

**Table S1.** RNA-seq dataset of transcriptomes of *Lbh*-null and wildtype outer hair cells.

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**Table S2:** Differentially expressed genes between *Lbh*-null and wildtype OHCs.

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**Table S3:** Significantly enriched genes associated with Wnt and Notch signaling.

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**Table S4:** Significantly enriched genes associated with cell cycle and transcription

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**Table S5:** Significantly enriched genes associated with DNA damage/repair and autophagy.

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