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A comparative study of age-related hearing loss in wild type and insulin-like growth factor I deficient mice

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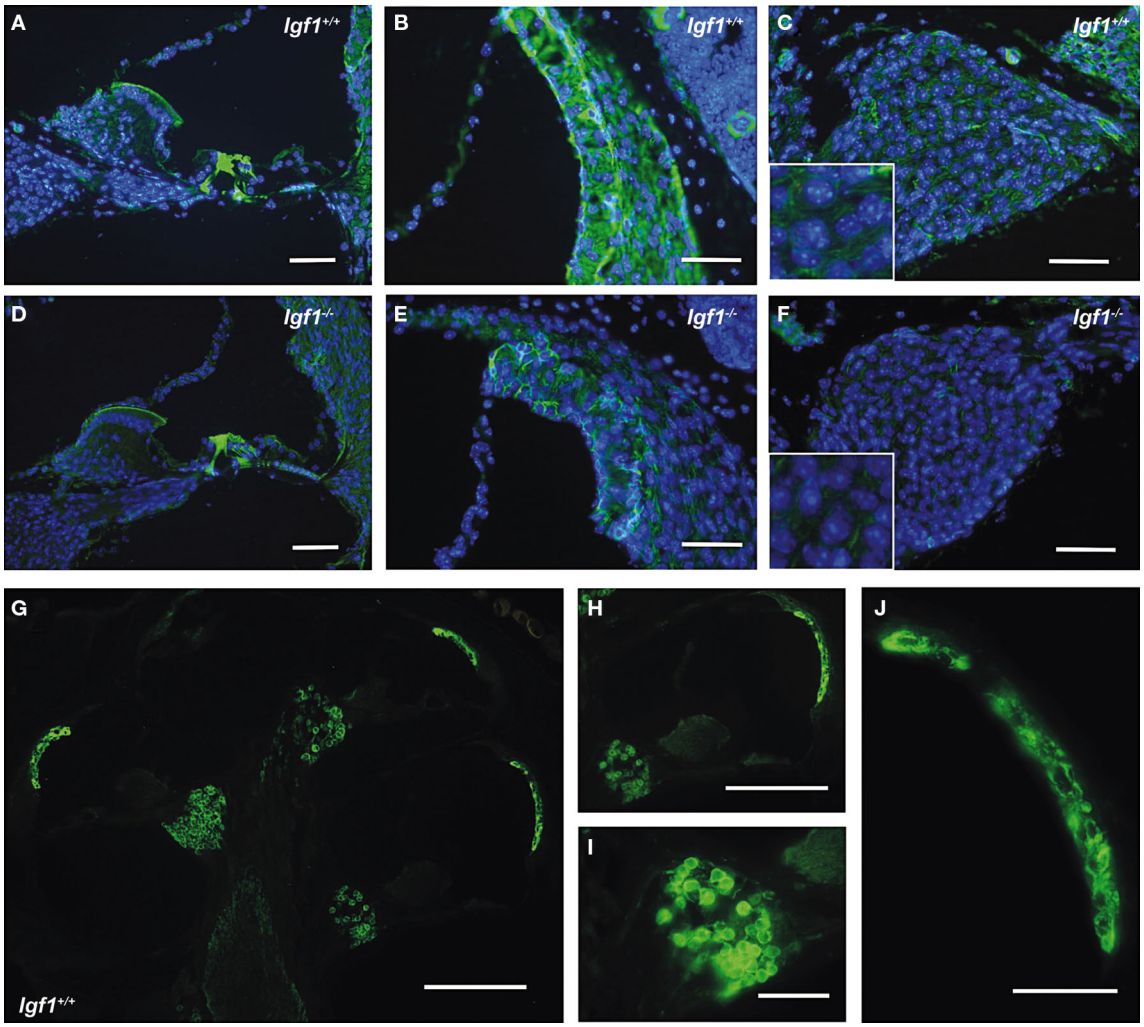

FIGURE S1 | Phalloidin histochemistry of cochlear sections from 7-month-old mice of both genotypes. (A–C) The basal turn of the cochlea was normal in wild type *Igf1*$^{+/+}$ mice, with phalloidin labeled hair cells (stereocilia and cuticular plate) and pillars of Corti. **(D–F)** The scala media and stria vascularis was smaller in *Igf1*$^{-/-}$ mice, although phalloidin labeling of the organ of Corti was normal. **(B,E)** The stria vascularis appeared normal in the wild type *Igf1*$^{+/+}$ mice, unlike that of the *Igf1*$^{-/-}$ mice. **(C,F)** The cochlear ganglion of wild type *Igf1*$^{+/+}$ and *Igf1*$^{-/-}$ null mice. The inset shows a detail of the nuclei of ganglion cells. Four to six mice per condition were analyzed. Scale bar 50 μm. Kir4.1 (KCNJ10) potassium channel immunohistochemistry **(G–J)** Kir4.1 expression in the wild type mice highlights the reduced density of neurons in the ganglia (more evident at the base of cochlea) and in some stria vascularis areas as a result of normal aging. The relative loss of expression in stria reflects the areas with fewer neurons in the ganglia).

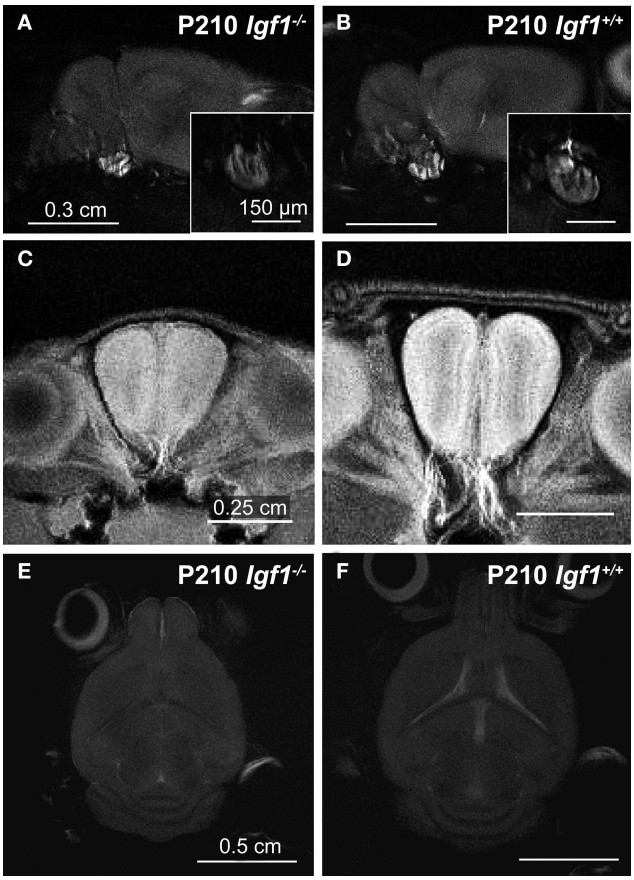

FIGURE S2 | Morphology of the cochlea and brain of mice from both genotypes was studied by MRI. (A,B) Note the different arrangement of the cochlea in parasagittal images (T2 weighted) of wild type and null mice, highlighting the different brain-cochlear angle. Inset shows the conformation of the cochlea in a horizontal view, where a deformed and smaller cochlea is shown in **(A)** compared with **(B)**. **(C,D)** The olfactory bulb was also altered in IGF-I deficient mice, with a loss of cytoarchitecture and of the characteristic laminar pattern evident in coronal brain sections (MRI T1). **(E,F)** Deficient mice also had a reduced ventricular system when compared to control animals, as seen in horizontal sections of the brain.

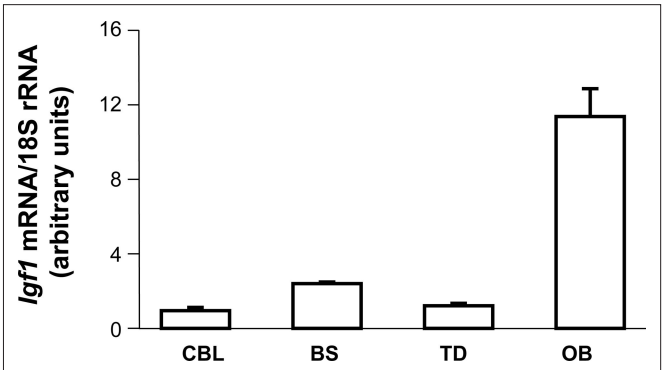

FIGURE S3 | IGF-I expression in the brain. IGF-I mRNA levels in different brain regions were measured by quantitative RT-PCR as indicated and normalized to the levels of the 18S ribosomal RNA. The results represent the mean ± s.d. Three to five mice per genotype were used. Brainstem (BS), olfactory bulb (OB), cerebellum (CBL), and the remainder of the telencephalic-diencephalic region (TD).