

**Supplemental Table 1S.**

Complete list of genes whose expression was significantly regulated in response to high fat lard feeding

Agilent accession number	Pvalue	Fold changes	NCBI accession number	Gene symbol	Genes name
A_51_P453043	0.00522	3.6	NM_030210	<i>Aacs</i>	acetoacetyl-CoA synthetase
A_51_P381683	0.00131	4.3	NM_007377	<i>Aatr</i>	apoptosis-associated tyrosine kinase
A_52_P161305	0.000112	0.5	NM_018811	<i>Abca8b</i>	ATP-binding cassette, sub-family A (ABC1), member 8b
A_52_P664506	0.0442	2.7	NM_019811	<i>Abhd2</i>	aldehyde dehydrogenase domain containing 2
A_52_P566718	0.000623	0.4	NM_019811	<i>Acas2</i>	acetyl-Coenzyme A synthetase 2 (ADP forming)
A_51_P213515	0.0297	2.6	NM_145368	<i>Acnat2</i>	acyl-coenzyme A amino acid N-acyltransferase 2
A_52_P72237	8.33E-05	3.6	NM_013798	<i>Actg</i>	actin, gamma, cytoplasmic
A_52_P240164	0.00642	0.4	NM_009622	<i>Adcy1</i>	adenylate cyclase 1
A_51_P462271	0.0309	0.4	NM_007424	<i>Agc1</i>	aggreclin 1
A_51_P306731	0.0029	2.5	NM_172715	<i>Agpat9</i>	1-acetylgeranyl-3-phosphate O-acyltransferase 9, transcript variant 1
A_51_P391616	2.81E-05	0.2	NM_027907	<i>Agxt2l1</i>	alanine-glyoxylate aminotransferase 2-like 1
A_52_P559066	0.0183	2.7	XM_131754	<i>Aim1l</i>	PREDICTED: Mus musculus absent in melanoma 1-like, transcript variant 1
A_51_P377826	0.008	2.1	AF224494	<i>Airap</i>	arsenite inducible RNA associated protein
A_51_P494125	0.00235	2.1	NM_007431	<i>Akp2</i>	alkaline phosphatase 2
A_52_P129756	0.00695	4.6	NM_020559	<i>Alas1</i>	aminolevulinic acid synthase 1
A_51_P220681	5.94E-05	0.3	NM_009657	<i>Aldoc</i>	aldolase 3, C isoform
A_51_P243168	0.00853	2.1	XM_655201	<i>Als2cr4</i>	PREDICTED: Mus musculus amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4, transcript variant 1
A_51_P293315	0.0209	2.1	NM_020033	<i>Ankd2</i>	ankyrin repeat domain 2 (stretch responsive muscle)
A_51_P397783	0.00193	0.4	XM_132758	<i>Anub1l</i>	Mus musculus AN1, ubiquitin-like, homolog (Xenopus laevis), transcript variant 1
A_51_P165342	0.00134	2.7	NM_007585	<i>Anxa2</i>	annexin A2
A_51_P327496	0.000188	4.3	NM_007468	<i>Apoa4</i>	apolipoprotein A-IV
A_51_P419319	0.00213	2.5	NM_009700	<i>Aqp4</i>	aquaporin 4
A_52_P267651	3.07E-05	0.1	NM_007489	<i>Arntl</i>	aryl hydrocarbon receptor nuclear translocator-like
A_51_P417651	0.00485	0.3	NM_027560	<i>Arroc2</i>	arrestin domain containing 2
A_52_P164136	0.00812	3.3	NM_178917	<i>Arroc3</i>	arrestin domain containing 3
A_51_P125745	0.00505	0.1	NM_012055	<i>Asns</i>	asparagine synthetase
A_52_P452689	0.000301	5	NM_007498	<i>Atf3</i>	activating transcription factor 3
A_51_P209736	0.00273	0.4	NM_153778	<i>Atah8</i>	atoh1 homolog 8 (Drosophila)
A_51_P504114	0.0116	0.5	NM_015804	<i>Atp11a</i>	ATPase, class VI, type 11A
A_51_P426792	0.00176	0.4	NM_018731	<i>Atp4a</i>	ATPase, H <sup>+</sup> /K <sup>+</sup> transporting, alpha polypeptide
A_51_P315042	0.00072	0.5	NM_016847	<i>Avpr1a</i>	arginine vasopressin receptor 1A
A_51_P272553	0.00352	2.3	NM_011498	<i>Bhlhb2</i>	basic helix-loop-helix domain containing, class B2
A_51_P393081	0.00381	3.2	NM_009812	<i>Bhlhb3</i>	basic helix-loop-helix domain containing, class B9
A_51_P373082	5.75E-05	0.4	NM_016778	<i>Bok</i>	Bcl-2-related ovarian killer protein
A_51_P340601	0.000876	0.3	NM_009770	<i>Btg3</i>	B-cell translocation gene 3
A_51_P221651	3.48E-05	0.5	NM_023341	<i>Cabc1</i>	chaperone, ABC1 activity of bc1 complex like
A_51_P382618	0.0128	0.4	NM_009810	<i>Casp3</i>	caspase 3, apoptosis related cysteine protease
A_51_P286737	0.0359	3.4	NM_011333	<i>Ccl2</i>	chemokine (C-C motif) ligand 2
A_51_P483512	0.0266	2.4	NM_013683	<i>Ccl5</i>	chemokine (C-C motif) ligand 5
A_51_P262766	0.00064	3.2	NM_007631	<i>Ccni1</i>	cyclin D1
A_51_P375146	0.0251	2.3	NM_007443	<i>Cd36</i>	CD36 antigen
A_51_P199135	0.0172	2.9	NM_009856	<i>Cd83</i>	CD83 antigen
A_51_P320852	2.38E-05	0.4	NM_007657	<i>Cd9</i>	CD9 antigen
A_51_P137336	0.00103	0.3	NM_009864	<i>Cdh1</i>	cadherin 1
A_51_P513573	7.83E-06	0.4	NM_145603	<i>Ces2</i>	carboxylesterase 2
A_51_P443339	6.67E-06	0.4	NM_133960	<i>Ces6</i>	carboxylesterase 6
A_52_P420045	0.00127	0.4	NM_013490	<i>Chka</i>	choline kinase alpha
A_51_P390021	0.00032	2.7	NM_144803	<i>Chra2</i>	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)
A_51_P490456	0.0122	3.8	NM_178373	<i>Cidec</i>	cell death-inducing DFFA-like effector c
A_52_P48681	0.00356	0.4	NM_016674	<i>Cldn1</i>	claudin 1
A_51_P246653	0.0321	2.7	NM_020008	<i>Clec7a</i>	C-type lectin domain family 7, member a
A_51_P304683	1.95E-05	0.3	NM_011802	<i>Clix</i>	caseinolytic protease X
A_52_P366525	3.95E-05	3.2	NM_026424	<i>Cog10b</i>	coenzyme Q10 homolog B (S. cerevisiae), transcript variant 2
A_52_P462296	0.000642	2.3	NM_007755	<i>Cpeb1</i>	cytoplasmic polyadenylation element binding protein 1
A_52_P13060	0.004	0.3	NM_009993	<i>Cpeb2</i>	cytoplasmic polyadenylation element binding protein 2
A_52_P625508	0.0145	2.8	NM_009845	<i>Crt1b</i>	carotene palmityltransferase 1b, muscle
A_51_P122246	0.00652	2.4	NM_023220	<i>Crtl2</i>	cysteine-rich with EGF-like domains 2
A_51_P325776	0.000536	0.3	NM_144942	<i>Csad</i>	cysteine sulfenic acid decarboxylase
A_52_P437662	0.021	0.2	NM_013884	<i>Cspg5</i>	chondroitin sulfate proteoglycan 5
A_51_P251357	3.77E-05	2.1	NM_016748	<i>Ctps</i>	cytidine 5'-triphosphate synthase
A_51_P432641	0.00032	4	NM_021274	<i>Cxcl10</i>	chemokine (C-X-C motif) ligand 10
A_51_P461665	0.00296	3.4	NM_008599	<i>Cxcl9</i>	chemokine (C-X-C motif) ligand 9
A_52_P595871	0.0242	0.4	NM_009993	<i>Cyp1a2</i>	cytochrome P450, family 1, subfamily a, polypeptide 2
A_52_P382149	0.00345	0.2	NM_007811	<i>Cyp26a1</i>	cytochrome P450, family 26, subfamily a, polypeptide 1
A_52_P472486	0.0124	0.2	NM_009999	<i>Cyp2b10</i>	cytochrome P450, family 2, subfamily b, polypeptide 10
A_51_P492339	0.00839	5	NM_007813	<i>Cyp2b13</i>	cytochrome P450, family 2, subfamily b, polypeptide 13
A_52_P289091	0.000175	17.8	NM_007813	<i>Cyp2b13</i>	cytochrome P450, family 2, subfamily b, polypeptide 13
A_51_P467076	0.000686	8.6	NM_010000	<i>Cyp2b9</i>	cytochrome P450, family 2, subfamily b, polypeptide 9
A_51_P447785	3.42E-05	0.1	NM_028089	<i>Cyp2c55</i>	cytochrome P450, family 2, subfamily c, polypeptide 55
A_51_P134142	1.95E-05	0.4	NM_145499	<i>Cyp2c70</i>	cytochrome P450, family 2, subfamily c, polypeptide 70
A_51_P335301	1.81E-05	0.2	NM_007818	<i>Cyp3a11</i>	cytochrome P450, family 3, subfamily a, polypeptide 11
A_51_P482051	8.75E-06	0.1	NM_007820	<i>Cyp3a16</i>	cytochrome P450, family 3, subfamily a, polypeptide 16
A_51_P341203	7.83E-06	0.2	NM_017396	<i>Cyp3a41</i>	cytochrome P450, family 3, subfamily a, polypeptide 41
A_52_P571006	1.95E-05	0.2	NM_177380	<i>Cyp3a44</i>	cytochrome P450, family 3, subfamily a, polypeptide 44
A_52_P257774	0.0126	2.4	NM_010011	<i>Cyp4a10</i>	cytochrome P450, family 4, subfamily a, polypeptide 10
A_52_P164161	0.002029	0.3	NM_020010	<i>Cyp51</i>	cytochrome P450, family 51
A_52_P84027	0.00268	9.6	NM_007824	<i>Cyp7a1</i>	cytochrome P450, family 7, subfamily a, polypeptide 1
A_51_P377557	0.00023	2.3	NM_029794	<i>D11Ert636e</i>	DNA segment, Chr 11, ERA10 Dot 636, expressed
A_52_P223809	0.000345	2.5	NM_030169	<i>D11Erp2e</i>	DNA segment, Chr 11, Lotar Hemmehausen 2, expressed
A_52_P630563	0.00319	0.5	NM_027852	<i>D5Wsu178e</i>	DNA segment, Chr 5, Wayne State University 178, expressed (D5Wsu178e)
A_51_P180492	0.000344	12.4	NM_016974	<i>Dbp</i>	D site albumin promoter binding protein
A_52_P327627	5.24E-05	2.6	NM_018831	<i>Dclre1a</i>	DNA cross-link repair 1A, PSO2 homolog
A_51_P116838	0.00138	0.3	NM_010024	<i>Dct</i>	dopachrome tautomerase
A_52_P63905	2.52E-05	0.5	NM_016672	<i>Ddc</i>	dopa decarboxylase
A_52_P536731	0.00409	0.2	NM_001004364	<i>Ddef2</i>	development and differentiation enhancing factor 2
A_51_P245796	0.00572	0.2	NM_029083	<i>Ddit4</i>	DNA-damage-inducible transcript 4
A_52_P535946	0.00401	0.3	NM_007896	<i>Dhcr7</i>	7-dehydrocholesterol reductase
A_51_P403477	0.0136	2	NM_007860	<i>Diol1</i>	diolase, iodothyronine, type 1
A_52_P310225	0.000629	2	NM_008298	<i>Dnaa1</i>	DnaJ (Hsp40) homolog, subfamily A, member 1
A_52_P369415	0.0329	2.4	NM_207649	<i>Dscr11l</i>	Down syndrome critical region gene 1-like 1
A_51_P495212	0.00018	0.4	NM_172442	<i>Dtx4</i>	deltex 4 homolog (Drosophila)
A_51_P502614	0.00678	2	NM_026268	<i>Dusp6</i>	dual specificity phosphatase 6
A_51_P455338	0.0309	2.4	NM_053113	<i>Ear1l</i>	eosinophil-associated, ribonuclease A family, member 11
A_51_P187842	0.0175	2.5	NM_028229	<i>Eif4e3</i>	eukaryotic translation initiation factor 4E member 3
A_51_P324633	1.61E-05	0.1	NM_007703	<i>Elovl3</i>	elongation of very long chain fatty acids 3
A_51_P401974	6.83E-05	2	NM_015744	<i>Engp2</i>	ectonucleotide pyrophosphatase/phosphodiesterase 2
A_52_P257426	9.14E-05	0.5	NM_133191	<i>Eps8l2</i>	EPS8-like 2
A_52_P317246	0.000696	3.3	NM_011935	<i>Esrrg</i>	estrogen-related receptor gamma
A_51_P117618	0.00563	0.2	NM_023154	<i>Ethel1</i>	ethylmalonic encephalopathy 1
A_51_P346893	0.00925	3.5	NM_019578	<i>Extl1</i>	exostosins (multiple)-like 1
A_51_P313381	0.000116	2.6	NM_007890	<i>Fabp2</i>	fatty acid binding protein 2, intestinal
A_51_P30074	0.0257	2.8	NM_021272	<i>Fabp7</i>	fatty acid binding protein 7, brain
A_52_P181733	5.41E-06	4	NM_153600	<i>Fam102a</i>	Mus musculus family with sequence similarity 102, member A
A_52_P21986	9.88E-05	0.5	NM_026062	<i>Fam69a</i>	family with sequence similarity 69, member A
A_51_P379798	3.73E-05	0.2	NM_134469	<i>Fdps</i>	farnesyl diphosphate synthetase
A_51_P148828	0.000125	2.4	NM_010197	<i>Fgf1</i>	fibroblast growth factor 1
A_52_P235347	0.00496	6.5	NM_020013	<i>Fgf21</i>	fibroblast growth factor 21
A_51_P361220	0.000188	2	NM_008055	<i>Fzd4</i>	frizzled homolog 4 (Drosophila)
A_52_P681391	0.00104	4.1	NM_008059	<i>G0S2</i>	GO/G1 switch gene 2
A_51_P296608	0.0316	3.7	NM_007836	<i>Gadd45a</i>	growth arrest and DNA-damage-inducible 45 alpha
A_51_P355629	0.00139	0.5	NM_008087	<i>Gas2</i>	growth arrest specific 2
A_51_P203955	0.00931	2.9	NM_010260	<i>Gbp2</i>	guanylate nucleotide binding protein 2
A_51_P165244	0.00131	3.6	NM_018734	<i>Gbp4</i>	guanylate nucleotide binding protein 4
A_51_P463846	0.000601	3.4	NM_145645	<i>Gbp6</i>	guanylate binding protein 6
A_52_P287456	0.0155	0.4	NM_145623	<i>Gca</i>	granulocin
A_52_P259537	0.00278	2.8	NM_010292	<i>Gck</i>	glucokinase
A_52_P532982	0.00846	0.4	NM_011819	<i>Gdf15</i>	growth differentiation factor 15
A_51_P311546	4.98E-05	3.4	NM_138595	<i>Glic</i>	glycine decarboxylase

A_51_P110323	0.000798	5	NM_008137	<i>Gna14</i>	guanine nucleotide binding protein, alpha 14
A_51_P383774	0.0334	0.4	NM_010314	<i>Gngt1</i>	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
A_51_P370700	0.016	0.4	NM_010324	<i>Got1</i>	glutamate oxaloacetate transaminase 1, soluble
A_51_P276943	8.75E-06	5.1	NM_016985	<i>Gpc1</i>	glypican 1
A_52_P566840	0.00311	0.1	NM_133778	<i>Gpr110</i>	G protein-coupled receptor 110
A_52_P141488	0.000197	0.3	NM_018869	<i>Gprk5</i>	G protein-coupled receptor kinase 5
A_51_P397934	9.82E-06	9.4	NM_130455	<i>Grin3b</i>	glutamate receptor, ionotropic, NMDA3B
A_51_P305140	0.00629	0.4	NM_008181	<i>Gsta1</i>	glutathione S-transferase, alpha 1
A_52_P458682	9.14E-05	0.2	NM_008182	<i>Gsta2</i>	glutathione S-transferase, alpha 2
A_51_P112223	2.81E-05	0.5	NM_010357	<i>Gsta4</i>	glutathione S-transferase, alpha 4
A_52_P415215	8.74E-05	0.5	NM_010358	<i>Gstm1</i>	glutathione S-transferase, mu 1
A_51_P454949	8.75E-06	0.5	NM_010359	<i>Gstm3</i>	glutathione S-transferase, mu 3
A_52_P415996	0.000135	0.4	NM_008184	<i>Gstm6</i>	glutathione S-transferase, mu 6
A_51_P374464	2.95E-05	0.4	NM_013541	<i>Gstp1</i>	glutathione S-transferase, pi 1
A_52_P391505	0.000143	0.1	NM_144513	<i>GT2</i>	GT2, imprinted maternally expressed untranslated mRNA
A_51_P199993	0.000812	0.5	NM_021896	<i>Gucy1a3</i>	guanylate cyclase 1, soluble, alpha 3
A_51_P134228	3.77E-05	2	NM_172563	<i>Hlf</i>	hepatic leukemia factor
A_52_P32287	3.41E-05	0.4	NM_008255	<i>Hmgcr</i>	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
A_51_P146941	5.95E-05	0.4	NM_035342	<i>Hmgcs1</i>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
A_51_P352303	0.000114	0.1	NM_011983	<i>Homer2</i>	homer homolog 2 (Drosophila)
A_52_P441634	0.000269	0.3	NM_177960	<i>Idi1</i>	isopentenyl-diphosphate delta isomerase
A_51_P391432	7.41E-05	2.2	NM_145449	<i>Ifi2712b</i>	interferon, alpha-inducible protein 27 like 2B
A_51_P327751	0.00173	5	NM_008331	<i>Ifit1</i>	interferon-induced protein with tetratricopeptide repeats 1
A_51_P359570	0.000394	3.6	NM_010501	<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3
A_51_P112355	0.000119	3.1	NM_018738	<i>Igtp</i>	interferon gamma induced GTPase
A_51_P357735	0.000466	3.8	NM_008382	<i>Inhbe</i>	inhibin beta E
A_52_P393392	0.000503	0.4	NM_153526	<i>Insp1</i>	insulin induced gene 1
A_52_P113250	0.00107	0.5	NM_178082	<i>Insg2</i>	insulin induced gene 2
A_51_P257058	0.000435	0.4	NM_029634	<i>Ip6k2</i>	inositol hexaphosphate kinase 2
A_52_P463936	0.0016	2.6	NM_015783	<i>Isg15</i>	ISG15 ubiquitin-like modifier
A_51_P364250	0.000969	0.5	NM_172471	<i>Ith5</i>	inter-alpha (globulin) inhibitor H5
A_51_P325914	7.72E-05	3.5	NM_010591	<i>Jun</i>	Jun oncogene
A_52_P570240	0.00577	2.1	NM_080303	<i>Kbtbd11</i>	transcript variant 1
A_51_P287198	0.0067	2.5	NM_033373	<i>Krt1-23</i>	keratin complex 1, acidic, gene 23
A_51_P303556	0.00565	2.8	NM_008484	<i>Lamb3</i>	lammin, beta 3
A_52_P257812	0.00702	1.3	NM_008590	<i>Lpl</i>	lipoprotein lipase
A_51_P267354	0.0123	0.4	NM_175478	<i>Lrn3</i>	leucine rich repeat and fibronectin type III domain containing 3
A_51_P437426	0.00274	2.1	NM_146069	<i>Lrrc33</i>	leucine rich repeat containing 33
A_51_P326685	0.0167	2.2	NM_176920	<i>Lrtm1</i>	leucine-rich repeats and transmembrane domains 1
A_51_P302358	0.000387	2.2	NM_008518	<i>Ltb</i>	lymphotoxin B
A_51_P343517	0.000876	3.4	NM_010742	<i>Ly6d</i>	lymphocyte antigen 6 complex, locus D
A_51_P179987	2.81E-05	0.5	NM_027985	<i>Mad2l2</i>	MAD2 mitotic arrest deficient-like 2
A_52_P547187	2.81E-05	0.4	NM_134645	<i>Map3k2d2</i>	MAP3K2 domain protein kinase kinase kinase 7 interacting protein 2
A_52_P541175	2.81E-05	2.3	NM_183195	<i>Marveld1</i>	MARVEL (membrane-associated) domain containing 1
A_51_P389539	8.33E-05	10.2	NM_054053	<i>Mass1</i>	monogenic, audiogenic seizure susceptibility 1
A_51_P196113	0.0108	0.4	NM_019945	<i>Mast1</i>	microtubule associated serine/threonine kinase 1
A_51_P186601	0.00144	0.5	M29546	<i>Me1</i>	Mouse MOD-1 null malic enzyme
A_51_P480390	0.00605	0.4	NM_008579	<i>Meig1</i>	meiosis expressed gene 1
A_52_P423810	0.0152	0.3	BC027282	<i>Mt1</i>	metallothionein 1 mRNA (cDNA clone MGC:27821 IMAGE:3483861), complete cds.
A_51_P139920	0.00611	2.3	NM_011844	<i>Mpl</i>	monocyte colony stimulating factor receptor
A_52_P364021	0.00172	4.9	NM_028713	<i>Mgat1</i>	monoglycosylidyl O-acyltransferase 1
A_52_P189772	0.00554	3.1	NM_194336	<i>Mpa2l</i>	macrophage activation 2 like
A_51_P228295	0.000306	0.3	NM_01001880	<i>Mpz1</i>	myelin protein zero-like 1
A_52_P525183	0.00217	2.7	NM_134188	<i>Mte1</i>	mitochondrial acyl-CoA thioesterase 1
A_51_P202623	0.00505	2.6	NM_028832	<i>Mterfd3</i>	MTERF domain containing 3
A_52_P167278	0.00375	3.1	NM_172308	<i>Mthfd1l</i>	methylene tetrahydrofolate dehydrogenase (NADP+ dependent)-like
A_52_P413947	0.0184	0.4	NM_010840	<i>Mthfr</i>	5,10-methylenetetrahydrofolate reductase
A_51_P405606	8.33E-05	0.2	NM_010884	<i>Ndr1</i>	N-myc downstream regulated gene 1
A_51_P501018	0.0129	0.4	NM_010892	<i>Nek2</i>	NIMA (never in mitosis gene a)-related expressed kinase 2
A_52_P20727	2.52E-05	2.1	NM_175340	<i>Nhlrc1</i>	NHL repeat containing 1
A_51_P315666	3.42E-05	0.3	NM_008695	<i>Nid2</i>	nidogen 2
A_51_P300666	0.0279	0.5	NM_153288	<i>Npb</i>	neuropeptide B
A_51_P159803	0.00245	2.4	NM_032002	<i>Nrg4</i>	neuregulin 4
A_51_P469285	0.0329	2.1	NM_008737	<i>Nrp1</i>	neuropilin 1
A_51_P326942	0.000179	0.2	NM_010947	<i>Nsdhl</i>	NAD(P) dependent steroid dehydrogenase-like
A_51_P193336	0.0443	0.3	NM_016773	<i>Nucb2</i>	nucleobandin 2
A_51_P437309	0.00512	2.3	NM_145209	<i>Oasl1</i>	2'-5' oligoadenylate synthetase-like 1
A_52_P436238	0.000615	2.1	NM_013614	<i>Odc1</i>	ornithine decarboxylase, structural 1
A_51_P434928	0.000209	0.5	NM_146287	<i>Olfrr114</i>	olfactory receptor 114
A_51_P368894	0.034	2.4	NM_008262	<i>Onecut1</i>	one cut domain, family member 1
A_51_P196844	2.93E-05	8.4	NM_027881	<i>Osbpl3</i>	oxysterol binding protein-like 3
A_52_P134075	4.72E-05	4	NM_024289	<i>Osbpl5</i>	oxysterol binding protein-like 5
A_52_P40934	0.000518	2.1	NM_198414	<i>Pact1</i>	proteoglycan and adipon receptor family member IX
A_51_P387235	1.95E-05	3	NM_021524	<i>Pber1</i>	pre-B-cell colony-enhancing factor 1
A_51_P124388	0.00897	0.4	NM_145977	<i>Pcanap6</i>	prostate cancer associated protein 6
A_51_P205286	1.21E-05	4.7	NM_008793	<i>Pcsk4</i>	proprotein convertase subtilisin/kexin type 4
A_51_P397673	0.000269	0.2	NM_153565	<i>Pcsk9</i>	proprotein convertase subtilisin/kexin type 9
A_51_P333839	8.17E-06	0.4	NM_019971	<i>Pdgfr</i>	platelet-derived growth factor, C polypeptide
A_52_P445958	0.0149	2.1	NM_172134	<i>Pdk</i>	pyridoxal (pyridoxine, vitamin B6) kinase
A_51_P282760	2.81E-05	11.6	NM_011068	<i>Per2</i>	period homolog 2 (Drosophila)
A_52_P34306	0.000182	2.1	NM_028730	<i>Pex26</i>	peroxisome biogenesis factor 26
A_52_P99848	0.0202	2	NM_008840	<i>Pik3cd</i>	phosphatidylinositol 3-kinase catalytic delta polypeptide, transcript variant 1
A_51_P511236	0.000227	2.7	NM_011085	<i>Pik3r1</i>	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1
A_51_P226655	0.0245	0.4	NM_011125	<i>Pltp</i>	phospholipid transfer protein
A_51_P492410	0.000159	0.4	NM_026784	<i>Pmvk</i>	phosphomevalonate kinase
A_52_P30451	0.0247	0.5	NM_016854	<i>Ppp1r3c</i>	protein phosphatase 1, regulatory (inhibitor) subunit 3C
A_51_P486217	0.0271	0.4	NM_176538	<i>Ppkwnk4</i>	protein kinase, lysine deficient 4
A_51_P369310	0.00104	2.3	NM_172892	<i>Prl3a2</i>	proteasome (prosome, macroprosome) subunit, beta type 9
A_51_P420489	0.00375	11.6	NM_134246	<i>Pte2a</i>	peroxisomal acyl-CoA thioesterase 2A
A_52_P215170	0.000572	3.2	NM_134247	<i>Pte2b</i>	peroxisomal acyl-CoA thioesterase 2B
A_51_P157406	0.0018	0.2	NM_008963	<i>Ptgds</i>	prostaglandin D2 synthase (brain)
A_52_P587378	0.00316	2.1	NM_011200	<i>Ptp4a1</i>	protein tyrosine phosphatase 4a1
A_51_P269792	0.00088	5.6	NM_090914	<i>Rad51ll1</i>	RAD51-like 1
A_52_P256771	0.00059	0.3	NM_090916	<i>Raet1a</i>	retinoic acid early transcript 1, alpha
A_52_P10063	0.000177	0.2	NM_198193	<i>Raet1e</i>	retinoic acid early transcript 1E
A_51_P469160	0.000168	0.3	NM_021557	<i>Rd11</i>	retinol dehydrogenase 11
A_51_P177762	0.00164	2.1	NM_153133	<i>Rdh9</i>	retinol dehydrogenase 9
A_52_P261868	0.0412	2.5	NM_134257	<i>Rgs3</i>	regulator of G-protein signaling 3 (Rgs3), transcript variant 2
A_51_P294288	0.000307	2.2	NM_146002	<i>Rhbd17</i>	rhuboid, veinlet-like 7 (Drosophila)
A_51_P386539	0.00591	0.4	NM_026301	<i>Rnf125</i>	ring finger protein 125
A_51_P247637	0.000835	0.3	NM_080563	<i>Rnf144</i>	ring finger protein 144
A_51_P272023	0.00461	2.5	NM_025786	<i>Rnf186</i>	ring finger protein 186
A_52_P670026	0.00232	2.8	NM_011068	<i>Rpl3a2</i>	ribosomal protein L3 (sodium/sulfate symporters), member 4
A_52_P379337	0.000211	2.1	NM_194054	<i>Rtn4</i>	reticulon 4
A_52_P94401	0.00563	0.5	NM_177708	<i>Rtn4r1</i>	reticulon 4 receptor-like 1
A_51_P209372	0.00972	0.5	NM_025436	<i>Sc4mol</i>	sterol-C4-methyl oxidase-like
A_52_P682382	0.0158	0.3	NM_099127	<i>Scd1</i>	stearoyl-Coenzyme A desaturase 1
A_51_P249335	0.00709	0.4	NM_145565	<i>Sds</i>	serine dehydratase
A_51_P431018	0.000558	0.4	NM_019444	<i>Selenbp2</i>	selenium binding protein 2
A_51_P383310	0.00521	3.7	NM_035550	<i>Sema5b</i>	semaphorin, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic tail
A_51_P050505	0.000503	0.2	NM_172892	<i>Slc13a1</i>	solute carrier family 13 (sodium/sulfate symporters), member 4
A_51_P221031	1.95E-05	2.7	NM_172838	<i>Slc16a12</i>	solute carrier family 16 (monocarboxylic acid transporters), member 12
A_51_P466633	0.000233	2.1	NM_011391	<i>Slc16a7</i>	solute carrier family 16 (monocarboxylic acid transporters), member 7
A_52_P163021	9.82E-06	3.8	NM_182959	<i>Slc17a8</i>	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8
A_51_P173445	6.83E-05	0.3	NM_136506	<i>Slc30a10</i>	PREDICTED: similar to solute carrier family 30 (zinc transporter), member 10 isoform a
A_51_P103222	8.62E-06	0.3	NM_028064	<i>Slc39a4</i>	solute carrier family 39 (zinc transporter), member 4
A_51_P442097	0.00528	2.6	NM_027868	<i>Slc41a3</i>	solute carrier family 41, member 3
A_52_P55661	3.49E-05	2.5	NM_177870	<i>Slc5a6</i>	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
A_51_P315931	2.93E-05	0.4	NM_033314	<i>Slc22a7</i>	solute carrier organic anion transporter family, member 2a1
A_51_P487298	0.00177	0.4	NM_139307	<i>Slit2</i>	Slit-like 2 (Drosophila)
A_52_P478025	0.00756	3.4	NM_021491	<i>Smpd3</i>	sphingomyelin phosphodiesterase 3, neutral
A_51_P214209	0.000203	2.3	NM_026282	<i>Spbc24</i>	spindle pole body component 24 homolog
A_52_P381484	0.00104	0.2	NM_133903	<i>Spon2</i>	spondin 2, extracellular matrix protein
A_51_P139678	0.0101	2.1	NM_092624	<i>Spr1a</i>	small proline-rich protein 1A

A_51_P450487	0.000138	0.2	NM_009270	<i>Sqle</i>	squalene epoxidase			
A_52_P562612	0.000118	0.4	NM_175283	<i>Srd5a1</i>	steroid 5 alpha-reductase 1			
A_51_P469951	3.53E-05	0.2	NM_153070	<i>Srgap3</i>	SLIT-ROBO Rho GTPase activating protein 3			
A_51_P300709	0.000132	2	NM_009272	<i>Srm</i>	spermidine synthase			
A_51_P352594	0.00198	0.5	NM_001001326	<i>St5</i>	suppression of tumorigenicity 5			
A_51_P431047	0.00415	3.7	NM_009182	<i>St8sia3</i>	ST8 alpha-N-acetylneuraminidase alpha-2,8-sialyltransferase 3			
A_52_P70255	0.000646	2.2	NM_009283	<i>Stat1</i>	signal transducer and activator of transcription 1			
A_51_P228574	0.0161	0.5	NM_146214	<i>Tat</i>	tyrosine aminotransferase			
A_52_P159276	0.00101	2.3	NM_145890	<i>Tcfcp2l2</i>	transcription factor CP2-like 2			
A_51_P450561	0.000236	2.8	NM_153484	<i>Tef</i>	thyrotroph embryonic factor			
A_51_P456208	0.0347	0.4	NM_011575	<i>Tff3</i>	trefoil factor 3, intestinal			
A_51_P341918	0.0329	2.6	NM_009366	<i>Tgfb14</i>	transforming growth factor beta 1 induced transcript 4, transcript variant 2			
A_52_P627816	0.0042	2	NM_019984	<i>Tgm1</i>	transglutaminase 1, K polypeptide			
A_52_P676510	0.00209	3	NM_011579	<i>Tgtp</i>	T-cell specific GTPase			
A_51_P226453	8.74E-05	3.3	NM_025590	<i>Thea</i>	thioesterase, adipose associated			
A_51_P194099	8.87E-05	5	NM_009381	<i>Thrsp</i>	thyroid hormone responsive SPOT14 homolog (Rattus)			
A_51_P452629	0.00837	2.1	NM_011905	<i>Tlr2</i>	toll-like receptor 2			
A_51_P461123	0.000166	2.7	AF186107	<i>Tlr5</i>	toll-like receptor 5			
A_52_P35064	5.16E-05	0.4	NM_028454	<i>Tm7sf2</i>	transmembrane 7 superfamily member 2			
A_52_P281543	0.0385	0.4	NM_175507	<i>Tmem20</i>	transmembrane protein 20			
A_51_P331207	0.00156	0.4	NM_025464	<i>Tmem218</i>	transmembrane protein 218			
A_51_P125842	0.000177	0.5	NM_145402	<i>Tmem51</i>	transmembrane protein 51			
A_52_P418477	0.0018	3.1	NM_009416	<i>Tpm2</i>	tropomyosin 2, beta			
A_52_P600274	0.0359	0.5	NM_175093	<i>Trib3</i>	tribbles homolog 3, transcript variant 2			
A_52_P303100	0.0232	2.5	NM_175130	<i>Trpm4</i>	transient receptor potential cation channel, subfamily M, member 4			
A_52_P65829	0.0193	2	NM_01124819	<i>Tsku</i>	tsukushin			
A_52_P303161	0.0013	0.2	NM_01124819	<i>Tuba8</i>	tubulin, alpha 8			
A_51_P103659	0.000449	0.2	NM_009450	<i>Tubb2</i>	tubulin, beta 2			
A_51_P315795	0.000144	0.5	NM_009451	<i>Tubb4</i>	tubulin, beta 4			
A_52_P163795	1.95E-05	0.5	NM_011655	<i>Tubb5</i>	tubulin, beta 5			
A_52_P186937	0.0161	2	NM_020557	<i>Tyki</i>	thymidylate kinase family LPS-inducible member			
A_52_P338066	4.97E-05	4.9	NM_023137	<i>Ubd</i>	ubiquitin D			
A_52_P198239	0.00437	0.4	XM_355202	<i>Ube2u</i>	transcript variant 1			
A_52_P156806	0.000646	0.2	NM_201644	<i>Ugt1a9</i>	UDP glucuronosyltransferase 1 family, polypeptide A9			
A_51_P245503	0.000491	0.5	NM_152811	<i>Ugt2b1</i>	UDP glucuronosyltransferase 2 family, polypeptide B1			
A_51_P294535	0.00011	3.2	NM_029770	<i>Unc5b</i>	unc-5 homolog B			
A_52_P259817	0.0455	2.6	NM_029692	<i>Upp2</i>	uridine phosphorylase 2			
A_51_P164219	0.000655	3.3	NM_011909	<i>Usp18</i>	ubiquitin specific protease 18			
A_51_P172663	0.00172	6.4	NM_016808	<i>Usp2</i>	ubiquitin specific protease 2			
A_52_P436628	0.000121	0.5	NM_011697	<i>Vegfb</i>	vascular endothelial growth factor B			
A_51_P278334	0.0035	2.5	NM_013703	<i>Vldlr</i>	very low density lipoprotein receptor			
A_51_P424332	0.000536	3	NM_011704	<i>Vnn1</i>	vanin 1			
A_51_P400217	0.000536	0.4	NM_016982	<i>Vpreb1</i>	pre-B lymphocyte gene 1			
A_51_P465211	0.00115	3.1	NM_026323	<i>Wfdc2</i>	WAP four-disulfide core domain 2			
A_51_P316951	9.13E-05	2.4	XM_620310	<i>Wipf3</i>	PREDICTED: Mus musculus WAS/WASL interacting protein family, member 3			
A_52_P85805	0.0327	2.9	NM_009525	<i>Wnt5b</i>	wingless-related MMTV integration site 5B			
A_51_P137991	9.32E-05	3.1	NM_009525	<i>Wnt5b</i>	wingless-related MMTV integration site 5B			
A_51_P184936	0.000616	4.8	NM_021394	<i>Zbp1</i>	Z-DNA binding protein 1			
A_51_P263419	0.00312	0.4	NM_011309	<i>Zfp30</i>	zinc finger protein 30			
A_51_P239236	3.77E-05	0.3	BC022940		acetyl-Coenzyme A carboxylase beta, mRNA (cDNA clone IMAGE:4009364), partial cds.			
A_51_P372550	0.000188	5.1	BC023116		cell growth regulator with EF hand domain 1mRNA (cDNA clone MGC:28551 IMAGE:4206019), complete cds.			
A_51_P268529	0.000293	0.3	AF045741		deoxyribonuclease II precursor mRNA			
A_52_P379277	0.00047	0.5	BC005527		ectonucleotide pyrophosphatase (cDNA clone IMAGE:3495326), partial cds.			
A_51_P455997	0.000203	0.1	Y13832		mRNA for GT12 protein			
A_52_P306357	0.00017	6.8	BC042707		prokineticin 1 with apparent retained intron (cDNA clone MGC:51604 IMAGE:4975079), complete cds.			
A_51_P420415	0.000379	0.4	BC073863		steroid 5 alpha-reductase 1 mRNA (cDNA clone MGC:100251 IMAGE:6807475), complete cds.			
A_52_P391130	0.00012	5.5	BC058749		synaptotagmin 2, mRNA (cDNA clone MGC:67830 IMAGE:6390688), complete cds.			
A_52_P289231	0.00351	0.4	SS7425		Mus sp. Fas antigen (lpr) mRNA, partial cds; and transposon Etn			
A_52_P376502	0.00157	0.2	BC025011		calcium/calmodulin-dependent protein kinase ID, (cDNA clone IMAGE:5052777), complete cds.			
A_52_P385824	0.00154	4.1	BC059307		sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, mRNA (cDNA clone IMAGE:5064213), partial cds.			
A_51_P452533	0.00134	2.9	BC035277		DNA segment, Chr 1, ERATO Doi 471, expressed, mRNA (cDNA clone IMAGE:5064213), partial cds.			
A_51_P267587	0.00107	3	BC052902		ganglioside-induced differentiation-associated-protein 10, mRNA (cDNA clone MGC:60602 IMAGE:30067675), complete cds.			
A_52_P289231	0.00351	0.4	SS7425		Mus sp. Fas antigen (lpr) mRNA, partial cds; and transposon Etn, complete sequence.			
A_52_P376502	0.00157	0.2	BC025011		calcium/calmodulin-dependent protein kinase ID, (cDNA clone IMAGE:5052777), complete cds.			
A_52_P385824	0.00154	4.1	BC059307		sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, mRNA (cDNA clone IMAGE:5064213), partial cds.			
A_51_P452533	0.00134	2.9	BC035277		DNA segment, Chr 1, ERATO Doi 471, expressed, mRNA (cDNA clone IMAGE:5064213), partial cds.			
A_51_P267587	0.00107	3	BC052902		ganglioside-induced differentiation-associated-protein 10, mRNA (cDNA clone MGC:60602 IMAGE:30067675), complete cds.			





