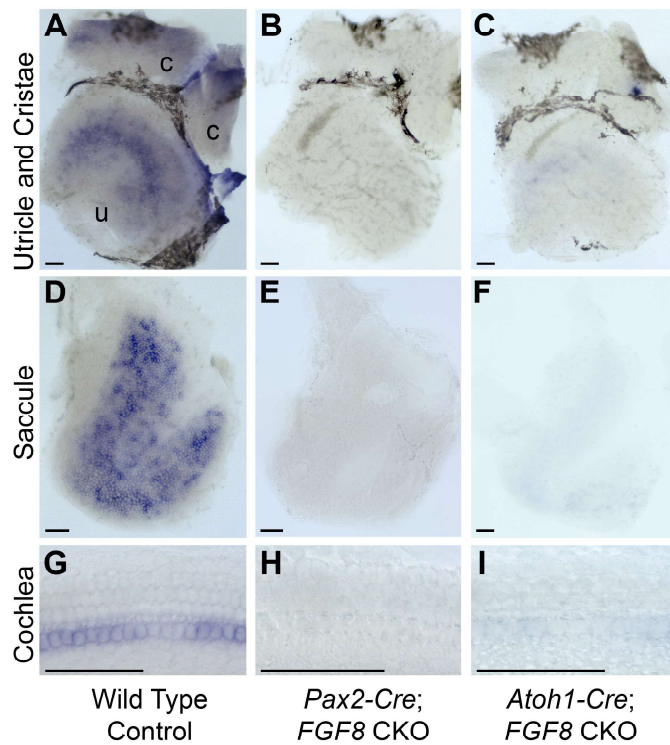
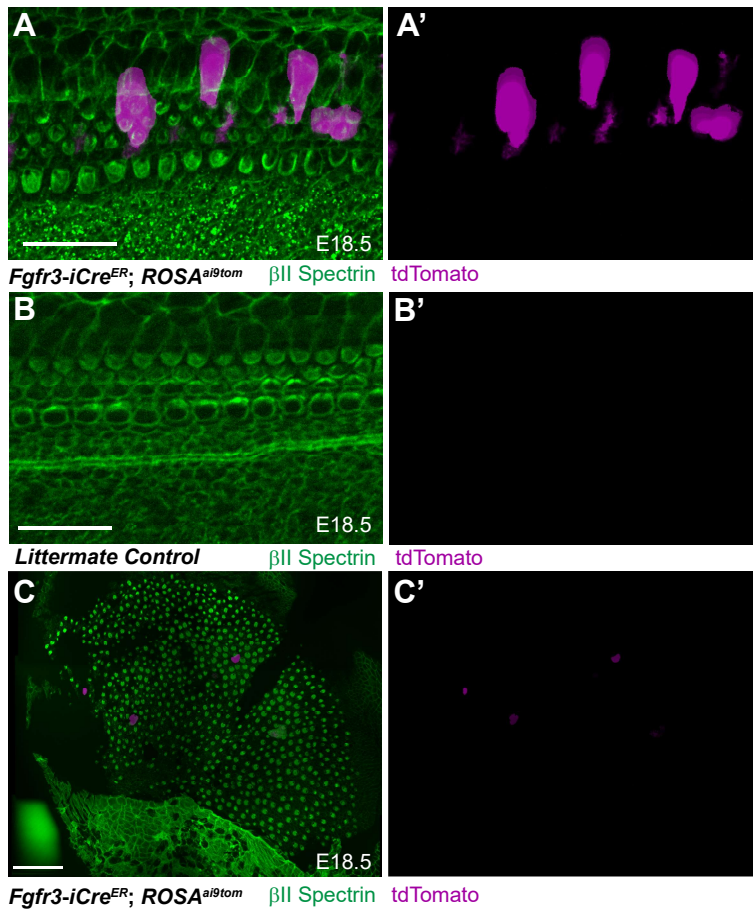


**Figure S1. Timecourse of  $Fgf8^{mcm}$  genetic labeling in the developing mouse utricle.** tdTomato labeling of utricular hair cells following a single dose of tamoxifen delivered at (A) E11.5, (B) E13.5, (C) E15.5 or (D) E17.5 and evaluated at E18.5. (E) tdTomato labeling of utricular hair cells following a single dose of tamoxifen delivered at P2 and evaluated at P14. Panels (A) and (D) are reprinted from primary figures. Scale bars: (50  $\mu$ m)



**Figure S2. *Fgf8* expression is abolished in *Pax2-Cre* and *Atoh1-Cre*; *Fgf8* CKOs**  
 (A) Wholemout ISH for *Fgf8* shows vestibular hair cell expression in littermate control utricle (u) and cristae (c), saccule (D), and inner hair cells (G) of the organ of Corti. (B,E,H) *Fgf8* mRNA is completely lost following gene deletion using *Pax2-Cre* in each of these sensory epithelia. (C,F) *Fgf8* mRNA is lost from the extrastricular regions of the utricle and saccule and the inner hair cells (I) of the organ of Corti following hair cell specific deletion using *Atoh1-Cre*. Brackets indicate the approximate boundaries of the striolar region. Scale bars: (50 $\mu$ m)



**Figure S3. Fgfr3 expression is absent from the majority of the utricle**

**(A)** Fgfr3-iCreER tdTomato labeling of cells in the organ of Corti following daily tamoxifen injections from E9.5 to E12.5. **(B)** Cre negative littermate control cochlea showing activation of the tdTomato reporter. **(C)** Fgfr3-iCreER shows minimal labeling of the utricle following the same tamoxifen regimen.  $\beta$ II-spectrin labeling shows the distribution of vestibular hair cells. Scale bars: 20 $\mu$ m (A,B); 50 $\mu$ m (C).

P14 (E11.5 Tam) from Fig. 6D

Utricle	tdTomato (+)	tdTomato(+) w/ Calyx	% Colocalized	Mean	83%
1	12	9	75%	STDEV	12%
2	12	11	92%	STDERROR	8%
				√N	1.4

P14 (E17.5 Tam) from Fig. 6D

Utricle	tdTomato (+)	tdTomato(+) w/ Calyx	% Colocalized	Mean	92%
1	360	354	98%	STDEV	6%
2	300	277	92%	STDERROR	3%
3	466	403	86%	√N	1.7

P14 (P2 Tam) from Fig. 6D

Utricle	tdTomato (+)	tdTomato(+) w/ Calyx	% Colocalized	Mean	90%
1	34	33	97%	STDEV	7%
2	445	374	84%	STDERROR	4%
3	464	419	90%	√N	1.7

**Table S1. Raw data used for quantification graphs presented in Figure 6**

P14 (P2 Tam) from Fig. 7D

Utricle	tdTomato (+)	tdTomato (+) w/ OPN	% Colocalized	Mean	86%
1	205	188	92%	STDEV	9%
2	206	187	91%	STDERROR	5%
3	45	34	76%	√N	1.7

P14 (P2 Tam) from Fig. 7D

Utricle	tdTomato (+)	tdTomato (+) w/ Calb2	% Colocalized	Mean	6%
1	28	1	4%	STDEV	5%
2	390	46	12%	STDERROR	3%
3	396	12	3%	√N	1.7

P14 (P2 Tam) from Fig. 7D

Utricle	tdTomato (+)	tdTomato (+) w/ Anxa4	% Colocalized	Mean	4%
1	149	9	6%	STDEV	2%
2	321	10	3%	STDERROR	1%
3	275	10	4%	√N	1.7

**Table S2. Raw data used for quantification graphs presented in Figure 7**

P14 from Fig. 8I

Utricle	Genotype	MyoVIIa	BIII Tubulin+MyoVIIa	% HCs with Calyx	Mean	61%
1	Littermate Control	778	511	66%	STDEV	4%
2	Littermate Control	845	486	58%	STDERROR	2%
3	Littermate Control	945	566	60%	√N	1.7

Utricle	Genotype	MyoVIIa	BIII Tubulin+MyoVIIa	% HCs with Calyx	Mean	61%
1	<i>Atoh1-Cre;Fgf8</i> CKO	955	525	55%	STDEV	5%
2	<i>Atoh1-Cre;Fgf8</i> CKO	914	575	63%	STDERROR	3%
3	<i>Atoh1-Cre;Fgf8</i> CKO	913	590	65%	√N	1.7

P14 from Fig. 8J

Utricle	Genotype	OPN	Mean	121
1	Littermate Control	138	STDEV	20
2	Littermate Control	99	STDERROR	12
3	Littermate Control	127	√N	1.73

Utricle	Genotype	OPN	Mean	93
1	<i>Pax2-Cre; Fgf8</i> CKO	149	STDEV	51
2	<i>Pax2-Cre; Fgf8</i> CKO	50	STDERROR	29
3	<i>Pax2-Cre; Fgf8</i> CKO	79	√N	1.73

P14 from Fig. 8J

Utricle	Genotype	OCM	Mean	123
1	Littermate Control	134	STDEV	17
2	Littermate Control	104	STDERROR	8
3	Littermate Control	140	√N	2.00
4	Littermate Control	114		

Utricle	Genotype	OCM	Mean	122
1	<i>Pax2-Cre; Fgf8</i> CKO	128	STDEV	10
2	<i>Pax2-Cre; Fgf8</i> CKO	110	STDERROR	6
3	<i>Pax2-Cre; Fgf8</i> CKO	128	√N	1.73

P14 from Fig. 8J

Utricle	Genotype	Mean LWSR	Mean	0.56
1	Littermate Control	0.51	STDEV	0.04
2	Littermate Control	0.57	STDERROR	0.02
3	Littermate Control	0.56	√N	2.45
4	Littermate Control	0.55		
5	Littermate Control	0.55		
6	Littermate Control	0.56		
7	Littermate Control	0.55		
8	Littermate Control	0.66		

Utricle	Genotype	Mean LWSR	Mean	0.54
1	<i>Pax2-Cre; Fgf8</i> CKO	0.56	STDEV	0.08
2	<i>Pax2-Cre; Fgf8</i> CKO	0.45	STDERROR	0.03
3	<i>Pax2-Cre; Fgf8</i> CKO	0.51	√N	2.45
4	<i>Pax2-Cre; Fgf8</i> CKO	0.70		
5	<i>Pax2-Cre; Fgf8</i> CKO	0.56		
6	<i>Pax2-Cre; Fgf8</i> CKO	0.49		
7	<i>Pax2-Cre; Fgf8</i> CKO	0.47		

**Table S3. Raw data used for quantification graphs presented in Figure 8**

Comparison of E18.5 *Pax2-Cre; Fgf8* CKO utricles to littermate controls for presence of Type I hair cells in the striola Oncomodulin and extrastriola with Osteopontin from Fig. 8J and Lateral extrastriolar width to striolar width ratio (LWSR) compared between E18.5 *Pax2-Cre; Fgf8* CKO utricles corresponding to Fig. 8J.