

1 **Rapid active zone remodeling consolidates presynaptic potentiation**

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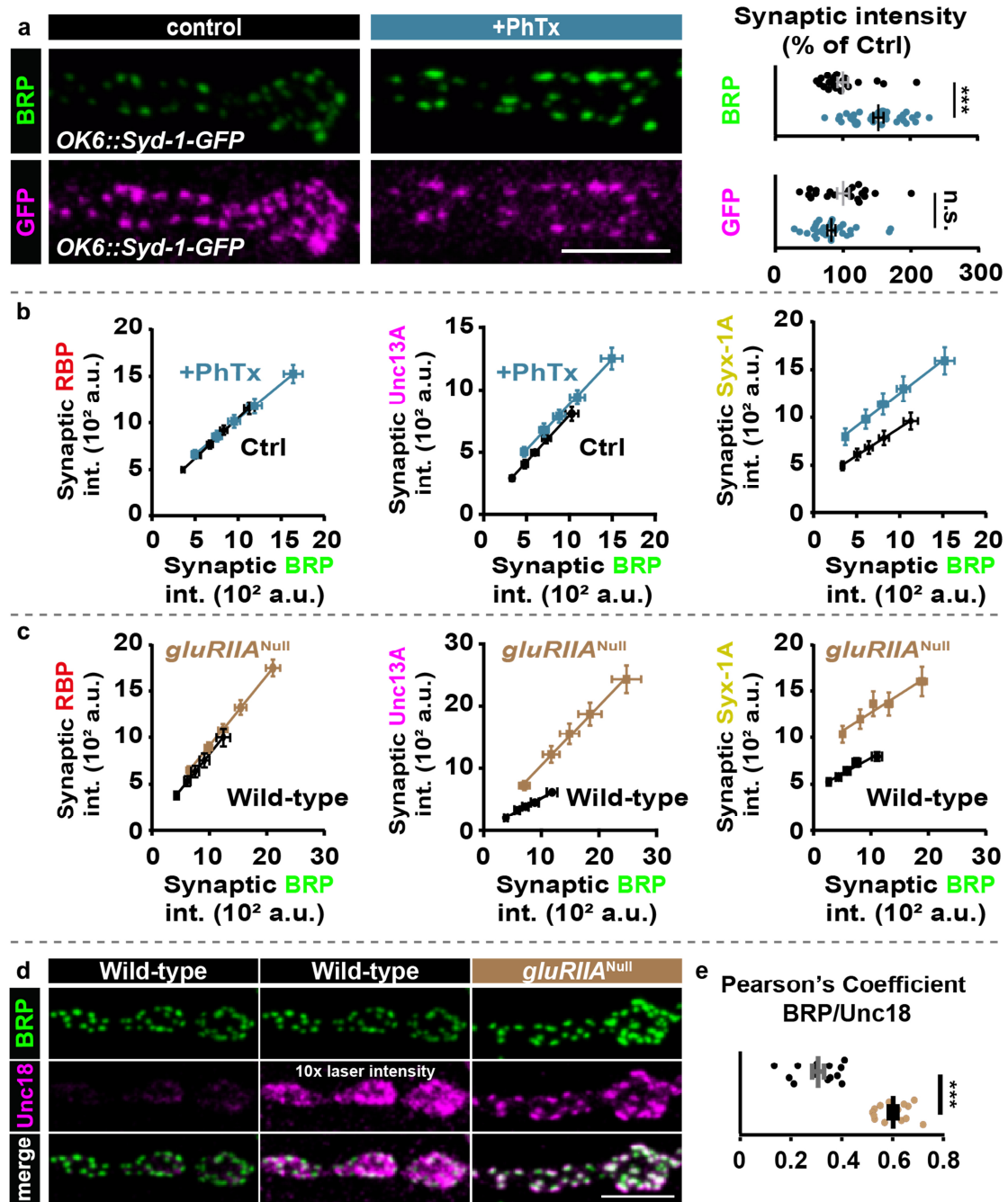
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12 **Supplemental figures, titles and legends**

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14 Supplementary Figure 1 – related to Figure 1



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16 **Supplementary Figure 1: Rapid and chronic homeostatic potentiation enhances AZ**
 17 **protein levels.**

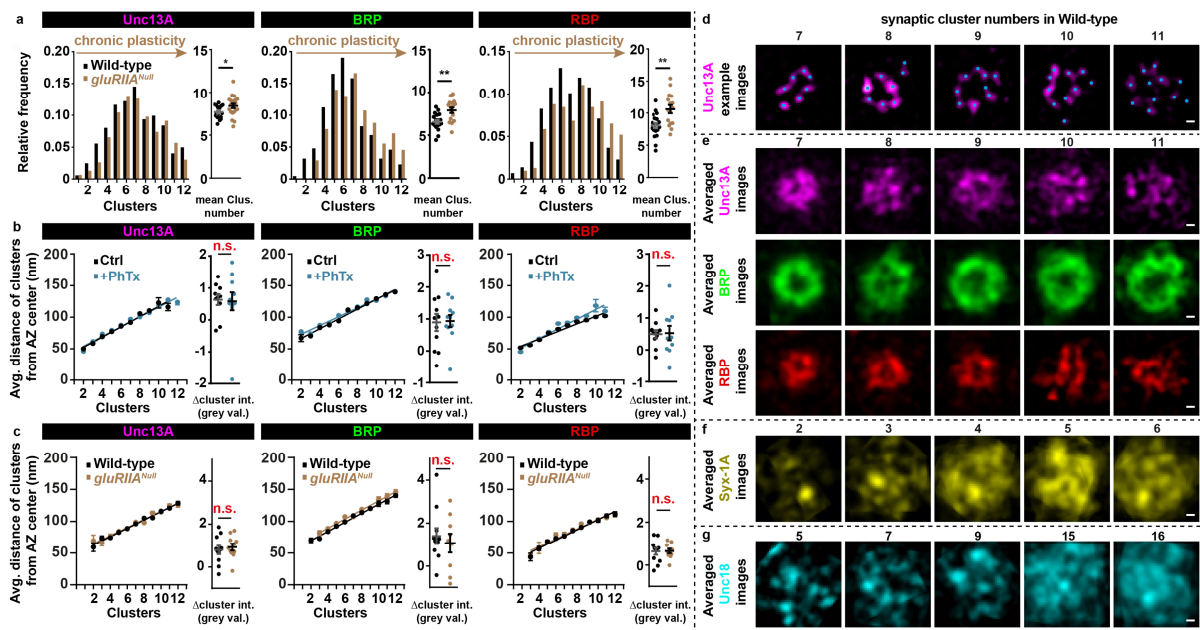
18 **(a)** Confocal images (left) and quantification (right) of synaptic BRP and GFP in
 19 motoneurons overexpressing Syd-1-GFP, labelled with the indicated antibodies. **(b,c)** Scatter
 20 plot of average BRP/RBP-, BRP/Unc13A- and BRP/Syx-1A-intensity levels of AZs binned

21 by their BRP intensity fit with regression lines for Ctrl (black) and PhTx (blue) treated (b)
22 and in Wild-type (black) and *gluRIIA*^{Null} mutant (light brown) (c) larvae. **(d)** Confocal scans
23 of muscle 4 NMJs of segment A2-4 from 3rd instar Wild-type and *gluRIIA*^{Null} larvae labelled
24 with the indicated antibodies. In the second Wild-type column, the laser intensity for Unc18
25 was increased tenfold. **(e)** Quantification of Pearson's correlation coefficient for BRP and
26 Unc18 in Wild-type (black) and *gluRIIA*^{Null} (light brown) larvae. Source data as exact
27 normalized and raw values, detailed statistics including sample sizes and P values are
28 provided in the Source Data file. Scale bars: (a,d) 5 μ m. Statistics: Mann-Whitney U test.
29 *** $P \leq 0.001$; n.s., not significant, $P > 0.05$. All panels show mean \pm s.e.m..

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32 **Supplementary Figure 2 – related to Figure 2**

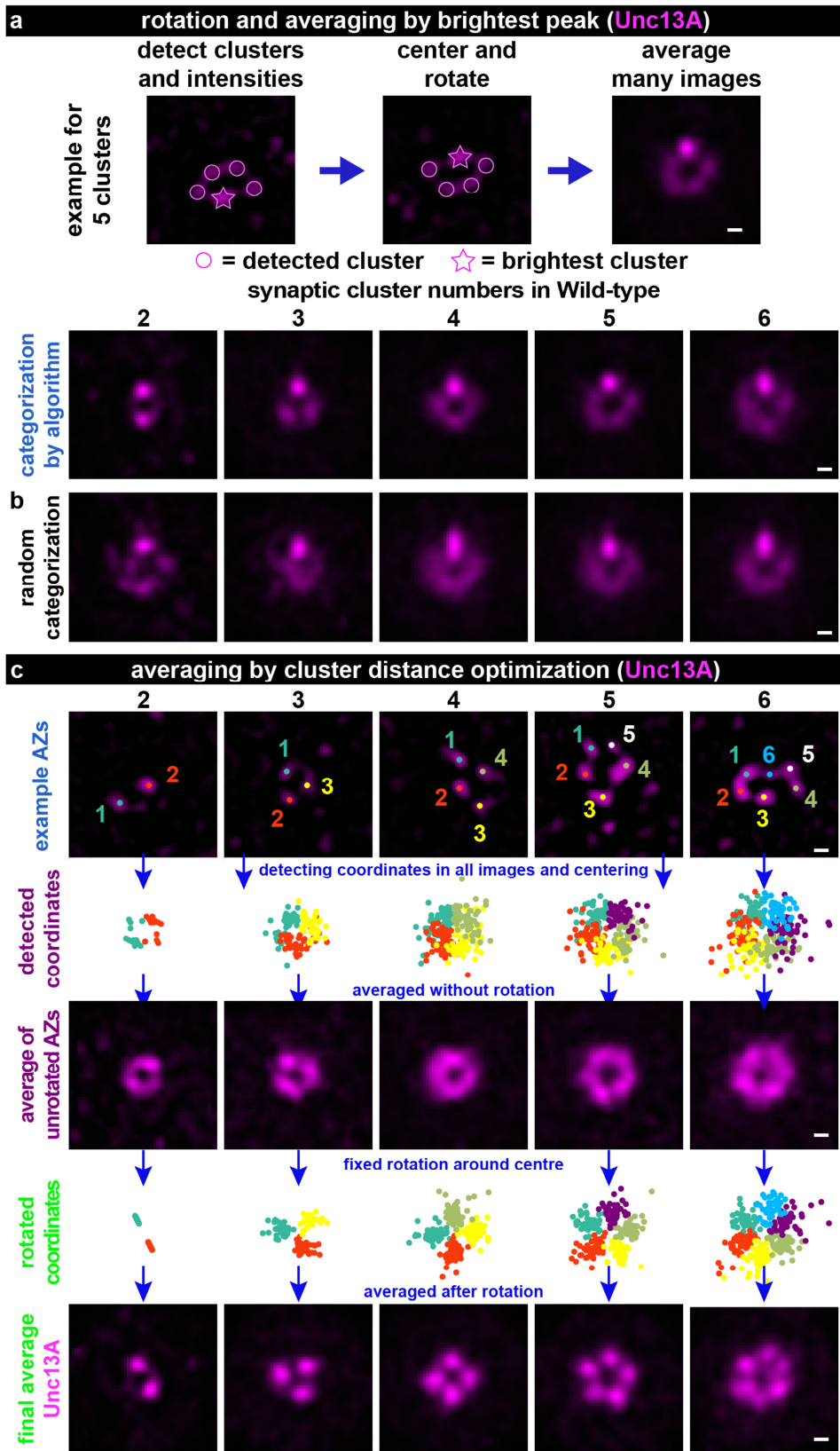


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34 **Supplementary Figure 2: Analysis of AZ nano-architecture**

35 **(a)** Frequency distribution of clusters (left) and average cluster number (right) of Unc13A,
 36 BRP and RBP in Wild-type (black) or *gluRIIA*^{Null} (light brown) larvae. **(b,c)** Average AZ
 37 radius (left) and cluster intensity change (right) of Unc13A, BRP and RBP without (Ctrl;
 38 black) and with 10 minutes PhTx (+PhTx; blue) treatment (b) and in Wild-type (black) or
 39 *gluRIIA*^{Null} (light brown) (c) larvae. **(d)** Example Unc13A STED-images of AZs with 7-11
 40 clusters. **(e)** Average of rotated STED images stained against Unc13A (magenta), BRP
 41 (green) and RBP (red) with 7-11 clusters. **(f,g)** Average of rotated STED images stained
 42 against Syx-1A with 2-6 clusters (e) or Unc18 with 5, 7, 9, 15 and 16 clusters (f). Source data
 43 as exact raw values, detailed statistics including sample sizes and P values are provided in the
 44 Source Data file. Scale bars: (d-g) 50 nm. Statistics: Mann-Whitney U test. **P ≤ 0.01; n.s.,
 45 not significant, P > 0.05. All panels show mean ± s.e.m..

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49 Supplementary Figure 3: AZ protein averaging procedures exemplified for Unc13A.

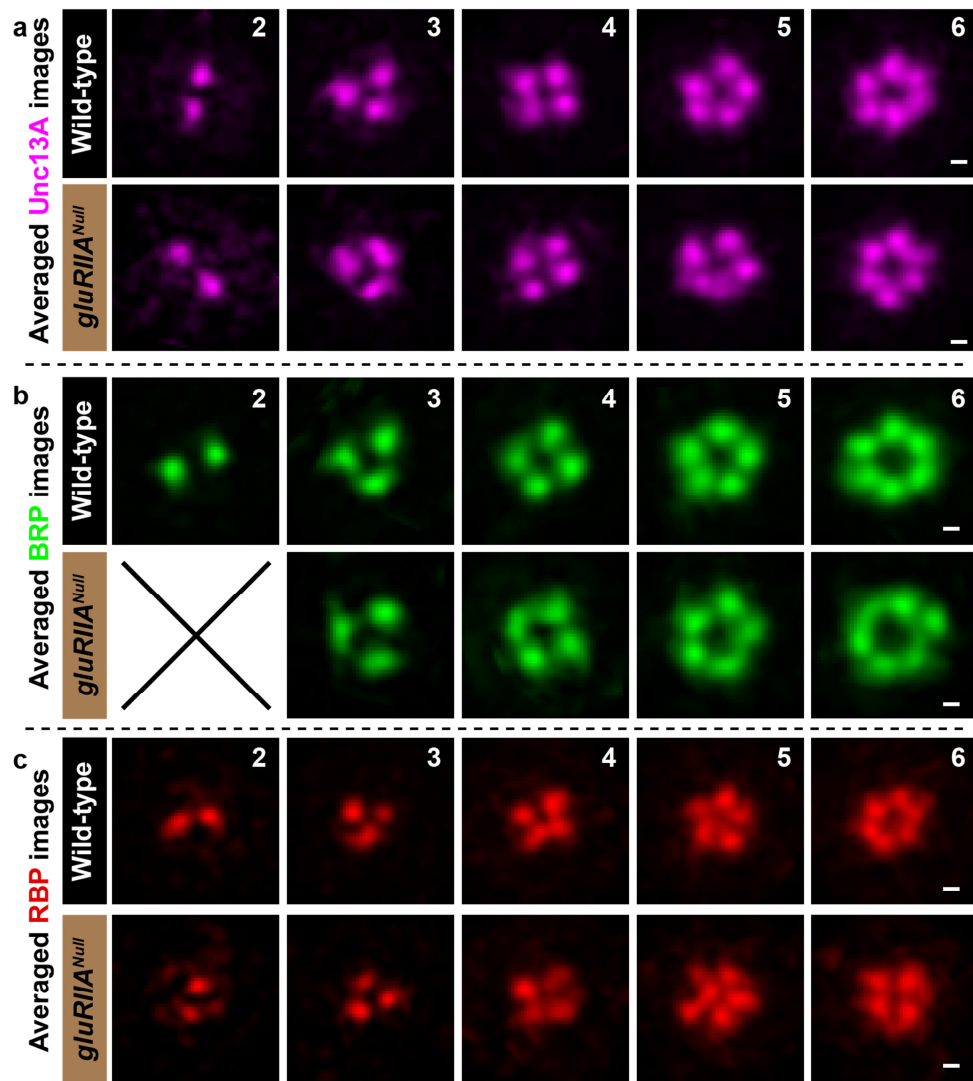
50 **(a,b)** Procedure 1: Single AZ STED images of Unc13A after categorization via peak finder
51 algorithm (a) or after random categorization (b) are centered and only the highest intensity
52 peak is considered for AZ rotation. Whole images are rotated to align the highest intensity
53 peak on the vertical midline between the top quadrants. Images are shown for 2 to 6 clusters.
54 **(c)** Averaging procedure of Unc13A-labelled single AZ images. The top row contains
55 example AZ with 2-6 Unc13A clusters, marked by colored dots. In the second row,
56 corresponding cluster positions from all AZ images containing the same number of clusters
57 are shown together; in each AZ, clusters are counted in a counter-clockwise manner and all
58 detected clusters from all images are shown by their rank in identical colors. Without further
59 processing, averaging these images reveal a circular fluorescence pattern, because of the
60 random localization of clusters in the different images (third row). Fixed rotation of cluster
61 positions per image optimizes the overlap between the clusters of all images, and averaging
62 of images then reveals a geometrical pattern (bottom row). Images are 510x510 nm. Scale
63 bars: 50 nm.

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67 **Supplementary Figure 4 – related to Figure 2**



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69 **Supplementary Figure 4: Chronic plasticity does not alter principle Unc13A/BRP/RBP**

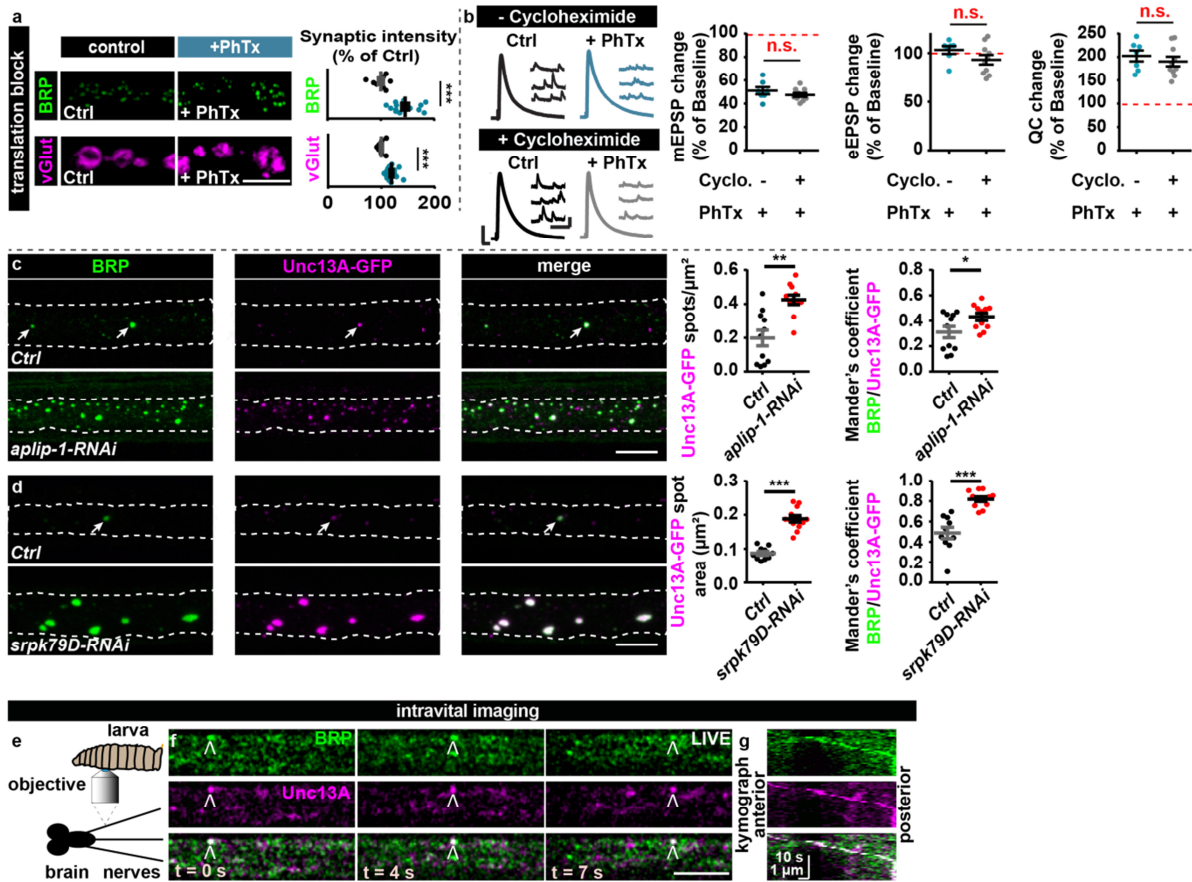
70 **single AZ protein architecture.**

71 **(a-c)** Averages of rotated STED images stained against Unc13A (a), BRP (b) and RBP (c)

72 with 2-6 modules in Wild-type or *glulRIIA*^{Null} larvae. Scale bars: 50 nm.

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74 **Supplementary Figure 5 – related to Figure 3**



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76 **Supplementary Figure 5: Translation block maintains PHP and AZ-remodeling,**

77 **Unc13A co-accumulates in the axons of 3rd instar larvae upon *aplip-1*-KD and *srpK79d*-**

78 **KD, BRP and Unc13A were seen to co-transport in motoneuronal axons.**

79 **(a)** Confocal images and quantification of AZ-fluorescence intensities at Wild-type NMJs

80 labelled with the indicated antibodies after translation blockage with Cycloheximide without

81 (Ctrl; black) and with 10 minutes PhTx (+PhTx; blue) treatment. Note that BRP AZ-levels

82 were not changed after 10 minutes of Cycloheximide treatment in comparison to untreated

83 NMJs (single BRP-AZ-levels without Cycloheximide: 1912 ± 109.3 a.u. vs. with

84 Cycloheximide: 1943 ± 57.88 a.u.; P-value 0.7945, Student's t-test). **(b)** (left) Representative

85 traces of eEPSP (evoked) and mEPSP (spont.) with or without the translation blocker

86 Cycloheximide, and after control (Ctrl; black) or PhTx (+PhTx; blue) treatment for 10

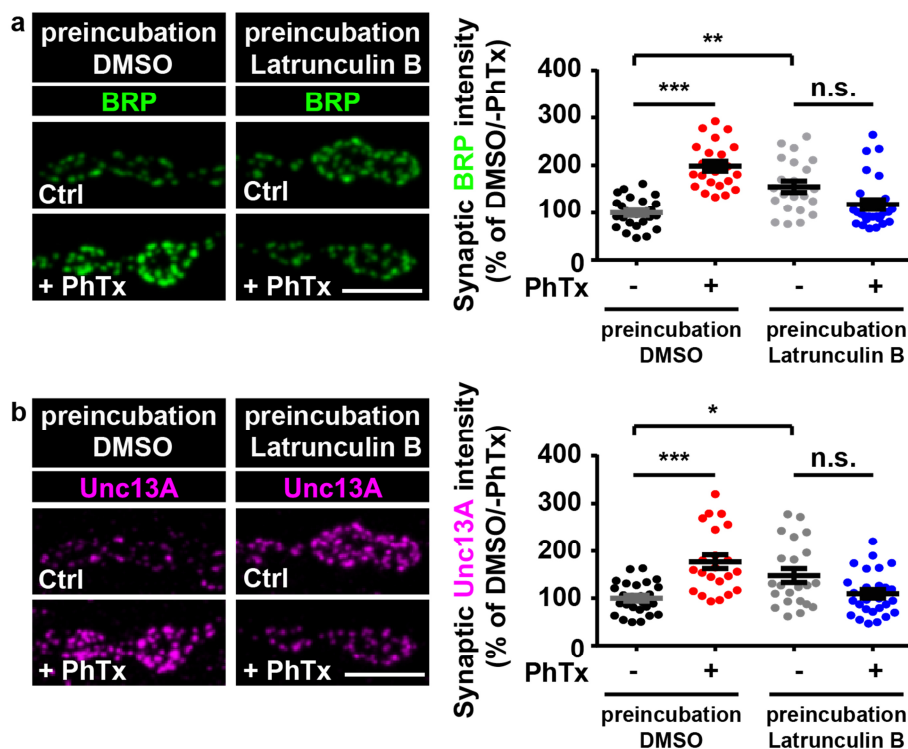
87 minutes. (right) Quantifications of percentage change of mEPSP amplitude, eEPSP amplitude

88 and quantal content (QC) in PhTx-treated Wild-type (blue) cells in the presence (+) or
89 absence (-) of Cycloheximide compared to baseline of each control treatment (without PhTx,
90 dashed red line corresponds to 100%/no change). **(c)** Nerve bundles of segments A1–A3 from
91 third instar larvae of the respective genotypes labeled with the antibodies indicated. Arrows
92 indicate axonal spots co-positive for BRP and Unc13A-GFP in the control situation.
93 Quantification of axonal Unc13A-GFP spots per μm^2 and Mander's overlap coefficient for
94 BRP and Unc13A-GFP. **(d)** Nerve bundles of segments A1–A3 from third instar larvae of the
95 genotypes indicated labeled with the antibodies indicated. Arrows point to axonal spots co-
96 positive for BRP and Unc13A-GFP in the control situation. Quantification of axonal
97 Unc13A-GFP spot area in μm^2 and Mander's overlap coefficient for BRP and Unc13A-GFP.
98 Dashed lines outline the axonal area. Exact values, detailed statistics including sample sizes
99 and P values are listed in Supplementary Table 1. **(e)** Intravital imaging procedure. **(f,g)** Live
100 imaging in intact third instar larvae (f) and dual-color kymograph (g) of axonal BRP (green)
101 and Unc13A (magenta) showed anterograde co-transport of both proteins. See also **Movie 1**.
102 Source data as exact normalized and raw values, detailed statistics including sample sizes and
103 P values are provided in the Source Data file. Scale bars: (b) eEPSP: 50 ms, 4 mV; mEPSP:
104 250 ms, 1 mV; (a,c,d) 5 μm . Statistics: Mann-Whitney U test. * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq$
105 0.001. n.s., not significant, $P > 0.05$. All panels show mean \pm s.e.m..

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108 **Supplementary Figure 6 – related to Figure 3**



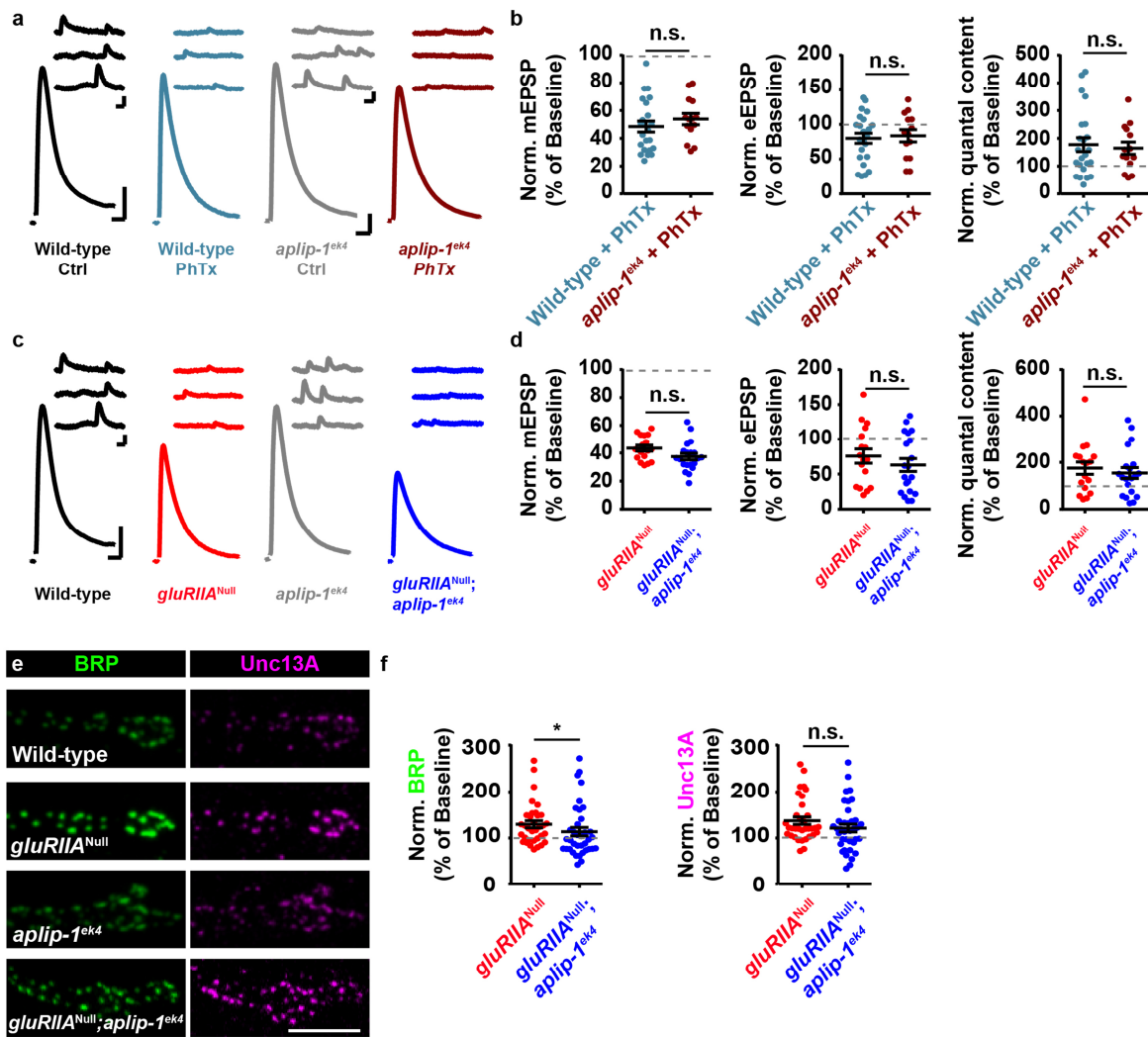
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110 **Supplementary Figure 6: Actin polymerization is required for rapid AZ-remodelling.**

111 **(a,b)** Confocal images and quantification of synaptic BRP or Unc13A intensities in % of
 112 DMSO/-PhTx without (preincubation DMSO) and with (preincubation Latrunculin B)
 113 labelled with the indicated antibodies without (Ctrl) and with 10 minutes PhTx (+PhTx)
 114 treatment. Source data as exact normalized and raw values, detailed statistics including
 115 sample sizes and P values are provided in the Source Data file. Scale bar: 5 μ m. Statistics:
 116 nonparametric one-way analysis of variance (ANOVA) test, followed by a Tukey's multiple
 117 comparison test. * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$; n.s., not significant, $P > 0.05$. All
 118 panels show mean \pm s.e.m..

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120 **Supplementary Figure 7 – related to Figure 5**



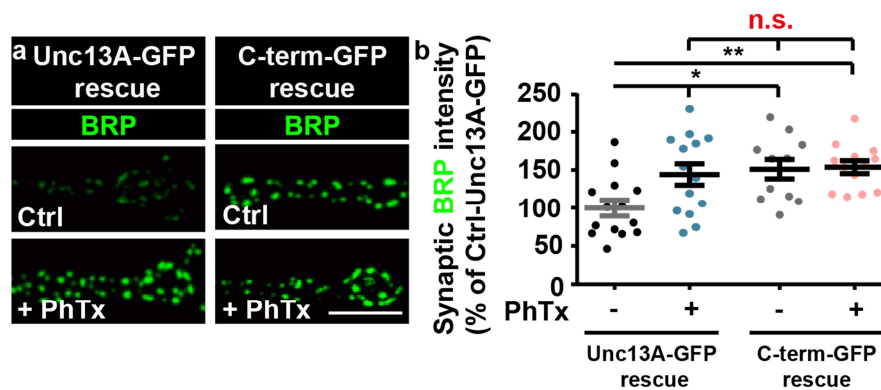
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122 **Supplementary Figure 7: Loss of Aplip-1 in *glurIIA*^{Null} mutants moderately (i.e. non-**
 123 **significantly at 5% level) impairs the expression of chronic homeostatic plasticity.**

124 **(a)** Representative traces of eEPSP (evoked) and mEPSP (spont.) of the indicated genotypes
 125 with and without PhTx-treatment. **(b)** Quantifications of percentage change of mEPSP
 126 amplitude, eEPSP amplitude and quantal content (QC) in PhTx-treated genotypes compared
 127 to baseline (no PhTx) for each genotype (dashed red line corresponds to 100%/no change).
 128 **(c,d)** Same as in (a,b) but for Wild-type (black), *glurIIA*^{Null} (red), *aplip-1*^{ek4} (grey) and
 129 *glurIIA*^{Null};*aplip-1*^{ek4} (blue) but compared to baseline values of Wild-type for *glurIIA*^{Null} and
 130 *aplip-1*^{ek4} for *glurIIA*^{Null};*aplip-1*^{ek4} (dashed red line corresponds to 100%/no change). **(e)**

131 Confocal of muscle 4 NMJs of abdominal segment 2-5 from 3rd instar larvae at Wild-type,
132 *gluRIIA*^{Null}, *aplip-1^{ek4}* and *gluRIIA*^{Null},*aplip-1^{ek4}* NMJs labelled with the indicated antibodies.
133 **(f)** Quantification of percentage change of synaptic BRP and Unc13A levels in *gluRIIA*^{Null}
134 (red) and *gluRIIA*^{Null};*aplip-1^{ek4}* (blue) mutants compared to baseline fluorescence values of
135 Wild-type for *gluRIIA*^{Null} and *aplip-1^{ek4}* for *gluRIIA*^{Null};*aplip-1^{ek4}* (dashed grey line
136 corresponds to 100%/no change). Source data as exact normalized and raw values, detailed
137 statistics including sample sizes and P values are provided in the Source Data file. See also
138 Supplementary figure 10 and 11 for non-normalized values. Scale bars: (a,c) eEPSP: 25 ms, 5
139 mV; mEPSP: 50 ms, 1 mV; (e) 5 μ m. Statistics: Student's T-test for all comparisons except
140 ((d) quantal content) and (f) where a Mann-Whitney U Test was performed. * $P \leq 0.05$; ** $P \leq$
141 0.01; *** $P \leq 0.001$; n.s., not significant, $P > 0.05$. All panels show mean \pm s.e.m..
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143 **Supplementary Figure 8 – related to Figure 6**

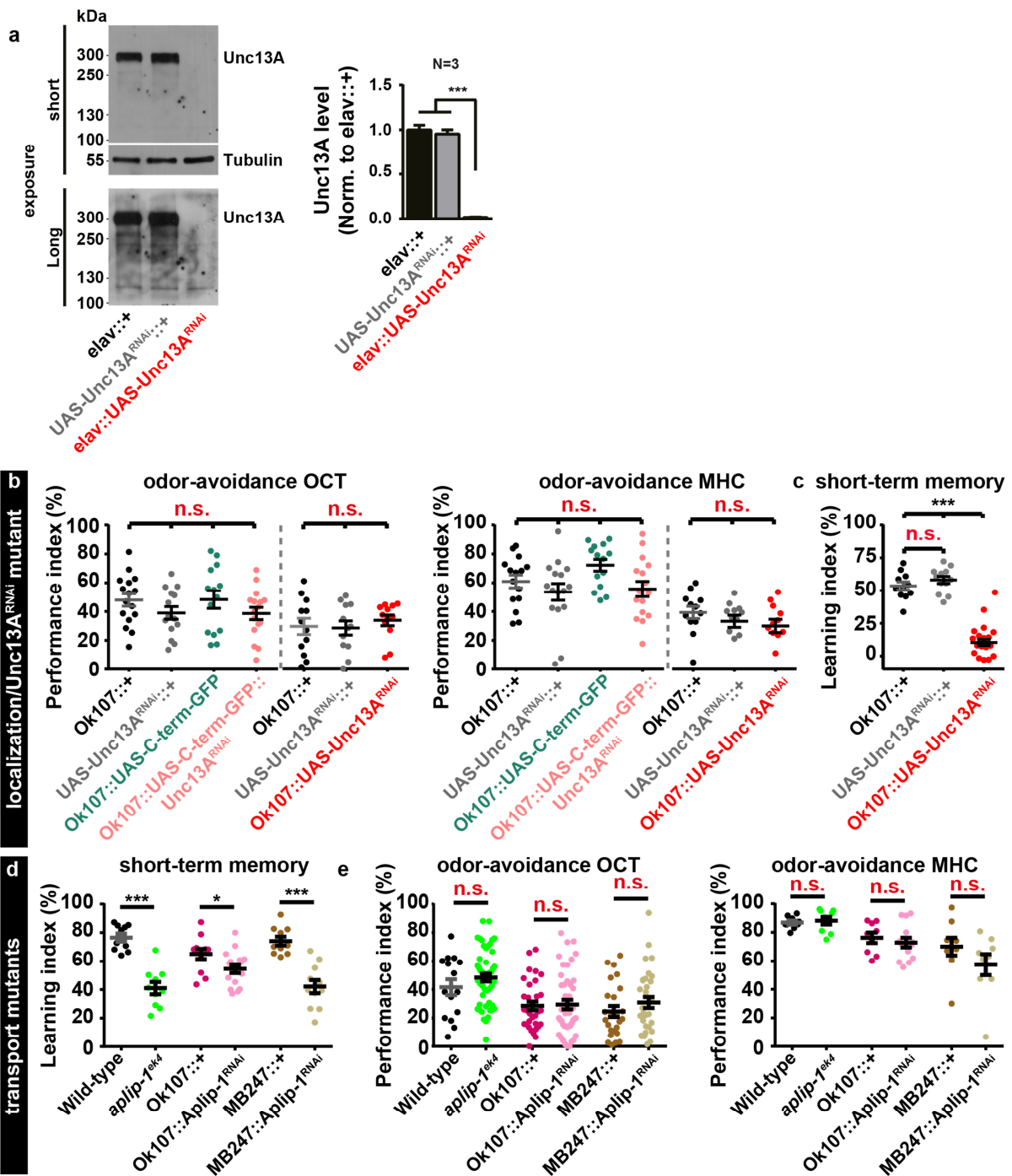


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145 **Supplementary Figure 8: Enhanced synaptic BRP levels and loss of AZ-remodeling at**
 146 ***unc13*^{Null} NMJs expressing the C-term GFP construct.**

147 **(a,b)** Confocal images and quantification of synaptic BRP intensities in % of Unc13A-GFP
 148 rescue at NMJs pan-neuronally re-expressing Unc13A-GFP or C-term-GFP in the *unc13*^{Null}
 149 background labelled with the indicated antibodies without (Ctrl; black (Unc13A-GFP rescue);
 150 grey (C-term-GFP rescue)) and with 10 minutes PhTx (+PhTx; blue (Unc13A-GFP rescue);
 151 light red (C-term-GFP rescue)) treatment. Source data as exact normalized and raw values,
 152 detailed statistics including sample sizes and P values are provided in the Source Data file.
 153 Scale bar: 5 μ m. Statistics: nonparametric one-way analysis of variance (ANOVA) test,
 154 followed by a Tukey's multiple comparison test. *P \leq 0.05; **P \leq 0.01; n.s., not significant,
 155 P > 0.05. All panels show mean \pm s.e.m..

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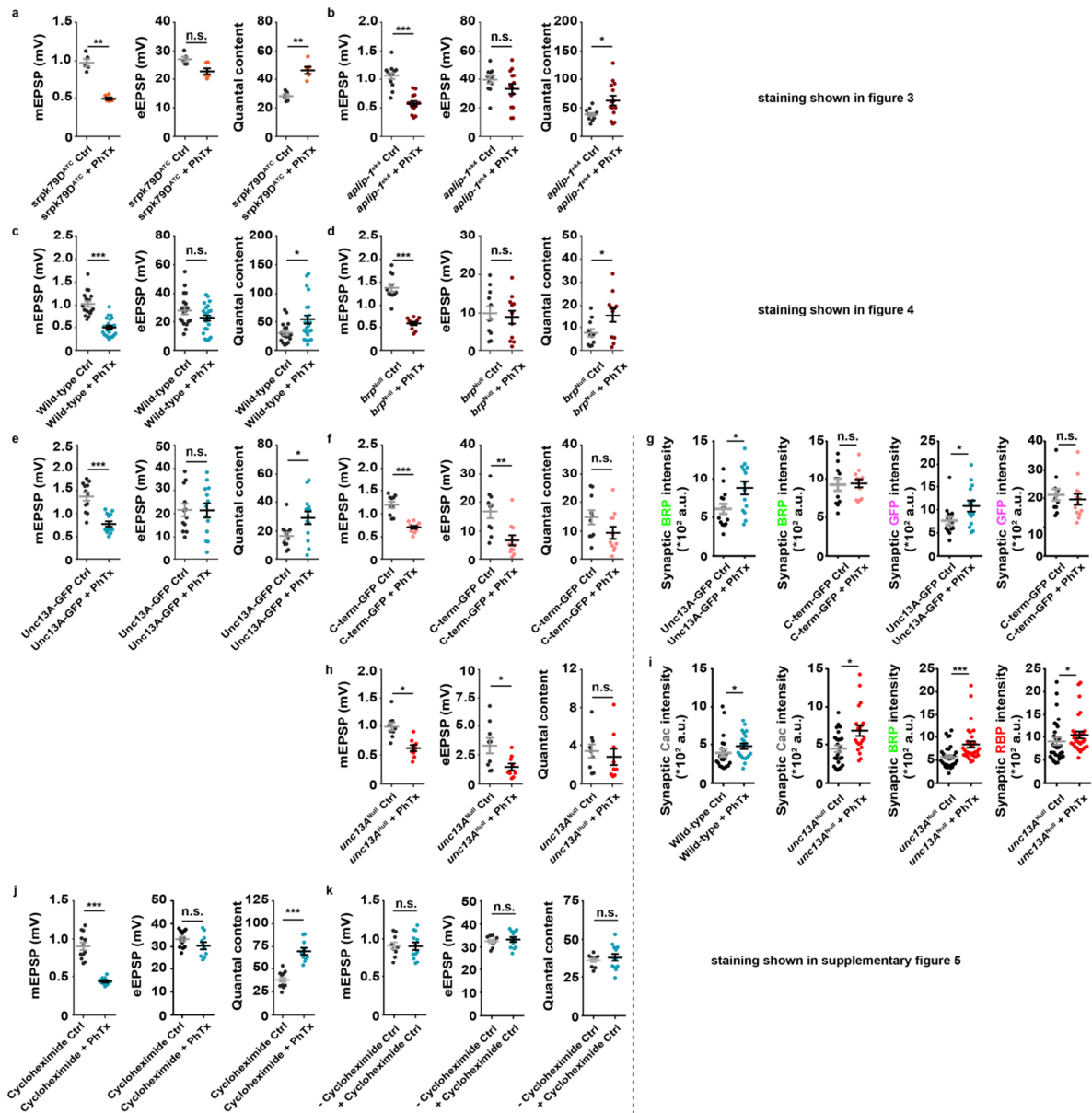
159 **Supplementary Figure 9: Efficiency of Unc13A-RNAi, odor avoidance controls for**
 160 **behavioral analyses and short-term memory impairment upon Unc13A-KD and in**
 161 **Aplip-1 mutants.**

162 **(a)** Whole brain western blot and quantification of Unc13A-levels normalized to driver-
 163 control of pan-neuronally expressed Unc13A^{RNAi} and control flies with short (top) and longer

164 exposure (bottom). **(b)** Quantification of odor-avoidance performance index of OCT (left) or
165 MHC (right) in the indicated genotypes. **(c)** Short-term memory scores after mushroom body-
166 specific Unc13A downregulation via locally driven RNAi expression (Ok107:: Unc13A^{RNAi})
167 compared to controls expressing the driver, but not the RNAi (Ok107::+) or the RNAi
168 without driver (UAS-Unc13A^{RNAi}::+). **(d)** Short-term memory scores in *aplip-1^{ek4}* mutant
169 flies compared to Wild-type and ones after mushroom body-specific Aclip-1 downregulation
170 via locally driven RNAi expression (Ok107::Aclip-1^{RNAi}) or (MB247::Aclip-1^{RNAi}) compared
171 to controls expressing the driver, but not the RNAi (Ok107::+ or MB247::+). **(e)**
172 Quantification of odor-avoidance performance index of OCT (left) or MHC (right) in the
173 indicated genotypes. Source data as exact normalized and raw values, detailed statistics
174 including sample sizes and P values are provided in the Source Data file. Statistics: (a-c)
175 nonparametric one-way analysis of variance (ANOVA) test, followed by a Tukey's multiple
176 comparison test. (d,e) Mann-Whitney U test. *P ≤ 0.05; ***P ≤ 0.001; n.s., not significant, P
177 > 0.05. All panels show mean ± s.e.m..

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179 **Supplementary Figure 10 – related to Figure 5, 6 and Supplementary Fig. 7**



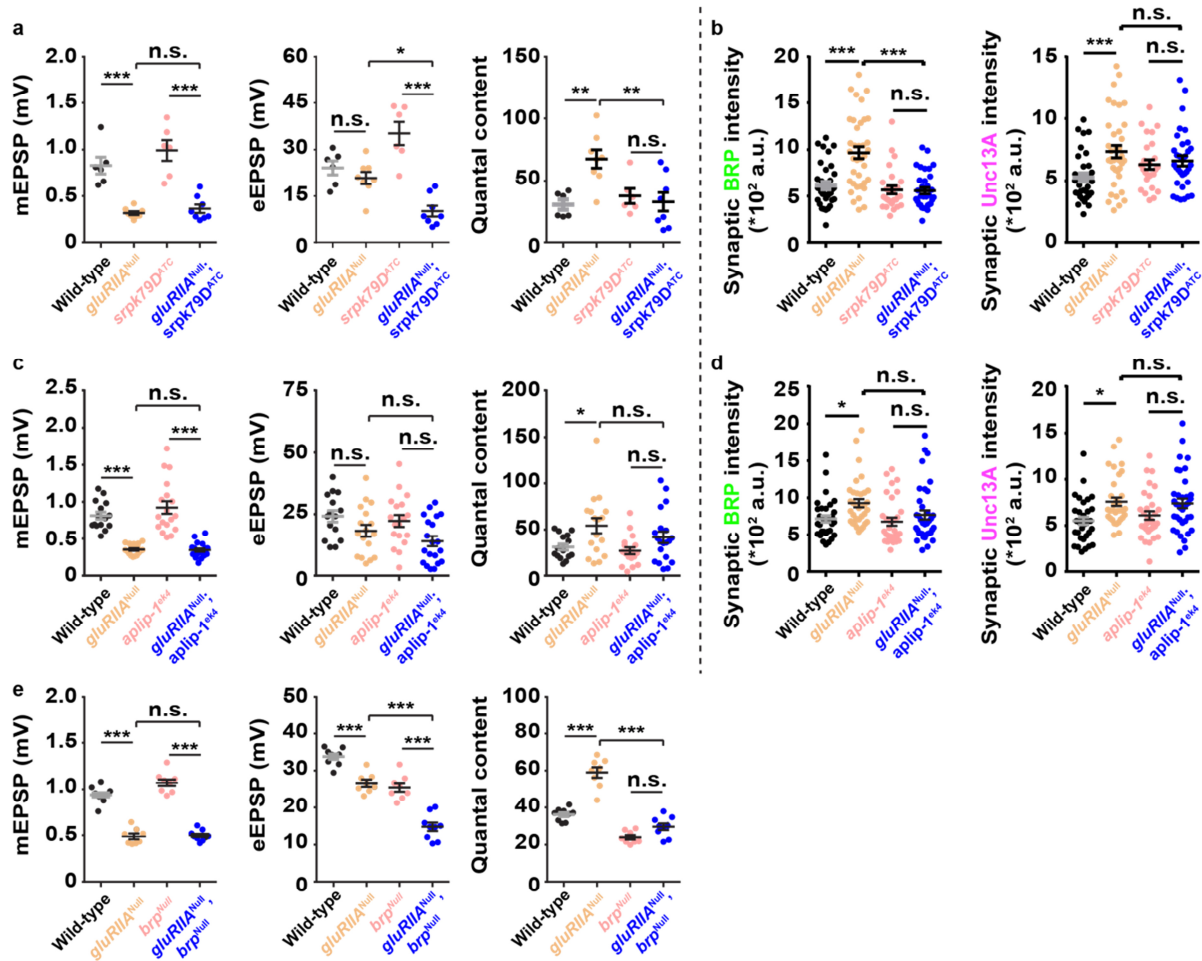
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181 **Supplementary Figure 10: Non-normalized values of electrophysiological and single AZ**
 182 **imaging experiments**

183 (a-f,h,j) Non-normalized values of mEPSP amplitude, eEPSP amplitude and quantal content
 184 without (Ctrl) and with (+PhTx) PhTx-treatment in the genotypes indicated. (g,i)
 185 Quantification of BRP, GFP, Cac or RBP AZ-levels in Ctrl and PhTx (+PhTx) treated
 186 animals of the indicated genotypes. (k) Non-normalized values of mEPSP amplitude, eEPSP
 187 amplitude and quantal content of cells without (-Cycloheximide) and with (+Cycloheximide)-

188 treatment. Statistics: Student's t test for all comparisons except for (a, g, i, j), quantal content
189 in (b, c, e, h and k), mEPSP in (d, f), and eEPSP in (f and h) where a Mann-Whitney U test
190 was performed. * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$; n.s., not significant, $P > 0.05$. All
191 panels show mean \pm s.e.m..

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195 **Supplementary Figure 11: Non-normalized values of electrophysiological and single AZ**
 196 **imaging experiments**

197 (a,c,e) Non-normalized values of mEPSP amplitude, eEPSP amplitude and quantal content in
 198 the genotypes indicated. (b,d) Quantification BRP and Unc13A AZ-levels in the genotypes
 199 indicated. Statistics: nonparametric one-way analysis of variance (ANOVA) test, followed by
 200 a Tukey's multiple comparison test. * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$; n.s., not
 201 significant, $P > 0.05$. All panels show mean \pm s.e.m..

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