APPENDIX

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Appendix Figure S1

Representative transmission electron microscopy images from serial cross sections of the hermaphrodite amphid sensory pore in WT, *rabs-5(ok1513)* and *vps-45(tm0246)* worms. The entire pore is shown in the large panels; individual cilia are shown at higher magnifications in the small panels. Red outline denotes the PCMCs. The schematics show the the section positions (colour coded) and the ultrastructure phenotypes observed. For simplicity, the cartoons of the pores in longitudinal orientation only show 3 out of the 10 channel axonemes. PCMC; periciliary membrane compartment. sMT; singlet microtubules.

Appendix Figure S2

A. Representative transmission electron microscopy images from serial cross sections of the male-specific cephalic (CEP and CEM) sensory pore in WT, *rabs-5(ok1513)* and *vps-45(tm0246)* worms. CEM and CEP cilia outlined in pink and yellow, respectively. Neighbouring OLQ cilium outlined in green. PCMC; periciliary membrane compartment. Left images show the entire pore; smaller right-hand images show indicated cilia at higher magnifications. Blue arrowheads denote vesicles in the PCMC of CEM cilia. Yellow arrowheads denote extracellular vesicles in the sensory pore lumen. Schematics show the

CEP, CEM and OLQ cilia and associated pores in longitudinal and cross section, and indicate the ultrastructural phenotypes observed, as well as the section positions (colour coded). Note that whilst the proximal and middle (doublets and singlets; (Silva et al. Curr Biol. 2017 Apr 3; 27(7):968-980)) portions of the mutant CEM cilia are normal, we cannot tell from our images if the distal portion is normal or not in the mutants.

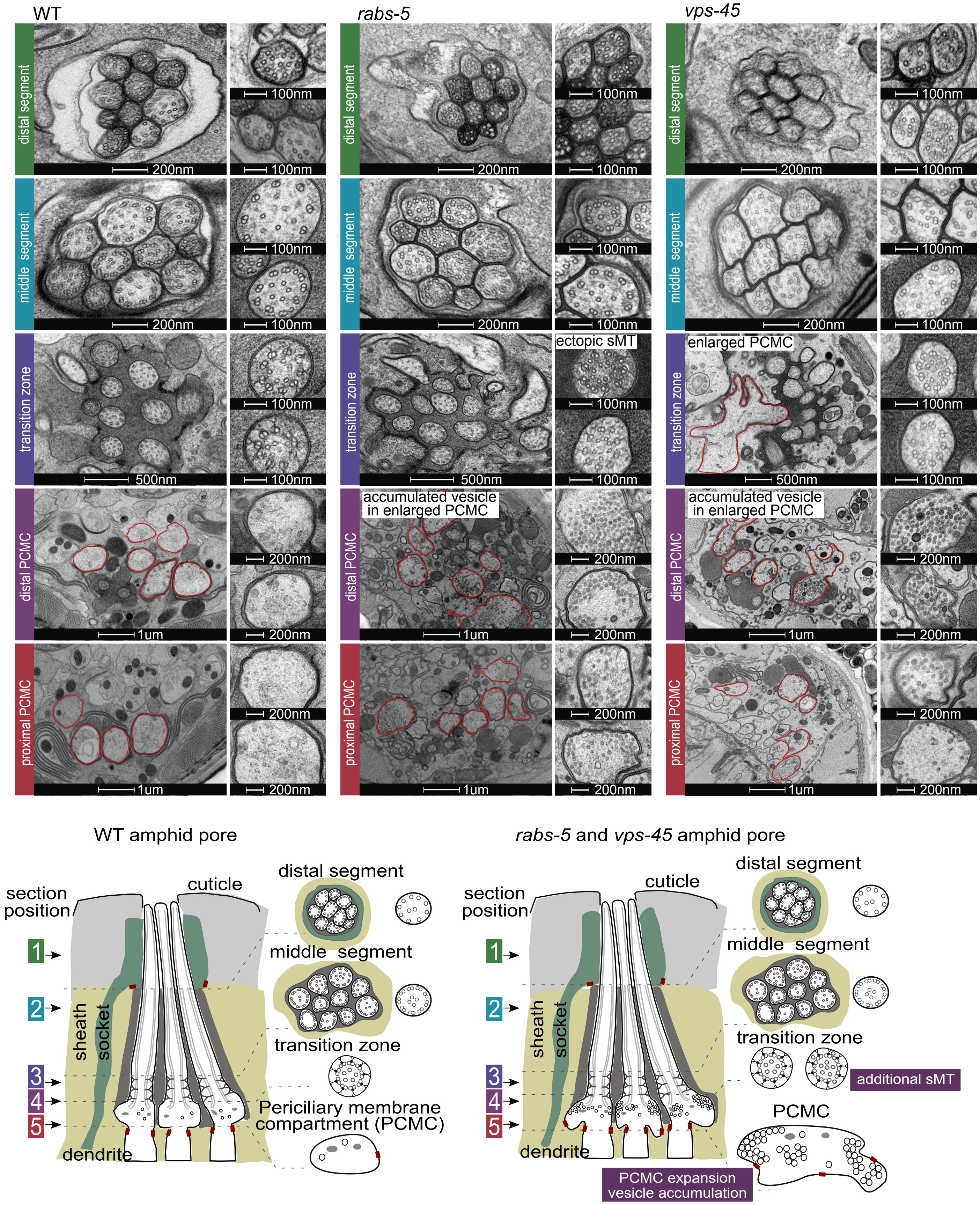
B. Representative transmission electron microscopy images from serial cross sections of the hermaphrodite inner labial sensory pore in WT, *rabs-5(ok1513)* and *vps-45(tm0246)* worms. IL1 cilium outlined in dark blue. IL2 cilium outlined in light blue.

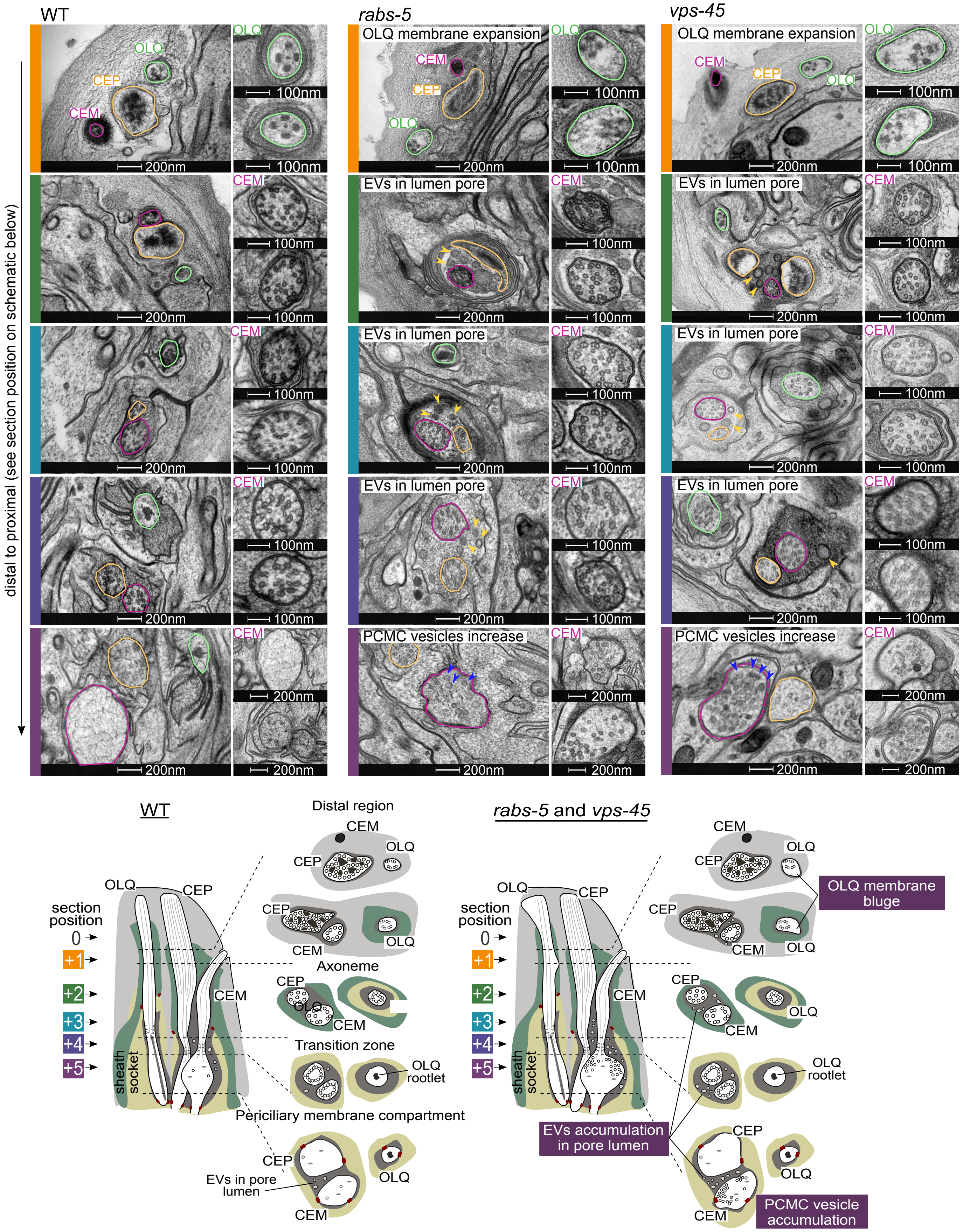
Appendix Table S1 List of *C. elegans* genes and corresponding alleles screened for cilium structure and function defects (**Fig 1A**).

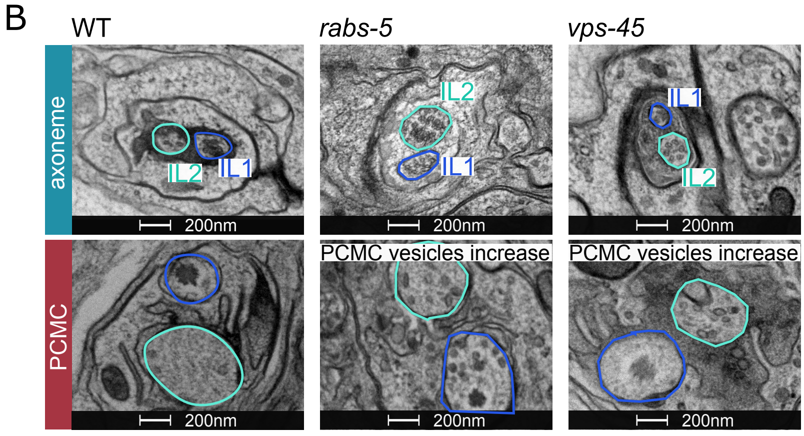
Appendix Table S2 *C. elegans* strains used in this study.

Appendix Table S3. Primer used in this study to genotype by PCR the indicated *C. elegans* mutant alleles.

Appendix Figure S1, related to Figure 4







Appendix Figure S2, related to Figure 4

Appendix Table S1:

List of *C. elegans* genes and corresponding alleles screened for cilium structure and function defects

C. elegans gene	allele	human orthologue	
arf-1.2	*ok796*	ARF1	ADP ribosylation factor 1
asm-2	*gk293929*	SMPD1	sphingomyelin phosphodiesterase 1
cav-1	*ok2089*	CAV1	caveolin 1
cav-2	*hc191*	CAV2	caveolin 2
dgk-1	*ok1462*	DGKQ	diacylglycerol kinase theta
eea-1	*ok1040*	EEA1	early endosome antigen 1
gta-1	*ok517*	GABAT	4-aminobutyrate aminotransferase
hyl-1	*ok976*	CERS6	ceramide synthase 6
hyl-2	*ok1766*	CERS4	ceramide synthase 4
M01E5.2	*ok2552*	MTG2	mitochondrial ribosome associated GTPase 2
mec-2	*e75*	STOM	stomatin
mtm-6	*ok330*	MTMR6	myotubularin related protein 6
mtm-9	*ok3523*	MTMR9	myotubularin related protein 9
mtr-4	*ok2642*	SKIV2L2	Ski2 like RNA helicase 2
nex-1	*gk148*	ANX13	annexin A13
nex-2	*ok764*	ANX7	annexin A7
nex-3	*gk385*	ANX5	annexin A5
nex-4	*gk102*	ANX6	annexin A6
num-1	*bc365*	NUMBL	NUMB like, endocytic adaptor protein
prmn-1	*gk545*	PROM1	prominin 1
rab-10	*ok1494*	RAB10	RAB10
rabn-5	*ok1555*	RABPT5	rabaptin-5, RAB GTPase binding effector protein 1
rabs-5	*ok1513*	RABSN	rabenosyn, RAB effector
rabx-5	*tm1215*	RABGEF1	rabex5, RAB guanine nucleotide exchange factor 1
ric-19	*ok833*	ICA1	islet cell autoantigen 1
ric-4	*md1088*	SNAP25	synaptosome associated protein 25
ric-8	*md1909*	RIC8A	RIC8 guanine nucleotide exchange factor A
rme-1	*b1045*	EHD1	EH domain containing 1
rme-2	*b1008*	LRP2	LDL receptor related protein 2
rme-6	*b1014*	GAPVD1	GTPase activating protein and VPS9 domains 1
rme-8	*b1023*	DNAJC13	DnaJ heat shock protein family (Hsp40) member C13
sax-7	*ok1244*	NRCAM	neuronal cell adhesion molecule
stn-2	*ok2417*	SNTG2	syntrophin gamma 2
syx-7	*gk338314*	STX12	syntaxin 12
tat-3	*gk819359*	ATP10A	ATPase phospholipid transporting 10A
tat-6	*ok1984*	ATP9B	ATPase phospholipid transporting 9B
tin-9.1	*ok2194*	TIMM9	translocase of inner mitochondrial membrane 9
tmem-135	*ok1646*	TMEM135	transmembrane protein 135
unc-1	*e94*	STOM	stomatin
unc-24	*e138*	STOML1	stomatin like 1
unc-44	*e362*	ANK1	ankyrin 1
vps-45	*tm0246*	VPS45	vacuolar protein sorting 45 homolog
vps-54	*ok1463*	VPS54	VPS54, GARP complex subunit
wdfy-2	*ok3592*	WDFY2	WD repeat and FYVE domain containing 2

Appendix Table S2: *C. elegans* strains used in this study

N2 (Bristol)

him-5(e1490)

osm-5(p813)

bbs-8(nx77)

arf-1.2(ok796)

asm-2 (gk293929)

cav-1(ok2089)

cav-2(hc191)

dgk-1(ok1462)

eea-1(ok1040)

gta-1 (ok517)

hyl-1(ok976)

hyl-2(ok1766)

M01E5.2 (ok2552)

mec-2(e75)

mtm-6 (ok330)

mtm-9 (ok3523)

mtr-4 (ok2642)

nex-1(gk148)

nex-2(ok764)

nex-3(gk385)

nex-4(gk102)

num-1(bc365)

prmn-1(gk545)

rab-10(ok1494)

rabn-5(ok1555)

rabs-5(ok1513)

rabx-5(tm1215)

ric-19(ok833)

ric-4(md1088)

ric-8(md1909)

rme-1(b1045)

rme-2(b1008)

rme-6(b1014)

rme-8(b1023)

sax-7(ok1244)

stn-2(ok2417)

syx-7 (gk338314)

tat-3(gk819359)

tat-6(ok1984)

tin-9.1(ok2194)

tmem-135 (ok1646)

unc-1(e94)

unc-24(e138)

unc-44(e362)

vps-45(tm0246)

vps-54 (ok1463)

wdfy-2(ok3592)

N2;*oqEx306[rabs-5* p::*gfp* + *unc122* p::*dsRed*]

rabs-5(ok1513 ;*oqEx307* [*rabs-5* p::*rabs-5* + *unc122* p::*dsRed*]

vps-45 (tm0246); oqEx308[arl-13 p::*vps45* + *unc122* p::*dsRed*]

rabs-5(ok1513) ;*oqEx401[arl-13* p::*rfp::rabs-5(WT)* + *unc122* p::*dsRed*]

rabs-5(ok1513) ;*oqEx402[arl-13* p::*rfp::rabs-5(ΔZN)* + *unc122* p::*dsRed*]

rabs-5(ok1513) ;*oqEx403[arl-13* p::*rfp::rabs-5(ΔFYVE)* + *unc122* p::*dsRed*]

rabs-5(ok1513 ;*oqEx404[arl-13* p::*rfp::rabs-5(ΔRBD)* + *unc122* p::*dsRed*]

N2;*oqEx405* [*arl-13* p::*rfp::rabs-5(WT)* + *unc122* p::*gfp*]

N2*;oqEx406* [*arl-13* p::*rfp::rabs-5(ΔZN)* + *unc122* p::*gfp*]

N2;*oqEx407[arl-13* p::*rfp::rabs-5(ΔFYVE)* + *unc122* p::*gfp*]

N2;*oqEx408[arl-13* p*::rfp::rabs-5(ΔRBD) + unc122* p::*gfp*]
N2;*oqEx409[arl-13* p*::vps-45::gfp + unc122* p::*dsRed*]
N2;*oqEx410[arl-13* p*::gfp::rab-5 + unc122* p::*dsRed*]
N2;*oqEx411[arl-13p::wdfy-2::gfp + unc122* p::*dsRed*]
N2;*oqEx412[arl-13* p*::rfp::eea-1 + unc122* p::*gfp*]
N2;*oqEx413[arl-13* p*::dpy-23::gfp + unc122* p::*dsRed]*
N2;*oqEx414[arl-13* p*::gfp::cav-1 + unc122* p::*dsRed*]
him-5(e1490 ;*oqEx415[pkd-2* p*::rfp::rabs-5(WT) +unc122* p::*dsRed*]
him-5(e1490 ;*oqEx416[pkd-2* p*::rfp::cav-1 +unc122* p::*dsRed*]
him-5(e1490 ;*oqEx417[pkd-2* p*::wdfy-2::rfp +unc122* p::*dsRed*]
N2;*oqEx418[str-2* p::*jbts-14::gfp + str-2::rfp + unc122* p::*gfp*]
N2;*oqEx204[arl-13* p::*gfp::rab-5(Q78L) + rol-6* (su1006)]
N2;*oqEx205[arl-13* p::*gfp ::rab-5(S33N) + rol-6* (su1006)]
him-5(e1490);myIs1[pkd-2::gfp + unc-122p::gfp] IV
N2;*oqEx58[arl-13* p*::arl-13::gfp + rol-6(su1006)*]
N2;oy*Ex[srbc-66::gfp + unc122* p*::dsRed]*
N2;*nxEx[tram-1::tdTomato + bbs-8* p*::mks-2::gfp + rol-6* (su1006)]
lin-15(n765 ;*kyIs141[osm-9::gfp + lin-15(+)*]
N2;*nxEx289[rpi-2::gfp + xbx-1 ::tdTomato + rol-6(su1006)*]
N2;*kyIs104[str-1* p*::gfp*]
N2;*mnIs17[osm-6* p::*osm-6 ::gfp*]

Appendix Table S3_Primer used for genotyping the indicated mutant allele

primer name	**primer sequence**	**allele genotyped**
cav-1_F	AGGCGAAGTTACATTAGGCTG	*cav-1(ok2089)*
cav-1_R	GCACTCTTTCTACGCAATCG	*cav-1(ok2089)*
cav-1_Pn	TGTGTCAGTAGGGAAATCGC	*cav-1(ok2089)*
eea-1_F	ATTTAAGCGGAACAGCCTCA	*eea-1(b1040)*
eea-1_R	CTTCCAATTCTCTTGCTCG	*eea-1(b1040)*
eea-1_Pn	GAAATCAGAGGGAATCCGG	*eea-1(b1040)*
rabs-5_F	GATTGGAGCAACTGGTTCAG	*rabs-5(ok1513)*
rabs-5_R	ATGATCCGTTTGTATTGTATCATC	*rabs-5(ok1513)*
rabs-5_Pn	CGGTAAAATTTCATCAGGAG	*rabs-5(ok1513)*
rabx-5_F	CGCTTAAGGAGAGTGGTGA	*rabx-5(tm1215)*
rabx-5 _R	ATTCTTCGCAAAATCCTGAC	*rabx-5(tm1215)*
rabx-5_Pn	CTCGCCATGCTTATCTGAC	*rabx-5(tm1215)*
rme-1_F	CTTATCCGGAGAAAAGCAAA	*rme1(b1045)*
rme-1_R	TACCATGAAGCAGTCGACC	*rme1(b1045)*
rme-1_Pn	GAATGATCCCAAATAGACACG	*rme1(b1045)*
rme-6(WT)_F	GCAATCATCAGTCCGC	*rme-6(b1014)*
rme-6(b1014)_F	GGCAATCATCAGTCCGT	*rme-6(b1014)*
rme-6_R	TTTCTAAAACTGACGTCCCTC	*rme-6(b1014)*
vps-45_F	AATGCAAATTCTCCTGCTCT	*vps-45(tm0246)*
vps-45_R	TTCAACTGCAACAATAGCG	*vps-45(tm0246)*
vps-45_Pn	ACAGTGTCATGCGCATTT	*vps-45(tm0246)*
wdfy-2_F	ATGATAGATCCGTTCGCCTG	*wdfy-2(ok3592)*
wdfy-2_R	AGAAGGGGCAGAGCAAAC	*wdfy-2(ok3592)*
wdfy-2_Pn	GAAAGTGGTCGGATTGAGAC	*wdfy-2(ok3592)*