

Supplementary Table 2. Identified proteins with expression significantly altered in the hippocampus of rats exposed to MeHg group (EG) vs. control group (CG)

^a Access Number	Protein name description	PLGS Score	Fold Change
P35213	14-3-3 protein beta/alpha	3217.24	-0.9231
P62260	14-3-3 protein epsilon	3971.27	-0.9418
P68511	14-3-3 protein eta	2305.94	-0.9231
P61983	14-3-3 protein gamma	6131.12	-0.9231
P68255	14-3-3 protein theta	288-0.38	-0.8694
P63102	14-3-3 protein zeta/delta	8270.35	-0.8521
P13233	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1277.06	-0.5169
Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial	44.35	2.05443
P38983	40S ribosomal protein SA	295.28	2.4596
P63039	60 kDa heat shock protein, mitochondrial	3810.85	1.10517
P19944	60S acidic ribosomal protein P1	2014.83	-0.9048
Q7TP92	Ab1-196	120.42	1.50682
Q9ER34	Aconitate hydratase, mitochondrial	907.99	-0.3263
P68035	Actin, alpha cardiac muscle 1	9131.88	-0.4677
P68136	Actin, alpha skeletal muscle	9169.15	-0.4677
P62738	Actin, aortic smooth muscle	8788.9	-0.4677
D3ZRN3	Actin, beta-like 2	3409.93	-0.4916
P60711	Actin, cytoplasmic 1	18154.38	-0.4724
P63259	Actin, cytoplasmic 2	18154.38	-0.4724
P63269	Actin, gamma-enteric smooth muscle	8788.9	-0.4677
Q4KLF8	Actin-related protein 2/3 complex subunit 5	371.36	3.00417
Q4V7C7	Actin-related protein 3	369.89	-0.5326
F8WG67	Acyl-CoA thioesterase 7, isoform CRA_a	386.59	-0.8106

P11030	Acyl-CoA-binding protein	1047.04	-0.7047
A0A0G2JSM7	Adducin 1 (Alpha), isoform CRA_b	305.89	-0.7945
M0RC66	Adenylate kinase isoenzyme 1	746.44	1.32313
Q08163	Adenylyl cyclase-associated protein 1	588.13	-0.8607
P84079	ADP-ribosylation factor 1	1766.91	-0.5379
P84082	ADP-ribosylation factor 2	1695.05	-0.5543
P61206	ADP-ribosylation factor 3	1766.91	-0.5326
P61751	ADP-ribosylation factor 4	1595.47	-0.5712
P84083	ADP-ribosylation factor 5	1595.47	-0.5769
P07943	Aldose reductase	103.57	-0.4868
G3V6Y6	Alpha-1,4 glucan phosphorylase	124.87	-0.6703
Q63028	Alpha-adducin	305.89	-0.7945
P85515	Alpha-centractin	346.97	-0.6977
P23565	Alpha-internexin	3961.57	1.28403
P54921	Alpha-soluble NSF attachment protein	975.67	-0.8353
P37377	Alpha-synuclein	4509.07	1.11628
A0A0G2K3U1	AMP deaminase	140.62	-0.4538
Q02356	AMP deaminase 2	140.62	-0.4449
F1LPP0	Amphiphysin	151.88	1.29693
M0R7C6	Ankyrin repeat domain 33	218.67	-0.5712
P02650	Apolipoprotein E	157.53	1.2214
B2RYJ7	ARP1 actin-related protein 1 homolog B	346.97	-0.657
Q78E60	Aryl hydrocarbon receptor nuclear translocator 2	60.63	2.85765
P13221	Aspartate aminotransferase, cytoplasmic	2964.88	-0.8106
P00507	Aspartate aminotransferase, mitochondrial	3225.35	-0.5434
Q5U318	Astrocytic phosphoprotein PEA-15	98.96	1.78604
F1LP05	ATP synthase subunit alpha	6096.17	1.2214
P15999	ATP synthase subunit alpha, mitochondrial	6323.49	1.2214

G3V6D3	ATP synthase subunit beta	12373.68	1.47698
P10719	ATP synthase subunit beta, mitochondrial	12373.68	1.47698
B1WBP7	ATP synthase subunit delta, mitochondrial	873.8	1.53726
P35435	ATP synthase subunit gamma, mitochondrial	343.16	1.10517
D4A133	ATPase H ⁺ -transporting V1 subunit A	2455.47	-0.827
D3ZZS8	ATPase H ⁺ -transporting V1 subunit B1	482.47	-0.7483
Q6P503	ATPase H ⁺ -transporting V1 subunit D	198.22	2.07508
Q52KS1	ATP-dependent 6-phosphofructokinase	213.93	-0.8521
P47858	ATP-dependent 6-phosphofructokinase, muscle type	121.8	-0.8353
P47860	ATP-dependent 6-phosphofructokinase, platelet type	180.23	-0.8187
P85969	Beta-soluble NSF attachment protein	1241.13	-0.8781
Q63754	Beta-synuclein	12707.9	1.17351
Q5HZA7	Bin1 protein	1175.82	1.1275
Q05175	Brain acid soluble protein 1	2074.98	1.50682
Q3ZB98	Breast carcinoma-amplified sequence 1 homolog	137.19	2.2034
G3V9G3	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_a	860.51	-0.6977
F1LUE2	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_c	875.11	-0.2209
F1LZG4	Calcium/calmodulin-dependent protein kinase type II subunit alpha	1800.28	-0.2346
P11730	Calcium/calmodulin-dependent protein kinase type II subunit gamma	312.81	-0.7047
P63055	Calmodulin regulator protein PCP4	1692.38	1.17351
D4ABV5	Calmodulin-2	8786.66	1.20925
Q5U206	Calmodulin-like protein 3	1989.73	1.10517
P18418	Calreticulin	702.79	1.15027
P12368	cAMP-dependent protein kinase type II-alpha regulatory subunit	220.18	-0.7558
P27139	Carbonic anhydrase 2	538.72	-0.8521
F1M642	CCR4-NOT transcription complex, subunit 6-like	241.66	-0.5273
G3V936	Citrate synthase	1830.18	-0.4317
Q8VHF5	Citrate synthase, mitochondrial	1602.76	-0.4449

F1M779	Clathrin heavy chain	199.04	-0.343
P11442	Clathrin heavy chain 1	97.55	-0.3465
P08081	Clathrin light chain A	243.32	2.29332
P08082	Clathrin light chain B	190.91	1.97388
B0BNA5	Coactosin-like protein	264.02	1.46228
P45592	Cofilin-1	9901.81	-0.9512
A0A096P6L9	Complement C5	205.62	-0.4868
D3ZPI8	Complement C8 gamma chain	142.08	-0.1809
P63041	Complexin-1	296.06	1.20925
P84087	Complexin-2	732.07	1.11628
P07335	Creatine kinase B-type	9604.02	1.17351
P25809	Creatine kinase U-type, mitochondrial	657.88	-0.7634
Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial	931.37	-0.5712
Q5M9I5	Cytochrome b-c1 complex subunit 6, mitochondrial	327.05	-0.8958
B2RYS2	Cytochrome b-c1 complex subunit 7	182.95	1.28403
P11240	Cytochrome c oxidase subunit 5A, mitochondrial	3687.85	1.1853
P12075	Cytochrome c oxidase subunit 5B, mitochondrial	1453.15	1.2586
P62898	Cytochrome c, somatic	940.1	1.16183
Q64559	Cytosolic acyl coenzyme A thioester hydrolase	386.59	-0.8025
P80254	D-dopachrome decarboxylase	2487.91	-0.9324
Q6MG13	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	143.83	-0.4066
A0A0G2KAY1	DEAH-box helicase 16	13-0.39	-0.522
Q62651	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	61.84	3.06485
Q6P725	Desmin	151.67	1.29693
G3V6P2	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex), isoform CRA_a	362.14	1.34986
Q6P6R2	Dihydrolipoyl dehydrogenase, mitochondrial	1245.81	-0.7118
P08461	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	588.04	-0.8958

Q01205	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	362.14	1.34986
P11348	Dihydropteridine reductase	1220.52	1.1275
Q62950	Dihydropyrimidinase-related protein 1	2225.35	-0.8958
P47942	Dihydropyrimidinase-related protein 2	14884.86	-0.9048
Q62952	Dihydropyrimidinase-related protein 3	773.62	-0.8958
Q9JHU0	Dihydropyrimidinase-related protein 5	88.68	-0.8781
A0A0G2K8Y5	Dihydropyrimidinase-related protein 5-like	83.79	-0.8781
P21575	Dynamin-1	1336.73	-0.7047
O35303	Dynamin-1-like protein	135.47	-0.3535
P39052	Dynamin-2	188.06	-0.7483
Q08877	Dynamin-3	16-0.01	-0.7483
M0R757	Elongation factor 1-alpha	1276.23	-0.8781
F1M6C2	Elongation factor 1-alpha 1 pseudogene	1254.04	-0.8694
P62632	Elongation factor 1-alpha 2	1599.24	-0.7334
P85834	Elongation factor Tu, mitochondrial	151.72	-0.8607
O35179	Endophilin-A1	951.5	1.08329
O88752	Epsilon 1 globin	2342.47	1.11628
O88339	Epsin-1	144.47	2.29332
D3ZAY2	Erythrocyte membrane protein band 4.1-like 2	56.99	-0.8958
Q5RKI1	Eukaryotic initiation factor 4A-II	193.81	1.16183
Q3B8Q2	Eukaryotic initiation factor 4A-III	115.69	1.55271
Q6P3V8	Eukaryotic translation initiation factor 4A1	171.59	1.24608
Q5XI72	Eukaryotic translation initiation factor 4H	123.98	1.37713
B2GUZ5	F-actin-capping protein subunit alpha-1	62.35	1.76827
A0A0G2KAM4	Fascin	273.28	-0.8437
P55053	Fatty acid-binding protein, epidermal	177.23	1.52196
A0A0G2K3Q6	Fructose-bisphosphate aldolase	5515.53	-0.7634

P05065	Fructose-bisphosphate aldolase A	4119.16	-0.5117
P09117	Fructose-bisphosphate aldolase C	5515.53	-0.7634
Q5PQK2	FUS RNA-binding protein	116.9	4.1787
D3ZSS5	G protein subunit alpha transducin 1	177.61	-0.644
D4AA42	G protein subunit alpha transducin 2	177.61	-0.6313
P07323	Gamma-enolase	4571.83	-0.9608
P47819	Glial fibrillary acidic protein	4905.74	1.24608
Q62669	Globin a1	1088.11	-0.657
A0A0G2JSW3	Globin a4	7369.64	-0.9231
A0A0G2JSV6	Globin c2	12758.02	1.09417
Q6P6V0	Glucose-6-phosphate isomerase	229.26	-0.4724
P10860	Glutamate dehydrogenase 1, mitochondrial	1778.92	-0.7711
P09606	Glutamine synthetase	2090.81	-0.419
G3V983	Glutathione S-transferase	548.37	-0.8607
P04905	Glutathione S-transferase Mu 1	642.5	-0.827
P08010	Glutathione S-transferase Mu 2	194.1	-0.7408
P04906	Glutathione S-transferase P	859.28	-0.8869
P08009	Glutathione S-transferase Yb-3	452.32	-0.7408
D3ZVQ8	Glutathione S-transferase, mu 6-like	176.48	-0.5117
B1WBQ8	Glyceraldehyde-3-phosphate dehydrogenase	1174.44	1.29693
Q9ESV6	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	1174.44	1.29693
P53534	Glycogen phosphorylase, brain form	151.8	-0.6771
P09811	Glycogen phosphorylase, liver form	99.04	-0.5712
PYGM_RABIT	Glycogen phosphorylase, muscle form	148.5	-0.6005
Q5EEY3	GTP-binding protein G-alpha-i2 splice variant b	170.17	-0.6313
Q9WTT6	Guanine deaminase	435.69	-0.657
P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1	184.73	-0.6376
P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2	184.73	-0.6505

P54311	Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-1	2833.24	-0.5016
P54313	Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-2	2061.65	-0.5599
P52287	Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-3	728.13	-0.3716
P08753	Guanine nucleotide-binding protein G(k) subunit alpha	184.73	-0.6376
P59215	Guanine nucleotide-binding protein G(o) subunit alpha	618.59	-0.5886
G3V8E8	Guanine nucleotide-binding protein G(olf) subunit alpha	170.17	-0.644
P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	174.06	-0.6376
Q63803	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	174.06	-0.6313
P29348	Guanine nucleotide-binding protein G(t) subunit alpha-3	203.11	-0.6376
Q63210	Guanine nucleotide-binding protein subunit alpha-12	189.18	-0.657
Q6Q7Y5	Guanine nucleotide-binding protein subunit alpha-13	189.18	-0.6376
O35353	Guanine nucleotide-binding protein subunit beta-4	1850.94	-0.4868
M0RBJ0	Guanine nucleotide-binding protein subunit gamma	4414.54	-0.4538
P0DMW0	Heat shock 70 kDa protein 1A	1181.2	-0.9231
P0DMW1	Heat shock 70 kDa protein 1B	1139.67	-0.9048
P55063	Heat shock 70 kDa protein 1-like	1102.2	-0.8781
Q5XHZ0	Heat shock protein 75 kDa, mitochondrial	368.35	-0.7634
P82995	Heat shock protein HSP 90-alpha	1118.22	-0.9048
P01946	Hemoglobin subunit alpha-1/2	12758.02	1.10517
P02091	Hemoglobin subunit beta-1	7369.64	-0.9324
P11517	Hemoglobin subunit beta-2	3781.96	1.1275
A0A0G2JTW9	Hemoglobin, beta adult major chain	1088.11	-0.6505
Q9JJ54	Heterogeneous nuclear ribonucleoprotein D0	117.32	1.87761
M0R9K1	Heterogeneous nuclear ribonucleoprotein K-like	205.04	1.43333
F1LQ48	Heterogeneous nuclear ribonucleoprotein L	63.02	1.64872
M0R6X5	Histone H2A	67.7	1.55271
P0C169	Histone H2A type 1-C	1246.7	1.34986
P0C170	Histone H2A type 1-E	1246.7	1.34986

Q64598	Histone H2A type 1-F	1246.7	1.34986
P0CC09	Histone H2A type 2-A	1246.7	1.33643
Q4FZT6	Histone H2A type 3	1246.7	1.34986
Q00728	Histone H2A type 4	1246.7	1.34986
M0RBQ5	Histone H2B	5432.61	1.63232
Q00715	Histone H2B type 1	5802.96	1.58407
Q00729	Histone H2B type 1-A	1223.1	1.59999
D3ZK97	Histone H3	741.51	1.11628
P84245	Histone H3.3	741.51	1.11628
P62804	Histone H4	7610.9	1.10517
P97697	Inositol monophosphatase 1	375.07	-0.7945
Q9JKU3	Intraflagellar transport protein 172 homolog	75.93	2.05443
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	558.52	-0.8187
P41565	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	741.17	-0.827
F1LNF7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	558.52	-0.827
Q6IFZ5	Keratin 76	73.38	3.09566
A0A0G2JW69	Keratin 78	55.76	3.70617
Q6IG11	Keratin 81	55.76	3.74342
A7M746	Keratin 83	55.76	3.81904
D3ZSY5	Keratin 84	71.11	3.74342
A7M777	Keratin 85	55.76	3.63279
A0A0G2QC11	Keratin 86	55.76	3.81904
Q6IG00	Keratin, type II cytoskeletal 4	55.76	3.49034
F7FFV2	Keratin, type II cytoskeletal 5	64.72	3.89619
Q6IG12	Keratin, type II cytoskeletal 7	55.76	4.80665
Q6IG03	Keratin, type II cytoskeletal 73	179.59	2.82922
Q6IG05	Keratin, type II cytoskeletal 75	55.76	3.85743
Q10758	Keratin, type II cytoskeletal 8	55.76	4.85496

Q6P7Q4	Lactoylglutathione lyase	185.87	1.43333
Q6AYX2	L-lactate dehydrogenase	197.74	-0.8025
P04642	L-lactate dehydrogenase A chain	2429.92	-0.6313
P42123	L-lactate dehydrogenase B chain	2515.2	-0.657
Q6TXF8	LRRGT00041	193.22	-0.5712
P30904	Macrophage migration inhibitory factor	3659.21	1.10517
O88989	Malate dehydrogenase, cytoplasmic	4452.33	-0.9231
P04636	Malate dehydrogenase, mitochondrial	14925.98	-0.8869
Q3KR86	MICOS complex subunit Mic60	352.44	-0.8437
D4A1Q2	Microtubule-associated protein	1430.72	1.10517
A0A0U1RS27	Microtubule-associated protein 2	123.59	1.55271
F1LQZ9	Microtubule-associated protein 6	310.6	1.20925
Q5XIT1	Microtubule-associated protein RP/EB family member 3	235.05	2.2705
O08839	Myc box-dependent-interacting protein 1	1181.27	1.1275
Q5XFW1	Myelin basic protein	5695.46	1.36343
P60203	Myelin proteolipid protein	1745.36	-0.0907
P62775	Myotrophin	112.18	1.37713
Q5RJQ4	NAD-dependent protein deacetylase sirtuin-2	518.37	-0.6977
D3ZG43	NADH dehydrogenase (Ubiquinone) Fe-S protein 3 (Predicted), isoform CRA_c	345.14	-0.7711
Q63362	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	233.59	-0.5769
Q5BK63	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	338.44	-0.1313
Q5XIH3	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	227.12	-0.8025
P19234	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	311.33	1.40495
D4A0T0	NADH:ubiquinone oxidoreductase subunit B10	325.3	1.13883
A0A0G2JWS2	Nebulette	74.68	10.6974
F1LQ81	N-ethylmaleimide sensitive fusion protein, isoform CRA_b	191.61	-0.5434
F1LNY3	Neural cell adhesion molecule 1	340.67	-0.4107

M0R9J4	Neuroendocrine secretory protein 55	170.17	-0.6313
P16884	Neurofilament heavy polypeptide	604.89	1.15027
P19527	Neurofilament light polypeptide	4999.24	1.59999
G3V7S2	Neurofilament medium polypeptide	1088.83	1.43333
D3ZTX2	NK2 homeobox 4	134.59	-0.357
A0A0G2JSV0	N-myc downstream regulated gene 2, isoform CRA_a	418.67	-0.6703
A0A0G2JSU4	N-myc downstream regulated gene 2, isoform CRA_b	418.67	-0.6907
D3ZSF3	Peptidyl-prolyl cis-trans isomerase	305.54	-0.8958
P10111	Peptidyl-prolyl cis-trans isomerase A	9173.66	-0.8187
G3V7I0	Peroxiredoxin 3	473.15	-0.6839
P35704	Peroxiredoxin-2	2886.1	-0.8958
Q9Z0V5	Peroxiredoxin-4	199.72	-0.0464
O35244	Peroxiredoxin-6	5921.94	1.1275
P31044	Phosphatidylethanolamine-binding protein 1	11950.35	1.2214
P16617	Phosphoglycerate kinase 1	4170.6	-0.9324
P16290	Phosphoglycerate mutase 2	174.36	-0.827
P0CG51	Polyubiquitin-B	2453.46	1.09417
F1LML2	Polyubiquitin-C	2453.46	1.09417
P54708	Potassium-transporting ATPase alpha chain 2	265.1	-0.463
A0A0G2JUG1	Predicted gene 5414	55.76	3.85743
P67779	Prohibitin	448.9	1.2586
D3ZFH6	Prohibitin, pseudogene 1	225.35	1.19722
Q5XIH7	Prohibitin-2	375.54	1.20925
Q9QXU9	ProSAAS	260.91	1.17351
P11598	Protein disulfide-isomerase A3	172.71	1.19722
Q5GFD9	Protein IMPACT	295.73	-0.7261
D3ZC07	Protein kinase N3	133.81	1.66529
Q8VBU2	Protein NDRG2	418.67	-0.6907

P04631	Protein S100-B	5909.12	1.06184
Q63945	Protein SET	118.74	1.61607
A0A140TAB9	Protein-L-isoaspartate O-methyltransferase	1931.79	1.16183
P22062	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	1944.29	1.15027
O35331	Pyridoxal kinase	168.67	1.91554
F7FKI5	Pyruvate dehydrogenase E1 component subunit alpha	382.41	-0.8106
P26284	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	382.41	-0.7945
A0A0G2KAM3	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3227.07	-0.8869
M0RD14	Pyruvate kinase	4589.29	-0.5543
P11980	Pyruvate kinase PKM	6418.95	-0.5434
P50398	Rab GDP dissociation inhibitor alpha	2968.98	-0.4317
P50399	Rab GDP dissociation inhibitor beta	1342.17	-0.5066
D4A823	RAD52 motif 1 (Predicted), isoform CRA_c	141.33	-0.357
F1LV89	Rap1 GTPase-activating protein	117.55	-0.3791
D3ZTA4	RCG26849, isoform CRA_a	269.88	1.82212
B5DFG5	RCG53214, isoform CRA_d	403.85	-0.8869
Q0ZFS8	RCG61099, isoform CRA_c	227.42	1.50682
Q5XI73	Rho GDP-dissociation inhibitor 1	1706.63	-0.9324
P10362	Secretogranin-2	75.52	1.23368
A0A0U1RRT8	Septin 6	403.85	-0.8694
B3GNI6	Septin-11	489.22	-0.9139
Q91Y81	Septin-2	197.54	1.30996
Q9WVC0	Septin-7	861.81	-0.8694
A0A0G2K7T5	Serine/threonine-protein phosphatase	412.68	-0.5769
Z4YNW7	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B	151.75	-0.3716
P36877	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	151.75	-0.3716

P20651	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	417.06	-0.5655
P62138	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	153.04	-0.4274
P62142	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	153.04	-0.4493
P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	153.04	-0.4232
P02770	Serum albumin	42.5	-0.8694
Q5EBB0	Similar to 14-3-3 protein sigma	2066.69	-0.9324
D3ZQL7	Similar to 25 kDa brain-specific protein (P25-alpha) (Predicted), isoform CRA_a	2393.8	1.09417
F1M9V3	Similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase)	342.69	1.24608
D4A5L9	Similar to Cytochrome c, somatic	940.1	1.16183
F1LUV3	Similar to glyceraldehyde-3-phosphate dehydrogenase	108.41	1.69893
G3V8S4	Sodium/potassium-transporting ATPase subunit alpha	265.1	-0.4677
P06685	Sodium/potassium-transporting ATPase subunit alpha-1	100.76	-0.3791
P06686	Sodium/potassium-transporting ATPase subunit alpha-2	117	-0.4148
P06687	Sodium/potassium-transporting ATPase subunit alpha-3	194.99	-0.3906
Q64541	Sodium/potassium-transporting ATPase subunit alpha-4	282.29	-0.4677
P07340	Sodium/potassium-transporting ATPase subunit beta-1	190.39	-0.3642
A0A0G2K2J7	Solute carrier family 25 member 12	575.25	-0.6126
A0A0G2JZ69	Spectrin alpha chain, non-erythrocytic 1	262.66	-0.9139
P13668	Stathmin	1007.82	1.53726
P21818	Stathmin-2	150.78	2.2034
P13086	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	358.74	-0.7334
F1LM47	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	199.01	-0.9139
D3ZEV8	Sushi domain containing 2 (Predicted), isoform CRA_a	110.36	-0.4724
G3V733	Synapsin II, isoform CRA_a	4056.34	-0.7483
P09951	Synapsin-1	3410.3	1.04081
Q63537	Synapsin-2	4056.34	-0.7483
F8WG75	Synaptosomal-associated protein	1087.23	1.2214

P60881	Synaptosomal-associated protein 25	1536.58	1.11628
P61765	Syntaxin-binding protein 1	2185.32	-0.3166
Q68FQ0	T-complex protein 1 subunit epsilon	233.25	-0.7558
Q05546	Tenascin-R	59.06	1.16183
Q9Z0V6	Thioredoxin-dependent peroxide reductase, mitochondrial	473.15	-0.6771
F1LPS8	Transcriptional activator protein Pur-alpha	1157.66	1.20925
A0A0G2K6I5	Transgelin	330.06	1.2214
Q5XFX0	Transgelin-2	126.47	-0.7408
P50137	Transketolase	219.59	-0.8694
P63029	Translationally-controlled tumor protein	278.37	1.89648
A0A0G2JWU1	Triosephosphate isomerase	7055.07	-0.8521
P70566	Tropomodulin-2	218.39	1.40495
Q63610	Tropomyosin alpha-3 chain	103.38	1.73325
F1LUM5	Tubulin alpha chain	1907.25	-0.5488
P68370	Tubulin alpha-1A chain	17536.7	-0.4404
Q6P9V9	Tubulin alpha-1B chain	15785.07	-0.4274
Q6AYZ1	Tubulin alpha-1C chain	14809.92	-0.4584
Q68FR8	Tubulin alpha-3 chain	13904.29	-0.436
Q5XIF6	Tubulin alpha-4A chain	12891.46	-0.436
Q6AY56	Tubulin alpha-8 chain	7545.25	-0.3679
Q4QQV0	Tubulin beta chain	13767.53	-0.4771
P85108	Tubulin beta-2A chain	21576.78	-0.4916
Q3KRE8	Tubulin beta-2B chain	21249.4	-0.4868
Q4QRB4	Tubulin beta-3 chain	19581.19	-0.4916
Q6P9T8	Tubulin beta-4B chain	23390.48	-0.4677
P69897	Tubulin beta-5 chain	20969.97	-0.4819
A0A0G2K2D6	Tubulin polymerization-promoting protein	2393.8	1.07251
Q6IG08	Type II keratin 23	55.76	3.81904

A0A0G2JVA8	Type II keratin Kb15	55.76	3.93535
D4AA63	Ubiquilin 2	62.64	2.03399
F1LU69	Ubiquitin B pseudogene 4	2047.21	1.10517
Q00981	Ubiquitin carboxyl-terminal hydrolase isozyme L1	2801.35	-0.8521
B2RYG6	Ubiquitin thioesterase OTUB1	313.49	1.69893
P62982	Ubiquitin-40S ribosomal protein S27a	2453.46	1.08329
P62986	Ubiquitin-60S ribosomal protein L40	2453.46	1.10517
Q9EQX9	Ubiquitin-conjugating enzyme E2 N	427.42	1.30996
A0A0G2K3Z9	Uncharacterized protein	73.37	1.13883
F1M1Y1	Uncharacterized protein	308.74	1.10517
F1M2S4	Uncharacterized protein	148.25	1.64872
A0A0G2K099	Uncharacterized protein	3186.49	1.2586
F1M2N4	Uncharacterized protein	2955.45	1.23368
A0A0G2K7R1	Uncharacterized protein	4677.37	1.55271
F1M4G6	Uncharacterized protein	2673.43	1.23368
D3ZEN2	Uncharacterized protein	2673.43	1.23368
F1LUI2	Uncharacterized protein	435.72	1.13883
A0A0G2JYY8	Uncharacterized protein	2083.45	-0.9231
D3ZME3	Uncharacterized protein	2083.45	-0.9324
Q9QUL6	Vesicle-fusing ATPase	191.61	-0.5543
P31000	Vimentin	308.71	1.08329
P81155	Voltage-dependent anion-selective channel protein 2	1235.06	-0.6505
Q9R1Z0	Voltage-dependent anion-selective channel protein 3	501.47	-0.6839
Q5M7T6	V-type proton ATPase subunit	291.59	-0.6505
P62815	V-type proton ATPase subunit B, brain isoform	826.52	-0.7945
P50408	V-type proton ATPase subunit F	396.23	1.78604
A0A0G2K2R1	V-type proton ATPase subunit G	190.55	1.59999
Q5RKI0	WD repeat-containing protein 1	460.14	-0.7866

G3V9G6

Zinc finger protein 111

44.33

14.154

^aAccession ID according to Uniport.org database.

Signs of + or – indicates up or down-regulation, respectively, when EG is compared to CG.