Control of stereocilia length during development of hair bundles

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Abbreviations: CV, coefficient of variation; F-actin, filamentous actin; Het, heterozygote; IHC, inner hair cell; KO, knockout; OHC, outer hair cell; P, postnatal day; PSF, point-spread function; SIM, structured illumination microscopy.

Abstract

Assembly of the hair bundle, the sensory organelle of the inner ear, depends on differential growth of actin-based stereocilia. Separate rows of stereocilia, labeled 1 through 3 from tallest to shortest, lengthen or shorten during discrete time intervals during development. We used lattice structured illumination microscopy and surface rendering of mouse apical inner hair cells to measure stereocilia dimensions during early postnatal development; these measurements revealed a sharp transition at postnatal day 8 between stage III (row 1 and 2 widening; row 2 shortening) and stage IV (final row 1 lengthening and widening). Tip proteins that determine row 1 lengthening did not accumulate simultaneously during stages III and IV; while the actin-bundling protein EPS8 peaked at the end of stage III, GNAI3 peaked several days later—in early stage IV—and GPSM2 peaked near the end of stage IV. To establish the contributions of key macromolecular assemblies to bundle structure, we examined mouse mutants that eliminated tip links (*Cdh23*^{v2J} or *Pcdh15*^{av3J}), transduction channels (*Tmie*^{KO}), or the row 1 tip complex (*Myo15a*^{sh2}). *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ bundles had adjacent stereocilia in the same row that were not matched in length, revealing that a major role of these cadherins is to synchronize lengths of side-by-side stereocilia. Use of the tip-link mutants also allowed us to distinguish the role of transduction from effects of transduction proteins themselves. While levels of GNAI3 and GPSM2, which stimulate stereocilia elongation, were greatly attenuated at the tips of *Tmie*$^{KO/KO}$ row 1 stereocilia, they accumulated normally in *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ stereocilia. These results reinforced the suggestion that the transduction proteins themselves facilitate localization of proteins in the row 1 complex. By contrast, EPS8 concentrates at tips of all *Tmie*$^{KO/KO}$, *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ stereocilia, correlating with the less polarized distribution of stereocilia lengths in these bundles. These latter results indicated that in wild-type hair cells, the transduction complex prevents accumulation of EPS8 at the tips of shorter stereocilia, causing them to shrink (row 2 and 3) or disappear (row 4 and microvilli). Reduced rhodamine-actin labeling at row 2 stereocilia tips of tip-link and transduction mutants suggests that transduction's role is to destabilize actin filaments there. These results suggest that regulation of stereocilia length occurs through EPS8, and that CDH23 and PCDH15 regulate stereocilia lengthening beyond their role in gating mechanotransduction channels.

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Introduction

Sensory hair cells of the inner ear are distinguished by the staircase arrangement of the ~100 stereocilia in their hair bundles, the sensory organelle that converts mechanical stimuli into electrical signals [1, 2]. The staircase architecture enables directional sensitivity of mechanotransduction [3] and increases

transduction sensitivity [4]. In the mature mammalian cochlea, stereocilia of inner hair cells (IHCs) and outer hair cells (OHCs) are arranged in three rows, albeit with distinct stereocilia lengths and widths [5].

During development, stereocilia in each row differentially widen and lengthen in specific phases [1, 6]. A complex of GPSM2 and GNAI3, coupled to MYO15A and EPS8 by WHRN, catalyzes lengthening of stereocilia beyond about a micrometer [7–9]; this complex concentrates exclusively in row 1. These five proteins undergo phase separation together, and the presence of GPSM2 both enhances phase separation and promotes F-actin bundling by EPS8 [10, 11], activity that presumably underlies stereocilia lengthening. Mutations in any of the genes encoding these five proteins leads to hair bundles that have short stereocilia and a minimal staircase, i.e., only very small changes of stereocilia length in successive rows [12].

Lengths of the shorter rows of stereocilia are regulated differently. Several other proteins, including TWF2, EPS8L2, and CAPZB, are found predominantly at row 2 tips [13–15]; these proteins have actin-filament capping activity, so their presence may slow lengthening. Stereocilia lacking *Capzb* are narrow, then shorten and disappear [14], suggesting that CAPZB (and its binding partner TWF2) contribute both to stereocilia widening but also length stability.

Tension in tip links, extracellular filaments that interconnect stereocilia rows, elicits transduction currents by opening cation-conducting mechanotransduction channels [2, 16]. Transduction regulates the final dimensions of stereocilia. Blockade of transduction channels elicits stereocilia shortening, suggesting a dynamic balance between actin polymerization and depolymerization [17]. Establishment of transduction currents requires the small membrane protein TMIE [18] and either TMC1 or TMC2, two channel-like proteins [19, 20]. An ordered stereocilia staircase still forms in mouse mutants lacking either *Tmie* or both *Tmc1* and *Tmc2* [18, 19], but row-specific distinctions of stereocilia width and length become more muted [6, 21]. The presence of transduction-channel proteins also regulates the localization of proteins specific for row 1 and row 2 [6]. Although row 1 lacks transduction [22], in transduction mutants, GNAI3 and GPSM2 do not accumulate substantially at row 1 tips in transduction mutants [6]. Significantly, transduction-channel proteins do localize to row 1 during early postnatal development [23].

Tip links are made up of dimers of CDH23, which project from the side of a taller stereocilium, and dimers of PCDH15, projecting from tips of short stereocilia [24–26]. The molecular motor MYO7A positions both molecules and tensions tip links [27–29]. All three of these proteins are members of the Usher I protein complex [30], and all are necessary for formation of tip links and activation of transduction. Mutant mouse lines lacking functional genes for *Cdh23* or *Pcdh15* develop ragged staircases, with stereocilia of irregular lengths but relatively uniform diameters [31–33]. Because tip links gate transduction channels [34], *Cdh23* and *Pcdh15* mutants lose both transduction and membrane tenting [33].

When tip links are under tension, the stereocilia membrane lifts off of the underlying F-actin core, a phenomenon called membrane tenting [34, 35]; once the membrane is pulled away, actin polymerization is enhanced, especially on the side of stereocilium where the tip link anchors [17, 36]. This phenomenon gives row 2 stereocilia a pronounced beveled shape [17, 36]. Tension in tip links thus promotes actin polymerization in the shorter stereocilia rows, independent of channel gating [37]. Lacking tip links, shorter stereocilia in homozygous *Cdh23* and *Pcdh15* mutants have rounded tips instead of beveled ones [33].

F-actin can be depolymerized at stereocilia tips due to the action of the ADF/CFL family members DSTN and CFL1 [38, 39]; these proteins sever actin filaments, which can lead to dissolution of actin structures [40]. Proteins in the ADF/CFL family typically associate with WDR1 (AIP1), which is located in stereocilia [41] and participates in length regulation [38]. DSTN and CFL1 are specifically located at row 2 stereocilia tips during early postnatal development, and this localization is disrupted in mutants lacking mechanotransduction [39]. Actin dynamics controlled by DSTN and CFL1 may underlie pruning of the shortest rows of stereocilia that occurs during hair-bundle maturation [42].

Thus at least five key multimolecular assemblies control stereocilia dimensions: (1) tip links, (2) transduction channels, (3) the row 1 complex, (4) row 2 cappers, and (5) actin-severing proteins. Each of these assemblies is activated at different times during development and is responsible for one or more steps of hair-bundle development. Here we defined with higher precision the changes in stereocilia dimensions during postnatal development of apical IHCs from postnatal day 0.5 (P0.5) to P21.5. Moreover, we used mutant mice to define more specifically the role of tip links on bundle development and the localization of tip-protein complexes. We examined stereocilia dimensions and row protein localization in *Pcdh15*^{av3J} and *Cdh23*^{v2J} null hair cells, as well as in *Tmie*^{KO} and *Myo15a*^{sh2} null hair cells. Besides gating transduction channels, we found that the tip-link proteins play an essential role in regulating stereocilia lengths; they also have a significant impact on accumulation of row-specific proteins at stereocilia tips, which in turn modulate stereocilia length. These observations complement previous results and provide us with a more comprehensive molecular understanding of bundle development.

Results

Quantitation of stereocilia actin-core dimensions using lattice structured illumination microscopy

We determined dimensions of stereocilia F-actin cores, labeled with fluorescent phalloidin, which were imaged in apical IHCs of C57BL/6 mice at precise times during early postnatal development. Our measurements should reflect native lengths and widths; dimensions of mildly-fixed, phalloidin-labeled stereocilia are not significantly different from dimensions of live stereocilia labeled with membrane dyes [43]. We improved resolution over conventional confocal microscopy by using lattice structured

illumination microscopy (lattice SIM) [44–46], which has a point-spread function (PSF) of ~150 nm under our conditions [46]; typical confocal microscopy PSFs are ~230 nm [47]. We rendered image surfaces from each phalloidin-stained hair bundle (Fig 1A-F); rendered surfaces are three-dimensional models of specific structures computed from stacks of images by pre-processing, segmentation, and connected-component labeling steps. We saved separate surfaces for each row 1, 2, or 3 stereocilium, as well as for some row 4 stereocilia and apical-surface microvilli (referred together as row 4+ stereocilia). Because of their relatively large sizes, row 1 and 2 stereocilia could be measured reliably; dimensions of row 3 and 4+ stereocilia and microvilli could also be measured, but required careful choices of rendering parameters and editing of surfaces after rendering.

Fig 1. **Stereocilia dimensions during development of C57BL/6J apical IHCs.**

A-F, Imaris reconstruction of phalloidin-labeled IHC stereocilia from indicated ages. Stereocilia surfaces are color-coded according to row; each box is 14 x 35 μm. Imaris reconstructions show overlapping hair bundles of adjacent cells, presumably an artefact of sample preparation. ***G-N,*** IHC stereocilia dimension measurements using reconstructed stereocilia surfaces. ***G***, Row 1 and 2 stereocilia length during development; center ten stereocilia in each row. Row 1 data were fit with a line with slope of zero from P0.5-P7.5 followed by an exponential climb from P7.5-P21.5; row 2 data were fit with an exponential decline. ***H***, Row 1 and 2 stereocilia width (center ten). In the panel, data for each row were fit with an exponential climb. The data could also be fit linearly; between P0.5 and P7.5, the slope for row 1 was 0.026 $\mu m \cdot day^{-1}$ (95% confidence interval of 0.025-0.026), while the row 2 slope was 0.034 $\mu m \cdot day^{-1}$ (95% confidence interval of 0.032-0.036). ***I***, Volume per individual row 1 or row 2 stereocilium (center ten). Data were fit with a linear increase from P0.5-P7.5, following by an exponential climb (row 1) or decline (row 2) from P7.5-P21.5. ***J***, Row 1 and 2 stereocilia cross-sectional area (center ten). Data were fit with a linear increase from P0.5-P7.5, followed by an exponential climb (row 1) or decline (row 2) from P7.5-P21.5. ***K***, Total stereocilia volume per cell using row 1, 2, and 3 stereocilia. Data were fit with an exponential climb. ***L***, Number of stereocilia per cell. Data were fit with an exponential decline. ***M***, Length difference between row 1 and row 2 stereocilia in the same column. Data were fit with a line with slope of zero from P0.5-P7.5, followed by an exponential climb from P7.5-P21.5. ***N***, Length difference between adjacent (side-by-side) stereocilia in the same row. Data were fit by exponential declines. For each plot, dimension measurements of stereocilia from each bundle were averaged to give an individual cell mean; then all means for individual cells (5-6 cells from each of 3-4 cochleas) were averaged and plotted ± SEM.

For row 1 and row 2, the variability in stereocilia length within each IHC hair bundle (represented by the coefficient of variation, CV) was high at P0.5 and declined by P7.5 (panel A in S1 Fig). The majority of length variability at intermediate ages during development was because the peripheral stereocilia in a row were systematically shorter than the central stereocilia of that row [6], a phenomenon that disappears by P11 [43] (depicted schematically in panels E-G of S1 Fig). We therefore restricted most of our measurements to the center ten stereocilia of each row (panel F of S1 Fig), which could be reliably carried out only with rows 1 and 2. By focusing on these center stereocilia, length variability was reduced significantly in row 1 and row 2 at all ages except P0.5 and was constant across development (panel B

154 in S1 Fig). The width CV for each bundle was also significantly lower for row 1 and especially row 2 for
155 the center ten stereocilia at most ages (panels C-D in S1 Fig).

156 **Stereocilia dimensions during stages III and IV of early postnatal development**

157 Tilney suggested that hair-bundle development in chickens could be divided into four stages [1]. While
158 these stages are present in apical IHCs of C57BL/6 mice [6], the temporal and spatial resolution of
159 previous measurements was insufficient to define transition points between the stages. We improved on
160 those measurements by (a) using the objective measurement approach described above, (b) including a
161 larger number of samples for each time point, and (c) expanding the number of time points examined
162 (Fig 1G-N). For length and width measurements, as well as individual stereocilium volumes, we
163 calculated the mean and CV for the center ten stereocilia of each row of a single bundle; each symbol
164 (each time point) in Fig 1G-N corresponds to data from 22-24 single hair cells from four different cochleas.
165 Total stereocilia volume and number measurements were made for all stereocilia in a bundle, also with
166 a total of 22-24 single-cell measurements from four cochleas.

167 As previously reported [48], the number of IHC stereocilia decreased between P0.5 and P21.5, eventually
168 reaching ~17 each of row 1 and row 2 stereocilia (Fig 1L). Row 1 stereocilia length remained constant
169 between P0.5 and P8.5, then increased exponentially through P21.5, nearly doubling in length over that
170 time period (Fig 1G). The transition between the flat and exponential regimes was sharp. By contrast,
171 row 2 lengths were greatest at P0.5; the length then decreased linearly until P8.5, when the length
172 stabilized (Fig 1G). Row 2 stereocilia widened about 30% faster than row 1 stereocilia (Fig 1H). The
173 difference in width between the rows at each time point was somewhat less than we previously estimated
174 using a different quantitation method [6]. The widening of row 1 over the entire developmental period was
175 fit by an exponential function, while row 2 started with exponential growth and switched to narrowing with
176 an exponential time course. The more sustained widening in row 1 stereocilia meant that they eventually
177 became about 20% wider than those in row 2 (Fig 1H).

178 If new actin filaments were added to a stereocilium at a constant rate, stereocilium cross-sectional area
179 (but not width) would grow linearly. Indeed, stereocilia cross-sectional area for IHCs increased linearly
180 between P0.5 and P8.5 (row 1) or P7.5 (row 2); after that time, row 1 area increased exponentially in row
181 1 and decreased exponentially in row 2 (Fig 1J). Again, the transition between the linear and exponential
182 regimes occurred sharply around P8 (Fig 1J).

183 The volume of each center ten row 1 or 2 IHC stereocilium increased linearly until P8.5 (row 1) or P7.5
184 (row 2); row 1 volume increased exponentially afterwards, while row 2 volume decreased exponentially
185 (Fig 1I). To measure total stereocilia volume in a hair bundle, we included all stereocilia from rows 1-3;
186 volume increased exponentially between P0.5 and P21.5 (Fig 1K), with no apparent transitions.

We also measured the difference in length between adjacent IHC stereocilia. The difference in length between adjacent row 1 and 2 stereocilia pairs—those that are in a single column along the tip-link axis—was constant at ~1 μm between P0.5 and P7.5, then increased exponentially to over 4 μm by P21.5 (Fig 1M). Unsurprisingly, this growth profile resembled that of row 1 lengthening, and was enhanced by the minor row 2 shortening over the same period. Immediately adjacent stereocilia (side-by-side) in a row were very similar in length (Fig 1N). Using the central ten stereocilia of each row, we measured the absolute value of the difference in length between each pair of adjacent stereocilia, then plotted the mean and CV for each hair bundle. Row 1 and row 2 stereocilia pairs showed a narrow distribution of length differences within a bundle, averaging approximately 0.3 μm (Fig 1N).

Using mouse mutants to dissect hair-bundle development

To understand the contribution of CDH23 and PCDH15 to hair-bundle development in IHCs, we investigated morphological features of hair bundles in postnatal apical IHCs from *Cdh23*^{v2J} and *Pcdh15*^{av3J} mice [32, 49–51]. These mouse lines are referred to here as “tip-link mutants,” and they also lack mechanotransduction because of the loss of tip links [33]. We confirmed that PCDH15 immunoreactivity was lost in *Pcdh15*$^{av3J/av3J}$ mice and CDH23 immunoreactivity was absent in *Cdh23*$^{v2J/v2J}$ mice (S2 Fig). To disentangle loss of tip links from loss of transduction, we also evaluated *Tmie*^{KO} mice, which represent the “transduction mutant” class; they phenocopy both the *Tmc1;Tmc2* double knockout and *Cib2* knockouts [18, 23]. Phenotypes shared by tip-link and transduction mutants most likely result from the loss of transduction, while phenotypes specific for tip-link mutants arise from the absence of the links themselves. We also analyzed *Myo15a*^{sh2} mice, which represent the "row 1 tip complex mutant" class; they largely phenocopy *Gpsm2*, *Gnai3*, *Eps8*, and *Whrn* mutants [9].

We examined hair-bundle structure, stereocilia shape, and presence of interstereocilia links using scanning electron microscopy of apical IHCs at P8.5, at the end of stage III (Fig 2). In heterozygote controls from each of the four mouse lines, bundle structure was similar with thick row 1 and 2 stereocilia and much thinner row 3 stereocilia (Fig 2A-D); moreover, stereocilia length in each row was relatively uniform. By contrast, in tip-link mutants, while distinct rows 1, 2, and 3 usually could be identified, rows were less orderly and stereocilia length in each row was irregular (Fig 2E-F). Row 1 and 2 stereocilia were still relatively thick, and row 3 stereocilia were generally considerably thicker than those of controls (Fig 2E-F). As previously reported, *Tmie*$^{KO/KO}$ bundles have stereocilia that are more uniform in length and width (Fig 2G).

Fig 2. Scanning electron microscopy of mutants showing links and tip profiles.

A-H, Scanning electron micrographs of single IHC hair bundles from P8.5 cochleas of indicated genotypes. For each genotype, top panel (labeled i) is a profile example and bottom panel (ii) is a top-down example. Panel widths, 6 μm. Inserts are 0.5 μm wide and are magnified three-fold on left; arrows indicate tip links. The insets in Ai, Bi, Ci, Di, and Gi all provide examples of beveled or pointed stereocilia tips; the insets in Ei, Fi, and Hi provide example of rounded tips. Some links were still present in both *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3j/av3J}$ bundles, but were not

located at the apices of a stereocilia tips. ***I-L***, Quantitation of number of stereocilia per hair bundle from scanning electron micrographs. Rows 1, 2, and 3 separately plotted; additional rows of stereocilia and microvilli on each cell's apical surface were also counted (row 4+). P values for unpaired t-tests are indicated.

While tip links were impossible to convincingly distinguish from other links at early developmental ages using scanning electron microscopy [52], total links in hair bundles were abundant in heterozygote controls, as well as *Tmie*$^{KO/KO}$ and *Myo15a*$^{sh2/sh2}$ mutants; by contrast, there were qualitatively fewer total links in *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ bundles, as reported previously [33]. Beveled row 2 tips were common in heterozygote control bundles and in *Tmie*$^{KO/KO}$ bundles (Fig 2A-D, G), consistent with tip links causing membrane tenting and increased actin polymerization [6, 18]. By contrast, row 2 tips of tip-link mutant stereocilia were rounded (Fig 2E-F), presumably because of the loss of tip links.

We examined scanning electron micrographs to determine the number of stereocilia in each row (Fig 2I-L). Pooled heterozygotes stereocilia from all four lines had 17.4 ± 0.3 row 1 stereocilia, 18.1 ± 0.3 row 2 stereocilia, 23.1 ± 0.5 row 3 stereocilia, and 51 ± 4 total stereocilia (mean ± SEM; n = 27 cells). The values of 17-18 row 1 and 2 stereocilia were very close to those estimated by lattice SIM at P7.5 (Fig 1L).

In IHCs homozygous for any of the four mutant alleles, the number of row 1 and row 2 stereocilia did not change significantly relative to heterozygotes (Fig 2I-L). In tip-link mutants, the number of row 3 stereocilia decreased significantly (Fig 2I-J); by contrast, the number of stereocilia in row 3 did not change in *Tmie*$^{KO/KO}$ hair bundles, although the number of row 4+ stereocilia (stereocilia associated with the bundle beyond row 3 and microvilli on the apical surface) decreased significantly (Fig 2K).

Increased variability in stereocilia dimensions of tip-link mutants

Although we previously measured stereocilia dimensions in transduction mutants [6], corresponding dimensions in tip-link mutants have yet to be systematically investigated. We therefore determined length, width, and volume of mutant IHC stereocilia from rendered lattice SIM images from P7.5, at the end of stage III, and P21.5, at the end of stage IV (Fig 3A-H). Stereocilia of tip-link mutants were less well regimented than those in controls, making assignment to rows 1, 2, and 3 more difficult. Proximity to the bare zone along the lateral edge of a hair bundle was used to assign row 1, with neighboring row assignments made medially from row 1. For length and width measurements, we calculated the mean and CV for the central ten stereocilia of each row; these were our single-cell data points (gray symbols). A cochlea measurement (colored symbols) was derived from mean or CV measurements from 5-6 single IHCs.

Fig 3. Stereocilia length in IHCs of mutants.

A-H, Imaris reconstruction of phalloidin-labeled stereocilia from *Cdh23*^{v2J} (A-B), *Pcdh15*^{av3J} (C-D), *Tmie*^{KO} (E-F), and *Myo15a*^{sh2} (G-H) IHCs at P7.5 and P21.5. Stereocilia surfaces are color-

259 coded according to row; scale bar in A (2 μm) applies to all panels. ***I-P,*** Average stereocilia
260 length (panels labeled i) and coefficient of variation for length (CV; ii). Length measurements
261 used reconstructed stereocilia surfaces. Lengths were determined for the center ten stereocilia
262 of each hair cell, and means for all ten stereocilia were plotted separately for rows 1 and 2 (gray
263 symbols). The cell means were averaged for each cochlea (5-6 cells per cochlea) and plotted
264 with colored symbols (4 cochleas per condition) [53]. Nested t-tests were used to compare the
265 cochlea values for each genotype [54]. P values are indicated and were bolded if <0.010. ***I-J***,
266 Length and length CV at P7.5 and P21.5 for *Cdh23*^{v2J}. ***M-N***, Length and length CV at P7.5 and
267 P21.5 for *Pcdh15*^{av3J}. ***K-L***, Length and length CV at P7.5 and P21.5 for *Tmie*^{KO}. ***O-P***, Length and
268 length CV at P7.5 and P21.5 for *Myo15a*^{sh2}.

269 At P7.5, average lengths of the central ten stereocilia in rows 1 and 2 changed only modestly between
270 heterozygote control and *Cdh23*$^{v2J/v2J}$ (Fig 3Ii) or *Pcdh15*$^{av3J/av3J}$ stereocilia (Fig 3Mi). By contrast, average
271 CV values for length (within each hair bundle) were significantly higher for mutant stereocilia, especially
272 those of row 2 (Fig 3Iii and 3Mii). By P21.5, average lengths were still similar between control and mutant
273 cells (Fig 3Ji and 3Ni); again, CV values were considerably higher for *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$
274 mutants, again most notably for row 2 (Fig 3Jii and 3Nii). Thus *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants
275 displayed higher variability of lengths of stereocilia in each IHC for rows 1 and 2 than controls, despite
276 having similar average lengths.

277 Stereocilia lengths in *Tmie*$^{KO/KO}$ mutants at P7.5 were also not significantly different from those of controls
278 (Fig 3Ki); by P21.5, however, row 1 stereocilia had lengthened considerably less than those of controls
279 (Fig 3Li). Variability in row 1 and 2 lengths was significantly greater in *Tmie*$^{KO/KO}$ stereocilia as compared
280 to controls (Fig 3Kii, 3Lii), although CV values were much less than those for tip-link mutants.

281 Stereocilia widths of the central ten stereocilia changed in *Pcdh15*$^{av3J/av3J}$, *Cdh23*$^{v2J/v2J}$, and *Tmie*$^{KO/KO}$
282 mutants; in each case, rows 1 and 2 widths were similar in controls but row 2 was reduced in width in
283 mutants (Fig 4Gi-Fi). Width variability increased significantly in tip-link mutants, especially in row 2
284 (Fig 4Aii-Dii); by contrast, width CV decreased in *Tmie*$^{KO/KO}$ mutants (Fig 4Eii-Fii). Row 2 width decreased
285 in all three mutants, suggesting that transduction promotes widening. However, widths were more
286 variable in the tip-link mutants, suggesting that CDH23-PCDH15 links between adjacent stereocilia might
287 also coordinate widening.

288 **Fig 4. Stereocilia width in mutants.**

289 Width measurements used reconstructed stereocilia surfaces. ***A-H,*** Average stereocilia width
290 (panels labeled i) and coefficient of variation for width (CV; ii) were determined for the center ten
291 stereocilia of each hair cell (gray symbols), separately for rows 1 and 2. Plotting and statistical
292 testing were as in Fig 3. ***I-J***, Width and width CV at P7.5 and P21.5 for *Cdh23*^{v2J}. ***M-N***, Width
293 and width CV at P7.5 and P21.5 for *Pcdh15*^{av3J}. ***K-L***, Width and width CV at P7.5 and P21.5 for
294 *Tmie*^{KO}. ***O-P***, Width and width CV at P7.5 and P21.5 for *Myo15a*^{sh2}.

295 **Adjacent stereocilia length coordination is disrupted in tip-link mutant IHCs**

296 An elevated CV for IHC stereocilia length for tip-link mutants (Fig 3) could arise from systematic variation
297 in length within a row or from stochastic variation within the row. To probe the source of high CV, we
298 used Imaris surfaces to measure the differences in length between adjacent (side-by-side) stereocilia of
299 row 1 or row 2 of *Cdh23*$^{v2J/v2J}$, *Pcdh15*$^{av3J/av3J}$, *Tmie*$^{KO/KO}$, and *Myo15a*$^{sh2/sh2}$ hair bundles. The average
300 difference in length was larger in tip-link mutants than in controls at P7.5 (row 1 in Fig 5Ci and row 2 in
301 Fig 5Ei; compare to Fig 1N), and was particularly large at P21.5 (Fig 5Di, Fi). CV values for the length
302 differences were high but similar for control and mutant stereocilia (Fig 5Cii-Fii). Because the length
303 differences were so small, the high CV values may simply reflect these small values relative to a
304 presumed absolute measurement error of similar magnitude. Altogether, the length-difference results
305 suggest that length variability is stochastic, and indicated that CDH23 and PCDH15 participate in
306 coordination of the lengths of adjacent stereocilia, both for row 1 and for row 2.

307 **Fig 5. Adjacent stereocilia length coordination in mutants.**

308 ***A***, Phalloidin-labeled stereocilia from P7.5 *Pcdh15*^{av3J} IHCs. Adjacent stereocilia in homozygous
309 mutant hair bundles are irregular in length. Panel widths: 30 μm. ***B***, Schematic showing
310 measurements made. For each pair of adjacent stereocilia in row 1 and, separately, in row 2,
311 we measured the difference in length between them (side-by-side stereocilia Δ length). For
312 example, Δ length for the pair indicated in panel B would be $|\text{length}_1 - \text{length}_2|$, or the absolute
313 value of the difference in lengths. In addition, for each row 1 – row 2 pair in a column, we
314 measured the difference in length between the two stereocilia (in-column stereocilia Δ length).
315 The brackets in panel B mark this length difference for the first row 1-row 2 stereocilia pair. ***C-***
316 ***H***, Difference in adjacent stereocilia length for *Cdh23*^{v2J}, *Pcdh15*^{av3J}, *Tmie*^{KO}, and *Myo15a*^{sh2}
317 mice using reconstructed stereocilia surfaces. Plotting and statistical testing were as in Fig 3. ***C-***
318 ***D***, Difference in length (Δ length) of side-by-side row 1 stereocilia at P7.5 and P21.5. ***E-F***,
319 Δ length of side-by-side row 2 stereocilia at P7.5 and P21.5. ***G-H***, Δ length of in-column
320 (adjacent row 1 and 2) stereocilia at P7.5 and P21.5.

321 *Tmie*$^{KO/KO}$ mutant IHCs showed a different pattern for adjacent stereocilia length differences (Fig 5C-F).
322 At P7.5, adjacent stereocilia length differences were similar in control and mutant hair bundles, both for
323 adjacent stereocilia in row 1 (Fig 5Ci) or in row 2 (Fig 5Ei) At P21.5, *Tmie*$^{KO/KO}$ mutants showed much
324 greater length variability for row 1 stereocilia (Fig 5Di), but not for row 2 (Fig 5Fi). These results suggest
325 that the lengths of adjacent row 2 stereocilia remain coordinated in *Tmie*$^{KO/KO}$ mutants, which still have
326 tip links, although row 1 coordination is reduced.

327 The difference in length between row 1 and row 2 stereocilia in a column was approximately the same
328 for tip-link mutants and heterozygotes at P7.5 (Fig 5G) and P21.5 (Fig 5H). By contrast, CV values were
329 much higher for tip-link mutants at both ages (Fig 5Gii, 5Hii). These results suggest that tip links also
330 control the relative difference in length between row 1 and row 2, perhaps indirectly through controlling
331 adjacent stereocilia lengths in the same row.

While *Tmie*$^{KO/KO}$ mutant IHCs had a similar in-column difference in length compared to heterozygotes at P7.5 (Fig 5G), that difference was much less in mutants than heterozygotes at P21.5 (Fig 5Hi), which corresponds to the reduced row 1 lengthening seen in these mutants (Fig 3). This reduced difference in length was accompanied by an increased CV for the difference, perhaps reflecting the reduced coordination among row 1 stereocilia (Fig 5Hii).

Myo15a* interacts genetically with *Pcdh15

As previously reported, stereocilia of *Myo15a*$^{sh2/sh2}$ IHC hair bundles were very short, and were more uniform in length and width than *Myo15a*^{sh2}/+ stereocilia (Fig 2G-H). Although they still support mechanotransduction [12], tips of *Myo15a*$^{sh2/sh2}$ IHCs were rounded (Fig 2H), perhaps because the minimal staircase prevented tip links from sufficiently tenting membranes off the tips of the shorter rows. The number of stereocilia in each row of *Myo15a*$^{sh2/sh2}$ bundles did not change appreciably (Fig 2L). As has been well documented [55], row 1 and 2 stereocilia lengths and widths were significantly reduced for *Myo15a*$^{sh2/sh2}$ mutants (Fig 3Oi, Pi; Fig 4Gi, Hi), associated with lower CV values (Fig 3Oii, Pii; Fig 4Gii-Hii). The adjacent stereocilia length differences for *Myo15a*$^{sh2/sh2}$ at P7.5 (Fig 5C, E) and P21.5 (Fig 5D, F) were considerably less than those of heterozygote controls. Likewise, the in-column difference in length for *Myo15a*$^{sh2/sh2}$ mutants was substantially lower than controls at both ages (Fig 5Gi, 5Hi); the CV for difference in length was increased substantially (Fig 5Hii, 5Hii), which may reflect errors in measuring these very short stereocilia.

We created double knockout *Pcdh15*$^{av3J/av3J}$;*Myo15a*$^{sh2/sh2}$ (*Pcdh15;Myo15a* DKO) mice to test for a genetic interaction between *Pcdh15* and *Myo15a* (Fig 6). In *Pcdh15*$^{av3J/av3J}$;*Myo15a*$^{sh2/sh2}$ IHC hair bundles, stereocilia were spread across the apical surface and were packed roughly hexagonally (Fig 6C), albeit not in a precise array as in *Pcdh15*^{av3J}/+;*Myo15a*$^{sh2/sh2}$ (*shaker 2* KO mice). Lengths and widths of row 1 and 2 *Pcdh15*$^{av3J/av3J}$;*Myo15a*$^{sh2/sh2}$ stereocilia were similar to those of *Pcdh15*^{av3J}/+;*Myo15a*$^{sh2/sh2}$ stereocilia (Fig 6D-E), although row 2 stereocilia were significantly shorter in the DKO bundles as compared to *sh2* KO bundles. *Pcdh15*$^{av3J/av3J}$;*Myo15a*$^{sh2/sh2}$ stereocilia showed a significant lateral-to-medial gradient in length, which was less apparent in *Pcdh15*^{av3J}/+;*Myo15a*$^{sh2/sh2}$ bundles. Row 2 stereocilia showed more length and width variation in DKO as compared to *sh2* KO bundles (Fig 6H-I), but the differences were not large.

Fig 6. *Pcdh15*^{av3J};*Myo15a*^{sh2} double knockout mice.

A-C, Phalloidin-labeled IHC hair bundles from *Pcdh15*^{av3J}/+;*Myo15a*^{sh2}/+ (Het;Het), *Pcdh15*^{av3J}/+;*Myo15a*$^{sh2/sh2}$ (Het;KO), and *Pcdh15*$^{av3J/av3J}$; *Myo15a*$^{sh2/sh2}$ (KO;KO) cochleas, Panels labeled i are single x-y planes from image stacks; panels labeled ii are x-z reslices from those stacks, with the region of the stack indicated with a yellow box in i. ***D-K***, Dimension measurements using reconstructed stereocilia surfaces. Plotting was as in Fig 3; statistical tests used one-way ANOVA analysis with the Šidák correction. ***D-E***, Length and CV length measurements. ***F-G***, Width and width CV measurements. ***H-I***, Difference in length (Δ length)

368 and CV for Δ length of side-by-side row 1 stereocilia. ***J-K***, Difference in length (Δ length) and
369 CV for Δ length of in-column (adjacent row 1 and 2) stereocilia.

370 The difference in length between adjacent stereocilia was similar in DKO hair bundles as compared to
371 *sh2* KO bundles (Fig 6F), with no significant differences in CV (Fig 6J). Likewise, the difference in length
372 between row 1 and 2 stereocilia in a single column was no different in DKO bundles than in *sh2* KO
373 bundles (Fig 6G, K). These results suggest that row 1 complex proteins are required to elongate
374 stereocilia before PCDH15-dependent links can help refine bundle architecture.

375 **Disrupted pruning of stereocilia and microvilli in mutants**

376 Mutations in tip-link genes also impacted the pruning of short rows of IHC stereocilia. In control hair cells,
377 row 3 stereocilia were obvious at P7.5 (Fig 7A-D) but were much harder to detect by P21.5 (Fig 7E-H).
378 Stereocilia and microvilli beyond row 3 (row 4+) were present at P7.5 (Fig 7A-D, K) but had nearly
379 completely disappeared by P21.5 (Fig 7E-H, L). By contrast, not only did the number of stereocilia in
380 rows 3 and 4+ increase in mutants (Fig 2I-L), but their length and diameter—and thus volume—also
381 increased in mutants (Fig 7). Row 3 and 4+ stereocilia lengths and widths, measured using Imaris surface
382 reconstructions, were quite variable since the phalloidin signal in these stereocilia in controls was very
383 low and therefore challenging to render. Instead, we measured surface volumes, which incorporated both
384 length and width, as they better reflected the overall F-actin amount in each stereocilium and were more
385 consistently measured from control IHCs (Fig 7I-L).

386 **Fig 7. Pruning of short stereocilia and microvilli in mutant IHCs.**
387 ***A-H***, Phalloidin labeling of P7.5 (A-D) and P21.5 (E-H) IHC hair bundles (i, heterozygotes; ii,
388 homozygotes). Arrows indicate extra rows of thicker stereocilia. Panel widths: 20 μm. ***I-***
389 ***L***, Individual stereocilium volumes (panels labeled i) and total volumes per cell for all stereocilia
390 in a row (ii). Row 3 (I-J) and row 4+ (K-L) are separately plotted. Volume measurements used
391 reconstructed stereocilia surfaces. Plotting and statistical testing were as in Fig 3.

392 In tip-link mutants, the volume of each row 3 stereocilium increased significantly at P7.5 compared to
393 controls, and that translated into a significant increase in total volume in all stereocilia of row 3 (Fig 7A-
394 B, I). This increase in individual and total volume for row 3 stereocilia was maintained at P21.5 for
395 *Pcdh15*$^{av3J/av3J}$ mutant hair bundles, but not for *Cdh23*$^{v2J/v2J}$ mutant bundles (Fig 7E-F, J). This
396 measurement was one of very few that distinguished the *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants. Row 4+
397 individual and total stereocilia volume also increased significantly in tip-link mutant IHCs at P7.5 (Fig 7K),
398 but was less striking at P21.5 (Fig 7L).

399 Reduced pruning and increased volume of row 3 and 4+ stereocilia was much more apparent in *Tmie*$^{KO/KO}$
400 and *Myo15a*$^{sh2/sh2}$ hair bundles (Fig 2K-L; Fig 7). As previously reported, *Tmie*$^{KO/KO}$ bundles had a
401 prominent row 3 and often additional rows (Fig 7C, G); *Myo15a*$^{sh2/sh2}$ bundles had 4-6 rows of stereocilia
402 (Fig 7D, H). At P7.5, individual and summed volumes of row 3 (Fig 7Ii-ii) and row 4+ (Fig 7Ki-ii) *Tmie*$^{KO/KO}$

403 and *Myo15a*$^{sh2/sh2}$ stereocilia were substantially and significantly increased over controls; this effect
404 remained at P21.5, although more dramatically for *Myo15a*$^{sh2/sh2}$ than *Tmie*$^{KO/KO}$ bundles (Fig 7Ji-ii, Li-ii).
405 These results showed that pruning of short rows of stereocilia was altered in all mutant bundles.

406 **Total hair-bundle volume does not change in mutants**

407 Total stereocilia volume per hair cell was not significantly different between *Cdh23*^{v2J}/+, *Pcdh15*^{av3J}/+,
408 *Tmie*^{KO}/+ heterozygotes and C57BL/6 wild-type mice at P7.5 and P21.5 (Fig 8). Despite the variability in
409 stereocilia number, length, and width, total stereocilia volumes in *Cdh23*$^{v2J/v2J}$, *Pcdh15*$^{av3J/av3J}$, and
410 *Tmie*$^{KO/KO}$ IHC hair bundles were statistically indistinguishable at P7.5 (Fig 8A). At P21.5, differences
411 between *Cdh23*^{v2J} and *Tmie*^{KO} controls and mutants were modest, albeit statistically significant (Fig 8B).
412 The similarity in stereocilia volume is broadly consistent with Tilney's proposal that each hair cell has a
413 constant amount of F-actin in its bundle, but cells deploy it differently depending on other factors [56].
414 Although *Myo15a* was an outlier at P21.5 (Fig 8B), actin and actin crosslinkers intended for stereocilia
415 may have been directed instead to cytocauds in the cell body [57].

416 **Fig 8. Total stereocilia volume in mutant IHCs.**

417 ***A-B***, Total stereocilia volume per hair bundle and volume CV for *Cdh23*^{v2J}, *Pcdh15*^{av3J}, *Tmie*^{KO}
418 and *Myo15a*^{sh2} IHCs. Volume measurements used reconstructed stereocilia surfaces. Plotting
419 was as in Fig 3; statistical tests used one-way ANOVA analysis with the Šidák correction. ***A***,
420 P7.5. No significant differences in volume between any of the genotypes. ***B***, P21.5. Modest
421 differences in total stereocilia volume were seen for *Cdh23*^{v2J}/+ vs. *Cdh23*$^{v2J/v2J}$ and *Tmie*^{KO}/+
422 vs. *Tmie*$^{KO/KO}$; a large difference in volume was seen for *Myo15a*^{sh2} IHCs.

423 **Localization of row 1 tip complex proteins in control and mutant IHCs**

424 Because proteins that localize to row 1 tips control stereocilia length, we examined in greater detail the
425 appearance of EPS8, GNAI3, and GPSM2 at the tips of C57BL/6 hair bundles (Fig 9) and at mutant
426 bundle tips (Figs 10-12). EPS8 increased at row 1 and 2 tips during stage III, then showed an initial
427 decrease and subsequent increase during stage IV (Fig 9I). GNAI3 was relatively low during stage III,
428 but increased to a peak at P10.5, near the beginning of stage IV (Fig 9J). By contrast, GPSM2 increased
429 modestly at the end of stage III but shot up substantially during late stage IV, peaking at P15.5 (Fig 9K).
430 GNAI3 and GPSM2 levels each dropped precipitously by P21.5 (Fig 9J-K). Our results showing
431 sequential accumulation of EPS8, then GNAI3, and finally GPSM2 at stereocilia tips are not consistent
432 with the earlier suggestion that the row 1 tip complex assembles simultaneously [9].

433 **Fig 9. Developmental expression of row 1 complex proteins in IHC stereocilia.**

434 ***A-D***, Localization of GPSM2 and EPS8 in P0.5, P7.5, P15.5, and P21.5 IHCs. ***E-F***, Localization
435 of GNAI3 and EPS8 in P0.5, P7.5, P15.5, and P21.5 IHCs. In A-B and E-F, images are
436 projections of horizontal slices with partially flattened hair bundles. In C-D and G-H, images are
437 projections of horizontal slices obtained at the level of row 1 tips only (top) or row 2 tips and row
438 shafts (bottom). Images in A-D were acquired in the same imaging session and used the same
439 acquisition, processing, and display parameters; the same holds for images in E-H. Panel

440 widths: A-H, 30 μm. ***I-J***, Quantitation of EPS8, GNAI3, and GPSM2 immunofluorescence at row
441 1 and 2 tips. Fluorescence was normalized to fluorescence at P7.5 (EPS8 and GNAI3) or P15.5
442 (GPSM2) to allow comparison between multiple experiments.

443 As in C57BL/6 stereocilia, in heterozygotes from mutant IHCs, GNAI3, GPSM2, and EPS8 were
444 concentrated at tips of row 1 stereocilia (Fig 10A-D, I-L). WHRN was also concentrated at row 1 tips in
445 heterozygotes (Fig 10E-H). In *Pcdh15*$^{av3J/av3J}$ IHCs, GNAI3 and GPSM2 remained concentrated at row 1
446 but EPS8 was seen at all stereocilia tips in similar amounts (Fig 10B, F, J). These results contrasted with
447 those from *Tmie*$^{KO/KO}$ IHCs, where GPSM2 and GNAI3 largely disappeared from hair bundles (Fig 10D,
448 L); WHRN intensity was reduced, but remained most abundant in row 1 (Fig 10H). EPS8 levels in shorter
449 rows of *Tmie*$^{KO/KO}$ IHCs increased substantially [6], but EPS8 was still most abundant in row 1 (Fig 10D,
450 H, L).

451 **Fig 10. Row 1 protein localization in mutant IHCs.**

452 ***A-D***, Localization of GNAI3 and EPS8 in *Pcdh15*^{av3J} and *Tmie*^{KO} heterozygotes and
453 homozygotes at P7.5. ***E-H***, Localization of WHRN and EPS8 in *Pcdh15*^{av3J} and *Tmie*^{KO}
454 heterozygotes and homozygotes at P7.5. ***I-L***, Localization of GNAI3 and EPS8 in *Pcdh15*^{av3J}
455 and *Tmie*^{KO} heterozygotes and homozygotes at P7.5. Arrows in B and D show high levels of row
456 2 EPS8 but not GNAI3. Images from all pairs of heterozygote and homozygote cochleas (A and
457 B, C and D, E and F, G and H, I and L) were acquired in the same session and used the same
458 acquisition, processing, and display parameters. All images are projections of horizontal slices;
459 projections that allow visualization of the entire hair bundle typically had stereocilia splayed
460 against the apical surface, especially at P15.5, which resulted in immunofluorescence signal
461 from stereocilia being overlaid on top of immunofluorescence signal from apical surfaces.
462 Arrows in B, F, and J show high levels of EPS8 in row 2 stereocilia of *Pcdh15*$^{av3J/av3J}$ IHCs.
463 Asterisks in D and L show reduced levels of GNAI3 and GPSM2 in *Tmie*$^{KO/KO}$ IHCs. Panel widths:
464 30 μm.

465 Quantitation of row 1 tip complex proteins allowed us to determine the distribution of these proteins
466 between row 1 and 2 stereocilia more thoroughly (Fig 11-12; S4 Fig). Total EPS8 at stereocilia tips was
467 not altered in tip-link mutants at P7.5 or P21.5 (Fig 11A-B); EPS8 decreased modestly but not significantly
468 in *Tmie*$^{KO/KO}$ hair bundles. Here we used fluorescence intensity normalized to heterozygote levels for
469 each age, which reduced signal variability but prevented us from comparing total fluorescence at different
470 ages.

471 **Fig 11. Distribution of EPS8 at tips of stereocilia in tip-link and transduction mutant IHCs.**

472 ***A-B***, EPS8 fluorescence average intensity per hair bundle for all measured stereocilia (row 1
473 and 2) for *Cdh23*^{v2J}, *Pcdh15*^{av3J}, and *Tmie*^{KO} hair cells at P7.5 (A) and P21.5 (B). Plotting and
474 statistical testing were as in Fig 3. ***C-F***, Frequency distribution of stereocilia length and EPS8 tip
475 intensity in *Cdh23*^{v2J} hair cells. ***G-J***, Frequency distribution of stereocilia length and EPS8 tip
476 intensity in *Pcdh15*^{av3J} hair cells. ***K-N***, Frequency distribution of stereocilia length and EPS8 tip
477 intensity in *Tmie*^{KO} hair cells. Stereocilia length measurements (B, D, F, H, J, L) and EPS8 tip
478 intensities (C, E, G, I, K, M) were from all row 1 and 2 stereocilia; distributions were fit with

479 double Gaussian functions. ***O-R***, Correlation of normalized EPS8 intensity with stereocilia
480 length. Data from individual rows were displayed with separate symbol colors but all data were
481 used for fits; data were fit with $y = a + b \cdot \exp(-k \cdot x)$, where y is stereocilia length, x is EPS
482 intensity, and a, b, and k are constants.

483 Frequency distribution plots, using normalized EPS8 intensities (signal at each tip divided by the total
484 signal for all row 1 and 2 stereocilia measured in the hair bundle), revealed how EPS8 was uniformly
485 targeted to stereocilia tips in tip-link mutants. Fitting each frequency distribution with a double Gaussian
486 function, two prominent peaks were detected in *Cdh23*^{v2J}/+ or *Pcdh15*^{av3J}/+ controls (blue data in Fig 11D,
487 F, H, J). By contrast, *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants each displayed a single distribution,
488 centered at a tip intensity/average = 1 (orange data in Fig 11 D, F, H, J). The convergence to a single
489 distribution was seen both at P7.5 (Fig 11D, H) and P21.5 (Fig 11F, J). These results confirmed the
490 relative uniformity of EPS8 at all stereocilia tips in tip-link mutants.

491 We also plotted the distribution of row 1 and 2 stereocilia lengths for each dataset; in homozygous
492 mutants, the length distributions were biased towards shorter stereocilia lengths and were broadened,
493 especially at P21.5 (Fig 11C, E, G, I). These results also show that a consequence of the increased
494 variability in row 1 and 2 lengths in the tip-link mutants is an increase in stereocilia of intermediate lengths
495 (Fig 11 C, E, G, I), in between average lengths for row 1 and 2 in the heterozygote controls. Thus, despite
496 their lack of length coordination within rows, hair bundles of tip-link mutants as a whole contain stereocilia
497 of more uniform lengths than those of controls.

498 In *Tmie*$^{KO/KO}$ hair bundles at P7.5, the EPS8 frequency distribution showed a broad double peak, unlike
499 the two well separated peaks in the *Tmie*^{KO}/+ control (Fig 11L; see also panel J in S5 Fig); the distribution
500 was weighted more towards high EPS8 tip/average values than in the tip-link mutant plots. At P7.5,
501 *Tmie*$^{KO/KO}$ showed a broad distribution of stereocilia length that was still fit with two Gaussians (Fig 11K).
502 EPS8 distribution and stereocilia length for *Tmie*$^{KO/KO}$ at P21.5 were broadly similar to those of
503 *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$. These results highlight the effect of loss of CDH23 or PCDH15 on EPS8;
504 while tip-link mutants have lost transduction, as have *Tmie*$^{KO/KO}$ bundles, the impact on EPS8 distribution
505 in the tip-link mutants is somewhat greater.

506 We also compared the EPS8 intensity at each tip with the length of that stereocilium at P15.5 (Fig 11O-
507 R). We found that these data were fit well with an exponential, showing that while the length of shorter
508 stereocilia was correlated with EPS8 intensity, beyond a certain EPS8 intensity, stereocilia length no
509 longer depended on EPS8 intensity. Loss of PCDH15 caused a broadening of this curve, although the
510 trend was still the same. Loss of TMIE did not change the shape of the curve but instead lowered the
511 plateau, reflecting the reduced stereocilia lengthening in these mutants. While more stereocilia had
512 intermediate EPS8 intensity in both mutants, stereocilia belonging to different rows were scattered along
513 the curve in the *Pcdh15*$^{av3J/av3J}$ mutants, reflecting the loss of row organization in these mutants. These

514 results suggested that EPS8 could influence stereocilia length, but only up to a certain length; this
515 maximal elongation may be regulated by mechanisms in addition to EPS8 levels.

516 Total GNAI3, GPSM2, and WHRN fluorescence at stereocilia tips was not affected in tip-link mutants (Fig
517 10A-B, E-F, I-J; Fig 12A-D; panels A-D in S4 Fig). In *Tmie*$^{KO/KO}$ mutants, as previously reported [6],
518 GNAI3, GPSM2, and WHRN fluorescence at stereocilia tips was considerably reduced (Fig 10C-D, G-H,
519 K-L), with statistically significant reductions for GNAI3 and WHRN at P7.5 (Fig 12A-B) and GPSM2 at
520 P15.5 (Fig 12C). These results confirm that TMIE (and TMC1/2) affect distribution of GNAI3, GPSM2 and
521 WHRN directly, not via transduction-mediated ion flux [6]. TMC2 still targeted to stereocilia in
522 *Pcdh15*$^{av3J/av3J}$ mutants, but TMC1 disappeared (S3 Fig), suggesting that TMC2 may be sufficient for
523 localization of GPSM2, GNAI3, and WHRN to row 1 tips.

524 **Fig 12. Distribution of GNAI3 and WHRN at tips of stereocilia in tip-link and transduction**
525 **mutant IHCs.**

526 ***A-B***, GNAI3 (A) and WHRN (B) fluorescence average intensity per hair bundle for all measured
527 stereocilia (row 1 and 2) for *Cdh23*^{v2J}, *Pcdh15*^{av3J}, and *Tmie*^{KO} hair cells at P7.5. Plotting and
528 statistical testing were as in Fig 3. ***C-F***, Frequency distribution of GNAI3 and WHRN tip intensity
529 in *Cdh23*^{v2J} hair cells. ***G-J*** Frequency distribution of GNAI3 and WHRN tip intensity in *Pcdh15*^{av3J}
530 hair cells. ***K-N***, Frequency distribution of GNAI3 and WHRN tip intensity in *Tmie*^{KO} hair cells. Tip
531 intensities for GNAI3 (E, G, I, K, M, O) and WHRN (F, H, J, L, N, P) were from all row 1 and 2
532 stereocilia; distributions were fit with double Gaussian functions.

533 In control hair bundles at P7.5, GNAI3 frequency distributions were very different from those of EPS8;
534 most stereocilia had little or no GNAI3, but a minority had a considerable amount (blue in Fig 12E and
535 panel Q in S4 Fig). This distribution matched the immunocytochemistry images, where GNAI3 was found
536 nearly exclusively at row 1 tips (Fig 10; S4 Fig). In *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants, the frequency
537 distribution was moderately altered; most stereocilia still had little or no GNAI3, but relatively larger
538 numbers had intermediate levels of signal (orange in Figs 12E and panel Q in S4 Fig). Even though
539 GNAI3 levels dropped significantly in *Tmie*$^{KO/KO}$ bundles (Fig 12A), the frequency distribution resembled
540 that of tip-link mutants (green in Fig 12I). The distribution of WHRN at P7.5 was similar to but broader
541 than that of GNAI3, and was altered similarly in tip-link and transduction mutants (Figs 12B, F, J and
542 panels N, R in S4 Fig). At P21.5, distribution of GNAI3 and WHRN among stereocilia tips was not altered
543 substantially in tip-link mutants (panels O-P and S-T in S4 Fig).

544 Total GPSM2 intensity was decreased significantly in stereocilia tips of P15.5 *Tmie*$^{KO/KO}$ mutants,
545 although EPS8 was not (Fig 12C-D). The distribution of GPSM2 at P15.5 in heterozygote stereocilia (Fig
546 12G, K) was similar to that of GNAI3 at P7.5 (Fig 12E, I), and the altered distribution in *Pcdh15*$^{av3J/av3J}$
547 and *Tmie*$^{KO/KO}$ mutants also resembled that of GNAI3 (Fig 12G, K).

548 Plots of stereocilia length against GPSM2 intensity (Fig 12M-P) were fit well with an exponential
549 relationship for both controls and mutants, similar to that seen with EPS8 (Fig 11O-R). The exponential

550 constant k was considerably smaller for the GPSM2 fits ($k \approx 3$) than for the EPS8 fits ($k \approx 8$), consistent
551 with GPSM2 tip accumulation only occurring in the longest stereocilia (i.e., row 1).

552 ***Tmie* does not interact genetically with *Pcdh15***

553 We created double knockout *Pcdh15*$^{av3J/av3J}$;*Tmie*$^{KO/KO}$ (*Pcdh15;Tmie* DKO) mice to clarify interaction
554 between *Pcdh15* and *Tmie* (S5 Fig). KO;KO hair bundles demonstrated unaltered EPS8 levels and a
555 single-Gaussian distribution, similar to that in tip-link mutants (panels I-J in S5 Fig). KO;KO bundles also
556 showed reduced GNAI3 levels and altered distribution as seen in *Tmie*$^{KO/KO}$ bundles (panels K-L in S5
557 Fig). KO;KO bundles shared features of both Het;KO and KO;Het bundles (panels A-D in S5 Fig).
558 Mutations in *Pcdh15* thus did not suppress transduction-mutant phenotypes, nor did mutations in *Tmie*
559 suppress phenotypes seen in tip-link mutants, indicating a lack of genetic interaction for these
560 phenotypes.

561 **Labeling stereocilia free barbed ends with rhodamine-actin**

562 Row 2 stereocilia shrink during stage III, then stabilize in length during stage IV (Fig 1G). Actin-filament
563 free ends, measured in permeabilized hair bundles using rhodamine-actin as a probe, were particularly
564 high at row 2 tips in control bundles during early postnatal development but decreased in cochleas of
565 transduction mutants or cochleas treated with transduction-channel blockers [39]. Results with tip-link
566 mutants (Fig 13A-B, G-H, M, P) were very similar to those obtained with *Tmie*$^{KO/KO}$ mutants [39] (Fig 13C-
567 D, I-J, N, Q). In *Pcdh15*^{av3J}/+ controls, the high level of row 2 labeling by rhodamine-actin seen in control
568 bundles at P7.5 (Fig 13A, M) had disappeared by P21.5 (Fig 13G, P); row 1 labeling was reduced as well
569 at P21.5 (Fig 13P). In *Pcdh15*$^{av3J/av3J}$ mutants at P7.5, rhodamine-actin labeling was relatively low, with
570 row 1 and 2 tips having similar intensities (Fig 13B, M). That pattern was relatively unchanged at P21.5
571 (Fig 13H, P).

572 **Fig 13. Free barbed end labeling of IHC stereocilia with rhodamine-actin.**

573 ***A-L***, Rhodamine-actin (Rh-actin) and phalloidin labeling of mutant IHC hair bundles at P7.5 and
574 P21.5. *Pcdh15*^{av3J} (A-B, G-H), *Tmie*^{KO} (C-D, I-J), and *Myo15a*^{sh2} (E-F, K-L). Arrows in A, C, and
575 E indicate high levels of row 2 rhodamine-actin labeling in P7.5 control IHC bundles; asterisks
576 in B, D,F, H, and J indicate similar rhodamine-actin levels at all stereocilia tips in P7.5 and P21.5
577 mutant IHC bundles. Panel widths: 24 μm. ***M-R***, Rh-actin tip intensity and intensity CV in
578 *Pcdh15*^{av3}, *Tmie*^{KO}, and *Myo15a*^{sh2} at P7.5 (M-O) and P21.5 (P-R). Plotting and statistical testing
579 were as in Fig 3.

580 By contrast, in *Myo15a*$^{sh2/sh2}$ mice, row 1 and row 2 rhodamine-actin labeling was elevated to the intensity
581 level seen in row 1 from control mice at P7.5 (Fig 13E-F, O); rhodamine-actin labeling then declined
582 precipitously in both rows by P21.5 (Fig 13K-L, R). Thus, during stage III, actin filament free ends appear
583 to be suppressed by the row 1 complex but enhanced by transduction; in turn, increased free ends
584 correlate with row 2 shortening.

585 **CAPZB no longer concentrates at P21.5 stereocilia tips in tip-link mutants**

586 After P10, CAPZB—and to a lesser extent, EPS8L2—shifts from the shafts of all stereocilia to concentrate
587 at row 2 tips in control hair bundles [6]; this shift does not occur in homozygous transduction mutants [6].
588 We confirmed results in *Tmie*^{KO} mice (Fig 14C-D, G-H) and showed further that CAPZB no longer
589 concentrated at row 1 or 2 tips in *Pcdh15*$^{av3J/av3J}$ IHCs (Fig 14A-B, G), instead remaining along stereocilia
590 shafts (asterisks in Fig 14B). By contrast, CAPZB concentrated at tips of both rows in relatively equal
591 amounts in in *Myo15a*$^{sh2/sh2}$ bundles (arrows in Fig 14F; Fig 14G).

592 **Fig 14. Row 2 protein localization in mutant IHCs.**

593 ***A-F***, Localization of CAPZB and EPS8L2 in *Pcdh15*^{av3J} (A-B), *Tmie*^{KO} (C-D), and *Myo15a*^{sh2} (E-
594 F) heterozygous and homozygous IHCs at P21.5. Arrows in A, C, and E show high levels of row
595 2 CAPZB in heterozygotes. In B, asterisks show CAPZB labeling along stereocilia shafts and
596 arrowheads show strong EPS8L2 labeling at row 1 and 2 tips. Arrows in F show CAPZB at tips
597 of all stereocilia in *Myo15a*$^{sh2/sh2}$. Panel widths: H-M, 30 μm. ***G-H***, Quantitation of CAPZB (G)
598 and EPS8L2 (H) average intensity in row 2 tips divided by the average intensity in row 1 tips in
599 heterozygotes and homozygotes at P21.5. Plotting and statistical testing were as in Fig 3.

600 EPS8L2 was present at both row 1 and row 2 tips in control hair bundles, with a modest bias towards
601 row 2; EPS8L2 was found at nearly equal levels in both rows of *Pcdh15*$^{av3J/av3J}$ and *Tmie*$^{KO/KO}$ IHC bundles
602 (Fig 14A-D, H; arrowheads in Fig 14B). In contrast to CAPZB, EPS8L2 was nearly completely absent
603 from *Myo15a*$^{sh2/sh2}$ bundles (Fig 14E-F). These results suggested that the presence of transduction and
604 the row 1 complex are required for selective targeting of CAPZB to row 2 tips during late development.
605 The appearance of CAPZB at tips by P21.5 was correlated with the decline in free barbed end labeling
606 at this age for both control and mutant bundles, suggesting that capping proteins, row 1 proteins, and
607 transduction all stabilize F-actin at stereocilia tips during stage IV.

608 ## Discussion

609 The results presented here support a comprehensive model that explains key steps of developmental
610 assembly of the apical IHC hair bundle (Fig 15). By increasing resolution for our measurements of
611 stereocilia dimensions, we defined more accurately Tilney's stages III and IV of stereocilia growth in
612 mouse hair cells and the point of transition between them [1]. These improvements were made possible
613 by boosting sampling frequency and increasing measurement precision using automated analysis. In
614 addition, use of four mouse mutant lines allowed us to determine what role the tip-link proteins,
615 transduction proteins, and the row 1 complex play in bundle development. Together the results provide
616 a picture of several simultaneous processes proceeding in parallel with significant interconnections
617 reinforcing key transitions.

Fig 15. Model for assembly of IHC hair bundle.

A, Left, stereocilia building blocks (combined actin and actin crosslinkers) increase continuously in IHCs throughout early postnatal development. Right, a spatial gradient of building blocks may also exist, with building blocks having greater access to row 1 stereocilia than to shorter rows. ***B***, PCDH15 and CDH23 maintain coordination of adjacent stereocilia lengths, presumably by triggering actin depolymerization when spontaneous stereocilia elongation interrupts the stable state. ***C-D***, Stage-dependent processes. ***C***, EPS8 is present at all stages of stereocilia growth. In stage II, EPS8 is present at all tips in approximate proportion to stereocilia length. In stage III and IV, EPS8 levels drop at row 2 tips while they remain constant at row 2 tips. ***D***, GPSM2 appears in row 1 stereocilia during stage II, and stimulates the row 1 complex sufficiently to drive this phase of lengthening. GPSM2 levels drop during stage II, when lengthening is arrested. If transduction proteins are present in the hair bundle, GPSM2 levels rise during stage IV, presumably leading to activation of EPS8 and actin-filament elongation. ***E***, At row 2, the actin-depolymerizing proteins DSTN and CFL1 (and their partner WDR1) are found diffusely in stereocilia. During stage III, transduction leads to localization of DSTN and CFL1 at row 2 tips, triggering actin-filament turnover and shrinkage of row 2. CAPZB and TWF2 are localized separately during this stage, but in stage IV both are found together at row 2 tips if transduction is active.

Steady growth of stereocilia building blocks and local regulation

In chick cochlea, hair bundles with widely varying numbers and dimensions of stereocilia still have the same total amount of F-actin in their bundles [56]. Similarly, we found that P7.5 bundles from mouse mutants with differing stereocilia number, length, and width still had the same total stereocilia volume. Moreover, in wild-type hair cells, the total stereocilia volume per bundle increased monotonically despite the very different growth behavior of individual stereocilia rows during stages III and IV. While cellular actin transcript and protein levels do not rise during early postnatal bundle development [58–60] (see also umgear.org), actin crosslinkers do increase in expression over this period [59, 61] (umgear.org); moreover, loss of crosslinkers affects stereocilia dimensions [61–63], and FSCN2 overexpression lengthens stereocilia [64]. A continually increasing supply of actin crosslinkers, including ESPN, FSCN2, and PLS1, may therefore steadily increase the supply of “building blocks” (i.e., actin plus actin crosslinkers) for stereocilia growth during early postnatal development.

These results suggest that hair cells continuously synthesize stereocilia building blocks and that local regulatory mechanisms then control how these building blocks are exploited. These local regulatory mechanisms must be switched on and off rapidly. Our results showed that during stage III, lengthening of stereocilia was completely inhibited; cross-sectional area grew linearly during this time, suggesting a constant rate of addition of actin filaments to the periphery of the stereocilia core. At P8, however, a sharp transition occurred; lengthening resumed then and proceeded exponentially for the next two weeks.

Stereocilia building blocks appear to be made available to the hair bundle in a lateral to medial gradient; even when tip links are not present and the row 1 complex is distributed to most stereocilia, a row 1

656 through row 3 gradient in length was still apparent. This gradient was even apparent in *Myo15a*$^{sh2/sh2}$
657 mutants, which lack the row 1 complex at any tips. A plausible explanation is that building blocks are
658 more accessible at the fonticulus, the aperture in the cuticular plate that the kinocilium extends through.
659 This region is not only filled with microtubules and vesicles [65] but also could be a region where soluble
660 molecules like actin monomers and crosslinkers more freely diffuse. The alternative explanation that
661 stereocilia growth starts later in shorter stereocilia is not supported by the comparison of row 1 and 2
662 kinetics in C57BL/6 hair cells (Fig 1).

663 **The row 1 tip complex controls lengthening in stages II and IV**

664 The biochemical properties of the row 1 tip complex, composed of EPS8, MYO15A, WHRN, GNAI3, and
665 GPSM2, suggest how the complex controls stereocilia length. EPS8 and MYO15A each can control actin
666 polymerization [66, 67], and early in development, the two proteins target to all stereocilia in amounts
667 approximately proportionally to stereocilia length [7]. Moreover, together both proteins form a phase-
668 separated complex that may promote actin polymerization [10]. In the absence of transduction [6] or tip
669 links (this work), the EPS8-MYO15A complex is no longer exclusively targeted to row 1 and instead
670 appears at all tips, also in proportion to length. These results suggest that the EPS8-MYO15A complex
671 is targeted to all tips, but that other events during development lead to their accumulation with the rest of
672 the complex members only at the tips of row 1.

673 In stereocilia, as long as functional RGS12 is present [68], GPSM2 and its partner GNAI3 are exclusively
674 found at row 1 tips [7, 8]; there, they assemble with the EPS8-MYO15A complex [7–9] using WHRN as
675 an adapter [9]. GPSM2 forms large protein condensates in vitro, both by itself and with the entire row 1
676 complex [11], and it is reasonable to suggest that GPSM2 drives the formation of similar condensates at
677 the tips of row 1 stereocilia. When the row 1 complex is formed, GPSM2 activates EPS8's F-actin
678 bundling activity, which likely promotes stereocilia lengthening [11]. GNAI3 can target to stereocilia tips
679 independently from other row 1 proteins [7], and may act as an adapter between the membrane at row 1
680 tips and the rest of the row 1 complex [11].

681 Previous characterization of the row 1 tip complex has not distinguished its activity during the two
682 lengthening stages of hair-bundle development [1]. In apical IHCs, stage II—initial lengthening of
683 stereocilia—occurred prior to our first measurements at P0.5. Tadenev and colleagues demonstrated
684 that GNAI3 and GPSM2 are indeed required for this initial lengthening stage. First, both proteins appear
685 at row I tips during stage II [9]. In addition, hair cells that express pertussis toxin, which inactivates all
686 GNAI isoforms, have very short stereocilia, as do *Gpsm2*-null hair cells [9]. These stereocilia are much
687 shorter than those of bundles at P0.5, which is at the end of stage II. Bundles lacking EPS8, MYO15A,
688 or WHRN each show the same short-stereocilia phenotype [69–71].

689 Although these simple knockouts do not probe later steps in development, our experiments suggest that
690 GNAI3 and GPSM2 are also required for the final stereocilia lengthening that occurs during stage IV.

691 GNAI3 and GPSM2 each build up at tips of row 1 stereocilia during stage IV, with GPSM2 peaking later
692 than GNAI3. *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants, which retain GNAI3 and GPSM2 in row 1, have
693 row 1 lengths nearly equal to those of controls. By contrast, *Tmie*$^{KO/KO}$ mutants, which do not accumulate
694 GNAI3 or GPSM2 in row 1 stereocilia during stage IV, have shorter row 1 stereocilia.

695 **Loss of CDH23 or PCDH15 leads to uncoordinated stereocilia lengthening**

696 Our experiments also revealed several specific functions for CDH23 and PCDH15, presumably as
697 heterotetrametric links, during development of apical IHC hair bundles. While CDH23-PCDH15 tip links
698 gate transduction channels and transduction impacts bundle development [6], we show here that CDH23
699 and PCDH15 are also essential for coordinating the lengths of adjacent stereocilia in the same row. While
700 we cannot rule out effects specific to CDH23 or PCDH15, the similarity in phenotype between *Cdh23*^{v2J}
701 and *Pcdh15*^{av3J} mouse lines and demonstrated interaction between them [26, 72, 73] makes it most likely
702 that roles for these two proteins, like length coordination, require their interaction.

703 CDH23 and PCDH15 have each been suggested to contribute to the transient lateral links [24, 26, 74,
704 75], and these links may be essential for coordinating adjacent stereocilia lengths. Transient lateral links
705 bridge the gap between adjacent stereocilia along their shafts and are prominent in mouse IHCs and
706 OHCs between E17.5 and P0; they begin to disappear after P0, and are no longer seen after P5 except
707 at stereocilia tips [76]. Although some links between adjacent stereocilia remain in both *Pcdh15*$^{av3J/av3J}$
708 and *Cdh23*$^{v2J/v2J}$ hair bundles (Fig 2), these are likely ankle links [76, 77].

709 Transient lateral links are similar to the thread-like links that interconnect the distal microvilli tips in the
710 intestinal brush border [78]; these links are composed of CDHR2 (PCDH24) and CDHR5, members of
711 the adhesion complex, and are essential for microvillar clustering and length uniformity [78]. Length
712 uniformity in microvilli of the brush border has been proposed to arise from stimulation of actin dynamics
713 through the adhesion complex or by physical constraints, as a link could prevent an adjacent microvillus
714 from elongating [79]. In IHCs, we propose that dimeric complexes of CDH23 and PCDH15 carry out the
715 same function throughout development.

716 Nevertheless, the morphology of *Pcdh15*^{av3J}*;Myo15a*^{sh2} DKO hair bundles was dissimilar to that of CACO-
717 2_{BBE} intestinal cells with shRNA knockdown of PCDH24; these latter cells had microvilli of widely differing
718 lengths that lacked hexagonal arrangement [78]. DKO bundles retained a modest gradient in stereocilia
719 length, despite the lack of tip links, and adjacent stereocilia were similar in length; while packed less
720 tightly than either *Pcdh15*^{av3J}/+;*Myo15a*^{sh2}/+ or *Pcdh15*^{av3J}/+;*Myo15a*$^{sh2/sh2}$ stereocilia, packing was still
721 hexagonal. The retention of length coordination, albeit to very short lengths, suggests that additional
722 mechanisms contribute to regulation of stereocilia length in addition to the row 1 complex and PCDH15.
723 Physical constraints of the overlying tectorial membrane probably do not contribute to length regulation;
724 when the tectorial membrane is eliminated genetically, IHC and OHC bundles retain their normal
725 morphology and stereocilia lengths are aligned [80, 81].

726 A system for aligning lengths of adjacent stereocilia may have evolved to produce optimal activation of
727 transduction channels. Alignment of stereocilia lengths in each row should coordinate transduction
728 channel gating and increase sensitivity. For small stimuli, the shear between two stereocilia can be
729 approximated by $x = \gamma \cdot X$ [82], where X is the displacement applied to the hair bundle's tip and γ is a
730 geometrical gain factor; x is the distance that the gating spring is stretched by the stimulus and hence is
731 the relevant activation delivered to the transduction channels [83]. In turn, $\gamma = S / L$, where S is the
732 spacing between stereocilia at their bases and L is the length of the stereocilia at the point of shear. In
733 wild-type bundles, spacing between adjacent stereocilia in a given row is constant within that row and
734 from bundle to bundle [82]. By contrast, in tip-link mutants, variability in L of row 2 will produce variability
735 in x; if a cell has variations in x with a constant X, channel open probabilities will vary, perhaps
736 considerably. In turn, variability in open probabilities will broaden the displacement-transduction current
737 relationship of the bundle and reduce sensitivity. Tight control of stereocilia length within a row is thus
738 required to maintain the hair cell's high sensitivity.

739 **Transduction proteins localize the row 1 complex**

740 Our results here confirm our previous suggestion that transduction proteins themselves regulate the
741 amount of GNAI3 and GPSM2 that accumulate at row 1 tips during stage IV [6]. While little GNAI3 (or
742 GPSM2) is found in row 1 of *Tmie*$^{KO/KO}$ mutant hair bundles, GNAI3 and GPSM2 concentrate relatively
743 normally in row 1 stereocilia in *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutants. Stage III and IV localization of
744 these proteins to row 1 tips occurs long after the initial lengthening of stereocilia adjacent to the kinocilium,
745 so transduction mediated through kinocilia-stereocilia links [84] is likely not responsible. TMIE and the
746 TMCs do localize to row 1 near tips during early postnatal development [23], and at least TMC2 is present
747 in row 1 in *Pcdh15*$^{av3J/av3J}$ mutants (S3 Fig).

748 Accordingly, GNAI3 or GPSM2 may bind directly or indirectly to TMC channels localized to tips of row 1
749 stereocilia during development (Fig 15E). This coupling could be mediated by the established CIB2-
750 WHRN interaction [85]; CIB2 is part of the transduction-channel complex [86–88] and WHRN interacts
751 with GPSM2 [9, 11]. TMC channels are no longer at row 1 tips in older stereocilia [89], so localization of
752 GNAI3 and GPSM2 to row 1 by the transduction complex may only be necessary at the beginning of
753 stage IV to initiate formation of a robust row 1 complex.

754 **Transduction controls actin dynamics at row 2 tips**

755 Transduction controls actin-regulatory mechanisms in row 2 differently than those in row 1; during stage
756 III, row 2 stereocilia shorten when row 1 lengthens, showing they respond differently during development,
757 and the complement of proteins at their tips differs from that at row 1 tips. Our results confirm the
758 observations of McGrath and colleagues, who demonstrated that row 2 tips transiently have abundant
759 free actin filaments ends, but not in *Tmie*$^{KO/KO}$ mutants nor in the presence of channel blockers [39].
760 *Pcdh15*$^{av3J/av3J}$ mutants also lose strong row 2 rhodamine-actin labeling, confirming that transduction
761 itself—rather than transduction proteins—is responsible for this effect.

762 Effects of transduction on protein localization likely occur because transduction channels are partially
763 open at rest during development [90], and because substantial Ca^{2+} entry occurs when channels are
764 open [16]. The steep local gradient of Ca^{2+} may in turn localize specific proteins to row 2 tips but not
765 elsewhere in the row 2 stereocilia.

766 Transduction recruits DSTN (ADF) and CFL1 to stereocilia tips [39], which may depend on local Ca^{2+}
767 entry (Fig 15F). Moreover, in many contexts, Ca^{2+} influx increases DSTN and CFL1 activity by activating
768 Ca^{2+}-dependent phosphatases [40]. In tip-link or transduction mutants, not only is the high level of
769 rhodamine-actin labeling at row 2 tips reduced, but rhodamine-actin labeling at row 1 tips also increases.
770 These results suggest that actin dynamics are regulated by transduction at both row 1 and row 2 tips, but
771 in opposite directions. Transduction contributes to the polarization of EPS8 into row 1, as both *Tmie*$^{KO/KO}$
772 and *Pcdh15*$^{av3J/av3J}$ mutants have relatively similar amounts of EPS8 in all tips; in this case, the similarity
773 in phenotype between the two mutants suggests that transduction currents themselves mediate EPS8
774 exclusion from the shorter rows. By preventing accumulation of EPS8 at row 2 tips, transduction could
775 thereby promote its accumulation at row 1, thus contributing to the polarization in actin dynamics between
776 the two rows.

777 These results suggest that transduction stimulates actin depolymerization at the tips of the shorter rows
778 [38, 39]. Moreover, by increasing actin dynamics, transduction thus also controls stereocilia remodeling
779 (row 2) or resorption (rows 3 and beyond) during development. A key question is why this model, which
780 suggests that transduction promotes row 2 shortening, is contradicted by experiments showing that
781 transduction-channel block stimulates row 2 shortening [17]. A plausible explanation for this discrepancy
782 is that these latter experiments were conducted on stage IV hair bundles [6]. Thus while transduction
783 promotes row 2 shortening during stage III, changes that occur during stage IV reverse the sign of
784 transduction's effect. The F-actin capping complex of CAPZB and TWF2 appears during stage IV only if
785 transduction is present [6], so the effect of blocking transduction during stage IV may be to dissociate the
786 capping complex and trigger stereocilia shortening.

787 **A model for hair-bundle length regulation during stages III and IV**

788 Our model for development of mouse IHC hair bundles (Fig 15) references Tilney's chick bundle
789 development model [1]; it also exploits key observations made in developing mouse cochlear hair cells
790 [7–9, 39] and biochemical studies of the row 1 complex [9, 11]. In this model, mouse bundles undergo
791 temporally segregated initial lengthening (stage II), widening (stage III) and final lengthening (stage IV)
792 steps. A key feature of bundle development is the creation of three stereocilia rows, each with unique
793 dimensions for their stereocilia. Establishment of these rows occurs when symmetry within the bundle is
794 broken, allowing distinct actin-regulatory mechanisms to control F-actin growth within individual
795 stereocilia rows.

796 At least two global mechanisms, not specific to any row, also regulate growth of hair bundles. Our results
797 suggest that the concentration of building blocks for stereocilia, including G-actin, actin crosslinkers, and
798 other essential actin cytoskeleton proteins, slowly increases in each hair cell over development. Even
799 when individual stereocilia rows show sharp transitions in lengthening and widening, there is little
800 evidence of any alteration in the rate of growth of total stereocilia volume. Thus the cell constantly
801 supplies stereocilia building blocks, and regulatory steps that are specific to individual rows leads to the
802 transitions in bundle-assembly modes. In all rows, EPS8 mediates incorporation of these building blocks
803 into growing stereocilia (Fig 15A). Another global mechanism is coordination of stereocilia length, which
804 occurs within each row because of the presence of CDH23 and PCDH15, presumably through the
805 transient lateral links (Fig 15B).

806 A key event during development of the bundle is the breaking of symmetry between the rows. Asymmetry
807 is created not only by increasing the length of row 1, but also by limiting the growth of the shorter rows.
808 The three main symmetry-breaking mechanisms that affect actin regulation are (a) establishment of the
809 row 1 complex by GNAI3 and GPSM2; (b) the appearance of tip links, which pull on the tips of the shorter
810 stereocilia but not on row 1 tips; and (c) appearance of transduction in the shorter rows. These
811 mechanisms in turn control three actin-regulatory processes: first, F-actin bundling and polymerization,
812 which lengthen or widen stereocilia; second, F-actin depolymerization, which shortens or thins stereocilia;
813 and finally, F-actin capping, which stabilizes filaments and hence stereocilia length. By locally altering
814 the balance of these three regulatory processes, stereocilia of varying dimensions can be created.

815 GPSM2 and GNAI3, which are only recruited to row 1, presumably boost EPS8 F-actin-bundling activity
816 to lengthen row 1 during stage II (Fig 15E). Given that they do not have GPSM2 and GNAI3, how do the
817 shorter rows lengthen during this stage? Transduction is not involved, as it only appears in apical IHCs
818 after P0 [52, 91], after stage II is complete (Fig 15C). These rows likely lengthen during stage II because
819 tip links are already present [76], and the tension they apply to the tips of the shorter stereocilia rows
820 causes membrane tenting, actin polymerization, and stereocilia lengthening [36]. This lengthening likely
821 is mediated by EPS8-MYO15A complexes, which are present at this early stage at row 2 and 3 tips [9].

822 GPSM2 and GNAI3 also control lengthening during stage IV (Fig 15E). While EPS8 levels are high across
823 stages III and IV, GPSM2 and GNAI3 levels are low during stage III widening. Towards the end of stage
824 III, however, GNAI3 begins to accumulate at row 1 tips, reaching a peak during early stage IV. This
825 accumulation depends on the presence of the transduction complex, and may be due to binding of GNAI3
826 to the complex at the tip of row 1, where it is transiently during development. GPSM2 appears at row 1
827 tips later during stage IV (Fig 15E), presumably requiring GNAI3 to establish its presence first, and
828 recruitment of GPSM2 may be directly responsible for the burst in lengthening that occurs then. During
829 stage IV, only row 1 of apical IHCs lengthens.

830 Tip links appear early in development of the hair bundle (Fig 15C), before the appearance of transduction
831 [48, 52, 92]. Tip-link tension pulls the membrane at the tip of the short stereocilium of the interconnected
832 pair away from the F-actin core beneath (tip-link tenting), which eliminates the membrane's suppression
833 of actin polymerization [93, 94]. Actin polymerization thus proceeds as the membrane is tented, allowing
834 stereocilia lengthening [36]. During stage II, the shorter rows may lengthen simultaneously with row 1,
835 but stereocilia in the shorter rows will be limited in their maximal length because the molecular motor
836 pulling on the tip link will run to the end of its track. Thus, bundles formed by the end of stage II have
837 multiple rows of thin stereocilia with a relatively short stereocilia staircase spacing (Fig 1A). Bundles
838 around P0 are also often tilted strongly in the negative direction [48, 52], which may occur when tip links
839 draw all of the stereocilia together. Negatively tilted bundles are especially apparent in OHCs. Because
840 of the different structures at each of their ends, tip links thus contribute to the distinction between row 1
841 and the shorter rows.

842 During stage III, the appearance of transduction (Fig 15C) allows for further divergence of row identity
843 (Fig 15F). Steady Ca^{2+} influx, due to the transduction channels being partially open at rest, is present at
844 all rows except row 1 [22]. DSTN and CFL1 are recruited to the tips of shorter stereocilia if transduction
845 is active, and these proteins may also be activated indirectly by entering Ca^{2+}. Activated DSTN and CFL1,
846 in turn, increase the turnover of actin filaments at tips of these rows, which may directly lead to both row
847 2 shortening and pruning (disappearance) of other rows. In addition, EPS8 declines at row 2 tips during
848 stage III (Fig 15D), further distinguishing these tips from those of row 1 stereocilia. The presence of
849 dynamic actin at row 2 tips may explain this decline. EPS8 may still target to the tips of shorter rows, but
850 could be released after filament severing by DSTN and CFL1. The F-actin capping protein EPS8L2
851 instead concentrates at row 2 tips [6, 15], and its mechanism of localization and function likely differs
852 from that of EPS8.

853 Changes in length of one row may affect the availability of building blocks for remaining rows, especially
854 later in development. For example, without robust lengthening of row 1 (e.g., in *Myo15a*$^{sh2/sh2}$ hair
855 bundles), more building blocks are available to thicken shorter stereocilia rows, which also stabilizes
856 them. If depolymerization activity is low due to a lack of transduction currents (e.g., in transduction or tip-
857 link mutants), supernumerary stereocilia can thicken. In addition, allocation of stereocilia building blocks
858 appears to extend along a lateral-medial gradient, such that the stereocilia closest to the lateral edge (the
859 bare zone) receive building blocks at a higher rate than those farthest away. Finally, the taller a
860 stereocilium, the farther it is from cytoplasmic pools of DSTN and CFL1 and cytoplasmic changes in Ca^{2+}.
861 Short stereocilia whose filaments are not capped by EPS8, EPS8L2, CAPZB, or TWF2 will be more
862 susceptible to resorption.

863 **How the mutant phenotypes arise**

864 The mutant phenotypes described here each result from failure in one or more of the three main
865 symmetry-breaking events that normally occur during development. In *Myo15a*$^{sh2/sh2}$ hair bundles, without

866 trafficking of the row 1 complex, stereocilia length asymmetry cannot be created; lengthening requires
867 EPS8, which is transported by MYO15A. The lack of lengthening of the taller rows frees stereocilia
868 building blocks; these building blocks are subsequently used to thicken rows 3 and 4+, as well as
869 eventually creating cytocauds. In addition, without mechanisms to uniquely distinguish row 1, all
870 stereocilia become similar to row 2. For example, all rows show high levels of rhodamine-actin
871 incorporation at tips and equal levels of accumulation of DSTN and CFL1. Moreover, all rows are equally
872 thickened and capping proteins, which usually enrich at row 2 (EPS8L2, CAPZB, TWF2), are present at
873 all rows, presumably slowly pruning of the shorter rows.

874 While *Tmie*$^{KO/KO}$ and tip-link mutants both lack transduction, they differ in the establishment of the other
875 two main symmetry-breaking events. In *Tmie*$^{KO/KO}$ mutants, members of the row 1 complex are still
876 present, but neither GPSM2 nor GNAI3 traffic efficiently to row 1 tips in the absence of transduction
877 proteins, at least during stage IV. Stage IV lengthening of row 1 stereocilia is therefore significantly
878 reduced as there is no additional stimulation of EPS8 activity in that row by GPSM2. Since row 1 still
879 grows taller than the other rows, both tip links and the lateral-medial gradient in building blocks contribute
880 to forming shallow gradients in length and width. In *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ tip-link mutants,
881 members of the row 1 complex still traffic and accumulate at normal levels at tips, so stage IV lengthening
882 continues to occur and taller stereocilia are created. Because kinocilial links are lost and hair bundles
883 change in shape, allocation of GNAI3, GPSM2, and WHRN becomes more variable; in some cases, they
884 are delivered to stereocilia beyond just those bordering the bare zone. More randomized allocation of
885 row 1 complex members and the varying positions of stereocilia across the lateral-medial resource
886 gradient may also create length variability.

887 Due to the loss of tip links, all stereocilia tips in *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ hair bundles develop a
888 rounded shape; the uniquely beveled tip of the shorter rows of both control and *Tmie*$^{KO/KO}$ stereocilia fails
889 to develop. EPS8 accumulates at more equal levels across all stereocilia tips in tip-link mutants as
890 compared to the *Tmie*$^{KO/KO}$ mutants, which may occur because all stereocilia develop the rounded tip
891 shape of row 1. In tip-link and transduction mutants, loss of transduction promotes equal but reduced
892 levels of DSTN/CFL1 activity at all tips. Although *Dstn;Cfl1* double-knockout mice retain a polarized EPS8
893 distribution [39], seemingly contradicting aspects of our model, the induction of the double knockout
894 occurred postnatally, after accumulation of EPS8 already occurred at row 1 tips. Regardless of the
895 mechanism, EPS8 accumulation and more equalized distribution of DSTN/CFL1 apparently allows some
896 supernumerary rows to thicken and persist.

897 **Conclusions**

898 Development of the hair bundle is guided by three symmetry-breaking events—the formation of the row 1
899 complex, the asymmetric distortion of the lower-stereocilium membrane caused by tip-link tension, and
900 the establishment of mechanotransduction only at stereocilia tips of shorter rows. During stages II, III,
901 and IV of bundle development, CDH23 and PCDH15 are essential for coordination of stereocilia length

within a row. During stage II, before transduction, lengthening of row 1 elicits lengthening of shorter rows because tip links under tension stimulate lengthening; in wild-type IHCs, this produces a bundle with three to four rows and an even staircase. Lengthening of row 1—and hence the short rows too—stops at the beginning of stage III, when transduction first appears. Stereocilia widen during stage III since building blocks continue to be supplied. During stage III, row 2 stereocilia (and row 3) shorten modestly due to the action of DSTN and CFL1 but also due to the exclusion of EPS8. The row 1 complex reassembles during stage IV in a stepwise manner, dependent on the expression of transduction proteins. Rapid growth of row 1 stereocilia does not occur until sufficient GPSM2 is present; these stereocilia then lengthen while those of the shorter rows continue to shrink. Thus the interplay of the row 1 complex and transduction creates the final apical IHC bundle, with its dramatic length differences between the rows.

Materials and Methods

Mice

All mouse studies were performed in accordance with the guidelines established by the Institutional Animal Care and Use Committees of Oregon Health & Science University (protocol #IP00000714). Animals were housed in individually ventilated cages (IVCs; Thoren) with a maximum of five animals per cage with food and water ad libitum. Breeder pairs were separated 16 to 18 days after crossing and single housed animals were provided with nesting material; pregnant dams were given breeder chow (5058 PicoLab; LabDiet) in place of standard chow (5LOD Irr Rodent; LabDiet). Mice were housed under barrier specific pathogen free conditions in accordance with OHSU IACUC. Mouse pups were assumed to be born at midnight, so animals used on the first day are referred to as P0.5. Data labeled as "P21.5" here refers to mice at weaning age; while most animals were P21.5 (including all animals used in Fig 1), we used a range of ages from P20.5-P25.5. Both male and female pups were used; because newborn mice cannot be sexed without genetic analysis, we used a mixture of sexes in all experiments. We analyzed IHCs from the basal half of the apical ~1/3 of the cochlea (17-33% of the cochlear length, measured from the apex; roughly the 125th IHC from the apex through the 250th), and we refer to them as apical IHCs.

For developmental analysis, we used C57BL/6J mice (RRID:IMSR_JAX:000664, Jackson Laboratories, Bar Harbor, ME). While C57BL/6J mice exhibit progressive hearing loss relative to other strains, at 1.5 months of age (i.e., older than the mice we used), auditory brainstem responses and cochlear hair cell preservation were identical to strains with excellent hearing, such as CBA/Ca [95]. All mutant mice were backcrossed for more than ten generations to C57BL/6J. The *Cdh23*^{v2J} line has been described previously [33, 50]; the *v2J* mutation changes a donor splice site and produces stop-codon containing mutant splice forms with that are predicted to produce truncated proteins lacking the transmembrane domain. The *av3J* mutation in *Pcdh15* also leads to a premature stop codon prior to the transmembrane domain [33, 49]. Accordingly, both *Cdh23*^{v2J} and *Pcdh15*^{av3J} are expected to be full null mutations [33]. The *Tmie*^{KO} line has been described previously [6, 18], as has *Myo15a*^{sh2} [55, 69].

Primary antibodies

Anti-GPSM2 Cat# HPA007327 (RRID: AB_1849941) from Sigma-Aldrich (St. Louis, MO). Rabbit polyclonal anti-GNAI3, directed against a C-terminal mouse GNAI3 peptide (KNNLKECGLY), was Cat# G4040 (RRID: AB_259896) from Sigma-Aldrich (St. Louis, MO). Mouse monoclonal anti-EPS8 (clone 15), against mouse EPS8 amino acids 628-821, was Cat# 610143; RRID: AB_397544 from BD Bioscience (San Jose, CA). Rabbit polyclonal anti-WHRN (#8127), against a C-terminal mouse WHRN peptide with an added cysteine (KERDYIDFLVTEFNVML-C), was from the Ulrich Müller lab. Mouse monoclonal anti-CAPZB2, against a C-terminal peptide of human CAPZB2, was Cat# AB6017 (RRID: AB_10806205) from EMD Millipore (Burlington, MA). Mouse monoclonal anti-EPS8L2, against human EPS8L2 amino acids 615-715, was Cat# ab57571 (RRID: AB_941458) from Abcam (Cambridge, UK).

948 Anti-PCDH15 (HL5614) was generated in rabbit and obtained from Zubair Ahmed and anti-CDH23 was
949 generated in goat by GenScript (Piscataway, NJ) against mouse CDH23 EC15/16 (CATRPAPPDRERQ)
950 (Indzhykulian et al, 2013).

951 **Immunofluorescence sample preparation**

952 Inner ears from C57BL/6J mice or mutant mice littermates dissected at the indicated ages in cold Hank's
953 balanced salt solution (Cat# 14025076, Thermo Fisher Scientific) supplemented with 5 mM HEPES, pH
954 7.4 (dissection buffer). To allow perfusion of the fixative, small openings were made within the periotic
955 bones.

956 For measurements of stereocilia dimensions from C57BL/6J or mutant mice using only phalloidin
957 (Figs 1, 3-8), ears were fixed in 4% formaldehyde (Cat# 1570, Electron Microscopy Sciences) in 1x PBS
958 for 0.5 – 1 hour at room temperature. Ears were washed in PBS, then cochleas were dissected out from
959 the periotic bone and the lateral wall was removed. After permeabilization in 0.2% Triton X-100 in 1x PBS
960 for 10 minutes at room temperature, cochleas were incubated with phalloidin (0.4 U/ml Alexa Fluor 488
961 phalloidin; Cat# A12379, Thermo Fisher Scientific) in 1x PBS for 12-16 hours at 4°C. Organs were
962 washed three times in PBS for 5 min per wash and mounted in Vectashield (Cat# H-1000, Vector
963 Laboratories).

964 For immunofluorescence using antibodies against row 1 or 2 proteins (Figs 8-11; S4 Fig), ears were fixed
965 in 4% formaldehyde (Cat# 1570, Electron Microscopy Sciences) in dissection buffer for 20-30 min at
966 room temperature. As noted previously, row 2 protein antibodies (EPS8L2, CAPZB) required fixation of
967 at most 20 min, whereas row 1 protein antibodies were not sensitive to fixative duration. Ears were
968 washed in PBS, then cochleas were dissected out from the periotic bone and the lateral wall was
969 removed. Cochleas were permeabilized in 0.2% Triton X-100 in 1x PBS for 10 min and blocked in 5%
970 normal donkey serum (Cat# 017-000-121, Jackson ImmunoResearch) diluted in 1x PBS (blocking buffer)
971 for 1 hr at room temperature. Organs were incubated overnight at 4°C with primary antibodies in blocking
972 buffer and then washed three times in 1x PBS. Dilutions were 1:500 for anti-GNAI3; 1:250 for anti-
973 GPSM2, anti-EPS8, anti-EPS8L2, anti-WHRN, anti-CAPZB. Tissue was then incubated with secondary
974 antibodies, which were 2 µg/ml donkey anti-rabbit Alexa Fluor 488 (Cat# A21206, Thermo Fisher
975 Scientific) and 2 µg/ml donkey anti-mouse Alexa Fluor 568 (Cat# A10037, Thermo Fisher Scientific); 1
976 U/ml CF405 phalloidin (Cat# 00034, Biotium) was also included for the 3-4 hr room temperature
977 treatment. Tissue was washed three times in PBS and mounted on a glass slide in ~50 µl of Vectashield
978 and covered with a #1.5 thickness 22 x 22 mm cover glass (Cat# 2850-22, Corning) or a #1.5 thickness
979 22 x 40 mm cover glass (Cat# CLS-1764-2240, Fisher Scientific).

980 Immunofluorescence using anti-CDH23 and anti-PCDH15 antibodies was performed as outlined
981 previously [96]. Briefly, ears were fixed in 4% formaldehyde (Cat# 1570, Electron Microscopy Sciences)
982 in dissection buffer for 20-30 min at room temperature then washed twice in calcium/magnesium free

983 HBSS (Cat# 14-175-095m Fisher Scientific). Tissue was blocked for 2 hours in 10% normal donkey
984 serum (Cat# 017-000-121, Jackson ImmunoResearch) diluted in calcium/magnesium free HBSS with
985 2 mM EDTA, and this blocking buffer was used for all antibody steps. Tissue was incubated overnight at
986 4°C with 1:100 anti-CDH23 and 1:200 anti-PCDH15, washed three times with calcium/magnesium-free
987 HBSS, then incubated for 2-3 hours at room temperature with 2 µg/ml donkey anti-goat Alexa Fluor 488
988 (Cat# A21206, Thermo Fisher Scientific), 2 µg/ml donkey anti-rabbit Alexa Fluor 568 (Cat# A10037,
989 Thermo Fisher Scientific), and 1 U/ml CF405 phalloidin (Cat# 00034, Biotium). Tissue was washed three
990 times in calcium/magnesium-free HBSS and mounted on a glass slide in ~50 µl of Vectashield and
991 covered with a #1.5 thickness 22 x 22 mm cover glass (Cat# 2850-22, Corning).

992 **Rhodamine-actin labeling**

993 Labeling of free barbed ends of actin filaments was performed as outlined [39]. Inner ears from C57BL/6J
994 mice or mutant mice littermates dissected at the indicated ages in cold Hank's balanced salt solution
995 (Cat# 14025076, Thermo Fisher Scientific) supplemented with 5 mM HEPES, pH 7.4 (dissection buffer).
996 Cochlea were dissected and lateral wall, Reissner's membrane, and tectorial membrane were removed.
997 Live tissue was then briefly washed in cytoskeletal buffer (20 mM HEPES, pH 7.4, 138 mM KCl, 4 mM
998 $MgCl_2$, 3 mM EGTA, 1% bovine serum albumin (Cat# A3803, Sigma Aldrich), 2 mM ATP (Cat#
999 10127531001, Sigma Aldrich), and 0.05% saponin (Cat# S7900, Sigma Aldrich) before incubating for
1000 5 minutes at room temperature in 40 ng/µl rhodamine-labeled actin (Cat# AR05, Cytoskeleton, Inc.)
1001 freshly prepared in cytoskeletal buffer. Samples were then washed in cytoskeletal buffer and fixed for
1002 1 hour at room temperature in 4% formaldehyde (Cat# 1570, Electron Microscopy Sciences) in PBS.
1003 Tissues were rinsed twice in PBS, then incubated for 1 hour at room temperature in 0.4 U/ml Alexa Fluor
1004 488 phalloidin (Cat# A12379, Thermo Fisher Scientific) diluted in PBS with 0.05% saponin. Tissue was
1005 washed three times in PBS and mounted on a glass slide in ~50 µl of Vectashield and covered with a
1006 #1.5 thickness 22 x 40 mm cover glass (Cat# CLS-1764-2240, Fisher Scientific).

1007 **Fluorescence microscopy**

1008 Structured illumination (SIM) images were acquired at 26-30°C with a 63X 1.4 NA oil immersion lens on
1009 a Zeiss lattice-based Elyra 7 microscope with dual PCO.edge 4.2 sCMOS cameras for detection.
1010 Illumination grid selection and z-spacing was guided by the software and kept consistent across images.
1011 Post-acquisition processing was performed with software-recommended standard filtering for the 488 nm
1012 channel, without baseline subtraction and with "scale to raw" checked. Contrast was manually adjusted
1013 to retain both dim and bright structures due to the high dynamic range of the phalloidin signal. Verification
1014 of channel alignment and measurement of the microscope point-spread function was carried out as
1015 previously described [46].

1016 Airyscan images were acquired at room temperature using a 63x, 1.4 NA Plan-Apochromat objective on
1017 a Zeiss 3-channel LSM980 laser-scanning confocal microscope equipped with an Airyscan.2 detector
1018 and run under ZEISS ZEN (v3.1, 64-bit software; Zeiss) acquisition software. Settings for x-y pixel

resolution, z-spacing, as well as pinhole diameter and grid selection, were set according to software-suggested settings for optimal Nyquist-based resolution. Raw data processing for Airyscan-acquired images was performed using manufacturer-implemented automated settings. Display adjustments in brightness and contrast and reslices and/or maximum intensity Z-projections were made in Fiji software (https://imagej.net/software/fiji/).

For cochlea imaging, for each stain, 2-4 images were acquired from 1-2 cochlea per genotype per age for each experiment, and experiments were conducted three to four times. Ears from control and mutant littermates or from different ages of C57BL/6J mice (of both sexes) were stained and imaged on the same days for each experiment to limit variability. Genotyping was performed either prior to dissection or performed on tails collected during dissection for younger animals (<P8). Genotypes were known by the experimenter during staining and image acquisition. During image acquisition, the gain and laser settings for the antibody and phalloidin signals were adjusted to reveal the staining pattern in control samples, and the corresponding KO samples used the same settings. Image acquisition parameters and display adjustments were kept constant across ages and genotypes for every antibody/fluorophore combination.

Image rendering and measurements of stereocilia dimensions

Surface rendering was carried out with Imaris software (imaris.oxinst.com; versions 9.7.0, 9.8.0, 9.9.0; Oxford Instruments); the rendered surfaces were stored as sparse voxel octrees [97], which allowed them to be manipulated and measured using Imaris. A batch processing file was created in Imaris and applied to each dataset. Within each batch, background subtraction was first performed in the image processing tab using a filter width of 1 μm for the phalloidin channel for all images. Volumetric surface areas of the stereocilia in each image were then created from the phalloidin channel using creation parameters guided by the program and edited as needed so that the phalloidin signal for each stereocilium was accurately surrounded by a surface. Due to the high dynamic range of the signal, and the low intensity of the signal in control row 3 or 4 stereocilia, creation parameters were guided to create the most accurate surfaces for row 1 and 2, which often left some low intensity row 3 or 4 stereocilia undetected. Manual cutting of any connected stereocilia surfaces was performed so that each stereocilium was modeled by a unique surface. For any visible stereocilia lacking a surface (most often in rows 3 or 4), a surface was created using the magic wand tool in the Create tab of Imaris. If the intensity of the stereocilium was too similar to the phalloidin intensity of the surrounding cuticular plate, a surface could often not be generated. Thus, row 3 and 4 stereocilia are only sparsely represented in older control hair bundles. Stereocilia surfaces were labeled as corresponding to each stereocilia row (1, 2, 3, or 4+) and as corresponding to each cell in the image. Measurements of Volume, BoundingBoxOO (object-oriented) Lengths, Number, and Position (x,y) for all labeled surfaces were exported from Imaris to Microsoft Excel. BoundingBoxOO lengths are generated within Imaris by considering the minimal rectangular box which fully encloses each object with no constraints to the orientation; the dimensions of that box are reported as Lengths A, B, and C, with A being the shortest principal axis and C the longest principal axis. To measure length and width

1055 of each stereocilium, object-oriented BoundingBoxOO Length C and the average of lengths A and B were
1056 used, respectively. For volume, we used the surface volume measurement provided by Imaris, which
1057 quantifies the amount of space each object occupies. The number of stereocilia and the sum of stereocilia
1058 volume per cell were calculated in Excel from the Imaris output. To measure the center 10 stereocilia, 10
1059 neighboring row 1 and row 2 stereocilia at the center of each bundle were selected within Imaris, and
1060 measurements for this subset were exported to Excel. Position (x,y) data could be used to determine
1061 neighboring stereocilia and calculate differences in dimensions for adjacent stereocilia within each row
1062 or adjacent row 1 and 2 stereocilia (Fig 5).

1063 Three-dimensional rendering of stereocilia and EPS8 and GPSM2 tip staining (Fig 11O-R and Fig 12M-
1064 P) from Airyscan z-stack images was also performed in Imaris using similar methods. Background
1065 subtraction was first performed in the image processing tab using a filter width of 1 μm for all channels
1066 for all images. Volumetric surface areas of the stereocilia in each image were then created from the
1067 phalloidin channel using creation parameters guided by the program and edited as needed so that the
1068 phalloidin signal for each stereocilium was accurately surrounded by a surface. Volumetric surface areas
1069 of the EPS8 or GPSM2 signals in each image were also created in their respective channels using
1070 creation parameters guided by the program and filtered to only include those with at least 0.01 overlap
1071 volume ratio with the phalloidin stereocilia surfaces, so that only EPS8/GPSM2 surfaces at stereocilia
1072 tips were included. All surfaces were manually edited to split any joining surfaces and create any surfaces
1073 that were missed for low intensity phalloidin, EPS8, or GPSM2 signals. Once all surfaces were edited,
1074 the two sets of surfaces were merged and the phalloidin and EPS8 or GPSM2 surfaces corresponding
1075 to each individual stereocilium were joined in the edit tab, creating a surface that encompassed both the
1076 phalloidin signal and tip complex signals for each stereocilium. E Each stereocilium surface was then
1077 labeled according to its row position. Thus, for each stereocilium we measured both the length
1078 (BoundingBoxOO Length C) and the corresponding intensity sum for each channel in the image, with the
1079 channel 1 (568 nm) intensity sum measuring EPS8 amount and the channel 2 (488 nm) measuring
1080 GPSM2 amount. These measurements were exported to Excel, pooled, and then plotted within Prism.

1081 **Quantitation of proteins at stereocilia tips**

1082 For Fig 9I-K, Fig 11A-N, Fig 12A-L, Fig 13M-R, and Fig 14G-H, quantitation of protein expression at row 1
1083 and 2 tips was carried out after importing Airyscan z-stacks into Fiji. For analysis of C57BL/6J mice
1084 throughout development, CAPZB and EPS8L2 in P21.5 mutants, and rhodamine-actin signal, summed
1085 z-projections of Airyscan stacks were made that included row 1 and row 2 tips in the same projection.
1086 For samples in which row 1 and 2 were in separate Z planes, separate Z-projections were made for row
1087 1 and row 2 tips. Regions of interest (ROIs) were selected at 10 (or more) row 1, and 10 (or more) row 2
1088 tips per hair bundle. ROIs were circles that encompassed most of each tip. Using Fiji's Measure function,
1089 the area and mean gray value were measured for each ROI; measurements were also made outside the
1090 stereocilia and above the epithelium to determine background. The total fluorescence signal in a tip (tip

signal) was thus area • mean gray value • minus total signal for the background. Tip signals below the background were assigned the value of 0, which were used in calculating averages.

For analysis of mutant mice in Figs 11-12, S4 Fig, and S5 Fig, due to increased length variability, regions of interest (ROIs) were selected at row 1 or row 2 tips within individual x-y slices from the z-stacks. Images were kept as multi-channel stacks and phalloidin was used to guide selection at the tip of each stereocilium. For these images, all row 1 and 2 stereocilia were measured within each cell. Measurements and calculation of tip signal were otherwise carried out as above. Mean intensities were calculated as the average tip intensity for all row 1 and row 2 stereocilia within each cell. Mean intensities were normalized to the average tip intensity for all row 1 and 2 stereocilia from all het cochlea imaged on the same day. Histograms were created in Prism using frequency distributions of the number of values, with a bin width of 0.2 μm. The distributions were fit with a least-squares regression for a sum of two Gaussians.

Data presentation and statistical analysis

For quantitation of length, width, and adjacent stereocilia length differences in Fig 1, we derived the data from the center ten stereocilia from each row. Volumes were instead calculated from Imaris volume measurements from all stereocilia in each hair bundle. The data were derived from 2 litters per time point, 2 cochleas per litter, 1 image per cochlea, and 3-6 cells per image; thus *n* (the number of cells) was 12-24, and *N* (the number of cochleas examined) was 4. Each point represents the mean ± standard deviation for all cell averages from all cochleas (i.e., *n* samples). Blinding of sample age was not possible as the age was obvious from the bundle and tissue morphology.

For quantitation in Figs 3-8, we compared measurements of dimensions between heterozygote and knockout hair cells. We carried out volume, length, and width measurements for each stereocilium, then derived adjacent stereocilia length and volume sum measurements. Blinding of samples was not possible as the mutant phenotypes are easily discerned. To avoid problems with pseudoreplication [53, 54, 98], we considered the five hierarchical levels in our data sets—litter, animal, cochlea, cell, and stereocilium. The two cochleas from each animal were analyzed independently; we did not track individual animals. Cochlea mounting, intensity of labeling reagents, distance from the coverslip (potentially leading to spherical aberration and decrease in signal), and exact position along the apical-basal gradient all substantially affected the measurements and had a greater influence than animal or litter. For length, width, and volume measurements, measurements from all stereocilia of each row were averaged, providing a single measurement per cell. For these figures, all data were derived from 2-3 litters per genotype, 1-2 cochleas per litter, 2 images per cochlea, 4 total cochlea images, 5-6 cells per image, all row 1 and 2 stereocilia for each hair cell, and some row 3 stereocilia for each hair cell. For each condition, *n* was 23-24 and *N* was 4. For length and width (and their corresponding CVs), we used the nested (hierarchical) t-test function in Prism to compare the results from heterozygote and knockout cochleas; while comparing the results from the 4 cochleas per condition, the nested t-test approach takes into account the structure of the data, i.e., the variance in individual cell measurements for each condition

[54]. For comparisons of dimensions of *Pcdh15*^{av3J}*;Myo15a*^{sh2} genotypes (Fig 6), as well as volume measurements for mutants and C57BL/6 (Fig 8), we used the nested one-way ANOVA function in Prism, adjusting for multiple comparisons using the Šidák correction [99].

For comparisons of intensity of row 1 tip proteins (Figs 11-12, S4 Fig), as well as rhodamine-actin labeling at row 1 and 2 tips (Fig 13) and row 2 protein intensities (Fig 14), we used nested t-tests as above. For comparisons of intensity of row 1 tip proteins in *Pcdh15*^{av3J}*;Tmie*^{KO} genotypes (S5 Fig), we used ordinary one-way ANOVA tests with the Tukey correction for multiple comparisons.

Data reporting

Underlying data (e.g., measurements of individual stereocilia in hair bundles) and aggregated data used to construct figures have been deposited in figshare:

Krey, JF, and Barr-Gillespie, PG. Control of stereocilia length during development of hair bundles. 2022. figshare. 10.6084/m9.figshare.21632636

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Supporting Information Legends

S1 Fig. Variability in stereocilia length and width measurements.

A, CVs for stereocilia length from all stereocilia at indicated ages. Blue lines in panels A-D show developmental trends for row 1 length or width CV. ***B***, CVs for stereocilia length from center ten stereocilia at indicated ages. P values from unpaired Student's t-tests comparing all row 1 stereocilia versus center ten row 1 stereocilia: P0.5, 0.1861; P1.5-P21.5, <0.0001. P values from unpaired Student's t-tests comparing length CVs for all row 2 stereocilia versus center ten row 2 stereocilia: P0.5, 0.4933; P1.5-P21.5, <0.0001. ***C***, CVs for stereocilia width from all stereocilia at indicated ages. ***D***, CVs for stereocilia width from center ten stereocilia at indicated ages. P values from unpaired Student's t-tests comparing length CVs for all row 1 stereocilia versus center ten row 1 stereocilia: P0.5, 0.0473; P1.5, <0.0001; P2.5, 0.0893; P3.5-P4.5, <0.0001; P5.5, 0.0001; P7.5, <0.0001; P10.5, 0.0038; P13.5, 0.0823; P16.5, 0.0126; P21.5, 0.118. P values from unpaired Student's t-tests comparing all row 2 stereocilia versus center ten row 2 stereocilia: P0.5-P21.5, <0.0001. ***E-G***, Models of stereocilia arrangement. A peripheral-to-central gradient of stereocilia length for row 1 and row 2 was seen at P7.5 (F; red gradient symbol), rather than uniform lengths (E; red line). Stereocilia lengths largely equalized by P21.5 (G).

S2 Fig. CDH23 and PCDH15 immunoreactivity in mouse tip-link mutants.

A-B, CDH23 and PCDH15 localization in *Cdh23*^{v2J}/+ (A) and *Cdh23*$^{v2J/v3J}$ (B) IHCs. ***C-D***, CDH23 and PCDH15 localization in *Pcdh15*^{av3J}/+ (C) and *Pcdh15*$^{av3J/av3J}$ (D) IHCs. Panel widths: 30 µm.

S3 Fig. Localization of TMC1-HA and TMC2-Myc in *Pcdh15*$^{av3J/av3J}$ mutant IHCs.

A, TMC1-HA in P7 *Tmc1*$^{HA/HA}$;*Pcdh15*^{av3J}/+ cochlea at the hair-bundle level. ***B***, TMC1-HA in same P7 *Tmc1*$^{HA/HA}$;*Pcdh15*^{av3J}/+ cochlea at the soma level. ***C***, TMC1-HA in P7 *Tmc1*$^{HA/HA}$;*Pcdh15*$^{av3J/av3J}$ cochlea (bundles). ***D***, TMC1-HA in same P7 *Tmc1*$^{HA/HA}$;*Pcdh15*$^{av3J/av3J}$ cochlea (somas). ***E***, TMC2-Myc in P4 *Tmc1*$^{Myc/Myc}$;*Pcdh15*^{av3J}/+ cochlea (bundles). ***F***, TMC2-Myc in P4 *Tmc1*$^{Myc/Myc}$;*Pcdh15*$^{av3J/av3J}$ cochlea (bundles). Panel widths: 35 µm.

S4 Fig. Localization of GNAI3 and WHRN in *Cdh23*$^{v2J/v2J}$ and *Pcdh15*$^{av3J/av3J}$ mutant IHCs.

A-L, Localization of row 1 complex proteins in *Cdh23*^{v2J} and *Pcdh15*^{av3J} heterozygotes and homozygotes IHCs. Panel widths: 30 µm. ***A-B***, GNAI3 and EPS8 in *Cdh23*^{v2J}/+ and *Cdh23*$^{v2J/v2J}$ at P7.5. ***C-D***, WHRN and EPS8 in *Cdh23*^{v2J}/+ and *Cdh23*$^{v2J/v2J}$ at P7.5. ***E-F***, GNAI3 and EPS8 in *Cdh23*^{v2J}/+ and *Cdh23*$^{v2J/v2J}$ at P21.5. ***G-H***, WHRN and EPS8 in *Cdh23*^{v2J}/+ and *Cdh23*$^{v2J/v2J}$ at P21.5. ***I-J***, GNAI3 and EPS8 in *Pcdh15*^{av3J}/+ and *Pcdh15*$^{av3J/av3J}$ at P21.5. ***K-L***, WHRN and EPS8 in *Pcdh15*^{av3J}/+ and *Pcdh15*$^{av3J/av3J}$ at P21.5. ***M-P***, GNAI3 and WHRN normalized fluorescence average intensity per hair bundle for all measured stereocilia (row 1 and 2) for *Cdh23*^{v2J} and *Pcdh15*^{av3J} IHCs at P7.5 and P21.5. Intensities were normalized to the heterozygote average for each genotype pair. Plotting and statistical testing were as in Fig 3. ***Q-T***, Frequency distribution of GNAI3 and WHRN tip intensity in *Cdh23*^{v2J} hair cells at P7.5 and P21.5.

1422 **S5 Fig. *Pcdh15^{av3J};Tmie^{KO}* double knockout mice.**

1423 ***A-D***, Scanning electron micrographs showing P8.5 IHC hair bundles from *Pcdh15^{av3J}*/+;*Tmie^{KO}*/+
1424 (Het;Het) *Pcdh15^{av3J}*/+;*Tmie$^{KO/KO}$* (Het;KO), *Pcdh15$^{av3J/av3J}$*;*Tmie^{KO}*/+ (KO;Het), and
1425 *Pcdh15$^{av3J/av3J}$*;*Tmie$^{KO/KO}$* (KO;KO) cochleas. ***E-H***, Localization of GNAI3 and EPS8 in IHCs of
1426 *Pcdh15^{av3J}*;*Tmie^{KO}* genotypes at P7.5. ***I***, EPS8 fluorescence average intensity per bundle for all
1427 measured stereocilia in bundles of each genotype. ***J,*** Frequency distribution of EPS8 tip intensity
1428 in bundles of each genotype. Het;Het and Het;KO distributions were fit with double Gaussians;
1429 KO;Het and KO;KO distributions were fit with single Gaussians. ***K***, GNAI3 fluorescence average
1430 intensity per bundle for all measured stereocilia in bundles of each genotype. ***L,*** Frequency
1431 distribution of GNAI3 tip intensity in bundles of each genotype. Distributions from each genotype
1432 were fit with double Gaussians. For statistical comparisons in I and K, we used ordinary one-
1433 way ANOVA tests with the Tukey correction.

1434

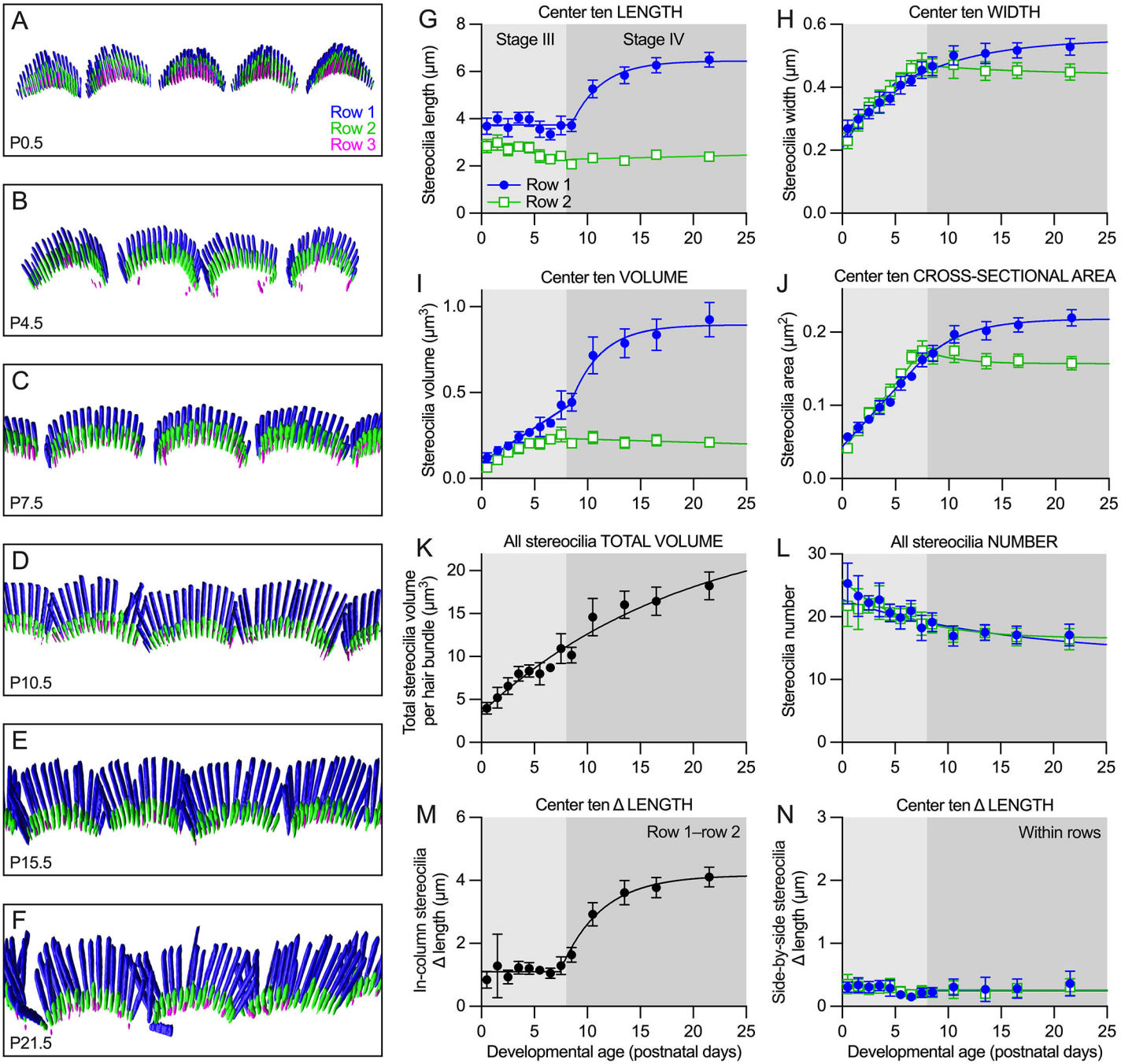

Figure 1
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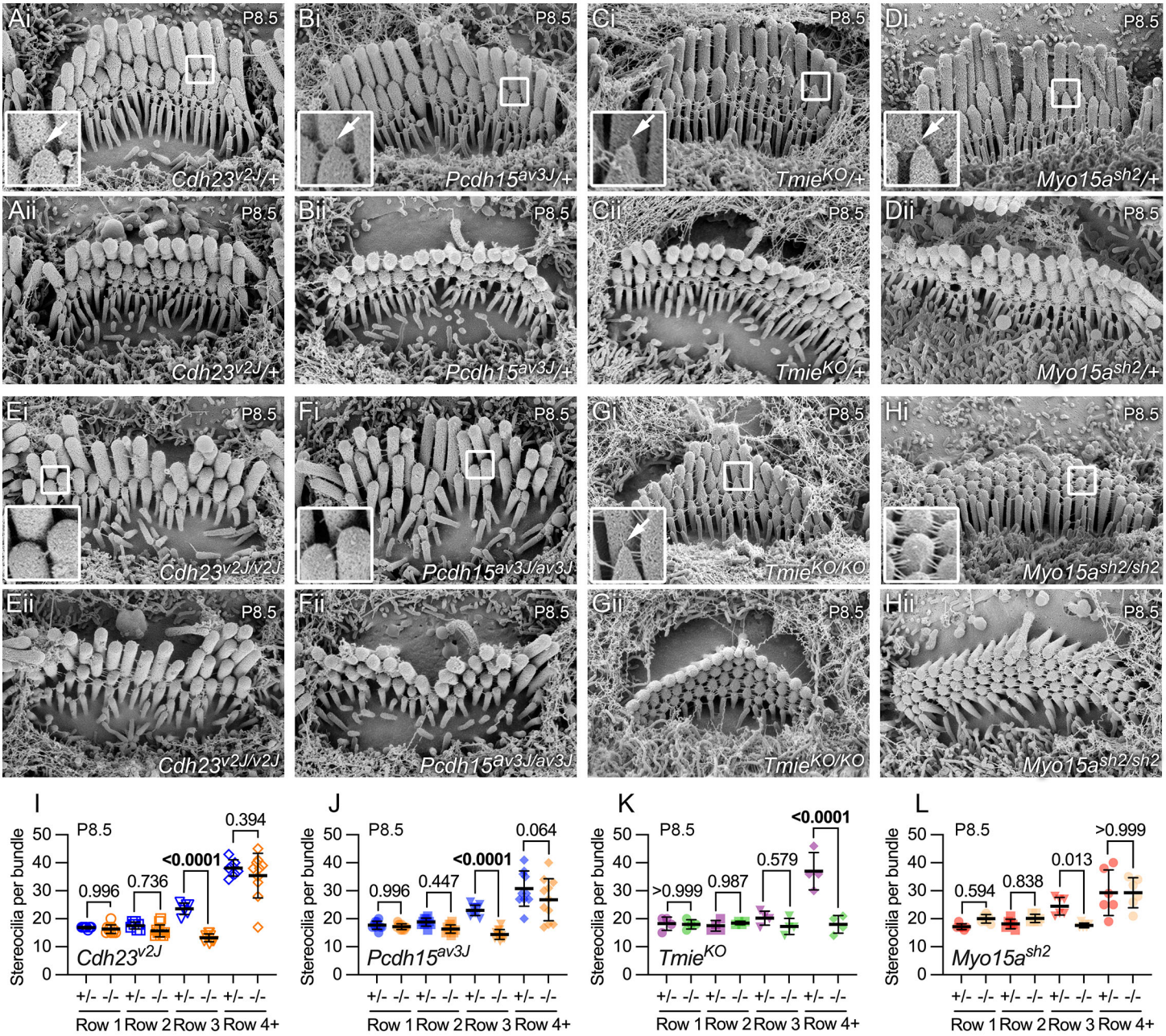

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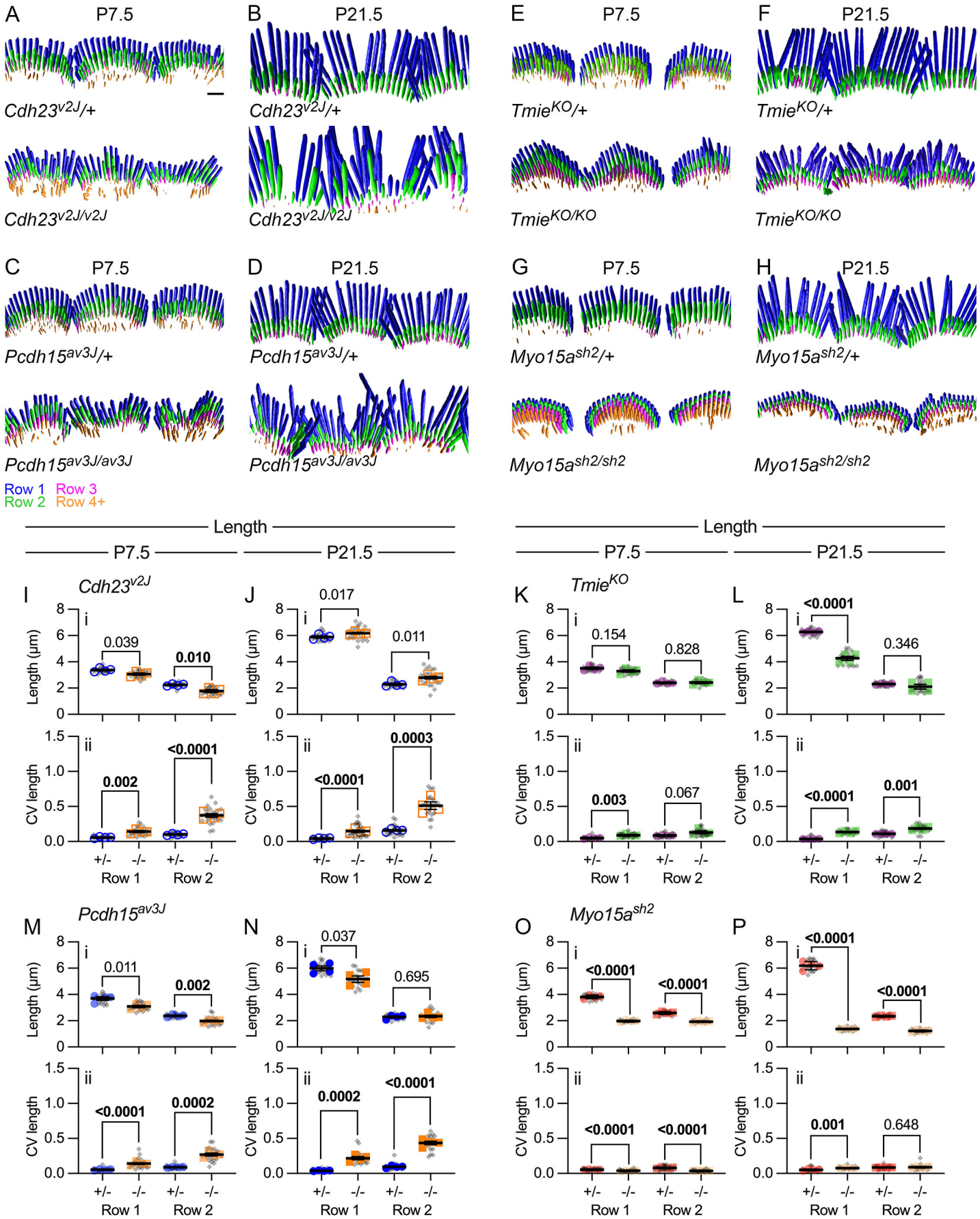

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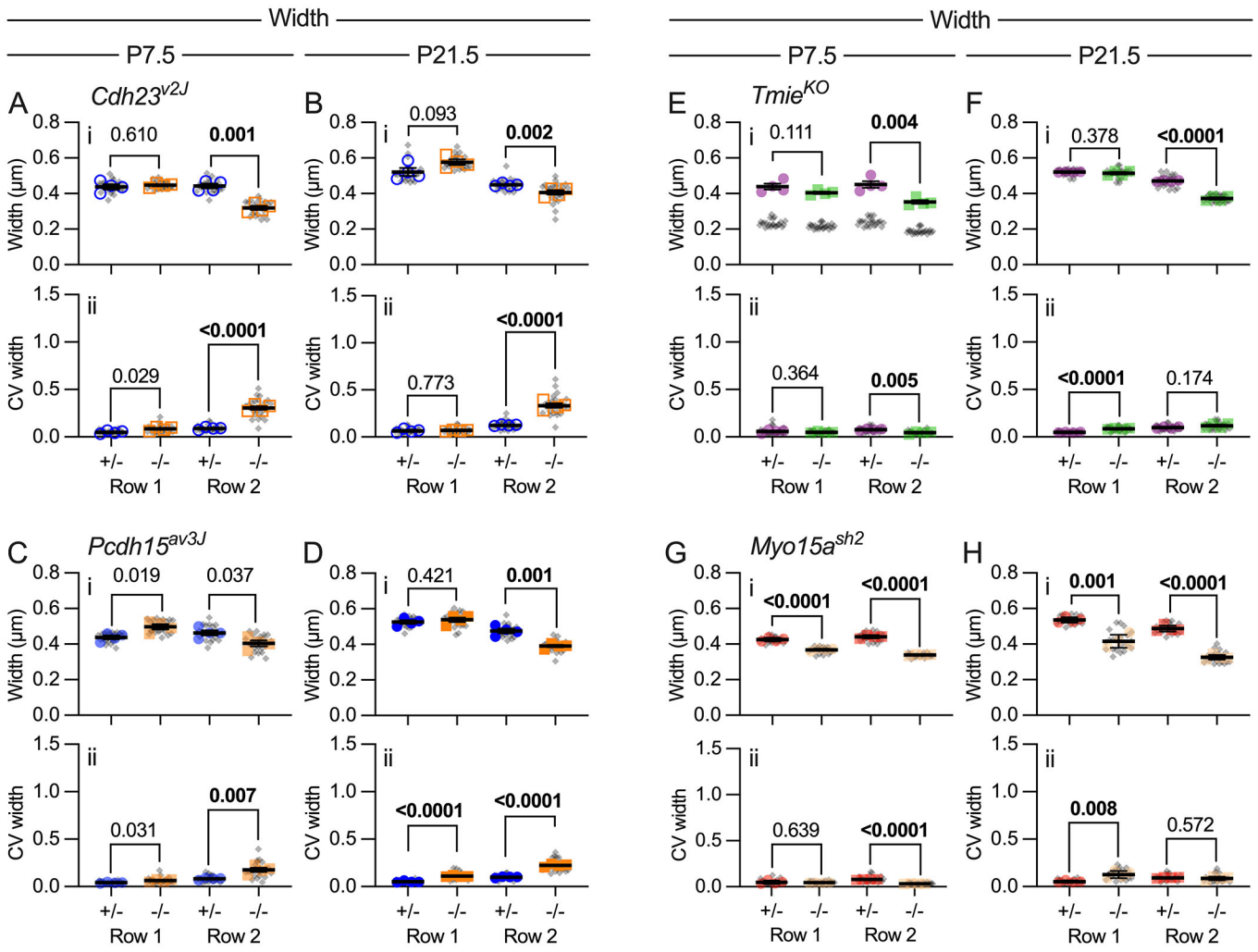

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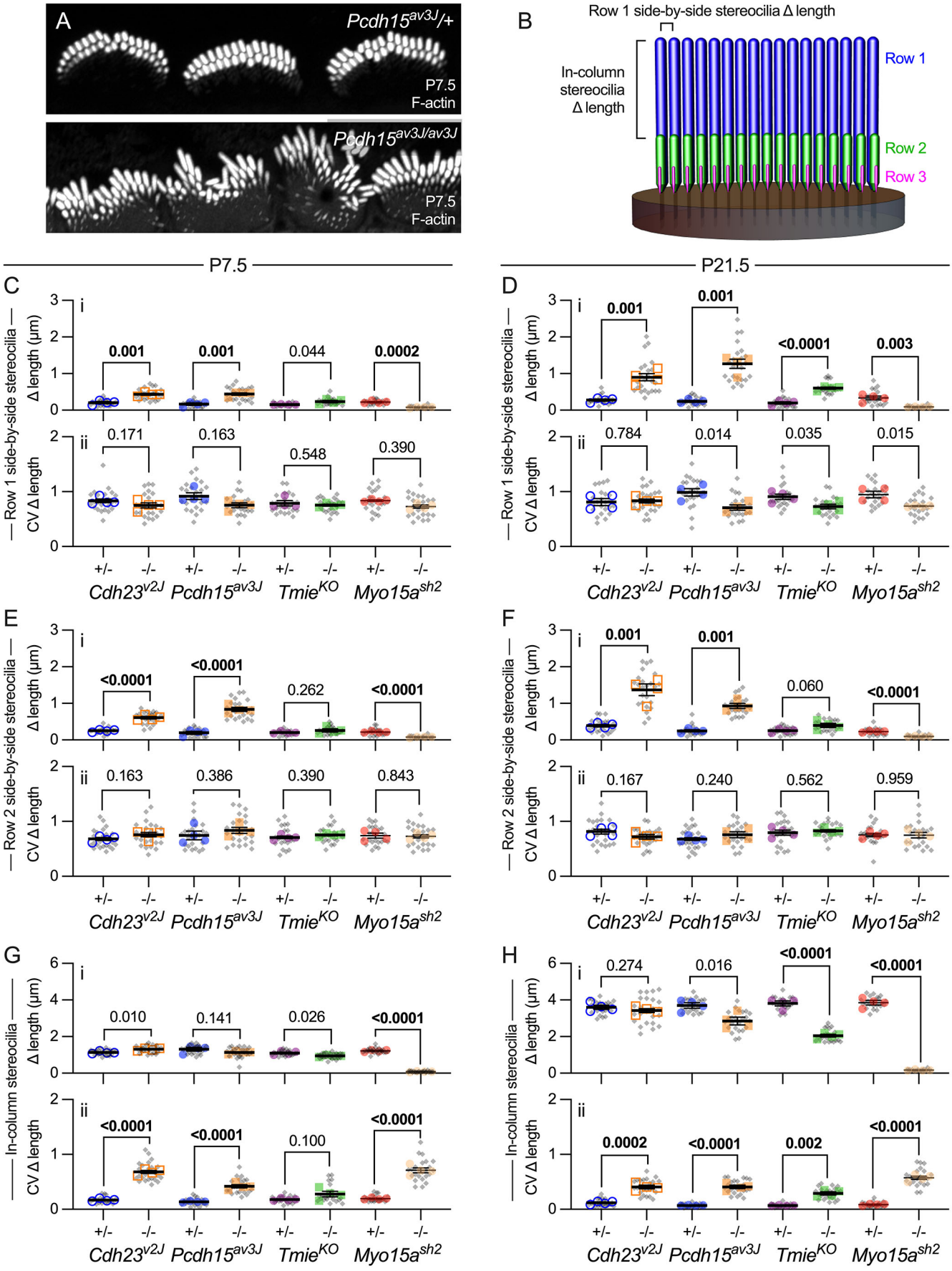

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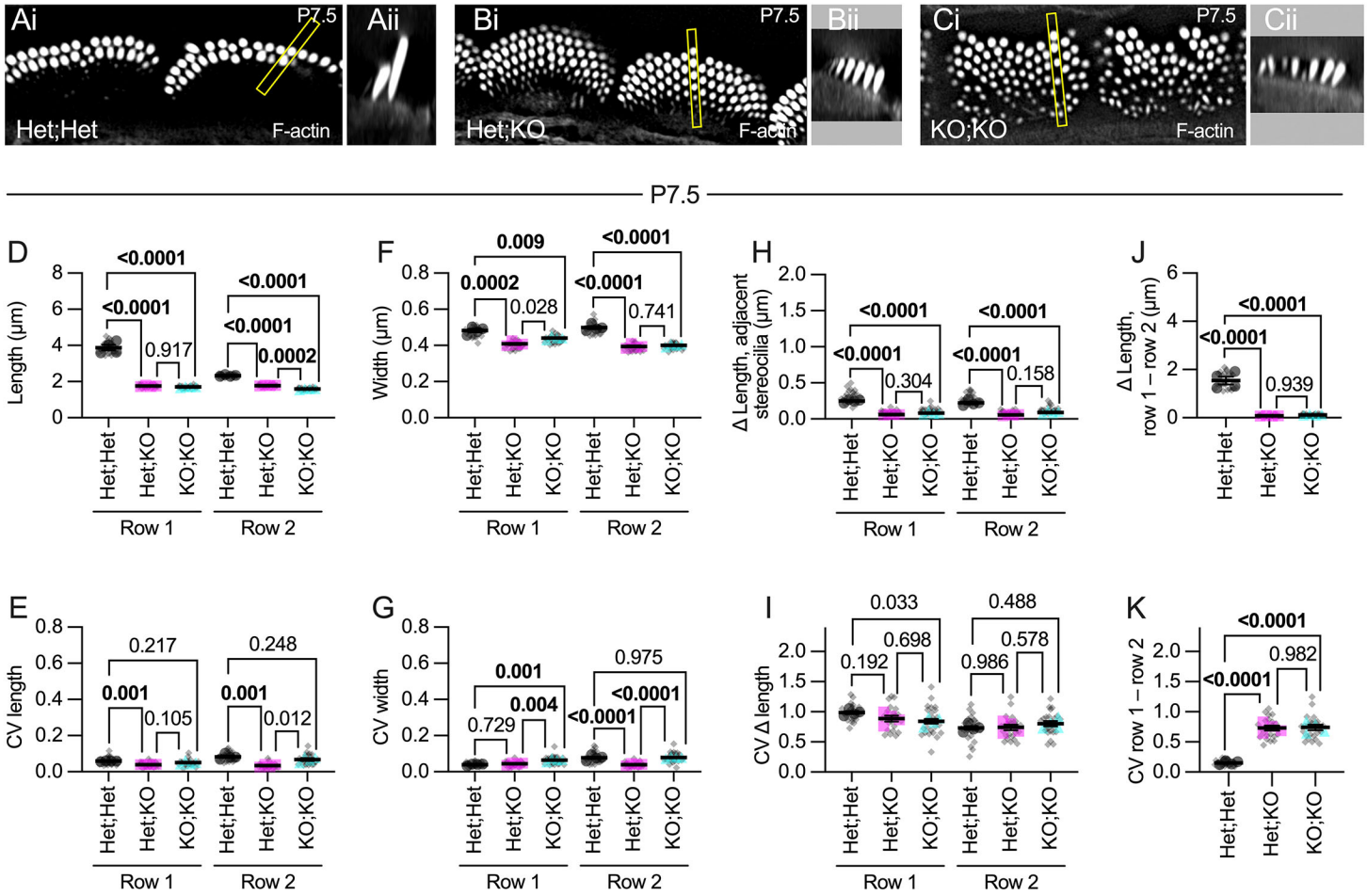

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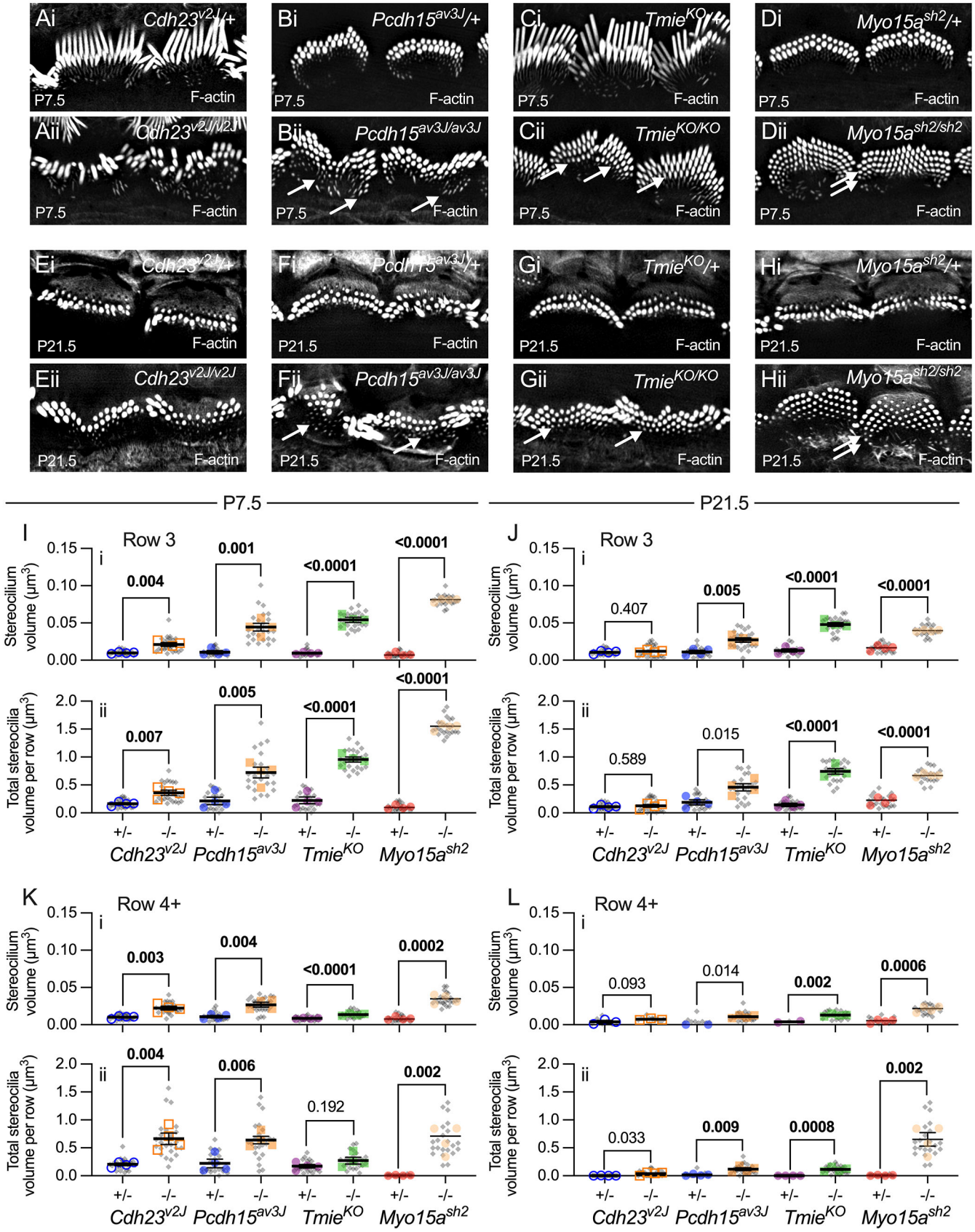

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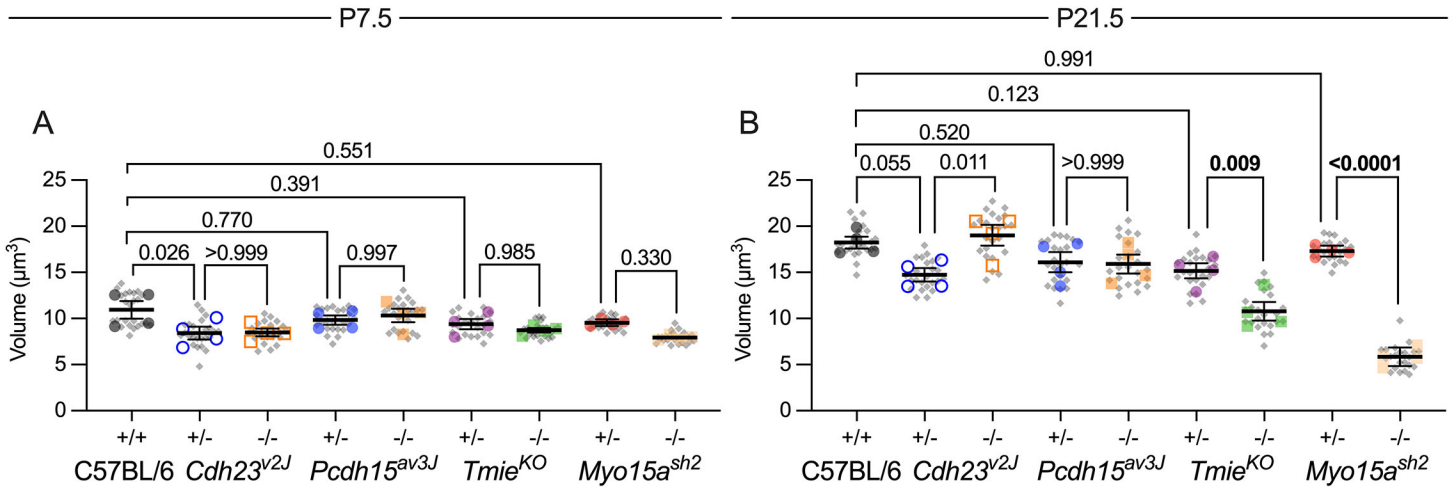

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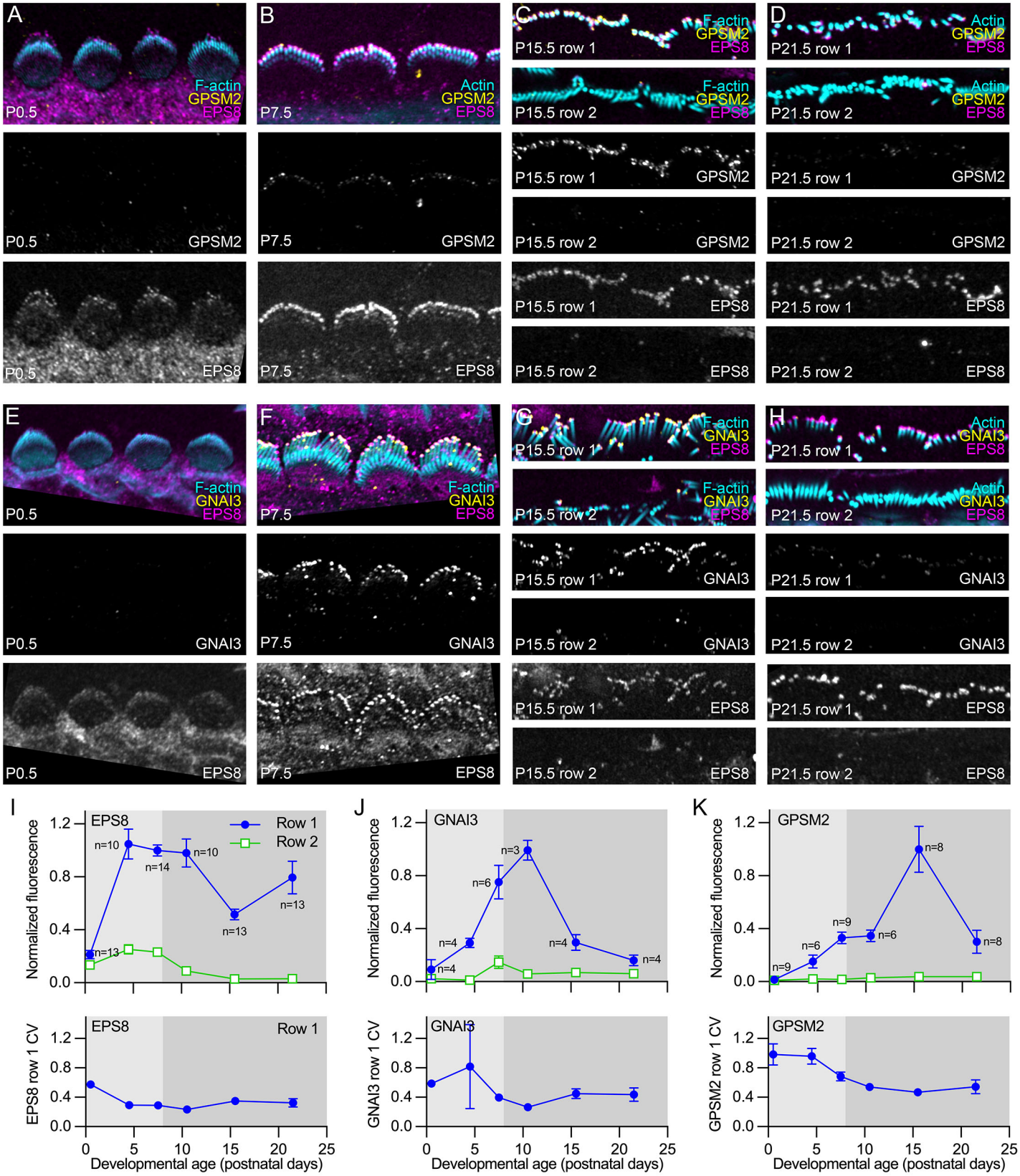

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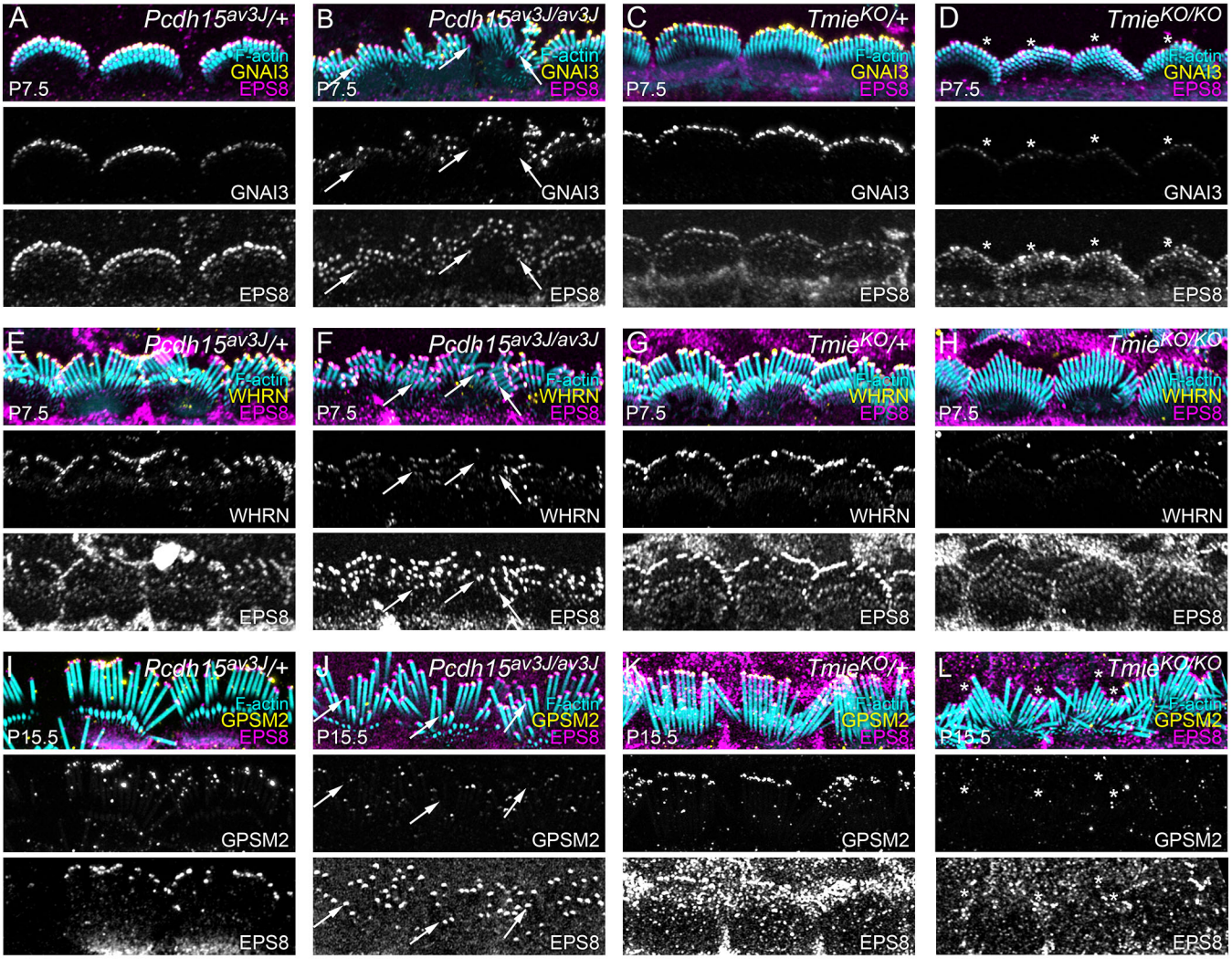

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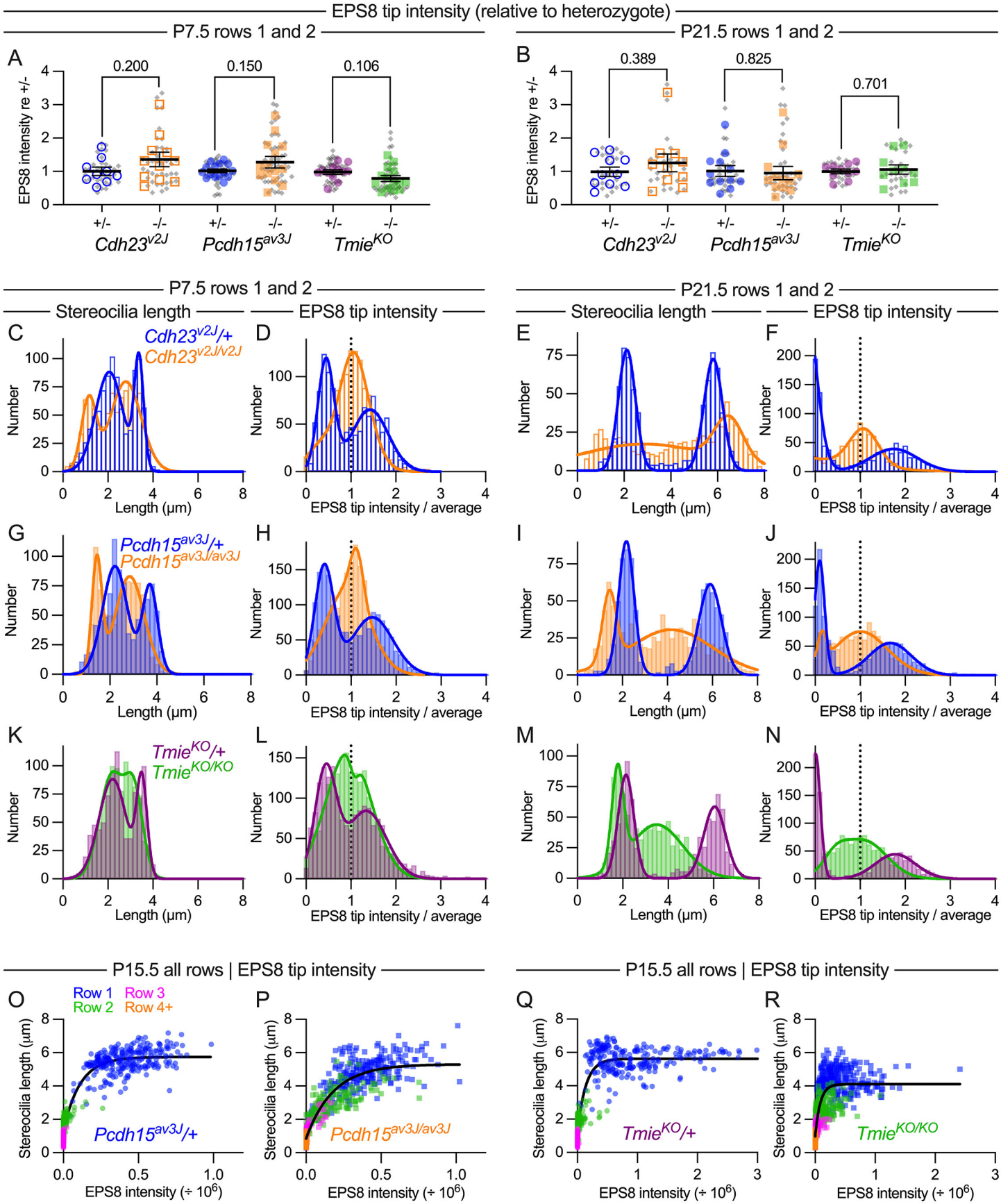

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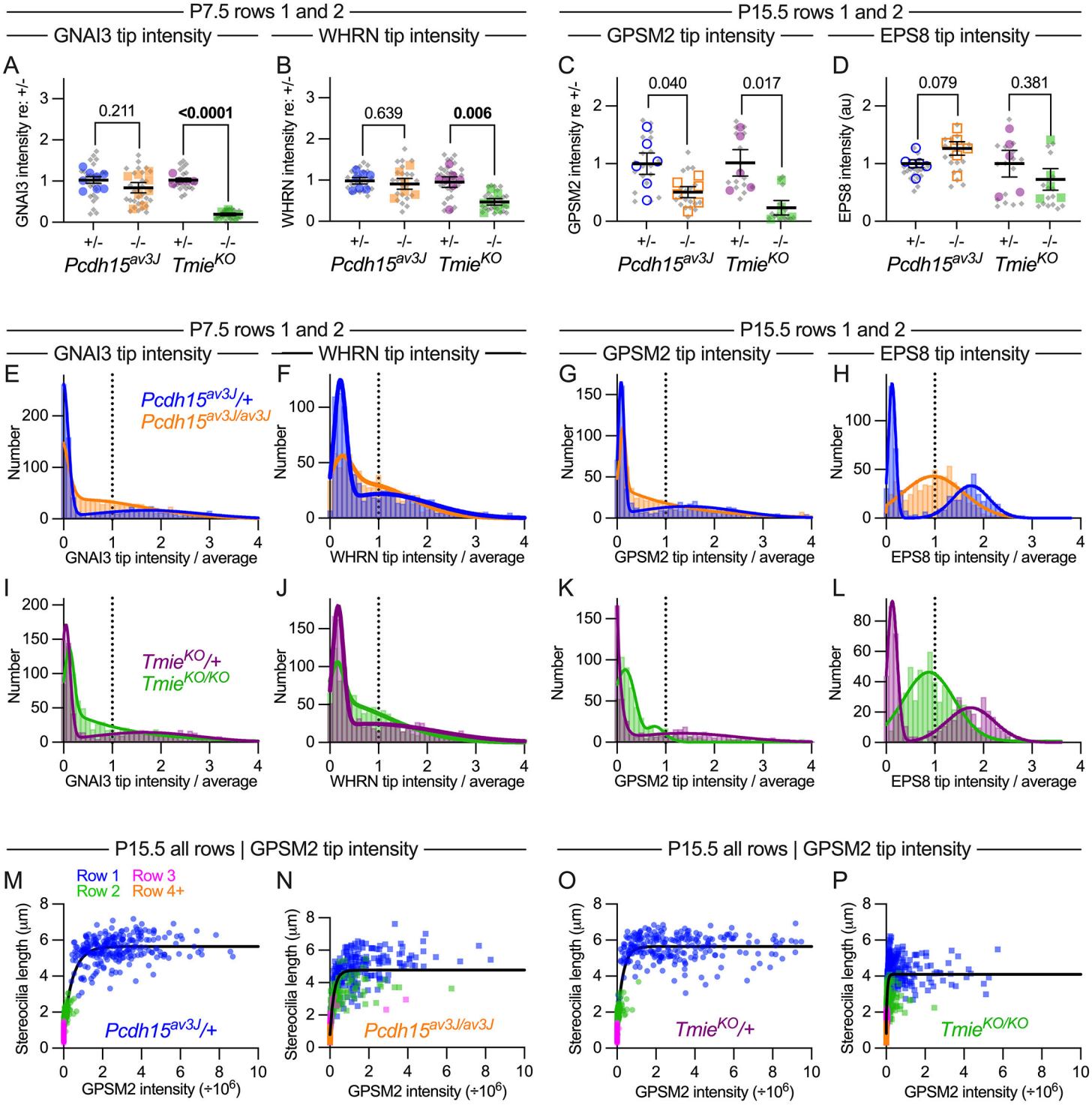

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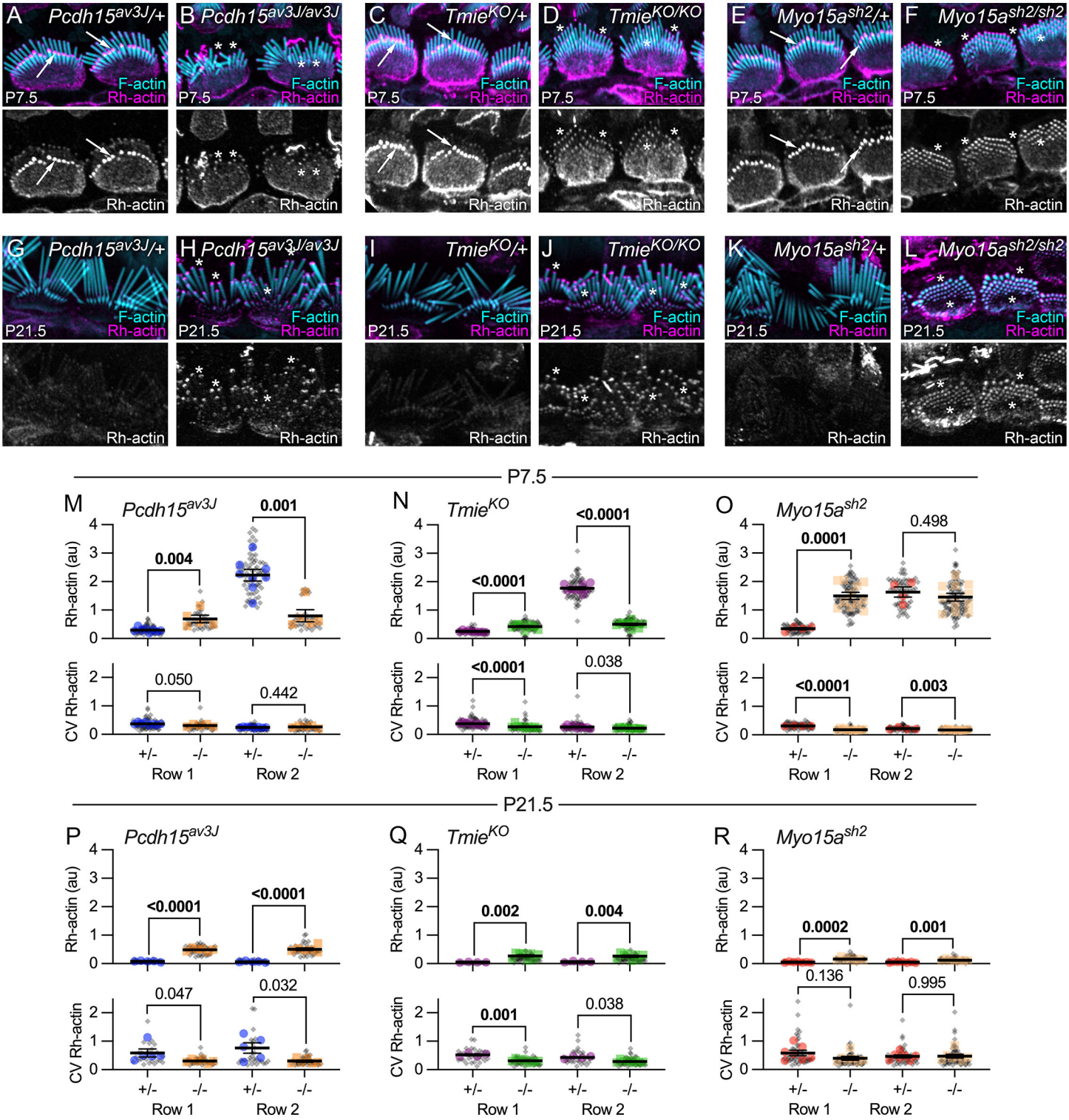

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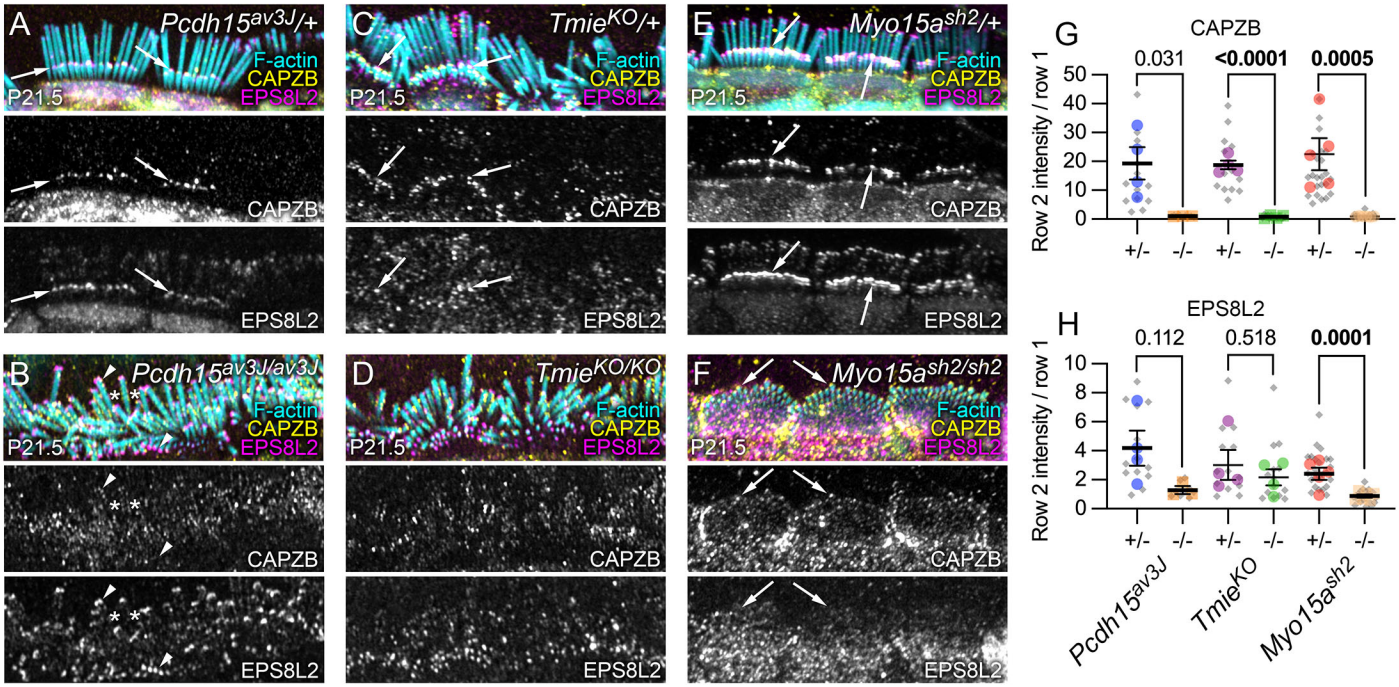

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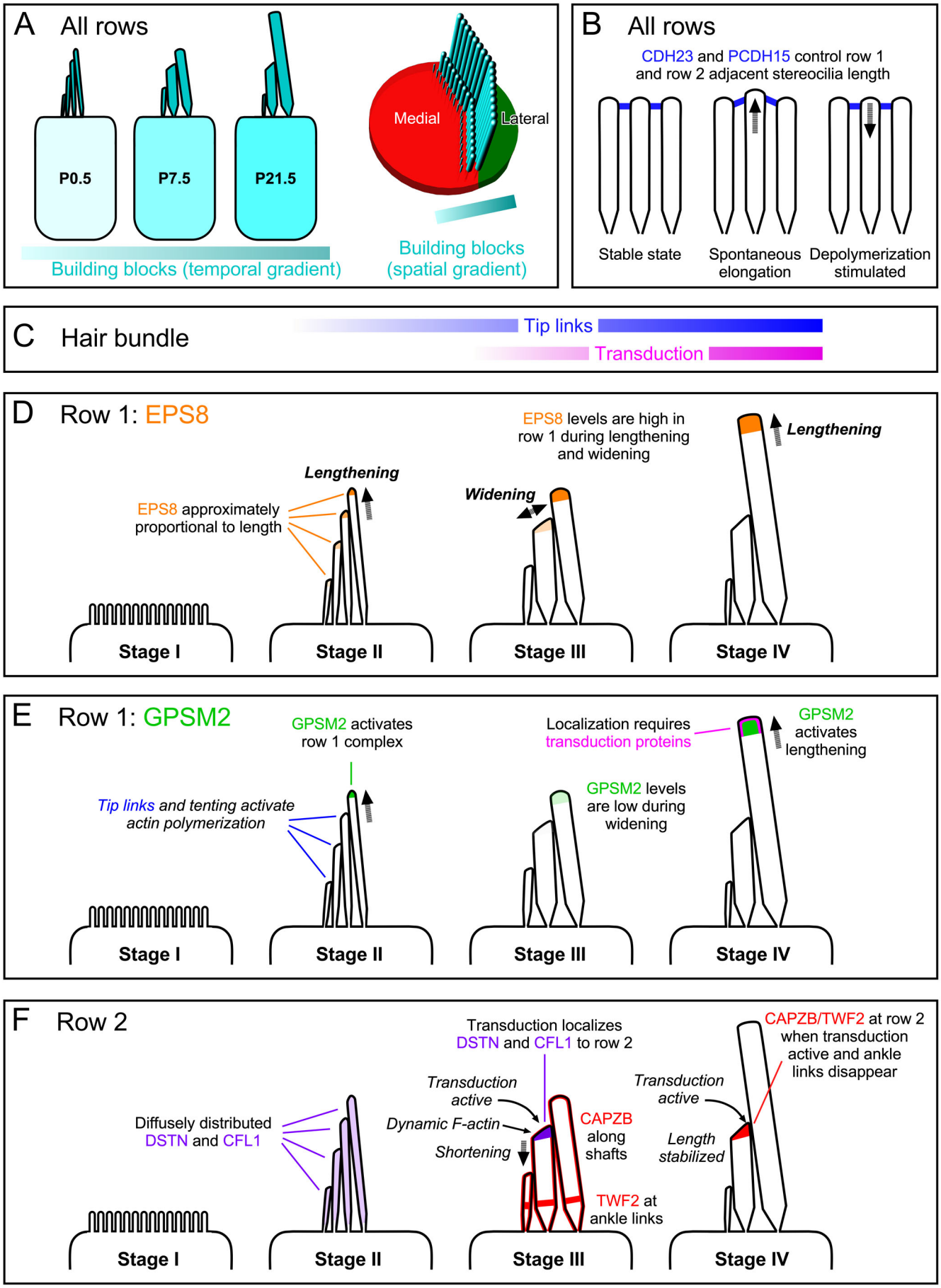

Figure 15
Krey et al.

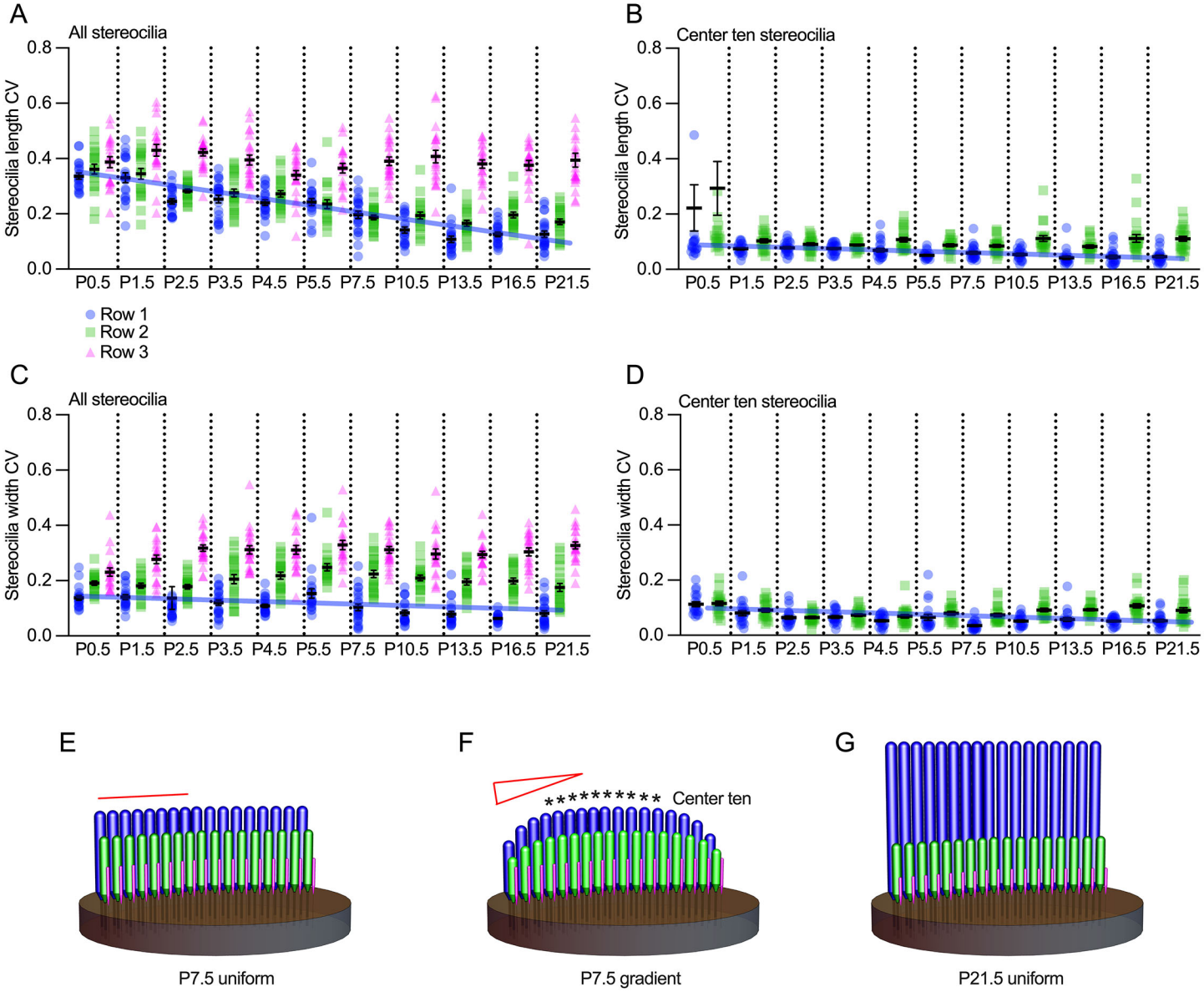

Figure S1
Krey et al.

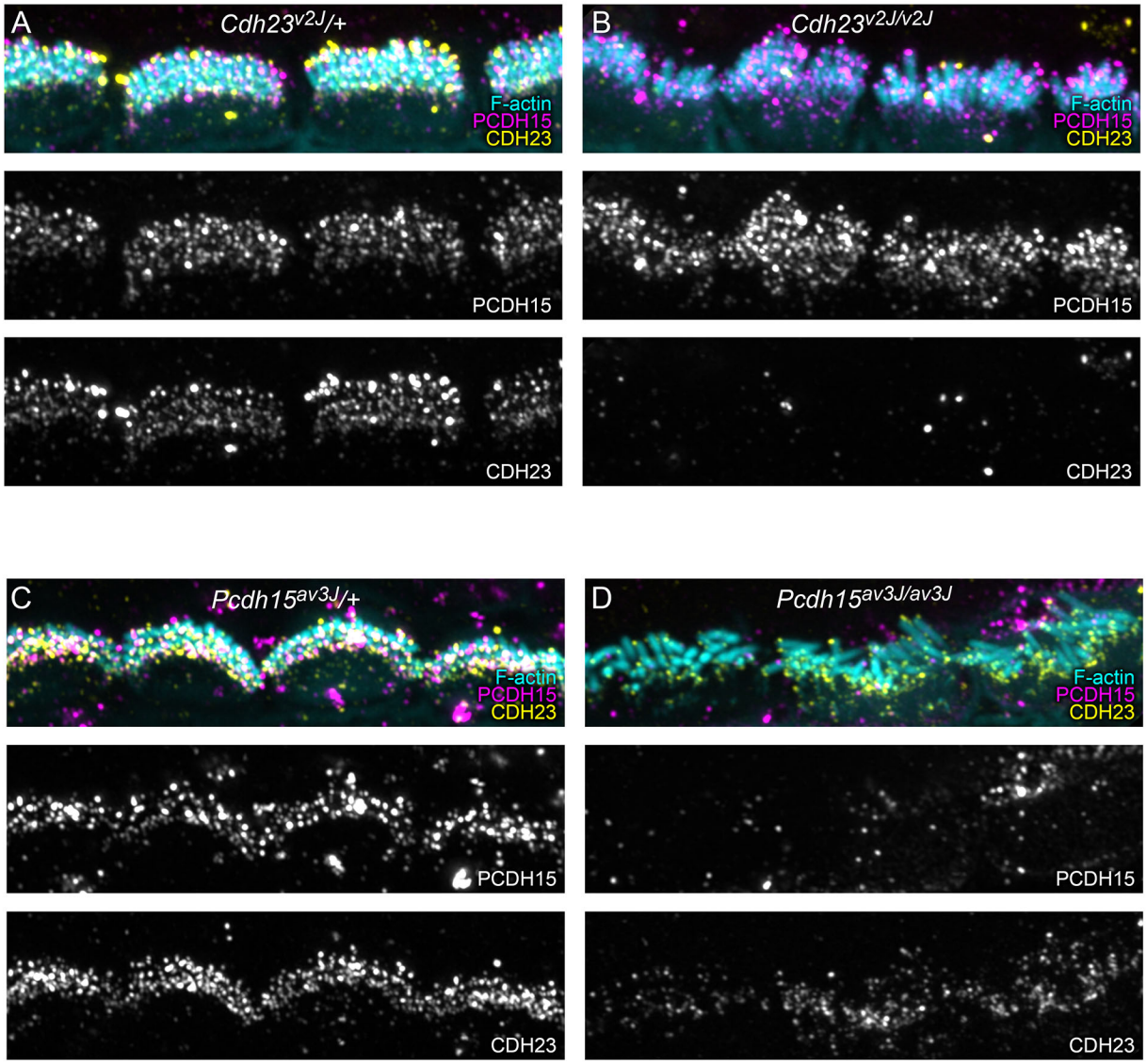

Figure S2
Krey et al.

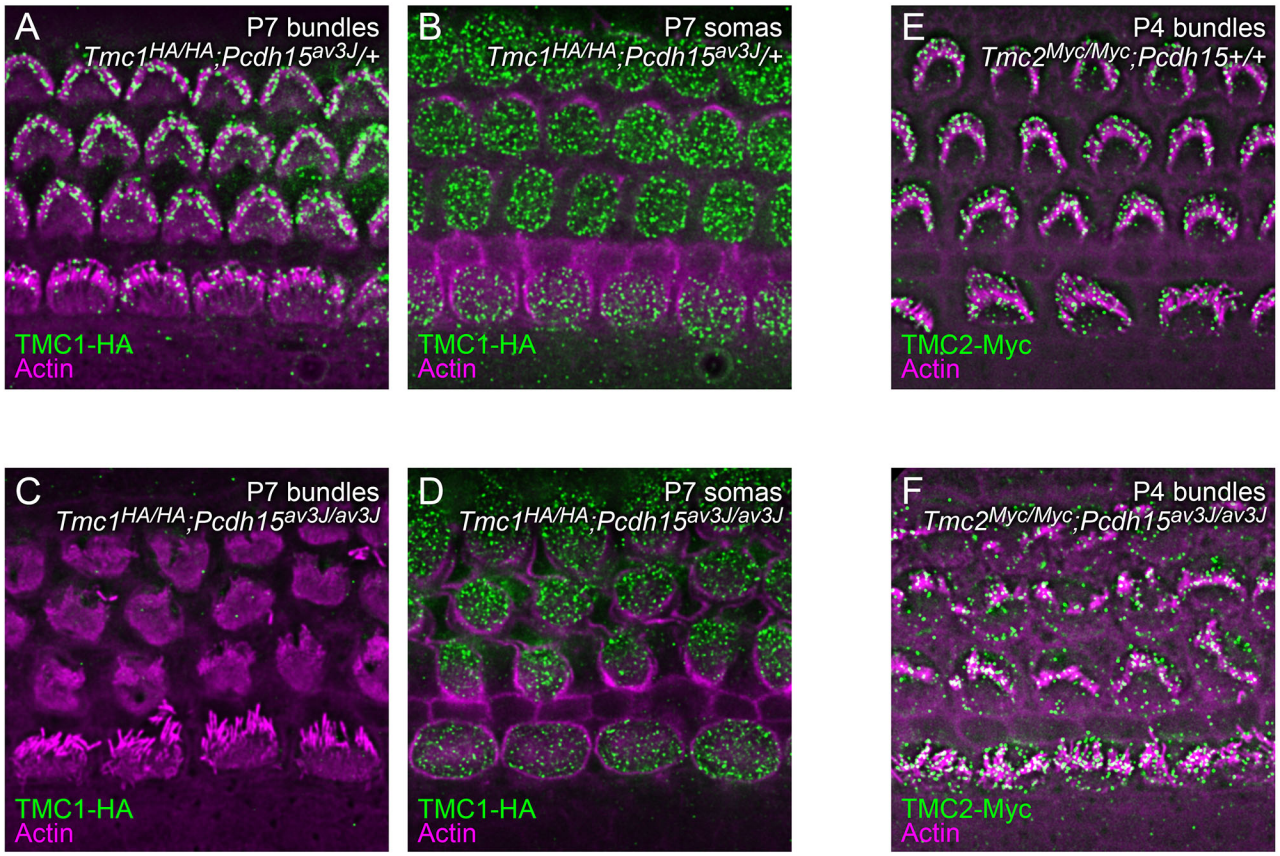

Figure S3
Krey et al.

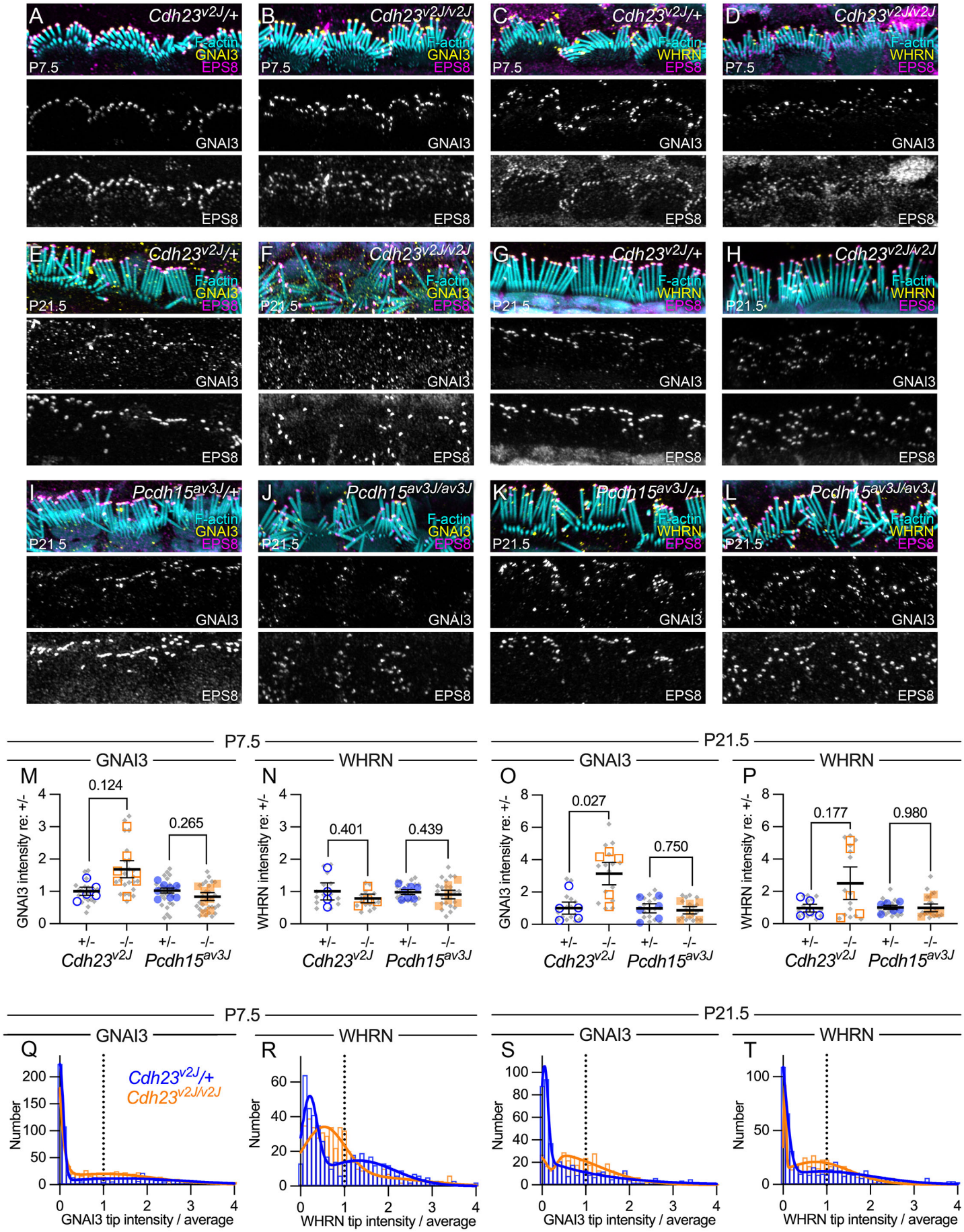

Figure S4
Krey et al.

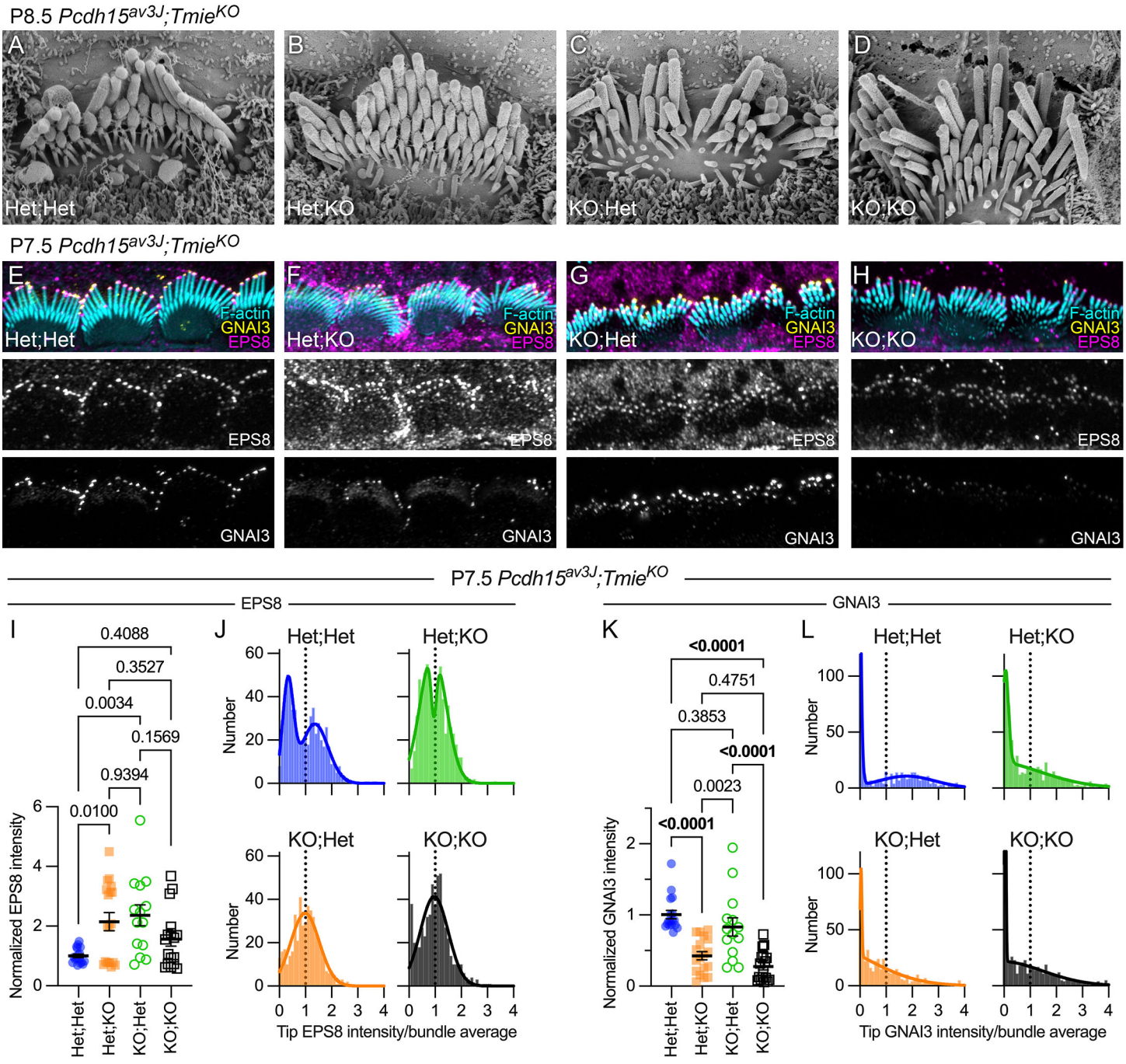

Figure S5
Krey et al.