Phosphatidylinositol 4,5-bisphosphate regulates cilium transition zone maturation in *Drosophila melanogaster*

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Brief summary statement: The authors show that the membrane phospholipid PIP_2 , and the kinase that produces PIP_2 called Skittles, are needed for normal ciliary transition zone morphology and function in the Drosophila male germline.

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¹ Abstract

Cilia are cellular antennae that are essential for human development and physiology. A large 2 number of genetic disorders linked to cilium dysfunction are associated with proteins that 3 localize to the ciliary transition zone (TZ), a structure at the base of cilia that regulates 4 trafficking in and out of the cilium. Despite substantial effort to identify TZ proteins and 5 their roles in cilium assembly and function, processes underlying maturation of TZs are not 6 rell understood. Here, we report a role for the membrane lipid phosphatidylinositol 4,5π 7 bisphosphate (PIP₂) in TZ maturation in the Drosophila melanogaster male germline. We show 8 that reduction of cellular PIP₂ levels by ectopic expression of a phosphoinositide phosphatase 9 or mutation of the type I phosphatidylinositol phosphate kinase Skittles induces formation of 10 longer than normal TZs. These hyperelongated TZs exhibit functional defects, including loss 11 of plasma membrane tethering. We also report that the onion rings (onr) allele of Drosophila 12 exo84 decouples TZ hyperelongation from loss of cilium-plasma membrane tethering. Our 13 results reveal a requirement for PIP₂ in supporting ciliogenesis by promoting proper TZ 14 maturation. 15

16 Introduction

Cilia are sensory organelles that are important for signalling in response to extracellular cues, 17 and for cellular and extracellular fluid motility [1, 2, 3, 4]. Consistent with their importance, 18 defects in cilium formation (i.e. ciliogenesis) are associated with genetic disorders known 19 as ciliopathies, which can display neurological, skeletal and fertility defects, in addition to 20 other phenotypes [5, 6, 7, 8]. Many ciliopathies are associated with mutations in proteins that 21 localize to the transition zone (TZ), the proximal-most region of the cilium that functions as a 22 diffusion barrier and regulates the bidirectional transport of protein cargo at the cilium base 23 [9, 10]. For example, the conserved TZ protein CEP290 is mutated in at least six different 24 ciliopathies [11] and is important for cilium formation and function in humans [12, 13] and 25 Drosophila [14]. Although the protein composition of TZs has been investigated in various 26 studies [15], the process of TZ maturation, through which it is converted from an immature 27 form to one competent at supporting cilium assembly, is relatively understudied. 28

Ciliogenesis begins with assembly of a nascent TZ at the tip of the basal body (BB) [9]. During 29 TZ maturation, its structure and protein constituents change, allowing for establishment of a 30 compartmentalized space, bounded by the ciliary membrane and the TZ, where assembly of the 31 axoneme, a microtubule-based structure that forms the ciliary core, and signalling can occur. In 32 Drosophila, nascent TZs first assemble on BBs during early G2 phase in primary spermatocytes 33 [16]. This occurs concomitantly with anchoring of cilia to the plasma membrane (PM), 34 microtubule remodelling within the TZ [17, 18], and establishment of a ciliary membrane that 35 will persist through meiosis [16] (Figure 1A). TZ maturation has been described in Paramecium 36 [19], Caenorhabditis elegans [20] and Drosophila [18], and is most readily observed by an 37 increase in TZ length in the Drosophila male germline. 38

³⁹ We previously showed that the membrane lipid phosphatidylinositol 4,5-bisphosphate (PIP₂) is ⁴⁰ essential for formation of the axoneme in the Drosophila male germline [21, 22]. PIP₂, which ⁴¹ is one of seven different phosphoinositides (PIPs) present in eukaryotes, localizes primarily

to the PM, where it is required for vesicle trafficking, among other processes [23]. PIP₂ has 42 recently been linked to cilium function. Although the ciliary membrane contains very little 43 PIP₂ due to the action of the cilium resident PIP phosphatase INPP5E, the base of the cilium 44 is enriched in PIP₂ [24]. Inactivation of INPP5E causes a build up of intraciliary PIP₂, which 45 disrupts transport of Hedgehog signalling proteins in vertebrates [25, 26, 27] and ion channels 46 involved in mechanotransduction in Drosophila [28]. In light of the current understanding 47 of PIP₂ as a modulator of cilium function, we sought to investigate the cause of defects we 48 had observed in axoneme assembly in Drosophila male germ cells with reduced levels of PIP₂ 49 [21, 22]. 50

51 Results

⁵² PIP₂ is essential for transition zone maturation

To investigate how reduction of cellular PIP₂ affects ciliogenesis in the Drosophila male 53 germline, we used transgenic flies expressing the Salmonella PIP phosphatase SigD under 54 control of spermatocyte-specific β_2 -tubulin promoter (hereafter β_2 t-SigD) [21]. To examine 55 whether axoneme defects in β_2 t-SigD [21] were caused by aberrant TZ function, we examined 56 localization of fluorescently-tagged versions of the core centriolar/BB protein Ana1 (CEP295 57 homolog) [29, 30] and the conserved TZ protein Cep290 [14] during early steps of cilium 58 assembly. Cep290 distribution appeared similar in control and β_2 t-SigD in early G2 phase, 59 when TZs are still immature. In contrast, Cep290-labelled TZs were significantly longer 60 in β_2 t-SigD compared to controls by late G2 phase, following the period of TZ maturation 61 (Figure 1B and 1C). Unlike Drosophila cep290 mutants, which contain longer than normal BBs 62 [14], Ana1 length was not affected in β_2 t-SigD, and we did not observe a strong correlation 63 between Cep290 and Ana1 lengths (Figure 1D). Consistent with this result, the ultrastructure 64 of BBs in β_2 t-SigD is normal, and localization of the centrillar marker GFP-PACT [31] is 65 similar, in controls and β_2 t-SigD [21]. In contrast, TZ proteins Chibby (Cby) [32] and Mks1 66

[33, 34] exhibited hyperelongation in β_2 t-SigD (Figure 1E), indicating that this phenotype is 67 not unique to Cep290. TZ hyperelongation was a highly penetrant phenotype (>70%) and 68 showed high correlation (>0.95) within syncytial germ cell cysts, suggestive of a dosage-based 69 response to a shared cellular factor, presumably SigD. Despite persistence of hyperelongated 70 TZs through meiosis, axonemes were able to elongate normally in post-meiotic cells (Figure 71 1F). Nonetheless, the ultrastructure of these axonemes is frequently aberrant, either lacking 72 nine-fold symmetry or containing triplet microtubules in addition to the usual doublets 73 [21]. 74

75 The type I PIP kinase Skittles regulates TZ length

Although PIP₂ is its major substrate in eukaryotic cells in vivo [35, 36, 37], SigD can de-76 phosphorylate multiple PIPs in vitro [38]. To address whether TZ hyperelongation observed 77 in β_2 t-SigD represented a physiologically relevant phenotype due to decreased PIP₂, we at-78 tempted to rescue this phenotype by co-expressing β_2 t-SigD with fluorescently-tagged Skittles 79 (Sktl) under control of β_2 -tubulin promoter. We found that Sktl expression was able to suppress 80 TZ hyperelongation in a cilium-autonomous manner (Figure 2A and 2B). Furthermore, the 81 BB/TZ protein Unc-GFP [39, 21], exhibited TZ hyperelongation at a low penetrance in *sktl*^{2.3} 82 mutant clones (Figure 2C), indicating that Sktl is important for TZ maturation. 83

Vertebrate type I PIP kinase PIPKI γ has previously been shown to be important for cilium 84 formation in cultured cells [40]. The two Drosophila PIPKIs, Sktl and PIP5K59B, arose from 85 recent duplication of the ancestral PIPKI gene, and are not orthologous to specific vertebrate 86 PIPKI isoforms (Figure 2D). Sktl has diverged more than its paralog PIP5K59B and seems 87 to be functionally related to PIPKI γ and the C. elegans PPK-1 in having roles at cilia [41]. 88 However, unlike the human PIPKI γ , which licenses TZ assembly by promoting CP110 removal 89 from BBs [40], our results suggest that Sktl functions in regulating TZ length but not TZ 90 assembly. Notably, neither inactivation nor overexpression of cp110 affects cilium formation in 91 Drosophila, and Cp110 is removed from BBs in early primary spermatocytes [42]. 92

⁹³ Hyperelongated transition zones exhibit functional defects

We next sought to examine whether TZ hyperelongation due to SigD expression affected TZ 94 function. Following meiosis in the Drosophila male germline, TZs detach from the BB and 95 migrate along the growing axoneme, maintaining a ciliary compartment at the distal-most 96 $\sim 5\mu$ m where tubulin is incorporated into the axoneme [14, 43]. As shown by Unc and Cep290 97 localization, TZs in β_2 t-SigD were frequently incapable of detaching from BBs and migrating 98 along axonemes despite axoneme and cell elongation (Figures 1E, 3A and 3B). Indeed, the 99 previously reported "comet-shaped" Unc-GFP localization in β_2 t-SigD [21] persists during cell 100 elongation after meiosis (Figure 3A, bottommost panel) despite elongation of the axoneme 101 (Figure 1E). 102

In Drosophila and humans, BBs consist of microtubule triplets [44, 45], whereas axonemes 103 contain microtubule doublets due to obstruction of C-tubules at the TZ [18]. Consistent 104 with a defect in this barrier and the presence of microtubule triplets in axonemes in β_2 t-SigD 105 [21], a subset of cilia (<5%) in β_2 t-SigD contained puncta of Ana1 at the distal tips of TZs 106 (Figure 3C). Treatment of germ cells with the microtubule-stabilizing drug Taxol increased the 107 penetrance of this phenotype from <5% in untreated cells to >25% in cells treated with 4 108 μ M Taxol (arrowheads in Figure 3D) without significantly affecting Cep290 length (Figure 109 3E). Taxol-treated controls did not exhibit TZ-distal Ana1 puncta (p < 0.01 at 5% penetrance). 110 Fluorescently-tagged Asterless (CEP152 homolog), a pericentriolar protein [46, 47], did not 111 localize to TZ-distal puncta in β_2 t-SigD (p < 0.01) suggesting that these TZ-distal sites are not 112 fully centriolar in protein composition. Taxol has been hypothesized to disrupt TZ maturation 113 by inhibiting microtubule remodelling in the Drosophila male germline [17]. Similar to 114 β_2 t-SigD, Taxol-treated male germ cells assemble extremely long axonemes that contain triplet 115 microtubules [17], further supporting a functional relationship between PIP₂ and microtubule 116 reorganization in TZ maturation. 117

¹¹⁸ The onion rings (onr) mutant decouples defects found in cells with reduced levels of ¹¹⁹ PIP₂

¹²⁰ Male flies homozygous for the *onion rings* (*onr*) mutant of Drosophila *exo84* are sterile and ¹²¹ exhibit defects in cell elongation and polarity similar to β_2 t-SigD [21]. Exo84 is a component ¹²² of the octameric exocyst complex, which binds PIP₂ and regulates membrane trafficking at the ¹²³ PM [48]. To investigate whether defects in TZ hyperelongation could be explained by defective ¹²⁴ Exo84 function, we examined TZs in *onr* mutants. Unlike β_2 t-SigD, *onr* did not display ¹²⁵ hyperelongated TZs (Figure 4A), suggesting that Exo84 is dispensable for TZ maturation.

Due to involvement of the exocyst in trafficking at the PM, we examined whether cilium-126 associated membranes were affected in β_2 t-SigD or *onr* mutants in a manner similar to *dilatory*; 127 cby mutants [33]. Dilatory (Dila), a conserved TZ protein, cooperates with Cby to assemble 128 TZs in the Drosophila male germline [33]. Whereas TZs in β_2 t-SigD and onr cells were able 129 to dock at the PM initially, they were unable to maintain membrane connections, and were 130 rendered cytoplasmic (Figure 4B and C), similar to TZs in dila; cby mutants. We found that 13 fluorescently-tagged Exo70, a PIP₂-binding exocyst subunit, localized to BBs (Figure 4D). Our 132 results suggest that the exocyst, and Exo84 in particular, regulates cilium-PM associations, 133 similar to PIP₂, and that TZ hyperelongation and loss of cilium-PM association are genetically 134 separable phenotypes. 135

136 Discussion

¹³⁷ The process of maturation of a TZ from a nascent form to a fully functional state, leading ¹³⁸ ultimately to axoneme assembly and ciliary signalling, requires orchestration of various pro-¹³⁹ teins and cellular pathways [9, 15]. Our results indicate that normal execution of this process ¹⁴⁰ requires PIP₂ and that depletion of PIP₂ induces TZs to grow longer than normal. Similar to β_2 t-¹⁴¹ SigD, Drosophila *dila; cby* and *cby* mutants display hyperelongated TZs [32, 33], whereas *mks1* ¹⁴² mutants have shorter TZs [34]. Because both Cby and Mks1 are hyperelongated in β_2 t-SigD

¹⁴³ cells, PIP₂ regulates TZ length independently of an effect on Cby or Mks1 recruitment.

We also show that hyperelongated TZs are dysfunctional. Similar to *dila*; *cby* [33] and *cep290* 144 [14] mutants, axonemes can assemble in β_2 t-SigD, albeit with aberrant ultrastructure [21], 14 despite the lack of functional TZs or membrane association. The presence of TZ-distal Ana1 146 puncta in β_2 t-SigD cells, without the increase in BB length seen in *cep290* mutants lacking 147 a functional TZ barrier, suggests that β_2 t-SigD expression selectively disrupts the ability of 148 TZs to restrict C-tubules and Ana1 without abolishing the TZ barrier entirely. CEP295, the 149 human Ana1 ortholog, regulates post-translational modification of centriolar microtubules 150 [49], which may explain the presence of Ana1 along with supernumerary microtubules in 151 β_2 t-SigD cells. Asterless (Asl), a pericentriolar protein important for centrosome formation 152 and centriole duplication [46, 47], did not exhibit this TZ-distal localization, possibly due to 153 differences dynamics of Ana1 and Asl loading onto centrioles [50, 51] or the more peripheral 154 nature of Asl within the centriole [46]. 155

The majority of PIP₂ at the PM is produced by PIPKIs [23, 52]. In this study, we showed 156 that mutation of the PIPKI Sktl induced hyperelongated TZs and that expression of Sktl 157 could suppress TZ hyperelongation in β_2 t-SigD, with some cells showing cilium-autonomous 158 suppression, suggesting Sktl might function in situ to regulate TZ length. In humans, PIPKI γ is 159 linked to lethal congenital contractural syndrome type 3 (LCCS3), which has been suggested 160 to represent a ciliopathy [40]. The recent discovery of a role for LCCS1-associated GLE1 16 protein in cilium function [53] corroborates this hypothesis. Our data support the idea that 162 PIPKIs might represent ciliopathy-associated genes or genetic modifiers of disease. 163

¹⁶⁴ Members of the exocyst complex such as Sec10 and Sec8 are important for cilium formation ¹⁶⁵ in cultured cell lines and zebrafish [54, 55, 56], but their precise roles in ciliogenesis are ¹⁶⁶ not well understood. The subunits Sec3 and Exo70 regulate exocyst targeting to the plasma ¹⁶⁷ membrane through a direct interaction with PIP₂ [48, 57]. We previously showed that the ¹⁶⁸ *onr* allele of Drosophila *exo84* phenocopies defects in cell polarity and elongation observed in ¹⁶⁹ β_2 t-SigD [22]. Here, we show that the *onr* mutation phenocopies the loss of cilium-membrane ¹⁷⁰ contacts in β_2 t-SigD, similar to *dila; cby* mutants [33], but not TZ hyperelongation. Thus, TZ ¹⁷¹ hyperelongation is not a prerequisite for the failure of cilium-PM association in male germ ¹⁷² cells, and Exo84 uniquely regulates the latter process, potentially by supplying membrane ¹⁷³ required to maintain cilium-PM association. This result is supported by the Drosophila *cep290* ¹⁷⁴ mutant, which lacks a functional TZ but retains cilium-PM association [14]. Notably, *EXOC8*, ¹⁷⁵ which encodes the human Exo84, has been linked to the ciliopathy Joubert syndrome [58], ¹⁷⁶ and a similar process might underlie defects in humans with mutations in *EXOC8*.

177 Methods

178 Transgenic flies

Drosophila stocks were cultured on cornmeal molasses agar medium at 25°C and 50% humidity. 179 Stocks expressing β_2 t::*Styp*\SigD (chromosome 3) and β_2 t::YFP-Sktl (chromosome 2) were 180 described previously [21, 59]. GFP-Exo70 was cloned into the low-level expression vector tv3 18 [59] and transgenic flies were generated using standard *P* element-mediated transformation. 182 Ana1-tdTomato (chromosome 2) and Cep290-GFP (chromosome 3) were provided by T. 183 Avidor-Reiss [14]. Sp/CvO; Unc-GFP was originally provided by M. Kernan [39]. Stocks 184 expressing GFP-tagged Chibby and Mks1 were provided by B. Durand [32, 33]. The onr 185 mutant was described previously [60]. Stocks for generating *sktl*^{2.3} clones were originally 186 provided by A. Guichet [61]. Clones were induced by heat shock for two hours on days 3, 4 187 and 5 after egg laying. w^{1118} was used as the wild-type control. 188

189 Antibodies

¹⁹⁰ The following primary antibodies were used for immunofluorescence at the indicated concen-¹⁹¹ trations: chicken anti-GFP IgY (abcam), 1:1000; rat anti-RFP IgG (5F8, ChromoTek), 1:1000; ¹⁹² rabbit anti-Centrin (C7736, Sigma-Aldrich), 1:500; mouse anti-acetylated α -tubulin 6-11-B (Sigma-Aldrich), 1:1000. Secondary antibodies were Alexa 488- and Alexa 568-conjugated
anti-mouse, anti-rabbit and anti-chicken IgG (Molecular Probes) at 1:1000. DAPI at 1:1000
was used to stain for DNA.

¹⁹⁶ *Fluorescence microscopy*

For live imaging, testes were dissected in phosphate buffered saline (PBS). To stain for DNA, intact testes were incubated in PBS with Hoechst 33342 (1:5000) for 5 minutes. Testes were transferred to a polylysine-coated glass slide (Thermo Fisher Scientific) in a drop of PBS, ruptured using a syringe needle and squashed under a glass coverslip using Kimwipes. The edges of the coverslip were sealed with nail polish and the specimen was visualized using an epifluorescence microscope (Zeiss Axioplan 2) with an Axiocam CCD camera. Cells were examined live whenever possible to avoid artefacts from immunostaining.

For Taxol treatments, testes from larvae or pupae expressing Ana1-tdTomato; Cep290-GFP were dissected into Shields and Sang M3 medium (Sigma-Aldrich) supplemented with a predefined concentration of Taxol (Sigma-Aldrich) in DMSO and incubated overnight in a humidified sterile chamber in the dark at room temperature. These were then squashed in PBS and imaged live.

For CellMask staining, cells were spilled from testes in M3 medium onto a sterilized glassbottom dish pre-treated with sterile polylysine solution to enable cells to adhere. CellMask Deep Red (Invitrogen) solution (20 μ g/mL) was added to the medium dropwise immediately before visualization under a confocal microscope.

For immunocytochemistry, testes were dissected in PBS, transferred to a polylysine-coated glass slide in a drop of PBS, ruptured with a needle, squashed and frozen in liquid nitrogen for 5 minutes. Slides were transferred to ice-cold methanol for 5-10 minutes for fixation. Samples were then permeabilized and blocked in PBS with 0.1% Triton-X and 0.3% bovine serum albumin, and incubated with primary antibodies overnight at 4°C, followed by three ²¹⁸ 5-minute washes with PBS, 1 hour incubation with secondary antibodies, and three 5-minute
²¹⁹ washes with PBS. Samples were mounted in Dako (Agilent) and imaged with a Zeiss Axioplan
²²⁰ 2 epifluorescence microscope or a Nikon A1R scanning confocal microscope (SickKids imaging
²²¹ facility).

222 Statistical methods

Statistical analysis and graphing was performed using R (version 3.4). A Gaussian jitter was 223 applied when plotting results in Figures 1 and 2 for clearer visualization of trends, but raw 224 data was used for all analyses. Statistical tests for "absence of phenotype" were computed 225 using a binomial test under the assumption that the probability of the phenotype occuring 226 was fixed. All t-tests were unpaired and two-sided with Welch's correction for unequal 227 variances. *n* represents the pooled number of samples (individual cilia) from multiple flies. 228 A significance level of 0.01 was fixed a priori for all classical analyses. All raw data and 229 code for analysis and plotting can be found online at http://www.github.com/alindgupta/ 230 germline-paper/. 23

232 Phylogenetic analysis

Candidate orthologs of Skittles and PIP5K9B were queried from Inparanoid (version 8.0) and
FlyBase (version FB2017_05). Poorly annotated protein sequences were confirmed to encode
type I phosphatidylinositol phosphate kinases using reciprocal BLAST search. Phylogeny.fr
(http://www.phylogeny.fr) [62] was used for phylogenetic reconstruction with T-Coffee for
multiple alignment and MrBayes for tree construction. The output was converted to a vector
image in Illustrator and colours were added for the purpose of illustration.

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246 Author contributions

A.G. and J.A.B. conceived the project. A.G. performed all the experiments and analyses, and
wrote the manuscript. L.F. generated GFP-Exo70 flies. J.A.B. edited the manuscript and
supervised the project.

Declaration of interests

²⁵¹ The authors declare no competing interests.

252 Figure legends

²⁵³ Figure 1. SigD expression induces transition zone hyperelongation.

- (A) Schematic diagram of the stages of ciliogenesis in the Drosophila male germline. Stages
 in parentheses correspond to those from [63].
- (B) β_2 t-SigD expression induces Cep290 hyperelongation in cilia at late G2 phase (white arrowheads).

- (C) Quantification of paired Ana1-Cep290 lengths in early and late G2 phase in spermatocytes (n > 30 and > 65 respectively).
- (D) Lengths of Ana1-tdTomato versus Cep290-GFP in control and β_2 t-SigD cells at late G2 phase from (C) showing negligible correlation. Regression lines are plotted in red, and the Pearson correlation coefficient (*r*) is indicated on the bottom-left.
- (E) β_2 t-SigD expression induces hyperelongation of the TZ proteins Chibby (Cby) and Mks1
- in late G2 phase (white arrowheads).
- (F) TZ hyperelongation persists through meiosis (white arrowhead) but does not affect
 axoneme outgrowth. Acetylated tubulin (AcTub) labels the axoneme.

²⁶⁷ Figure 2. Sktl is important for transition zone maturation.

- (A) Expression of full-length Sktl can suppress β_2 t-SigD-induced TZ hyperelongation in a cilium-autonomous manner. Images were chosen to demonstrate varying levels of rescue of Cep290-GFP length in β_2 t-YFP-Sktl; β_2 t-SigD. White arrowheads mark rescued Cep290 distribution for comparison.
- (B) Quantification of Cep290 and Ana1 lengths from control, β_2 t-SigD from (A) and β_2 t-YFP-Sktl; β_2 t-SigD (n = 100).
- (C) $sktl^{2.3}$ clones exhibit TZ hyperelongation (white arrowheads), as marked by Unc-GFP (left). Quantification of Unc-GFP lengths in control (n = 53), $sktl^{2.3}$ (n = 31) and β_2 t-SigD (n = 51) spermatocytes at late G2 phase (right).

(D) Phylogenetic tree of PIP5Ks showing evolutionary conservation of cilium-associated 277 functions. Scale bar (bottom) represents expected amino acid substitutions per site. 278 Branch support values are shown in red (a value of 1 indicates maximum support). Black 279 arrows represent previous evidence of involvement in cilium-associated functions (from 280 [40]). Black arrowhead indicates Sktl. Abbreviations: Cele (*Caenorhabditis elegans*), 281 Spur (Strongylocentrotus purpuratus), Amel (Apis mellifera), Aaeg (Aedes aegypti), Dana 282 (Drosophila ananassae), Dmel (Drosophila melanogaster), Hsap (Homo sapiens), Mmus 283 (Mus musculus), Xtro (Xenopus tropicalis), Cint (Ciona intestinalis), Scer (Saccharomyces 284

285	cerevisiae).

²⁸⁶ Figure 3. Hyperelongated transition zones display functional defects.

(A) Unc-GFP is unable to detach from the basal body and migrate in spermatids expressing β_2 t-SigD (white arrowhead). Cell elongation in spermatids is concomitant with elongation of the mitochondrial derivative (dark organelles in the phase-contrast images). Insets show phase-contrast images corresponding to the region shown in the fluorescence images.

(B) Cep290 is unable to detach and migrate from the basal body at the onset of axoneme assembly in β_2 t-SigD spermatids (white arrowhead). Insets show phase contrast images corresponding to the region shown in the fluorescence images, with the elongating mitochondrial derivative delineated by a yellow dashed line.

- (C) Structured illumination micrographs of β_2 t-SigD cells showing TZ-distal puncta of the centriolar protein Ana1 (yellow arrowheads).
- (D) Treatment of control and β_2 t-SigD cells with the microtubule stabilizing drug Taxol. Images demonstrate the variety in Cep290 distribution. Yellow arrowheads mark TZdistal Ana1.

(E) Quantification of Cep290 lengths in Taxol-treated control and β_2 t-SigD cells from (D) (*n* is between 30 and 40).

Figure 4. The onion rings (onr) allele of exo84 decouples TZ hyperlongation from loss of plasma membrane contacts.

- (A) onr mutant cells do not display hyperelongated acetylated tubulin signal at the cilium
 (white arrowhead). Acetylated tubulin marks the axoneme, which colocalizes with the
 TZ in spermatocytes [34].
- (B) Cells expressing β_2 t-SigD fail to maintain cilium-PM tethering despite initially anchoring to the PM. The PM is marked with CellMask, a cell impermeable dye.
- 310 (C) onr mutants do not maintain PM-cilium tethering.

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311 (D) GFP-tagged Exo70 localizes to BBs in spermatocytes.

List of Abbreviations

β_2 t-SigD	SigD driven by the male germline-specific β_2 -tubulin promoter
PIP ₂	phosphatidylinositol 4,5-bisphosphate
PIP	phosphoinositide, also known as phosphatidylinositol phosphate
TZ	transition zone
BB	basal body
PM	plasma membrane
onr	onion rings (an allele of exo84)

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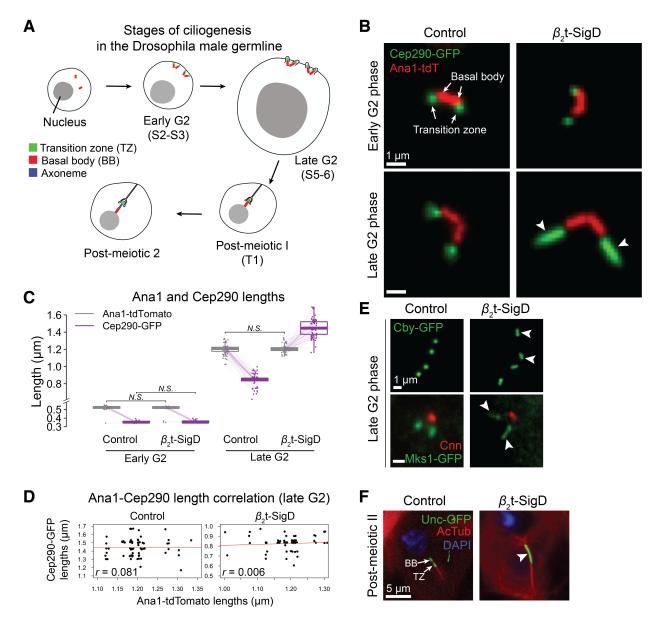
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Figures

Figure 1





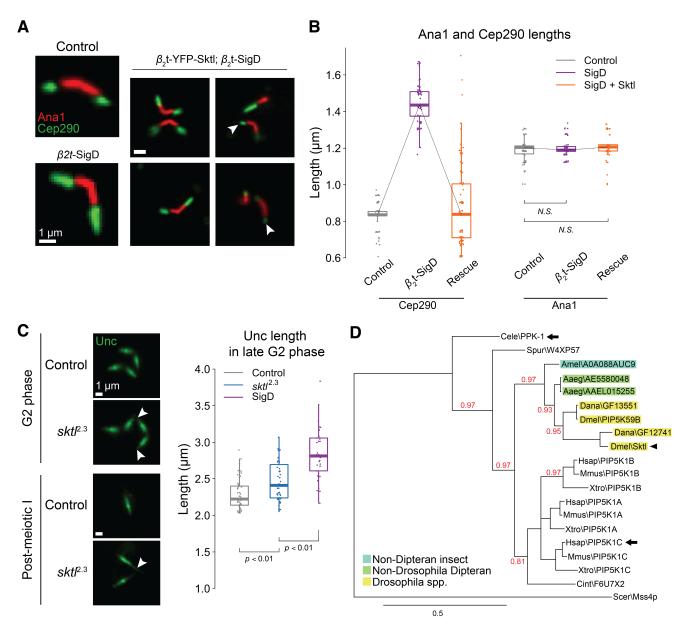


Figure 3

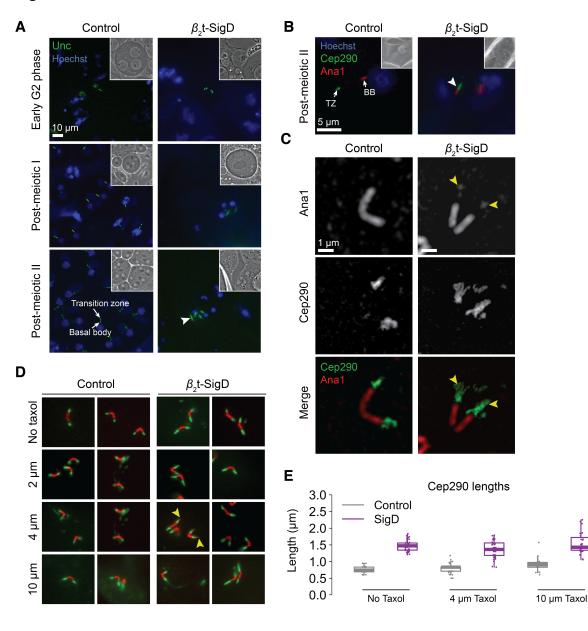


Figure 4

