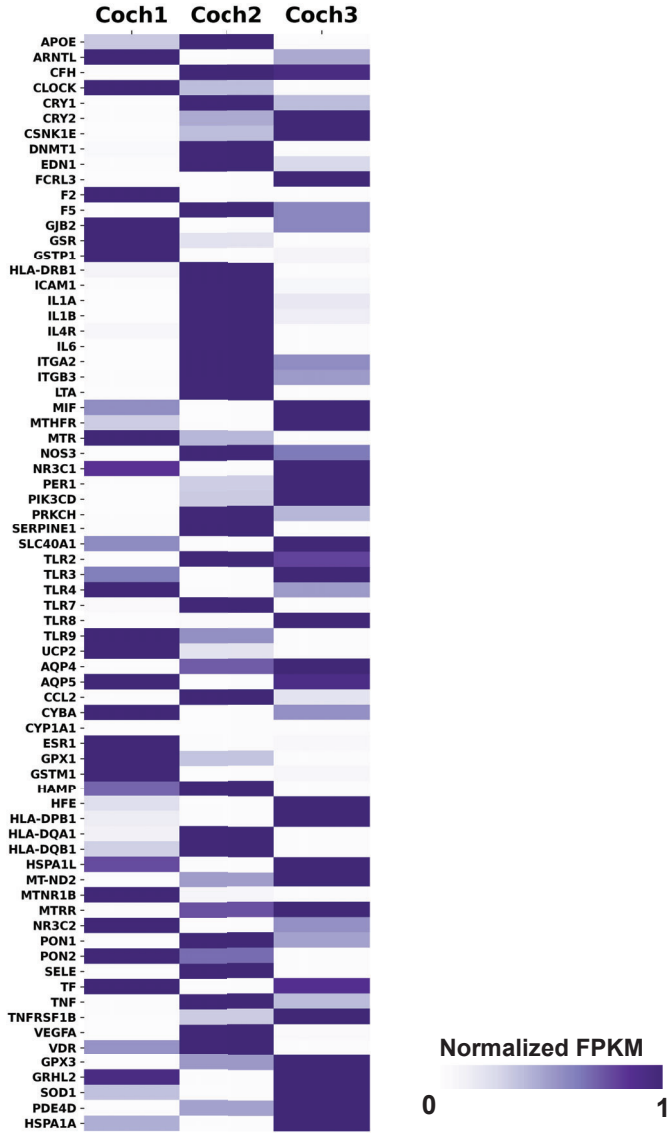**Suppl. Digital Content, Figure 3.** SSNHL genes expressed in human cochlea bulk RNA-Seq

Suppl. Digital Content 8, Figure 3. Expression of SSNHL-investigated genes in the adult human cochlea utilizing bulk RNA-Seq from human cochlea specimens obtained during vestibular schwannoma surgery (Schrauwen et al., 2016). Heatmap displays 3 human cochlea samples along the horizontal axis and SSNHL-investigated genes along the vertical axis. The darker the bar the more highly expressed the gene is in a given cell. One caveat to these data is that while bulk RNA-Seq may identify highly expressed genes, cell type-specific gene expression may be missed in bulk RNA-Seq datasets as compared to single-cell RNA-Seq datasets.

Methods:

Data availability. Published bulk human cochlea RNA-Seq dataset obtained from patients undergoing surgery for vestibular schwannoma was utilized (Schrauwen et al., 2016) and are available at the following link for download (https://www.tgen.org/home/research/research-divisions/neurogenomics/supplementary-data/inner-ear-transcriptome.aspx).

Visualization of Human cochlea bulk RNA-Seq. Raw FPKM data were downloaded as described above (file name: HumanEar_FPKM_gene_RNASTAR.xlsx). Gene ensemble id's were converted to gene symbols based on human genome reference (GRCh38.p13). FPKM values were scaled by min-max scaling before plotting. Heatmap was plotted by Seaborn (v0.10.1).