Table S1. QPCR primers

Gene	**Forward**	**Reverse**
Foxp1	CGAATGTTTGCTTACTTCCGACGC	ACTTCATCCACTGTCCATACTGCC
Foxp2	GCCAGGCTGTGAAAGCATATGTGA	CATTTGCACTCGACATTGGGCAGT
Sox2	TGCACATGGCCCAGCACT	TTCTCCAGTTCGCAGTCCAG
Sox9	AGACCAGTACCCGCATCTGCACAA	TCTCTTCTCGCTCTCGTTCAGCA
Nkx2.1	TCCTCGGAAAGACAGCATCAGCTT	TCGTGTGCTTTGGACTCATCGACA
Scgb1a1	ATACCCTCCCACAAGAGACCAGGATA	ACACAGGGCAGTGACAAGGCTTTA
Scgb3a2	GCTGGTATCTATCTTTCTGCTGGTG	ACAACAGGGAGACGGTTGATGAGA
Cbr2	TGAATTTCAGTGGCCTGAGGG	ACTTTGGCTCCTGAGGCGT
Foxj1	AGTGGATCACGGACAACTTCTGCT	TTCTCCCGAGGCACTTTGATGAAG
Tubb4b	AACCCGGCACCATGGACTCTGT	TGCCTGCTCCGGATTGACCAAATA
Stat6	GGCCACCATCAGACAAATACTTCAAGGG	TTGAGTTCTTCCTGCTTCCGATGG
Spdef	TTGTGGGCGAGGTCCTGAAAGATA	AAAGCCACTTCTGCACGTTACCAG
Agr2	ACCGGCTCTACGCTTATGAACCTT	AAGTCCACAGTGCTTCTGCCTTCT
Muc5ac	TCGTACCATGAACACCGCTCTGAT	AGGTGGGATGATGGTCACCCTATT
Muc5b	ATGGGCAGCAGAAACTGGAGCTG	TCTGACTGTCTCCGGTGAGTTCTA
Muc2	TGACACCATCTACCTCACCCACAA	TGGTGTAGGCATCGTTCTTCTCA
Foxa3	ATGCTGGGCTCAGTGAAGATGGA	AAGGTCATGTAGGAGTTGAGAGGG
Clca3	TATGAGGGCATCGTCATCGCCATA	GAGGCCTGAGTCACCATGTCCTTTAT
Tff2	TTTGGGACTGCATGCTCTGGTAGA	AGCCACAGTTCTTTCTGTTGTGGG
Ascl1	GAGGAACAAGAGCTGCTGGACTTT	TGACGTCGTTGGCGAGAAACACTA
Sftpc/Spc	ACCCTGTGTGGAGAGCTACCA	TTTGCGGAGGGTCTTTCCT
Hes1	AAAGCCTATCATGGAGAAGAGGCG	GGAATGCCGGGAGCTATCTTTCTT
Hes5	CGTCAGCTACCTGAAACACAGCAA	AGTAGCCCTCGCTGTAGTCCT
Hey1	CTTGCAGATGACTGTGGATCACCT	AAACTCCGATAGTCCATAGCCAGG
Hey2	TTTGAAGATGCTCCAGGCTACAGG	AGCACTCTCGGAATCCAATGCTCA
Pofut1	TGTTCACAGGCATTTCCTTCAGCG	AGTGCGAGCACAGGATGCTCTTT
Notch1	TTGAGATGCTCCCAGCCAAGT	AGGATTGGAGTCCTGGCATCGTT
Notch2	CGTCAGACTGGCGACTTCACTTT	TCGTCGATATTCCGCTCACAGGT
Notch3	ATGTGCAAATGGAGGTCGGTGC	TGAGTGGCAAGGGTCTTCCAG
Notch4	TGCTGCTCTTGCCACTCAATTTCC	TCAGGCAGGTGCCTCCGTT
Dll1	AAGATGTGCGACCCTGGCTGGAAA	CAGTATCCATGTTGGTCATCACACCC
Dll3	TTTACCTGGGCCTGGACCTTGTGAT	GCACATTCAAAGGAGCCAGAGGTT
Dll4	AGTGTGCCTGCGATGAGGGAT	ATTCTTGCACGGAGAGTGGTGAGT
Jag1	ACCGTAATCGCATCGTACTGCCTT	ATTACTGGAATCCCAGGCCTCCACC
Jag2	TCGTCATTCCCTTTCAGTTCGCCT	ATCTGGAGTGGTGTCATTGTCCCAG
AGR2 (human)	CCAGAAATTGGCAGAGCAGTTTGTCC	TACTGGCCATCAGGAGAAAGGTGT

Table S2. Microarray analysis of *Shh-cre* control and *Foxp1/4*^{ShhcreDKO} mutant lungs at E14.5			
Gene symbol	**gene_assignment**	**Ab folds**	**Fold-change (KO vs. control)**
EG665955	FJ556972 // EG665955 // predicted gene, EG665955 // 5 B3 // 665955	36.4	-36.4
Xist	NR_001463 // Xist // inactive X specific transcripts // X D // 213742 /// NR_001	4.76199	-4.76199
Zfp125	ENSMUST00000079237 // Zfp125 // zinc finger protein 125 // --- // 22651 /// AJ00	2.91934	-2.91934
Cthrc1	NM_026778 // Cthrc1 // collagen triple helix repeat containing 1 // 15 C // 6858	2.77058	-2.77058
n/a	---	2.53775	-2.53775
Cym	NM_001111143 // Cym // chymosin // 3 F2.3 // 229697 /// BC147477 // Cym // chymo	2.5251	-2.5251
A2m	alpha-2-macroglobulin	2.27946	-2.27946
n/a	---	2.27944	-2.27944
Trim12	NM_023835 // Trim12 // tripartite motif-containing 12 // 7 E3 // 76681 /// ENSMU	2.19746	-2.19746
Lamp3	NM_177356 // Lamp3 // lysosomal-associated membrane protein 3 // 16 A3 // 239739	2.11631	-2.11631
G730007D18Rik	AK144596 // G730007D18Rik // RIKEN cDNA G730007D18 gene // --- // 100038502	1.98571	-1.98571
n/a	---	1.96031	-1.96031
Ascl1	NM_008553 // Ascl1 // achaete-scute complex homolog 1 (Drosophila) // 10 C1 // 1	1.93527	-1.93527
Serpina6	NM_007618 // Serpina6 // serine (or cysteine) peptidase inhibitor, clade A, memb	1.89658	-1.89658
Cps1	NM_001080809 // Cps1 // carbamoyl-phosphate synthetase 1 // 1 C3|1 43.4 cM // 22	1.87436	-1.87436
n/a	---	1.86076	-1.86076
Gm7120	NM_001039244 // Gm7120 //	1.84847	-1.84847

	predicted gene 7120 // 13 D2.3 // 633640 /// ENSMUST00		
Acp1	NM_001110239 // Acp1 // acid phosphatase 1, soluble // 12 A2 // 11431 /// NM_021	1.81548	-1.81548
n/a	---	1.81062	-1.81062
Nr1h5	NM_198658 // Nr1h5 // nuclear receptor subfamily 1, group H, member 5 // 3 F2.2	1.80988	-1.80988
Alb	NM_009654 // Alb // albumin // 5 E1|5 50.0 cM // 11657 /// ENSMUST00000031314 //	1.79378	-1.79378
Cbr2	NM_007621 // Cbr2 // carbonyl reductase 2 // 11 E2|11 72.5 cM // 12409 /// ENSMU	1.77952	-1.77952
4833420G17Rik	NM_001113550 // 4833420G17Rik // RIKEN cDNA 4833420G17 gene // 13 D2.3 // 67392	1.7695	-1.7695
Pgcp	NM_018755 // Pgcp // plasma glutamate carboxypeptidase // 15 B3.2 // 54381 /// N	1.7594	-1.7594
4933409K07Rik	BC059060 // 4933409K07Rik // RIKEN cDNA 4933409K07 gene // 4 A5 // 108816 /// BC	1.75297	-1.75297
Serinc2	NM_172702 // Serinc2 // serine incorporator 2 // 4 D2.2 // 230779 /// BC031720 /	1.74251	-1.74251
Art4	NM_026639 // Art4 // ADP-ribosyltransferase 4 // 6 G1|6 66.5 cM // 109978 /// EN	1.73703	-1.73703
Mgp	NM_008597 // Mgp // matrix Gla protein // 6 G1 // 17313 /// ENSMUST00000032342 /	1.69343	-1.69343
Scgb3a2	NM_054038 // Scgb3a2 // secretoglobin, family 3A, member 2 // 18 C-D // 117158 /	1.69	-1.69
C030030A07Rik	NM_001039558 // C030030A07Rik // RIKEN cDNA C030030A07 gene // 6 G1 // 654818 //	1.65654	-1.65654
2610044O15Rik	---	1.64385	-1.64385
Anxa1	NM_010730 // Anxa1 // annexin A1 // 19 B|19 18.0 cM // 16952 ///	1.60904	-1.60904

	ENSMUST00000025		
St6gal2	NM_172829 // St6gal2 // beta galactoside alpha 2,6 sialyltransferase 2 // 17 C /	1.6045	-1.6045
Cntn4	NM_001109749 // Cntn4 // contactin 4 // 6 E2 // 269784 /// NM_173004 // Cntn4 //	1.59978	-1.59978
n/a	---	1.59207	-1.59207
n/a	---	1.59207	-1.59207
Nr1h5	nuclear receptor subfamily 1, group H, member 5	1.591	-1.591
Lect1	NM_010701 // Lect1 // leukocyte cell derived chemotaxin 1 // 14 D3 // 16840 ///	1.58707	-1.58707
9130008F23Rik	NM_027834 // 9130008F23Rik // RIKEN cDNA 9130008F23 gene // 17 C // 71583 /// EN	1.58396	-1.58396
Pcdhb11	NM_053136 // Pcdhb11 // protocadherin beta 11 // 18 B3 // 93882 /// ENSMUST00000	1.5822	-1.5822
5730407I07Rik	ENSMUST00000069422 // 5730407I07Rik // RIKEN cDNA 5730407I07 gene // --- // 7051	1.57093	-1.57093
Gstm6	NM_008184 // Gstm6 // glutathione S-transferase, mu 6 // 3 F2.3 // 14867 /// ENS	1.56977	-1.56977
n/a	---	1.5673	-1.5673
Plcd3	phospholipase C, delta 3	1.5528	-1.5528
AK041797	---	1.5528	-1.5528
C030011O14Rik	---	1.5528	-1.5528
n/a	---	1.5528	-1.5528
n/a	---	1.5528	-1.5528
n/a	---	1.5528	-1.5528
n/a	---	1.5528	-1.5528
Qpct	NM_027455 // Qpct // glutaminyl-peptide cyclotransferase (glutaminyl cyclase) //	1.54484	-1.54484
Ccl28	NM_020279 // Ccl28 // chemokine (C-C motif) ligand 28 // --- // 56838 /// ENSMUS	1.52822	-1.52822
Gm8840	XR_032645 // Gm8840 // predicted gene 8840 // 1 C3 // 667842	1.51585	-1.51585

Gm9078	XR_031413 // Gm9078 // predicted gene 9078 // X C3 // 668271	1.50366	-1.50366
Gabra5	NM_176942 // Gabra5 // gamma-aminobutyric acid (GABA) A receptor, subunit alpha	1.50264	1.50264
E330027M22Rik	AK054458 // E330027M22Rik // RIKEN cDNA gene, E330027M22Rik // --- // 100038419	1.50502	1.50502
n/a	---	1.51105	1.51105
Fgf14	NM_207667 // Fgf14 // fibroblast growth factor 14 // 14 E5|14 59.0 cM // 14169 /	1.51452	1.51452
Rprl2	NR_004439 // Rprl2 // ribonuclease P RNA-like 2 // --- // 19784	1.51685	1.51685
Plac9	NM_207229 // Plac9 // placenta specific 9 // 14 B // 211623 /// BC032982 // Plac	1.51819	1.51819
Snord33	NR_001277 // Snord33 // small nucleolar RNA, C/D box 33 // 7 B4 // 27208	1.52073	1.52073
n/a	---	1.52452	1.52452
Zfp868	NM_172754 // Zfp868 // zinc finger protein 868 // 8 B3.3 // 234362 /// NM_001045	1.52483	1.52483
Snora44	AF357394 // Snora44 // small nucleolar RNA, H/ACA box 44 // 4|4 // 100217418	1.52484	1.52484
BC030870	ENSMUST00000098713 // BC030870 // cDNA sequence BC030870 // --- // 407795	1.52645	1.52645
snRNA	---	1.52858	1.52858
Rmrp	NR_001460 // Rmrp // RNA component of mitochondrial RNAase P // 4 B1 // 19782	1.53004	1.53004
snRNA	---	1.53176	1.53176
Fam183b	NM_029283 // Fam183b // family with sequence similarity 183, member B // 11 B1.3	1.53187	1.53187
Ccdc115	NM_027159 // Ccdc115 // coiled-coil domain containing 115 // 1 B // 69668 /// EN	1.53255	1.53255
Gm10484	AK142929 // Gm10484 // predicted	1.53306	1.53306

	gene 10484 // --- // 100038503		
Snhg1	AK051045 // Snhg1 // small nucleolar RNA host gene (non-protein coding) 1 // 19	1.53383	1.53383
Gm9282	XR_033945 // Gm9282 // predicted gene 9282 // 12 A1.3 // 668645 /// XR_034054 //	1.53816	1.53816
Capsl	NM_029341 // Capsl // calcyphosine-like // 15 A1 // 75568 /// ENSMUST00000042360	1.53888	1.53888
snRNA	---	1.54879	1.54879
Trappc2l	NM_021502 // Trappc2l // trafficking protein particle complex 2-like // 8 E1 //	1.55072	1.55072
Snora34	AF357396 // Snora34 // small nucleolar RNA, H/ACA box 34 // 15|15 // 100217417	1.55249	1.55249
Slc34a2	NM_011402 // Slc34a2 // solute carrier family 34 (sodium phosphate), member 2 //	1.55307	1.55307
Pcsk6	NM_011048 // Pcsk6 // proprotein convertase subtilisin/kexin type 6 // 7 C|7 28.	1.56027	1.56027
Ear2	NM_007895 // Ear2 // eosinophil-associated, ribonuclease A family, member 2 // 1	1.57029	1.57029
Phxr4	BC107288 // Phxr4 // per-hexamer repeat gene 4 // 9 A1 // 18689 /// X12806 // Ph	1.57534	1.57534
Matn2	NM_016762 // Matn2 // matrilin 2 // 15 B3.3 // 17181 /// ENSMUST00000022947 // M	1.5794	1.5794
Efhc1	EU520262 // Efhc1 // EF-hand domain (C-terminal) containing 1 // 1 A5 // 71877 /	1.58143	1.58143
Vsig1	NM_030181 // Vsig1 // V-set and immunoglobulin domain containing 1 // X F1 // 78	1.59441	1.59441
Cubn	NM_001081084 // Cubn // cubilin (intrinsic factor-cobalamin receptor) // 2 A1|2	1.60886	1.60886
Kdm5d	NM_011419 // Kdm5d // lysine (K)-	1.60974	1.60974

	specific demethylase 5D // Y A1 // 20592 /// EN		
Acvr1c	NM_001111030 // Acvr1c // activin A receptor, type IC // 2 C1.1 // 269275 /// NM	1.6164	1.6164
Fgf1	NM_010197 // Fgf1 // fibroblast growth factor 1 // 18 B3|18 19.0 cM // 14164 ///	1.61827	1.61827
Rassf9	NM_146240 // Rassf9 // Ras association (RalGDS/AF-6) domain family (N-terminal)	1.62071	1.62071
Rnu2	NR_004414 // Rnu2 // U2 small nuclear RNA // --- // 19848 /// NR_004414 // Rnu2	1.62103	1.62103
Kcnip4	NM_030265 // Kcnip4 // Kv channel interacting protein 4 // 5 B3 // 80334 /// ENS	1.63221	1.63221
Dkk1	NM_010051 // Dkk1 // dickkopf homolog 1 (Xenopus laevis) // 19 C2 // 13380 /// E	1.63962	1.63962
snRNA	---	1.66388	1.66388
B230354O11Rik	AK046228 // B230354O11Rik // RIKEN cDNA B230354O11 gene // 12 A1.3 // 668468 ///	1.66391	1.66391
AW112010	EF660528 // AW112010 // expressed sequence AW112010 // 19 A // 107350 /// ENSMUS	1.67792	1.67792
Adam28	NM_010082 // Adam28 // a disintegrin and metallopeptidase domain 28 // 14 D2 //	1.69066	1.69066
AK009175	---	1.69391	1.69391
Abhd1	abhydrolase domain containing 1	1.6956	1.6956
Trip6	thyroid hormone receptor interactor 6	1.71235	1.71235
snRNA	---	1.72719	1.72719
unknown cDNA	---	1.73924	1.73924
Pcdh10	NM_001098171 // Pcdh10 // protocadherin 10 // 3 C // 18526 /// NM_011043 // Pcdh	1.74845	1.74845
mitochondrion	---	1.77531	1.77531
Rny1	NR_004419 // Rny1 // RNA, Y1 small cytoplasmic, Ro-associated //	1.8161	1.8161

	6|6 54.3 cM //		
Naaladl2	XM_975226 // Naaladl2 // N-acetylated alpha-linked acidic dipeptidase-like 2 //	1.82424	1.82424
Bend6	NM_177235 // Bend6 // BEN domain containing 6 // 1 B // 320705 /// ENSMUST000000	1.86022	1.86022
Emb	NM_010330 // Emb // embigin // 13 D2.3 // 13723 /// ENSMUST00000022242 // Emb //	1.86958	1.86958
Ccdc67	NM_181816 // Ccdc67 // coiled-coil domain containing 67 // 9 A2 // 234964 /// EN	1.8701	1.8701
Gtf3c2/Mpv17 transgene	---	1.87106	1.87106
Gm9943	ENSMUST00000067349 // Gm9943 // predicted gene 9943 // --- // 100036531 /// ENSM	1.88364	1.88364
1700003M02Rik	NM_027041 // 1700003M02Rik // RIKEN cDNA 1700003M02 gene // 4 A5 // 69329 /// EN	1.88947	1.88947
1700011H14Rik	BC026534 // 1700011H14Rik // RIKEN cDNA 1700011H14 gene // 14 C1 // 67082 /// EN	1.91853	1.91853
Gm606	BC086669 // Gm606 // predicted gene 606 // 16 B2 // 239789 /// ENSMUST0000008983	1.9554	1.9554
Gm10664	ENSMUST00000098718 // Gm10664 // predicted gene 10664 // --- // 100038489	1.98689	1.98689
Clca4	NM_139148 // Clca4 // chloride channel calcium activated 4 // 3 H2-H3 // 229927	2.02107	2.02107
mitochondrion	---	2.02263	2.02263
Ddx3y	NM_012008 // Ddx3y // DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked // Y A1	2.04613	2.04613
snRNA	---	2.04892	2.04892
snRNA	---	2.04892	2.04892
Meig1	NM_008579 // Meig1 // meiosis expressed gene 1 // 2 A1 // 104362 /// ENSMUST0000	2.05128	2.05128

Cldn8	NM_018778 // Cldn8 // claudin 8 // 16 C3.3 // 54420 /// ENSMUST00000049697 // Cl	2.06801	2.06801
Kcnj13	NM_001110227 // Kcnj13 // potassium inwardly-rectifying channel, subfamily J, me	2.10826	2.10826
snRNA	---	2.12772	2.12772
Uty	NM_009484 // Uty // ubiquitously transcribed tetratricopeptide repeat gene, Y ch	2.21234	2.21234
Cpa3	NM_007753 // Cpa3 // carboxypeptidase A3, mast cell // 3 A2|3 13.2 cM // 12873 /	2.28783	2.28783
LOC677548	XR_034974 // LOC677548 // similar to Hippocalcin-like protein 1 (Visinin-like pr	2.28948	2.28948
Hdc	NM_008230 // Hdc // histidine decarboxylase // 2 E5-G // 15186 /// ENSMUST000000	2.31709	2.31709
Agr2	NM_011783 // Agr2 // anterior gradient 2 (Xenopus laevis) // 12 A3 // 23795 ///	2.53228	2.53228
Gm4638	XM_001480931 // Gm4638 // predicted gene 4638 // 14 D3|14 // 100043775 /// XM_00	2.60111	2.60111
LOC280487	X16670 // LOC280487 // pol polyprotein // 13 A3.1 // 280487	2.60111	2.60111
Ear1	NM_007894 // Ear1 // eosinophil-associated, ribonuclease A family, member 1 // 1	2.65703	2.65703
mitochondrion	---	2.72734	2.72734
Eif2s3y	NM_012011 // Eif2s3y // eukaryotic translation initiation factor 2, subunit 3, s	2.81909	2.81909
mitochondrion	---	3.34419	3.34419
Tecrl	NM_153801 // Tecrl // trans-2,3-enoyl-CoA reductase-like // 5 E1 // 243078 /// E	3.55249	3.55249
Habp2	NM_146101 // Habp2 // hyaluronic acid binding protein 2 // 19 D2 // 226243 /// E	4.85063	4.85063
mitochondrion	---	5.2727	5.2727

mitochondrion	---	5.71257	5.71257
mitochondrion	---	6.1976	6.1976