

## *Supplementary Material*

# **Dysregulation of parvalbumin expression in the Cntnap2<sup>-/-</sup> mouse model of autism spectrum disorder**

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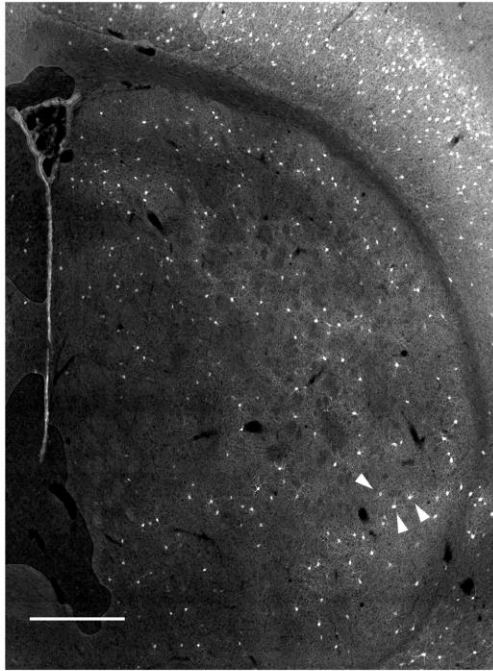
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## **Supplementary Figures**

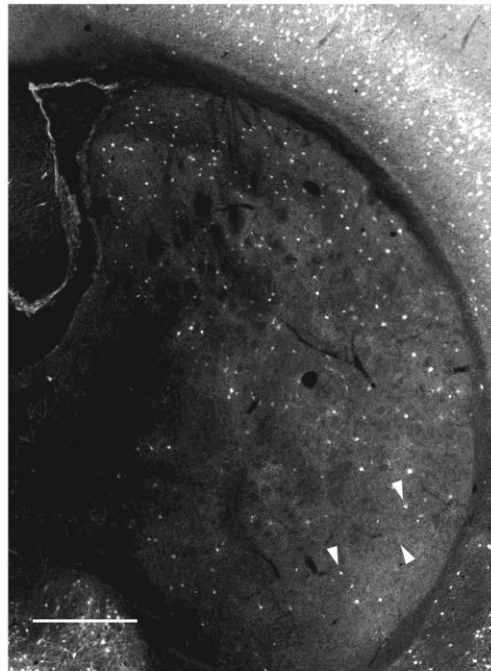
## Striatum

Parvalbumin (PV)

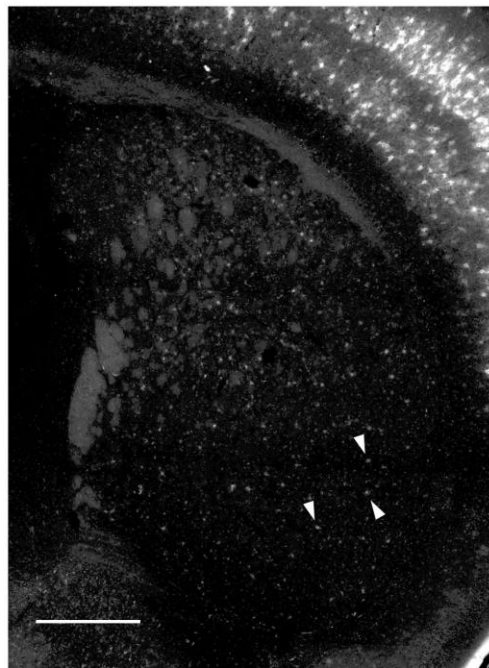
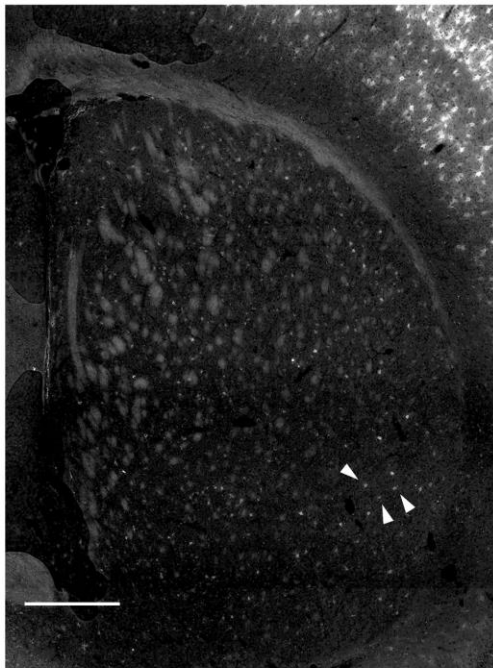
WT



*Cntnap2*<sup>-/-</sup>

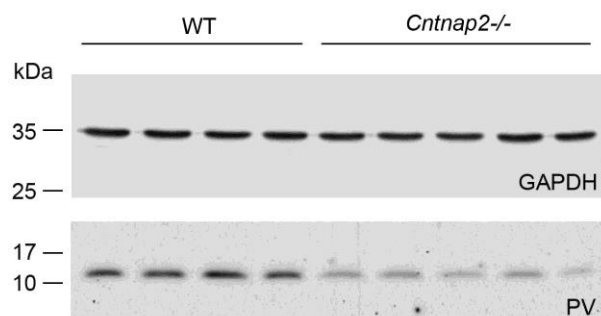


Vicia Villosa Agglutinin (VVA)

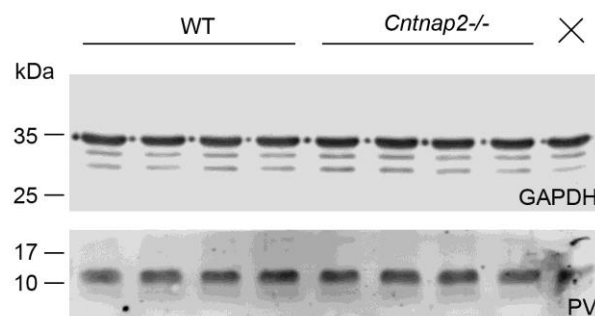


**Suppl. Figure 1: (A)** VVA staining of the corresponding striatal sections shown in Figure 1. VVA<sup>+</sup> cells are indicated with arrowheads. One VVA<sup>+</sup> cell (lower right) in the *Cntnap2*<sup>-/-</sup> group appears to be negative for PV. Scale bar 500  $\mu$ m.

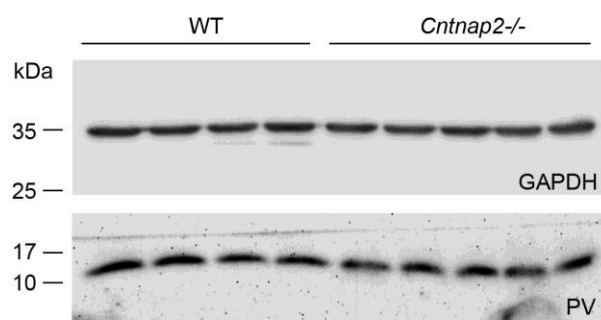
### Striatum PND25



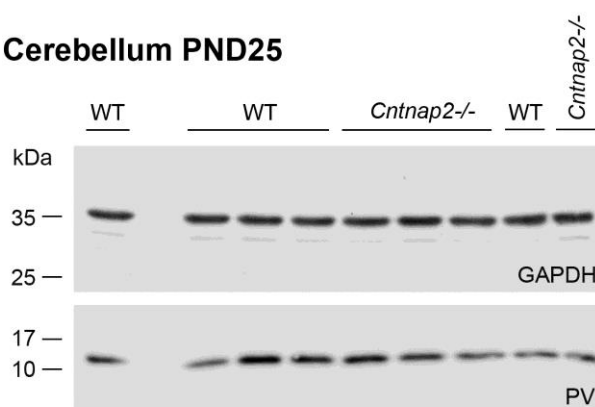
### Cortex PND25



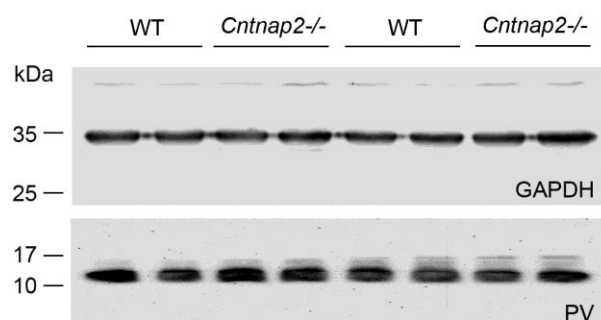
### Hippocampus PND25



### Cerebellum PND25

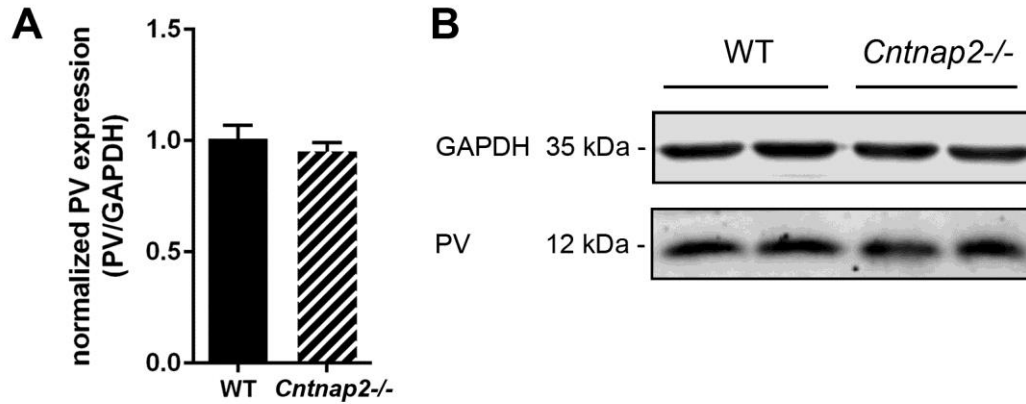


### Cortex PND70

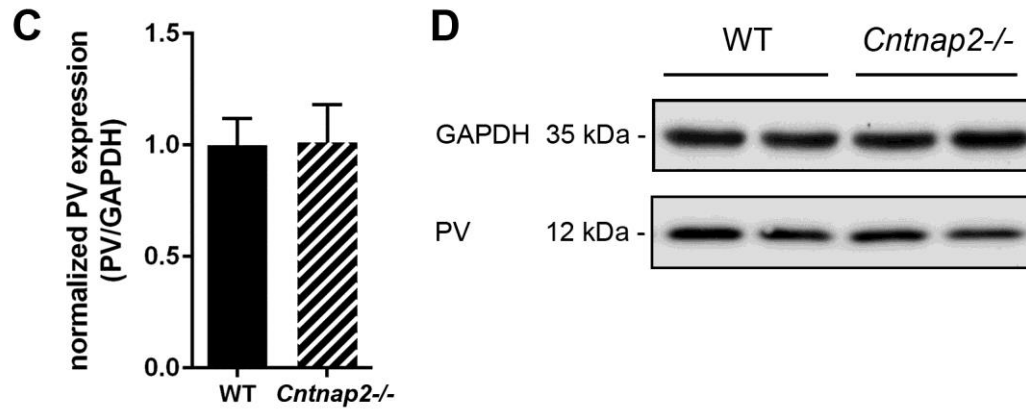


**Suppl. Figure 2:** Complete uncropped images of the Western blots shown in the manuscript.

## Hippocampus PND25

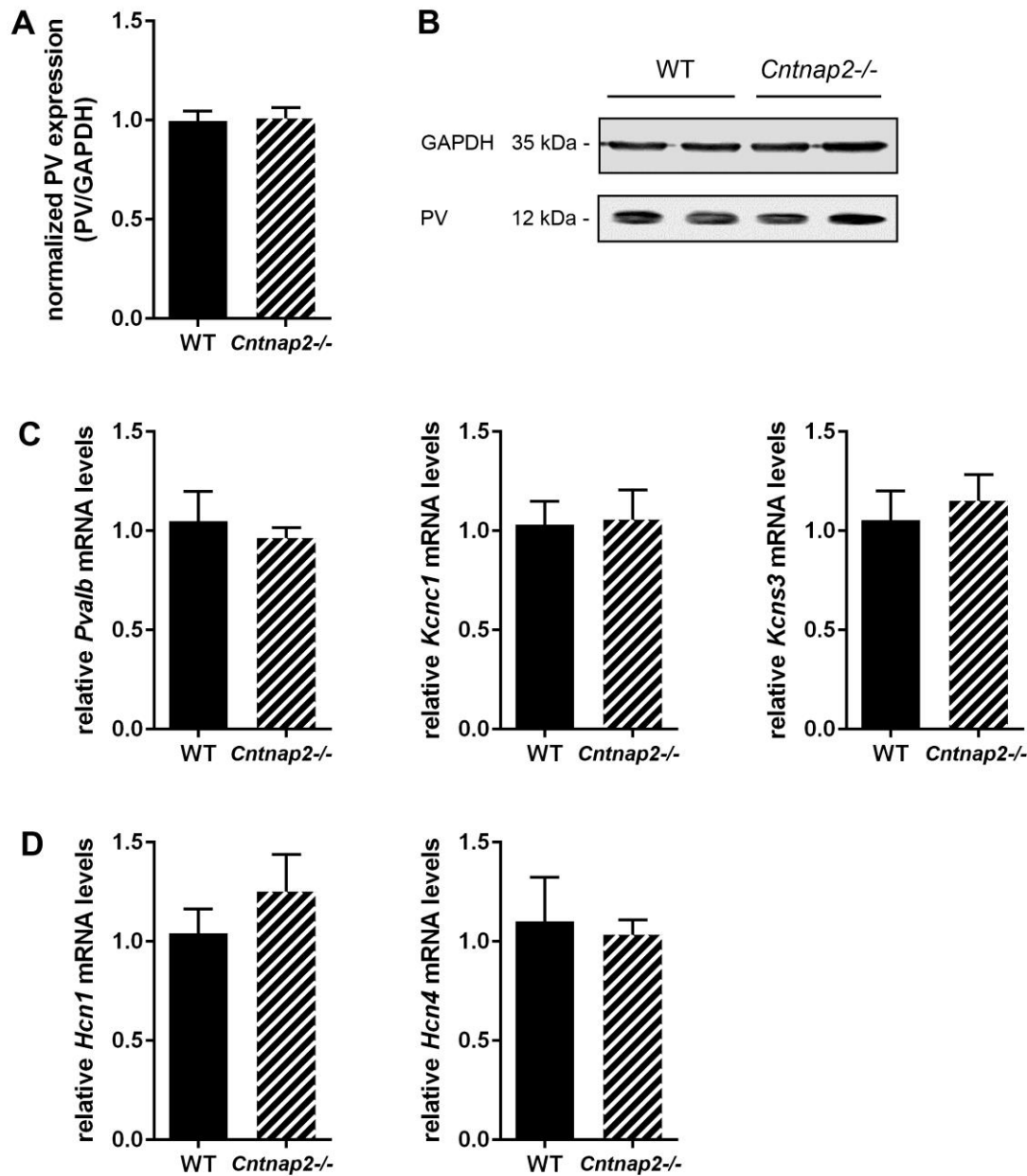


## Cerebellum PND25



**Supplementary Figure 3:** Quantitative Western blot analysis of (A) hippocampal and (C) cerebellar samples of PND25 WT and *Cntnap2*<sup>-/-</sup> mice (N = 5 mice each). Quantification of PV protein levels is shown. GAPDH signals served as loading controls and were used for the normalization of PV protein signals. Results are expressed as a percentage of normalized PV/GAPDH signals in the WT group. Representative Western blot signals for PV and GAPDH are shown for the (B) hippocampus and (D) cerebellum. All data are expressed as mean  $\pm$  SEM.

## Cortex PND70



**Suppl. Figure 4:** (A) Quantitative Western blot analysis of cortical samples of PND70 WT and *Cntnap2*<sup>-/-</sup> mice (N = 5 mice each). Quantification of PV protein levels is shown. GAPDH signals served as loading controls and were used for the normalization of PV protein signals. Results are expressed as a percentage of normalized PV/GAPDH signals in the WT group. (B) Representative Western blot signals for PV and GAPDH are shown. (C and D) RT-qPCR values from cortical samples of WT and *Cntnap2*<sup>-/-</sup> PND70 mice representing mRNA levels for (C) **Left: *Pvalb*; Middle: *Kcnc1*; Right: *Kcns3***, (D) **Left: *Hcn1*; Right: *Hcn4***. Signals were normalized to *Rn18S* mRNA levels and expressed as fold change compared to WT (N = 5 mice each). All data are expressed as mean  $\pm$  SEM.