Supporting Information

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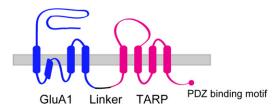


Fig. S1. The diagram of construction of the GluA1-TARP tethered receptor. The C-tail of GluA1 (blue) was fused to the N terminus of TARP (red) with a short segment of linker sequence (black). The PDZ-binding motif is highlighted by a filled circle.

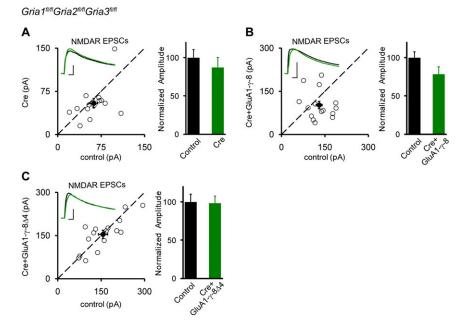


Fig. S2. NMDAR-mediated synaptic transmission is intact in experiments where AMPARs are knocked out or replaced with GluA1-TARP tethered receptors. Simultaneous dual whole-cell recordings from a transfected CA1 pyramidal neuron and a neighboring wild-type one from P17–P21 acute slices as in Fig. 1 *A*–C. Open and filled circles represent amplitudes of NMDAR-EPSCs (the current amplitudes were measured 100 ms after stimulation) for single pairs and mean \pm SEM, respectively. (*Insets*) Sample current traces from control (black) and experimental (green) cells. (Scale bars: 100 pA and 25 ms for representative traces.) Bar graphs show normalized EPSC amplitudes (mean \pm SEM) (Cre: *A*, *n* = 14, 87.31 \pm 13.21% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P* > 0.05; Cre+GluA1- γ -8: *B*, *n* = 15, 78.46 \pm 9.91% control, *P*

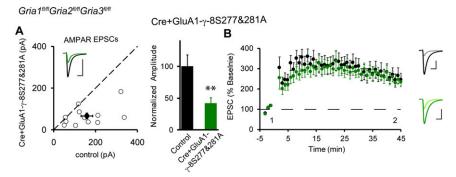


Fig. S3. Phosphorylation of γ -8 is involved in synaptic trafficking of the tethered GluA1 receptor but not required for LTP. The endogenous AMPARs were replaced with GluA1- γ -8(S277&281A) as in Fig. 1*B*. (*A*) Open and filled circles represent amplitudes of AMPAR-EPSCs for single pairs and mean \pm SEM, respectively. (*Insets*) Sample current traces from control (black) and experimental (green) cells. (Scale bars: 100 pA and 25 ms for representative traces.) Bar graphs show normalized EPSC amplitudes (mean \pm SEM) (*n* = 12, 41.84 \pm 8.50% control, ***P* < 0.005) presented in scatter plots. (*B*) LTP of GluA1- γ -8(S277&281A) replacement neurons (*n* = 10) is similar to neighboring wild-type cells. The data are shown as the percentage of the respective baseline before LTP induction (mean \pm SEM). Sample traces show EPSCs before and 30 min after LTP induction in paired control (black) and replacement neurons (green). (Scale bars: 100 pA and 25 ms.) All of the statistical analyses are compared with respective control neurons by the two-tailed Wilcoxon signed-rank sum test.

Wild-type Rat

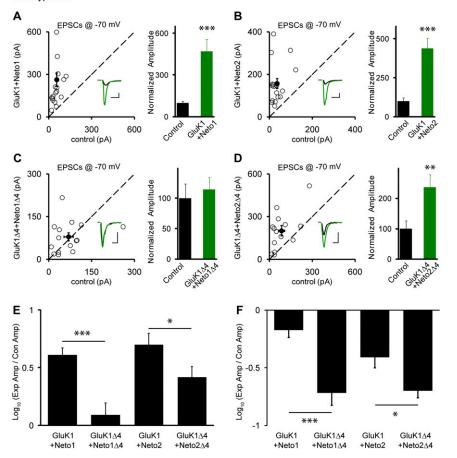


Fig. 54. PDZ-binding motif-mediated interaction is required for synaptic targeting of GluK1/Neto receptors. Rat hippocampal slice cultures were biolistically transfected with indicated constructs, and dual whole-cell recordings were applied to examine evoked EPSCs. (*A–D*) Open and filled circles represent amplitudes of EPSCs for single pairs and mean \pm SEM, respectively. (*Insets*) Sample current traces from control (black) and experimental (green) cells. [Scale bars: 100 pA and 25 ms (*A* and *B*) and 50 pA and 25 ms (*C* and *D*) for representative traces.] Bar graphs show normalized EPSC amplitudes (mean \pm SEM) (GluK1/Neto1: *A*, *n* = 19, 470.65 \pm 85.60% control, ****P* < 0.0005; GluK1/Neto2: *B*, *n* = 17, 689.52 \pm 195.16% control, ****P* < 0.0005; GluK1Δ4/Neto1Δ4: *C*, *n* = 15, 114.09 \pm 20.36% control, *P* > 0.05; GluK1Δ4/Neto2Δ4: *D*, *n* = 14, 236.51 \pm 41.54% control, ***P* < 0.005) presented in scatter plots. All of the statistical analyses are compared with respective control neurons by the two-tailed Wilcoxon signed-rank sum test. (*E*) Logarithm summary of the EPSC amplitudes ratio between the experimental and respective control neurons (mean \pm SEM) for the above four experimental groups [GluK1/Neto1 (0.61 \pm 0.06) vs. GluK1Δ4/Neto1Δ4 (0.09 \pm 0.11), ****P* < 0.001; GluK1/Neto2 (0.70 \pm 0.10) vs. GluK1Δ4/Neto2Δ4 (0.42 \pm 0.09), **P* < 0.05]. All statistical analyses of the different groups are tested using the Mann–Whitney *U* test. It should be noted that the raw data of GluK1/Neto1 and GluK1/Neto2 (-0.41 \pm 0.09) vs. GluK1Δ4/Neto2Δ4 (-0.70 \pm 0.006), **P* < 0.05]. All statistical analyses of the different groups are tested using the Mann–Whitney *U* test.

Gria1^{##}Gria2^{##}Gria3^{##}

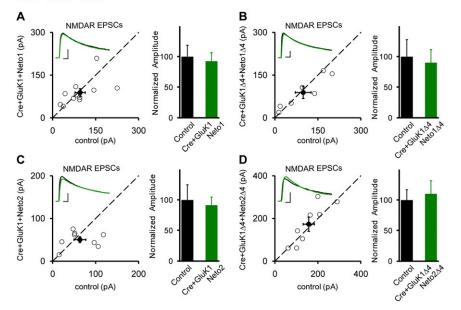


Fig. S5. NMDAR-mediated synaptic transmission is intact in experiments where AMPARs were replaced with KARs. The same experimental procedure was followed as in Fig. 3 A1-D1 except that open and filled circles represent amplitudes of NMDAR-EPSCs (the current amplitudes were measured 100 ms after stimulation) for single pairs and mean \pm SEM, respectively. *Insets* show sample current traces from control (black) and experimental (green) cells. (Scale bars are 50 pA and 25 ms for representative traces.) Bar graphs show normalized EPSC amplitudes (mean \pm SEM) (GluK1/Neto1: *A*, *n* = 11, 92.39 \pm 14.28% control, *P* > 0.05; GluK1/A4/Neto1 Δ 4: *B*, *n* = 7, 89.96 \pm 21.60% control, *P* > 0.05; GluK1/Neto2: *C*, *n* = 8, 91.55 \pm 13.09% control, *P* > 0.05; GluK1 Δ 4/Neto1 Δ 4: *D*, *n* = 8, 11.02 \pm 21.19% control, *P* > 0.05; presented in scatter plots. All of the statistical analyses are compared with respective control neurons by the two-tailed Wilcoxon signed-rank sum test.