

## SUPPLEMENTARY MATERIAL

Supplementary Figures S1 to S7

Supplementary Tables S1 and S2

### Supplementary Figure Legends

**Fig. S1. MicroCT imaging analysis in *Tgfb2<sup>f/f</sup>;K14-Cre* mice. (A-L)** MicroCT images from E18.5 *Tgfb2<sup>f/f</sup>* control (A-F) and *Tgfb2<sup>f/f</sup>;K14-Cre* (G-L) mice, arranged from the anterior to posterior. Images of (B,D,F,H,J,L) are enlarged from (A,C,E,G,J,K), respectively. Yellow arrows indicate cleft palate. Scale bars, 1.0 mm in (A,C,E,G,J,K); 250  $\mu$ m in (B,D,F,H,J,L).

**Fig. S2. Comparison of palate development in *Tgfb2<sup>f/f</sup>* control and *Tgfb2<sup>f/f</sup>;K14-Cre* mice. (A-Y)** Coronal images of H&E staining from the anterior to posterior of *Tgfb2<sup>f/f</sup>* control (A-C,G-I,M-O,S-U) and *Tgfb2<sup>f/f</sup>;K14-Cre* (D-F,J-L,P-R,V-X) mice at the indicated developmental stages. Red lines on the schematic drawings (Y) show the position of the sections. Scale bars, 200  $\mu$ m.

**Fig. S3. Apoptotic activity is not altered in *Tgfb2<sup>f/f</sup>;K14-Cre* mice. (A-F)** H&E staining (A, B), BrdU staining (C, D), and immunofluorescent staining with MyHC (green) and BrdU (red) (E, F) of *Tgfb2<sup>f/f</sup>* control (A,C,E) and *Tgfb2<sup>f/f</sup>;K14-Cre* (B,D,F) mice at E15.5. Dotted lines indicate outline of the TVP. Scale bars, 50  $\mu$ m (**G**) Quantification of the number of BrdU-labeled nuclei in the TVP of E15.5 *Tgfb2<sup>f/f</sup>* control (white bar) and *Tgfb2<sup>f/f</sup>;K14-Cre* (black bar) mice. Three samples per genotype were analyzed. \*, p<0.05. (**H-M**) TUNEL assay of the soft palate of *Tgfb2<sup>f/f</sup>* control (H,I,L) and *Tgfb2<sup>f/f</sup>;K14-Cre* (J,K,M) mice at E15.5 (H-K) and E16.5 (L,M). Insets (I,K) show higher magnification of (H,K), respectively. Scale bars, 100  $\mu$ m

**Fig. S4. Cleft soft palate in  $Tgfb2^{fl/fl};K14-Cre;Irf6^{Tg}$  mice.** (A-L) H&E staining of  $Tgfb2^{fl/fl}$  control (A,D,G,J),  $Tgfb2^{fl/fl};K14-Cre$  (B,E,H,K), and  $Tgfb2^{fl/fl};K14-Cre;Irf6^{Tg}$  (C,F,I,L) mice at E15.5 and E18.5. Scale bars, 200  $\mu\text{m}$ . (M) Quantitative RT-PCR analyses of *Dkk1* and *Dkk4* in the palates of E15.5  $Tgfb2^{fl/fl}$  control (blue bars),  $Tgfb2^{fl/fl};K14-Cre$  (red bars), and  $Tgfb2^{fl/fl};K14-Cre;Irf6^{Tg}$  (green bars) mice. Three samples were analyzed for each experiment. \*\*\* $, p<0.001$ ; \* $, p<0.05$ ; NS, not significant.

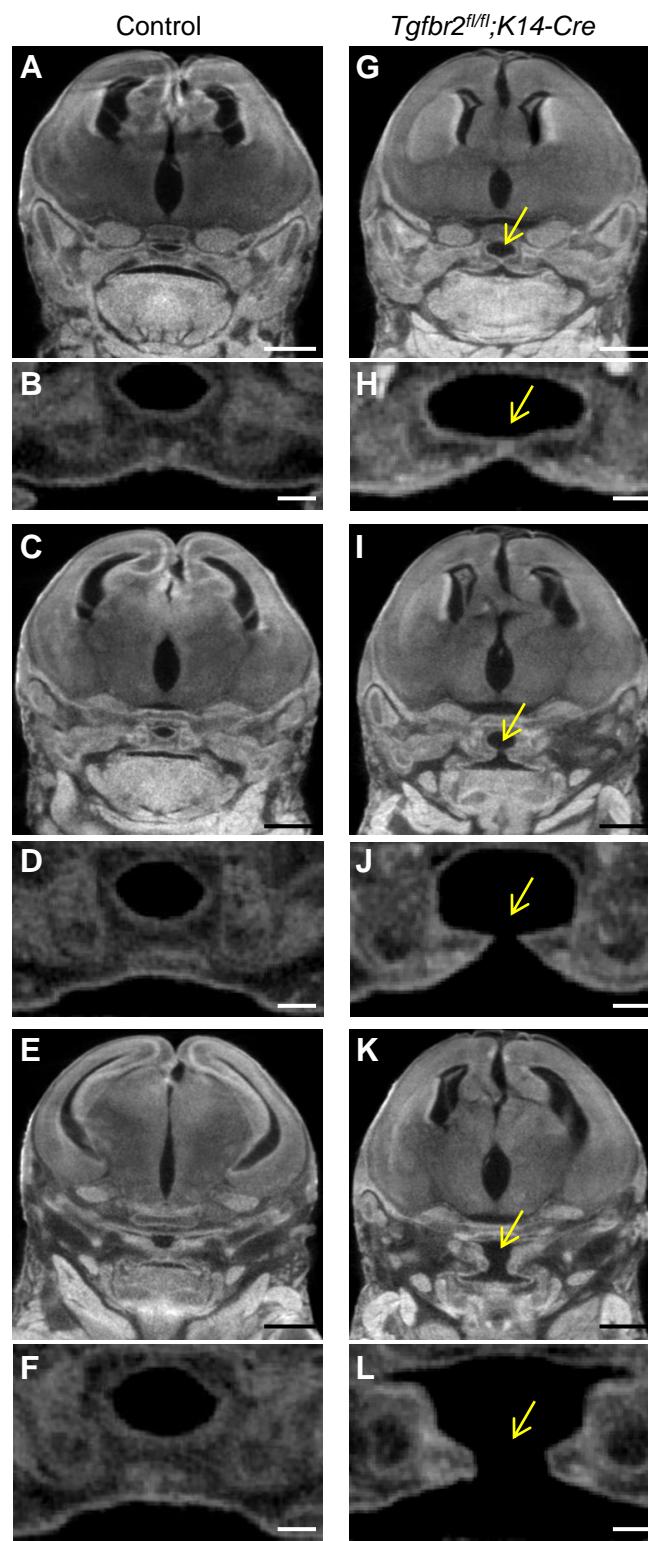
**Fig. S5. Heat map image of TGF $\beta$  signaling pathway in the anterior versus posterior palate of E15.5 wild type mice.** Anterior and posterior portions of the secondary palate from E15.5 wild type mice. Six samples per group were analyzed.

**Fig. S6. Soft palate development in  $Tgfb2^{fl/fl};Wnt1-Cre$  mice.** (A,B) Oral view of E18.5  $Tgfb2^{fl/fl}$  control (A) and  $Tgfb2^{fl/fl};Wnt1-Cre$  (B) mice. Yellow dotted lines indicate the pterygoid plate. Blue dotted lines indicate the end of the soft palate. (C-J) H&E staining of E18.5  $Tgfb2^{fl/fl}$  control (C,D,G,H),  $Tgfb2^{fl/fl};Wnt1-Cre$  (E,F,I,J) mice. Boxed areas in (C,E,G,I) are enlarged in (D,F,H,J), respectively. Scale bars, 500  $\mu\text{m}$  in (C,E,G,I); 50  $\mu\text{m}$  in (D,F,H,J). Ptr, pterygoid plate. (K) Quantitative RT-PCR analyses of *Dkk2* and *Limd1* in the palates of E15.5  $Tgfb2^{fl/fl}$  control (white bars) and  $Tgfb2^{fl/fl};Wnt1-Cre$  (black bars) mice. Three samples were analyzed for each experiment. \*\*\* $, p<0.001$ ; \* $, p<0.05$ .

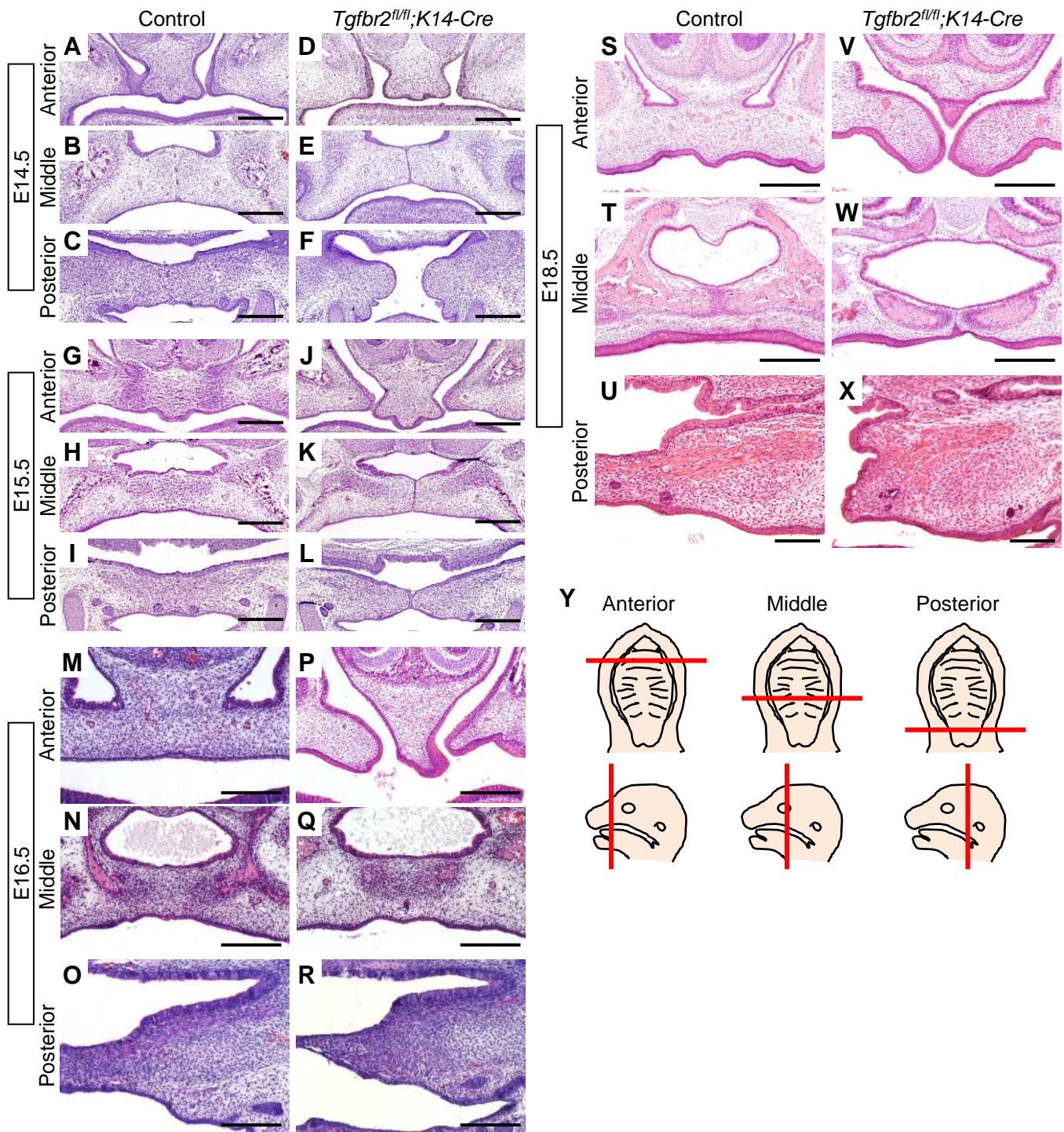
**Fig. S7. Heat map image of canonical WNT signaling pathway in  $Tgfb2^{fl/fl};Wnt1-Cre$  palate.**

Palatal shelves from E14.5  $Tgfb2^{fl/fl}$  control and  $Tgfb2^{fl/fl};Wnt1-Cre$  mice. Five samples per genotype were analyzed.

**Fig. S1**



**Fig. S2**



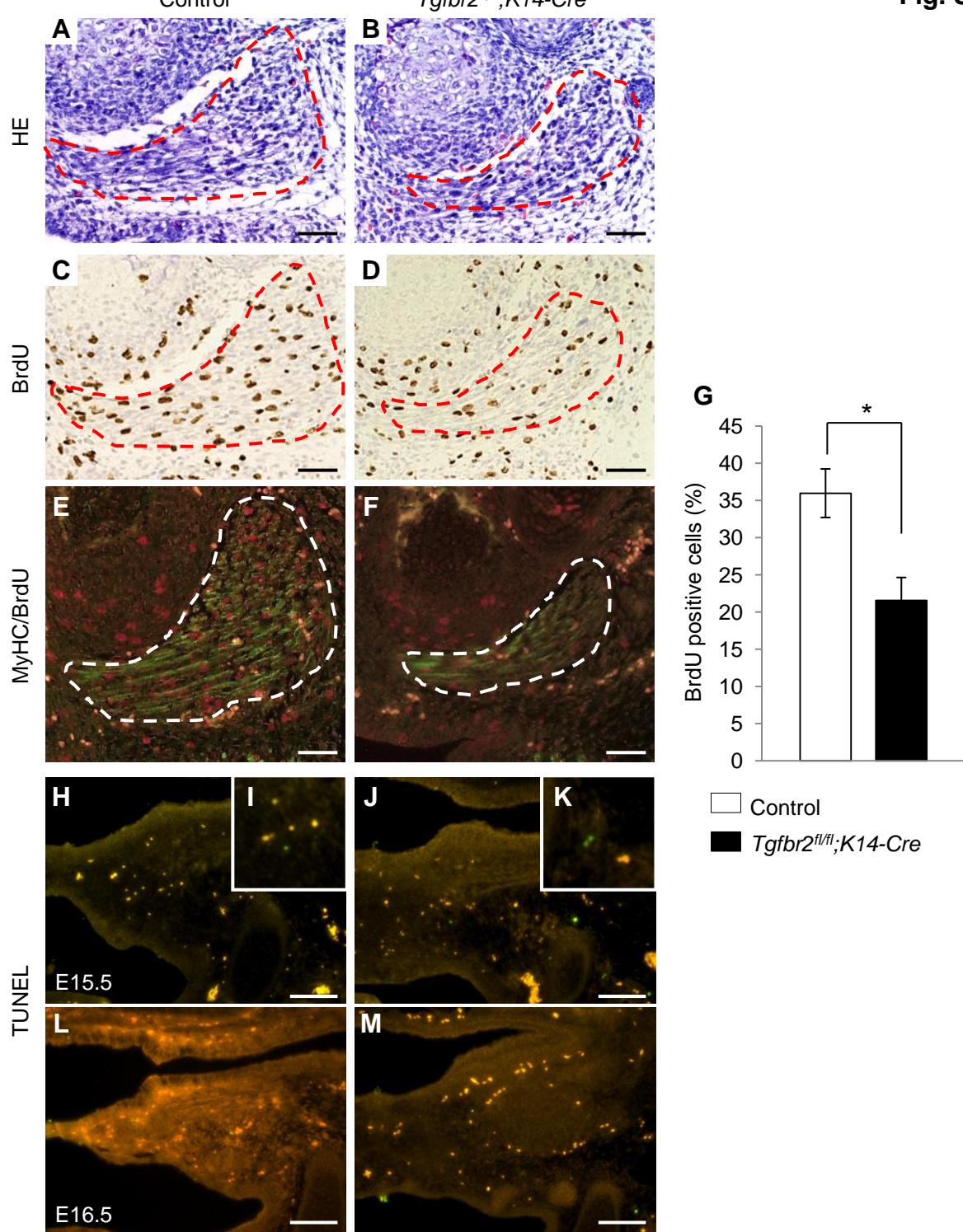
**Fig. S3**

Fig. S4

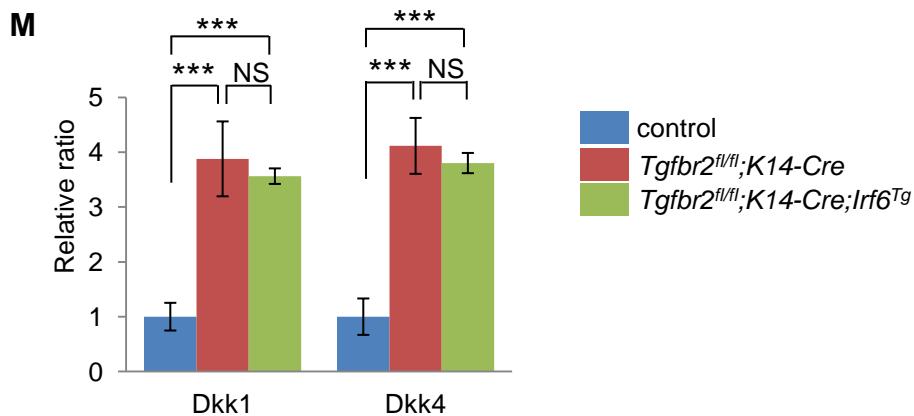
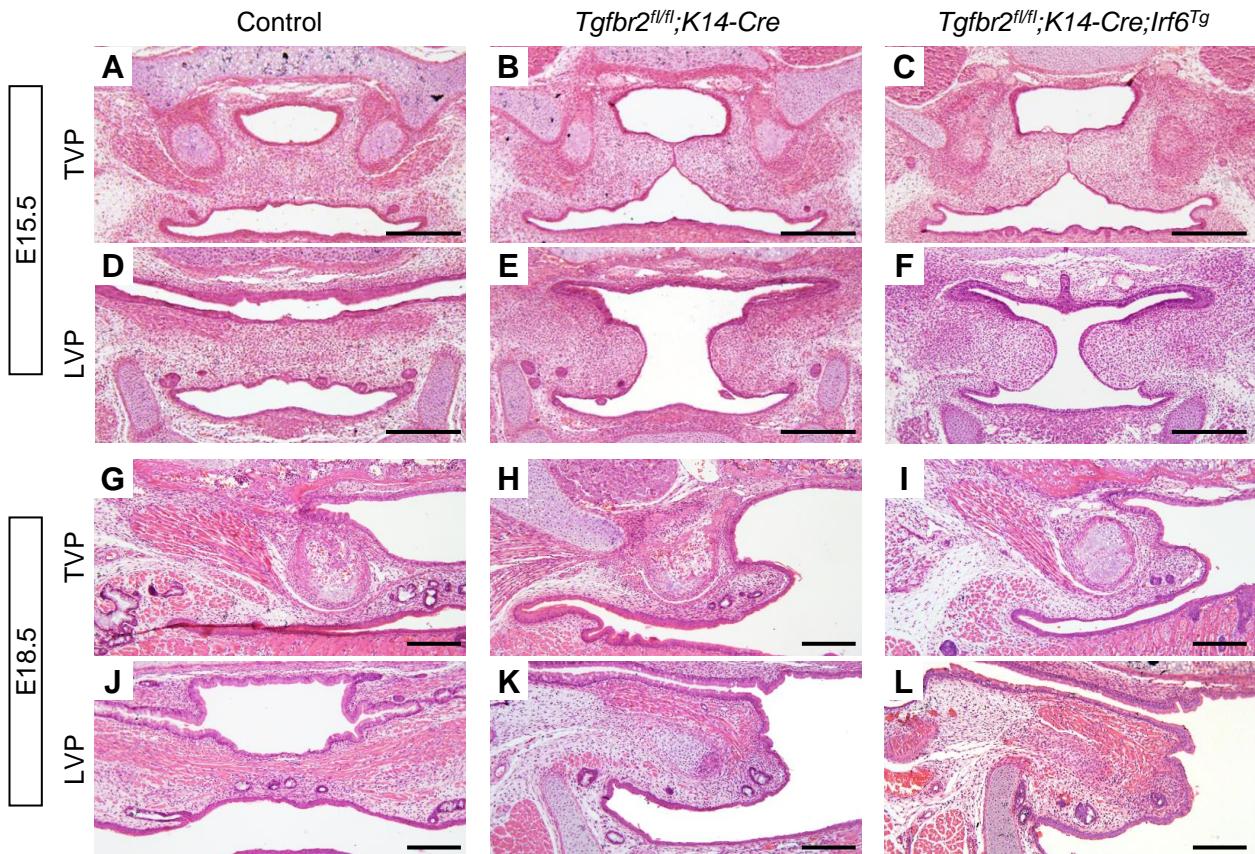


Fig. S5

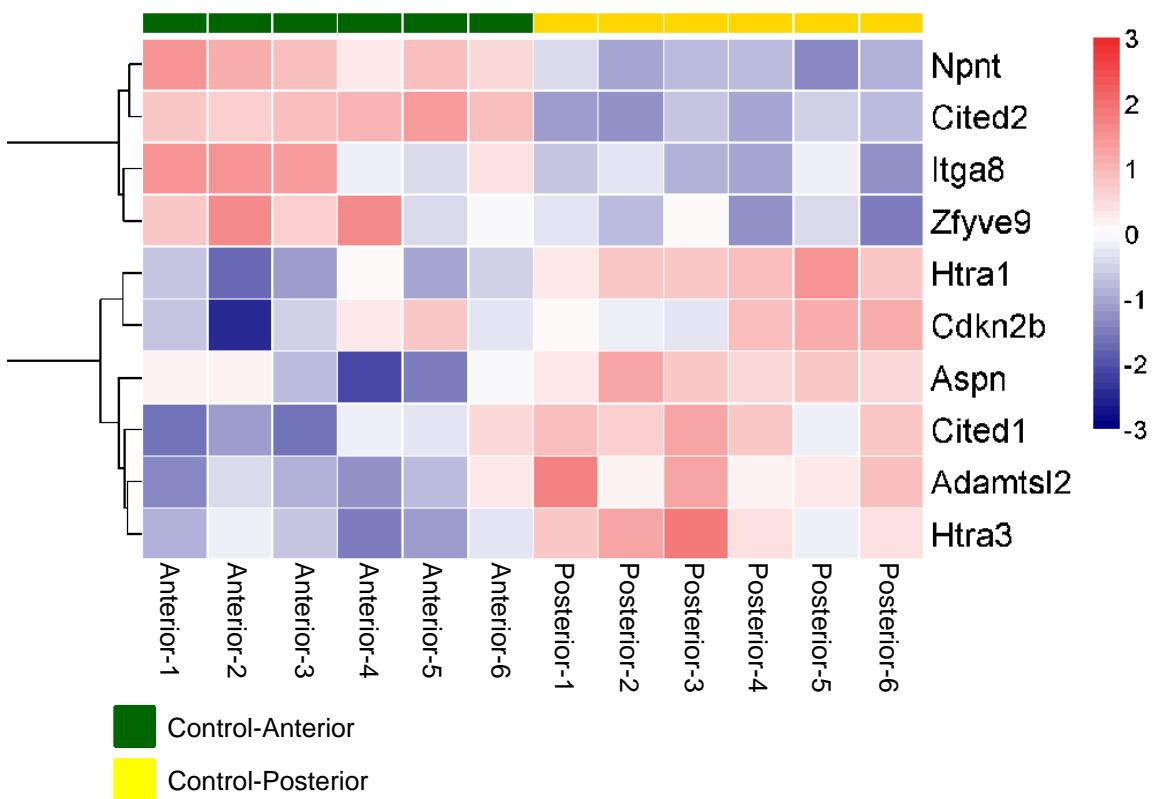
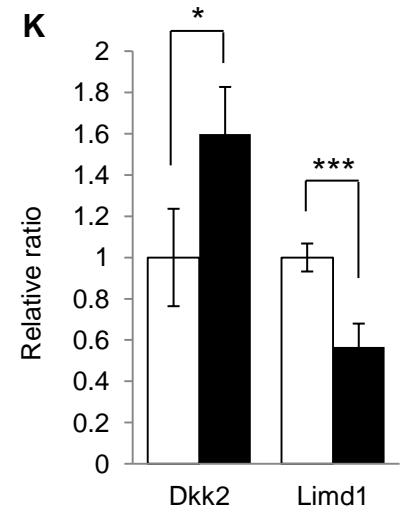
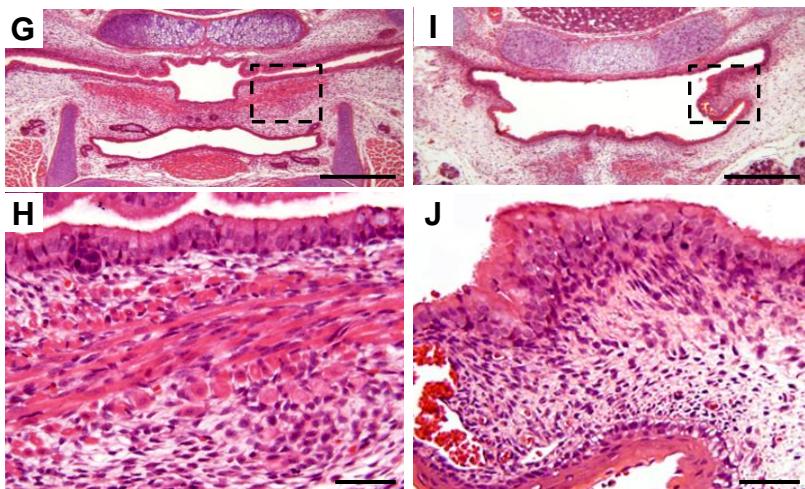
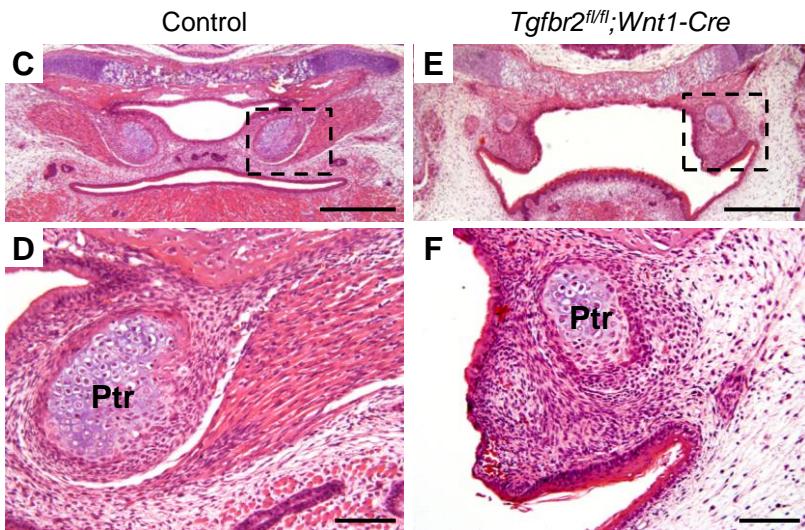
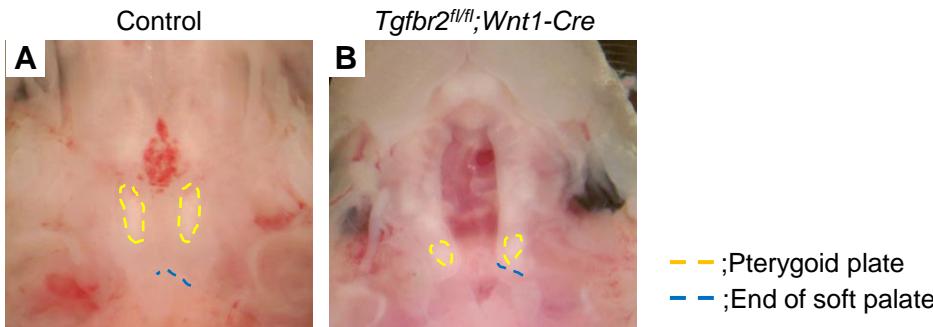
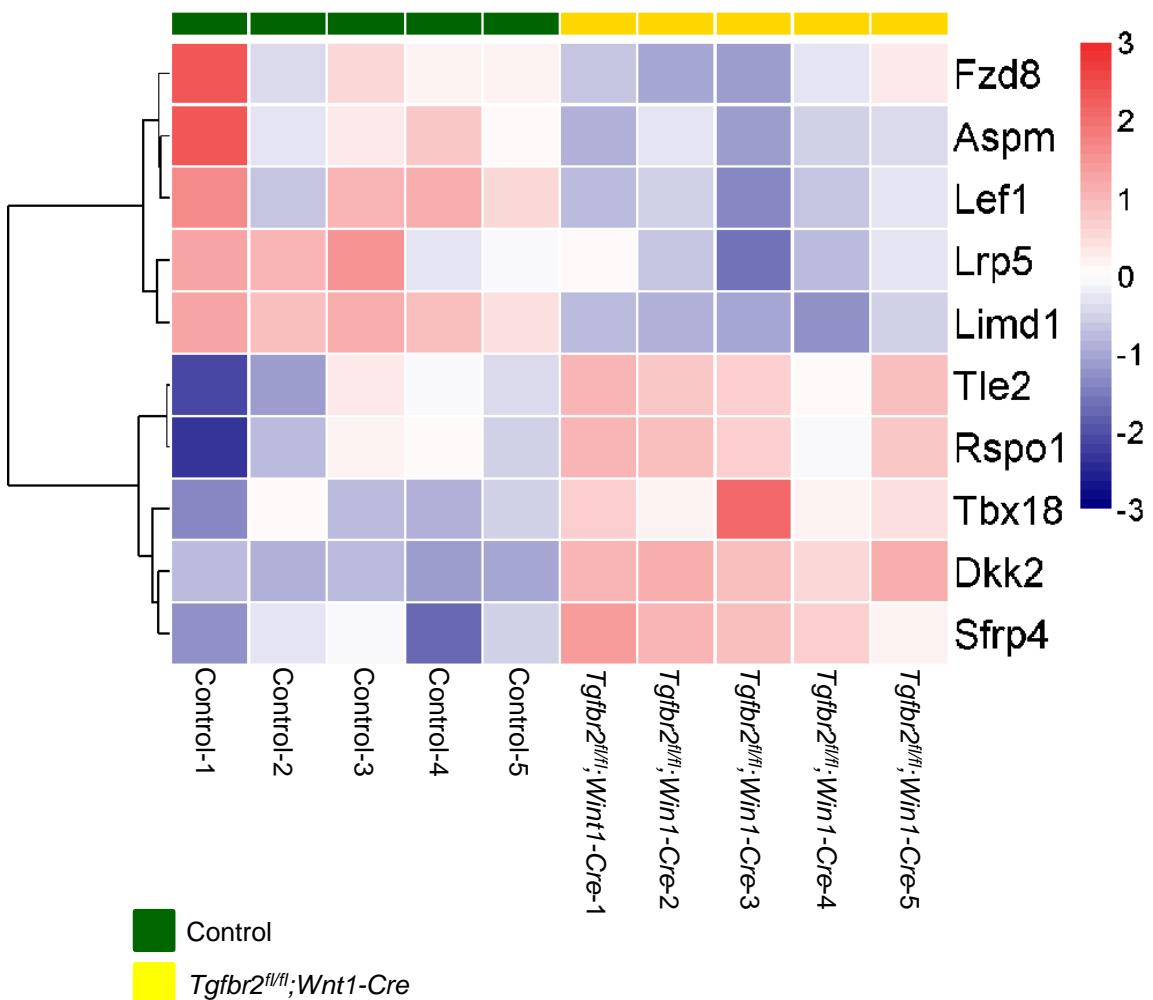


Fig. S6



□ Control  
■ *Tgfbr2<sup>fl/fl</sup>;Wnt1-Cre*

Fig. S7



Supplementary Table 1. Up-regulated genes in the soft palate of *Tgfb2<sup>fl/fl</sup>;Wnt1-Cre* mice at E15.5

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1416645_a_at	Afp	9.94	448.87	45.149	0.000
1425614_x_at	H2-D1	16.98	242.07	14.256	0.000
1422588_at	Krt6b	34.18	438.47	12.829	0.001
1436879_x_at	Afp	9.13	93.19	10.203	0.000
1454608_x_at	Ttr	15.31	131.94	8.617	0.000
1443746_x_at	Dmp1	284.76	2133.51	7.492	0.008
1449133_at	Sprr1a	88.45	642.80	7.268	0.001
1455913_x_at	Ttr	11.57	80.86	6.988	0.000
1427651_x_at	H2-D1	17.11	118.96	6.951	0.000
1422253_at	Col10a1	18.99	129.91	6.842	0.037
1416646_at	Afp	28.58	191.28	6.694	0.001
1426175_a_at	Tpsab1	25.08	160.92	6.416	0.000
1449466_at	Clec3b	53.81	330.09	6.134	0.000
1443745_s_at	Dmp1	547.08	3172.86	5.800	0.031
1439483_at	Al506816	19.11	110.34	5.773	0.000
1437344_x_at	Krt13	160.11	916.35	5.723	0.006
1425447_at	Dkk4	30.67	171.78	5.602	0.010
1455848_at	Tmprss11a	65.32	354.39	5.425	0.004
1435760_at	Csta	12.43	66.08	5.318	0.000
1422454_at	Krt13	906.58	4717.33	5.203	0.005
1417614_at	Ckm	380.21	1957.40	5.148	0.015
1422401_at	Sprr3	52.63	270.32	5.136	0.000
1435761_at	BC100530	239.97	1190.49	4.961	0.013
1459737_s_at	Ttr	16.98	83.61	4.925	0.001
1429540_at	Cnfn	44.85	212.08	4.728	0.000
1430567_at	Spink5	10.72	50.66	4.727	0.000
1421979_at	Phex	164.99	777.59	4.713	0.001
1440852_at	Idi2	18.66	86.77	4.651	0.001
1452544_x_at	H2-D1	77.37	352.51	4.556	0.000
1417461_at	Cap1	414.68	1873.95	4.519	0.000
1457936_at	Mapk8	22.26	100.57	4.518	0.000
1453801_at	Them5	21.06	91.71	4.355	0.003
1451258_at	Psca	44.21	191.84	4.339	0.000
1451447_at	Cuedc1	43.16	186.89	4.330	0.000
1426005_at	Dmp1	93.77	404.75	4.316	0.012
1431035_at	Daam1	32.57	127.82	3.925	0.000
1441863_x_at	Krt13	82.94	315.29	3.801	0.039
1418735_at	Krt4	835.48	3171.82	3.796	0.002
1436329_at	Egr3	33.47	126.31	3.774	0.001
1460285_at	Itga9	88.98	325.27	3.655	0.000
1444638_at	Ttn	24.30	86.78	3.571	0.046
1437517_x_at	Serpibnb3a	13.26	46.68	3.521	0.001
1438394_x_at	Krt4	1360.77	4755.36	3.495	0.001
1419527_at	Comp	41.11	143.34	3.486	0.039
1436755_at	Itih5	37.74	131.57	3.486	0.003
1450633_at	Calm4	51.19	176.82	3.454	0.003
1418511_at	Dpt	454.80	1562.51	3.436	0.002
1429159_at	Itih5	222.65	764.76	3.435	0.000
1456498_at	Itga4	20.14	68.89	3.421	0.003
1433804_at	Jak1	66.01	224.56	3.402	0.000
1419082_at	Serpibnb2	21.20	70.38	3.320	0.044

Supplementary Table 1. Up-regulated genes in the soft palate of *Tgfb2<sup>fl/fl</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
X00686_3_at	---	3337.28	11047.70	3.310	0.001
1449937_at	Pp11r	48.82	158.61	3.249	0.027
1417462_at	Cap1	198.94	644.81	3.241	0.000
1441946_at	Itih5	78.35	253.70	3.238	0.005
1438683_at	Wasf2	77.14	249.39	3.233	0.000
1418172_at	Hebp1	530.32	1702.26	3.210	0.000
1425538_x_at	Ceacam1	141.73	454.30	3.205	0.017
1435998_at	Ccnb1ip1	17.21	55.07	3.200	0.000
1418189_s_at	Malat1	1251.13	3997.75	3.195	0.001
1444083_at	Ttn	64.31	205.41	3.194	0.047
1445226_at	BC023969	32.06	102.14	3.186	0.000
1415931_at	Igf2	145.18	459.23	3.163	0.000
1438207_at	Gbf1	32.96	104.08	3.158	0.000
1454660_at	1100001E04Rik	133.22	420.45	3.156	0.038
1438840_x_at	Apoa1	35.55	111.07	3.125	0.009
1435639_at	2610528A11Rik	89.92	279.45	3.108	0.040
1458000_at	Dsg1a	44.86	138.95	3.098	0.013
1457266_at	---	90.45	278.96	3.084	0.000
1456120_at	Secisbp2l	40.74	125.58	3.083	0.000
1422908_at	Atp1b4	168.28	513.48	3.051	0.041
1421933_at	Cbx5	70.52	214.66	3.044	0.000
1450009_at	Ltf	94.66	287.47	3.037	0.040
1419276_at	Enpp1	27.70	83.55	3.016	0.001
1453084_s_at	Col22a1	335.23	1005.85	3.001	0.022
1449938_at	Pp11r	75.24	224.72	2.986	0.039
1435129_at	---	687.11	2049.12	2.982	0.001
1457359_at	Inpp4b	16.84	50.07	2.972	0.000
1441955_s_at	LOC676674	60.03	177.69	2.960	0.040
1440248_at	Casc4	23.79	69.99	2.942	0.003
1437127_at	A630033E08Rik	41.91	122.66	2.927	0.000
1419150_at	Myf6	57.20	167.41	2.927	0.044
1455201_x_at	Apoa1	33.33	97.24	2.918	0.003
1449894_at	Lrrc18	20.58	60.05	2.917	0.021
1418608_at	Calm13	485.22	1415.16	2.917	0.038
1426268_at	C130090K23Rik	31.42	91.45	2.911	0.000
1451999_at	Ldb3	87.15	252.99	2.903	0.045
1448469_at	Nid1	125.58	357.23	2.845	0.001
1426152_a_at	Kitl	66.32	187.82	2.832	0.008
1428301_at	100041874	260.52	735.83	2.824	0.008
1452470_at	Cep350	44.47	125.30	2.818	0.001
1422123_s_at	Ceacam1	267.60	752.61	2.812	0.015
1427797_s_at	EG665955	46.41	129.36	2.787	0.037
1450494_x_at	Ceacam1	150.93	420.46	2.786	0.026
1441125_at	Setd5	21.17	58.76	2.775	0.000
1428781_at	Dmkn	618.32	1704.69	2.757	0.041
1423594_a_at	Ednrb	93.47	257.24	2.752	0.001
1434227_at	Krtdap	615.10	1685.47	2.740	0.037
1417160_s_at	Expi	44.56	120.46	2.703	0.046
1427711_a_at	Ceacam1	20.52	55.25	2.693	0.039
1421153_at	Loxl4	53.17	143.06	2.691	0.003
1446342_at	2310001H17Rik	10.21	27.16	2.660	0.000

Supplementary Table 1. Up-regulated genes in the soft palate of *Tgfb2<sup>fl/fl</sup>*; *Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1431281_at	Dysfip1	32.97	87.63	2.658	0.042
1418188_a_at	Malat1	667.65	1769.07	2.650	0.011
1417979_at	Tnmd	221.27	585.50	2.646	0.007
1442075_at	Al314604	36.45	96.32	2.642	0.010
1450078_at	Nrk	234.37	617.57	2.635	0.012
1423669_at	Col1a1	1881.55	4954.59	2.633	0.003
1422749_at	Ly6g6c	30.49	80.00	2.624	0.037
1425675_s_at	Ceacam1	45.58	119.11	2.613	0.039
1417814_at	Pla2g5	33.91	88.54	2.611	0.000
1427630_x_at	Ceacam1	107.88	281.00	2.605	0.030
1424808_at	Lama4	19.11	49.33	2.582	0.000
1422672_at	Sprr1b	9.26	23.90	2.580	0.024
1456088_at	Xiap	67.78	174.60	2.576	0.000
1421955_a_at	Nedd4	2204.01	5673.27	2.574	0.000
1427306_at	Ryr1	44.49	114.04	2.563	0.039
1444504_at	Dhrs7c	73.61	188.17	2.556	0.046
1443921_at	Ranbp3l	27.43	70.06	2.554	0.005
1425764_a_at	Bcat2	81.35	207.23	2.547	0.000
1440339_at	Enpp1	38.38	97.67	2.545	0.011
1421413_a_at	Pdlim5	95.05	239.49	2.520	0.040
1448228_at	Lox	1198.61	3019.95	2.520	0.006
1428909_at	A130040M12Rik	54.42	136.65	2.511	0.004
1455516_at	---	34.40	86.19	2.506	0.000
1460256_at	Car3	250.08	626.22	2.504	0.010
1448602_at	Pygm	70.13	175.53	2.503	0.041
1416930_at	Ly6d	647.24	1616.63	2.498	0.040
1443832_s_at	Sdpr	214.55	534.88	2.493	0.012
1457262_at	Smg1	58.12	144.84	2.492	0.000
1418175_at	Vdr	42.70	105.88	2.479	0.001
1448415_a_at	Sema3b	116.30	286.83	2.466	0.000
1450377_at	LOC640441	73.61	180.78	2.456	0.002
1434722_at	Ampd1	44.40	108.86	2.452	0.046
1429700_at	3110040M04Rik	13.53	33.16	2.451	0.003
1421851_at	Mtap1b	47.81	116.90	2.445	0.010
1430841_at	3300002P13Rik	34.03	83.15	2.443	0.029
1421290_at	Hspb7	29.04	70.79	2.438	0.002
1434927_at	Hspb7	30.50	74.28	2.436	0.006
1452731_x_at	100041874	158.81	386.02	2.431	0.037
1427371_at	Abca8a	166.42	401.91	2.415	0.001
1420360_at	Dkk1	209.73	506.44	2.415	0.045
1436544_at	Atp10d	110.88	267.69	2.414	0.000
1438363_at	Pnmal2	43.19	103.40	2.394	0.006
1427919_at	Srpx2	41.84	100.10	2.392	0.004
1419233_x_at	Apoa1	57.00	136.35	2.392	0.025
1450179_at	Sost	43.93	105.03	2.391	0.001
1419232_a_at	Apoa1	28.34	67.45	2.380	0.004
1422866_at	Col13a1	130.37	309.15	2.371	0.032
1451878_a_at	Jmy	16.72	39.58	2.367	0.002
1419560_at	Lipc	23.35	55.12	2.361	0.000
1417933_at	Igfbp6	46.31	108.95	2.353	0.043

Supplementary Table 1. Up-regulated genes in the soft palate of *Tgfb2<sup>fl/fl</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1455466_at	Gpr133	61.49	144.57	2.351	0.041
1423578_at	Col11a2	153.16	359.65	2.348	0.043
1419312_at	Atp2a1	211.31	495.97	2.347	0.040
1449880_s_at	Bglap-rs1	358.51	840.48	2.344	0.039
1418690_at	Ptprz1	12.93	30.23	2.337	0.002
1448367_at	Sdf4	69.84	162.91	2.333	0.000
1450051_at	Atrx	92.47	215.57	2.331	0.006
1417355_at	Peg3	1739.46	4049.63	2.328	0.001
1422546_at	Ilf3	109.77	255.46	2.327	0.000
1455593_at	Apob	14.14	32.89	2.326	0.008
1460302_at	Thbs1	254.61	591.19	2.322	0.000
1420408_a_at	Abcc9	13.41	31.10	2.318	0.009
1441384_at	Gadl1	32.06	74.17	2.313	0.003
1449862_a_at	Pi4k2b	47.72	110.02	2.305	0.042
1438588_at	Plagl1	65.30	150.42	2.303	0.007
1440150_at	Tgm3	59.79	137.64	2.302	0.005
1420097_at	D13Ertd787e	48.82	112.34	2.301	0.048
1459897_a_at	Sbsn	377.74	867.01	2.295	0.011
1450093_s_at	Zbtb7a	87.03	198.69	2.283	0.000
1459804_at	Crebbp	23.60	53.72	2.276	0.006
1430786_at	1110002E22Rik	99.86	227.28	2.276	0.048
1426498_at	Kdm5c	31.44	71.42	2.272	0.004
1437904_at	Rbm45	241.28	547.63	2.270	0.008
1436858_at	Mbnl2	168.51	381.77	2.265	0.000
1418280_at	Klf6	120.21	271.88	2.262	0.007
1443621_at	Xaf1	12.87	29.04	2.256	0.040
1447360_at	Tsc22d1	8.46	19.02	2.248	0.006
1452284_at	Ptprz1	242.38	544.68	2.247	0.000
1441111_at	---	132.26	296.37	2.241	0.047
1422481_at	Krt1	177.77	397.80	2.238	0.050
1435752_s_at	Abcc9	152.96	341.97	2.236	0.037
1416321_s_at	Prelp	48.50	108.09	2.229	0.010
1423886_at	Lamc1	58.00	129.13	2.226	0.000
1423760_at	Cd44	396.54	876.01	2.209	0.009
1436731_at	Zfp385b	108.83	239.66	2.202	0.023
1433745_at	Trio	554.71	1214.96	2.190	0.000
1427177_at	Fyco1	110.44	241.53	2.187	0.000
1425544_at	Plekha5	75.70	165.43	2.185	0.000
1427950_at	Rnf160	47.30	103.35	2.185	0.001
1418176_at	Vdr	57.82	125.61	2.172	0.000
1417552_at	Fap	371.18	805.10	2.169	0.007
1453345_at	Nipal1	49.46	106.95	2.162	0.026
1416455_a_at	Cryab	282.48	609.94	2.159	0.041
1459929_at	Zfp568	52.52	112.93	2.150	0.039
1436399_s_at	Nrk	70.13	150.75	2.150	0.037
1428662_a_at	Hopx	511.14	1096.35	2.145	0.038
1432269_a_at	Sh3kbp1	27.14	58.19	2.144	0.004
1436521_at	Slc36a2	46.92	100.55	2.143	0.010
1429357_at	Fam135a	17.05	36.49	2.141	0.000
1417626_at	Pde4dip	85.20	181.14	2.126	0.047

Supplementary Table 1. Up-regulated genes in the soft palate of *Tgfb2<sup>fl/fl</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1436037_at	Itga4	141.28	300.21	2.125	0.004
1422834_at	Kcnd2	18.43	39.16	2.125	0.030
1426285_at	Lama2	200.51	424.72	2.118	0.002
1427789_s_at	Gnas	34.04	71.91	2.113	0.012
1417956_at	Cidea	48.21	101.65	2.109	0.010
1442819_at	Rhbdl2	75.17	158.42	2.108	0.002
1449311_at	Bach1	81.79	172.32	2.107	0.000
1441333_at	---	8.22	17.29	2.104	0.026
1440879_at	Abca9	171.87	360.80	2.099	0.004
1438271_at	Lpp	43.09	90.43	2.099	0.024
1423407_a_at	Fbln2	730.79	1531.86	2.096	0.001
1416697_at	Dpp4	74.63	156.41	2.096	0.002
1431211_s_at	Them5	42.84	89.62	2.092	0.034
1449716_s_at	Nrd1	123.86	258.72	2.089	0.000
1424112_at	Igf2r	1161.71	2422.21	2.085	0.000
1460125_at	---	84.77	176.69	2.084	0.050
1439630_x_at	Sbsn	350.13	729.08	2.082	0.027
1432393_a_at	Thg11	154.49	321.52	2.081	0.000
1420371_at	Sntb2	42.08	87.46	2.078	0.028
1419088_at	Timp3	48.12	99.83	2.074	0.000
1449434_at	Car3	1806.24	3742.59	2.072	0.040
1460426_at	Pde4dip	27.36	56.62	2.069	0.002
1451382_at	Chac1	70.37	145.59	2.069	0.014
1425218_a_at	Scgb3a2	91.29	188.87	2.069	0.000
1423065_at	Dnmt3a	282.70	584.68	2.068	0.002
1439555_at	Rlf	23.32	48.08	2.061	0.003
1449396_at	Aoc3	32.04	66.02	2.060	0.042
1429400_at	Clcn5	549.96	1131.26	2.057	0.003
1422882_at	Sypl	84.53	173.70	2.055	0.000
1429332_at	4632427E13Rik	11.42	23.39	2.049	0.004
1427019_at	Ptprz1	158.97	325.13	2.045	0.000
1456351_at	Brd8	44.60	91.20	2.045	0.000
1437536_at	Fkrp	29.29	59.70	2.039	0.003
1456537_at	A930033H14Rik	20.85	42.50	2.038	0.000
1425338_at	Plcb4	22.56	45.97	2.038	0.001
1415964_at	Scd1	179.70	366.19	2.038	0.000
1421190_at	Gabrb3	9.31	18.96	2.036	0.005
1416062_at	Tbc1d15	107.12	217.77	2.033	0.000
1450068_at	Baz1b	35.87	72.93	2.033	0.038
1434605_at	Eif5b	191.91	389.83	2.031	0.001
1420417_at	Gm2521	39.17	79.53	2.030	0.001
1449563_at	Cntn1	50.58	102.66	2.030	0.038
1437422_at	Sema5a	221.75	448.32	2.022	0.011
1456863_at	Epha4	12.11	24.45	2.019	0.002
1438667_at	5730410E15Rik	55.36	111.62	2.016	0.037
1451204_at	Scara5	148.39	298.52	2.012	0.020
1416551_at	Atp2a2	674.81	1353.21	2.005	0.017
1418403_at	Adam19	51.42	103.11	2.005	0.000
1419292_at	Htra3	266.66	534.14	2.003	0.001
1457270_at	Gas7	68.42	136.99	2.002	0.002
1419703_at	Col5a3	49.39	98.86	2.002	0.047

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1438955_x_at	Ppif	149.78	74.85	-2.001	0.001
1429222_at	Pus3	69.75	34.85	-2.001	0.007
1436726_s_at	Sptlc1	434.96	216.77	-2.007	0.044
1437132_x_at	Nedd9	680.57	338.40	-2.011	0.014
1453977_at	Exoc4	19.46	9.67	-2.013	0.000
1416886_at	C1d	190.39	94.56	-2.013	0.001
1416422_a_at	Ssb	598.06	296.29	-2.019	0.030
1416476_a_at	Ube2d2	4564.64	2251.26	-2.028	0.039
1419401_at	Asb13	67.54	33.24	-2.032	0.039
1418487_at	Ripk4	271.18	133.45	-2.032	0.017
1452713_a_at	Snrnp40	4596.19	2252.37	-2.041	0.027
1418656_at	Lsm5	3774.38	1848.42	-2.042	0.008
1429145_at	Nhlrc2	238.43	116.63	-2.044	0.037
1434578_x_at	LOC100045999	8210.53	4012.54	-2.046	0.040
1435164_s_at	Uba3	1567.23	764.50	-2.050	0.039
1423747_a_at	Pdk1	1090.85	531.76	-2.051	0.041
1436600_at	Tox3	526.01	256.40	-2.052	0.011
1425149_a_at	Pdcl	1353.03	657.97	-2.056	0.001
1459646_at	Hs3st6	204.99	99.41	-2.062	0.000
1438841_s_at	Arg2	33.18	16.05	-2.068	0.029
1438921_at	Atr	33.84	16.34	-2.071	0.000
1443153_at	Trip11	31.19	15.04	-2.073	0.000
1433568_at	Papd4	357.26	171.98	-2.077	0.017
1454951_at	Zfp606	352.63	169.62	-2.079	0.016
1441107_at	Dmrta2	755.30	363.03	-2.081	0.037
1459742_at	---	20.38	9.74	-2.094	0.000
1428162_at	4933421E11Rik	421.67	201.41	-2.094	0.004
1460244_at	Upb1	103.56	49.45	-2.094	0.001
1460399_at	Ccdc117	223.68	106.76	-2.095	0.000
1416152_a_at	Sfrs3	2665.79	1269.02	-2.101	0.009
1437914_at	E2f6	234.06	110.96	-2.109	0.000
1438349_at	Zfp229	259.13	122.78	-2.111	0.011
1434636_at	Homez	82.48	39.07	-2.111	0.028
1435252_at	B3galt6	123.88	58.65	-2.112	0.009
1429372_at	Sox11	751.69	354.20	-2.122	0.000
1455261_at	Luc7l	254.64	119.89	-2.124	0.000
1434045_at	Cdkn1b	1059.02	498.16	-2.126	0.003
1454838_s_at	Pkdcc	2387.09	1122.67	-2.126	0.018
1438659_x_at	Chchd6	1828.70	858.15	-2.131	0.006
1449482_at	Hist3h2ba	751.11	351.96	-2.134	0.039
1453136_at	Fbxo30	179.28	83.66	-2.143	0.037
1435523_s_at	2700089E24Rik	225.66	105.19	-2.145	0.040
1437490_x_at	LOC640502	407.39	189.86	-2.146	0.044
1424694_at	2010011I20Rik	202.03	93.93	-2.151	0.000
1426471_at	Zfp52	303.63	140.98	-2.154	0.000
1452593_a_at	Tceb1	206.37	95.80	-2.154	0.001
1437164_x_at	Atp5o	4214.53	1951.96	-2.159	0.023
1423422_at	Asb4	744.38	344.55	-2.160	0.007
1420726_x_at	Tmlhe	100.98	46.59	-2.167	0.032
1433757_a_at	Nisch	229.98	105.99	-2.170	0.002

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1428603_at	Gm16039	663.80	305.67	-2.172	0.000
1429436_at	Prpf40a	419.59	193.03	-2.174	0.008
1430135_at	Dnase2a	65.60	30.07	-2.182	0.001
1439558_at	Zfp317	122.29	56.03	-2.183	0.009
1439428_x_at	Gmds	178.21	81.64	-2.183	0.041
1440342_at	G530011O06Rik	49.96	22.87	-2.185	0.000
1460354_a_at	Mrpl13	2124.04	971.75	-2.186	0.005
1456735_x_at	Acpl2	1394.07	637.12	-2.188	0.000
1449128_at	Ccdc43	186.17	84.91	-2.193	0.027
1435532_at	LOC100048362	143.52	65.46	-2.193	0.020
1437168_at	RP23-12I24.6	156.03	71.01	-2.197	0.048
1434067_at	Al662270	105.60	47.98	-2.201	0.004
1451511_at	Hibch	85.34	38.63	-2.209	0.033
1444248_at	Rcn2	73.89	33.38	-2.213	0.000
1416267_at	Scoc	901.23	405.79	-2.221	0.041
1438511_a_at	1190002H23Rik	466.76	210.08	-2.222	0.001
1428224_at	Hnrpd1	522.25	234.68	-2.225	0.037
1422881_s_at	Sypl	1541.88	692.09	-2.228	0.044
1445274_at	Zfp781	92.39	41.46	-2.228	0.000
1430569_at	Ttc9c	97.70	43.84	-2.229	0.050
1452091_a_at	Rbm28	448.07	200.94	-2.230	0.000
1455433_at	3110048L19Rik	258.18	115.62	-2.233	0.003
1440353_at	Ntf5	394.34	176.34	-2.236	0.042
1418525_at	Pcm1	198.79	88.85	-2.237	0.002
1454842_a_at	B3galnt2	340.41	152.05	-2.239	0.012
1429335_at	Snapc1	315.36	140.75	-2.240	0.000
1418190_at	Pon1	91.34	40.72	-2.243	0.007
1425495_at	Zfp62	286.18	127.48	-2.245	0.044
1435435_at	Ctnnbp2	145.71	64.83	-2.248	0.001
1460218_at	Cd52	419.37	186.20	-2.252	0.000
1451181_at	Tmem121	360.94	159.95	-2.257	0.000
1441890_x_at	Tmeff1	172.27	76.25	-2.259	0.024
1429490_at	Rif1	245.85	108.26	-2.271	0.012
1439475_at	Zfp429	131.73	57.94	-2.274	0.000
1423804_a_at	Idi1	535.69	235.11	-2.279	0.030
1441941_x_at	Serpinb5	526.83	231.06	-2.280	0.047
1456736_x_at	Mff	3806.07	1666.54	-2.284	0.001
1428304_at	Esco2	251.37	110.00	-2.285	0.031
1440125_at	A530054K11Rik	42.90	18.65	-2.300	0.008
1434014_at	Atg4c	228.01	99.07	-2.301	0.000
1452426_x_at	---	18.15	7.88	-2.304	0.000
1437286_x_at	1110020G09Rik	91.25	39.55	-2.307	0.042
1454885_at	BC063263	130.14	56.38	-2.308	0.001
1418138_at	Sult1d1	25.77	11.14	-2.314	0.000
1448609_at	Tst	1326.02	572.34	-2.317	0.040
1436684_a_at	Riok2	605.18	261.05	-2.318	0.001
1453070_at	Pcdh17	267.68	114.84	-2.331	0.042
1456698_s_at	Hnrpd1	2775.18	1189.48	-2.333	0.039
1441797_at	---	45.26	19.32	-2.342	0.005
1456244_x_at	Glx3	3061.48	1305.02	-2.346	0.002

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1455883_a_at	Lrrtm1	861.38	366.58	-2.350	0.042
1416179_a_at	Rdx	3278.56	1393.00	-2.354	0.048
1433866_x_at	Prdx1	7822.40	3323.55	-2.354	0.044
1447202_at	1200009F10Rik	110.23	46.81	-2.355	0.000
1424409_at	Cldn23	646.43	274.17	-2.358	0.043
1457278_at	6720489N17Rik	48.87	20.73	-2.358	0.000
1454402_at	3110048L19Rik	16.16	6.85	-2.358	0.001
1451931_x_at	H2-L	618.59	262.19	-2.359	0.010
1430357_at	H3f3b	260.50	110.39	-2.360	0.024
1453749_at	2610507I01Rik	92.48	39.18	-2.361	0.001
1435471_at	Zfp708	127.00	53.74	-2.363	0.000
1449152_at	Cdkn2b	204.15	86.37	-2.364	0.005
1447977_x_at	3100002L24Rik	272.29	115.01	-2.368	0.001
1424264_at	Med6	528.68	223.24	-2.368	0.022
1429285_at	Serpina9	95.28	40.19	-2.371	0.038
1438487_s_at	Zzz3	485.96	204.73	-2.374	0.044
1418428_at	Kif5b	1080.43	454.94	-2.375	0.046
1438455_at	Pabpc4l	335.48	141.13	-2.377	0.040
1447825_x_at	Pcdh8	301.33	126.68	-2.379	0.005
1437711_x_at	Gm6742	3135.44	1317.05	-2.381	0.049
1450140_a_at	Cdkn2a	32.96	13.72	-2.402	0.001
1437461_s_at	Rnpc3	521.14	215.89	-2.414	0.001
1450896_at	Arhgap5	478.50	197.91	-2.418	0.039
1438786_a_at	2610021A01Rik	252.83	104.56	-2.418	0.011
1426593_a_at	Fbxo22	1295.73	534.25	-2.425	0.039
1417208_at	Amacr	428.89	176.08	-2.436	0.000
1428586_at	Tmem41b	236.23	96.63	-2.445	0.042
1453245_at	9130024F11Rik	117.56	47.84	-2.458	0.000
1453040_at	Mcart6	195.08	79.33	-2.459	0.000
1423487_at	Cript	27.81	11.31	-2.459	0.000
1418499_a_at	Kcne3	496.40	201.21	-2.467	0.000
1426243_at	Cth	279.81	113.40	-2.467	0.000
1454642_a_at	Commd3	1880.03	761.69	-2.468	0.038
1438754_at	---	50.90	20.56	-2.475	0.001
1457044_at	Macc1	172.56	69.41	-2.486	0.006
1454701_at	4930503L19Rik	138.52	55.53	-2.494	0.040
1437152_at	Mex3b	1512.21	605.64	-2.497	0.038
1436981_a_at	Ywhaz	646.91	259.06	-2.497	0.039
1423832_at	Prkag2	106.59	42.58	-2.503	0.003
1451065_a_at	Ddx39	2234.19	891.38	-2.506	0.020
1438984_x_at	Psmb4	5731.91	2281.86	-2.512	0.042
1437911_at	6330416L07Rik	147.37	58.66	-2.512	0.000
1447837_x_at	Polh	535.60	213.09	-2.513	0.005
1425315_at	Dock7	53.18	21.10	-2.520	0.001
1416826_a_at	Med20	879.44	346.86	-2.535	0.000
1453568_at	Dapl1	917.86	361.88	-2.536	0.015
1428375_at	4932415G12Rik	111.20	43.83	-2.537	0.000
1452348_s_at	Gm2785	57.55	22.68	-2.538	0.008
1437285_at	1110020G09Rik	73.00	28.73	-2.540	0.024
1447703_x_at	Zfp593	688.95	270.23	-2.549	0.000

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1454898_s_at	Iah1	776.86	304.24	-2.553	0.010
1425646_at	BC016495	62.76	24.51	-2.560	0.000
1423792_a_at	Cmtm6	450.31	175.70	-2.563	0.046
1452876_x_at	2610044O15Rik	167.59	64.91	-2.582	0.004
1424292_at	Depdc1a	547.72	211.48	-2.590	0.002
1456032_x_at	Gm8203	4913.88	1896.96	-2.590	0.039
1436330_x_at	Gm7072	229.29	87.12	-2.632	0.000
1439442_x_at	Yars2	329.23	125.07	-2.632	0.005
1451683_x_at	H2-D1	81.72	30.98	-2.638	0.000
1448716_at	Hba-x	504.97	190.72	-2.648	0.012
1416290_a_at	Psmc4	4243.79	1602.07	-2.649	0.024
1436390_a_at	Clcc1	508.30	191.33	-2.657	0.041
1420725_at	Tmlhe	120.72	45.36	-2.661	0.009
1423142_a_at	Gtpbp4	704.05	263.93	-2.668	0.040
1433453_a_at	Abtb2	515.24	192.19	-2.681	0.039
1455384_x_at	D030056L22Rik	607.57	226.24	-2.686	0.000
1438922_x_at	Gm5256	1275.03	468.95	-2.719	0.014
1450717_at	Ang	92.82	34.10	-2.722	0.000
1458667_at	Ninl	40.83	14.98	-2.726	0.022
1435661_at	Als2cr4	808.81	295.86	-2.734	0.045
1428693_at	2610044O15Rik	181.56	66.25	-2.741	0.002
1444589_at	Gm4944	136.37	49.74	-2.742	0.000
1429007_at	Slc35b2	163.69	59.22	-2.764	0.000
1452083_a_at	Pja1	760.74	275.14	-2.765	0.039
1439406_x_at	Fars2	166.66	60.26	-2.766	0.018
1456862_at	Six4	332.30	119.39	-2.783	0.043
1428490_at	C1galt1	407.23	146.15	-2.786	0.001
1431708_a_at	Tia1	149.23	52.94	-2.819	0.014
14117845_at	Cldn6	558.47	197.65	-2.826	0.009
1439753_x_at	Six4	329.77	116.63	-2.828	0.047
1423640_at	Synpr	206.45	72.96	-2.830	0.001
1428738_a_at	D14Ertd449e	2276.36	797.75	-2.853	0.000
1431225_at	---	690.79	242.01	-2.854	0.007
1425545_x_at	H2-D1	722.88	252.52	-2.863	0.045
1434150_a_at	Higd1c	826.16	286.31	-2.886	0.008
1455213_at	Tmsb15b1-Tmsb15b2	1388.94	476.22	-2.917	0.000
1438360_x_at	Gm5256	1499.51	513.93	-2.918	0.021
1456746_a_at	Cd99l2	231.46	79.28	-2.919	0.038
1435682_at	Lars2	364.83	124.39	-2.933	0.000
1437987_at	---	89.93	30.59	-2.939	0.000
1434236_at	Zdhhc20	594.25	199.93	-2.972	0.039
1455648_at	---	293.40	98.05	-2.992	0.000
1451784_x_at	H2-D1	706.03	234.49	-3.011	0.042
1460434_at	Fundc2	302.14	100.27	-3.013	0.000
1456467_s_at	Nlk	145.68	48.28	-3.018	0.019
1422606_at	C1qtnf3	784.46	259.58	-3.022	0.042
1448872_at	Reg3g	744.31	245.36	-3.034	0.038
1437313_x_at	Hmgb2	4118.52	1355.14	-3.039	0.041
1420622_a_at	Hspa8	7052.32	2318.07	-3.042	0.039
1416166_a_at	Prdx4	2313.23	756.27	-3.059	0.040

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
1456097_a_at	Itgb3bp	398.91	130.36	-3.060	0.000
1431686_a_at	Gmfb	147.67	47.84	-3.087	0.000
1436298_x_at	Paics	2290.72	732.79	-3.126	0.050
1449153_at	Mmp12	112.92	36.00	-3.137	0.021
1435370_a_at	Ces3	193.32	61.61	-3.138	0.009
1438758_at	Adi1	599.72	191.02	-3.140	0.000
1419453_at	Uchl5	36.92	11.71	-3.152	0.000
1427151_at	Qser1	227.94	72.19	-3.158	0.049
1437172_x_at	Hadhb	1823.31	575.36	-3.169	0.047
1434700_at	G2e3	156.28	49.23	-3.175	0.000
1428414_at	Ccny	206.58	64.91	-3.182	0.000
1417222_a_at	Tmem123	1657.00	509.39	-3.253	0.048
1452473_at	Prr15	536.93	164.81	-3.258	0.020
1424573_at	Tmed5	912.33	277.63	-3.286	0.041
1425926_a_at	Otx2	162.01	49.09	-3.300	0.021
1429527_a_at	Plscr1	487.60	146.57	-3.327	0.008
1423436_at	Gsta3	613.77	183.26	-3.349	0.041
1453985_at	0610007P08Rik	77.55	23.11	-3.355	0.000
1451190_a_at	Sbk1	2057.35	612.96	-3.356	0.019
1454725_at	Tra2a	2486.09	734.41	-3.385	0.012
1437995_x_at	7-Sep	3904.94	1153.42	-3.386	0.040
14117769_at	Psmc6	301.35	88.47	-3.406	0.013
1459714_at	---	63.37	18.51	-3.424	0.000
1418940_at	Sult1b1	108.15	31.51	-3.432	0.000
1422916_at	Fgf21	130.80	38.00	-3.442	0.000
1417408_at	F3	1362.93	389.93	-3.495	0.043
1416911_a_at	Akirin1	1372.78	392.03	-3.502	0.039
1447868_x_at	Glrx3	204.34	58.33	-3.503	0.002
1455292_x_at	Rsl1	258.81	73.82	-3.506	0.000
1435884_at	Itsn1	286.63	81.00	-3.539	0.043
1421144_at	Rpgrip1	533.11	150.06	-3.553	0.000
1456532_at	Pdgfd	202.55	56.92	-3.558	0.016
1417051_at	Pcdh8	256.02	71.00	-3.606	0.000
1417069_a_at	Gmfb	354.91	98.04	-3.620	0.000
AFFX-DapX-3_at	---	6325.54	1714.60	-3.689	0.000
1429712_at	Gm14288	1108.28	297.76	-3.722	0.000
AFFX-ThrX-3_at	---	1576.30	420.50	-3.749	0.003
1430979_a_at	Prdx2	2061.53	540.40	-3.815	0.000
1460628_at	Eme2	53.14	13.93	-3.815	0.000
AFFX-r2-Bs-dap-3_at	---	6912.36	1811.01	-3.817	0.000
1457588_at	C76213	70.16	18.27	-3.840	0.000
AFFX-r2-Bs-thr-3_s_at	---	2235.19	578.84	-3.862	0.001
1437850_a_at	Cnbp	3296.98	849.45	-3.881	0.043
1460713_at	BC048355	478.54	122.88	-3.894	0.000
1459835_s_at	Dnaja1	1862.60	473.10	-3.937	0.039
1435702_s_at	Ywhae	2675.97	679.09	-3.940	0.033
AFFX-DapX-M_at	---	4183.48	1054.96	-3.966	0.000
1434452_x_at	Eif2a	855.86	215.53	-3.971	0.041

Supplementary Table 2. Down-regulated genes in the soft palate of *Tgfb2<sup>f/f</sup>;Wnt1-Cre* mice at E15.5  
 (Continued)

Probe ID	Gene Symbol	Geo Mean WT	Geo Mean Mutant	MUT POST /WT POST	FDR
AFFX-r2-Bs-thr-M_s_at	---	1126.88	276.39	-4.077	0.002
1429691_at	Ptpn2	376.57	90.80	-4.147	0.000
AFFX-PheX-3_at	---	872.55	206.92	-4.217	0.001
AFFX-r2-Bs-dap-M_at	---	4504.20	1052.55	-4.279	0.000
AFFX-ThrX-5_at	---	593.43	129.78	-4.572	0.007
1457352_x_at	Svopl	95.99	20.80	-4.615	0.000
AFFX-r2-Bs-thr-5_s_at	---	631.82	134.39	-4.702	0.011
1437502_x_at	Cd24a	3584.35	762.00	-4.704	0.044
14117797_a_at	1810019J16Rik	504.94	106.61	-4.736	0.001
1416187_s_at	Pnrc2	3101.09	633.71	-4.894	0.040
AFFX-ThrX-M_at	---	836.86	169.63	-4.933	0.001
1439059_at	BC031748	136.24	27.49	-4.957	0.007
AFFX-r2-Bs-dap-5_at	---	2362.96	476.40	-4.960	0.003
1449033_at	Tnfrsf11b	180.27	36.30	-4.966	0.009
1460668_at	Gal	987.26	194.42	-5.078	0.001
1437128_a_at	A630033E08Rik	97.35	19.03	-5.116	0.000
1439780_at	Rpl7l1	230.12	44.84	-5.131	0.001
AFFX-r2-Bs-phe-3_at	---	1213.76	235.88	-5.146	0.000
1456688_at	---	55.99	10.82	-5.174	0.000
AFFX-DapX-5_at	---	1746.51	334.87	-5.215	0.002
1448973_at	Sult1d1	93.95	17.69	-5.311	0.000
1437726_x_at	C1qb	902.07	165.92	-5.437	0.000
AFFX-LysX-3_at	---	1167.31	212.73	-5.487	0.000
AFFX-LysX-M_at	---	587.92	103.49	-5.681	0.000
AFFX-PheX-M_at	---	835.21	144.51	-5.780	0.000
1439415_x_at	Gm5963	1162.09	200.25	-5.803	0.040
1437262_x_at	Bcas2	329.20	56.34	-5.843	0.031
1422716_a_at	Acp1	580.72	97.23	-5.972	0.038
1436107_at	Lsm8	122.19	19.16	-6.379	0.000
AFFX-r2-Bs-lys-3_at	---	535.14	83.66	-6.397	0.000
1447831_s_at	Mtmm7	133.12	20.75	-6.416	0.000
1438238_at	2010315B03Rik	184.53	27.73	-6.655	0.000
AFFX-r2-Bs-phe-M_at	---	1073.56	157.93	-6.798	0.000
AFFX-r2-Bs-lys-5_at	---	599.70	83.29	-7.200	0.000
1434171_at	Zfp874	177.10	24.53	-7.219	0.000
AFFX-r2-Bs-lys-M_at	---	627.02	86.64	-7.237	0.000
AFFX-PheX-5_at	---	719.05	95.45	-7.534	0.000
1438936_s_at	Ang	614.05	80.75	-7.605	0.001
1436717_x_at	Hbb-y	8663.57	1132.87	-7.647	0.000
AFFX-r2-Bs-phe-5_at	---	1193.76	153.75	-7.764	0.000
1436823_x_at	Hbb-y	8727.03	1117.78	-7.807	0.000
1423696_a_at	Psmd6	3460.08	418.31	-8.272	0.000
1434280_at	---	1007.31	121.60	-8.284	0.000
1450621_a_at	Hbb-y	3818.24	459.11	-8.317	0.000
AFFX-LysX-5_at	---	411.97	48.75	-8.450	0.000
1438937_x_at	Ang	238.65	27.81	-8.582	0.000
1435514_at	Lztf1	110.14	10.97	-10.041	0.000
1452239_at	Gt(ROSA)26Sor	359.15	28.96	-12.400	0.000