<table>
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<th>Title</th>
<th>A role for sorting nexin 27 in AMPA receptor trafficking( Figures )</th>
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<tr>
<td>Author(s)</td>
<td>Loo, Li Shen; Tang, Ning; Al-Haddawi, Muthafar; Stewart Dawe, Gavin; Hong, Wanjin</td>
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<tr>
<td>Date</td>
<td>2014</td>
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<td>URL</td>
<td><a href="http://hdl.handle.net/10220/19359">http://hdl.handle.net/10220/19359</a></td>
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Figure 1
Figure 2

(a) GFP-SNX27, mCh-PSD95, Merge

Inset

(b) SNX27, synaptophysin, merge

Figure 2
Figure 3

GFPSNX27  mCherryPSD95  merge

∆PDZ

∆PX

∆RA

Fluorescence units

Fluorescence units

Fluorescence units

distance (um)

distance (um)

distance (um)
Figure 4

(a) Rab5
SNX27
Merge

(b) TfR
SNX27
Merge
Rab11
SNX27
Merge

(c) 0:00 0:05 0:10 0:15 0:20 0:25 0:30 0:35 min

(d) 0:00 0:05 0:10 0:15 0:20 min

(e) Displacement (um)
dendrite spine

(f) SNX27 spine translocation events:

N spine translocation/total spine

Basal Gly

Figure 4
Figure 5

**Panel a**
Images showing the progression of events labeled 0:00, 2:50, 5:00, 7:50, and 10:00 min.

**Panel b**
Graph illustrating the change in GFP/mCh signal over time (0.0 to 11.0) with two conditions: Gly and Gly/APV.

**Panel c**
Images comparing WT and SNX27-/- conditions under different saturation, basal, Gly, and Gly/APV conditions.

**Panel d**
Bar graph showing intracellular AII-Tf (AFU) levels under Basal, Gly, and Gly/APV conditions for WT and SNX27-/- conditions, with a significant difference indicated by **.**
Figure 6

(a) Synaptosome fraction

(b) TX-insoluble (PSD) fraction

** Relative GluN1 levels

<table>
<thead>
<tr>
<th></th>
<th>synaptosomes</th>
<th>PSD fraction</th>
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</thead>
<tbody>
<tr>
<td>+/+</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>-/-</td>
<td>0.6**</td>
<td>0.6**</td>
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** Indicates statistical significance.
Figure 7

(a) Western blot analysis showing the expression of K-ras, H-ras, and N-ras. The blots are probed with IgG and IP:SNX27. The blots are normalized to input and IBSNX27.

(b) Immunofluorescence images showing the expression of SNX27, KRas, and their merge. The images are taken under basal and Gly conditions. The Pearson's coefficient is significantly higher under Gly compared to basal conditions.

(c) Graph showing the normalized intensity of K-ras/CaM over time. The data is normalized to IP:CaM and IB:CaM.
Figure 8

(a) Western blot analysis showing the interaction of GluA1, GluA2, SAP97, PSD95, and SNX27 with myc-tagged SNX27. The blots were probed with antibodies specific to each protein. The blot shows a marked increase in the intensity of the GluA1 and GluA2 bands upon co-immunoprecipitation (IP) with myc-SNX27.

(b) Western blot analysis for GluA2 showing the interaction with myc-SNX27. The blot reveals a significant increase in the GluA2 band intensity in the IP lane compared to the input lane.

(c) Summary table showing the expression levels of Myc-SNX27 and Myc-SNX27ΔPDZ with GFP GluA1 C-tail in the presence and absence of myc. The normalized intensity ratios are calculated and presented in a bar graph.

(d) Graph showing the normalized intensity ratio of GluA1 and K-ras over time after glycine treatment. The ratio is plotted against time, and significant differences are indicated by asterisks.

(e) Western blot analysis and graph showing the expression levels of GluA1 and SNX27 in different conditions involving ACSF, Gly, Gly/KN93, Gly/FTI276, and Gly/FTI277. The normalized intensity ratios are compared, with significant differences highlighted by asterisks.
Figure 9
Figure 10