

Supporting Information

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SI Materials and Methods

For in situ hybridization, *Atf5*^{+/+} and *Atf5*^{+/-} embryonic stage 18.5 embryos or heads from postnatal day 0 *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice were harvested, fixed in 4% (wt/vol) paraformaldehyde at 4 °C overnight, infused with 25% (wt/vol)

sucrose in 1× PBS overnight, embedded in optimal cutting temperature (OCT) compound, and cryosectioned at 18 μm. Digoxigenin-labeled riboprobes against *Atf5* and *LacZ* were used to perform in situ hybridization, as described previously (1).

1. Wang SZ, et al. (2006) An oligodendrocyte-specific zinc-finger transcription regulator cooperates with Olig2 to promote oligodendrocyte differentiation. *Development* 133(17):3389–3398.

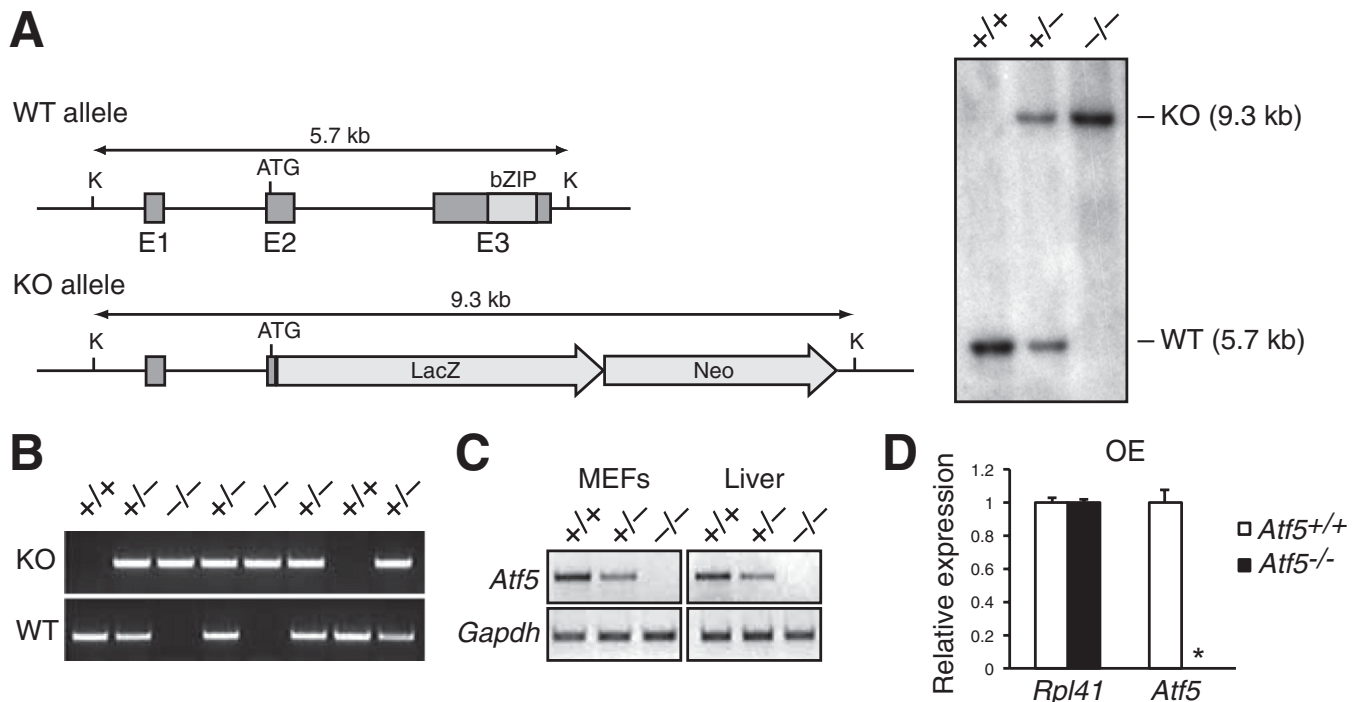


Fig. S1. Validation of *Atf5*^{-/-} mice. (A) (Left) Schematic diagrams of the wild-type (WT) and knockout (KO) *Atf5* alleles. To generate the KO allele, a LacZ-Neo cassette was inserted in frame and replaced most of exon 1 (E1) and all of exons 2 and 3 (E2 and E3, respectively). The gene replacement results in an increase in length of a KpnI restriction fragment that encompasses the *Atf5* locus from 5.7 kb (WT allele) to 9.3 kb (KO allele). K represents the KpnI sites; ATG represents the translation start site; bZIP denotes the basic region leucine zipper domain. (Right) Southern blot analysis of the *Atf5* locus in *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. (B) PCR genotyping of a litter of *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice from an *Atf5*^{+/-} intercross. (C) RT-PCR analysis of *Atf5* expression in mouse embryonic fibroblasts (MEFs) (Left) and liver (Right) of *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. *Gapdh* was monitored as a control. (D) qRT-PCR analysis of *Atf5* expression in OE derived from *Atf5*^{+/+} and *Atf5*^{-/-} mice. *Rpl41* was monitored as a control. The results were normalized to the expression level in *Atf5*^{+/+} mice, which was set to 1. **P* < 0.05.

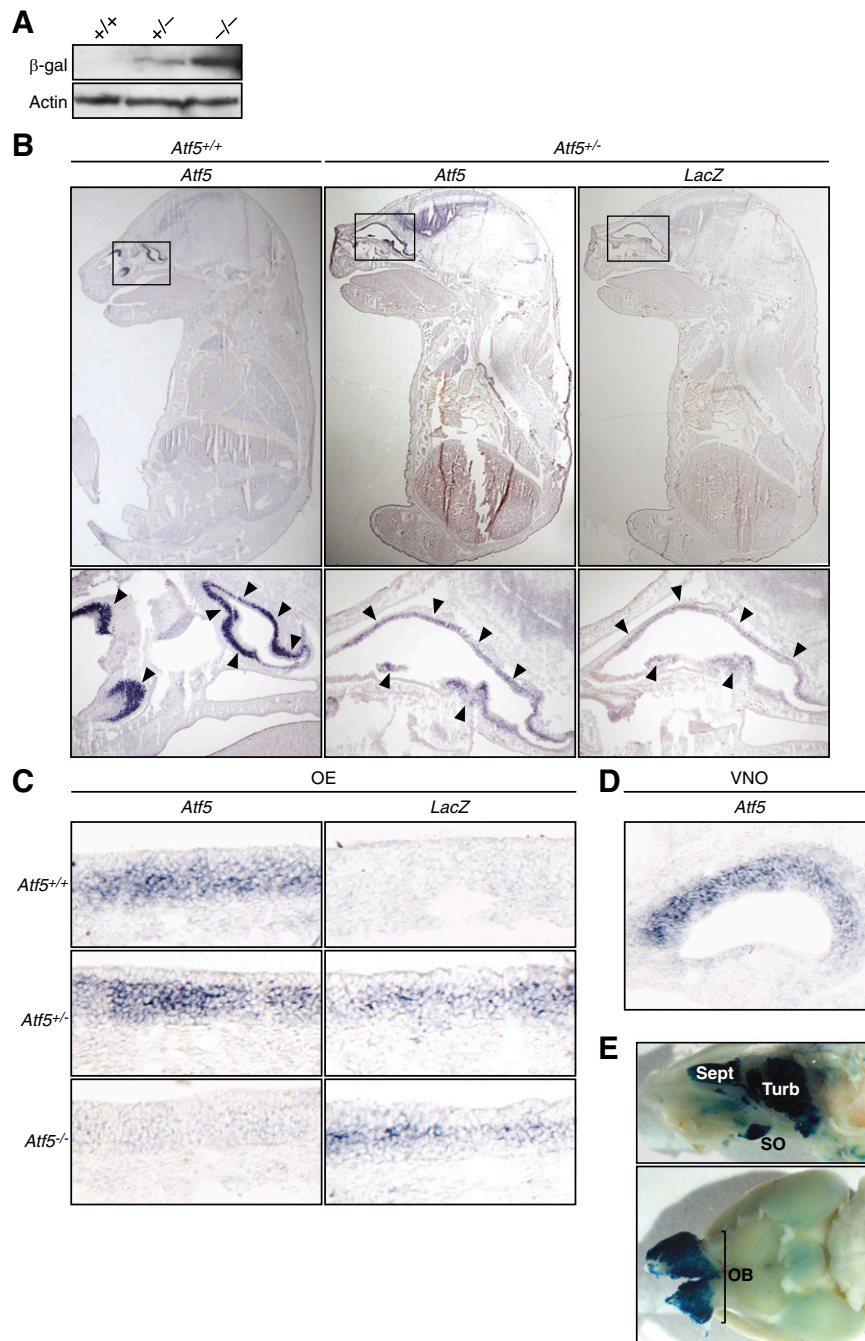


Fig. S2. Further characterization of *Atf5* expression by in situ hybridization analysis and β -gal immunoblot analysis and activity assays. (A) Immunoblot analysis monitoring β -gal levels in *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. Actin was monitored as a loading control. (B) In situ hybridization monitoring *Atf5* and *LacZ* expression on a sagittal section of *Atf5*^{+/+} and *Atf5*^{+/-} whole embryonic stage 18.5 embryos. Upper, magnification 0.8 \times ; Lower, magnification 5 \times . Inset highlights the region that is shown in the Lower image. Arrowheads denote positive staining. (C) In situ hybridization monitoring *Atf5* and *LacZ* expression in the olfactory epithelium (OE) of postnatal day 0 (P0) *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. Magnification 100 \times . (D) In situ hybridization monitoring *Atf5* expression in the vomeronasal organ (VNO) of a P0 *Atf5*^{+/+} mouse. Magnification 100 \times . (E) Whole-mount β -gal activity assay on a sagittal section of the nose (Upper) and a bottom view of the brain (Lower) of a 10-mo-old *Atf5*^{+/-} mouse. Sept, septum; Turb, turbinates; SO, septal organ; OB, olfactory bulb. Magnification 8 \times .

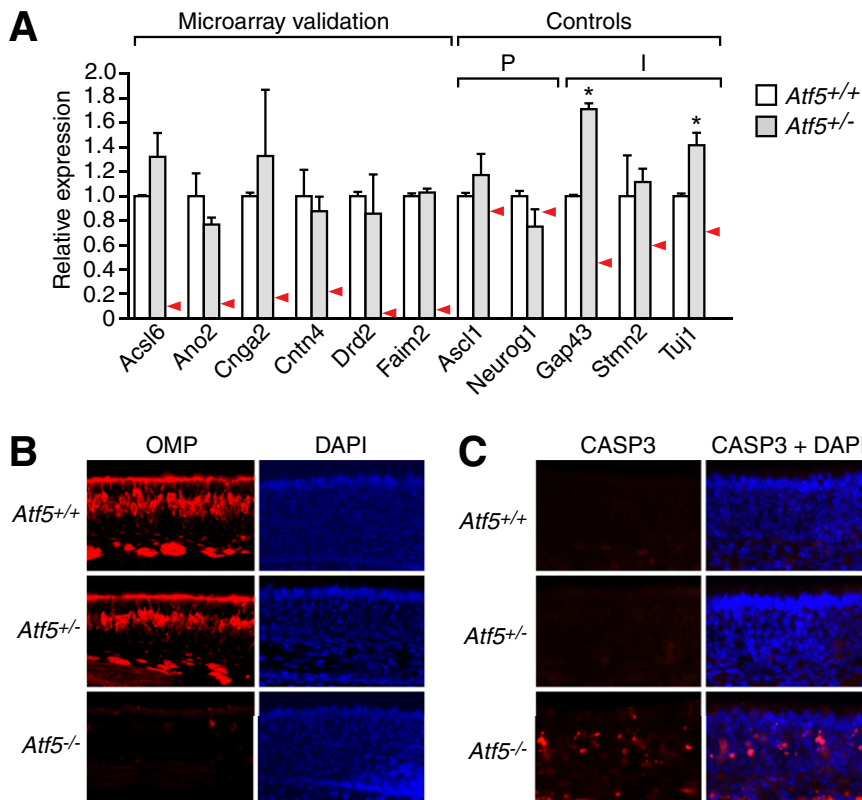


Fig. 56. Similarity in olfactory sensory neuron (OSN)-specific gene expression and OMP and cleaved caspase 3 (CASP3) staining between *Atf5*^{+/+} and *Atf5*^{+/-} mice. (A) qRT-PCR analysis monitoring gene expression in olfactory epithelium (OE) of postnatal day 0 (P0) *Atf5*^{+/+} and *Atf5*^{+/-} mice. The results were normalized to the expression level in *Atf5*^{+/+} mice, which was set to 1. Red arrowheads indicate the relative expression of each gene in *Atf5*^{-/-} mice, as shown in Fig. 4B. P, progenitor markers; I, immature OSN markers. **P* < 0.05. The results show that expression of OSN-specific genes was similar in *Atf5*^{+/+} and *Atf5*^{+/-} mice. (B) Immunofluorescence monitoring OMP staining in the OE of P0 *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. (Right) DAPI images. Magnification 20 \times . (C) Immunofluorescence monitoring cleaved CASP3 staining in the OE of P0 *Atf5*^{+/+}, *Atf5*^{+/-}, and *Atf5*^{-/-} mice. Merged images are shown in the absence and presence of DAPI. Magnification 20 \times .

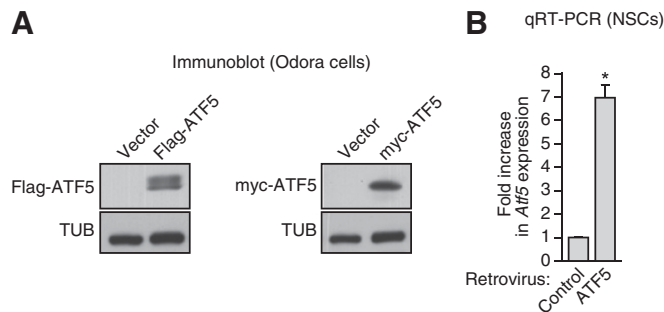


Fig. 57. Confirmation of ectopic *Atf5* expression. (A) Immunoblot analysis monitoring Flag-ATF5 (Left) and myc-ATF5 (Right) levels in rat Odora cells transfected with empty vector and Flag-ATF5 or myc-ATF5. Tubulin was monitored as a loading control. (B) qRT-PCR analysis monitoring expression of *Atf5* in mouse neural stem cells (NSCs) transduced with a retrovirus that expresses ATF5 or empty virus control. Fold increase in *Atf5* expression is given relative to the empty virus control, which was set at a value of 1. **P* < 0.05.

