

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Adad1	adenosine deaminase domain containing 1 (testis specific)	0.0086	0.0059	0.0888	2.39	2.15	2.11
Epm2aip1	EFM2A (atofin) interacting protein 1	0.0005	0.0002	0.0447	1.46	1.73	1.32
4530429F24Rik	RIKEN cDNA 4530429F24 gene	0.0011	0.0068	0.1122	1.73	1.61	1.3
Pdhx	pyruvate dehydrogenase complex, component X	0.0078	0.0012	0.0134	1.17	1.21	1.18
Pknox1a	protein kinase, cAMP dependent regulatory, type 1, alpha	0.0076	0.0094	0.0191	1.16	1.2	1.17
Ncor1	nuclear receptor co-repressor 1	0.0044	0.0001	0.3212	-1.2	-1.41	1.12
Dennm4a	DENM4AD domain containing 4A	0.0080	0.0034	0.4320	1.45	-1.39	-1.09
Sympo2	sympo2	0.0076	0.0004	0.1429	1.31	1.22	-1.1
Txlna	taxilin alpha	0.0074	0.0091	0.0803	-1.27	-1.26	-1.19
Kdm3b	KDM3B lysine (K)-specific demethylase 3B	0.0007	0.0072	0.0957	-1.39	-1.26	-1.2
Aox1	aldehyde oxidase 1	0.0009	0.0041	0.0128	-1.37	-1.36	-1.21
Khl23	kelch-like 23 (Drosophila)	0.0051	0.0002	0.0646	-1.46	-1.65	-1.22
Exi1	exostosin (multiple) 1	0.0005	0.0031	0.0115	-1.48	-1.42	-1.22
Foxo1	forkhead box O1	0.0011	0.0023	0.1076	1.49	-1.48	-1.24
Cyp2d34	cytochrome P450, family 2, subfamily d, polypeptide 34	0.0030	0.0005	0.2951	-1.63	-3.21	-1.25
Cilp3	CAP-GLY domain containing linker protein 3	0.0044	0.0000	0.0297	-1.24	-1.7	-1.4
Zfp628	zinc finger protein 528	0.0001	0.0038	0.2157	-6.35	-2.97	-1.62
C23003516Rik	RIKEN cDNA C23003516 gene	0.0000	0.0046	0.0433	3.85	-1.77	-1.82
Amn	amniotless	0.0000	0.0002	0.0130	-4.78	-3.39	-2.05
Muc16	imucin 16	0.0004	0.0624	0.0010	4.91	2.07	4.94
Ly6d	lymphocyte antigen 6 complex, locus D	0.0030	0.0377	0.0096	2.9	2.8	2.58
Tmem40	transmembrane protein 40	0.0073	0.0511	0.0058	1.91	1.93	2.22
Zkda	zinc finger, X-linked, duplicated A	0.0015	0.0241	0.0011	1.44	1.46	1.58
Gatpb2	GA repeat binding protein, beta 2	0.0047	0.1926	0.0037	1.41	1.17	1.5
Smc5	structural maintenance of chromosomes 5	0.0051	0.0603	0.0012	1.27	1.26	1.34
Dst	dystonin	0.0074	0.0980	0.0040	-1.39	1.13	1.27
Ikar5	IKAROS family zinc finger 5	0.0016	0.3258	0.0056	1.38	1.11	1.26
Ncaa1	nuclear receptor coactivator 1	0.0004	0.0519	0.0054	1.49	1.26	1.25
Copz1	coatamer protein complex, subunit zeta 1	0.0006	0.0586	0.0045	1.13	1.1	1.21
Rhot1	ras homolog gene family, member T1	0.0100	0.0519	0.0004	1.12	1.09	1.2
Aarsd1	alanyl-tRNA synthetase domain containing 1	0.0081	0.4284	0.0034	1.2	1.05	1.14
Eif1	eukaryotic translation initiation factor 1	0.0001	0.2372	0.0019	1.15	-1.05	-1.1
Hena	hexameric A	0.0005	0.0224	0.0002	1.17	-1.11	-1.19
G3bp2	GTPase activating protein (SH3 domain) binding protein 2	0.0020	0.0611	0.0001	-1.38	-1.19	-1.39
Adipor2	adiponectin receptor 2	0.0023	0.0226	0.0006	-1.43	-1.26	-1.77
2310050P20Rik	RIKEN cDNA 2310050P20 gene	0.0000	0.0615	0.0044	-3.08	-1.49	-1.83
Zbtb5	zinc finger and BTB domain containing 5	0.0056	0.1059	0.0022	-1.42	-1.83	-1.19
Kl	kl	0.1835	0.0000	0.0003	3.5	7.25	6.19
Gm1568	predicted gene 1568	0.0285	0.0060	0.0022	5.08	5.53	5.32
Gm4814	predicted gene 4814	0.0368	0.0000	0.0006	3.34	5.52	4.28
Lca5l	Leber congenital amaurosis 5-like	0.2994	0.0081	0.0062	1.98	3.4	4.22
Lph	lipase, member H	0.9951	0.0087	0.0007	1	2.77	3.82
2900047A07Rik	RIKEN cDNA 2900047A07 gene	0.1296	0.0001	0.0007	1.84	3.57	3.81
2900042E19Rik	RIKEN cDNA 2900042E19 gene	0.2715	0.0004	0.0052	2.16	3.32	3.36
Sic25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14	0.7069	0.0001	0.0000	1.2	3.07	3.07
Trem2	triggering receptor expressed on myeloid cells 2	0.0960	0.0003	0.0029	2.77	3.26	2.81
Pdp1cb	protein phosphatase 1, catalytic subunit, beta isoform	0.5300	0.0000	0.0004	-1.13	2.73	2.65
4530431B20Rik	RIKEN cDNA 4530431B20 gene	0.0762	0.0001	0.0001	2.84	2.64	2.65
Gm7536	predicted gene 7536	0.2148	0.0000	0.0002	-1.42	2.71	2.64
Tsld2	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	0.3073	0.0001	0.0001	1.06	2.46	2.56
4921525O09Rik	RIKEN cDNA 4921525O09 gene	0.2068	0.0065	0.0006	2.12	2.67	2.53
4830429F24Rik	RIKEN cDNA 4830429F24 gene	0.4388	0.0000	0.0002	1.12	3.08	2.43
4921510106Rik	RIKEN cDNA 4921510106 gene	0.0351	0.0084	0.0086	2.66	2.39	2.67
Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	0.2212	0.0000	0.0006	1.22	2.25	2.38
Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	0.1132	0.0003	0.0002	-1.62	2.41	2.38
BC016423	cDNA sequence BC016423	0.6040	0.0000	0.0000	-1.09	2.22	2.37
Mib1	mindbomb homolog 1 (Drosophila)	0.4337	0.0016	0.0014	1.12	2.19	2.33
LOC100303644	hypothetical LOC100303644	0.0511	0.0045	0.0041	2.24	2.73	2.27
Calcng2	calcium channel, voltage-dependent, gamma subunit 2	0.9666	0.0003	0.0032	-1.02	2.5	2.24
Pdia4	protein disulfide isomerase associated 4	0.0899	0.0002	0.0037	-1.76	3.06	2.22
Itgb1bp3	integrin beta 1 binding protein 3	0.7106	0.0013	0.0007	-1.08	1.73	2.22
AI131651	expressed sequence AI131651	0.0188	0.0064	0.0077	-2.94	1.86	2.21
Tes5-ps	testis derived transcript 3, pseudogene	0.272	0.0002	0.0005	1.32	2.16	2.16
AA407881	expressed sequence AA407881	0.0423	0.0000	0.0000	1.42	2.35	2.16
Lepr	leptin receptor	0.8628	0.0058	0.0052	-1.05	2.09	2.14
9330156P08Rik	RIKEN cDNA 9330156P08 gene	0.3074	0.0024	0.0004	1.26	2.22	2.13
Tao1	TAO kinase	0.1763	0.0000	0.0000	-1.24	2.2	2.11
Croc1	chromodomain helicase DNA binding protein 1	0.8599	0.0017	0.0017	1.02	2.12	2.11
Yod1	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae)	0.2750	0.0038	0.0022	-1.16	2.39	2.1
10-Sep	septin 10	0.5783	0.0019	0.0010	-1.13	1.86	2.07
Sirbp	spermatid perinuclear RNA binding protein	0.8871	0.0001	0.0024	1.03	1.72	2.07
Lypla1	lysophospholipase 1	0.8089	0.0000	0.0001	-1.01	2.39	2.06
Sdc4	syndecan 4	0.8935	0.0009	0.0008	-1.02	2.03	2.06
Zfp120	zinc finger protein 120	0.0905	0.0000	0.0001	1.29	2.35	2.04
Dnaic3	DnaI (Hsp40) homolog, subfamily C, member 3	0.8340	0.0000	0.0000	-1.01	1.87	2.04
Mgst3	microsomal glutathione S-transferase 3	0.3301	0.0000	0.0000	-1.2	2.16	2.02
C78692	expressed sequence C78692	0.1973	0.0000	0.0006	1.16	2.36	1.97
Haus2	HAUS augmin-like complex, subunit 2	0.056	0.0006	0.0007	1.37	1.95	1.95
Slc38a4	solute carrier family 38, member 4	0.5364	0.0024	0.0003	-1.05	2.34	1.95
Col4a3	collagen, type IV, alpha 3	0.1255	0.0080	0.0012	1.43	1.82	1.94
Ddo	D-aspartate oxidase	0.1325	0.0000	0.0000	1.2	2.12	1.93
9330159F19Rik	RIKEN cDNA 9330159F19 gene	0.2769	0.0005	0.0075	-1.21	2.47	1.92
Ppil3	peptidyl isomerase (cyclophilin)-like 3	0.7575	0.0001	0.0005	-1.03	1.85	1.92
Tceb1	transcription elongation factor B (SII), polypeptide 1	0.1915	0.0006	0.0000	1.13	1.83	1.91
Ugt2	UDP-glucose glycosyltransferase 2	0.2785	0.0015	0.0078	-1.23	2.15	1.91
130004C03	hypothetical LOC403343	0.6679	0.0075	0.0071	1.11	1.87	1.9
Pgil	phosphatidylinositol glycan anchor biosynthesis, class F	0.3029	0.0023	0.0003	1.15	1.94	1.89
Gtf3c4	general transcription factor IIC, polypeptide 4	0.3892	0.0000	0.0000	-1.19	1.72	1.89
Blzf1	basic leucine zipper nuclear factor 1	0.4504	0.0000	0.0000	-1.06	2.11	1.89
Ociad2	OCA domain containing 2	0.0629	0.0000	0.0000	1.15	1.9	1.89
Farsb	phenylalanyl-tRNA synthetase, beta subunit	0.1439	0.0010	0.0001	1.15	1.77	1.88
Camap1	calmodulin regulated spectrin-associated protein 1	0.8881	0.0003	0.0000	1.02	2.25	1.87
Oub1	OTU domain, ubiquitin aldehyde binding 1	0.0507	0.0004	0.0089	1.96	1.86	1.86
Mett11b	methyltransferase like 11B	0.0528	0.0003	0.0003	1.17	1.7	1.86
Vglt3	vestigial like 3 (Drosophila)	0.9533	0.0002	0.0006	1.01	1.87	1.85
2900053A13Rik	RIKEN cDNA 2900053A13 gene	0.4139	0.0000	0.0000	-1.03	1.83	1.85
Cope6	COP6 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	0.0341	0.0000	0.0000	1.13	1.89	1.85
Poi2f1	polymerase (RNA) II (DNA directed) polypeptide F	0.7374	0.0034	0.0034	-1.04	1.78	1.84
Dleu2	deleted in lymphocytic leukemia, 2	0.6105	0.0000	0.0001	1.07	2.06	1.83
Zfp518	zinc finger protein 518	0.9435	0.0026	0.0008	1.01	1.62	1.83
Ergic2	ERGIC and golgi 2	0.6965	0.0000	0.0001	-1.04	1.99	1.82
Sap30	sap3 associated polypeptide	0.1709	0.0043	0.0015	-1.16	1.47	1.82
Usp9b	ubiquitin specific peptidase 9, X chromosome	0.8323	0.0003	0.0005	-1.06	1.74	1.82
Pldn5	profoldin 5	0.4242	0.0000	0.0000	1.05	1.96	1.82
C130034I24Rik	RIKEN cDNA C130034I24 gene	0.2561	0.0026	0.0001	1.2	1.72	1.82
Mrps34	mitochondrial ribosomal protein S34	0.8224	0.0003	0.0000	-1.02	1.82	1.81
Erbp2ip	Erbp2 interacting protein	0.3543	0.0000	0.0001	-1.05	2.04	1.81
Hdh2	haloacid dehalogenase-like hydrolase domain containing 2	0.1886	0.0000	0.0000	1.07	1.93	1.81
Zfp367	zinc finger protein 367	0.4004	0.0001	0.0007	-1.13	1.82	1.81
7-Mar	membrane-associated ring finger (C3HC4) 7	0.4323	0.0000	0.0000	1.03	1.78	1.81
Mfap3l	microfilament-associated protein 3-like	0.5306	0.0005	0.0009	-1.06	1.64	1.8
Cope4	COP4 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	0.4584	0.0001	0.0000	1.09	1.89	1.8
Psmc1	proteasome, macropain 1 2S subunit, ATPase 1	0.3871	0.0000	0.0000	-1.02	1.89	1.79
Haus1	HAUS augmin-like complex, subunit 1	0.1364	0.0001	0.0002	1.21	1.75	1.79
Itch	itchy, E3 ubiquitin protein ligase	0.8208	0.0001	0.0015	-1.04	1.89	1.78
Calcr1	calcitonin receptor-like	0.5667	0.0038	0.0010	1.08	1.79	1.77
Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	0.0194	0.0000	0.0000	-1.1	1.85	1.77
Cutc	cutc copper transporter homolog (E. coli)	0.0649	0.0000	0.0000	1.2	1.83	1.77
Clec2d	C-type lectin domain family 2, member d	0.6299	0.0063	0.0035	-1.09	1.7	1.77
Usp53	ubiquitin specific peptidase 53	0.2028	0.0031	0.0006	1.14	1.76	1.77
Rgmd2	RNA (guanine 9-) methyltransferase domain containing 2	0.0477	0.0002	0.0048	1.34	1.78	1.76
Cik4	CDC like kinase 4	0.6702	0.0016	0.0000	-1.03	1.87	1.76
Polydm1	polydm1	0.3683	0.0000	0.0004	1	1.46	1.75
Cpeb2	cytoplasmic polyadenylation element binding protein 2	0.6076	0.0000	0.0028	-1.04	1.9	1.75
Fbxo30	F-box protein 30	0.0744	0.0087	0.0017	1.25	1.66	1.75
Calm3	calmodulin 3	0.9600	0.0000	0.0001	-1	1.83	1.75
Tm7a2	transmembrane 7 superfamily member 2	0.0436	0.0029	0.0051	1.36	1.93	1.75
Dcc4	dedicator of cytokinesis 4	0.7092	0.0015	0.0016	-1.07	1.87	1.73
Tbp1	TATA box binding protein-like 1	0.4151	0.0005	0.0010	1.14	1.81	1.73
Lpt1	lipoyltransferase 1	0.7153	0.0001	0.0003	1.04	2.03	1.72
Rps20	ribosomal protein S20	0.9486	0.0022	0.0000	-1.01	1.71	1.72
Ocd1d2	discoidin, CUB and LCCL domain containing 2	0.6209	0.0001	0.0002	-1.08	1.54	1.72
Fam46a	family with sequence similarity 46, member A	0.8995	0.0010	0.0054	1.05	1.6	1.72

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Cdc56	coiled-coil domain containing 56	0.3280	0.0000	0.0001	-1.12	1.82	1.71
Atg4a	autophagy-related 4A (yeast)	0.2314	0.0000	0.0000	1.04	1.76	1.71
Fmrb4b	FERM domain containing 4B	0.4757	0.0074	0.0083	-1.2	1.91	1.71
Hmrbp2	heterogeneous nuclear ribonucleoprotein H2	0.6793	0.0002	0.0001	-1.03	1.7	1.71
Mrlp55	mitochondrial ribosomal protein L55	0.8082	0.0000	0.0004	1.02	1.79	1.71
Dhw2	DTW domain containing 2	0.3448	0.0098	0.0001	-1.12	1.67	1.71
Slc5a1	solute carrier organic anion transporter family, member 5A1	0.2530	0.0003	0.0000	1.09	1.55	1.7
Zfp644	zinc finger protein 644	0.4256	0.0012	0.0003	1.08	1.75	1.7
Cep290	centrosomal protein 290	0.4175	0.0032	0.0016	-1.16	2.24	1.69
A430102J17Rik	RIKEN cDNA A430102J17 gene	0.6240	0.0003	0.0001	1.04	1.74	1.69
Ktbbd4	Kelch repeat and BTB (POZ) domain containing 4	0.1417	0.0006	0.0003	1.19	1.73	1.69
Vcan	versican	0.5518	0.0078	0.0006	-1.1	1.62	1.69
Mpp5	membrane protein, palmitoylated 5 (MAGUR p55 subfamily member 5)	0.2421	0.0081	0.0022	1.65	1.69	1.69
4830466K18Rik	RIKEN cDNA 4830466K18 gene	0.0149	0.0003	0.0044	1.37	1.63	1.69
Gak3b	glycogen synthase kinase 3 beta	0.3058	0.0000	0.0002	-1.07	1.8	1.68
D230044B12Rik	RIKEN cDNA D230044B12 gene	0.5777	0.0016	0.0075	-1.09	1.59	1.68
Gdc1	GC-rich sequence DNA-binding factor 1	0.9957	0.0001	0.0002	-1	1.62	1.68
Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	0.8484	0.0017	0.0085	-1.02	1.64	1.68
Rbm3	RNA binding motif protein 3	0.2910	0.0094	0.0051	1.14	1.56	1.68
Rbm8a	RNA binding motif protein 8a	0.7030	0.0000	0.0000	1.03	1.76	1.68
Snrpd3	small nuclear ribonucleoprotein D3	0.0255	0.0003	0.0081	1.27	1.98	1.67
Bat1	blocked early in transport 1 homolog (S. cerevisiae)	0.0607	0.0001	0.0008	1.18	1.68	1.67
Wdr33	WD repeat domain 33	0.8903	0.0000	0.0000	1.02	1.76	1.67
Tulp4	tubby like protein 4	0.5997	0.0000	0.0000	-1.04	1.61	1.67
2900009J20Rik	RIKEN cDNA 2900009J20 gene	0.6313	0.0002	0.0024	-1.06	1.59	1.67
C730026J16	hypothetical protein C730026J16	0.1408	0.0003	0.0001	1.12	1.66	1.67
Pls3	plastin 3 (T-isoform)	0.4363	0.0012	0.0002	-1.08	1.67	1.67
Akr6	ADP-ribosylation factor 6	0.8776	0.0001	0.0008	-1.02	1.69	1.66
Skip1a	S-phase kinase-associated protein 1A	0.0158	0.0000	0.0007	-1.36	1.85	1.66
Vwa5a	von Willebrand factor A domain containing 5A	0.4846	0.0002	0.0045	1.08	1.66	1.66
Zfp472	zinc finger protein 472	0.0427	0.0002	0.0004	1.43	1.52	1.65
Cot1	coactonin-like 1 (Drosophila)	0.8854	0.0001	0.0066	1.01	1.67	1.65
Deaf1	differentially expressed in 184F-10	0.8852	0.0001	0.0000	1.01	1.72	1.65
Lcor	ligand dependent nuclear receptor corepressor	0.8476	0.0003	0.0000	-1.02	1.7	1.65
Mmadhc	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	0.6965	0.0000	0.0000	-1.02	1.65	1.65
Mobk1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	0.3337	0.0003	0.0000	-1.08	1.68	1.65
Lsm14b	LSM14 homolog B (SCD6, S. cerevisiae)	0.5436	0.0000	0.0001	1.06	1.68	1.65
Pmr2	proline-rich nuclear receptor coactivator 2	0.4272	0.0000	0.0000	1.42	1.74	1.64
Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	0.9247	0.0034	0.0018	-1.01	1.62	1.64
Sic25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	0.2505	0.0017	0.0066	-1.16	1.75	1.64
C230091D08Rik	RIKEN cDNA C230091D08 gene	0.7621	0.0014	0.0064	1.05	1.7	1.64
Trab2	transformer 2 beta homolog (Drosophila)	0.3080	0.0000	0.0000	-1.09	1.66	1.64
Commdb	COMM domain containing 8	0.8146	0.0000	0.0004	1.01	1.75	1.64
Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	0.9353	0.0006	0.0089	-1.01	1.46	1.63
Yme1l1	YME1-like 1 (S. cerevisiae)	0.9381	0.0000	0.0016	-1.01	1.95	1.63
Rpp14	ribonuclease P 14 subunit (human)	0.0342	0.0000	0.0000	1.11	1.67	1.63
1110059E24Rik	RIKEN cDNA 1110059E24 gene	0.0685	0.0011	0.0004	-1.25	1.81	1.63
Ankrk32	ankyrin repeat domain 32	0.4875	0.0003	0.0005	1.01	1.72	1.63
Mbnl2	muscleblind-like 2	0.1894	0.0000	0.0000	1.06	1.74	1.63
Ptpn12	protein tyrosine phosphatase, non-receptor type 12	0.7877	0.0002	0.0006	-1.02	1.62	1.62
Ktbbd10	Kelch repeat and BTB (POZ) domain containing 10	0.0794	0.0000	0.0001	-1.42	1.73	1.62
Ppf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.6172	0.0032	0.0010	-1.05	1.64	1.62
Zfp407	zinc finger protein 407	0.0667	0.0026	0.0031	1.2	1.5	1.62
Tspan8	tetraspanin 8	0.6400	0.0001	0.0022	-1.05	1.64	1.62
Aatf	apoptosis antagonizing transcription factor	0.5138	0.0050	0.0017	1.09	1.61	1.62
Aak1	AP2 associated kinase 1	0.9293	0.0007	0.0005	1.01	1.59	1.62
Cnot2	CCR4-NOT transcription complex, subunit 2	0.5956	0.0002	0.0004	1.06	1.7	1.62
Nnmat3	nicotinamide nucleotide adenyltransferase 3	0.0816	0.0056	0.0028	1.16	1.39	1.61
Ilf2	interleukin enhancer binding factor 2	0.2391	0.0068	0.0049	-1.18	1.5	1.61
Xpo7	exportin 7	0.1677	0.0002	0.0008	1.2	1.8	1.61
Morf42	mortality factor 4 like 2	0.0183	0.0000	0.0000	1.12	1.7	1.61
Apc	adenomatous polyposis coli	0.3108	0.0001	0.0000	1.07	1.67	1.61
Srsf10	serine/arginine-rich splicing factor 10	0.2857	0.0013	0.0014	-1.08	1.62	1.61
Itgav	integrin alpha V	0.2892	0.0009	0.0002	-1.1	1.46	1.61
Nr3c2	nuclear receptor subfamily 3, group C, member 2	0.0831	0.0086	0.0003	1.23	1.29	1.6
Hmrbp3	heterogeneous nuclear ribonucleoprotein A3	0.7078	0.0023	0.0037	-1.04	1.53	1.6
Dmrt1	Dmrt-like 1	0.1844	0.0001	0.0014	-1.13	1.8	1.6
Epf1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	0.2150	0.0002	0.0005	-1.14	1.68	1.6
1110004F10Rik	RIKEN cDNA 1110004F10 gene	0.3189	0.0000	0.0000	-1.09	1.74	1.6
2310010M20Rik	RIKEN cDNA 2310010M20 gene	0.1815	0.0002	0.0025	-1.31	2.1	1.6
Olfec2a	oligonucleotide/oligosaccharide-binding fold containing 2A	0.5408	0.0000	0.0006	-1.06	1.67	1.6
Home1	home1 homolog 1 (Drosophila)	0.7985	0.0007	0.0000	-1.02	1.59	1.59
Wapal	wings apart-like homolog (Drosophila)	0.3896	0.0000	0.0000	1.02	1.49	1.59
Col4a3bp	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0.6845	0.0000	0.0000	1.04	1.59	1.59
Aab15	ankyrin repeat and SOCS box-containing 15	0.5075	0.0044	0.0012	-1.08	1.71	1.59
Cu12	cullin 2	0.4596	0.0000	0.0000	-1.03	1.48	1.59
Aib48100	expressed sequence Aib48100	0.2995	0.0008	0.0013	-1.1	1.45	1.59
Acad5	acyl-Coenzyme A binding domain containing 5	0.8336	0.0000	0.0014	1.06	1.66	1.59
C1d	C1D nuclear receptor co-repressor	0.1358	0.0000	0.0000	-1.14	1.66	1.58
Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	0.1972	0.0000	0.0003	1.11	1.66	1.58
B230118H07Rik	RIKEN cDNA B230118H07 gene	0.8638	0.0000	0.0000	-1.01	1.51	1.58
Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	0.1904	0.0001	0.0010	1.09	1.7	1.58
Pp1	partner of NOB1 homolog (S. cerevisiae)	0.0875	0.0000	0.0000	1.11	1.74	1.58
Arl5b	ADP-ribosylation factor-like 5B	0.4970	0.0023	0.0001	1.06	1.42	1.58
Rpp30	ribonuclease P/MRP 30 subunit (human)	0.5364	0.0000	0.0000	1.03	1.54	1.58
Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	0.9331	0.0013	0.0065	1.01	1.79	1.58
Srx13	sorting nexin 13	0.8604	0.0014	0.0000	1.01	1.57	1.58
Naa15	N-acylserine/threonine transferase 15, NAA auxiliary subunit	0.1041	0.0058	0.0001	1.27	1.7	1.58
Tlcr9c	tetratricopeptide repeat domain 9C	0.6955	0.0003	0.0001	1.02	1.55	1.58
Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, aminoacidate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.5334	0.0021	0.0000	-1.07	1.36	1.58
Aasdhpt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.0512	0.0000	0.0006	-1.23	1.6	1.57
5830443J22Rik	RIKEN cDNA 5830443J22 gene	0.1859	0.0057	0.0032	1.22	1.63	1.57
Ttc1615	TTC16 family, member 15	0.8517	0.0000	0.0000	1.02	1.69	1.57
Ints5	integrator complex subunit 5	0.3787	0.0000	0.0000	-1.06	1.67	1.57
3110048L19Rik	zinc finger pseudogene	0.4751	0.0010	0.0013	1.08	1.46	1.57
Vamp7	vesicle-associated membrane protein 7	0.1196	0.0001	0.0001	1.17	1.67	1.57
BC049807	cDNA sequence BC049807	0.5165	0.0049	0.0080	1.12	1.7	1.57
Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	0.3874	0.0001	0.0002	-1.17	1.63	1.57
2310002L09Rik	RIKEN cDNA 2310002L09 gene	0.2978	0.0001	0.0002	1.1	1.7	1.57
Serinc1	serine incorporator 1	0.3224	0.0000	0.0000	1.05	1.67	1.57
Aab11	ankyrin repeat and SOCS box-containing 11	0.1787	0.0000	0.0002	1.13	1.69	1.57
Aaa11	N-acylserine/threonine amidohydrolase 1	0.7047	0.0003	0.0006	1.04	1.61	1.57
Orca1	origin recognition complex, subunit 4-like (S. cerevisiae)	0.3999	0.0001	0.0000	1.06	1.7	1.57
Gatad1	GATA zinc finger domain containing 1	0.8825	0.0000	0.0000	1.01	1.57	1.57
Tmod1	tropomodulin 1	0.6051	0.0007	0.0002	1.05	1.6	1.57
Srsf5	serine/arginine-rich splicing factor 5	0.1477	0.0023	0.0017	1.15	1.65	1.56
Rictor	RPTOR independent companion of MTOR, complex 2	0.4213	0.0004	0.0065	-1.09	1.54	1.56
0610009D07Rik	RIKEN cDNA 0610009D07 gene	0.2004	0.0000	0.0000	-1.07	1.69	1.56
Bzw1	basic leucine zipper and W2 domains 1	0.6029	0.0001	0.0003	1.04	1.6	1.56
Tcf12	transcription factor 12	0.1551	0.0018	0.0008	-1.1	1.51	1.56
Comm2	COMM domain containing 2	0.8884	0.0002	0.0000	-1.01	1.51	1.56
Itrp12	inositol 1,4,5-trisphosphate receptor interacting protein-like 2	0.6705	0.0060	0.0051	-1.05	1.41	1.56
Acr6	ARF6 actin-related protein 6 homolog (yeast)	0.3505	0.0003	0.0004	-1.11	1.54	1.56
Tmod3	tropomodulin 3	0.3267	0.0063	0.0026	1.14	1.67	1.56
Cmt6	CKLF-like MARVEL transmembrane domain containing 6	0.4232	0.0073	0.0008	-1.1	1.36	1.56
Tm4sf1	transmembrane 4 superfamily member 1	0.7834	0.0086	0.0054	-1.03	1.39	1.56
Cank1a1	casein kinase 1, alpha 1	0.5359	0.0000	0.0001	1.03	1.73	1.56
Apl62	amyloid beta (Aβ) precursor protein-binding, family B, member 2	0.1863	0.0010	0.0004	1.14	1.41	1.56
Mrlp48	mitochondrial ribosomal protein L48	0.8523	0.0002	0.0001	1.02	1.57	1.56
Timm17a	translocase of inner mitochondrial membrane 17a	0.3514	0.0000	0.0000	1.03	1.61	1.56
Med13	mediator complex subunit 13	0.9805	0.0002	0.0012	1	1.49	1.56
Ikar2	IKAROS family zinc finger 2	0.4375	0.0009	0.0012	-1.1	1.6	1.55
Hsd2	hydroxysteroid dehydrogenase like 2	0.7296	0.0007	0.0001	1.04	1.41	1.55
Wdr61	WD repeat domain 61	0.6610	0.0000	0.0003	-1.02	1.63	1.55
Khl9	Kelch-like 9 (Drosophila)	0.2227	0.0000	0.0013	1.05	1.63	1.55
Aco19	acyl-CoA thioesterase 9	0.1419	0.0000	0.0000	1.1	1.53	1.55
Sharpin	SHANK-associated RH domain interacting protein	0.4021	0.0000	0.0006	1.07	1.64	1.54
Pst1a	protection of telomeres 1A	0.0773	0.0000	0.0014	1.26	1.54	1.54
4833408D11Rik	RIKEN cDNA 4833408D11 gene	0.1984	0.0048	0.0074	1.19	1.75	1.54
Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	0.4211	0.0001	0.0000	1.05	1.52	1.54
Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0.9238	0.0000	0.0000	-1	1.5	1.54
Pcm1	pericentriolar material 1	0.8738	0.0063	0.0013	1.01	1.25	1.54
Synrip	synaptobrevin binding, cytoplasmic RNA interacting protein	0.3591	0.0000	0.0001	1.05	1.48	1.54

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Mrp1	mitochondrial ribosomal protein L1	0.5837	0.0000	0.0008	1.05	1.71	1.54
Otu4	OTU domain containing 4	0.1288	0.0005	0.0003	-1.13	1.44	1.54
Prosm10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.9276	0.0001	0.0000	1.01	1.76	1.54
D7Ertd715e	DNA segment, Chr 7, ERATO Dcl 715, expressed	0.5059	0.0003	0.0000	-1.06	1.51	1.54
1110028C15Rik	RIKEN cDNA 1110028C15 gene	0.3482	0.0008	0.0001	-1.07	1.7	1.54
Trpm7	transient receptor potential cation channel, subfamily M, member 7	0.6859	0.0048	0.0004	1.04	1.39	1.54
Ccnc	cyclin C	0.3444	0.0000	0.0000	1.06	1.48	1.54
Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	0.8768	0.0001	0.0000	-1.01	1.47	1.53
BC013529	cDNA sequence BC013529	0.1283	0.0000	0.0000	-1.08	1.53	1.53
DnaJ7	DnaJ (Hsp40) homolog, subfamily C, member 7	0.0811	0.0001	0.0000	-1.12	1.44	1.53
Cdc42	cell division cycle 42 homolog (S. cerevisiae)	0.5166	0.0001	0.0017	1.07	1.71	1.53
Tor1a2	torsin A interacting protein 2	0.8269	0.0005	0.0001	-1.02	1.47	1.53
Mitf1	mitochondrial transitional release factor 1-like	0.8732	0.0006	0.0004	1.05	1.48	1.53
Arhgap20	Rho GTPase activating protein 20	0.0215	0.0001	0.0005	1.13	1.31	1.53
Org1	developmentally regulated GTP binding protein 1	0.9080	0.0000	0.0000	-1	1.59	1.53
Zfp825	zinc finger protein 825	0.8498	0.0041	0.0045	1.04	1.58	1.53
C1galt1c1	C1GALT1-specific chaperone 1	0.3661	0.0001	0.0032	-1.06	1.47	1.53
Ppt1	palmitoyl protein thioesterase 1	0.8881	0.0028	0.0007	-1.06	1.46	1.53
Par1	presenilin associated, rhomboid-like	0.0622	0.0000	0.0000	1.09	1.48	1.53
Anxa7	annexin A7	0.3313	0.0001	0.0002	1.08	1.69	1.53
Psmb2	proteasome (prosome, macropain) subunit, beta type 2	0.2003	0.0001	0.0001	-1.15	1.51	1.53
Birc6	baculoviral IAP repeat-containing 6	0.1119	0.0001	0.0036	1.17	1.66	1.53
Ssb	Spoken syndrome antigen B	0.3012	0.0005	0.0000	1.01	1.62	1.53
4933434E20Rik	RIKEN cDNA 4933434E20 gene	0.5137	0.0003	0.0004	1.05	1.65	1.53
Tmx2	thioredoxin-related transmembrane protein 2	0.4328	0.0013	0.0011	-1.11	1.4	1.53
Pds5b	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	0.0780	0.0005	0.0004	1.16	1.41	1.52
Zfp799	zinc finger protein 799	0.8473	0.0076	0.0057	-1.02	1.47	1.52
Sacm1	SAC1 (suppressor of actin mutations 1, homolog)/like (S. cerevisiae)	0.1082	0.0001	0.0000	1.06	1.64	1.52
Rars	arginyl-tRNA synthetase	0.1488	0.0003	0.0001	1.17	1.56	1.52
Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	0.8818	0.0013	0.0017	-1.02	1.46	1.52
Romo1	reactive oxygen species modulator 1	0.1636	0.0000	0.0001	1.07	1.64	1.52
Cdc127	coiled-coil domain containing 127	0.8079	0.0001	0.0033	1.02	1.6	1.52
Fam116a	family with sequence similarity 116, member A	0.8821	0.0002	0.0022	1.01	1.51	1.52
Rbm15	RNA binding motif protein 15	0.4476	0.0001	0.0007	1.09	1.66	1.52
Poli3k	polymerase (RNA) III (DNA directed) polypeptide K	0.3439	0.0001	0.0002	1.08	1.68	1.52
Mrps22	mitochondrial ribosomal protein S22	0.0167	0.0000	0.0000	1.14	1.6	1.52
Ostc	oligosaccharyltransferase complex subunit	0.5369	0.0000	0.0000	-1.03	1.57	1.52
Serpinb5a	serine (or cysteine) peptidase inhibitor, clade B, member 5a	0.4712	0.0005	0.0000	1.04	1.66	1.52
Zfp110	zinc finger protein 110	0.2174	0.0000	0.0000	-1.08	1.61	1.52
Zfp715	zinc finger protein 715	0.5091	0.0000	0.0002	1.03	1.45	1.51
Apix	apertaxin	0.1035	0.0011	0.0002	-1.13	1.47	1.51
Ipo11	importin 11	0.2260	0.0041	0.0002	1.11	1.43	1.51
Ccch1	cyclin H	0.3045	0.0001	0.0004	1.07	1.49	1.51
0610037P05Rik	RIKEN cDNA 0610037P05 gene	0.6410	0.0000	0.0000	-1.03	1.57	1.51
Pecr	peroxisomal trans-2-enoyl-CoA reductase	0.2040	0.0008	0.0001	1.13	1.52	1.51
Arfgap2	ADP-ribosylation factor GTPase activating protein 2	0.4511	0.0000	0.0001	-1.06	1.79	1.51
Osepp	O-sialosylcochaperone endopeptidase	0.4333	0.0014	0.0002	1.1	1.59	1.51
Odr4	odrin	0.2137	0.0004	0.0000	-1.06	1.37	1.51
Rnf115	ring finger protein 115	0.7585	0.0002	0.0015	1.01	1.55	1.51
Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	0.7035	0.0002	0.0027	-1.07	1.65	1.51
Lymr1	LYR motif containing 1	0.0979	0.0001	0.0016	1.22	1.66	1.51
Brc3	BRCA1/BRCA2-containing complex, subunit 3	0.3383	0.0001	0.0000	1.06	1.72	1.51
Zfp644	zinc finger and BTB domain containing 44	0.4026	0.0008	0.0000	1.47	1.51	1.51
Vtn	vitronectin	0.1261	0.0032	0.0010	1.15	1.34	1.51
Cnbp	cellular nucleic acid binding protein	0.1549	0.0000	0.0000	1.05	1.59	1.51
Fh1	fumarate hydratase 1	0.2528	0.0001	0.0000	1.07	1.45	1.51
Fdps	farnesyl diphosphate synthetase	0.1753	0.0003	0.0047	1.16	1.61	1.51
Usp34	ubiquitin specific peptidase 34	0.3609	0.0001	0.0000	-1.04	1.46	1.5
Rock2	Rho-associated coiled-coil containing protein kinase 2	0.0594	0.0001	0.0004	1.15	1.47	1.5
Gldc1	glycosyltransferase-like domain containing 1	0.4455	0.0003	0.0007	1.06	1.41	1.5
Kif	kit ligand	0.4909	0.0037	0.0009	1.06	1.38	1.5
Phf14	PHD finger protein 14	0.2453	0.0002	0.0003	-1.09	1.46	1.5
Pcd3	peroxiredoxin 3	0.2132	0.0001	0.0002	-1.1	1.54	1.5
D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	0.0408	0.0075	0.0001	1.16	1.51	1.5
4921524J17Rik	RIKEN cDNA 4921524J17 gene	0.4077	0.0000	0.0000	1.1	1.57	1.5
Piar1	protein prenyltransferase alpha subunit repeat containing 1	0.4061	0.0000	0.0000	1.09	1.68	1.5
Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	0.7138	0.0017	0.0033	1.05	1.49	1.5
Ncaa2	nuclear receptor coactivator 2	0.0108	0.0022	0.0002	-1.18	1.36	1.5
Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	0.3108	0.0000	0.0003	1.09	1.63	1.5
Rdm1	RAD52 motif 1	0.5022	0.0019	0.0000	1.07	1.4	1.5
Mna11	menage a trois 1	0.1924	0.0003	0.0002	1.08	1.38	1.5
Glt1	glutamine fructose-6-phosphate transaminase 1	0.4876	0.0000	0.0000	-1.04	1.43	1.5
Snmp48	small nuclear ribonucleoprotein 48 (U1/U12)	0.3417	0.0037	0.0000	-1.06	1.46	1.5
Nrcks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.5685	0.0001	0.0000	-1.02	1.53	1.5
Nol11	nucleolar protein 11	0.2914	0.0001	0.0000	1.04	1.65	1.5
Pign	phosphatidylinositol glycan anchor biosynthesis, class N	0.0830	0.0021	0.0000	1.15	1.31	1.5
Arhgap5	Rho GTPase activating protein 5	0.2444	0.0000	0.0005	-1.09	1.55	1.5
Rck2	RCK kinase 2 (yeast)	0.1779	0.0001	0.0014	-1.13	1.76	1.5
Klhl7	kelch-like 7 (Drosophila)	0.7415	0.0007	0.0006	1.04	1.41	1.5
Usp14	ubiquitin specific peptidase 14	0.3342	0.0000	0.0003	1.08	1.57	1.5
Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	0.0287	0.0009	0.0001	1.21	1.46	1.5
Znfp624	zinc metalloproteinase, STE24 homolog (S. cerevisiae)	0.4601	0.0001	0.0000	-1.05	1.48	1.5
Sf3b5	splicing factor 3b, subunit 5	0.3426	0.0015	0.0008	-1.1	1.57	1.5
Prc1	proline-rich coiled-coil 1	0.1754	0.0011	0.0014	-1.18	1.28	1.5
Thoc1	THO complex 1	0.0787	0.0000	0.0000	1.11	1.58	1.5
3830406C13Rik	RIKEN cDNA 3830406C13 gene	0.8018	0.0005	0.0089	1.03	1.65	1.5
Zfp68	zinc finger protein 68	0.4207	0.0007	0.0011	1.08	1.54	1.49
Rpl6	ribosomal protein L6	0.0198	0.0000	0.0000	1.15	1.6	1.49
Fubp3	far upstream element (FUSE) binding protein 3	0.3108	0.0068	0.0037	-1.18	1.65	1.49
5730494N06Rik	RIKEN cDNA 5730494N06 gene	0.3345	0.0000	0.0000	1.05	1.39	1.49
Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	0.6180	0.0072	0.0063	1.1	1.48	1.49
DnaJ1	DnaJ (Hsp40) homolog, subfamily A, member 1	0.4454	0.0042	0.0047	-1.09	1.62	1.49
Zfp639	zinc finger protein 639	0.2892	0.0015	0.0028	1.13	1.4	1.49
Cbx3	cortexin 3	0.0609	0.0001	0.0099	1.35	1.61	1.49
Hist3h2a	histone cluster 3, H2a	0.0146	0.0026	0.0001	1.14	1.36	1.49
2410002022Rik	RIKEN cDNA 2410002022 gene	0.5851	0.0007	0.0038	-1.07	1.54	1.49
Dhps	deoxyhypusine synthase	0.2876	0.0002	0.0005	-1.07	1.56	1.49
Rps19	ribosomal protein S19	0.8386	0.0008	0.0003	1.02	1.57	1.49
Mki67p	Mki67 (FHA domain) interacting nucleolar phosphoprotein	0.5624	0.0010	0.0004	1.05	1.49	1.48
Trim23	tripartite motif-containing 23	0.9553	0.0013	0.0013	-1.01	1.51	1.48
Zfp33	zinc finger and BTB domain containing 33	0.7461	0.0049	0.0003	-1.03	1.44	1.48
Psm2	proteasome (prosome, macropain) subunit, alpha type 2	0.4828	0.0000	0.0000	1.02	1.42	1.48
Rcap	BRCA2 and CDKN1A interacting protein	0.8996	0.0011	0.0013	1.04	1.41	1.48
Zfp655	zinc finger protein 655	0.4959	0.0038	0.0000	-1.04	1.42	1.48
Shfm1	split hand/foot malformation (ectrodactyly) type 1	0.1847	0.0005	0.0055	-1.23	1.67	1.48
Uba3	ubiquitin-like modifier activating enzyme 3	0.7664	0.0007	0.0025	1.03	1.6	1.48
Fam119x	family with sequence similarity 119, X-linked	0.1720	0.0083	0.0004	-1.19	1.37	1.48
Kctd7	kelch repeat and BTB (POZ) domain containing 7	0.7400	0.0001	0.0007	1.08	1.45	1.48
Ok	gusking	0.5488	0.0034	0.0007	1.08	1.34	1.48
Nl5c3	5'-nucleotidase, cytosolic III	0.3627	0.0002	0.0000	1.06	1.47	1.48
Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	0.0635	0.0002	0.0000	1.09	1.45	1.48
Nup35	nucleoporin 35	0.1329	0.0000	0.0006	1.24	1.69	1.48
Dendb1b	DEAD-box domain containing 1B	0.5803	0.0000	0.0004	1.04	1.34	1.48
Al597468	expressed sequence Al597468	0.0145	0.0000	0.0002	-1.16	1.68	1.48
Zfp51	zinc finger protein 51	0.2206	0.0001	0.0003	-1.11	1.48	1.48
Clyb1	citrate lyase beta like	0.6103	0.0032	0.0052	1.05	1.38	1.48
Fam179b	family with sequence similarity 179, member B	0.9198	0.0072	0.0007	1.01	1.29	1.47
Ythd5	YTH domain family 5	0.3893	0.0005	0.0001	-1.08	1.49	1.47
DnaJ12	DnaJ (Hsp40) homolog, subfamily C, member 12	0.7610	0.0001	0.0000	1.02	1.41	1.47
Srsf3	serine/arginine-rich splicing factor 3	0.0296	0.0005	0.0004	-1.16	1.54	1.47
Yip7	Yip1 domain family, member 7	0.9212	0.0001	0.0001	1.01	1.39	1.47
Ttc1	telantactopeptide repeat domain 1	0.4733	0.0002	0.0005	1.05	1.53	1.47
5730617P06Rik	RIKEN cDNA 5730617P06 gene	0.8183	0.0000	0.0002	1.14	1.55	1.47
Uso1	USO1 homolog, vesicle docking protein (yeast)	0.1996	0.0002	0.0000	1.06	1.28	1.47
Cpsf6	cleavage and polyadenylation specific factor 6	0.3896	0.0001	0.0000	-1.03	1.49	1.47
Bpgm	2,3-bisphosphoglycerate mutase	0.2037	0.0028	0.0021	1.16	1.45	1.47
Abca8	ATP-binding cassette, sub-family A (ABC1), member 8	0.8288	0.0001	0.0001	-1.02	1.46	1.47
Mrps18c	mitochondrial ribosomal protein S18c	0.0975	0.0001	0.0000	-1.08	1.62	1.47
Kctd3	potassium channel tetramerisation domain containing 3	0.1905	0.0000	0.0058	-1.13	1.69	1.47
Rnf144b	ring finger protein 144b	0.7198	0.0004	0.0076	-1.03	1.48	1.47
Gm11517	ubiquitin A-52 residue ribosomal protein fusion product 1 pseudogene	0.7200	0.0050	0.0005	1.03	1.47	1.47
1300003B13Rik	RIKEN cDNA 1300003B13 gene	0.9105	0.0005	0.0009	1.01	1.46	1.47
Al06	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-glucosyltransferase)	0.1891	0.0001	0.0011	1.14	1.75	1.47

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Endrb	endothelin receptor type B	0.3957	0.0001	0.0007	1.12	1.65	1.47
Lym5	LYR motif containing 5	0.8899	0.0005	0.0000	-1.01	1.35	1.47
Gm16039	predicted gene 16039	0.2937	0.0002	0.0006	-1.13	1.6	1.47
Fbxl5	F-box and leucine-rich repeat protein 5	0.5658	0.0063	0.0003	-1.04	1.34	1.47
Higd1b	HIG1 domain family, member 1B	0.2254	0.0002	0.0044	1.16	1.76	1.47
Svip	small VCP/p97-interacting protein	0.1692	0.0000	0.0001	-1.09	1.53	1.47
1810074P20Rik	RIKEN cDNA 1810074P20 gene	0.1776	0.0062	0.0032	1.15	1.4	1.47
Rangrf	RAN guanine nucleotide release factor	0.0651	0.0000	0.0002	1.12	1.47	1.47
Fcl1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0.0348	0.0003	0.0001	1.18	1.35	1.47
Ppp23c	protein phosphatase 2, regulatory subunit B', gamma	0.6020	0.0000	0.0001	1.02	1.5	1.47
Ppat	phosphoribosyl pyrophosphate amidotransferase	0.6335	0.0015	0.0072	1.07	1.94	1.47
Stoml2	stomatol (Epo7/2)-like 2	0.6911	0.0004	0.0002	1.03	1.45	1.46
Ttc33	tetratricopeptide repeat domain 33	0.8706	0.0001	0.0001	1.01	1.47	1.46
Fam120a	family with sequence similarity 120, member A	0.9345	0.0000	0.0000	-1	1.46	1.46
Mrp150	mitochondrial ribosomal protein L50	0.7051	0.0006	0.0029	-1.05	1.6	1.46
Zfyve16	zinc finger, FYVE domain containing 16	0.8763	0.0088	0.0013	-1.02	1.4	1.46
Ppf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	0.8975	0.0029	0.0010	1.01	1.65	1.46
Igfc04	immunoglobulin superfamily, DCC subclass, member 4	0.2843	0.0004	0.0016	1.02	1.62	1.46
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.7004	0.0013	0.0004	-1.04	1.5	1.46
Morf41	mortality factor 4 like 1	0.5619	0.0001	0.0002	-1.04	1.51	1.46
Xpo1	exportin 1, CRM1 homolog (yeast)	0.3272	0.0007	0.0004	1.08	1.38	1.46
Nlr2	nrlase family, member 2	0.3100	0.0001	0.0003	1.09	1.54	1.45
Sclcp	synexin binding protein	0.3854	0.0002	0.0041	-1.08	1.51	1.45
Atpev1c1	ATPase, H ⁺ transporting, lysosomal V1 subunit C1	0.1332	0.0004	0.0002	1.1	1.43	1.45
Fam136a	family with sequence similarity 136, member A	0.7480	0.0000	0.0000	-1.02	1.61	1.45
Neun3	NOL1/NOP2/Sun domain family member 3	0.5232	0.0001	0.0007	-1.04	1.38	1.45
Asb5	ankyrin repeat and SOCS box-containing 5	0.2474	0.0000	0.0002	1.07	1.61	1.45
Vrlb	vesicle transport through interaction with t-SNAREs 16 homolog	0.4833	0.0000	0.0000	-1.05	1.45	1.45
Polr2	polymerase (RNA) II (DNA directed) polypeptide J	0.1497	0.0001	0.0010	1.11	1.55	1.45
Trp53bp1	transformation related protein 53 binding protein 1	0.0202	0.0000	0.0060	-1.21	1.54	1.45
Impa1	inositol (myo)-1(or 4)-monophosphatase 1	0.2309	0.0002	0.0000	1.08	1.52	1.45
Ube2d2	ubiquitin-conjugating enzyme E2D (putative) 2	0.0336	0.0005	0.0012	-1.32	1.29	1.45
Usp1	ubiquitin-specific peptidase 1	0.0582	0.0006	0.0000	-1.1	1.35	1.45
Senp8	SUMO/sentrin specific peptidase 8	0.5017	0.0004	0.0014	1.07	1.56	1.45
Tob1	transducer of ErbB-2.1	0.5540	0.0000	0.0004	1.05	1.68	1.45
Zfp386	zinc finger protein 386 (Kruppel-like)	0.0120	0.0003	0.0002	-1.19	1.52	1.45
Gtaz1	general transcription factor II A, 1	0.6743	0.0048	0.0065	1.05	1.53	1.45
U11W509b	DNA segment C.11, Wayne State University 99, expressed	0.8617	0.0011	0.0025	1.61	1.45	1.45
Sec24a	Sec24 related gene family, member A (S. cerevisiae)	0.2791	0.0000	0.0056	-1.1	1.59	1.45
Tmed2	transmembrane emp24 domain trafficking protein 2	0.1858	0.0000	0.0000	-1.12	1.44	1.45
2310007O11Rik	RIKEN cDNA 2310007O11 gene	0.9035	0.0014	0.0034	1.01	1.52	1.45
Rars2	arginyl-tRNA synthetase 2, mitochondrial	0.4759	0.0000	0.0000	-1.04	1.41	1.45
Apo3d	apolipoprotein D	0.3385	0.0000	0.0001	1.08	1.75	1.44
Tmem41b	transmembrane protein 41B	0.3794	0.0006	0.0007	-1.06	1.43	1.44
Clint1	clathrin interactor 1	0.2273	0.0000	0.0000	-1.06	1.41	1.44
Tbc1d8b	TBC1 domain family, member 8B	0.9725	0.0007	0.0003	1	1.35	1.44
Foxo3	forkhead box O3	0.5048	0.0082	0.0051	-1.08	1.61	1.44
U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	0.1487	0.0001	0.0007	-1.13	1.5	1.44
Trappc1	trafficking protein particle complex 1	0.9653	0.0025	0.0012	1	1.36	1.44
Cdad1	cytidine and dCMP deaminase domain containing 1	0.6237	0.0015	0.0002	-1.04	1.39	1.44
Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.8281	0.0011	0.0002	1.01	1.44	1.44
Mbt1	muscleblind-like 1 (Drosophila)	0.0151	0.0002	0.0000	1.17	1.43	1.44
Rpl1	Rpl1 Part RNA polymerase II complex component, homolog (S. cerevisiae)	0.3438	0.0001	0.0001	1.06	1.4	1.44
Mrp31	mitochondrial ribosomal protein S31	0.0565	0.0002	0.0001	1.13	1.39	1.44
Rpa1	replication protein A1	0.5762	0.0001	0.0001	-1.04	1.47	1.44
A430005L14Rik	RIKEN cDNA A430005L14 gene	0.5926	0.0016	0.0001	1.04	1.28	1.44
Ahl1	AFAP/RMZ family, member 1	0.3685	0.0053	0.0014	-1.11	1.39	1.44
Ras1b	RAS related protein 1b	0.8796	0.0001	0.0001	1.5	1.44	1.44
Eif4e	eukaryotic translation initiation factor 4E	0.5556	0.0000	0.0001	1.04	1.6	1.44
Mycbp	c-myc binding protein	0.7980	0.0063	0.0003	1.03	1.39	1.44
Sumo1	SMT3 suppressor of mit two 3 homolog 1 (yeast)	0.3075	0.0002	0.0001	1.06	1.43	1.44
4833403P05Rik	RIKEN cDNA 4833403P05 gene	0.5862	0.0053	0.0023	-1.06	1.38	1.44
Polyr2k	polymerase (RNA) II (DNA directed) polypeptide K	0.8410	0.0000	0.0016	1.02	1.44	1.44
Dld	dihydrodipicolinate dehydrogenase	0.3572	0.0001	0.0004	1.05	1.45	1.43
Bmpr2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	0.5629	0.0000	0.0000	1.03	1.43	1.43
Rio1	RIO kinase 1 (yeast)	0.3683	0.0081	0.0021	1.11	1.56	1.43
Zfp758	zinc finger protein 758	0.9226	0.0077	0.0049	-1.02	1.45	1.43
Lap3	leucine aminopeptidase 3	0.3703	0.0000	0.0000	-1.05	1.49	1.43
2010107E04Rik	RIKEN cDNA 2010107E04 gene	0.0487	0.0012	0.0010	1.21	1.43	1.43
Sic9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0.2997	0.0004	0.0000	1.04	1.44	1.43
Capza2	capping protein (actin filament) muscle Z-line, alpha 2	0.2032	0.0000	0.0001	-1.08	1.41	1.43
Gloa4	glyoxalase domain containing 4	0.0388	0.0000	0.0005	-1.1	1.4	1.43
Fam12b	family with sequence similarity 12, member B	0.8496	0.0002	0.0000	1.34	1.43	1.43
Mthfd2l	methyltetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0.3485	0.0001	0.0005	-1.11	1.72	1.43
Pdzd8	PDZ domain containing 8	0.9139	0.0032	0.0025	1.01	1.44	1.43
Uba2	ubiquitin-like modifier activating enzyme 2	0.4835	0.0001	0.0003	-1.05	1.57	1.43
Snap23	synaptosomal-associated protein 23	0.0785	0.0004	0.0015	1.15	1.67	1.43
Lrp	limb and neural pates	0.4137	0.0011	0.0007	1.07	1.58	1.43
Gm10786	predicted gene 10786	0.9370	0.0018	0.0010	-1.01	1.43	1.42
Btaf1	BTAf1 RNA polymerase II, B-TFIIID transcription factor-associated, (Mot1) homolog, S. cer	0.1591	0.0011	0.0003	1.1	1.38	1.42
Icdh3a	isocitrate dehydrogenase 3 (NAD+) alpha	0.0565	0.0000	0.0001	1.09	1.48	1.42
H2-K62	H2-K62 region expressed gene 2	0.3238	0.0001	0.0005	1.08	1.49	1.42
Denn	densin-regulated protein	0.1923	0.0016	0.0002	-1.06	1.42	1.42
Rnf149	ring finger protein 149	0.0586	0.0001	0.0009	-1.09	1.5	1.42
Nars	asparaginyl-tRNA synthetase	0.8636	0.0001	0.0000	-1.01	1.35	1.42
0610007C21Rik	RIKEN cDNA 0610007C21 gene	0.6667	0.0000	0.0017	1.02	1.52	1.42
Tubd1	tubulin, delta 1	0.9161	0.0006	0.0019	1.01	1.4	1.42
Nlr1	major histocompatibility complex, class I-related	0.8096	0.0005	0.0019	1.07	1.49	1.42
Kdm5a	[lysine (K)-specific demethylase 5A	0.2140	0.0028	0.0027	-1.1	1.44	1.42
Snu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	0.5091	0.0037	0.0000	1.03	1.38	1.42
Prex2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	0.0126	0.0002	0.0050	-1.25	1.54	1.42
Uim1d1	Uim1d1 C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	0.0214	0.0010	0.0002	-1.15	1.3	1.42
D830001B02	hypothetical protein D830001B02	0.1837	0.0012	0.0007	1.16	1.66	1.42
Spc3	spinal peptidase complex subunit 3 homolog (S. cerevisiae)	0.8409	0.0002	0.0000	-1.02	1.56	1.42
Map3k2	mitogen-activated protein kinase kinase kinase 2	0.5061	0.0020	0.0024	-1.09	1.58	1.42
Slag2	stromal antigen 2	0.6238	0.0001	0.0001	1.03	1.47	1.42
Seik	selenoprotein K	0.0786	0.0003	0.0003	1.15	1.42	1.42
Paskd2	PASKY kinase domains 2	0.1340	0.0002	0.0089	-1.15	1.64	1.42
Mrp14	mitochondrial ribosomal protein L14	0.4987	0.0002	0.0001	1.07	1.27	1.42
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	0.2278	0.0000	0.0000	1.04	1.5	1.42
Azn1	antizyme inhibitor 1	0.8276	0.0038	0.0067	1.02	1.39	1.42
Hif1a	hypoxia inducible factor 1, alpha subunit	0.0960	0.0000	0.0006	-1.17	1.57	1.42
Sic2a1	solute carrier family 2 (facilitated glucose transporter), member 1	0.0596	0.0048	0.0038	-1.3	1.53	1.42
Paip1	polyadenylate binding protein-interacting protein 1	0.3978	0.0000	0.0005	1.11	1.71	1.42
Rpf2	ribosome production factor 2 homolog (S. cerevisiae)	0.9741	0.0005	0.0001	1	1.42	1.42
Smchd1	SMC hinge domain containing 1	0.4159	0.0004	0.0056	-1.09	1.58	1.42
Hectd1	HECT domain containing 1	0.8980	0.0063	0.0005	1.01	1.22	1.41
Umy1c	Uim1d1 domain containing 1C	0.9753	0.0021	0.0011	1.37	1.41	1.41
Zfp422-rs1	zinc finger protein 422, related sequence 1	0.6448	0.0099	0.0076	1.05	1.37	1.41
Ino80d	INO80 complex subunit D	0.3839	0.0003	0.0001	1.06	1.43	1.41
Psenen	presenilin enhancer 2 homolog (C. elegans)	0.1998	0.0000	0.0003	1.1	1.49	1.41
Spy2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	0.8864	0.0039	0.0091	-1.02	1.48	1.41
Phylae1	patatin-like phospholipase domain containing 8	0.0336	0.0008	0.0000	1.17	1.52	1.41
Casp12	caspase 12	0.1223	0.0006	0.0000	-1.13	1.48	1.41
1110034B05Rik	RIKEN cDNA 1110034B05 gene	0.9202	0.0003	0.0043	-1.01	1.5	1.41
Smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	0.2590	0.0017	0.0001	-1.19	1.23	1.41
Dnm1	dynamitin 1-like	0.6395	0.0000	0.0000	-1.02	1.36	1.41
Mpx2	multiple PEX domain protein	0.3997	0.0036	0.0007	-1.07	1.27	1.41
Acyp1	acylphosphatase 1, erythrocyte (common) type	0.3783	0.0002	0.0048	1.1	1.52	1.41
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	0.2892	0.0002	0.0001	-1.16	1.45	1.41
Aimp2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	0.6108	0.0009	0.0003	1.05	1.55	1.41
Glo1	glyoxalase 1	0.9789	0.0005	0.0021	1	1.47	1.41
Fam103a1	family with sequence similarity 103, member A1	0.1889	0.0000	0.0001	1.05	1.59	1.41
Ankrd10	ankyrin repeat domain 10	0.4375	0.0032	0.0071	1.08	1.5	1.41
Uqcrl0	ubiquinol-cytochrome c reductase, complex III subunit X	0.5984	0.0002	0.0002	1.03	1.42	1.41
Art3	ADP-ribosyltransferase 3	0.4813	0.0000	0.0003	1.07	1.6	1.41
Cdc123	cell division cycle 123 homolog (S. cerevisiae)	0.1045	0.0000	0.0001	1.12	1.4	1.41
Cas1	CAS1 domain containing 1	0.1428	0.0001	0.0001	-1.09	1.41	1.41
BC088983	cDNA sequence BC088983	0.4271	0.0096	0.0023	1.1	1.31	1.41
Pfnd4	prefoldin 4	0.3101	0.0011	0.0049	-1.08	1.37	1.41
Rbm18	RNA binding motif protein 18	0.5239	0.0000	0.0002	1.03	1.43	1.41
8430410K20Rik	RIKEN cDNA 8430410K20 gene	0.5411	0.0001	0.0000	-1.04	1.39	1.41
Hs6b3	heat shock protein 3	0.4489	0.0076	0.0011	1.06	1.27	1.41

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Spcc52	signal peptidase complex subunit 2 homolog (S. cerevisiae)	0.9529	0.0001	0.0004	1	1.44	1.4
Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	0.0523	0.0001	0.0000	1.1	1.32	1.4
Hscap11	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	0.8396	0.0001	0.0000	1.03	1.42	1.4
Atps5	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit 5	0.1426	0.0001	0.0006	1.09	1.5	1.4
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	0.5173	0.0018	0.0028	1.07	1.49	1.4
Cript	cysteine-rich PDZ-binding protein	0.1502	0.0000	0.0001	1.08	1.47	1.4
Ucl1	ubiquitin-fold modifier conjugating enzyme 1	0.6524	0.0000	0.0000	-1.03	1.4	1.4
Pdpk1	3-phosphoinositide dependent protein kinase 1	0.0661	0.0011	0.0047	-1.27	1.4	1.4
Chmp5	chromatin modifying protein 5	0.7097	0.0014	0.0086	-1.04	1.55	1.4
PsmA7	proteasome (prosome, macropain) subunit, alpha type 7	0.0711	0.0000	0.0000	-1.1	1.45	1.4
Yip6	Yip1 domain family, member 6	0.3346	0.0001	0.0001	1.06	1.33	1.4
Trps1	trichorhinophthalangeal syndrome 1 (human)	0.0522	0.0086	0.0014	-1.23	1.56	1.4
Znf11	zinc finger, H1T domain containing 1	0.7846	0.0011	0.0022	-1.02	1.45	1.4
Rnf13	ring finger protein 13	0.3403	0.0000	0.0000	1.03	1.49	1.4
Abce1	ATP-binding cassette, sub-family E (OABP), member 1	0.3080	0.0020	0.0016	1.11	1.38	1.4
Srfbp1	serum response factor binding protein 1	0.0771	0.0010	0.0053	1.18	1.39	1.4
Rab5a	RAB5A, member RAS oncogene family	0.5575	0.0000	0.0000	1.03	1.47	1.4
Krt11	ADP-ribosylation factor-like 1	0.0536	0.0002	0.0003	1.18	1.39	1.4
Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0.7731	0.0026	0.0048	-1.03	1.45	1.4
Dhrs7c	dehydrogenase/reductase (SDR family) member 7C	0.5098	0.0003	0.0009	1.06	1.44	1.4
Myf6	myogenic factor 6	0.1616	0.0001	0.0000	1.12	1.66	1.4
Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	0.1438	0.0015	0.0004	1.12	1.44	1.4
Cherp	calcium homeostasis endoplasmic reticulum protein	0.3787	0.0003	0.0019	-1.03	1.89	1.4
Psm6	proteasome (prosome, macropain) subunit, beta type 6	0.6692	0.0012	0.0005	-1.01	1.34	1.4
Nt5dc1	5'-nucleotidase domain containing 1	0.0595	0.0047	0.0016	-1.21	1.29	1.4
Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	0.1589	0.0003	0.0001	-1.09	1.46	1.4
Nik6la	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.8908	0.0005	0.0040	-1.02	1.66	1.39
Ptbp2	polycomb target binding protein 2	0.0273	0.0017	0.0041	1.49	1.39	1.4
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide)	0.8672	0.0016	0.0000	-1.01	1.37	1.39
1500011K16RIK	RIKEN cDNA 1500011K16 gene	0.8538	0.0022	0.0009	1.01	1.35	1.39
Tmx4	thioredoxin-related transmembrane protein 4	0.0252	0.0003	0.0000	-1.11	1.26	1.39
Vamp8	vesicle-associated membrane protein 8	0.7388	0.0018	0.0016	-1.04	1.26	1.39
PsmA1	proteasome (prosome, macropain) subunit, alpha type 1	0.8435	0.0000	0.0000	1.02	1.39	1.39
Pcna	proliferating cell nuclear antigen	0.8577	0.0000	0.0000	1.01	1.37	1.39
Sema3c	sema domain, immunoglobulin domain (Iq), short basic domain, secreted, (semaphorin) 3	0.2037	0.0000	0.0001	1.06	1.36	1.39
Eif3	eukaryotic translation initiation factor 3, subunit L	0.9392	0.0000	0.0000	1	1.42	1.39
Pcmtd2	protein-L-isopartate (D-aspartate) O-methyltransferase domain containing 2	0.8699	0.0005	0.0003	1.01	1.47	1.39
Bcap31	B cell-associated protein 31	0.1895	0.0003	0.0015	-1.11	1.42	1.39
Acs4	acyl-CoA synthetase long-chain family member 4	0.7677	0.0000	0.0012	-1.04	1.46	1.39
1110012L19RIK	RIKEN cDNA 1110012L19 gene	0.3007	0.0001	0.0001	1.06	1.52	1.39
Zbtb41	zinc finger and BTB domain containing 41 homolog	0.3496	0.0000	0.0003	-1.04	1.41	1.39
6330403M23RIK	RIKEN cDNA 6330403M23 gene	0.1280	0.0006	0.0002	1.1	1.38	1.39
Upr2	UPF2 regulator of nonsense transcripts homolog (yeast)	0.1917	0.0016	0.0015	-1.13	1.32	1.39
Rpl12	ribosomal protein L12	0.3369	0.0003	0.0002	1.07	1.46	1.39
Rhoq	ras homolog gene family, member Q	0.0642	0.0002	0.0001	-1.13	1.41	1.39
Hars	histidyl-IRNA synthetase	0.9285	0.0002	0.0037	-1.01	1.5	1.39
281008M24RIK	RIKEN cDNA 281008M24 gene	0.6444	0.0001	0.0000	-1.02	1.44	1.39
1110050L19RIK	RIKEN cDNA 1110050L19 gene	0.0081	0.0001	0.0003	-1.06	1.39	1.39
Eapp	E2F-associated phosphoprotein	0.1200	0.0003	0.0031	1.08	1.47	1.39
Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.2019	0.0004	0.0041	-1.18	1.67	1.39
Wdr75	WD repeat domain 75	0.7815	0.0032	0.0056	1.02	1.33	1.39
Csde1	cold shock domain containing E1, RNA binding	0.0554	0.0005	0.0007	-1.27	1.36	1.38
Gmfb	glia maturation factor, beta	0.3389	0.0017	0.0005	1.46	1.36	1.38
Larp4	La ribonucleoprotein domain family, member 4	0.9889	0.0023	0.0004	-1	1.22	1.38
Calr3	calreticulin 3	0.3284	0.0016	0.0007	-1.08	1.43	1.38
Gl(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	0.0925	0.0030	0.0084	1.22	1.51	1.38
Cbr4	carbonyl reductase	0.7510	0.0000	0.0000	-1.02	1.45	1.38
Nbsm2	N-5 adenine-specific DNA methyltransferase 2 (putative)	0.3413	0.0002	0.0000	1.06	1.42	1.38
Atp7a	ATPase, Cu++ transporting, alpha polypeptide	0.9679	0.0043	0.0020	-1	1.42	1.38
Rnf160	ring finger protein 160	0.6106	0.0003	0.0000	1.03	1.34	1.38
Matr3	matrin 3	0.9766	0.0003	0.0003	-1	1.35	1.38
Zfp889	zinc finger protein 889	0.7368	0.0003	0.0011	-1.04	1.32	1.38
Trfnd	Trfnd, Ccr 7, Rcnk18 c	0.8489	0.0006	0.0008	1.03	1.49	1.38
Scd1	Sec1 family domain containing 1	0.7877	0.0032	0.0041	1.02	1.37	1.38
4930420K17RIK	RIKEN cDNA 4930420K17 gene	0.0973	0.0098	0.0043	-1.28	1.48	1.38
Slam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0.2769	0.0032	0.0061	1.09	1.48	1.38
Ankle2	ankyrin repeat and LEM domain containing 2	0.4577	0.0012	0.0025	-1.06	1.33	1.38
Eif2a	eukaryotic translation initiation factor 2a	0.0005	0.0000	0.0000	1.04	1.51	1.38
Tipr1	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	0.5974	0.0094	0.0021	1.05	1.37	1.38
Eya1	eyes absent 1 homolog (Drosophila)	0.2205	0.0000	0.0013	-1.11	1.63	1.38
Itim2a	integral membrane protein 2A	0.4505	0.0004	0.0013	-1.03	1.61	1.38
2810422J05RIK	RIKEN cDNA 2810422J05 gene	0.8856	0.0022	0.0002	-1.01	1.32	1.38
Satz	serpinase	0.8141	0.0016	0.0000	-1.02	1.36	1.38
Adal	adenosine deaminase-like	0.1146	0.0093	0.0046	1.17	1.35	1.38
Sabp1	single-stranded DNA binding protein 1	0.3160	0.0041	0.0056	-1.1	1.45	1.38
Ufp2	UFM1-specific peptidase 2	0.0378	0.0015	0.0002	1.24	1.33	1.38
Narf	nuclear prelamin A recognition factor	0.0536	0.0041	0.0016	-1.21	1.23	1.38
1810026B05RIK	RIKEN cDNA 1810026B05 gene	0.8908	0.0006	0.0002	-1.03	1.5	1.37
Rsc2	arginine/serine-rich coiled-coil 2	0.3789	0.0041	0.0001	1.04	1.27	1.37
Crot	carbamate O-octanoyltransferase	0.2745	0.0002	0.0020	1.1	1.6	1.37
Mthfd1	methyltetrahydrofolate dehydrogenase (NADP+ dependent), methyltetrahydrofolate	0.1477	0.0004	0.0020	-1.1	1.32	1.37
Scir	secretin receptor	0.7743	0.0056	0.0071	-1.05	1.42	1.37
Snx14	sorting nexin 14	0.8386	0.0005	0.0031	-1.01	1.5	1.37
Vdac3	voltage-dependent anion channel 3	0.1622	0.0001	0.0000	1.06	1.39	1.37
Pcnp	PEST proteolytic signal containing nuclear protein	0.4386	0.0009	0.0018	-1.07	1.42	1.37
Pias1	protein inhibitor of activated STAT 1	0.5276	0.0053	0.0018	1.05	1.39	1.37
1700021F05RIK	RIKEN cDNA 1700021F05 gene	0.1005	0.0005	0.0003	-1.11	1.46	1.37
Fbxo22	F-box protein 22	0.1961	0.0029	0.0049	-1.16	1.5	1.37
Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	0.3667	0.0000	0.0000	-1.03	1.41	1.37
Zfyve9	zinc finger, FYVE domain containing 9	0.2764	0.0079	0.0000	1.06	1.21	1.37
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	0.0776	0.0001	0.0002	1.14	1.41	1.37
Zfp207	zinc finger protein 207	0.0547	0.0001	0.0061	1.24	1.56	1.37
Samd8	sterile alpha motif domain containing 8	0.8867	0.0000	0.0000	1.03	1.47	1.37
Apool	apolipoprotein O-like	0.0625	0.0000	0.0001	1.09	1.4	1.37
Npm1	nucleophosmin 1	0.3231	0.0003	0.0020	1.07	1.51	1.37
Med21	mediator complex subunit 21	0.3719	0.0001	0.0039	-1.1	1.54	1.37
Pp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0.6352	0.0007	0.0001	1.02	1.27	1.37
Rn3	RN3 RNA polymerase I transcription factor homolog (yeast)	0.2806	0.0005	0.0011	1.08	1.34	1.36
Lars	leucyl-tRNA synthetase	0.1758	0.0000	0.0007	-1.09	1.55	1.36
Gabarap2	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2	0.9902	0.0000	0.0004	1	1.43	1.36
Atfrip1	ADP-ribosylation factor related protein 1	0.6802	0.0015	0.0011	-1.03	1.34	1.36
Mios	missing occyte, meiosis regulator, homolog (Drosophila)	0.0927	0.0056	0.0032	1.19	1.33	1.36
BC003966	cDNA sequence BC003966	0.8297	0.0002	0.0002	-1.04	1.44	1.36
Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	0.7853	0.0006	0.0086	1.03	1.49	1.36
Gm5081	predicted gene 5081	0.5624	0.0000	0.0004	-1.03	1.38	1.36
Calm2	calmodulin 2	0.6555	0.0010	0.0009	-1.04	1.45	1.36
Tmem208	transmembrane protein 208	0.6546	0.0009	0.0002	1.04	1.35	1.36
1110020G09RIK	RIKEN cDNA 1110020G09 gene	0.8534	0.0048	0.0008	1.03	1.28	1.36
Oycs	cytochrome c, somatic	0.6603	0.0000	0.0000	1.03	1.47	1.36
Bnip2	BCL2/adenovirus E1B interacting protein 2	0.4515	0.0003	0.0012	-1.05	1.37	1.36
Fam98b	family with sequence similarity 98, member B	0.5294	0.0007	0.0010	-1.03	1.37	1.36
Fam165b	family with sequence similarity 165, member B	0.6183	0.0008	0.0076	1.05	1.42	1.36
Psm5	proteasome (prosome, macropain) subunit, non-ATPase 5	0.0521	0.0004	0.0007	1.06	1.41	1.36
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	0.1319	0.0065	0.0011	-1.13	1.29	1.36
Eps15	epidermal growth factor receptor pathway substrate 15	0.8884	0.0002	0.0000	1.01	1.32	1.36
Hdgt	hepatoma-derived growth factor	0.0501	0.0018	0.0032	-1.21	1.28	1.36
Rab18	RAB18, member RAS oncogene family	0.0991	0.0000	0.0002	1.1	1.36	1.36
Nm14a	NM14A (SC26.5, S. cerevisiae)	0.4013	0.0001	0.0001	1.07	1.45	1.36
Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	0.9246	0.0012	0.0002	1.01	1.5	1.36
Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	0.7178	0.0004	0.0002	1.02	1.46	1.36
Mbtps2	membrane-bound transcription factor peptidase, site 2	0.4228	0.0049	0.0003	1.03	1.19	1.35
Phf5a	PHD finger protein 5A	0.7162	0.0009	0.0001	1.02	1.44	1.35
Ns2	NS2 ribosome biogenesis homolog (S. cerevisiae)	0.4016	0.0000	0.0012	1.06	1.46	1.35
Asb14	ankyrin repeat and SOCS box-containing 14	0.5337	0.0000	0.0001	1.04	1.47	1.35
Hipk3	homeodomain interacting protein kinase 3	0.0647	0.0001	0.0001	1.08	1.28	1.35
Srsf7	serine/arginine-rich splicing factor 7	0.5639	0.0016	0.0024	-1.06	1.43	1.35
Asb12	ankyrin repeat and SOCS box-containing 12	0.4282	0.0002	0.0027	1.07	1.47	1.35
Kdelr2	KDEL (yeast Asp-Asp) endoplasmic reticulum protein retention receptor 2	0.0865	0.0004	0.0009	1.08	1.44	1.35
Ppp25c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.0408	0.0051	0.0017	-1.19	1.24	1.35
Chac2	ChaC, cation transport regulator homolog 2 (E. coli)	0.3464	0.0003	0.0083	-1.08	1.41	1.35
Luc7l3	LUC7-like 3 (S. cerevisiae)	0.5957	0.0017	0.0001	1.02	1.34	1.35
Atg3	autophagy-related 3 (yeast)	0.0331	0.0003	0.0001	-1.13	1.31	1.35
Naa30	N(alpha)-acetyltransferase 30, NatC catalytic subunit	0.3997	0.0000	0.0001	-1.05	1.41	1.35

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Rrbt1	ras responsive element binding protein 1	0.3601	0.0021	0.0025	-1.09	1.44	1.35
1110067022Rik	RIKEN cDNA 1110067022 gene	0.9788	0.0024	0.0005	-1	1.37	1.35
Rpl7l1	ribosomal protein L7, class 1	0.7692	0.0050	0.0003	-1.03	1.33	1.35
Apoo	apolipoprotein O	0.0435	0.0001	0.0001	1.15	1.35	1.35
Sdhaf2	succinate dehydrogenase complex assembly factor 2	0.1355	0.0017	0.0008	1.13	1.52	1.35
Papola	poly (A) polymerase alpha	0.8726	0.0007	0.0098	1.01	1.45	1.35
Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	0.3782	0.0037	0.0003	1.04	1.22	1.35
Atf2	activator 1 transcription factor 2	0.4853	0.0006	0.0001	1.04	1.36	1.35
Ccq3	coenzyme Q3 homolog, methyltransferase (yeast)	0.6482	0.0000	0.0003	1.04	1.51	1.35
Dram2	VDNA-damage regulated autophagy modulator 2	0.2320	0.0000	0.0001	1.07	1.47	1.35
Trks	tyrosine kinase, TRF1-interacting ankyrin-related ADP-ribose polymerase	0.6043	0.0087	0.0025	1.06	1.24	1.35
Ubr1	ubiquitin protein ligase E3 component n-recognin 1	0.9150	0.0004	0.0000	-1.01	1.29	1.35
Adam10	alpha disintegrin and metalloproteinase domain 10	0.1422	0.0000	0.0003	-1.1	1.44	1.35
Sirt1	sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	0.9186	0.0023	0.0055	1.01	1.39	1.35
Gimn	glomulin, FKBP associated protein	0.9502	0.0009	0.0081	-1.02	1.57	1.35
Osgp1	O-sialoglycoprotein endopeptidase-like 1	0.2827	0.0017	0.0015	1.09	1.35	1.34
Fam86a	family with sequence similarity 96, member A	0.9129	0.0005	0.0025	-1.01	1.42	1.34
Sfr1	suppression of tumorigenicity 7-like	0.1876	0.0002	0.0000	1.13	1.39	1.34
Cdc27	cell division cycle 27 homolog (S. cerevisiae)	0.8747	0.0046	0.0020	1.01	1.3	1.34
Psm4d	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	0.1520	0.0000	0.0007	1.09	1.37	1.34
Hspb2	heat shock protein 2	0.1473	0.0010	0.0016	1.07	1.45	1.34
Wdr26	WD repeat domain 26	0.2843	0.0027	0.0028	1.1	1.23	1.34
BC020557	cDNA sequence BC020557	0.8207	0.0022	0.0007	1.03	1.31	1.34
Hax1	HCLS1 associated X-1	0.7406	0.0042	0.0008	1.02	1.35	1.34
Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	0.8682	0.0013	0.0010	-1.01	1.3	1.34
Psmg3	proteasome (prosome, macropain) assembly chaperone 3	0.0342	0.0044	0.0067	1.21	1.2	1.34
Psm6b	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	0.3654	0.0000	0.0004	1.04	1.51	1.34
Scap2b	S cell receptor associated protein 2b	0.2995	0.0005	0.0001	1.06	1.26	1.34
Haus3	HAUS augmin-like complex, subunit 3	0.5647	0.0014	0.0005	1.06	1.25	1.34
Funcd1	FUN14 domain containing 1	0.6353	0.0020	0.0005	-1.03	1.3	1.34
Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.3989	0.0001	0.0025	-1.04	1.47	1.34
Brb8	bromodomain containing 8	0.0115	0.0007	0.0002	1.26	1.45	1.34
Tmed5	transmembrane emp24 protein transport domain containing 5	0.7395	0.0003	0.0011	-1.02	1.35	1.34
Dcaf13	DOB1 and CUL4 associated factor 13	0.8291	0.0005	0.0000	-1.01	1.32	1.34
Hsbp1	heat shock factor binding protein 1	0.7674	0.0000	0.0001	-1.02	1.39	1.34
Ca2nd2f1	calcium channel, voltage-dependent, alpha2/delta subunit 1	0.5205	0.0018	0.0026	1.03	1.31	1.34
Txncd12	thioredoxin domain containing 12 (endoplasmic reticulum)	0.4753	0.0001	0.0001	1.04	1.34	1.34
2610030H08Rik	RIKEN cDNA 2610030H08 gene	0.8207	0.0022	0.0007	1.03	1.25	1.34
Phb	prohibitin	0.2406	0.0000	0.0001	1.08	1.39	1.34
Tmem9b	TMEM9 domain family, member B	0.0592	0.0097	0.0002	1.15	1.28	1.34
Tbce	tubulin-specific chaperone E	0.2098	0.0001	0.0002	1.06	1.4	1.34
Skil	SKI-like	0.3221	0.0056	0.0044	-1.1	1.31	1.34
Gpn3	GPN-loop GTPase 3	0.4976	0.0003	0.0100	1.04	1.36	1.34
Skv2l2	superkiller viral-like activity 2-like 2 (S. cerevisiae)	0.4038	0.0000	0.0001	1.07	1.4	1.34
Pja2	praja 2, RING-H2 motif containing	0.0156	0.0000	0.0002	-1.17	1.3	1.34
3110073H01Rik	RIKEN cDNA 3110073H01 gene	0.2373	0.0047	0.0001	-1.05	1.16	1.34
Case11	chromosome segregation 1-like (S. cerevisiae)	0.5258	0.0022	0.0036	-1.06	1.33	1.33
Nudt2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	0.8301	0.0000	0.0000	1.02	1.34	1.33
Epc2	enhancer of polycomb homolog 2 (Drosophila)	0.4562	0.0001	0.0013	1.02	1.22	1.33
Zfp58	zinc finger protein 58	0.0234	0.0015	0.0013	-1.3	1.46	1.33
Ralgapb	Ral GTPase activating protein, beta subunit (non-catalytic)	0.6970	0.0041	0.0002	-1.02	1.25	1.33
Tmem49	transmembrane protein 49	0.6349	0.0002	0.0003	-1.01	1.43	1.33
Lgalis8	lectin, galactose binding, soluble 8	0.4333	0.0038	0.0082	1.07	1.34	1.33
Detn	desmin	0.5977	0.0005	0.0008	1.04	1.37	1.33
DeWsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	0.0739	0.0001	0.0005	-1.1	1.41	1.33
Afr4	AF4/FR2 family, member 4	0.8554	0.0003	0.0009	-1.01	1.3	1.33
Mip63	mitochondrial ribosomal protein 63	0.0422	0.0030	0.0011	1.11	1.24	1.33
Sypl	synaptophysin-like protein	0.8702	0.0012	0.0008	1.09	1.38	1.33
Ccl4	chaperonin containing Tcp1, subunit 4 (delta)	0.1203	0.0000	0.0000	1.1	1.35	1.33
Atf7ip	activating transcription factor 7 interacting protein	0.0315	0.0055	0.0042	1.11	1.2	1.33
Fxr1	fragile X mental retardation gene 1, autosomal homolog	0.6953	0.0000	0.0003	1.02	1.31	1.33
Clasp1	CLIP associating protein 1	0.1751	0.0054	0.0064	-1.15	1.31	1.33
Rbx1	radixin	0.8482	0.0020	0.0045	-1.42	1.34	1.33
Gpbp1	GC-rich promoter binding protein 1	0.3600	0.0001	0.0000	1.03	1.37	1.33
Exosc8	exosome component 8	0.8589	0.0000	0.0000	1.01	1.47	1.33
Appl1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	0.5609	0.0041	0.0003	-1.02	1.41	1.33
Arctn1	archan 1	0.1271	0.0001	0.0000	1.08	1.28	1.33
Trp12	thyroid hormone receptor interactor 12	0.3835	0.0010	0.0003	-1.02	1.24	1.33
Psm14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0.9902	0.0006	0.0009	-1	1.29	1.33
Rbpj	recombination signal binding protein for immunoglobulin kappa J region	0.6740	0.0036	0.0020	-1.02	1.24	1.33
Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.2143	0.0000	0.0000	1.08	1.44	1.33
Elfin	eukaryotic translation initiation factor 3, subunit H	0.0218	0.0000	0.0000	1.11	1.38	1.33
Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	0.3985	0.0006	0.0008	-1.07	1.32	1.33
Abhd11	abhydrolase domain containing 11	0.2879	0.0053	0.0001	1.07	1.2	1.33
Btf3l4	basic transcription factor 3-like 4	0.9938	0.0002	0.0009	1	1.36	1.33
Mip59	mitochondrial ribosomal protein S9	0.9322	0.0047	0.0064	-1.01	1.32	1.32
Fam86a	family with sequence similarity 96, member A	0.8644	0.0000	0.0000	1.01	1.32	1.32
Osgp1d	oxysterol binding protein-like 7	0.2485	0.0001	0.0005	-1.07	1.34	1.32
1110018J18Rik	RIKEN cDNA 1110018J18 gene	0.8330	0.0092	0.0027	-1.01	1.38	1.32
Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.1375	0.0003	0.0005	-1.09	1.39	1.32
Lmbd1	LMBR1 domain containing 1	0.5609	0.0001	0.0004	-1.04	1.39	1.32
Mip49	mitochondrial ribosomal protein L49	0.1326	0.0069	0.0065	1.18	1.31	1.32
Usp2	UDP-glucose pyrophosphatase 2	0.0312	0.0002	0.0017	1.16	1.36	1.32
4833433P14Rik	RIKEN cDNA 4833433P14 gene	0.0745	0.0001	0.0002	1.11	1.31	1.32
Rab23	RAB23, member RAS oncogene family	0.8694	0.0023	0.0015	1.01	1.33	1.32
Cdk7	cyclin-dependent kinase 7	0.9836	0.0054	0.0018	1	1.32	1.32
Vps35	vacuolar protein sorting 35	0.5759	0.0000	0.0000	-1.01	1.34	1.32
Lgalis1	lectin, galactose binding, soluble 1	0.9872	0.0002	0.0013	-1.12	1.35	1.32
Pxmp3	peroxisomal membrane protein 3	0.5451	0.0000	0.0022	1.04	1.47	1.32
Mip15	mitochondrial ribosomal protein L15	0.3576	0.0002	0.0000	1.04	1.37	1.32
Fkbp3	FK506 binding protein 3	0.5204	0.0016	0.0040	1.04	1.33	1.32
DeK	DEK oncogene (DNA binding)	0.8966	0.0035	0.0013	-1.01	1.32	1.32
Nhp2f1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0.9246	0.0002	0.0012	-1	1.41	1.32
Nip7	nucleic acid import 7 homolog (S. cerevisiae)	0.4293	0.0017	0.0040	1.09	1.45	1.32
Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.1770	0.0007	0.0003	-1.09	1.36	1.32
Fbxo3	F-box protein 3	0.8803	0.0000	0.0002	1.01	1.39	1.32
Pdc3	phosphatidylcholine transferase 3	0.3823	0.0005	0.0006	1.05	1.4	1.32
Elfin	eukaryotic translation initiation factor 3, subunit E	0.3956	0.0001	0.0004	1.06	1.39	1.32
Mip11	mitochondrial ribosomal protein L11	0.5898	0.0000	0.0000	-1.02	1.38	1.32
Hicf2	host cell factor C2	0.4347	0.0014	0.0023	1.04	1.38	1.32
Vps54	vacuolar protein sorting 54 (yeast)	0.2852	0.0036	0.0003	-1.11	1.14	1.32
Usp47	ubiquitin specific peptidase 47	0.0735	0.0043	0.0010	1.13	1.21	1.32
Syap1	synapse associated protein 1	0.9687	0.0045	0.0015	-1	1.32	1.32
Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	0.2362	0.0005	0.0040	-1.13	1.29	1.32
Ipo7	importin 7	0.2864	0.0062	0.0002	1.08	1.22	1.32
Lgr4	leucine-rich repeat-containing G protein-coupled receptor 4	0.7706	0.0002	0.0013	-1.02	1.3	1.32
Sepp1	selenoprotein P, plasma, 1	0.0417	0.0002	0.0001	1.1	1.32	1.31
Heat3	HEAT repeat containing 3	0.7292	0.0100	0.0039	1.02	1.2	1.31
Rab28	RAB28, member RAS oncogene family	0.6666	0.0006	0.0002	-1.02	1.23	1.31
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	0.0287	0.0018	0.0010	1.17	1.32	1.31
Tipin	timeless interacting protein	0.2525	0.0025	0.0016	-1.1	1.29	1.31
Usp45	ubiquitin specific peptidase 45	0.2768	0.0000	0.0004	-1.08	1.34	1.31
Fam128	family with sequence similarity 92, member A	0.2127	0.0006	0.0002	-1.12	1.27	1.31
Lmo7	LIM domain only 7	0.3506	0.0024	0.0057	-1.05	1.29	1.31
Cnot8	CCR4-NOT transcription complex, subunit 8	0.1263	0.0058	0.0060	1.19	1.33	1.31
Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	0.4193	0.0002	0.0000	1.03	1.33	1.31
Naa50	N(alpha)-acetyltransferase 50, NADc catalytic subunit	0.0696	0.0003	0.0003	1.1	1.37	1.31
Fgfr1	fibroblast growth factor receptor 1	0.4337	0.0050	0.0042	-1.11	1.37	1.31
Zfp493	zinc finger protein 493	0.9441	0.0018	0.0079	-1.01	1.5	1.31
Lrrc40	leucine rich repeat containing 40	0.7954	0.0003	0.0011	1.04	1.53	1.31
Phlp	pleckstrin homology domain interacting protein	0.7057	0.0010	0.0025	-1.03	1.41	1.31
Tmem106b	transmembrane protein 106b	0.3293	0.0023	0.0001	1.07	1.2	1.31
Cnmp1b	chromatin modifying protein 1b	0.3720	0.0023	0.0049	1.08	1.29	1.31
Exosc1	exosome component 1	0.0893	0.0003	0.0005	1.18	1.37	1.31
Chchd1	coiled-coil-helix-coiled-coil-helix domain containing 1	0.1042	0.0000	0.0000	1.07	1.33	1.31
Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	0.0251	0.0054	0.0041	1.19	1.3	1.31
Pcdh9b	protocadherin gamma cluster	0.0672	0.0001	0.0028	1.32	1.6	1.31
Cry2	crystallin, zeta	0.7812	0.0028	0.0040	1.02	1.44	1.31
2610030H08Rik	RIKEN cDNA 2610030H08 gene	0.3631	0.0026	0.0000	1.03	1.24	1.31
Elf4a2	eukaryotic translation initiation factor 4A2	0.3222	0.0000	0.0005	-1.07	1.44	1.31
Dox21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.8131	0.0018	0.0007	1.02	1.37	1.31
Brix1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	0.9620	0.0004	0.0026	-1.1	1.47	1.31
Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	0.0517	0.0000	0.0004	-1.13	1.47	1.31

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Scarb2	scavenger receptor class B, member 2	0.6393	0.0004	0.0012	1.03	1.26	1.31
Cyt1	cytochrome c-1	0.0734	0.0010	0.0001	1.11	1.32	1.31
1610020D17Rik	RIKEN cDNA 1610020D17 gene	0.0816	0.0005	0.0003	1.04	1.35	1.31
Atp1b3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	0.0870	0.0018	0.0039	1.12	1.31	1.3
Ufm1	ubiquitin-fold modifier 1	0.1874	0.0003	0.0078	-1.13	1.46	1.3
Cuedc2	CUE domain containing 2	0.7110	0.0003	0.0058	1.03	1.33	1.3
Slmap	sarcolemma associated protein	0.8720	0.0010	0.0001	-1	1.21	1.3
Pomp	proteasome component 9	0.7692	0.0001	0.0005	1.02	1.38	1.3
Ubl4	ubiquitin-like 4	0.0961	0.0008	0.0000	1.06	1.31	1.3
Med4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	0.0528	0.0016	0.0009	1.2	1.34	1.3
Ints8	integrator complex subunit 8	0.2481	0.0052	0.0020	1.09	1.39	1.3
Mps33	mitochondrial ribosomal protein S33	0.5750	0.0005	0.0006	-1.04	1.29	1.3
Exoc3	exosome component 3	0.2001	0.0017	0.0013	-1.06	1.34	1.3
Chfr	checkpoint with forkhead and ring finger domains	0.1896	0.0006	0.0000	-1.07	1.36	1.3
Rpl34	ribosomal protein L34	0.0849	0.0000	0.0002	1.08	1.37	1.3
Pfdn2	prefoldin 2	0.3206	0.0000	0.0059	-1.11	1.47	1.3
Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	0.7704	0.0007	0.0009	1.02	1.33	1.29
Pus10	pseudouridylate synthase 10	0.1407	0.0000	0.0001	1.13	1.28	1.29
Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	0.2472	0.0015	0.0022	-1.08	1.3	1.29
Vps28	vacuolar protein sorting 28 (yeast)	0.0863	0.0001	0.0003	1.11	1.32	1.29
Xiap	X-linked inhibitor of apoptosis	0.2338	0.0018	0.0003	1.06	1.26	1.29
Elf2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	0.9093	0.0002	0.0032	1.01	1.43	1.29
Snarcc1	SWI/SNF related, matrix associated, activator dependent regulator of chromatin, subfamily c	0.0912	0.0002	0.0014	1.13	1.3	1.29
Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0.4889	0.0004	0.0008	-1.04	1.33	1.29
Cik1	CDC-like kinase 1	0.4496	0.0012	0.0056	1.07	1.45	1.29
493043202Rik	RIKEN cDNA 493043202 gene	0.9938	0.0015	0.0092	-1	1.41	1.29
Cttnb1	catenin (cadherin associated protein), beta 1	0.2647	0.0064	0.0014	-1.07	1.21	1.29
Armc3	armadillo repeat contain, X-linked 3	0.4327	0.0010	0.0000	1.04	1.35	1.29
Usp1	ubiquitin specific peptidase 1	0.8790	0.0001	0.0008	-1.01	1.33	1.29
Myf9	myosin, light polypeptide 9, regulatory	0.2108	0.0094	0.0038	1.13	1.42	1.29
Vbp1	von Hippel-Lindau binding protein 1	0.3383	0.0005	0.0004	1.07	1.39	1.29
MAK16	MAK16 homolog (S. cerevisiae)	0.0694	0.0001	0.0044	1.16	1.4	1.29
Ssp1	sarcomeric RNA activator	0.1323	0.0000	0.0000	1.12	1.53	1.29
Eif1ax	eukaryotic translation initiation factor 1A, X-linked	0.6456	0.0000	0.0005	1.02	1.34	1.29
Trappc2	trafficking protein particle complex 2	0.8016	0.0044	0.0053	-1.02	1.3	1.29
Hnmpk	heterogeneous nuclear ribonucleoprotein K	0.0847	0.0000	0.0000	-1.09	1.46	1.29
Spop	speckle-type POZ protein	0.9174	0.0048	0.0003	-1	1.17	1.29
Ighp1	immunoglobulin (cD76A) binding protein 1	0.8619	0.0007	0.0010	-1.01	1.54	1.29
Ube2f	ubiquitin-conjugating enzyme E2f (putative)	0.5226	0.0092	0.0017	-1.06	1.31	1.29
Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.3212	0.0014	0.0022	-1.07	1.4	1.29
Ragd	Ras-related GTP binding D	0.7016	0.0008	0.0006	1.03	1.37	1.29
Akip1	thymoma viral proto-oncogene 1 interacting protein	0.7783	0.0006	0.0000	-1.02	1.24	1.29
1110020B05Rik	RIKEN cDNA 1110020B05 gene	0.0114	0.0001	0.0001	-1.14	1.3	1.29
Rpl11	ribosomal protein L11	0.8822	0.0001	0.0001	1.01	1.32	1.29
Otd6b	OTU domain containing 6B	0.5233	0.0004	0.0052	1.06	1.33	1.29
Exoc7	exosome component 7	0.9798	0.0002	0.0088	1	1.36	1.29
Hbp1	high mobility group box transcription factor 1	0.4066	0.0004	0.0004	1.07	1.38	1.29
Zfp44	zinc finger homeodomain 4	0.0209	0.0003	0.0042	-1.11	1.3	1.29
D030074E01Rik	RIKEN cDNA D030074E01 gene	0.3161	0.0006	0.0035	-1.05	1.25	1.29
Atp6v1b2	ATPase, H ⁺ transporting, lysosomal V1 subunit B2	0.0850	0.0002	0.0004	1.12	1.46	1.28
Cldn12	claudin 12	0.4317	0.0007	0.0004	-1.07	1.33	1.28
Tmem126a	transmembrane protein 126A	0.1060	0.0000	0.0001	1.08	1.33	1.28
Rpl8	ribosomal protein L8	0.0129	0.0000	0.0002	1.15	1.3	1.28
Exoc3	exocyst complex component 3	0.9491	0.0076	0.0095	1.01	1.28	1.28
Oxr1	oxidation resistance 1	0.6968	0.0004	0.0006	-1.01	1.22	1.28
Rpl7a	ribosomal protein L7A	0.0251	0.0001	0.0004	1.13	1.33	1.28
Pfz2	profilin 2	0.7174	0.0006	0.0019	1.03	1.37	1.28
Hock3	hock homolog 3 (Drosophila)	0.8389	0.0006	0.0004	-1.04	1.28	1.28
Rap1a	RAS-related protein-1a	0.6412	0.0001	0.0017	-1.03	1.45	1.28
Cct6a	chaperonin containing Tcp1, subunit 6a (zeta)	0.4919	0.0012	0.0006	-1.04	1.34	1.28
Eed	embryonic ectoderm development	0.7938	0.0014	0.0048	1.02	1.36	1.28
Tmem33	transmembrane protein 33	0.6089	0.0008	0.0056	1.04	1.42	1.28
Commd3	CCMD domain containing 3	0.3740	0.0001	0.0006	1.02	1.32	1.28
Hnrlp1	heterogeneous nuclear ribonucleoprotein L-like	0.1781	0.0033	0.0043	-1.1	1.31	1.28
Gpcpd1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	0.0388	0.0003	0.0002	1.13	1.27	1.28
Rpl1	ribosome production factor 1 homolog (S. cerevisiae)	0.2906	0.0004	0.0036	1.1	1.46	1.28
Laptm4a	lysosomal-associated protein transmembrane 4A	0.9228	0.0004	0.0031	-1.01	1.33	1.28
Oat	ornithine aminotransferase	0.7969	0.0002	0.0003	1.02	1.29	1.28
Cct3	chaperonin containing Tcp1, subunit 3 (gamma)	0.5372	0.0008	0.0019	-1.04	1.34	1.28
Sic3oa6	solute carrier family 30 (zinc transporter), member 6	0.3648	0.0035	0.0019	-1.06	1.33	1.28
Fam192a	family with sequence similarity 192, member A	0.7822	0.0029	0.0036	1.04	1.26	1.28
Carlk2	carbohydrate kinase domain containing	0.5981	0.0031	0.0025	-1.04	1.33	1.28
Emg1	EMG1 nuclear protein homolog (S. cerevisiae)	0.3791	0.0001	0.0000	1.06	1.31	1.28
Tmem60	transmembrane protein 60	0.3607	0.0021	0.0035	1.03	1.26	1.28
Imp3	IMP3, U3 small nuclear ribonucleoprotein, homolog (yeast)	0.0612	0.0041	0.0011	1.14	1.37	1.28
2610001J05Rik	RIKEN cDNA 2610001J05 gene	0.4062	0.0002	0.0060	-1.05	1.32	1.27
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	0.3748	0.0054	0.0025	1.15	1.35	1.27
Schp1	Schwannian interacting protein 1	0.8796	0.0001	0.0003	-1.06	1.51	1.27
Zfp871	zinc finger protein 871	0.4034	0.0024	0.0000	1.03	1.23	1.27
2310035C23Rik	RIKEN cDNA 2310035C23 gene	0.6290	0.0048	0.0075	1.04	1.27	1.27
Mmgt1	membrane magnesium transporter 1	0.2109	0.0000	0.0001	1.06	1.31	1.27
Ndufb3	NAADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0.4739	0.0057	0.0006	1.04	1.2	1.27
Opm1l	CLPTM1-like	0.3016	0.0002	0.0002	1.29	1.27	1.27
Nanp	N-acetylneuraminic acid phosphorylase	0.8743	0.0024	0.0043	1.02	1.36	1.27
Sub1	SUB1 homolog (S. cerevisiae)	0.3383	0.0004	0.0004	1.06	1.44	1.27
Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	0.0819	0.0039	0.0060	1.1	1.2	1.27
Hnmpa0	heterogeneous nuclear ribonucleoprotein A0	0.0137	0.0024	0.0014	1.1	1.27	1.27
Gna3	guanine nucleotide binding protein (G protein), alpha inhibiting 3	0.9129	0.0002	0.0042	-1.01	1.32	1.27
Psm4	proteasome (prosome, macropain) subunit, beta type 4	0.0749	0.0000	0.0001	1.08	1.34	1.27
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	0.0974	0.0000	0.0005	-1.1	1.34	1.27
Pdcd10	programmed cell death 10	0.2811	0.0000	0.0018	1.04	1.33	1.27
Mapkap1	MAPK scaffold protein 1	0.3313	0.0004	0.0092	-1.06	1.38	1.27
Atp5f1	ATP synthase F1F0-transferring, mitochondrial F0 complex, subunit c1 (subunit 9)	0.8057	0.0001	0.0018	1.06	1.23	1.27
Mfsd1	major facilitator superfamily domain containing 1	0.7217	0.0009	0.0069	1.03	1.37	1.27
Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	0.8596	0.0014	0.0087	1.01	1.36	1.27
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	0.0252	0.0011	0.0082	-1.24	1.42	1.27
Hnfs3	histidine triad nucleotide binding protein 3	0.3625	0.0032	0.0035	1.06	1.24	1.27
Opa3	cytoplasmic polyadenylation element binding protein 3	0.8622	0.0043	0.0000	-1	1.15	1.27
Mfsd3	major facilitator superfamily domain containing 3	0.2342	0.0024	0.0010	1.13	1.32	1.27
Psmc8	proteasome (prosome, macropain) 26S subunit, ATPase, 6	0.3091	0.0006	0.0015	1.06	1.26	1.27
Clic	clathrin, heavy polypeptide (Hc)	0.1539	0.0012	0.0001	-1.09	1.27	1.27
Zc3h12c	zinc finger CCHC type containing 12C	0.7968	0.0044	0.0038	1.02	1.2	1.27
Pitp1	pituitary tumor-transforming gene 1	0.4939	0.0008	0.0004	1.04	1.23	1.27
Hnmpc	heterogeneous nuclear ribonucleoprotein C	0.9898	0.0006	0.0061	-1	1.35	1.27
3230401D17Rik	RIKEN cDNA 3230401D17 gene	0.5919	0.0008	0.0001	1.03	1.36	1.27
Atad1	ATPase family, AAA domain containing 1	0.1152	0.0015	0.0044	-1.14	1.36	1.26
Mps32	mitochondrial ribosomal protein S23	0.2979	0.0009	0.0055	1.08	1.33	1.26
Tmem70	transmembrane protein 70	0.8536	0.0021	0.0020	-1.01	1.28	1.26
Serbp1	serpine1 mRNA binding protein 1	0.3717	0.0013	0.0014	1.06	1.2	1.26
Cst6	cystatin E/M	0.5421	0.0002	0.0087	-1.07	1.41	1.26
Rnft1	ring finger protein, transmembrane 1	0.3302	0.0005	0.0087	1.05	1.35	1.26
Capza1	capping protein (actin filament) muscle Z-line, alpha 1	0.1458	0.0012	0.0016	-1.07	1.28	1.26
Magt1	magnesium transporter	0.8823	0.0016	0.0074	-1.22	1.38	1.26
Zfand6	zinc finger, AN1-type domain 6	0.0451	0.0035	0.0014	-1.14	1.26	1.26
Mtap	methylthioadenosine phosphorylase	0.2103	0.0000	0.0016	-1.07	1.37	1.26
Uqcrc	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	0.8774	0.0021	0.0100	-1.01	1.38	1.26
Ywhaf	tyrosine 3-monooxygenase/tyrosinase 5-monooxygenase activation protein, eta polypeptide	0.0463	0.0000	0.0082	1.1	1.26	1.26
Cc2d3b	coiled-coil domain containing 3b	0.7051	0.0016	0.0011	-1.02	1.21	1.26
Mct5	malignant T cell amplified sequence 1	0.8530	0.0002	0.0004	-1.01	1.26	1.26
Nampt	nicotinamide phosphoribosyltransferase	0.5817	0.0016	0.0040	1.04	1.39	1.26
Edem3	ER degradation enhancer, mannosidase alpha-like 3	0.2386	0.0007	0.0068	1.06	1.22	1.26
2700060E02Rik	RIKEN cDNA 2700060E02 gene	0.0937	0.0001	0.0002	1.1	1.36	1.26
Tmem83	transmembrane 83 superfamily member 3	0.9547	0.0004	0.0010	-1	1.32	1.26
HistH2bc	histone cluster 1, H2bc	0.1863	0.0003	0.0038	1.08	1.4	1.26
2810405K02Rik	RIKEN cDNA 2810405K02 gene	0.4895	0.0071	0.0064	-1.06	1.36	1.26
Mterf1	MTERF domain containing 1	0.0637	0.0004	0.0073	-1.1	1.29	1.26
Pel1	pellino 1	0.7978	0.0040	0.0074	-1.02	1.37	1.26
Mcew	methylcrotonyl CoA epimerase	0.9416	0.0008	0.0001	-1	1.18	1.26
Rab33b	RAB33B, member of RAS oncogene family	0.1116	0.0000	0.0041	-1.12	1.34	1.25
Ppp1cc	protein phosphatase 1, catalytic subunit, gamma isoform	0.8214	0.0002	0.0009	1.01	1.36	1.25
Bola1	BOLA-like 1 (E. coli)	0.6189	0.0057	0.0042	1.03	1.24	1.25
Pob	polymerase (DNA directed), beta	0.3373	0.0001	0.0001	-1.03	1.29	1.25
2810407Y02Rik	RIKEN cDNA 2810407Y02 gene	0.0172	0.0042	0.0028	-1.19	1.24	1.25

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Mmactb	methylmalonic aciduria cblC type, with homocystinuria	0.7261	0.0004	0.0062	-1.02	1.51	1.25
Pamc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	0.2730	0.0006	0.0042	1.07	1.3	1.25
Spr14	sprawl related protein 14	0.2642	0.0001	0.0001	-1.04	1.24	1.25
Trappc4	trafficking protein particle complex 4	0.8262	0.0011	0.0010	1.01	1.35	1.25
2900010M23Rik	RIKEN cDNA 2900010M23 gene	0.1029	0.0003	0.0007	1.07	1.2	1.24
Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	0.0127	0.0001	0.0004	1.16	1.24	1.24
Cast2	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	0.9736	0.0001	0.0001	1	1.2	1.24
H2atz	H2A histone family, member Z	0.4103	0.0003	0.0001	1.03	1.24	1.24
Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	0.8281	0.0001	0.0007	-1.01	1.27	1.24
Elf1	ET4-like factor 1	0.1726	0.0045	0.0093	-1.17	1.29	1.24
Aga	asparaginylglucosaminidase	0.8030	0.0039	0.0077	1.01	1.29	1.24
DnaJ15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.6822	0.0003	0.0003	1.02	1.25	1.24
Rod1d3	roadblock domain containing 3	0.0393	0.0003	0.0011	-1.12	1.31	1.24
Znfn2	zinc finger, MYM-type 2	0.9277	0.0006	0.0047	1.01	1.33	1.24
Rpap2	RNA polymerase II associated protein 2	0.3174	0.0003	0.0069	1.12	1.41	1.24
Ube3a	ubiquitin protein ligase E3A	0.9472	0.0051	0.0078	1	1.43	1.24
Ptc3	pentatricopeptide repeat domain 3	0.3429	0.0070	0.0035	1.06	1.2	1.24
Calc30l	calcium binding protein 39-like	0.8164	0.0003	0.0010	-1.03	1.29	1.24
Akap9	A kinase (PRKA) anchor protein (yttaa) 9	0.4739	0.0095	0.0047	1.04	1.23	1.24
Hprt	hypoxanthine guanine phosphoribosyl transferase	0.0201	0.0013	0.0034	-1.14	1.26	1.24
Egr	epidermal growth factor	0.4090	0.0100	0.0075	-1.07	1.21	1.24
LOC820419	zinc finger protein 669-like	0.9380	0.0075	0.0048	1	1.2	1.24
Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0.1865	0.0006	0.0084	1.1	1.22	1.23
1810013L24Rik	RIKEN cDNA 1810013L24 gene	0.6424	0.0009	0.0043	-1.03	1.23	1.23
Fastkd5	FAST kinase domains 5	0.3273	0.0004	0.0063	1.05	1.31	1.23
Polim5	PDZ and LIM domain 5	0.1555	0.0006	0.0091	1.12	1.4	1.23
Alp5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	0.9102	0.0014	0.0002	1.01	1.23	1.23
Apa1	apoptosis associated protein complex AP-4, sigma 1	0.3291	0.0003	0.0007	1.05	1.32	1.23
Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	0.5343	0.0024	0.0000	-1.02	1.26	1.23
Mtch2	mitochondrial carrier homolog 2 (C. elegans)	0.0500	0.0000	0.0000	1.06	1.37	1.23
Snrp2	small nuclear ribonucleoprotein D2	0.9718	0.0001	0.0003	-1	1.26	1.23
Rab1	RAB1, member RAS oncogene family	0.8264	0.0001	0.0051	1.01	1.31	1.23
Pkia	protein kinase, alpha	0.8793	0.0027	0.0010	-1.02	1.22	1.23
Mrf	mitochondrial ribosome recycling factor	0.2074	0.0003	0.0030	1.06	1.39	1.23
Mrlp24	mitochondrial ribosomal protein L24	0.0212	0.0001	0.0001	1.08	1.29	1.23
Pdx1	peroxiredoxin 1	0.7131	0.0003	0.0006	-1.02	1.26	1.23
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	0.1473	0.0036	0.0025	1.09	1.24	1.23
Znfx2	zinc finger, main type	0.4882	0.0001	0.0000	1.02	1.34	1.23
Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	0.5093	0.0060	0.0017	1.03	1.21	1.23
Vamp4	vesicle-associated membrane protein 4	0.5781	0.0022	0.0037	-1.02	1.27	1.23
6330577E15Rik	RIKEN cDNA 6330577E15 gene	0.2765	0.0021	0.0005	1.07	1.27	1.23
Thrap3	thyroid hormone receptor associated protein 3	0.8698	0.0046	0.0017	-1.01	1.21	1.23
Rpl32	ribosomal protein L32	0.2442	0.0003	0.0007	1.06	1.3	1.23
Dpy19l4	dpy-19-like 4 (C. elegans)	0.3482	0.0012	0.0006	-1.06	1.24	1.23
Pamb1	proteasome (prosome, macropain) subunit, beta type 1	0.5049	0.0002	0.0007	1.03	1.27	1.22
2310016M24Rik	RIKEN cDNA 2310016M24 gene	0.6357	0.0013	0.0007	-1.02	1.23	1.22
Mrgp25	mitochondrial ribosomal protein S25	0.7967	0.0010	0.0045	-1.02	1.29	1.22
Atp6v1g1	ATPase V1+transferring, lysosomal V1 subunit G1	0.1093	0.0003	0.0001	-1.08	1.34	1.22
Cwc15	CWC15 homolog (S. cerevisiae)	0.2791	0.0007	0.0048	1.06	1.27	1.22
Mrlp51	mitochondrial ribosomal protein L51	0.3323	0.0010	0.0059	1.06	1.32	1.22
Acact1	acetyl-Coenzyme A acetyltransferase 1	0.1660	0.0039	0.0002	-1.1	1.17	1.22
Hspa9	heat shock protein 9	0.2543	0.0000	0.0002	1.03	1.26	1.22
Elle	eukaryotic translation initiation factor 6	0.8219	0.0006	0.0008	1.02	1.21	1.22
Lanc12	LanC (bacterial antibiotic synthetase component C)-like 2	0.5355	0.0055	0.0064	1.04	1.17	1.22
Der12	Der1-like domain family, member 2	0.2894	0.0002	0.0086	-1.08	1.4	1.22
Kpna2	karyopherin (importin) alpha 2	0.4955	0.0007	0.0057	-1.05	1.37	1.22
Mrgp10	mitochondrial ribosomal protein S10	0.0934	0.0085	0.0092	-1.16	1.27	1.22
Spdc	sarcoglycan, beta (dystrophin-associated glycoprotein)	0.3876	0.0008	0.0077	1.04	1.26	1.22
Tmx1	thioredoxin-related transmembrane protein 1	0.8477	0.0006	0.0020	1.01	1.31	1.22
Rai24d1	ribosomal L24 domain containing 1	0.7154	0.0006	0.0000	-1.04	1.35	1.22
Aaf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.9552	0.0048	0.0005	-1	1.35	1.22
AU022870	expressed sequence AU022870	0.3045	0.0058	0.0039	1.06	1.23	1.22
Synj2bap	synaptojanin 2 binding protein	0.0712	0.0056	0.0020	1.1	1.2	1.22
Rbx1	ring-box 1	0.6268	0.0004	0.0002	-1.02	1.26	1.21
2010106G01Rik	RIKEN cDNA 2010106G01 gene	0.6660	0.0010	0.0065	1.02	1.23	1.21
Riesd	Rieske (Fe-S) domain containing	0.3985	0.0002	0.0053	1.06	1.34	1.21
Med30	mediator complex subunit 30	0.9454	0.0005	0.0036	-1.01	1.27	1.21
Gsp1	G protein pathway suppressor 1	0.3527	0.0015	0.0012	1.05	1.21	1.21
Rpl19	ribosomal protein L19	0.0989	0.0001	0.0002	1.07	1.23	1.21
Ppa1	pyrophosphatase (inorganic)	0.4985	0.0025	0.0052	-1.04	1.21	1.21
Sorbs2	sorbin and SH3 domain containing 2	0.2805	0.0034	0.0007	1.11	1.19	1.21
Calm1	calmodulin 1	0.5053	0.0004	0.0005	-1.03	1.29	1.21
Sclaf1	succinate dehydrogenase complex, subunit D, integral membrane protein	0.1847	0.0090	0.0048	1.02	1.28	1.21
Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0.4572	0.0076	0.0019	1.03	1.26	1.21
Rpl26	ribosomal protein L26	0.1664	0.0004	0.0010	1.08	1.24	1.21
Slc30a4	solute carrier family 30 (zinc transporter), member 4	0.9068	0.0009	0.0059	1.01	1.28	1.21
Mina	myc induced nuclear antigen	0.4668	0.0028	0.0028	1.04	1.29	1.21
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0.0589	0.0019	0.0079	1.1	1.27	1.21
Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	0.1096	0.0032	0.0011	1.11	1.22	1.21
Rps7	ribosomal protein S7	0.0353	0.0037	0.0064	1.16	1.23	1.21
Ghrpr	glyoxylate reductase/hydroxypyruvate reductase	0.1741	0.0020	0.0011	1.12	1.28	1.21
Psmg2	proteasome (prosome, macropain) assembly chaperone 2	0.2873	0.0073	0.0010	-1.06	1.2	1.21
Mtpap	mitochondrial pol(A) polymerase	0.3774	0.0003	0.0040	-1.03	1.2	1.21
Fundc2	FUN14 domain containing 2	0.3160	0.0013	0.0086	1.08	1.31	1.21
Mrlp12	mitochondrial ribosomal protein L12	0.0775	0.0094	0.0021	1.08	1.24	1.21
Zbtb46	zinc finger and BTB domain containing 46	0.1001	0.0046	0.0051	1.13	1.52	1.21
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.5657	0.0011	0.0002	1.02	1.17	1.19
Pdgfra	platelet derived growth factor receptor, alpha polypeptide	0.8914	0.0004	0.0025	-1.03	1.18	1.19
Exosc4	exosome component 4	0.2839	0.0061	0.0020	1.06	1.27	1.19
Rps15	ribosomal protein S15	0.3068	0.0022	0.0010	1.07	1.2	1.19
Pirg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	0.0325	0.0002	0.0020	1.15	1.33	1.19
Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)	0.0854	0.0001	0.0011	-1.1	1.31	1.19
Tcnp	thioredoxin interacting protein	0.3723	0.0086	0.0048	1.06	1.21	1.19
Tjp1	tight junction protein 1	0.0353	0.0046	0.0025	-1.08	1.12	1.19
Adnp	activity-dependent neuroprotective protein	0.2310	0.0000	0.0006	-1.06	1.19	1.19
Rpl18	ribosomal protein L18	0.0108	0.0028	0.0059	1.14	1.21	1.18
Ktn1	kinesin 1	0.0816	0.0093	0.0032	1.12	1.11	1.18
Apx1	apurinic/apyrimidinic endonuclease 1	0.3570	0.0031	0.0040	-1.03	1.18	1.18
Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	0.5559	0.0050	0.0043	-1.03	1.19	1.18
Pam12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	0.7666	0.0004	0.0009	1.02	1.2	1.18
Vps26a	vacuolar protein sorting 26 homolog A (yeast)	0.4191	0.0022	0.0091	1.03	1.23	1.18
Cox5b	cytochrome c oxidase, subunit Vb	0.2693	0.0068	0.0050	1.09	1.2	1.18
2510033E04Rik	RIKEN cDNA 2510033E04 gene	0.2894	0.0016	0.0017	1.07	1.25	1.18
Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	0.6324	0.0016	0.0007	1.02	1.17	1.18
Mikn1	muskelin 1, intracellular mediator containing kelch motifs	0.3313	0.0031	0.0023	1.06	1.22	1.17
Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	0.5506	0.0014	0.0067	1.04	1.19	1.17
H2atz	H2A histone family, member Z	0.0912	0.0043	0.0081	1.14	1.19	1.17
6330409N04Rik	RIKEN cDNA 6330409N04 gene	0.8890	0.0049	0.0081	1.03	1.18	1.17
Golga7	golgi autoantigen, golgin subfamily a, 7	0.0739	0.0013	0.0074	-1.11	1.26	1.17
Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	0.5129	0.0001	0.0094	1.05	1.31	1.17
Brp44l	brain protein 44-like	0.1755	0.0001	0.0008	1.05	1.27	1.17
Mrlp16	mitochondrial ribosomal protein L16	0.2229	0.0045	0.0040	1.05	1.18	1.16
Acrb	ATP8 acid-related protein 8 homolog (S. cerevisiae)	0.0482	0.0007	0.0006	1.12	1.15	1.16
Suc1a2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	0.1050	0.0040	0.0016	1.06	1.14	1.16
Ppp4r2	protein phosphatase 4, regulatory subunit 2	0.4719	0.0069	0.0032	1.06	1.14	1.16
Nop16	NOP16 nuclear protein homolog (yeast)	0.1735	0.0076	0.0059	-1.09	1.19	1.16
Sec23a	SEC23A (S. cerevisiae)	0.2601	0.0021	0.0042	1.05	1.17	1.16
Pacs	phosphatidylinositol-3-OH kinase class I domain containing 1	0.1097	0.0089	0.0012	1.06	1.19	1.16
Pgk1	phosphoglycerate kinase 1	0.0387	0.0003	0.0058	1.17	1.22	1.15
Glx3	glutaredoxin 3	0.0978	0.0052	0.0014	1.08	1.24	1.15
Cetn2	centrin 2	0.9816	0.0003	0.0046	-1	1.2	1.15
Ino80c	INO80 complex subunit C	0.0384	0.0064	0.0009	1.11	1.11	1.15
Slm2	stromal interaction molecule 2	0.1922	0.0055	0.0081	1.11	1.1	1.15
Bnip3	BCL2/adenovirus E1B interacting protein 3	0.2744	0.0012	0.0032	1.06	1.1	1.11
Taz	tafazzin	0.2230	0.0010	0.0048	1.04	1.12	1.11
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	0.0539	0.0084	0.0028	1.07	1.18	1.12
Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	0.2184	0.0005	0.0037	1.07	1.26	1.16
BC046404	cDNA sequence BC046404	0.4714	0.0007	0.0086	1.05	1.23	1.16
Fkbp1a	FK506 binding protein 1a	0.7394	0.0000	0.0003	1.01	1.23	1.18
Parp1	poly (ADP-ribose) polymerase family, member 1	0.7003	0.0026	0.0072	-1.02	1.22	1.18
Cbara1	calcium binding atopy-related autoantigen 1	0.3515	0.0060	0.0069	-1.05	1.25	1.19
Gabarap	gamma-aminobutyric acid receptor associated protein	0.0201	0.0004	0.0002	1.07	1.14	1.19
Cacoph	calcium channel, voltage-dependent, gamma subunit 8	0.1100	0.0002	0.0076	1.06	1.31	1.19

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Cdc37	cell division cycle 37 homolog (S. cerevisiae)	0.5926	0.0028	0.0070	1.03	-1.24	-1.19
Cyb5b1	cytochrome b5 reductase 1	0.0223	0.0011	0.0021	-1.12	-1.22	-1.19
Uba1	ubiquitin-like modifier activating enzyme 1	0.0153	0.0001	0.0080	1.08	-1.29	-1.2
Rps10	ribosomal protein S10	0.4682	0.0075	0.0026	1.04	-1.17	-1.2
Vdac1	voltage-dependent anion channel 1	0.1491	0.0008	0.0030	1.08	-1.25	-1.2
Auh	AU RNA binding protein/enoyl-Coenzyme A hydratase	0.3765	0.0009	0.0019	1.03	-1.21	-1.2
Clcn4-2	chloride channel 4-2	0.8007	0.0006	0.0096	-1.01	-1.42	-1.2
Pex19	peroxisomal biogenesis factor 19	0.7835	0.0032	0.0011	-1.02	-1.37	-1.21
Brd4	bromodomain containing 4	0.3222	0.0001	0.0052	-1.07	-1.38	-1.21
Ankrd27	ankyrin repeat domain 27 (VPS9 domain)	0.2786	0.0002	0.0022	-1.1	-1.28	-1.22
H1f0	H1 histone family, member 0	0.0165	0.0016	0.0026	-1.17	-1.25	-1.22
Aq3d1	adaptor-related protein complex 3, delta 1 subunit	0.4574	0.0005	0.0041	-1.04	-1.38	-1.22
Elf5	eukaryotic translation initiation factor 5B	0.1499	0.0001	0.0093	1.08	-1.47	-1.22
Suox	sulfite oxidase	0.9194	0.0000	0.0011	1.01	-1.29	-1.23
Tmem134	transmembrane protein 134	0.3116	0.0013	0.0010	-1.05	-1.2	-1.23
Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase/hydroxyacyl-Coenzyme A dehydratase	0.5296	0.0003	0.0017	1.04	-1.36	-1.23
LOC100047863	similar to lymphocyte-specific adaptor protein Lnk	0.4574	0.0003	0.0075	1.05	-1.54	-1.23
0610031306Rk	RIKEN cDNA 0610031306 gene	0.4363	0.0016	0.0042	-1.06	-1.32	-1.23
Mpdn	MPN domain containing	0.7293	0.0004	0.0097	-1.03	-1.36	-1.23
Six1	sine oculis-related homeobox 1 homolog (Drosophila)	0.1172	0.0002	0.0022	-1.14	-1.26	-1.23
Tubg1	tubulin, gamma 1	0.0760	0.0001	0.0010	1.16	-1.26	-1.24
Hlbadh	3-hydroxyisobutyrate dehydrogenase	0.5316	0.0050	0.0079	-1.04	-1.26	-1.24
Prkd	paroxysmal nonkinetogenic dyskinesia	0.7883	0.0028	0.0080	1.02	-1.32	-1.24
Cog10a	coenzyme Q10 homolog A (yeast)	0.2327	0.0001	0.0002	1.08	-1.33	-1.24
Strn3	striatin, calmodulin binding protein 3	0.1674	0.0000	0.0005	-1.04	-1.31	-1.24
Tspan3	tetraspanin 3	0.0273	0.0001	0.0005	-1.14	-1.27	-1.24
Rrp1	ribosomal RNA processing 1 homolog (S. cerevisiae)	0.2301	0.0001	0.0041	1.04	-1.22	-1.24
Cox1b	COX1b cytochrome c oxidase assembly homolog (S. cerevisiae)	0.7303	0.0003	0.0058	-1.02	-1.4	-1.24
Gng5	guanine nucleotide binding protein (G protein), gamma 5	0.0793	0.0032	0.0084	1.13	-1.3	-1.25
Ankrd23	ankyrin repeat domain 23	0.1801	0.0011	0.0044	1.11	-1.29	-1.25
2310042D19Rk	RIKEN cDNA 2310042D19 gene	0.5816	0.0005	0.0075	1.06	-1.41	-1.25
Vps4a	vacuolar protein sorting 4a (yeast)	0.0396	0.0001	0.0064	1.12	-1.44	-1.25
Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	0.4296	0.0040	0.0018	1.02	-1.34	-1.26
2610024G14Rk	RIKEN cDNA 2610024G14 gene	0.6539	0.0007	0.0026	-1.04	-1.4	-1.26
BC024814	cDNA sequence BC024814	0.2458	0.0016	0.0059	1.08	-1.34	-1.26
Gler	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	0.1109	0.0004	0.0000	1.15	-1.23	-1.26
Supl8h	suppressor of Ty 5 homolog (S. cerevisiae)	0.5385	0.0060	0.0051	-1.04	-1.24	-1.26
Oas2-ps	ornithine decarboxylase antizyme 2, pseudogene	0.2843	0.0002	0.0085	1.05	-1.46	-1.27
Gpx4	glutathione peroxidase 4	0.2165	0.0000	0.0006	-1.05	-1.41	-1.27
Fez2	fasciculation and elongation protein zeta 2 (zyglin II)	0.3352	0.0009	0.0045	-1.07	-1.39	-1.27
1810031K17Rk	RIKEN cDNA 1810031K17 gene	0.1020	0.0052	0.0019	1.15	-1.27	-1.27
Erp1c3	ERGIC and golgi 3	0.6318	0.0047	0.0026	1.02	-1.24	-1.27
Uba1f1	Uba1 previtellogenesis domain containing 1	0.8036	0.0004	0.0007	1.03	-1.4	-1.27
Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	0.8013	0.0021	0.0011	-1.02	-1.29	-1.27
Sic35b1	solute carrier family 35, member B1	0.6302	0.0010	0.0012	-1.02	-1.28	-1.27
Mrlp9	mitochondrial ribosomal protein L9	0.3803	0.0001	0.0008	1.04	-1.37	-1.28
Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	0.0822	0.0000	0.0004	-1.09	-1.41	-1.28
Adx1	adrenomedullin 1 (alpha)	0.8796	0.0002	0.0048	-1.01	-1.36	-1.28
Cdc42ep3	CD042 effector protein (Rho GTPase binding) 3	0.5753	0.0001	0.0067	-1.04	-1.45	-1.28
Adi1	acreductone dioxygenase 1	0.2562	0.0056	0.0089	-1.09	-1.35	-1.28
Abhd4	abhydrolase domain containing 4	0.0251	0.0026	0.0019	1.14	-1.24	-1.28
Naca	nascent polypeptide-associated complex alpha polypeptide	0.0523	0.0000	0.0089	1.13	-1.57	-1.28
Wdr81	WD repeat domain 81	0.3708	0.0038	0.0093	-1.07	-1.48	-1.29
Al318807	expressed sequence Al318807	0.5589	0.0014	0.0014	1.02	-1.28	-1.28
Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	0.0186	0.0003	0.0023	1.14	-1.41	-1.28
Hrc	histidine rich calcium binding protein	0.4576	0.0009	0.0017	1.04	-1.27	-1.29
Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0.1779	0.0007	0.0020	1.08	-1.34	-1.29
Pgi	phosphatidylglycerol anchor biosynthesis, class I	0.8849	0.0018	0.0032	-1.01	-1.31	-1.29
Tmem214	transmembrane protein 214	0.0259	0.0095	0.0048	1.21	-1.39	-1.29
Golga2	golgi autoantigen, golgin subfamily a, 2	0.1373	0.0005	0.0039	1.09	-1.46	-1.29
Map2k5	mitogen-activated protein kinase kinase 5	0.4996	0.0003	0.0081	1.03	-1.35	-1.29
Ar2	ADP-ribosylation factor-like 2	0.4488	0.0018	0.0002	1.04	-1.25	-1.29
Nudcd3	NudC domain containing 3	0.1246	0.0004	0.0086	1.09	-1.34	-1.29
Ctsa	cathepsin A	0.4802	0.0015	0.0034	1.04	-1.33	-1.29
Rab22a	RAB22A, member RAS oncogene family	0.5204	0.0071	0.0021	1.06	-1.24	-1.29
Piges2	prostaglandin E synthase 2	0.9256	0.0001	0.0083	-1.01	-1.5	-1.29
Rnf181	ring finger protein 181	0.2425	0.0001	0.0007	-1.08	-1.39	-1.29
Gpr107	G protein-coupled receptor 107	0.2765	0.0003	0.0017	1.06	-1.42	-1.3
Mfn2	mitofusin 2	0.3475	0.0001	0.0005	1.04	-1.48	-1.3
Mknr2	makorin, ring finger protein, 2	0.7889	0.0006	0.0043	1.02	-1.41	-1.3
Ndnf2	neodin-like 2	0.0682	0.0005	0.0076	-1.13	-1.31	-1.3
Pkn2	pyruvate kinase, muscle	0.0354	0.0017	0.0023	1.15	-1.33	-1.3
Mcart1	mitochondrial carrier triple repeat 1	0.8172	0.0001	0.0032	-1.02	-1.39	-1.3
Ecat	ECST1 homolog (Drosophila)	0.1710	0.0001	0.0012	1.12	-1.3	-1.3
Ak3	adenylate kinase 3	0.6821	0.0001	0.0078	1.03	-1.47	-1.3
Ryr1	ryanodine receptor 1, skeletal muscle	0.0704	0.0002	0.0058	1.12	-1.52	-1.31
Dusp13	dual specificity phosphatase 13	0.0148	0.0027	0.0050	1.18	-1.36	-1.31
Glaib1	lectin, galactose binding, soluble 9	0.3867	0.0067	0.0075	1.05	-1.37	-1.31
Cdc124	coiled-coil domain containing 124	0.2166	0.0022	0.0003	1.05	-1.27	-1.31
Hagh	hydroxyacyl glutathione hydrolase	0.8090	0.0000	0.0001	-1.01	-1.33	-1.31
Ier3ip1	immediate early response 3 interacting protein 1	0.2724	0.0003	0.0012	-1.06	-1.4	-1.31
Txn2	thioredoxin 2	0.4528	0.0006	0.0003	1.04	-1.36	-1.31
C14bp	complement component 1, q subcomponent binding protein	0.0528	0.0004	0.0008	1.09	-1.35	-1.31
Nfi	neurofibromatosis 1	0.3047	0.0080	0.0000	1.07	-1.25	-1.31
Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	0.5394	0.0000	0.0012	1.03	-1.39	-1.31
Cfb	clathrin, light polypeptide (Lcb)	0.8033	0.0036	0.0001	1.01	-1.23	-1.31
Wsb2	WD repeat and SOCS box-containing 2	0.1500	0.0000	0.0008	-1.1	-1.53	-1.32
Aqp16f1	aquaporin-related 16-like 1 (yeast)	0.0617	0.0003	0.0033	1.13	-1.56	-1.32
Bop1	block of proliferation 1	0.2268	0.0025	0.0022	1.1	-1.41	-1.32
Podxl	podocalyxin-like	0.8045	0.0001	0.0064	-1.02	-1.76	-1.32
Akap1	A kinase (PRKA) anchor protein 1	0.1734	0.0014	0.0062	-1.16	-1.47	-1.32
1500002020Rk	RIKEN cDNA 1500002020 gene	0.1989	0.0007	0.0020	1.06	-1.31	-1.32
Co2	coenzyme Q2 homolog, prenyltransferase (yeast)	0.9857	0.0000	0.0005	-1	-1.4	-1.32
Clnb	cellular lipofuscinosis, neuronal 6	0.2712	0.0007	0.0030	1.1	-1.52	-1.32
Stom	stomatin	0.1323	0.0058	0.0002	-1.08	-1.27	-1.33
Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2	0.1436	0.0012	0.0038	-1.13	-1.39	-1.33
Rab1b	RAB1B, member RAS oncogene family	0.4486	0.0006	0.0003	-1.04	-1.29	-1.33
Mast2	microtubule associated serine/threonine kinase 2	0.0377	0.0003	0.0086	1.16	-1.4	-1.33
Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12b	0.2636	0.0000	0.0009	-1.08	-1.54	-1.33
Dirc2	disrupted in renal carcinoma 2 (human)	0.1706	0.0001	0.0007	1.09	-1.43	-1.33
Foxp1	forkhead box P1	0.5847	0.0020	0.0096	-1.05	-1.56	-1.33
Zfp12	Zinc finger protein 212	0.8601	0.0056	0.0061	-1.01	-1.34	-1.33
Aic	5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	0.1097	0.0001	0.0006	-1.09	-1.46	-1.33
Atp8b2	ATPase, class I, type B8, member 2	0.0760	0.0076	0.0076	-1.17	-1.25	-1.33
Fem1a	feminization 1 homolog a (C. elegans)	0.0527	0.0023	0.0062	1.17	-1.44	-1.33
Poidip2	polymerase (DNA-directed), delta interacting protein 2	0.0235	0.0000	0.0021	1.12	-1.59	-1.33
Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	0.3387	0.0001	0.0003	-1.03	-1.45	-1.33
Th1f	TH1-like homolog (Drosophila)	0.3333	0.0004	0.0043	1.09	-1.51	-1.33
Fam98c	family with sequence similarity 98, member C	0.2291	0.0013	0.0068	1.09	-1.48	-1.33
Sarp1	structure specific recognition protein 1	0.8929	0.0000	0.0097	-1.01	-1.75	-1.33
Tsc2d1	TSC22 domain family, member 1	0.0392	0.0000	0.0057	1.13	-1.59	-1.33
Ppp2r3a	protein phosphatase 2, regulatory subunit B', alpha	0.5488	0.0011	0.0003	-1.03	-1.26	-1.33
Ptt23	PTT23 finger protein 23	0.2097	0.0002	0.0038	1.06	-1.45	-1.33
Exoc4	exocyst complex component 4	0.0232	0.0005	0.0029	-1.19	-1.43	-1.34
Lamp1	lysosomal-associated membrane protein 1	0.9184	0.0001	0.0007	-1	-1.51	-1.34
Dus1f	dihydropyrimidine synthase 1-like (S. cerevisiae)	0.1623	0.0051	0.0090	1.12	-1.42	-1.34
Sic35a3	solute carrier family 35, member E3	0.8000	0.0015	0.0013	-1.02	-1.44	-1.34
016w92126	cDNA sequence 016w92126, Brigham & Women's Genetics 0212 expressed	0.9857	0.0000	0.0005	-1	-1.4	-1.34
Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	0.1270	0.0002	0.0009	1.08	-1.41	-1.34
Zkscan17	zinc finger with KRAB and SCAN domains 17	0.3547	0.0060	0.0086	-1.08	-1.47	-1.34
Camk2b	calcium/calmodulin-dependent protein kinase II, beta	0.4867	0.0000	0.0013	1.03	-1.58	-1.34
Atxn7l3	ataxin 7-like 3	0.4447	0.0002	0.0028	-1.02	-1.45	-1.34
Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	0.2989	0.0003	0.0019	1.05	-1.48	-1.34
Nenr	neuron derived neurotrophic factor	0.0778	0.0009	0.0007	-1.11	-1.36	-1.34
Psmc1	proteasome (prosome, macropain) 26 subunit, alpha	0.8037	0.0078	0.0003	-1.01	-1.28	-1.34
Nfe2l1	nuclear factor, erythroid derived 2, like 1	0.2759	0.0003	0.0012	1.08	-1.57	-1.34
Ramp1	receptor (calcitonin) activity modifying protein 1	0.7168	0.0015	0.0040	1.04	-1.47	-1.35
Maik	v-maf myeloblastic leukemia factor-3/avian myeloblastosis virus oncogene family, protein K (avian)	0.8073	0.0001	0.0080	-1.02	-1.57	-1.35
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform	0.0347	0.0001	0.0001	1.15	-1.4	-1.35
Zfp397	zinc finger protein 397	0.1473	0.0019	0.0018	1.25	-1.32	-1.35
Rilp1	Rab interacting lysosomal protein-like 1	0.1221	0.0001	0.0002	1.11	-1.4	-1.35
1110003008Rk	RIKEN cDNA 1110003008 gene	0.2747	0.0002	0.0052	1.06	-1.63	-1.35
Elf3c	eukaryotic translation initiation factor 3, subunit C	0.2880	0.0000	0.0004	1.06	-1.59	-1.35

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	0.8459	0.0001	0.0034	1.02	-1.54	-1.35
1110014N23Rik	RIKEN cDNA 1110014N23 gene	0.2968	0.0017	0.0079	1.13	-1.51	-1.35
Cyp2	carbamate carboxylesterase 2	0.2976	0.0005	0.0032	-1.07	-1.52	-1.35
Abhd14a	abhydrolase domain containing 14A	0.4237	0.0076	0.0047	1.07	-1.31	-1.35
4632411B12Rik	RIKEN cDNA 4632411B12 gene	0.1142	0.0005	0.0031	1.11	-1.48	-1.36
Senp3	SUMO/sentrin specific peptidase 3	0.9005	0.0007	0.0021	-1.01	-1.41	-1.36
Tcea3	transcription elongation factor A (SII), 3	0.0662	0.0009	0.0032	1.22	-1.48	-1.36
Ube2r1	ubiquitin-conjugating enzyme E2 variant 1	0.3553	0.0010	0.0035	1.04	-1.36	-1.36
Tacc2	transforming, acidic coiled-coil containing protein 2	0.1244	0.0002	0.0021	1.13	-1.5	-1.36
Daxx	Fas death domain-associated protein	0.2477	0.0004	0.0003	1.12	-1.47	-1.36
Slc41a3	solute carrier family 41, member 3	0.1202	0.0001	0.0001	-1.09	-1.44	-1.36
Znrf12-ps	zinc finger, HIT domain containing 2, pseudogene	0.0476	0.0017	0.0059	-1.2	-1.47	-1.36
Hdcf1	host cell factor C1	0.8192	0.0000	0.0035	1.01	-1.72	-1.36
Rab6	RAB6, member RAS oncogene family	0.3761	0.0000	0.0001	1.03	-1.6	-1.36
Mef2d	myocyte enhancer factor 2D	0.0689	0.0000	0.0018	1.09	-1.76	-1.36
Ankrd13c	ankyrin repeat domain 13c	0.6761	0.0000	0.0001	1.02	-1.62	-1.36
Smad1	MAD homolog 1 (Drosophila)	0.0326	0.0005	0.0020	-1.2	-1.48	-1.36
Sp2	Sp2 transcription factor	0.7253	0.0028	0.0004	-1.04	-1.6	-1.36
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate bind	0.3579	0.0021	0.0005	-1.05	-1.3	-1.36
Tmcc3	transmembrane and coiled coil domains 3	0.3128	0.0000	0.0025	1.07	-1.68	-1.37
Ubxn1	UBX domain protein 1	0.0804	0.0029	0.0004	1.09	-1.36	-1.37
Onaib2	DnaJ (Hsp40) homolog, subfamily B, member 2	0.3602	0.0002	0.0029	1.05	-1.47	-1.37
Timm17b	translocase of inner mitochondrial membrane 17b	0.2893	0.0003	0.0011	1.04	-1.29	-1.37
Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	0.0579	0.0000	0.0014	1.09	-1.62	-1.37
Gcc1	golgi coiled coil 1	0.0972	0.0011	0.0028	-1.11	-1.39	-1.37
Eif3b	eukaryotic translation initiation factor 3, subunit B	0.1757	0.0012	0.0001	1.09	-1.44	-1.37
Timp2	tissue inhibitor of metalloproteinase 2	0.5028	0.0024	0.0057	-1.07	-1.44	-1.37
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	0.7635	0.0000	0.0014	-1.02	-1.37	-1.37
Gse1	genetic suppressor element 1	0.5737	0.0002	0.0094	1.04	-1.57	-1.37
Tpm2	tropomyosin 2, beta	0.7168	0.0002	0.0003	1.04	-1.42	-1.37
Islr	immunoglobulin superfamily containing leucine-rich repeat	0.8111	0.0000	0.0002	1.02	-1.55	-1.37
Piknd1	plexin D1	0.2552	0.0006	0.0086	-1.13	-1.5	-1.37
Smnbl2	smnblin-like 2	0.8445	0.0008	0.0009	-1.01	-1.31	-1.37
Nprl3	nitrogen permease regulator-like 3 (S. cerevisiae)	0.0482	0.0001	0.0001	1.11	-1.57	-1.38
Snx15	sorting nexin 15	0.8924	0.0013	0.0032	-1.01	-1.42	-1.38
Ivd	isovaleryl coenzyme A dehydrogenase	0.0320	0.0004	0.0013	-1.22	-1.43	-1.38
Mpsr15	mitochondrial ribosomal protein S15	0.4371	0.0076	0.0003	1.06	-1.27	-1.38
Argp1	arginine and proline rich protein 1	0.0717	0.0017	0.0002	1.37	-1.36	-1.38
Mill6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated	0.4312	0.0000	0.0007	-1.06	-1.5	-1.38
Pkag3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	0.7017	0.0005	0.0030	1.06	-1.66	-1.38
Camk1	calcium/calmodulin-dependent protein kinase I	0.6106	0.0009	0.0025	-1.04	-1.54	-1.38
Fam63a	family with sequence similarity 63, member A	0.6109	0.0008	0.0052	1.04	-1.54	-1.38
Erl3	exoribinase 3	0.0546	0.0005	0.0038	1.13	-1.39	-1.38
Pikfb4	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	0.4767	0.0003	0.0006	1.06	-1.53	-1.38
Aab2	ankyrin repeat and SOCS box-containing 2	0.4508	0.0098	0.0082	1.07	-1.44	-1.38
Claa	clathrin, light polypeptide (Lca)	0.8741	0.0035	0.0020	1.02	-1.4	-1.38
2210411K11Rik	RIKEN cDNA 2210411K11 gene	0.3990	0.0059	0.0051	-1.11	-1.41	-1.38
Gd1	guanine diphosphate (GDP) dissociation inhibitor 1	0.1101	0.0008	0.0010	1.06	-1.26	-1.38
Scamp2	secretory carrier membrane protein 2	0.2403	0.0004	0.0009	1.08	-1.54	-1.38
Tjp1	tight junction associated protein 1	0.0559	0.0000	0.0000	1.21	-1.63	-1.38
Gli2	general transcription factor II	0.2645	0.0000	0.0004	-1.06	-1.48	-1.38
Setd1b	SET domain containing 1B	0.2640	0.0002	0.0030	-1.12	-1.58	-1.38
Bcd1	bicentration of chromosomes in cell division 1	0.1894	0.0000	0.0003	1.06	-1.53	-1.38
Zcchc11	zinc finger, CCHC domain containing 11	0.1296	0.0002	0.0003	1.09	-1.48	-1.39
Rab3gap1	RAB3 GTPase activating protein subunit 1	0.2940	0.0007	0.0005	-1.08	-1.34	-1.39
Bin1	bridging integrator 1	0.2395	0.0013	0.0026	-1.08	-1.42	-1.39
Kctd10	potassium channel tetramerization domain containing 10	0.2161	0.0036	0.0052	1.09	-1.39	-1.39
Cybb3	cytochrome b5 reductase 3	0.3672	0.0012	0.0088	1.06	-1.51	-1.39
Yrdc	yrdc domain containing (E.coli)	0.6979	0.0007	0.0037	-1.03	-1.38	-1.39
Atp6v0e2	ATPase, H+ transporting, lysosomal V0 subunit E2	0.4337	0.0002	0.0007	-1.03	-1.33	-1.39
Slc43a2	solute carrier family 43, member 2	0.8609	0.0003	0.0008	1.02	-1.67	-1.39
Zfp574	zinc finger protein 574	0.9982	0.0028	0.0083	1	-1.41	-1.39
Ubxn2a	UBX domain protein 2A	0.8859	0.0003	0.0011	-1.01	-1.33	-1.39
Icm1	isoprenylcysteine carboxyl methyltransferase	0.2429	0.0003	0.0056	1.11	-1.61	-1.39
Ube2h	ubiquitin-conjugating enzyme E2H	0.8883	0.0000	0.0030	-1.01	-1.7	-1.39
Gkap1	G kinase anchoring protein 1	0.3400	0.0005	0.0050	-1.05	-1.47	-1.39
Fam76a	family with sequence similarity 76, member A	0.1934	0.0006	0.0001	-1.04	-1.4	-1.39
Axm11	axmin 7-like 1	0.4317	0.0012	0.0097	-1.06	-1.61	-1.39
Ehd4	EH-domain containing 4	0.3757	0.0001	0.0005	1.06	-1.68	-1.4
Smg5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	0.3889	0.0017	0.0006	1.03	-1.54	-1.4
Mmp2	matrix metalloproteinase 2	0.6651	0.0003	0.0014	-1.06	-1.39	-1.4
Ona27	DnaJ (Hsp40) homolog, subfamily C, member 27	0.5827	0.0000	0.0075	1.03	-2.09	-1.4
Zcchc24	zinc finger, CCHC domain containing 24	0.8236	0.0000	0.0000	1.04	-1.42	-1.4
Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	0.0785	0.0000	0.0006	-1.12	-1.65	-1.4
Ak1	adenylate kinase 1	0.1557	0.0003	0.0028	1.1	-1.59	-1.4
Zbtb20	zinc finger and BTB domain containing 20	0.4835	0.0003	0.0024	-1.04	-1.62	-1.4
Lmf1	lipase maturation factor 1	0.1819	0.0044	0.0012	1.23	-1.52	-1.4
Psp115a	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0.1144	0.0008	0.0010	1.11	-1.34	-1.4
D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	0.7122	0.0021	0.0006	1.02	-1.25	-1.4
Eprs	glutamyl-prolyl-tRNA synthetase	0.2835	0.0001	0.0043	-1.08	-1.71	-1.4
Tsn	translin	0.0485	0.0014	0.0046	1.26	-1.62	-1.41
4-Sep	Septin 4	0.2034	0.0000	0.0051	-1.1	-1.75	-1.41
Pk4a	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	0.8386	0.0008	0.0032	-1.04	-1.53	-1.41
Cank1g2	casein kinase 1, gamma 2	0.3597	0.0000	0.0003	1.05	-1.61	-1.41
Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	0.0678	0.0038	0.0013	1.15	-1.41	-1.41
Bag3	BCL2-associated athanogene 3	0.9454	0.0000	0.0000	-1	-1.57	-1.41
Atp13a2	ATPase type 13A2	0.9799	0.0011	0.0010	1	-1.46	-1.41
Spn1	spnifer homolog 1 (Drosophila)	0.7406	0.0003	0.0007	-1.03	-1.61	-1.41
Dennd4b	DENN/MAD0 domain containing 4B	0.1936	0.0000	0.0029	1.07	-1.68	-1.41
Letm1	leucine zipper-EF-hand containing transmembrane protein 1	0.5259	0.0014	0.0032	1.05	-1.55	-1.41
Acsm1	acyl-CoA synthetase short-chain family member 1	0.3235	0.0070	0.0072	1.16	-1.62	-1.41
Cdc25a	cell division cycle 25 homolog A (S. pombe)	0.2518	0.0062	0.0037	-1.22	-1.35	-1.41
Pclt1	pellonin 1	0.0496	0.0000	0.0002	1.06	-1.56	-1.41
Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	0.0485	0.0012	0.0007	1.16	-1.39	-1.41
Tgfb3	transforming growth factor, beta 3	0.2447	0.0001	0.0038	1.07	-1.62	-1.41
Jun	Jun oncogene	0.4898	0.0006	0.0027	1.08	-1.47	-1.41
Cc2d2a	coiled-coil and C2 domain containing 2A	0.0485	0.0050	0.0021	-1.27	-1.59	-1.41
Nuclm1	nuclear mitotic apparatus protein 1	0.0476	0.0009	0.0082	-1.19	-1.54	-1.41
C85492	expressed sequence C85492	0.5991	0.0083	0.0039	1.05	-1.36	-1.42
Cbx5	chromobox homolog 5 (Drosophila HP1a)	0.7444	0.0011	0.0066	1.02	-1.54	-1.42
Mlec	malectin	0.8165	0.0000	0.0015	-1.02	-1.57	-1.42
Ogfr1	opioid growth factor receptor-like 1	0.7883	0.0008	0.0012	1.02	-1.47	-1.42
Fam36a	family with sequence similarity 36, member A	0.4867	0.0038	0.0028	-1.06	-1.39	-1.42
Ncdn	neurochondrin	0.7012	0.0018	0.0097	1.05	-1.68	-1.42
Tbc1d10b	TBC1 domain family, member 10b	0.4533	0.0001	0.0010	1.04	-1.76	-1.42
Arfgap1	ADP-ribosylation factor GTPase activating protein 1	0.3794	0.0047	0.0069	-1.1	-1.46	-1.42
Npr2	natruric peptide receptor 2	0.3778	0.0000	0.0006	1.06	-1.94	-1.42
Herpud2	HERPUD family member 2	0.4708	0.0001	0.0018	1.09	-1.53	-1.42
Srsf4	serine/arginine-rich splicing factor 4	0.0203	0.0000	0.0000	-1.14	-1.47	-1.42
Aamp	angio-associated migratory protein	0.1638	0.0001	0.0000	1.05	-1.34	-1.42
Polg	polymerase (DNA directed), gamma	0.0149	0.0000	0.0005	1.21	-1.63	-1.43
Alpk3	alpha-kinase 3	0.3484	0.0000	0.0027	1.06	-1.94	-1.43
Tmem107	transmembrane protein 107	0.8077	0.0001	0.0009	1.06	-1.32	-1.43
Tmem131	transmembrane protein 131	0.9464	0.0000	0.0001	1	-1.59	-1.43
Kdm4a	lysine (K)-specific demethylase 4A	0.8388	0.0086	0.0009	-1.02	-1.39	-1.43
Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	0.5991	0.0000	0.0030	1.04	-1.8	-1.43
Scrbp	scribbled homolog (Drosophila)	0.8794	0.0002	0.0045	-1.02	-1.8	-1.43
Exocb6	exocyst complex component B6	0.8310	0.0046	0.0022	1.04	-1.56	-1.43
Puf60	poly-U binding splicing factor 60	0.2424	0.0000	0.0000	1.04	-1.65	-1.43
Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	0.5400	0.0000	0.0020	1.03	-1.89	-1.43
Amot1	angiomotin-like 1	0.1923	0.0000	0.0075	-1.08	-1.7	-1.43
Unk	unlabeled homolog (Drosophila)	0.7159	0.0019	0.0061	-1.03	-2.01	-1.43
Gfrc2	general transcription factor IIC, polypeptide 2, beta	0.2652	0.0002	0.0027	1.07	-1.67	-1.43
Dnajc30	DnaJ (Hsp40) homolog, subfamily C, member 30	0.0630	0.0001	0.0000	-1.07	-1.57	-1.43
Rab35	RAB35, member RAS oncogene family	0.1340	0.0021	0.0009	-1.1	-1.55	-1.43
Ascc1	activating signal cointegrator 1 complex subunit 1	0.2440	0.0001	0.0063	1.08	-1.64	-1.43
Atp13a1	ATPase type 13A1	0.9297	0.0003	0.0005	1.01	-1.5	-1.43
Psp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	0.0741	0.0001	0.0002	1.1	-1.53	-1.44
Prex1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	0.3556	0.0001	0.0063	-1.16	-1.87	-1.44
Ppm1j	protein phosphatase 1J	0.0164	0.0001	0.0002	1.15	-1.57	-1.44
1700008J07Rik	RIKEN cDNA 1700008J07 gene	0.2271	0.0000	0.0004	1.09	-1.81	-1.44
Mlycd	malonyl-CoA decarboxylase	0.7033	0.0027	0.0003	1.04	-1.39	-1.44
Rais	X-rel reticulendotheliosis viral oncogene homolog A (avian)	0.4461	0.0001	0.0012	-1.05	-1.78	-1.44

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Shisa2	shisa homolog 2 (Xenopus laevis)	0.3447	0.0001	0.0010	1.05	-1.54	-1.44
Rcsd1	RCS domain containing 1	0.6295	0.0003	0.0012	1.04	-1.62	-1.44
Tub52c	tubulin beta 2C	0.2454	0.0014	0.0042	1.15	-1.57	-1.44
Lztr1	leucine zipper-like transcriptional regulator, 1	0.1578	0.0098	0.0033	1.2	-1.31	-1.44
Stab1	stabilin 1	0.3220	0.0004	0.0066	-1.19	-1.35	-1.44
Ccdc136	coiled-coil domain containing 136	0.0991	0.0036	0.0009	1.13	-1.27	-1.44
Slc44a2	solute carrier family 44, member 2	0.1139	0.0000	0.0012	-1.09	-1.68	-1.44
Ccdc172	coiled-coil domain containing 172	0.0010	0.0022	0.0004	-1.15	-1.3	-1.44
Txndc17	thioredoxin domain containing 17	0.9777	0.0001	0.0002	1	-1.26	-1.44
Traf3	TNF receptor-associated factor 3	0.3756	0.0000	0.0010	-1.06	-1.68	-1.44
Psm3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	0.8503	0.0000	0.0007	-1.01	-1.62	-1.44
Sdr39a1	short chain dehydrogenase/reductase family 39A, member 1	0.0745	0.0016	0.0017	1.14	-1.47	-1.44
Khgap17	Rho GTPase activating protein 17	0.8795	0.0008	0.0005	-1.02	-1.49	-1.44
Nt5m	5'-3'-nucleotidase, mitochondrial	0.7078	0.0055	0.0048	-1.03	-1.41	-1.45
Fam189a2	family with sequence similarity 189, member A2	0.3091	0.0004	0.0035	1.07	-1.51	-1.45
Pcnx3	pecanex-like 3 (Drosophila)	0.4598	0.0000	0.0012	1.04	-1.57	-1.45
Pasp	prospasin	0.1987	0.0000	0.0000	-1.04	-1.51	-1.45
Xpc8	exportin 8	0.2686	0.0001	0.0086	1.1	-1.72	-1.45
Sash1	SAM and SH3 domain containing 1	0.4784	0.0014	0.0016	-1.1	-1.47	-1.45
Glt25d1	glycosyltransferase 25 domain containing 1	0.6117	0.0004	0.0027	1.04	-1.73	-1.45
Mosc2	MOCO sulphurase C-terminal domain containing 2	0.7971	0.0083	0.0014	-1.01	-1.37	-1.45
Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	0.9630	0.0044	0.0026	-1.01	-1.48	-1.45
Mvp	major vault protein	0.1184	0.0010	0.0001	1.14	-1.5	-1.45
Ncl6	nucleolar protein family 6 (RNA-associated)	0.9691	0.0002	0.0086	1.01	-1.79	-1.45
Cry2	cryptochrome 2 (photolyase-like)	0.6184	0.0049	0.0030	1.07	-1.5	-1.45
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0.0892	0.0008	0.0002	-1.19	-1.47	-1.45
2400001E08Rik	RIKEN cDNA 2400001E08 gene	0.7462	0.0001	0.0026	-1.04	-1.56	-1.45
Col6a1	collagen type VI, alpha 1	0.8705	0.0006	0.0030	-1.02	-1.45	-1.45
Pcbp1	poly(RC) binding protein 1	0.3762	0.0000	0.0000	1.05	-1.44	-1.45
Myrn	myopalladin	0.2184	0.0001	0.0016	1.07	-1.61	-1.45
Ipk61	inositol hexaphosphate kinase 1	0.3949	0.0000	0.0078	-1.08	-1.7	-1.45
Adnrk1	adrenergic receptor kinase, beta 1	0.9336	0.0017	0.0015	1.01	-1.6	-1.46
Ac3b8	acyl-CoA oxidase 3 binding domain containing 5	0.3094	0.0001	0.0001	-1.08	-1.55	-1.46
Dist	dihydropyrimidine S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.1647	0.0000	0.0003	1.09	-1.7	-1.46
Ralb1	ralA binding protein 1	0.7748	0.0001	0.0008	1.02	-1.56	-1.46
Eef2	eukaryotic translation elongation factor 2	0.0682	0.0000	0.0002	1.12	-1.64	-1.46
Slc2a8	solute carrier family 2, (facilitated glucose transporter), member 8	0.7490	0.0003	0.0017	-1.03	-1.75	-1.46
Cry2	cryptochrome 2	0.1175	0.0002	0.0009	1.08	-1.36	-1.46
Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0.0971	0.0003	0.0010	1.14	-1.59	-1.46
Btrc	beta-transducin repeat containing protein	0.6812	0.0061	0.0045	1.05	-1.59	-1.46
Top1	topoisomerase (DNA) I	0.0816	0.0008	0.0012	-1.16	-1.49	-1.46
Ccdc88c	coiled-coil domain containing 88C	0.6215	0.0001	0.0027	-1.04	-1.66	-1.46
Rapsn	receptor-associated protein of the synapse	0.2336	0.0016	0.0089	1.12	-1.56	-1.46
Ctsd	cathepsin D	0.1032	0.0000	0.0000	-1.08	-1.53	-1.46
Lrp10	low-density lipoprotein receptor-related protein 10	0.1968	0.0001	0.0003	1.07	-1.65	-1.46
Flywh1	FLYWH-type zinc finger 1	0.7409	0.0000	0.0000	1.02	-1.59	-1.47
Gm10397	predicted gene 10397	0.1010	0.0000	0.0002	1.04	-1.57	-1.47
Klhl22	kelch-like 22 (Drosophila)	0.1195	0.0006	0.0005	-1.11	-1.44	-1.47
Sec61a1	SecE1 alpha 1 subunit (S. cerevisiae)	0.6936	0.0037	0.0043	-1.04	-1.62	-1.47
Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	0.3272	0.0002	0.0019	1.09	-1.54	-1.47
Spnb1	spectrin beta 1	0.1728	0.0000	0.0023	1.17	-1.75	-1.47
Ubxn6	UBX domain protein 6	0.9832	0.0013	0.0067	1	-1.7	-1.47
Map2k3	mitogen-activated protein kinase kinase 3	0.3273	0.0002	0.0006	1.06	-1.54	-1.47
Fam63b	family with sequence similarity 63, member B	0.0430	0.0013	0.0012	1.11	-1.31	-1.47
Zfp524	zinc finger protein 524	0.3428	0.0063	0.0042	1.07	-1.46	-1.47
Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	0.5622	0.0014	0.0012	-1.05	-1.48	-1.47
Tctb7	tetratricopeptide repeat domain 7B	0.0648	0.0001	0.0023	1.14	-1.96	-1.47
1600014C10Rik	RIKEN cDNA 1600014C10 gene	0.4343	0.0001	0.0002	1.07	-1.46	-1.47
1110038D17Rik	RIKEN cDNA 1110038D17 gene	0.5649	0.0000	0.0006	1.05	-1.62	-1.47
Plekha3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	0.1906	0.0003	0.0041	-1.16	-1.72	-1.47
Angel2	angel homolog 2 (Drosophila)	0.9255	0.0032	0.0011	-1.01	-1.37	-1.48
Adrm1	adhesion regulating molecule 1	0.5509	0.0000	0.0000	1.03	-1.68	-1.48
Corasp2	coral reassembly stacking protein 2	0.2513	0.0001	0.0001	1.03	-1.48	-1.48
Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.0600	0.0005	0.0008	1.16	-1.48	-1.48
Nrx1	NLR family member X1	0.4940	0.0001	0.0004	-1.07	-1.7	-1.48
6430571L13Rik	RIKEN cDNA 6430571L13 gene	0.1562	0.0009	0.0095	1.16	-1.58	-1.48
Pp5c6	protein phosphatase 5, catalytic subunit	0.0198	0.0005	0.0002	1.22	-1.55	-1.48
Zfp524	zinc finger RNA binding protein 524	0.7221	0.0001	0.0001	1.04	-1.54	-1.48
Rras	Harvey rat sarcoma oncogene, subgroup R	0.5891	0.0003	0.0002	-1.03	-1.54	-1.48
Robo4	roundabout homolog 4 (Drosophila)	0.2324	0.0056	0.0049	1.13	-1.44	-1.48
Rnf220	ring finger protein 220	0.0210	0.0027	0.0013	1.23	-1.6	-1.49
Thap11	THAP domain containing 11	0.2179	0.0010	0.0045	1.1	-1.6	-1.49
Sec18a	SEC16 homolog A (S. cerevisiae)	0.3541	0.0001	0.0002	1.04	-1.55	-1.49
Tip53np2	transformation related protein 53 inducible nuclear protein 2	0.1343	0.0000	0.0019	1.07	-1.84	-1.49
Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	0.9970	0.0010	0.0004	1	-1.5	-1.49
Rtkn	rhotein	0.4781	0.0007	0.0077	1.06	-1.54	-1.49
Daglb	diacylglycerol lipase, beta	0.1857	0.0061	0.0031	1.13	-1.39	-1.49
Nosp1	nitric oxide synthase interacting protein	0.9724	0.0003	0.0001	1	-1.4	-1.49
Dut	deoxyuridine triphosphatase	0.5115	0.0020	0.0015	-1.09	-1.58	-1.49
Cog5	coenzyme Q5 homolog, methyltransferase (yeast)	0.3790	0.0015	0.0003	-1.05	-1.46	-1.49
Gpr146	G protein-coupled receptor 146	0.3335	0.0011	0.0010	1.08	-1.64	-1.49
Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	0.8655	0.0006	0.0027	1.02	-1.76	-1.49
Pla2g6	phospholipase A2, group 6	0.0449	0.0003	0.0037	1.17	-1.79	-1.49
Smurf1	SMAD specific E3 ubiquitin protein ligase 1	0.0301	0.0045	0.0084	-1.25	-1.33	-1.49
Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	0.0525	0.0074	0.0010	-1.25	-1.63	-1.5
Sid2	SID1 transmembrane family, member 2	0.5174	0.0000	0.0000	-1.03	-1.57	-1.5
Slc38a3	solute carrier family 38, member 3	0.5083	0.0006	0.0024	1.11	-1.81	-1.5
Sec31a	SEC31 homolog A (S. cerevisiae)	0.7917	0.0004	0.0004	1.02	-1.57	-1.5
Ubr4	ubiquitin protein ligase E3 component n-recogin 4	0.1148	0.0049	0.0006	-1.12	-1.57	-1.5
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.2040	0.0000	0.0001	1.11	-1.58	-1.5
Hspb1	heat shock protein 1	0.2928	0.0009	0.0000	1.1	-1.53	-1.5
Tps2	protein-tyrosine sulfotransferase 2	0.2636	0.0007	0.0003	-1.07	-1.42	-1.5
1700021K19Rik	RIKEN cDNA 1700021K19 gene	0.8002	0.0001	0.0002	1.05	-1.5	-1.5
Carns1	carbamoyl synthase 1	0.4994	0.0046	0.0006	1.03	-1.49	-1.5
Akr7a5	aldo-keto reductase family 7, member A5 (afatoxin aldehyde reductase)	0.4066	0.0000	0.0002	1.05	-1.7	-1.5
Nes	nestin	0.7553	0.0006	0.0081	-1.04	-1.44	-1.5
Srsf12p1	serine/arginine-rich splicing factor 12, interacting protein 1	0.3301	0.0002	0.0007	-1.07	-1.52	-1.5
Sreb2	sterol regulatory element binding factor 2	0.8224	0.0007	0.0051	1.03	-1.68	-1.5
Osr	amplified in osteosarcoma	0.2640	0.0048	0.0015	-1.12	-1.39	-1.5
Gdps1	glycerophosphodiester phosphodiesterase domain containing 1	0.2012	0.0012	0.0039	-1.2	-1.61	-1.5
4933426M11Rik	RIKEN cDNA 4933426M11 gene	0.2314	0.0000	0.0011	1.09	-1.88	-1.5
Zfp787	zinc finger protein 787	0.2206	0.0000	0.0003	-1.07	-1.88	-1.5
Dnajc21	DNAJ (Hsp40) homolog, subfamily C, member 21	0.2702	0.0000	0.0009	1.08	-1.66	-1.5
Adcy9	adenylyl cyclase 9	0.6876	0.0000	0.0017	1.03	-2.06	-1.5
Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	0.8098	0.0000	0.0000	1.02	-1.56	-1.5
Trio	triple functional domain (PTPRF interacting)	0.1339	0.0025	0.0001	1.24	-1.36	-1.51
Lamb2	laminin, beta 2	0.8695	0.0013	0.0025	-1.01	-1.65	-1.51
P3cd1	programmed cell death 1	0.8313	0.0000	0.0015	-1.04	-1.77	-1.51
Dpf2	D4, zinc and double PHD fingers family 2	0.0590	0.0000	0.0000	-1.09	-1.7	-1.51
Plekha1	pleckstrin homology domain containing, family M (with RUN domain) member 1	0.6763	0.0030	0.0059	-1.04	-1.65	-1.51
Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	0.3869	0.0001	0.0027	1.06	-1.64	-1.51
Ccdc22	coiled-coil domain containing 22	0.5362	0.0005	0.0004	1.05	-1.68	-1.51
Upr1	UPR1 regulator of nonsense transcripts homolog (yeast)	0.3896	0.0014	0.0005	-1.11	-2.28	-1.51
Dync1h1	dynein cytoplasmic 1 heavy chain 1	0.0180	0.0001	0.0005	-1.25	-1.58	-1.51
Prkab	protein kinase, cAMP dependent, catalytic, beta	0.6835	0.0017	0.0062	-1.03	-1.49	-1.51
Cank2a2	casein kinase 2, alpha prime polypeptide	0.6661	0.0001	0.0021	1.03	-1.61	-1.51
Arhgap27	Rho GTPase activating protein 27	0.4780	0.0002	0.0084	-1.09	-1.75	-1.51
Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	0.3003	0.0005	0.0056	-1.01	-1.71	-1.51
Ube2q1	ubiquitin-conjugating enzyme E2Q (putative) 1	0.9344	0.0001	0.0019	-1.01	-1.73	-1.51
Fbxw4	F-box and WD-40 domain protein 4	0.2277	0.0002	0.0021	1.11	-1.83	-1.52
Pcbp2	poly(RC) binding protein 2	0.1528	0.0000	0.0001	1.07	-1.63	-1.52
Rxb1	retinoid X receptor beta 1	0.0868	0.0004	0.0009	-1.27	-1.66	-1.52
Wnk2	WWK (lysine deficient protein kinase) family 2	0.1433	0.0001	0.0034	1.21	-1.75	-1.52
Phid3	pleckstrin homology-like domain, family A, member 3	0.4946	0.0023	0.0001	1.06	-1.53	-1.52
Stub1	STIP1 homology and U-Box containing protein 1	0.0302	0.0000	0.0000	1.09	-1.6	-1.52
Rptor	regulatory associated protein of MTOR, complex 1	0.9052	0.0000	0.0013	1.01	-1.55	-1.52
Ccdc52	coiled-coil domain containing 52	0.0127	0.0032	0.0022	-1.34	-1.46	-1.52
Pis1	Pis1 interacting zinc finger protein 1	0.3056	0.0001	0.0004	1.04	-1.64	-1.52
Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.3969	0.0000	0.0000	-1.04	-1.6	-1.52
Pgrmc2	progesterone receptor membrane component 2	0.7531	0.0027	0.0059	1.03	-1.68	-1.52
Setd5	SET domain containing 5	0.4548	0.0008	0.0085	-1.09	-1.92	-1.52
Slc41a1	solute carrier family 41, member 1	0.5970	0.0002	0.0056	-1.05	-1.95	-1.52
E230208H17Rik	RIKEN cDNA E230208H17 gene	0.1397	0.0000	0.0015	1.1	-1.54	-1.52

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Rnf216	ring finger protein 216	0.5179	0.0000	0.0000	-1.06	-2.01	-1.52
Gn11	guanine nucleotide binding protein-like 1	0.2095	0.0024	0.0024	-1.14	-1.54	-1.52
Ppil1	peptidylprolyl isomerase F (cyclophilin F)	0.7690	0.0024	0.0033	-1.03	-1.54	-1.52
Mfsd5	major facilitator superfamily domain containing 5	0.4163	0.0009	0.0015	1.06	-1.59	-1.53
Tom12	target of myb1-like 2 (chicken)	0.6832	0.0020	0.0013	1.04	-1.46	-1.53
Ralgds	ral guanine nucleotide dissociation stimulator	0.2556	0.0031	0.0086	-1.14	-1.8	-1.53
Smnrc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c	0.6787	0.0028	0.0016	1.04	-1.48	-1.53
Hef1	heparin-binding epGF related with YPRW motif-like	0.016	0.0003	0.0004	1.91	-1.21	-1.53
ST3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	0.4590	0.0084	0.0088	1.1	-1.53	-1.53
DnaJ5	DnaJ (Hsp40) homolog, subfamily B, member 5	0.4832	0.0039	0.0062	-1.09	-1.64	-1.53
2510006D16Rik	RIKEN cDNA 2510006D16 gene	0.1140	0.0002	0.0003	1.12	-1.65	-1.53
Mamstr	MEF2 activating motif and SAP domain containing transcriptional regulator	0.0385	0.0011	0.0002	1.24	-1.51	-1.53
Axcas3	ATP-binding cassette, sub-family A (ABC1), member 3	0.0890	0.0012	0.0038	1.35	-2.25	-1.53
Plekhh3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	0.8369	0.0012	0.0047	-1.02	-1.69	-1.53
Grif1	glucocorticoid receptor DNA binding factor 1	0.3041	0.0001	0.0081	1.1	-2.03	-1.53
Mxra7	matrix-remodelling associated 7	0.1323	0.0002	0.0099	-1.16	-1.61	-1.53
Ccdc85b	coiled-coil domain containing 85b	0.7079	0.0004	0.0040	-1.04	-1.7	-1.53
Spta	small glutamine-rich tetrapeptide repeat (TPR)-containing, alpha	0.0469	0.0016	0.0007	1.15	-1.51	-1.53
ORF19	open reading frame 19	0.2498	0.0000	0.0003	1.05	-1.59	-1.53
Tgfbp1	transforming growth factor, beta receptor associated protein 1	0.4832	0.0000	0.0011	1.07	-1.97	-1.54
Rvra	retinoid X receptor alpha	0.2938	0.0000	0.0031	1.08	-1.92	-1.54
Cksr1	connector enhancer of kinase suppressor of Ras 1	0.1606	0.0029	0.0084	1.17	-1.76	-1.54
Pum1	pumilio 1 (Drosophila)	0.0896	0.0006	0.0001	-1.14	-1.54	-1.54
Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	0.9667	0.0000	0.0001	1	-1.74	-1.54
Zfp213	zinc finger protein 213	0.2355	0.0010	0.0014	-1.09	-2.13	-1.54
Mon1a	MON1 homolog A (yeast)	0.3959	0.0010	0.0022	-1.07	-1.81	-1.54
Cttnbp2nl	CTNBP2 N-terminal like	0.4233	0.0050	0.0016	1.07	-1.54	-1.54
Taf6	TAF8 (polymerase II, TATA box binding protein (TBP)-associated factor	0.0375	0.0042	0.0034	-1.04	-1.54	-1.54
Ankrd13a	ankyrin repeat domain 13a	0.3275	0.0042	0.0080	1.11	-1.55	-1.54
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	0.4112	0.0000	0.0000	1.03	-1.69	-1.54
Pknox2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.9765	0.0002	0.0014	-1	-1.69	-1.55
Nbph1	nephronophthisis 1 (juvenile) homolog (human)	0.2159	0.0033	0.0085	1.21	-1.52	-1.55
Rexn2	REX2 RNA export factor 2 (homolog (S. cerevisiae)	0.7242	0.0000	0.0003	1.01	-1.57	-1.55
Gsr	glutathione reductase	0.0130	0.0006	0.0000	-1.16	-1.54	-1.55
Pxx	PX domain containing serine/threonine kinase	0.3584	0.0006	0.0035	1.08	-1.67	-1.55
Smyd4	SET and MYND domain containing 4	0.0210	0.0037	0.0022	-1.35	-1.52	-1.55
Traf1	TRAF type zinc finger domain containing 1	0.7752	0.0003	0.0005	-1.02	-1.58	-1.55
N-acet1	N-acetylglucosamine acetylhydrolase 2	0.2207	0.0033	0.0046	-1.1	-1.29	-1.55
Casc3	cancer susceptibility candidate 3	0.8684	0.0000	0.0000	-1.01	-1.91	-1.55
Pabpc1	poly(A) binding protein, cytoplasmic	0.6639	0.0009	0.0001	1.04	-1.61	-1.55
Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	0.6764	0.0002	0.0001	1.02	-1.56	-1.55
Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	0.0860	0.0007	0.0005	-1.21	-1.57	-1.55
Soc3sta13	solute carrier family 38 (metanion transporter), member 13	0.3032	0.0042	0.0038	1.13	-1.57	-1.55
Ifi203	interferon activated gene 203	0.8655	0.0035	0.0029	-1.02	-1.51	-1.55
Mgat1	mannoside acetylglucosaminyltransferase 1	0.3603	0.0000	0.0007	1.08	-1.79	-1.55
Fkrp	fukutin related protein	0.0792	0.0000	0.0000	1.12	-1.73	-1.55
E130308A19Rik	RIKEN cDNA E130308A19 gene	0.2918	0.0028	0.0037	1.09	-1.62	-1.56
Anapc11	anaphase promoting complex subunit 11	0.8935	0.0035	0.0003	1.04	-1.68	-1.56
Cntm8	CKLF-like MARVEL transmembrane domain containing 8	0.4227	0.0013	0.0091	-1.2	-2.45	-1.56
Nat6	N-acetyltransferase 6	0.8951	0.0010	0.0009	-1.01	-1.48	-1.56
Nef	N-ethylmaleimide sensitive fusion protein	0.6343	0.0000	0.0002	-1.03	-1.69	-1.56
Lmf2	lipase maturation factor 2	0.5443	0.0003	0.0005	1.06	-1.64	-1.56
Pfr2	phosphatidylserine transferase 2	0.8894	0.0002	0.0021	1.01	-1.94	-1.56
Sys1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	0.0545	0.0001	0.0001	-1.14	-1.63	-1.56
Traab1	TraB domain containing	0.0892	0.0019	0.0043	1.18	-1.77	-1.56
Ankrd13b	ankyrin repeat domain 13b	0.3266	0.0070	0.0025	1.12	-1.54	-1.56
Dda1	DET1 and DDB1 associated 1	0.8802	0.0037	0.0028	-1.01	-1.49	-1.56
Sib1	sirtuin homolog 2 domain-containing transforming protein B	0.3405	0.0013	0.0087	-1.15	-1.67	-1.56
Smap2	stromal membrane-associated GTPase-activating protein 2	0.4258	0.0059	0.0091	-1.09	-1.59	-1.56
Axin2	axin2	0.9547	0.0002	0.0026	-1	-1.89	-1.56
Chd7	chromodomain helicase DNA binding protein 7	0.1794	0.0038	0.0013	-1.19	-1.88	-1.56
Ttp11	tufelin interacting protein 11	0.3721	0.0000	0.0000	1.03	-1.5	-1.56
Mta1	metastasis associated 1	0.8336	0.0003	0.0002	1.04	-1.52	-1.56
Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12c	0.8796	0.0011	0.0041	-1.02	-2.32	-1.56
Oplah	5-oxoprolinase (ATP-hydrolysing)	0.0416	0.0000	0.0023	-1.17	-2.02	-1.57
Eif3a	eukaryotic translation initiation factor 3, subunit A	0.0403	0.0000	0.0000	-1.08	-1.5	-1.57
Smnrc4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a	0.2207	0.0000	0.0002	1.04	-1.81	-1.57
Hmbx1	homeobox 1	0.1295	0.0002	0.0004	1.14	-1.75	-1.57
Kif21a	kinesin family member 21A	0.0215	0.0002	0.0003	-1.24	-1.66	-1.57
Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	0.4546	0.0001	0.0001	1.06	-1.73	-1.57
Pknoxh	protein kinase C substrate 80K-H	0.0972	0.0007	0.0000	1.14	-1.32	-1.57
Brp	BRCA1 associated protein	0.1956	0.0045	0.0023	1.12	-1.47	-1.57
Uaf2	upstream transcription factor 2	0.0426	0.0009	0.0002	1.14	-1.95	-1.57
Zfp142	zinc finger protein 142	0.7996	0.0017	0.0072	-1.02	-1.74	-1.57
Hpn	hepsin	0.2860	0.0012	0.0076	1.09	-2.15	-1.57
Mknk2	MAP kinase-interacting serine/threonine kinase 2	0.9668	0.0001	0.0000	1	-1.59	-1.57
Kat2a	(lysine) acetyltransferase 2A	0.9294	0.0000	0.0004	-1	-1.62	-1.57
Hmg206	high mobility group 201	0.1396	0.0023	0.0003	1.16	-1.68	-1.57
Mapkap5	MAP kinase-activated protein kinase 5	0.7598	0.0000	0.0002	1.01	-1.8	-1.57
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0.7538	0.0002	0.0018	-1.02	-1.84	-1.57
Mapkbp1	mitogen-activated protein kinase binding protein 1	0.4872	0.0002	0.0026	-1.06	-2.05	-1.58
Hap4	hyaluronate acid binding protein 4	0.2434	0.0001	0.0002	1.1	-1.99	-1.58
Atp2a	ATP2C autophagy related 2 homolog A (S. cerevisiae)	0.2217	0.0011	0.0005	1.14	-1.87	-1.58
Bcas3	breast carcinoma amplified sequence 3	0.4057	0.0000	0.0001	1.04	-2.21	-1.58
Capns1	calpain, small subunit 1	0.8487	0.0000	0.0000	-1.01	-1.74	-1.58
Gata2b	GATA zinc finger domain containing 2b	0.6253	0.0000	0.0053	1.04	-1.87	-1.58
Phf1	PHD finger protein 1	0.0939	0.0005	0.0046	1.14	-1.74	-1.58
Vdsu21	WD repeat, S441 and U-box domain containing 1	0.1967	0.0003	0.0001	1.09	-1.54	-1.58
Sic45a4	solute carrier family 45, member 4	0.9920	0.0000	0.0003	1	-1.85	-1.58
Anxa6	annexin A6	0.8030	0.0002	0.0020	-1.02	-1.73	-1.58
Ypel3	yyppee-like 3 (Drosophila)	0.8240	0.0036	0.0038	1.03	-1.59	-1.58
Orp2	developmentally regulated GTP binding protein 2	0.8525	0.0022	0.0057	-1.03	-1.93	-1.58
Ubp1	upregulator of cell proliferation	0.8013	0.0002	0.0004	1.05	-1.54	-1.58
Rgmb	RCM domain family, member B	0.1576	0.0000	0.0000	1.14	-1.98	-1.58
Mapk3	mitogen-activated protein kinase 3	0.4248	0.0009	0.0016	1.07	-1.77	-1.58
Pygo2	pygopus 2	0.5069	0.0005	0.0009	-1.06	-1.78	-1.58
Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	0.1174	0.0004	0.0008	1.16	-1.6	-1.6
Krtge7f	keratinocyte growth factor exchange factor (GEF7)	0.1365	0.0000	0.0004	1.09	-2.07	-1.6
Zfp768	zinc finger protein 768	0.0914	0.0000	0.0000	1.12	-1.61	-1.6
Klc4	kinesin light chain 4	0.3569	0.0007	0.0046	-1.09	-1.74	-1.6
Dax54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	0.8037	0.0000	0.0011	-1.02	-2	-1.6
0610040J01Rik	RIKEN cDNA 0610040J01 gene	0.6979	0.0006	0.0082	1.04	-1.86	-1.6
Ushap1	usher syndrome 1C binding protein 1	0.7780	0.0000	0.0089	-1.03	-1.95	-1.6
Tbc1d2b	TBC1 domain family, member 2b	0.6774	0.0013	0.0023	-1.06	-1.81	-1.6
St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylglucosaminide alpha-2	0.8838	0.0047	0.0044	1.02	-1.49	-1.6
Vamp1	vesicle-associated membrane protein 1	0.5215	0.0030	0.0046	1.07	-1.61	-1.6
Pap16	poly (ADP-ribose) polymerase family, member 16	0.0387	0.0066	0.0072	-1.33	-1.7	-1.6
Ipo13	importin 13	0.0764	0.0000	0.0002	1.12	-1.89	-1.6
Snta1	syntrophin, acidic 1	0.0270	0.0000	0.0001	1.17	-1.73	-1.6
Nr2f6	nuclear receptor subfamily 2, group F, member 6	0.5532	0.0002	0.0034	-1.06	-2.19	-1.6
Phc2	polyhomeotic-like 2 (Drosophila)	0.7460	0.0001	0.0016	1.03	-1.86	-1.6
Hsf1	heat shock factor 1	0.0228	0.0007	0.0000	1.14	-1.55	-1.6
Khlh17	ketch-like 17 (Drosophila)	0.2965	0.0011	0.0082	-1.13	-1.6	-1.6
Pncr1	proline-rich nuclear receptor coactivator 1	0.1895	0.0004	0.0003	1.18	-1.53	-1.6
Limd1	LIM domains containing 1	0.6786	0.0003	0.0015	1.03	-1.96	-1.6
Wbp1	WW domain binding protein 1	0.6617	0.0000	0.0008	1.03	-1.98	-1.61
Bcl2l13	BCL2-like 13 (apoptosis facilitator)	0.4800	0.0001	0.0001	-1.05	-1.86	-1.61
Rab11b	RAB11B, member RAS oncogene family	0.1096	0.0000	0.0000	-1.07	-1.61	-1.61
Esrra	estrogen related receptor, alpha	0.5546	0.0001	0.0002	1.04	-1.51	-1.61
Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	0.0113	0.0001	0.0004	1.24	-1.62	-1.61
Supf6h	suppressor of Ty 6 homolog (S. cerevisiae)	0.1316	0.0000	0.0000	1.14	-1.88	-1.61
Sf3b2	splicing factor 3b, subunit 2	0.3820	0.0008	0.0009	1.08	-1.76	-1.61
Nbsc23	S-nucleoside domain containing 3	0.2225	0.0006	0.0085	1.1	-2.02	-1.61
Eif1b	eukaryotic translation initiation factor 1b	0.0534	0.0000	0.0000	1.09	-1.58	-1.61
2310003H01Rik	RIKEN cDNA 2310003H01 gene	0.5057	0.0000	0.0000	-1.08	-1.82	-1.61
Repin1	replication initiator 1	0.0152	0.0000	0.0000	-1.15	-1.94	-1.61
Ube2o	ubiquitin-conjugating enzyme E2O	0.2398	0.0000	0.0016	1.08	-1.97	-1.61
Nhl1	myeloid/lymphoid mixed-lineage leukemia 1	0.2432	0.0000	0.0023	1.1	-1.95	-1.61
Tbc1d9b	TBC1 domain family, member 9b	0.3727	0.0002	0.0012	-1.08	-1.76	-1.61
Socs7	suppressor of cytokine signaling 7	0.2930	0.0005	0.0048	-1.12	-1.91	-1.61
Sipa1	signal-induced proliferation associated gene 1	0.0261	0.0004	0.0078	-1.32	-1.98	-1.61
Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	0.3401	0.0007	0.0009	-1.08	-1.53	-1.61
Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	0.1495	0.0000	0.0000	1.08	-1.74	-1.62

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Gas6	growth arrest specific 6	0.5121	0.0000	0.0007	1.02	-1.81	-1.62
Epb4.1	erythrocyte protein band 4.1	0.3595	0.0008	0.0003	1.06	-1.54	-1.62
Coro1	coronin 1	0.0891	0.0015	0.0008	1.23	-1.5	-1.62
Actr1b	ARP1 actin-related protein 1 homolog B, centractin (yeast)	0.1654	0.0000	0.0018	1.12	-2.18	-1.62
Igfbp3	insulin-like growth factor binding protein 3	0.2848	0.0069	0.0066	1.16	-1.61	-1.62
Mel1	male-specific lethal 1 homolog (Drosophila)	0.0764	0.0010	0.0038	1.21	-1.81	-1.62
Epn2	epsin 2	0.8692	0.0000	0.0005	1.01	-2.03	-1.62
Rgs2	rat guanine nucleotide dissociation stimulator-like 2	0.1937	0.0000	0.0000	1.06	-1.76	-1.62
Gna12	guanine nucleotide binding protein, alpha 12	0.2123	0.0011	0.0002	-1.17	-1.75	-1.62
Adprh	ADP-ribosylarginine hydrolase	0.1134	0.0000	0.0000	-1.1	-1.55	-1.62
Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	0.4166	0.0004	0.0083	1.12	-2.45	-1.62
Tecpr1	tectonin beta-propeller repeat containing 1	0.0231	0.0015	0.0019	-1.25	-1.68	-1.62
Zsdc	ZAD family zinc finger C	0.8716	0.0012	0.0089	-1.02	-1.82	-1.62
Tmem143	transmembrane protein 143	0.3910	0.0036	0.0008	-1.09	-1.61	-1.62
Fastk	Fas-activated serine/threonine kinase	0.8649	0.0003	0.0005	1.01	-1.72	-1.62
Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	0.6662	0.0006	0.0001	1.02	-1.48	-1.62
Tns1	tensin 1	0.4432	0.0000	0.0009	1.11	-2	-1.62
Naa16	N(omega)-acetyltransferase 16, Naa1 auxiliary subunit	0.1401	0.0017	0.0005	1.28	-1.37	-1.62
Rbms2	RNA binding motif, single stranded interacting protein 2	0.6208	0.0000	0.0001	-1.02	-1.75	-1.62
Gatsl2	GATS protein-like 2	0.1127	0.0000	0.0001	-1.05	-1.99	-1.62
Fam108c	family with sequence similarity 108, member C	0.6307	0.0001	0.0030	-1.03	-1.8	-1.62
Keap1	kelch-like ECH-associated protein 1	0.4866	0.0000	0.0003	-1.06	-1.96	-1.63
Rps8l2	ribosomal protein S6 kinase, polypeptide 2	0.0190	0.0068	0.0031	1.29	-1.74	-1.63
061009O20R1K	RIKEN cDNA 061009O20 gene	0.6000	0.0008	0.0011	1.04	-1.75	-1.63
Tmbim6	transmembrane BAX inhibitor motif containing 6	0.2021	0.0000	0.0000	-1.06	-1.76	-1.63
Pdgfrb	platelet derived growth factor, B polypeptide	0.5473	0.0001	0.0006	-1.04	-1.99	-1.63
rp8	retinitis pigmentosa 8 (human)	0.4437	0.0014	0.0042	-1.09	-1.78	-1.63
Ube2t2	ubiquitin-conjugating enzyme E2R 2	0.3108	0.0000	0.0000	-1.05	-1.72	-1.63
Zfp775	zinc finger protein 775	0.2618	0.0006	0.0022	-1.12	-1.66	-1.63
Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	0.4940	0.0008	0.0023	1.08	-1.7	-1.63
Ccdc90a	coiled-coil domain containing 90A	0.5950	0.0010	0.0028	-1.06	-1.57	-1.63
1700025G04R1K	RIKEN cDNA 1700025G04 gene	0.1379	0.0001	0.0008	1.18	-1.89	-1.64
Glyp3	glycose 6 phosphatase, catalytic 3	0.8926	0.0000	0.0007	1.09	-1.74	-1.64
Cltu2	cytosolic thiouridylase subunit 2 homolog (S. pombe)	0.3449	0.0045	0.0053	1.12	-1.91	-1.64
Rusc1	RUN and SH3 domain containing 1	0.5607	0.0025	0.0048	1.09	-1.98	-1.64
Slaf6	signal transducer and activator of transcription 6	0.7882	0.0024	0.0008	1.03	-1.47	-1.64
Fam193a	family with sequence similarity 193, member A	0.2783	0.0005	0.0009	1.1	-1.68	-1.64
Acas4	acyl-Coenzyme A dehydrogenase, short chain	0.0867	0.0000	0.0000	-1.17	-1.63	-1.64
lpsk2	inositol hexaphosphate kinase 2	0.1708	0.0056	0.0040	1.19	-1.62	-1.64
Hhail	hedgehog acyltransferase-like	0.6397	0.0001	0.0012	1.04	-1.82	-1.64
Pelo	pelota homolog (Drosophila)	0.2319	0.0009	0.0034	1.16	-1.8	-1.64
Rho12	ras homolog gene family, member T2	0.0127	0.0000	0.0000	1.18	-1.65	-1.64
Bcl7b	B-cell CLL/lymphoma 7B	0.3076	0.0000	0.0000	1.06	-1.71	-1.64
Fbxw5	F-box and WD-40 domain protein 5	0.0111	0.0000	0.0002	1.21	-1.82	-1.64
Khlh21	kelch-like 21 (Drosophila)	0.6916	0.0000	0.0000	1.03	-1.96	-1.65
Gys1	glycogen synthase 1, muscle	0.1080	0.0000	0.0004	1.11	-2.05	-1.65
Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	0.5014	0.0084	0.0020	-1.09	-1.53	-1.65
130000101R1K	RIKEN cDNA 130000101 gene	0.2302	0.0000	0.0022	-1.12	-1.95	-1.65
Gmps	guanine monophosphate synthetase	0.3970	0.0000	0.0000	-1.05	-1.53	-1.65
Nr1h2	nuclear receptor subfamily 1, group H, member 2	0.2393	0.0004	0.0026	-1.12	-1.9	-1.65
Bcl7c	B-cell CLL/lymphoma 7C	0.7244	0.0000	0.0000	1.02	-1.8	-1.65
Ccdc86	coiled-coil domain containing 86	0.9980	0.0003	0.0009	-1	-1.51	-1.65
Dna12	DnaJ (Hsp40) homolog, subfamily B, member 12	0.0710	0.0001	0.0004	1.19	-1.55	-1.65
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	0.8581	0.0018	0.0047	1.02	-1.76	-1.65
Pbxp1	pre-B-cell leukemia transcription factor interacting protein 1	0.0372	0.0001	0.0014	1.2	-1.94	-1.65
Fyn	Fyn proto-oncogene	0.8454	0.0007	0.0001	1.02	-1.47	-1.65
Cdh15	cadherin 15	0.8283	0.0072	0.0074	-1.03	-1.64	-1.65
Card10	cardiac troponin domain family, member 10	0.8136	0.0004	0.0027	-1.02	-2.07	-1.65
Vps72	vacuolar protein sorting 72 (yeast)	0.5818	0.0000	0.0001	-1.03	-1.87	-1.65
Eya3	eyes absent 3 homolog (Drosophila)	0.2444	0.0003	0.0001	-1.08	-1.74	-1.65
Lrrc38	leucine rich repeat containing 38	0.2158	0.0004	0.0029	-1.15	-1.87	-1.65
Pgo	phosphoglycolate phosphatase	0.4458	0.0000	0.0008	1.05	-2.02	-1.65
Phar2a	protein kinase, cAMP dependent regulatory, type II alpha	0.1286	0.0000	0.0001	1.11	-1.75	-1.66
Marveld1	MARVEL (membrane-associated) domain containing 1	0.1408	0.0042	0.0093	-1.24	-1.88	-1.66
Kif1c	kinesin family member 1C	0.9331	0.0000	0.0001	-1.01	-1.77	-1.66
Nos1	nitric oxide synthase 1, neuronal	0.1504	0.0036	0.0058	1.17	-1.73	-1.66
Anks1	ankyrin repeat and SAM domain containing 1	0.4533	0.0002	0.0020	1.06	-1.92	-1.66
Vash1	vashon 1	0.3829	0.0000	0.0014	-1.1	-1.76	-1.66
Atad3a	ATPase family, AAA domain containing 3A	0.3081	0.0014	0.0028	1.11	-1.8	-1.66
Dlx2	deltex 2 homolog (Drosophila)	0.0199	0.0078	0.0032	-1.41	-1.98	-1.66
Fbin2	fibulin 2	0.4660	0.0003	0.0004	1.07	-1.67	-1.66
Fgf6	fibroblast growth factor 6	0.0249	0.0013	0.0047	-1.25	-1.6	-1.66
Agp2	aspartate-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	0.3927	0.0000	0.0000	-1.06	-1.67	-1.66
Nav2	neuron navigator 2	0.2100	0.0001	0.0001	-1.09	-1.75	-1.66
Midn	midnolin	0.4178	0.0000	0.0001	1.05	-1.89	-1.66
Tcf3	transcription factor E3	0.2909	0.0033	0.0099	-1.19	-2.12	-1.66
Dhr7	17-dehydrocholesterol reductase	0.2466	0.0005	0.0005	1.12	-2.19	-1.66
231004Y10R1K	RIKEN cDNA 231004Y10 gene	0.8612	0.0000	0.0007	1.04	-1.82	-1.66
Lonp1	lon peptidase 1, mitochondrial	0.0614	0.0000	0.0000	1.17	-2.01	-1.66
Obsl	obscurin-like 1	0.4091	0.0004	0.0058	-1.12	-2.18	-1.67
Ube3b	ubiquitin protein ligase E3B	0.3798	0.0000	0.0000	1.04	-2.07	-1.67
Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	0.0159	0.0000	0.0000	1.22	-1.92	-1.67
Map2d2	MAP2 microtubule associated protein 2 (yeast)	0.8356	0.0047	0.0038	1.05	-1.71	-1.67
Lemd2	LEM domain containing 2	0.8977	0.0009	0.0012	-1.01	-1.67	-1.67
Cttnbp1	catenin beta interacting protein 1	0.0145	0.0026	0.0002	-1.31	-1.38	-1.67
Sox18	SRY-box containing gene 18	0.9747	0.0012	0.0091	-1	-1.74	-1.67
Ccdc123	coiled-coil domain containing 123	0.4275	0.0078	0.0092	-1.12	-1.56	-1.67
Sna15	serine/arginine-rich splicing factor 15	0.3597	0.0000	0.0034	-1.08	-2.92	-1.67
P2y2	purinergic receptor P2Y, G-protein coupled 2	0.0316	0.0016	0.0019	1.37	-1.89	-1.67
Tln1	talin 1	0.2892	0.0001	0.0001	1.07	-1.76	-1.67
Itga7	integrin alpha 7	0.7937	0.0001	0.0000	1.01	-1.66	-1.67
Tbra	thyroid hormone receptor alpha	0.6436	0.0001	0.0004	-1.03	-1.83	-1.67
Fam53a	family with sequence similarity 53, member A	0.3474	0.0000	0.0000	1.05	-1.9	-1.67
Fbxw8	F-box and WD-40 domain protein 8	0.1104	0.0001	0.0004	1.11	-1.71	-1.67
Eif4g1	eukaryotic translation initiation factor 4, gamma 1	0.3238	0.0003	0.0025	-1.11	-1.99	-1.67
Cyht2	cytohesin 2	0.5903	0.0015	0.0022	1.06	-1.76	-1.68
Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	0.5929	0.0000	0.0002	1.03	-2.02	-1.68
Leng1	leukocyte receptor cluster (LRC) member 1	0.2380	0.0024	0.0082	-1.18	-1.67	-1.68
Star10	START domain containing 10	0.5254	0.0000	0.0000	1.04	-1.91	-1.68
2810453J06R1K	RIKEN cDNA 2810453J06 gene	0.9834	0.0001	0.0001	-1	-1.66	-1.68
Med13l	mediator complex subunit 13-like	0.0935	0.0001	0.0000	1.24	-1.55	-1.68
Flo	fat mass and obesity associated	0.7289	0.0000	0.0001	1.02	-1.9	-1.68
Adcy6	adenylyl cyclase 6	0.8401	0.0008	0.0034	-1.02	-2.05	-1.68
Acpat6	1-acetylcoenzyme A:phosphate O-acetyltransferase 6 (lysophosphatidic acid acyltransferase, ze	0.6809	0.0019	0.0001	-1.04	-1.48	-1.68
Srebf1	sterol regulatory element binding transcription factor 1	0.2807	0.0000	0.0041	-1.13	-2.15	-1.68
Hdac5	histone deacetylase 5	0.3013	0.0000	0.0002	1.07	-2.33	-1.69
Eif2c1	eukaryotic translation initiation factor 2C, 1	0.6556	0.0013	0.0002	-1.03	-1.65	-1.69
Kctd2	potassium channel tetramerisation domain containing 2	0.9524	0.0007	0.0000	-1	-1.65	-1.69
Pdim4	PDZ and LIM domain 4	0.5632	0.0036	0.0017	-1.06	-1.51	-1.69
Myk4	myosin light chain kinase family, member 4	0.3584	0.0001	0.0000	1.07	-1.83	-1.69
Sorbs3	sorbin and SH3 domain containing 3	0.0106	0.0001	0.0000	1.27	-1.63	-1.69
Kpna6	karyopherin (importin) alpha 6	0.9652	0.0000	0.0014	-1	-2.39	-1.69
Stat3	signal transducer and activator of transcription 3	0.8297	0.0000	0.0000	1.04	-1.53	-1.69
Adamts4	ADAMTS-like 4	0.1467	0.0006	0.0034	1.22	-1.96	-1.69
Eef1a2	eukaryotic translation elongation factor 1 alpha 2	0.1321	0.0000	0.0000	1.1	-1.81	-1.69
Zfand3	zinc finger, AN1-type domain 3	0.9758	0.0000	0.0006	1	-1.92	-1.69
Myh14	myosin, heavy polypeptide 14	0.8010	0.0005	0.0009	-1.02	-1.8	-1.69
Hc1	hypermethylated in cancer 1	0.2123	0.0004	0.0004	-1.1	-2.08	-1.69
2300009A05R1K	RIKEN cDNA 2300009A05 gene	0.0926	0.0000	0.0003	1.15	-1.8	-1.69
Tex264	testis expressed gene 264	0.3308	0.0013	0.0007	1.09	-1.65	-1.69
Fkbp4	FK506 binding protein 4	0.0458	0.0000	0.0000	1.13	-1.65	-1.69
Rnf123	ring finger protein 123	0.1041	0.0001	0.0011	1.13	-1.91	-1.7
Trapp3	trafficking protein particle complex 3	0.4809	0.0000	0.0001	1.04	-2.09	-1.7
Shz2b	SHZ2 adaptor protein 1	0.3557	0.0001	0.0016	1.07	-1.89	-1.7
Nucb1	nucleobindin 1	0.2777	0.0005	0.0009	1.12	-1.78	-1.7
Atg4c	autophagy-related 4C (yeast)	0.3281	0.0011	0.0001	-1.09	-1.68	-1.7
PHF21A	PHD finger protein 21A	0.1633	0.0011	0.0001	-1.11	-1.57	-1.7
Ras11b3	RAB11 family interacting protein 3 (class II)	0.8652	0.0000	0.0002	-1.14	-2.43	-1.7
Gnao1	guanine nucleotide binding protein, alpha O	0.5522	0.0008	0.0012	1.1	-1.76	-1.7
Rere	arginine glutamic acid dipeptide (RE) repeats	0.9506	0.0000	0.0002	-1	-2.37	-1.7
Acin1	apoptotic chromatin condensation inducer 1	0.9734	0.0000	0.0001	-1	-2.11	-1.71
Acpat3	1-acetylcoenzyme A:phosphate O-acetyltransferase 3	0.6443	0.0007	0.0005	1.04	-1.71	-1.71
Rib3	ribbed-like homeodomain transcription factor 3	0.7831	0.0032	0.0037	1.04	-1.65	-1.71

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	0.3110	0.0004	0.0005	1.09	-1.74	-1.71
Egln2	EGln2 homolog 2 (C. elegans)	0.1817	0.0000	0.0000	1.09	-1.73	-1.71
Arhgap2	Rho GTP dissociation inhibitor (GDI) alpha	0.1106	0.0000	0.0000	1.09	-1.68	-1.71
Man2c1	mannosidase, alpha, class 2C, member 1	0.6150	0.0002	0.0002	1.03	-1.55	-1.71
Crelid1	cysteine-rich with EGF-like domains 1	0.6917	0.0016	0.0027	-1.04	-1.71	-1.71
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	0.4237	0.0049	0.0027	1.1	-1.54	-1.72
Zc3h18	zinc finger CCHC-type containing 18	0.0176	0.0018	0.0002	1.16	-1.33	-1.72
Pilpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0.7646	0.0001	0.0001	-1.03	-1.67	-1.72
Nuc41	nucleolar complex associated 4 homolog (S. cerevisiae)	0.5602	0.0052	0.0060	-1.06	-1.52	-1.72
Pbx2	pre B-cell leukemia transcription factor 2	0.0837	0.0000	0.0006	-1.14	-1.81	-1.72
Igf1r	insulin-like growth factor 1 receptor	0.0200	0.0001	0.0011	1.52	-1.99	-1.72
BC032203	cDNA sequence BC032203	0.3651	0.0005	0.0001	1.1	-1.58	-1.72
Nup62	nucleoporin 62	0.8702	0.0032	0.0024	-1.02	-1.63	-1.72
Gtf2rid1	general transcription factor II I repeat domain-containing 1	0.7689	0.0001	0.0002	-1.02	-1.73	-1.72
Dusp28	dual specificity phosphatase 28	0.3729	0.0025	0.0025	1.09	-1.59	-1.72
Impad1	inositol monophosphatase domain containing 1	0.0776	0.0096	0.0012	-1.23	-1.34	-1.72
Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0.1700	0.0000	0.0001	-1.07	-2.14	-1.72
Pr24	proline rich 24	0.8886	0.0000	0.0001	1.04	-2.15	-1.72
Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	0.1495	0.0032	0.0026	-1.22	-1.75	-1.73
Med24	mediator complex subunit 24	0.2817	0.0062	0.0007	1.1	-1.59	-1.73
Adam33	alpha disintegrin and metalloproteinase domain 33	0.8302	0.0017	0.0007	1.02	-1.49	-1.73
Fam131a	family with sequence similarity 131, member A	0.3699	0.0000	0.0005	1.05	-1.82	-1.73
Pp2	palmitoyl protein thioesterase 2	0.8717	0.0016	0.0086	-1.02	-1.89	-1.73
Pura	purine rich element binding protein A	0.0213	0.0023	0.0011	-1.32	-1.74	-1.73
Slc26a6	solute carrier family 26, member 6	0.0140	0.0000	0.0001	-1.19	-1.81	-1.73
Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	0.7623	0.0037	0.0002	-1.04	-1.49	-1.73
Coro6	coronin 6	0.0542	0.0000	0.0000	1.2	-2.24	-1.73
Smn1	survival motor neuron 1	0.3412	0.0001	0.0001	1.06	-1.86	-1.73
Sars2	seryl-aminoacyl-tRNA synthetase 2	0.6141	0.0000	0.0003	1.04	-2.64	-1.73
Rai1	retinoic acid induced 1	0.2570	0.0004	0.0019	1.13	-2.08	-1.73
Fzdb	frizzled homolog 8 (Drosophila)	0.1646	0.0053	0.0049	-1.15	-1.58	-1.73
Brd3	bromodomain containing 3	0.3685	0.0000	0.0000	1.03	-1.83	-1.73
Etic	Ellis van Creveld gene homolog (human)	0.9889	0.0000	0.0007	-1	-1.83	-1.73
Cxcr5	CXCR5 finger 5	0.6687	0.0000	0.0009	-1.05	-2.3	-1.73
Trim3	tripartite motif-containing 3	0.7394	0.0000	0.0000	1.02	-1.87	-1.73
Lox1	lysyl oxidase-like 1	0.2010	0.0023	0.0040	-1.24	-1.79	-1.74
Nacc2	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	0.0579	0.0001	0.0006	-1.14	-1.85	-1.74
ATP6v1a	ATPase V1H transporting, lysosomal V1 subunit A	0.1434	0.0024	0.0010	-1.22	-1.56	-1.74
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	0.9715	0.0000	0.0000	-1	-1.73	-1.74
Slc25a39	solute carrier family 25, member 39	0.2611	0.0013	0.0021	1.15	-2.17	-1.74
1110038B12Rik	RIKEN cDNA 1110038B12 gene	0.9951	0.0001	0.0013	1	-1.58	-1.74
Gnb2	guanine nucleotide binding protein (G protein), beta 2	0.9597	0.0002	0.0008	1	-1.98	-1.74
Rnf10	ring finger protein 10	0.0617	0.0000	0.0004	1.16	-2.07	-1.74
Jag2	jagged 2	0.1293	0.0016	0.0013	-1.18	-1.73	-1.74
Iqsec1	IQ motif and Sec7 domain 1	0.1125	0.0002	0.0004	-1.15	-1.94	-1.74
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	0.6391	0.0086	0.0000	1.04	-1.48	-1.74
Rbm19	RNA binding motif protein 19	0.2569	0.0010	0.0056	-1.14	-2.09	-1.75
Spr	sepiapterin reductase	0.3217	0.0086	0.0013	-1.1	-1.44	-1.75
Rora	RAR-related orphan receptor alpha	0.7051	0.0001	0.0016	-1.05	-1.39	-1.75
Dexi	dexamethasone-induced transcript	0.0985	0.0000	0.0000	1.12	-2.22	-1.75
Zmynd8	zinc finger, MYND-type containing 8	0.4508	0.0002	0.0003	1.08	-2.1	-1.75
Elr3a	ELF3 homolog A (S. cerevisiae)	0.9325	0.0000	0.0002	1	-2.08	-1.75
Nklr1	NKX1 (neurogenic leukemia)/myocardin-like 1	0.8790	0.0000	0.0004	1.02	-2.32	-1.75
Cenpv	centromere protein V	0.4629	0.0001	0.0000	1.06	-1.65	-1.75
Prip4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	0.2851	0.0018	0.0015	-1.14	-1.71	-1.75
Zfp414	zinc finger protein 414	0.4490	0.0001	0.0004	-1.07	-1.98	-1.75
Slc38a1	solute carrier family 38 (proton/amino acid symporter), member 1	0.0577	0.0009	0.0041	-1.25	-2.39	-1.75
Phid1r	pleckstrin homology-like domain, family A, member 1	0.0337	0.0002	0.0002	-1.36	-1.63	-1.75
2310022A10Rik	RIKEN cDNA 2310022A10 gene	0.5763	0.0023	0.0006	1.05	-1.57	-1.75
Fads1	fatty acid desaturase 1	0.3573	0.0092	0.0081	-1.18	-1.63	-1.75
1300018117Rik	RIKEN cDNA 1300018117 gene	0.8124	0.0000	0.0000	1.01	-2.06	-1.75
Cd151	CD151 antigen	0.8577	0.0074	0.0015	-1.02	-1.52	-1.75
Fam3b	family with sequence similarity 33, member B	0.1899	0.0004	0.0014	-1.16	-2.36	-1.75
Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	0.3674	0.0037	0.0074	-1.14	-2.02	-1.75
Rps6ka1	ribosomal protein S6 kinase polypeptide 1	0.8944	0.0009	0.0018	1.01	-2.24	-1.75
Chad	chondroadherin	0.2155	0.0086	0.0061	-1.42	-1.75	-1.75
Urc68	leucine rich repeat containing 68	0.8486	0.0000	0.0002	-1.01	-2.04	-1.75
Tp53l1	transformation related protein 53 inducible protein 11	0.2222	0.0010	0.0017	-1.17	-1.85	-1.75
Srsf2p	serine/arginine-rich splicing factor 2, interacting protein	0.0903	0.0027	0.0003	-1.25	-1.48	-1.76
Inpp1	inositol polyphosphate phosphatase-like 1	0.0156	0.0002	0.0000	-1.25	-1.9	-1.76
Bat5	HLA-B associated transcript 5	0.3147	0.0000	0.0001	1.06	-2.02	-1.77
Nat15	N-acetyltransferase 15 (GUNS-related, putative)	0.0956	0.0000	0.0001	-1.08	-1.86	-1.77
Fam65a	family with sequence similarity 65, member A	0.4315	0.0009	0.0005	-1.05	-2.25	-1.77
Rhog	ras homolog gene family, member G	0.4276	0.0001	0.0002	1.08	-1.59	-1.77
Slk40	serine/threonine kinase 40	0.3925	0.0001	0.0001	-1.08	-1.8	-1.77
2700081015Rik	RIKEN cDNA 2700081015 gene	0.1893	0.0055	0.0029	-1.18	-1.81	-1.77
Ntn1	neurturin	0.4484	0.0065	0.0026	-1.11	-1.79	-1.77
Ehfp11	Eh1 domain binding protein 1-like 1	0.3293	0.0000	0.0003	1.06	-2.19	-1.77
2310061104Rik	RIKEN cDNA 2310061104 gene	0.2073	0.0003	0.0013	1.13	-1.95	-1.78
Pcy2	phosphate cytidylyltransferase 2, ethanolamine	0.0475	0.0072	0.0007	-1.36	-1.48	-1.78
Jsrp1	junctional sarcoplasmic reticulum protein 1	0.0461	0.0002	0.0002	1.16	-1.78	-1.78
Kcng4	potassium voltage-gated channel, subfamily G, member 4	0.6197	0.0016	0.0021	-1.08	-1.95	-1.78
F6a	factor 6-associated gene A	0.7657	0.0015	0.0081	-1.06	-2.56	-1.78
Gna12	guanine nucleotide binding protein (G protein), alpha inhibiting 2	0.2730	0.0000	0.0000	-1.05	-1.88	-1.78
Plekhl1	pleckstrin homology domain containing, family J member 1	0.1958	0.0050	0.0005	1.11	-1.51	-1.78
Asap2	ARF GAP with SH3 domain, ankyrin repeat and PH domain 2	0.6938	0.0000	0.0002	-1.05	-2.59	-1.78
Mlxip	MLX interacting protein-like	0.3438	0.0000	0.0002	1.08	-2.45	-1.78
Pex11a	peroxisomal biogenesis factor 11 alpha	0.4989	0.0000	0.0023	-1.08	-1.75	-1.79
593043B04Rik	RIKEN cDNA 593043B04 gene	0.4784	0.0001	0.0000	-1.05	-1.85	-1.79
Neur11a	neuronalized homolog 1A (Drosophila)	0.0502	0.0000	0.0002	1.16	-1.98	-1.79
Alch4a1	aldehyde dehydrogenase 4 family, member A1	0.2333	0.0060	0.0071	1.18	-1.78	-1.79
Eng	engoglin	0.5720	0.0006	0.0022	1.07	-1.97	-1.79
P2y1a	platelet derived growth factor, alpha	0.0528	0.0008	0.0005	-1.23	-1.78	-1.8
Mgm1	mitochondrial, ring finger 1	0.2176	0.0000	0.0003	1.07	-2.01	-1.8
Clec18a	C-type lectin domain family 18, member A	0.2917	0.0000	0.0000	1.06	-2.15	-1.8
Crtap	cartilage associated protein	0.1663	0.0008	0.0008	-1.23	-1.96	-1.8
Dusp7	dual specificity phosphatase 7	0.2569	0.0022	0.0033	1.19	-2.08	-1.8
Spz7	spastic paraplegia 7 homolog (human)	0.8032	0.0000	0.0000	1.01	-2.15	-1.8
Cldsp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	0.3276	0.0000	0.0000	1.03	-2.11	-1.8
Zfp628	zinc finger protein 628	0.7903	0.0000	0.0001	-1.02	-1.88	-1.8
Pknox1	plexin A1	0.9075	0.0000	0.0001	1.01	-1.97	-1.8
Rgp1	RGF1 retrograde golgi transport homolog (S. cerevisiae)	0.6886	0.0000	0.0012	-1.03	-2.4	-1.8
Kdm4b	lysine (K)-specific demethylase 4b	0.2427	0.0060	0.0088	1.16	-2.01	-1.8
Oral1	ORAI calcium release-activated calcium modulator 1	0.6329	0.0001	0.0003	-1.05	-1.88	-1.8
Foxn3	forkhead box N3	0.0430	0.0000	0.0001	1.15	-2.26	-1.81
Rbm25	RNA binding motif protein 25	0.2930	0.0002	0.0000	-1.11	-1.51	-1.81
Foxo4	forkhead box O4	0.3831	0.0004	0.0009	1.1	-1.94	-1.81
Smardc3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d	0.0126	0.0000	0.0000	1.11	-2.09	-1.81
Akt1s1	AKT1 substrate 1 (proline-rich)	0.1188	0.0002	0.0002	1.12	-1.83	-1.81
Ufsp1	UFM1-specific peptidase 1	0.1524	0.0012	0.0023	1.18	-2.04	-1.81
Adpgk	ADP-dependent glucokinase	0.9428	0.0005	0.0020	-1.01	-2.36	-1.81
Olfec2b	oligonucleotide/oligosaccharide-binding fold containing 2B	0.3725	0.0000	0.0000	1.05	-1.8	-1.82
Des	desmin	0.2129	0.0000	0.0000	1.07	-2.16	-1.82
Mtap7d1	microtubule-associated protein 7 domain containing 1	0.5678	0.0000	0.0001	-1.04	-2.03	-1.82
Cldnd1	claudin domain containing 1	0.2462	0.0005	0.0001	-1.11	-1.51	-1.82
4930402E16Rik	RIKEN cDNA 4930402E16 gene	0.2484	0.0006	0.0005	-1.12	-1.67	-1.82
Chfr8	CTF8 chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	0.1392	0.0038	0.0029	1.17	-1.81	-1.82
Denn1f1a	DENND1F domain containing 1A	0.3847	0.0000	0.0015	1.1	-2.56	-1.82
Pkd1	polycystic kidney disease 1 homolog	0.7111	0.0006	0.0010	1.06	-2.07	-1.82
Klf15	Kruppel-like factor 15	0.7680	0.0086	0.0046	-1.03	-1.56	-1.82
Dyrk1b	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	0.0472	0.0000	0.0000	1.18	-2.1	-1.82
Pfkb1	pleckstrin homology-like domain, family B, member 1	0.5183	0.0000	0.0003	1.06	-2.51	-1.82
Fndc5	fibronectin type III domain containing 5	0.8376	0.0000	0.0005	1.02	-2.57	-1.82
Med15	mediator complex subunit 15	0.2290	0.0041	0.0013	1.13	-1.63	-1.82
Gata2a2	GATA zinc finger domain containing 2A	0.2042	0.0000	0.0002	1.1	-2.19	-1.82
Eid2	EP300 interacting inhibitor of differentiation 2	0.9018	0.0010	0.0027	1.02	-2.01	-1.82
Stom1	stomatin-like 1	0.5080	0.0012	0.0001	1.1	-1.72	-1.82
Cals	Calstactin B-like lymphoma b	0.8036	0.0007	0.0000	-1.02	-1.65	-1.82
Abhd8	abhydrolase domain containing 8	0.9807	0.0001	0.0061	1	-3.54	-1.82
Drp1	Dr1 associated protein 1 (negative cofactor 2 alpha)	0.0211	0.0000	0.0000	1.18	-1.79	-1.83
Ilrak1	interleukin-1 receptor-associated kinase 1	0.7525	0.0000	0.0001	-1.02	-1.69	-1.83
Shc1	src homology 2 domain-containing transforming protein C1	0.0484	0.0001	0.0002	-1.15	-2.07	-1.83
Nceps	aminopeptidase puromycin sensitive	0.8239	0.0006	0.0014	1.05	-2.03	-1.83

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Hgs	HGF-regulated tyrosine kinase substrate	0.2279	0.0000	0.0000	1.1	-1.81	-1.83
Fam129b	family with sequence similarity 129, member B	0.7256	0.0007	0.0013	1.05	-1.8	-1.84
Tmem201	transmembrane protein 201	0.3846	0.0001	0.0000	-1.1	-2.11	-1.84
Creg1	cellular repressor of E1A-stimulated genes 1	0.0893	0.0001	0.0000	-1.18	-1.67	-1.84
Dcaakd	dephospho-CoA kinase domain containing	0.8174	0.0001	0.0053	-1.02	-1.95	-1.84
Pacs2	phosphotransferase domain containing	0.9900	0.0014	0.0028	1	-1.98	-1.84
Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	0.9748	0.0001	0.0032	-1	-2.81	-1.85
Dpp9	diacylglycerol phosphatase 9	0.0477	0.0003	0.0019	-1.31	-1.99	-1.85
Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	0.1298	0.0000	0.0005	1.17	-2.19	-1.85
Emi3	echinoderm microtubule associated protein like 3	0.0175	0.0042	0.0007	-1.42	-1.5	-1.85
Nr2f2	nuclear receptor subfamily 2, group F, member 2	0.2766	0.0037	0.0011	1.17	-1.64	-1.85
Man2b1	mannosidase 2, alpha B1	0.5071	0.0006	0.0016	-1.07	-1.96	-1.85
Rbm38	RNA binding motif protein 38	0.4928	0.0000	0.0001	1.05	-2.25	-1.85
Fhd1	formin homology 2 domain containing 1	0.4504	0.0001	0.0008	1.08	-2.65	-1.85
Sic9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0.0781	0.0007	0.0012	1.3	-1.99	-1.85
Zbed6	zinc finger, BED domain containing 6	0.2484	0.0021	0.0015	-1.17	-1.24	-1.86
Jph2	junctophilin 2	0.8168	0.0000	0.0000	-1.01	-2.37	-1.86
Kcnq4	potassium voltage-gated channel, subfamily Q, member 4	0.0389	0.0001	0.0014	1.2	-2.29	-1.86
Plcb2	phospholipase B domain containing 2	0.9902	0.0003	0.0013	-1	-2.22	-1.86
H19	H19 fetal liver mRNA	0.6956	0.0004	0.0015	1.04	-2.5	-1.86
Sh3bgr3	SH3 domain binding glutamic acid-rich protein-like 3	0.0150	0.0007	0.0004	-1.38	-1.73	-1.86
Arba	ADP-ribosylation factor-like 8A	0.6238	0.0001	0.0001	1.04	-1.92	-1.86
Impd1	inosine 5'-phosphate dehydrogenase 1	0.3216	0.0028	0.0014	-1.1	-1.86	-1.86
Bloc1s3	biogenesis of lysosome-related organelles complex-1, subunit 3	0.1753	0.0007	0.0011	-1.21	-1.94	-1.86
Zfp703	zinc finger protein 703	0.3942	0.0032	0.0063	-1.13	-1.96	-1.86
Frat2	frequently rearranged in advanced T-cell lymphomas 2	0.1440	0.0003	0.0013	-1.19	-1.86	-1.87
Cu11	Castias B-lineage lymphoma-like 1	0.7908	0.0008	0.0001	-1.02	-1.42	-1.87
BC03012A226Rik	RIKEN cDNA BC03012A22 gene	0.2007	0.0004	0.0003	1.06	-1.9	-1.87
Al480526	expressed sequence AL480526	0.0543	0.0004	0.0003	1.22	-1.76	-1.87
Erp29	endoplasmic reticulum protein 29	0.8657	0.0066	0.0046	1.02	-1.76	-1.87
Ubn1	ubiquitin 1	0.0316	0.0004	0.0001	-1.21	-1.44	-1.87
Akap3	AKAP with GTPase domain, ankyrin repeat and PH domain 3	0.1773	0.0012	0.0031	1.16	-2.44	-1.87
Dcn1	chondrin 1	0.0856	0.0000	0.0004	1.19	-2.34	-1.87
Aldh2	aldehyde dehydrogenase 2, mitochondrial	0.3228	0.0012	0.0021	-1.12	-1.97	-1.87
Sf1	splicing factor 1	0.7357	0.0000	0.0000	1.01	-1.98	-1.87
Zfp710	zinc finger protein 710	0.5709	0.0001	0.0016	-1.05	-2	-1.88
Plec	plectin	0.0649	0.0000	0.0003	1.16	-2.84	-1.88
Tmem150a	transmembrane protein 150A	0.0327	0.0000	0.0000	1.16	-2.07	-1.88
Lynx1	Ly6/neurotoxin 1	0.6360	0.0000	0.0000	-1.02	-2.15	-1.88
Ramp2	receptor (calcitonin) activity modifying protein 2	0.1095	0.0004	0.0003	1.24	-1.58	-1.88
Acs3	acyl-CoA synthetase family member 3	0.1285	0.0000	0.0005	-1.11	-2.27	-1.88
Sic6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	0.8455	0.0023	0.0044	1.02	-1.88	-1.88
BC017612	cDNA sequence BC017612	0.8138	0.0023	0.0017	-1.4	-2.04	-1.89
Lime1	Lck interacting transmembrane adaptor 1	0.9869	0.0030	0.0008	-1	-1.92	-1.89
Wiz	widely-interspaced zinc finger motifs	0.3280	0.0002	0.0002	1.11	-2.15	-1.89
Zbtb22	zinc finger and BTB domain containing 22	0.5554	0.0000	0.0002	-1.04	-2.1	-1.89
Chmp1a	chromatin modifying protein 1A	0.5312	0.0004	0.0006	1.06	-1.86	-1.89
Pap3	paternally expressed 3	0.5347	0.0006	0.0003	-1.08	-1.37	-1.89
Parp4	poly (ADP-ribose) polymerase family, member 4	0.4936	0.0000	0.0002	1.08	-2.17	-1.89
Ank1	ankyrin 1, erythroid	0.4059	0.0000	0.0001	1.06	-1.84	-1.89
Wbp7	WW domain binding protein 7	0.0906	0.0000	0.0000	1.12	-2.24	-1.89
Pdxp	pyridoxal (pyridoxine, vitamin B6) phosphatase	0.4447	0.0013	0.0019	-1.06	-1.7	-1.9
Zc3h7b	zinc finger CCH1 type containing 7B	0.8952	0.0000	0.0000	1.01	-2.29	-1.9
Serinc2	serine incorporator 2	0.1969	0.0001	0.0003	1.13	-2.15	-1.9
Zfp516	zinc finger protein 516	0.6224	0.0095	0.0030	-1.05	-1.7	-1.9
Usp21	ubiquitin specific peptidase 21	0.4515	0.0000	0.0000	-1.05	-1.97	-1.9
Igf2bp1	insulin-like growth factor binding protein 7	0.7338	0.0000	0.0000	1.02	-2.06	-1.9
Scarb1	scavenger receptor class B, member 1	0.3077	0.0013	0.0080	-1.15	-2.27	-1.9
Plp5k1c	phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma	0.1203	0.0001	0.0000	1.25	-2.01	-1.91
Ehfd2	EF hand domain containing 2	0.6520	0.0051	0.0084	-1.06	-2.15	-1.91
Sic9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0.1576	0.0021	0.0011	-1.16	-1.87	-1.91
Plp4k2b	phosphatidylinositol 5-phosphate 4-kinase, type II, beta	0.9834	0.0000	0.0002	1	-2.47	-1.92
Ccnb3	cyclin D3	0.8355	0.0000	0.0054	-1.03	-1.79	-1.92
Rpap1	RNA polymerase II associated protein 1	0.2078	0.0000	0.0003	1.09	-2.41	-1.92
Eid1	EP300 interacting inhibitor of differentiation 1	0.7317	0.0007	0.0003	1.04	-1.89	-1.92
Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	0.8210	0.0001	0.0000	1.03	-2.07	-1.93
Arrb2	arrestin, beta 2	0.0493	0.0001	0.0093	-1.29	-3.11	-1.93
CD3004610Rik	RIKEN cDNA CD3004610f gene	0.1614	0.0000	0.0001	-1.19	-2.19	-1.93
Cd99	CD99 antigen	0.5023	0.0004	0.0020	-1.1	-2.18	-1.93
Zfp598	zinc finger protein 598	0.9299	0.0000	0.0000	1.01	-2	-1.93
Prkd	protein kinase C, delta	0.3047	0.0009	0.0001	-1.14	-1.74	-1.93
Arap1	ARFAP with RhoGAP domain, ankyrin repeat and PH domain 1	0.9964	0.0001	0.0006	1	-3.52	-1.93
D4Ertd206e	cDNA segment, Chr 4, ERATO Dcl 292, expressed	0.8005	0.0000	0.0005	-1.04	-2.05	-1.93
Scyl1	SCY1-like 1 (S. cerevisiae)	0.1476	0.0000	0.0000	1.09	-2.01	-1.93
Thop1	thimet oligopeptidase 1	0.6550	0.0000	0.0003	1.04	-2.61	-1.94
Itfg2	integrin alpha FG-GAP repeat containing 2	0.4406	0.0000	0.0004	1.07	-2.01	-1.94
Cd99l2	CD99 antigen-like 2	0.0781	0.0000	0.0000	-1.17	-1.93	-1.94
Nipbl	Nipped-B homolog (Drosophila)	0.3314	0.0000	0.0000	1.07	-1.68	-1.94
Synpo2l	synaptopodin 2-like	0.8888	0.0000	0.0001	1.01	-2.59	-1.95
Spac	secreted acidic cysteine rich glycoprotein	0.1641	0.0020	0.0025	-1.27	-1.9	-1.95
Farsa	phenylalanyl-tRNA synthetase, alpha subunit	0.7615	0.0001	0.0000	-1.04	-2.14	-1.95
Aebp1	AE binding protein 1	0.4011	0.0006	0.0006	1.14	-2.16	-1.95
Kctd17	potassium channel domain containing 17	0.8387	0.0000	0.0084	-1.08	-2.53	-1.95
Tbkbp1	TBK1 binding protein 1	0.5761	0.0001	0.0001	-1.06	-2.11	-1.95
Prdm2	PR domain containing 2, with ZNF domain	0.0161	0.0030	0.0016	-1.48	-1.83	-1.95
Ext1	extostoses (multiple)-like 1	0.4484	0.0000	0.0002	-1.08	-2.18	-1.95
Pkl	phosphofructokinase, liver, B-type	0.1078	0.0001	0.0015	-1.24	-2.97	-1.95
Dgap2	daps, large homolog associated protein 4 (Drosophila)	0.0126	0.0000	0.0000	1.22	-2.65	-1.95
Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0.3015	0.0001	0.0002	1.11	-2.01	-1.96
Zfhx3	zinc finger homeobox 3	0.8322	0.0003	0.0016	-1.03	-2.16	-1.96
Crtc1	CREB regulated transcription coactivator 1	0.0879	0.0015	0.0006	-1.21	-2.08	-1.96
Myk2	myosin, light polypeptide kinase 2, skeletal muscle	0.0852	0.0000	0.0001	1.19	-2.27	-1.96
Ubr2	ubiquitin protein ligase E3 component n-recognin 2	0.0347	0.0000	0.0000	-1.13	-1.85	-1.96
Ifitm3	interferon induced transmembrane protein 3	0.6944	0.0004	0.0001	-1.03	-1.71	-1.96
Z310044H10Rik	RIKEN cDNA Z310044H10 gene	0.4919	0.0000	0.0000	-1.06	-1.87	-1.96
Znr1f	zinc and ring finger 1	0.1247	0.0000	0.0000	-1.14	-2.14	-1.96
Z310022B05Rik	RIKEN cDNA Z310022B05 gene	0.3941	0.0001	0.0001	-1.08	-2.23	-1.97
Gp4	gap junction protein, alpha 4	0.1302	0.0025	0.0081	-1.34	-2.57	-1.97
Srm2	serine/arginine repetitive matrix 2	0.1148	0.0006	0.0000	-1.13	-1.53	-1.97
Zfp580	zinc finger protein 580	0.5853	0.0001	0.0001	1.04	-2.01	-1.97
Dcn1	dynactin 1	0.5505	0.0000	0.0001	1.04	-2.43	-1.97
Wnt4	wingless-related MMV integration site 4	0.5373	0.0001	0.0002	-1.08	-2.2	-1.97
CD3043bD06Rik	RIKEN cDNA CD3043bD06 gene	0.0516	0.0000	0.0002	-1.38	-2.1	-1.97
Myo18a	myosin XVIIIa	0.8738	0.0001	0.0001	1.01	-2.12	-1.97
Trim28	tripartite motif-containing 28	0.4623	0.0000	0.0000	-1.04	-2.05	-1.98
Poi3f	polymerase (RNA) III (DNA directed) polypeptide F	0.8202	0.0022	0.0010	1.03	-1.81	-1.98
Ubpap2	ubiquitin-associated protein 2	0.0623	0.0000	0.0000	1.1	-2.15	-1.98
BC017647	cDNA sequence BC017647	0.3036	0.0000	0.0000	1.06	-2.28	-1.98
Rad23a	RAD23a homolog (S. cerevisiae)	0.9350	0.0000	0.0000	1.01	-2.37	-1.98
Sic27a1	solute carrier family 27 (fatty acid transporter), member 1	0.0561	0.0000	0.0007	-1.25	-2.64	-1.98
Kcnb1	potassium voltage-gated channel, Shab-related subfamily, member 1	0.6765	0.0002	0.0003	1.05	-2.36	-1.98
Mtap1a	microtubule-associated protein 1A	0.5093	0.0025	0.0002	-1.06	-1.61	-1.98
Trim7	tripartite motif-containing 7	0.3972	0.0001	0.0008	-1.00	-2.09	-1.98
Phf12	PHD finger protein 12	0.3030	0.0023	0.0088	-1.27	-3.03	-1.99
Fxr2	fragile X mental retardation, autosomal homolog 2	0.4168	0.0000	0.0000	1.04	-2.25	-1.99
Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)	0.1290	0.0014	0.0009	1.18	-1.7	-1.99
Vars	valyl-tRNA synthetase	0.1848	0.0000	0.0000	1.13	-1.96	-1.99
Cd22a1	collagen, type XXII, alpha 1	0.0736	0.0001	0.0003	-1.25	-2.42	-1.99
Zyx	zyxin	0.0859	0.0002	0.0000	1.14	-1.89	-1.99
Lrrc2	leucine rich repeat containing 2	0.3074	0.0007	0.0001	-1.17	-1.56	-1.99
Gaa	glucosidase, alpha, acid	0.4481	0.0003	0.0003	1.08	-2.02	-2
Ltr	lymphotxin B receptor	0.5151	0.0005	0.0004	-1.06	-1.94	-2
Nhs2	NHS-like 2	0.4593	0.0001	0.0000	1.05	-1.73	-2
Ankrd9	ankyrin repeat domain 9	0.0434	0.0000	0.0000	1.23	-2.04	-2
Zfp746	zinc finger protein 746	0.2387	0.0014	0.0050	1.16	-1.83	-2
Eif4e3	eukaryotic translation initiation factor 4E member 3	0.0843	0.0092	0.0015	-1.3	-1.64	-2
Flt4	FMS-like tyrosine kinase 4	0.8855	0.0003	0.0003	-1.01	-1.68	-2.01
Mpat2	mannitol-6-phosphate adenylyltransferase 2	0.4702	0.0003	0.0007	-1.08	-2.04	-2.01
Npep1	aminopeptidase-like 1	0.0670	0.0000	0.0001	1.16	-2.1	-2.01
Magix	MAGI family member, X-linked	0.3941	0.0000	0.0000	1.04	-2.19	-2.01
Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c	0.9105	0.0000	0.0006	-1.01	-2.4	-2.02
Pnm1	phosphomannomutase 1	0.7761	0.0001	0.0000	1.03	-2.01	-2.02
Mvfr8	myosin, heavy polypeptide 8, non-muscle	0.1289	0.0001	0.0001	-1.29	-1.98	-2.02

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Cdh13	cadherin 13	0.0321	0.0000	0.0000	1.18	-2.41	-2.02
Dab2ip	disabled homolog 2 (Drosophila) interacting protein	0.7460	0.0002	0.0008	1.04	-2.38	-2.02
Tricop	TRIO and F-actin-binding protein	0.8399	0.0000	0.0001	1.03	-2.13	-2.03
Spns2	spinster homolog 2 (Drosophila)	0.0570	0.0009	0.0004	1.35	-1.95	-2.03
Fam168a	family with sequence similarity 168, member A	0.5055	0.0000	0.0000	1.04	-1.96	-2.03
Bri3	brain protein 13	0.1529	0.0000	0.0001	1.13	-2.67	-2.04
Tmem25	transmembrane protein 25	0.0285	0.0005	0.0056	-1.76	-2.79	-2.04
Gpsm3	G-protein signaling modulator 3 (AGSS-like, C. elegans)	0.3330	0.0017	0.0017	-1.21	-2.05	-2.04
2310061J03Rik	RIKEN cDNA 2310061J03 gene	0.3331	0.0018	0.0028	-1.14	-1.98	-2.04
Synpo	synaptopodin	0.1824	0.0000	0.0000	1.09	-2.74	-2.05
Zfp651	zinc finger protein 651	0.7717	0.0000	0.0000	1.02	-2.19	-2.05
Mocs3	polybrominated cofactor synthesis 3	0.3560	0.0000	0.0000	1.08	-1.72	-2.05
Pevs1	peroxisomal biogenesis factor 6	0.3101	0.0000	0.0000	-1.06	-2.21	-2.05
Tmem52	transmembrane protein 52	0.5601	0.0002	0.0000	1.11	-1.85	-2.05
1110036O03Rik	RIKEN cDNA 1110036O03 gene	0.0162	0.0005	0.0006	-1.27	-1.46	-2.06
Tusc1	tumor suppressor candidate 1	0.3390	0.0033	0.0043	-1.18	-2.11	-2.06
Gpx3	glutathione peroxidase 3	0.2226	0.0000	0.0001	1.18	-2.14	-2.06
Gnd5	G protein-coupled receptor kinase 5	0.1304	0.0046	0.0081	-2.11	-2.06	-2.06
Cspg4	chondroitin sulfate proteoglycan 4	0.1413	0.0011	0.0025	-1.26	-2.42	-2.06
Myop	Myb-related transcription factor, partner of profilin	0.6612	0.0014	0.0010	1.04	-2	-2.06
2310021P13Rik	RIKEN cDNA 2310021P13 gene	0.7160	0.0000	0.0001	1.03	-3.39	-2.07
Phr1	PHD and ring finger domains 1	0.2181	0.0008	0.0002	1.14	-2.19	-2.07
Icam	basal cell adhesion molecule	0.3813	0.0006	0.0051	1.15	-1.99	-2.07
Tncr18	trinucleotide repeat containing 18	0.7436	0.0000	0.0001	1.05	-2.27	-2.07
Fgfr1	fibroblast growth factor receptor 1	0.1924	0.0005	0.0014	1.19	-2.38	-2.07
Lrsam1	leucine rich repeat and sterile alpha motif containing 1	0.3923	0.0005	0.0036	1.09	-1.75	-2.08
Tor1aip1	torsin A interacting protein 1	0.4567	0.0002	0.0003	-1.09	-2.03	-2.08
Zfp498	zinc finger protein 498	0.3654	0.0017	0.0003	1.12	-2.06	-2.08
Gdm	glutamate-cysteine ligase, modifier subunit	0.0383	0.0009	0.0009	-1.35	-1.86	-2.09
Hr	hairless	0.5986	0.0002	0.0001	1.07	-2.27	-2.09
Ring1	ring finger protein 1	0.1130	0.0000	0.0004	1.15	-2.77	-2.09
Ahd1	A1 hook, DNA binding motif, containing 1	0.4395	0.0004	0.0033	-1.2	-2.71	-2.09
6230424C14Rik	RIKEN cDNA 6230424C14 gene	0.1173	0.0000	0.0016	-1.23	-2.22	-2.09
Fkbp8	FK506 binding protein 8	0.5976	0.0000	0.0000	1.04	-2.3	-2.09
Atg9a	autophagy-related 9A (yeast)	0.5022	0.0000	0.0000	1.05	-2.19	-2.1
Tmc22	transmembrane and coiled-coil domains 2	0.7003	0.0000	0.0002	-1.03	-2.63	-2.1
Atxn2	ataxin 2-like	0.9182	0.0004	0.0003	-1.01	-2.27	-2.1
C2448	C2448 antigen, endosialin	0.9273	0.0022	0.0045	1.02	-2.5	-2.1
Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	0.4001	0.0000	0.0000	1.06	-2.25	-2.1
Sh3r2	SH3 domain containing ring finger 2	0.4236	0.0034	0.0026	-1.2	-2.04	-2.1
Irf8	interferon regulatory factor 8	0.0702	0.0001	0.0003	1.17	-2.42	-2.11
Tada3	transcriptional adaptor 3	0.1431	0.0018	0.0010	1.16	-2.05	-2.11
Wdr6	WD repeat domain 6	0.1765	0.0006	0.0008	-1.25	-2.11	-2.11
Mfsd4	major facilitator superfamily domain containing 4	0.0123	0.0016	0.0013	-1.5	-2.4	-2.11
Zfp362	zinc finger protein 362	0.5368	0.0000	0.0000	-1.05	-2.41	-2.11
Phactr2	phosphatase and actin regulator 2	0.5996	0.0010	0.0002	-1.05	-1.81	-2.12
Aes	amino-terminal enhancer of split	0.5677	0.0000	0.0000	1.05	-2.22	-2.12
Plo2	pellonin 2	0.8926	0.0000	0.0000	-1.03	-2.59	-2.13
Samd4b	sterile alpha motif domain containing 4B	0.9874	0.0001	0.0005	-1	-2.09	-2.13
Pxn	paxillin	0.4396	0.0000	0.0000	1.03	-2.29	-2.13
Rhb	ras homolog gene family, member B	0.8767	0.0033	0.0018	-1.02	-1.93	-2.13
Sf3a2	splicing factor 3a, subunit 2	0.9027	0.0004	0.0006	-1.01	-2.49	-2.13
Igfbp4	insulin-like growth factor binding protein 4	0.8276	0.0004	0.0087	-1.08	-2.22	-2.13
Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (v)	0.6756	0.0000	0.0000	1.02	-2.33	-2.14
Prikac	protein kinase, cAMP dependent, catalytic, alpha	0.5249	0.0000	0.0000	1.03	-2.6	-2.15
Lingo3	leucine rich repeat and Ig domain containing 3	0.4408	0.0005	0.0033	1.15	-2.61	-2.15
Lphn1	latrophilin 1	0.0389	0.0000	0.0000	-1.22	-2.37	-2.15
Irf2bp1	interferon regulatory factor 2 binding protein 1	0.3291	0.0001	0.0000	-1.08	-2.2	-2.16
Ganc	glucosidase, alpha; neutral C	0.9802	0.0000	0.0000	1	-2.99	-2.16
Trim8	tripartite motif-containing 8	0.3124	0.0000	0.0000	1.06	-2.11	-2.16
Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	0.2428	0.0032	0.0088	-1.2	-2.85	-2.16
Amdhd2	amidohydrolase domain containing 2	0.4987	0.0022	0.0027	-1.11	-1.86	-2.16
Sfr	serum response factor	0.2086	0.0000	0.0000	2.35	-2.17	-2.17
Ino80b	INO80 complex subunit B	0.6569	0.0001	0.0094	-1.09	-2.96	-2.18
Metn	metenrin, glial cell differentiation regulator	0.2875	0.0000	0.0000	-1.08	-2.4	-2.19
Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	0.5569	0.0008	0.0003	-1.05	-2.05	-2.19
Slc4a2	solute carrier family 4 (anion exchanger), member 2	0.0921	0.0001	0.0001	-1.21	-2.34	-2.19
Cpb6	chromobox homolog 6	0.9023	0.0000	0.0005	1.01	-2.97	-2.19
Piscr3	phospholipid scramblase 3	0.2958	0.0005	0.0001	-1.1	-1.94	-2.2
Steap3	STEAP family member 3	0.7464	0.0059	0.0097	1.05	-2.54	-2.2
4930404K06Rik	RIKEN cDNA 4930404K06 gene	0.3702	0.0007	0.0088	-1.27	-3.14	-2.2
Zfp316	zinc finger protein 316	0.5466	0.0004	0.0009	-1.06	-2.06	-2.21
Gatz3	glutathione S-transferase, theta 3	0.9126	0.0087	0.0081	-1.02	-1.55	-2.21
Szt2	seizure threshold 2	0.8226	0.0068	0.0005	1.04	-1.85	-2.21
Tnxb	tenascin XB	0.6024	0.0021	0.0060	-1.08	-2.19	-2.21
Sim2	single-minded homolog 2 (Drosophila)	0.2018	0.0003	0.0007	1.18	-2.56	-2.21
Tatdn2	TatD DNase domain containing 2	0.2454	0.0001	0.0009	-1.13	-2.07	-2.21
Dapk3	death-associated protein kinase 3	0.3070	0.0003	0.0005	-1.08	-1.97	-2.21
Efcab4a	EF-hand calcium binding domain 4A	0.7066	0.0010	0.0012	-1.06	-2.66	-2.22
A730011L01Rik	RIKEN cDNA A730011L01 gene	0.7804	0.0006	0.0030	-1.05	-3	-2.22
Pims	parathyrimosin	0.8182	0.0003	0.0004	-1.02	-2.06	-2.22
Opa3	optic atrophy 3 (human)	0.0377	0.0000	0.0000	-1.22	-2.23	-2.23
Gabbr1	gamma-aminobutyric acid (GABA) B receptor, 1	0.7723	0.0002	0.0002	-1.04	-2.1	-2.23
Ncstn	nicastatin	0.2500	0.0002	0.0002	-1.13	-2.23	-2.23
Mink1	misshapen-like kinase 1 (zebrafish)	0.9807	0.0001	0.0001	-1	-2.38	-2.23
Hoxc10	homeobox C10	0.0115	0.0001	0.0000	-1.41	-1.98	-2.24
Pim3	proliferation inducing myeloid 3	0.1224	0.0022	0.0037	1.38	-2.09	-2.24
Khrp	KH-type helix-loop-helix regulatory protein	0.0152	0.0009	0.0019	-2.87	-2.24	-2.24
Stim1	stromal interaction molecule 1	0.1951	0.0001	0.0003	-1.15	-2.35	-2.24
Tbc1d13	TBC1 domain family, member 13	0.2907	0.0035	0.0022	-1.17	-1.97	-2.24
Pofut2	protein O-fucosyltransferase 2	0.4411	0.0001	0.0008	1.07	-2.73	-2.24
Smtn	smoothenin	0.8177	0.0000	0.0000	1.02	-2.43	-2.24
Rnf51	ring finger protein 51	0.9735	0.0011	0.0000	-1	-1.6	-2.25
Lmna	lamin A	0.1698	0.0000	0.0000	1.1	-2.64	-2.25
Ski	ski sarcoma viral oncogene homolog (avian)	0.3632	0.0002	0.0003	1.09	-2.39	-2.26
Vamp2	vesicle-associated membrane protein 2	0.2192	0.0001	0.0001	1.11	-2.25	-2.26
Sox13	SRV-box containing gene 13	0.3451	0.0004	0.0021	1.09	-2.5	-2.27
Scap	SREBF chaperone	0.1495	0.0000	0.0000	1.16	-3.13	-2.27
Calr	calreticulin	0.8469	0.0000	0.0000	1.01	-2.28	-2.27
Zmiz2	zinc finger, MIZ-type containing 2	0.4851	0.0000	0.0000	1.04	-2.84	-2.27
Dmwd	dystrophin myotonia-containing WD repeat motif	0.1954	0.0000	0.0000	1.08	-2.3	-2.27
Spred2	sprouty-related, EVH1 domain containing 2	0.0163	0.0000	0.0000	-1.27	-2.6	-2.28
Lbi	limb-bud and heart	0.3796	0.0000	0.0000	-1.07	-3.24	-2.28
Rasa4	RAS p21 protein activator 4	0.6123	0.0000	0.0000	1.06	-3.14	-2.28
Itgb6	integrin beta 6	0.0520	0.0000	0.0000	-1.3	-1.75	-2.29
Prr12	proline rich 12	0.4000	0.0027	0.0021	-1.15	-2.11	-2.3
Lbx1	ladybird homeobox homolog 1 (Drosophila)	0.3714	0.0000	0.0005	-1.1	-2.98	-2.3
Khrgef1	Rho guanine nucleotide exchange factor (GEF) 1	0.8867	0.0000	0.0001	-1.04	-2.66	-2.3
Cuedc1	CUE domain containing 1	0.3488	0.0000	0.0000	-1.06	-2.66	-2.3
Ubiqul4	ubiquitin 4	0.4183	0.0001	0.0003	-1.08	-2.9	-2.3
S100pbp	S100P binding protein	0.0960	0.0002	0.0004	-1.21	-2.71	-2.3
Rps9ka4	ribosomal protein S6 kinase, polypeptide 4	0.7056	0.0041	0.0020	1.08	-2.25	-2.31
Rbm42	RNA binding motif 42	0.0426	0.0009	0.0000	1.06	-2.41	-2.31
4833447P13Rik	RIKEN cDNA 4833447P13 gene	0.2763	0.0041	0.0002	-1.28	-1.53	-2.31
Col4a2	collagen, type IV, alpha 2	0.9451	0.0007	0.0007	1.01	-2.26	-2.31
Rcor1	REST corepressor 1	0.0446	0.0000	0.0001	-1.14	-1.83	-2.32
Dazap1	DAZ associated protein 1	0.0792	0.0000	0.0000	1.16	-2.08	-2.32
Gstf1	glutathione S-transferase A resistance factor 1	0.1533	0.0000	0.0001	1.13	-2.74	-2.32
Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	0.1888	0.0002	0.0008	1.16	-2.48	-2.32
Snx24	sorting nexin 24	0.0711	0.0002	0.0000	-1.21	-1.99	-2.32
Slc25a42	solute carrier family 25, member 42	0.5606	0.0000	0.0000	-1.03	-2.77	-2.33
Csnk1e	casein kinase 1, epsilon	0.7553	0.0000	0.0000	-1.02	-2.45	-2.33
C242ep1	C24242 effect protein (Rho GTPase binding) 1	0.1872	0.0015	0.0018	-1.23	-2.22	-2.34
Rhg	RFGN O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.6707	0.0011	0.0015	-1.06	-2.72	-2.35
Zbtb7b	zinc finger and BTB domain containing 7B	0.9338	0.0009	0.0012	1.01	-3.06	-2.35
Ston2	stonin 2	0.0189	0.0000	0.0000	1.14	-2.94	-2.36
BC068474	cDNA sequence BC068474	0.3466	0.0000	0.0000	1.05	-2.15	-2.37
Scn1b	sodium channel, voltage-gated, type 1, beta	0.3434	0.0000	0.0000	1.04	-2.51	-2.37
Pgap2	post-GPI attachment to proteins 2	0.3886	0.0000	0.0000	-1.06	-1.98	-2.38
Furin	furin (paired basic amino acid cleaving enzyme)	0.8810	0.0000	0.0000	1.02	-2.34	-2.38
Sbf1	SET binding factor 1	0.0593	0.0000	0.0001	1.2	-2.54	-2.38
Med16	mediator complex subunit 16	0.3087	0.0000	0.0000	1.09	-2.86	-2.39
Cic	capicua homolog (Drosophila)	0.3460	0.0000	0.0000	1.09	-2.61	-2.39

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Bai22	HLA-B associated transcript 2-like 2	0.7758	0.0017	0.0004	1.04	-1.54	-2.39
Scy	selenocysteine lyase	0.8025	0.0004	0.0011	-1.04	-2.21	-2.4
Ubp4	latent transforming growth factor beta binding protein 4	0.8824	0.0011	0.0005	1.08	-3.28	-2.4
Gpatch8	G patch domain containing 8	0.3329	0.0000	0.0000	1.09	-2.26	-2.41
Shank3	SH3/ankyrin domain gene 3	0.3406	0.0001	0.0002	1.09	-2.88	-2.41
Rph3a1	rabphilin 3A-like (without C2 domains)	0.9135	0.0003	0.0004	-1.01	-2.35	-2.41
Plac2a	phosphatidylinositol 4-kinase type 2 alpha	0.9070	0.0068	0.0004	-1.02	-1.89	-2.41
Nas31	nucleolar associated 1, BEN and BTB (POZ) domain containing	0.3796	0.0000	0.0001	1.1	-2.82	-2.41
Dok4	docking protein 4	0.0759	0.0057	0.0054	-1.36	-2.05	-2.42
Cdk16	cyclin-dependent kinase 16	0.0550	0.0001	0.0001	1.2	-2.65	-2.44
Ppp6r1	protein phosphatase 6, regulatory subunit 1	0.3570	0.0006	0.0006	1.11	-2.6	-2.44
Zfp358	zinc finger protein 358	0.0399	0.0002	0.0003	1.24	-2.71	-2.44
F2d4	frizzled homolog 4 (Drosophila)	0.2038	0.0051	0.0016	-1.32	-1.96	-2.44
Cygb	cytoglobin	0.8009	0.0044	0.0082	-1.04	-2.72	-2.45
Rab5c	RAB5C, member RAS oncogene family	0.9427	0.0018	0.0012	1.01	-1.98	-2.45
E2f4	E2F transcription factor 4	0.5204	0.0000	0.0000	1.06	-2.63	-2.45
Khr18	kelch-like 18 (Drosophila)	0.3022	0.0001	0.0000	-1.09	-2.91	-2.46
6430527G18Rik	RIKEN cDNA 6430527G18 gene	0.0620	0.0001	0.0001	1.15	-2.03	-2.46
Comt1	catechol-O-methyltransferase 1	0.0386	0.0002	0.0002	-1.31	-2.35	-2.46
Pitpm2	phosphatidylinositol transfer protein, membrane-associated 2	0.1007	0.0000	0.0000	-1.17	-2.81	-2.47
Col4a1	collagen, type IV, alpha 1	0.6458	0.0006	0.0004	-1.07	-2.32	-2.47
Asb10	ankyrin repeat and SOCS box-containing 10	0.2520	0.0001	0.0000	-1.12	-2.2	-2.47
Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	0.0506	0.0000	0.0000	1.23	-3.03	-2.49
Tsga13	testis specific gene A13	0.9484	0.0007	0.0040	1.01	-2.88	-2.52
Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	0.7038	0.0000	0.0000	-1.02	-2.69	-2.52
Parv6	parvin, beta	0.8004	0.0000	0.0000	1.03	-3.09	-2.52
Tgm2	transglutaminase 2, C polypeptide	0.8338	0.0000	0.0000	-1.02	-2.68	-2.52
Trak1	trafficking protein, kinase binding 1	0.3638	0.0000	0.0000	-1.19	-2.52	-2.53
Sphk2	sphingosine kinase 2	0.3141	0.0003	0.0001	-1.11	-2.23	-2.53
Fam116b	family with sequence similarity 116, member B	0.8784	0.0006	0.0003	1.02	-2.23	-2.53
Atf5	activating transcription factor 5	0.2880	0.0000	0.0000	-1.14	-3.21	-2.54
9130404D08Rik	RIKEN cDNA 9130404D08 gene	0.5288	0.0000	0.0000	1.09	-2.09	-2.54
Syrn1	synovial sarcoma synovial sarcoma 1, synoviolin	0.3547	0.0000	0.0000	1.04	-2.47	-2.56
Ubi7	ubiquitin-like 7 (bone marrow stromal cell-derived)	0.8920	0.0000	0.0000	-1.01	-2.44	-2.56
Mbd3	methyl-CpG binding domain protein 3	0.1221	0.0000	0.0000	1.13	-2.64	-2.58
Ncor2	nuclear receptor co-repressor 2	0.5519	0.0000	0.0000	1.04	-3.51	-2.58
Wbp2	WW domain binding protein 2	0.0868	0.0000	0.0000	1.05	-2.67	-2.58
Rest	REST, silencing transcription factor	0.4347	0.0013	0.0001	-1.13	-2.58	-2.59
Bai2	HLA-B associated transcript 2	0.2472	0.0000	0.0000	1.04	-2.89	-2.59
Susd2	sushi domain containing 2	0.4514	0.0069	0.0053	-1.17	-2.43	-2.58
Pnpl2	patatin-like phospholipase domain containing 2	0.8034	0.0013	0.0021	-1.04	-2.91	-2.59
Ace	angiotensin converting enzyme (peptidyl-dipeptidase A) 1	0.1775	0.0000	0.0000	1.12	-2.7	-2.59
Kdelr1	KDEL (Yp48-Cy5) Leu-endorphin endoplasmic reticulum protein retention receptor 1	0.2845	0.0000	0.0000	-1.08	-2.89	-2.6
Htra3	HTRA serine peptidase 3	0.3281	0.0007	0.0015	-1.18	-3.29	-2.6
Vapb	vesicle-associated membrane protein, associated protein B and C	0.0752	0.0001	0.0001	-1.26	-2.63	-2.62
Srcap	Src2-related CREBBP activator protein	0.7151	0.0070	0.0004	-1.07	-1.77	-2.62
Pa2g4	proliferation-associated 2G4	0.0348	0.0000	0.0000	-1.17	-2.33	-2.63
Hsf4	heat shock transcription factor 4	0.3547	0.0001	0.0001	1.14	-2.68	-2.63
Cntrf	ciliary neurotrophic factor receptor	0.1914	0.0001	0.0001	-1.28	-2.53	-2.63
Tcf1b	transcription factor EB	0.6519	0.0000	0.0000	1.02	-2.66	-2.64
Bak1	BCL2-antagonist/killer 1	0.0305	0.0000	0.0000	1.15	-3.13	-2.65
Alp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	0.2122	0.0000	0.0000	1.13	-2.97	-2.65
Numb1	protein tyrosine phosphatase 4a3	0.8051	0.0028	0.0016	-1.28	-2.68	-2.66
Ptp4a3	protein tyrosine phosphatase 4a3	0.0540	0.0000	0.0000	1.15	-3.02	-2.66
Calcoo1	calcium binding and coiled coil domain 1	0.8184	0.0000	0.0000	1.01	-2.68	-2.66
Cdh5	cadherin 5	0.0592	0.0000	0.0000	-1.17	-3.3	-2.67
Hnmp1	heterogeneous nuclear ribonucleoprotein L	0.1581	0.0000	0.0000	-1.32	-2.82	-2.67
Pigt	phosphatidylinositol glycan anchor biosynthesis, class 1	0.7886	0.0008	0.0008	1.07	-2.93	-2.67
Tenc1	tenascin like C1 domain-containing phosphatase	0.6462	0.0004	0.0029	1.06	-4.11	-2.68
Hs1bp3	HCLS1 binding protein 3	0.2193	0.0009	0.0024	-1.23	-2.85	-2.69
Fam114a2	family with sequence similarity 114, member A2	0.7534	0.0001	0.0000	-1.03	-2.24	-2.69
Raver1	ribonucleoprotein, PTB-binding 1	0.1525	0.0000	0.0001	1.08	-4.18	-2.72
Zfp425	zinc finger protein 425	0.0383	0.0003	0.0003	-1.36	-2.68	-2.72
Hspg2	perlecan (heparan sulfate proteoglycan 2)	0.3384	0.0000	0.0000	-1.1	-2.96	-2.74
Leng8	leukocyte receptor cluster (LRC) member 8	0.2055	0.0000	0.0000	-1.11	-2.84	-2.74
9330161A08Rik	RIKEN cDNA 9330161A08 gene	0.1297	0.0006	0.0006	-1.27	-3.17	-2.75
Foxp4	forkhead box P4	0.0917	0.0012	0.0004	-1.27	-2.98	-2.75
Irbp2	ITB (POZ) domain containing 2	0.3863	0.0003	0.0010	1.01	-3.89	-2.76
Mu1	mitochondrial ubiquitin ligase activator of NFKB 1	0.4601	0.0000	0.0000	1.08	-3.39	-2.76
Mdga1	MAM domain containing glycosylphosphatidylinositol anchor 1	0.5285	0.0072	0.0007	1.09	-2.37	-2.77
Erf2c2	eukaryotic translation initiation factor 2C, 2	0.9563	0.0001	0.0000	1.01	-2	-2.78
Seih8	SET domain containing (lysine methyltransferase) 8	0.8833	0.0000	0.0000	-1.01	-3.25	-2.78
Rnf126	ring finger protein 126	0.0227	0.0001	0.0001	-1.34	-2.19	-2.79
Calcob1	calcium channel, voltage-dependent, beta 1 subunit	0.4347	0.0002	0.0002	1.1	-3.24	-2.8
Spock2	sparc osteonectin, cwcv and kazal-like domains proteoglycan 2	0.8596	0.0011	0.0004	-1.03	-2.27	-2.8
Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	0.5528	0.0057	0.0056	-1.16	-3.38	-2.81
Fam108a	family with sequence similarity 108, member A	0.0714	0.0000	0.0000	1.11	-3.14	-2.81
Khrndb	kelch domain containing 8b	0.0219	0.0001	0.0043	-1.17	-6.42	-2.82
Mapt	microtubule-associated protein tau	0.0624	0.0000	0.0000	1.15	-2.83	-2.83
Notch4	Notch gene homolog 4 (Drosophila)	0.3431	0.0004	0.0004	1.14	-3.04	-2.83
Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	0.7778	0.0003	0.0003	-1.04	-2.74	-2.83
Ndn	nicotinic homolog (zebrafish)	0.6435	0.0004	0.0005	1.06	-2.78	-2.83
Rnf11	ring finger protein 11	0.8441	0.0000	0.0000	1.02	-2.87	-2.84
Capn1	calpain 1	0.6345	0.0000	0.0000	1.03	-3.31	-2.85
Plekho2	pleckstrin homology domain containing, family O member 2	0.4136	0.0000	0.0000	-1.05	-2.29	-2.86
Epn1	epsin 1	0.1797	0.0000	0.0000	1.07	-3.55	-2.86
Znfhc8	zinc finger, D/HHC domain containing 8	0.2831	0.0000	0.0000	-1.17	-2.92	-2.86
Hra	histone cell cycle regulation distinctive homolog A (S. cerevisiae)	0.8913	0.0006	0.0006	1.04	-2.86	-2.86
Tie1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	0.0109	0.0000	0.0000	-1.16	-2.93	-2.86
D11Erd717e	DNA segment, Chr 11, ERATO Doi 717, expressed	0.6481	0.0035	0.0008	-1.07	-1.91	-2.88
Zbtb39	zinc finger and BTB domain containing 39	0.6810	0.0001	0.0001	-1.04	-2.34	-2.89
Lnc20	leucine rich repeat containing 20	0.2852	0.0000	0.0000	1.11	-2.84	-2.94
Znfhc18	zinc finger, D/HHC domain containing 18	0.3098	0.0000	0.0000	-1.01	-3.35	-2.94
Ppp2r3d	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta	0.1536	0.0004	0.0001	-1.32	-3.39	-2.95
Sic25a23	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 23	0.2803	0.0009	0.0010	-1.14	-3.16	-2.96
Vat1	vesicle amine transport protein 1 homolog (T. californica)	0.8795	0.0001	0.0015	-1.02	-6.25	-3
Fgf7	c-fos induced growth factor	0.2770	0.0010	0.0010	-1.21	-2.86	-3.02
Map2k2	mitogen-activated protein kinase kinase 2	0.2740	0.0000	0.0000	1.06	-3.63	-3.03
Fntb	farnesyltransferase, CAAX box, beta	0.3310	0.0000	0.0000	1.09	-2.7	-3.06
Rusc2	RUN and SH3 domain containing 2	0.9537	0.0000	0.0002	1.01	-2.98	-3.07
Npr1	natriuretic peptide receptor 1	0.1732	0.0004	0.0003	-1.15	-2.61	-3.09
Nbl1	neuroblastoma, suppression of tumorigenicity 1	0.9864	0.0000	0.0017	-1	-4.04	-3.11
Tnm32	tripartite motif containing 32	0.3803	0.0000	0.0000	-1.03	-3.09	-3.11
Six2	sine oculis-related homeobox 2 homolog (Drosophila)	0.7358	0.0001	0.0000	1.05	-2.76	-3.13
Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	0.6233	0.0000	0.0000	-1.05	-2.87	-3.14
1110054M08Rik	RIKEN cDNA 1110054M08 gene	0.8610	0.0000	0.0000	1.02	-3.2	-3.14
Vegfb	vascular endothelial growth factor B	0.4101	0.0000	0.0000	1.07	-3.47	-3.16
Mapre3	microtubule-associated protein, RPIEB family, member 3	0.0216	0.0000	0.0000	1.23	-3.41	-3.17
Pcdh1	protocadherin 1	0.5408	0.0090	0.0025	-1.17	-2.31	-3.18
Lfng	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.3075	0.0031	0.0053	-1.27	-4.7	-3.18
Fbrs	fibrosin	0.6230	0.0000	0.0005	1.07	-4.43	-3.19
Gain2	UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylglucosaminyltransferase 2	0.6751	0.0000	0.0000	1.04	-2.72	-3.2
Ppp11b6a	protein phosphatase 1, regulatory (inhibitor) subunit 1b6a	0.0106	0.0000	0.0005	-1.44	-5.23	-3.26
Cd300g	CD300 antigen like family member G	0.1001	0.0001	0.0002	-1.24	-3.39	-3.26
Ece1	endothelin converting enzyme 1	0.5685	0.0009	0.0001	-1.09	-1.95	-3.28
Glt1	G protein-coupled receptor kinase-interactor 1	0.1571	0.0000	0.0000	1.08	-3.57	-3.28
9330066F20Rik	RIKEN cDNA 9330066F20 gene	0.3334	0.0003	0.0001	1.1	-2.18	-3.29
2310026I24Rik	RIKEN cDNA 2310026I24 gene	0.2895	0.0000	0.0000	1.08	-2.53	-3.3
Tgfb1	transforming growth factor, beta 1	0.8713	0.0009	0.0014	1.03	-4.63	-3.31
Cpox	coproporphyrinogen oxidase	0.2683	0.0000	0.0000	1.14	-3.19	-3.35
Ptpn21	protein tyrosine phosphatase, non-receptor type 21	0.4697	0.0000	0.0000	1.05	-3.77	-3.35
Poox12	podocalyxin-like 2	0.5309	0.0000	0.0000	-1.03	-4.17	-3.35
Syt12	synaptobrevin 12	0.0719	0.0014	0.0088	-1.36	-2.63	-3.36
Coro2b	coronin, actin binding protein, 2b	0.0522	0.0011	0.0003	-1.41	-2.63	-3.38
Jund	Jun proto-oncogene related gene d	0.7900	0.0007	0.0001	-1.04	-2.41	-3.38
Zfp385a	zinc finger protein 385A	0.4382	0.0053	0.0053	-1.16	-2.85	-3.38
Cdc57	coiled-coil domain containing 57	0.3470	0.0000	0.0000	1.05	-4.63	-3.38
Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	0.0887	0.0000	0.0000	-1.14	-4.42	-3.41
Akna	AT-hook transcription factor	0.1594	0.0053	0.0026	-1.42	-2.79	-3.42
Fam101b	family with sequence similarity 101, member B	0.0114	0.0000	0.0000	-1.48	-3.03	-3.44
Cnrf3	CCR4-NOT transcription complex, subunit 3	0.4344	0.0001	0.0003	1.11	-5.14	-3.44
Test1	testis specific protein kinase 1	0.8511	0.0000	0.0000	1.01	-4.09	-3.45
Zfp865	zinc finger protein 865	0.1556	0.0001	0.0000	-1.14	-2.94	-3.45

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Rgma	RCM domain family, member A	0.4774	0.0000	0.0000	-1.06	-4.38	-3.45
Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	0.0494	0.0000	0.0000	1.19	-3.25	-3.48
Sdp	sane acute-binding protein homolog (Drosophila)	0.3834	0.0001	0.0001	1.41	2.94	-3.6
Pcbp4	poly(RC) binding protein 4	0.2608	0.0000	0.0000	1.09	-4.38	-3.5
Anid3b	AT rich interactive domain 3B (BRIGHT-like)	0.7152	0.0000	0.0020	1.07	-5.99	-3.53
Fam57b	family with sequence similarity 57, member B	0.8302	0.0000	0.0002	1.03	-5.91	-3.61
Cabin1	calciuretin binding protein 1	0.2557	0.0003	0.0001	-1.15	-2.23	-3.61
Cd424ep4	CD424 effector protein (Rho GTPase binding) 4	0.8532	0.0006	0.0008	1.09	-3.26	-3.66
Notch3	Notch gene homolog 3 (Drosophila)	0.1256	0.0000	0.0000	1.19	-4.01	-3.66
Zfp579	zinc finger protein 579	0.8946	0.0000	0.0000	1.01	-4.06	-3.68
Zfp395	zinc finger protein 395	0.0831	0.0000	0.0000	-1.12	-5.54	-3.74
Hoxa4	homeobox A4	0.6493	0.0000	0.0002	1.06	-3.73	-3.75
Nr1f1	nuclear receptor subfamily 1, group D, member 1	0.7652	0.0000	0.0001	1.05	-6.47	-3.8
A230071A22Rik	RIKEN cDNA A230071A22 gene	0.2414	0.0002	0.0001	-1.17	-2.35	-3.81
Ap2a1	adaptor protein complex AP-2, alpha 1 subunit	0.4755	0.0000	0.0000	1.06	-4.72	-3.83
Car2bp	cysteine and glycine-rich protein 2 binding protein	0.5962	0.0041	0.0004	-1.14	-2.28	-3.92
Ctfa23	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0.0229	0.0000	0.0000	-1.38	-4.39	-3.96
Col1a1	collagen, type I, alpha 1	0.3716	0.0007	0.0010	-1.19	-3.78	-3.97
Bcat2	branched chain aminotransferase 2, mitochondrial	0.6500	0.0001	0.0001	1.06	-4.36	-4.01
Fam110a	family with sequence similarity 110, member A	0.5015	0.0042	0.0073	-1.19	-4.72	-4.05
E2f2	E2F transcription factor 2	0.2644	0.0079	0.0033	-1.53	-3.64	-4.12
Tpcn1	two pore channel 1	0.2380	0.0000	0.0000	-1.1	-4.21	-4.24
Raz23b	RAZ23b homolog (S. cerevisiae)	0.2327	0.0000	0.0000	-1.1	-4.33	-4.27
Snfb2	syntrophin, basic 2	0.0319	0.0034	0.0008	-1.58	-2.72	-4.31
Sta	steroid sulfatase	0.9461	0.0010	0.0017	1.01	-5.85	-4.39
Unc5a	unc-5 homolog A (C. elegans)	0.9016	0.0009	0.0008	1.02	-3.66	-4.41
Gm12689	predicted gene 12689	0.5048	0.0036	0.0028	-1.22	-4.48	-4.47
Mann1t1	mannosyl transferase, alpha class 1B, member 1	0.7538	0.0000	0.0000	1.05	-3.98	-4.46
Baz2a	bromodomain adjacent to zinc finger domain, 2A	0.1088	0.0000	0.0000	-1.15	-2.01	-4.51
Kdm6b	KDM1 lysine (K)-specific demethylase 6B	0.8195	0.0006	0.0005	-1.04	-4.25	-4.53
Wdct1	WD and tetrapeptide repeats 1	0.6109	0.0000	0.0000	1.05	-4.77	-4.58
Map3k10	mitogen-activated protein kinase kinase kinase 10	0.7994	0.0006	0.0003	-1.05	-3.95	-4.62
C19orf18	expressed sequence C19orf18	0.4657	0.0000	0.0000	-1.18	-3.63	-4.64
Plov1	prostate tumor over expressed gene 1	0.3074	0.0002	0.0000	1.11	-3.75	-4.67
Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	0.7742	0.0002	0.0002	-1.05	-5.04	-4.85
Poir2a	polymerase (RNA) II (DNA directed) polypeptide A	0.3859	0.0000	0.0000	-1.06	-5.7	-4.89
Kdm2a	lysine (K)-specific demethylase 2A	0.2243	0.0000	0.0000	-1.11	-5.22	-4.96
Maz	5.8 kb zinc finger protein (purine-binding transcription factor)	0.6897	0.0000	0.0000	-1.16	-5.3	-5.0
Nfic	nuclear factor IIC	0.0596	0.0000	0.0000	-1.14	-5.84	-5.35
Phospho1	phosphatase, orphan 1	0.2237	0.0004	0.0005	1.21	-5.84	-5.4
Scaf1	SR-related CTD-associated factor 1	0.0861	0.0000	0.0000	1.19	-5.46	-5.44
Dusp23	dual specificity phosphatase 23	0.4500	0.0000	0.0000	1.05	-4.43	-5.74
Mmp15	matrix metalloproteinase 15	0.8516	0.0000	0.0000	1.06	-6.31	-5.64
Klc2	kinesin light chain 2	0.5136	0.0000	0.0000	1.04	-3.84	-6.25
Arhgap10	Rho GTPase activating protein 10	0.0367	0.0000	0.0000	1.28	-6.38	-6.35
Mpz	myelin protein zero	0.6883	0.0001	0.0001	1.05	-5.67	-6.39
Ppard	peroxisome proliferator activator receptor delta	0.4113	0.0000	0.0000	1.1	-5.64	-6.41
Ras2b	RAS2b family, member 2	0.3727	0.0000	0.0000	-1.11	-6.46	-6.48
Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	0.1740	0.0000	0.0000	1.11	-8.57	-6.62
Anpep	alanine (membrane) aminopeptidase	0.2548	0.0000	0.0000	1.21	-6.31	-7.25
Tmem109	transmembrane protein 109	0.1482	0.0000	0.0000	1.11	-7.61	-7.31
Dmpk	dystrophin myotonic-protein kinase	0.0605	0.0000	0.0000	-1.21	-14.54	-10.21
Mark4	MAP/kinectin-like affinity-regulating kinase 4	0.4856	0.0004	0.0040	1.18	-27.84	-11.16
Lrp5	low density lipoprotein receptor-related protein 5	0.6824	0.0000	0.0000	-1.06	-10.3	-14.44
4930572J05Rik	RIKEN cDNA 4930572J05 gene	0.1367	0.0000	0.0000	-1.25	-8.55	-15.39
Palm	paralectmin	0.6540	0.0032	0.0011	-1.11	-5.16	-17.9
2700094K13Rik	RIKEN cDNA 2700094K13 gene	0.0001	0.0000	0.0000	3.77	4.17	4.25
Gp1	glutathione peroxidase 1	0.0000	0.0000	0.0000	2.98	3.55	3.3
Sepw1	selenoprotein W, muscle 1	0.0000	0.0000	0.0000	3.28	2.21	2.1
15-Sep	selenoprotein	0.0001	0.0000	0.0000	1.42	1.74	1.72
Vps4b	vacuolar protein sorting 4b (yeast)	0.0065	0.0000	0.0001	-1.27	1.92	1.71
Eif5	eukaryotic translation initiation factor 5	0.0081	0.0000	0.0002	-1.28	1.61	1.63
Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	0.0000	0.0000	0.0003	1.31	1.85	1.61
3110001022Rik	RIKEN cDNA 3110001022 gene	0.0077	0.0037	0.0046	1.45	1.63	1.6
Cdkn1b	cyclin-dependent kinase inhibitor 1B	0.0054	0.0004	0.0049	-1.71	2	1.59
Selm	selenoprotein M	0.0002	0.0004	0.0072	1.66	1.6	1.54
Dbr1	debranching enzyme homolog 1 (S. cerevisiae)	0.0051	0.0044	0.0015	-1.33	1.32	1.45
Ratggb1b	RAS geranylgeranyl transferase 1, subunit 1	0.0000	0.0000	0.0000	1.26	1.5	1.42
Mrps11	mitochondrial ribosomal protein S11	0.0087	0.0026	0.0027	1.31	1.52	1.42
Urod	uroporphyrinogen decarboxylase	0.0031	0.0000	0.0000	1.1	1.44	1.38
Stx12	syntaxin 12	0.0050	0.0001	0.0000	1.12	1.27	1.35
Pvt1	ribosomal protein L7	0.0039	0.0002	0.0001	1.21	1.42	1.32
Pwp1	PWP1 homolog (S. cerevisiae)	0.0000	0.0000	0.0002	1.09	1.05	1.31
Mrlp42	mitochondrial ribosomal protein L42	0.0031	0.0002	0.0002	1.15	1.3	1.31
Rps5	ribosomal protein S5	0.0043	0.0002	0.0001	1.2	1.23	1.27
Tcp1	T-complex protein 1	0.0064	0.0001	0.0006	1.14	1.25	1.27
Sec13	SEC13 homolog (S. cerevisiae)	0.0062	0.0001	0.0003	1.16	1.33	1.26
Pmrtf	protein arginine N-methyltransferase 7	0.0051	0.0000	0.0009	1.13	1.31	1.24
Prip39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	0.0004	0.0031	0.0017	1.32	1.28	1.22
Paip2	polyadenylate-binding protein-interacting protein 2	0.0020	0.0051	0.0057	-1.55	1.31	1.2
2410015M20Rik	RIKEN cDNA 2410015M20 gene	0.0092	0.0062	0.0059	1.14	1.16	1.18
Uqcrcf1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0.0038	0.0076	0.0026	1.19	1.12	1.15
Sdhb	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0.0064	0.0001	0.0003	1.11	1.16	1.15
Dazap2	DAZ associated protein 2	0.0070	0.0016	0.0036	-1.13	-1.16	-1.11
Nrbp1	nuclear receptor binding protein 1	0.0006	0.0000	0.0057	1.38	-1.45	-1.22
Pde4dp	phosphodiesterase 4D interacting protein (myomegalin)	0.0086	0.0002	0.0064	1.15	-1.43	-1.22
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	0.0083	0.0002	0.0086	1.73	-1.4	-1.23
Pphn1	periplan	0.0000	0.0005	0.0001	-1.26	-1.19	-1.24
Pymg	myosin glycocy phosphorylase	0.0077	0.0006	0.0042	1.17	-1.36	-1.26
Phb2	prohibitin 2	0.0007	0.0000	0.0002	1.18	-1.34	-1.28
Arpc2	actin related protein 2/3 complex, subunit 2	0.0012	0.0004	0.0002	-1.31	-1.29	-1.29
Obscn	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0.0066	0.0001	0.0069	1.22	-1.55	-1.29
Tmm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	0.0056	0.0011	0.0086	1.13	-1.33	-1.3
Ogdn	oxoglutarate dehydrogenase (lipamide)	0.0041	0.0001	0.0008	1.19	-1.51	-1.31
Tmtt1	TRMT1 tRNA methyltransferase 1 homolog (S. cerevisiae)	0.0047	0.0024	0.0078	1.27	-1.38	-1.34
Ldb3	LIM domain binding 3	0.0041	0.0000	0.0003	1.17	-1.45	-1.34
Irf2	interferon-related developmental regulator 2	0.0028	0.0001	0.0030	1.34	-1.67	-1.37
Bmyc	brain expressed myelocytomatosis oncogene	0.0086	0.0072	0.0022	1.25	-1.47	-1.36
Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	0.0078	0.0004	0.0014	1.27	-1.4	-1.38
Tat	thiosulfate sulfurtransferase, mitochondrial	0.0056	0.0003	0.0061	-1.22	-1.55	-1.39
Rala	v-rat simian leukemia viral oncogene homolog A (ras related)	0.0006	0.0014	0.0004	1.29	-1.39	-1.4
Flt1	flightless 1 homolog (Drosophila)	0.0052	0.0000	0.0014	1.16	-1.76	-1.43
Sec2b	SEC2B homolog (S. cerevisiae)	0.0000	0.0004	0.0002	1.31	-1.35	-1.44
Chd8	chromodomain helicase DNA binding protein 8	0.0086	0.0002	0.0007	-1.28	-1.64	-1.47
9430021M05Rik	RIKEN cDNA 9430021M05 gene	0.0003	0.0001	0.0037	-2.68	-2.2	-1.5
Dcn2	dynactin 2	0.0090	0.0000	0.0000	1.12	-1.54	-1.53
Scnm1	sex comb on midleg homolog 1	0.0069	0.0000	0.0017	1.16	-1.89	-1.56
Dag1	dystroglycan	0.0005	0.0000	0.0002	2.06	-2.02	-1.61
Osgn1	oxidative stress induced growth inhibitor 1	0.0084	0.0059	0.0046	-1.27	-1.57	-1.62
Rsad1	radical S-adenosyl methionine domain containing 1	0.0004	0.0000	0.0020	-1.32	-1.81	-1.65
Cxcl14	chemokine (C-X-C motif) ligand 14	0.0012	0.0000	0.0003	1.35	-2.16	-1.69
Mett11	methyltransferase like 1	0.0078	0.0005	0.0000	-1.33	-1.59	-1.7
Tmem179b	transmembrane protein 179b	0.0046	0.0003	0.0000	-1.22	-1.61	-1.7
Map3k7	mitogen-activated protein kinase kinase kinase 7	0.0050	0.0001	0.0003	1.32	-1.67	-1.71
Satb1	special AT-rich sequence binding protein 1	0.0022	0.0000	0.0001	-1.18	-2.19	-1.72
Rhbtd1	rhomboid, veinlet-like 1 (Drosophila)	0.0009	0.0000	0.0000	1.28	-1.84	-1.74
Ttc28	tetratricopeptide repeat domain 28	0.0033	0.0000	0.0000	1.29	-1.85	-1.82
Ras3	HLA-B-associated transcript 3	0.0031	0.0000	0.0000	1.16	-2.27	-1.86
Mapkapk2	MAP kinase-activated protein kinase 2	0.0014	0.0000	0.0000	1.22	-2.58	-1.99
R3hdm2	R3H domain containing 2	0.0050	0.0000	0.0000	1.16	-2.68	-2.08
Tbcel	tubulin folding cofactor E-like	0.0055	0.0000	0.0000	-1.18	-2.98	-2.34
Gdc	glutamate-cysteine ligase, catalytic subunit	0.0022	0.0000	0.0000	-1.45	-1.98	-2.35
Dusp10	dual specificity phosphatase 10	0.0073	0.0006	0.0019	1.78	-2.74	-2.46
Lmo4	LIM domain only 4	0.0044	0.0001	0.0001	-1.49	-2.36	-2.68
Nudt11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.0059	0.0021	0.0039	-1.84	-4	-3.12
Cpt1c	carbamate palmitoyltransferase 1c	0.0058	0.0006	0.0016	-1.93	-2.61	-3.19
B930041F14Rik	RIKEN cDNA B930041F14 gene	0.0020	0.0005	0.0002	-1.68	-2.18	-3.33