

Supplementary table S2 Differentially expressed annotated genes with  $p < 0.05$  in lungs of rats treated with a 1% quercetin diet (n=6) as compared to rats treated with a control diet (n=6).

***Metabolism***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Adh1	alcohol dehydrogenase 1	NM_019286	0.021	1.11
Ldhc	lactate dehydrogenase 3, C chain	NM_017266	0.048	-1.14
Ephx2	epoxide hydrolase 2, cytoplasmic	BM986667	0.008	-1.20
Coq6_predicted	coenzyme Q6 homolog (yeast) (predicted)	XM_216748	0.034	1.13
Chi3l1	chitinase 3-like 1	AA926356	0.013	-1.18
Man2c1	mannosidase, alpha, class 2C, member 1	NM_139256	0.011	1.19
Cav3	caveolin 3	NM_019155	0.044	1.18
Lpl	lipoprotein lipase	NM_012598	0.020	1.22
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	NM_022594	0.008	1.16
Acaa2	acetyl-Coenzyme A acyltransferase 2	NM_130433	0.013	1.19
Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	NM_017340	0.046	1.19
Pcca	propionyl-coenzyme A carboxylase, alpha polypeptide	XM_341383	0.022	1.15
Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	NM_053535	0.022	-1.23

Thtpa	thiamine triphosphatase	NM_0010076 82	0.043	-1.17
Glul	glutamine synthetase 1	NM_017073	0.043	1.22
Sulf1	sulfatase 1	BF567631	0.018	-1.13
Pld1	phospholipase D1	NM_030992	0.023	1.14
Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	NM_017080	0.035	1.13
Pld3_predicted	phospholipase D3 (predicted)	BQ211430	0.028	-1.13
Dhdds_predicted	dehydrololichyl diphosphate synthase (predicted)	AI145286	0.045	-1.06
Dbt	dihydrolipoamide branched chain transacylase E2	XM_342328	0.030	-1.07
Pcsk1	proprotein convertase subtilisin/kexin type 1	NM_017091	0.044	1.09
Arse_predicted	arylsulfatase E (chondrodysplasia punctata 1) (predicted)	XM_227066	0.036	-1.11
Scot-S	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1	BF285225	0.039	-1.21
Dpysl3	dihydropyrimidinase-like 3	BG665445	0.002	1.26
Hibadh	3-hydroxyisobutyrate dehydrogenase	XM_342686	0.028	1.12
Srebf1	sterol regulatory element binding factor 1	XM_213329	0.013	-1.09
Noxo1_predicted	NADPH oxidase organizer 1 (predicted)	XM_220221	0.019	1.25
Apobec3_predicted	apolipoprotein B editing complex 3 (predicted)	XM_235485	0.016	-1.11
CYP2A2	hepatic steroid hydroxylase IIA2	M33313	0.012	1.26
CYP2A2	hepatic steroid hydroxylase IIA2	M33313	0.030	1.25

Phgdhl1	phosphoglycerate dehydrogenase like 1	AW142488	0.050	1.14
Retsat	all-trans-13,14-dihydroretinol saturase	NM_145084	0.015	1.22
PFK-A	Phosphofructo-1-kinase isozyme A	AI071717	0.043	-1.12
Aco1	aconitase 1	NM_017321	0.007	1.18
Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	NM_173094	0.009	1.16
Uros_predicted	uroporphyrinogen III synthase (predicted)	XM_219416	0.034	-1.08

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***Transport***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
ANT2	ADP, ATP carrier protein, fibroblast isoform	AI411329	0.005	-1.14
Muted_predicted	Muted_predicted; muted (predicted)	XM_225255	0.028	1.09
Xlas	XLas protein	NM_021845	0.025	1.17
Cacng6	calcium channel, voltage-dependent, gamma subunit 6	NM_080694	0.006	1.23
Accn2	amiloride-sensitive cation channel 2, neuronal	AJ006519	0.041	-1.10
Cacng7	calcium channel, voltage-dependent, gamma subunit 7	NM_080695	0.013	-1.24
Pdzk1	PDZ domain containing 1	NM_031712	0.047	1.09
Sorbs1_predicted	sorbin and SH3 domain containing 1 (predicted)	AW917667	0.007	1.21
LOC49826	similar to Golgin 45	BC079114	0.024	1.05

Steap2_predicted	six transmembrane epithelial antigen of prostate 2	AA957889	0.026	1.09
Clic2_predicted	chloride intracellular channel 2 (predicted)	NM_0010096 51	0.033	-1.30
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	BI297089	0.001	-1.22
Prkwnk4	protein kinase, lysine deficient 4	AW142701	0.035	1.12
Kcnk1	potassium channel, subfamily K, member 1	NM_021688	0.016	1.15
LOC245960	potassium channel regulator 1	NM_139101	0.039	1.20
Vps39_predicted	vacuolar protein sorting 39 (yeast) (predicted)	XM_342500	0.005	1.14
XM_223589	similar to Clast4 protein	XM_223589	0.018	-1.15
Atp6v1c2	ATPase, H+ transporting, V1 lysosomal subunit C, isoform 2	XM_343129	0.048	1.18
Slc22a1	solute carrier family 22 (organic cation transporter), member 1	NM_012697	0.046	-1.09
Slc10a1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	AA999182	0.047	-1.10
Vdac1	voltage-dependent anion channel 1	NM_031353	0.016	1.07
Cyp4f4	cytochrome P450 4F4	NM_173123	0.043	-1.25
Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	NM_138515	0.021	1.11
Txndc5_predicted	thioredoxin domain containing 5 (predicted)	XM_225257	0.028	1.19
Cln8	ceroid-lipofuscinosis, neuronal 8	NM_0010076 86	0.011	-1.18
Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	NM_019225	0.049	1.28

Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	NM_013031	0.020	1.18
Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	NM_019283	0.042	1.12
Atp6v1h_predicted	ATPase, H <sup>+</sup> transporting, lysosomal 50/57kDa, V1 subunit H (predicted)	AI548908	0.019	-1.12
Col9a1_predicted	procollagen, type IX, alpha 1 (predicted)	XM_223124	0.048	-1.12
Apom	apolipoprotein M	NM_019373	0.016	-1.25
Kdelr1_predicted	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 (predicted)	XM_341860	0.032	1.14
Cpne7_predicted	copine VII (predicted)	XM_341711	0.044	-1.06
Slco1a2	solute carrier organic anion transporter family, member 1A2	NM_030838	0.043	1.11
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	AF452728	0.048	1.09

### *Immune response*

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Znf179	zinc finger protein 179	NM_138613	0.046	-1.22
Lat	linker for activation of T cells	NM_030853	0.042	1.11
Gbp3_predicted	guanylate nucleotide binding protein 3 (predicted)	XM_227762	0.043	-1.09
LOC500449	similar to SHP2-interacting transmembrane adaptor protein	BC088199	0.043	1.09
Colec12	collectin sub-family member 12	XM_341574	0.012	-1.14

LOC361454	Chemokine C-C motif receptor-like 1 adjacent	CB546044	0.001	-1.17
Cd59	CD59 antigen	NM_012925	0.029	1.09
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	XM_341842	0.045	1.08
Ccl12_predicted	chemokine (C-C motif) ligand 12 (predicted)	XM_213425	0.007	-1.28
Ccr2	chemokine receptor CCR2 gene	NM_021866	0.030	-1.12
C1qg_predicted	complement component 1, q subcomponent, gamma polypeptide (predicted)	NM_0010085 24	0.018	1.12
Il18rap	interleukin 18 receptor accessory protein	NM_184047	0.036	-1.24
Crp	C-reactive protein, petaxin related	NM_017096	0.024	-1.14
C9	complement component 9	NM_057146	0.049	-1.25
Dmbt1	deleted in malignant brain tumors 1	XM_219318	0.029	-1.12
Cd2bp2_predicted	CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	TC473940	0.032	1.07
Cd68_predicted	CD68 antigen (predicted)	XM_213372	0.031	1.09
LOC361399	similar to autoantigen	XM_341677	0.029	-1.15
Z75902	Immunoglobulin, epsilon chain, variable region (clone Hg32)	Z75902	0.010	1.86

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***DNA repair***

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<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
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Tyms	thymidylate synthase	NM_019179	0.004	-1.24
Blm_predicted	Bloom syndrome (predicted)	XM_344913	0.014	-1.15
Rad1_predicted	RAD1 homolog (S. pombe) (predicted)	XM_215497	0.041	1.08
Ruvbl2_predicted	RuvB-like 2 (E. coli) (predicted)	XM_214951	0.039	1.07
Pnkp	polynucleotide kinase 3' -phosphatase	NM_0010042 59	0.001	1.14
Xpc_predicted	xeroderma pigmentosum, complementation group C (predicted)	XM_232194	0.007	1.13
Mbd4_predicted	methyl-CpG binding domain protein 4 (predicted)	XM_342742	0.004	-1.30
Pms2_predicted	postmeiotic segregation increased 2 (S. cerevisiae) (predicted)	XM_213712	0.027	1.17

### ***Apoptosis***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Bcl2	B-cell leukemia/lymphoma 2	NM_016993	0.011	-1.12
Nme6	expressed in non-metastatic cells 6, protein (nucleoside diphosphate kinase)	AI014074	0.006	-1.12
App	amyloid beta (A4) precursor protein	AI412064	0.025	-1.17
Casp14_predicted	caspase 14 (predicted)	ENSRNOT00 000009833	0.004	-1.15
Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	NM_181086	0.049	1.14
Col4a3	collagen, type IV, alpha 3	XM_343607	0.036	1.10

Dnase1	deoxyribonuclease I	BM389034	0.032	1.14
Rit1_predicted	Ras-like without CAAX 1 (predicted)	BF406174	0.006	-1.13
Rabl4_predicted	RAB, member of RAS oncogene family-like 4 (predicted)	AW525988	0.032	-1.10
Rasgrp2_predicted	RAS guanyl releasing protein 2 (calcium and DAG-regulated) (predicted)	XM_342003	0.015	-1.13
Rras2_predicted	related RAS viral (r-ras) oncogene homolog 2 (predicted)	BU758451	0.033	-1.08

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***Cell adhesion/structure***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Arhgap8	Rho GTPase activating protein 8	NM_0010042 42	0.031	-1.10
Pcdhgc3	protocadherin gamma subfamily C, 3	XM_341600	0.031	-1.18
Igsf4a_predicted	immunoglobulin superfamily, member 4A (predicted)	AA900645	0.009	1.13
Igsf4a_predicted	immunoglobulin superfamily, member 4A (predicted)	XM_343385	0.039	1.11
Catnal1_predicted	catenin alpha-like 1 (predicted)	XM_216386	0.012	1.30
Cyr61	cysteine rich protein 61	NM_031327	0.024	1.17
Opcml	opioid-binding protein/cell adhesion molecule-like	NM_053848	0.024	-1.08
Spon1	spondin 1	NM_172067	0.043	1.17
LOC314490	similar to DiGeorge syndrome protein C	XM_234588	0.042	-1.11



LOC309745	similar to alpha T-catenin	XM_228133	0.033	1.08
Ilk	integrin linked kinase	NM_133409	0.022	1.13
Ecm2_predicted	extracellular matrix protein 2, female organ and adipocyte specific (predicted)	XM_214443	0.030	1.20
Actl7b_predicted	actin-like 7b (predicted)	XM_232919	0.050	-1.21
Krt2-8	keratin complex 2, basic, gene 8	BF281337	0.006	-1.20
Tubgcp3_predicted	tubulin, gamma complex associated protein 3 (predicted)	XM_225013	0.045	1.06
Neb_predicted	nebulin (predicted)	XM_229925	0.019	1.19
Nolc1	ucleolar and coiled-body phosphoprotein 1	NM_022869	0.042	1.10
Supt16h_predicted	suppressor of Ty 16 homolog ( <i>S. cerevisiae</i> ) (predicted)	AA850372	0.029	1.15
Ankrd27_predicted	ankyrin repeat domain 27 (VPS9 domain) (predicted)	XM_341843	0.042	-1.11
Coro1b	coronin, actin-binding protein, 1B	NM_019222	0.016	1.17
Asb16_predicted	ankyrin repeat and SOCS box-containing 16 (predicted)	AW530584	0.010	-1.16

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### ***Receptors***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Lancl1	lanC (bacterial lantibiotic synthetase component C)-like 1	BF549735	0.049	-1.13
Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	NM_053936	0.049	1.15

Grm3	glutamate receptor, metabotropic 3	XM_342626	0.013	1.12
Lphn3	calcium-independent alpha-latrotoxin receptor homolog 3	NM_130822	0.041	1.07
Has1	hyaluronan synthase1	NM_172323	0.043	1.14
P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	NM_057124	0.028	-1.13
Olr1271	olfactory receptor 1271	NM_173300	0.034	-1.09
Olr1319	olfactory receptor 1319 (predicted)	NM_0010004 70	0.024	-1.13
Olr1350	olfactory receptor 1350 (predicted)	NM_0010007 52	0.004	-1.14
Olr1380	olfactory receptor 1380 (predicted)	NM_0010008 57	0.014	-1.08
Olr193	olfactory receptor 193 (predicted)	NM_0010001 86	0.028	-1.18
Olr197	olfactory receptor 197 (predicted)	NM_0010001 88	0.005	-1.10
Olr557	olfactory receptor 557 (predicted)	NM_0010006 69	0.019	-1.16
Olr725	olfactory receptor 725 (predicted)	NM_0010005 14	0.042	-1.18
Olr830	olfactory receptor 830 (predicted)	NM_0010009 00	0.017	-1.12
Olr867	olfactory receptor 867 (predicted)	NM_0010004 12	0.023	-1.16
Olr92	olfactory receptor 92 (predicted)	NM_0010001 40	0.049	-1.18
Rgs5	regulator of G-protein signaling 5	NM_019341	0.048	-1.15

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**Protein modification**

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Zc3hdc1_predicted	zinc finger CCCH type domain containing 1 (predicted)	BI285978	0.038	-1.11
Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	NM_173312	0.035	-1.25
Gypc_predicted	glycophorin C (Gerbich blood group) (predicted)	AY234182	0.001	1.15
Ephb6_predicted	Eph receptor B6 (predicted)	XM_231650	0.035	-1.08
Rpl19	ribosomal protein L19	BE115955	0.029	-1.10
LOC302430	similar to Eukaryotic translation initiation factor 4B (eIF-4B)	XM_228592	0.026	1.10
Ppif	peptidylprolyl isomerase F (cyclophilin F)	AA875449	0.043	-1.16
Hspb2	heat shock 27kD protein 2	NM_130431	0.047	-1.09
Hspcb	heat shock 90kDa protein 1, beta	AI236795	0.009	-1.20
LOC362758	similar to Peptidylprolyl isomerase-like 2	XM_343085	0.018	1.10
Hsp105_predicted	heat shock protein 105 (predicted)	XM_213699	0.020	-1.27
Hspca	heat shock protein 1, alpha	NM_175761	0.048	-1.21
LOC301252	similar to heat shock protein 84 - mouse	XM_215591	0.040	-1.09
Prickle1	prickle-like 1 (Drosophila)	XM_235609	0.010	-1.15
LOC305342	similar to mKIAA1413 protein	XM_223405	0.025	-1.08
Sumo1_predicted	SMT3 suppressor of mif two 3 homolog 1 (yeast)	AA850550	0.049	-1.11

	(predicted)			
Gphn	gephyrin	NM_022865	0.035	1.12
Kcmf1_predicted	potassium channel modulatory factor 1 (predicted)	XM_216171	0.023	1.16
Ecel1	endothelin converting enzyme-like 1	NM_021776	0.014	-1.16
Mme	membrane metallo endopeptidase	NM_012608	0.017	1.13
Afg3l2_predicted	AFG3(ATPase family gene 3)-like 2 (yeast) (predicted)	XM_225866	0.035	1.12
Fosb_predicted	FBJ osteosarcoma oncogene B (FosB)	XM_218419	0.047	-1.13
Smarcal1_predicted	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (predicted)	XM_237241	0.048	1.18
Ssr2_predicted	signal sequence receptor, beta (predicted)	BQ211506	0.019	-1.14
Pja2	praja 2, RING-H2 motif containing	NM_138896	0.010	1.09
BRAP2	BRCA1-associated protein	BF284618	0.007	-1.15
Herc1_predicted	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	XM_236362	0.038	1.16
Herc3_predicted	hect domain and RLD 3 (predicted)	BG668746	0.012	1.23
LOC312688	similar to ubiquitin specific protease UBP43	XM_347056	0.021	-1.12
Ube2q_predicted	ubiquitin-conjugating enzyme E2Q (putative) (predicted)	XM_215612	0.025	1.14
LOC362294	MKIAA0010 protein	AW144296	0.038	1.14
LOC362736	HECT domain containing protein 1	AA924584	0.035	-1.10

Rnf121_predicted	ring finger protein 121 (predicted)	XM_238909	0.018	1.15
Bap1_predicted	Brca1 associated protein 1 (predicted)	XM_224614	0.017	-1.10

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***Regulation of transcription***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Fubp3_predicted	far upstream element (FUSE) binding protein 3 (predicted)	AI137378	0.047	1.14
Dmrt1	doublesex and mab-3 related transcription factor 1	NM_053706	0.034	-1.14
Runx2	runt related transcription factor 2	AF053953	0.050	-1.14
Arid1a_predicted	AT rich interactive domain 1A (Swi1 like) (predicted)	AA900926	0.018	1.26
Ncor2_predicted	nuclear receptor co-repressor 2 (predicted)	XM_341072	0.049	-1.05
Tfdp2_predicted	transcription factor Dp-2 (E2F dimerization partner 2) (predicted)	XM_217232	0.047	1.12
Jund	Jun D proto-oncogene	NM_138875	0.025	1.12
YT521	splicing factor YT521-B	NM_133423	0.046	-1.16
Phtf1	putative homeodomain transcription factor 1	XM_342306	0.042	-1.22
LOC313588	similar to Smad nuclear interacting protein	XM_233518	0.044	1.06
Mtdh	metadherin	NM_133398	0.045	1.19
Zfp111	zinc finger protein 111	NM_133323	0.035	1.06

LOC314600	similar to zinc finger protein 422, related sequence 1	XM_234860	0.040	-1.11
Hnrpd	heterogeneous nuclear ribonucleoprotein D	NM_024404	0.042	1.14
Myt1_predicted	myelin transcription factor 1 (predicted)	XM_342605	0.044	-1.13
Lass3_predicted	LAG1 longevity assurance homolog 3 ( <i>S. cerevisiae</i> ) (predicted)	XM_218749	0.027	-1.15
Crsp3_predicted	cofactor required for Sp1 transcriptional activation, subunit 3 (predicted)	XM_220093	0.032	1.19

***Cell proliferation/differentiation***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
LOC498574	similar to Spindlin	XM_224608	0.018	-1.08
Fhl1	four and a half LIM domains 1	BC061782	0.008	1.21
Efna5	ephrin A5	NM_053903	0.040	-1.08
Drb1	developmentally regulated RNA-binding protein 1	NM_153306	0.046	1.12
Ebaf2	endometrial bleeding associated factor	NM_0010075	0.015	-1.11
Fgf8	fibroblast growth factor 8	56 NM_133286	0.044	1.07
Pdgfa	platelet derived growth factor, alpha	NM_012801	0.035	1.18
Hgf	hepatocyte growth factor	AW917931	0.014	1.10
LOC317322	similar to glypican 4	BQ190716	0.025	-1.17

Ivl	involucrin gene	NM_022195	0.035	-1.14
Stk6	serine/threonine kinase 6	NM_153296	0.024	1.17
Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	NM_013223	0.031	1.13
LOC294513	similar to DnaJ (Hsp40) homolog, subfamily B, member 12	TC481420	0.015	1.11
Bdnf	brain derived neurotrophic factor	NM_012513	0.019	1.12
Igfbp3	insulin-like growth factor binding protein 3	NM_012588	0.003	1.24
Fmip_predicted	Fms interacting protein (predicted) (Fmip_predicted)	XM_341250	0.033	1.14
Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	AA859324	0.020	1.10
Cdc7_predicted	cell division cycle 7 ( <i>S. cerevisiae</i> ) (predicted)	XM_341183	0.035	1.15

### ***Signalling***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Adcyap1	adenylate cyclase activating polypeptide 1	NM_016989	0.039	-1.16
Vsnl1	visinin-like 1	NM_012686	0.034	-1.20
Mertk	c-mer proto-oncogene tyrosine kinase	NM_022943	0.047	1.12
Mast2_predicted	microtubule associated serine/threonine kinase 2 (predicted)	XM_233782	0.025	-1.11
Map2k4_predicted	mitogen activated protein kinase kinase 4 (predicted)	CA510796	0.005	1.21

Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	XM_345627	0.047	-1.10
Zdhhc13_predicted	zinc finger, DHHC domain containing 13 (predicted)	XM_344895	0.038	1.09

### ***RNA processing***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
SMN1	survival of motor neuron 1, telomeric	BF391279	0.022	-1.12
Rnps1_predicted	ribonucleic acid binding protein S1 (predicted)	XM_237758	0.012	1.12
Sf3b1	splicing factor 3b, subunit 1	BF523561	0.046	1.26
Srrm1_predicted	serine/arginine repetitive matrix 1 (predicted)	XM_233556	0.042	1.12
Taf3_predicted	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	XM_225559	0.025	-1.20
Pop5_predicted	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (predicted)	XM_213794	0.034	1.14
Wars_predicted	tryptophanyl-tRNA synthetase (predicted)	XM_234566	0.046	-1.09

### ***Miscellaneous***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Sequence ID</b>	<b>p-Value</b>	<b>Ratio</b>
Serpinc1_predicted	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1 (predicted)	XM_222802	0.039	-1.08
LOC500450	similar to tropomyosin 1, embryonic fibroblast	CA338648	0.030	1.17



MBH1	BarH-like 2 homeobox protein (Bar-class homeodomain protein MBH1) (Homeobox protein B-H1),	NM_022956	0.049	-1.16
Zfp262_predicted	zinc finger protein 262 (predicted)	XM_233529	0.048	-1.23
Ttn	titin	XM_342452	0.014	-1.09
Lama2_predicted	laminin, alpha 2 (predicted)	XM_219866	0.025	1.17
LOC307465	similar to karyopherin (importin) alpha 2	XM_225973	0.024	1.12
Cirbp	cold inducible RNA binding protein	NM_031147	0.034	1.10
Prlpa	prolactin-like protein A	NM_017036	0.030	-1.19
Stk25	serine/threonine kinase 25 (STE20 homolog, yeast)	NM_184049	0.013	1.21
Otos	otospiralin	NM_139188	0.002	-1.21
Best5	Best5 protein	AI045512	0.022	-1.11
Gtl3_predicted	gene trap locus 3 (predicted)	AW920916	0.029	1.14
Sca1	spinocerebellar ataxia 1 homolog (human)	NM_012726	0.035	-1.16
Tpra40	transmembrane domain protein regulated in adipocytes	NM_053534	0.023	1.14
Prlpc1	prolactin-like protein C 1	NM_020079	0.013	-1.17
Prlpd	prolactin-like protein D	NM_022537	0.049	1.10
Tparl_predicted	TPA regulated locus (predicted)	AW140440	0.045	1.15
Nicn1	Nicolin 1	AW433572	0.011	-1.18
Thap11_predicted	THAP domain protein 11 (HRIHFB2206)	BF548596	0.031	1.11

Mak10	corneal wound healing related protein	NM_133324	0.037	1.15
Ppm1h_predicted	protein phosphatase 1H (PP2C domain containing) (predicted)	XM_235200	0.023	-1.19
Papd1_predicted	PAP associated domain containing 1 (predicted)	XM_225468	0.028	1.07
Prnpip1_predicted	prion protein interacting protein 1 (predicted)	XM_342890	0.050	1.08
Rg9mtd1_predicted	RNA (guanine-9-) methyltransferase domain containing 1 (predicted)	NM_0010083 37	0.047	1.19
Serf2_predicted	small EDRK-rich factor 2 (predicted)	BC081918	0.037	1.15
Spag8_predicted	sperm associated antigen 8 (predicted)	XM_342826	0.036	1.20
Spg6_predicted	spastic paraplegia 6 (autosomal dominant) (predicted)	XM_218719	0.037	-1.12
Tcte1_predicted	t-complex-associated testis expressed 1 (predicted)	XM_236941	0.008	-1.12
Tm7sf1_predicted	transmembrane 7 superfamily member 1 (predicted)	XM_237907	0.000	1.26
Tnfrsf26_predicted	tumor necrosis factor receptor superfamily, member 26 (predicted)	XM_341968	0.019	-1.11
LOC501250	similar to Reticulocalbin 1 precursor	XM_343735	0.044	1.14
LOC302864	similar to transmembrane protein 32	XM_229191	0.044	-1.19
LOC310460	similar to SH3-containing guanine nucleotide exchange factor	XM_227201	0.014	-1.12
LOC315663	similar to synaptotagmin-like homologue lacking C2 domains-b	XM_236272	0.015	-1.13
LOC314251	erythroid spectrin beta	NM_212522	0.018	-1.20
LOC363393	similar to GTPase activating protein testicular GAP1	XM_347133	0.032	1.19

Zg16	zymogen granule protein 16	NM_134409	0.030	-1.17
Zp4	zona pellucida glycoprotein 4	NM_172330	0.014	-1.16
Rnf166	ring finger protein 166	NM_0010022 79	0.046	1.17
Zfp521_predicted	zinc finger protein 521 (predicted)	XM_226153	0.030	-1.06
Zswim1_predicted	zinc finger, SWIM domain containing 1 (predicted)	TC485502	0.021	1.17

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