

# Quantification of 3-dimensional morphology of craniofacial mineralized tissue defects in Tgfb2/Osx-Cre mice

Running title: 3D modeling in orofacial CT images

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## footnote

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## Disclosures

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Quantification of 3-dimensional morphology of craniofacial mineralized tissue defects in  
Tgfr2/Osx-Cre mice

**ABSTRACT**

Craniofacial morphology is affected by the growth, development, and 3-dimensional (3-D) relationship of mineralized structures including the skull, jaws, and teeth. Despite fulfilling different purposes within this region, cranial bones and tooth dentin are derived from mesenchymal cells that are affected by perturbations within the TGF- $\beta$  signaling pathway. TGFBR2 encodes a transmembrane receptor that is part of the canonical, SMAD-dependent TGF- $\beta$  signaling pathway and mutations within this gene are associated with Loeys-Dietz syndrome, a condition which often presents with craniofacial signs including craniosynostosis and cleft palate. To investigate the role of Tgfr2 in immature, but committed, mineralized tissue forming cells, we analyzed postnatal craniofacial morphology in mice with conditional Tgfr2 deletion in Osx-expressing cells. Novel application of a 3-D shape-based comparative technique revealed that Tgfr2 in Osx-expressing cells results in impaired postnatal molar root and anterior cranial growth. These findings support those from studies using similar Tgfr2 conditional knockout models, highlights the anomalous facial and dental regions/structures using tomographic imaging-based techniques, and provides insight into the role of Tgfr2 during postnatal craniofacial development.

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31 Keywords: 3D modeling, Morphometry, Tgfr2, Tissue Engineering

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## 35 **1. INTRODUCTION**

36 Growth and development of specialized structures within the craniofacial complex  
37 requires dynamic coordination between the cells of multiple organs and tissues. Among these  
38 elements are the teeth, jaws, and cranial skeleton, all mineralized structures which significantly  
39 affect function (e.g. communication and eating) and appearance (e.g. facial profile, proportions,  
40 and symmetry) within this region. Craniofacial morphology of human patients can be  
41 quantitatively described via cephalometric analyses that rely on linear and angular measurements  
42 between standardized radiographic landmarks <sup>1,2</sup>. However, reduced dimensionality (i.e. from 3  
43 to 2-dimensions) may obscure critical shape-based differences in complete structures. Volume  
44 rendering from tomographic imaging (e.g. CT, MRI, or  $\mu$ CT) circumvents this issue by  
45 permitting 3-D shape-based comparisons that provide detailed insight into the etiology of  
46 anomalous craniofacial states.

47 Though among the most common birth defects, the genetic cause of many craniofacial  
48 anomalies remains unknown. However, mutations in TGFBR2 have been associated with Loey-  
49 Dietz syndrome, a condition which can present with connective tissue defects and craniofacial  
50 signs including craniosynostosis and cleft palate <sup>3,4</sup>. TGFBR2 is part of the canonical, SMAD-  
51 dependent TGF- $\beta$  signaling pathway and encodes a constitutively active transmembrane  
52 serine/threonine tyrosine kinase receptor that initiates downstream signaling by forming a  
53 heterotetrameric complex with TGFBR1 <sup>5</sup>. The TGF- $\beta$  superfamily encompasses 2 receptor types  
54 and multiple ligands such as TGF- $\beta$ s (e.g. TGF-  $\beta$ 1, TGF-  $\beta$ 2, TGF-  $\beta$ 3), bone morphogenetic  
55 proteins (BMPs), activins, and growth and differentiation factors (GDFs) that interact with other  
56 pathways to influence mineralized tissue development. Specifically, studies using Tgfr2 loss of  
57 function animal models suggest a critical role during the development of structures (e.g. teeth,  
58 jaw, and cranial skeleton) that impact overall craniofacial morphology. Phenotypic observations

59 include cleft palate, absent or defective calvaria components, reduced and/or defective  
60 mandibular process morphology, abnormal molar root, and abnormal dentin formation <sup>6-11</sup>.

61 Mesenchymal cells are multipotent cells that, upon differentiation, contribute to multiple  
62 craniofacial structures including bones and teeth. Commitment to a bone-forming osteoblastic or  
63 dentin-forming odontoblastic lineage corresponds with the expression of Osterix/SP7 (*Osx*), a  
64 transcription factor that restricts chondrogenic differentiation and acts downstream of *Runx2*,  
65 another key regulator of bone formation <sup>12</sup>. Despite critical spatial, functional, and gene  
66 expression differences between mature osteoblasts and odontoblasts, Cre-recombinase  
67 expression driven by the *Osx* promoter allows targeted gene knockout in immature, but  
68 committed, mineralized tissue forming cells <sup>13</sup>. Such *Osx* Cre-recombinase based excisional  
69 approaches also circumvent perinatal lethality issues observed in other tissue specific conditional  
70 knockout models thereby allowing investigation into gene function and craniofacial morphology  
71 at postnatal time points <sup>6,8</sup>. Multiple studies documented that *Osx*-Cre mediated *Tgfr2* deletion  
72 leads to shortened molar root, hypomorphic cementum, and reduced bone volume and bone  
73 density <sup>11,14,15</sup>.

74 In the present study, using mice with *Osx*-Cre mediated *Tgfr2* deletion, we focus our  
75 studies in 3-dimensional morphology to highlight insight into the etiology of anomalous  
76 craniofacial states, but have not been characterized. Our analyses at postnatal day 26 correspond  
77 to near-maximal skull growth and indicate that *Tgfr2* affects anterior skull, palate, skull base,  
78 mandibular, and molar root morphology. These results critically corroborate the craniofacial  
79 phenotypic outcomes of conditional *Osx*-Cre mediated *Tgfr2* deletion reported in other studies  
80 <sup>9,11</sup> while also highlighting a useful method for quantitatively comparing the 3-dimensional  
81 morphology of mineralized structures.

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## 84 **2. MATERIALS AND METHODS**

### 85 **2.1 Animal Model**

86 All animals and experiments were performed in accordance with the policies and federal laws for  
87 the judicious use of vertebrate animals, as approved by the University Committee on Use and  
88 Care of Animals at the University of Michigan. Conditional knockout mice for *Tgfr2* were  
89 created through Cre-lox recombination driven by the *Osx* promoter. Mice that did not carry the

90 Osx-Cre transgene (i.e. Osx-Cre<sup>-</sup>), and therefore did not have Tgfr2 deletions, were designated  
91 as “control” animals and compared against their Osx-Cre<sup>+</sup> (conditional knockout or “cKO”)  
92 littermates. All analyses were performed at postnatal day 26 (P26).

93

94 **2.2 Micro-CT (μCT)** Micro-CT scanning of fixed heads was performed at the University of  
95 Michigan using a Micro-CT core (μCT40 Scanco Medical, Bassersdorf, Switzerland). Scan  
96 settings were the following: voxel size 18μm, 55kVp, 109μA, 0.5mm AL filter, and integration  
97 time 500ms.

98

### 99 **2.3 Image Analysis**

100 Structures of interest were segmented and converted to 3D mesh models from micro-CT data  
101 using ITK-SNAP (itksnap.org, open source software developed by grants and contracts from the  
102 United States National Institutes of Health). Shape comparisons against a single reference model  
103 (i.e. control mouse structure/s of interest) were then performed using tools developed in 3D  
104 Slicer (slicer.org, open source software). Briefly, landmarks (see Tables 1-3) were placed (“CMF  
105 Reg tool”) thereby allowing for model superimposition based on the minimization of Euclidean  
106 distance between similar surface points. The distances between corresponding landmarks were  
107 measured using the “Q3DC tool”. The distances between closest points on the model surfaces  
108 were also calculated using “Model to Model Distance tool” which were then used to generate a  
109 heatmap (“Shape Population Viewer tool”) that illustrated regions/surfaces which differed from  
110 the reference model based on point to point alignment.

111

112

## 113 **3. RESULTS**

### 114 **Craniofacial dysmorphism is observed in Tgfr2<sup>fl/fl</sup>/Osx-Cre mice**

115 Disruption of Tgfr2 by Osx-Cre resulted in altered craniofacial morphology that was  
116 apparent at P26. Most pronounced were reductions in skull and incisor size, the latter of which  
117 appeared either missing or unerupted upon initial inspection (Figure 1A-H). Tomographic and  
118 lateral radiographic analysis confirmed the presence of diminutive upper and lower incisors  
119 which likely contributed to an anterior open bite phenotype (Figure 1C, D, G, H, I). Also  
120 apparent was posterior widening of the interfrontal suture and porosities within the frontal bone

121 suggestive of lower mineral content (Figure 1I). Though these collective phenotypic differences  
122 indicate changes in the anterior facial morphology of cKO mice, the inability to localize specific  
123 regions of change represents a limitation of 2-dimensional cephalometric analysis. We therefore  
124 employed qualitative 3-dimensional whole skull alignment which both highlighted  
125 anteroposterior skull shortening and implicated deficiencies within structures anterior of the  
126 coronal suture (Figure 1J).

127

### 128 **Anterior skull defects are observed in $Tgfb2^{fl/fl}$ /Osx-Cre mice**

129 Shape-based 3-dimensional analysis indicated a high degree of morphologic difference in  
130 anterior regions of cKO mouse skulls (Figure 2, top). Whole skull superimposition revealed that  
131 the area surrounding the intersection of the frontonasal and interfrontal sutures was a “hotspot”  
132 of morphologic change (Figure 2, middle). Likewise, significant changes in shape were seen in  
133 the maxilla and became progressively worse when moving anterior from the transverse palatine  
134 suture (Figure 2, bottom). Importantly, these observations (i.e., differences along sutures within  
135 the anterior facial region) corroborated those from our 2-dimensional analysis thereby supporting  
136 quantitative 3-dimensional analysis as an improved method for assessing phenotypic changes.  
137 Despite its utility in shape-based data visualization, a limitation of this technique can also be  
138 seen along the zygomatic arch which, due to its long, narrow shape, is sensitive to model  
139 superimposition (Figure 2, bottom).

140

### 141 **Morphologic differences are present along the mandibular periphery in $Tgfb2^{fl/fl}$ /Osx-Cre** 142 **mice**

143 Broad differences in craniofacial appearance (e.g. facial profile) are affected by the size,  
144 shape, and position of skull components. Besides the ossicles of the inner ear, the mandible is the  
145 only mobile skull bone and plays a critical role in both mastication and the determination of  
146 facial profile. Shape-based analyses of cKO mice validated suspicions of shortened mandibles  
147 and revealed deficiencies at the condyloid process, coronoid process, angular process, and  
148 incisor alveolus (Figure 3). Despite reductions in overall jaw size, these structures were not  
149 grossly misshapen in cKO mice. Rather, the position of these structures along the periphery of  
150 the mandible and the proportional but scaled-down appearance of the mandible indicated  
151 impaired growth following  $Tgfb2$  disruption.

152

153 **Anterior skull length is shorter, but skull base morphology is not significantly affected in**  
154 **Tgfb<sup>fl/fl</sup>/Osx-Cre mice**

155 The skull base is a midline structure that connects the facial skeleton with posterior  
156 elements of the skull and aberrant skull base morphology has been found to contribute to other  
157 syndromic facies. Analysis of the skull base revealed that skull base is proportionally shorter as  
158 if scaled down to the smaller skull size in the cKO mice (Figure 4A and 4B). Differences in skull  
159 morphology and facial profile were therefore due to differences in the anterior skull (e.g. facial  
160 skeleton and palate) and not secondary effects (i.e., restricted anterior and superior growth of the  
161 facial skeleton) of disproportional skull base shortening. However, though shape-based analyses  
162 seemingly indicate differences along the presphenoid and anterior portions of the greater wings  
163 of the sphenoid, these can be disregarded and attributed to an inherent limitation during image  
164 segmentation; tomographic image resolution restricts differentiation of fine anatomic structures.  
165 As such, “hotspots” were seen along the periphery of anterior structures in both control and cKO  
166 mice (Figure 4C).

167

168 **Molar root morphology is more affected than the crowns in Tgfb<sup>fl/fl</sup>/Osx-Cre mice**

169 Facial height, and therefore appearance, is a byproduct of mandibular morphology (e.g.  
170 mandibular angle) and vertical dimension of occlusion (VDO), the superior-inferior relationship  
171 of the jaws. VDO is determined by tooth size and alignment as this space in dentate organisms is  
172 primarily occupied by the crowns of molar teeth. Crown surface features (i.e. cusps, ridges, and  
173 fossae) are highly complex and harmonious inter-arch relationship exists when there is  
174 interposition of these features. Analysis of mandibular first and second molars revealed that  
175 shape-based differences in cKO mouse molars were more pronounced at the root apices  
176 compared to the crowns (Figure 5A and 5B). Therefore, craniofacial morphological differences  
177 are driven by skull elements and not coronal dysmorphism. Whether Tgfb<sup>fl/fl</sup> plays a direct role in  
178 root elongation or if the root phenotype observed in this study represents outcomes of cell (i.e.  
179 odontoblast and bone producing mesenchyme) interactions cannot be determined using the  
180 current model and 3-dimensional analytic technique.

181

182

183 **4. DISCUSSION**

184 Multiple previous studies demonstrated that *Osx-Cre* mediated *Tgfr2* deletion leads to  
185 various types of abnormalities in mineralized tissues. With most of previous histological analysis  
186 being focused on the mechanism leading to abnormal odontoblast and osteoblast differentiation,  
187 our 3-dimensional morphological analysis provides a complementing insight into the etiology of  
188 anomalous craniofacial states<sup>11,14,15</sup>. Model segmentation and digital superimposition from  
189 tomographic imaging allows for the unbiased, 3-dimensional shape-based comparison of  
190 structures of interest. Such analyses provide detailed insight regarding regions or sources  
191 underlying abnormal craniofacial morphology beyond the capabilities of standard cephalometric  
192 tracing and analysis<sup>1,2</sup>. While tomographic imaging (e.g. cone beam CT) has become more  
193 common in clinical dentistry, increased radiation exposure and the high cost of imaging  
194 equipment limits 3-D analysis to either small areas of interest (e.g. single teeth) or cases  
195 involving extensive surgical reconstruction. Despite inherent limitations related to image  
196 resolution, comparative heatmaps based on superimposed models provide quantitative,  
197 straightforward, and visually attractive representations of morphology-based data.

198 Gross phenotypic differences (i.e. anterior open bite and reduced overall skull size)  
199 observed in *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mice are attributable to small incisor size and disruption of  
200 structures/regions proximal to the nasofrontal, interfrontal, and transverse palatine sutures. This  
201 suggests that *Tgfr2* may influence overall craniofacial morphology by maintaining suture  
202 patency and supporting growth in the anterior facial region. These observations were critical  
203 findings of the present study because: (1) small, non-occluding incisors and skulls were  
204 consistent with other studies using a similar *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mouse model<sup>9,11</sup> and (2) the  
205 application of our shape-based analysis permitted identification of specific craniofacial regions  
206 with morphologic dissimilarities. It was noted by previous studies that *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO  
207 mice have normal size of the skull and mandible at the new born stage<sup>11</sup>. Therefore, the noted  
208 small skull and mandible are due to affected postnatal growth due to *Tgfr2* loss of function. In  
209 previous studies, *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mice develop dwarfism due to the decrease  
210 chondrocyte proliferation in the growth plate<sup>11</sup>. Given that skull base elongation is through  
211 endochondral ossification, the shortened skull base in *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO is likely due to the  
212 decreased chondrocyte proliferation in two synchondroses of the skull base. *Tgfr2* loss of  
213 function mediated by *Osx-Cre* leads to decreased proliferation and slow maturation of pre-



214 osteoblast<sup>11</sup>, which is not directly helpful to explain the small skull and mandible. Cranial  
215 sutures serve as signaling centers for skull bone growth and their premature fusion restricts  
216 postnatal calvaria growth, a hallmark of craniosynostosis<sup>16</sup> and the mechanism controlling  
217 mandible growth remains elusive. Though sutures in *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mice were not  
218 histologically evaluated to confirm premature fusion, we would expect craniosynostosis due to  
219 the known contribution of reduced TGF- $\beta$  signaling in premature suture fusion<sup>17,18</sup> and the  
220 craniofacial signs (i.e. craniosynostosis and abnormal palatal shape) in patients with Loeys-Dietz  
221 syndrome, a condition associated with *TGFBR2* mutations<sup>4,15</sup>. Additionally, *Tgfr2* is expressed  
222 in both cranial sutures and developing tooth buds thereby suggesting potential involvement their  
223 development<sup>19</sup>. Patients with Loeys-Dietz syndrome are also described as having dental findings  
224 including malocclusions, dental crowding, affected mandibular projection, and delayed eruption  
225 of permanent incisors, all traits which could affect facial profile and contribute to an anterior  
226 open bite similar to observations in mice.

227 Like reduced skull and incisor size, molar root dysmorphism is a consistent characteristic  
228 of *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mice<sup>11</sup>. Tooth formation requires spatiotemporally coordinated  
229 interaction between cells of different origin (i.e. epithelium-derived ameloblasts and  
230 mesenchyme-derived odontoblasts) and root formation initiates (postnatally in mice) after crown  
231 completion<sup>20,21</sup>. This process involves coordination of both enamel epithelium, Hertwig's  
232 epithelial root sheath (HERS) and mesenchyme. Root growth begins with the apical migration  
233 and fusion of the inner and outer enamel epithelium into HERS. The epithelial derived HERS  
234 subsequently affects root morphology as well as root dentin formation through its interaction  
235 with mesenchymal cells of the dental papilla. It was documented previously that *Tgfr2<sup>fl/fl</sup>/Osx-*  
236 *Cre* cKO mice have delayed elongation and disorganization in HERS<sup>11</sup>. Since *Osx-Cre* target  
237 into mesenchyme of tooth, the affected HERS is secondarily due to the affected odontoblast  
238 differentiation. In our study, the morphological analysis showcases the short, dysmorphic molar  
239 roots in *Tgfr2<sup>fl/fl</sup>/Osx-Cre* cKO mice suggests that *Tgfr2* in committed odontoblasts within the  
240 dental papilla is important for postnatal root elongation and dentin development. This influence  
241 of *Tgfr2* on dentin development and tooth morphology is further supported by observations of  
242 dysmorphic crown dentin formation in alternative *Tgfr2*-cKO mouse models<sup>6,8</sup>.

243 The localized effects of conditional *Tgfr2* knockout on skull and tooth morphology are  
244 interesting considering how *Osx* is expressed as early as e13.5 and conditional gene knockout

245 should, presumably, affect all *Osx*-expressing skull components and coronal and radicular dentin  
246 alike<sup>12,13</sup>. However, we believe that *Tgfr2* plays important roles during postnatal mineralized  
247 tissue formation because morphologically affected regions undergo significant growth and  
248 development after birth. As previously discussed, root formation is a postnatal (through  
249 approximately P26) event in mice and differences were seen in root but not crown morphology.  
250 Similarly, the murine facial skeleton during the first month of life grows more relative to the  
251 cranium and was another “hotspot” of morphologic difference<sup>22</sup>. Conversely, we did not see  
252 significant differences in skull base morphology, a region with proportionality little anterior-  
253 posterior growth through P30. *Tgfr2* in *Osx*-expressing cells was also found to be dispensable  
254 during prenatal but not postnatal femur growth<sup>15</sup>. We therefore believe that morphologic  
255 differences reflect postnatal-specific differences caused by *Tgfr2* deficiency and not a  
256 secondary effect of the *Osx* promoter used to drive Cre-recombinase based excision.

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258

## 259 **5. CONCLUSION**

260 We hereby present findings that corroborate and expand upon prior findings using a  
261 similar *Tgfr2*<sup>fl/fl</sup>/*Osx*-Cre cKO mouse model by identifying specific regions of morphologic  
262 change in the anterior skull, mandible and molar roots. Superimposition of 3D models  
263 constructed from tomographic imaging presents a useful tool for determining the etiology of  
264 changes to craniofacial morphology and application of this technique critically expounds the role  
265 of *Tgfr2* during postnatal development of mineralized tissues in the craniofacial region.

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## 325 **FIGURE LEGENDS**

326

327 **Figure 1.** Comparison of gross craniofacial morphology. (A-H) External morphology and lateral  
328 cephalometric radiography. *Tgfr2*-cKO mice (bottom, E-H) had reduced anterior-posterior skull  
329 length and erupted incisor length at postnatal day 26 (P26). Noted findings were diminished skull  
330 size and an anterior open bite in *Tgfr2*-cKO mice. (I) Whole skull tomographic imaging  
331 confirmed the presence of diminutive upper and lower incisors and suggested potential  
332 shortening of the jaws and the presence of interfrontal suture pathology in *Tgfr2*-cKO mice. (J)  
333 Whole skull tomographic imaging-based comparison of craniofacial morphology. Posterior  
334 alignment of whole Control vs. *Tgfr2*-cKO (purple vs. green, respectively) skulls illustrated  
335 differences in overall size and the morphology of facial skeletal structures.

336

337 **Figure 2.** Shape-based 3-dimensional comparison of whole skull morphology. (Top) Heatmaps  
338 generated from shape-based comparisons of entire skulls indicated “hotspots” of change located  
339 in the anterior skulls of *Tgfr2*-cKO mice (bottom row). (Middle) Magnified views of the  
340 interfrontal suture and anterior skull regions that exhibited significant morphologic dissimilarity.  
341 (Bottom) Magnified views of the transverse palatine suture and palatal regions that exhibited  
342 significant morphologic dissimilarity. Green indicates morphologic similarity (i.e., no change)  
343 whereas warm (e.g., yellow-to-red) and cool (e.g., cyan-to-violet) colors indicate the degree of  
344 reduction or increase, respectively, in Euclidean distances between similar surface points. A  
345 single control mouse (i.e., Ct 4) was used as reference to generate the comparative heatmaps for  
346 control samples (i.e., Ct 1 through 4; top rows) and *Tgfr2*-cKO samples (i.e., mt 1 through 4;  
347 bottom rows) in each panel.

348

349 **Figure 3.** Comparison of mandibular morphology. Heatmaps generated from shape-based  
350 mandibular comparisons reflect observations of reduced lower jaw size in *Tgfr2*-cKO mice  
351 (bottom row) compared to control counterparts (top row). “Hotspots” of significantly dissimilar  
352 morphology (i.e., regions colored purple and yellow) were located along the periphery and  
353 include the condyloid process, coronoid process, angular process, and incisor alveolus. Green  
354 indicates morphologic similarity (i.e., no change) whereas warm (e.g., fuchsia-to-red) and cool  
355 (e.g., cyan-to-violet) colors indicate reduction or increase, respectively, in Euclidean distances  
356 between similar surface points. A single control mouse (i.e., Sample ID 7) was used as reference  
357 to generate the comparative heatmaps for control samples (i.e., Sample IDs 2, 3, 6, 7; top rows)  
358 and *Tgfr2*-cKO samples (i.e., Sample IDs 4, 5, 8, 9; bottom rows) in each panel.

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360

361 **Figure 4.** Comparison of skull base morphology. (A) Representative skull base with landmarks  
362 corresponding to those listed in Table 2. (B) Magnified overlay of elements defining the inferior  
363 skull base indicated proportional shortening of the skull base in *Tgfr2*-cKO mice (yellow).  
364 Structures are bound by points 1, 2, 4, and 7 shown in Table 2 and Figure 4A. Spheno-occipital  
365 synchondrosis (SOS) is located between the basioccipital and basisphenoid. Intersphenoid  
366 synchondrosis (ISS) is located between the basisphenoid and presphenoid. (C) Heatmaps  
367 generated from shape-based comparisons of skull base morphology between Control and *Tgfr2*-

368 cKO mice (top vs. bottom row, respectively) illustrated differences along the anterior wings of  
369 the alisphenoid. Green indicates morphologic similarity (i.e., no change) whereas warm (e.g.,  
370 yellow-to-red) and cool (e.g., cyan-to-violet) colors indicate reduction or increase, respectively,  
371 in Euclidean distances between similar surface points. A single control mouse (i.e., Ct 3) was  
372 used as reference to generate the comparative heatmaps for control samples (i.e., Ct 1 through 4;  
373 top rows) and Tgfr2-cKO samples (i.e., mt 1 through 4; bottom rows) in each panel.

374  
375 **Figure 5.** Comparison of mandibular molar morphology. (A) Representative molars with  
376 landmarks corresponding to those listed in Table 3. (B) Heatmaps generated from shape-based  
377 comparisons of molar morphology between Control and Tgfr2-cKO mice highlighted  
378 differences in root length. Non-significant differences in coronal features were observed. Green  
379 indicates morphologic similarity (i.e., no change) whereas warm (e.g., yellow-to-red) and cool  
380 (e.g., cyan-to-violet) colors indicate reduction or increase, respectively, in Euclidean distances  
381 between similar surface points. A single control mouse (i.e., Ct 3) was used as reference to  
382 generate the comparative heatmaps for control samples (i.e., Ct 1 through 4; top rows) and  
383 Tgfr2-cKO samples (i.e., mt 1 through 4; bottom rows) in each panel.

384  
385  
386 **Table 1.** Mandibular landmarks used to superimpose digital models and generate heatmaps in  
387 Figure 3.

388  
389 **Table 2.** Cranial base landmarks used to superimpose digital models and generate heatmaps in  
390 Figure 4.

391  
392 **Table 3.** Mandibular molar landmarks used to superimpose digital models and generate  
393 heatmaps in Figure 5.

Table 1. Mandibular Points Legend

Point 1	Most anterior point on alveolus
Point 2	Most superior, posterior condyle
Point 3	Most distal point on angular process
Point 4	Most superior point on coronoid process
Point 5	Most superior point of antegonial notch
Point 6	Distal point of molar alveolus
Point 7	Anterior point of molar alveolus
Point 8	Greatest concavity along posterior border

Table 2. Cranial Base Points Legend

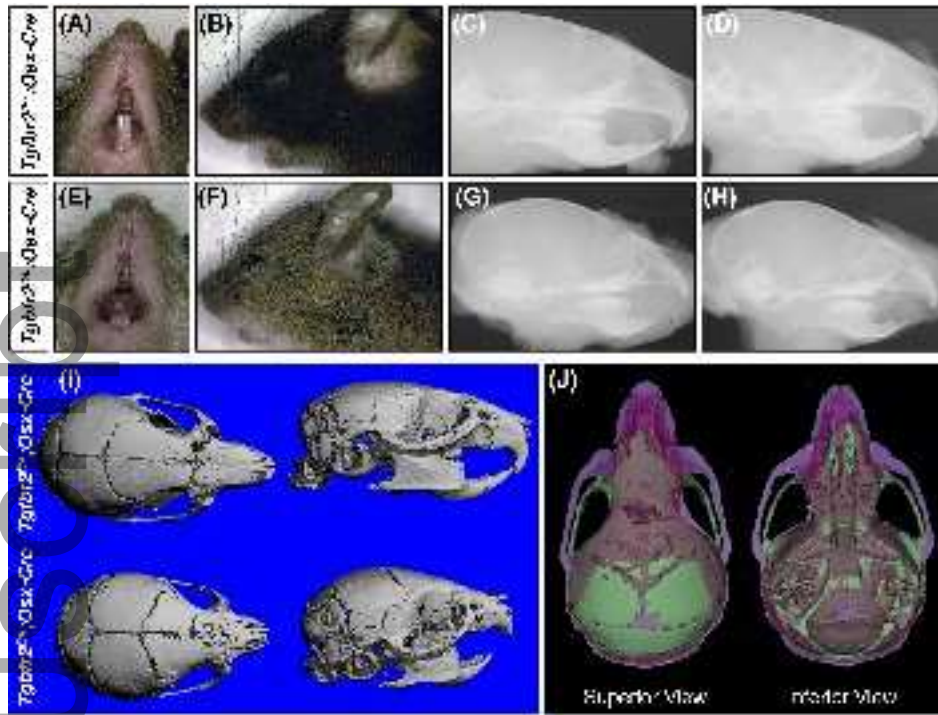
Point 1	Most anterior point of the indentation in the center of the presphenoid
Point 2	Most anterior point on the anterior projection on the presphenoid
Point 3	Postero-medial point of the inferior portion of the left alisphenoid
Point 4	Most antero-lateral point on corner of the basioccipital at the basioccipital synchondrosis
Point 5	Mid-point on the anterior margin of the foramen magnum, taken on squamosal occipital
Point 6	Most infero-lateral point on the squamous occipital
Point 7	Mid-point on the posterior margin of the foramen magnum, taken on basioccipital

Table 3. Mandibular Molar Points Legend

Point 1	Middle buccal surface
Point 2	Middle lingual surface
Point 3	Mesial contact point
Point 4	Distal contact point
Point 5	Mesio-buccal cusp tip
Point 6	Disto-buccal cusp tip
Point 7	Mesio-buccal root apex

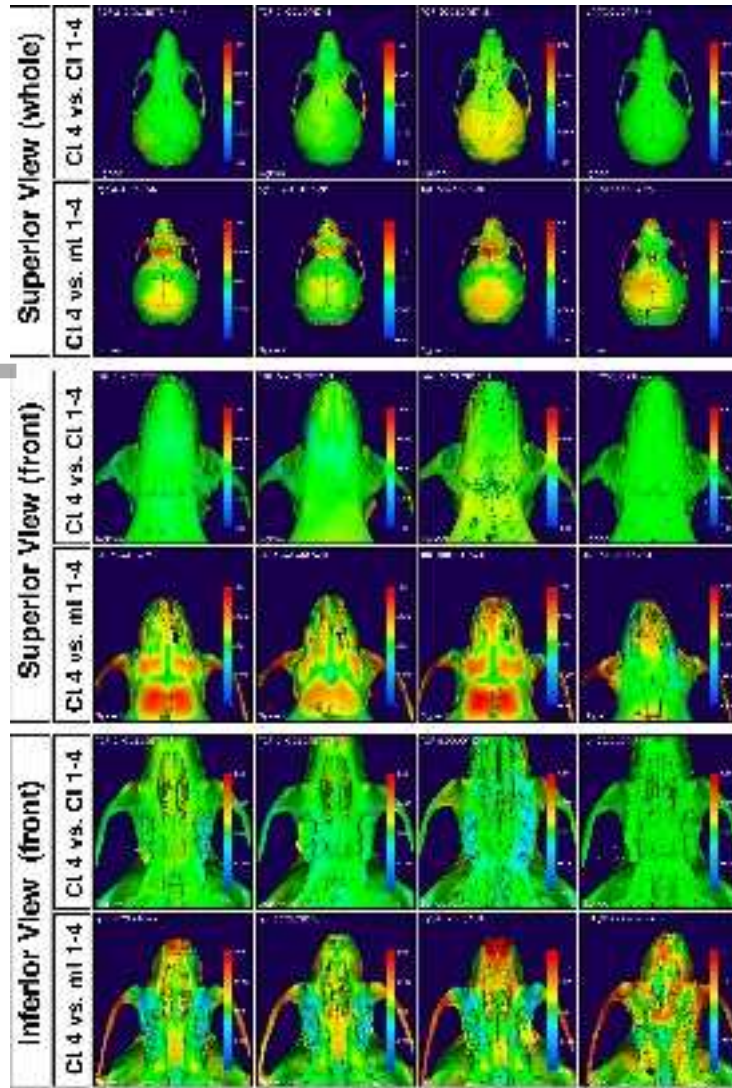
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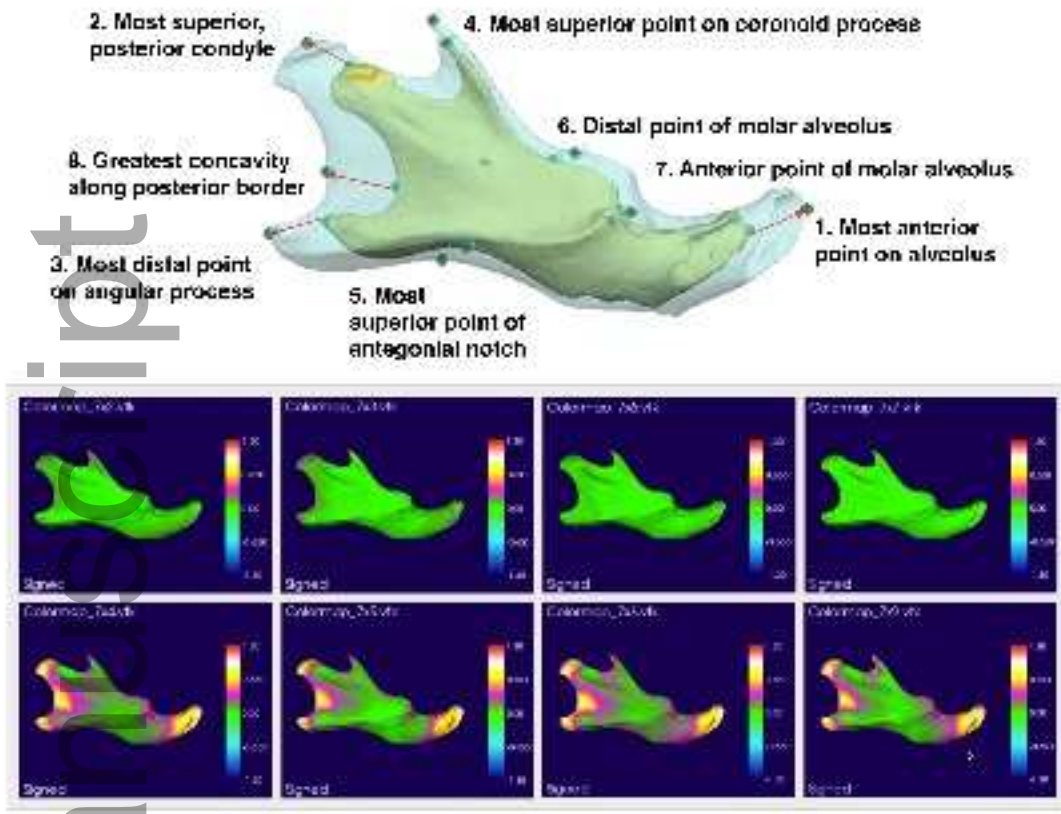
Snider, Louie et al., Figure 1

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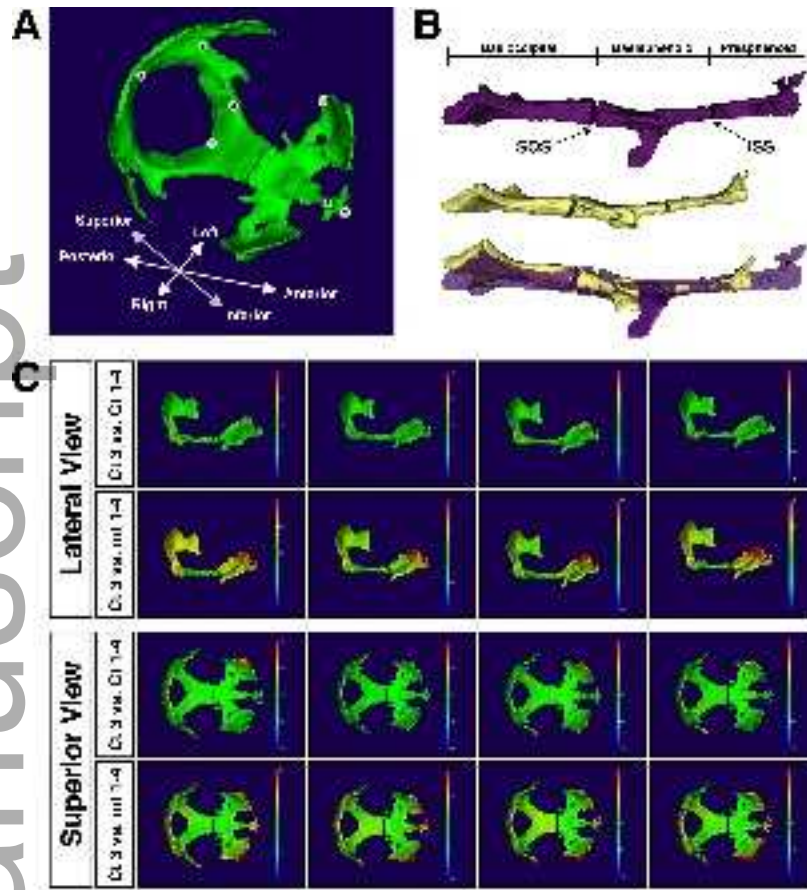
Snider, Louie et al., Figure 2

osi2\_1099\_f2.tif



Snider, Louie et al., Figure 3

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Snider, Louie et al., Figure 4

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Snider, Louie et al., Figure 5

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