

VIP17/MAL Expression Modulates Epithelial Cyst Formation and Ciliogenesis

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Running Title: VIP17/MAL Modulates Cyst and Cilium Formation

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ABSTRACT:

The polarized organization of epithelial cells is required for vectorial solute transport and may be altered in renal cystic diseases. Vesicle integral protein of 17 kD (VIP17/MAL) is involved in apical vesicle transport. VIP17/MAL overexpression *in vivo* results in renal cystogenesis of unknown etiology. Renal cystogenesis can occur as a consequence of defects of the primary cilium. To explore the role of VIP17/MAL in renal cystogenesis and ciliogenesis, we examined the polarization and ciliary morphology of wild-type and VIP17/MAL-overexpressing MDCK renal epithelial cells grown in two-dimensional (2D) and three-dimensional (3D) cyst culture. VIP17/MAL is apically localized when expressed in cells maintained in 2D and 3D culture. VIP17/MAL-overexpressing cells produce more multi-lumen cysts compared to controls. While the distributions of basolateral markers are not affected, VIP17/MAL expression results in aberrant sorting of the apical marker gp135 to the primary cilium. VIP17/MAL overexpression is also associated with shortened or absent cilia. Immunofluorescence analysis performed on kidney sections from VIP17/MAL transgenic mice also demonstrates fewer and shortened cilia within dilated lumens ($p < 0.01$). These studies demonstrate that VIP17/MAL overexpression results in abnormal cilium and cyst development, *in vitro* and *in vivo*, suggesting that VIP17/MAL overexpressing mice may develop cysts secondary to a ciliary defect.

KEY WORDS: cystogenesis, polycystic kidney disease, epithelial trafficking

INTRODUCTION:

Vesicular integral protein of 17 kD (VIP17/MAL), also known as myelin and lymphocyte protein (MAL) and myelin vesicular protein of 17 kD (MVP), is a 17kD proteolipid involved in the transport and delivery of carrier vesicles to the apical plasma membrane domains of polarized epithelial cells.(9, 42, 61) Originally identified over 20 years ago through a search for genes that are differentially expressed during human T-cell development, VIP17/MAL is also produced in oligodendrocytes and Schwann cells, and in epithelial cells of the thyroid, kidney, stomach, and large intestine.(25, 32) In addition, VIP17/MAL is expressed in cultured polarized epithelial cells, including the renal MDCK cell line, a model system for studying epithelial polarity.(36, 61)

The VIP17/MAL gene encodes a non-glycosylated integral membrane protein with four predicted transmembrane domains. In epithelial cells, VIP17/MAL is localized predominantly at the apical plasma membrane.(19) VIP17/MAL contains multiple hydrophobic segments and, in contrast to most other integral membrane proteins, is highly soluble in organic solvents. This behavior accounts for the designation of VIP17/MAL as a proteolipid. (1) Moreover, in all of the cell types in which it is expressed, VIP17/MAL is present in glycolipid- and cholesterol-enriched membrane (GEM) domains or “rafts”.(25, 32, 35, 61) As incorporation into GEM domains at the level of the TGN may be responsible for the apical sorting of a number of proteins, it is possible that VIP17/MAL may facilitate the organization of apical cargo into microdomains to facilitate their targeting and transport.(9, 42, 47, 61)

When VIP17/MAL levels are suppressed *in vitro* through treatment of cultured epithelial cells with RNAi, the ordinarily apically-localized influenza hemagglutinin

protein accumulates in the Golgi complex with diminished apical expression and partial missorting to the basolateral membrane.(9, 42, 61) In contrast, when VIP17/MAL is overexpressed *in vitro*, net membrane delivery to the apical surface appears to be enhanced, and as a consequence VIP17/MAL overexpressing MDCK cells have excess or enlarged apical membranes.(9) When grown in three-dimensional culture, MDCK cells in which VIP17/MAL expression has been decreased by RNAi manifest abnormal cyst formation as well as atypical ciliogenesis.(53) These studies collectively suggest that VIP17/MAL is involved in the accurate trafficking of a sub-group of proteins to the apical surface in MDCK cells as well as in epithelial morphogenesis.

When VIP17/MAL is overexpressed under the control of its own promoter in transgenic animals *in vivo*, the epithelial cells lining distal nephron segments in the mouse kidney also appear to exhibit abnormal morphology. They manifest a pseudostratified appearance with amplified apical membranes that balloon into the tubule lumina. In addition, these animals develop renal cysts, although the histology of these cysts differs from that characteristic of Autosomal Dominant Polycystic Kidney Disease (ADPKD).(18) In these transgenic mice, renal expression of VIP17/MAL is greatest in the collecting duct, although staining can also be detected in other tubule segments.(19, 23) The collecting duct also expresses aquaporin-2 (AQP2), the water channel that is trafficked from an intracellular vesicular compartment to the apical plasma membrane in response to the antidiuretic hormone, arginine vasopressin. VIP17/MAL co-localizes and interacts with AQP-2 in the renal collecting duct.(23) In LLC-PK₁ cells, expression of VIP17/MAL increases surface expression of AQP2 by decreasing the rate of the channel's endocytic internalization.(23) Moreover, in cultured cells *in vitro*, vasopressin

induces the expression of VIP17/MAL, which may facilitate the apical trafficking or retention of newly synthesized AQP2.(24) The VIP17/MAL-mediated increase in apical AQP2 expression may be due to decreased endocytosis from the apical surface and/or the increased exocytosis of AQP2 from recycling endosomes.(6) These studies collectively suggest that VIP17/MAL overexpression results in an imbalance between apical membrane formation and internalization.

It is unclear why VIP17/MAL transgenic mice develop renal cystic disease. However, it is well-established that renal cystogenesis occurs in association with defects of the primary cilium, a specialized compartment of the apical membrane with a protein and phospholipid composition that is distinct from that of the remainder of the apical membrane.(44) A number of genetic diseases are attributable to mutations in the genes encoding proteins involved in cilia function. Many of these “ciliopathies” include among their rosters of characteristic symptoms the presence of renal cysts. (29, 38, 48, 52, 56, 57, 59) We wondered, therefore, whether the cystic phenotype observed in VIP17/MAL overexpressing mice might be attributable to possible effects of this overexpression on the formation or function of primary cilia.

To explore the role of VIP17/MAL in renal cystogenesis and ciliogenesis, we examined the morphology and polarization of wild-type and VIP17/MAL overexpressing MDCK cells grown in two-dimensional and three-dimensional culture. In addition, we evaluated the cilia in both wild-type and VIP17/MAL overexpressing MDCK cells. Our *in vitro* and *in vivo* studies demonstrate that both epithelial morphogenesis and ciliary structure are profoundly perturbed in cells that overexpress VIP17/MAL. These

130 observations suggest an explanation for the renal cystic phenotype observed in
131 VIP17/MAL transgenic mice.

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MATERIALS AND METHODS:

Cell Culture, Cell Lines, and Transfection

MDCK type II cells were cultured in α -MEM (GIBCO) supplemented with 10% fetal bovine serum, 2mM L-glutamine, 50U/ml penicillin, and 50 ug/ml streptomycin, in a humidified incubator with 5% CO₂. VIP17/MAL overexpressing MDCK cells were similarly cultured. Three independent clones of VIP17/MAL overexpressing MDCK cells were generated and examined for these studies.

The coding sequence for VIP17/MAL (NM_005434.4) was inserted into pcDNATM 3.1⁺ vector (Invitrogen, Carlsbad, CA) using NheI and XbaI. A Flag sequence was subsequently inserted at the amino-terminus by PCR amplification using the primers F-5'-

GCCCAAGCTTATGGACTACAAGGACGACGATGACAAGGCCCCCGCAGCGG
CGACGGGG-3' (Flag epitope in bold, HindIII site underlined) and R-5'-
GCGCCTCGAGTTATGAAGACTTCCATCTGAT-3' (KpnI site underlined) and subcloned as previously described.(23)

MDCK cells were stably transfected with Lipofectamine 2000 (Invitrogen). Clones were selected by growth in medium supplemented with 1.6 mg/mL Zeomycin and screened by immunofluorescence.

In vitro cystogenesis

Briefly, 1 x 10⁵ MDCK or VIP17/MAL overexpressing cells were suspended in Matrigel (BD Biosciences, Inc.) per the protocol previously described by Grantham et al.(31) All suspensions were co-incubated with MDCK culture medium as described

above, with media being replaced every other day. Matrigel suspensions were then placed at 95° Celsius until melted, at which point the cysts were allowed to settle to the bottom of the well for image capture by light microscopy. For cyst immunofluorescence, cysts were retained within the gel.

Immunofluorescence in two-dimensions and three-dimensions

Cells on coverslips were washed twice with cold PBS (Sigma-Aldrich) with 1mM MgCl₂ and 100 μM CaCl₂ (PBS²⁺) and fixed for 30 minutes in 4% PFA at room temperature. Cells were subsequently washed with PBS²⁺ and then permeabilized with permeabilization buffer (0.3% Triton X-100/0.1% BSA in PBS). Cells were incubated for 1 hour with anti-acetylated alpha tubulin (Sigma) followed by incubation with fluorescein isothiocyanate- or rhodamine-conjugated anti-rat IgG (Molecular Probes). Nuclei were stained with propidium iodide when required. Cells were visualized on a Zeiss LSM 780 confocal microscope.

Immunofluorescence on three-dimensional cysts was performed as previously described by O'Brien et al.(37) Briefly cysts were fixed with 4% PFA for 30 minutes, permeabilized in 0.025% saponin for 30 minutes, quenched for 10 min with 7mM NH₄Cl, 20mM glycine, in PBS²⁺ (pH8) and then incubated overnight with primary antibody to anti-ZO-1 (Chemicon), anti-E-cadherin (Sigma), anti-β-catenin (Sigma), anti-FLAG (Sigma), anti-gp58 (gift of Ira Mellman) or anti-gp135 (gift of Ira Mellman) as indicated, diluted in goat serum. Cysts were washed for 2-4 hours with saponin in PBS²⁺ and incubated with secondary antibodies overnight. All other details of three-dimensional immunofluorescence are the same as those outlined in the protocol for

immunofluorescence analysis of cells grown in two-dimensions that is described above.

Cells were visualized using confocal microscopy (Zeiss LSM 780) at 40x and 63x.

Images were processed using LSM Image Viewer (Carl Zeiss, Inc.)

Quantitative RT-PCR.

RNA from WT and VIP17-overexpressing MDCK cells was purified using the RNeasy

kit (Qiagen, Germany). cDNA was synthesized using Superscript III Reverse

Transcriptase (Invitrogen) according to the manufacturer's instructions. Quantitative RT-

PCR was performed using the QuantiTect SYBR Green PCR kit (Qiagen). Initial

denaturation was performed for 10 min at 95°C, and amplification was performed for 40

cycles, at 95°C for 30 s, 57°C for 1 min, and 72°C for 1 min. To amplify exogenous

human VIP17, the primers 5'-GTACATAATTGGAGCCCACGGTGGGA-3' (sense) and

5'-AAGCCGTCTTGCATCGTGATGGT-3' (antisense) were used, resulting in a 135-bp

product. To amplify endogenous canine VIP17, the primers 5'-

CACCACAGCCCTGCTTGTCTGT-3' (sense) and 5'-

TCCCAATGGTGGCCAAAGCTTCC-3' (antisense) were used, resulting in a 143-bp

product. The products were confirmed by agarose gel electrophoresis, and quantified

using the $\Delta\Delta C_T$ method with β -actin as a reference gene. VIP17 expression in WT

MDCK cells was normalized to 1.

Immunohistochemistry

Both wild-type and VIP-17/MAL transgenic mouse kidneys were fixed in 4%

paraformaldehyde before being immersed in 30% sucrose and then embedded in

OCT.(19) Cryosections (5 μ M) were obtained, and sections were then processed for immunofluorescence experiments. Briefly, sections were washed three times in TBS, and then incubated for 5 minutes in TBS with 1% SDS before being washed in TBS again. Following blocking in Goat Serum Dilution Buffer (GSDB; 10% goat serum, 1% Triton X-100, and 10 mM glycine in PBS supplemented with 100 μ M CaCl_2 and 1 mM MgCl_2 (PBS^{++})), sections were incubated with a rabbit polyclonal antibody to ADP-ribosylation factor-like protein 13B (ARL13B) (7) (kind gift of Dr. S. Weatherbee, Yale University, used at 1:1,000) and a mouse monoclonal antibody to Na,K-ATPase (41) (Millipore, used at 1:400) diluted in GSDB. Sections were then washed again in TBS before being incubated with an anti-rabbit rhodamine and anti-mouse FITC secondary antibody (also diluted in GSDB) for 1 hour at room temperature. After a final set of washes in TBS, sections were examined and pictures were taken using a Leica confocal microscope.

Ciliary length was quantitated using NIS Elements Imaging Software (Nikon). Only unfolded cilia were used for quantitation, with 3 cilia measured per mouse from 3 control and 3 VIP17/MAL transgenic mice for a total n of 9 per condition.

Statistical Analysis

We calculated the statistical significance of differences in results using unpaired Student's t-tests. We considered a p-value less than 0.05 to be statistically significant.

RESULTS:

VIP17/MAL overexpressing MDCK cells display apical localization of VIP17/MAL.

To investigate the role of VIP17/MAL in epithelial polarization and cyst formation, we used Madin Darby canine kidney (MDCK) cells, a model system extensively employed for *in vitro* studies of epithelial membrane polarization. These cultured renal epithelial cells were stably transfected with a cDNA encoding the VIP17/MAL protein tagged with a FLAG epitope at its amino terminus. Three independent clones of VIP/MAL overexpressing MDCK cells were examined. Quantitative PCR using primers sets designed to detect expression of either the endogenous canine VIP17/MAL transcript or the transcript produce from the transfected human VIP/17 MAL construct indicated that the transfected cells express ~175 fold higher levels of VIP17/MAL mRNA than do untransfected cells. To determine the sub-cellular localization of the VIP17/MAL protein, we performed immunofluorescence studies on fully differentiated and intact monolayers of MDCK cells (**Figure 1a**). Using an antibody directed against the FLAG-epitope, we observed that the VIP17/MAL protein is present primarily on the apical membranes of MDCK cells, consistent with prior reports.(9, 61) Interestingly, the VIP17/MAL protein was detected over the entire apical surface and was apparently able to access the “exclusion zones” that surround the bases of cilia.(17) Consistent with this observation, the overexpressed VIP17/MAL protein could also be detected in a punctate distribution in some but not all cilia (**Figure 1c**). Western blot analysis of protein extracts prepared from these cells (**Figure 1b**) using both monoclonal and polyclonal anti-FLAG antibodies detects a protein with the anticipated size of 17kD.

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247 *VIP17/MAL overexpressing cysts have altered morphology.*

248 The presence of amplified apical membranes in VIP17/MAL overexpressing
249 MDCK cells grown in two-dimensional culture suggests that VIP17/MAL plays a role in
250 regulating vesicular traffic to and from the apical membrane.(9, 42, 61) To evaluate the
251 effect of VIP17/MAL on epithelial morphogenesis, VIP17/MAL overexpressing MDCK
252 cells and wild-type MDCK cells were suspended in a three-dimensional collagen matrix
253 and allowed to form cysts spontaneously as previously described.(31) While
254 untransfected MDCK cells generally formed cysts surrounding a single lumen, cysts
255 produced by VIP17/MAL overexpressing cells were significantly more likely to exhibit
256 multiple lumens (**Figure 2a**). The difference in lumen number is quantified in **Figure 2b**
257 ($p<0.01$). Both proliferative rate and the level of the mTOR activity have been shown to
258 be elevated in the context of renal cystic disease (8, 51), so we assessed the proliferation
259 rate and mTOR activity in VIP17/MAL overexpressing MDCK cells by
260 immunofluorescence staining for Ki67 and western blotting for phospho-S6 kinase,
261 respectively. This analysis revealed no differences between the wild type and
262 VIP17/MAL overexpressing cells (not shown). It is interesting and perhaps somewhat
263 surprising to note that a similar multiple lumen phenotype is observed with MDCK cells
264 in which VIP17/MAL expression has been reduced through treatment with RNAi.(53)
265 While the mechanisms responsible for multiple lumen formation in the context of
266 VIP17/MAL knockdown and overpression may not be identical, together these results
267 suggest that a specific level of VIP17/MAL expression is required in order to drive the

cavitation process responsible for MDCK cyst lumen formation towards the production of a single central lumen.

E-cadherin, β -catenin, gp58 and ZO-1 expression in VIP17/MAL overexpressing cysts is similar to that of control MDCK cysts.

The multiple lumen formation that we observed in VIP17/MAL overexpressing cell cysts could, in principle, arise as a consequence of a defect in the function of membrane protein polarity or sorting pathways. To assess this possibility, we examined the distribution and expression of several markers of epithelial polarity. E-cadherin is a calcium-dependent cell adhesion molecule, which binds to a catenin protein complex (α and β) to mediate cell-cell adhesion, and polarized epithelium formation.(54, 58) Polycystin-1, one of two proteins implicated in ADPKD, interacts with the E-cadherin complex containing β -catenin, and a large body of evidence suggests that aberrant β -catenin mediated Wnt signaling may be involved in cystogenesis.(4, 22, 27, 43, 45, 46, 50)

To test whether the localization of E-cadherin and β -catenin is disrupted in VIP17/MAL overexpressing cell cysts, immunofluorescence studies were performed, and protein localization was evaluated by laser scanning confocal microscopy. There is normal basolateral localization of E-cadherin in both WT (**Figure 3a**) and VIP17/MAL overexpressing cell cysts (**Figure 4a**). Under normal circumstances, β -catenin localizes to the perinuclear cytoplasm or to the basolateral membrane, where it engages with E-cadherin.(26) In cysts formed from wild-type MDCK cells (**Figure 3b**) or VIP17/MAL overexpressing cells (**Figure 4b**), β -catenin retains its classic distribution along the

basolateral membrane. Finally, immunofluorescence was used to assess the distribution of the basolateral marker antigen identified as gp58, which is the β -subunit of the Na,K-ATPase. This protein also retains a basolateral distribution independent of VIP17/MAL overexpression (**Figures 3c, 4c**). (3, 20) We conclude that VIP17/MAL overexpression does not affect the distribution of E-cadherin, β -catenin, or gp58 in an *in vitro* model of cystogenesis.

Zona occludens 1 (ZO-1) is a classic structural component of tight junctions in MDCK cells.(2) The integrity of the tight junction is important for establishing the extent and nature of the paracellular ion permeability barrier, which in turn plays a role in the mechanisms responsible for luminal fluid secretion.(13, 60) We therefore examined the localization of ZO-1 in cysts composed of wild-type MDCK cells or VIP17/MAL overexpressing MDCK cells. By immunofluorescence and confocal imaging, ZO-1 was abundantly expressed and properly localized to tight junctions in both cyst types (data not shown). We conclude that VIP17/MAL expression does not have an obvious effect on ZO-1 localization.

VIP17/MAL overexpression results in apical accumulation of gp135 with aberrant localization of this protein to the primary cilium.

Gp135, also known as podocalyxin, is endogenously expressed and localized to the apical membrane in MDCK cells.(33) VIP17/MAL overexpression results in increased apical expression of the influenza virus hemagglutinin, among other proteins (9). In VIP17/MAL overexpressing MDCK cysts, immunofluorescence localization of gp135 reveals a surprising alteration in this protein's distribution. In control MDCK

cells, gp135 is not present in the cilium that extends from the apical surface, accounting for the characteristic pattern of “ciliary exclusion” that is observed when the pattern of gp135 localization is observed in the apical surfaces of MDCK cells viewed en face.⁽¹⁷⁾ Interestingly, it appears that gp135 localizes to the primary cilium in VIP17/MAL overexpressing MDCK cells grown in three-dimensional cyst culture (**Figure 5a**). This behavior was also detected in two-dimensional cultures, in which we determined that VIP17/MAL overexpression correlates with ciliary localization of gp135 (**Figure 5b**). Gp135 is notably absent from the cilia of control MDCK cells grown either under two or three dimensional culture conditions (**Figure 5a and b**).

VIP17/MAL overexpression results in shortened or absent cilia in vitro and in vivo.

Since VIP17/MAL transgenic mice are reported to develop renal cysts, and susceptibility to the formation of renal cysts is frequently associated with perturbations that produce ciliary defects, we next examined the cilia of MDCK cysts grown *in vitro*. Untransfected MDCK cells and VIP17/MAL overexpressing MDCK cells were both suspended in a collagenous matrix, and immunofluorescence analysis, employing an antibody directed against acetylated tubulin, was used to visualize the ciliary axoneme. As shown in **Figure 6**, we found that MDCK cell cysts demonstrated long cilia that extended well into the lumen, consistent with our previous observations and those of others.⁽⁵⁵⁾ In contrast, cysts produced by VIP17/MAL overexpressing cells displayed stunted or absent cilia. Moreover, even when present, primary cilia did not appear to be protruding extensively into the lumen. Therefore, we conclude that VIP17/MAL

overexpression perturbs cilia formation, extension or stability in a model of renal epithelial cells grown in 3D culture *in vitro*.

We also evaluated the primary cilia of kidneys isolated from transgenic VIP17/MAL overexpressing mice (**Figure 7**). Immunofluorescence analysis was performed on the kidneys of adult mice using an anti-ARL13B antibody (7) to label the cilium and an anti-Na,K-ATPase antibody (41) to identify the basolateral membrane. ARL13B is the ciliary protein mutated in Joubert syndrome (5). In parallel with our *in vitro* findings, we readily observed the presence of long, protruding cilia within the lumina of the renal tubules of wild type control mice of the same genetic strain. In contrast, cilia were significantly stunted or absent in the dilated lumina/cysts of the renal tubules of in tissue from a VIP17/MAL overexpressing transgenic mouse model. The average lengths of these cilia were roughly half of those measured in similar renal tubule segments of wild type animals (6 μ M versus 12 μ M, $p < 0.01$). These studies suggest that VIP17/MAL overexpression results in the development of abnormal cilia.

DISCUSSION:

We find that VIP17/MAL overexpression results in abnormal cilia and cyst development in renal epithelial cells, *in vitro* and *in vivo*. In the well-studied MDCK cell culture model of *in vitro* epithelial cystogenesis, VIP17/MAL overexpressing cells formed multi-lumen cysts more frequently than did control cells, and their cilia were either shortened or absent. The VIP17/MAL transgenic mice are known to develop renal cysts (18), and we show that the cilia in these structures are also diminished in number and size as compared to those found in association with the epithelial cells of renal tubules from wild type animals. These phenotypes are present in the context of normal sorting of basolateral membrane proteins, including E-cadherin, β -catenin, the Na,K-ATPase and ZO-1. In contrast, the distribution of the apical marker protein gp135 is markedly abnormal in the VIP/MAL over-expressing cells. The presence of this polypeptide on the apical surface appears to be increased and, most importantly, it is no longer excluded from the cilium in the VIP17/MAL over-expressing cells. This observation suggests that over-expression of VIP17/MAL perturbs the formation or maintenance of the barrier that normally maintains the unique composition of the ciliary membrane by preventing intermixing of apical and ciliary membrane components.(30)

VIP17/MAL has been proposed to facilitate the apical delivery of several newly synthesized membrane proteins, including influenza hemagglutinin, gp80, and gp114.(9, 42) This function is supported by *in vitro* studies in which decreased levels of VIP17/MAL result in aberrant trafficking of these apical proteins to the basolateral membrane in MDCK monolayers. In contrast, overexpression of VIP17/MAL in this same cultured epithelial model system leads to expansion of the apical plasma membrane

375 surface area, suggesting increased delivery or decreased retrieval of apical
376 components.(9, 42, 61)

377 VIP17/MAL has been shown to decrease the rate of endocytosis of the aquaporin-
378 2 water channel and thus to stabilize its residence in the apical plasma membrane.(23) It
379 is therefore possible that an imbalance in the rates of endocytosis and exocytosis is
380 responsible for the capacity of VIP17/MAL overexpression to induce the development of
381 amplified renal epithelial cell membranes.(18) In contrast to the flattened cyst lining
382 epithelia observed in the most common renal cystic disease, ADPKD, the cells lining the
383 cysts of VIP17/MAL overexpressing mice exhibit ballooning or blebbing of the apical
384 membrane into the cyst lumen, with a pseudostratified morphology.(18) Collectively,
385 these data support the premise that VIP17/MAL may contribute to cystogenesis through
386 perturbations in the structure of the apical membrane induced by disrupting the strict
387 balance between endocytosis and exocytosis that normally determines the surface area of
388 the apical plasma membrane domain.

389 In genetic polycystic kidney diseases, including autosomal dominant polycystic
390 kidney disease, autosomal recessive polycystic kidney disease, and the nephronophthoses,
391 the proteins encoded by the responsible genes are often localized to the primary
392 cilium.(49) Renal cysts are therefore common features of the “ciliopathies”, the family
393 of genetic diseases attributable to perturbations on genes whose protein products
394 contribute to ciliary structure or function. The common mechanism underlying these
395 diseases involves disruption of the primary cilium or proteins that co-localize with it.(39)
396 The primary cilium is formed when the designated mother centriole is modified to
397 assume its role as the basal body beneath the cell’s apical surface.(40) Ciliogenesis

ensues, with the cell directing necessary cargo to the tip of the cilium in a process known as intraflagellar transport.

Ciliopathies can result from either abnormal transport of proteins within the cilium or from disrupted delivery of vesicles from intracellular compartments to the base of the cilium. (10, 16) Recent data suggests that while targeting of ciliary proteins to the cilium may occur via lateral transport from within the cell's apical membrane (34), there is also a component of targeted exocytosis to the base of the cilium.(15) This cargo navigates through or across the peri-ciliary membrane or ciliary necklace and is subsequently trafficked into the cilium.(28) While VIP17/MAL has not previously been implicated in ciliary trafficking, a number of other proteins similarly implicated in epithelial polarity have been shown to be involved in ciliogenesis.(11, 12, 14, 62) It is also worth noting that recent studies have shown that Septin 2, a guanosine triphosphatase is located at the base of the ciliary membrane and is thought to be part of a diffusion barrier that maintains the unique composition of the ciliary membrane.(21) When Septin 2 is absent, the structure of the ciliary membrane is destroyed and abnormal or abrogated ciliary growth occurs.

When VIP17/MAL was overexpressed in cultured MDCK cells *in vitro*, we noted that cilia were also shortened and compositionally altered, with aberrant sorting of gp135 to the cilium. These observations suggest the interesting interpretation that the barrier regulating ciliary protein trafficking had been disrupted. According to this model, VIP17/MAL overexpression may either perturb the sorting of those proteins to the cilium that are required for maintaining the ciliary barrier, or VIP17/MAL may itself directly disturb this boundary. Regardless, given this disturbance, it is perhaps expected that

ciliary structure and thereby function is altered, leading to shortened and developmentally altered cilia, such as those seen in Figures 6, and to an *in vivo* phenotype that bears the hallmarks of a ciliopathy (Figure 7). It is important to note that our analysis of ciliary length in wild type and VIP17/MAL overexpressing kidneys was limited to a relatively small number of specimens, and thus the results need to be interpreted with caution. Nevertheless, our data suggest the novel possibility that VIP17/MAL overexpression produces renal cysts *in vivo* by inducing the production of over-abundant apical membrane, which in turn disrupts the composition and structure of the cilium. Thus, the cysts observed in VIP17/MAL overexpression may be seen as arising as the consequence of a “secondary ciliopathy.”

These studies highlight the relationship between epithelial cell polarization and ciliogenesis, which results in cystogenesis when disrupted. VIP17/MAL appears to be a central component involved in both of these processes. When evaluated collectively, these data suggest a connection between cilia formation, post-Golgi sorting mechanisms, and epithelial cell polarization in renal cystogenesis.

GRANTS:

This work was supported by NIH MSTP TG 5T32GM07205 and F30DK083221 to VT and NIH DK57328 and DK17433 to MJC. These studies made use of imaging resources provided through the Center for Polycystic Kidney disease Research at Yale (NIH DK090744)

AUTHOR CONTRIBUTIONS:

V.T. designed and performed the experiments and wrote the manuscript. K.M. and M.C. assisted with and helped to analyze the *in vitro* and *ex vivo* experiments, respectively. N.S-W. developed the VIP17/MAL overexpressing mouse model. MJC directed the project and assisted with manuscript preparation.

DISCLOSURES:

The authors of this manuscript have no conflicts of interests or disclosures.

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FIGURE LEGENDS:

Figure 1: Stable VIP17/MAL expression.

a) Immunofluorescence analysis of MDCK cells stably transfected with Flag-VIP17/MAL. The apical localization of VIP17/MAL is revealed with poly-Flag (red) in both *en face* extended depth of focus (bottom panel) and in XZ cross section (top panel) images. b) Western blot analysis of MDCK cell lines stably transfected with VIP17/MAL. A specific band is detected at 17kD. c) VIP17/MAL (green) is detectable in a punctate pattern in some but not all cilia (labeled with anti-acetylated tubulin; red) in transfected MDCK cells.

Figure 2: VIP17/MAL overexpression alters morphology of cultured MDCK cysts.

(a) Representative images of WT MDCK (top) and VIP17/MAL overexpressing MDCK (bottom) cysts, acquired by light microscopy, demonstrating more multi-lumen (arrows) cysts produced by cells overexpressing VIP17/MAL. b) Quantitation of microscopic images revealing an increased incidence of multilumen cysts derived from VIP17/MAL overexpressing MDCK cells** $p < 0.01$ (n=100 cysts)

Figure 3: Localization of basolateral membrane markers in three-dimensional WT MDCK cell cysts.

Immunofluorescence analysis of representative wild type MDCK cell cysts demonstrates the localization of (a) E-cadherin, (b) β -catenin, and (c) gp58 (green) at the basolateral membrane. Propidium iodide (blue) was used to label nuclei. Merged color images are depicted in the right hand panel. All scale bars depicted are 20 μ m.

Figure 4: Basolateral membrane marker expression is unchanged by overexpression of VIP17/MAL.

Immunofluorescence analysis of representative VIP17/MAL overexpressing MDCK cell cysts with antibodies to the basolateral markers (a) E-cadherin, (b) β -catenin, and (c) gp58 (green) demonstrates normal basolateral localization, similar to that detected in control MDCK cysts. Hoescht staining (blue) was used to label nuclei. Mono-FLAG (red) indicates VIP17/MAL expression. Merged color images are depicted in the right hand panel. All scale bars depicted are 20 μ m.

Figure 5: VIP17/MAL overexpression results in gp135 apical localization and ciliary localization in an in vitro cyst culture model.

(a) Representative WT MDCK (top) and VIP17/MAL overexpressing cell cysts (bottom) depicting expression of the apical marker gp135 (red) at the apical membrane (thick arrow) and in the cilium (thin arrow) (alpha-tubulin; green) in cells expressing VIP17/MAL. (b) Gp135 (red) is present in the primary cilia of VIP17/MAL overexpressing MDCK cells grown in 2D (thin arrows, bottom panel), but is notably absent from WT MDCK cilia and from the ciliary exclusion zones in the apical membranes of WT MDCK cells (thin arrows, top panel). Orthogonal images of the individual cilia indicated by the arrow heads are shown in the upper right corners of the top and bottom panels. All scale bars depicted are 10 μ M.

Figure 6: VIP17/MAL overexpression results in aberrant ciliogenesis in an in vitro three-dimensional cyst culture model.

MDCK cells suspended in Matrigel were analyzed by immunofluorescence to localize acetylated tubulin (green). Nuclei are labeled with propidium iodide (red). Prominent cilia are seen protruding into the apical lumen in wild-type MDCK cysts (top), while very few, shortened cilia are seen in VIP17/MAL overexpressing cysts (bottom). Arrows point to multi-lumen cysts.

Figure 7: VIP17/MAL transgenic mice have abnormal cilia.

Immunofluorescence analysis to detect cilia in control (CTRL) and VIP17/MAL transgenic mice. Renal sections were labeled with antibody directed against the ciliary protein, Arl13b (red) and the Na,K-ATPase (green). Control mice display readily detectable, long cilia protruding into the distal tubule lumen, while VIP17/MAL transgenic mice display fewer and smaller cilia within their dilated lumina/cysts. Scale bars (lower right of both panels) are 10 μ M.

Figure 1

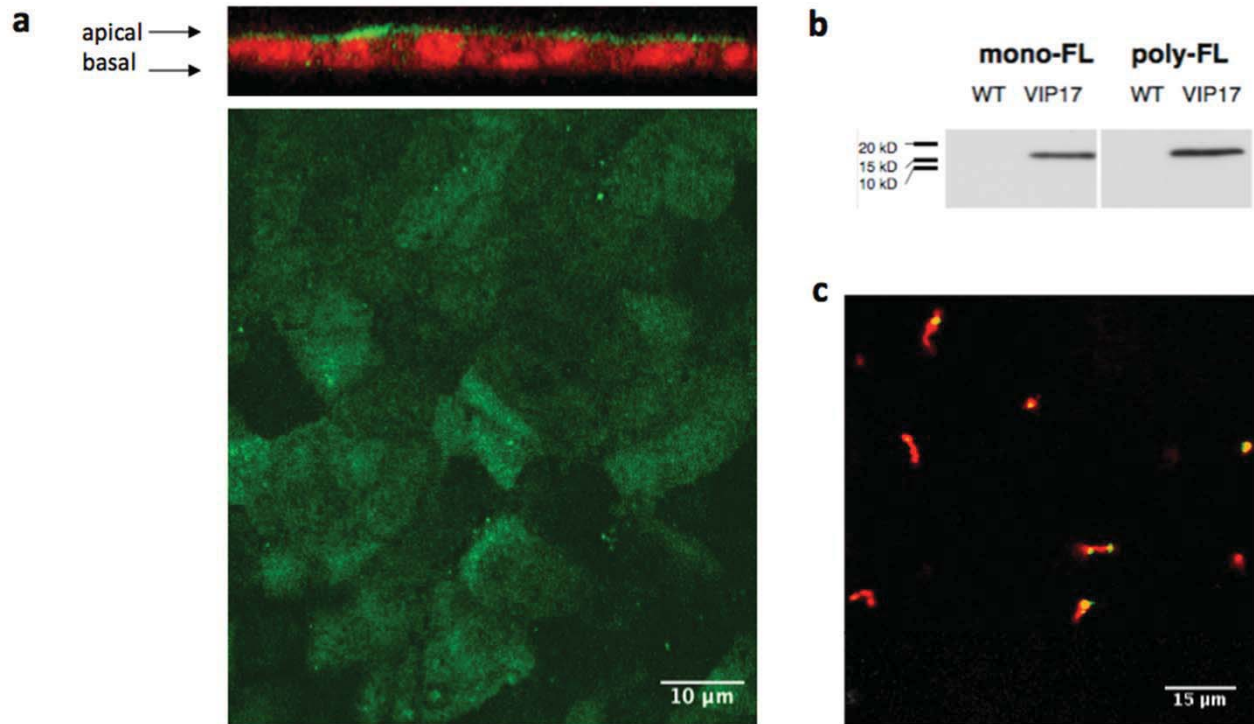


Figure 2

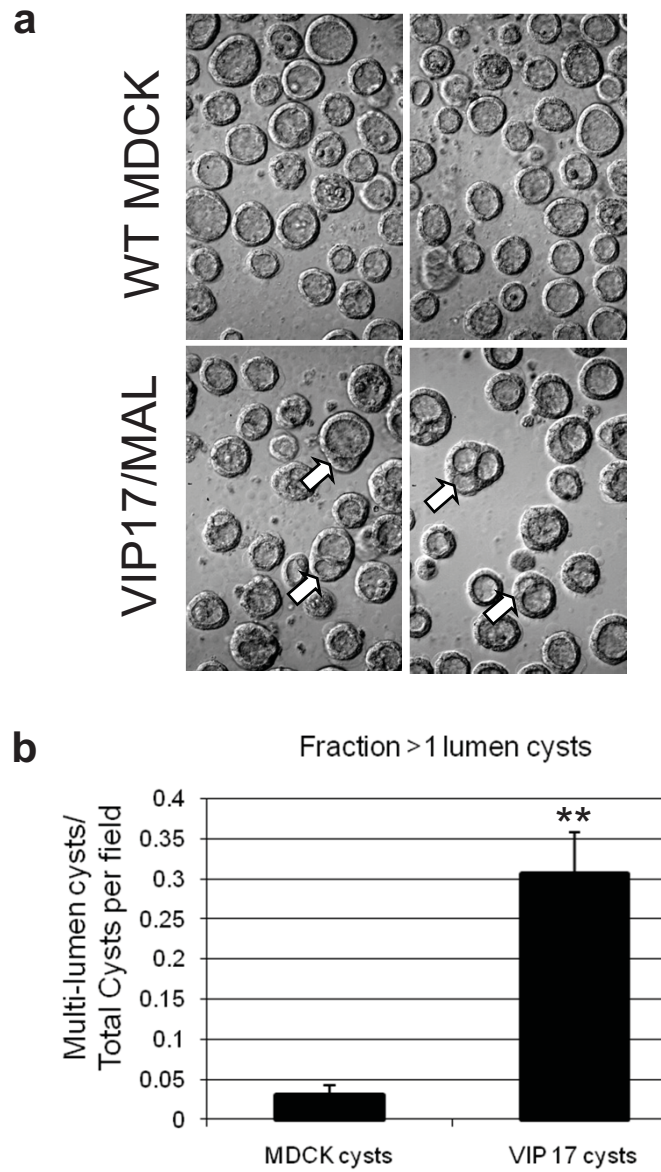


Figure 3

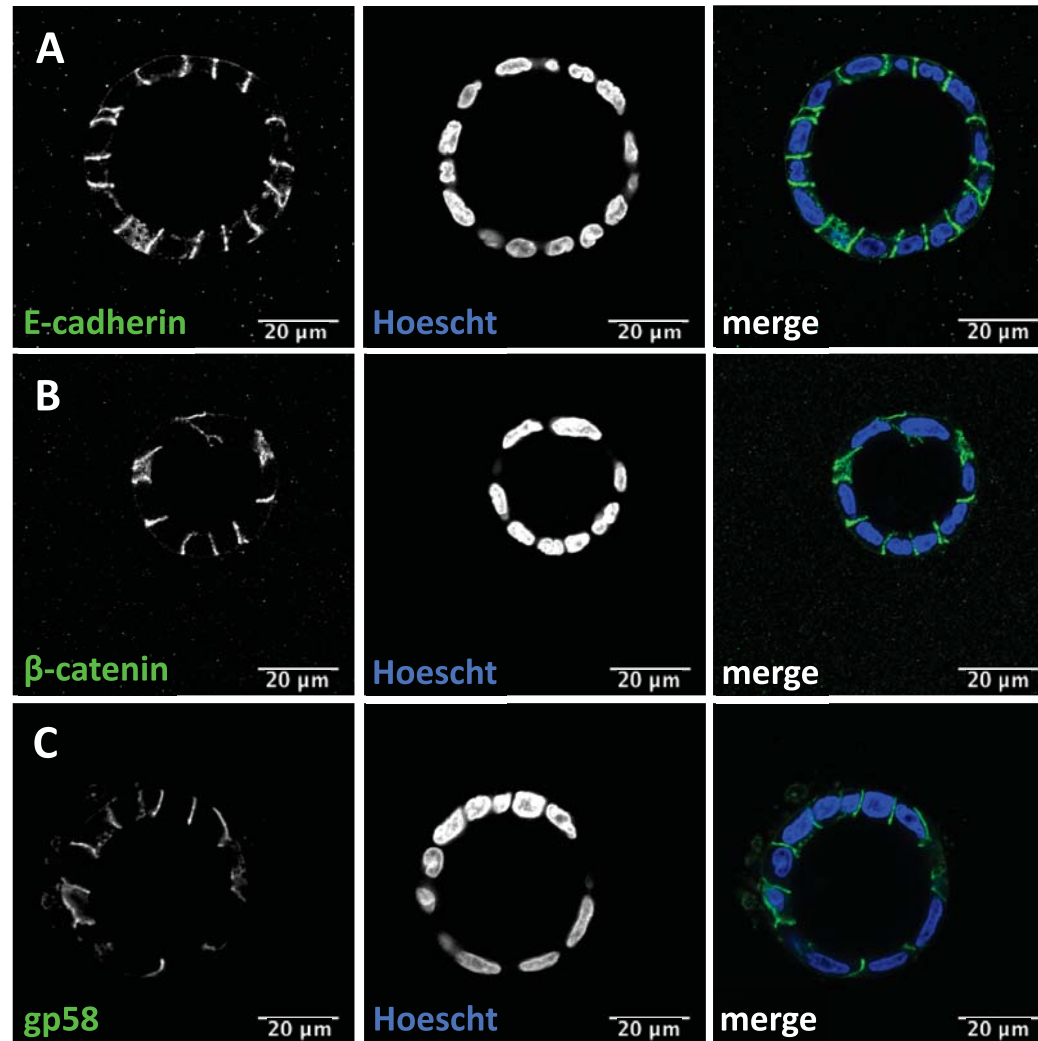


Figure 4

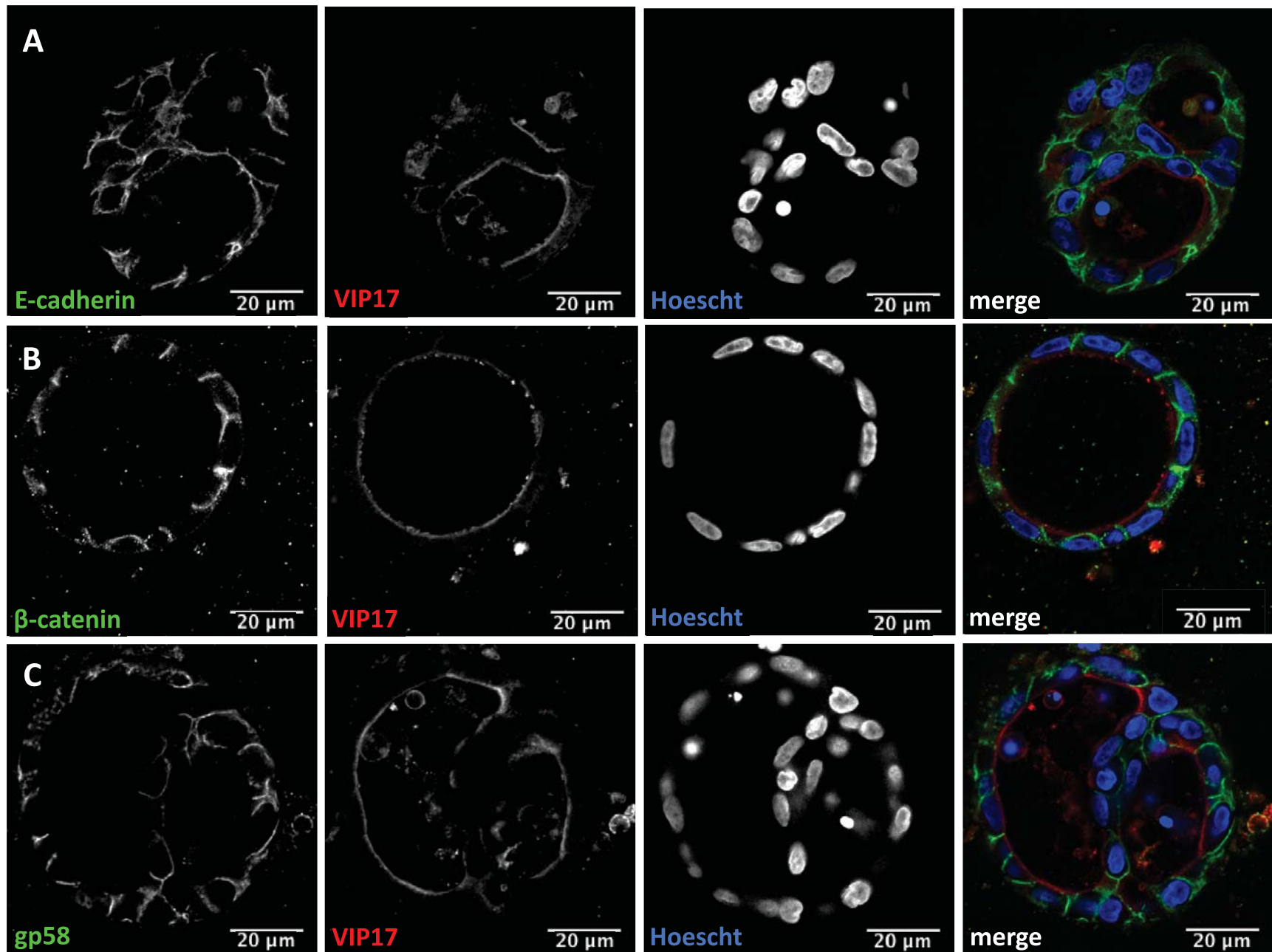


Figure 5

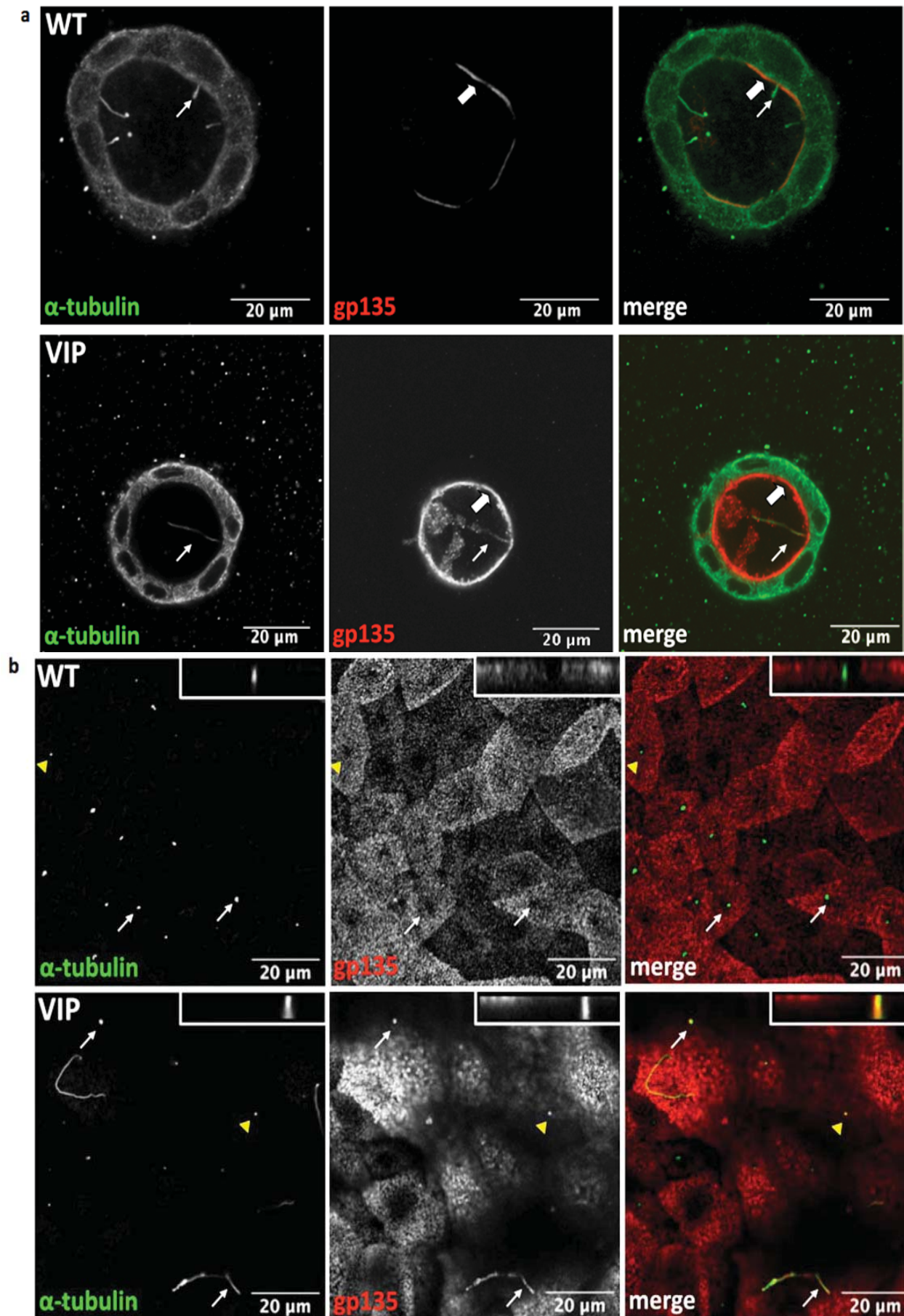


Figure 6

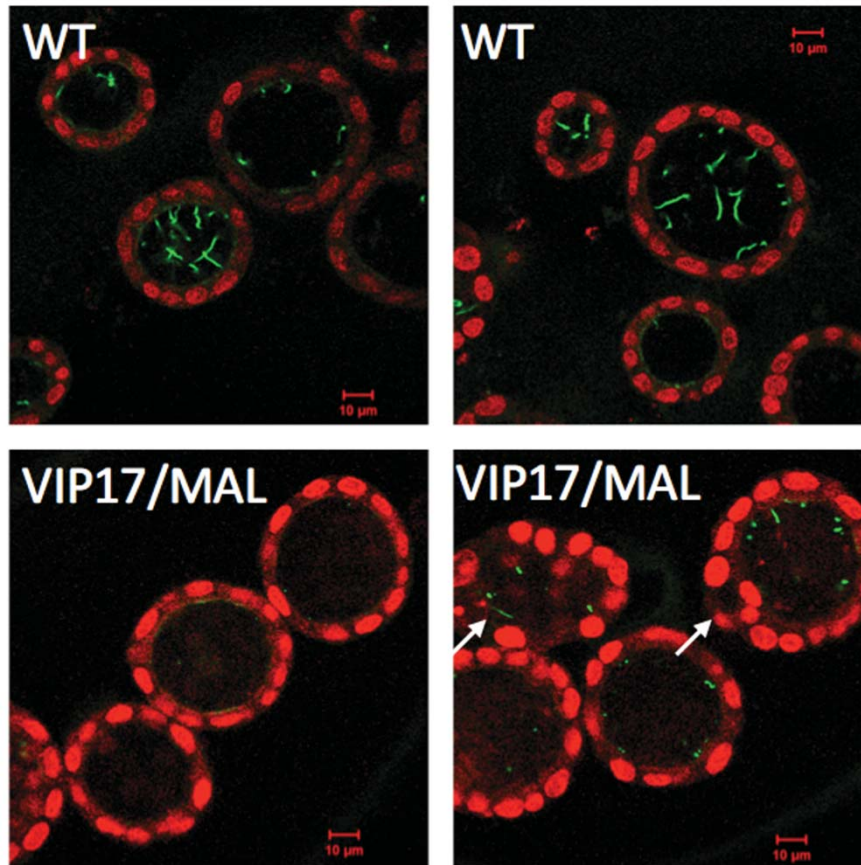


Figure 7

