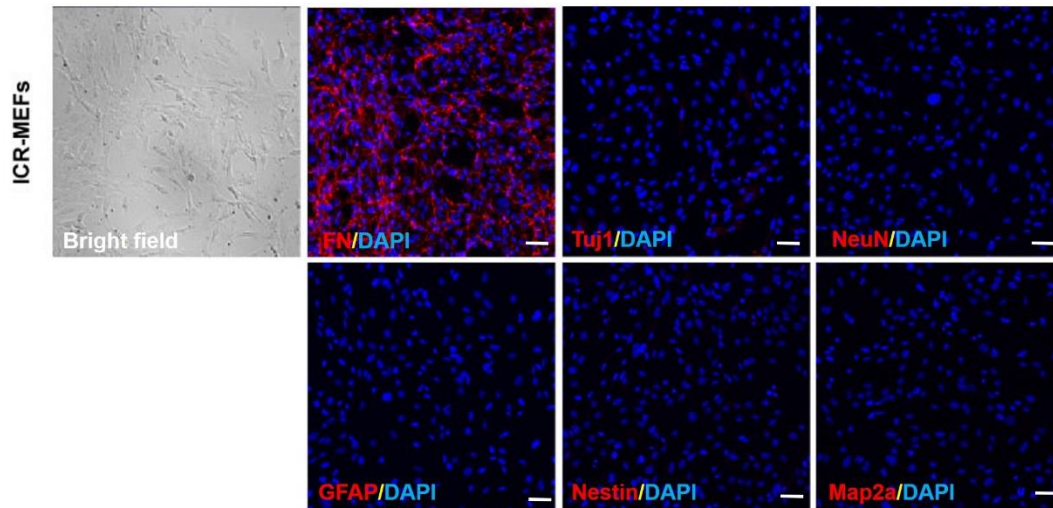**Supplemental Figure Legends:**
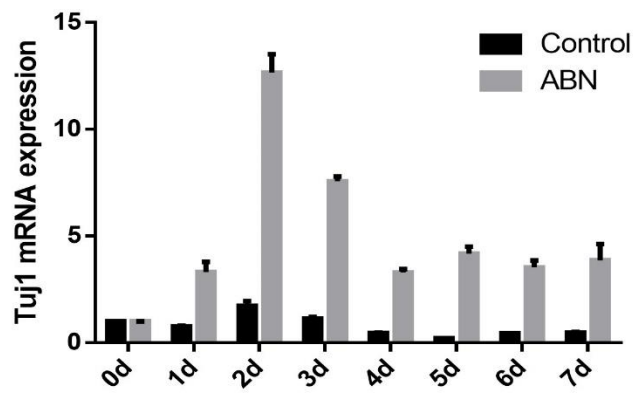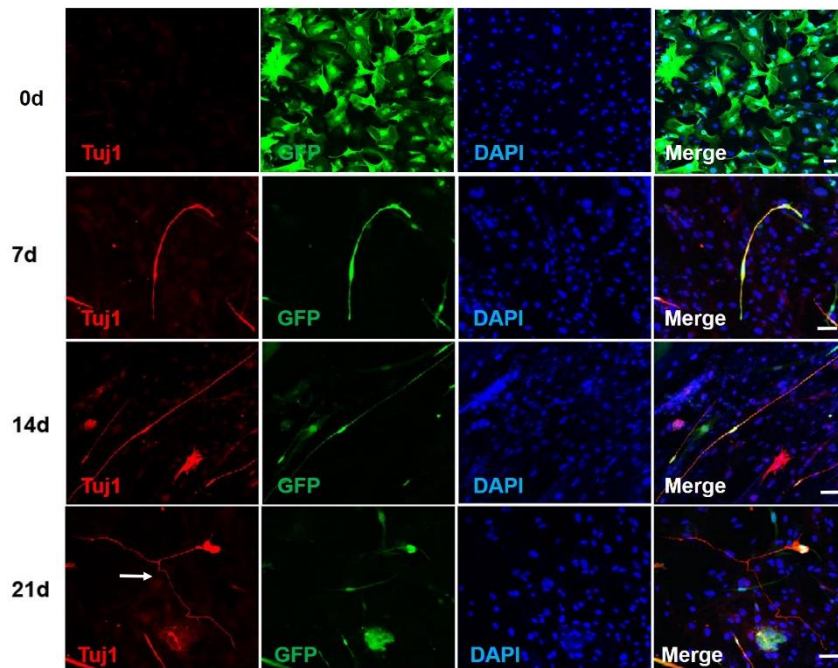**Figure. S1**

**A**



**B**



**FIGURE S1.** (*A*) Immunofluorescence staining to identify MEFs. (*B*) Quantitative real-time PCR analysis of *Tuj1* expression during ABN-induced transdifferentiation. The experiments were repeated 3 times.
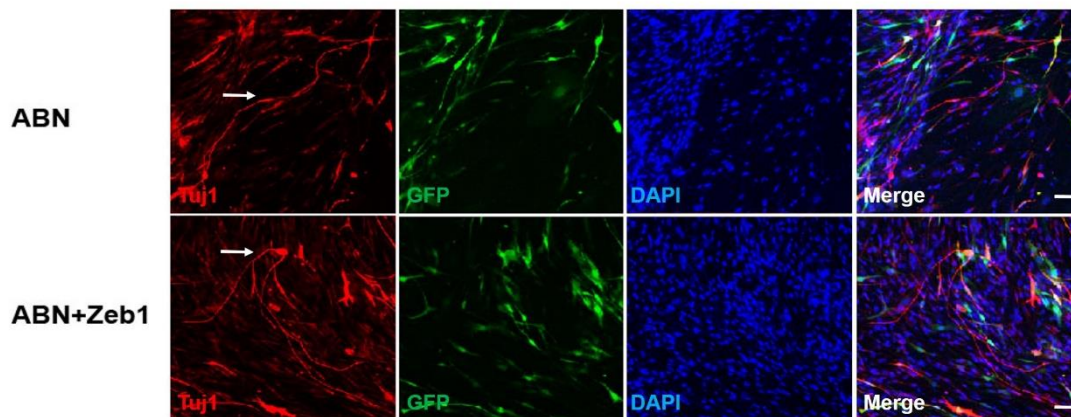
**Figure. S2**

**A**



**B**



**FIGURE S2.** (*A*) Immunostaining of TUJ1 on days 7, 14 and 21 of transdifferentiation (ABN + *Zeb1* group). Scale bar, 50 μm. (*B*) Immunostaining of multipolar iN cells at 21-days post-infection. Scale bar, 50 μm.
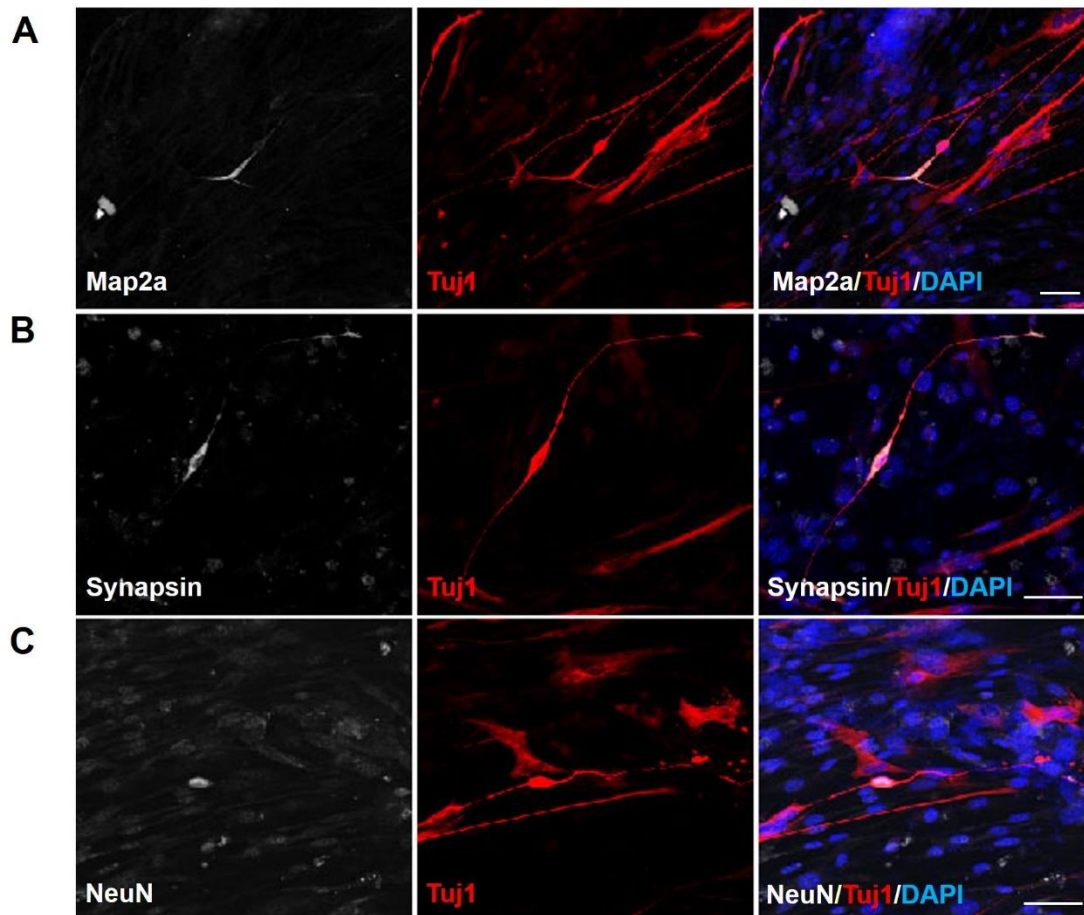
**Figure. S3**



**FIGURE S3.** Characterization of mature iN cells by neuronal markers. (*A-C*) Immunostaining analysis one week post-infection using the indicated antibodies. *Map2a*, *Synapsin* and *NeuN*, pan-neuronal markers. Scale bar, 50 μm.
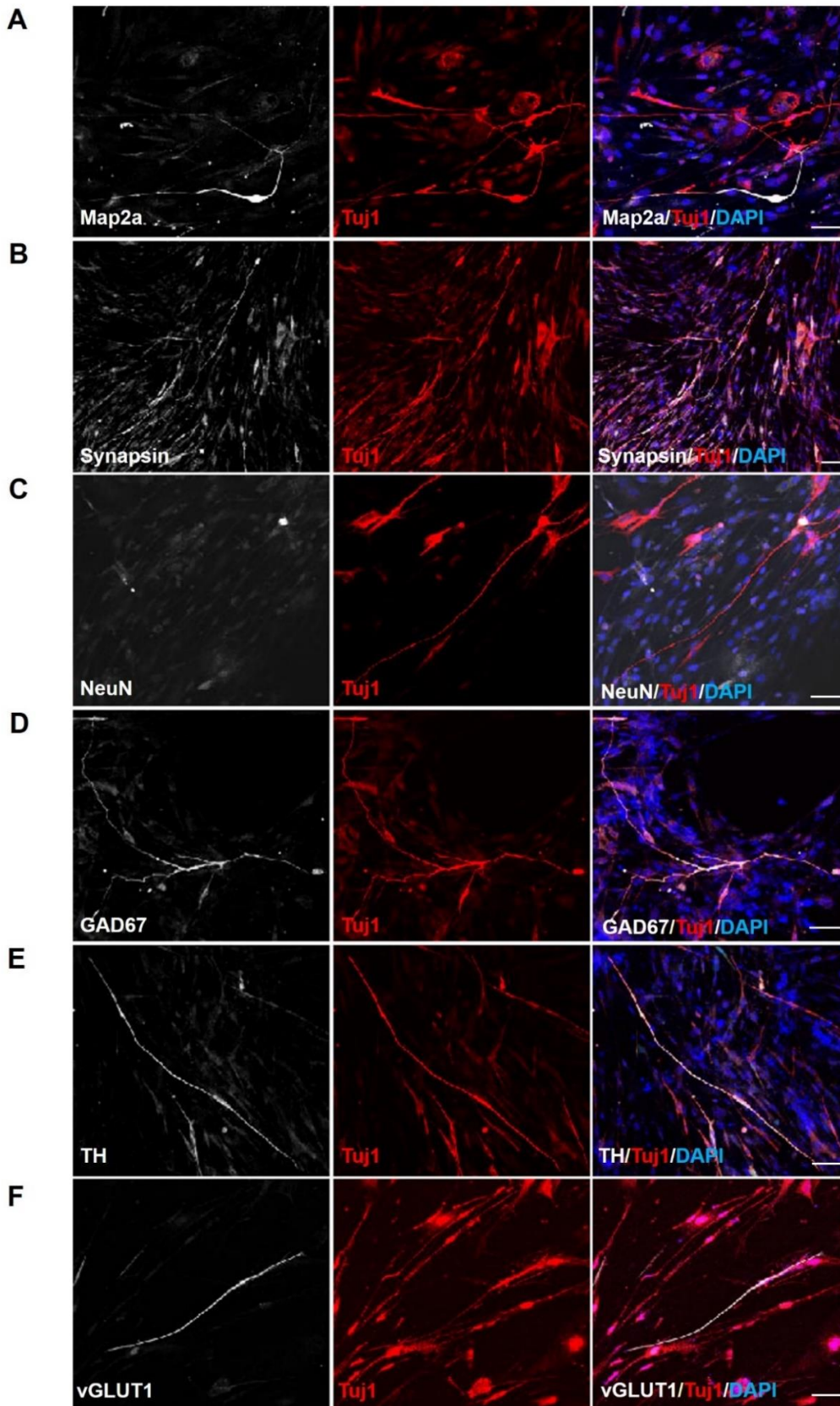
**Figure. S4**

**FIGURE S4.** Characterization of mature iN cells by neuronal markers. (*A-F*) Immunostaining analysis three weeks post-infection using the indicated antibodies. *Map2a*, *Synapsin* and *NeuN*, pan-neuronal markers. *GAD67*, inhibitory neuron marker; Tyrosine hydroxylase (*TH*), dopaminergic neuron marker; *vGLUT1*, excitatory neuron marker. Scale bar, 50 μm.
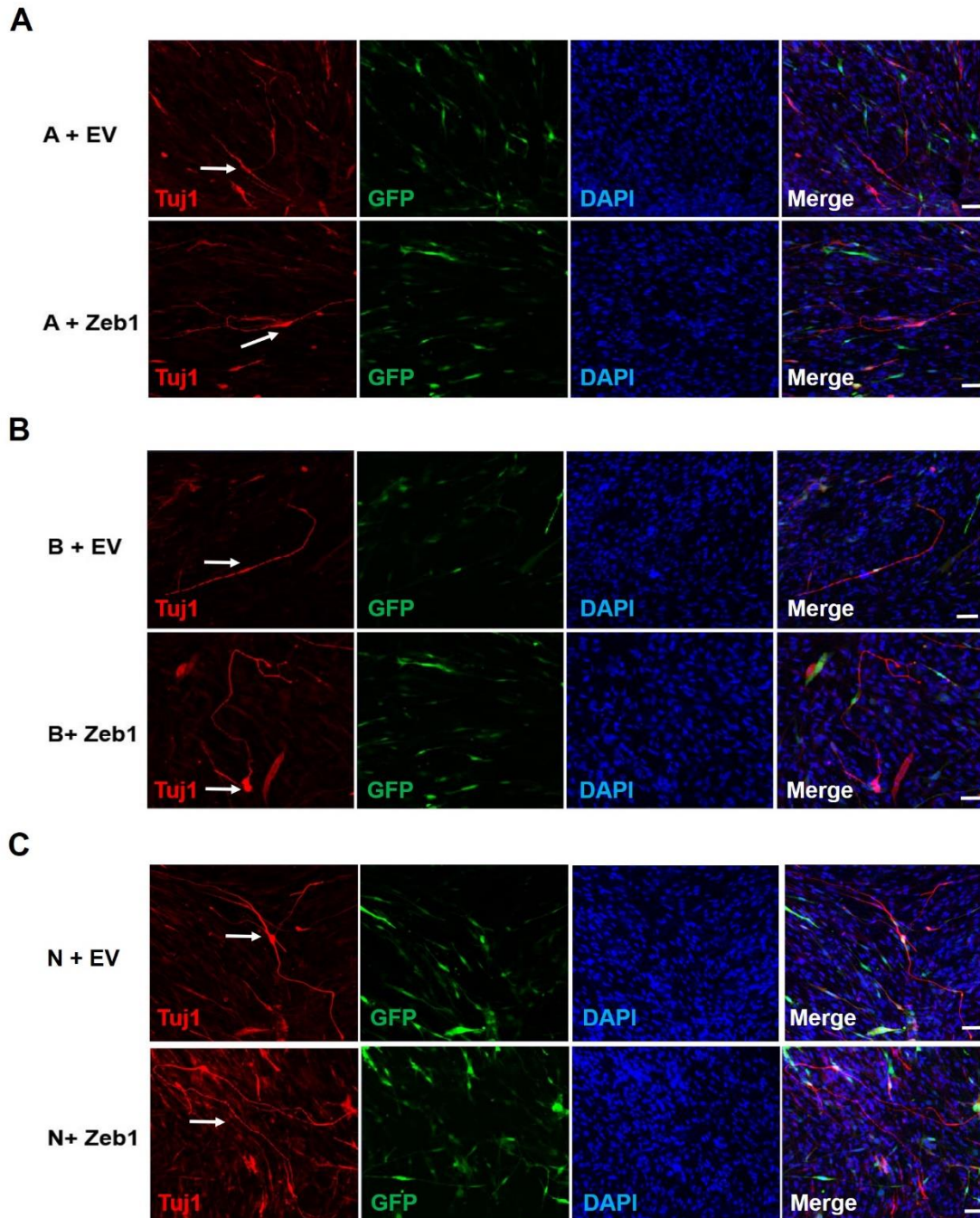
**Figure. S5**



**FIGURE S5.** Bipolar iN cells generated by single transcription factors with or without *Zeb1*. (*A-C*) Immunofluorescence staining of TUJ1 in the indicated groups. Scale bars, 50 μm.
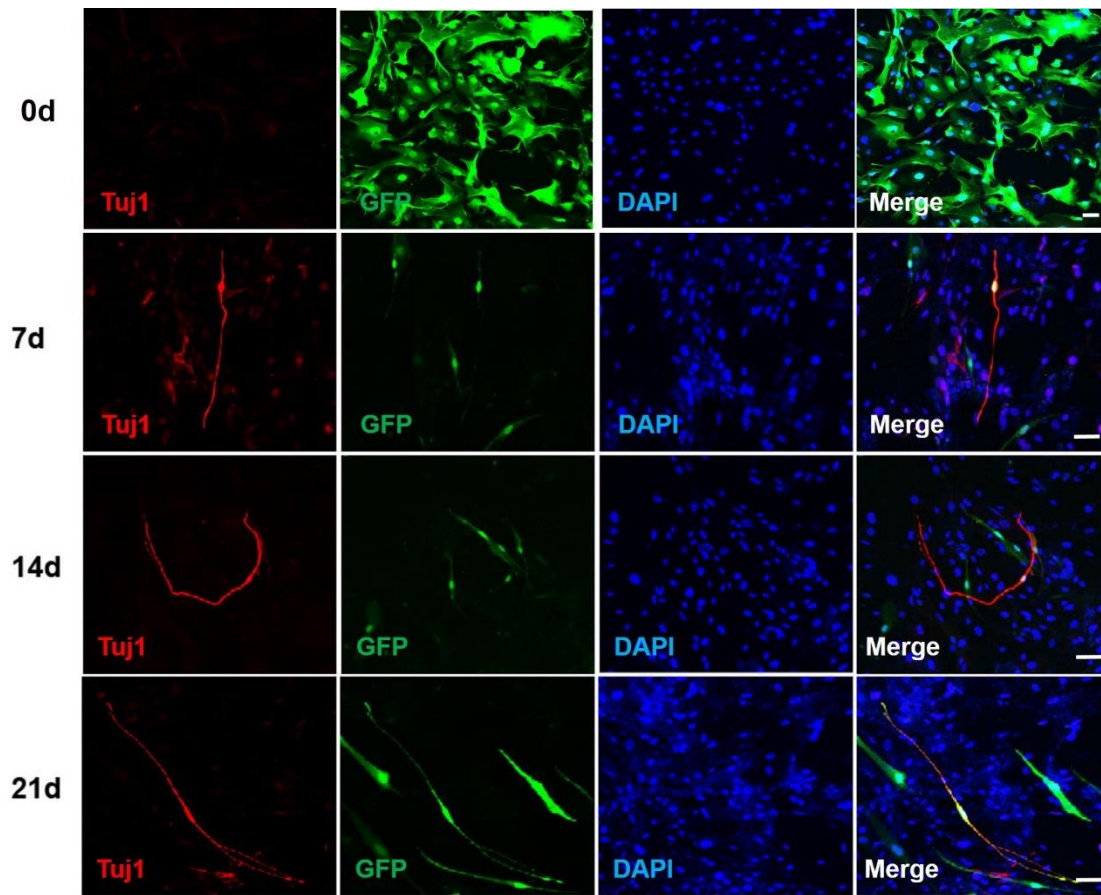
**Figure. S6**



**FIGURE S6.** Immunofluorescence staining of TUJ1 on days 7, 14 and 21 of transdifferentiation with *Zeb1* alone. Scale bar, 50 μm.
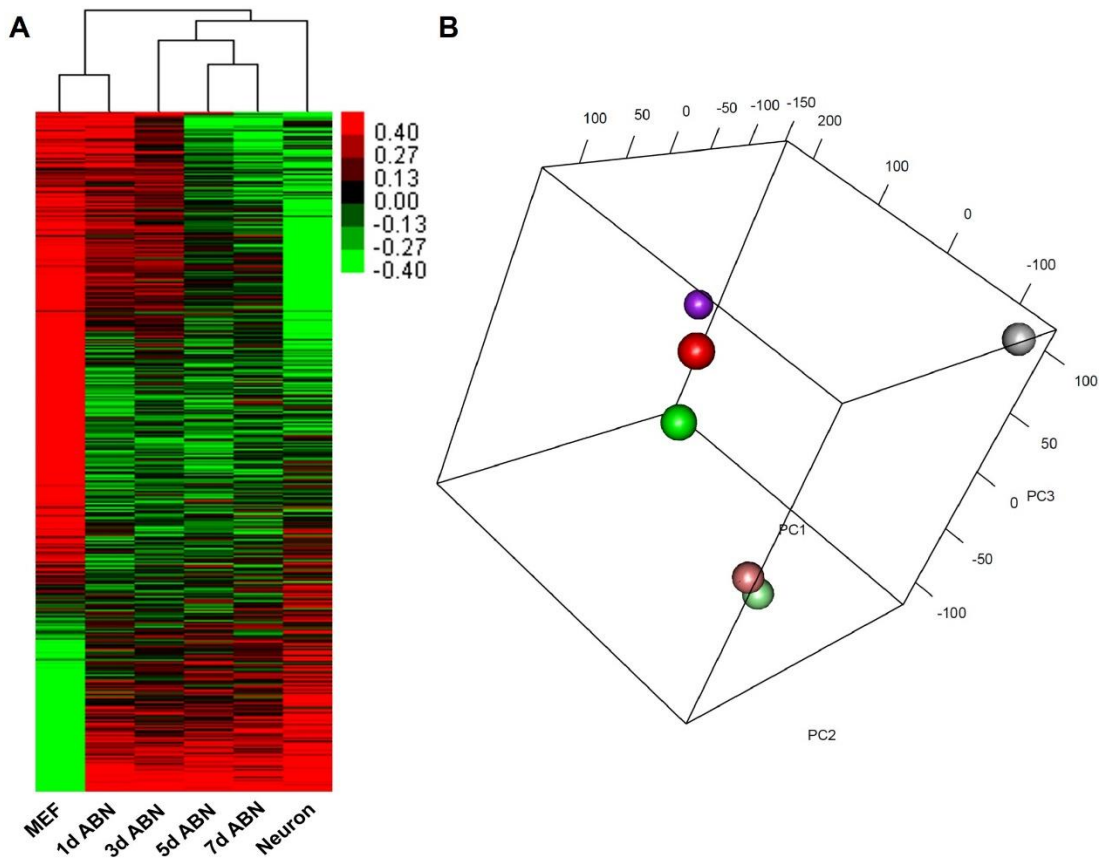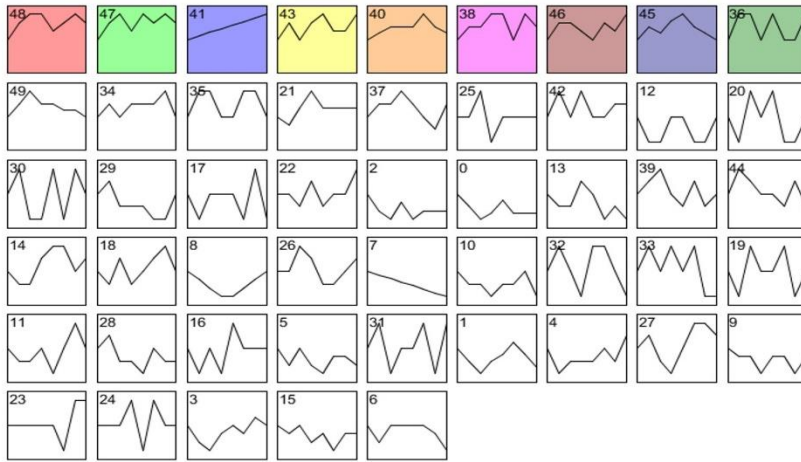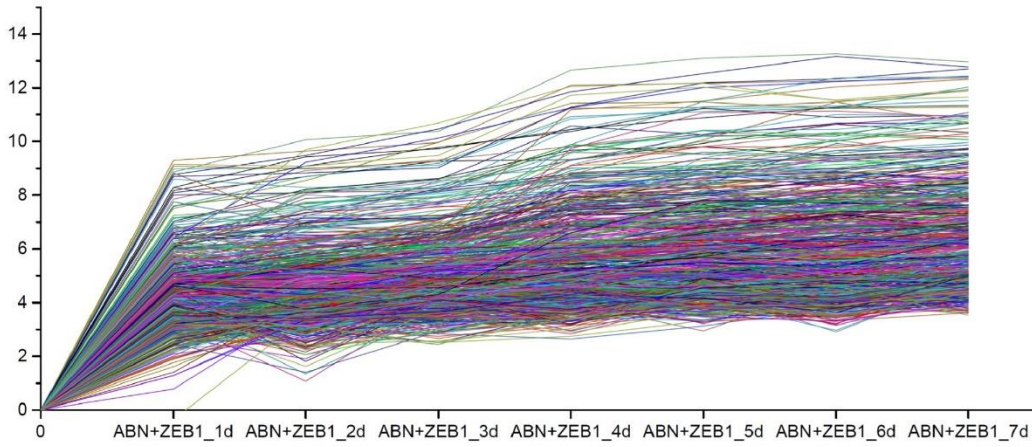
**Figure. S7**



**FIGURE S7.** (*A*) Hierarchical clustering analysis of the whole-genome profiles of ABN groups. Primary neurons were isolated from the hippocampus of a newborn pup. iN cells were harvested at the indicated time points. (*B*) Principle component analysis (PCA) of the indicated samples. Light green, 2d ABN; Light red, 2d ABN + *Zeb1*; Green, 7d ABN; Red, 7d ABN + *Zeb1*; Gray, MEF; Purple, Neuron;

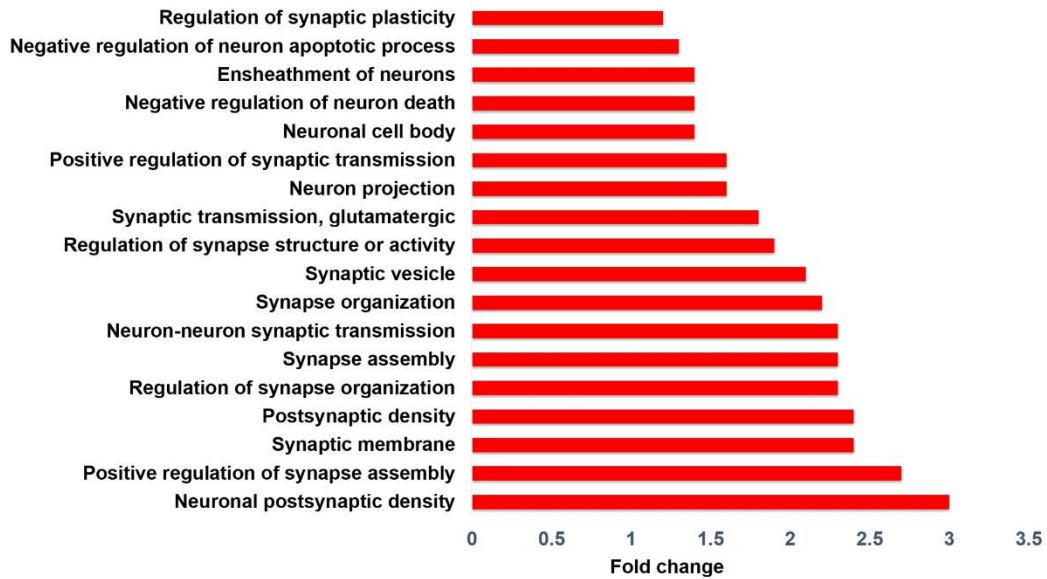**A**



**B**



**C**



Fold change

**FIGURE S8.** Short Time-series Expression Miner (STEM) analysis. (*A*) Selected STEM profiles. The colored squares indicate significance. (*B*) Profile 41 (0, 1, 2, 3, 4, 5, 6, 7); 710 genes assigned; 42.3 genes expected; *P* value = 0.00 (significant). (*C*) Gene ontology analysis of the 710 up-regulated genes.