



**Supplementary Information for**

**Cell-type-specific, multi-color labeling of endogenous proteins  
with split fluorescent protein tags in *Drosophila***

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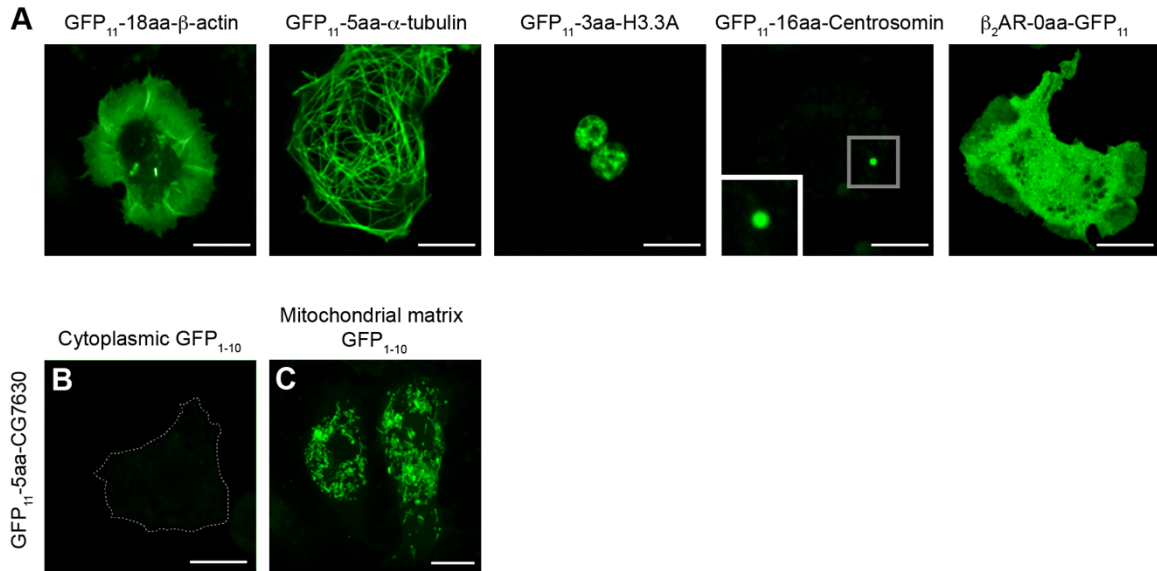
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Legends for Movies S1 to S2  
SI References

**Other supplementary materials for this manuscript include the following:**

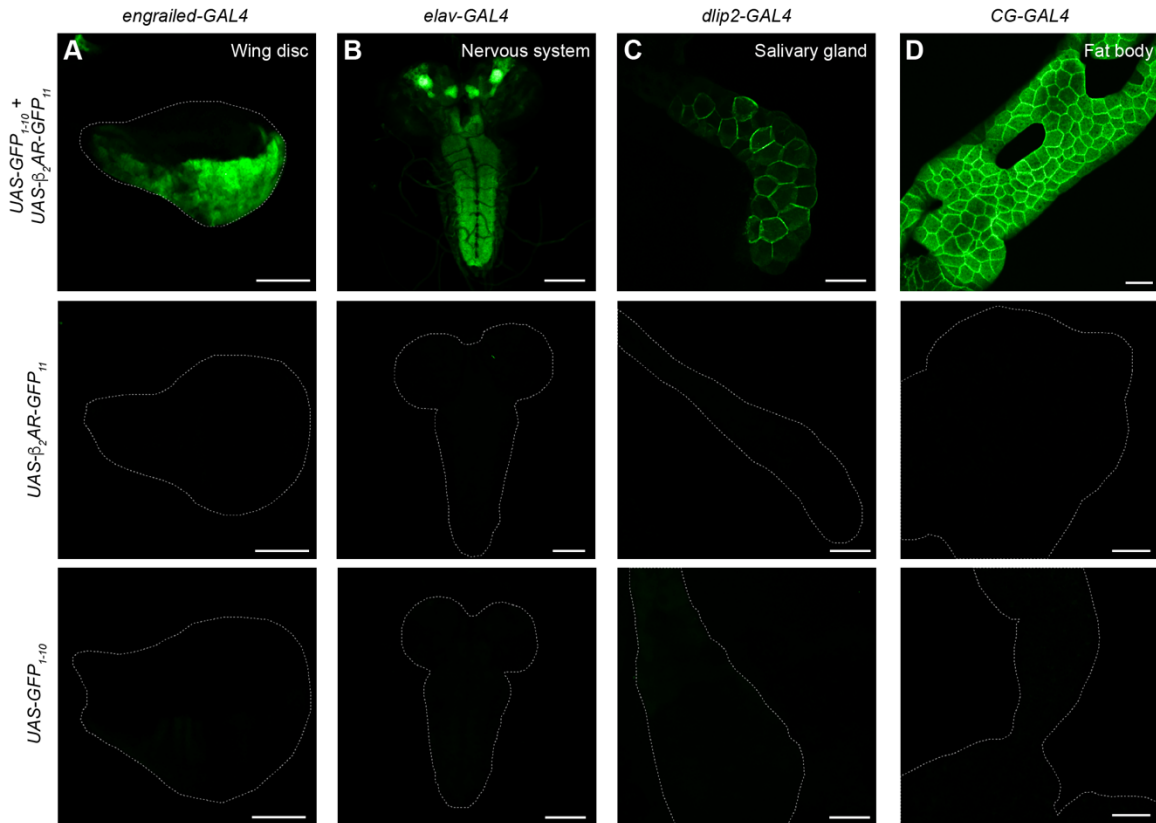
Movies S1 to S2



**Fig. S1 | Labeling of cellular proteins with GFP<sub>11</sub>-tag in S2 cells**

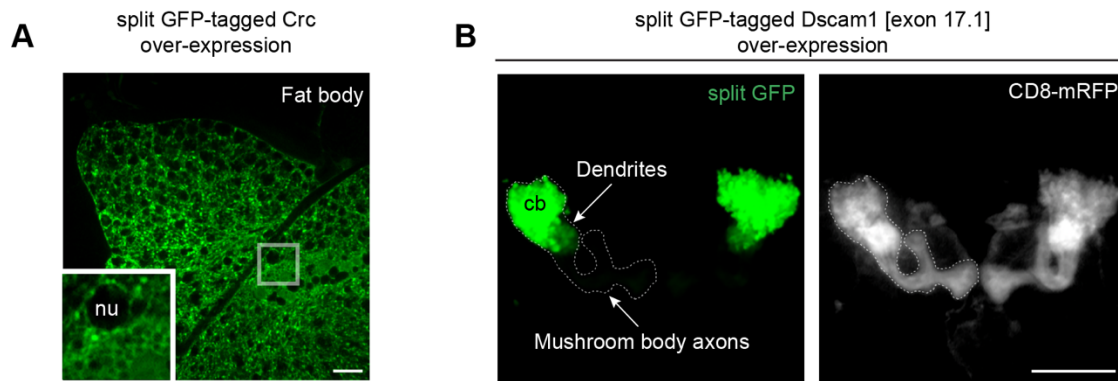
(A) Representative images of S2 cells co-expressing GFP<sub>1-10</sub> with GFP<sub>11</sub> fused to various cellular proteins. For each fusion, the linker length is indicated in the figure. (B) The expression of cytoplasmic GFP<sub>1-10</sub> shows that there is no reconstituted signal from GFP<sub>11</sub>-tagged CG7630. CG7630 is known to localize to the mitochondrial matrix (1). (C) CG7630-GFP<sub>11</sub> in S2 cells co-expressing GFP<sub>1-10</sub><sup>mitochondrial matrix</sup> leads to localization pattern similar to that obtained by the CG7630-HA fusion (1). Scale bars, 10 μm.

Over-expression of split GFP-tagged  $\beta_2$ AR in different tissues



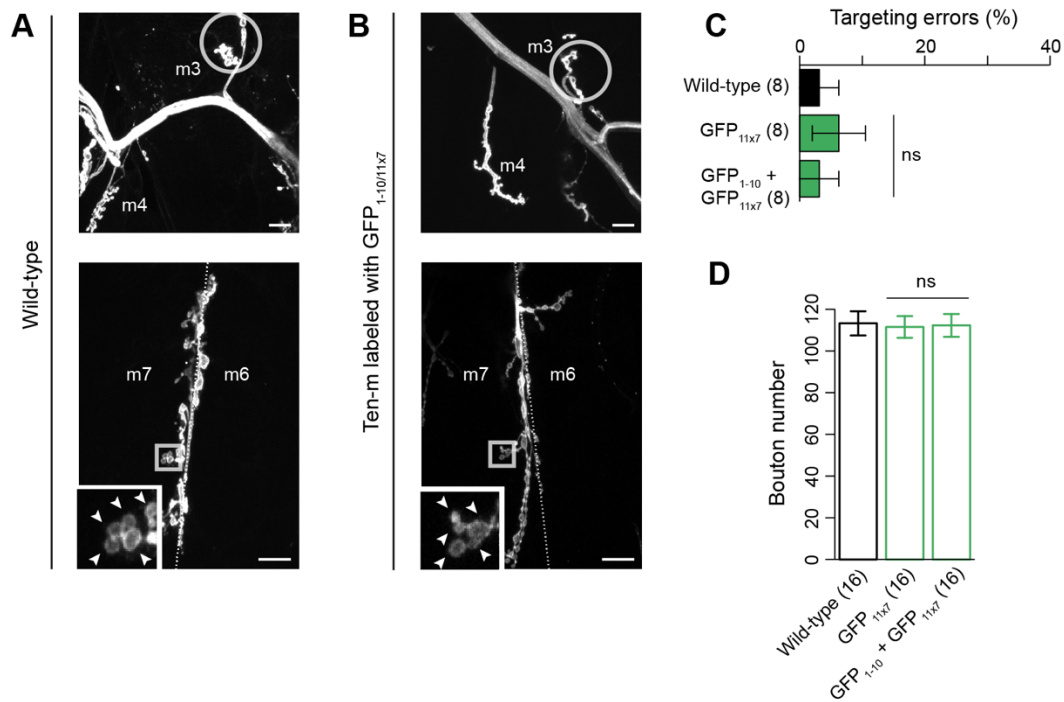
**Fig. S2 | Validation of the split GFP<sub>1-10/11</sub> system in flies**

Top panels (**A-D**): Confocal projections showing *GAL4*-driven split GFP expression in larval tissues. We simultaneously expressed *UAS-GFP<sub>1-10</sub>* and *UAS- $\beta_2$ AR-GFP<sub>11</sub>* under the control of various *GAL4* drivers. Middle and bottom panels (**A-D**): Representative images of larval tissues over-expressing either *UAS- $\beta_2$ AR-GFP<sub>11</sub>* (middle panels) or *UAS-GFP<sub>1-10</sub>* (bottom panels) under the control of these *GAL4* drivers. We show that neither GFP<sub>1-10</sub> nor  $\beta_2$ AR-GFP<sub>11</sub> produces fluorescence in these tissues. The images were taken with the same acquisition settings. The tissues (outlined by white dash lines) are oriented to the anterior to the top. Scale bars, 100  $\mu$ m.



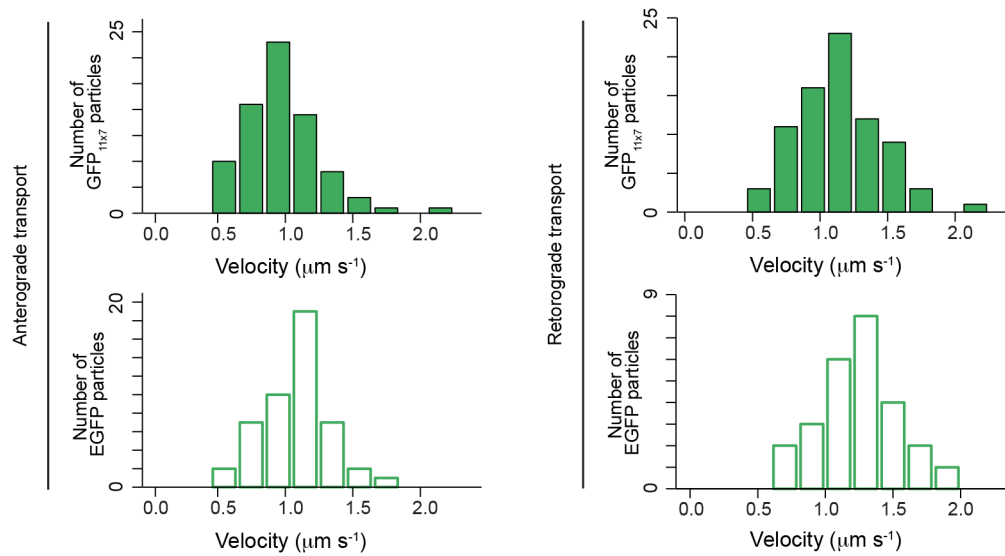
**Fig. S3 | Tagging an ER luminal protein and the extracellular domain of a transmembrane protein with GFP<sub>11</sub>-tag**

(A-B) An ER-targeted GFP<sub>1-10</sub> (GFP<sub>1-10</sub><sup>sec</sup>) labels an ER luminal protein (GFP<sub>11</sub>-Calreticulin) in the larval fat body or the extracellular domain of a plasma membrane protein (GFP<sub>11</sub>-Dscam1 [exon 17.1]) in the larval brain. (A, inset) Calreticulin is localized to the ER and the nuclear membrane (nu). (B) *CD8* (a cell membrane marker) and *dscam1* [exon 17.1] are co-expressed under the control of *201Y-GAL4*. Dscam1 [exon 17.1] is preferentially localized in dendrites and cell bodies (cb), while CD8 is distributed throughout cell bodies, dendrites, and axons. Images for different fluorophores were collected sequentially to avoid crosstalk between color channels. Scale bars, 100 μm.



**Fig. S4 | Evaluation of the function of Ten-m in homozygous protein trap lines**

(A-B) Representative NMJs in segment A2 stained with antibodies to the enzyme horseradish peroxidase (HRP). Larvae with either GFP<sub>11x7</sub> or GFP<sub>1-10/11x7</sub>-labeled Ten-m do not show any phenotype at the NMJs, suggesting that the tandem tag does not disturb the function of Ten-m. Circles indicate the innervation on muscle 3. Arrowheads in the zoomed insets indicate individual boutons. (C) Quantification of the hemisegment percentage with failed ‘muscle 3’ innervation. (D) Quantification of bouton numbers on muscles 6 and 7. For each quantification,  $n = 8$  larvae; 16 NMJs. ns, not significant as compared to wild-type. Scale bars, 20  $\mu$ m.



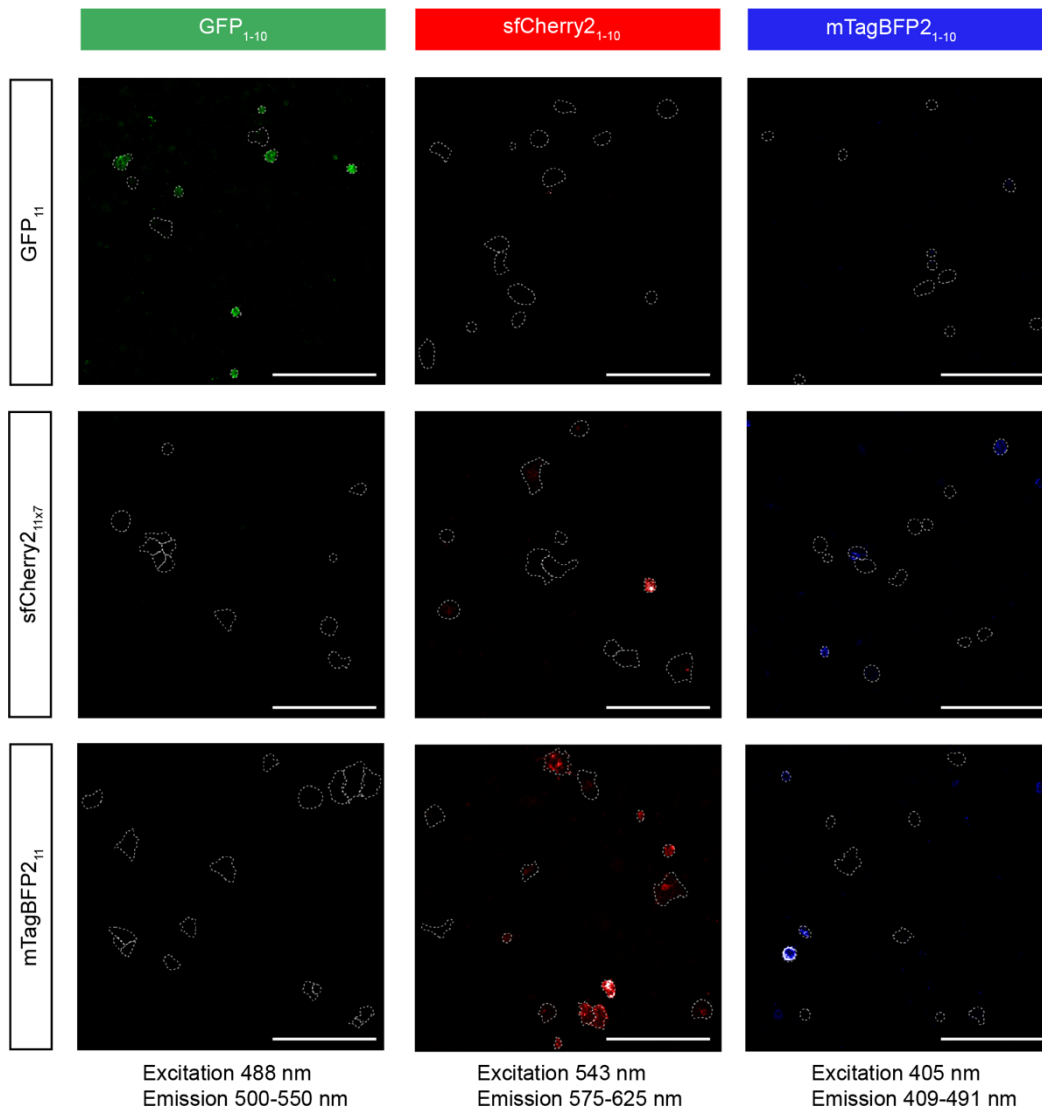
**Fig. S5 | Quantification of Ten-m transport along larval motor axons**

Velocity frequency distribution of Ten-m tagged with either GFP<sub>11x7</sub> or full-length EGFP. There is no statistical difference between the two different labeling approaches for either anterograde or retrograde velocity. A summary graph is shown in **Fig. 1J**.



**Fig. S6 | Engineering new split FPs for protein labeling in *Drosophila* cells**

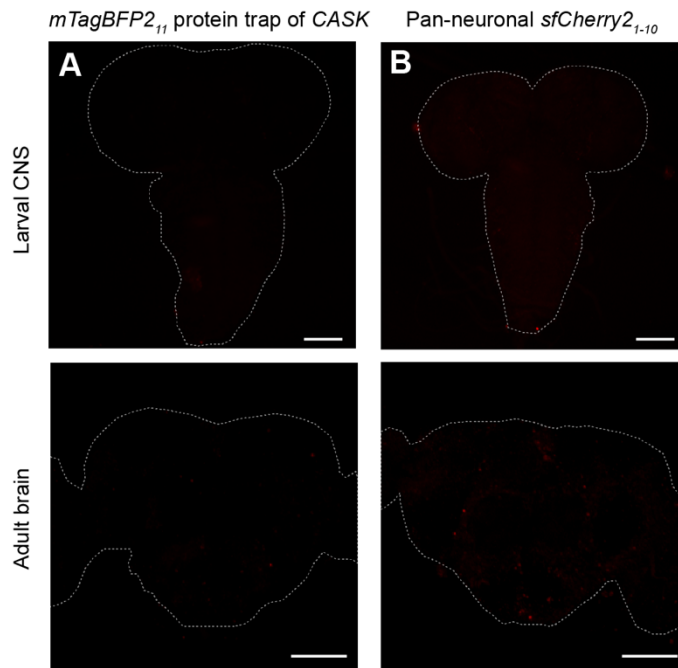
Fluorescence images of S2 cells co-expressing CD8-mIFP (an infrared FP-tagged membrane marker) with mNeonGreen2<sub>1-10/11</sub>, mApple<sub>1-10/11</sub>, sfCherry3V<sub>1-10/sfCherry2</sub><sub>11</sub>, mKate2<sub>1-10/11</sub>, E2-Crimson<sub>1-10/11</sub>, or spacer inserted mCardinal. Dashed lines encircle IFP-positive cells. Scale bars, 100  $\mu$ m.



**Fig. S7 | Characterizing the binding properties of the three FP<sub>1-10/11</sub> pairs (i.e., GFP<sub>1-10/11</sub>, sfCherry2<sub>1-10/11</sub>, and mTagBFP2<sub>1-10/11</sub>)**

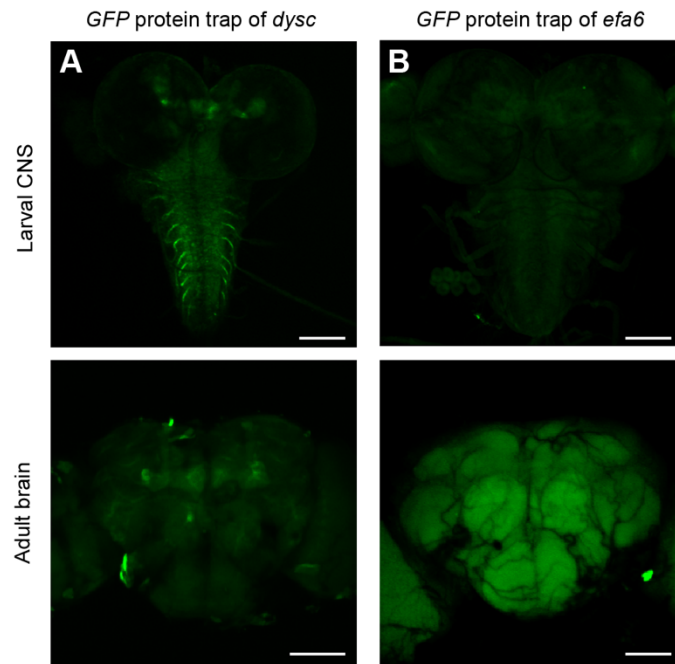
We tested each of the FP<sub>11</sub> fragments to complement all of the FP<sub>1-10</sub> fragments. We calculated the percentage of split FP-positive cells in the IFP-positive population. A summary chart is shown in **Fig. 3A**. Dashed lines encircle IFP-positive cells. Scale bars, 100  $\mu$ m.





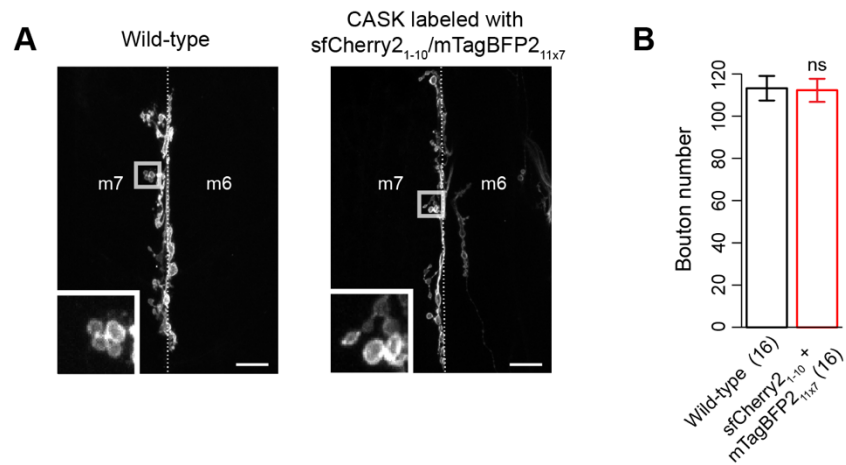
**Fig. S8 | Background fluorescence in larval and adult brains from sfCherry2<sub>1-10</sub> or mTagBFP2<sub>11</sub>**

(A-B) Fluorescence images of larval (top panels) and adult fly brains (bottom panels). We show that neither mTagBFP2<sub>11</sub> nor sfCherry2<sub>1-10</sub> by themselves produce visible fluorescence as negative controls. Dashed lines encircle the brains. Images in A-B and Fig. 4 were taken with the same acquisition settings. Scale bars, 100  $\mu$ m.



**Fig. S9 | GFP protein trap lines of *dysc* and *efa6***

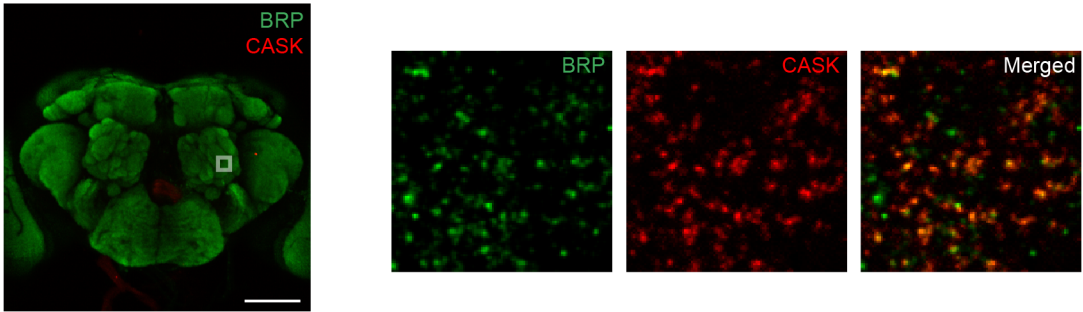
(A-B) Fluorescence images of two different GFP trap lines. Expression and localization of GFP-tagged *Dysc* and *Efa6* proteins are detected in neuronal tracts throughout the CNS during the larval (top panels) and adult (bottom panels) stages. Scale bars, 100  $\mu\text{m}$ .



**Fig. S10 | Function of sfCherry2<sub>1-10</sub>/mTagBFP2<sub>11x7</sub>-tagged CASK at NMJs**

**(A)** Representative NMJs stained for the presynaptic membrane maker HRP. **(B)** Quantification of bouton numbers on muscles 6 and 7 in segment A2. In a previous study, Sun *et al.* have demonstrated that *CASK* mutations cause an increase in bouton number (2). In contrast, the homozygous *TagBFP*<sub>11x7</sub> line of *CASK* with a pan-neuronal expression of *sfCherry2*<sub>1-10</sub> has shown no significant difference in bouton number from wild-type. Scale bars, 20 μm.

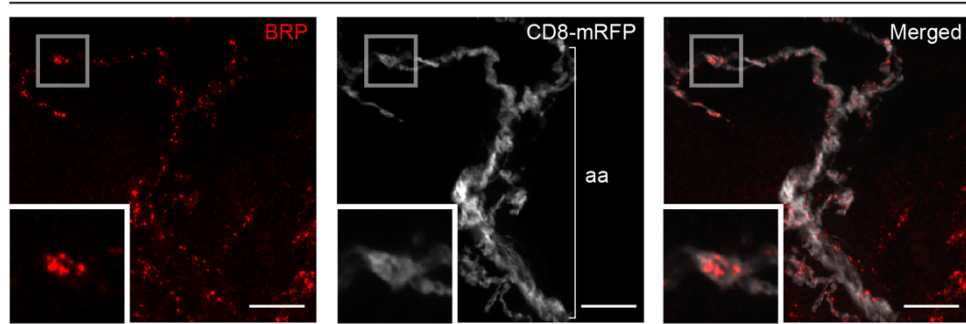
ORN-specific labeling of CASK  
with sfCherry2<sub>1-10</sub>/mTagBFP2<sub>11x7</sub>



**Fig. S11 | Co-labeling of presynaptic sites in Or47b-expressing ORNs using anti-BRP and cell-type-specific CASK labeling**

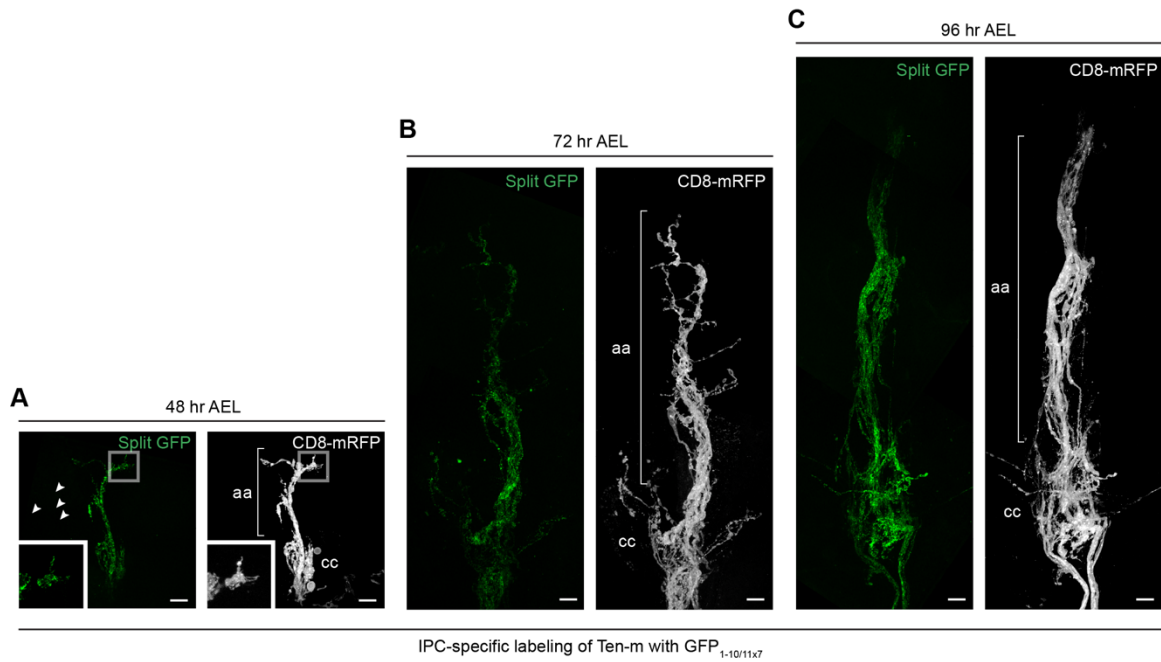
Representative images of ORNs stained with anti-BRP and expressing sfCherry2<sub>1-10</sub> via *Or47b-GAL4* in an *mTagBFP2<sub>11x7</sub>* line of *CASK*. A boxed region is shown in higher magnification in the right columns. Scale bar, 100  $\mu$ m.

72 hr after egg laying (AEL)



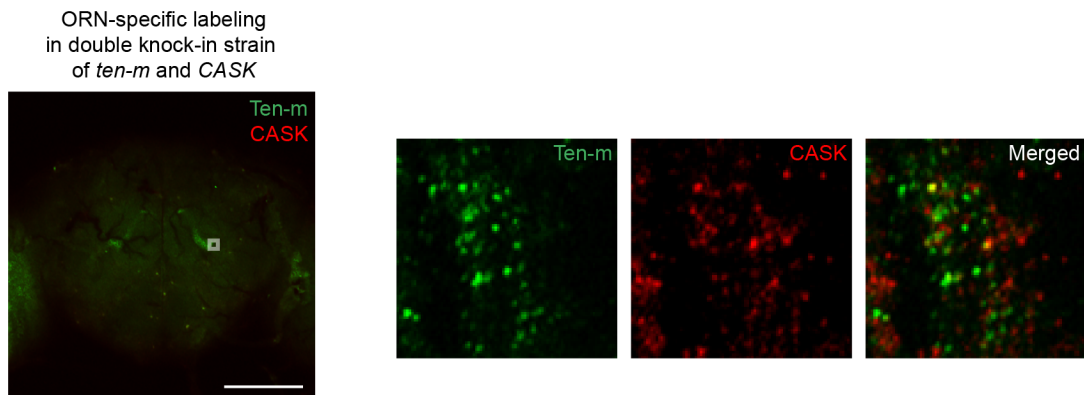
**Fig. S12 | BRP puncta accumulation at IPC axonal terminals**

Partial view of the axonal terminals of IPCs. IPCs expressing *mCD8-mRFP* were co-labeled with anti-BRP. The inset shows a higher magnification confocal image of BRP puncta in the axonal terminals. aa, anterior aorta. Scale bars, 10  $\mu$ m.



**Fig. S13 | Localization of Ten-m in IPC axons at different stages of larval development**

(A-C) A  $GFP_{11x7}$  line of *Ten-m* was crossed with an IPC-specific line of  $GFP_{1-10}$ . Ten-m is localized to axons of IPC during larval stages. Arrowheads (A, inset) mark Ten-m puncta in the terminals. aa, anterior aorta; cc, corpora cardiaca. Scale bars, 10  $\mu$ m.



**Fig.S14 | Dual-color labeling of Ten-m and CASK in Or47b-expressing ORNs**

Representative images of Or47b-expressing ORNs. Ten-m and CASK's localization patterns labeled with two orthogonal split FP systems are shown with higher magnification in the right panels (the inset at the left panel). Ten-m puncta only slightly overlap with CASK puncta in the axonal terminals. Scale bars, 100  $\mu\text{m}$ .

**Table S1****Properties of red-colored split FPs used in this study**

	<b>sfCherry2<sub>1-10</sub> + sfCherry2<sub>11</sub></b>	<b>sfCherry2<sub>1-10</sub> + TagBFP2<sub>11</sub></b>
<b>EC at peak (M<sup>-1</sup>cm<sup>-1</sup>)</b>	82,500	76,200
<b>QY</b>	0.22	0.19
<b>Brightness<sup>a</sup></b>	18,150	14,478

EC, extinction coefficient; QY, quantum yield. <sup>a</sup> Calculated as the product of EC and QY.



**Table S2**

**Nucleotide sequences of *mTagBFP2*<sub>1-10/11</sub>, *GFP*<sub>1-10/11</sub>, *mNeonGreen2*<sub>1-10/11</sub>, *mApple*<sub>1-10/11</sub>, *sfCherry2*<sub>1-10/11</sub>, *mKate2*<sub>1-10/11</sub>, *E2-Crimson*<sub>1-10/11</sub>, and *spacer-inserted mCardinal***

<b>FP<sub>1-10/11</sub></b>	<b>Sequence (5'-3')</b>
<i>mTagBFP2</i> <sub>1-10</sub>	<b>ATG</b> AGCGAGCTGATTAAGGAGAACATGCACATGAAGCT GTACATGGAGGGCACCGTGGACAACCATCACTTCAAGT GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCAC CCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTC TCCCCTTCGCCTTCGACATCCTGGCTACTAGCTTCCTCT ACGGCAGCAAGACCTTCATCAACCACACCCAGGGCATC CCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACA TGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGC TGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGC CTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCACA TCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTG GGAGGCCTTCACCGAGACGCTGTACCCCGCTGACGGC GGCCTGGAAGGCAGAAACGACATGGCCCTGAAGCTCGT GGGCGGGAGCCATCTGATCGCAAACGCCAAGACCACAT ATAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCTG GCGTCTACTATGTGGACTACAGACTGGAAAGAATCAAG GAGGCCAACAACT <b>TAA</b>
<i>mTagBFP2</i> <sub>11</sub>	TCTGAGACCTACGTCGAGCAGCACGAGGTGGCAGTGGC CAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAAGC TTAAT
<i>GFP</i> <sub>1-10</sub>	<b>ATG</b> TCCAAAGGAGAAGAAGTGTGTTACCGGTGTTGTGCCA ATTTTGGTTGAACTCGATGGTGTGATGTCAACGGACATAAG TTCTCAGTGAGAGGCGAAGGAGAAGGTGACGCCACCAT TGGAAAATTGACTCTTAAATTCATCTGTACTACTGGTAAA CTTCCTGTACCATGGCCGACTCTCGTAACAACGCTTACG TACGGAGTTCAGTGCTTTTTCGAGATACCCAGACCATATG AAAAGACATGACTTTTTTAAAGTCGGCTATGCCTGAAGGT TACGTGCAAGAAAGAACAATTTTCGTTCAAAGATGATGGA AAATATAAACTAGAGCAGTTGTAAATTTGAAGGAGATA CTTTGGTTAACCGCATTGAACTGAAAGGAACAGATTTTA AAGAAGATGGTAATATTCTTGGACACAACTCGAATACA ATTTTAATAGTCATAACGTATACATCACTGCTGATAAGCA AAAGAACGGAATTAAGCGAATTTACAGTACGCCATAA TGTAGAAGATGGCAGTGTTCAACTTGCCGACCATTACCA ACAAAACACCCCTATTGGAGACGGTCCGGTACTTCTTCC TGATAATCACTACCTCTCAACACAAACAGTCCTGAGCAA AGATCCAAATGAAAA <b>TAA</b>
<i>GFP</i> <sub>11</sub>	CGTGACCACATGGTCTTCATGAGTATGTAAATGCTGCT GGGATTACA

(Table continues)

<i>mNeonGreen2<sub>1-10</sub></i>	<p> <b>ATG</b>GTGAGCAAGGGTGAGGAGGATAACATGGCCTCTCT  CCCAGCGACTCATGAGTTACACATCTTTGGCTCCATCAA  CGGTGTGGACTTTGACATGGTGGGTCAGGGTACCGGCA  ATCCAAATGATGGTTATGAGGAGTTAAACCTGAAGTCCA  CCAAGGGTGACCTCCAGTTCTCCCCCTGGATTCTGGTC  CCTCATATCGGGTATGGCTTCCATCAGTACCTGCCCTAC  CCTGACGGGATGTGCGCTTTCCAGGCCGCCATGGTAGA  TGGCTCCGGATACCAAGTCCATCGCACAAATGCAGTTTGA  AGATGGTGCCTCCCTTACTGTAACTACCGCTACACCTA  CGAGGGAAGCCACATCAAAGGAGAGGCCAGGTGATG  GGGACTGGTTTCCCTGCTGACGGTCCTGTGATGACCAA  CACGCTGACCGCTGCGGACTGGTGCATGTCGAAGAAGA  CTTACCCCAACGACAAAACCATCATCAGTACCTTTAAGT  GGAGTTACACCACTGTAAATGGCAAACGCTACCGGAGC  ACTGCGCGGACCACCTACACCTTTGCCAAGCCAATGGC  GGCTAACTATCTGAAGAACCAGCCGATGTACGTGTTCC  GTAAGACGGAGCTCAAGCACTCCATG<b>TAA</b> </p>
<i>mNeonGreen2<sub>11</sub></i>	<p> ACCGAGCTCAACTTCAAGGAGTGGCAAAGGCCTTTAC  CGATATGATG </p>
<i>mApple<sub>1-10</sub></i>	<p> <b>ATG</b>GTGAGCAAGGGCGAGGAGAATAACATGGCCATCAT  CAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGGCT  CCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGG  CGAGGGCCGCCCTACGAGGCCTTTCAGACCGCTAAGC  TGAAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGG  GACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAGGTC  TACATTAAGCACCCAGCCGACATCCCCGACTACTTCAAG  CTGTCCTTCCCCGAGGGCTTCAGGTGGGAGCGCGTGAT  GAACTTCGAGGACGGCGGCATTATTCACGTTAACCAGG  ACTCCTCCCTGCAGGACGGCGTGTTTCATCTACAAGGTG  AAGCTGCGCGGCACCAACTTCCCCTCCGACGGCCCCGT  AATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCGAG  GAGCGGATGTACCCCGAGGACGGCGCCCTGAAGAGCG  AGATCAAGAAGAGGCTGAAGCTGAAGGACGGCGGCCA  CTACGCCGCCGAGGTCAAGACCACCTACAAGGCCAAGA  AGCCCGTGACGCTGCCCGGCGCCTACATCGTGCACATC  AAGTTGGACATCGTGTCCACAACGAGGAC<b>TAA</b> </p>
<i>mApple<sub>11</sub></i>	<p> TACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCG  CCTACTCCACCGGCGGCATGGACGAGCTGTACAAG </p>

(Table continues)

<i>sfCherry2<sub>1-10</sub></i>	<p> <b>ATG</b>GAGGAGGACAACATGGCCATCATCAAGGAGTTCAT  GAGATTC AAGGTGCACATGGAGGGCAGCGTGAACGGC  CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCACC  CCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGAC  CAAGGGCGGGCCCCCTGCCCTTCGCCTGGGACATCCTGA  GCCCCCAGTTCATGTACGGCAGCAAGGCCTACGTGAAG  CACCCCGCCGACATCCCCGACTACCTGAAGCTGAGCTT  CCCCGAGGGCTTCACCTGGGAGAGAGTGATGAACTTCG  AGGACGGCGGCGTGGTGACCGTGACCCAGGACAGCAG  CCTGCAGGACGGCCAGTTCATCTACAAGGTGAAGCTGC  TGGGCATCAACTTCCCCAGCGACGGCCCCGTGATGCAG  AAGAAGACCATGGGCTGGGAGGCCAGCACCGAGAGAA  TGTACCCCGAGGACGGCGCCCTGAAGGGCGAGATCAA  CCAGAGACTGAAGCTGAAGGACGGCGGCCACTACGAC  GCCGAGGTGAAGACCACCTACAAGGCCAAGAAGCCCGT  GCAGCTGCCCGGCGCCTACAACGTGGACATCAAGCTGG  ACATCACCAGCCACAACGAGGACT<b>TAA</b> </p>
<i>sfCherry2<sub>11</sub></i>	<p> TACACCATCGTGGAGCAGTATGAACGTGCAGAGGCTCG  CCATTCCACA </p>
<i>mKate2<sub>1-10</sub></i>	<p> <b>ATG</b>GTGAGCGAGCTGATTAAGGAGAACATGCACATGAA  GCTGTACATGGAGGGCACCGTGAACAACCACCACTTCA  AGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGG  CACCCAGACCATGAGAATCAAGGCGGTGAGGGCGGC  CCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTC  ATGTACGGCAGCAAAACCTTCATCAACCACCCAGGG  CATCCCCGACTTCTTTAAGCAGTCCTTCCCCGAGGGCTT  CACATGGGAGAGAGTCAACCACATACGAAGACGGGGGC  GTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACG  GCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAAC  TTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTC  GGCTGGGAGGCCTCCACCGAGACCCTGTACCCCGCTG  ACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCTGAA  GCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGA  CCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGA  TGCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGA  ATCAAGGAGGCCGACAA<b>TAA</b> </p>
<i>mKate2<sub>11</sub></i>	<p> GAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCA  GATACTGCGACCTCCCTAGCAA<b>ACTGGGGC</b>CACAGA </p>

(Table continues)

<i>E2-Crimson<sub>1-10</sub></i>	<p> <b>ATG</b>GATAGCACTGAGAACGTCATCAAGCCCTTCATGCG  CTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACG  AGTTCGAGATCGAGGGCGTGGGCGAGGGCAAGCCCTA  CGAGGGCACCCAGACCGCCAAGCTGCAAGTGACCAAG  GGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCC  CCAGTTCTTCTACGGCTCCAAGGCGTACATCAAGCACC  CCGCCGACATCCCCGACTACCTCAAGCAGTCCTTCCCC  GAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGA  CGGCGGCGTGGTGACCGTGACCCAGGACTCCTCCCTG  CAGGACGGCACCCCTCATCTACCACGTGAAGTTCATCGG  CGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGA  AGACTCTGGGCTGGGAGCCCTCCACTGAGCGCAACTAC  CCCCGCGACGGCGTGCTGAAGGGCGAGAACCACATGG  CGCTGAAGCTGAAGGGCGGCGGCCACTACCTGTGTGA  GTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGAAGC  TGCCCGGCTACCACTACGTGGACTACAAGCTCGACATC  ACCTCCCACAACGAGGACT<b>TAA</b> </p>
<i>E2-Crimson<sub>11</sub></i>	<p> TACACCGTGGTGGAGCAGTACGAGCGCGCCGAGGCC  GCCACCACCTGTTCCAG </p>
<i>Spacer-inserted mCardinal</i>	<p> <b>ATG</b>GTGAGCAAGGGCGAGGAGCTGATCAAGGAGAACAT  GCACATGAAGCTGTACATGGAAGGCACCGTGAACAACC  ACCACTTCAAGTGCACCACCGAAGGGGAGGGCAAGCCC  TACGAGGGCACCCAGACCCAGAGGATTAAGGTGGTGG  GGGAGGCCCCCTGCCGTTTCGCATTCGACATCCTGGCCA  CCTGCTTTATGTACGGGAGCAAGACCTTCATCAACCACA  CCCAGGGCATCCCCGATTTCTTTAAGCAGTCCTTCCCTG  AGGGCTTCACATGGGAGAGAGTCAACACATACGAAGAC  GGGGGCGTGCTTACCGTTACCCAGGACACCAGCCTCCA  GGACGGCTGCTTGATCTACAACGTCAAGCTCAGAGGGG  TGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAA  CACTCGGCTGGGAGGCCACCACCGAGACCCTGTACCC  CGCTGACGGCGGCCTGGAAGGCAGATGCGACATGGCC  CTGAAGCTCGTGGGCGGGGGCCACCTGCACTGCAACC  TGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACC  TCAAGATGCCCGGCGTCTACTTTGTGGACCGCAGACTG  GAAAGAATCAAGGAGGCCGACAAT<b>GGTGGTGGCGGATC</b>  <b>AGAAGGAGGCGGTAGCGGGGGCCCTGGTTCGGGAGG</b>  <b>GGAAGGTTCTGCTGGGGGAGGGAGCGCTGGCGGGGG</b>  <b>GTCTGAGACCTACGTGAGCAGCACGAGGTGGCTGTGG</b>  CCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAAA  CTTAATGGCATGGACGAGCTGTACAAG<b>TAA</b> </p>

**30-aa spacer**  
Start or stop codon

**Table S3****Amino acid sequences of mTagBFP2<sub>1-10/11</sub>, GFP<sub>1-10/11</sub>, and sfCherry2<sub>1-10/11</sub>**

<b>FP<sub>1-10/11</sub></b>	<b>aa. sequence</b>
mTagBFP2 <sub>1-10</sub>	MSELIKENMHMKLYMEGTVDNHHFKCTSEGEGKPYEGTQTMRI KVEGGPLPFAFDILATSFLYGSKTFINHTQGIPDFFKQSFPEGFT WERVTTYEDGGVLTATQDTSLQDGCLIYVVKIRGVNFTSNGPVM QKKTLGWEAFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT YRSKPKAKNLKMPGVVYVDYRLERIKEANN
mTagBFP2 <sub>11</sub>	SETYVEQHEVAVARYCDLPSKLGHKLN
mTagBFP2 <sub>11x7</sub>	MSETYVEQHEVAVARYCDLPSKLGHKLN <b>GGSGG</b> SETYVEQHEV AVARYCDLPSKLGHKLN <b>GGSGG</b> SETYVEQHEVAVARYCDLPSK LGHKLN <b>GGSGG</b> SETYVEQHEVAVARYCDLPSKLGHKLN <b>GGSG</b> <b>G</b> SETYVEQHEVAVARYCDLPSKLGHKLN <b>GGSGG</b> SETYVEQHEV AVARYCDLPSKLGHKLN <b>GGSGG</b> SETYVEQHEVAVARYCDLPSK LGHKLN
GFP <sub>1-10</sub>	MSKGEELFTGVVPIVELDGDVNGHKFSVRGEGEGDATIGKLT KFICTTGKLPVPWPTLVTTLYGVQCFSRYPDHMKRHDFFSAM PEGYVQERTISFKDDGKYKTRAVVKFEGDTLVNRIELKGTDFKE DGNILGHKLEYNFNHNVIYITADKQKNGIKANFTVRHNVEDGSV QLADHYQQNTPIGDGPVLLPDNHYLSTQTVLSKDPNEK
GFP <sub>11</sub>	RDHMLHEVNAAGIT
GFP <sub>11x7</sub>	MRDHMLHEVNAAGIT <b>GGSGGR</b> RDHMLHEVNAAGIT <b>GGSG</b> <b>GRD</b> HMLHEVNAAGIT <b>GGSGGR</b> RDHMLHEVNAAGIT <b>GGSG</b> <b>GRD</b> HMLHEVNAAGIT <b>GGSGGR</b> RDHMLHEVNAAGIT <b>GGSG</b> <b>GRD</b> HMLHEVNAAGIT
sfCherry2 <sub>1-10</sub>	MEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGHPYEGTQ TAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSF PEGFTWERVMNFEDEGGVVTVTQDSSLQDGQFIYKVKLLGINFPS DGPVMQKKTMGWEASTERMYPEDGALKGEINQRLKLDGGHY DAEVKTTYKAKKPVQLPGAYNVDIKLDITSHNED
sfCherry2 <sub>11</sub>	YTIVEQYERAEARHST
sfCherry2 <sub>11x7</sub>	MYTIVEQYERAEARHST <b>GGSGGY</b> TIVEQYERAEARHST <b>GGSGG</b> YTIVEQYERAEARHST <b>GGSGGY</b> TIVEQYERAEARHST <b>GGSGGY</b> TIVEQYERAEARHST <b>GGSGGY</b> TIVEQYERAEARHST <b>GGSGGY</b> TIVEQYERAEARHST

**5-aa spacer**

**Table S4****List of the oligonucleotides and gene fragments used in this study**

<b>Oligonucleotide or gene fragment</b>	<b>Sequence (5'-3')</b>
GFP <sub>11</sub> -Histone H3.3A gene fragment	GGGAATTGGGAATTCACCATGGCACGTAC CAAGCAAACAGCCCGTAAATCGACCGGAG GCAAGGCGCCCCGCAAGCAGCTGGCCACC AAGGCGGCCCGTAAATCGGCGCCATCCAC CGGCGGAGTGAAGAAGCCACATCGCTACC GTCCTGGAACGGTGGCCCTGCGTGAGATT CGTCGCTACCAGAAGTCCACGGAGCTGCT CATCCGCAAGCTGCCGTTCCAGCGTCTGG TGCGCGAGATAGCCAGGACTTCAAGACC GATCTGCGCTTCCAGTCGGCGGCCATTGG AGCCCTACAGGAGGCCAGCGAGGCGTACC TGGTCGGTCTGTTGAGGACACCAATCTGT GCGCCATTCACGCCAAGCGCGTCACCATT ATGCCAAGGACATCCAGCTGGCCAGACG CATCCGTGGCGAGCGGGCCGGTGGATCG <b>CGTGACCACATGGTCCTTCATGAGTATGT</b> <b>AAATGCTGCTGGGATTACATAG</b> ATCTGCG GCCGCGG
pACUH-Centrosomin [1-1440] (F)	GGGAATTGGGAATTCACCATGAATAGTAAT CGAACGTC
pACUH-Centrosomin [1-1440] (R)	AATAGAGTACAGAATGCCAGC
Centrosomin [1420-1440]-GFP <sub>11</sub> gene fragment	CTGGCATTCTGTACTCTATTAGCAGCGGTG GAGCAAGCGCAGCCAGTGGTAGCGCGGAT CCACCGGTCGCCACCC <b>CGTGACCACATGGT</b> <b>CCTTCATGAGTATGTAAATGCTGCTGGGAT</b> <b>TACATA</b> AGATCTGCGGCCGCGG
pACUH-β <sub>2</sub> AR-GFP <sub>11</sub> (F)	TTAACAGATCTTGCGGCCGCATGCGGCTCT GCATCCCGCAGGTGCTGTTG
pACUH-β <sub>2</sub> AR-GFP <sub>11</sub> (R)	CACAAAGATCCTCTAGAT <b>TTATGTAATCCCA</b> <b>GCAGCATTACATACTCATGAAGGACCAT</b> <b>GTGGTCACGCAGCAGTGAGTCATTTGTA</b> CT ACAATTCCT
<sup>[1]</sup> pACUH-GFP <sub>1-10</sub> <sup>sec</sup> (F)	ACTTCCGCGCCACCTGTTC
<sup>[1]</sup> pACUH-GFP <sub>1-10</sub> <sup>sec</sup> (F)	GGTGGCGGCGGAAG <b>TTAG</b> TCTAGAGGATC TTTGTG

*(Table continues)*

pACUH-GFP <sub>1-10</sub> <sup>mitochondrial matrix</sup> (F)	ATGTCCAAAGGAGAAGAACT
pACUH-GFP <sub>1-10</sub> <sup>mitochondrial matrix</sup> (R)	TCGAGCCGCGGCCGCTTACAGATCCTCTT CTGAGATGAGTTTTTGTTCACCTCCTCCGC CACCTTTTTCATTTGGATCTTTGC
COXVIII gene fragment	ATGTCCGTCCTGACGCCGCTGCTGCTGCG GGGCTTGACAGGCTCGGCCCGGCCGGCTC CCAGTGCCGCGCGCCAAGATCCATTCGTT G
<sup>[2]</sup> pACUH-mCherry-GFP <sub>11</sub> (F)	GTGAGCAAGGGCGAGGAGGAT
<sup>[2]</sup> pACUH-mCherry-GFP <sub>11</sub> (R)	TCGAGCCGCGGCCGCTATGTAATCCAG <b>CAGCATTACATACTCATGAAGGACCATG</b> TGGTCACGACTTCTCCGCCACCCTTGTA CAGCTCGTCCATGC
<sup>[2]</sup> CG7630 gene fragment	ATGTTGGTTAAGCACATTGTCAAGCAGGG GCTTCTGCTCAAGAACGCTGGCGTTTTGT CGCGTGCCGCTTACCACGGTGGACATGGT CCCCACTCCACCATGAACGATCTGCCCGT GCCCCGCTGGAGACTGGAAGGAGCAGCAC AGCCAGAAGAACGCCAAGTACAATGCCCG GCTCATCACTGGCATTCTCGTCCTGGCCG GCACTATTGGATTCTGAAATCTTCTGGTA TCATCCACTTCAACTACTACGCGCCCAAG AGCCTGGAC
<sup>[3]</sup> pBS-Dscam1 [1-1684] (F)	GGGAATTGGGAATTCACCATGAATATGCC CAACGAACGC
<sup>[3]</sup> pBS-Dscam1 [1-1684] (R)	AGCTAGGGTCTGACTACCAC
<sup>[3]</sup> pBS-GFP <sub>11</sub> -Dscam1 [1-1684] (F)	GGTGC GGCGCAGGAGCCCGTGACCACA <b>TGGTCCTTCA</b>
<sup>[3]</sup> pBS-GFP <sub>11</sub> -Dscam1 [1-1684] (R)	TGCGCCGGCTCCAGCCCCTGTAATCCCA <b>GCAGCATTTACA</b>
<sup>[3]</sup> pACUH-GFP <sub>11</sub> -Dscam1 [1-1684] (F)	GCCAATCCCCCAGATGCC
<sup>[3]</sup> pACUH-GFP <sub>11</sub> -Dscam1 [1-1684] (R)	GCTCCAGACAATCGAATCG
<sup>[3]</sup> pACUH-GFP <sub>11</sub> -Dscam1 [1685-6463] (F)	CGATTGATTGTCTGGGAGC
<sup>[3]</sup> pACUH-GFP <sub>11</sub> -Dscam1 [1685-6463] (R)	GCGGCCGCGAGATCTGTTAACTTACACTGC CATAGTATCGTAGGC
<sup>[4]</sup> pACUH-sfCherry2 <sub>11</sub> -β-actin (F)	TCCGGACTCAGATCTGGC
<sup>[4]</sup> pACUH-sfCherry2 <sub>11</sub> -β-actin (R)	TGTGGAATGGCGAGCCTC
<sup>[4]</sup> pACUH-sfCherry2 <sub>11x7</sub> -β-actin (F)	TCCGGACTCAGATCTGGC
<sup>[4]</sup> pACUH-sfCherry2 <sub>11x7</sub> -β-actin (R)	CGTGGAGTGTCTGCCTC

(Table continues)

<sup>[4]</sup> pACUH-sfCherry2 <sub>11x7</sub> -sfGFP-β-act (F)	GGGAATTGGGAATTCATGTACACCATCGT G
<sup>[4]</sup> pACUH-sfCherry2 <sub>11x7</sub> -sfGFP-β-act (R)	GGTGGCGACCTCGAGCGGTAGCGCCGTG GAGTGTCTGCCTCTGC
pACUH-β <sub>2</sub> AR-sfCherry <sub>11</sub> (F)	TTAACAGATCTTGC GGCCGC <b>ATG</b> CGGCTC TGCATCCCGCAGGTGCTGTTG
pACUH-β <sub>2</sub> AR-sfCherry <sub>11</sub> (R)	CTTCACAAAGATCCTCTAGAT <b>TTA</b> GCCGCC <b>GGTGTGTGTCTGCCCTCGGCTCTCTCGT</b> <b>ACTGCTCCACGATGGTGTACAGCAGTGAG</b> TCATTTGTA CTAC
pACUH-CD8-sfCherry <sub>11</sub> (F)	CGTTAACAGATCTTGC GGCCGC <b>ATG</b> GCCT CACC
pACUH-CD8-sfCherry <sub>11</sub> (R)	CTTCACAAAGATCCTCTAGAT <b>CTA</b> GCCGCC <b>GGTGTGTGTCTGCCCTCGGCTCTCTCGT</b> <b>ACTGCTCCACGATGGTGTAGCGGCTGTG</b> GTAGCAGATGAGAG
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mNG2 <sub>11</sub> (F)	GGGAATTCGTTAACAGATCT <b>ATGA</b> AATCCCA AGAGCGAAGTCCTCATTGCA
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mNG2 <sub>11</sub> (R)	CCTTCACAAAGATCCTCTAGAT <b>TTACATCAT</b> <b>ATCGGTA AAGGCCTTTTGCCACTCCTTGA</b> <b>AGTTGAGCTCGGTCATAGCATAGAGCCCC</b> ACTGCA
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mKT2 <sub>11</sub> (F)	GGGAATTCGTTAACAGATCT <b>ATGA</b> AATCCCA AGAGCGAAGTCCTCATTGCA
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mKT2 <sub>11</sub> (R)	CCTTCACAAAGATCCT <b>CTA</b> GATTATCTGTG <b>CCCCAGTTTGCTAGGGAGGTCGCAGTAT</b> <b>CTGGCCACAGCCACCTCGTGCTGCTCGA</b> <b>CGTAGGTCTCCATAGCATAGAGCCCCACT</b> GCA
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mCrim <sub>11</sub> (F)	GGGAATTCGTTAACAGATCT <b>ATGA</b> AATCCCA AGAGCGAAGTCCTCATTGCA
<sup>[5]</sup> pACUH-CD4-IFP-T2A-HO-mCrim <sub>11</sub> (R)	CCTTCACAAAGATCCTCTAGAT <b>TTACTGGAA</b> <b>CAGGTGGTGGCGGGCCTCGGCGCGCTCG</b> <b>TACTGCTCCACCACGGTGTACATAGCATA</b> GAGCCCCACTGCA
<sup>[6]</sup> pACUH-mApple <sub>11</sub> -sfGFP (F)	ATAGGGAATTGGGAATTCTACACCATCGT <b>GGAACAGTACGAACGCGCCGAGGGCCG</b> <b>CCACTCCACCGGCGGCATGGACGAGCTG</b> <b>TACAAGATG</b> GTGAGCAAGGGCGAGGAGC TG
<sup>[6]</sup> pACUH-mApple <sub>11</sub> -sfGFP (R)	TCACGGCGGCCGCAAGATCTCTTGTACAG CTCGTCCATGCCGTGAGT

(Table continues)



<sup>[7]</sup> pACUH-TagBFP2 <sub>11</sub> -GFP/Emerald (F)	GGGAATTCGTTAACAGATCT <b>ATG</b> TCTGAGACCTACGTCGAGCAGCAGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAAC <b>TGGGGCACAAGCTTAATGGTGGCTCTATG</b> GTGAGCAAG
<sup>[7]</sup> pACUH-mTagBFP2 <sub>11</sub> -Emerald-Clc (R)	CCTTCACAAAGATCCTCTAGAC <b>CTA</b> GCGGGA <b>CAGTG</b>
<sup>[7]</sup> pACUH-mTagBFP2 <sub>11</sub> -sfGFP-β-act (R)	CCTTCACAAAGATCCTCTAGACTAGAAAGCA <b>TTTGC</b>
<sup>[7]</sup> pACUH-mTagBFP2 <sub>11</sub> -β-actin (F)	TCCGGACTCAGATCTGGC
<sup>[7]</sup> pACUH-mTagBFP2 <sub>11</sub> -β-actin (R)	ATTAAGCTTGTGCCCCAG
<sup>[8]</sup> pACUH-mEmerald-Tub-TagBFP2 <sub>11</sub> (F)	GGGAATTCGTTAACAGATCT <b>ATG</b> GTGAGCAAGGGC
<sup>[8]</sup> pACUH-mEmerald-Tub-TagBFP2 <sub>11</sub> (R)	CCTTCACAAAGATCCTCTAGAT <b>TTAATTAAGCTTGTGCCCCAGTTTGCTAGGGAGGTGCGAGTATCTGGCCACTGCCACCTCGTGCTGCTCGACGTAGGTCTCAGAGTATTCCTCTCCTTCTTCCTCA</b>
mTagBFP2 <sub>11</sub> -Histone H3.3A gene fragment	GGGAATTGGGAATTCACC <b>ATG</b> GCACGTACCAAGCAAACAGCCCGTAAATCGACCGGAGGCAAGGCGCCCCGCAAGCAGCTGGCCACC <b>AAGGCGGCCCGTAAATCGGCGCCATCCACCGGCGGAGTGAAGAAGCCACATCGCTACCGTCTGGAACGGTGGCCCTGCGTGAGATT</b> CGTTCGCTACCAGAAGTCCACGGAGCTGCTCATCCGCAAGCTGCCGTTCCAGCGTCTGGTGCAGGATAGCCCAGGACTTCAAGACCGATCTGCGCTTCCAGTCGGCGGCCATTGGAGCCCTACAGGAGGCCAGCGAGGCGTACCTGGTTCGGTCTGTTTCGAGGACACCAATCTGTGCGCCATTCACGCCAAGCGCGTCAACATTATGCCCAAGGACATCCAGCTGGCCAGACGCATCCGTGGCGAGCGGGCCGGTGGATCG <b>GAGACCTACGTCGAGCAGCAGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAA</b> ACTGGGGCACAAGCTTAAT <b>TAG</b> ATCTGCGGCCGCGG

### Split FP<sub>11</sub>-tag

Start or stop codon

(F)orward primer

(R)everse primer

<sup>[1]</sup> *pACUH-GFP<sub>1-10</sub><sup>sec</sup>* was generated by deleting the SEHDEL sequence of *pACUH-SP-GFP<sub>1-10</sub>-SEHDEL* used in previous work (3).

<sup>[2]</sup> *mCherry* was amplified by PCR from *pcDNA3.1-mCherry-CAAX* with a 3' primer encoding *GFP<sub>11</sub>* and cloned together with the *CG7630* gene fragment into the EcoRI/NotI sites of *pACUH*.

[3] *pACUH-GFP<sub>11</sub>-Dscam1* was generated in two steps. First, DNA from the extracellular domain was subcloned into *pBluescript (pBS-Dscam1 [1-1684 nucleotide])*, and PCR-based mutagenesis of the plasmid using Q5 polymerase was used to create *pBS-GFP<sub>11</sub>-Dscam1 [1-1684]*. Second, *GFP<sub>11</sub>-Dscam1 [1-1684]* and the remainder of *Dscam1 (Dscam1 [1685-6463])* were individually amplified by PCR. The two PCR products were ligated into the EcoRI/BglII sites of *pACUH*

[4] An *sfCherry2<sub>11x7</sub>-β-actin* construct was generated from *pACUH-sfGFP-β-actin (3)*. The *sfCherry2<sub>11x7</sub>* fragment was introduced into this plasmid, replacing *sfGFP*. An *sfCherry2<sub>11</sub>-β-actin* construct was made by replacing *sfCherry2<sub>11x7</sub>* with *sfCherry2<sub>11</sub>*.

[5] Using *pACU2\_CD4-mIFP T2A HO1* (plasmid 72441, Addgene) as a template, the *CD4-mIFP T2A HO1* region was amplified by PCR with a 3' primer encoding *FP<sub>11</sub>*, and inserted between the BglII/XbaI sites of *pACUH*.

[6] *sfGFP* was amplified by PCR from *pACUH-β<sub>2</sub>AR-sfGFP* with a 5' primer encoding *mApple<sub>11</sub>*, and cloned into the EcoRI/BglII sites of *pACUH*.

[7] *mTagBFP2<sub>11</sub>-mEmerald-Clc* and *mTagBFP2<sub>11</sub>-sfGFP-β-actin* were PCR-amplified from *mEmerald-Clathrin-15* (plasmid 54040, Addgene) and *pACUH-sfGFP-β-actin (3)*, respectively, and inserted into the BglII/XbaI sites of *pACUH*. *pACUH-mTagBFP2<sub>11</sub>-β-actin* was constructed by deleting the *sfGFP* sequence in *pACHU-mTagBFP2<sub>11</sub>-sfGFP-β-actin*.

[8] *mEmerald-α-tubulin* was PCR-amplified from *mEmerald-Tubulin-C-18* (plasmid 54292, Addgene) with a 3' primer encoding *mTagBFP2<sub>11</sub>*. We cloned the resulting fragment into the BglII/XbaI sites of *pACUH*.

**Table S5****Amino acid sequences of spacer-inserted red-colored split FPs**

<b>FP<sub>1-10/11</sub></b>	<b>aa. sequence</b>
Spacer-inserted sfCherry2 <sub>1-10/11</sub>	MEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGHPYEGTQ TAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSF PEGFTWERVMNFEDGGVVTVTQDSSLQDGQFIYKVKLLGINFPS DGPVMQKKTMGWEASTERMYPEDGALKGEINQRLKLDGGHY DAEVKTTYKAKKPVQLPGAYNVDIKLDITSHNED <b>GGGGSEGGGS</b> <b>GGPGSGGEGSAGGGSAGGGS</b> YTIVEQYERAEARHSTHHHHHH
Spacer-inserted sfCherry2 <sub>1-10/</sub> mTagBFP2 <sub>11</sub>	MEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGHPYEGTQ TAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSF PEGFTWERVMNFEDGGVVTVTQDSSLQDGQFIYKVKLLGINFPS DGPVMQKKTMGWEASTERMYPEDGALKGEINQRLKLDGGHY DAEVKTTYKAKKPVQLPGAYNVDIKLDITSHNED <b>GGGGSEGGGS</b> <b>GGPGSGGEGSAGGGSAGGGS</b> SETYVEQHEVAVARYCDLPSKL GHKLNHHHHHH

**30-aa spacer***His<sub>x6</sub>-tag*

**Table S6**  
**Specific genotypes in each experiment used in this study**

Figure	Genotype
Fig. 1C	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11</sup> ; <i>1</i>
Fig. 1D	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i>
Fig. 1F	w; <i>Or47b-Gal4</i> UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i>
Fig. 1G	w; <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i>
Fig. 1H	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i>
Fig. 1I	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i> (top)
Fig. 1J	yw; <i>MkPT-GFSTF</i> ; <i>1</i> Ter-nlM102844-GFSTF; <i>1</i> (bottom)
Fig. 2B	w; UAS- <i>stCherry2</i> <sup>1-10</sup> / +; UAS- <i>mCD8-stCherry</i> <sup>11</sup> / <i>elav-GAL4</i>
Fig. 4A	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / UAS- <i>stCherry2</i> <sup>1-10</sup> ; <i>elav-GAL4</i> / <i>MkPT-ntTagBFP2</i> <sup>11</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11</sup> ; <i>0</i>
Fig. 4B	yw; <i>MkPT-GFSTF</i> ; <i>0</i> CASKIM100989-GFSTF; <i>0</i> / TM6
Fig. 4C	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / UAS- <i>stCherry2</i> <sup>1-10</sup> ; + / <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 4D	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / UAS- <i>stCherry2</i> <sup>1-10</sup> ; <i>elav-GAL4</i> / <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> dy <sup>sc</sup> [M101694- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 4E	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / UAS- <i>stCherry2</i> <sup>1-10</sup> ; <i>elav-GAL4</i> / <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> elaf6[M100261- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 4G	w; <i>Or47b-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> ; UAS- <i>CD4-tGFP</i> / <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 5A	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / UAS- <i>stCherry2</i> <sup>1-10</sup> ; <i>elav-GAL4</i> UAS-GFP <sup>1-10</sup> / <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 5C	w; <i>dilp2-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Fig. 5A	w; <i>engrailed-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (top)
Fig. 5A	w; <i>engrailed-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO (bottom)
Fig. 5A	w; <i>engrailed-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO (bottom)
Fig. 5A	w; <i>elav-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (top)
Fig. 5A	w; <i>elav-GAL4</i> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (middle)
Fig. 5A	w; <i>elav-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO (bottom)
Fig. 5A	w; <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (top)
Fig. 5A	w; <i>dilp2-GAL4</i> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (middle)
Fig. 5A	w; <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> / CyO (bottom)
Fig. 5A	w; CG-GAL4 UAS-GFP <sup>1-10</sup> / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (top)
Fig. 5A	w; CG-GAL4 / CyO; UAS- $\beta$ -2-AR-GFP <sup>11</sup> / TM6B (middle)
Fig. 5A	w; CG-GAL4 UAS-GFP <sup>1-10</sup> / CyO (bottom)
Fig. 5A	w; CG-GAL4 / UAS-GFP <sup>1-10</sup> ; UAS- <i>Calcitriol</i> -GFP <sup>11</sup> / TM6B
Fig. 5A	w; 201Y-GAL4 / UAS-GFP <sup>1-10</sup> ; UAS-GFP <sup>11</sup> ; <i>Discant1</i> [exon 17.1] / TM6B
Fig. 5A	yw;
Fig. 5A	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i>
Fig. 5A	w; // CyO; <i>MkPT-ntTagBFP2</i> <sup>11</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11</sup> ; <i>0</i> / TM3
Fig. 5A	w; <i>elav-GAL4</i> / +; UAS- <i>stCherry2</i> <sup>1-10</sup> / +
Fig. 5A	yw; <i>MkPT-GFSTF</i> ; <i>0</i> dy <sup>sc</sup> [M102729-GFSTF; <i>0</i>
Fig. 5A	yw; <i>MkPT-GFSTF</i> ; <i>0</i> Elaf6[M100261-GFSTF; <i>0</i> / TM6
Fig. 5A	yw; (left)
Fig. 5A	w; <i>elav-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> / CyO; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> (right)
Fig. 5A	w; <i>Or47b-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> ; <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> / TM3
Fig. 5A	w; <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> / <i>dilp2-GAL4</i> UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i>
Fig. 5A	w; <i>Or47b-GAL4</i> UAS- <i>stCherry2</i> <sup>1-10</sup> ; UAS-GFP <sup>1-10</sup> / <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; <i>MkPT-ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i> CASKIM101748- <i>ntTagBFP2</i> <sup>11x7</sup> ; <i>0</i>
Video S1	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; UAS-GFP <sup>11</sup> - <i>actin</i>
Video S2	w; <i>elav-GAL4</i> / UAS-GFP <sup>1-10</sup> ; <i>MkPT-GFP</i> <sup>11x7</sup> ; <i>1</i> Ter-nlM107828-GFP <sup>11x7</sup> ; <i>1</i> ; UAS- <i>mCD8-mRFP</i>
Video S2	yw; <i>MkPT-GFSTF</i> ; <i>1</i> Ter-nlM102844-GFSTF; <i>1</i>

## Legends for Movies S1 to S2

### **Movie S1. Movie of split GFP-tagged actin in axonal growth cones**

Time-lapse movie shows dynamic filopodia activity in SNb (segmental nerve b) motor growth cones in an hour 13 AEL embryo co-expressing *GFP<sub>1-10</sub>* and *GFP<sub>11</sub>-β-actin* under the control of *e/av-GAL4*. Images were acquired every 10 sec in a single plane.

Arrowheads indicate individual filopodia. Scale bar, 10 μm.

### **Movie S2. Movie of Ten-m axonal transport in motor axons of 3<sup>rd</sup> instar larva**

Time-lapse movie shows retrograde and anterograde transport of Ten-m tagged with *GFP<sub>1-10/11x7</sub>* (top) and full-length GFP (bottom) in larval motor axons. Axon bundles are aligned with cell bodies on the left and axon terminals on the right. Images were acquired every 0.5 sec. Arrowheads indicate Ten-m puncta which are transported along axons. Scale bar, 5 μm.

## SI References

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