1, APBA2, DBNL, DLG3, DLGAP1, DLGAP3, DLGAP4, EPB41L1, EPB41L5, GRIN1, GRIN2A, GRIN2B, GRM1, GRM5, HOMER1, HOMER2, LIN7A, LIN7B, LIN7C, LRRTM1, LRRTM2, LRRTM3, NLGN2, NLGN3, NLGN4X, NRXN2, NRXN3, PDLIM5, SHANK1, SHANK2, SHANK3, SIPA1L1, STX1A, STXBP1, SYT1, SYT12, SYT7
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	0.0066	1.6770	54	GSPT1, GSPT2, NCBP1, NCBP2, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, UPF1
Major pathway of rRNA processing in the nucleolus and cytosol	0.0170	1.6524	57	CSNK1E, DDX21, DIS3, EXOSC10, EXOSC2, NCL, NOP58, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, UTP20

Table S3: Significantly enriched Reactome pathways for proteins ranked by log₂(fold-change) in children (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
SRP-dependent cotranslational protein targeting to membrane	0.0066	1.6277	59	DDOST, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPN1, RPN2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SRP14, SRP54, SRP68, SRP72, SRP9, SRPRA, SRPRB
Formation of a pool of free 40S subunits	0.0135	1.6177	59	EIF1AX, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	0.0101	1.6121	64	DCP1A, EIF4A3, GSPT1, GSPT2, MAGOH, NCBP1, NCBP2, PPP2R1A, PPP2R2A, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SMG1, SMG5, SMG6, SMG8, UPF1, UPF2
Cytosolic tRNA aminoacylation	0.0406	-1.9795	18	AARS1, AIMP1, AIMP2, DARS1, EEF1E1, EPRS1, FARSB, GARS1, KARS1, LARS1, MARS1, NARS1, QARS1, RARS1, TARS1, VARS1, WARS1, YARS1
Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	0.0374	-2.0533	6	YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ
Glycolysis	0.0406	-2.0706	16	ALDOA, ALDOC, BPGM, ENO1, ENO2, GAPDH, GNPDA1, GNPDA2, HK1, PFKL, PFKM, PFKP, PGAM1, PGK1, PGM2L1, PGP

Table S4: Significantly enriched Reactome pathways for proteins ranked by log2(fold-change) in adults

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Formation of the cornified envelope	0.0000	2.3246	25	CAPN1, CAPNS1, CASP14, DSC1, DSG1, DSP, FLG, JUP, KRT13, KRT14, KRT16, KRT17, KRT27, KRT5, KRT6A, KRT6B, KRT7, KRT71, KRT72, KRT77, KRT78, KRT80, PKP1, PKP4, TGM1
Striated Muscle Contraction	0.0049	1.9296	9	ACTN2, MYH6, MYL2, MYL3, TMOD1, TMOD2, TPM3, TPM4, VIM
Response of EIF2AK4 (GCN2) to amino acid deficiency	0.0000	1.9125	61	ASNS, EIF2AK4, EIF2S1, EIF2S2, EIF2S3, FAU, GCN1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Peptide chain elongation	0.0000	1.8765	57	EEF1A1, EEF2, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Selenocysteine synthesis	0.0000	1.8676	56	EEFSEC, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Eukaryotic Translation Termination	0.0000	1.8663	59	APEH, FAU, GSPT1, GSPT2, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, TRMT112

Table S4: Significantly enriched Reactome pathways for proteins ranked by log2(fold-change) in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Viral mRNA Translation	0.0000	1.8662	56	DNAJC3, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Common Pathway of Fibrin Clot Formation	0.0210	1.8545	5	F13A1, FGA, FGB, PROS1, SERPINE2
Major pathway of rRNA processing in the nucleolus and cytosol	0.0000	1.8443	65	CSNK1D, CSNK1E, DDX21, DIS3, EXOSC10, FAU, FBL, MTREX, NCL, NOP58, PELP1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Formation of the ternary complex, and subsequently, the 43S complex	0.0005	1.8438	37	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	0.0000	1.8327	59	FAU, GSPT1, GSPT2, NCBP1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, UPF1

Table S4: Significantly enriched Reactome pathways for proteins ranked by log₂(fold-change) in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
L13a-mediated translational silencing of Ceruloplasmin expression	0.0000	1.8244	72	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Formation of a pool of free 40S subunits	0.0000	1.8086	66	EIF1AX, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
GTP hydrolysis and joining of the 60S ribosomal subunit	0.0000	1.8009	74	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, EIF5, EIF5B, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Translation initiation complex formation	0.0046	1.7389	40	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA

Table S4: Significantly enriched Reactome pathways for proteins ranked by log2(fold-change) in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Ribosomal scanning and start codon recognition	0.0039	1.7078	41	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, EIF5, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
SRP-dependent cotranslational protein targeting to membrane	0.0007	1.7038	66	DDOST, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPN1, RPN2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SRP14, SRP54, SRP68, SRP72, SRP9, SRPRA, SRPRB, SSR4
45 Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	0.0012	1.6942	69	DCP1A, EIF4A3, FAU, GSPT1, GSPT2, MAGOH, NCBP1, PPP2R1A, PPP2R2A, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SMG1, SMG5, SMG6, SMG8, UPF1, UPF2
mRNA Splicing - Major Pathway	0.0009	1.6543	71	BCAS2, BUD31, CDC5L, CPSF3, CPSF7, CSTF2, DDX42, DHX15, DHX9, DNAJC8, EFTUD2, EIF4A3, ELAVL1, FIP1L1, FUS, HNRNPA0, HNRNPA2B1, HNRNPA3, HNRNPF, HNRNPH1, HNRNPH2, HNRNPK, HNRNPL, HNRNPR, HSPA8, LSM2, LSM3, LSM6, MAGOH, MTREX, NCBP1, NUDT21, PCBP1, PCBP2, PHF5A, PLRG1, POLR2A, POLR2J, PPIL1, PPIL3, PRPF19, PRPF6, PRPF8, RBM22, RBMX, SF1, SF3A1, SF3A3, SF3B1, SF3B2, SF3B3, SF3B5, SNRNP200, SNRNP70, SNRPA, SNRPA1, SNRPB, SNRPB2, SNRPD1, SNRPD2, SNRPD3, SRSF10, SRSF3, SRSF6, SRSF7, SRSF9, TRA2B, U2AF1, U2AF2, WBP11, XAB2

Table S4: Significantly enriched Reactome pathways for proteins ranked by log₂(fold-change) in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Regulation of expression of SLITs and ROBOs	0.0005	1.6232	98	CUL2, EIF4A3, ELOB, ELOC, FAU, GSPT1, GSPT2, MAGOH, NCBP1, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB3, PSMB4, PSMB5, PSMB6, PSMB7, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMD1, PSMD11, PSMD12, PSMD13, PSMD14, PSMD2, PSMD3, PSMD4, PSMD5, PSMD6, PSMD7, PSMD8, PSME1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SLIT1, UPF2, USP33
Activation of Matrix Metalloproteinases	0.0138	-1.9916	4	COL18A1, ELANE, MMP9, PLG
Collagen chain trimerization	0.0123	-2.2167	8	COL11A1, COL12A1, COL14A1, COL18A1, COL1A1, COL4A2, COL6A2, COL6A3
Regulation of Complement cascade	0.0002	-2.6783	11	C1QC, C3, C4BPA, C4BPB, CFH, CLU, ELANE, IGHG1, IGKC, IGLC2, PROS1

Table S5: Significantly enriched WikiPathways for proteins ranked by log2(fold-change) in children

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Disruption of postsynaptic signaling by CNV	0.0066	1.8221	28	ARC, CAMK2A, CAMK2B, CAMK2D, CYFIP1, DLG1, DLG2, DLGAP1, FMR1, GRIN1, GRIN2A, GRIN2B, GRM1, HOMER1, MAPK1, MAPK3, NLGN2, NLGN3, NLGN4X, NRXN1, NRXN2, NRXN2, NRXN3, RPH3A, RYR2, SHANK1, STX1A, YWHAG
Oxidative phosphorylation	0.0146	1.7258	33	ATP5F1A, ATP5F1B, ATP5F1D, ATP5ME, ATP5PB, ATP5PD, ATP5PF, ATP5PO, ATP6AP1, DMAC2L, NDUFA10, NDUFA2, NDUFA3, NDUFA4, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFB1, NDUFB4, NDUFB6, NDUFB7, NDUFB8, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS8
Cytoplasmic ribosomal proteins	0.0066	1.6689	55	MRPL19, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36A, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS6KA1, RPS6KA3, RPS6KB1, RPS7, RPS8, RPS9, RPSA
Electron transport chain: OXPHOS system in mitochondria	0.0212	1.5995	55	ATP5F1A, ATP5F1B, ATP5F1C, ATP5F1D, ATP5IF1, ATP5ME, ATP5PB, ATP5PD, ATP5PF, ATP5PO, COX4I1, COX5A, COX5B, COX6B1, COX6C, COX7A2, COX7A2L, COX7C, DMAC2L, MT-CO2, NDUFA10, NDUFA12, NDUFA2, NDUFA3, NDUFA4, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFB1, NDUFB3, NDUFB4, NDUFB6, NDUFB7, NDUFB8, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS8, SDHA, SDHB, SLC25A4, SLC25A5, SLC25A6, UQCRCB, UQCRC1, UQCRC2, UQCRFS1, UQCRQ
Glutathione metabolism	0.0374	-2.0714	6	G6PD, GCLM, GSR, GSS, IDH1, OPLAH
Glycolysis in senescence	0.0406	-2.1152	6	G6PD, GAPDH, LDHA, PGK1, PKM, PKM

Table S6: Significantly enriched WikiPathways for proteins ranked by log2(fold-change) in adults

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Cardiac progenitor differentiation	0.0101	1.9537	9	GSK3B, KIT, MEF2C, MYH6, MYL2, NCAM1, NCAM1, SIRPA, THY1
Cytoplasmic ribosomal proteins	0.0002	1.7786	59	MRPL19, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS6KA1, RPS6KA3, RPS6KB1, RPS7, RPS8, RPS9, RPSA
mRNA processing	0.0003	1.7768	61	CELF1, CELF2, CELF4, CPSF3, CSTF2, DDX1, DDX20, DHX15, DHX9, DICER1, DNAJC8, EFTUD2, FUS, HNRNPA2B1, HNRNPH1, HNRNPH2, HNRNPK, HNRNPL, HNRNPR, LSM2, NCBP1, NONO, NUDT21, NXF1, PCBP2, PHF5A, POLR2A, PRPF4B, PRPF6, PRPF8, PTBP2, RBMX, SF3A1, SF3A3, SF3B1, SF3B2, SF3B3, SF3B5, SFPQ, SMC1A, SNRNP70, SNRPA, SNRPA1, SNRPB, SNRPB2, SNRPD1, SNRPD2, SNRPD3, SRP54, SRPK2, SRSF10, SRSF3, SRSF6, SRSF7, SRSF9, SUGP2, SUPT5H, TMED10, TRA2B, U2AF1, U2AF2
Blood clotting cascade	0.0002	-2.5175	6	F8A1, FGA, FGB, FGG, PLG, VWF

Table S7: Significantly enriched Reactome pathways for proteins ranked by VIP4p in children

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Transferrin endocytosis and recycling	0.0000	2.4855	12	ATP6AP1, ATP6V0A1, ATP6V0C, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H
Ion channel transport	0.0000	2.4397	12	ATP6AP1, ATP6V0A1, ATP6V0C, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H
ROS and RNS production in phagocytes	0.0000	2.4168	11	ATP6V0A1, ATP6V0C, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H
Insulin receptor recycling	0.0000	2.3663	13	ATP6AP1, ATP6V0A1, ATP6V0C, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H, INSR
Miscellaneous transport and binding events	0.0011	2.0849	9	ADD1, ADD2, ADD3, AZGP1, DMTN, LRRC8A, LRRC8B, LRRC8D, PIP
Formation of the cornified envelope	0.0005	2.0022	26	CAPN1, CAPNS1, CASP14, CSTA, DSC1, DSG1, DSP, FLG, JUP, KRT13, KRT14, KRT16, KRT17, KRT25, KRT27, KRT5, KRT6A, KRT6B, KRT7, KRT71, KRT77, KRT78, KRT80, PKP2, PKP4, TGM1
Amino acids regulate mTORC1	0.0037	1.9094	24	ATP6V0C, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H, CASTOR2, FLCN, LAMTOR1, LAMTOR2, LAMTOR5, MIOS, MTOR, RHEB, RPTOR, RRAGA, RRAGC, SEH1L, SH3BP4, SZT2
Mitochondrial translation elongation	0.0087	1.7260	36	DAP3, GFM1, MRPL1, MRPL11, MRPL13, MRPL14, MRPL15, MRPL16, MRPL19, MRPL22, MRPL38, MRPL41, MRPL44, MRPL46, MRPL47, MRPL48, MRPL49, MRPL54, MRPL9, MRPS11, MRPS15, MRPS2, MRPS22, MRPS25, MRPS26, MRPS30, MRPS31, MRPS35, MRPS36, MRPS5, MRPS6, MRPS7, MRPS9, PTCD3, TSFM, TUFM
COPI-independent Golgi-to-ER retrograde traffic	0.0238	1.7237	32	ACTR10, ACTR1A, AGPAT3, BICD1, CAPZA1, CAPZA2, DCTN1, DCTN2, DCTN4, DCTN6, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNLL1, DYNLL2, PAFAH1B1, PAFAH1B3, PLA2G6, RAB18, RAB3GAP1, RAB3GAP2, RAB6A, RAB6B, TUBA4A, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB6, TUBB8
Mitochondrial translation termination	0.0135	1.7105	35	DAP3, GFM2, MRPL1, MRPL11, MRPL13, MRPL14, MRPL15, MRPL16, MRPL19, MRPL22, MRPL38, MRPL41, MRPL44, MRPL46, MRPL47, MRPL48, MRPL49, MRPL54, MRPL9, MRPS11, MRPS15, MRPS2, MRPS22, MRPS25, MRPS26, MRPS30, MRPS31, MRPS35, MRPS36, MRPS5, MRPS6, MRPS7, MRPS9, MRRF, PTCD3

Table S7: Significantly enriched Reactome pathways for proteins ranked by VIP4p in children (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Mitochondrial translation initiation	0.0286	1.6920	35	DAP3, MRPL1, MRPL11, MRPL13, MRPL14, MRPL15, MRPL16, MRPL19, MRPL22, MRPL38, MRPL41, MRPL44, MRPL46, MRPL47, MRPL48, MRPL49, MRPL54, MRPL9, MRPS11, MRPS15, MRPS2, MRPS22, MRPS25, MRPS26, MRPS30, MRPS31, MRPS35, MRPS36, MRPS5, MRPS6, MRPS7, MRPS9, MTIF2, MTIF3, PTC3
RHOB GTPase cycle	0.0393	1.6391	35	ABR, ACTC1, ANLN, ARHGAP1, ARHGAP21, ARHGAP26, ARHGAP32, ARHGAP35, ARHGAP39, ARHGAP5, ARHGEF1, ARHGEF11, ARHGEF12, ARHGEF25, BCR, CAV1, CAVIN1, DAAM1, DIAPH1, FLOT1, FLOT2, JUP, MCF2L, MYO9A, OPHN1, PCDH7, PIK3R1, PIK3R2, PREX1, RHPN2, ROCK2, SLK, STOM, TJP2, VAV2
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	0.0496	1.5442	54	GSPT1, GSPT2, NCBP1, NCBP2, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, UPF1
DNA methylation	0.0499	-1.9435	6	H2AC20, H2AX, H2AZ2, H2BC21, H3-3A, H4-16
B-WICH complex positively regulates rRNA expression	0.0496	-2.0590	8	DDX21, H2AC20, H2AX, H2AZ2, H2BC21, H3-3A, H4-16, SF3B1

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Formation of the cornified envelope	0.0002	2.0357	25	CAPN1, CAPNS1, CASP14, DSC1, DSG1, DSP, FLG, JUP, KRT13, KRT14, KRT16, KRT17, KRT27, KRT5, KRT6A, KRT6B, KRT7, KRT71, KRT72, KRT77, KRT78, KRT80, PKP1, PKP4, TGM1
Ion channel transport	0.0112	1.9531	11	ATP6AP1, ATP6V0A1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H
Selenocysteine synthesis	0.0000	1.9335	56	EEFSEC, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Viral mRNA Translation	0.0000	1.9087	56	DNAJC3, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Peptide chain elongation	0.0000	1.9071	57	EEF1A1, EEF2, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	0.0000	1.8956	59	FAU, GSPT1, GSPT2, NCBP1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, UPF1

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Response of EIF2AK4 (GCN2) to amino acid deficiency	0.0000	1.8864	61	ASNS, EIF2AK4, EIF2S1, EIF2S2, EIF2S3, FAU, GCN1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Cytosolic tRNA aminoacylation	0.0060	1.8757	19	AARS1, AIMP1, AIMP2, DARS1, EEF1E1, EPRS1, FARSB, GARS1, IARS1, KARS1, LARS1, MARS1, NARS1, QARS1, RARS1, TARS1, VARS1, WARS1, YARS1
Eukaryotic Translation Termination	0.0000	1.8733	59	APEH, FAU, GSPT1, GSPT2, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, TRMT112
PI5P Regulates TP53 Acetylation	0.0352	1.8691	5	MAP2K6, PIN1, PIP4K2A, PIP4K2B, PIP4K2C
Selenoamino acid metabolism	0.0228	1.8584	11	AIMP1, AIMP2, DARS1, EEF1E1, EPRS1, IARS1, KARS1, LARS1, MARS1, QARS1, RARS1
Major pathway of rRNA processing in the nucleolus and cytosol	0.0000	1.8295	65	CSNK1D, CSNK1E, DDX21, DIS3, EXOSC10, FAU, FBL, MTREX, NCL, NOP58, PELP1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
L13a-mediated translational silencing of Ceruloplasmin expression	0.0000	1.8239	72	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Insulin receptor recycling	0.0351	1.8194	12	ATP6AP1, ATP6V0A1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H, INSR
Formation of a pool of free 40S subunits	0.0000	1.8180	66	EIF1AX, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
GTP hydrolysis and joining of the 60S ribosomal subunit	0.0000	1.8177	74	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, EIF5, EIF5B, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Regulation of expression of SLITs and ROBOs	0.0000	1.8142	98	CUL2, EIF4A3, ELOB, ELOC, FAU, GSPT1, GSPT2, MAGOH, NCBP1, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB3, PSMB4, PSMB5, PSMB6, PSMB7, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMD1, PSMD11, PSMD12, PSMD13, PSMD14, PSMD2, PSMD3, PSMD4, PSMD5, PSMD6, PSMD7, PSMD8, PSME1, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SLIT1, UPF2, USP33
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	0.0000	1.8062	69	DCP1A, EIF4A3, FAU, GSPT1, GSPT2, MAGOH, NCBP1, PPP2R1A, PPP2R2A, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SMG1, SMG5, SMG6, SMG8, UPF1, UPF2
Transferrin endocytosis and recycling	0.0469	1.8018	12	ATP6AP1, ATP6V0A1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1G2, ATP6V1H, TFRC
Complex I biogenesis	0.0037	1.7753	34	ACAD9, ECSIT, MT-ND5, NDUFA10, NDUFA11, NDUFA12, NDUFA13, NDUFA2, NDUFA5, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFAF2, NDUFAF3, NDUFAF4, NDUFAF6, NDUFB1, NDUFB10, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB9, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS8, NUBPL

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
SRP-dependent cotranslational protein targeting to membrane	0.0002	1.7439	66	DDOST, FAU, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL36AL, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPN1, RPN2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA, SRP14, SRP54, SRP68, SRP72, SRP9, SRPRA, SRPRB, SSR4
Formation of the ternary complex, and subsequently, the 43S complex	0.0046	1.7347	37	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
55 Translation initiation complex formation	0.0058	1.7191	40	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
Ribosomal scanning and start codon recognition	0.0046	1.6918	41	EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3A, EIF3B, EIF3D, EIF3E, EIF3F, EIF3I, EIF3J, EIF3K, EIF3L, EIF3M, EIF4A1, EIF4A2, EIF4H, EIF5, FAU, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS7, RPS8, RPSA
mRNA Splicing - Major Pathway	0.0020	1.6449	71	BCAS2, BUD31, CDC5L, CPSF3, CPSF7, CSTF2, DDX42, DHX15, DHX9, DNAJC8, EFTUD2, EIF4A3, ELAVL1, FIP1L1, FUS, HNRNPA0, HNRNPA2B1, HNRNPA3, HNRNPF, HNRNPH1, HNRNPH2, HNRNPK, HNRNPL, HNRNPR, HSPA8, LSM2, LSM3, LSM6, MAGOH, MTREX, NCBP1, NUDT21, PCBP1, PCBP2, PHF5A, PLRG1, POLR2A, POLR2J, PPIL1, PPIL3, PRPF19, PRPF6, PRPF8, RBM22, RBMX, SF1, SF3A1, SF3A3, SF3B1, SF3B2, SF3B3, SF3B5, SNRNP200, SNRNP70, SNRPA, SNRPA1, SNRPB, SNRPB2, SNRPD1, SNRPD2, SNRPD3, SRSF10, SRSF3, SRSF6, SRSF7, SRSF9, TRA2B, U2AF1, U2AF2, WBP11, XAB2

Table S8: Significantly enriched Reactome pathways for proteins ranked by VIP4p in adults (*continued*)

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Cargo recognition for clathrin-mediated endocytosis	0.0170	1.6138	42	AAK1, AP2A1, AP2A2, AP2M1, APOB, ARRB1, CLTA, CLTB, COPS2, COPS3, COPS4, COPS5, COPS7A, EGFR, EPN1, EPS15, EPS15L1, GPS1, GRK2, GRK3, HGS, ITSN1, ITSN2, PICALM, REPS1, REPS2, SGIP1, SH3GL1, SH3GL2, SH3GL3, SH3KBP1, SNAP91, STAM, STAM2, STON2, SYT1, SYT11, TFRC, TOR1A, UBQLN1, UBQLN2, VAMP7

Table S9: Significantly enriched WikiPathways for proteins ranked by VIP4p in children

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Proximal tubule transport	0.0035	1.9518	17	ABCB1, ABCG2, ATP1A1, ATP1B1, ATP6V0C, ATP6V1A, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1F, ATP6V1G1, ATP6V1H, CA4, SLC20A2, SLC2A1, SLC3A2, SLC4A4
Pathogenic Escherichia coli infection	0.0468	1.6529	29	ABL1, ARPC1A, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, CDC42, CTTN, EZR, FYN, ITGB1, NCK1, NCK2, NCL, PRKCA, RHOA, ROCK2, TUBA4A, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB6, TUBB8, WASL, YWHAQ, YWHAZ
Nonalcoholic fatty liver disease	0.0345	1.5366	69	AKT1, AKT2, AKT3, CDC42, COX4I1, COX5A, COX5B, COX6B1, COX6C, COX7A2, COX7A2L, COX7C, CYC1, EIF2S1, GSK3A, IKBKB, INSR, IRS1, IRS2, ITCH, MAP3K5, MAPK8, MAPK9, MT-CO2, NDUFA10, NDUFA12, NDUFA13, NDUFA2, NDUFA3, NDUFA4, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFB1, NDUFB3, NDUFB4, NDUFB6, NDUFB7, NDUFB8, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS8, PIK3CA, PIK3CB, PIK3R1, PIK3R2, PRKAA1, PRKAA2, PRKAB2, PRKAG1, PRKAG2, RAC1, RELA, SDHA, SDHB, TRAF2, UQCRB, UQCRC1, UQCRC2, UQCRFS1, UQCRQ

Table S10: Significantly enriched WikiPathways for proteins ranked by VIP4p in adults

Pathway	Adjusted p-value	Norm. Enrich. Score	# genes	Genes
Cytoplasmic ribosomal proteins	0.0005	1.7328	59	MRPL19, RPL10, RPL10A, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL19, RPL21, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL28, RPL3, RPL30, RPL34, RPL35, RPL35A, RPL36, RPL37A, RPL38, RPL4, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP2, RPS10, RPS11, RPS12, RPS13, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS26, RPS27, RPS28, RPS3, RPS3A, RPS4X, RPS6, RPS6KA1, RPS6KA3, RPS6KB1, RPS7, RPS8, RPS9, RPSA
Oxidative phosphorylation	0.0117	1.7186	36	ATP5F1A, ATP5F1B, ATP5F1D, ATP5ME, ATP5PB, ATP5PD, ATP5PF, ATP5PO, ATP6AP1, DMAC2L, MT-ND5, NDUFA10, NDUFA11, NDUFA2, NDUFA4, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFB1, NDUFB10, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB9, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS8
mRNA processing	0.0046	1.6127	61	CELF1, CELF2, CELF4, CPSF3, CSTF2, DDX1, DDX20, DHX15, DHX9, DICER1, DNAJC8, EFTUD2, FUS, HNRNPA2B1, HNRNPH1, HNRNPH2, HNRNPK, HNRNPL, HNRNPR, LSM2, NCBP1, NONO, NUDT21, NXF1, PCBP2, PHF5A, POLR2A, PRPF4B, PRPF6, PRPF8, PTBP2, RBMX, SF3A1, SF3A3, SF3B1, SF3B2, SF3B3, SF3B5, SFPQ, SMC1A, SNRNP70, SNRPA, SNRPA1, SNRPB, SNRPB2, SNRPD1, SNRPD2, SNRPD3, SRP54, SRPK2, SRSF10, SRSF3, SRSF6, SRSF7, SRSF9, SUGP2, SUPT5H, TMED10, TRA2B, U2AF1, U2AF2