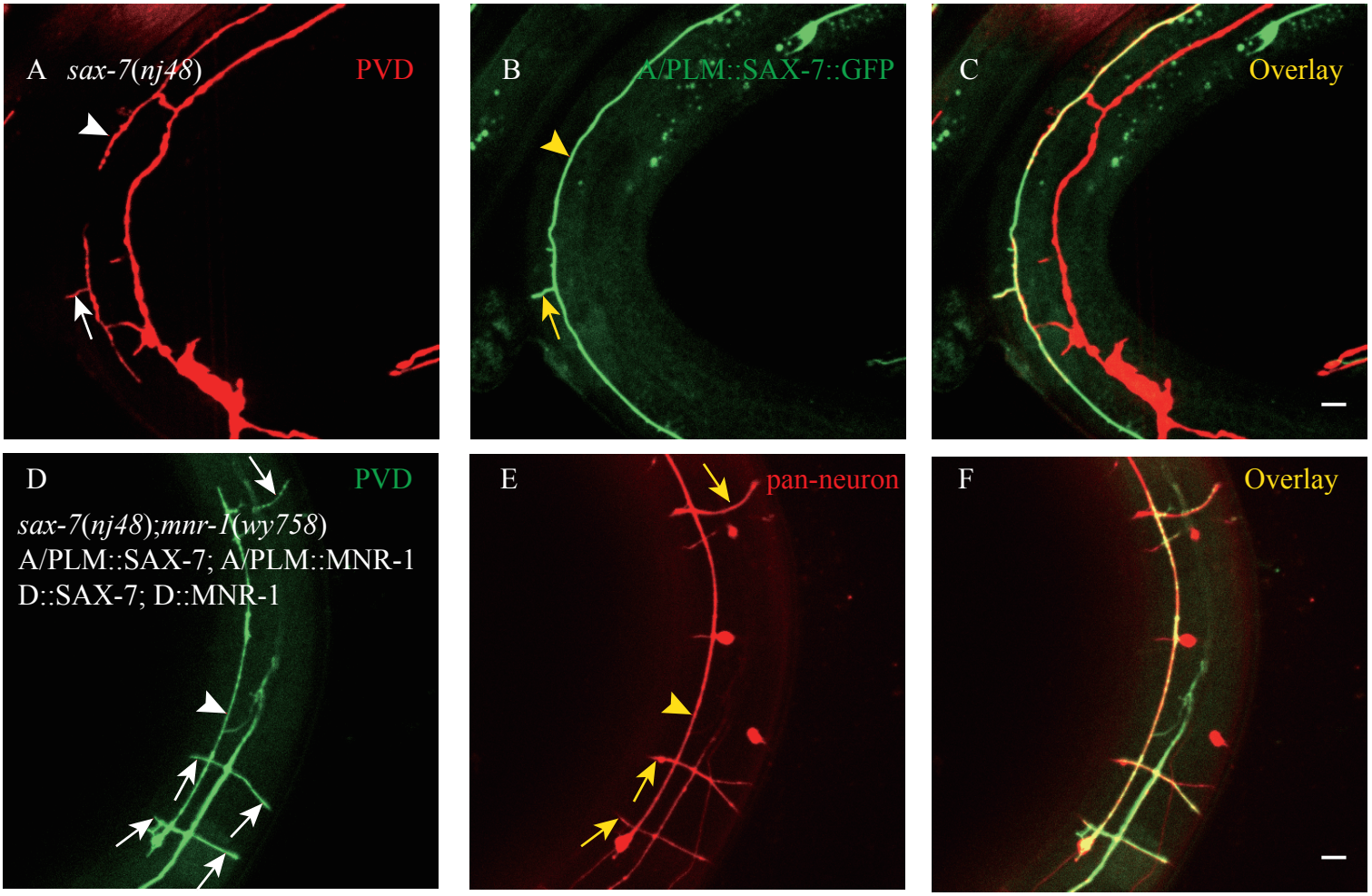
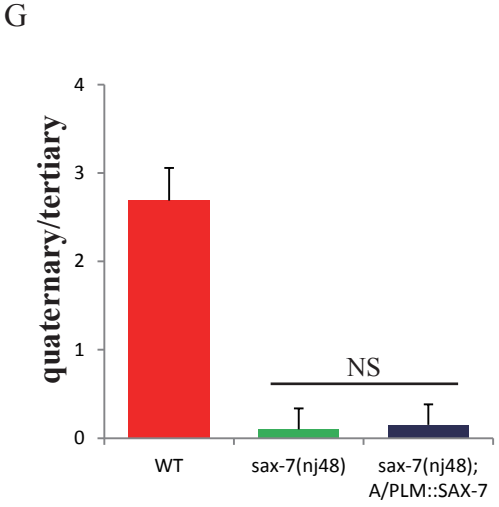
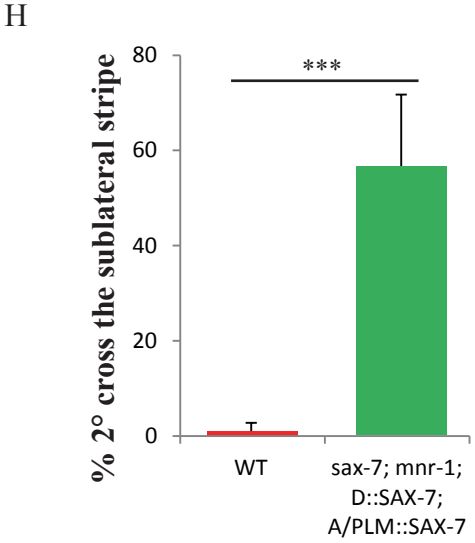
Fig. S1


A sax-7(nj48) PVD
B A/PLM::SAX-7::GFP
C Overlay
D PVD
sax-7(nj48);mnr-1(wy758)
A/PLM::SAX-7; A/PLM::MNR-1
D::SAX-7; D::MNR-1
E pan-neuron
F Overlay


G
quaternary/tertiary
4
3
2
1
0
NS
WT
sax-7(nj48)
sax-7(nj48); A/PLM::SAX-7


H
% 2° cross the sublateral stripe
80
60
40
20
0
***
WT
sax-7; mnr-1; D::SAX-7; A/PLM::SAX-7

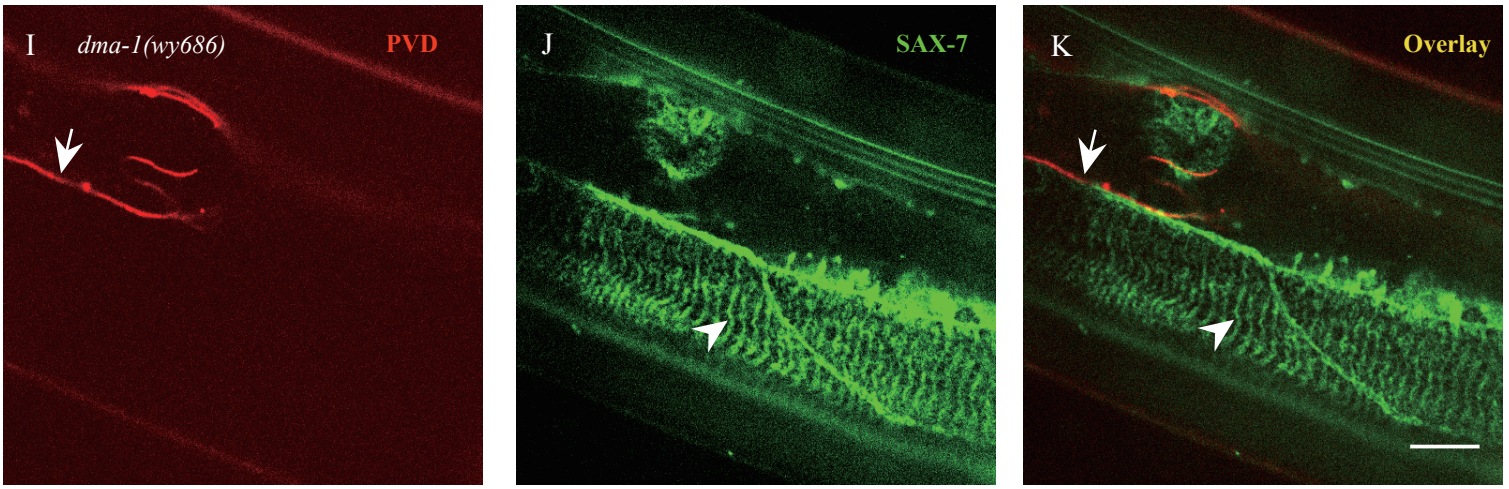
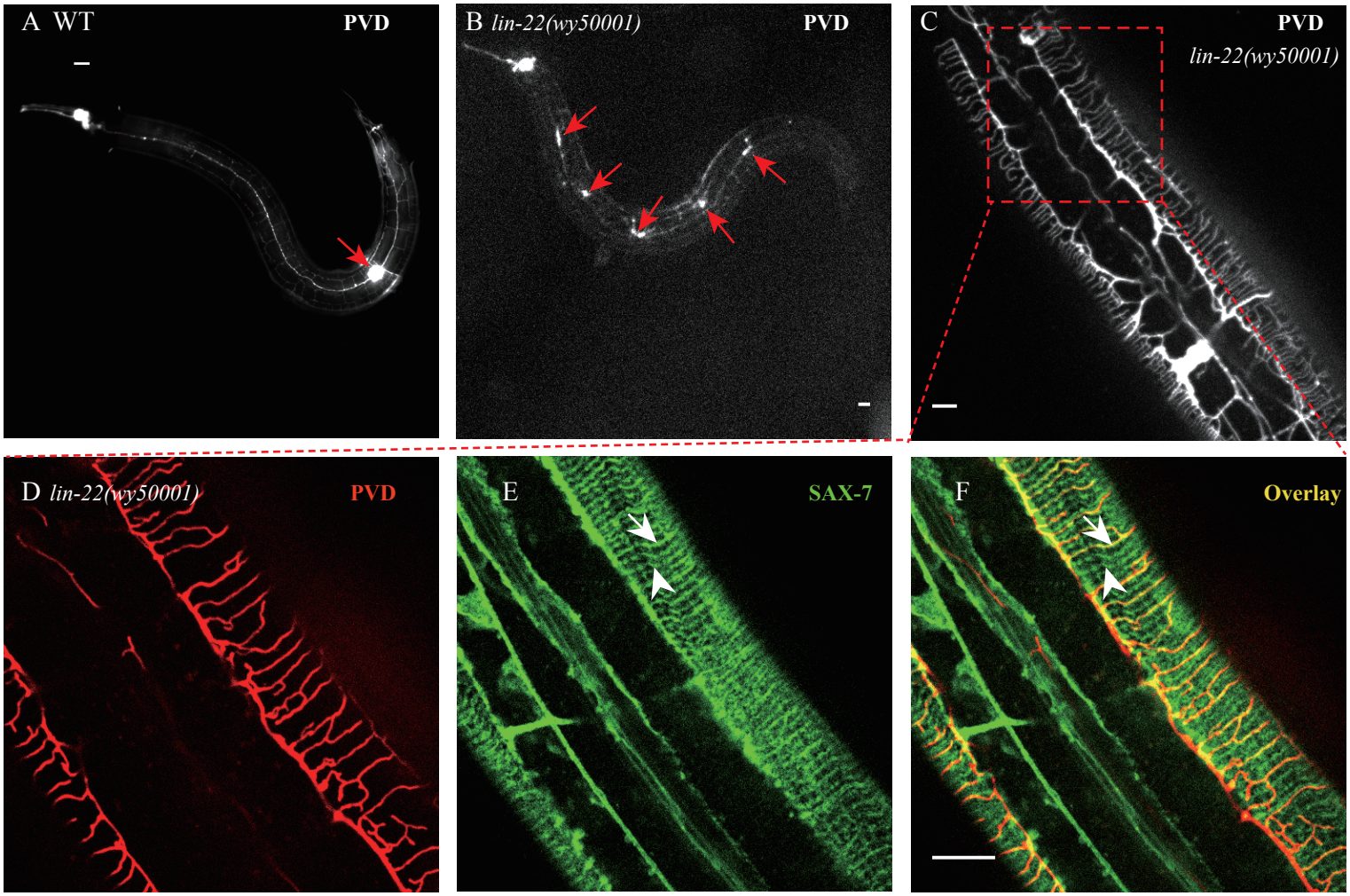
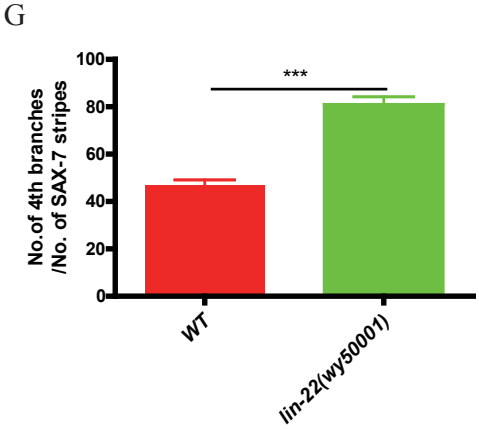

I dma-1(wy686) PVD
J SAX-7
K Overlay

Fig. S2


A WT
PVD
B lin-22(wy50001)
PVD
C
PVD
lin-22(wy50001)
D lin-22(wy50001)
PVD
E
SAX-7
F
Overlay


G
No.of 4th branches /No. of SAX-7 stripes
100
80
60
40
20
0
***
WT
lin-22(wy50001)

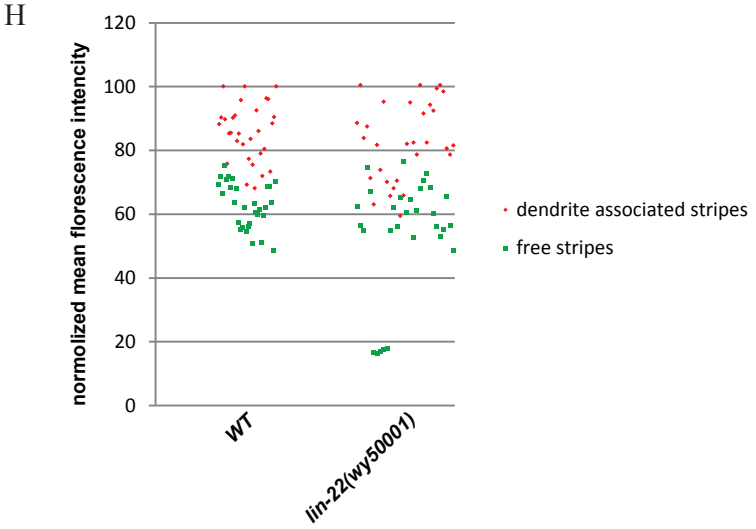

H
normolized mean florescence intencity
120
100
80
60
40
20
0
WT
lin-22(wy50001)
dendrite associated stripes
free stripes

Fig. S3

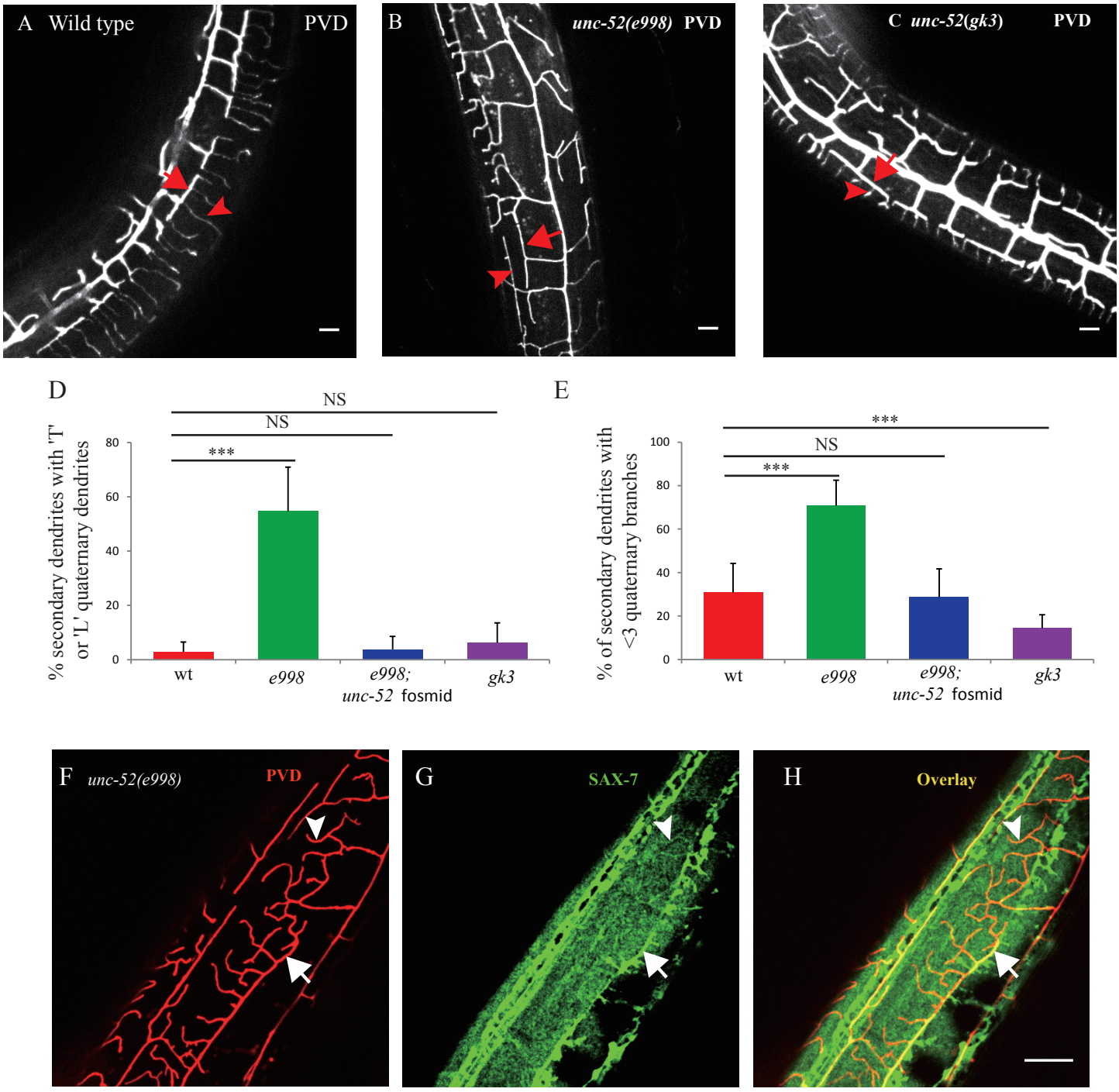

A Wild type PVD
B unc-52(e998) PVD
C unc-52(gk3) PVD
D
% secondary dendrites with 'T' or 'L' quaternary dendrites
NS
NS
***
0
20
40
60
80
wt
e998
e998; unc-52 fosmid
gk3
E
% of secondary dendrites with <3 quaternary branches
***
NS
***
0
20
40
60
80
100
wt
e998
e998; unc-52 fosmid
gk3
F unc-52(e998) PVD
G SAX-7
H Overlay

Fig. S4

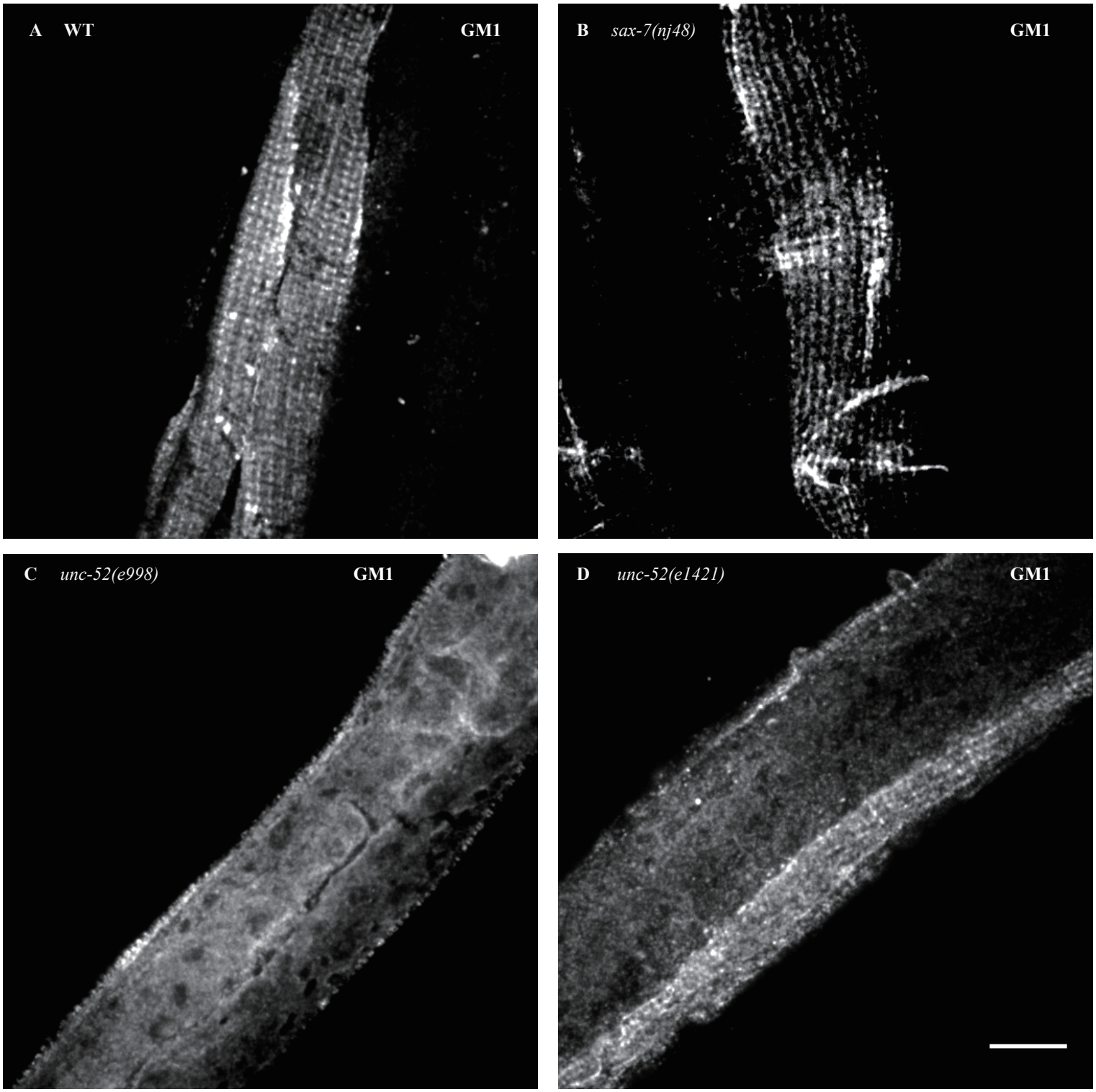
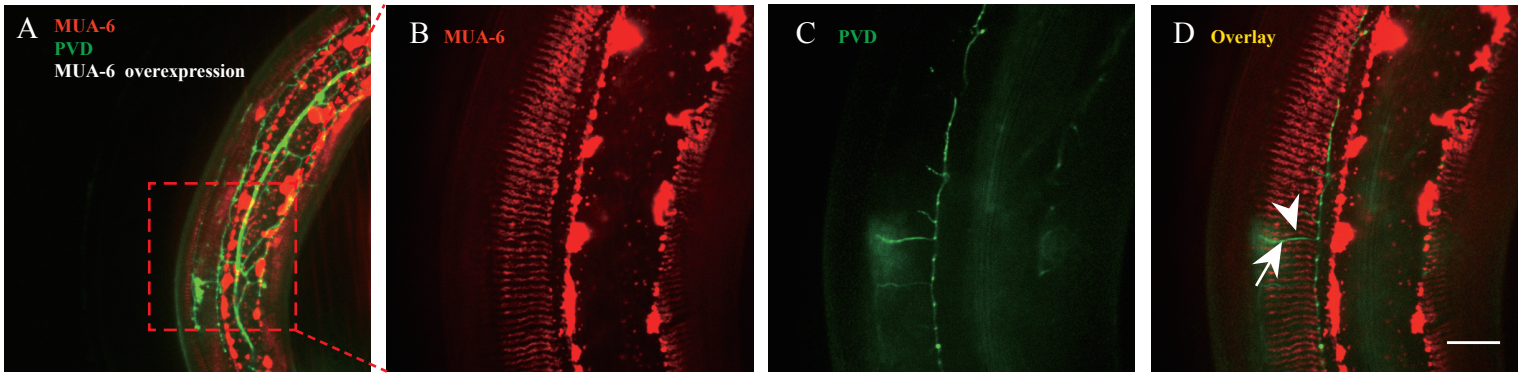
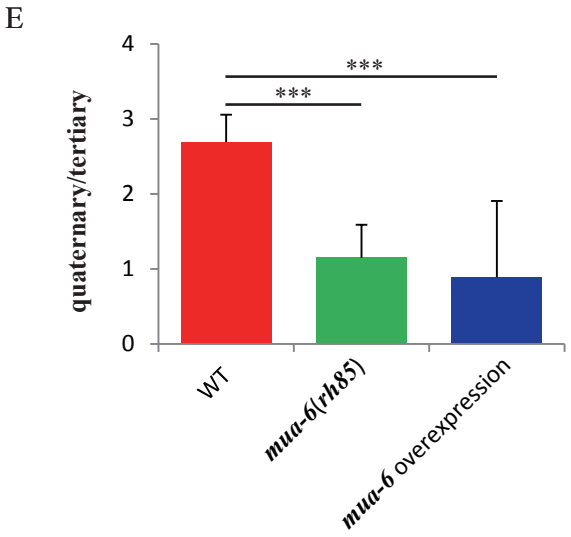


Fig. S5


A
MUA-6
PVD
MUA-6 overexpression
B MUA-6
C PVD
D Overlay


E
quaternary/tertiary
4
3
2
1
0
***
***
WT
mua-6(rh85)
mua-6 overexpression

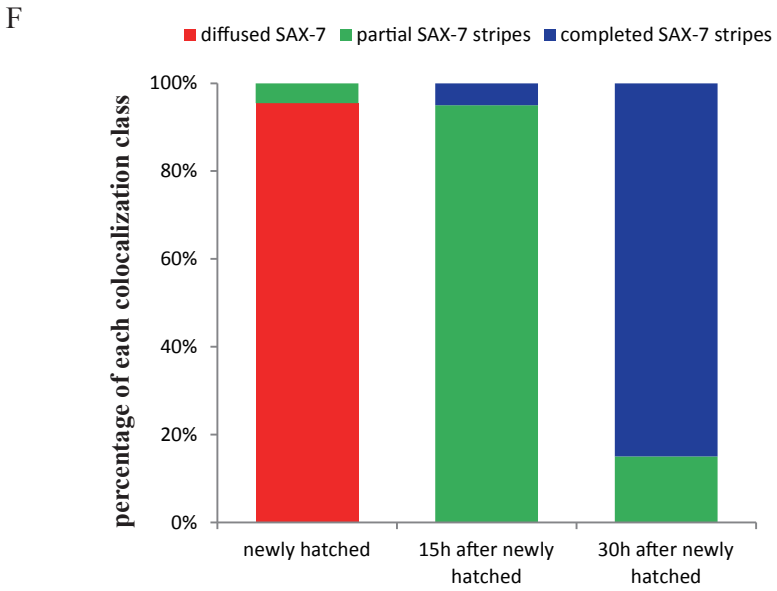

F
diffused SAX-7
partial SAX-7 stripes
completed SAX-7 stripes
percentage of each colocalization class
100%
80%
60%
40%
20%
0%
newly hatched
15h after newly hatched
30h after newly hatched

Fig. S1, related to Fig. 1. Gain-of-function SAX-7 manipulations generate predictable patterns of 4° dendrites

A-C) Confocal images of *sax-7*(*nj48*) mutant expressing PVD::mCherry and A/PLM::SAX-7::GFP. White arrowhead shows one PVD 3° branch, and yellow arrowhead indicates the PLM neurite. Yellow arrow marks the synaptic branch of PLM, and the white arrow shows a PVD branch that follows the synaptic branch of PLM. D-F) Confocal images of *sax-7*(*nj48*); *mnr-1*(*wy758*) double mutant expressing SAX-7 and MNR-1 (SAX-7's co-ligand) together in the D type neurons (DD and VD) and the A/PLM neurons. Yellow arrows indicate the commissures of D type neurons, and the white arrows show the PVD dendrites that follow the D type neurons' commissures. Yellow arrowheads indicate the ALM neurites, and the white arrowheads show the PVD 3° branch. G) Quantification of ratio between 4° and 3° branch of worms that SAX-7 ectopically expressed in A/PLM. H) Quantification of the ratio that 2° branches cross the sub-lateral line when *sax-7* ectopically expressed in D type neuron. Error bars, SEM. ***$p < 0.001$ by Student's t test. NS: not significant. n>20 for each genotype. I-K) Confocal images of *dma-1*(*wy686*) mutant expressing hypodermal SAX-7::YFP and PVD::mCherry. Arrow indicates the 3° branch and arrowhead shows one of the SAX-7 stripes. n=20. Scale bar is 10 μm.

Fig. S2, related to Fig. 1. *lin-22* worms produce five PVDs and have denser 4° branches but still follow the SAX-7 stripes

A-B) Confocal images of young adult wild type and *lin-22* (*wy50001*) worm. The arrows indicate the cell bodies of PVDs. C-F) A *lin-22* (*wy50001*) worm expressing both PVD::mCherry and P*dpy-7*::SAX-7::YFP. Note that all the PVD 4^o branches (red) co-localized with SAX-7 stripes

(green). Arrows indicate a SAX-7 stripe that is colocalized with a PVD branch. Arrowheads indicate a "free" SAX-7 stripe. G) Quantification of co-localization of PVD 4° branches and SAX-7 stripes. Y-axis means the average ratio of PVD 4° branches number/SAX-7 stripes number in one field around cell body. Error bars, SEM. ***p <0.001 by Student's t test. n=20. H) Quantification of mean florescence intensity of SAX-7 stripes in dendrite associated stripes and "free" ones. Ten SAX-7 stripes in every worm were chosen randomly to measure the mean florescence intensity using ImageJ for this quantification. n=3. Error bars, SEM. ***p < 0.001 by Student's t test. Scale bar is 10 μm.

Fig. S3, related to Fig. 2. *unc-52*(*e998*) affects PVD dendrites and SAX-7 pattern, while *unc-52*(*gk3*) does not affect PVD dendrites development

A-C) Florescent images of young adult wild type, *unc-52*(*e998*) and *unc-52*(*gk3*) expressing PVD::GFP. Arrow indicates one 3° branch and arrowhead shows one 4° branch. Scale bar is 10 μm. D) Quantification of the percentage of the 2° branches which contain "L" or "T" shaped 4° branches in *unc-52*(*e998*), *unc-52*(*e998*) and the *unc-52* genomic DNA rescued worm, and *unc-52*(*gk3*) mutant. E) Quantification of percentage of the 2° branches which contain less than three 4° branches in *unc-52*(*e998*), *unc-52*(*e998*) and the *unc-52* genomic DNA rescued worm, and *unc-52*(*gk3*) mutant. Error bars, SEM. ***p < 0.001 by ANOVA. NS: not significant. n>20 for each genotype. F-H) Confocal images of *unc-52*(*e998*). In *unc-52*(*e998*) mutants the disorganized SAX-7 stripes were always followed by the disorganized PVD 4° branches. Arrows indicate the PVD tertiary branch and the SAX-7 sub-lateral tripe. Arrowheads mark one of the PVD quaternary branch and the co-localized SAX-7 stripe. Scale bar is 10 μm.

Fig. S4, related to Fig. 3. UNC-52 antibody staining is affected in *unc-52* mutants but not *sax-7*(*nj48*)

A-D) GM1 antibody staining confocal images of young adult animals of wild type, *sax-7*(*nj48*), *unc-52*(*e1421*) and *unc-52*(*e998*). Compared with wild type, *sax-7*(*nj48*) did not change the regular pattern of UNC-52 (illustrated by GM1 staining). In *unc-52*(*e1421*) and *unc-52*(*e998*) the staining of UNC-52 was greatly reduced and the fluorescence becomes diffusely localized. n>10 for each genotype. Scale bar is 10 μm.

Fig. S5, related to Fig. 6. Overexpression MUA-6 blocked PVD 4° branches growth

A-D) Confocal images of overexpressed MUA-6::mCherry and PVD::GFP. Arrow indicates one PVD 4° branch and arrowhead shows one FO stripe. E) Quantification of 4° branches in *mua-6*(*rh85*) and *mua-6* overexpression worms. Error bars, SEM. ***p < 0.001 by ANOVA. n>20. *mua-6*(*rh85*) mutant was very sick and also disrupted 2° and 3° branches, therefore, only identifiable 3° branches were quantified. F) Quantification of the SAX-7 stripes formation time. Diffused SAX-7 means no stripes were observed; partial SAX-7 stripes means SAX-7 stripes formed in some regions; completed SAX-7 stripes means SAX-7 stripes formed in all the regions. n=20 for each stage. Scale bar is 10 μm.

Table S1, related to experimental procedures "*C. elegans* Strains, Genetics and RNAi" section. Mutant Alleles and Transgenes Used in This Study

A. Mutant alleles

Allele	Reference
unc-52(e998)	*(Gregory P. Mullen et al., 1999)*
unc-52(e1421)	*(Gregory P. Mullen et al., 1999)*
sax-7(nj48)	*(Xintong Dong et al.,2013)*
lin-22(wy50001)	This study
dma-1(wy686)	*(Liu and Shen, 2012)*
mua-6(rh85)	*(Vera Hapiak et al.,2003)*

B. Integrated transgenes

Allele	Chromosome	Constructs	Co-injection marker
wyIs50001	X	pXD26(15ng/ul),pOL036(5ng/ul)	P*odr-1*::RFP
wyIs50005	?	pOL036(20ng/ul),POL057(5ng/ul)	P*odr-1*::RFP

C. Extrachromosomal arrays

Allele	Constructs	Co-injection marker
wyEx5147	pXD28(15ng/ul),pOL036(15ng/ul)	P*odr-1*::RFP
wyEx5312	pXD30(15ng/ul),pOL036(15ng/ul)	P*odr-1*::RFP
wyEx6519	pXD26(15ng/ul),pOL036(5ng/ul)	P*odr-1*::RFP
wyEx6522	pXD26(0.1ng/ul),pOL036(5ng/ul)	P*odr-1*::RFP
wyEx50017	*unc-52* genomic DNA(25ng/ul)	P*egl-17*::myri-mCherry
wyEx50028	pXM41(30ng/ul),pXM3(20ng/ul)	
wyEx50029	pXM41(6ng/ul),pOL057(15ng/ul)	
wyEx50030	pXM41(6ng/ul),pOL020(50ng/ul)	
wyEx50034	pXM41(30ng/ul),pOL057(15ng/ul)	

Table S2, related to experimental procedures "Molecular Biology and Transgenes" section. Plasmid Used in This Study

Plasmid	Genotype
pOL020	*ser-2*Prom3::myr-GFP
pXD26	P*dpy-7*::SAX-7S::YFP
pOL036	*ser-2*Prom3::myr-Cherry
pOL057	P*dpy-7*::SAX-7S::GFP
pXD28	P*dpy-7*::SAX-7S Del Ex::YFP
pXD30	P*dpy-7*::SAX-7S Del Cyto::YFP
pXM3	*ser-2*Prom3::GFP
pXM41	P*mua-6*::MUA-6::Cherry