

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Iqk-V19-20	immunoglobulin kappa chain variable 19 (V19)-20	0.0078	0.0046	0.0139	6.48	3.13	6.11
1700095J03Rik	RIKEN cDNA 1700095J03 gene	0.0091	0.0029	0.0655	3.51	4.32	2.11
Mast3	microtubule associated serine/threonine kinase 3	0.0003	0.0008	0.0176	1.8	1.81	1.96
9630019E01Rik	RIKEN cDNA 9630019E01 gene	0.0035	0.0043	0.0412	1.67	2.12	1.77
Rab38	RAB38, member of RAS oncogene family	0.0024	0.0057	0.0238	2.1	2.12	1.7
AI506816	expressed sequence AI506816	0.0076	0.0061	0.2661	2.77	2.97	1.66
AU022297	expressed sequence AU022297	0.0055	0.0000	0.0995	1.72	2.2	1.6
Hgf	hepatocyte growth factor	0.0064	0.0065	0.2119	2.16	2.35	1.44
Plekhh1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	0.0079	0.0003	0.0116	1.37	1.86	1.42
Utp23	UTP23, small subunit (SSU) processome component, homolog (yeast)	0.0052	0.0088	0.0243	1.42	1.26	1.42
Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	0.0001	0.0000	0.0100	-1.29	1.54	1.37
Ddb1	DDB1 and CUL4 associated factor 5	0.0042	0.0026	0.0347	1.26	1.35	1.35
5830443J22Rik	RIKEN cDNA 5830443J22 gene	0.0003	0.0023	0.1055	1.37	1.34	1.33
Urgcp	upregulator of cell proliferation	0.0035	0.0014	0.1392	1.29	1.28	1.24
1700094D03Rik	RIKEN cDNA 1700094D03 gene	0.0057	0.0003	0.5435	1.52	1.88	1.21
Smcr7l	Smith-Magenis syndrome chromosome region, candidate 7-like (human)	0.0096	0.0009	0.0577	1.18	1.32	1.2
Tshz1	teashirt zinc finger family member 1	0.0040	0.0025	0.2860	1.24	1.22	1.09
9430008C03Rik	RIKEN cDNA 9430008C03 gene	0.0016	0.0025	0.8851	1.42	1.42	1.03
2310040G24Rik	RIKEN cDNA 2310040G24 gene	0.0041	0.0028	0.7347	-1.57	-1.37	-1.03
Secisbp2l	SECIS binding protein 2-like	0.0070	0.0003	0.1522	-1.13	-1.22	-1.07
Amp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.0068	0.0002	0.1689	-1.15	-1.22	-1.08
Farsb	phenylalanyl-tRNA synthetase, beta subunit	0.0071	0.0028	0.2154	-1.34	-1.53	-1.13
Mocos	molybdenum cofactor sulfurase	0.0025	0.0042	0.0230	-1.29	-1.25	-1.15
Hemk1	HemK methyltransferase family member 1	0.0069	0.0024	0.1921	-1.34	-1.54	-1.17
Comtd1	catechol-O-methyltransferase domain containing 1	0.0062	0.0083	0.0532	-1.33	-1.55	-1.17
Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	0.0050	0.0087	0.0227	-1.35	-1.21	-1.17
Thns2	threonine synthase-like 2 (bacterial)	0.0021	0.0033	0.0230	-1.32	-1.34	-1.18
Prkaq1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0.0060	0.0028	0.0603	-1.35	-1.34	-1.2
Psmc5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	0.0070	0.0074	0.0199	-1.33	-1.38	-1.26
Cdcp1	CUB domain containing protein 1	0.0075	0.0016	0.0195	-1.38	-1.63	-1.28
Ttl12	tubulin tyrosine ligase-like family, member 12	0.0086	0.0002	0.0124	-1.22	-1.55	-1.35
Gstm2	glutathione S-transferase, mu 2	0.0043	0.0008	0.0948	-1.57	-1.91	-1.36
1700012B15Rik	RIKEN cDNA 1700012B15 gene	0.0018	0.0056	0.0273	-1.42	-1.42	-1.38
Ran	RAN, member RAS oncogene family	0.0053	0.0013	0.0148	-1.54	-1.64	-1.45
9130409J23Rik	RIKEN cDNA 9130409J23 gene	0.0080	0.0039	0.0249	-1.85	-1.83	-1.47
5330421C15Rik	RIKEN cDNA 5330421C15 gene	0.0022	0.0024	0.0173	-1.4	-1.73	-1.49
Haus1	HAUS augmin-like complex, subunit 1	0.0020	0.0074	0.0389	-1.36	-1.35	-1.5
AF529169	cDNA sequence AF529169	0.0039	0.0054	0.0897	-3.53	-3.03	-1.67
Gpx2	glutathione peroxidase 2	0.0032	0.0092	0.0112	-6.23	-3.64	-3.1
D8ErtD56e	DNA segment, Chr 8, ERATO Doi 56, expressed	0.0037	0.0879	0.0090	8.71	4.53	6.14
1700012A03Rik	RIKEN cDNA 1700012A03 gene	0.0055	0.0319	0.0087	2.03	2.46	2.59
Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	0.0039	0.0656	0.0037	2.01	2.21	2.41
1700026H06Rik	RIKEN cDNA 1700026H06 gene	0.0058	0.0198	0.0045	2.04	2.27	2.34
Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	0.0042	0.0826	0.0056	1.77	1.46	2.26
Tdrd1	tudor domain containing 1	0.0065	0.0179	0.0062	1.63	1.84	2.21
Cyp4a14	cytochrome P450, family 4, subfamily a, polypeptide 14	0.0020	0.0154	0.0048	2.33	2.13	2.03
Rab42-ps	RAB42, member RAS oncogene family, pseudogene	0.0059	0.0422	0.0057	2.43	1.72	1.93
Cyp2c37	cytochrome P450, family 2, subfamily c, polypeptide 37	0.0038	0.0439	0.0002	1.55	1.55	1.8
Mgmt	O-6-methylguanine-DNA methyltransferase	0.0090	0.8706	0.0087	1.88	1.04	1.58
Ube2u	ubiquitin-conjugating enzyme E2U (putative)	0.0040	0.1773	0.0052	1.64	1.25	1.55
Slc37a4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	0.0041	0.0381	0.0011	1.39	1.3	1.5
Imp2l2	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.0016	0.0168	0.0006	1.27	1.28	1.5
Rnf26	ring finger protein 26	0.0009	0.0194	0.0025	1.38	1.34	1.49
Uqcrb	ubiquinol-cytochrome c reductase binding protein	0.0046	0.0112	0.0000	1.2	1.25	1.48
Dpyd	dihydropyrimidine dehydrogenase	0.0017	0.0284	0.0017	1.37	1.41	1.45
1700052M09Rik	RIKEN cDNA 1700052M09 gene	0.0000	0.5999	0.0092	1.4	1.06	1.44
Topors	topoisomerase I binding, arginine/serine-rich	0.0090	0.0793	0.0088	1.4	1.25	1.44
Asb7	ankyrin repeat and SOCS box-containing 7	0.0069	0.1153	0.0014	1.2	1.35	1.43
Ulk1	Unc-51 like kinase 1 (C. elegans)	0.0004	0.1281	0.0019	1.36	1.22	1.41
Dnaic19	DnaJ (Hsp40) homolog, subfamily C, member 19	0.0038	0.4175	0.0034	1.2	1.08	1.4
Antrx2	anthrax toxin receptor 2	0.0060	0.1175	0.0011	1.26	1.33	1.4
Cml2	camello-like 2	0.0028	0.0381	0.0054	1.32	1.3	1.38
Gulo	gulonolactone (L-) oxidase	0.0023	0.0158	0.0007	1.38	1.27	1.37
Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1	0.0031	0.0272	0.0062	1.3	1.22	1.36
Sart3	squamous cell carcinoma antigen recognized by T-cells 3	0.0024	0.2752	0.0054	1.46	1.23	1.28
Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0.0062	0.0129	0.0011	1.15	1.31	1.25
Atp5f2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	0.0030	0.8376	0.0079	1.17	1.02	1.17
Psmc1	proteasome (prosome, macropain) 26S subunit, alpha	0.0051	0.0356	0.0098	-1.26	-1.18	-1.19
Fkbp2	FK506 binding protein 2	0.0027	0.2969	0.0014	-1.18	-1.08	-1.21
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0.0005	0.0140	0.0052	-1.32	-1.21	-1.21
Dync1h1	dynein cytoplasmic 1 heavy chain 1	0.0007	0.2639	0.0000	-1.18	-1.05	-1.23
Lars	leucyl-tRNA synthetase	0.0073	0.0993	0.0021	-1.21	-1.2	-1.27
Cnot7	CCR4-NOT transcription complex, subunit 7	0.0022	0.0104	0.0004	-1.29	-1.29	-1.27
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	0.0024	0.0280	0.0002	-1.24	-1.13	-1.27
Cdip1	CDP-diacylglycerol-inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	0.0066	0.1175	0.0027	-1.19	-1.08	-1.3
Sort1	sortilin 1	0.0013	0.0565	0.0085	-1.27	-1.3	-1.32
Lmo4	LIM domain only 4	0.0004	0.0199	0.0043	-1.6	-1.22	-1.35
Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.0022	0.0173	0.0002	-1.22	-1.43	-1.38
Dpp7	dipeptidylpeptidase 7	0.0073	0.0234	0.0044	-1.35	-1.38	-1.39
Aql	amylol-1,6-glucosidase, 4-alpha-glucanotransferase	0.0084	0.0386	0.0014	-1.33	-1.26	-1.4
Myi6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0.0091	0.8599	0.0042	-1.38	-1.02	-1.42
Samd4	sterile alpha motif domain containing 4	0.0031	0.1169	0.0090	-1.86	-1.27	-1.49
Cdt1	chromatin licensing and DNA replication factor 1	0.0079	0.0667	0.0035	-1.36	-1.31	-1.51
Birc3	baculoviral IAP repeat-containing 3	0.0018	0.1257	0.0014	-1.57	-1.25	-1.51
Sdc4	syndecan 4	0.0060	0.8848	0.0045	1.37	-1.02	-1.51
Gclc	glutamate-cysteine ligase, catalytic subunit	0.0032	0.0214	0.0089	-1.71	-1.28	-1.51
Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member	0.0049	0.0226	0.0010	-1.54	-1.38	-1.58
Rfx5	regulatory factor X, 5 (influences HLA class II expression)	0.0011	0.0340	0.0004	-1.45	-1.36	-1.59
Mtmr2	myotubularin related protein 2	0.0049	0.0230	0.0002	-1.33	-1.59	-1.62
Hip1r	huntingtin interacting protein 1 related	0.0073	0.0130	0.0088	-1.57	-1.62	-1.74
Amn	amniotless	0.0057	0.0102	0.0091	-2.17	-2.66	-1.92
4930595D18Rik	RIKEN cDNA 4930595D18 gene	0.0024	0.0288	0.0041	-1.77	-1.53	-2.02
Mik1	mixed lineage kinase domain-like	0.0059	0.0333	0.0025	-1.8	-1.86	-2.44
Rhbf2	rhomboid 5 homolog 2 (Drosophila)	0.0001	0.7323	0.0005	-3.6	-1.11	-3.37
Hsd3b5	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5	0.0542	0.0012	0.0010	9.09	11.02	13.81
D18ErtD201e	DNA segment, Chr 18, ERATO Doi 201, expressed	0.2077	0.0055	0.0041	3.11	8.04	8.2
Gm8350	predicted gene 8350	0.0646	0.0008	0.0001	4.09	4.93	7.72
Vps13c	vacuolar protein sorting 13C (yeast)	0.2548	0.0026	0.0020	2.5	8.44	6.55
B3gal12	UDP-Gal:beta-GlcNAc beta 1,3-galactosyltransferase, polypeptide 2	1.0000	0.0019	0.0073	1	3.96	5.68
4930565D16Rik	RIKEN cDNA 4930565D16 gene	0.0126	0.0076	0.0001	4.14	5.71	5.47
Susd4	sushi domain containing 4	0.0221	0.0056	0.0011	2.67	4.52	4.58
Fam19a5	family with sequence similarity 19, member A5	0.5043	0.0023	0.0022	1.32	3.27	3.89
Ras10a	RAS-like, family 10, member A	0.3872	0.0082	0.0066	1.39	2.86	3.33
Fam55b	family with sequence similarity 55, member B	0.1150	0.0056	0.0002	1.94	2.62	3.17

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Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
2310069B03Rik	RIKEN cDNA 2310069B03 gene	0.2409	0.0065	0.0022	1.74	2.54	3.07
Gna14	guanine nucleotide binding protein, alpha 14	0.0127	0.0073	0.0007	1.81	2.11	2.99
Ythd2	YTH domain family 2	0.3234	0.0000	0.0000	1.19	2.53	2.75
Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.0930	0.0005	0.0003	1.39	2.72	2.73
Dnaia4	DnaJ (Hsp40) homolog, subfamily A, member 4	0.0640	0.0000	0.0010	1.66	3.37	2.7
4930553M12Rik	RIKEN cDNA 4930553M12 gene	0.8810	0.0055	0.0054	1.08	2.27	2.7
Cnot6l	CCR4-NOT transcription complex, subunit 6-like	0.0148	0.0000	0.0003	1.27	2.38	2.59
Fgfr1	fibroblast growth factor receptor 1	0.5389	0.0017	0.0022	1.2	2.37	2.53
Lrp5	low density lipoprotein receptor-related protein 5	0.8467	0.0013	0.0004	-1.05	2.58	2.48
Rad23b	RAD23b homolog (S. cerevisiae)	0.6159	0.0000	0.0000	1.05	2.04	2.36
Dusp23	dual specificity phosphatase 23	0.4315	0.0001	0.0001	1.12	1.93	2.33
Dio1	deriodinase, iodothyronine, type I	0.0549	0.0019	0.0004	1.86	2.34	2.32
Kihl28	kelch-like 28 (Drosophila)	0.0433	0.0093	0.0066	1.31	2.11	2.31
Cyp2c55	cytochrome P450, family 2, subfamily c, polypeptide 55	0.0474	0.0026	0.0000	1.66	1.46	2.3
Fam128b	family with sequence similarity 128, member B	0.1096	0.0041	0.0007	1.37	1.87	2.29
Psme3	proteasome (prosome, macropain) 28 subunit, 3	0.4232	0.0000	0.0000	1.09	2.15	2.29
Sulf2	sulfatase 2	0.3792	0.0000	0.0000	1.24	2.49	2.27
Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	0.0736	0.0001	0.0002	1.35	2	2.26
Tnp3	transportin 3	0.8601	0.0001	0.0000	1.02	2.27	2.21
Spata2L	spermatogenesis associated 2-like	0.0757	0.0014	0.0000	1.47	1.77	2.19
Cpox	coproporphyrinogen oxidase	0.4775	0.0015	0.0000	1.1	2.05	2.16
Foxo4	forkhead box O4	0.1260	0.0012	0.0000	1.31	1.9	2.1
Zc3h3	zinc finger CCCH type containing 3	0.2884	0.0091	0.0068	1.37	1.98	2.07
Slco1a1	solute carrier organic anion transporter family, member 1a1	0.0297	0.0002	0.0004	2.07	2.04	2.04
Od3	outer dense fiber of sperm tails 3	0.5363	0.0088	0.0058	-1.14	2.06	2.01
1700018L02Rik	RIKEN cDNA 1700018L02 gene	0.0366	0.0005	0.0051	1.66	2.11	1.96
Nup62	nucleoponin 62	0.0824	0.0021	0.0009	1.22	2.2	1.94
Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	0.7719	0.0021	0.0008	1.04	1.88	1.93
Snmp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0.7862	0.0003	0.0001	-1.03	1.8	1.92
Nceh1	arylamide deacetylase-like 1	0.0417	0.0003	0.0024	2.09	2.05	1.92
Scaf1	SR-related CTD-associated factor 1	0.9231	0.0000	0.0007	1.02	1.96	1.91
Nfic	nuclear factor I/C	0.7007	0.0004	0.0010	1.07	2.19	1.91
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0.1828	0.0022	0.0011	-1.14	2.04	1.91
Scly	selenocysteine lyase	0.1003	0.0000	0.0002	1.16	1.98	1.9
Mett5d1	methyltransferase 5 domain containing 1	0.0424	0.0004	0.0064	1.56	1.84	1.9
Ncma00081	non-protein coding RNA 81	0.0634	0.0000	0.0008	1.27	1.71	1.89
Homer2	homer homolog 2 (Drosophila)	0.0868	0.0002	0.0007	1.29	2.21	1.88
Furin	furin (paired basic amino acid cleaving enzyme)	0.3985	0.0002	0.0000	1.07	1.89	1.87
Arhgap10	Rho GTPase activating protein 10	0.1073	0.0083	0.0055	1.73	1.53	1.87
Naa16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	0.5725	0.0009	0.0004	-1.11	1.64	1.85
Limd1	LIM domains containing 1	0.0549	0.0006	0.0001	1.22	2.04	1.84
Uba6	ubiquitin-like modifier activating enzyme 6	0.7282	0.0003	0.0001	1.06	1.54	1.83
Mga	MAX gene associated	0.1066	0.0064	0.0018	1.29	1.57	1.83
Traf4	TNF receptor associated factor 4	0.1948	0.0016	0.0003	1.23	1.41	1.82
Mhas1	malignant fibrous histiocytoma amplified sequence 1	0.1008	0.0000	0.0016	1.23	1.73	1.81
C77805	expressed sequence C77805	0.0934	0.0034	0.0057	1.38	1.8	1.8
Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	0.2935	0.0000	0.0005	1.38	2.59	1.8
Med13l	mediator complex subunit 13-like	0.4062	0.0000	0.0004	1.17	1.82	1.79
Fam63b	family with sequence similarity 63, member B	0.1000	0.0079	0.0015	1.37	1.47	1.78
Raver1	ribonucleoprotein, PTB-binding 1	0.8420	0.0046	0.0024	1.02	1.74	1.77
Mil5	myeloid/lymphoid or mixed-lineage leukemia 5	0.1720	0.0021	0.0000	-1.05	1.69	1.77
Npc1	Niemann Pick type C1	0.0298	0.0034	0.0010	1.19	1.68	1.77
Grtp1	GH regulated TBC protein 1	0.0516	0.0057	0.0001	1.27	1.76	1.76
Mgat2	mannoside acetylglucosaminyltransferase 2	0.0314	0.0004	0.0012	1.26	1.75	1.75
Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	0.9102	0.0003	0.0007	1.01	1.61	1.75
Kdm6b	KDM1 lysine (K)-specific demethylase 6B	0.0756	0.0003	0.0060	-1.23	2.08	1.74
Asb6	ankyrin repeat and SOCS box-containing 6	0.0620	0.0042	0.0004	1.41	1.55	1.73
Nr2f2	nuclear receptor subfamily 2, group F, member 2	0.1963	0.0079	0.0076	1.21	1.55	1.73
Zfp36l2	zinc finger protein 36, C3H type-like 2	0.0393	0.0009	0.0058	1.29	1.73	1.73
Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	0.4707	0.0034	0.0004	-1.09	1.73	1.72
Rnf11	ring finger protein 11	0.7312	0.0002	0.0013	1.05	1.78	1.71
Srx16	sorting nexin 16	0.2374	0.0021	0.0075	1.16	1.88	1.71
Alg11	asparagine-linked glycosylation 11 homolog (yeast, alpha-1,2-mannosyltransferase)	0.7592	0.0034	0.0037	-1.03	1.47	1.7
Slc25a23	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 23	0.6299	0.0001	0.0002	1.04	1.72	1.69
Isq20	interferon-stimulated protein	0.3190	0.0090	0.0022	1.2	1.85	1.68
Aoh1a	anterior pharynx defective 1a homolog (C. elegans)	0.2029	0.0086	0.0045	1.17	2.04	1.67
Exoc4	exocyst complex component 4	0.0318	0.0006	0.0015	1.29	1.94	1.67
Mospd3	motile sperm domain containing 3	0.7228	0.0063	0.0002	1.05	1.52	1.67
Epn1	epsin 1	0.1589	0.0016	0.0017	1.2	1.71	1.66
Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0.0903	0.0081	0.0086	1.44	1.51	1.66
Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)	0.0344	0.0076	0.0020	1.3	1.48	1.66
Fam108a	family with sequence similarity 108, member A	0.0600	0.0001	0.0001	1.11	1.58	1.66
Qpct	glutamyl-peptide cyclotransferase (glutamyl cyclase)	0.0255	0.0048	0.0011	1.41	1.69	1.66
Mrps36	mitochondrial ribosomal protein S36	0.5880	0.0048	0.0002	1.06	1.41	1.66
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	0.2613	0.0001	0.0032	1.07	1.71	1.65
Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	0.1593	0.0009	0.0003	1.3	1.72	1.65
Ccdc97	coiled-coil domain containing 97	0.2300	0.0013	0.0025	1.18	1.6	1.65
Brn3	brain protein 13	0.6568	0.0046	0.0005	-1.04	1.51	1.64
Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	0.8949	0.0001	0.0002	1.01	1.58	1.64
Phlpp1	PH domain and leucine rich repeat protein phosphatase 1	0.0346	0.0006	0.0001	1.28	1.62	1.64
Tnfrsf81	tumor necrosis factor, alpha-induced protein 8-like 1	0.0509	0.0021	0.0051	1.39	1.43	1.64
Ethd2	EF hand domain containing 2	0.0425	0.0008	0.0007	1.3	1.95	1.64
Abhd1	abhydrolase domain containing 1	0.2523	0.0006	0.0009	1.17	1.69	1.63
Cxxc5	CXXC finger 5	0.4387	0.0047	0.0005	1.1	1.49	1.63
Srd5a1	steroid 5 alpha-reductase 1	0.0437	0.0036	0.0003	1.38	1.63	1.62
Ccdc72	coiled-coil domain containing 72	0.1396	0.0002	0.0000	1.08	1.57	1.62
Ass1	argininosuccinate synthetase 1	0.2413	0.0024	0.0004	1.27	1.6	1.6
Foxn3	forkhead box N3	0.0385	0.0005	0.0011	-1.14	1.77	1.6
2310022B05Rik	RIKEN cDNA 2310022B05 gene	0.4229	0.0033	0.0008	1.1	1.47	1.6
Pnkd	paroxysmal nonkinesigenic dyskinesia	0.4600	0.0045	0.0008	1.08	1.43	1.6
Gbf1	golgi-specific brefeldin A-resistance factor 1	0.9165	0.0001	0.0000	1.01	1.46	1.6
Mobk13	MOB1, Mps One Binder kinase activator-like 3 (yeast)	0.4016	0.0002	0.0001	-1.08	1.65	1.6
Zdhc21	zinc finger, DHHC domain containing 21	0.0726	0.0038	0.0036	1.36	1.68	1.59
Nfe2l2	nuclear factor, erythroid derived 2, like 2	0.9862	0.0072	0.0024	1	1.48	1.59
Dcakd	dephospho-CoA kinase domain containing	0.3103	0.0024	0.0009	1.14	1.59	1.59
Nosip	nitric oxide synthase interacting protein	0.1718	0.0005	0.0001	1.19	1.43	1.58
2300009A05Rik	RIKEN cDNA 2300009A05 gene	0.6151	0.0008	0.0011	1.04	1.75	1.58
Rhbd1	rhomboid family 1 (Drosophila)	0.5238	0.0001	0.0003	1.09	1.64	1.57
Wbp2	VW domain binding protein 2	0.3822	0.0000	0.0000	1.07	1.61	1.57
Fam114a2	family with sequence similarity 114, member A2	0.5065	0.0006	0.0039	-1.08	1.68	1.57
Top1	topoisomerase (DNA) I	0.0196	0.0018	0.0005	1.23	1.47	1.56
C430003N24Rik	RIKEN cDNA C430003N24 gene	0.2796	0.0088	0.0028	1.23	1.68	1.55
Fnip1	folliculin interacting protein 1	0.8751	0.0059	0.0006	1.02	1.62	1.55
Car8	carbonic anhydrase 8	0.2756	0.0073	0.0015	1.1	1.48	1.55

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Slc25a44	solute carrier family 25, member 44	0.2796	0.0018	0.0037	1.19	1.62	1.55
Gm5918	predicted gene 5918	0.6181	0.0026	0.0042	1.06	1.53	1.54
Dexi	dexamethasone-induced transcript	0.0606	0.0044	0.0001	1.22	1.68	1.54
2610024G14Rik	RIKEN cDNA 2610024G14 gene	0.5592	0.0016	0.0003	1.03	1.31	1.54
Trim32	tripartite motif-containing 32	0.5941	0.0045	0.0027	-1.06	1.38	1.54
Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	0.0801	0.0061	0.0031	1.27	1.57	1.53
Rgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	0.3442	0.0000	0.0003	1.15	1.84	1.53
Rtp3	receptor transporter protein 3	0.2304	0.0033	0.0021	1.11	1.52	1.53
Rab43	RAB43, member RAS oncogene family	0.2279	0.0019	0.0005	1.18	1.48	1.53
Dirc2	disrupted in renal carcinoma 2 (human)	0.2955	0.0095	0.0004	1.19	1.47	1.53
Slco1b2	solute carrier organic anion transporter family, member 1b2	0.1344	0.0014	0.0004	1.1	1.33	1.53
Tm2d2	TM2 domain containing 2	0.2790	0.0000	0.0000	1.11	1.54	1.52
Vegfb	vascular endothelial growth factor B	0.3380	0.0088	0.0016	-1.16	1.38	1.52
Bcar3	breast cancer anti-estrogen resistance 3	0.8342	0.0003	0.0001	-1.02	1.48	1.52
Ammecr1l	AMME chromosomal region gene 1-like	0.8375	0.0077	0.0002	1.01	1.33	1.52
Hdac11	histone deacetylase 11	0.2265	0.0086	0.0001	1.1	1.44	1.52
Rfx1	regulatory factor X, 1 (influences HLA class II expression)	0.0677	0.0021	0.0013	1.24	1.57	1.52
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	0.3249	0.0004	0.0000	1.13	1.43	1.52
Lgals9	lectin, galactose binding, soluble 9	0.1490	0.0029	0.0000	1.13	1.28	1.51
Reep5	receptor accessory protein 5	0.3591	0.0003	0.0008	-1.12	1.71	1.51
Pdik1l	PDLIM1 interacting kinase 1 like	0.6764	0.0010	0.0008	1.04	1.41	1.51
Tbc1d13	TBC1 domain family, member 13	0.6363	0.0085	0.0075	1.06	1.53	1.51
Phf2	putative homeodomain transcription factor 2	0.4691	0.0083	0.0087	1.12	1.5	1.51
Syni2bp	synaptotagmin 2 binding protein	0.0101	0.0000	0.0000	1.24	1.44	1.51
Hnf4a	hepatic nuclear factor 4, alpha	0.0305	0.0032	0.0005	1.32	1.54	1.5
Slc25a45	solute carrier family 25, member 45	0.0302	0.0024	0.0032	1.42	1.43	1.5
Alpl	alkaline phosphatase, liver/bone/kidney	0.0572	0.0050	0.0021	1.22	1.47	1.5
0610030E20Rik	RIKEN cDNA 0610030E20 gene	0.0229	0.0064	0.0032	1.35	1.44	1.5
Whamm	WAS protein homolog associated with actin, golgi membranes and microtubules	0.2534	0.0075	0.0035	1.1	1.29	1.5
Txndc17	thioredoxin domain containing 17	0.7337	0.0002	0.0001	1.03	1.46	1.5
D5Ert798e	DNA segment, Chr 5, ERATO Doi 798, expressed	0.4510	0.0003	0.0024	1.21	1.6	1.49
Rnf10	ring finger protein 10	0.8777	0.0001	0.0007	-1.01	1.47	1.49
Rere	arginine glutamic acid dipeptide (RE) repeats	0.8378	0.0076	0.0003	1.03	1.26	1.49
Fndc4	fibronectin type III domain containing 4	0.0689	0.0012	0.0000	1.16	1.33	1.48
Tmem107	transmembrane protein 107	0.1164	0.0074	0.0088	1.18	1.47	1.48
Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.6148	0.0029	0.0006	1.06	1.35	1.48
Arsb	arylsulfatase B	0.4676	0.0058	0.0001	-1.04	1.39	1.48
Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	0.0434	0.0023	0.0001	1.26	1.52	1.48
4833441D16Rik	RIKEN cDNA 4833441D16 gene	0.4724	0.0048	0.0012	1.07	1.58	1.48
Kif5b	kinesin family member 5B	0.9986	0.0000	0.0001	-1	1.54	1.48
Kif1c	kinesin family member 1C	0.0446	0.0001	0.0004	1.23	1.57	1.47
Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	0.0601	0.0000	0.0005	1.13	1.52	1.47
Mavs	mitochondrial antiviral signaling protein	0.2252	0.0083	0.0002	1.11	1.46	1.46
Bcl2l13	BCL2-like 13 (apoptosis facilitator)	0.6625	0.0011	0.0009	1.05	1.65	1.46
C80913	expressed sequence C80913	0.0201	0.0005	0.0001	1.28	1.47	1.46
Midn	midnolin	0.4540	0.0061	0.0034	1.09	1.77	1.46
Rab6	RAB6, member RAS oncogene family	0.8270	0.0022	0.0006	1.01	1.41	1.46
Sertad2	SERTA domain containing 2	0.0912	0.0012	0.0077	1.19	1.53	1.46
Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	0.0414	0.0014	0.0069	1.21	1.67	1.45
Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	0.1099	0.0050	0.0001	-1.11	1.63	1.45
Pin4	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	0.0537	0.0001	0.0000	1.2	1.4	1.45
Hoxp	HOP homeobox	0.1777	0.0024	0.0062	1.34	1.66	1.45
Fbxw8	F-box and WD-40 domain protein 8	0.0369	0.0004	0.0001	1.25	1.35	1.45
Rps27l	ribosomal protein S27-like	0.9900	0.0026	0.0000	1	1.35	1.45
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0.0420	0.0001	0.0014	1.16	1.43	1.45
Zdhdc9	zinc finger, DHHC domain containing 9	0.6588	0.0006	0.0002	1.03	1.37	1.45
Opa3	optic atrophy 3 (human)	0.7948	0.0030	0.0049	-1.03	1.55	1.44
Fam176a	family with sequence similarity 176, member A	0.0790	0.0022	0.0000	1.14	1.27	1.44
Hagh	hydroxyacyl glutathione hydrolase	0.2892	0.0009	0.0000	1.05	1.42	1.44
Vav2	vav 2 oncogene	0.2702	0.0006	0.0000	1.09	1.34	1.44
Prpf8	pre-mRNA processing factor 8	0.2010	0.0009	0.0000	1.11	1.32	1.44
Spred2	sprouty-related, EVH1 domain containing 2	0.5130	0.0006	0.0003	1.06	1.53	1.44
Stard3	START domain containing 3	0.3261	0.0011	0.0015	1.1	1.67	1.43
Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	0.4340	0.0062	0.0012	1.08	1.29	1.43
C730029A08Rik	RIKEN cDNA C730029A08 gene	0.2070	0.0018	0.0044	1.33	1.67	1.43
Npepps	aminopeptidase puromycin sensitive	0.9739	0.0000	0.0008	1	1.53	1.43
Nrbf2	nuclear receptor binding factor 2	0.2769	0.0059	0.0006	1.12	1.42	1.43
Shb	src homology 2 domain-containing transforming protein B	0.0339	0.0002	0.0067	1.39	1.43	1.43
Ccnq1	cyclin G1	0.0105	0.0035	0.0033	1.24	1.42	1.42
Atg4c	autophagy-related 4C (yeast)	0.8401	0.0007	0.0062	1.01	1.52	1.42
Pcdc5	programmed cell death 5	0.2177	0.0056	0.0017	-1.11	1.35	1.42
Stradb	STE20-related kinase adaptor beta	0.0237	0.0007	0.0007	1.14	1.37	1.42
Map3k3	mitogen-activated protein kinase kinase kinase 3	0.1043	0.0081	0.0077	1.12	1.5	1.41
Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	0.7222	0.0033	0.0049	1.02	1.28	1.41
Rod1	ROD1 regulator of differentiation 1 (S. pombe)	0.3062	0.0000	0.0071	1.08	1.62	1.41
Cog4	component of oligomeric golgi complex 4	0.0302	0.0099	0.0019	1.18	1.19	1.41
Calr	calreticulin	0.0296	0.0008	0.0002	1.22	1.46	1.41
Pigr	polymeric immunoglobulin receptor	0.0606	0.0011	0.0094	1.3	1.51	1.41
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0.7698	0.0033	0.0026	-1.04	1.47	1.41
Fgfr3	fibroblast growth factor receptor 3	0.1570	0.0026	0.0077	1.14	1.44	1.39
Gm672	predicted gene 672	0.0144	0.0055	0.0001	1.3	1.5	1.39
Ogfr1	opioid growth factor receptor-like 1	0.0299	0.0001	0.0012	1.24	1.45	1.39
Ptdss2	phosphatidylserine synthase 2	0.4976	0.0036	0.0047	-1.08	1.45	1.39
Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	0.1209	0.0004	0.0001	1.08	1.4	1.39
Obfc2b	oligonucleotide/oligosaccharide-binding fold containing 2B	0.2155	0.0089	0.0003	1.12	1.35	1.38
Smad4	MAD homolog 4 (Drosophila)	0.0186	0.0021	0.0013	1.22	1.4	1.38
Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0.5704	0.0016	0.0048	1.07	1.28	1.38
Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	0.2170	0.0061	0.0013	1.1	1.35	1.38
Lipc	lipase, hepatic	0.0203	0.0034	0.0015	1.3	1.36	1.38
Rwdd1	RWD domain containing 1	0.5214	0.0001	0.0009	1.03	1.31	1.37
Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	0.0164	0.0050	0.0015	1.22	1.33	1.37
Card6	caspase recruitment domain family, member 6	0.0570	0.0003	0.0016	1.18	1.37	1.37
Gpr125	G protein-coupled receptor 125	0.8534	0.0088	0.0026	-1.02	1.46	1.37
Till4	tubulin tyrosine ligase-like family, member 4	0.0810	0.0099	0.0029	1.34	1.31	1.37
Hist1h2bc	histone cluster 1, H2bc	0.0151	0.0000	0.0001	1.15	1.44	1.37
Poli2i	polymerase (RNA) II (DNA directed) polypeptide 1	0.3893	0.0090	0.0004	1.05	1.24	1.37
Tacc1	transforming, acidic coiled-coil containing protein 1	0.3640	0.0003	0.0006	1.13	1.54	1.36
Ier3ip1	immediate early response 3 interacting protein 1	0.0761	0.0025	0.0008	1.12	1.33	1.36
Sash1	SAM and SH3 domain containing 1	0.7132	0.0002	0.0081	-1.05	1.55	1.36
Hccs	holocytochrome c synthetase	0.7863	0.0100	0.0017	-1.02	1.31	1.36
Pxn	paxillin	0.0569	0.0004	0.0027	1.1	1.29	1.36
2510006D16Rik	RIKEN cDNA 2510006D16 gene	0.4833	0.0025	0.0002	1.06	1.27	1.36
Oaf	OAF homolog (Drosophila)	0.1012	0.0036	0.0000	1.22	1.34	1.36
Gpr155	G protein-coupled receptor 155	0.1395	0.0008	0.0028	1.18	1.39	1.36

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Tpp1	tripeptidyl peptidase 1	0.0366	0.0079	0.0007	-1.24	1.38	1.36
Mogs	mannosyl-oligosaccharide glucosidase	0.6109	0.0022	0.0015	-1.04	1.33	1.36
Lactb	lactamase, beta	0.8059	0.0014	0.0010	-1.02	1.34	1.36
Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	0.5207	0.0071	0.0002	1.07	1.34	1.35
Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	0.3142	0.0002	0.0011	1.11	1.46	1.35
Sec62	SEC62 homolog (S. cerevisiae)	0.9482	0.0000	0.0000	-1	1.39	1.35
Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	0.3645	0.0041	0.0072	1.11	1.41	1.34
Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0.3569	0.0036	0.0003	1.06	1.23	1.34
Naprt1	nicotinate phosphoribosyltransferase domain containing 1	0.2729	0.0027	0.0034	1.1	1.39	1.34
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	0.1229	0.0002	0.0020	1.15	1.29	1.34
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	0.1012	0.0060	0.0009	1.15	1.49	1.34
D2Ert0612e	DNA segment, Chr 2, ERATO D01 612, expressed	0.2990	0.0049	0.0078	1.18	1.5	1.34
Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	0.0973	0.0037	0.0040	1.15	1.35	1.34
Fto	fat mass and obesity associated	0.0616	0.0000	0.0009	1.18	1.27	1.34
Drp1	Dr1 associated protein 1 (negative cofactor 2 alpha)	0.2413	0.0028	0.0032	-1.09	1.31	1.33
Txndc15	thioredoxin domain containing 15	0.6348	0.0055	0.0004	1.04	1.21	1.33
Map2k3	mitogen-activated protein kinase kinase 3	0.7761	0.0000	0.0014	1.01	1.19	1.33
Hpn	hepsin	0.3164	0.0000	0.0001	1.03	1.34	1.33
Mil110	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, RAB11a, member RAS oncogene family	0.5411	0.0003	0.0003	1.03	1.31	1.33
Rab11a	RAB11a, member RAS oncogene family	0.6167	0.0100	0.0005	1.03	1.27	1.33
Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypept	0.0253	0.0005	0.0000	1.16	1.3	1.32
Dmtf1	cyclin D binding myb-like transcription factor 1	0.1160	0.0021	0.0010	1.09	1.27	1.32
Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	0.5130	0.0006	0.0057	1.03	1.3	1.32
Cbl1l	Casitas B-lineage lymphoma-like 1	0.3084	0.0028	0.0031	1.13	1.36	1.31
Atg16l1	autophagy-related 16-like 1 (yeast)	0.4168	0.0050	0.0036	1.04	1.3	1.31
Efr3a	EFR3 homolog A (S. cerevisiae)	0.3423	0.0067	0.0010	1.07	1.25	1.31
Ilk	integrin linked kinase	0.8346	0.0029	0.0039	-1.01	1.33	1.31
Kdm2a	lysine (K)-specific demethylase 2A	0.4149	0.0002	0.0015	-1.07	1.69	1.3
Argl1	arginine and glutamate rich 1	0.2873	0.0054	0.0001	-1.06	1.23	1.3
Dpp8	dipeptidylpeptidase 8	0.6426	0.0001	0.0032	-1.03	1.4	1.3
BC017647	cDNA sequence BC017647	0.3201	0.0037	0.0026	1.19	1.67	1.3
Larp1b	La ribonucleoprotein domain family, member 1B	0.4678	0.0017	0.0008	-1.04	1.22	1.3
Eif1	eukaryotic translation initiation factor 1	0.1015	0.0015	0.0004	1.1	1.27	1.3
Purb	purine rich element binding protein B	0.4945	0.0004	0.0037	1.06	1.53	1.3
Tln1	talin 1	0.9970	0.0008	0.0016	-1	1.3	1.3
Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.8518	0.0006	0.0010	-1.01	1.3	1.3
Cpsf7	cleavage and polyadenylation specific factor 7	0.5661	0.0079	0.0014	-1.05	1.23	1.3
Proc	protein C	0.0170	0.0009	0.0001	1.11	1.23	1.3
Nbr1	neighbor of Brca1 gene 1	0.4035	0.0084	0.0032	1.03	1.21	1.3
Flii	flightless I homolog (Drosophila)	0.9598	0.0012	0.0003	1	1.21	1.29
Fam134a	family with sequence similarity 134, member A	0.2662	0.0044	0.0086	1.08	1.36	1.29
Sirt7	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	0.1542	0.0073	0.0071	1.09	1.26	1.28
1110008F13Rik	RIKEN cDNA 1110008F13 gene	0.3692	0.0013	0.0013	-1.05	1.27	1.28
Zfxh3	zinc finger homeobox 3	0.8107	0.0058	0.0085	1.02	1.36	1.28
Sic25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	0.8362	0.0073	0.0006	-1.01	1.22	1.28
Rab9	RAB9, member RAS oncogene family	0.2880	0.0005	0.0038	1.05	1.26	1.28
Arhgap21	Rho GTPase activating protein 21	0.3952	0.0030	0.0085	-1.08	1.48	1.28
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	0.1721	0.0071	0.0006	1.11	1.19	1.28
2510039O18Rik	RIKEN cDNA 2510039O18 gene	0.5766	0.0042	0.0007	1.03	1.27	1.28
Mtmr14	myotubularin related protein 14	0.0181	0.0021	0.0089	1.29	1.37	1.28
Set	SET translocation	0.2138	0.0003	0.0011	1.07	1.28	1.27
Man2b1	mannosidase 2, alpha B1	0.6929	0.0031	0.0010	-1.02	1.27	1.27
Zfr	zinc finger RNA binding protein	0.1442	0.0061	0.0057	1.13	1.23	1.26
Man1a	mannosidase 1, alpha	0.0466	0.0054	0.0070	1.19	1.26	1.26
Snx24	sorting nexin 24	0.0312	0.0027	0.0079	-1.24	1.36	1.26
Mapkapk2	MAP kinase-activated protein kinase 2	0.6970	0.0078	0.0096	1.05	1.23	1.25
Eif1b	eukaryotic translation initiation factor 1B	0.9524	0.0024	0.0007	-1	1.22	1.25
Nadk	NAD kinase	0.3452	0.0049	0.0016	1.04	1.22	1.25
Pepd	peptidase D	0.7931	0.0064	0.0036	-1.02	1.21	1.24
Surf1	surfeit gene 1	0.3355	0.0073	0.0031	1.04	1.22	1.24
Cd164	CD164 antigen	0.0153	0.0024	0.0026	1.18	1.2	1.24
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	0.1492	0.0013	0.0000	1.08	1.2	1.24
Cp	ceruloplasmin	0.1601	0.0027	0.0044	1.16	1.44	1.23
Bat2	HLA-B associated transcript 2	0.7268	0.0002	0.0051	-1.03	1.32	1.23
Ahcy1	S-adenosylhomocysteine hydrolase-like 1	0.0996	0.0080	0.0049	1.08	1.21	1.22
Prkacb	protein kinase, cAMP dependent, catalytic, beta	0.0555	0.0002	0.0012	1.12	1.29	1.22
Mapk14	mitogen-activated protein kinase 14	0.3324	0.0032	0.0030	1.07	1.29	1.22
Gapv1	GTPase activating protein and VPS9 domains 1	0.2429	0.0003	0.0003	1.06	1.35	1.21
Eif2c2	eukaryotic translation initiation factor 2C, 2	0.0467	0.0000	0.0038	1.22	1.58	1.21
Myt4	MYST histone acetyltransferase monocytic leukemia 4	0.0350	0.0001	0.0007	1.1	1.27	1.21
Arlgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	0.0372	0.0008	0.0013	1.09	1.19	1.21
Acp1	acid phosphatase 1, soluble	0.2080	0.0039	0.0000	1.05	1.13	1.21
Copa	coatamer protein complex subunit alpha	0.6048	0.0012	0.0028	-1.03	1.2	1.21
Scarb1	scavenger receptor class B, member 1	0.0161	0.0006	0.0026	1.29	1.35	1.21
Cst3	cystatin C	0.5400	0.0013	0.0075	1.04	1.34	1.21
Rbm28	RNA binding motif protein 28	0.8790	0.0025	0.0071	1.01	1.24	1.2
Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0.6462	0.0020	0.0021	1.04	1.25	1.2
Arcp2	actin related protein 2/3 complex, subunit 2	0.9371	0.0003	0.0058	-1	1.32	1.2
1110005A03Rik	RIKEN cDNA 1110005A03 gene	0.7950	0.0004	0.0099	-1.02	1.29	1.19
Stk40	serine/threonine kinase 40	0.5939	0.0012	0.0020	-1.04	1.23	1.18
Trmprs6	transmembrane serine protease 6	0.9766	0.0017	0.0054	1	1.24	1.18
Dtnbp1	dystrobrevin binding protein 1	0.0426	0.0086	0.0024	1.09	1.21	1.17
Cd82	CD82 antigen	0.9612	0.0001	0.0061	-1	1.23	1.17
Vps25	vacuolar protein sorting 25 (yeast)	0.2936	0.0064	0.0053	1.06	1.17	1.17
Zfp874	zinc finger protein 874	0.3592	0.0025	0.0084	1.07	1.14	1.16
Arlh2	ariadne homolog 2 (Drosophila)	0.7426	0.0099	0.0088	1.02	1.15	1.15
1810027O10Rik	RIKEN cDNA 1810027O10 gene	0.0172	0.0001	0.0005	1.19	1.21	1.15
Os9	amplified in osteosarcoma	0.4119	0.0024	0.0096	1.05	1.31	1.15
Gns	glucosamine (N-acetyl)-6-sulfatase	0.6499	0.0025	0.0020	1.03	1.2	1.14
Pabpc1	poly(A) binding protein, cytoplasmic 1	0.1942	0.0011	0.0091	-1.05	1.25	1.1
Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	0.0632	0.0007	0.0014	-1.08	-1.17	-1.13
Nqin	neugrin, neurite outgrowth associated	0.0116	0.0075	0.0003	-1.15	-1.24	-1.13
Mcf2	multiple coagulation factor deficiency 2	0.0702	0.0017	0.0004	-1.05	-1.12	-1.13
Chmp5	chromatin modifying protein 5	0.1187	0.0054	0.0073	-1.12	-1.18	-1.15
Mrp11	mitochondrial ribosomal protein L11	0.9196	0.0018	0.0076	-1.01	-1.22	-1.15
Tpi1	triosephosphate isomerase 1	0.5811	0.0016	0.0048	-1.05	-1.22	-1.16
Pgk1	phosphoglycerate kinase 1	0.4240	0.0002	0.0002	-1.02	-1.17	-1.16
Trappc4	trafficking protein particle complex 4	0.2588	0.0035	0.0077	-1.1	-1.24	-1.17
Gsta3	glutathione S-transferase, alpha 3	0.2175	0.0054	0.0006	-1.09	-1.33	-1.18
BC052040	cDNA sequence BC052040	0.9120	0.0082	0.0090	1.02	-1.47	-1.18
Diablo	diablo homolog (Drosophila)	0.1973	0.0023	0.0008	-1.08	-1.18	-1.19
Dtymk	deoxythymidylate kinase	0.5714	0.0020	0.0090	-1.04	-1.31	-1.2
Ssbp1	single-stranded DNA binding protein 1	0.1202	0.0008	0.0016	-1.09	-1.29	-1.2
Rpl12	ribosomal protein L12	0.1306	0.0076	0.0026	-1.11	-1.34	-1.21

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Phb	prohibitin	0.6979	0.0003	0.0025	-1.02	-1.38	-1.21
Yars	tyrosyl-tRNA synthetase	0.0551	0.0038	0.0023	-1.15	-1.24	-1.22
C1d	C1D nuclear receptor co-repressor	0.7809	0.0014	0.0057	-1.02	-1.33	-1.22
Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	0.0136	0.0001	0.0054	-1.14	-1.28	-1.22
Pfdn5	prefoldin 5	0.5316	0.0054	0.0031	-1.03	-1.28	-1.22
Ccdc104	coiled-coil domain containing 104	0.1464	0.0000	0.0063	-1.09	-1.57	-1.22
Ssrp1	structure specific recognition protein 1	0.1424	0.0008	0.0041	-1.1	-1.25	-1.22
Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0.1561	0.0063	0.0047	-1.1	-1.42	-1.23
Psmc2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0.0941	0.0083	0.0064	-1.11	-1.29	-1.23
Mgat1	mannoside acetylglucosaminyltransferase 1	0.5298	0.0012	0.0007	1.03	-1.19	-1.23
Sqstm1	sequestosome 1	0.0299	0.0016	0.0017	-1.13	-1.33	-1.24
Usp19	ubiquitin specific peptidase 19	0.1173	0.0034	0.0001	-1.09	-1.21	-1.24
Yip1	Yip1 domain family, member 1	0.0793	0.0005	0.0045	-1.12	-1.32	-1.24
Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	0.4887	0.0049	0.0060	-1.06	-1.31	-1.24
Racd1	rod1 (required for cell differentiation) homolog 1 (S. pombe)	0.3876	0.0013	0.0069	-1.07	-1.36	-1.24
Las1	LAS1-like (S. cerevisiae)	0.1129	0.0016	0.0016	-1.11	-1.41	-1.24
Fam120a	family with sequence similarity 120, member A	0.3911	0.0021	0.0017	1.04	-1.2	-1.25
Rpl3	ribosomal protein L3	0.0934	0.0002	0.0004	-1.06	-1.31	-1.25
Gpx4	glutathione peroxidase 4	0.0119	0.0006	0.0051	-1.19	-1.34	-1.25
Gart	phosphoribosylglycinamide formyltransferase	0.1005	0.0020	0.0028	-1.1	-1.36	-1.25
Cryz1	crystallin, zeta (quinone reductase)-like 1	0.8820	0.0004	0.0070	-1.01	-1.33	-1.26
H2-Ke6	H2-K region expressed gene 6	0.0959	0.0006	0.0093	-1.12	-1.36	-1.26
Ncl	nucleolin	0.3097	0.0025	0.0013	-1.07	-1.34	-1.26
Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	0.7433	0.0026	0.0043	1.02	-1.29	-1.26
Tip2	tripeptidyl peptidase II	0.0137	0.0007	0.0079	-1.18	-1.29	-1.27
Hint2	histidine triad nucleotide binding protein 2	0.6354	0.0004	0.0014	-1.05	-1.33	-1.27
Sptlc1	serine palmitoyltransferase, long chain base subunit 1	0.0361	0.0074	0.0091	-1.12	-1.36	-1.27
Psmc5	proteasome (prosome, macropain) subunit, alpha type 5	0.0200	0.0010	0.0022	-1.16	-1.31	-1.27
Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	0.6971	0.0030	0.0060	-1.03	-1.13	-1.28
Cd1d1	CD1d1 antigen	0.5214	0.0041	0.0054	-1.04	-1.21	-1.28
Nit1	nitrilase 1	0.6938	0.0008	0.0003	1.02	-1.28	-1.28
Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.3232	0.0013	0.0071	-1.1	-1.52	-1.29
Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.6695	0.0086	0.0042	-1.03	-1.24	-1.29
Gnb1	guanine nucleotide binding protein (G protein), beta 1	0.0392	0.0017	0.0092	-1.12	-1.23	-1.29
Ranbp1	RAN binding protein 1	0.0342	0.0014	0.0083	-1.16	-1.36	-1.29
Ilf1	interferon-induced protein with tetratricopeptide repeats 1	0.7004	0.0014	0.0053	-1.05	-1.57	-1.29
Parl	presenilin associated, rhomboid-like	0.1545	0.0001	0.0007	-1.11	-1.4	-1.29
Mrpl55	mitochondrial ribosomal protein L55	0.1407	0.0081	0.0058	1.13	-1.21	-1.29
Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	0.5753	0.0024	0.0000	-1.03	-1.25	-1.29
Etha1	EF hand domain family A1	0.3330	0.0066	0.0093	-1.11	-1.45	-1.3
Tmem120a	transmembrane protein 120A	0.9540	0.0000	0.0044	1	-1.39	-1.3
Mrpl12	mitochondrial ribosomal protein L12	0.4894	0.0033	0.0018	-1.08	-1.32	-1.3
Hnmpu	heterogeneous nuclear ribonucleoprotein U	0.1260	0.0003	0.0002	-1.12	-1.39	-1.3
9430016H08Rik	RIKEN cDNA 9430016H08 gene	0.0154	0.0009	0.0033	-1.22	-1.49	-1.3
8430419L09Rik	RIKEN cDNA 8430419L09 gene	0.5056	0.0009	0.0018	-1.1	-1.27	-1.3
Smc3	structural maintenance of chromosomes 3	0.4241	0.0015	0.0075	-1.08	-1.52	-1.31
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	0.0651	0.0034	0.0012	-1.15	-1.27	-1.31
2610101N10Rik	RIKEN cDNA 2610101N10 gene	0.1253	0.0013	0.0002	-1.06	-1.3	-1.31
Asqr1	asialoglycoprotein receptor 1	0.2811	0.0051	0.0000	-1.07	-1.33	-1.31
Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	0.0929	0.0001	0.0001	-1.07	-1.28	-1.31
Tcf3	transcription factor E3	0.1734	0.0089	0.0061	-1.15	-1.28	-1.31
Usp14	ubiquitin specific peptidase 14	0.0291	0.0002	0.0077	-1.23	-1.66	-1.31
Zmat2	zinc finger, matrin type 2	0.2372	0.0004	0.0005	-1.1	-1.43	-1.32
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	0.8190	0.0021	0.0004	-1.01	-1.28	-1.32
Slc12a2	solute carrier family 12, member 2	0.0171	0.0063	0.0060	-1.18	-1.18	-1.32
Myq1	melanocyte proliferating gene 1	0.0463	0.0008	0.0003	-1.09	-1.32	-1.32
Galk1	galactokinase 1	0.0163	0.0024	0.0018	-1.26	-1.46	-1.33
Nagk	N-acetylglucosamine kinase	0.0294	0.0000	0.0001	-1.2	-1.34	-1.33
Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	0.9251	0.0073	0.0006	-1.01	-1.21	-1.33
Cltc	clathrin, heavy polypeptide (Hc)	0.0981	0.0009	0.0024	-1.12	-1.39	-1.33
Ai314180	expressed sequence Ai314180	0.2831	0.0008	0.0092	-1.05	-1.35	-1.33
Krt18	keratin 18	0.2132	0.0050	0.0015	-1.14	-1.44	-1.34
U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	0.2806	0.0025	0.0039	-1.07	-1.49	-1.34
Ptplad1	protein tyrosine phosphatase-like A domain containing 1	0.0200	0.0012	0.0001	-1.14	-1.31	-1.34
Tmod3	tropomodulin 3	0.0276	0.0026	0.0012	-1.2	-1.4	-1.34
111002G09Rik	RIKEN cDNA 111002G09 gene	0.2097	0.0019	0.0014	-1.08	-1.57	-1.35
Ogfd1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0.0268	0.0087	0.0005	-1.21	-1.21	-1.35
Ogfd2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.9787	0.0010	0.0002	1	-1.33	-1.35
Spop	speckle-type POZ protein	0.2748	0.0034	0.0002	1.04	-1.27	-1.35
Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	0.0150	0.0019	0.0023	-1.26	-1.34	-1.36
Phyh1	phytanoyl-CoA dioxygenase domain containing 1	0.0116	0.0024	0.0047	-1.19	-1.35	-1.36
Fam158a	family with sequence similarity 158, member A	0.1171	0.0004	0.0002	-1.18	-1.5	-1.36
Cyfp1	cytoplasmic FMR1 interacting protein 1	0.2329	0.0022	0.0036	-1.16	-1.27	-1.37
Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	0.2555	0.0076	0.0023	-1.09	-1.29	-1.37
2810422J05Rik	RIKEN cDNA 2810422J05 gene	0.3658	0.0077	0.0036	-1.09	-1.3	-1.37
Morc2a	microorchidia 2A	0.1116	0.0008	0.0053	-1.13	-1.34	-1.37
Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0.2325	0.0000	0.0000	-1.07	-1.38	-1.39
Tm7sf2	transmembrane 7 superfamily member 2	0.0985	0.0031	0.0059	-1.15	-1.48	-1.39
Coq7	demethyl-Q 7	0.0145	0.0014	0.0059	-1.33	-1.6	-1.4
2900010J23Rik	RIKEN cDNA 2900010J23 gene	0.2570	0.0058	0.0098	-1.11	-1.52	-1.4
Osgep	O-sialoglycoprotein endopeptidase	0.0625	0.0013	0.0017	-1.15	-1.33	-1.41
Psmc7	proteasome (prosome, macropain) subunit, alpha type 7	0.9818	0.0003	0.0000	-1	-1.36	-1.41
Pias1	protein inhibitor of activated STAT 1	0.5891	0.0043	0.0085	-1.04	-1.38	-1.41
D530039A21Rik	RIKEN cDNA D530039A21 gene	0.0156	0.0077	0.0084	-1.45	-1.43	-1.41
Rnaseh2b	ribonuclease H2, subunit B	0.0797	0.0039	0.0001	-1.23	-1.37	-1.41
Usp42	ubiquitin specific peptidase 42	0.4126	0.0016	0.0038	-1.1	-1.3	-1.41
Bsg	basigin	0.3853	0.0036	0.0009	-1.09	-1.37	-1.41
Ggct	gamma-glutamyl cyclotransferase	0.8713	0.0012	0.0012	-1.02	-1.4	-1.41
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	0.1004	0.0096	0.0022	-1.12	-1.59	-1.43
Rps19	ribosomal protein S19	0.1172	0.0003	0.0010	-1.13	-1.51	-1.44
Iltb1	integrin beta 1 (fibronectin receptor beta)	0.7691	0.0001	0.0006	1.02	-1.5	-1.44
Snhg1	small nucleolar RNA host gene (non-protein coding) 1	0.3706	0.0013	0.0018	-1.07	-1.4	-1.44
Exosc4	exosome component 4	0.4057	0.0048	0.0005	1.05	-1.38	-1.44
Tm4sf1	transmembrane 4 superfamily member 1	0.0211	0.0049	0.0040	-1.32	-1.48	-1.44
Cks2	CDC28 protein kinase regulatory subunit 2	0.0621	0.0028	0.0001	-1.24	-1.45	-1.45
Mett17a1	methyltransferase like 7A1	0.1043	0.0028	0.0071	-1.16	-1.49	-1.45
BC021614	cDNA sequence BC021614	0.0334	0.0035	0.0003	-1.2	-1.52	-1.45
Pold4	polymerase (DNA-directed), delta 4	0.1779	0.0042	0.0054	-1.16	-1.47	-1.46
Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0.1919	0.0018	0.0073	-1.1	-1.43	-1.46
Nsa2	NSA2 ribosome biogenesis homolog (S. cerevisiae)	0.3560	0.0008	0.0002	-1.06	-1.41	-1.47
Slc22a18	solute carrier family 22 (organic cation transporter), member 18	0.0801	0.0003	0.0013	-1.21	-1.52	-1.47
Mrps25	mitochondrial ribosomal protein S25	0.8767	0.0008	0.0008	-1.01	-1.37	-1.48
Raga	Ras-related GTP binding A	0.0404	0.0017	0.0087	-1.13	-1.77	-1.48
Pef1	penta-EF hand domain containing 1	0.0981	0.0009	0.0033	-1.16	-1.57	-1.48

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Inpp5k	inositol polyphosphate 5-phosphatase K	0.0640	0.0005	0.0004	-1.21	-1.64	-1.49
2310037124Rik	RIKEN cDNA 2310037124 gene	0.0160	0.0099	0.0009	-1.28	-1.29	-1.51
Mrpl50	mitochondrial ribosomal protein L50	0.0331	0.0017	0.0022	-1.22	-1.78	-1.51
Rwdd4a	RWD domain containing 4A	0.5489	0.0092	0.0008	-1.03	-1.29	-1.51
Arnt	aryl hydrocarbon receptor nuclear translocator	0.3019	0.0095	0.0088	-1.16	-1.43	-1.53
Pot1a	protection of telomeres 1A	0.3656	0.0001	0.0033	-1.09	-1.72	-1.53
Cebpz	CCAAT/enhancer binding protein zeta	0.6497	0.0002	0.0001	-1.05	-1.4	-1.53
Swap70	SWA-70 protein	0.1069	0.0006	0.0091	-1.27	-1.73	-1.53
Luc7l3	LUC7-like 3 (S. cerevisiae)	0.2211	0.0000	0.0000	-1.12	-1.47	-1.54
Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	0.0241	0.0010	0.0001	-1.26	-1.53	-1.54
4933411D12Rik	RIKEN cDNA 4933411D12 gene	0.9539	0.0084	0.0028	1.01	-1.35	-1.55
Stard3nl	STARD3 N-terminal like	0.0579	0.0005	0.0022	-1.3	-1.74	-1.55
Msl2	male-specific lethal 2 homolog (Drosophila)	0.1049	0.0071	0.0000	-1.15	-1.27	-1.55
Srsf5	serine/arginine-rich splicing factor 5	0.0182	0.0004	0.0050	-1.26	-1.63	-1.56
Ttc5	tetratricopeptide repeat domain 5	0.1397	0.0006	0.0001	-1.2	-1.59	-1.57
Tmx2	thioredoxin-related transmembrane protein 2	0.1484	0.0017	0.0003	-1.15	-1.43	-1.57
Strbp	spermatid perinuclear RNA binding protein	0.0305	0.0010	0.0032	-1.39	-1.7	-1.58
2700022O18Rik	RIKEN cDNA 2700022O18 gene	0.4623	0.0027	0.0079	-1.09	-1.94	-1.58
Srsf9	serine/arginine-rich splicing factor 9	0.1773	0.0019	0.0005	-1.12	-1.72	-1.58
Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	0.1086	0.0009	0.0015	-1.14	-1.61	-1.58
Tsn	translin	0.1966	0.0061	0.0015	-1.11	-1.42	-1.59
G3bp1	Ras-GTPase-activating protein SH3-domain binding protein 1	0.2789	0.0042	0.0052	-1.1	-1.66	-1.59
F11r	F11 receptor	0.3774	0.0029	0.0002	-1.11	-1.48	-1.61
Thoc4	THO complex 4	0.0291	0.0072	0.0021	-1.27	-1.71	-1.62
Chd4	chromodomain helicase DNA binding protein 4	0.0521	0.0008	0.0005	-1.2	-1.59	-1.62
Rsad2	radical S-adenosyl methionine domain containing 2	0.2598	0.0016	0.0002	-1.13	-1.61	-1.63
Ssbp3	single-stranded DNA binding protein 3	0.6396	0.0070	0.0047	-1.04	-1.55	-1.63
Vat1	vesicle amine transport protein 1 homolog (T. californica)	0.0186	0.0062	0.0075	-1.4	-1.52	-1.64
AU015603	expressed sequence AU015603	0.9414	0.0015	0.0042	1.01	-1.87	-1.66
Snrnp70	small nuclear ribonucleoprotein 70 (U1)	0.2378	0.0051	0.0049	-1.14	-1.65	-1.66
Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.0207	0.0059	0.0020	-1.28	-1.48	-1.66
Insig1	insulin induced gene 1	0.3864	0.0007	0.0002	-1.12	-1.66	-1.67
Rasa2	RAS p21 protein activator 2	0.0276	0.0002	0.0003	-1.26	-1.94	-1.68
10-Sep	septin 10	0.2585	0.0011	0.0005	-1.13	-1.51	-1.68
Nrarp	Notch-regulated ankyrin repeat protein	0.0790	0.0094	0.0084	-1.48	-1.61	-1.68
Pfdr2	prefoldin 2	0.1077	0.0078	0.0009	-1.17	-1.73	-1.68
Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0.9487	0.0062	0.0002	1.02	-1.45	-1.69
Acdk4	aaRF domain containing kinase 4	0.3972	0.0069	0.0030	-1.14	-1.57	-1.69
Acr5	ARP5 actin-related protein 5 homolog (yeast)	0.0802	0.0016	0.0066	-1.28	-2.23	-1.7
Ubf1	ubiquitin family domain containing 1	0.0811	0.0038	0.0018	-1.18	-1.64	-1.7
Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	0.0257	0.0000	0.0002	-1.2	-1.76	-1.7
Wip1	WD repeat domain, phosphoinositide interacting 2	0.1548	0.0003	0.0001	-1.16	-1.64	-1.7
Rictor	RPTOR independent companion of MTOR, complex 2	0.2448	0.0028	0.0005	-1.11	-1.62	-1.71
Gm7072	predicted gene 7072	0.5401	0.0001	0.0015	1.1	-1.64	-1.72
Wdr1	WD repeat domain 1	0.2739	0.0042	0.0002	-1.17	-1.57	-1.73
Rsl1	remodeling and spacing factor 1	0.6019	0.0054	0.0010	-1.04	-1.43	-1.73
Mthfd2	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cycle	0.0209	0.0008	0.0008	-1.51	-2	-1.74
Dsp	desmoplakin	0.0706	0.0011	0.0001	-1.13	-1.52	-1.76
Tmed2	transmembrane emp24 domain trafficking protein 2	0.3508	0.0005	0.0000	-1.05	-1.53	-1.76
Tmem167b	transmembrane protein 167B	0.7102	0.0039	0.0003	-1.06	-1.74	-1.77
Rho	rhodopsin	0.5275	0.0038	0.0023	-1.06	-1.66	-1.79
Wac	WW domain containing adaptor with coiled-coil	0.0852	0.0023	0.0008	1.16	-1.35	-1.8
Pop25e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	0.1233	0.0098	0.0006	1.2	-1.52	-1.81
Slk25	serine/threonine kinase 25 (yeast)	0.2222	0.0001	0.0002	-1.18	-1.89	-1.81
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	0.9686	0.0004	0.0005	1.01	-1.95	-1.82
4932431P20Rik	RIKEN cDNA 4932431P20 gene	0.5103	0.0052	0.0003	1.07	-1.43	-1.84
Snord104	small nucleolar RNA, C/D box 104	0.6071	0.0036	0.0013	1.06	-1.94	-1.84
Rnf149	ring finger protein 149	0.6831	0.0000	0.0001	1.02	-1.96	-1.85
A1cf	APOBEC1 complementation factor	0.1474	0.0071	0.0014	-1.18	-1.66	-1.85
Psmb2	proteasome (prosome, macropain) subunit, beta type 2	0.1063	0.0049	0.0012	-1.2	-1.86	-1.85
Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0.0357	0.0080	0.0007	-1.26	-1.75	-1.86
Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	0.0117	0.0010	0.0009	-1.48	-1.84	-1.88
Nacc2	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	0.0968	0.0014	0.0002	-1.33	-1.71	-1.89
A1987944	expressed sequence A1987944	0.1861	0.0001	0.0000	-1.11	-2.07	-1.89
Dync1l1	dynein cytoplasmic 1 light intermediate chain 1	0.2116	0.0074	0.0040	-1.23	-1.8	-1.89
Nop58	NOP58 ribonucleoprotein homolog (yeast)	0.5097	0.0003	0.0001	-1.06	-2	-1.91
Camsap1	calmodulin regulated spectrin-associated protein 1	0.2494	0.0023	0.0002	1.1	-1.78	-1.94
2510022D24Rik	RIKEN cDNA 2510022D24 gene	0.5693	0.0089	0.0036	-1.09	-1.71	-1.98
AY036118	cDNA sequence AY036118	0.4862	0.0001	0.0000	-1.05	-1.91	-2
Mps1	mercaptopyruvate sulfurtransferase	0.0362	0.0002	0.0000	1.23	-1.78	-2.01
Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	0.4634	0.0059	0.0001	-1.06	-1.56	-2.01
Tm4sf4	transmembrane 4 superfamily member 4	0.9575	0.0050	0.0006	-1.02	-1.8	-2.02
Seps2	selenophosphate synthetase 2	0.7844	0.0010	0.0003	1.04	-1.77	-2.03
Ilf2	interleukin enhancer binding factor 2	0.0615	0.0010	0.0006	-1.23	-2.07	-2.03
9430034N14Rik	RIKEN cDNA 9430034N14 gene	0.0917	0.0000	0.0041	1.19	-1.72	-2.05
Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	0.0416	0.0073	0.0004	-1.35	-1.55	-2.06
Cdkn1b	cyclin-dependent kinase inhibitor 1B	0.3944	0.0019	0.0001	-1.08	-1.43	-2.08
Adnp2	ADNP homeobox 2	0.3055	0.0028	0.0021	-1.23	-2.39	-2.08
Plekha5	pleckstrin homology domain containing, family A member 5	0.0795	0.0038	0.0077	1.09	-1.96	-2.17
Gcap14	granule cell antiserum positive 14	0.0326	0.0034	0.0000	-1.4	-1.47	-2.2
Minpp1	multiple inositol polyphosphate histidine phosphatase 1	0.1673	0.0003	0.0000	-1.17	-2.11	-2.21
Fmo4	flavin containing monooxygenase 4	0.2938	0.0009	0.0026	-1.24	-2.8	-2.28
Setd4	SET domain containing 4	0.0616	0.0047	0.0008	-1.67	-2.12	-2.3
Thoc2	THO complex 2	0.7591	0.0005	0.0000	-1.02	-1.84	-2.45
3110047M12Rik	RIKEN cDNA 3110047M12 gene	0.1513	0.0044	0.0038	1.66	-2.19	-2.5
Hnnpab	heterogeneous nuclear ribonucleoprotein A/B	0.2315	0.0008	0.0008	-1.21	-2.5	-2.5
A1131651	expressed sequence A1131651	0.5893	0.0036	0.0023	-1.09	-2.18	-2.5
Zbtb4	zinc finger and BTB domain containing 4	0.1455	0.0009	0.0001	-1.18	-1.89	-2.53
Sox6	SRY-box containing gene 6	0.0707	0.0000	0.0000	-1.22	-2.26	-2.59
Usf1	upstream transcription factor 1	0.0933	0.0010	0.0004	-1.42	-2.22	-2.64
Gprc5c	G protein-coupled receptor, family C, group 5, member C	0.3469	0.0028	0.0024	-1.21	-2.75	-2.71
Otu2	OTU domain, ubiquitin aldehyde binding 2	0.0859	0.0005	0.0051	-1.74	-4.72	-2.75
Net1	neuroepithelial cell transforming gene 1	0.0344	0.0006	0.0004	-1.38	-2.7	-2.75
2810043O03Rik	RIKEN cDNA 2810043O03 gene	0.0412	0.0019	0.0015	-1.55	-2.54	-2.77
C80998	expressed sequence C80998	0.0935	0.0043	0.0013	-1.32	-1.99	-2.79
Pfn1	profilin 1	0.1422	0.0050	0.0002	-1.28	-2.29	-2.8
Gm3426	predicted gene 3426	0.0874	0.0064	0.0097	-1.87	-3.32	-2.86
D330013E07Rik	RIKEN cDNA D330013E07 gene	0.5091	0.0006	0.0014	1.11	-2.99	-2.88
Fam19a2	family with sequence similarity 19, member A2	0.0952	0.0000	0.0000	-1.49	-3.27	-2.9
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	0.0268	0.0001	0.0002	-1.45	-2.81	-2.97
Tif1	transcription termination factor, RNA polymerase I	0.1598	0.0063	0.0003	-1.28	-2.03	-2.99
6430537K16Rik	RIKEN cDNA 6430537K16 gene	0.1690	0.0001	0.0027	-1.47	-5.71	-3
Srp72	signal recognition particle 72	0.5382	0.0000	0.0000	-1.02	-2.99	-3.19
Uroc1	urocanase domain containing 1	0.4074	0.0011	0.0000	-1.25	-2.58	-3.27

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
3300002A11Rik	RIKEN cDNA 3300002A11 gene	0.0401	0.0015	0.0009	-1.74	-2.78	-3.34
Gtpbp5	GTP binding protein 5	0.5893	0.0011	0.0001	-1.08	-2.62	-3.51
Mapre2	microtubule-associated protein, RP/EB family, member 2	0.2584	0.0018	0.0012	-1.3	-3.1	-3.71
2610002D18Rik	RIKEN cDNA 2610002D18 gene	0.1979	0.0017	0.0001	-1.39	-2.79	-3.84
Arhgap9	Rho GTPase activating protein 9	0.1052	0.0083	0.0040	-1.75	-2.94	-3.87
Pparc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	0.1478	0.0000	0.0000	1.45	-2.88	-4.57
Slc6a20b	solute carrier family 6 (neurotransmitter transporter), member 20B	0.9757	0.0098	0.0095	-1.01	-5.21	-5.13
Cc2d1b	coiled-coil and C2 domain containing 1B	0.0277	0.0021	0.0007	-1.67	-3.2	-5.19
Nudt11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.0822	0.0039	0.0031	-2.18	-5.16	-5.22
Zfp612	zinc finger protein 612	0.0258	0.0000	0.0000	-1.42	-4.08	-8.5
Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0.5758	0.0002	0.0000	-1.08	-3.8	-11.02
Gpr87	G protein-coupled receptor 87	0.0004	0.0022	0.0041	3.76	4.51	6.73
2700094K13Rik	RIKEN cDNA 2700094K13 gene	0.0000	0.0000	0.0000	5.7	5.74	6.25
C030013E06Rik	RIKEN cDNA C030013E06 gene	0.0039	0.0001	0.0001	2.36	3.42	3.66
Sepw1	selenoprotein W, muscle 1	0.0000	0.0051	0.0001	4.24	4.24	3.61
Anpep	alanyl (membrane) aminopeptidase	0.0008	0.0000	0.0000	1.21	2.65	2.43
Txnrd2	thioredoxin reductase 2	0.0027	0.0008	0.0000	1.99	2.12	2.3
Gpx1	glutathione peroxidase 1	0.0000	0.0000	0.0000	2.37	2.32	2.3
Gpx3	glutathione peroxidase 3	0.0063	0.0003	0.0077	1.73	2.63	2.26
Med16	mediator complex subunit 16	0.0057	0.0002	0.0001	1.26	1.94	2.22
Seik	selenoprotein K	0.0000	0.0001	0.0001	2.12	1.8	2.08
BC031353	cDNA sequence BC031353	0.0013	0.0079	0.0097	1.58	1.65	2.03
1110054M08Rik	RIKEN cDNA 1110054M08 gene	0.0093	0.0005	0.0009	1.34	1.85	1.99
Wdsb1	WD repeat, SAM and U-box domain containing 1	0.0018	0.0029	0.0003	1.3	1.69	1.75
2010107H07Rik	RIKEN cDNA 2010107H07 gene	0.0083	0.0015	0.0009	1.37	1.6	1.69
Sepx1	selenoprotein X 1	0.0000	0.0000	0.0000	1.48	1.73	1.69
15-Sep	selenoprotein	0.0000	0.0000	0.0000	1.56	1.58	1.66
Cotl1	coactosin-like 1 (Dictyostelium)	0.0010	0.0069	0.0029	1.77	1.36	1.63
1600002H07Rik	RIKEN cDNA 1600002H07 gene	0.0000	0.0047	0.0014	1.78	1.75	1.63
Sxbp6	syntaxin binding protein 6 (amisyn)	0.0083	0.0090	0.0008	1.5	1.38	1.63
Trim8	tripartite motif-containing 8	0.0042	0.0001	0.0000	1.21	1.57	1.55
2810407C02Rik	RIKEN cDNA 2810407C02 gene	0.0001	0.0000	0.0001	1.44	1.5	1.52
Gphn	gephyrin	0.0039	0.0020	0.0002	1.19	1.34	1.49
Col18a1	collagen, type XVIII, alpha 1	0.0008	0.0002	0.0032	1.33	1.4	1.47
Ict1	immature colon carcinoma transcript 1	0.0096	0.0060	0.0001	1.19	1.27	1.43
Brd3	bromodomain containing 3	0.0080	0.0007	0.0005	1.24	1.46	1.43
Ptp4a1	protein tyrosine phosphatase 4a1	0.0028	0.0012	0.0074	1.41	1.62	1.42
Tst	thiosulfate sulfurtransferase, mitochondrial	0.0032	0.0000	0.0000	1.3	1.25	1.38
Klhl2	kelch-like 2, Mayven (Drosophila)	0.0059	0.0007	0.0000	1.2	1.37	1.36
Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	0.0026	0.0028	0.0001	1.26	1.28	1.36
Ifitm3	interferon induced transmembrane protein 3	0.0094	0.0048	0.0016	1.37	1.31	1.33
Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.0067	0.0000	0.0004	1.28	1.75	1.33
Dctpp1	dCTP pyrophosphatase 1	0.0006	0.0051	0.0050	1.24	1.18	1.3
Ptpf	protein tyrosine phosphatase, receptor type, F	0.0011	0.0011	0.0002	1.28	1.31	1.29
Pigs	phosphatidylinositol glycan anchor biosynthesis, class S	0.0100	0.0025	0.0045	1.14	1.29	1.28
Cadps2	Ca2+-dependent activator protein for secretion 2	0.0002	0.0032	0.0054	1.6	1.4	1.27
Txnrd1	thioredoxin reductase 1	0.0015	0.0057	0.0082	1.42	1.33	1.25
Cib1	calcium and integrin binding 1 (calmyrin)	0.0014	0.0001	0.0001	1.19	1.32	1.24
Cox5a	cytochrome c oxidase, subunit Va	0.0004	0.0001	0.0001	1.15	1.18	1.23
Phyh	phytanoyl-CoA hydroxylase	0.0074	0.0051	0.0002	1.15	1.18	1.22
F5	coagulation factor V	0.0055	0.0001	0.0005	1.12	1.24	1.15
Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0.0027	0.0002	0.0010	-1.14	-1.2	-1.19
Psmb5	proteasome (prosome, macropain) subunit, beta type 5	0.0001	0.0002	0.0013	-1.34	-1.29	-1.2
Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein	0.0054	0.0004	0.0098	-1.24	-1.32	-1.2
Akr1c13	aldo-keto reductase family 1, member C13	0.0012	0.0000	0.0017	-1.24	-1.33	-1.26
Slc35d1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), r	0.0008	0.0014	0.0056	-1.43	-1.4	-1.26
Bcap31	B-cell receptor-associated protein 31	0.0005	0.0014	0.0000	-1.18	-1.32	-1.27
Fil1	ferritin light chain 1	0.0057	0.0069	0.0095	-1.35	-1.34	-1.29
Tbce	tubulin-specific chaperone E	0.0008	0.0003	0.0014	-1.47	-1.45	-1.32
2310061C15Rik	RIKEN cDNA 2310061C15 gene	0.0017	0.0028	0.0014	-1.29	-1.34	-1.32
Oxsr1	oxidative-stress responsive 1	0.0071	0.0051	0.0033	-1.38	-1.42	-1.34
4930402H24Rik	RIKEN cDNA 4930402H24 gene	0.0001	0.0040	0.0020	-1.8	-1.39	-1.34
Tkt	transketolase	0.0033	0.0062	0.0023	-1.6	-1.5	-1.34
Pgd	phosphogluconate dehydrogenase	0.0024	0.0011	0.0028	-1.43	-1.53	-1.35
C2cd2	C2 calcium-dependent domain containing 2	0.0060	0.0005	0.0004	-1.22	-1.5	-1.36
Creb3	cAMP responsive element binding protein 3	0.0044	0.0001	0.0002	-1.17	-1.37	-1.37
Gss	glutathione synthetase	0.0007	0.0015	0.0004	-1.5	-1.48	-1.38
Tmem62	transmembrane protein 62	0.0011	0.0037	0.0018	-1.33	-1.32	-1.38
Impact	imprinted and ancient	0.0017	0.0027	0.0074	-1.5	-1.43	-1.38
Ephx1	epoxide hydrolase 1, microsomal	0.0058	0.0089	0.0043	-1.55	-1.37	-1.38
Mvp	major vault protein	0.0088	0.0023	0.0023	-1.35	-1.33	-1.39
Anxa7	annexin A7	0.0017	0.0014	0.0002	-1.28	-1.41	-1.4
C730048C13Rik	RIKEN cDNA C730048C13 gene	0.0043	0.0000	0.0000	-1.33	-1.44	-1.41
Thoc5	THO complex 5	0.0086	0.0018	0.0041	-1.3	-1.48	-1.42
Skp1a	S-phase kinase-associated protein 1A	0.0032	0.0031	0.0018	-1.31	-1.37	-1.42
Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	0.0007	0.0000	0.0000	-1.27	-1.57	-1.44
Ugt2b35	UDP glucuronosyltransferase 2 family, polypeptide B35	0.0001	0.0001	0.0001	-1.6	-1.56	-1.44
Bivrb	biliverdin reductase B (flavin reductase (NADPH))	0.0008	0.0006	0.0012	-1.97	-1.78	-1.46
Epb4.11i	erythrocyte protein band 4.1-like 1	0.0045	0.0001	0.0093	-1.35	-1.51	-1.47
Atplf1	ATPase inhibitory factor 1	0.0002	0.0018	0.0003	-1.38	-1.43	-1.49
Ces1	carboxylesterase 1	0.0016	0.0005	0.0008	-1.58	-1.76	-1.53
Gsr	glutathione reductase	0.0009	0.0012	0.0013	-1.58	-1.59	-1.57
Atf4	activating transcription factor 4	0.0040	0.0078	0.0087	-1.58	-1.71	-1.59
Cpeb3	cytoplasmic polyadenylation element binding protein 3	0.0067	0.0002	0.0002	-1.39	-1.63	-1.59
Capza2	capping protein (actin filament) muscle Z-line, alpha 2	0.0081	0.0018	0.0002	-1.14	-1.53	-1.6
Aox1	aldehyde oxidase 1	0.0018	0.0042	0.0077	-2.2	-1.8	-1.64
Akr1c19	aldo-keto reductase family 1, member C19	0.0003	0.0016	0.0014	-1.97	-1.66	-1.69
Pir	pirin	0.0018	0.0004	0.0005	-1.67	-1.82	-1.7
Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0.0002	0.0002	0.0002	-1.89	-1.79	-1.72
Pparg	peroxisome proliferator activated receptor gamma	0.0000	0.0000	0.0005	-2.05	-2.24	-1.73
Ddc	dopa decarboxylase	0.0002	0.0019	0.0004	-1.84	-1.78	-1.74
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.0004	0.0004	0.0004	-1.48	-2.1	-1.76
Hexa	hexosaminidase A	0.0006	0.0010	0.0000	-1.58	-1.48	-1.77
Cars	cysteinyln-IRNA synthetase	0.0031	0.0002	0.0000	-1.52	-1.78	-1.78
Ugdh	UDP-glucose dehydrogenase	0.0004	0.0001	0.0002	-1.85	-1.87	-1.83
Gsta4	glutathione S-transferase, alpha 4	0.0000	0.0002	0.0001	-2.62	-2.12	-1.87
2700089E24Rik	RIKEN cDNA 2700089E24 gene	0.0041	0.0036	0.0001	-1.3	-1.6	-1.89
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	0.0026	0.0001	0.0004	-1.47	-1.73	-1.89
Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0.0001	0.0000	0.0002	-1.96	-2.33	-1.89
Gm14964	predicted gene 14964	0.0013	0.0013	0.0019	-2.88	-2.11	-1.92
Irak2	interleukin-1 receptor-associated kinase 2	0.0035	0.0061	0.0001	-1.55	-1.5	-1.93
LOC630729	similar to Glutathione reductase, mitochondrial precursor (GR) (GRase)	0.0019	0.0049	0.0008	-1.65	-2.01	-1.94
Extl1	exostosins (multiple)-like 1	0.0001	0.0062	0.0014	-1.8	-2.07	-2.12
Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	0.0014	0.0021	0.0010	-2.05	-2.14	-2.12

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

Gene Symbol	Gene Title	p-value (SM)	p-value (SS)	p-value (YS)	FC (SM)	FC (SS)	FC (YS)
Mbni3	muscleblind-like 3 (Drosophila)	0.0018	0.0035	0.0013	-1.62	-1.76	-2.22
Gsta2	glutathione S-transferase, alpha 2 (Yc2)	0.0001	0.0003	0.0001	-3.47	-2.71	-2.25
Htatip2	HIV-1 tat interactive protein 2, homolog (human)	0.0000	0.0000	0.0000	-1.95	-2.19	-2.26
Gstm4	glutathione S-transferase, mu 4	0.0002	0.0001	0.0001	-2.29	-2.81	-2.29
Nqo1	NAD(P)H dehydrogenase, quinone 1	0.0036	0.0028	0.0020	-2.04	-2.43	-2.3
Srp54b	signal recognition particle 54B	0.0025	0.0000	0.0018	-2.25	-6.16	-2.31
Uap1l1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	0.0035	0.0087	0.0002	-1.74	-1.95	-2.35
Tsku	tsukushin	0.0009	0.0007	0.0000	-1.87	-2.12	-2.49
C730027H18Rik	RIKEN cDNA C730027H18 gene	0.0083	0.0005	0.0006	-1.74	-2.85	-2.68
Slc48a1	solute carrier family 48 (heme transporter), member 1	0.0000	0.0000	0.0000	-2.79	-2.67	-2.68
Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	0.0002	0.0039	0.0001	-1.58	-2.22	-2.71
Mgst3	microsomal glutathione S-transferase 3	0.0003	0.0001	0.0000	-2.26	-3.63	-3.4
Cbr1	carbonyl reductase 1	0.0000	0.0000	0.0000	-3.78	-3.44	-3.52
Gstm3	glutathione S-transferase, mu 3	0.0000	0.0000	0.0000	-3.89	-5.45	-3.97
Osbpl3	oxysterol binding protein-like 3	0.0017	0.0030	0.0051	-10.21	-5.75	-4.44
Psat1	phosphoserine aminotransferase 1	0.0001	0.0000	0.0000	-3.46	-6.98	-10.57
Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	0.0017	0.0018	0.0017	-13.46	-12.24	-13.03
Cbr3	carbonyl reductase 3	0.0014	0.0015	0.0015	-37.08	-26.08	-27.6