

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
9630023C09Rik	:RIKEN cDNA 9630023C09 gene	0.0000	0.0012	0.1311	5.52	8.25	5.37
B830012L14Rik	:RIKEN cDNA B830012L14 gene	0.0058	0.0000	0.0699	2.94	4.68	2.32
D130084N16Rik	:RIKEN cDNA D130084N16 gene	0.0060	0.0003	0.0337	1.88	2.39	2.28
5930422O12Rik	:RIKEN cDNA 5930422O12 gene	0.0086	0.0002	0.0404	2.07	2.93	2.22
2900034C19Rik	:RIKEN cDNA 2900034C19 gene	0.0038	0.0000	0.0496	2.1	5.81	2.15
6720477C19Rik	:RIKEN cDNA 6720477C19 gene	0.0015	0.0001	0.0704	2.32	3.31	2.11
C80998	:expressed sequence C80998	0.0014	0.0000	0.1367	2.4	3.51	2.07
6430537K16Rik	:RIKEN cDNA 6430537K16 gene	0.0077	0.0002	0.2091	2.16	3.1	2.01
D3Erd740e	:DNA segment, Chr 3, ERATO Doi 740, expressed	0.0087	0.0003	0.0251	1.64	2.15	1.91
3100002H09Rik	:RIKEN cDNA 3100002H09 gene	0.0062	0.0051	0.2091	2.1	2.99	1.89
5031426D15Rik	:RIKEN cDNA 5031426D15 gene	0.0006	0.0000	0.2801	2.89	6.27	1.8
8030445P17Rik	:RIKEN cDNA 8030445P17 gene	0.0090	0.0009	0.0254	1.81	2.21	1.78
AU019559	:expressed sequence AU019559	0.0080	0.0001	0.0750	1.77	2.58	1.78
D530037H12Rik	:RIKEN cDNA D530037H12 gene	0.0032	0.0012	0.0464	1.9	1.95	1.74
2810043O03Rik	:RIKEN cDNA 2810043O03 gene	0.0015	0.0000	0.1905	2.2	3.1	1.73
1500032P08Rik	:RIKEN cDNA 1500032P08 gene	0.0040	0.0018	0.0940	2.12	2.43	1.71
A930013F10Rik	:RIKEN cDNA A930013F10 gene	0.0033	0.0001	0.0603	1.87	2.54	1.7
Pcdh15	:protocadherin 15	0.0049	0.0002	0.0389	1.9	1.7	1.66
4732423E21Rik	:RIKEN cDNA 4732423E21 gene	0.0014	0.0000	0.1203	2.14	3.1	1.63
Cdc45	:coiled-coil domain containing 45	0.0029	0.0036	0.0464	1.66	1.68	1.52
D230019N24Rik	:RIKEN cDNA D230019N24 gene	0.0077	0.0012	0.1115	1.71	2.17	1.51
Dlx6os2	:Dlx6 opposite strand transcript 2	0.0059	0.0003	0.1654	1.66	2.15	1.51
D930001B02	:hypothetical protein D930001B02	0.0029	0.0000	0.1870	1.7	2.21	1.51
9930017N22Rik	:RIKEN cDNA 9930017N22 gene	0.0089	0.0001	0.1618	1.7	2.1	1.49
2010111O1Rik	:RIKEN cDNA 2010111O1 gene	0.0073	0.0043	0.0452	1.48	1.55	1.49
Hs3st3a1	:heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	0.0060	0.0092	0.3114	2.2	2.38	1.49
Slc18a2	:solute carrier family 18 (vesicular monoamine), member 2	0.0010	0.0004	0.1598	-2.76	-3.12	1.49
Chuk	:conserved helix-loop-helix ubiquitous kinase	0.0020	0.0000	0.0675	1.58	2.02	1.48
Dusp11	:dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	0.0063	0.0037	0.0220	1.46	1.53	1.47
9330156P08Rik	:RIKEN cDNA 9330156P08 gene	0.0027	0.0001	0.1277	1.7	2.09	1.45
Norna00081	:non-protein coding RNA 81	0.0020	0.0016	0.0594	-1.46	-1.39	1.45
2900055J20Rik	:RIKEN cDNA 2900055J20 gene	0.0099	0.0002	0.1219	1.61	2.2	1.44
DnaJ21	:DnaJ (Hsp40) homolog, subfamily C, member 21	0.0038	0.0017	0.0267	1.33	1.45	1.44
H2-T24	:histocompatibility 2, T region locus 24	0.0055	0.0036	0.2303	-2.12	-1.66	1.43
9230108I15Rik	:RIKEN cDNA 9230108I15 gene	0.0025	0.0013	0.1249	1.76	1.98	1.4
Leprel2	:leprecan-like 2	0.0017	0.0070	0.0278	1.66	1.55	1.39
Nktr	:natural killer tumor recognition sequence	0.0013	0.0018	0.0152	1.56	1.42	1.39
Gcfc1	:GC-rich sequence DNA-binding factor 1	0.0034	0.0012	0.0116	1.31	1.45	1.38
Snhg3	:small nucleolar RNA host gene (non-protein coding) 3	0.0099	0.0013	0.0940	1.3	1.49	1.35
9230104K21Rik	:RIKEN cDNA 9230104K21 gene	0.0079	0.0047	0.1323	1.63	1.87	1.35
3110082D06Rik	:RIKEN cDNA 3110082D06 gene	0.0052	0.0058	0.0573	1.57	1.64	1.34
Phyhd1	:phytanoyl-CoA dioxygenase domain containing 1	0.0038	0.0009	0.0125	1.36	1.44	1.34
Shank2	:SH3/ankyrin domain gene 2	0.0031	0.0000	0.0155	1.43	1.56	1.34
2610030P05Rik	:RIKEN cDNA 2610030P05 gene	0.0006	0.0004	0.2165	2.09	1.89	1.34
Luc7i3	:LUC7-like 3 (S. cerevisiae)	0.0059	0.0003	0.0106	1.21	1.39	1.33
Cdv3	:carnitine deficiency-associated gene expressed in ventricle 3	0.0027	0.0011	0.0384	1.23	1.31	1.32
Arglu1	:arginine and glutamate rich 1	0.0019	0.0001	0.0178	1.29	1.56	1.31
Prkg2	:protein kinase, GMP-dependent, type II	0.0015	0.0042	0.1194	1.53	1.68	1.31
Zmym5	:zinc finger, MYM-type 5	0.0014	0.0013	0.0228	1.37	1.36	1.31
6330418B08Rik	:RIKEN cDNA 6330418B08 gene	0.0003	0.0002	0.3489	2.19	2.35	1.31
Fyco1	:FYVE and coiled-coil domain containing 1	0.0002	0.0000	0.3492	2.21	2.85	1.31
C130015C19	:hypothetical LOC403342	0.0050	0.0019	0.2403	1.83	1.91	1.3
Pcgr6	:polycomb group ring finger 6	0.0030	0.0007	0.1064	1.45	1.56	1.3
Micalcl	:MICAL C-terminal like	0.0091	0.0015	0.4572	1.53	1.6	1.29
Dvl1	:dishevelled, dsh homolog 1 (Drosophila)	0.0018	0.0000	0.0460	1.23	1.65	1.29
Ncan	:neurocan	0.0003	0.0001	0.0723	1.62	1.62	1.29
Cdc14b	:CDC14 cell division cycle 14 homolog B (S. cerevisiae)	0.0022	0.0035	0.0452	1.4	1.39	1.28
4933427D14Rik	:RIKEN cDNA 4933427D14 gene	0.0006	0.0015	0.0369	1.39	1.32	1.28
Ddx26b	:DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	0.0057	0.0081	0.0900	1.45	1.4	1.27
Golga4	:golgi autoantigen, golgin subfamily a, 4	0.0013	0.0021	0.0551	1.34	1.38	1.27
Homer1	:homer homolog 1 (Drosophila)	0.0071	0.0006	0.2568	1.28	1.46	1.26
Igf1	:insulin-like growth factor 1	0.0047	0.0002	0.0433	1.35	1.39	1.26
Gbas	:glioblastoma amplified sequence	0.0028	0.0003	0.0186	1.3	1.49	1.26
Arfp1	:ADP-ribosylation factor related protein 1	0.0037	0.0006	0.0867	1.17	1.3	1.25
6720462K09Rik	:RIKEN cDNA 6720462K09 gene	0.0025	0.0009	0.1879	1.68	1.85	1.24
Chm	:choroidemia	0.0024	0.0006	0.0166	1.21	1.46	1.24
Vps37a	:vacuolar protein sorting 37A (yeast)	0.0020	0.0005	0.0414	1.3	1.38	1.24
Inpp5b	:inositol polyphosphate-5-phosphatase B	0.0006	0.0011	0.0170	1.26	1.43	1.24
Atxn7	:ataxin 7	0.0043	0.0003	0.0655	1.37	1.48	1.23
Shc3	:src homology 2 domain-containing transforming protein C3	0.0035	0.0032	0.0322	1.36	1.17	1.23
Cnnm4	:cyclin M4	0.0016	0.0002	0.3595	-1.51	-2.11	1.23
Abcg1	:ATP-binding cassette, sub-family G (WHITE), member 1	0.0007	0.0058	0.0109	1.23	1.16	1.23
Cacng2	:calcium channel, voltage-dependent, gamma subunit 2	0.0068	0.0000	0.2103	1.34	1.37	1.22
Hnmp1	:heterogeneous nuclear ribonucleoprotein H1	0.0015	0.0001	0.0279	1.19	1.4	1.22
B3gal1	:UDP-Gal:beta-GlcNAc beta 1,3-galactosyltransferase, polypeptide 1	0.0014	0.0008	0.2609	-1.82	-1.72	1.22
Inpp4a	:inositol polyphosphate-4-phosphatase, type I	0.0097	0.0002	0.1108	1.24	1.37	1.2
Rere	:arginine glutamic acid dipeptide (RE) repeats	0.0082	0.0010	0.0366	1.29	1.28	1.2
Mtmr12	:myotubularin related protein 12	0.0020	0.0058	0.0104	1.25	1.29	1.2
Mafg	:v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	0.0000	0.0000	0.4421	1.83	2.03	1.2
Arrdc2	:arrestin domain containing 2	0.0018	0.0028	0.1040	1.32	1.36	1.19
Katna1	:katanin p60 (ATPase-containing) subunit A1	0.0100	0.0019	0.2036	1.25	1.39	1.18
Usp16	:ubiquitin specific peptidase 16	0.0064	0.0044	0.0570	1.14	1.16	1.18
Pcdhb16	:protocadherin beta 16	0.0060	0.0006	0.4357	-1.68	-1.8	1.18
4930455F23Rik	:RIKEN cDNA 4930455F23 gene	0.0033	0.0002	0.0293	1.17	1.22	1.18
Spry2	:sprouty homolog 2 (Drosophila)	0.0014	0.0035	0.0150	-1.23	-1.24	1.18
2700023E23Rik	:RIKEN cDNA 2700023E23 gene	0.0064	0.0001	0.2025	1.38	1.79	1.17
2510002D24Rik	:RIKEN cDNA 2510002D24 gene	0.0044	0.0049	0.2731	1.53	1.42	1.17
Endod1	:endonuclease domain containing 1	0.0022	0.0001	0.4908	-1.59	-2.08	1.17
Pggt1b	:protein geranylgeranyltransferase type I, beta subunit	0.0012	0.0002	0.0864	1.25	1.39	1.17
Rad52	:RAD52 homolog (S. cerevisiae)	0.0005	0.0030	0.0221	1.34	1.27	1.17
Nab1	:Ngf-A binding protein 1	0.0008	0.0007	0.0837	1.24	1.35	1.16
Med1	:mediator complex subunit 1	0.0008	0.0000	0.3320	-1.97	-2	1.16
Unc80	:unc-80 homolog (C. elegans)	0.0051	0.0018	0.1152	1.19	1.25	1.15
Plk3ca	:phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0.0023	0.0000	0.2420	1.41	1.5	1.15
Samd5	:sterile alpha motif domain containing 5	0.0100	0.0009	0.5687	-1.6	-2.2	1.14
1500002C15Rik	:RIKEN cDNA 1500002C15 gene	0.0016	0.0034	0.6763	-1.87	-2.77	1.14
Polb	:polymerase (DNA directed), beta	0.0004	0.0000	0.1266	1.2	1.38	1.14
Uba6	:ubiquitin-like modifier activating enzyme 6	0.0000	0.0003	0.2249	1.34	1.39	1.14
Zeb2	:zinc finger E-box binding homeobox 2	0.0076	0.0022	0.5523	-1.71	-1.71	1.13
Fbxo32	:F-box protein 32	0.0049	0.0016	0.6461	-1.85	-2.33	1.13
Gm4455	:predicted gene 4455	0.0020	0.0001	0.3665	-1.52	-1.58	1.13
Slc20a1	:solute carrier family 20, member 1	0.0009	0.0003	0.0738	1.16	1.16	1.13
Eny2	:enhancer of yellow 2 homolog (Drosophila)	0.0005	0.0000	0.4024	-1.5	-1.63	1.13
Runx11f	:runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	0.0002	0.0003	0.1007	1.39	1.48	1.13
Klhl28	:kelch-like 28 (Drosophila)	0.0002	0.0000	0.1922	-1.53	-1.53	1.13
Mudeng	:MU-2/AP1M2 domain containing, death-inducing	0.0072	0.0001	0.2230	-1.31	-1.5	1.12

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Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Fam65a	family with sequence similarity 65, member A	0.0063	0.0070	0.2288	1.3	1.26	1.12
Zdhc24	zinc finger, DHHC domain containing 24	0.0050	0.0017	0.1690	1.26	1.38	1.12
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor	0.0026	0.0017	0.1887	-1.29	-1.28	1.12
Ddhd2	DDHD domain containing 2	0.0005	0.0090	0.1057	1.16	1.19	1.12
Psmc10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.0069	0.0071	0.0750	-1.12	1.14	1.11
Snhg12	small nucleolar RNA host gene 12	0.0010	0.0000	0.0301	1.17	1.35	1.11
Mltf6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0.0005	0.0031	0.0990	1.19	1.18	1.11
G3bp2	GTPase activating protein (SH3 domain) binding protein 2	0.0043	0.0000	0.3107	-1.28	-1.3	1.1
Larp1	La ribonucleoprotein domain family, member 1	0.0012	0.0060	0.1790	1.15	1.14	1.1
Apc	adenomatosis polyposis coli	0.0012	0.0009	0.0467	1.1	1.19	1.1
Scn8a	sodium channel, voltage-gated, type VIII, alpha	0.0062	0.0006	0.0834	1.13	1.13	1.09
Tro	trophinin	0.0060	0.0025	0.3198	1.23	1.2	1.09
Kif1b	kinesin family member 1B	0.0010	0.0001	0.0636	1.16	1.25	1.09
Pcdhgc4	protocadherin gamma subfamily C, 4	0.0006	0.0048	0.7392	2.16	1.71	1.09
Slc38a1	solute carrier family 38, member 1	0.0070	0.0000	0.6080	-1.45	-1.81	1.08
Rictor	RPTOR independent companion of MTOR, complex 2	0.0031	0.0005	0.2549	1.14	1.22	1.08
Cd55	CD55 antigen	0.0022	0.0000	0.2775	1.39	1.63	1.08
Lass4	LAG1 homolog, ceramide synthase 4	0.0010	0.0004	0.6900	1.39	1.46	1.08
Epas1	endothelial PAS domain protein 1	0.0065	0.0052	0.3340	1.2	1.28	1.07
Arhgap32	Rho GTPase activating protein 32	0.0052	0.0000	0.6371	-1.36	-1.78	1.07
Pura	purine rich element binding protein A	0.0041	0.0001	0.7095	1.31	1.59	1.07
Pcmd1	protein-L-isospartate (D-aspartate) O-methyltransferase domain containing	0.0041	0.0011	0.4516	-1.21	-1.26	1.07
Scn2a1	sodium channel, voltage-gated, type II, alpha 1	0.0032	0.0037	0.0830	1.14	1.11	1.07
Celf5	CUGBP, Elav-like family member 5	0.0006	0.0022	0.1146	1.24	1.15	1.07
Zfp148	zinc finger protein 148	0.0069	0.0000	0.5348	-1.3	-1.47	1.06
1200016B10Rik	RIKEN cDNA 1200016B10 gene	0.0060	0.0010	0.6775	1.31	1.29	1.06
Sp1	trans-acting transcription factor 1	0.0058	0.0000	0.7121	-1.63	-1.94	1.06
6430547I21Rik	RIKEN cDNA 6430547I21 gene	0.0055	0.0002	0.6874	1.54	1.64	1.06
Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	0.0031	0.0000	0.7258	-1.73	-2.75	1.06
Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta	0.0025	0.0000	0.4090	1.13	1.28	1.06
Wipf2	WAS/WASL interacting protein family, member 2	0.0023	0.0024	0.6952	1.37	1.28	1.06
Gtbbp2	GTP binding protein 2	0.0011	0.0014	0.4004	1.28	1.26	1.06
G3bp1	Ras-GTPase-activating protein SH3-domain binding protein 1	0.0049	0.0088	0.5212	1.18	1.18	1.05
Chd8	chromodomain helicase DNA binding protein 8	0.0030	0.0007	0.7225	1.42	1.46	1.05
Celf2	CUGBP, Elav-like family member 2	0.0023	0.0001	0.5333	1.31	1.4	1.05
Pbrm1	polybromo 1	0.0020	0.0085	0.5306	1.28	1.32	1.05
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.0000	0.0001	0.7374	1.43	1.5	1.05
Bicd2	bicaudal D homolog 2 (Drosophila)	0.0095	0.0005	0.2584	1.15	1.14	1.04
Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	0.0077	0.0013	0.4968	1.36	1.24	1.04
Rims2	regulating synaptic membrane exocytosis 2	0.0064	0.0000	0.8774	1.58	1.8	1.04
Trpc5	transient receptor potential cation channel, subfamily C, member 5	0.0058	0.0006	0.8296	-1.82	-2.07	1.04
Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyl	0.0050	0.0001	0.7826	-1.37	-1.85	1.04
Dst	dystonin	0.0044	0.0000	0.7222	1.4	1.42	1.04
4632415L05Rik	RRS1 ribosome biogenesis regulator homolog pseudogene	0.0037	0.0018	0.7689	-1.5	-1.42	1.04
Dixdc1	DIX domain containing 1	0.0031	0.0055	0.3647	1.12	1.19	1.04
Kctd12b	potassium channel tetramerisation domain containing 12b	0.0015	0.0061	0.7765	-1.89	-1.62	1.04
7630402I04Rik	RIKEN cDNA 7630402I04 gene	0.0007	0.0005	0.7925	-1.71	-1.98	1.04
Mett11d1	methyltransferase 11 domain containing 1	0.0002	0.0089	0.7186	1.43	1.39	1.04
4930402H24Rik	RIKEN cDNA 4930402H24 gene	0.0000	0.0001	0.7540	1.59	1.46	1.04
Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.0064	0.0076	0.8290	1.22	1.22	1.03
Tmem151b	transmembrane protein 151B	0.0019	0.0002	0.7307	1.32	1.29	1.03
Naa15	N(alpha)-acetyltransferase 15, NAtA auxiliary subunit	0.0010	0.0001	0.6919	-1.35	-1.52	1.03
Rap2b	RAP2B, member of RAS oncogene family	0.0004	0.0001	0.8440	-1.68	-1.63	1.03
Anapc5	anaphase-promoting complex subunit 5	0.0002	0.0006	0.4769	1.16	1.09	1.03
Smad5	MAD homolog 5 (Drosophila)	0.0088	0.0005	0.8959	-1.36	-1.6	1.02
Dnajb14	DnaJ (Hsp40) homolog, subfamily B, member 14	0.0073	0.0002	0.9366	-1.85	-2.25	1.02
Lpin2	lipin 2	0.0002	0.0004	0.8029	1.26	1.22	1.02
A930026I22Rik	RIKEN cDNA A930026I22 gene	0.0083	0.0043	0.8890	-1.17	-1.23	1.01
Abl2	abl-interactor 2	0.0081	0.0004	0.9452	-1.3	-1.5	1.01
Pdap1	PDGFA associated protein 1	0.0067	0.0006	0.9155	-1.22	-1.25	1.01
Xpo4	exportin 4	0.0052	0.0010	0.9364	-1.68	-2.05	1.01
Fam81a	family with sequence similarity 81, member A	0.0049	0.0002	0.9228	-1.57	-2	1.01
Fam63b	family with sequence similarity 63, member B	0.0046	0.0001	0.9174	-1.42	-1.57	1.01
Gabbr1	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1	0.0035	0.0000	0.9411	1.33	1.51	1.01
Hils1	histone H1-like protein in spermatids 1	0.0004	0.0024	0.9819	-1.78	-1.72	1
Ppat	phosphoribosyl pyrophosphate amidotransferase	0.0054	0.0023	0.9486	-1.34	-1.48	-1.01
6330407J23Rik	RIKEN cDNA 6330407J23 gene	0.0010	0.0001	0.9506	1.36	1.35	-1.01
Camsap1	calmodulin regulated spectrin-associated protein 1	0.0099	0.0015	0.9110	1.53	1.59	-1.02
Slpi	secretory leukocyte peptidase inhibitor	0.0059	0.0083	0.9473	-1.53	-1.52	-1.02
Fam92a	family with sequence similarity 92, member A	0.0018	0.0082	0.4330	-1.09	1.13	-1.02
Nbr1	neighbor of Brca1 gene 1	0.0015	0.0080	0.5222	-1.06	-1.07	-1.02
Tmem167	transmembrane protein 167	0.0008	0.0000	0.8030	-1.46	-1.49	-1.02
Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	0.0034	0.0074	0.7354	-1.16	-1.23	-1.03
Zc4h2	zinc finger, C4H2 domain containing	0.0005	0.0019	0.4127	-1.17	-1.1	-1.03
Fam69a	family with sequence similarity 69, member A	0.0005	0.0002	0.7163	-1.18	-1.3	-1.03
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	0.0063	0.0002	0.6724	-1.35	-1.48	-1.04
Ubi3	ubiquitin-like 3	0.0016	0.0001	0.6167	-1.27	-1.35	-1.04
Impad1	inositol monophosphatase domain containing 1	0.0006	0.0001	0.8273	-1.67	-1.65	-1.04
Bzw2	basic leucine zipper and W2 domains 2	0.0006	0.0002	0.7610	1.55	1.6	-1.04
Fut9	fucosyltransferase 9	0.0000	0.0092	0.2931	-1.26	-1.15	-1.04
Samd12	sterile alpha motif domain containing 12	0.0100	0.0002	0.8217	-1.77	-3.38	-1.05
Gmps	guanine monophosphate synthetase	0.0068	0.0002	0.7588	-1.38	-1.87	-1.05
Klf15	Kruppel-like factor 15	0.0066	0.0064	0.3865	1.29	1.34	-1.05
Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	0.0052	0.0004	0.7785	1.31	1.33	-1.05
Sart1	squamous cell carcinoma antigen recognized by T-cells 1	0.0034	0.0002	0.3495	-1.13	-1.22	-1.05
1600012F09Rik	RIKEN cDNA 1600012F09 gene	0.0009	0.0011	0.4838	-1.31	-1.2	-1.05
Actr2	ARP2 actin-related protein 2 homolog (yeast)	0.0073	0.0074	0.4817	1.17	1.16	-1.06
Arhgap5	Rho GTPase activating protein 5	0.0066	0.0025	0.3198	-1.2	-1.18	-1.06
Ptges3	prostaglandin H synthase 3 (cytosolic)	0.0027	0.0041	0.1574	-1.13	-1.16	-1.06
Zc3h15	zinc finger CCCH-type containing 15	0.0006	0.0011	0.5188	-1.44	-1.36	-1.06
A230046K03Rik	RIKEN cDNA A230046K03 gene	0.0006	0.0000	0.5999	-1.44	-1.49	-1.06
Usp15	ubiquitin specific peptidase 15	0.0069	0.0025	0.3144	-1.29	-1.28	-1.07
Lnp	limb and neural patterns	0.0046	0.0038	0.2154	-1.17	-1.25	-1.07
Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	0.0045	0.0002	0.5613	-1.48	-1.7	-1.07
Hcfc1	host cell factor C1	0.0030	0.0022	0.0419	1.19	-1.14	-1.07
Romo1	reactive oxygen species modulator 1	0.0029	0.0043	0.1392	-1.15	1.11	-1.07
Mia3	melanoma inhibitory activity 3	0.0013	0.0001	0.6556	-1.76	-2.33	-1.07
Sesn3	sestrin 3	0.0003	0.0000	0.7382	-2.33	-2.82	-1.07
Fbxo16	F-box protein 16	0.0033	0.0069	0.5078	-1.59	-1.6	-1.08
Ubn1	ubiquitin 1	0.0028	0.0000	0.1944	-1.35	-1.53	-1.08
Kif1a	kinesin family member 1A	0.0025	0.0091	0.2465	1.24	-1.24	-1.08
Bptf	bromodomain PHD finger transcription factor	0.0018	0.0013	0.4224	1.21	1.28	-1.08
Tmem30a	transmembrane protein 30A	0.0018	0.0000	0.4027	-1.32	-1.54	-1.08
Wdr37	WD repeat domain 37	0.0067	0.0014	0.1001	-1.15	-1.24	-1.09
Cldnd1	claudin domain containing 1	0.0057	0.0000	0.4141	-1.34	-2.1	-1.1
Rabl3	RAB, member of RAS oncogene family-like 3	0.0042	0.0020	0.2298	-1.25	-1.4	-1.1

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
6330509M05Rik	RIKEN cDNA 6330509M05 gene	0.0041	0.0002	0.6969	1.54	1.75	-1.1
Pus3	pseudouridine synthase 3	0.0020	0.0100	0.3729	-1.24	-1.35	-1.1
Arhgef9	CDC42 guanine nucleotide exchange factor (GEF) 9	0.0019	0.0001	0.4629	-1.26	-1.57	-1.1
Myo10	myosin X	0.0008	0.0003	0.3370	-1.37	-1.54	-1.1
Nfe2l3	nuclear factor, erythroid derived 2, like 3	0.0000	0.0054	0.1437	-1.69	-1.31	-1.1
Huwe1	HECT, UBA and WWE domain containing 1	0.0053	0.0014	0.0405	1.11	-1.2	-1.11
Ccdc71	coiled-coil domain containing 71	0.0049	0.0054	0.1431	-1.26	-1.21	-1.11
Bat1a	HLA-B-associated transcript 1A	0.0003	0.0021	0.0327	1.06	-1.09	-1.11
Pde1a	phosphodiesterase 1A, calmodulin-dependent	0.0094	0.0028	0.2386	-1.32	-1.44	-1.12
B3gal2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	0.0039	0.0008	0.3978	-1.51	-1.62	-1.12
Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	0.0017	0.0001	0.2881	-1.5	-1.58	-1.12
Fyttd1	forty-two-three domain containing 1	0.0002	0.0001	0.3563	-1.56	-1.64	-1.12
Rbm27	RNA binding motif protein 27	0.0065	0.0000	0.2972	-1.19	-1.45	-1.13
Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.0035	0.0051	0.0392	-1.13	-1.2	-1.13
3000002C10Rik	glyceraldehyde-3-phosphate dehydrogenase pseudogene	0.0086	0.0005	0.0904	-1.19	-1.32	-1.14
Prr5l	proline rich 5 like	0.0084	0.0003	0.2640	-1.32	-1.64	-1.14
Ythdf2	YTH domain family 2	0.0003	0.0001	0.1303	-1.33	-1.44	-1.14
Gqps1	geranylgeranyl diphosphate synthase 1	0.0027	0.0003	0.0797	-1.33	-1.42	-1.15
Pcdh10	protocadherin 10	0.0025	0.0001	0.1328	-1.16	-1.29	-1.16
Plcb3	phospholipase C, beta 3	0.0015	0.0012	0.0782	-1.67	-1.49	-1.16
Rhobtb3	Rho-related BTB domain containing 3	0.0013	0.0000	0.4048	-2.19	-2.82	-1.16
Slu7	SLU7 splicing factor homolog (S. cerevisiae)	0.0046	0.0083	0.2899	1.36	1.34	-1.17
Nrg1	neuregulin 1	0.0089	0.0016	0.1281	-1.23	-2.17	-1.18
Lpar1	lysophosphatidic acid receptor 1	0.0045	0.0011	0.0599	-1.28	-1.42	-1.18
Clcc1	chloride channel CLIC-like 1	0.0043	0.0080	0.0144	-1.22	-1.18	-1.19
Rab14	RAB14, member RAS oncogene family	0.0081	0.0000	0.3550	1.41	1.5	-1.2
Mal2	mal, T-cell differentiation protein 2	0.0047	0.0004	0.0335	-1.19	-1.36	-1.2
Pdcd6ip	programmed cell death 6 interacting protein	0.0038	0.0000	0.0405	-1.25	-1.53	-1.2
Stx1b	syntaxin 1B	0.0017	0.0037	0.0204	1.18	-1.24	-1.2
Rdh11	retinol dehydrogenase 11	0.0018	0.0001	0.1986	-1.44	-1.84	-1.21
Fam115a	family with sequence similarity 115, member A	0.0039	0.0025	0.0170	-1.3	-1.32	-1.22
Lrp1	low density lipoprotein receptor-related protein 1	0.0023	0.0013	0.0105	1.15	-1.19	-1.22
Zfp868	zinc finger protein 868	0.0030	0.0068	0.0179	-1.13	-1.19	-1.23
Cpd	carboxypeptidase D	0.0029	0.0000	0.1542	-1.67	-2.42	-1.24
Pias1	protein inhibitor of activated STAT 1	0.0004	0.0032	0.1322	1.36	1.29	-1.24
Griin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)	0.0007	0.0000	0.4526	1.76	1.88	-1.25
Hdgf	hepatoma-derived growth factor	0.0074	0.0007	0.4203	1.48	1.49	-1.26
Ppp2r3a	protein phosphatase 2, regulatory subunit B", alpha	0.0029	0.0000	0.0551	-1.38	-1.91	-1.26
Setd8	SET domain containing (lysine methyltransferase) 8	0.0085	0.0062	0.3042	1.42	1.56	-1.27
Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	0.0028	0.0003	0.0405	-1.55	-2.11	-1.29
Cnec2	cyclin E2	0.0056	0.0005	0.0431	-1.43	-1.57	-1.31
Srp72	signal recognition particle 72	0.0083	0.0002	0.2446	1.51	1.6	-1.32
Cttnbp2nl	CTTNBP2 N-terminal like	0.0075	0.0023	0.0131	-1.32	-1.48	-1.44
Ptpn4	protein tyrosine phosphatase, non-receptor type 4	0.0066	0.0000	0.0143	-1.39	-2.57	-1.48
Tmem180	transmembrane protein 180	0.0033	0.0018	0.1733	1.54	-2.8	-1.63
Zc3h6	zinc finger CCCH type containing 6	0.0007	0.0082	0.0201	-1.37	-1.46	-1.66
Gprin2	G protein regulated inducer of neurite outgrowth 2	0.0010	0.0050	0.0114	-1.47	-1.64	-1.67
A930018P22Rik	RIKEN cDNA A930018P22 gene	0.0035	0.0006	0.0271	-3.15	-3.88	-1.77
Gpr165	G protein-coupled receptor 165	0.0019	0.0048	0.0219	-2.35	-2.99	-1.95
C79999	expressed sequence C79999	0.0001	0.0620	0.0018	3.5	2.44	4.76
Mmp20	matrix metalloproteinase 20 (enamelysin)	0.0005	0.8043	0.0012	3.72	1.19	3.31
C130098B18Rik	RIKEN cDNA C130098B18 gene	0.0045	0.0315	0.0081	1.53	1.6	2.09
Ins15	insulin-like 5	0.0060	0.0121	0.0055	1.31	1.46	1.63
4933424B01Rik	RIKEN cDNA 4933424B01 gene	0.0081	0.0170	0.0012	1.25	1.22	1.48
Ncoa3	nuclear receptor coactivator 3	0.0066	0.0128	0.0033	1.27	1.3	1.44
Dlk2	delta-like 2 homolog (Drosophila)	0.0049	0.0626	0.0030	1.5	1.3	1.4
Ehbp1	EH domain binding protein 1	0.0067	0.0204	0.0048	1.16	1.19	1.35
Tcerq1	transcription elongation regulator 1 (CA150)	0.0086	0.1830	0.0005	1.17	1.09	1.31
Sgk3	serum/glucocorticoid regulated kinase 3	0.0040	0.0271	0.0057	1.31	1.33	1.3
Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	0.0004	0.0560	0.0030	1.22	1.17	1.3
Chd9	chromodomain helicase DNA binding protein 9	0.0037	0.0136	0.0023	1.19	1.24	1.28
Prp38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	0.0080	0.0218	0.0022	1.23	1.3	1.27
Eral1	Era (G-protein)-like 1 (E. coli)	0.0017	0.3146	0.0029	1.34	1.09	1.26
Jak2	Janus kinase 2	0.0023	0.0137	0.0005	1.18	1.14	1.25
Mapkbp1	mitogen-activated protein kinase binding protein 1	0.0007	0.1034	0.0060	1.3	1.1	1.25
Taf1a	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	0.0009	0.0109	0.0071	1.52	1.46	1.24
Taz	tafazzin	0.0029	0.0531	0.0048	1.19	1.12	1.23
Papd7	PAP associated domain containing 7	0.0042	0.0158	0.0037	1.21	1.15	1.21
Tub	tubby candidate gene	0.0037	0.0147	0.0065	1.19	1.2	1.21
Pcsk7	proprotein convertase subtilisin/kexin type 7	0.0007	0.0126	0.0069	1.24	1.23	1.17
Cog6	component of oligomeric golgi complex 6	0.0005	0.0163	0.0013	1.16	1.1	1.17
Macf1	microtubule-actin crosslinking factor 1	0.0006	0.0513	0.0023	1.17	1.11	1.15
Dctn6	dynactin 6	0.0003	0.1939	0.0030	-1.19	-1.05	1.14
Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	0.0018	0.4142	0.0076	1.13	1.03	1.12
Cep120	centrosomal protein 120	0.0031	0.1657	0.0082	1.14	1.08	1.08
Dek	DEK oncogene (DNA binding)	0.0015	0.3063	0.0046	-1.1	1.06	-1.09
Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	0.0036	0.6859	0.0065	-1.14	-1.02	-1.11
Ip6k1	inositol hexaphosphate kinase 1	0.0052	0.3298	0.0085	1.14	-1.07	-1.12
Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	0.0062	0.0199	0.0017	-1.18	-1.1	-1.13
Calu	calumenin	0.0070	0.3397	0.0037	1.07	-1.04	-1.14
Rps11	ribosomal protein S11	0.0027	0.2801	0.0091	-1.15	-1.05	-1.14
Dpp9	dipeptidylpeptidase 9	0.0087	0.0166	0.0027	1.26	1.1	-1.15
Ehmt2	euchromatic histone lysine N-methyltransferase 2	0.0006	0.2364	0.0092	1.21	-1.06	-1.15
2900010M23Rik	RIKEN cDNA 2900010M23 gene	0.0074	0.0236	0.0068	-1.1	-1.12	-1.16
Psmc1	protease (prosome, macropain) 26S subunit, ATPase 1	0.0042	0.0312	0.0033	-1.14	-1.09	-1.16
Comt1	catechol-O-methyltransferase 1	0.0029	0.0326	0.0055	1.12	-1.16	-1.17
Trim28	tripartite motif-containing 28	0.0023	0.0880	0.0020	1.12	-1.06	-1.17
Tram111	translocation associated membrane protein 1-like 1	0.0100	0.0998	0.0041	-1.15	-1.1	-1.18
Ola1	Obg-like ATPase 1	0.0094	0.0127	0.0027	-1.18	-1.15	-1.18
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0.0002	0.1736	0.0032	1.16	-1.05	-1.19
Repin1	replication initiator 1	0.0048	0.8804	0.0024	1.21	-1.01	-1.21
Cpsf1	cleavage and polyadenylation specific factor 1	0.0001	0.0556	0.0009	1.19	-1.12	-1.21
Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	0.0021	0.0261	0.0030	-1.1	-1.11	-1.24
Dalrd3	DALR anticodon binding domain containing 3	0.0007	0.6973	0.0057	1.25	-1.02	-1.24
D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	0.0096	0.1791	0.0004	-1.13	-1.04	-1.25
Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	0.0078	0.0825	0.0001	-1.11	-1.1	-1.29
Pde2a	phosphodiesterase 2A, cGMP-stimulated	0.0098	0.0152	0.0041	1.17	-1.23	-1.3
Nt5c3l	5'-nucleotidase, cytosolic III-like	0.0048	0.1598	0.0007	-1.19	-1.24	-1.3
Sqrdl	sulfide quinone reductase-like (yeast)	0.0070	0.6796	0.0051	-1.2	-1.04	-1.33
Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	0.0087	0.0471	0.0064	1.14	-1.1	-1.34
Git1	G protein-coupled receptor kinase-interactor 1	0.0007	0.0364	0.0001	1.39	-1.33	-1.35
Podxl2	podocalyxin-like 2	0.0084	0.0272	0.0075	1.25	-1.21	-1.36
Aglb3	ATP/GTP binding protein-like 3	0.0079	0.0138	0.0007	-1.42	-1.36	-1.39
Gcn11	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	0.0059	0.1470	0.0082	1.31	-1.25	-1.4
Arf6ip5	ADP-ribosylation factor-like 6 interacting protein 5	0.0059	0.3232	0.0001	-1.22	-1.06	-1.4
Pcsk1n	proprotein convertase subtilisin/kexin type 1 inhibitor	0.0080	0.0452	0.0015	1.17	-1.14	-1.41

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Dynl12	dynein light chain LC8-type 2	0.0097	0.0601	0.0001	-1.13	-1.08	-1.42
Capn5	calpain 5	0.0078	0.4530	0.0059	1.32	-1.07	-1.44
Hnmpab	heterogeneous nuclear ribonucleoprotein A/B	0.0016	0.0296	0.0036	-1.62	-1.22	-1.46
Sepw1	selenoprotein W, muscle 1	0.0003	0.0293	0.0002	1.38	-1.33	-1.5
Mir425	microRNA 425	0.0082	0.0847	0.0037	-1.57	-1.34	-1.51
Rgs3	regulator of G-protein signaling 3	0.0055	0.0124	0.0003	-1.2	-1.31	-1.51
Ssbp3	single-stranded DNA binding protein 3	0.0009	0.1426	0.0042	1.52	1.09	-1.68
Lix1	limb expression 1 homolog (chicken)	0.0039	0.0890	0.0002	-1.3	-1.26	-1.69
Hyou1	hypoxia up-regulated 1	0.0072	0.2605	0.0019	1.25	-1.19	-1.82
Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0.0069	0.0853	0.0000	-1.29	-1.28	-2.21
Tmem154	transmembrane protein 154	0.0020	0.0622	0.0082	-4.5	-1.95	-4.61
4933425L06Rik	RIKEN cDNA 4933425L06 gene	0.0154	0.0013	0.0013	4.99	7.54	5.89
Krtap31-1	keratin associated protein 31-1	0.0842	0.0076	0.0050	2.72	2.59	4.05
5033423O07Rik	RIKEN cDNA 5033423O07 gene	0.1275	0.0004	0.0010	2.28	3.15	3.99
A530058O07Rik	RIKEN cDNA A530058O07 gene	0.0397	0.0083	0.0090	2.23	3.84	3.91
Ugt2b35	UDP glucuronosyltransferase 2 family, polypeptide B35	0.0364	0.0050	0.0030	2.28	2.56	2.92
4930595D18Rik	RIKEN cDNA 4930595D18 gene	0.0392	0.0036	0.0001	1.64	2.17	2.8
Ccr12	chemokine (C-C motif) receptor-like 2	0.0231	0.0061	0.0026	2.04	2.64	2.77
5330406M23Rik	RIKEN cDNA 5330406M23 gene	0.0134	0.0000	0.0077	2.02	3.49	2.77
AW556556	expressed sequence AW556556	0.0275	0.0003	0.0044	1.79	3.45	2.42
Tm6sf2	transmembrane 6 superfamily member 2	0.8082	0.0070	0.0024	1.1	2.4	2.4
6330417A16Rik	RIKEN cDNA 6330417A16 gene	0.1428	0.0000	0.0021	1.27	3.67	2.35
Al605517	expressed sequence Al605517	0.1668	0.0061	0.0004	1.41	1.84	2.34
6430709C05Rik	RIKEN cDNA 6430709C05 gene	0.0625	0.0068	0.0018	1.6	2.17	2.32
Phxr1	per-hexamer repeat gene 1	0.0614	0.0098	0.0003	1.34	1.69	2.32
8430437O03Rik	RIKEN cDNA 8430437O03 gene	0.0254	0.0078	0.0017	1.57	2.01	2.3
LOC100134980	hypothetical LOC100134980	0.0383	0.0001	0.0008	1.55	2.54	2.28
8030425K09Rik	RIKEN cDNA 8030425K09 gene	0.1256	0.0090	0.0006	1.46	1.87	2.23
A130009122Rik	RIKEN cDNA A130009122 gene	0.0432	0.0008	0.0064	1.76	2.35	2.23
5830443J22Rik	RIKEN cDNA 5830443J22 gene	0.1557	0.0089	0.0044	1.29	1.77	2.16
C230007H23Rik	RIKEN cDNA C230007H23 gene	0.8921	0.0010	0.0063	1.03	2.06	2.12
LOC552902	hypothetical LOC552902	0.2112	0.0086	0.0040	1.32	1.92	2.08
9430064K01Rik	RIKEN cDNA 9430064K01 gene	0.0292	0.0093	0.0012	1.72	2.14	2.06
Gm3626	predicted gene 3626	0.0236	0.0005	0.0030	1.62	2.27	2.04
Pcdhg@	protocadherin gamma cluster	0.3538	0.0095	0.0025	1.2	1.72	2.03
B430203124Rik	RIKEN cDNA B430203124 gene	0.0446	0.0053	0.0063	1.53	1.81	2.01
Zkscan3	zinc finger with KRAB and SCAN domains 3	0.2043	0.0001	0.0059	1.25	2.13	2
Fmn2	formin 2	0.0170	0.0016	0.0005	1.56	1.81	2
9430034F23Rik	RIKEN cDNA 9430034F23 gene	0.0118	0.0000	0.0097	1.56	2.03	1.99
Rbm6	RNA binding motif protein 6	0.1303	0.0089	0.0015	1.34	1.62	1.97
3110045A19Rik	RIKEN cDNA 3110045A19 gene	0.0652	0.0066	0.0002	1.42	1.69	1.96
1110006E14Rik	RIKEN cDNA 1110006E14 gene	0.0254	0.0002	0.0003	1.4	2.6	1.95
Fam60a	family with sequence similarity 60, member A	0.0220	0.0008	0.0059	1.58	2.1	1.94
DXErt223e	DNA segment, Chr X, ERATO Doi 223, expressed	0.1760	0.0006	0.0057	1.3	2.07	1.93
A230006K03Rik	RIKEN cDNA A230006K03 gene	0.0191	0.0079	0.0011	1.57	1.68	1.93
5830456J23Rik	RIKEN cDNA 5830456J23 gene	0.0217	0.0004	0.0072	1.66	2.39	1.92
4633401B06Rik	RIKEN cDNA 4633401B06 gene	0.0372	0.0027	0.0001	1.31	1.64	1.9
A930035E12Rik	RIKEN cDNA A930035E12 gene	0.0140	0.0036	0.0090	1.81	2.27	1.88
Al415730	expressed sequence Al415730	0.0514	0.0076	0.0044	1.34	1.5	1.86
C80258	expressed sequence C80258	0.0320	0.0080	0.0007	1.45	1.83	1.84
C130034I24Rik	RIKEN cDNA C130034I24 gene	0.0292	0.0062	0.0069	1.6	1.8	1.84
4930447C04Rik	RIKEN cDNA 4930447C04 gene	0.0193	0.0084	0.0026	1.5	1.56	1.84
9030425L15Rik	RIKEN cDNA 9030425L15 gene	0.0184	0.0009	0.0040	1.61	1.89	1.84
Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	0.0209	0.0005	0.0004	1.51	1.92	1.83
B430007K19Rik	RIKEN cDNA B430007K19 gene	0.1526	0.0021	0.0011	1.28	1.54	1.8
B230117O15Rik	RIKEN cDNA B230117O15 gene	0.1554	0.0086	0.0043	1.43	1.94	1.79
Arhgap4	Rho GTPase activating protein 4	0.0439	0.0035	0.0012	1.7	1.81	1.79
B230214O09Rik	RIKEN cDNA B230214O09 gene	0.0190	0.0006	0.0027	1.5	2.03	1.75
D230040J21Rik	RIKEN cDNA D230040J21 gene	0.0161	0.0004	0.0053	1.69	2.14	1.75
A230061C15Rik	RIKEN cDNA A230061C15 gene	0.1185	0.0062	0.0070	1.34	1.8	1.74
A130012E19Rik	RIKEN cDNA A130012E19 gene	0.1991	0.0049	0.0059	1.26	1.83	1.73
Prp4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.0142	0.0002	0.0003	1.32	1.78	1.73
Tmem86b	transmembrane protein 86B	0.1416	0.0074	0.0051	1.45	1.68	1.72
Ccdc51	coiled-coil domain containing 51	0.1198	0.0015	0.0055	1.31	1.35	1.7
Taf1d	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, D	0.1545	0.0028	0.0037	1.3	1.87	1.69
Eml5	echinoderm microtubule associated protein like 5	0.0412	0.0026	0.0007	1.31	1.54	1.68
Gm2590	predicted gene 2590	0.0363	0.0030	0.0077	1.42	1.85	1.67
Adamts20	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motifs	0.4285	0.0009	0.0018	1.11	1.77	1.66
CD59a	CD59a antigen	0.0776	0.0019	0.0089	1.33	1.55	1.65
Cdc7	cell division cycle 7 (S. cerevisiae)	0.0130	0.0061	0.0004	1.3	1.62	1.65
LOC552906	hypothetical LOC552906	0.0648	0.0073	0.0004	1.34	1.44	1.63
Aph1a	anterior pharynx defective 1a homolog (C. elegans)	0.9291	0.0002	0.0000	-1.01	1.47	1.62
D130023J23Rik	RIKEN cDNA D130023J23 gene	0.3490	0.0023	0.0087	1.15	1.6	1.62
D2Ert612e	DNA segment, Chr 2, ERATO Doi 612, expressed	0.0106	0.0037	0.0047	1.49	1.67	1.62
A430102J17Rik	RIKEN cDNA A430102J17 gene	0.0279	0.0021	0.0080	1.46	1.81	1.61
Fubp1	far upstream element (FUSE) binding protein 1	0.0349	0.0028	0.0026	1.37	1.54	1.6
5830427D02Rik	RIKEN cDNA 5830427D02 gene	0.8580	0.0001	0.0018	-1.02	1.93	1.56
A130022J15Rik	RIKEN cDNA A130022J15 gene	0.3782	0.0084	0.0033	1.13	1.64	1.56
BC006779	cDNA sequence BC006779	0.0584	0.0024	0.0016	1.26	1.6	1.56
4933416O17Rik	RIKEN cDNA 4933416O17 gene	0.1357	0.0084	0.0080	-1.27	-1.99	1.54
AU041474	expressed sequence AU041474	0.0508	0.0019	0.0052	1.31	1.78	1.54
Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	0.2855	0.0043	0.0038	1.12	1.63	1.53
Al120166	expressed sequence Al120166	0.0211	0.0054	0.0012	1.28	1.48	1.52
Ankrd10	ankyrin repeat domain 10	0.0198	0.0004	0.0067	1.31	1.64	1.52
Fam114a2	family with sequence similarity 114, member A2	0.0809	0.0002	0.0000	1.21	1.43	1.5
C80068	expressed sequence C80068	0.0268	0.0078	0.0049	1.35	1.66	1.5
Srsf12	serine/arginine-rich splicing factor 12	0.0143	0.0009	0.0014	1.3	1.68	1.5
Tcf20	transcription factor 20	0.0706	0.0018	0.0074	1.15	1.4	1.49
Pde7a	phosphodiesterase 7A	0.0608	0.0011	0.0004	1.21	1.48	1.49
Kank2	KN motif and ankyrin repeat domains 2	0.4941	0.0012	0.0016	1.11	1.63	1.47
Rbm41	RNA binding motif protein 41	0.3993	0.0050	0.0002	1.07	1.3	1.47
Ubp1	upstream binding protein 1	0.0140	0.0020	0.0005	1.23	1.5	1.47
Plas	phosphoribosylformylglycinamide synthase (FGAR amidotransferase)	0.3205	0.0041	0.0000	1.05	1.22	1.46
Pin4	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	0.8596	0.0043	0.0009	1.01	1.37	1.44
Sfrs18	serine/arginine-rich splicing factor 18	0.0159	0.0007	0.0055	1.3	1.5	1.44
Sgms1	sphingomyelin synthase 1	0.7313	0.0002	0.0004	1.03	1.5	1.43
Ptpn2	protein tyrosine phosphatase, non-receptor type 2	0.1081	0.0000	0.0005	1.16	1.55	1.43
Mdn1	midasin homolog (yeast)	0.0911	0.0029	0.0009	1.19	1.46	1.43
Gxylt1	glucoside xylosyltransferase 1	0.5190	0.0011	0.0006	1.06	1.38	1.42
Al503301	expressed sequence Al503301	0.0389	0.0025	0.0044	1.24	1.46	1.42
2810403A07Rik	RIKEN cDNA 2810403A07 gene	0.0178	0.0063	0.0054	1.29	1.34	1.42
Sipa1l1	signal-induced proliferation-associated 1 like 1	0.5039	0.0005	0.0013	1.06	1.48	1.4
D19Ert132e	DNA segment, Chr 19, ERATO Doi 132, expressed	0.0660	0.0093	0.0089	1.24	1.47	1.4
Mapksp1	MAPK scaffold protein 1	0.8036	0.0002	0.0003	1.02	1.44	1.39
Phf14	PHD finger protein 14	0.1541	0.0002	0.0009	1.11	1.42	1.39
Bbs1	Bardet-Biedl syndrome 1 (human)	0.0975	0.0000	0.0001	1.17	1.46	1.38

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Lix1	Lix1-like	0.0931	0.0038	0.0027	1.25	1.47	1.38
2310001H12Rik	RIKEN cDNA 2310001H12 gene	0.0101	0.0008	0.0023	1.27	1.47	1.38
Bbs5	Bardet-Biedl syndrome 5 (human)	0.3518	0.0088	0.0017	1.08	1.27	1.37
2810055G20Rik	RIKEN cDNA 2810055G20 gene	0.0497	0.0021	0.0066	1.18	1.7	1.37
Paip2	polyadenylate-binding protein-interacting protein 2	0.8689	0.0013	0.0044	-1.01	1.4	1.36
Igdcc4	immunoglobulin superfamily, DCC subclass, member 4	0.4295	0.0004	0.0026	-1.05	1.44	1.36
Tra2a	transformer 2 alpha homolog (Drosophila)	0.1398	0.0099	0.0036	1.13	1.39	1.36
Tbc1d24	TBC1 domain family, member 24	0.1129	0.0002	0.0091	1.14	1.43	1.36
Lcor	ligand dependent nuclear receptor corepressor	0.0235	0.0020	0.0038	1.18	1.33	1.36
2810026P18Rik	RIKEN cDNA 2810026P18 gene	0.0114	0.0023	0.0034	1.25	1.49	1.36
2810455D13Rik	RIKEN cDNA 2810455D13 gene	0.1851	0.0063	0.0009	1.09	1.3	1.35
Sdcccag1	serologically defined colon cancer antigen 1	0.1639	0.0001	0.0006	-1.03	1.2	1.35
Las1l	LAS1-like (S. cerevisiae)	0.0946	0.0067	0.0012	1.12	1.24	1.35
Srsf6	serine/arginine-rich splicing factor 6	0.0119	0.0011	0.0087	1.18	1.35	1.35
BC016423	cDNA sequence BC016423	0.0648	0.0085	0.0020	1.16	1.25	1.34
Amy1	amylase 1, salivary	0.0440	0.0032	0.0020	1.2	1.32	1.34
Rps25	ribosomal protein S25	0.2549	0.0060	0.0046	1.08	1.23	1.33
Dgkz	diacylglycerol kinase zeta	0.2417	0.0000	0.0025	1.09	1.45	1.33
Smc6	structural maintenance of chromosomes 6	0.0162	0.0008	0.0040	1.12	1.19	1.33
Hnrnpul2	heterogeneous nuclear ribonucleoprotein U-like 2	0.0159	0.0012	0.0000	1.1	1.21	1.33
Med20	mediator complex subunit 20	0.6865	0.0023	0.0082	1.02	1.36	1.32
Tubk2	tau tubulin kinase 2	0.1605	0.0062	0.0004	1.09	1.15	1.32
Jakmp3	janus kinase and microtubule interacting protein 3	0.0729	0.0013	0.0091	1.16	1.39	1.32
Ino80d	INO80 complex subunit D	0.0419	0.0020	0.0001	1.11	1.21	1.32
Mlt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0.0189	0.0077	0.0066	1.21	1.29	1.32
Hook3	hook homolog 3 (Drosophila)	0.2420	0.0075	0.0074	1.09	1.28	1.31
Rbm8a	RNA binding motif protein 8a	0.1149	0.0002	0.0003	-1.06	1.42	1.31
Ccdc82	coiled-coil domain containing 82	0.0807	0.0065	0.0066	1.14	1.26	1.31
Zfp329	zinc finger protein 329	0.0523	0.0034	0.0032	1.2	1.35	1.31
Mettl3	methyltransferase like 3	0.0236	0.0000	0.0069	1.17	1.34	1.31
Wdr61	WD repeat domain 61	0.4634	0.0000	0.0013	-1.03	1.35	1.3
Rbm10	RNA binding motif protein 10	0.4561	0.0001	0.0058	1.03	1.38	1.3
Rps6ka3	ribosomal protein S6 kinase polypeptide 3	0.2152	0.0020	0.0001	1.09	1.23	1.3
2810037O22Rik	RIKEN cDNA 2810037O22 gene	0.1554	0.0040	0.0002	1.07	1.25	1.3
Frm4b	FERM domain containing 4B	0.1435	0.0010	0.0028	-1.09	1.4	1.3
Jmjd1c	jumonji domain containing 1C	0.0405	0.0099	0.0016	1.13	1.3	1.3
Dlc1	deleted in liver cancer 1	0.0143	0.0068	0.0042	1.14	1.21	1.3
Ifrd1	interferon-related developmental regulator 1	0.3064	0.0054	0.0060	1.05	1.31	1.29
Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	0.2396	0.0001	0.0000	1.06	1.26	1.29
Casc4	cancer susceptibility candidate 4	0.0980	0.0028	0.0005	1.13	1.25	1.29
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	0.6198	0.0000	0.0009	-1.03	1.36	1.28
Uhrf1bp1l	UHRF1 (ICBP90) binding protein 1-like	0.0705	0.0080	0.0042	1.07	1.15	1.28
Hmgn3	high mobility group nucleosomal binding domain 3	0.0651	0.0000	0.0041	1.13	1.39	1.28
Zfp871	zinc finger protein 871	0.0549	0.0017	0.0020	1.11	1.33	1.28
Wasl	Wiskott-Aldrich syndrome-like (human)	0.9093	0.0049	0.0100	1.01	1.32	1.27
Trp53bp1	transformation related protein 53 binding protein 1	0.0945	0.0000	0.0061	1.08	1.54	1.27
Seld7	SET domain containing (lysine methyltransferase) 7	0.0402	0.0003	0.0000	1.08	1.23	1.27
Ythdc1	YTH domain containing 1	0.0313	0.0091	0.0031	1.12	1.23	1.27
Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	0.7689	0.0002	0.0013	1.02	1.42	1.26
Parq	poly (ADP-ribose) glycohydrolase	0.5873	0.0051	0.0016	1.03	1.21	1.26
Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)	0.2504	0.0000	0.0000	1.05	1.26	1.26
Ralgps2	Rai GEF with PH domain and SH3 binding motif 2	0.0444	0.0024	0.0083	1.14	1.34	1.26
Brdw1	bromodomain and WD repeat domain containing 1	0.0143	0.0066	0.0057	1.23	1.24	1.26
Tada2a	transcriptional adaptor 2A	0.0100	0.0081	0.0061	1.29	1.28	1.26
Zfp715	zinc finger protein 715	0.8516	0.0004	0.0027	-1	1.31	1.25
Prp31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	0.8320	0.0060	0.0051	1.01	1.24	1.25
Ube3a	ubiquitin protein ligase E3A	0.4079	0.0038	0.0069	1.05	1.24	1.25
A830039N20Rik	RIKEN cDNA A830039N20 gene	0.2417	0.0008	0.0079	1.05	1.2	1.25
Sec11a	SEC11 homolog A (S. cerevisiae)	0.1653	0.0058	0.0015	1.07	1.26	1.25
Atad2b	ATPase family, AAA domain containing 2B	0.1327	0.0043	0.0068	1.1	1.43	1.25
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	0.0416	0.0001	0.0017	1.11	1.27	1.25
Rabggtb	RAB geranylgeranyl transferase, b subunit	0.9690	0.0016	0.0040	1	1.27	1.24
Rab2b	RAB2B, member RAS oncogene family	0.8730	0.0009	0.0019	1.01	1.37	1.24
Dnajc8	DnaJ (Hsp40) homolog, subfamily C, member 8	0.2897	0.0001	0.0050	1.04	1.33	1.24
Pias2	protein inhibitor of activated STAT 2	0.2578	0.0005	0.0009	1.05	1.18	1.24
Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0.2285	0.0006	0.0008	-1.06	1.27	1.24
Rpl23	ribosomal protein L23	0.9608	0.0002	0.0033	1	1.34	1.23
Gas5	growth arrest specific 5	0.0795	0.0000	0.0032	1.07	1.43	1.23
Pkd2	polycystic kidney disease 2	0.0641	0.0011	0.0005	1.18	1.19	1.23
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor 2	0.7564	0.0024	0.0042	1.02	1.28	1.22
Slpr3	sphingosine-1-phosphate receptor 3	0.3778	0.0000	0.0004	1.04	1.41	1.22
Prp38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	0.3159	0.0003	0.0083	-1.04	1.22	1.22
Rgs5	regulator of G-protein signaling 5	0.2008	0.0080	0.0013	1.07	1.17	1.22
Mobk1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	0.1428	0.0017	0.0082	1.12	1.26	1.22
Unkl	unkempt-like (Drosophila)	0.0484	0.0048	0.0067	1.1	1.11	1.22
Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.0271	0.0070	0.0041	1.15	1.22	1.22
D15Erd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	0.0110	0.0034	0.0062	1.16	1.16	1.22
Yip5	Yip1 domain family, member 5	0.7701	0.0036	0.0001	1.01	1.12	1.21
2010107E04Rik	RIKEN cDNA 2010107E04 gene	0.6258	0.0001	0.0074	1.02	1.33	1.21
Rpl37	ribosomal protein L37	0.1101	0.0007	0.0005	-1.06	1.22	1.21
2810407C02Rik	RIKEN cDNA 2810407C02 gene	0.4883	0.0005	0.0003	1.02	1.22	1.2
Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	0.2603	0.0018	0.0032	-1.04	1.2	1.19
Hnrnpk	heterogeneous nuclear ribonucleoprotein K	0.2579	0.0056	0.0025	-1.06	1.15	1.2
Lnpep	leucyl/cystinyl aminopeptidase	0.0725	0.0000	0.0003	1.09	1.29	1.2
Akr1e1	aldo-keto reductase family 1, member E1	0.7464	0.0000	0.0026	1.02	1.4	1.19
Tic21b	tetratricopeptide repeat domain 21B	0.7265	0.0100	0.0068	1.02	1.2	1.19
Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	0.4416	0.0059	0.0039	-1.03	1.18	1.19
Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	0.3951	0.0068	0.0085	1.05	1.2	1.19
Npc2	Niemann Pick type C2	0.3781	0.0014	0.0011	1.04	1.3	1.19
Ccs	copper chaperone for superoxide dismutase	0.2773	0.0014	0.0042	1.07	1.28	1.19
Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0.1233	0.0020	0.0094	1.1	1.4	1.19
Rps7	ribosomal protein S7	0.1157	0.0049	0.0010	-1.07	1.19	1.19
Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding)	0.0902	0.0081	0.0062	1.07	1.2	1.19
Pttg1	pituitary tumor-transforming gene 1	0.0606	0.0000	0.0011	-1.17	-1.19	1.19
Rb1cc1	RB1-inducible coiled-coil 1	0.1894	0.0011	0.0016	1.05	1.12	1.18
Mbnl2	muscleblind-like 2	0.0780	0.0004	0.0001	-1.06	1.18	1.18
Sub1	SUB1 homolog (S. cerevisiae)	0.0608	0.0089	0.0021	-1.12	1.15	1.18
Rab18	RAB18, member RAS oncogene family	0.6571	0.0022	0.0074	-1.03	1.2	1.17
Scarb2	scavenger receptor class B, member 2	0.5090	0.0004	0.0005	1.02	1.17	1.17
Klhl24	kelch-like 24 (Drosophila)	0.3290	0.0092	0.0042	1.04	1.16	1.17
Ociad1	OClA domain containing 1	0.0152	0.0001	0.0051	1.14	1.4	1.17
Sms	spermine synthase	0.0881	0.0081	0.0080	1.09	1.15	1.16
Abxn7l3b	ataxin 7-like 3B	0.0802	0.0000	0.0063	1.13	1.56	1.16
Rbx1	ring-box 1	0.0782	0.0001	0.0022	-1.08	1.2	1.16
Coq7	demethyl-Q 7	0.9886	0.0000	0.0028	1	1.35	1.15
Ati2	atlastin GTPase 2	0.7290	0.0039	0.0019	-1.01	1.15	1.15

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Tulp4	tubby like protein 4	0.4390	0.0000	0.0061	1.04	1.26	1.15
Wdfy2	WD repeat and FYVE domain containing 2	0.0183	0.0033	0.0011	1.21	1.24	1.15
Rpl12	ribosomal protein L12	0.1958	0.0091	0.0031	-1.09	1.24	1.14
Sap18	Sin3-associated polypeptide 18	0.0960	0.0007	0.0066	1.08	1.25	1.14
C78339	expressed sequence C78339	0.2766	0.0003	0.0008	-1.03	1.16	1.13
Rdx	radixin	0.2310	0.0017	0.0084	-1.05	1.22	1.13
Braf	Braf transforming gene	0.2072	0.0067	0.0051	1.06	1.19	1.13
Etnk1	ethanolamine kinase 1	0.0764	0.0035	0.0017	1.06	1.13	1.13
Cdc123	cell division cycle 123 homolog (S. cerevisiae)	0.1207	0.0001	0.0001	-1.07	1.15	1.12
Papd5	PAP associated domain containing 5	0.1970	0.0010	0.0068	1.06	1.2	1.11
Bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	0.3066	0.0002	0.0005	1.02	1.13	1.1
Srp19	signal recognition particle 19	0.0537	0.0011	0.0090	-1.09	1.16	1.09
Set	SET translocation	0.5433	0.0002	0.0014	-1.02	-1.21	-1.12
Spryd3	SPRY domain containing 3	0.2079	0.0026	0.0034	1.06	-1.21	-1.12
Wdr47	WD repeat domain 47	0.4634	0.0071	0.0030	1.03	-1.16	-1.13
Asns	asparagine synthetase	0.3619	0.0083	0.0038	-1.05	-1.14	-1.14
Tspyl5	testis-specific protein, Y-encoded-like 5	0.1037	0.0003	0.0071	-1.12	-1.36	-1.14
Hccs	holocytochrome c synthetase	0.0700	0.0011	0.0004	-1.11	-1.12	-1.14
Uba1	ubiquitin-like modifier activating enzyme 1	0.7337	0.0002	0.0002	-1.01	-1.17	-1.15
Txndc16	thioredoxin domain containing 16	0.3388	0.0091	0.0023	-1.05	-1.12	-1.15
Fasn	fatty acid synthase	0.2192	0.0002	0.0020	1.05	-1.14	-1.15
Ctsb	cathepsin B	0.3856	0.0017	0.0068	-1.03	-1.13	-1.16
Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	0.8975	0.0016	0.0012	-1	-1.32	-1.17
Csrp1	cysteine and glycine-rich protein 1	0.4974	0.0096	0.0024	1.03	-1.12	-1.17
Uchl1	ubiquitin carboxy-terminal hydrolase L1	0.3635	0.0082	0.0017	-1.05	-1.14	-1.17
Rela	rv-rel reticuloendotheliosis viral oncogene homolog A (avian)	0.3455	0.0089	0.0088	-1.05	-1.16	-1.17
Tcea1	transcription elongation factor A (SII) 1	0.2012	0.0048	0.0037	-1.05	-1.24	-1.17
Zc3h14	zinc finger CCHC type containing 14	0.1741	0.0030	0.0065	-1.07	-1.21	-1.17
Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	0.0289	0.0002	0.0010	-1.11	-1.29	-1.17
Ado	2-aminoethanethiol (cysteamine) dioxygenase	0.0193	0.0017	0.0083	-1.14	-1.23	-1.17
Mmd	monocyte to macrophage differentiation-associated	0.0144	0.0028	0.0023	-1.15	-1.16	-1.17
9030624J02Rik	RIKEN cDNA 9030624J02 gene	0.4903	0.0092	0.0000	1.02	-1.16	-1.18
Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana)	0.4139	0.0060	0.0030	-1.03	-1.13	-1.18
Trim3	tripartite motif-containing 3	0.3265	0.0011	0.0036	1.04	-1.4	-1.18
Puf60	poly-U binding splicing factor 60	0.2124	0.0010	0.0042	1.07	-1.17	-1.18
Vps39	vacuolar protein sorting 39 (yeast)	0.1276	0.0081	0.0045	1.08	-1.12	-1.18
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	0.1148	0.0091	0.0017	-1.05	-1.1	-1.18
Sars	seryl-aminoacyl-tRNA synthetase	0.8264	0.0064	0.0086	1.01	-1.21	-1.19
Fyn	Fyn proto-oncogene	0.8109	0.0013	0.0011	-1.01	-1.18	-1.19
Aars	alanine-tRNA synthetase	0.7811	0.0002	0.0002	1.02	-1.28	-1.19
Kat5	K(lysine) acetyltransferase 5	0.3144	0.0002	0.0041	-1.05	-1.24	-1.19
Nol4	nucleolar protein 4	0.1669	0.0041	0.0052	-1.07	-1.2	-1.19
Sf3a1	splicing factor 3a, subunit 1	0.6441	0.0091	0.0006	-1.02	-1.26	-1.2
Wbp11	WW domain binding protein 11	0.4591	0.0010	0.0007	-1.02	-1.14	-1.2
Ptms	parathymosin	0.3419	0.0041	0.0074	-1.04	-1.26	-1.2
Tom1l2	target of myb1-like 2 (chicken)	0.2264	0.0082	0.0026	1.05	-1.21	-1.2
Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	0.1991	0.0001	0.0001	1.03	-1.17	-1.2
Api5	apoptosis inhibitor 5	0.0722	0.0010	0.0039	-1.09	-1.29	-1.2
Ubl4	ubiquitin-like 4	0.0195	0.0011	0.0006	-1.06	-1.1	-1.2
Flo	fat mass and obesity associated	0.9586	0.0082	0.0050	-1	-1.19	-1.21
Aff3	AF4/FMR2 family, member 3	0.9249	0.0095	0.0061	-1	-1.14	-1.21
Pkm2	pyruvate kinase, muscle	0.7807	0.0080	0.0005	-1.01	-1.15	-1.21
Zfand2a	zinc finger, AN1-type domain 2A	0.6888	0.0060	0.0005	-1.01	-1.17	-1.21
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	0.6037	0.0002	0.0013	1.02	-1.32	-1.21
Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	0.4344	0.0006	0.0042	-1.03	-1.18	-1.21
Vps33a	vacuolar protein sorting 33A (yeast)	0.3274	0.0088	0.0076	-1.07	-1.22	-1.21
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	0.2707	0.0100	0.0035	-1.06	-1.16	-1.21
Mboat7	membrane bound O-acyltransferase domain containing 7	0.1571	0.0070	0.0017	-1.09	-1.22	-1.21
Celsr3	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	0.0990	0.0055	0.0086	1.11	-1.19	-1.21
Eftud2	elongation factor Tu GTP binding domain containing 2	0.0706	0.0095	0.0045	1.12	-1.23	-1.21
Dcaf11	DDB1 and CUL4 associated factor 11	0.0483	0.0082	0.0000	1.06	-1.09	-1.21
Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	0.0460	0.0011	0.0040	1.1	-1.42	-1.21
Mxi1	Max interacting protein 1	0.9027	0.0094	0.0012	1	-1.17	-1.22
Tecr	trans-2,3-enoyl-CoA reductase	0.1484	0.0060	0.0043	-1.1	-1.21	-1.22
Tbc1d10b	TBC1 domain family, member 10b	0.1255	0.0033	0.0028	1.06	-1.17	-1.22
Adap1	ArfGAP with dual PH domains 1	0.0650	0.0007	0.0050	1.13	-1.44	-1.22
Scamp5	secretory carrier membrane protein 5	0.0282	0.0075	0.0021	1.08	-1.17	-1.22
Atp9a	ATPase, class II, type 9A	0.0255	0.0084	0.0014	1.09	-1.2	-1.22
Eif3l	eukaryotic translation initiation factor 3, subunit L	0.7823	0.0033	0.0014	-1.02	-1.14	-1.23
Tubb2c	tubulin, beta 2C	0.5188	0.0054	0.0072	1.03	-1.2	-1.23
Plekha7	pleckstrin homology domain containing, family B (evectins) member 2	0.5181	0.0015	0.0015	-1.03	-1.17	-1.23
C230096C10Rik	RIKEN cDNA C230096C10 gene	0.3637	0.0083	0.0052	-1.05	-1.2	-1.23
2510012J08Rik	RIKEN cDNA 2510012J08 gene	0.2690	0.0048	0.0055	1.07	-1.18	-1.23
C1stn1	calystenine 1	0.2577	0.0035	0.0060	1.06	-1.29	-1.23
Slc44a2	solute carrier family 44, member 2	0.1579	0.0007	0.0027	1.1	-1.42	-1.23
2010107G23Rik	RIKEN cDNA 2010107G23 gene	0.1054	0.0034	0.0006	-1.07	-1.17	-1.23
Syng1	synaptogyrin 1	0.0543	0.0035	0.0034	1.07	-1.17	-1.23
Mgat2	mannoside acetylglucosaminyltransferase 2	0.0106	0.0004	0.0066	-1.21	-1.39	-1.23
Pa2g4	proliferation-associated 2G4	0.9602	0.0035	0.0014	1	-1.27	-1.24
Acvr1b	activin A receptor, type 1B	0.8075	0.0061	0.0020	-1.02	-1.16	-1.24
C630004H02Rik	RIKEN cDNA C630004H02 gene	0.6461	0.0001	0.0033	1.02	-1.4	-1.24
Gstm7	glutathione S-transferase, mu 7	0.5112	0.0023	0.0055	-1.05	-1.25	-1.24
Fbxo2	F-box protein 2	0.3462	0.0051	0.0025	1.05	-1.16	-1.24
Tm9sf4	transmembrane 9 superfamily protein member 4	0.2868	0.0034	0.0081	-1.05	-1.23	-1.24
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	0.2865	0.0060	0.0024	-1.07	-1.2	-1.24
Gna12	guanine nucleotide binding protein, alpha 12	0.2264	0.0055	0.0028	1.08	-1.18	-1.24
Hk1	hexokinase 1	0.1271	0.0007	0.0000	1.05	-1.21	-1.24
Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	0.0788	0.0000	0.0001	-1.16	-1.3	-1.24
Flot2	flotillin 2	0.0460	0.0000	0.0056	1.09	-1.42	-1.24
2410016O06Rik	RIKEN cDNA 2410016O06 gene	0.0317	0.0029	0.0001	-1.09	-1.22	-1.24
Smad3	SMAD3 related, matrix associated, actin dependent regulator of chromatin	0.8332	0.0051	0.0001	-1.01	-1.18	-1.25
Chrm2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	0.3262	0.0022	0.0012	1.06	-1.26	-1.25
Cpsf2	cleavage and polyadenylation specific factor 2	0.1858	0.0006	0.0011	-1.08	-1.36	-1.25
Sdhaf1	succinate dehydrogenase complex assembly factor 1	0.0727	0.0034	0.0067	1.08	-1.1	-1.25
Slc35a4	solute carrier family 35, member A4	0.0694	0.0006	0.0080	-1.09	-1.31	-1.25
Mid1p1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	0.0361	0.0007	0.0002	-1.07	-1.23	-1.25
Crelp1	cysteine-rich with EGF-like domains 1	0.9403	0.0072	0.0045	-1	-1.17	-1.26
D3Bwg0562e	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	0.8986	0.0018	0.0051	-1	-1.17	-1.26
Nckip5d	NCK interacting protein with SH3 domain	0.3792	0.0010	0.0005	1.05	-1.25	-1.26
Tmem38a	transmembrane protein 38A	0.1662	0.0066	0.0021	1.1	-1.28	-1.26
Fbxl15	F-box and leucine-rich repeat protein 15	0.1415	0.0050	0.0022	-1.07	-1.22	-1.26
Gorasp2	golgi reassembly stacking protein 2	0.8801	0.0081	0.0001	1.01	-1.14	-1.27
Fa2h	fatty acid 2-hydroxylase	0.8531	0.0088	0.0050	-1.01	-1.31	-1.27
Btdb6	BTB (POZ) domain containing 6	0.7185	0.0009	0.0024	1.02	-1.27	-1.27
Lgi3	leucine-rich repeat LGI family, member 3	0.3781	0.0098	0.0042	1.03	-1.29	-1.27
Plec	plectin	0.3119	0.0009	0.0022	1.06	-1.31	-1.27

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	0.2974	0.0005	0.0046	1.05	-1.49	-1.27
Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	0.2796	0.0004	0.0030	1.05	-1.28	-1.27
Zfp707	zinc finger protein 707	0.1918	0.0041	0.0058	-1.09	-1.29	-1.27
Zfp580	zinc finger protein 580	0.0911	0.0035	0.0058	-1.11	-1.32	-1.27
Mtdh	metadherin	0.0367	0.0002	0.0006	-1.1	-1.35	-1.27
Bcan	brevican	0.0151	0.0054	0.0000	1.15	-1.22	-1.27
Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)	0.9590	0.0087	0.0070	-1.01	-1.23	-1.28
Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0.8294	0.0000	0.0001	-1.01	-1.36	-1.28
Wars	tryptophanyl-tRNA synthetase	0.8136	0.0038	0.0013	1.01	-1.23	-1.28
0610011L14Rik	RIKEN cDNA 0610011L14 gene	0.7755	0.0051	0.0023	-1.02	-1.34	-1.28
AU020094	expressed sequence AU020094	0.7397	0.0045	0.0045	-1.02	-1.32	-1.28
Eno2	enolase 2, gamma neuronal	0.6528	0.0010	0.0013	1.02	-1.27	-1.28
Kdm2a	lysine (K)-specific demethylase 2A	0.3473	0.0031	0.0049	1.07	-1.25	-1.28
Ptprn	protein tyrosine phosphatase, receptor type, N	0.2218	0.0011	0.0004	1.06	-1.36	-1.28
Phyh1pl	phytanoyl-CoA hydroxylase interacting protein-like	0.2076	0.0020	0.0048	1.07	-1.3	-1.28
Cbx4	chromobox homolog 4 (Drosophila Pc class)	0.2025	0.0000	0.0000	-1.07	-1.25	-1.28
Arfp2	ADP-ribosylation factor interacting protein 2	0.1472	0.0061	0.0009	1.07	-1.12	-1.28
Trim46	tripartite motif-containing 46	0.1276	0.0013	0.0092	1.12	-1.33	-1.28
Eid1	EP300 interacting inhibitor of differentiation 1	0.1209	0.0012	0.0011	-1.07	-1.26	-1.28
Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	0.1008	0.0019	0.0084	-1.1	-1.39	-1.28
Chrm1	cholinergic receptor, muscarinic 1, CNS	0.0618	0.0038	0.0004	1.11	-1.15	-1.28
Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0.8677	0.0004	0.0010	1.01	-1.3	-1.29
Ctsd	cathepsin D	0.5927	0.0020	0.0014	1.02	-1.24	-1.29
Add1	adducin 1 (alpha)	0.5855	0.0005	0.0004	-1.02	-1.27	-1.29
Atp5sl	ATP5S-like	0.5156	0.0068	0.0027	1.04	-1.25	-1.29
Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	0.4809	0.0007	0.0031	1.06	-1.37	-1.29
Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.3442	0.0005	0.0014	1.04	-1.29	-1.29
Otd7a	OTU domain containing 7A	0.2991	0.0086	0.0009	-1.07	-1.28	-1.29
Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0.2750	0.0053	0.0041	-1.09	-1.28	-1.29
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	0.2024	0.0011	0.0003	1.06	-1.26	-1.29
Evl	Ena-vasodilator stimulated phosphoprotein	0.2000	0.0069	0.0003	1.06	-1.14	-1.29
Tbc1d5	TBC1 domain family, member 5	0.1325	0.0013	0.0026	-1.11	-1.29	-1.29
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.1211	0.0005	0.0007	-1.12	-1.29	-1.29
Syt11	synaptotagmin XI	0.9603	0.0014	0.0000	-1	-1.17	-1.3
Rgmb	RGM domain family, member B	0.8249	0.0026	0.0007	1.01	-1.46	-1.3
Vsm2l	V-set and transmembrane domain containing 2-like	0.6497	0.0018	0.0058	-1.03	-1.5	-1.3
Ergic3	ERGIC and golgi 3	0.4630	0.0036	0.0007	1.04	-1.22	-1.3
Lanc1	LanC (bacterial lantibiotic synthetase component C)-like 1	0.4362	0.0086	0.0011	-1.07	-1.21	-1.3
Kctd13	potassium channel tetramerisation domain containing 13	0.3116	0.0042	0.0011	-1.04	-1.17	-1.3
Spnb1	spectrin beta 1	0.1142	0.0046	0.0048	-1.08	-1.25	-1.3
Cyp46a1	cytochrome P450, family 46, subfamily a, polypeptide 1	0.0943	0.0004	0.0013	1.09	-1.35	-1.3
Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member	0.0312	0.0054	0.0006	1.08	-1.27	-1.3
Pnkd	paroxysmal nonkinesigenic dyskinesia	0.8656	0.0051	0.0078	1.01	-1.35	-1.31
Ascc1	activating signal cointegrator 1 complex subunit 1	0.6139	0.0025	0.0050	-1.04	-1.35	-1.31
Stub1	STIP1 homology and U-Box containing protein 1	0.6043	0.0010	0.0003	1.03	-1.19	-1.31
Gpr26	G protein-coupled receptor 26	0.5719	0.0051	0.0038	-1.07	-1.31	-1.31
Itns1	intersectin 1 (SH3 domain protein 1A)	0.1353	0.0037	0.0095	-1.13	-1.41	-1.31
Sh3glb2	SH3-domain GRB2-like endophilin B2	0.0478	0.0016	0.0010	1.12	-1.28	-1.31
Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	0.0238	0.0071	0.0005	1.14	-1.23	-1.31
Pspc1	paraspeckle protein 1	0.0186	0.0064	0.0018	-1.14	-1.27	-1.31
Wtap	Wilms' tumour 1-associating protein	0.0133	0.0043	0.0002	-1.15	-1.2	-1.31
Rcc2	regulator of chromosome condensation 2	0.4370	0.0030	0.0023	-1.05	-1.3	-1.32
Gpi1	glucose phosphate isomerase 1	0.3996	0.0009	0.0003	1.03	-1.17	-1.32
Actr1a	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	0.3754	0.0032	0.0000	1.03	-1.15	-1.32
Rtn2	reticulon 2 (Z-band associated protein)	0.3513	0.0075	0.0003	1.05	-1.22	-1.32
Far2	fatty acyl CoA reductase 2	0.3089	0.0098	0.0029	-1.09	-1.31	-1.32
Fiz1	Flt3 interacting zinc finger protein 1	0.2143	0.0003	0.0000	-1.07	-1.35	-1.32
Drp1	developmentally regulated GTP binding protein 1	0.1695	0.0005	0.0002	-1.06	-1.21	-1.32
Tmem179	transmembrane protein 179	0.1539	0.0041	0.0004	1.08	-1.17	-1.32
Zfr	zinc finger RNA binding protein	0.1298	0.0001	0.0002	-1.08	-1.41	-1.32
Gcsh	glycine cleavage system protein H (aminomethyl carrier)	0.0680	0.0017	0.0002	-1.07	-1.18	-1.32
Eif3c	eukaryotic translation initiation factor 3, subunit C	0.0666	0.0095	0.0000	1.11	-1.14	-1.32
Kctd17	potassium channel tetramerisation domain containing 17	0.8669	0.0045	0.0042	1.01	-1.29	-1.33
Trpc4ap	transient receptor potential cation channel, subfamily C, member 4 associated	0.6929	0.0004	0.0005	1.02	-1.39	-1.33
Tbc1d25	TBC1 domain family, member 25	0.6171	0.0008	0.0052	-1.04	-1.36	-1.33
Reep2	receptor accessory protein 2	0.4247	0.0000	0.0021	-1.05	-1.48	-1.33
Fndc4	fibronectin type III domain containing 4	0.3951	0.0003	0.0002	1.03	-1.21	-1.33
Xpot	xportin, tRNA (nuclear export receptor for tRNAs)	0.2870	0.0061	0.0042	-1.1	-1.33	-1.33
Ogdh	oxoglutarate dehydrogenase (lipoamide)	0.2604	0.0003	0.0003	1.04	-1.43	-1.33
Scand1	SCAN domain-containing 1	0.2583	0.0064	0.0010	-1.05	-1.15	-1.33
Pcsk2	proprotein convertase subtilisin/kexin type 2	0.2456	0.0009	0.0060	-1.07	-1.4	-1.33
Mgm1	mahogunin, ring finger 1	0.1011	0.0029	0.0022	1.14	-1.32	-1.33
Gnb2	guanine nucleotide binding protein (G protein), beta 2	0.0546	0.0055	0.0022	1.12	-1.23	-1.33
Rel2	REL2-like 2	0.8738	0.0021	0.0010	-1.01	-1.32	-1.34
Dapk3	death-associated protein kinase 3	0.8268	0.0056	0.0050	1.02	-1.44	-1.34
Fbxo44	F-box protein 44	0.7874	0.0024	0.0006	1.02	-1.34	-1.34
Hspbp1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	0.7629	0.0000	0.0005	-1.01	-1.42	-1.34
C2cd2l	C2 calcium-dependent domain containing 2-like	0.6475	0.0041	0.0059	-1.03	-1.36	-1.34
Spnb3	spectrin beta 3	0.0645	0.0051	0.0006	1.15	-1.3	-1.34
Calcoco1	calcium binding and coiled coil domain 1	0.0122	0.0004	0.0098	-1.17	-1.68	-1.34
Sympk	symplesin	0.7183	0.0002	0.0006	1.02	-1.46	-1.35
Rab11b	RAB11B, member RAS oncogene family	0.6467	0.0009	0.0001	1.01	-1.22	-1.35
Mtap1s	microtubule-associated protein 1S	0.4259	0.0036	0.0003	1.04	-1.2	-1.35
Sf3b4	splicing factor 3b, subunit 4	0.3827	0.0018	0.0021	-1.05	-1.39	-1.35
Dbn1	debrin 1	0.3700	0.0056	0.0008	1.05	-1.24	-1.35
Nudc	nuclear distribution gene C homolog (Aspergillus)	0.2182	0.0009	0.0008	-1.06	-1.22	-1.35
Cpt1c	carnitine palmitoyltransferase 1c	0.1562	0.0006	0.0001	1.07	-1.19	-1.35
Ati3	atlastin GTPase 3	0.1327	0.0052	0.0003	1.05	-1.18	-1.35
Usp11	ubiquitin specific peptidase 11	0.0633	0.0002	0.0030	-1.1	-1.44	-1.35
Dos	downstream of Shk11	0.0146	0.0006	0.0086	1.19	-1.43	-1.35
Srebf1	sterol regulatory element binding transcription factor 1	0.9725	0.0096	0.0015	-1	-1.21	-1.36
Med16	mediator complex subunit 16	0.8910	0.0002	0.0030	-1.01	-1.46	-1.36
Exoc6b	exocyst complex component 6B	0.8250	0.0031	0.0013	1.01	-1.58	-1.36
Efn3	ephrin A3	0.5190	0.0002	0.0008	-1.03	-1.34	-1.36
Copg	coatamer protein complex, subunit gamma	0.5143	0.0009	0.0003	-1.04	-1.32	-1.36
Rap1gap	Rap1 GTPase-activating protein	0.3066	0.0068	0.0086	1.11	-1.46	-1.36
Brd2	bromodomain containing 2	0.2387	0.0001	0.0000	1.05	-1.29	-1.36
Gbf1	golgi-specific brefeldin A-resistance factor 1	0.1861	0.0070	0.0064	1.1	-1.34	-1.36
Actr1b	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	0.1536	0.0006	0.0001	1.08	-1.48	-1.36
Epha4	Eph receptor A4	0.0248	0.0099	0.0044	-1.23	-1.26	-1.36
Fam160a2	family with sequence similarity 160, member A2	0.0155	0.0003	0.0010	-1.12	-1.3	-1.36
Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	0.0116	0.0012	0.0037	1.19	-1.47	-1.36
Slc48a1	solute carrier family 48 (heme transporter), member 1	0.9716	0.0017	0.0006	1	-1.26	-1.37
Sncb	synuclein, beta	0.9420	0.0008	0.0004	1	-1.45	-1.37
Ggt7	gamma-glutamyltransferase 7	0.7840	0.0011	0.0004	1.02	-1.35	-1.37
Cacng3	calcium channel, voltage-dependent, gamma subunit 3	0.6881	0.0019	0.0054	-1.03	-1.66	-1.37

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Cln3	calyntenin 3	0.6259	0.0018	0.0013	-1.04	-1.43	-1.37
Fam102a	family with sequence similarity 102, member A	0.2082	0.0038	0.0018	1.05	-1.22	-1.37
Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	0.0881	0.0060	0.0045	1.11	-1.39	-1.37
Il34	interleukin 34	0.0603	0.0029	0.0005	-1.2	-1.29	-1.37
Urgcp	upregulator of cell proliferation	0.6309	0.0011	0.0085	1.04	-1.44	-1.38
BC024814	cDNA sequence BC024814	0.5440	0.0066	0.0010	-1.04	-1.34	-1.38
LOC100045546	similar to Id4	0.4968	0.0002	0.0042	-1.05	-1.33	-1.38
Camk1	calcium/calmodulin-dependent protein kinase I	0.4946	0.0015	0.0003	1.03	-1.41	-1.38
Cd99	CD99 antigen	0.3068	0.0018	0.0076	-1.07	-1.36	-1.38
Sorcs2	sortilin-related VPS10 domain containing receptor 2	0.2976	0.0021	0.0041	-1.11	-1.44	-1.38
Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)	0.1796	0.0002	0.0047	-1.11	-1.69	-1.38
Gns	glucosamine (N-acetyl)-6-sulfatase	0.0328	0.0041	0.0000	1.11	-1.17	-1.38
P4htm	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	0.0135	0.0002	0.0003	1.1	-1.21	-1.38
Prkaca	protein kinase, cAMP dependent, catalytic, alpha	0.8480	0.0001	0.0006	-1.01	-1.5	-1.39
Sez6	seizure related gene 6	0.4700	0.0009	0.0029	1.04	-1.5	-1.39
Gprn1	G protein-regulated inducer of neurite outgrowth 1	0.2891	0.0003	0.0003	1.06	-1.56	-1.39
Sfxn1	sideroflexin 1	0.2202	0.0002	0.0009	-1.07	-1.46	-1.39
Gatad2b	GATA zinc finger domain containing 2B	0.1748	0.0019	0.0002	-1.05	-1.16	-1.39
Dctn1	dynactin 1	0.1394	0.0003	0.0010	1.09	-1.46	-1.39
Eri3	exoribonuclease 3	0.0722	0.0026	0.0005	1.09	-1.26	-1.39
Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	0.0330	0.0012	0.0010	-1.16	-1.28	-1.39
Tmem132a	transmembrane protein 132A	0.5015	0.0004	0.0001	1.04	-1.37	-1.4
Tmem151a	transmembrane protein 151A	0.4649	0.0098	0.0016	1.04	-1.41	-1.4
Rhbd1	rhomboid, veinlet-like 1 (Drosophila)	0.4577	0.0002	0.0006	1.04	-1.3	-1.4
Mast2	microtubule associated serine/threonine kinase 2	0.3843	0.0048	0.0003	1.07	-1.39	-1.4
Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	0.3814	0.0083	0.0034	-1.08	-1.4	-1.4
Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	0.3297	0.0007	0.0099	-1.08	-1.48	-1.4
Obfc2b	oligonucleotide/oligosaccharide-binding fold containing 2B	0.2852	0.0030	0.0002	1.05	-1.37	-1.4
Rad23a	RAD23a homolog (S. cerevisiae)	0.1552	0.0085	0.0010	1.08	-1.24	-1.4
Rusc1	RUN and SH3 domain containing 1	0.0975	0.0005	0.0000	1.14	-1.27	-1.4
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	0.0604	0.0055	0.0001	1.12	-1.25	-1.4
Slc25a44	solute carrier family 25, member 44	0.0420	0.0000	0.0098	-1.2	-2.24	-1.4
Tcfcp2	transcription factor CP2	0.0282	0.0017	0.0011	-1.2	-1.33	-1.4
Vamp2	vesicle-associated membrane protein 2	0.0253	0.0002	0.0000	1.12	-1.49	-1.4
Calr	calreticulin	0.6656	0.0026	0.0036	-1.04	-1.51	-1.41
Tmem201	transmembrane protein 201	0.4762	0.0003	0.0006	-1.06	-1.44	-1.41
Cfl1	cofilin 1, non-muscle	0.3647	0.0044	0.0002	1.04	-1.34	-1.41
Kat2a	K(lysine) acetyltransferase 2A	0.2660	0.0000	0.0000	1.04	-1.28	-1.41
Evi5l	ecotropic viral integration site 5 like	0.2352	0.0007	0.0006	1.07	-1.48	-1.41
Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	0.0611	0.0001	0.0001	-1.1	-1.4	-1.41
Neurl1a	neuronalized homolog 1A (Drosophila)	0.0199	0.0035	0.0008	1.17	-1.29	-1.41
Caly	calcyon neuron-specific vesicular protein	0.9648	0.0000	0.0002	-1	-1.23	-1.42
Ar8b	ADP-ribosylation factor-like 8B	0.8745	0.0024	0.0001	-1.01	-1.21	-1.42
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	0.7766	0.0010	0.0010	-1.02	-1.46	-1.42
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor	0.7279	0.0082	0.0028	-1.02	-1.26	-1.42
Spat2	spermatogenesis associated 2	0.7087	0.0007	0.0007	-1.02	-1.38	-1.42
Txndc5	thioredoxin domain containing 5	0.3555	0.0037	0.0003	1.06	-1.25	-1.42
Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	0.3053	0.0013	0.0000	-1.05	-1.19	-1.42
Fbxo31	F-box protein 31	0.1053	0.0000	0.0037	-1.09	-1.46	-1.42
Dennd1a	DENN/MADD domain containing 1A	0.1013	0.0002	0.0055	-1.14	-1.45	-1.42
Agap3	1-acylglycerol-3-phosphate O-acyltransferase 3	0.0904	0.0034	0.0038	1.28	-1.37	-1.42
Psme3	proteasome (prosome, macropain) 28 subunit, 3	0.0627	0.0019	0.0017	-1.16	-1.42	-1.42
Pitpm1	phosphatidylinositol transfer protein, membrane-associated 1	0.0171	0.0021	0.0006	1.15	-1.37	-1.42
Clp3	CAP-GLY domain containing linker protein 3	0.8810	0.0006	0.0009	1.01	-1.48	-1.43
Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin	0.5391	0.0005	0.0016	1.03	-1.41	-1.43
Snx32	sorting nexin 32	0.5024	0.0004	0.0003	1.06	-1.5	-1.43
Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	0.3648	0.0033	0.0016	1.08	-1.35	-1.43
B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	0.1338	0.0026	0.0004	1.1	-1.37	-1.43
Fntb	farnesyltransferase, CAAX box, beta	0.0365	0.0016	0.0040	1.14	-1.47	-1.43
Dnm1	dynamitin 1	0.9811	0.0005	0.0004	1	-1.46	-1.44
Myo18a	myosin XVIIIa	0.8747	0.0000	0.0001	-1.01	-1.43	-1.44
Mtap7d1	microtubule-associated protein 7 domain containing 1	0.6970	0.0000	0.0000	-1.01	-1.35	-1.44
Nol6	nucleolar protein family 6 (RNA-associated)	0.4857	0.0005	0.0096	-1.08	-1.96	-1.44
Mras	muscle and microspikes RAS	0.3290	0.0014	0.0044	1.07	-1.68	-1.44
Sez6l2	seizure related 6 homolog like 2	0.0604	0.0030	0.0009	1.15	-1.34	-1.44
Igslf21	immunoglobulin superfamily, member 21	0.9695	0.0006	0.0027	-1	-1.46	-1.45
Aplp1	amyloid beta (A4) precursor-like protein 1	0.5887	0.0002	0.0001	1.02	-1.55	-1.45
Rnf123	ring finger protein 123	0.5517	0.0032	0.0070	1.05	-1.39	-1.45
Cbx1	cortixin 1	0.3298	0.0001	0.0005	1.05	-1.48	-1.45
Asna1	arsenate transporter, ATP-binding, homolog 1 (bacterial)	0.0551	0.0004	0.0003	-1.13	-1.6	-1.45
Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	0.0171	0.0004	0.0094	-1.35	-2.01	-1.45
Trim32	tripartite motif-containing 32	0.8699	0.0022	0.0003	1.01	-1.2	-1.46
Pld3	phospholipase D family, member 3	0.5973	0.0001	0.0001	1.03	-1.3	-1.46
Alg2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	0.4105	0.0007	0.0000	1.06	-1.37	-1.46
Gm3579	predicted gene 3579	0.1228	0.0008	0.0019	-1.15	-1.61	-1.46
Snapp2	small nuclear RNA activating complex, polypeptide 2	0.0310	0.0057	0.0008	-1.15	-1.25	-1.46
L1cam	L1 cell adhesion molecule	0.0107	0.0057	0.0009	1.27	-1.29	-1.46
Nrsn2	neurensin 2	0.8455	0.0052	0.0042	1.03	-1.62	-1.47
Rtn4r1	reticulon 4 receptor-like 1	0.7909	0.0080	0.0019	-1.02	-1.32	-1.47
Faim2	Fas apoptotic inhibitory molecule 2	0.7725	0.0010	0.0001	1.02	-1.53	-1.47
Myh9	myosin, heavy polypeptide 9, non-muscle	0.7655	0.0035	0.0056	1.02	-1.29	-1.47
Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	0.5523	0.0046	0.0000	-1.02	-1.18	-1.47
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	0.3266	0.0001	0.0000	-1.03	-1.32	-1.47
Rab40b	Rab40b, member RAS oncogene family	0.0170	0.0011	0.0000	-1.15	-1.3	-1.47
AU040320	expressed sequence AU040320	0.9833	0.0006	0.0001	-1	-1.3	-1.48
Ncapd2	non-SMC condensin II complex, subunit H2	0.6667	0.0002	0.0001	-1.03	-1.33	-1.48
Nr2f6	nuclear receptor subfamily 2, group F, member 6	0.3688	0.0061	0.0020	-1.1	-1.36	-1.48
Ctsz	cathepsin Z	0.1413	0.0037	0.0005	-1.13	-1.3	-1.48
Ptges2	prostaglandin H synthase 2	0.0905	0.0016	0.0006	-1.11	-1.33	-1.48
Mcrs1	microspherule protein 1	0.3056	0.0004	0.0000	-1.07	-1.55	-1.49
Tmem59l	transmembrane protein 59-like	0.2121	0.0016	0.0001	-1.07	-1.25	-1.49
Hdac11	histone deacetylase 11	0.9994	0.0002	0.0002	-1	-1.4	-1.5
Zbtb45	zinc finger and BTB domain containing 45	0.2100	0.0002	0.0007	-1.08	-1.33	-1.5
Bat3	HLA-B-associated transcript 3	0.0162	0.0000	0.0000	1.1	-1.46	-1.5
2610110G12Rik	RIKEN cDNA 2610110G12 gene	0.1725	0.0002	0.0053	-1.11	-1.66	-1.51
Palm	paralemmmin	0.0453	0.0083	0.0029	1.24	-1.55	-1.51
Sephs2	selenophosphate synthetase 2	0.0228	0.0095	0.0003	-1.2	-1.31	-1.51
Atg9a	autophagy-related 9A (yeast)	0.5578	0.0000	0.0001	1.03	-1.77	-1.52
Epb4.9	erythrocyte protein band 4.9	0.3778	0.0006	0.0004	-1.06	-1.39	-1.52
Pcbp4	poly(rC) binding protein 4	0.2048	0.0001	0.0001	1.06	-1.45	-1.52
Epn1	epsin 1	0.1735	0.0074	0.0001	1.09	-1.51	-1.52
Adrbk1	adrenergic receptor kinase, beta 1	0.1052	0.0041	0.0003	1.12	-1.44	-1.52
Osbp2	oxysterol binding protein 2	0.4848	0.0001	0.0083	-1.03	-1.58	-1.53
Rbm42	RNA binding motif protein 42	0.4525	0.0001	0.0000	-1.03	-1.39	-1.53
Rad23b	RAD23b homolog (S. cerevisiae)	0.3865	0.0061	0.0014	1.1	-1.5	-1.53
Pfkf	phosphofructokinase, liver, B-type	0.3392	0.0012	0.0002	1.05	-1.52	-1.53

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Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Gdap11	ganglioside-induced differentiation-associated protein 1-like 1	0.1254	0.0041	0.0001	-1.08	-1.22	-1.53
Usf1	upstream transcription factor 1	0.0840	0.0003	0.0012	-1.08	-1.39	-1.53
Pltp	phospholipid transfer protein	0.0398	0.0010	0.0014	1.12	-1.61	-1.53
Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	0.0245	0.0000	0.0004	1.16	-1.72	-1.53
Rogdi	rogdi homolog (Drosophila)	0.9382	0.0008	0.0001	1.01	-1.33	-1.54
Pdpx	pyridoxal (pyridoxine, vitamin B6) phosphatase	0.8998	0.0003	0.0000	1.01	-1.3	-1.54
Zfp385a	zinc finger protein 385A	0.8315	0.0001	0.0028	1.02	-1.94	-1.54
Smap2	stromal membrane-associated GTPase-activating protein 2	0.2428	0.0000	0.0000	-1.05	-1.51	-1.54
Coro1c	coronin, actin binding protein 1C	0.1417	0.0004	0.0057	-1.15	-1.84	-1.54
Pef1	penta-EF hand domain containing 1	0.0552	0.0001	0.0004	-1.08	-1.37	-1.54
Slc25a23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member	0.9468	0.0006	0.0012	-1.01	-1.52	-1.55
Br3	brain protein I3	0.8150	0.0019	0.0001	1.02	-1.28	-1.55
Arhgdia	Rho GDP dissociation inhibitor (GDI) alpha	0.3397	0.0002	0.0007	1.04	-1.51	-1.55
St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactos	0.2742	0.0022	0.0000	-1.04	-1.61	-1.55
Rab1b	RAB1B, member RAS oncogene family	0.0806	0.0000	0.0003	-1.12	-1.63	-1.55
Syp	synaptophysin	0.5494	0.0001	0.0000	1.02	-1.81	-1.56
Ssbp4	single stranded DNA binding protein 4	0.4565	0.0017	0.0001	-1.03	-1.33	-1.56
Testk1	testis specific protein kinase 1	0.4307	0.0018	0.0061	1.06	-1.47	-1.56
Trmp1	TMF1-regulated nuclear protein 1	0.2791	0.0013	0.0001	1.06	-1.3	-1.56
Ptk2b	PTK2 protein tyrosine kinase 2 beta	0.0571	0.0001	0.0001	1.07	-1.42	-1.56
Syn1	synapsin I	0.9933	0.0013	0.0006	-1	-1.42	-1.57
Tcf3	transcription factor E3	0.9928	0.0095	0.0004	1	-1.33	-1.57
Raver1	ribonucleoprotein, PTB-binding 1	0.3689	0.0004	0.0047	-1.1	-1.63	-1.57
Actl6b	actin-like 6B	0.0400	0.0041	0.0003	1.16	-1.5	-1.57
Dmwd	dystrophin myotonia-containing WD repeat motif	0.5691	0.0011	0.0024	-1.05	-1.61	-1.58
Plekjh1	pleckstrin homology domain containing, family J member 1	0.5266	0.0002	0.0005	-1.05	-1.63	-1.59
Zdhc8	zinc finger, DHHC domain containing 8	0.6622	0.0027	0.0072	1.04	-1.65	-1.6
Drp1	Dr1 associated protein 1 (negative cofactor 2 alpha)	0.1834	0.0000	0.0000	-1.07	-1.48	-1.6
Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0.0297	0.0079	0.0006	-1.22	-1.35	-1.6
Dlg4	discs, large homolog 4 (Drosophila)	0.2614	0.0013	0.0001	-1.1	-1.41	-1.61
Ring1	ring finger protein 1	0.0659	0.0067	0.0002	1.18	-1.47	-1.61
Man1b1	mannosidase, alpha, class 1B, member 1	0.9704	0.0036	0.0051	-1	-1.77	-1.62
Ap2m1	adaptor protein complex AP-2, mu 1	0.1862	0.0000	0.0000	-1.08	-1.67	-1.62
Arpc4	actin related protein 2/3 complex, subunit 4	0.2405	0.0000	0.0000	-1.05	-1.62	-1.63
Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	0.6561	0.0047	0.0042	1.05	-1.46	-1.64
Rhob	ras homolog gene family, member B	0.1231	0.0016	0.0000	-1.1	-1.51	-1.64
Bsq	basigin	0.0680	0.0013	0.0002	-1.15	-1.46	-1.64
C1qtnf4	C1q and tumor necrosis factor related protein 4	0.0643	0.0006	0.0002	1.13	-1.32	-1.64
Atcay	ataxia, cerebellar, Cayman type homolog (human)	0.5546	0.0001	0.0000	-1.05	-1.6	-1.65
Fam108a	family with sequence similarity 108, member A	0.0308	0.0004	0.0001	1.13	-1.45	-1.65
Fads6	fatty acid desaturase domain family, member 6	0.0163	0.0000	0.0002	-1.21	-1.75	-1.65
Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	0.6368	0.0003	0.0063	1.06	-2.41	-1.66
Mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1	0.3001	0.0001	0.0000	-1.05	-1.67	-1.66
Rbm11	RNA binding motif protein 11	0.1074	0.0031	0.0004	-1.16	-1.44	-1.66
Mocs3	molybdenum cofactor synthesis 3	0.8072	0.0001	0.0005	-1.02	-1.89	-1.67
Bcl7c	B-cell CLL/lymphoma 7C	0.7319	0.0057	0.0007	1.04	-1.36	-1.67
Klc2	kinesin light chain 2	0.4717	0.0089	0.0022	1.06	-1.53	-1.67
Pygo1	pygopus 1	0.0181	0.0047	0.0019	-1.36	-1.45	-1.67
Ncstn	nicastatin	0.6880	0.0048	0.0013	1.04	-1.67	-1.7
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform	0.5643	0.0020	0.0012	1.04	-1.48	-1.7
Med24	mediator complex subunit 24	0.0444	0.0011	0.0000	-1.13	-1.53	-1.7
Tubb4	tubulin, beta 4	0.8776	0.0001	0.0002	1.01	-1.88	-1.71
Aes	amino-terminal enhancer of split	0.8053	0.0002	0.0001	1.02	-1.64	-1.71
C530028O21Rik	RIKEN cDNA C530028O21 gene	0.1461	0.0004	0.0001	1.15	-1.8	-1.72
Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotranspo	0.0672	0.0004	0.0001	1.19	-1.9	-1.72
Arsb	arylsulfatase B	0.3822	0.0027	0.0000	-1.05	-1.3	-1.73
BC018242	cDNA sequence BC018242	0.3693	0.0084	0.0042	1.1	-1.66	-1.74
Cntrf	ciliary neurotrophic factor receptor	0.2270	0.0007	0.0013	-1.11	-1.63	-1.74
Ap2b1	adaptor-related protein complex 2, beta 1 subunit	0.1123	0.0009	0.0001	-1.09	-1.54	-1.74
Psd	pleckstrin and Sec7 domain containing	0.0829	0.0088	0.0003	1.16	-1.25	-1.75
Cgref1	cell growth regulator with EF hand domain 1	0.3284	0.0035	0.0013	1.13	-1.35	-1.76
Baalc	brain and acute leukemia, cytoplasmic	0.0289	0.0089	0.0050	-1.5	-1.49	-1.76
Bat2	HLA-B associated transcript 2	0.0729	0.0008	0.0001	1.13	-1.59	-1.78
Pde4b	phosphodiesterase 4B, cAMP specific	0.4595	0.0000	0.0000	-1.04	-1.47	-1.81
Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	0.7722	0.0012	0.0001	1.02	-1.45	-1.82
Smyd5	SET and MYND domain containing 5	0.7071	0.0051	0.0031	-1.04	-1.58	-1.84
Clip2	CAP-GLY domain containing linker protein 2	0.0387	0.0000	0.0007	-1.21	-2.81	-1.84
Olfm2	olfactomedin 2	0.5169	0.0004	0.0008	-1.06	-2.12	-1.85
Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	0.1275	0.0004	0.0001	1.12	-1.73	-1.85
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	0.2780	0.0004	0.0000	-1.09	-2.09	-1.86
Tmem98	transmembrane protein 98	0.0264	0.0002	0.0001	-1.29	-2.02	-1.86
Pglvrp1	peptidoglycan recognition protein 1	0.2565	0.0041	0.0017	-1.2	-2.24	-1.87
Foxp4	forkhead box P4	0.6173	0.0072	0.0050	-1.09	-1.74	-1.89
Phyhip	phytanoyl-CoA hydroxylase interacting protein	0.3811	0.0001	0.0000	1.06	-1.93	-1.91
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	0.0545	0.0008	0.0009	-1.32	-1.93	-1.92
Ap2a1	adaptor protein complex AP-2, alpha 1 subunit	0.0909	0.0027	0.0002	1.22	-1.71	-1.94
Rab5c	RAB5C, member RAS oncogene family	0.0232	0.0029	0.0004	-1.31	-1.6	-1.94
Chrm3	cholinergic receptor, muscarinic 3, cardiac	0.2214	0.0060	0.0037	-1.28	-1.75	-1.99
Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	0.5578	0.0007	0.0015	-1.07	-2.1	-2
Ubi7	ubiquitin-like 7 (bone marrow stromal cell-derived)	0.8039	0.0001	0.0000	-1.02	-2.08	-2.01
Zfp395	zinc finger protein 395	0.3652	0.0000	0.0081	-1.14	-9.82	-2.05
Nrgn	neurogranin	0.6756	0.0002	0.0001	1.06	-1.89	-2.06
Nell2	NEL-like 2 (chicken)	0.8126	0.0007	0.0002	1.02	-1.86	-2.14
BC056474	cDNA sequence BC056474	0.3934	0.0000	0.0001	-1.09	-2.47	-2.23
Gfap	glial fibrillary acidic protein	0.8059	0.0079	0.0097	-1.05	-2.53	-2.5
Igfbp5	insulin-like growth factor binding protein 5	0.6960	0.0014	0.0012	1.06	-2.28	-2.54
Mt3	metallothionein 3	0.4556	0.0007	0.0002	-1.11	-2.63	-2.89
Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	0.1801	0.0000	0.0000	-1.14	-3.23	-3.15
Arhgap10	Rho GTPase activating protein 10	0.6981	0.0001	0.0002	1.06	-4.1	-3.56
Cacng8	calcium channel, voltage-dependent, gamma subunit 8	0.0456	0.0079	0.0013	-1.59	-2.26	-3.56
4930578M01Rik	RIKEN cDNA 4930578M01 gene	0.0094	0.0087	0.0012	4.11	4.51	7.17
C77626	expressed sequence C77626	0.0031	0.0008	0.0047	3.54	3.89	4.08
4832406H04Rik	RIKEN cDNA 4832406H04 gene	0.0026	0.0000	0.0014	1.94	5.02	3.72
6720420G18Rik	RIKEN cDNA 6720420G18 gene	0.0089	0.0024	0.0005	2.21	3.01	3.11
B430316J06Rik	RIKEN cDNA B430316J06 gene	0.0076	0.0023	0.0040	1.87	2.85	2.97
2900018E21Rik	RIKEN cDNA 2900018E21 gene	0.0024	0.0001	0.0058	1.82	2.5	2.48
Yod1	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae)	0.0069	0.0006	0.0002	1.75	2.25	2.46
3110080E11Rik	RIKEN cDNA 3110080E11 gene	0.0047	0.0022	0.0068	2.38	2.64	2.34
A130064L14Rik	RIKEN cDNA A130064L14 gene	0.0081	0.0002	0.0015	1.71	2.13	2.33
2900009J20Rik	RIKEN cDNA 2900009J20 gene	0.0025	0.0000	0.0000	1.31	2.76	2.3
B830008J18Rik	RIKEN cDNA B830008J18 gene	0.0067	0.0003	0.0081	1.92	2.48	2.23
9130002K18Rik	RIKEN cDNA 9130002K18 gene	0.0051	0.0080	0.0036	1.92	2.17	2.22
Mom1	MORN repeat containing 1	0.0052	0.0009	0.0045	1.94	2.62	2.18
2900046L07Rik	RIKEN cDNA 2900046L07 gene	0.0093	0.0002	0.0015	1.81	2.56	2.13
Aak1	AP2 associated kinase 1	0.0017	0.0001	0.0018	1.48	2.45	2.13
A230055J12Rik	RIKEN cDNA A230055J12 gene	0.0052	0.0010	0.0063	1.93	2.03	2.12

Online Resource 1. Genes changed in expression by at least two diets (p<0.01) in cerebral cortex

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
9630005C17Rik	:RIKEN cDNA 9630005C17 gene	0.0005	0.0000	0.0009	2.04	2.71	2.1
Tet2	:tet oncogene family member 2	0.0088	0.0000	0.0007	1.55	2.65	2.08
Ap1ar	:adaptor-related protein complex 1 associated regulatory protein	0.0086	0.0001	0.0074	1.66	2.54	2.03
6720427H10Rik	:RIKEN cDNA 6720427H10 gene	0.0003	0.0002	0.0005	2	2.01	1.96
2900084O13Rik	:RIKEN cDNA 2900084O13 gene	0.0073	0.0014	0.0074	1.82	2.29	1.94
Trps1	:trichorhinophalangeal syndrome I (human)	0.0035	0.0003	0.0022	1.71	2.27	1.88
Stag1	:stromal antigen 1	0.0010	0.0001	0.0087	2.01	2.56	1.88
4930456A14Rik	:RIKEN cDNA 4930456A14 gene	0.0006	0.0002	0.0075	1.93	2.28	1.85
2810416A17Rik	:RIKEN cDNA 2810416A17 gene	0.0006	0.0006	0.0034	1.93	2.23	1.83
C130057M05Rik	:RIKEN cDNA C130057M05 gene	0.0065	0.0020	0.0012	1.57	1.92	1.82
Unc13b	:unc-13 homolog B (C. elegans)	0.0074	0.0008	0.0004	1.49	1.82	1.75
A830010M09Rik	:RIKEN cDNA A830010M09 gene	0.0015	0.0004	0.0083	1.99	2.31	1.73
Son	:Son DNA binding protein	0.0050	0.0000	0.0038	1.39	2.16	1.69
Rbm33	:RNA binding motif protein 33	0.0063	0.0057	0.0030	1.45	1.56	1.63
Al414108	:expressed sequence Al414108	0.0029	0.0012	0.0014	1.46	1.44	1.62
Tia1	:cytotoxic granule-associated RNA binding protein 1	0.0089	0.0001	0.0006	1.48	1.89	1.59
Vmn2r29	:vomeronasal 2, receptor 29	0.0041	0.0022	0.0016	1.36	1.55	1.59
Snhg11	:small nucleolar RNA host gene 11 (non-protein coding)	0.0015	0.0020	0.0027	1.6	1.63	1.59
Man2c1	:mannosidase, alpha, class 2C, member 1	0.0030	0.0001	0.0010	1.35	1.76	1.51
Glt8d1	:glycosyltransferase 8 domain containing 1	0.0065	0.0002	0.0005	1.25	1.56	1.5
Akap8	:A kinase (PRKA) anchor protein 8	0.0011	0.0009	0.0012	1.41	1.57	1.5
Nek1	:NIMA (never in mitosis gene a)-related expressed kinase 1	0.0087	0.0002	0.0004	1.26	1.51	1.47
Ccnt2	:cyclin T2	0.0080	0.0023	0.0004	1.25	1.44	1.44
Fam178a	:family with sequence similarity 178, member A	0.0041	0.0008	0.0025	1.38	1.59	1.43
Spag1	:sperm associated antigen 1	0.0035	0.0019	0.0053	1.66	2.02	1.43
Rbm5	:RNA binding motif protein 5	0.0002	0.0000	0.0001	1.35	1.39	1.41
Eif2c3	:eukaryotic translation initiation factor 2C, 3	0.0033	0.0069	0.0055	1.26	1.34	1.38
Map4k5	:mitogen-activated protein kinase kinase kinase 5	0.0005	0.0000	0.0002	1.26	1.3	1.38
Nin	:ninein	0.0003	0.0054	0.0041	1.34	1.38	1.38
Snrnp70	:small nuclear ribonucleoprotein 70 (U1)	0.0006	0.0000	0.0004	1.38	1.51	1.37
Eif2s3y	:eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	0.0027	0.0009	0.0092	1.38	1.74	1.36
Pxdn	:peroxidasin homolog (Drosophila)	0.0014	0.0006	0.0019	1.47	1.39	1.36
Ssh2	:slingshot homolog 2 (Drosophila)	0.0035	0.0004	0.0066	1.25	1.31	1.34
Smg1	:SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	0.0039	0.0003	0.0061	1.47	1.51	1.33
Zfc3h1	:zinc finger, C3H1-type containing	0.0013	0.0053	0.0030	1.23	1.2	1.33
Mirg	:miRNA containing gene	0.0021	0.0004	0.0015	1.3	1.38	1.32
Chd2	:chromodomain helicase DNA binding protein 2	0.0019	0.0052	0.0001	1.2	1.33	1.32
Zfp280d	:zinc finger protein 280D	0.0009	0.0006	0.0024	1.18	1.3	1.31
Ddx50	:DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	0.0049	0.0013	0.0055	1.19	1.32	1.29
Psme4	:proteasome (prosome, macropain) activator subunit 4	0.0001	0.0008	0.0054	1.38	1.23	1.28
Ing1	:inhibitor of growth family, member 1	0.0011	0.0012	0.0016	1.24	1.34	1.27
Usp31	:ubiquitin specific peptidase 31	0.0057	0.0013	0.0030	1.26	1.33	1.26
Taf1	:TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.0041	0.0032	0.0063	1.21	1.22	1.26
Peg3	:paternally expressed 3	0.0010	0.0004	0.0005	1.22	1.22	1.26
Dpm2	:dolichol-phosphate (beta-D) mannosyltransferase 2	0.0048	0.0004	0.0003	1.18	1.27	1.25
Zfp445	:zinc finger protein 445	0.0004	0.0006	0.0031	1.27	1.28	1.25
Lrrprc	:leucine-rich PPR-motif containing	0.0073	0.0058	0.0012	1.17	1.25	1.22
Phf15	:PHD finger protein 15	0.0059	0.0016	0.0049	1.2	1.34	1.22
2310058N22Rik	:RIKEN cDNA 2310058N22 gene	0.0048	0.0085	0.0025	1.19	1.21	1.22
Tia1	:Tia1 cytotoxic granule-associated RNA binding protein-like 1	0.0073	0.0003	0.0003	1.2	1.26	1.21
Rbm39	:RNA binding motif protein 39	0.0004	0.0034	0.0008	1.14	1.25	1.2
Senp6	:SUMO/sentrin specific peptidase 6	0.0063	0.0030	0.0006	1.24	1.22	1.16
Arhgap21	:Rho GTPase activating protein 21	0.0002	0.0090	0.0007	1.23	1.15	1.14
Kidins220	:kinase D-interacting substrate 220	0.0041	0.0012	0.0083	1.12	1.16	1.13
Mgea5	:meningioma expressed antigen 5 (hyaluronidase)	0.0081	0.0039	0.0054	1.12	1.15	1.12
Aldh5a1	:aldehyde dehydrogenase family 5, subfamily A1	0.0036	0.0018	0.0086	1.17	1.13	1.09
Gdi2	:guanosine diphosphate (GDP) dissociation inhibitor 2	0.0099	0.0061	0.0005	-1.1	-1.13	-1.11
Rala	:v-ras simian leukemia viral oncogene homolog A (ras related)	0.0004	0.0003	0.0099	-1.21	-1.18	-1.14
Tsc22d2	:TSC22 domain family, member 2	0.0008	0.0033	0.0058	-1.2	-1.18	-1.16
Nrcam	:neuron-glia-CAM-related cell adhesion molecule	0.0032	0.0000	0.0083	-1.11	-1.29	-1.18
Gpr162	:G protein-coupled receptor 162	0.0071	0.0081	0.0043	-1.16	-1.17	-1.2
Rab12	:RAB12, member RAS oncogene family	0.0005	0.0001	0.0026	-1.17	-1.31	-1.21
Id2	:inhibitor of DNA binding 2	0.0070	0.0027	0.0006	-1.25	-1.29	-1.27
Grif1	:glucocorticoid receptor DNA binding factor 1	0.0000	0.0085	0.0069	-1.17	-1.21	-1.27
Mtap1a	:microtubule-associated protein 1 A	0.0087	0.0074	0.0037	-1.15	-1.29	-1.28
Tspyl1	:testis-specific protein, Y-encoded-like 1	0.0065	0.0001	0.0014	-1.21	-1.38	-1.29
Sbf1	:SET binding factor 1	0.0026	0.0010	0.0010	-1.18	-1.32	-1.32
Zswim1	:zinc finger, SWIM domain containing 1	0.0046	0.0001	0.0010	-1.19	-1.51	-1.36
Hnnpul1	:heterogeneous nuclear ribonucleoprotein U-like 1	0.0084	0.0009	0.0002	-1.24	-1.32	-1.39
Zfp60	:zinc finger protein 60	0.0006	0.0000	0.0000	-1.32	-1.75	-1.41
Zfp574	:zinc finger protein 574	0.0066	0.0013	0.0001	-1.19	-1.43	-1.44
Mapk8ip3	:mitogen-activated protein kinase 8 interacting protein 3	0.0017	0.0002	0.0000	-1.19	-1.39	-1.44
Fam134c	:family with sequence similarity 134, member C	0.0016	0.0016	0.0002	-1.21	-1.18	-1.45
Tiparp	:TCDL-inducible poly(ADP-ribose) polymerase	0.0009	0.0023	0.0044	-1.7	-1.65	-1.45
Atp6v1a	:ATPase, H+ transporting, lysosomal V1 subunit A	0.0021	0.0003	0.0002	-1.24	-1.36	-1.49
Scap	:SREBF chaperone	0.0043	0.0010	0.0006	-1.2	-1.27	-1.52
Grin1	:glutamate receptor, ionotropic, NMDA1 (zeta 1)	0.0035	0.0002	0.0001	-1.18	-1.54	-1.52
Suox	:sulfite oxidase	0.0011	0.0008	0.0006	-1.36	-1.4	-1.52
Arhgap33	:Rho GTPase activating protein 33	0.0072	0.0060	0.0008	-1.29	-1.53	-1.56
Lip12	:lipoyl(octanoyl) transferase 2 (putative)	0.0095	0.0048	0.0026	-1.29	-1.39	-1.57
Sprn	:shadow of prion protein	0.0043	0.0013	0.0001	-1.26	-1.4	-1.58
1700020114Rik	:RIKEN cDNA 1700020114 gene	0.0004	0.0006	0.0017	-1.79	-1.68	-1.58
Gm5113	:predicted gene 5113	0.0075	0.0004	0.0069	-1.59	-1.76	-1.66
Zfp146	:zinc finger protein 146	0.0005	0.0010	0.0001	-1.61	-1.32	-1.72
AA409289	:expressed sequence AA409289	0.0045	0.0061	0.0005	-2.42	-2.46	-3.68