Supplemental Figure S1: (A) Immunoblot analysis of third instar larval homogenate using anti-Arfip antibody demonstrates that D42-Gal4 can drive the expression of Arfip from the arfip^{P1} insertion resulting in increases Arfip protein level by ~50-60% compared to wild type. Graph represents the quantification of Arfip protein normalized to actin of the indicated genotypes. (B) Immunoblots of co-immunoprecipitation analysis from S2 cells co-expressing FLAG-DNGlued and HA-Arfip fusion proteins incubated with anti-FLAG antibody coated beads. Inclusion of a competing FLAG peptide during incubation with beads completely abolished binding of Arfip-HA. Cell lysate of S2 cells co-expressing FLAG-DNGlued and HA-Arfip is shown as input. (C) Immunoblots of co-immunoprecipitation analysis from S2 cells coexpressing Arfip^{BAR}-FLAG and Arf6-HA fusion proteins incubated with anti-FLAG antibody coated beads. Inclusion of a competing FLAG peptide during incubation with beads completely abolished binding of Arf6-HA. Analysis of S2 cells expressing only Arf6-HA showed very low levels of non-specific binding to FLAG beads. Cell lysate of S2 cells coexpressing Arfip^{BAR}-FLAG and Arf6-HA or only Arf6-HA shows equivalent amount of protein materials added in each co-immunoprecipitation experiment.

Supplemental Movie S1: Live imaging of axonal transport of syb-GFP vesicles in wild type larvae. Representative movie of axonal tracts from a *OK6/UAS-syb-GFP;* +/+ larvae. The larval VNC is located to the left of the movie.

Supplemental Movie S2: Live imaging of axonal transport of syb-GFP vesicles in *arfip*^{12/71}

mutant larvae. Representative movie of axonal tracts from a *OK6/UAS-syb-GFP; arfip*^{12/71}

larvae. The larval VNC is located to the left of the movie.

Supplemental Material

Table S1: Molecular and genetic information for inserts altering synapse growth						
Insertion	Mutar	t Mutan	t Insert ³	Predicted	Predicted function ⁵	
Genotype	гуре	Class		Gene		
Enhancers						
<i>P{EP}CG17184^{EY118/4}</i>	E2	L/G	5' UTR	CG17184	Membrane trafficking	
<i>P</i> { <i>XP</i> } <i>CG</i> 17184 ^{d04252}	E2	L	3' UTR	CG17184	Membrane trafficking	
<i>P{EP}EY12448</i>	E2	n.d.	n.d.	none	n.a.	
PBac{PB}fan ^{c04756}	E2	L/G	5′	fan	vesicle-associated	
P{EP}EY20330	E2	G	5′	CG13813	Kinase activity	
P{EP}klar ^{EY01576}	E1	L	CDS	klar	MT transport	
P{EP}bbg ^{EY05191}	E1	L	CDS	bbg	Disc development	
PBac{PB}Sirt2 ^{c03323}	E1	L/G	5' UTR	Sirt2	Histone deacetylase	
<i>P{EP}EY06888</i>	E1	n.d.	n.d.	none	n.a.	
$P{EP}GRHR^{EY11371}$	E1	L/G	5' UTR	GRHR	Peptide receptor	
Suppressors ¹						
P{EP}nesd ^{EY11086}	S 3	L/G	5' UTR	nesd	CHO binding	
<i>P{EP}Coop</i> ^{EY13293}	S 3	L/G	5' UTR	Соор	RNA transcription	
$P{EP}CG42575^{EY04050}$	S2	L/G	5' UTR	CG42575	Transporter Activity	
$P\{EP\}B4^{EY14645}$	S2	L	Intron	B4	Disc development	
$P{EP}CG4562^{EY09703}$	S1	L/G	5' UTR	CG4562	Transporter Activity	
$P{EP}TM9SF4^{EY00960}$	S1	L/G	5' UTR	CG7364	Transporter Activity	

All data collected from P-element screen consisting of the indicated single copy insertion in trans to the *D42*, *DNGlued* recombinant chromosome. Insertion genotypes obtained from Flybase.org.

^T– Refers to the effects of inserts on viability when in trans to *D42*, *DNGlued* at 25C. Enhancers (E) *enhance* the effects of the *D42*, *DNGlued* allele on viability, and suppressors (S) have the opposite effects on viability. 1= weakest, 3= strongest. The lethality due to one copy of the *D42*, *DNGlued* is ~30%. Note that E2 = 100% lethality and E1 = < 60% lethality. S3 = 100% viability.

²–Predicted mutant class of insertion based on P-element type and location of insertion. L equals loss-of-function and G equals gain-of-function. Because many of the P-elements landed in 5' UTR, inserts could be either L or G (L/G).

³ – Refers to the position of the insert in the reported gene based on genetic information provided by Flybase.org. UTR=untranslated mRNA, CDS=coding sequence of mRNA. 5' refers to insertion site relative to gene.

⁴– Candidate genes predicted by the proximal location of insert and genes determined from the physical map data present at Flybase.org for each insert. # indicates insert location verified by iPCR.

⁵– Gene function data obtained from Flybase.org for gene listed in predicted gene column.

Table S2: Syb-GFP vesicle axonal transport analyses						
Genotype ¹	n ²	% particles moving ³	Axonal Density ⁴			
wt	43	55.8	0.0673			
	(8)	(76/136)	(0.0037)			
arfip ^{12/71}	56	57.6	0.0586			
	(11)	(90/156)	(0.0028)			

¹-Refers only to the genotype of 3rd chromosome, both genotypes have the following 2nd chromosome genotype: *OK6-Gal4/UAS-syb-GFP*.

²-Indicates the total number of axons analyzed for movement and density. The number of animals analyzed is presented within the parenthesis.

³-Represents the percentage of particles within a given region of interest that move in either direction during acquisition.

⁴-Represents the average number of syb-GFP transport vesicles per length of axon (particle/um). Values are not significantly different between wt and *arfip* mutants.



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