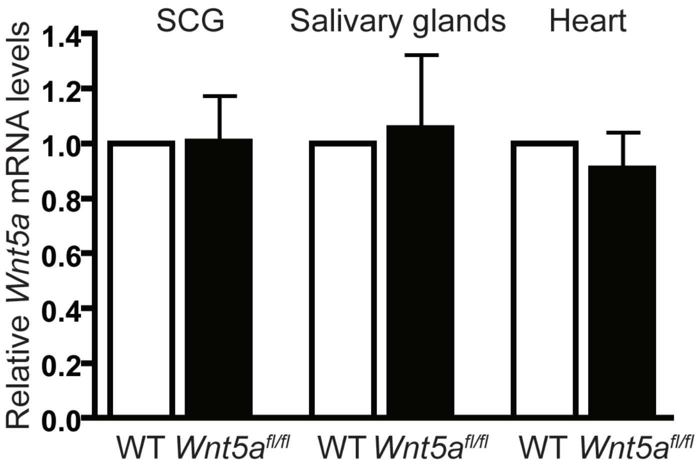
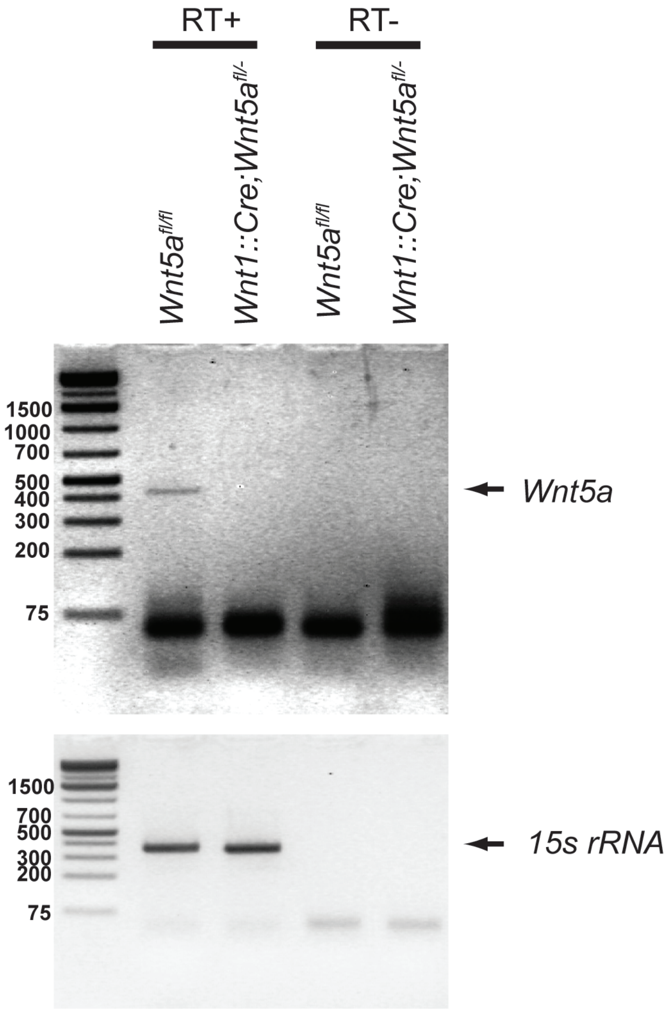
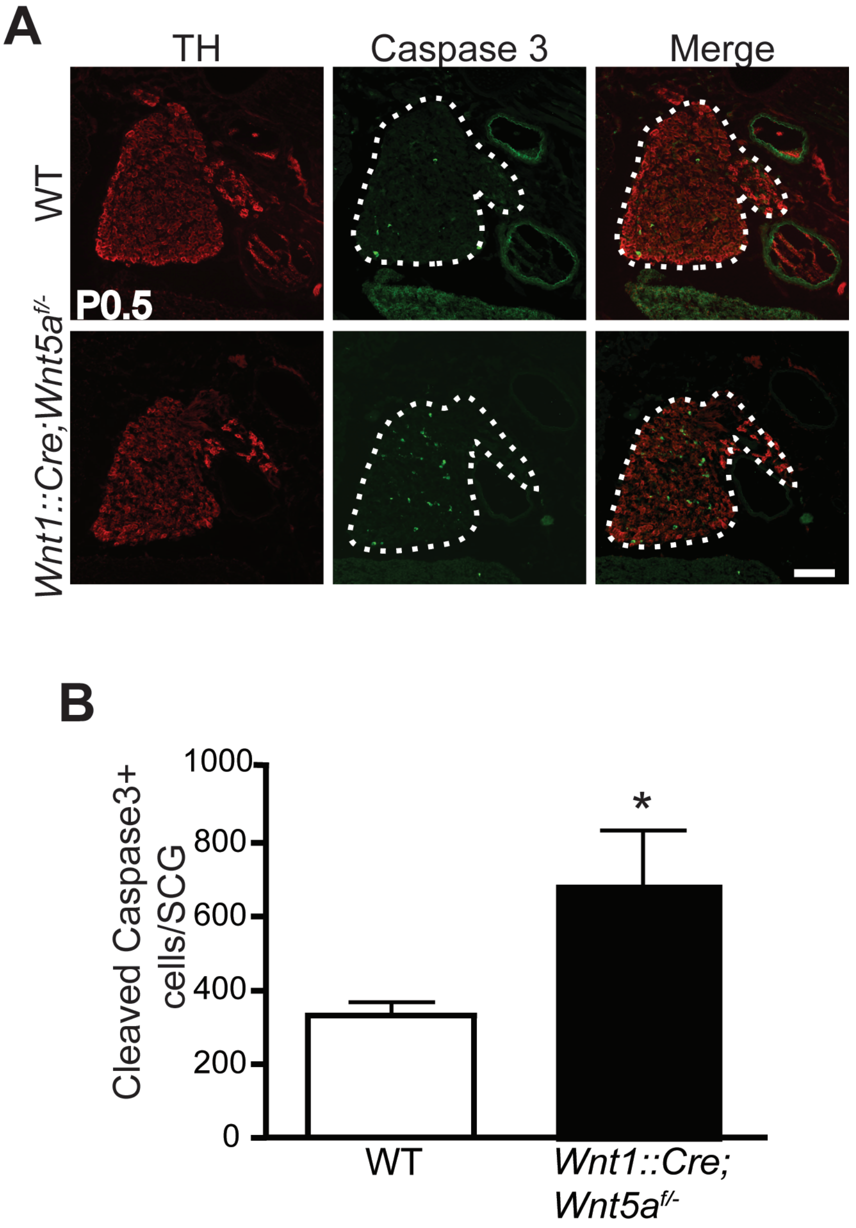


Supplementary Fig 1. Normal *Wnt5a* expression in floxed (*Wnt5a*$^{fl/fl}$) mice. Quantitative real-time PCR analyses show that *Wnt5a* transcript levels in the superior cervical ganglia (SCG), salivary glands and hearts from *Wnt5a*$^{fl/fl}$ mice are not significantly different compared to wild-type mice (C57BL/6) at P0.5. SCGs and salivary glands were harvested from n=6 wild-type and *Wnt5a*$^{fl/fl}$ mice. Hearts were dissected from n=4 wild-type and n=8 *Wnt5a*$^{fl/fl}$ mice. Values are the mean ± s.e.m.



Supplementary Fig 2. RT-PCR analysis of *Wnt5a* mRNA in *Wnt1::Cre;Wnt5a*$^{fl/-}$ and *Wnt5a*$^{fl/fl}$ sympathetic ganglia. *Wnt5a* mRNA was detected using primers that target 5'untranslated region to exon 3 of the *Wnt5a* gene, generating a product of 423bp (*Wnt5a*-F: 5'-AAGGCTTAACCCCGACGCTTC-3' and *Wnt5a*-R: 5'-ATCTCCGATGCCGGAACTGGT-3'). 15S rRNA sequence was used as a control (15S rRNA-F: 5'-TTCCGCAAGTTCACCTACC-3' and 15S rRNA-R: 5'-CGGGCCGGCCATGCTTTACG-3'). The absence of a PCR product in *Wnt1::Cre;Wnt5a*$^{fl/-}$ sympathetic ganglia suggests that the *Wnt5a* transcript missing exon 2, likely, undergoes nonsene mediated decay.



Supplementary Fig 3. Enhanced apoptosis in *Wnt1::Cre;Wnt5a*$^{fl/-}$ sympathetic ganglia. Cleaved caspase-3 immunofluorescence shows increased apoptosis in P0.5 *Wnt1::Cre;Wnt5a*$^{fl/-}$ SCGs as compared to wild-type ganglia. Dashed lines outline the superior cervical ganglia (SCG). Tissue sections have also been stained with TH to reveal the SCG. Scale bar, 100 μm. Values are the mean ± SEM; n=4 embryos for wild-type and n=3 for *Wnt1-Cre;Wnt5a*$^{fl/-}$, $^*p<0.03$.