



Supplementary Figure 1. Correlation of epithelial seam degeneration, cell death, and *Tgfb3* and *Mmp13* expression in E14.5 mice. (A-C) Histological analysis of wild-type embryos reveals a fully formed epithelial seam which is beginning to degenerate (A). Similarly, in *Irf6*^{+R84C};*Jag2*^{+ΔDSL} embryos, regions of epithelial degeneration between the palate and the tongue are apparent (arrowed in B). Further posteriorly, epithelial degeneration is more extensive and epithelial triangles are present (arrowed in C). (D-F) Immunofluorescence analysis for activated caspase 3 in adjacent sections to those depicted in A, B and C, respectively reveals extensive cell death in the midline epithelial seam of wild-type embryos (D) and in the region of epithelial degeneration in *Irf6*^{+R84C};*Jag2*^{+ΔDSL} littermates (arrowed in E and F). (G-L) At a slightly earlier time-point than shown in A-F, when the epithelia are still intact, *Tgfb3* and *Mmp13* are expressed in the midline epithelial seam of wild-type embryos (G,J). In *Irf6*^{+R84C};*Jag2*^{+ΔDSL} embryos, *Tgfb3* and *Mmp13* are expressed in regions of presumptive epithelial degeneration (arrowed in H,I,K,L). p, palate; t, tongue. Scale bars: 100 μm.