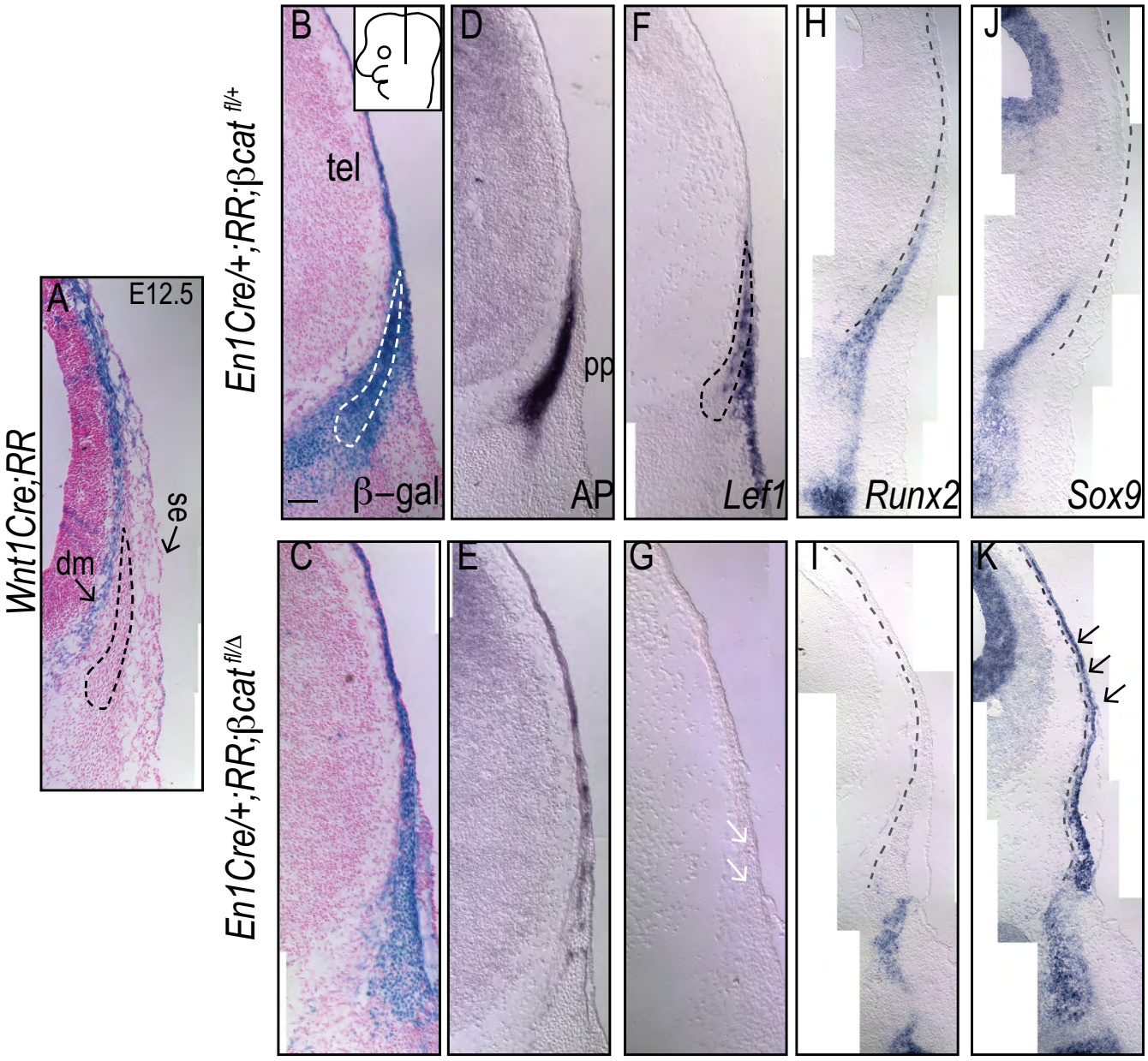

Fig. S1. β-catenin is required for cranial bone fate in paraxial mesoderm osteoprogenitor cells. X-Gal (**A-C**) and AP (**D**,**E**) staining or in situ hybridization (**F-K**) on tissue sections. Dashed lines, skull progenitors (A,B,F) or *En1Cre* lineage (H-K). White arrows indicate absent *Lef1* expression (G). Black arrows point to ectopic *Sox9* expression (K). Inset (B) shows plane of section. Tel, telencephalon; dm, dura mater; se, surface ectoderm; pp, parietal bone progenitor cells. Scale bar: 100 μm.

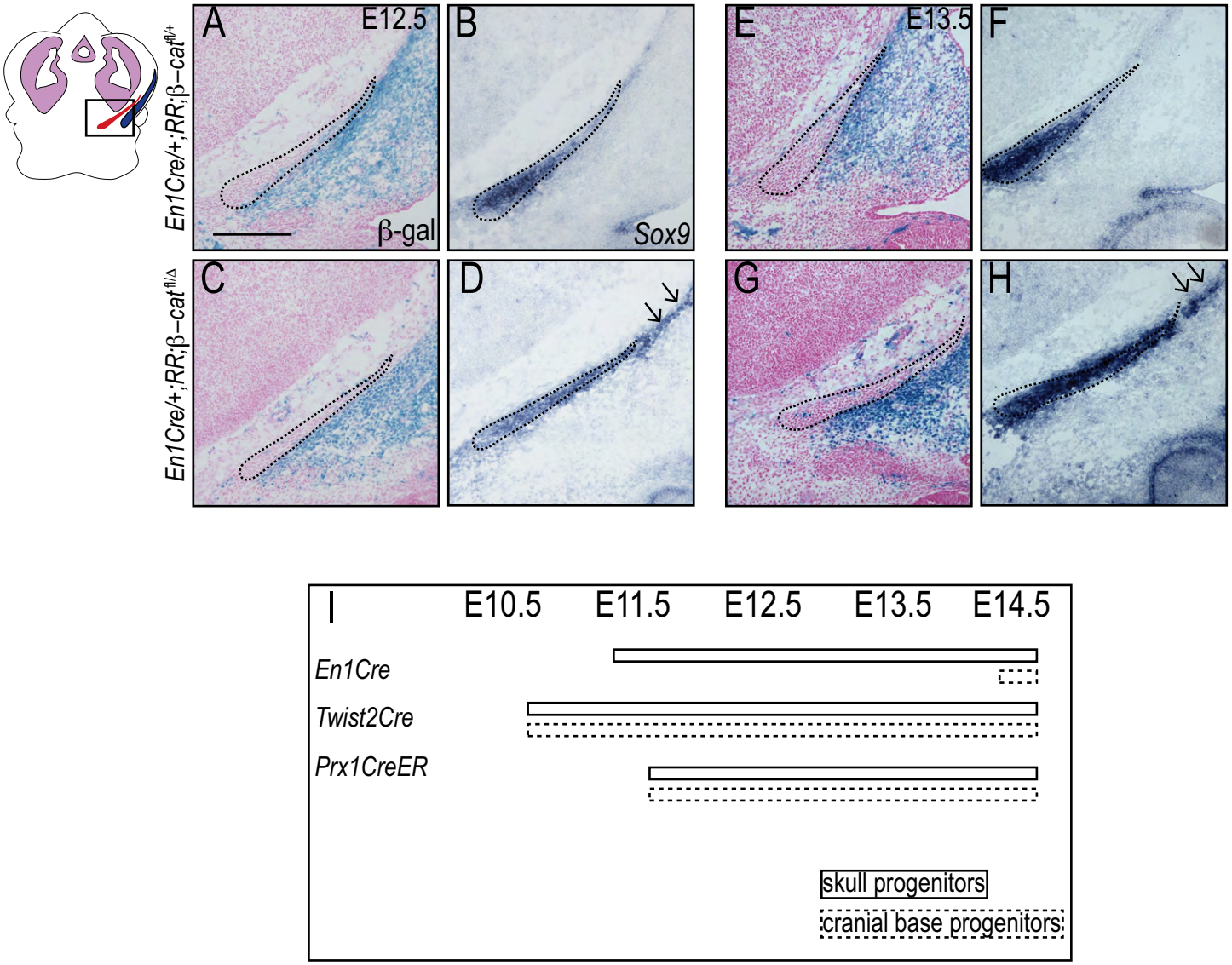

Fig. S2. Lack of contribution of *En1Cre* lineage to skull base and description of temporal differences in Cre activity. (**A-H**) X-Gal staining (A,C,E,G) or in situ hybridization (B,D,F,H) on coronal sections. Arrows (D,H) indicate ectopic *Sox9* expression. (**I**) Onset of Cre recombinase activity for the lines used in this study. Scale bar: 100 μm.

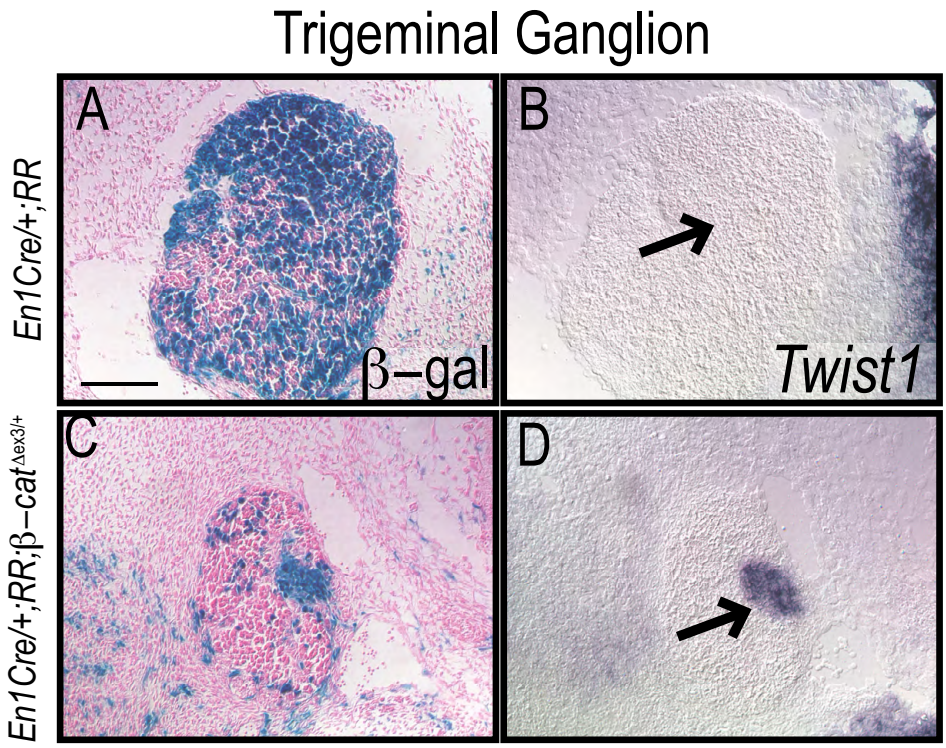

Fig. S3. β**-catenin is sufficient for ectopic *Twist1* expression.** Coronal tissue sections through trigeminal ganglia stained with X-Gal (**A**,**C**) or hybridized with mRNA probes (**B**,**D**). Arrows indicate area of ectopic expression. Scale bar: 100 μm.

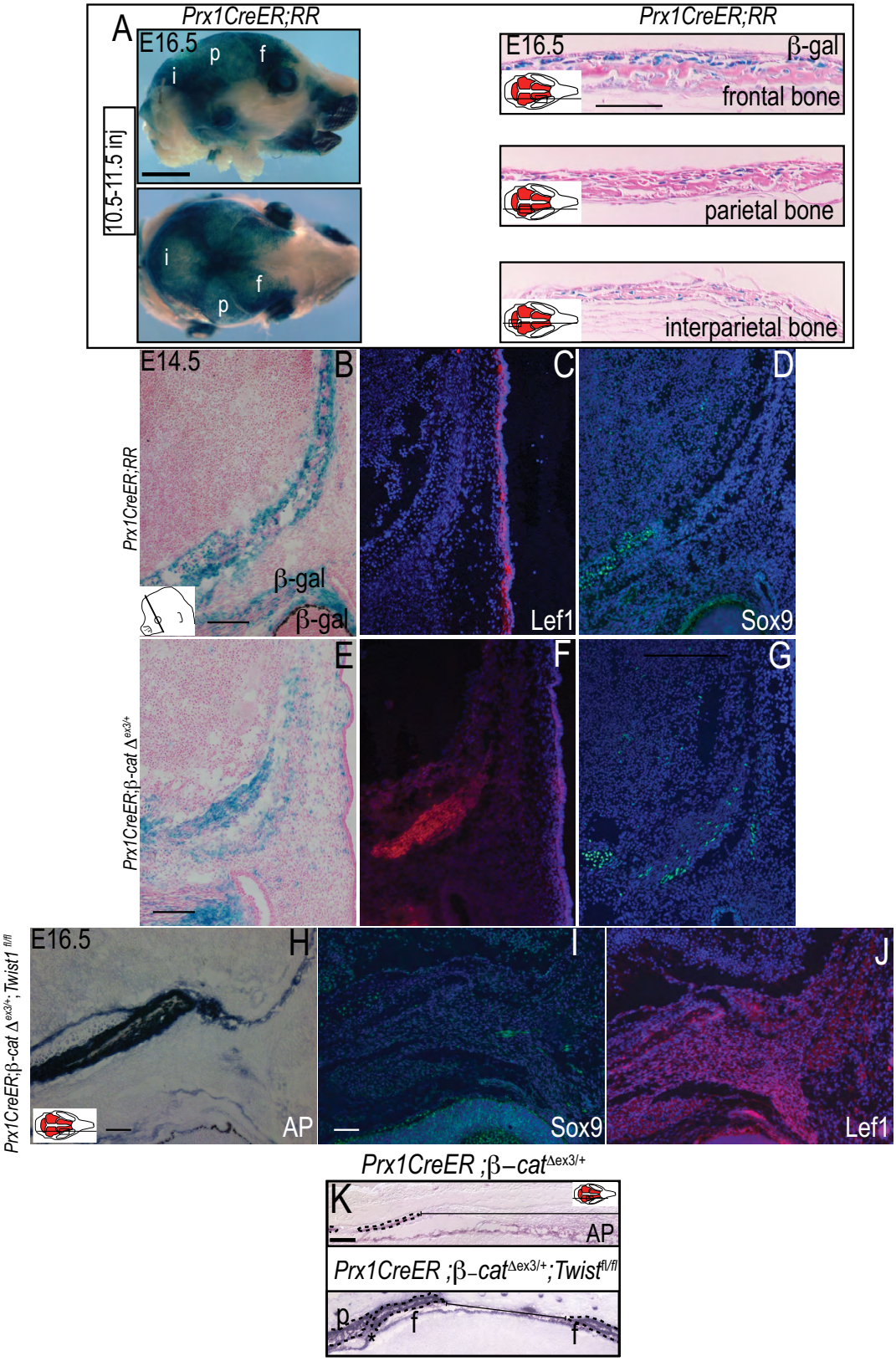

Fig. S4. Activation of β-catenin results in Lef1 expression; deletion of *Twist1* restores AP in Lef1-expressing cells. (**A**,**B**,**E**) Whole-mount X-Gal staining performed with skin removed and sagittal (A) or coronal (B,E) sections counterstained with Eosin. (**C**,**D**,**F**,**G**,**I**,**J**) Immunofluorescence on sections. (**H**,**K**) AP staining on sections. (K) Black brackets indicate missing bone, black dashed lines indicate AP^{+} bone, and asterisk indicates the coronal suture. Scale bars: 100 μm for tissue sections; 25 mm for whole-mounts.

Table S1. Primer sequences used for ChIP-qPCR

H3K4me1, β-catenin ChIP-Twist1 qPCR			
Twist1 -62	E1	ATGGGTGGCAGAGGTGATTA	CATGGGCTCCCATTTATAGC
Twist1 -60	E2	TTAGCCAGAGATCCCCGATT	CCTTGTGCCATTCATCATCA
Twist1 -22	E3	CCTTCTCCCCATCATTGAAA	ACCATGCCAGCCTTTTGTAT
Twist1 -18	E4	TGGACTTTGCCGAAAAGAAA	ACCTCCCGGTTCCTATTGAG
Twist1 -4.5	E5	CTCTTGTGGTCACTGGCAAA	TCCTACTCTCAGCCCTCCAA
Twist1 -3	E6	GAAAACAAAGCCCCTTGTGA	AGGCTTCTGTCAATCTGGTGA
Twist1 +5	E7	AACCCCCGCTTAATGTTCTT	ACCTGCCATAGGCTCCTTTT
Twist1 +10	E8	CTACACCCCAACCCTTGGT	GACACTCCACCCCTCAAATC
Twist1 +16	E9	TGAAATGTAACCCTGGTCCAA	TCAGCATTCAAGAGCCAAAA
Twist1 -1.7	P1-A	GGCACACTGTGGTCATTGTC	AAACTCTGGGGTGTGGAATG
Twist1 -1.8	P1-B	GGGTTTACTGGCCTCAGAAGA	CTGGGTCCTGCTGAAGCTCT
Twist1 -1.9	P1-C	CTTTGGTCCAACCCAGAAAG	GCTGAGGACCTTGCTAAACG
Twist1 -75	NT1	TGTGATAAGGCACCACCTCA	GCCCTGCTCTTCAAACTCAC
Twist1 -37	NT2	CAGGACAAGAGGAAGCAACC	ATGCACAACAGCACCACAAT
Twist1 -26	NT3	TCTGCAATTAGCCTTCTTTCC	AGCTAACAGCCCTGGTTTTG
Twist1 -8	NT4	CTGCACAATGCTGGTGTTCT	TGGCAAATGGAGAATGATGA

Twist ChIP-Sox9 qPCR		
	F:	R:
3'UTR 1	AAGCACATTTTCCCTGGTTG	AAAAATGAAAACTTCTCCTTACAAAA
3'UTR 2	TTTTTCACGCAGCCCTAAGT	AAAAATGAAAACTTCTCCTTACAAAA
3'UTR 4	CAAGCACATTTTCCCTGGTT	CGCTGGTATTCAGGGAGGTA
NT1	GGTTTTGAAACGATGTGCAG	TGTGTATCGGAGCCACCTG
NT2	TAGCCGACAAGGTTGGTTTT	ACTGTGTATCGGAGCCACCT
NT4	CGCTGTAGCACAAGGACAGA	TCAGCTAGCGTAGCCTCCTC
Promoter1	AGCGCCTCTGCTAAGTGC	ATGAAGGGGTCCAGGAGATT
Promoter2	CCGGTTTCGTTCTCTGTTTT	GCGGGCACTTAGCAGAGG
Promoter3	GGGAGCGACAACTTTACCAG	AGGAGGGAGGGAAAACAGAG