

SUPPLEMENTARY TABLES

Supplementary Table I: Transcriptional reporter plasmids derived from 5'-regulatory regions of genes.

<u>Promoter –Luciferase Constructs</u>	<u>5' Regulatory Region</u>	<u>Plasmid (R.E. Sites)</u>	<u>Description</u>
Mouse SP-A, <i>Sftpa</i> -0.45-luc	-399/+45 bps	pGL3 (Hind III / Pst I)	1
Mouse SP-B, <i>Sftpb</i> -1.8-luc	-1797/+42 bps	pGL3 (Hind III / Sal I)	2
Mouse SP-C, <i>Sftpc</i> -4.8-luc	-4800/+18 bps	pGL2 (Xho I / Xho I)	3
Mouse Abca3, <i>Abca3</i> -2.6-luc	-2591/+11	pGL3 (Kpn I / Xho I)	This Study
Mouse Foxa1, <i>Foxa1</i> -3.4-luc	-3400/+47 bps	pGL3 (Sac I / Xma I)	This Study
Mouse Foxa2, <i>Foxa2</i> -1.6-luc	-1529/+68	pGL3 (Nhe I / Hind III)	4

Supplemental References for Table I

1. Bruno, M.D., Korfhagen, T.R., Liu, C., Morrisey, E.E. & Whitsett, J.A. GATA-6 activates transcription of surfactant protein A. *J Biol Chem* **275**, 1043-9 (2000).
2. Sever-Chroneos, Z., Bachurski, C.J., Yan, C. & Whitsett, J.A. Regulation of mouse SP-B gene promoter by AP-1 family members. *Am J Physiol* **277**, L79-88 (1999).
3. Kelly, S.E., Bachurski, C.J., Burhans, M.S. & Glasser, S.W. Transcription of the lung-specific surfactant protein C gene is mediated by thyroid transcription factor 1. *J Biol Chem* **271**, 6881-8 (1996).
4. Kaestner, K.H., Montoliu, L., Kern, H., Thulke, M. & Schutz, G. Universal beta-galactosidase cloning vectors for promoter analysis and gene targeting. *Gene* **148**, 67-70 (1994).

Supplementary Table II: Oligonucleotides used in EMSA, ChIP and Real-Time PCR Assays.

Oligonucleotide Name	Oligonucleotide Sequence
<u>Oligonucleotides Used in EMSA</u>	
<i>Abca3</i>	
NFAT-II Sense	5'-GTGTCACCTTTGGAAAAAAGT-3'
NFAT-II Antisense	5'-GTGTACTTTTTTCCAAAGTG-3'
NFAT-III Sense	5'-GGGTGATTCTGGAAAATACA-3'
NFAT-III Antisense	5'-TGTGTGTATTTCCAGAATC-3'
<i>Foxa1</i>	
NFAT-IV Sense	5'-GGTTTCTCTTTTTTTCCTTT-3'
NFAT-IV Antisense	5'-GGTTAAAGGAAAAAAGAGAA-3'
NFAT-V Sense	5'-GGTTCCTTTTTTTCCTTTTCT-3'
NFAT-V Antisense	5'-GGTTAGAAAAGGAAAAAAG-3'
NFAT-VI Sense	5'-GGTTCCTATTTTTCTTTTCT-3'
NFAT-VI Antisense	5'-GGTTAGAAAAGGAAAAATAGG-3'
<i>IL-2</i>	
IL-2 Sense	5'-CAATTGGAAAATTTTAT-3'
IL-2 Antisense	5'-TGATAAAAATTTTCCAAT-3'
<i>rTg</i>	
TTF-1 Sense	5'-CACTGCCCAGTCAAGTGTCTTGAACA-3'
TTF-1 Antisense	5'-TGTTCAAGAACACTTGACTGGGCAGTG-3'
<u>Oligonucleotides Used in ChIP</u>	
<i>Sfipb</i> Promoter (Forward)	5'-AAACAAAAAAGCAGATCTCGTG-3'
<i>Sfipb</i> Promoter (Reverse)	5'-CCCCCTTACTTAAAAATCCTCTGA-3'
<i>Abca3</i> Promoter (Forward)	5'-TGAAGGAACCACAACCCCT-3'
<i>Abca3</i> Promoter (Reverse)	5'-AGGCTGTAACATCAAGAATCTCACTT-3'
<i>Gapdh</i> Promoter (Forward)	5'-ATTTATGGCCACATCCCTAAG-3'
<i>Gapdh</i> Promoter (Reverse)	5'-TTTGTCTACGGGACGAGGCT-3'
<u>Oligonucleotides Used in Real-Time PCR</u>	
<i>Pla2g1b</i> cDNA Primer (Forward)	5'-CAGGCGCTGCTGCACACAG-3'
<i>Pla2g1b</i> cDNA Primer (Reverse)	5'-GTC TAA GTC GTC CAC TGG GGT GC-3',
<i>Aytl2</i> cDNA(Forward)	5'-GGC TCC ACA TTC CTC CTC CTA CTT TG-3'
<i>Aytl2</i> cDNA(Reverse)	5'-ATC TCC TCC ACT GTC TTC CTT CG- 3'
<i>β-actin</i> (Forward)	5'-TGG AAT CCT GTG GCA TCC ATG AAA C-3'
<i>β-actin</i> (Forward)	5'-TAA AAC GCA GCT CAG TAA CAG TCC G-3'.

Supplementary Table III: Differentially expressed genes in lungs of mice after deletion of *Cnb1* vs. control littermates.

Systematic	common	genebank	Ratio	T-Test	description	GO Bio
1429626_at	Sfltpa1	NM_023134	-43.09	0.00000449	Surfactant-associated protein A1	phosphate transport; regulation of liquid surface tension; respiratory gaseous exchange
1415964_at	Scd1	NM_009127	-25.22	0.00000839	Stearoyl-Coenzyme A desaturase 1	fatty acid biosynthesis
1418190_at	Pon1	NM_011134	-15.02	0.000402	Paraoxonase 1	cholesterol metabolism; circulation; response to toxin
1418818_at	Aqp5	NM_009701	-13.60	7.14E-07	Aquaporin 5	transport; water transport
1458719_at	Bltd9	NM_172618	-7.81	0.000761	BTB (POZ) domain containing 9	cell adhesion
1449015_at	Retnla	NM_020509	-7.37	0.000469	Resistin like alpha	
1419407_at	Hc	NM_010406	-5.02	0.00307	Hemolytic complement	complement activation; complement activation, alternative pathway; complement activation, classical pathway; cytolysis
1416854_at	Slc34a2	NM_011402	-4.92	0.00138	Solute carrier family 34 (sodium phosphate), member 2	phosphate transport
1426215_at	Ddc	NM_016672	-4.66	0.000074	Dopa decarboxylase	amino acid and derivative metabolism; amino acid metabolism; catecholamine biosynthesis
1417388_at	Bex2	NM_009749	-4.25	0.0000486	Brain expressed X-linked 2	
1460470_at	Acox1	NM_028765	-4.20	0.0000219	Acyl-Coenzyme A oxidase-like	protein targeting
1448964_at	S100g	NM_009789	-4.12	0.0034	S100 calcium binding protein G	
1451359_at	BC005662	NM_145376	-3.96	0.00000849	CDNA sequence BC005662	muscle development; phospholipid biosynthesis
1460258_at	Lect1	NM_010701	-3.75	0.00176	Leukocyte cell derived chemotaxin 1	
1418108_at	Plekhh1	NM_133244	-3.67	0.000442	synonyms: Mbf, RTKN2, B130039D23Rik; membrane bound factor	8284 // positive regulation of cell proliferation // inferred from direct assay // 30097 // hemopoiesis
1440849_at	6330417G04Rik	BE647762	-3.66	0.0000693	RAS protein-specific guanine nucleotide-releasing factor 2	
1429076_a_a	Gdgd2	NM_023608	-3.53	0.000348	Glycerophosphodiester phosphodiesterase domain containing 2	glycerol metabolism
1448397_at	Gjtb6	NM_008128	-3.51	0.000343	Gap junction membrane channel protein beta 6	cell communication; cell-cell signaling; ear morphogenesis; perception of sound
1446764_at	Wnt3a	C77101	-3.50	0.00132	Wingless-related MMTV integration site 3A	16055 // Wnt receptor signaling pathway // inferred from electronic annotation
1447845_s_a	Vnn1	NM_011704	-2.94	0.00514	Vanin 1	nitrogen compound metabolism
1450371_at	Tshb	NM_009432	-2.63	0.00569	Thyroid stimulating hormone, beta subunit	
1416200_at	9230117N10Rik	NM_133775	-2.63	0.0083	RIKEN cDNA 9230117N10 gene	biological_process unknown
1437028_at	Sfltba	NM_147779	-2.57	0.00827	Surfactant associated protein B	lipid metabolism; regulation of liquid surface tension; respiratory gaseous exchange; sphingolipid metabolism
1431788_at	1700008G05Rik	BC030910	-2.52	0.0013	RIKEN cDNA 1700008G05 gene	
1424479_at	Cst8	NM_009978	-2.50	0.00863	Cystatin 8 (cystatin-related epididymal spermatogenic)	
1444480_at	Prkag3	NM_153744	-2.49	0.00315	Protein kinase, AMP-activated, gamma 3 non-catalytic subunit	
1430792_at	Wwir1	AK014334	-2.47	0.0205	WW domain containing transcription regulator 1	protein amino acid phosphorylation
1441050_at	5730526G10Rik	AK042046	-2.46	0.00399	RIKEN cDNA 5730526G10 gene	
1417070_at	Cyp4v3	NM_133969	-2.45	0.00342	Kallikrein B, plasma 1	biological_process unknown
1435610_at	C130034118Rik	NM_177233	-2.41	0.00939	RIKEN cDNA C130034118 gene	
1460238_at	Msln	NM_018857	-2.38	0.00126	Mesothelin	
1452270_s_a	Cubn	XM_130038	-2.35	0.0000145	Cubilin (intrinsic factor-cobalamin receptor)	receptor mediated endocytosis; tRNA aminoacylation for protein translation
1425496_at	Abca3	NM_013855	-2.33	0.000673	ATP-binding cassette, sub-family A (ABC1), member 3	transport
1449152_at	Cdkn2b	NM_007670	-2.32	0.000816	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	cell cycle; negative regulation of cell cycle; regulation of transcription, DNA-dependent
1423367_at	Wnt7a	NM_009527	-2.30	0.000504	Wingless-related MMTV integration site 7A	Wnt receptor signaling pathway; cell-cell signaling; development; embryonic limb morphogenesis; frizzled-2 signaling
1422550_a_a	Mtap6	NM_010837	-2.26	0.00071	Microtubule-associated protein 6	microtubule-based process
1429355_at	3300001K11Rik	XM_156349	-2.22	0.0116	RIKEN cDNA 3300001K11 gene	
1448949_at	Car4	NM_007607	-2.18	0.00251	Carbonic anhydrase 4	one-carbon compound metabolism
1446007_at	Bmp1	BM231135	-2.17	0.00039	Bone morphogenetic protein 1	9887 // organogenesis // inferred from electronic annotation
1458381_at	Cllic5	NM_172621	-2.17	0.000106	Chloride intracellular channel 5	chloride transport; ion transport
1449939_s_a	Dlk1	NM_010052	-2.14	0.000167	Delta-like 1 homolog (Drosophila)	
1442752_at	Opcml	CF579117	-2.14	0.00741	Opioid binding protein/cell adhesion molecule-like	7155 // cell adhesion // inferred from electronic annotation
1456793_at	4930443F05Rik	BC063103	-2.11	0.0108	Cytokine like 1	
1427747_a_a	Lcn2	NM_008491	-2.09	0.0242	Lipocalin 2	transport
1435026_at	Spock2	NM_052994	-2.05	0.000829	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	
1417933_at	Igfbbp6	NM_008344	-2.04	0.000134	Insulin-like growth factor binding protein 6	regulation of cell growth
1452320_at	Lrp2	NM_130308	-2.04	0.00669	Low density lipoprotein receptor-related protein 2	6766 // vitamin metabolism // inferred from mutant phenotype // 6898 // receptor mediated endocytosis
1451287_s_a	2810003C17Rik	NM_145144	-2.02	0.000598	RIKEN cDNA 2810003C17 gene	
1419079_at	Scnn1g	NM_011326	-2.01	0.000925	Sodium channel, nonvoltage-gated 1 gamma	ion transport; sodium ion transport
1422983_at	Iltgb6	NM_021359	-2.00	0.0012	Integrin beta 6	cell adhesion; cell-matrix adhesion; integrin-mediated signaling pathway
1447301_at		XM_138063	-1.99	0.000333	Gene model 258, (NCBI)	
1456922_at	4933437K13Rik	NM_028964	-1.99	0.0217	RIKEN cDNA 4933437K13 gene	7242 // PX; intracellular signaling cascade; 1.6e-13 // extended: Unknown
1442587_at	C130076O07Rik	AK051190	-1.94	0.0383	RIKEN cDNA C130076O07 gene	7155 // cell adhesion // inferred from electronic annotation
1451857_a_a	5730593N15Rik	NM_175263	-1.93	0.00127	RIKEN cDNA 5730593N15 gene	
1429953_at	2210011C24Rik	AA030229	-1.93	0.0045	RIKEN cDNA 2210011C24 gene	
1456392_at	Negr1	NM_177274	-1.92	0.00164	Neuronal growth regulator 1	cell adhesion
1457548_at	Adams16	AK030315	-1.92	0.00186	A disintegrin-like and metalloprotease (repolyrin type) with thrombospondin type 1 motif, 6	
1442067_at	Ror1	BU512899	-1.92	0.00105	Receptor tyrosine kinase-like orphan receptor 1	7275 // development // inferred from electronic annotation
1449166_at	S100a14	NM_025393	-1.91	0.00303	S100 calcium binding protein A14	
1451674_at	Slc12a5	NM_020333	-1.90	0.000788	Solute carrier family 12, member 5	amino acid transport; chloride transport; ion transport; potassium ion transport; sodium ion transport; synaptic transmission
1421821_at	Ldlr	NM_010700	-1.89	0.00155	Low density lipoprotein receptor	cholesterol homeostasis; cholesterol metabolism; endocytosis; lipid transport

1450029_s_at	IlgA9	NM_133721	-1.88	0.00166	Integrin alpha 9	cell adhesion; cell-matrix adhesion; integrin-mediated signaling pathway
1429123_at	Rab27a	NM_023635	-1.88	0.000255	RAB27A, member RAS oncogene family	blood coagulation; protein transport; small GTPase mediated signal transduction; vesicle-mediated transport
1419647_a_at	Ier3	NM_133662	-1.85	0.00202	Immediate early response 3	
1417408_at	F3	NM_010171	-1.85	0.00985	Coagulation factor III	blood coagulation
1432885_at	4632432E15Rik	AK014604	-1.85	0.00739	RIKEN full-length enriched library, clone:4632432E15	
1431300_at	3110007P09Rik	NM_144906	-1.84	0.0114	RIKEN cDNA 3110007P09 gene	
1418778_at	9030408N13Rik	NM_025779	-1.84	0.00336	RIKEN cDNA 9030408N13 gene	
1458934_at	D5Ert0505e	BG068094	-1.83	0.0119	Mus musculus cDNA clone H3061F11 3', mRNA sequence.	
1423647_a_at	Zdhhc3	NM_026917	-1.81	0.0000568	Zinc finger, DHHC domain containing 3	protein targeting; proteolysis and peptidolysis
1438511_a_at	1190002H23Rik	NM_025427	-1.80	0.0000236	RIKEN cDNA A130038J17 gene	cell cycle
1417611_at	Tmem37	NM_019432	-1.80	0.00517	Transmembrane protein 37	ion transport
1449455_at	Hck	NM_010407	-1.80	0.000637	Hemopoietic cell kinase	intracellular signaling cascade; protein amino acid phosphorylation
1417821_at	D17H6S56E-5	NM_033075	-1.80	0.00132	DNA segment, Chr 17, human D6S56E 5	
1439790_at	Serpnb9	NM_009256	-1.79	0.00122	Serine (or cysteine) proteinase inhibitor, clade B, member 9	
1430306_a_at	Alp6v1c2	NM_133699	-1.79	0.00178	ATPase, H+ transporting, V1 subunit C, isoform 2	proton transport
1451416_a_at	Tgm1	NM_019984	-1.78	0.00168	Transglutaminase 1, K polypeptide	organogenesis; peptide cross-linking; protein metabolism; protein modification
1441467_at	Tm4s9	BB307636	-1.78	0.0103	Transmembrane 4 superfamily member 9	7155 // cell adhesion // inferred from sequence or structural similarity
1456487_at	D11Bwg1392e	BC050125	-1.77	0.00399	Adenylyl cyclase 1	adenylyl cyclase activation; cAMP biosynthesis; cyclic nucleotide biosynthesis; intracellular signaling cascade
1420955_at	Vsn1	NM_012038	-1.77	0.0343	Visinin-like 1	
1436142_at	3526401B18Rik	AK014386	-1.77	0.0000167	RIKEN cDNA 3526401B18 gene	
1439045_x_at	Mlac2d1	NM_028924	-1.76	0.000951	Membrane targeting (tandem) C2 domain containing 1	transport
1433184_at	Cacna1c	AK020162	-1.76	0.000448	Calcium channel, voltage-dependent, L type, alpha 1C subunit	
1459713_s_at	AU040576	NM_178642	-1.76	0.00282	Expressed sequence AU040576	
1422790_at	Nppc	NM_010933	-1.75	0.0189	Natriuretic peptide precursor type C	cGMP biosynthesis
1421093_at	Slc7a10	NM_017394	-1.75	0.0427	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 10	amino acid transport; neutral amino acid transport
1439311_at	B830012L14Rik	AK053394	-1.75	0.00849	RIKEN cDNA B830012L14 gene	
1418639_at	Sftpc	NM_011359	-1.73	0.00112	Surfactant associated protein C	regulation of liquid surface tension; respiratory gaseous exchange
1430012_at	1110050K14Rik	AK087264	-1.73	0.000699	RIKEN cDNA 1110050K14 gene	
1448365_at	2610002K22Rik	NM_025568	-1.72	0.000402	RIKEN cDNA 2610002K22 gene	6364 // rRNA processing // inferred from electronic annotation // 6396 // RNA processing
1444845_at	Scfd1	AK129238	-1.72	0.00854	Sec1 family domain containing 1	15031 // protein transport // inferred from electronic annotation
1439819_at	Clsc	BG070233	-1.72	0.00195	Cathepsin C	6508 // proteolysis and peptidolysis // inferred from electronic annotation
1450224_at	Col4a3	NM_007734	-1.72	0.000924	Procollagen, type IV, alpha 3	cell adhesion
1421786_at	Ppp3r1	NM_024459	-1.71	0.000904	Protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	epithelial to mesenchymal transition; heart development
1429286_at	1190003M12Rik	BE864968	-1.71	0.00246	RIKEN cDNA 1190003M12 gene	
1422256_at	Sstr2	NM_009217	-1.70	0.00501	Somatostatin receptor 2	G-protein coupled receptor protein signaling pathway; G-protein signaling, adenylyl cyclase inhibiting pathway
1450276_a_at	Scin	NM_009132	-1.69	0.0135	Scinderin	
1420847_a_at	Fgfr2	NM_010207	-1.69	0.000133	Fibroblast growth factor receptor 2	bone mineralization; cell-cell signaling; positive regulation of cell proliferation; protein amino acid phosphorylation
1456481_at	D9Ert0280e	NM_177775	-1.69	0.0166	DNA segment, Chr 9, ERATO Doi 280, expressed	
1418464_at	Matn4	NM_013592	-1.68	0.00166	Matriin 4	
1436987_at	5430433G21Rik	AK044859	-1.68	0.000621	RIKEN cDNA 5430433G21 gene	
1425272_at	Emp2	NM_007929	-1.68	0.00248	Epithelial membrane protein 2	
1421404_at	Cxcl15	NM_011339	-1.66	0.0106	Chemokine (C-X-C motif) ligand 15	chemotaxis; hemopoiesis; immune response; inflammatory response; neutrophil chemotaxis; signal transduction
1422804_at	Serpnb6b	NM_011454	-1.66	0.000145	Serine (or cysteine) proteinase inhibitor, clade B, member 6b	
1415916_a_at	Mthfd1	NM_138745	-1.65	0.000606	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent)	amino acid biosynthesis; folic acid and derivative biosynthesis; histidine biosynthesis; histidine catabolism;
1429292_a_at	2310046K01Rik	NM_027172	-1.65	0.00345	RIKEN cDNA 2310046K01 gene	
1415823_at	Scd2	NM_009128	-1.65	0.000113	Stearoyl-Coenzyme A desaturase 2	fatty acid biosynthesis; lipid biosynthesis
1434733_at	Slk36	NM_172657	-1.64	0.00195	synonyms: FU, MGS58023, B930045J24, 1700112N14Rik;	6468 // protein amino acid phosphorylation // inferred from sequence or structural similarity
1457589_at	D430038H04Rik	BC030299	-1.64	0.00445	RIKEN cDNA D430038H04 gene	
1424408_at	Lims2	NM_144862	-1.64	0.00783	Expressed sequence AI853548	
1456344_at	Tnc	NM_011607	-1.64	0.0321	Tenascin C	biological_process unknown
1460454_at	2010001H14Rik	NM_027227	-1.64	0.00599	RIKEN cDNA 2010001H14 gene	
1432418_a_at	Ckml1	NM_009897	-1.64	0.0191	Creatine kinase, mitochondrial 1, ubiquitous	
1422603_at	Rnase4	NM_021472	-1.64	0.0000156	Ribonuclease, RNase A family 4	
1425831_at	Zfp101	NM_009542	-1.63	0.0211	Zinc finger protein 101	
1431094_at	Rll1	XM_356599	-1.63	0.00183	Mus musculus retrotransposon-like 1 (Rll1), mRNA.	
1450082_s_at	Etv5	NM_023794	-1.63	0.0157	Ets variant gene 5	organogenesis
1434794_at	Rhof	NM_175092	-1.63	0.0000433	Ras homolog gene family, member f	actin filament organization; small GTPase mediated signal transduction
1442494_at	E130209G04Rik	AW519757	-1.63	0.00313	Ubiquitin protein ligase E3 component n-recogrin 2	7141 // male meiosis I // inferred from mutant phenotype
1425970_a_at	Ros1	NM_011282	-1.62	0.00201	Ros1 proto-oncogene	cellular physiological process; protein amino acid phosphorylation; regulation of cell cycle
1452993_at	5430416O09Rik	NM_027789	-1.62	0.0186	RIKEN cDNA 5430416O09 gene	
1448136_at	Enpp2	NM_015744	-1.62	0.00167	Ectonucleotide pyrophosphatase/phosphodiesterase 2	nucleotide metabolism
1458635_at	4832428D23Rik	NM_0207281	-1.62	0.0208	RIKEN cDNA 4832428D23 gene	
1457198_at	Nrp	AA673443	-1.62	0.000633	Mus musculus cDNA clone IMAGE:1024249 5', mRNA sequence.	
1436398_at	Lef1	AK084363	-1.62	0.000401	Lymphoid enhancer binding factor 1	16055 // Wnt receptor signaling pathway // inferred from electronic annotation

1417178_at	Semcap2	NM_016867	-1.62	0.00694	SemaF cytoplasmic domain associated protein 2	7242 // PDZ:intracellular signaling cascade;1.5e-06 // extended:Unknown
1422837_at	Scel	NM_022886	-1.61	0.000831	Sciellin	
1419435_at	Aox1	NM_009676	-1.61	0.0106	Aldehyde oxidase 1	electron transport
1436070_at	1110008E19Rik	CB248061	-1.61	0.00267	RIKEN cDNA 8030475D13 gene [Mus musculus]	
1433959_at	9630048M01Rik	NM_177086	-1.61	0.0197	RIKEN cDNA 9630048M01 gene	mRNA processing: nuclear mRNA splicing, via spliceosome
1418489_a_at	Calcr1	NM_018782	-1.61	0.000657	Calcitonin receptor-like	G-protein coupled receptor protein signaling pathway
1440847_at	Mlss1	NM_144800	-1.60	0.00502	Metastasis suppressor 1	actin filament organization: actin filament polymerization
1421375_a_at	S100a6	NM_011313	-1.60	0.000591	S100 calcium binding protein A6 (calcyclin)	cell cycle: cell proliferation: regulation of cell cycle
1444810_at	Acac	CA526571	-1.60	0.00991	Hypothetical protein E130101M22	
1444266_at	Hod	CA976946	-1.60	0.024	Hypothetical protein E130218H05	7507 // heart development // inferred from mutant phenotype
1454678_s_at	A130022J15Rik	NM_175313	-1.59	0.0018	RIKEN cDNA A130022J15 gene	
1443300_at	Notch3	NM_008716	-1.59	0.00442	Notch gene homolog 3 (Drosophila)	cell differentiation: development: regulation of development: regulation of transcription, DNA-dependent
1457935_at	Sdcccag33l	AK029270	-1.59	0.0147	Serologically defined colon cancer antigen 33 like	
1423174_a_at	Pard6b	NM_021409	-1.59	0.00216	Par-6 (partitioning defective 6) homolog beta (C. elegans)	cell cycle: cytokinesis: intracellular signaling cascade
1429298_at	Ddah1	NM_026993	-1.59	0.00311	Dimethylarginine dimethylaminohydrolase 1	nitric oxide biosynthesis: protein amino acid nitrosylation
1451236_at	Rerg	NM_181988	-1.59	0.00203	RAS-like, estrogen-regulated, growth-inhibitor	
1456547_at	Ski	CA872770	-1.58	0.00408	Sloan-Kettering viral oncogene homolog	30326 // embryonic limb morphogenesis // inferred from mutant phenotype
1424109_a_at	Glo1	NM_025374	-1.58	0.00664	Glyoxalase 1	carbohydrate metabolism
1418478_at	Lmo1	NM_057173	-1.58	0.00131	LIM domain only 1	cell proliferation: cellular physiological process: development
1436520_at	na	XM_356601	-1.58	0.0265	Similar to KIAA2019 protein (LOC382641), mRNA	
1440091_at	Mrg1	NM_010825	-1.57	0.00032	Myeloid ecotropic viral integration site-related gene 1	eye morphogenesis: regulation of transcription, DNA-dependent
1424567_at	6330415F13Rik	NM_027533	-1.57	0.00174	RIKEN cDNA 6330415F13 gene	
1441972_at	6230424C14Rik	AK078961	-1.57	0.0208	RIKEN cDNA 6230424C14 gene	
1449308_at	C6	NM_016704	-1.57	0.022	Complement component 6	complement activation
1439426_x_at	Lzp-s	NM_013590	-1.56	0.00572	P lysozyme structural	carbohydrate metabolism: cell wall catabolism: cytolysis: defense response to bacteria
1425834_a_at	Gpam	NM_008149	-1.56	0.000259	Glycerol-3-phosphate acyltransferase, mitochondrial	fatty acid metabolism: phospholipid biosynthesis: positive regulation of body size
1460194_at	Phyh	NM_010726	-1.56	0.000467	Phytanoyl-CoA hydroxylase	fatty acid alpha-oxidation
1434292_at	A930034L06Rik	NM_175692	-1.56	0.00257	RIKEN cDNA A930034L06 gene	
1441058_at	Itpkb	AK050506	-1.56	0.0133	Inositol 1,4,5-trisphosphate 3-kinase B	MAPKKK cascade: T-cell differentiation: cell surface receptor linked signal transduction: positive regulation of Ras protein
1433471_at	Tcf7	NM_009331	-1.56	0.000856	Transcription factor 7, T-cell specific	Wnt receptor signaling pathway: regulation of apoptosis: regulation of cell proliferation: regulation of transcription
1444767_at	Gnas	AK076536	-1.56	0.00802	RIKEN cDNA A930027G11 gene	
1419578_at	Mbl1	NM_010775	-1.55	0.000794	Mannose binding lectin, liver (A)	complement activation, classical pathway: phosphate transport
1449476_at	Rage	NM_011973	-1.55	0.00138	Renal tumor antigen	protein amino acid phosphorylation
1431364_a_at	2810047C21Rik	BC026878	-1.55	0.0415	RIKEN cDNA 2810047C21 gene	
1433743_at	Dach1	NM_007826	-1.55	0.00004	Dachshund 1 (Drosophila)	development: regulation of transcription: regulation of transcription, DNA-dependent
1423006_at	Pim1	NM_008842	-1.55	0.0164	Proviral integration site 1	protein amino acid phosphorylation
1442845_at	2810489O06Rik	AK085840	-1.55	0.00041	RIKEN cDNA 2810489O06 gene	
1426758_s_at	Gli2	NM_144513	-1.55	0.00199	GTL2, imprinted maternally expressed untranslated mRNA	
1446715_at	Abca13	AY160971	-1.55	0.0202	ATP-binding cassette, sub-family A (ABC1), member 13	protein targeting: transport
1450822_at	Lyzs	NM_017372	-1.54	0.0106	Lysozyme	carbohydrate metabolism: cell wall catabolism: cytolysis: defense response to bacteria
1441013_at	C130089K02Rik	BE952079	-1.54	0.00833	RIKEN cDNA C130089K02 gene	
1454806_at	D12Erd553e	NM_029758	-1.54	0.000886	DNA segment, Chr 12, ERATO Doi 553, expressed	
1445148_at	Akr1b3	AK049014	-1.54	0.00966	Aldo-keto reductase family 1, member B3 (aldose reductase)	
1453055_at	Sema6d	NM_172537	-1.54	0.00181	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	development: neurogenesis
1416203_at	Aqp1	NM_007472	-1.53	0.00193	Aquaporin 1	transport: water transport
1445535_at	D8Erd594e	BG063117	-1.53	0.0144	DNA segment, Chr 8, ERATO Doi 594, expressed	
1459947_at	Txndc5	AK028958	-1.53	0.015	Thioredoxin domain containing 5	30509 // BMP signaling pathway // inferred from direct assay
1440635_at	2410003B16Rik	BB534971	-1.53	0.0256	RIKEN cDNA 2410003B16 gene	
1457030_at	Mirg	AK077315	-1.53	0.000704	MIRNA containing gene	
1434582_at	D14Erd171e	NM_177814	-1.53	0.00169	DNA segment, Chr 14, ERATO Doi 171, expressed	
1420417_at	Sema3a	NM_009152	-1.53	0.0102	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	development: negative regulation of axon extension; neurogenesis
1445395_at	Al875142	BM932656	-1.53	0.00149	Expressed sequence Al875142	
1455280_at	Frem1	AK051925	-1.52	0.0013	Fras1 related extracellular matrix protein 1	7160 // cell-matrix adhesion // inferred from mutant phenotype
1442305_at	Gtpbp2	NM_019581	-1.52	0.0152	GTP binding protein 2	protein biosynthesis: translational elongation
1433445_x_at	Hmgcs1	NM_145942	-1.52	0.00483	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	C21-steroid hormone biosynthesis: acetyl-CoA metabolism: cholesterol biosynthesis: regulation of transcription
1452899_at	Rlan	AB063319	-1.52	0.0000361	RNA imprinted and accumulated in nucleus	biological_process unknown
1457898_at	Kcng5	AA617573	-1.52	0.00838	Potassium voltage-gated channel, subfamily Q, member 5	6812 // cation transport // inferred from electronic annotation
1435292_at	Tbc1d4	BU517771	-1.52	0.00293	TBC1 domain family, member 4	7275 // development // inferred from electronic annotation
1459617_at	Mapk14	AI552949	-1.52	0.00501	Mitogen activated protein kinase 14	77 // DNA damage checkpoint // inferred from mutant phenotype
1435927_at	E030003N15Rik	XM_128129	-1.51	0.00219	RIKEN cDNA E030003N15 gene	
1452514_a_at	Kit	NM_021099	-1.51	0.00466	Kit oncogene	autophosphorylation: cell differentiation: cell proliferation: cellular physiological process: chemotaxis
1430967_at	3110080O07Rik	AV169086	-1.51	0.0246	Mus musculus cDNA clone 3110080O07	
1438783_at	Tmepal	AW742560	-1.51	0.000104	Transmembrane, prostate androgen induced RNA	
1438279_at	Dpp4	NM_010074	-1.51	0.0197	Dipeptidylpeptidase 4	proteolysis and peptidolysis

1438235_at	Crlf3	BE988213	-1.51	0.0259	Cytokine receptor-like factor 3	
1445860_at	1110014F12Rik	NM_026743	-1.50	0.0165	RIKEN cDNA 1110014F12 gene	
1458058_at	Bcas3	AK078571	-1.50	0.0168	Breast carcinoma amplified sequence 3	
1437700_at	Schp1	NM_013928	-1.50	0.0024	Schwannomin interacting protein 1	
1450684_at	Etv1	NM_007960	-1.50	0.00485	Ets variant gene 1	axon guidance; mechanosensory behavior; muscle development; regulation of transcription, DNA-dependent
1424613_at	Gprc5b	NM_022420	1.50	0.00316	G protein-coupled receptor, family C, group 5, member B	G-protein coupled receptor protein signaling pathway
1435264_at	Emilin2	NM_145158	1.50	0.000956	Elastin microfibril interfacier 2	cell adhesion
1439649_at	4933429I20Rik	NM_172875	1.50	0.0045	RIKEN cDNA 4933429I20 gene	polyamine biosynthesis
1421074_at	Cyp7b1	NM_007825	1.50	0.034	Cytochrome P450, family 7, subfamily b, polypeptide 1	cholesterol metabolism; electron transport
1419045_at	2310067G05Rik	NM_025877	1.50	0.00162	RIKEN cDNA 2310067G05 gene	
1416111_at	Cd83	NM_009856	1.50	0.000188	CD83 antigen	
1448265_x_at	Eva1	NM_007962	1.50	0.00269	Epithelial V-like antigen 1	cell adhesion
1454742_at	Rasgef1b	NM_145839	1.50	0.0000467	RasGEF domain family, member 1B	cytokinesis
1455731_at	Slc29a3	NM_023596	1.50	0.000137	Solute carrier family 29 (nucleoside transporters), member 3	transport
1421076_at	Sertad3	NM_133210	1.50	0.000189	DNA Segment, Chr 1, Mouse Genome Informatics 51	
1451371_at	1110025G12Rik	NM_029844	1.50	0.0357	RIKEN cDNA 1110025G12 gene	
1417130_s_at	Angptl4	NM_020581	1.50	0.00733	Angiopoietin-like 4	negative regulation of apoptosis
1449056_at	E330009J07Rik	NM_175528	1.50	0.00107	RIKEN cDNA E330009J07 gene	
1447101_at	Rnf122	BE447516	1.50	0.00553	Ring finger protein 122	
1453599_at	2610206G21Rik	AK011901	1.51	0.0217	RIKEN full-length enriched library, clone:2610206G21 G254	
1426022_a_at	Vill	NM_011700	1.51	0.0207	Villin-like	cytoskeleton organization and biogenesis
1425245_a_at	Rgs11	BC049910	1.52	0.00103	Regulator of G-protein signaling 11	G-protein coupled receptor protein signaling pathway; intracellular signaling cascade; signal transduction
1437811_x_at	Cot11	AV312368	1.52	0.01	Coactosin-like 1 (Dictyostellium)	
1427082_at	4632417N05Rik	NM_028725	1.52	0.00645	RIKEN cDNA 4632417N05 gene	
1416368_at	Gsta4	NM_010357	1.52	0.0289	Glutathione S-transferase, alpha 4	
1418799_a_at	Col17a1	NM_007732	1.52	0.00102	Procollagen, type XVII, alpha 1	cell adhesion; phosphate transport
1426471_at	Zfp52	NM_144515	1.52	0.00501	Zinc finger protein 52	regulation of transcription, DNA-dependent
1439266_a_at	Polr3k	NM_025901	1.52	0.0105	Polymerase (RNA) III (DNA directed) polypeptide K	RNA elongation; regulation of transcription, DNA-dependent
1416933_at	Por	NM_008898	1.53	0.000135	P450 (cytochrome) oxidoreductase	electron transport
1417266_at	Ccl6	NM_009139	1.53	0.00165	Chemokine (C-C motif) ligand 6	chemotaxis; immune response; signal transduction
1422808_s_at	Dock2	NM_033374	1.53	0.00494	Dedicator of cyto-kinesis 2	T-cell activation; T-cell proliferation; alpha-beta T-cell activation; alpha-beta T-cell proliferation; chemotaxis
1420715_a_at	Pparg	NM_011146	1.53	0.0109	Peroxisome proliferator activated receptor gamma	adipocyte differentiation; inflammatory response; negative regulation of transcription from Pol II promoter
1430148_at	Rab19	NM_011226	1.53	0.000121	RAB19, member RAS oncogene family	protein transport; small GTPase mediated signal transduction
1420905_at	Il17r	NM_008359	1.53	0.0000647	Interleukin 17 receptor	cell surface receptor linked signal transduction
1423613_at	Ssfa2	NM_080558	1.53	0.0000877	Sperm specific antigen 2	
1424404_at	0610040J01Rik	NM_029554	1.54	0.000354	RIKEN cDNA 0610040J01 gene	
1454906_at	Rarb	NM_011243	1.54	0.00356	Retinoic acid receptor, beta	regulation of transcription, DNA-dependent; ureteric bud development
1453102_at	Firt3	NM_178382	1.54	0.00416	Fibronectin leucine rich transmembrane protein 3	chemotaxis
1448553_at	Myh7	NM_080728	1.54	0.00787	Myosin, heavy polypeptide 7, cardiac muscle, beta	cytoskeleton organization and biogenesis; muscle development; protein amino acid alkylation; striated muscle contraction
1448415_a_at	Sema3b	NM_009153	1.54	0.00454	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	development; neurogenesis
1424824_at	9630044O09Rik	NM_198014	1.54	0.0123	RIKEN cDNA 9630044O09 gene	
1422542_at	Gpr34	NM_011823	1.54	0.00736	G protein-coupled receptor 34	G-protein coupled receptor protein signaling pathway
1445815_at	Fzd8	NM_008058	1.55	0.00283	Frizzled homolog 8 (Drosophila)	G-protein coupled receptor protein signaling pathway; Wnt receptor signaling pathway; development
1439768_x_at	Sema4f	NM_011350	1.55	0.0278	Sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	development; neurogenesis
1455610_at	Dmn	NM_183312	1.55	0.00261	Desmuslin	biological_process unknown
1417047_at	Prom2	NM_138750	1.55	0.00851	Prominin 2	electron transport
1448591_at	Clss	NM_021281	1.55	0.00147	Cathepsin S	proteolysis and peptidolysis
1460188_at	Hcph	NM_013545	1.56	0.0015	Hemopoietic cell phosphatase	cytokine, chemokine mediated signaling pathway; intracellular signaling cascade; protein amino acid dephosphorylation
1436905_x_at	Lap1m5	NM_010686	1.56	0.0000187	Lysosomal-associated protein transmembrane 5	
1448956_at	Stard10	NM_019990	1.56	0.0000884	START domain containing 10	
1433963_a_at	BC032204	NM_153795	1.56	0.00489	CDNA sequence BC032204	cell adhesion; tRNA splicing
1455451_at	Al449310	BCG242920	1.56	0.00266	Expressed sequence AI449310	
1434980_at	Pik3r5	BF720745	1.56	0.0206	Phosphoinositide-3-kinase, regulatory subunit 5, p101	
1434913_at	Hmgcl1	NM_173731	1.56	0.00265	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	
1444396_at	Trp53inp2	NM_178111	1.56	0.0227	Tumor protein p53 inducible nuclear protein 2	
1449351_s_at	Pdgfr	NM_019971	1.56	0.00638	Platelet-derived growth factor, C polypeptide	organogenesis; platelet-derived growth factor receptor signaling pathway; positive regulation of cell proliferation
1437835_a_at	0610011L14Rik	NM_026661	1.56	0.014	RIKEN cDNA 0610011L14 gene	
1455735_at	Ap1s3	NM_183027	1.57	0.0195	Adaptor-related protein complex AP-1, sigma 3	biological_process unknown
1448871_at	Mapk13	NM_011950	1.57	0.00247	Mitogen activated protein kinase 13	cell cycle; protein amino acid phosphorylation
1421326_at	Csf2rb2	NM_007781	1.57	0.0128	Colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	
1417422_at	Gnmt	NM_010321	1.57	0.000204	Glycine N-methyltransferase	
1420712_a_at	Hpn	NM_008281	1.57	0.00056	Hepsin	proteolysis and peptidolysis
1423024_at	Eat2	NM_012009	1.57	0.00496	EWS/FLI1 activated transcript 2	intracellular signaling cascade
1448617_at	Cd53	NM_007651	1.57	0.0167	CD53 antigen	

1434089_at	Synpo	XM_129030	1.57	0.000867	synaptopodin	
1416124_at	Ccnd2	NM_009829	1.57	0.00427	Cyclin D2	cell cycle; cytokinesis; regulation of cell cycle
1422836_at	Mbnl3	NM_134163	1.57	0.00337	Muscleblind-like 3 (Drosophila)	development; negative regulation of myoblast differentiation
1434118_at	O610009K11Rik	NM_026689	1.57	0.0103	RIKEN cDNA O610009K11 gene	
1421952_at	Capn6	NM_007603	1.57	0.00137	Calpain 6	proteolysis and peptidolysis
1434864_at	Nipa1	NM_153578	1.57	0.00671	Non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	
1448227_at	Grb7	NM_010346	1.57	0.00359	Growth factor receptor bound protein 7	intracellular signaling cascade; signal transduction
1451407_at	Jam4	NM_028078	1.58	0.000708	Junction adhesion molecule 4	cell-cell adhesion
1440147_at	Lgi2	NM_144945	1.58	0.00081	Leucine-rich repeat LGI family, member 2	
1418118_at	Slc22a1	NM_009202	1.58	0.0303	Solute carrier family 22 (organic cation transporter), member 1	cation transport
1434109_at	Sh3bgrl2	NM_172507	1.58	0.0225	SH3 domain binding glutamic acid-rich protein like 2	
1418219_at	Il15	NM_008357	1.58	0.000636	Interleukin 15	NK T-cell proliferation; extrathymic T-cell selection; immune response; lymph gland development
1433504_at	Pygb	NM_153781	1.58	0.000202	Brain glycogen phosphorylase	carbohydrate metabolism; glycogen metabolism
1424927_at	Gilpr1	NM_028608	1.58	0.0212	GLI pathogenesis-related 1 (glioma)	
1419132_at	Tlr2	NM_011905	1.59	0.00104	Toll-like receptor 2	cell surface receptor linked signal transduction; immune response; inflammatory response
1443928_at	A1462064	BF453416	1.59	0.00177	Mus musculus cDNA clone IMAGE:3821985 5', mRNA sequence.	
1455660_at	Csf2rb1	NM_007780	1.59	0.000467	Colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage)	
1416986_a_a	Ptpns1	NM_007547	1.59	0.00756	RIKEN cDNA 2900076A13 gene	actin filament organization; cell motility; cell-matrix adhesion; cytoskeleton organization and biogenesis; phagocytosis
1418842_at	Hcls1	NM_008225	1.59	0.0224	Hematopoietic cell specific Lyn substrate 1	
1433678_at	A1132321	NM_178911	1.59	0.000386	Expressed sequence A1132321	lipid catabolism
1441516_a_a	C130050O18Rik	NM_177000	1.59	0.0033	RIKEN cDNA C130050O18 gene	
1416554_at	Pdlim1	NM_016861	1.60	0.000109	PDZ and LIM domain 1 (elfin)	regulation of transcription
1417789_at	Ccl11	NM_011330	1.60	0.0158	Small chemokine (C-C motif) ligand 11	chemotaxis; immune response; inflammatory response; signal transduction
1448561_at	Ncf2	NM_010877	1.60	0.00908	Neutrophil cytosolic factor 2	NADP catabolism; superoxide metabolism
1427076_at	Mpeg1	L20315	1.60	0.00428	Macrophage expressed gene 1	
1459299_at	A430065P19Rik	NM_177376	1.60	0.0184	RIKEN cDNA A430065P19 gene	
1450387_s_a	Ak4	NM_009647	1.61	0.00301	Adenylate kinase 4	
1450241_a_a	Evi2a	NM_010161	1.61	0.0229	Ecotropic viral integration site 2a	cell growth and/or maintenance
1439048_at	2900078E11Rik	AK046773	1.62	0.00257	RIKEN cDNA 2900078E11 gene	
1436989_s_a	Slc12a6	NM_133648	1.62	0.0063	RIKEN cDNA E330013P08 gene	amino acid transport; chloride transport; ion transport; potassium ion transport; sodium ion transport
1435917_at	Ociad2	BC044883	1.62	0.0013	OClA domain containing 2	
1427327_at	Pllra	NM_153510	1.62	0.00365	Paired immunoglobulin-like type 2 receptor alpha	signal transduction
1419534_at	Olr1	NM_138648	1.62	0.0188	Oxidized low density lipoprotein (lectin-like) receptor 1	
1422178_a_a	Rab17	NM_008998	1.62	0.0164	RAB17, member RAS oncogene family	protein transport; small GTPase mediated signal transduction
1420980_at	Pak1	NM_011035	1.62	0.000304	P21 (CDKN1A)-activated kinase 1	dendrite morphogenesis; protein amino acid phosphorylation
1418809_at	Pira6	NM_011087	1.62	0.0273	Paired-Ig-like receptor A1	biological_process unknown
1433966_x_a	Asns	NM_012055	1.62	0.0146	Asparagine synthetase	amino acid biosynthesis; asparagine biosynthesis; glutamine metabolism
1427126_at	Hspa1a	XM_207062	1.63	0.00511	heat shock protein, 70 kDa	DNA repair; response to heat; telomere maintenance
1420699_at	Clec3f12	NM_020008	1.63	0.0023	C-type lectin domain family 7, member a	cell surface receptor linked signal transduction; cell-cell adhesion; detection of yeast; phagocytosis, engulfment
1430834_at	C030038J10Rik	BB359379	1.63	0.00526	Mus musculus cDNA clone C030038J10 3', mRNA sequence.	
1450058_at	Asph	NM_023066	1.63	0.00176	Aspartate-beta-hydroxylase	
1421969_a_a	Faah	NM_010173	1.63	0.00204	Fatty acid amide hydrolase	
1449429_at	Fkbp1b	NM_016863	1.64	0.00161	FK506 binding protein 1b	protein folding
1425619_s_a	Dsg2	NM_007883	1.64	0.000244	Desmoglein 2	cell adhesion; homophilic cell adhesion
1449058_at	Gli1	NM_010296	1.64	0.00177	GLI-Kruppel family member GLI1	regulation of transcription, DNA-dependent; signal transduction; spermatogenesis
1428031_at	Gpr24	NM_145132	1.65	0.00185	G protein coupled receptor 24	G-protein coupled receptor protein signaling pathway; neuropeptide signaling pathway
1443664_s_a	Z310047N01Rik	CB587604	1.65	0.00215	RIKEN cDNA Z310047N01 gene	
1416246_a_a	Coro1a	NM_009898	1.65	0.0028	Coronin, actin binding protein 1A	
1435323_a_a	Oact1	NM_153546	1.65	0.00439	O-acyltransferase (membrane bound) domain containing 1	
1425109_at	BC010552	NM_145394	1.65	0.000154	CDNA sequence BC010552	
1417689_a_a	Map17	NM_026018	1.65	0.00477	Membrane-associated protein 17	biological_process unknown
1425767_a_a	Six4	NM_011382	1.65	0.00229	Sine oculis-related homeobox 4 homolog (Drosophila)	development; regulation of transcription, DNA-dependent
1449544_a_a	Kcnh2	NM_013569	1.65	0.0000572	Potassium voltage-gated channel, subfamily H (eag-related), member 2	cation transport; circulation; muscle contraction; potassium ion transport; regulation of heart contraction rate
1434372_at	AW112010	AA726875	1.66	0.0206	Expressed sequence AW112010	
1453754_at	4930429A08Rik	AK043160	1.66	0.00605	RIKEN cDNA 4930429A08 gene	
1455531_at	A930031D07Rik	NM_172510	1.66	0.0333	RIKEN cDNA A930031D07 gene	
1437078_at	Vps52	AK051732	1.66	0.00816	Vacuolar protein sorting 52 (yeast)	
1420819_at	Sla	NM_009192	1.66	0.00155	Src-like adaptor	intracellular signaling cascade
1423147_at	Mat1a	NM_133653	1.67	0.00929	Methionine adenosyltransferase 1, alpha	one-carbon compound metabolism
1419631_at	Was	NM_009515	1.67	0.00549	Wiskott-Aldrich syndrome homolog (human)	T-cell activation; actin filament polymerization; actin filament-based movement; actin polymerization
1428111_at	Slc38a4	NM_027052	1.67	0.00131	Solute carrier family 38, member 4	amino acid transport
1420464_s_a	Pirb	NM_011095	1.67	0.0126	Paired-Ig-like receptor B	B-cell homeostasis; B-cell mediated immunity; cytokine and chemokine mediated signaling pathway; dendritic cell growth
1429274_at	Z310010M24Rik	NM_027990	1.67	0.000504	RIKEN cDNA Z310010M24 gene	
1448898_at	Ccl9	NM_011338	1.68	0.0031	Chemokine (C-C motif) ligand 9	chemotaxis; immune response; signal transduction

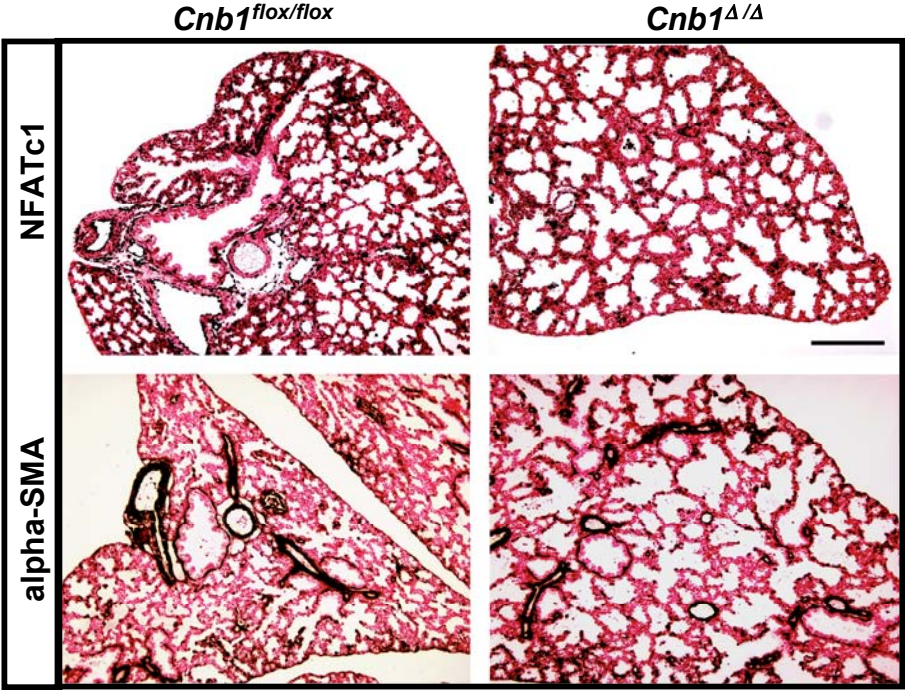
1418283_at	Cldn4	NM_009903	1.68	0.00946	Claudin 4	
1453509_at	Lypdc2	A1529499	1.68	0.00212	Ly6/Plaur domain containing 2	
1425407_s_at	Clec3f6	NM_011999	1.68	0.0107	C-type lectin domain family 4, member a2	
1457349_at	na	XM_126988	1.68	0.00198	Gene model 69, (NCBI)	
1437150_at	1700012H17Rik	NM_173426	1.69	0.0000334	RIKEN cDNA 1700012H17 gene	
1451764_at	Marveld3	NM_028584	1.69	0.00105	MARVEL (membrane-associating) domain containing 3	
1460197_a_a	Tnfalp9	NM_054098	1.69	0.00488	Tumor necrosis factor, alpha-induced protein 9	6810 // transport // inferred from electronic annotation /// 6118 // F420_oxidored;electron transport
1427942_at	Pamci	NM_146240	1.69	0.00266	Peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor	neuropeptide signaling pathway
1452966_at	9130430L19Rik	AK020296	1.70	0.00435	RIKEN cDNA 9130430L19 gene	
1427892_at	Myo1g	NM_178440	1.70	0.0124	Myosin IG	
1449164_at	Cd68	NM_009853	1.70	0.00339	CD68 antigen	
1427008_at	4732452J19Rik	NM_172448	1.70	0.000124	RIKEN cDNA 4732452J19 gene	
1457753_at	Tlr13; Gm713	NM_205820	1.70	0.00612	Mus musculus toll-like receptor 13 (Tlr13), mRNA.	
1418321_at	Dci	NM_010023	1.71	0.00042	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	fatty acid beta-oxidation; fatty acid metabolism
1419627_s_at	Clec3f10	NM_020001	1.72	0.0042	C-type lectin domain family 4, member n	heterophilic cell adhesion
1436345_at	5730559C18Rik	BC052416	1.72	0.0303	RIKEN cDNA 5730559C18 gene	
1450792_at	Tyrobp	NM_011662	1.72	0.00105	TYRO protein tyrosine kinase binding protein	
1429831_at	Plk3ap1	NM_031376	1.72	0.00215	Phosphoinositide-3-kinase adaptor protein 1	
1438325_at	Evi1	NM_007963	1.72	0.000331	Ecotropic viral integration site 1	development; regulation of transcription, DNA-dependent
1450240_a_a	Sytl1	NM_031393	1.73	0.0013	Synaptotagmin-like 1	hydrogen transport; intracellular protein transport
1425452_s_at	AW125753	NM_029007	1.73	0.000334	Expressed sequence AW125753	7507 // heart development // inferred from mutant phenotype
1430700_a_a	Pla2g7	NM_013737	1.74	0.0241	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	inflammatory response; lipid catabolism
1437085_at	D630039A03Rik	NM_178727	1.74	0.000133	RIKEN cDNA D630039A03 gene	
1421187_at	Ccr2	NM_009915	1.74	0.0043	Chemokine (C-C motif) receptor 2	
1439634_at	4930505D03Rik	BC059081	1.74	0.000468	RIKEN cDNA 4930505D03 gene	G-protein coupled receptor protein signaling pathway; cellular defense response (sensu Vertebrata); chemotaxis
1422552_at	Reprimo	NM_023396	1.74	0.0000162	Reprimo, TP53 dependant G2 arrest mediator candidate	cell cycle arrest; regulation of mitotic cell cycle
1423891_at	Gstl3	NM_133994	1.74	0.000716	Glutathione S-transferase, theta 3	glutathione metabolism
1450678_at	Itgb2	NM_008404	1.75	0.00177	Integrin beta 2	cell adhesion; cell-matrix adhesion; cellular extravasation; development; integrin-mediated signaling pathway
1452473_at	E130201N16Rik	NM_030024	1.75	0.00317	RIKEN cDNA E130201N16 gene	
1438884_at	D830007B15Rik	AK077061	1.75	0.000137	RIKEN cDNA D830007B15 gene	
1438097_at	Rab20	NM_011227	1.75	0.0000849	RAB20, member RAS oncogene family	protein transport; small GTPase mediated signal transduction
1422953_at	Fpr1	NM_008039	1.76	0.0147	Formyl peptide receptor, related sequence 2	6935 // chemotaxis // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway
1424737_at	Thrsp	NM_009381	1.76	0.0216	Thyroid hormone responsive SPOT14 homolog (Rattus)	
1444262_at	2210020M01Rik	BY704006	1.77	0.00617	RIKEN cDNA 2210020M01 gene	
1419537_at	Tcfec	NM_031198	1.77	0.00508	Transcription factor EC	development; regulation of transcription, DNA-dependent
1434354_at	Maob	NM_172778	1.78	0.000121	Monoamine oxidase B	electron transport
1418601_at	Aldh1a7	NM_011921	1.78	0.000405	Aldehyde dehydrogenase family 1, subfamily A7	metabolism; retinal metabolism
1419599_s_at	Ms4a6d	NM_026835	1.78	0.00107	Membrane-spanning 4-domains, subfamily A, member 11	
1455923_at	Kctd8	NM_175519	1.79	0.000487	Potassium channel tetramerisation domain containing 8	
1430247_at	Daam2	AK122266	1.79	0.00266	Dishevelled associated activator of morphogenesis 2	
1460218_at	Cd52	NM_013706	1.80	0.00126	CD52 antigen	
1417268_at	Cd14	NM_009841	1.80	0.00246	CD14 antigen	immune response; inflammatory response
1438555_x_at	Muc4	NM_080457	1.80	0.0155	RIKEN cDNA 4933405I11 gene	cell-matrix adhesion
1418496_at	Foxa1	NM_008259	1.80	0.0000722	Forkhead box A1	regulation of transcription, DNA-dependent
1420697_at	Slc15a3	NM_023044	1.81	0.0259	Solute carrier family 15, member 3	oligopeptide transport
1417845_at	Cldn6	NM_018777	1.81	0.00537	Claudin 6	
1453041_at	Tp53f5	NM_178381	1.81	0.0036	Tumor protein p53 inducible protein 5	
1430612_at	1810033B17Rik	AK087121	1.82	0.00616	RIKEN cDNA 1810033B17 gene	
1436712_at	Pla2g4c	XM_149881	1.82	0.00162	egg and early embryo abundant protein; CPLA2-gamma;	biological_process unknown
1427301_at	Cd48	NM_007649	1.83	0.014	CD48 antigen	
1444589_at		NM_177596	1.83	0.00256	Hypothetical protein 6720451E15	
1419608_a_a	Mia1	NM_019394	1.84	0.000695	Melanoma inhibitory activity 1	cell-matrix adhesion; extracellular matrix organization and biogenesis
1435697_s_at	Pscdbp	NM_139200	1.84	0.00208	Pleckstrin homology, Sec7 and coiled-coil domains, binding protein	regulation of cell adhesion
1434877_at	Nptx1	NM_008730	1.85	0.00268	Neuronal pentraxin 1	
1422411_s_at	Ear1	NM_007895	1.85	0.0107	Eosinophil-associated, ribonuclease A family, member 1	chemotaxis
1434049_at	Entpd3	NM_178676	1.85	0.000501	Ectonucleoside triphosphate diphosphohydrolase 3	nucleoside diphosphate catabolism; nucleoside triphosphate catabolism
1429954_at	3110037K17Rik	NM_153197	1.86	0.0103	C-type lectin domain family 4, member a3	
1438493_at	4933433K01Rik	XM_110919	1.86	0.0000559	RIKEN cDNA 4933433K01 gene	
1454942_at	Niban	NM_022018	1.87	0.000435	Niban protein	biological_process unknown
1436178_at	Leprel1	NM_173379	1.87	0.000783	Leprecan-like 1	
1426657_s_at	Phgdh	NM_016966	1.88	0.00173	3-phosphoglycerate dehydrogenase	L-serine biosynthesis
1417618_at	Ilth2	NM_010582	1.88	0.0328	Inter-alpha trypsin inhibitor, heavy chain 2	hyaluronan metabolism
1418668_at	Bucs1	NM_054094	1.88	0.000719	Butyryl Coenzyme A synthetase 1	fatty acid biosynthesis; metabolism
1417957_a_a	9030418M05Rik	NM_133681	1.89	0.00385	Tetraspan 1	

1429524_at	Myo1f	NM_008660	1.89	0.00326	synonym: C33006B10Rik; go_component: myosin [goid 0016459]	7010 // cytoskeleton organization and biogenesis // inferred from electronic annotation
1448978_at	Ngef	NM_019867	1.89	0.000187	Neuronal guanine nucleotide exchange factor	cellular physiological process
1422772_at	C1galt1	NM_052993	1.90	0.000484	Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	O-glycan processing, core 1
1431362_a_a	Smoc2	NM_022315	1.91	0.000457	SPARC related modular calcium binding 2	biological_process unknown
1430128_a_a	Dp111	NM_139292	1.91	0.0000222	Deleted in polyposis 1-like 1	
1450781_at	Hmg2	NM_010441	1.92	0.00199	High mobility group AT-hook 2	DNA packaging; chromosome organization and biogenesis (sensu Eukaryota); regulation of transcription, DNA-dependent
1419321_at	F7	NM_010172	1.94	0.000953	Coagulation factor VII	blood coagulation; metabolism; proteolysis and peptidolysis
1450220_a_a	Spdef	NM_013891	1.94	0.00479	SAM pointed domain containing ets transcription factor	regulation of transcription, DNA-dependent
1448609_at	Tst	NM_009437	1.95	0.00342	Thiosulfate sulfurtransferase, mitochondrial	sulfate transport
1441975_at	Acpp	NM_019807	1.97	0.0209	Acid phosphatase, prostate	biological_process unknown
1424208_at	Ptger4	NM_008965	1.97	0.00396	Prostaglandin E receptor 4 (subtype EP4)	G-protein coupled receptor protein signaling pathway; G-protein signaling, adenylate cyclase activating pathway
1456621_at	D430015B01Rik	NM_153574	1.98	0.000118	RIKEN cDNA D430015B01 gene	
1424155_at	Fabp4	NM_024406	1.99	0.00079	Fatty acid binding protein 4, adipocyte	transport
1419394_s_a	S100a8	NM_013650	2.00	0.00163	S100 calcium binding protein A8 (calgranulin A)	chemotaxis
1453510_s_a	4930589M24Rik	XM_125625	2.00	0.000805	RIKEN cDNA 4930589M24 gene	
1449091_at	Cldn8	NM_018778	2.00	0.00488	Claudin 8	
1452262_at	Grpel2	NM_021296	2.01	0.000118	GrpE-like 2, mitochondrial	protein folding
1436778_at	Cybb	NM_007807	2.02	0.000163	Cytochrome b-245, beta polypeptide	electron transport
1418961_at	1110005F07Rik	NM_025383	2.04	0.000759	RIKEN cDNA 1110005F07 gene	
1417481_at	Ramp1	NM_016894	2.05	0.00343	Receptor (calictonin) activity modifying protein 1	G-protein coupled receptor protein signaling pathway; intracellular protein transport; regulation of G-protein pathway
14242101_at	A930017N06Rik	NM_175522	2.08	0.00722	RIKEN cDNA A930017N06 gene	
1436256_at	Grpel2	NM_021296	2.10	0.000367	GrpE-like 2, mitochondrial	protein folding
1418393_a_a	Itga7	NM_008398	2.11	0.000336	Integrin alpha 7	cell adhesion; cell-matrix adhesion; cellular morphogenesis; integrin-mediated signaling pathway
1418186_at	Gstt1	NM_008185	2.15	0.0023	Glutathione S-transferase, theta 1	glutathione metabolism
1424477_at	BC019731	NM_144914	2.16	0.0000334	CDNA sequence BC019731	
1421195_at	Cckar	NM_009827	2.16	0.00000794	Cholecystokinin A receptor	G-protein coupled receptor protein signaling pathway
1435227_at	Bcl11b	NM_021399	2.19	0.00068	B-cell leukemia/lymphoma 11B	lymph gland development; negative regulation of cell proliferation; regulation of transcription, DNA-dependent
1458683_at	Sirpb	NM_178792	2.20	0.00569	Signal-regulatory protein beta	intracellular signaling cascade; positive regulation of phagocytosis
1439204_at	Scn3a	NM_018732	2.23	0.00181	sodium channel, voltage-gated, type III, alpha polypeptide	cation transport
1419766_at	Snf1k	NM_010831	2.34	0.0153	SNF1-like kinase	protein amino acid phosphorylation
1450928_at	Idb4	NM_031166	2.39	0.000764	Inhibitor of DNA binding 4	
1422634_a_a	Vsig2	NM_020518	2.46	0.0000165	V-set and immunoglobulin domain containing 2	biological_process unknown
1418374_at	Fxyd3	NM_008557	2.50	0.00000574	FXFD domain-containing ion transport regulator 3	ion transport
1437344_x_a	Krt11-13	NM_010662	2.56	0.024	Keratin complex 1, acidic, gene 13	cytoskeleton organization and biogenesis
1418724_at	Cfli	NM_007686	2.56	0.00461	Complement component factor i	complement activation; complement activation, classical pathway; proteolysis and peptidolysis
1435984_at	1110033F14Rik	CA328457	2.57	0.00851	RIKEN cDNA 1110033F14 gene	
1454402_at	3110048L19Rik	AK032425	2.61	0.00000258	RIKEN cDNA 3110048L19 gene	
1438567_at	Amaco	NM_172840	2.61	0.000478	VWA-like domains, matrilins and collagens	biological_process unknown
1448906_at	Cdh16	NM_007663	2.71	0.000221	Cadherin 16	cell adhesion; homophilic cell adhesion; tRNA aminoacylation for protein translation
1427492_at	Pof1b	NM_181579	2.74	0.00143	Premature ovarian failure 1B	
1450808_at	Fpr1	NM_013521	2.79	0.00607	Formyl peptide receptor 1	G-protein coupled receptor protein signaling pathway; chemotaxis
1438707_at	Alp13a4	NM_172613	2.80	0.000419	ATPase type 13A4	
1437355_at	Zcchc5	NM_199468	2.86	0.000063	Zinc finger, CCHC domain containing 5	
1421118_a_a	Gpr56	NM_018882	2.95	0.000631	G protein-coupled receptor 56	G-protein coupled receptor protein signaling pathway; metabolism; neuropeptide signaling pathway
1416456_a_a	2200003E03Rik	NM_023186	3.02	0.00297	RIKEN cDNA 2200003E03 gene	carbohydrate metabolism; chitin catabolism; chitin metabolism; polysaccharide catabolism
1455893_at	2610028F08Rik	NM_172815	3.38	0.00203	RIKEN cDNA 2610028F08 gene	protein amino acid phosphorylation; transmembrane receptor protein tyrosine kinase signaling pathway
1429950_at	Unc5cl	NM_152823	3.39	0.0000415	Unc-5 homolog C (C. elegans)-like	signal transduction
1449494_at	Rab3c	NM_023852	3.40	0.00298	RAB3C, member RAS oncogene family	intracellular protein transport; regulation of exocytosis; small GTPase mediated signal transduction
1416626_at	Pla2g1b	NM_011107	3.48	0.00012	Phospholipase A2, group IB, pancreas	cell proliferation; lipid catabolism; phospholipid catabolism; response to stress
1419118_at	2900093B09Rik	NM_021387	3.68	0.000423	RIKEN cDNA 2900093B09 gene	
1419325_at	Nmu	NM_019515	4.13	0.00365	Neuromedin U	neuropeptide signaling pathway; regulation of smooth muscle contraction
1419063_at	Ugt8	NM_011674	5.22	0.0000043	UDP-glucuronosyltransferase 8	glycolipid biosynthesis; metabolism; myelination
1451602_at	Snx6	NM_026998	6.79	0.00124	Sorting nexin 6	intracellular protein transport
1416842_at	Gstm5	NM_010360	7.28	0.0000119	Glutathione S-transferase, mu 5	metabolism
1437128_a_a	C730040L01Rik	AK046205	8.58	0.0000467	RIKEN cDNA C730040L01 gene	
1451612_at	Mt1	NM_013602	18.45	4.87E-08	Metallothionein 1	metal ion homeostasis; nitric oxide mediated signal transduction; zinc ion homeostasis

Supp. Table IV

Symbol	Cnb1	Foxa2	Titf11
Aqp5	-13.59766	-2.0876827	-3.12428
BC005662	-3.9554483	-3.8314176	-2.438277
Cckar	2.16372265	-1.7889088	1.9435294
Gsta4	1.51970273	1.866	2.621074
Hc	-5.0169294	-11.337868	-4.270418
Lyzs	-1.5436105	-2.0366599	-2.1202
Lzp-s	-1.5641306	-5.5555556	-1.991255
Pon1	-15.024086	-4.0650407	-20.35411
Rnase4	-1.6359133	-1.7006803	-2.57323
Scd1	-25.221696	-14.792899	-9.733572
Sftpa	-43.09	-12.72	-6.54
Slc34a2	-4.9167304	-2.020202	-2.188111
Zdhhc3	-1.8062683	-1.8903592	-2.580154
0610040J01	1.53590695	1.823	.
2900093B09	3.67672591	1.66	.
4732452J19	1.70072064	1.582	.
5730593N15	-1.9330605	-1.7331023	.
9030408N13	-1.8365175	-1.9230769	.
Abca3	-2.4813346	-1.8450185	.
Aldh1a7	1.77755272	1.568	.
Aox1	-1.6069522	-1.6556291	.
Atp6v1c2	-1.7852542	-1.6207455	.
Bex2	-4.2544706	-15.673981	.
Bmp1	1.82623808	1.708	.
Cdh16	2.71125033	2.582	.
Cst8	-2.5025795	-2.9069767	.
Cyp4v3	-2.4467775	-1.7699115	.
Ddc	-4.6612611	-1.6722408	.
Dlk1	-2.1415354	-2.9498525	.
Fabp4	1.99067583	2.212	.
Fgfr2	-1.6994399	-1.6694491	.
Foxa1	1.80263399	1.945	.
Gdpd2	-3.5337953	-1.6393443	.
Gjb6	-3.509747	-3.5714286	.
Gpam	-1.5640689	-1.6638935	.
Gpr56	2.95172889	1.74	.
Grpel2	2.10052762	2.519	.
Gstm5	7.28056326	8.821	.
Gstt1	2.14842253	1.575	.
Gstt3	1.74333695	1.872	.
Gtl2	-1.6862925	-2.0576132	.
Hmga2	1.91511408	1.694	.
Hmgcs1	-1.5796981	-1.7006803	.
Itga7	2.1112114	1.886	.
Itga9	-1.8796782	-1.5822785	.
Ldlr	-1.8870322	-1.5060241	.
Mt1	18.4537443	5.623	.
Mtac2d1	-1.7638195	1.525	.
Myh6	1.54246899	2.361	.
Pim1	3.62	1.614	.
Pla2g1b	3.56813119	2.144	.
Plekhk1	-3.6680805	-1.6313214	.
Pygb	1.58186329	1.837	.
Rab27a	-1.8755537	-1.7152659	.
Retnla	-7.3683145	-2.1691974	.
S100a14	-1.9149669	-1.8939394	.
Scel	-1.6120619	-2.1008403	.

Scin	-1.6944307	-1.9646365	.
Sftpb	-2.5675918	-1.6393443	.
Slc12a5	-1.8953234	-1.8621974	.
Smoc2	1.90859479	1.532	.
Synpo	1.57161762	1.643	.
Tgm1	-1.7804689	-1.5479876	.
Tst	1.95008406	1.922	.
Vnn1	-2.9356117	-1.9083969	.
Zfp52	1.52169891	2.16	.
1200008O12	.	-1.6750419	2.3084064
6530401D17	.	1.612	-3.314454
Car8	.	-2.0408163	-2.305594
Edil3	.	-1.5822785	-3.120172
li	.	2.388	1.9064244
Kif2c	.	-1.5037594	2.0185999
Mlc1	.	1.93	-3.020604
Pcx	.	1.585	-2.127272
Plscr2	.	2.021	-3.823655
Pnliprp1	.	-10.695187	2.1084799
Pvrl3	.	1.645	-2.257927
Rrm2	.	-1.8903592	3.9290502
Scgb1a1	.	-3.003003	-3.377231
Sftpd	.	1.678	1.5300821
Slc6a14	.	1.97	-2.529342
1190002H23	-1.8012873	.	-3.02612
2310046K01	-1.6493628	.	-2.13891
5430416O09	-1.6217703	.	-2.188478
6330415F13	-1.5689371	.	-2.080249
9630044O09	1.54395812	.	2.8303028
Aqp1	-1.5336705	.	-4.360525
Calb3	-4.1218266	.	-9.189717
Car4	-2.1795504	.	-3.069074
Cd14	1.79773292	.	2.306142
Cdkn2b	-2.3159481	.	-4.121626
Clic5	-2.1656251	.	-2.961609
Ear1	1.86110888	.	-3.213657
Emp2	-1.6771732	.	-2.300317
Enpp2	-1.6217545	.	-2.453219
Evi1	1.72365107	.	1.4384804
Fxyd3	2.50079509	.	3.2666573
Hck	-1.7989307	.	-2.534641
Ier3	-1.8487108	.	-2.157818
Lcn2	-2.0933698	.	4.758385
Lrp2	-2.0360357	.	-4.836787
Matn4	-1.6844828	.	-3.538602
Pard6b	-1.5880964	.	-3.398555
Pr1	-1.8004246	.	-3.124577
Scnn1g	-2.0073511	.	-8.958706
Serpnb6b	-1.6581997	.	-2.705273
Serpnb9	-1.7860088	.	-2.795924
Tshb	-2.6340968	.	-12.60515
Ugt8	5.22005472	.	2.4342933



SUPPLEMENTARY FIGURE LEGEND

Supplementary Figure 1: NFATc1 staining of the pulmonary vascular endothelium revealed normal capillary bed in close apposition to the epithelial cells in control (*Cnb1^{flx/flx}*) mice. In lungs of *Cnb1^{Δ/Δ}* mice, while NFATc1 staining was observed, the pulmonary capillaries were less developed and were embedded in thick mesenchyme at E18.5. α -SMA staining was unaltered; suggesting that lack of CNB1 in the respiratory epithelial cells does not affect the formation of pulmonary arteries and bronchiolar smooth muscle development at E18.5. Scale = 200 μ m.