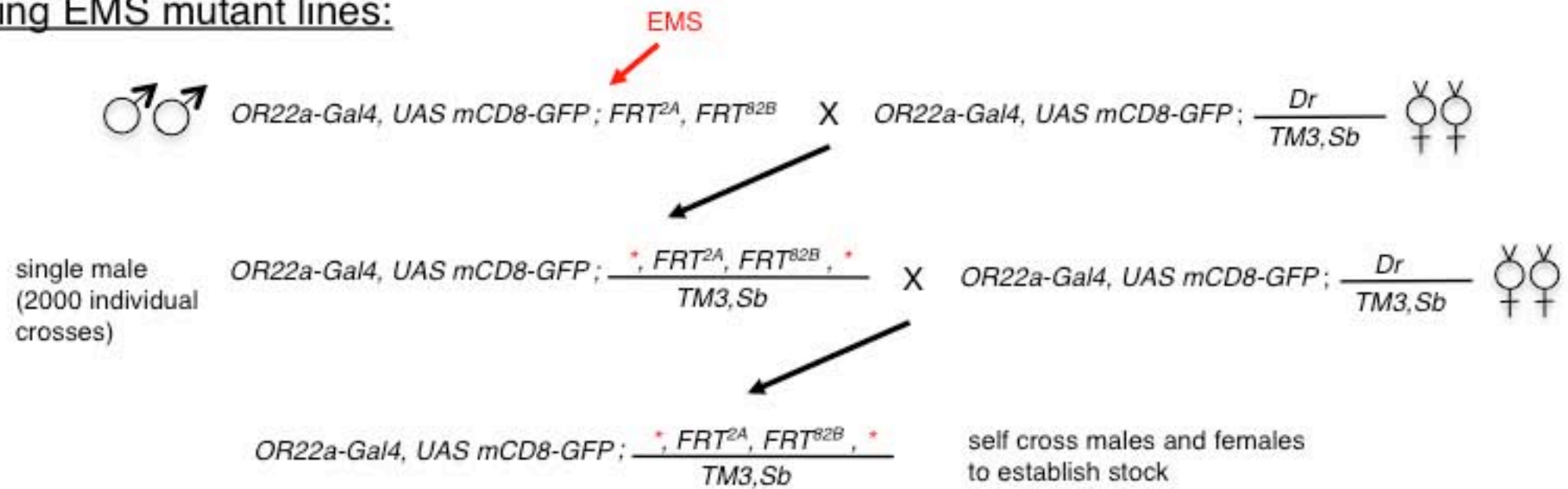
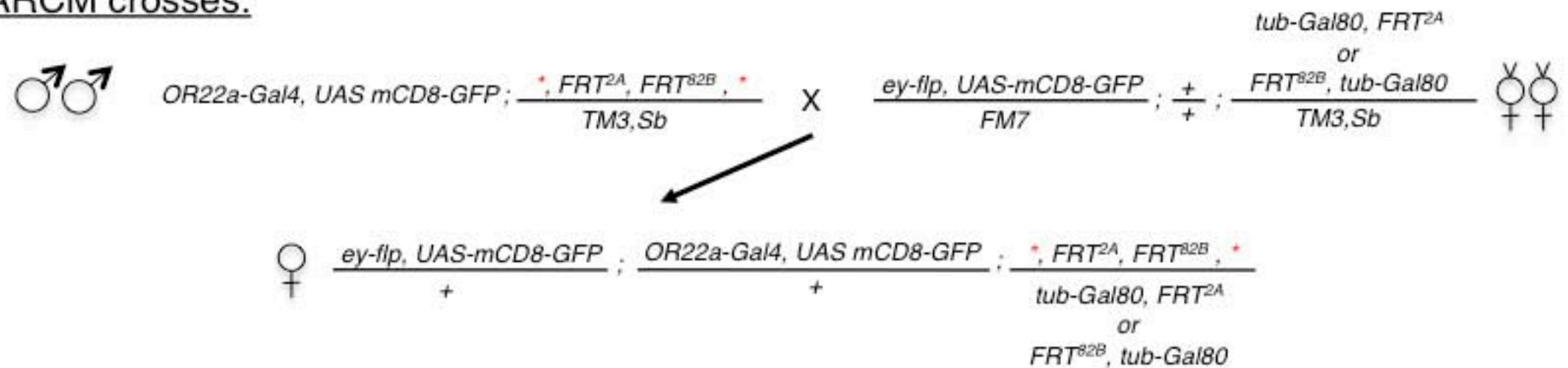


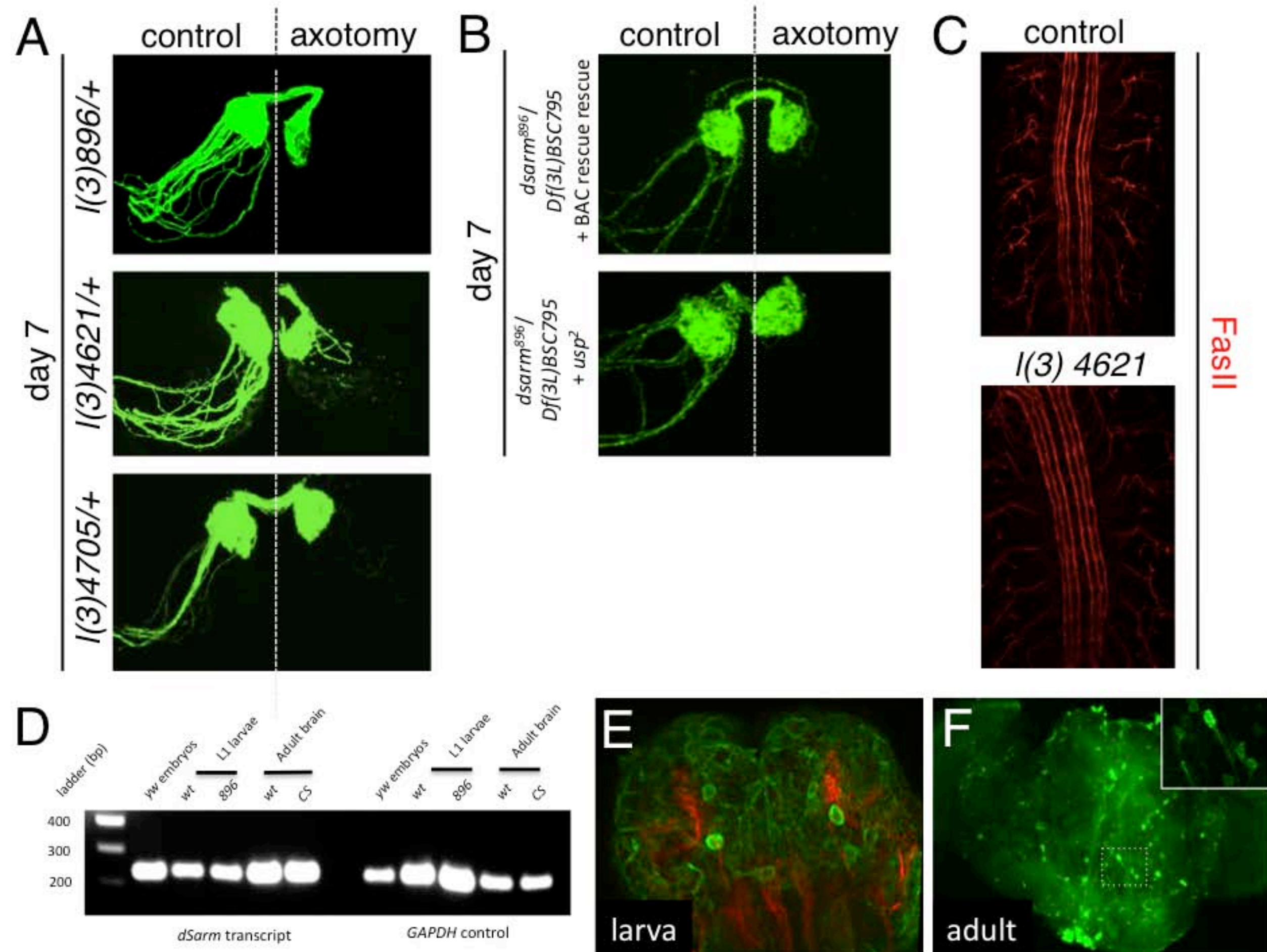
### A. Generating EMS mutant lines:



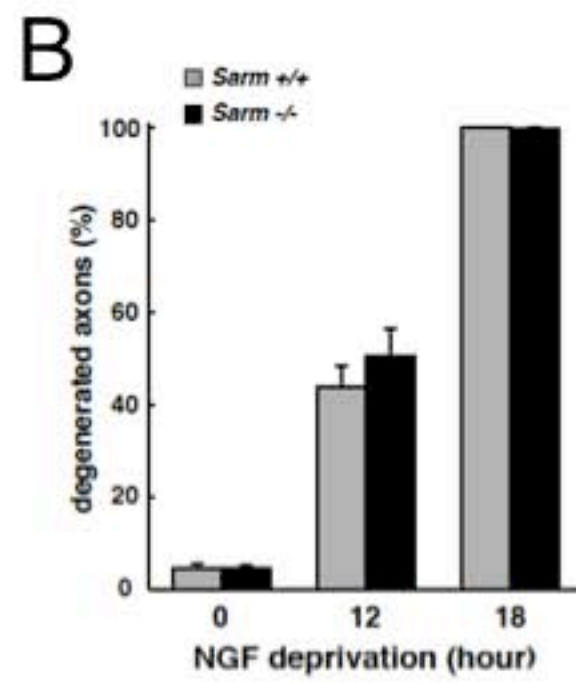
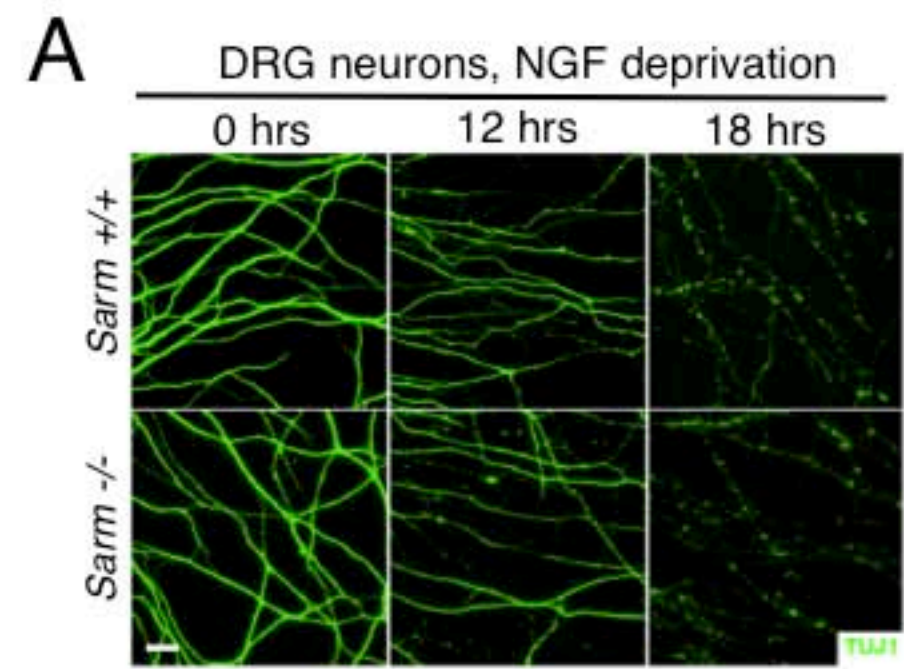
### B. MARCM crosses:



- 1) collect females only
- 2) clones generated in OR22a<sup>+</sup> ORN axons (by *ey-flp*)
- 3) unilateral ablation → assay severed axon integrity at 7 days

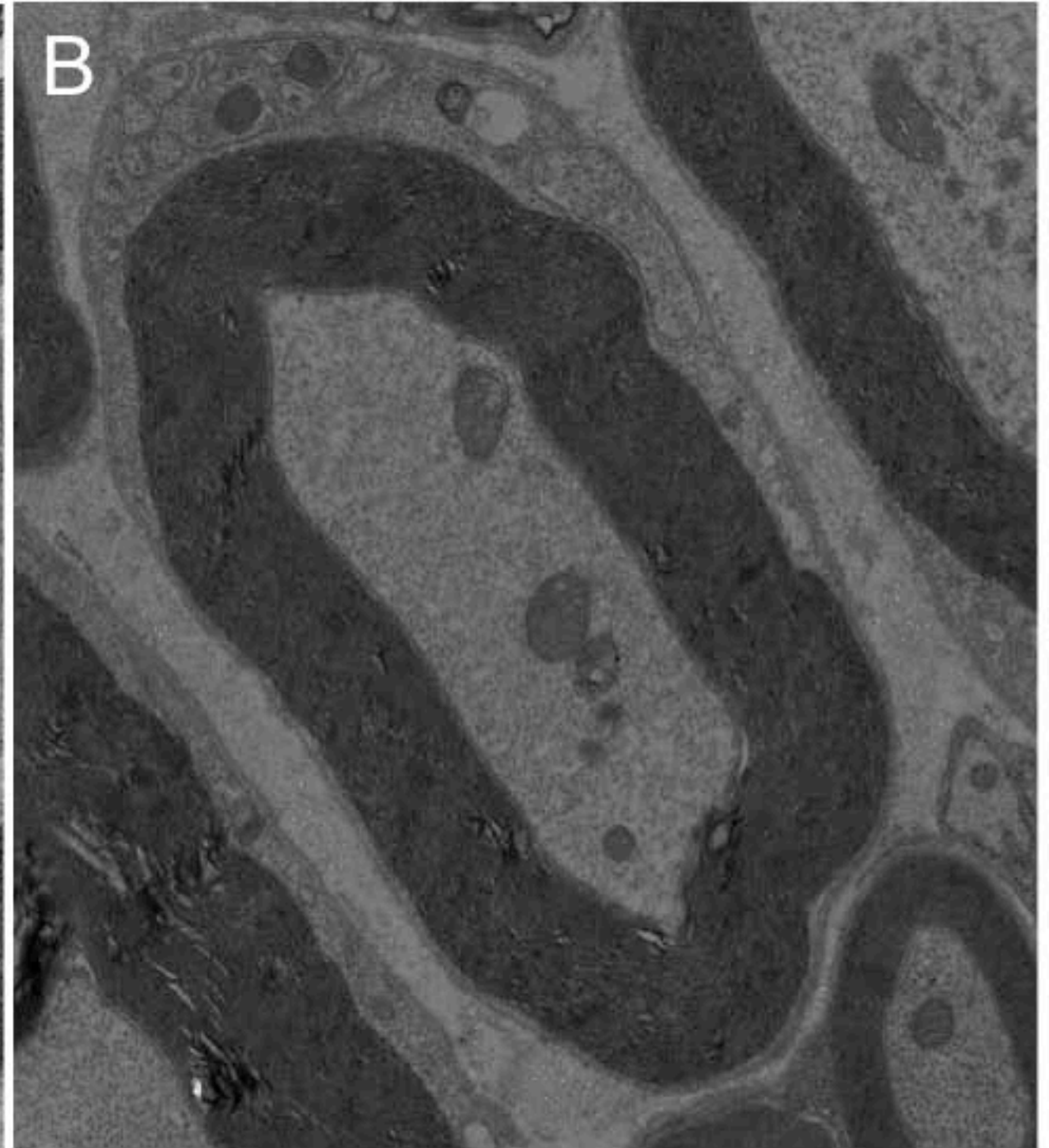
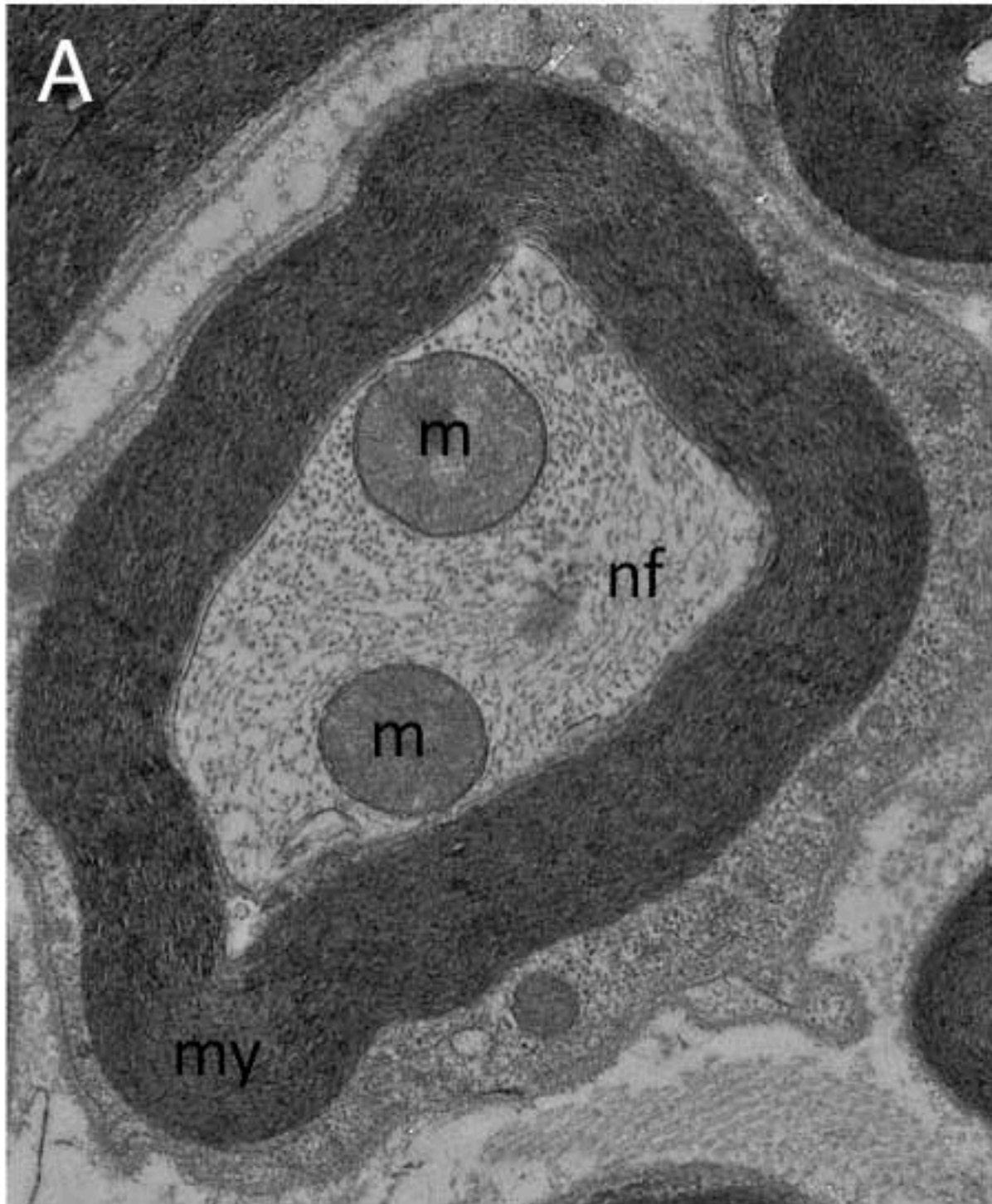


Supplementary Figure 2

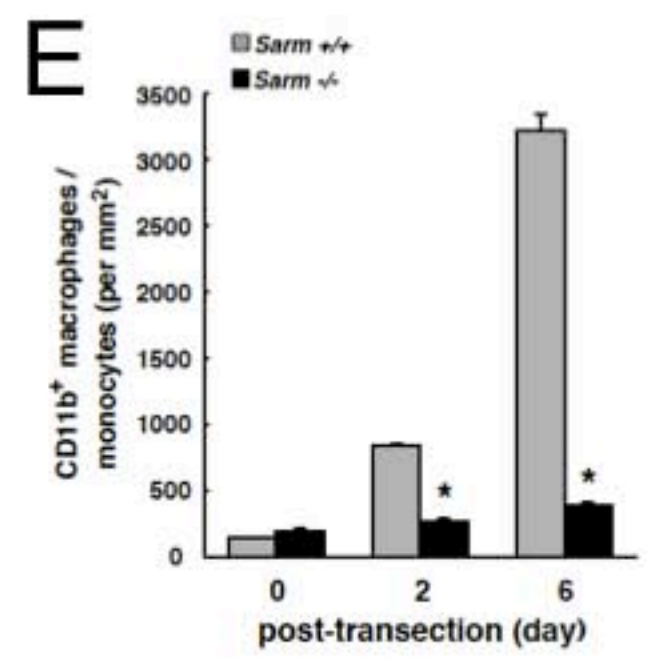
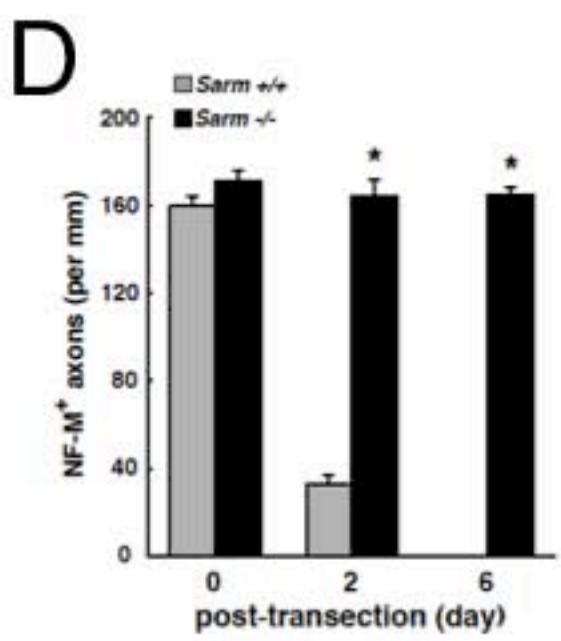
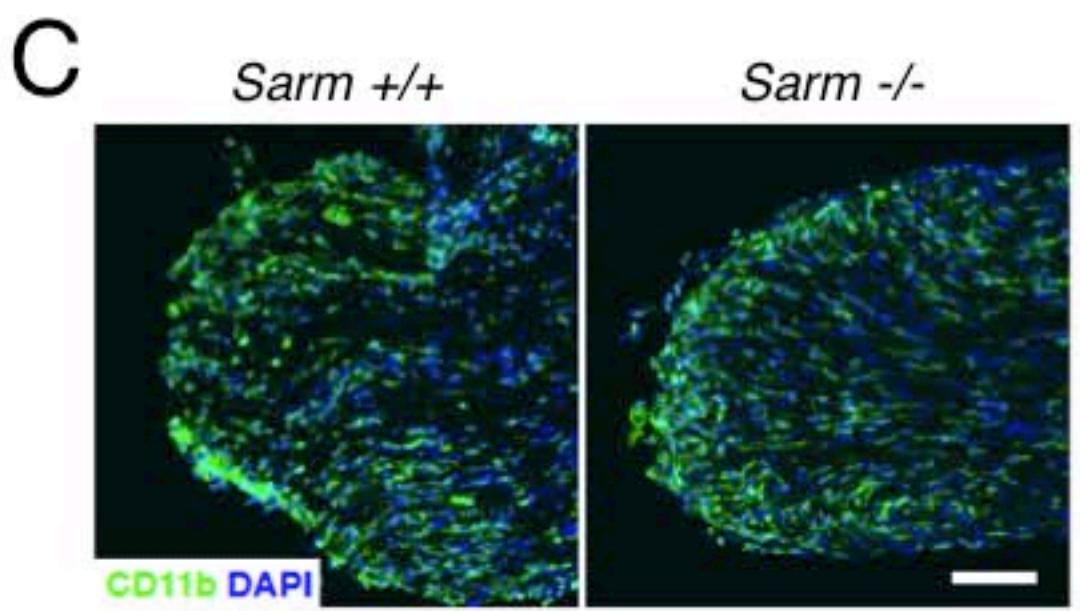
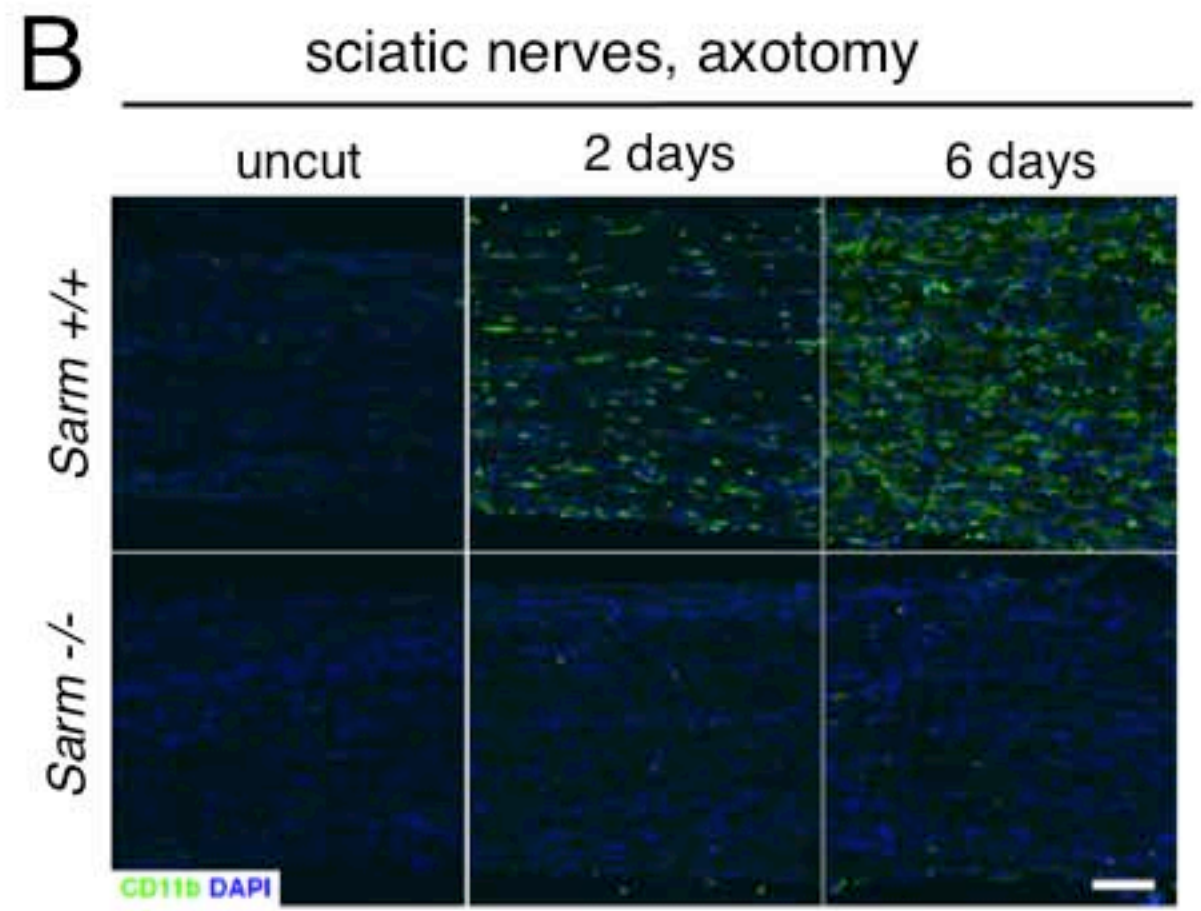
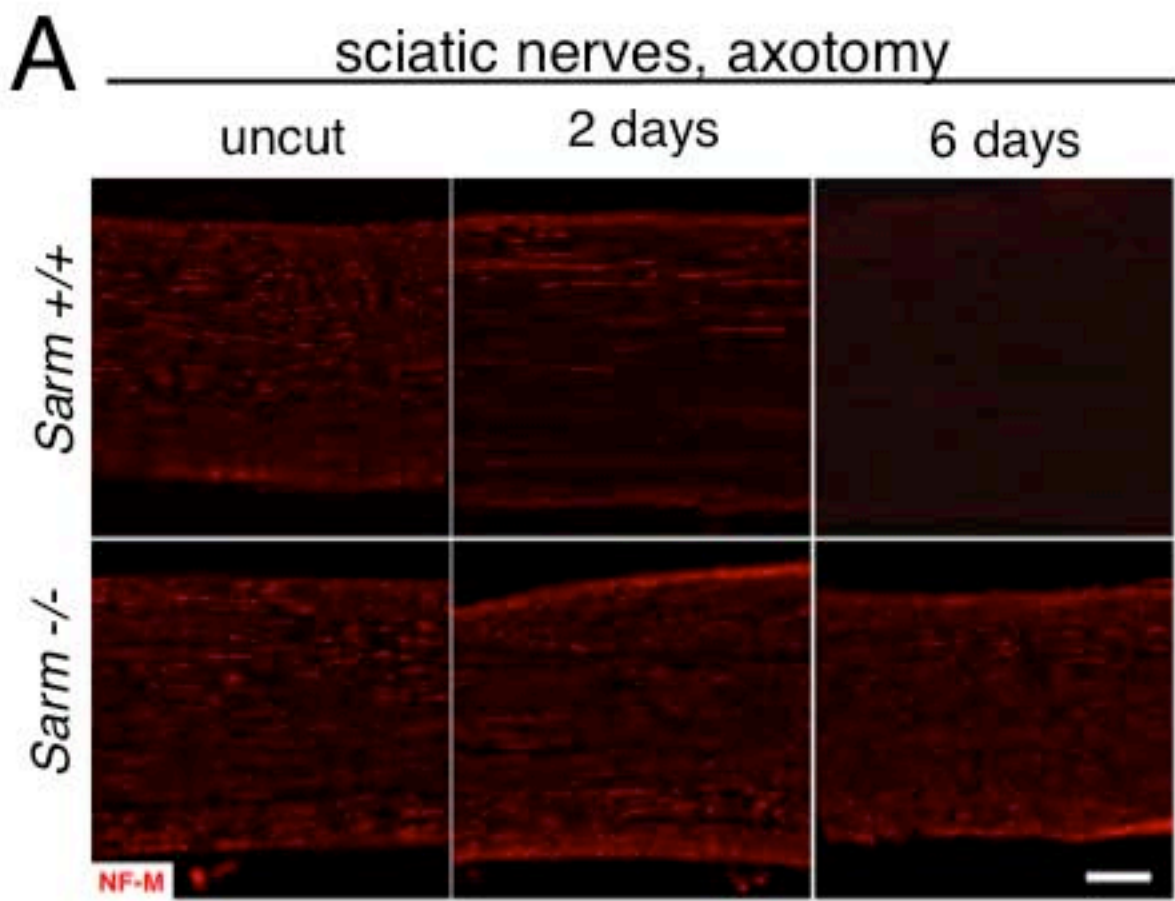


Supplementary  
Figure 3





Supplementary Figure 4



Supplementary Figure 5



## Supplementary Table 1: Mutants tested that fail to suppress Wallerian Degeneration

Gene	Mutant Allele	Allele Type
ASK1	DN	OE
Atg1	$\Delta$ 3D	LOF
Atg1	KQ #5B DN	OE
Atg1	68 DN	OE
Atg1	EP3009	LOF
Atg1	KG03098	LOF
Atg1	EP3348	LOF
Atg2	EP3697	LOF
Atg6	00096	LOF
Atg7	d77	LOF
Atg7	d14	LOF
Atg18	KG03098	LOF
Bsk/Jnk	DN	OE
buffy	H37	LOF
cullin-3	mds1	LOF
cullin-3	UAS	OE
cyt-c d	bln1	LOF
damm	f02209	LOF
dark	CD4	hypomorph

Gene	Mutant Allele	Allele Type
dark	CD8	hypomorph
debcl	E36	LOF
debcl	W105	hypomorph
diAP/thread	th1	LOF
diAP/thread	FL	OE
diAP2	G2326	OE
Dronc	DN	OE
Dronc	51	LOF
drp1	KG03815	LOF
Hsp22	EP(3)3247	OE
ik2	DN	OE
omi/htra2	FL	OE
omi/htra2	$\Delta$ 07	LOF
p35	FL	OE
pmn	FL	OE
puckered	FL	OE
roc1b	dc3	LOF
SOD1	FL	OE
TOR	TED DN	OE

All mutants or misexpression constructs were crossed into a background where a subset of ORNs were labeled with GFP. Constructs tested for overexpression phenotypes were co-expressed with GFP. ORN axons were severed, and axon degeneration and clearance from the brain was assayed 7 days after axotomy. LOF = reported amorphic loss of function allele; OE = overexpression construct; DN = dominant negative; FL = full length gene.

**Supplementary Table 2** – Production of MARCM clones and persistence of severed axons in mutant backgrounds

<b>mosaic chromosome</b>	<b>number of axons (uninjured)*</b>	<b>number of axons 7 days after axotomy*</b>
<i>wild type</i>	11.08 +/-1.52	0
<i>l(3)896</i>	4.71 +/-1.76	5.43 +/-2.12
<i>l(3)4621</i>	7.44 +/-0.66	6.13 +/-0.74
<i>l(3)4705</i>	4.94 +/-0.85	5.00 +/-1.61

\*Represents number of individual axon fibers identified in z-stacks from confocal imaging of entire antennal lobe. n≥10 antennal lobes for all.

**Supplementary Table 3 – Identification of *dsarm* through re-sequencing of mutant genomes**

	One mutant line (# of genes)	Any two mutant lines (maximum # of genes)	All three mutant lines (# of genes)
Unique coding variants; genome wide	92 (I(3)896) 997 (I(3)46210) 272 (I(3)4705)	166	6
Unique coding variants; chromosome 3L	34 (I(3)896) 132 (I(3)46210) 46 (I(3)4705)	8	3
+ nonsynonymous or splice site and heterozygous changes	17 (I(3)896) 66 (I(3)46210) 23 (I(3)4705)	2	1