

Table S1. Primers (5' to 3')

	Forward	Reverse	Expected band size (bp)
<b>Genotyping*</b>			
<i>lft88</i>	BY598: GCCTCCTGTTTCTTGACAACAGTG	BY919: GGTCTAACAAGTAAGCCAGTGTT BY956: CTGCACCAGCCATTTCTCTAAGTCATGTA	loxP, 370; Wt, 350; null, 270
<i>Cre</i>	BY1208: CCGTTTGCCGGTCTGGGGCGGCATGG	BY1209: CGCGCGGCTCCGACACGGGCACTG	Cre <sup>+</sup> , 750
<i>Kif3a</i>	BY951: AGGGCAGACGGAAGGGTGG	BY950: TCTGTGAGTTTGTGACCAGCC BY952: TGGCAGGTCAATGGACGCAG	loxP, 490; Wt, 360; null, 200
<i>mTmG</i>	BY3010: CTCTGCTGCCTCCTGGCTTCT	BY3011: CGAGGCGGATCACAAGCAATA BY3012: TCAATGGGCGGGGGTCTGTT	Wt, 330; transgene, 250
<i>ROSA</i>	BY33: AGCAGAAGCCTGCGATGTC BY1281: GGCTTAAAGGCTAACCTGATGTG	BY34: GTCAGACGATTCATTGGCAC BY1283: GGAGCGGGAGAAATGGATATG	Wt, 374; <i>lacZ</i> , 300
<i>Smo</i>	BY2110: AGTGCCTTGGTTCCGACAGAC BY2112: GAGGTAAACCTAGGGCTTCTG	BY2111: TAGCCCACAAAACAAATGCCACTC BY2113: CTGCCACGCTGTCAATACCG	Wt, 372; <i>Smo</i> , 600
<i>Ptch1-lacZ</i>	BY3147: TGGGGTGGGATTAGATAAATGCC BY3149: CTGCGGCAAGTTTTGGTTG	BY3148: TGTCTGTGTGTGCTCCTGAATCAC BY3150: AGGGCTTCTCGTTGGCTACAAG	Wt, 217; <i>Ptch1</i> , 501
<b>qRT</b>			
<i>lft88</i>	BY3617: TGGCCAACGACCTGGAGATTAACA	BY3616: ATAGCTGCTGGCTTGGGCAAATTC	
<i>Gli1</i>	BY3331: TCGACCTGCAAACCGTAATCC	BY3332: TCCTAAAGAAGGGCTCATGGTA	
<i>Ptch1</i>	BY1095: ATAACAGGCAATGGAAGTTGGAAC	BY1096: AATCTGGGTCGGCTGGGTTGAGGC	
<i>Gapdh</i>	BY3271: GGGTGTGAACCACGAGAAAT	BY3272: ACACATTGGGGGTAGGAACA	
<i>B2m</i>	BY3434: ATGAGGGAGATCGTGACAT	BY3435: CCCCTGAGCGGACACTGT	
Wt, wild type. *There can be one or two forward or reverse primers in certain reactions.			