**SUPPLEMENTAL INFORMATION**

Supplemental Figures 1 to 10

Supplemental Tables 1 to 3

## Supplemental Methods

*Microarray analysis*. Total RNA samples (1 μg per sample) were converted into biotin-labeled cRNA using the GeneChip® IVT Labeling Kit and standard protocols recommended by Affymetrix. Fragmented cDNA was applied to GeneChip® Mouse Genome 430 2.0 Arrays (Affymetrix) that contain probe sets designed to detect over 39,000 transcripts. Microarrays were hybridized, processed and scanned, as previously described using the manufacturer's recommended conditions (1). WebArray software was used to generate scaled log2 transformed gene expression values using the RMA algorithm (2, 3). Probes sets showing >1.5-fold differential expression with a <5% FDR were identified through LIMMA (Liner Models for Microarray Data)-based liner model statistical analysis and FDR calculations made using the SPLOSH (spacings LOESS histogram) method. All scaled gene expression scores and .cel files are available at the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) repository http://www.ncbi.nih.gov/geo/ under Series Accession Number GSE22989.

*Mass spectrometry; trypsin digestion and liquid chromatography tandem mass spectrometry (LC–MS/MS).* Samples were separated by 1-D polyacrylamide gel, and stained with Coomassie Blue to visualize bands. Individual bands were excised and tryptic digests were analyzed by LC–MS/MS in the University of Southern California, Proteomics

Core Facility, as described previously (4). Mass analysis was performed with a ThermoFinnigan LCQ Deca XP Plus ion trap mass spectrometer equipped with a nanospray ion source using a 4.5 cm long metal needle (Hamilton; 950-00954) in a data-dependent acquisition mode. Protein identification was obtained with the MS/MS search software Mascot 1.9 (Matrix Science) with confirmatory or complementary analyses with TurboSequest as implemented in the Bioworks Browser 3.2, build 41 (ThermoFinnigan) (4).

*Micro-CT analysis.* Micro-CT analysis was performed using SCANCO μCT50 at the University of Southern California Molecular Imaging Center. The micro-CT images were acquired with the x-ray source at 70 kVp and 250 μA. The data were collected at a high resolution of 20 μm. The reconstruction was done with AVIZO 6 (Visualization Sciences Group).

**Supplemental Figures**

**Supplemental Figure 1**

Identification of molecules with increased expression in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. (**A**) LacZ staining of *Wnt1-Cre* mice carrying the *R26R* reporter gene at E13.5. Palatal shelves were dissected for the preparation of primary MEPM cells (indicated by yellow dashed lines). Bar, 50 μm. (**B**) Cell sorting by fluorescein di-β-d-galactopyranoside to detect MEPM cells carrying the *R26R* reporter gene. Primary MEPM cells derived from the palates of both *Tgfbr2*$^{fl/+}$*;Wnt1-Cre* and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice are

composed of over 93% CNC-derived cells. (**C**) Coomassie staining of extracts from primary MEPM cells of *Tgfbr2*$^{fl/fl}$, *Tgfbr2*$^{fl/+}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. Altered bands were identified by mass spectrometry analyses.

**Supplemental Figure 2**

TGF-β2-mediated TβRIII/β-spectrin complex formation in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* cells. (**A** and **B**) Immunoblotting (IB) analysis of immunoprecipitation (IP) products using the indicated antibodies derived from IgG control beads, or MEPM cell extracts from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice with (+) or without (-) TGF-β2 treatment. Bar graphs (right) show the ratios of indicated molecules after quantitative densitometry of immunoblotting data. *Tgfbr2*$^{fl/fl}$ (white bars) and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* (black bars).

**Supplemental Figure 3**

No indication of activation of BMP signaling in the absence of *Tgfbr2*. (**A**) Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with TGF-β2 (10 ng/ml) for indicated time (0–120 minutes). C, (control) indicated genotype MEPM cells treated with BMP5 (10 ng/ml) for one hour. (**B**) Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with BMP5 (10 ng/ml) for indicated time (0–120 minutes).

**Supplemental Figure 4**

TAK1 activates p38 MAPK in *Tgfbr2* mutant cells. (**A** and **B**; left to right) Immunoblotting (IB) analysis of TAK1 or TAB1 in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with control, *Tak1* or *Tab1* siRNA. Bar graphs show quantitation of siRNA data. Immunoblotting analysis of phosphorylated p38 (P-p38) and p38 in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with indicated siRNA and cultured with (+) or without (-) TGF-β2 (10 ng/ml) for 30 minutes. C: *Tgfbr2*$^{fl/fl}$ control with TGF-β2 for 30 minutes. Bar graphs show the ratios of phosphorylated p38 relative to p38 after quantitative densitometry of immunoblotting data. Control siRNA (black bars), target siRNA (gray bars).

**Supplemental Figure 5**

No other type II receptor is involved in the activation of TAK1 in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* cells. (**A–C**; left to right) Immunoblotting (IB) analysis of BMPRII, ACVRIIA or ACVRIIB in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with indicated siRNAs. Bar graphs show quantitation of the siRNA data. Immunoblotting analysis of phosphorylated TAK1 (P-TAK1) and TAK1 in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with indicated siRNAs cultured with (+) or without (-) TGF-β2 (10 ng/ml) for 30 minutes. C: *Tgfbr2*$^{fl/fl}$ control with TGF-β2 for 30 minutes. Bar graphs (far right) show the ratios of phosphorylated TAK1 relative to TAK1 after quantitative densitometry of immunoblotting data. Control siRNA (black bars), target siRNA (gray bars).

**Supplemental Figure 6**

TβRI/TβRIII assembly in the absence of *Tgfbr2* functions to induce TAK1 phosphorylation in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* cells. (**A–C**; left to right) Immunoblotting analysis of phosphorylated TAK1 (P-TAK1) and TAK1 in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with the indicated siRNA and cultured with TGF-β2 (10 ng/ml) for indicated time. Bar graphs show the ratios of phosphorylated TAK1 relative to TAK1 after quantitative densitometry of immunoblotting data. Control siRNA (black bars), target siRNA (gray bars). Immunoblotting (IB) analysis of TβRIII or TβRI or β-spectrin in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with control or *Tgfbr3* or *Tgfbr1* or *Spnb* siRNA. Bar graphs (far right) show quantitation of siRNA data. Control siRNA (black bars), target siRNA (gray bars).

**Supplemental Figure 7**

Micro-CT analysis of skull bones in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tgfb2*$^{+/-}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/+}$ newborn mice. (**A**) Three dimensional micro-CT images of the maxilla and palate of *Tgfbr2*$^{fl/fl}$, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tgfb2*$^{+/-}$ newborn mice. P, palatine bone; pp, palatal process of maxilla. (**B**) Three dimensional micro-CT images of the maxilla and palate of *Tgfbr2*$^{fl/fl}$ control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/+}$, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/fl}$, and *Tgfbr2*$^{fl/+}$*;Wnt1-Cre;Alk5*$^{fl/fl}$ newborn mice. P, palatine bone; pp, palatal process of maxilla.

**Supplemental Figure 8**

Haploinsufficiency of TAK1 in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice rescues cleft palate. (**A**) Morphologies of E16.5 *Tgfbr2*$^{fl/fl}$ control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ mice. Bottom views show macroscopic appearance of palates at E16.5. Arrowheads indicate calvaria defects. Arrow indicates cleft palate, and open arrows indicate normal palates. Palates were scored as normal or cleft. (**B**) Hematoxylin and eosin staining of sections of control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ palates at E16.5. Arrows indicate palate. Bar, 50 μm. (**C**) Immunoblotting analysis of E16.5 *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* (lane 1), *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ (lane 2), and control (lane 3) palates.

**Supplemental Figure 9**

Effect of TGF-β1 and TGF-β3 on the alternative TGF-β signaling. Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with TGF-β1 (10 ng/ml) or TGF-β3 (10 ng/ml) for indicated time (0–120 minutes).

**Supplemental Figure 10**

p38 autophosphorylation contributes to further p38 MAPK activation. Immunoblotting analyses of indicated molecules in primary MEPM cells of *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with (+) or without (-) p38 MAPK inhibitor SB203580. P-p38, phosphorylated p38. Bar graphs (right) show the ratios of phosphorylated p38 relative to

p38 after quantitative densitometry of immunoblotting data. *Tgfbr2*$^{fl/fl}$ (white bars) and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* (black bars).

**Supplemental Tables**

**Supplemental Table 1**

Up-regulated genes in the palate of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice at E14.5. These genes were identified with the selection criteria of genes showing >1.5-fold change with a <5% FDR, as described in the Experimental procedures section. CKO refers to *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice and WT refers to *Tgfbr2*$^{fl/fl}$ control mice. Log(2)-transformed gene expression scores are provided along with geometric means and FDR calculations.

**Supplemental Table 2**

Down-regulated genes in the palate of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice at E14.5. These genes were identified with the selection criteria of genes showing >1.5-fold change with a <5% FDR. CKO refers to *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice and WT refers to *Tgfbr2*$^{fl/fl}$ control mice. Log(2)-transformed gene expression scores are provided along with geometric means and FDR calculations.

**Supplemental Table 3**

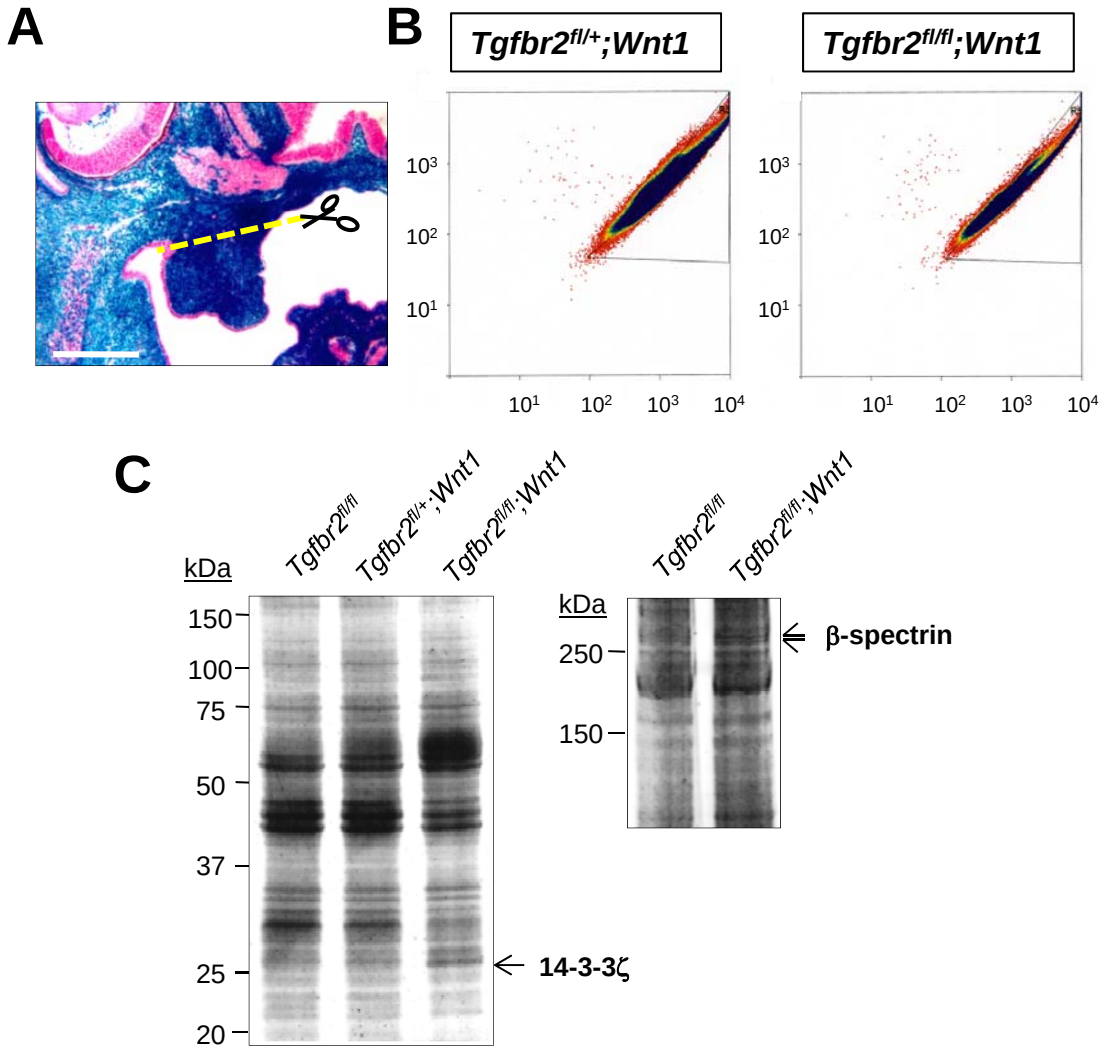
Mass spectrometry analysis in the MEPM cells of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. These molecules were identified using mass spectrometry with extracts from MEPM cells of E13.5 *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. #1 shows data from the approximately 30

kDa-band in Supplemental Figure 1C, and #2 shows data from the approximately 270 kDa-band in Supplemental Figure 1C.

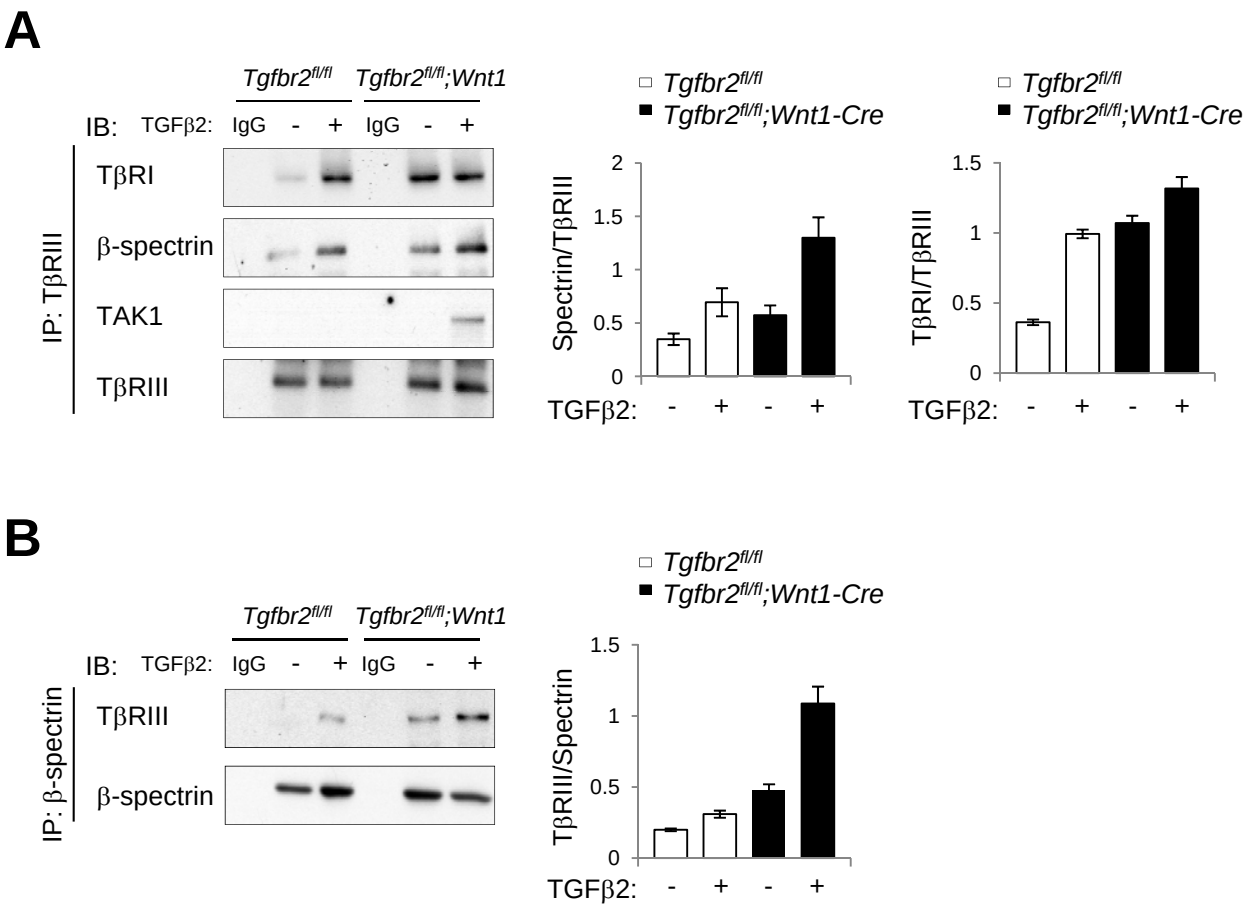
**Supplemental references**


1. Karaman MW, *et al.* (2003) Comparative analysis of gene-expression patterns in human and African great ape cultured fibroblasts. *Genome Res* 13(7):1619-1630.
2. Xia X, McClelland M, & Wang Y (2005) WebArray: an online platform for microarray data analysis. *BMC Bioinformatics* 6:306.
3. Wang Y, McClelland M, & Xia XQ (2009) Analyzing microarray data using WebArray. *Cold Spring Harb Protoc* 2009(8):pdb prot5260.
4. Gallaher TK, Wu S, Webster P, & Aguilera R (2006) Identification of biofilm proteins in non-typeable Haemophilus Influenzae. *BMC Microbiol* 6:65.

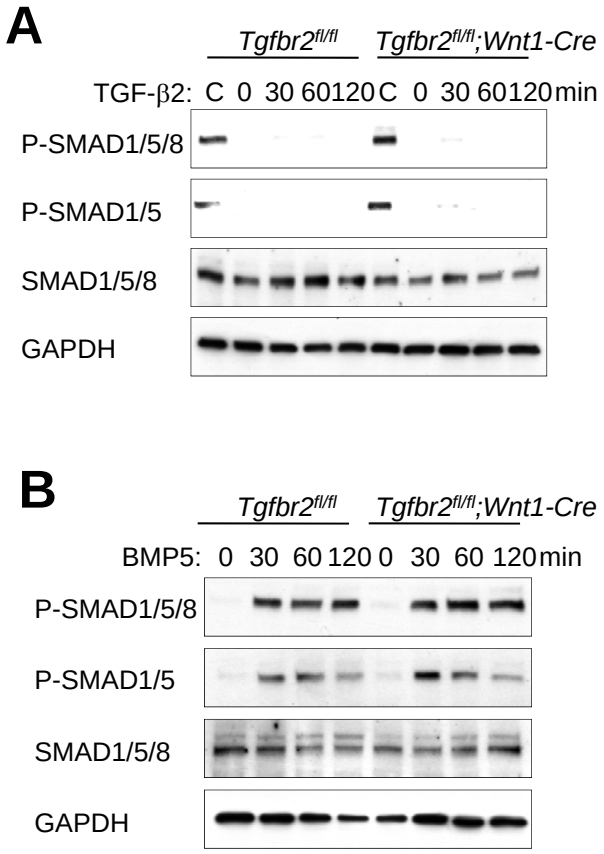
# Supplementary Figure 1. Iwata *et al*.




**Supplemental Figure 1**
Identification of molecules with increased expression in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. (**A**) LacZ staining of *Wnt1-Cre* mice carrying the *R26R* reporter gene at E13.5. Palatal shelves were dissected for the preparation of primary MEPM cells (indicated by yellow dashed lines). Bar, 50 μm. (**B**) Cell sorting by fluorescein di-β-d-galactopyranoside to detect MEPM cells carrying the *R26R* reporter gene. Primary MEPM cells derived from the palates of both *Tgfbr2*$^{fl/+}$*;Wnt1-Cre* and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice are composed of over 93% CNC-derived cells. (**C**) Coomassie staining of extracts from primary MEPM cells of *Tgfbr2*$^{fl/fl}$, *Tgfbr2*$^{fl/+}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. Altered bands were identified by mass spectrometry analyses.




**Supplemental Figure 2**
TGF-β2-mediated TβRIII/β-spectrin complex formation in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* cells. (**A** and **B**) Immunoblotting (IB) analysis of immunoprecipitation (IP) products using the indicated antibodies derived from IgG control beads, or MEPM cell extracts from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice with (+) or without (-) TGF-β2 treatment. Bar graphs (right) show the ratios of indicated molecules after quantitative densitometry of immunoblotting data. *Tgfbr2*$^{fl/fl}$ (white bars) and *Tgfbr2*$^{fl/fl}$;*Wnt1-Cre* (black bars).

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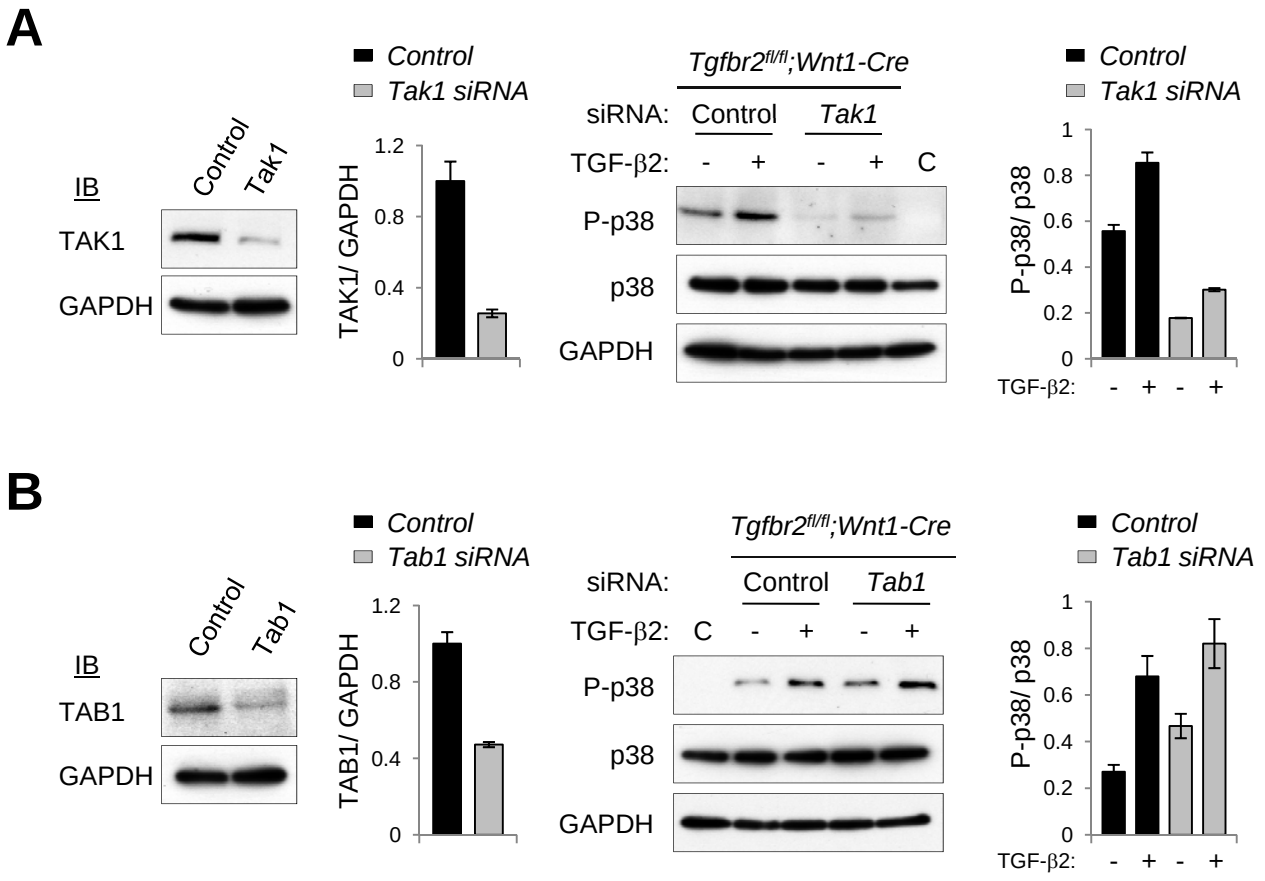
No indication of activation of BMP signaling in the absence of *Tgfbr2*. (**A**) Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with TGF-β2 (10 ng/ml) for indicated time (0–120 minutes). C, (control) indicated genotype MEPM cells treated with BMP5 (10 ng/ml) for one hour. (**B**) Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with BMP5 (10 ng/ml) for indicated time (0–120 minutes).

# Supplementary Figure 4. Iwata *et al*.

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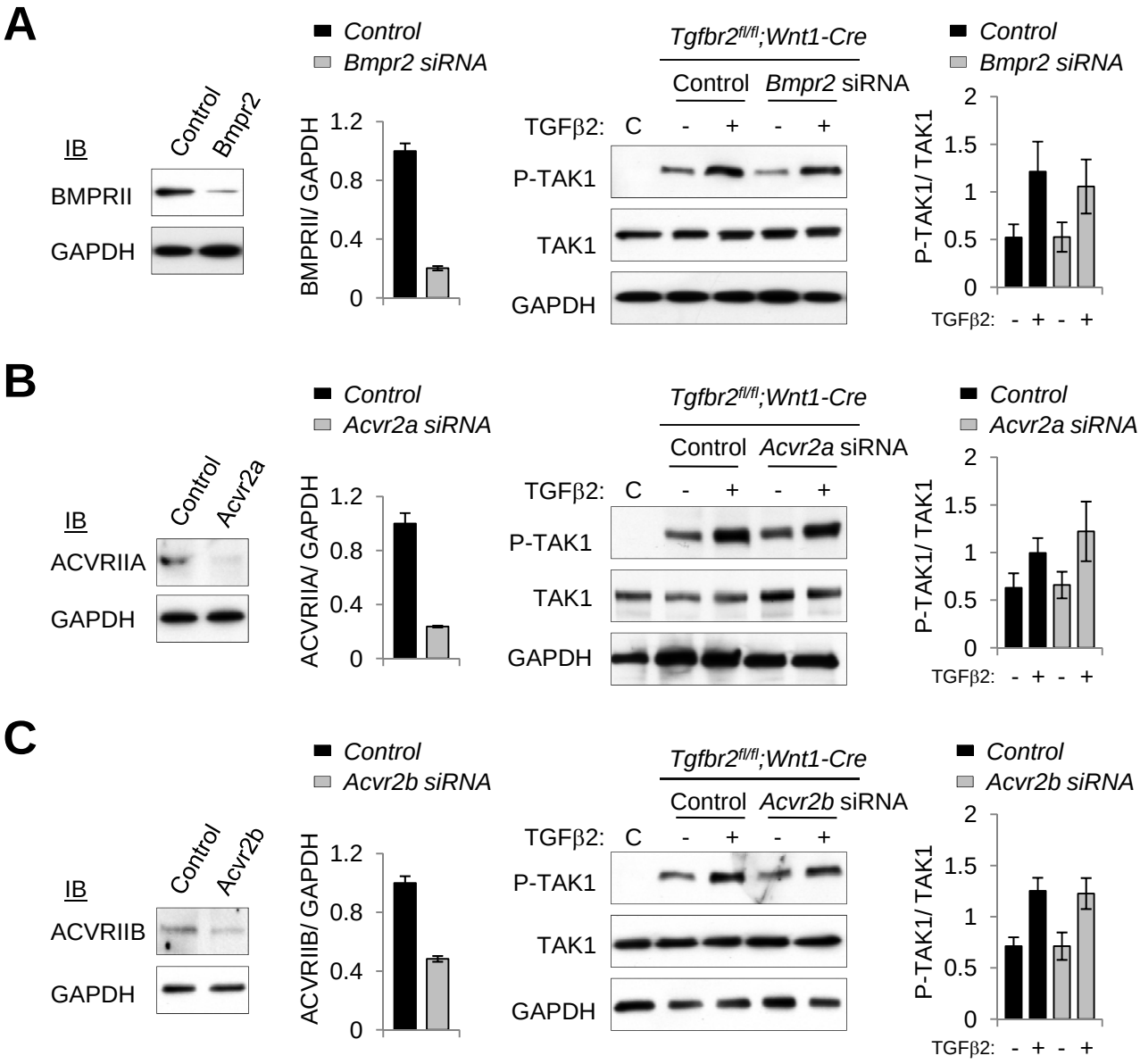


**Supplemental Figure 5**

No other type II receptor is involved in the activation of TAK1 in *Tgfbr2$^{fl/fl}$;Wnt1-Cre* cells. (**A**–**C**; left to right) Immunoblotting (IB) analysis of BMPRRII, ACVRIIA or ACVRIIB in primary MEPM cells from *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice treated with indicated siRNAs. Bar graphs show quantitation of the siRNA data. Immunoblotting analysis of phospho-TAK1 (P-TAK1) and TAK1 in primary MEPM cells from *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice treated with indicated siRNAs cultured with (+) or without (-) TGF-β2 (10 ng/ml) for 30 minutes. C: *Tgfbr2$^{fl/fl}$* control with TGF-β2 for 30 minutes. Bar graphs (far right) show the ratios of phopho-TAK1 relative to TAK1 after quantitative densitometry of immunoblotting data. Control siRNA (black bars), target siRNA (gray bars).

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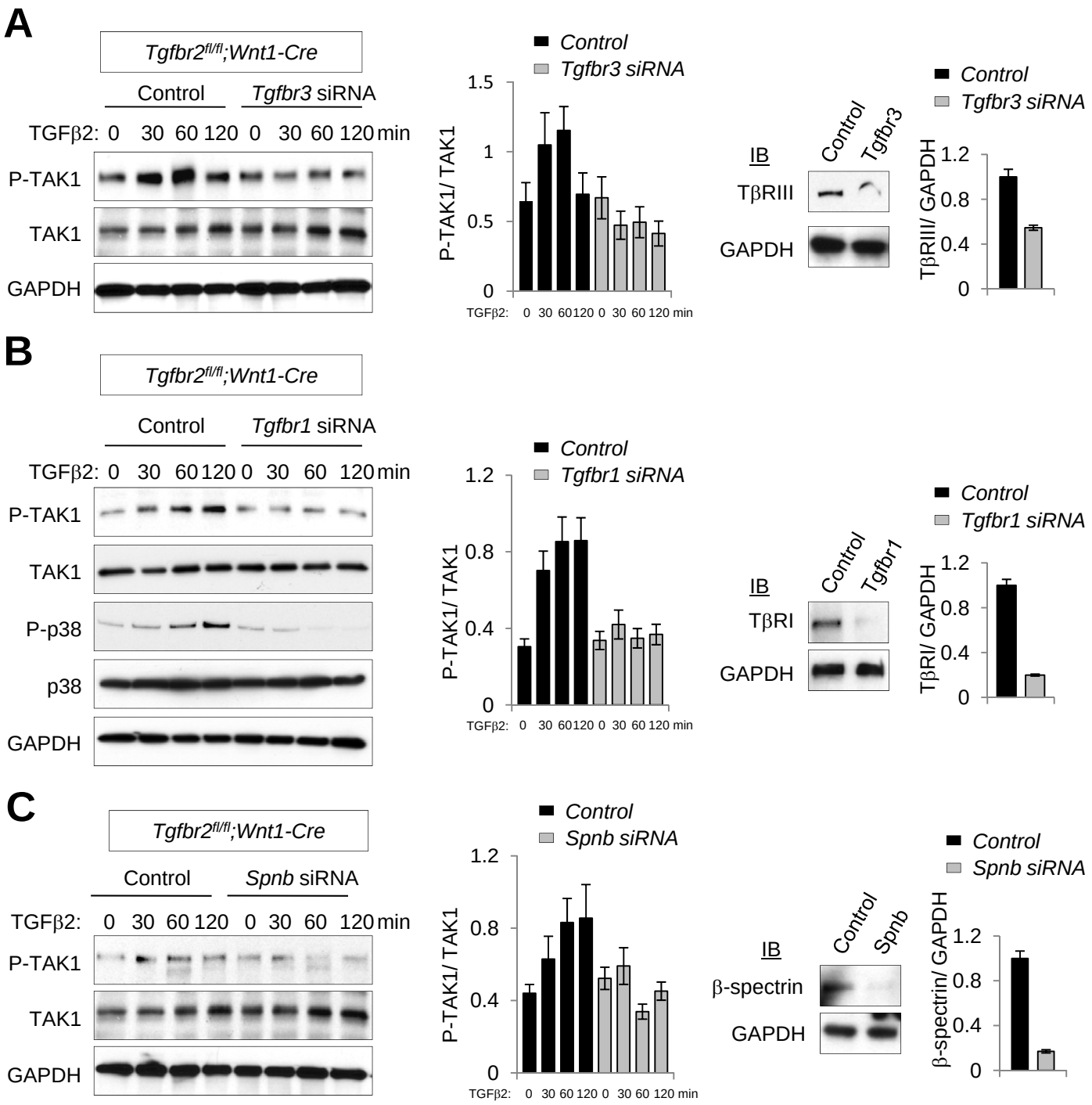


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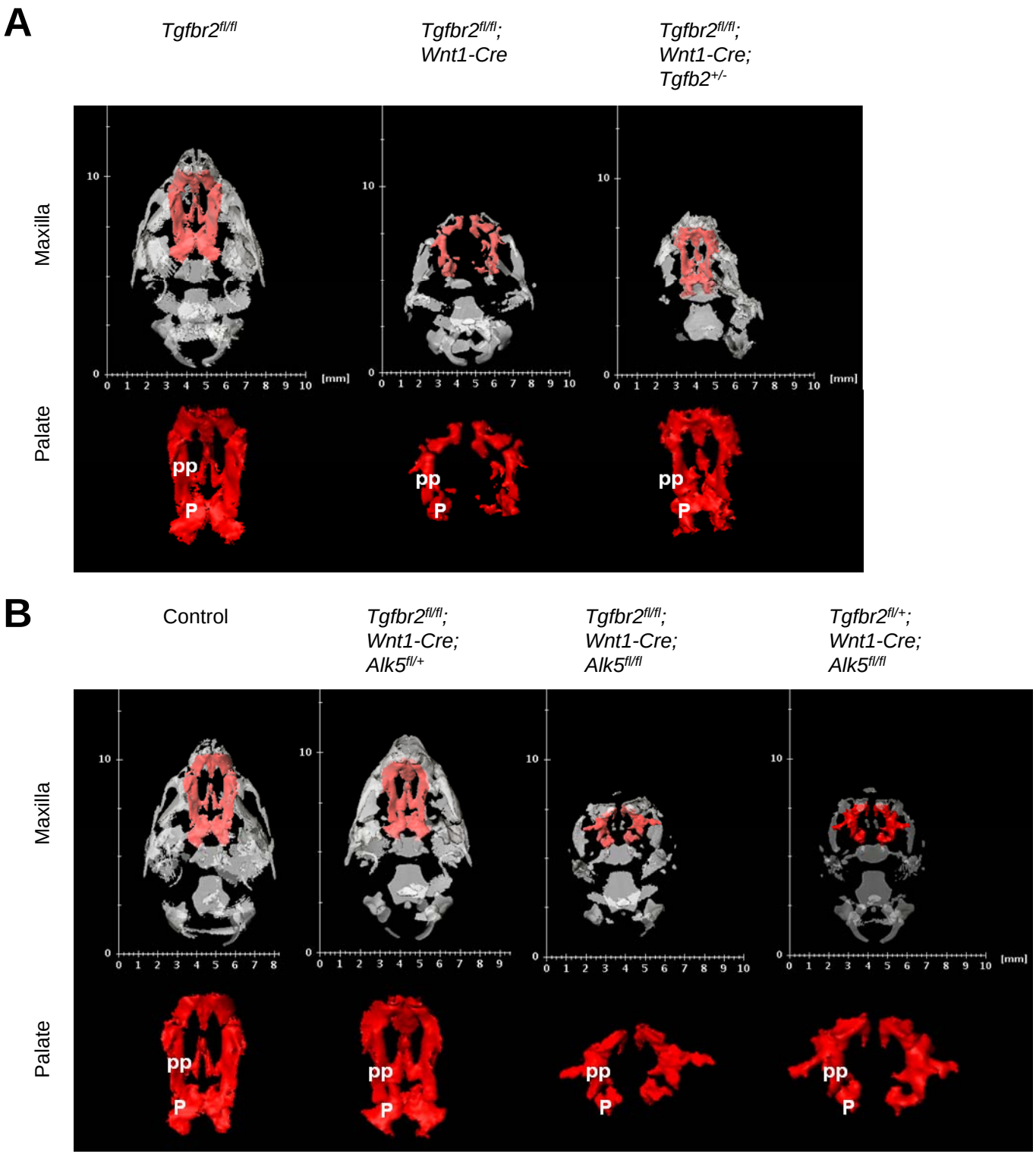
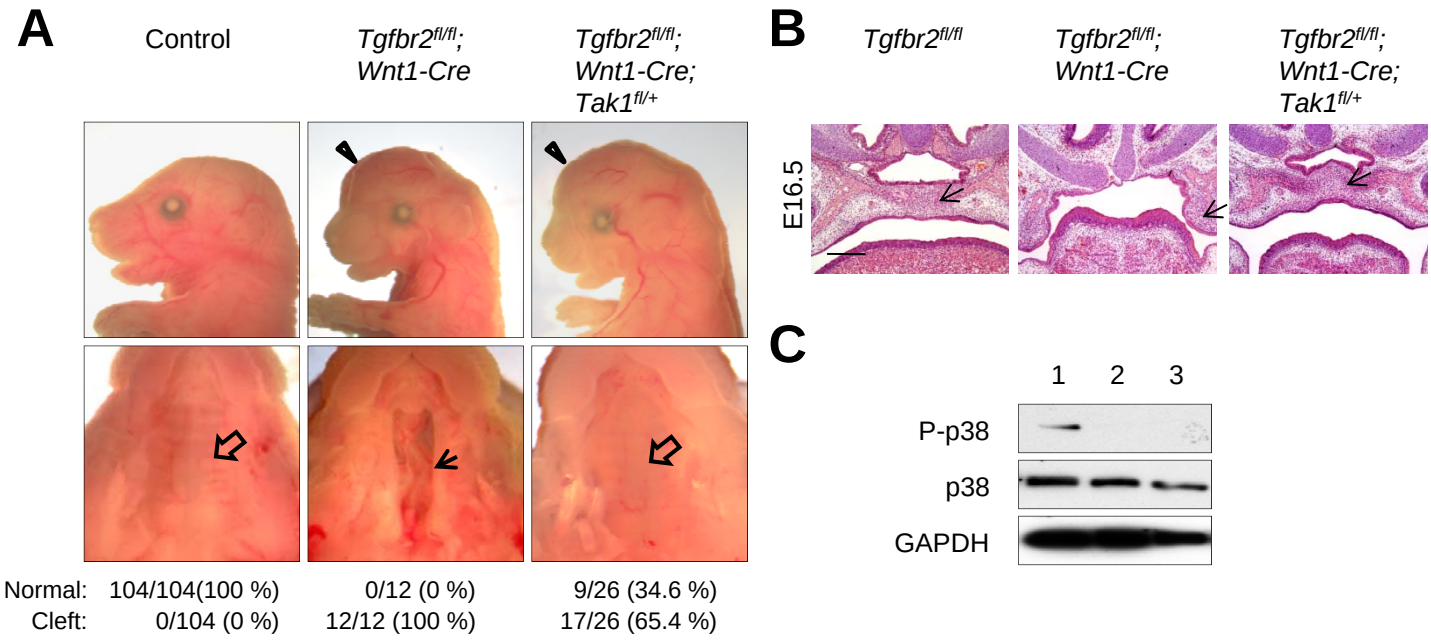
TβRI/TβRIII assembly in the absence of *Tgfbr2* functions to induce TAK1 phosphorylation in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* cells. (**A**–**C**; left to right) Immunoblotting analysis of phosphorylated TAK1 (P-TAK1) and TAK1 in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with the indicated siRNA and cultured with TGF-β2 (10 ng/ml) for indicated time. Bar graphs show the ratios of phosphorylated TAK1 relative to TAK1 after quantitative densitometry of immunoblotting data. Control siRNA (black bars), target siRNA (gray bars). Immunoblotting (IB) analysis of TβRIII or TβRI or β-spectrin in primary MEPM cells from *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with control or *Tgfbr3* or *Tgfbr1* or *Spnb* siRNA. Bar graphs (far right) show quantitation of siRNA data. Control siRNA (black bars), target siRNA (gray bars).

# Supplementary Figure 7. Iwata *et al*.




**Supplemental Figure 7**
Micro-CT analysis of skull bones in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tgfb2*$^{+/-}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/+}$ newborn mice. (**A**) Three dimensional micro-CT images of the maxilla and palate of *Tgfbr2*$^{fl/fl}$, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tgfb2*$^{+/-}$ newborn mice. P, palatine bone; pp, palatal process of maxilla. (**B**) Three dimensional micro-CT images of the maxilla and palate of *Tgfbr2*$^{fl/fl}$ control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/+}$, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Alk5*$^{fl/fl}$, and *Tgfbr2*$^{fl/+}$*;Wnt1-Cre;Alk5*$^{fl/fl}$ newborn mice. P, palatine bone; pp, palatal process of maxilla.

# Supplementary Figure 8. Iwata *et al*.

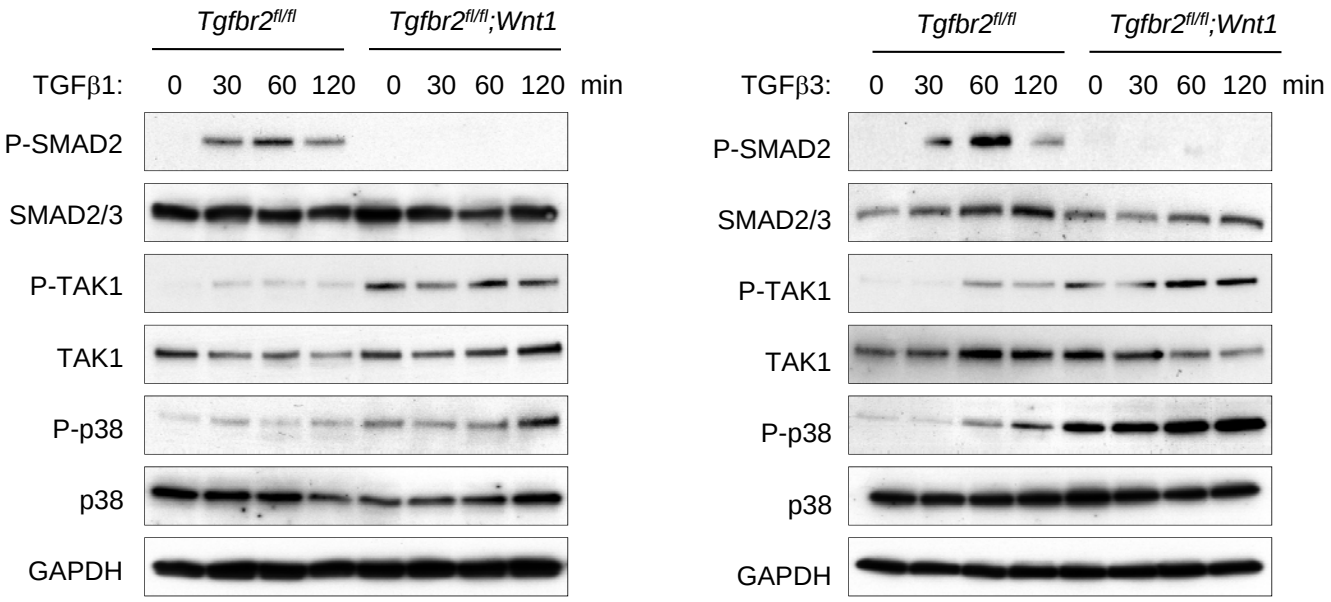



| | Control | *Tgfbr2*$^{fl/fl}$; *Wnt1-Cre* | *Tgfbr2*$^{fl/fl}$; *Wnt1-Cre; Tak1*$^{fl/+}$ |
|---|---|---|---|
| Normal: | 104/104(100 %) | 0/12 (0 %) | 9/26 (34.6 %) |
| Cleft: | 0/104 (0 %) | 12/12 (100 %) | 17/26 (65.4 %) |

**Supplemental Figure 8**

Haploinsufficiency of TAK1 in *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice rescues cleft palate. (**A**) Morphologies of E16.5 *Tgfbr2*$^{fl/fl}$ control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ mice. Bottom views show macroscopic appearance of palates at E16.5. Arrowheads indicate calvaria defects. Arrow indicates cleft palate, and open arrows indicate normal palates. Palates were scored as normal or cleft. (**B**) Hematoxylin and eosin staining of sections of control, *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre*, and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ palates at E16.5. Arrows indicate palate. Bar, 50 μm. (**C**) Immunoblotting analysis of E16.5 *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* (lane 1), *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre;Tak1*$^{fl/+}$ (lane 2), and control (lane 3) palates.

# Supplementary Figure 9. Iwata *et al*.




**Supplemental Figure 9**
Effect of TGF-β1 and TGF-β3 on the alternative TGF-β signaling. Immunoblotting analysis of indicated molecules in primary MEPM cells from *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice cultured with TGF-β1 (10 ng/ml) or TGF-β3 (10 ng/ml) for indicated time (0–120 minutes).

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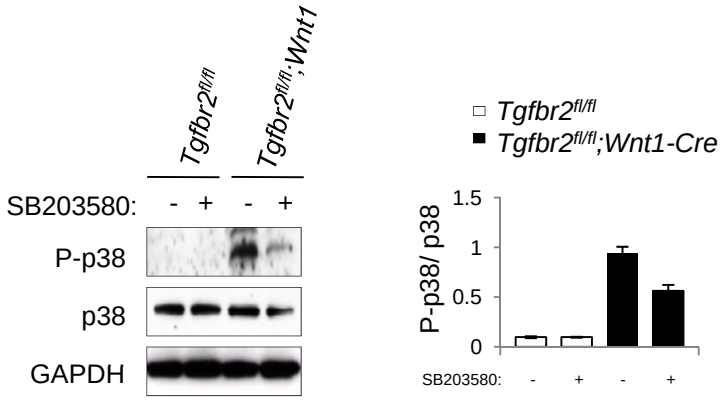


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p38 autophosphorylation contributes to further p38 MAPK activation. Immunoblotting analyses of indicated molecules in primary MEPM cells of *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice treated with (+) or without (-) p38 MAPK inhibitor SB203580. P-p38, phosphorylated p38. Bar graphs (right) show the ratios of phosphorylated p38 relative to p38 after quantitative densitometry of immunoblotting data. *Tgfbr2*$^{fl/fl}$ (white bars) and *Tgfbr2*$^{fl/fl}$;*Wnt1-Cre* (black bars).

Supplementary Table 1. Up-regulated genes in the palate of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice at E14.5

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1435603_at | Sned1 | 1668 | 417 | 4.00 | 0.001 |
| 1447258_at | --- | 315 | 81 | 3.88 | 0.013 |
| 1423410_at | Meig1 | 270 | 77 | 3.51 | 0.009 |
| 1458586_at | --- | 204 | 62 | 3.30 | 0.020 |
| 1422454_at | Krt13 | 389 | 129 | 3.02 | 0.023 |
| 1430762_at | 4833427G06Rik | 310 | 109 | 2.84 | 0.007 |
| 1454713_s_at | Hdc | 172 | 62 | 2.78 | 0.009 |
| 1432083_a_at | Lrrc23 | 651 | 243 | 2.68 | 0.003 |
| 1428987_at | Dynlrb2 | 1287 | 482 | 2.67 | 0.012 |
| 1447386_at | --- | 35 | 13 | 2.63 | 0.023 |
| 1458104_a_at | Ccdc153 | 103 | 40 | 2.58 | 0.006 |
| 1460107_at | Fam154b | 86 | 33 | 2.57 | 0.001 |
| 1446424_at | Dnahc12 | 77 | 30 | 2.55 | 0.019 |
| 1439194_at | C030048H21Rik | 111 | 44 | 2.52 | 0.005 |
| 1460138_at | --- | 121 | 50 | 2.43 | 0.002 |
| 1452804_at | Morn5 | 191 | 79 | 2.40 | 0.010 |
| 1430781_at | Ak7 | 203 | 86 | 2.36 | 0.002 |
| 1443127_at | 9630021D06Rik | 284 | 122 | 2.32 | 0.024 |
| 1439093_at | --- | 261 | 113 | 2.30 | 0.013 |
| 1451796_s_at | Hdc | 235 | 103 | 2.29 | 0.010 |
| 1434983_at | Ccdc108 | 104 | 46 | 2.28 | 0.000 |
| 1436111_at | E030011K20Rik | 99 | 44 | 2.28 | 0.034 |
| 1417643_at | Rsph1 | 393 | 173 | 2.27 | 0.022 |
| 1458708_at | --- | 407 | 179 | 2.27 | 0.044 |
| 1436787_x_at | 1110069O07Rik | 327 | 144 | 2.27 | 0.004 |
| 1436675_at | Wdr63 | 89 | 40 | 2.26 | 0.017 |
| 1429106_at | 4921509J17Rik | 291 | 132 | 2.20 | 0.011 |
| 1456555_at | Ccdc67 | 952 | 439 | 2.17 | 0.031 |
| 1428984_a_at | 1700012B09Rik | 105 | 49 | 2.16 | 0.009 |
| 1423396_at | Agt | 179 | 83 | 2.16 | 0.000 |
| 1445885_at | Ube2d2 | 196 | 91 | 2.16 | 0.019 |
| 1457214_at | --- | 114 | 53 | 2.16 | 0.042 |
| 1436786_at | 1110069O07Rik | 316 | 147 | 2.15 | 0.001 |
| 1437096_at | Ttc29 | 56 | 26 | 2.14 | 0.033 |
| 1453121_at | Tekt4 | 132 | 62 | 2.11 | 0.032 |
| 1455379_at | Dnali1 | 148 | 70 | 2.10 | 0.003 |
| 1426231_at | Vit | 166 | 79 | 2.09 | 0.000 |
| **1438303_at** | **Tgfb2** | **295** | **143** | **2.07** | **0.001** |
| 1441863_x_at | Krt13 | 25 | 12 | 2.02 | 0.001 |
| 1434905_at | Ndufa4l2 | 1080 | 534 | 2.02 | 0.001 |
| 1429181_at | 1700009P17Rik | 723 | 360 | 2.01 | 0.040 |
| 1459311_at | Pde4d | 43 | 22 | 2.00 | 0.048 |
| 1422750_a_at | Zmynd10 | 239 | 121 | 1.98 | 0.032 |
| 1438763_at | Dnahc2 | 128 | 65 | 1.97 | 0.008 |
| 1445452_at | Traf1 | 78 | 40 | 1.96 | 0.000 |
| 1445727_at | Ube3a | 205 | 105 | 1.96 | 0.033 |
| **1450923_at** | **Tgfb2** | **1262** | **645** | **1.95** | **0.002** |
| 1441306_at | 6820408C15Rik | 178 | 92 | 1.94 | 0.009 |
| 1429907_at | 1700094D03Rik | 570 | 296 | 1.92 | 0.002 |
| 1428089_at | Slitrk1 | 104 | 54 | 1.92 | 0.017 |
| 1453176_a_at | 4933404M02Rik | 54 | 28 | 1.92 | 0.004 |
| 1435487_at | Grid2 | 128 | 68 | 1.89 | 0.001 |
| 1438394_x_at | Krt4 | 356 | 188 | 1.89 | 0.039 |
| 1418735_at | Krt4 | 282 | 149 | 1.89 | 0.006 |
| 1427371_at | Abca8a | 337 | 179 | 1.88 | 0.000 |
| 1457541_at | Akap14 | 81 | 43 | 1.88 | 0.012 |
| 1442495_at | --- | 150 | 80 | 1.88 | 0.044 |
| 1453951_a_at | D19Ertd652e | 74 | 40 | 1.87 | 0.000 |
| 1456978_s_at | D19Ertd652e | 25 | 13 | 1.87 | 0.011 |

Supplementary Table 1. Up-regulated genes in the palate of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice at E14.5 (Continued)

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1432075_a_at | Tekt1 | 373 | 199 | 1.87 | 0.039 |
| 1441707_at | Psma3 | 207 | 112 | 1.84 | 0.013 |
| 1416713_at | Tppp3 | 608 | 330 | 1.84 | 0.036 |
| 1439711_at | --- | 87 | 47 | 1.84 | 0.010 |
| 1422727_at | Nme5 | 401 | 219 | 1.83 | 0.032 |
| 1419149_at | Serpine1 | 90 | 49 | 1.83 | 0.000 |
| 1438466_at | Dnahc7b | 87 | 48 | 1.82 | 0.011 |
| 1457693_a_at | 6430537H07Rik | 135 | 75 | 1.81 | 0.040 |
| 1429842_at | Mdh1b | 45 | 25 | 1.81 | 0.037 |
| 1456958_at | C230072F16Rik | 76 | 42 | 1.80 | 0.004 |
| 1418253_a_at | Hspa4l | 326 | 182 | 1.79 | 0.017 |
| 1423933_a_at | 1600029D21Rik | 167 | 93 | 1.79 | 0.020 |
| 1437344_x_at | Krt13 | 62 | 35 | 1.79 | 0.050 |
| 1460045_at | Cdh7 | 115 | 64 | 1.78 | 0.014 |
| 1456711_at | 4932425I24Rik | 63 | 35 | 1.78 | 0.010 |
| 1422561_at | Adamts5 | 328 | 185 | 1.78 | 0.000 |
| 1438122_at | 2900006K08Rik | 155 | 87 | 1.78 | 0.041 |
| 1455859_at | A330021E22Rik | 174 | 98 | 1.77 | 0.001 |
| 1457034_at | D14Abb1e | 383 | 216 | 1.77 | 0.028 |
| **1450922_a_at** | **Tgfb2** | **957** | **544** | **1.76** | **0.000** |
| 1435121_at | Dio3os | 384 | 218 | 1.76 | 0.000 |
| 1458385_at | Hspa4l | 112 | 64 | 1.75 | 0.012 |
| 1428599_at | Kndc1 | 108 | 62 | 1.75 | 0.007 |
| 1454254_s_at | 1600029D21Rik | 130 | 75 | 1.74 | 0.015 |
| 1442025_a_at | --- | 66 | 38 | 1.74 | 0.003 |
| 1453152_at | Mamdc2 | 259 | 150 | 1.73 | 0.016 |
| 1415894_at | Enpp2 | 400 | 231 | 1.73 | 0.000 |
| 1445787_at | 5033413D22Rik | 81 | 47 | 1.73 | 0.005 |
| 1460482_at | 3110047P20Rik | 151 | 88 | 1.72 | 0.004 |
| 1441218_at | Ttc21a | 45 | 26 | 1.72 | 0.016 |
| 1424041_s_at | C1s | 145 | 85 | 1.72 | 0.005 |
| 1429780_at | Ccdc39 | 24 | 14 | 1.70 | 0.012 |
| 1442029_at | Kcnq1ot1 | 482 | 284 | 1.70 | 0.018 |
| 1436785_a_at | 1110069O07Rik | 286 | 169 | 1.70 | 0.003 |
| 1456970_at | --- | 90 | 54 | 1.68 | 0.025 |
| 1429816_at | Armc3 | 96 | 58 | 1.68 | 0.037 |
| 1430970_a_at | Morn3 | 47 | 28 | 1.67 | 0.015 |
| 1429130_at | Ttc25 | 82 | 49 | 1.67 | 0.013 |
| 1429781_s_at | Ccdc39 | 308 | 185 | 1.67 | 0.009 |
| 1448136_at | Enpp2 | 1041 | 625 | 1.67 | 0.000 |
| 1442894_at | Dnahc6 | 137 | 83 | 1.66 | 0.045 |
| 1457694_at | 6430537H07Rik | 89 | 54 | 1.65 | 0.003 |
| 1427018_at | Tsnaxip1 | 95 | 57 | 1.65 | 0.005 |
| 1456945_at | Nudt6 | 667 | 404 | 1.65 | 0.002 |
| 1425506_at | Mylk | 845 | 516 | 1.64 | 0.014 |
| 1432513_a_at | 1700001C02Rik | 76 | 46 | 1.64 | 0.018 |
| 1416625_at | Serping1 | 444 | 272 | 1.63 | 0.000 |
| 1417333_at | Rasa4 | 99 | 61 | 1.63 | 0.001 |
| **1423250_a_at** | **Tgfb2** | **1160** | **714** | **1.62** | **0.000** |
| 1445576_at | Rsph10b2 | 40 | 25 | 1.62 | 0.045 |
| 1419874_x_at | Zbtb16 | 73 | 45 | 1.62 | 0.002 |
| 1436662_at | Sorcs1 | 29 | 18 | 1.61 | 0.003 |
| 1441113_at | A430071A18Rik | 139 | 86 | 1.61 | 0.004 |
| 1443223_at | --- | 75 | 47 | 1.60 | 0.021 |
| 1442184_at | --- | 39 | 25 | 1.60 | 0.028 |
| 1435992_at | Iqca | 54 | 34 | 1.60 | 0.010 |
| 1421436_at | Grid2 | 74 | 47 | 1.59 | 0.007 |
| 1450716_at | Adamts1 | 921 | 582 | 1.58 | 0.019 |

Supplementary Table 1. Up-regulated genes in the palate of *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice at E14.5 (Continued)

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1429058_at | Tmem107 | 2806 | 1774 | 1.58 | 0.005 |
| 1456404_at | Adamts5 | 154 | 97 | 1.58 | 0.000 |
| 1419703_at | Col5a3 | 113 | 72 | 1.58 | 0.000 |
| 1455973_at | Gm11992 | 22 | 14 | 1.58 | 0.009 |
| 1421375_a_at | S100a6 | 1545 | 982 | 1.57 | 0.001 |
| 1459078_at | --- | 70 | 45 | 1.57 | 0.029 |
| 1435148_at | Atp1b2 | 283 | 180 | 1.57 | 0.000 |
| 1420512_at | Dkk2 | 862 | 550 | 1.57 | 0.000 |
| 1447556_x_at | 1700094D03Rik | 178 | 114 | 1.56 | 0.001 |
| 1427183_at | Efemp1 | 916 | 586 | 1.56 | 0.001 |
| 1446204_at | --- | 89 | 57 | 1.56 | 0.023 |
| 1460043_at | --- | 18 | 12 | 1.55 | 0.028 |
| **1433795_at** | **Tgfbr3** | **1182** | **762** | **1.55** | **0.027** |
| 1449010_at | Hspa4l | 217 | 140 | 1.55 | 0.034 |
| 1442464_at | Fbxl20 | 140 | 91 | 1.54 | 0.017 |
| 1424909_at | Lrrc46 | 175 | 114 | 1.54 | 0.026 |
| 1417704_a_at | Arhgap6 | 74 | 48 | 1.54 | 0.001 |
| 1430217_at | Lrguk | 22 | 14 | 1.53 | 0.007 |
| 1429419_at | 2310007A19Rik | 119 | 78 | 1.52 | 0.032 |
| 1428083_at | Neat1 | 386 | 254 | 1.52 | 0.038 |
| 1442472_at | Ttc21a | 71 | 47 | 1.52 | 0.010 |
| 1433691_at | Ppp1r3c | 816 | 537 | 1.52 | 0.013 |
| 1441708_at | Spag16 | 67 | 44 | 1.52 | 0.034 |
| 1445639_at | 9130014G24Rik | 12 | 8 | 1.51 | 0.001 |
| 1421425_a_at | Rcan2 | 237 | 157 | 1.51 | 0.000 |
| 1447839_x_at | Adm | 149 | 99 | 1.51 | 0.002 |
| 1441743_at | Pax3 | 271 | 180 | 1.51 | 0.003 |
| 1458269_at | Pcdh9 | 161 | 107 | 1.51 | 0.012 |
| 1426303_at | B4galt7 | 74 | 49 | 1.51 | 0.025 |
| 1427053_at | Abi3bp | 282 | 187 | 1.50 | 0.007 |
| 1453168_at | 1700029J07Rik | 53 | 35 | 1.50 | 0.040 |
| 1451059_at | Zfp474 | 70 | 47 | 1.50 | 0.004 |

**Supplemental Table 1**
Up-regulated genes in the palate of *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice at E14.5. These genes were identified with the selection criteria of genes showing >1.5-fold change with a <5% FDR, as described in the Experimental procedures section. CKO refers to *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice and WT refers to *Tgfbr2$^{fl/fl}$* control mice. Log(2)-transformed gene expression scores are provided along with geometric means and FDR calculations.

Supplementary Table 2. Down-regulated genes in the palate of *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice at E14.5

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1417450_a_at | Tacc3 | 288 | 435 | -1.51 | 0.000 |
| 1422731_at | Limd1 | 473 | 717 | -1.51 | 0.000 |
| 1417445_at | Ndc80 | 191 | 289 | -1.51 | 0.002 |
| 1453748_a_at | Kif23 | 120 | 182 | -1.52 | 0.005 |
| 1416120_at | Rrm2 | 574 | 872 | -1.52 | 0.001 |
| 1438718_at | Fgf9 | 74 | 112 | -1.52 | 0.011 |
| 1424118_a_at | Spc25 | 637 | 967 | -1.52 | 0.006 |
| 1448566_at | Slc40a1 | 195 | 296 | -1.52 | 0.006 |
| 1422016_a_at | Cenph | 247 | 376 | -1.52 | 0.002 |
| 1438571_at | Bub1 | 85 | 129 | -1.52 | 0.000 |
| 1435678_at | 2610017I09Rik | 268 | 409 | -1.53 | 0.000 |
| 1431087_at | Spc24 | 463 | 707 | -1.53 | 0.000 |
| 1423450_a_at | Hs3st1 | 107 | 163 | -1.53 | 0.002 |
| 1422909_at | Smc6 | 66 | 101 | -1.53 | 0.037 |
| 1424278_a_at | Birc5 | 895 | 1367 | -1.53 | 0.000 |
| 1448752_at | Car2 | 217 | 331 | -1.53 | 0.019 |
| 1418754_at | Adcy8 | 79 | 121 | -1.53 | 0.029 |
| 1416299_at | Shcbp1 | 735 | 1125 | -1.53 | 0.031 |
| 1434789_at | Depdc1b | 149 | 228 | -1.53 | 0.000 |
| 1437260_at | Mmrn1 | 119 | 182 | -1.53 | 0.000 |
| 1421731_a_at | Fen1 | 310 | 475 | -1.53 | 0.000 |
| 1420707_a_at | Traip | 106 | 163 | -1.53 | 0.020 |
| 1422252_a_at | Cdc25c | 113 | 173 | -1.54 | 0.001 |
| 1426298_at | Irx2 | 39 | 59 | -1.54 | 0.018 |
| 1451419_at | Spsb4 | 34 | 52 | -1.54 | 0.002 |
| 1416575_at | Cdc45l | 145 | 224 | -1.54 | 0.000 |
| 1422024_at | Fli1 | 128 | 198 | -1.54 | 0.014 |
| 1417911_at | Ccna2 | 915 | 1415 | -1.55 | 0.000 |
| 1428304_at | Esco2 | 206 | 318 | -1.55 | 0.026 |
| 1429734_at | 4632434I11Rik | 145 | 224 | -1.55 | 0.024 |
| 1450112_a_at | Gas2 | 352 | 547 | -1.55 | 0.001 |
| 1452598_at | Gins1 | 337 | 525 | -1.56 | 0.002 |
| 1439695_a_at | Kif20b | 302 | 470 | -1.56 | 0.004 |
| 1418027_at | Exo1 | 98 | 153 | -1.56 | 0.001 |
| 1444443_at | --- | 53 | 82 | -1.56 | 0.005 |
| 1452961_at | 1200009O22Rik | 196 | 306 | -1.56 | 0.006 |
| 1452314_at | Kif11 | 271 | 424 | -1.56 | 0.002 |
| 1438307_at | Hmgb2 | 59 | 92 | -1.56 | 0.012 |
| 1450780_s_at | Hmga2 | 1174 | 1840 | -1.57 | 0.017 |
| 1429499_at | Fbxo5 | 490 | 768 | -1.57 | 0.007 |
| 1424797_a_at | Pitx2 | 719 | 1129 | -1.57 | 0.043 |
| 1447363_s_at | Bub1b | 393 | 617 | -1.57 | 0.000 |
| 1435054_at | Eme1 | 159 | 251 | -1.57 | 0.000 |
| 1416258_at | Tk1 | 407 | 640 | -1.57 | 0.000 |
| 1417939_at | Rad51ap1 | 88 | 139 | -1.58 | 0.003 |
| 1443906_at | Cd55 | 72 | 114 | -1.58 | 0.001 |
| 1429171_a_at | Ncapg | 216 | 342 | -1.58 | 0.002 |
| 1424046_at | Bub1 | 652 | 1030 | -1.58 | 0.002 |
| 1439510_at | Sgol1 | 175 | 278 | -1.58 | 0.000 |
| 1451128_s_at | Kif22 | 357 | 565 | -1.58 | 0.000 |
| 1448995_at | Pf4 | 264 | 419 | -1.58 | 0.016 |
| 1416076_at | Ccnb1 | 560 | 887 | -1.58 | 0.000 |
| 1434767_at | C79407 | 301 | 477 | -1.58 | 0.007 |
| 1427768_s_at | Myl3 | 22 | 35 | -1.59 | 0.006 |
| 1424971_at | Ccdc99 | 259 | 411 | -1.59 | 0.000 |
| 1417061_at | Slc40a1 | 220 | 350 | -1.59 | 0.000 |
| 1448466_at | Cdca5 | 208 | 330 | -1.59 | 0.000 |
| 1452040_a_at | Cdca3 | 692 | 1102 | -1.59 | 0.000 |
| 1453053_at | 2610036L11Rik | 129 | 206 | -1.60 | 0.007 |
| 1454877_at | Sertad4 | 836 | 1335 | -1.60 | 0.000 |
| 1417506_at | Gmnn | 527 | 843 | -1.60 | 0.001 |

Supplementary Table 2. Down-regulated genes in the palate of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice at E14.5 (Continued)

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1424991_s_at | Tyms | 568 | 912 | -1.61 | 0.008 |
| 1450496_a_at | 2810433K01Rik | 170 | 274 | -1.61 | 0.008 |
| 1454904_at | Mtm1 | 629 | 1012 | -1.61 | 0.025 |
| 1417019_a_at | Cdc6 | 205 | 331 | -1.61 | 0.000 |
| 1449877_s_at | Kifc1 | 139 | 224 | -1.61 | 0.002 |
| 1456863_at | Epha4 | 30 | 48 | -1.62 | 0.041 |
| 1451418_a_at | Spsb4 | 73 | 118 | -1.62 | 0.000 |
| 1437137_at | Fam70a | 158 | 257 | -1.62 | 0.039 |
| 1416802_a_at | Cdca5 | 462 | 751 | -1.62 | 0.000 |
| 1459646_at | Hs3st6 | 100 | 163 | -1.63 | 0.008 |
| 1424375_s_at | Gimap4 | 169 | 275 | -1.63 | 0.000 |
| 1452458_s_at | Ppil5 | 202 | 329 | -1.63 | 0.005 |
| 1434877_at | Nptx1 | 22 | 35 | -1.63 | 0.045 |
| 1460011_at | Cyp26b1 | 239 | 390 | -1.63 | 0.000 |
| 1418492_at | Grem2 | 199 | 327 | -1.64 | 0.000 |
| 1422851_at | Hmga2 | 1473 | 2418 | -1.64 | 0.014 |
| 1423813_at | Kif22 | 159 | 262 | -1.64 | 0.000 |
| 1455224_at | Angptl1 | 283 | 466 | -1.65 | 0.000 |
| 1456077_x_at | Cdc25c | 92 | 152 | -1.65 | 0.006 |
| 1431751_a_at | Mpped2 | 458 | 759 | -1.66 | 0.011 |
| 1418026_at | Exo1 | 180 | 300 | -1.66 | 0.000 |
| 1416043_at | Nasp | 156 | 260 | -1.67 | 0.001 |
| 1419083_at | Tnfsf11 | 19 | 31 | -1.69 | 0.023 |
| 1429404_at | 2010317E24Rik | 52 | 88 | -1.69 | 0.014 |
| 1428142_at | Etv5 | 173 | 292 | -1.69 | 0.011 |
| 1431043_at | Kbtbd5 | 47 | 79 | -1.69 | 0.035 |
| 1460314_s_at | Hist1h3a | 228 | 387 | -1.70 | 0.000 |
| 1423463_a_at | D2Ertd750e | 188 | 319 | -1.70 | 0.000 |
| 1452912_at | Dscc1 | 210 | 358 | -1.70 | 0.025 |
| 1421421_at | Angptl1 | 169 | 290 | -1.71 | 0.000 |
| 1430574_at | Cdkn3 | 124 | 215 | -1.73 | 0.015 |
| 1428029_a_at | H2afv | 1662 | 2880 | -1.73 | 0.013 |
| 1449298_a_at | Pde1a | 79 | 138 | -1.74 | 0.015 |
| 1450482_a_at | Pitx2 | 224 | 389 | -1.74 | 0.006 |
| 1447227_at | --- | 29 | 51 | -1.74 | 0.013 |
| 1435682_at | Lars2 | 139 | 242 | -1.74 | 0.000 |
| 1436948_a_at | Fam70a | 237 | 414 | -1.74 | 0.000 |
| 1423854_a_at | Rasl11b | 839 | 1505 | -1.79 | 0.000 |
| 1439078_at | Klhl4 | 178 | 320 | -1.80 | 0.013 |
| 1428922_at | 1200009O22Rik | 302 | 550 | -1.82 | 0.000 |
| 1433845_x_at | Dusp9 | 29 | 54 | -1.83 | 0.000 |
| 1436596_at | H2afv | 84 | 155 | -1.84 | 0.032 |
| 1450886_at | Gsg2 | 75 | 140 | -1.86 | 0.016 |
| 1416164_at | Fbln5 | 795 | 1491 | -1.88 | 0.000 |
| 1435532_at | LOC100048362 | 63 | 120 | -1.91 | 0.004 |
| 1454137_s_at | Hfe2 | 52 | 101 | -1.93 | 0.028 |
| 1443115_at | --- | 29 | 56 | -1.94 | 0.010 |
| 1423852_at | Shisa2 | 110 | 223 | -2.02 | 0.003 |
| 1450781_at | Hmga2 | 423 | 863 | -2.04 | 0.046 |
| 1452004_at | Calca | 59 | 125 | -2.11 | 0.023 |
| 1438238_at | 2010315B03Rik | 42 | 89 | -2.12 | 0.003 |
| 1454737_at | Dusp9 | 19 | 40 | -2.12 | 0.000 |
| 1458607_at | --- | 18 | 39 | -2.14 | 0.000 |
| 1457163_at | D730035F11Rik | 59 | 126 | -2.14 | 0.001 |
| 1416776_at | Crym | 61 | 132 | -2.15 | 0.027 |
| 1434013_at | Ablim3 | 33 | 71 | -2.16 | 0.018 |
| 1436867_at | Srl | 143 | 315 | -2.20 | 0.029 |
| 1449388_at | Thbs4 | 63 | 139 | -2.22 | 0.008 |
| 1452352_at | Ctla2b | 33 | 75 | -2.25 | 0.005 |
| 1456397_at | Cdh4 | 118 | 269 | -2.28 | 0.000 |
| 1449422_at | Cdh4 | 94 | 225 | -2.40 | 0.000 |
| 1438567_at | Vwa2 | 52 | 126 | -2.42 | 0.001 |

Supplementary Table 2. Down-regulated genes in the palate of *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice at E14.5 (Continued)

| AFFY_ID | Symbol | CKO Geo Mean | WT Geo Mean | CKO/WT Ratio | FDR |
|---|---|---|---|---|---|
| 1448554_s_at | Myh6 | 25 | 60 | -2.43 | 0.001 |
| 1450407_a_at | Anp32a | 502 | 1223 | -2.44 | 0.005 |
| 1451263_a_at | Fabp4 | 19 | 45 | -2.45 | 0.005 |
| 1417979_at | Tnmd | 90 | 225 | -2.51 | 0.025 |
| 1439658_at | Lmod3 | 14 | 36 | -2.55 | 0.028 |
| 1418769_at | Myoz2 | 43 | 116 | -2.69 | 0.018 |
| 1417023_a_at | Fabp4 | 30 | 83 | -2.79 | 0.000 |
| 1444083_at | Ttn | 58 | 174 | -2.98 | 0.029 |
| 1419606_a_at | Tnnt1 | 147 | 467 | -3.18 | 0.030 |
| 1450917_at | Myom2 | 26 | 83 | -3.19 | 0.034 |
| 1420757_at | Myf5 | 14 | 44 | -3.20 | 0.004 |
| 1441667_s_at | Smyd1 | 11 | 37 | -3.24 | 0.014 |
| 1448553_at | Myh7 | 47 | 152 | -3.25 | 0.000 |
| 1438175_x_at | Myom2 | 24 | 92 | -3.77 | 0.011 |
| 1448327_at | Actn2 | 75 | 283 | -3.77 | 0.026 |
| 1418155_at | Myot | 19 | 71 | -3.85 | 0.015 |
| 1457435_x_at | Myom2 | 41 | 188 | -4.56 | 0.014 |
| 1420884_at | Sln | 41 | 220 | -5.35 | 0.024 |
| 1418095_at | Smpx | 19 | 105 | -5.41 | 0.009 |
| 1435585_at | Tceal7 | 24 | 186 | -7.74 | 0.014 |
| 1435514_at | Lztfl1 | 11 | 105 | -9.53 | 0.000 |

**Supplemental Table 2**

Down-regulated genes in the palate of *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice at E14.5. These genes were identified with the selection criteria of genes showing >1.5-fold change with a <5% FDR. CKO refers to *Tgfbr2$^{fl/fl}$;Wnt1-Cre* mice and WT refers to *Tgfbr2$^{fl/fl}$* control mice. Log(2)-transformed gene expression scores are provided along with geometric means and FDR calculations.

Supplementary Table 3. Mass spectrometry analysis in the MEPM cells of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice

#1

| Mass | Score | Peptides matched | Protein |
|---|---|---|---|
| 32883 | 285 | 16 | Solute carrier family 25 |
| **32230** | **227** | **23** | **Similar to 14-3-3ζ protein** |
| **27754** | **186** | **22** | **14-3-3ζ protein** |
| 28814 | 141 | 8 | Phosphoglycerate mutase 1 |
| 28069 | 126 | 17 | 14-3-3β protein |
| 28285 | 104 | 20 | 14-3-3γ protein |
| 20848 | 92 | 9 | H1 histone family, member O |

#2

| Mass | Score | Peptides matched | Protein |
|---|---|---|---|
| **274052** | **1153** | **104** | **Spectrin beta 2 isoform 1** |
| 269665 | 669 | 46 | Talin 1 |
| 280325 | 639 | 62 | Filamin alpha |
| 272368 | 621 | 51 | Fibronectin 1 |
| 285170 | 451 | 34 | Spectrin alpha 2 |
| 41766 | 365 | 38 | Actin gamma |
| 272257 | 265 | 16 | Fatty acid synthase |

**Supplemental Table 3**
Mass spectrometry analysis in the MEPM cells of *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. These molecules were identified using mass spectrometry with extracts from MEPM cells of E13.5 *Tgfbr2*$^{fl/fl}$ and *Tgfbr2*$^{fl/fl}$*;Wnt1-Cre* mice. #1 shows data from the approximately 30 kDa-band in Supplemental Figure 1C, and #2 shows data from the approximately 270 kDa-band in Supplemental Figure 1C.