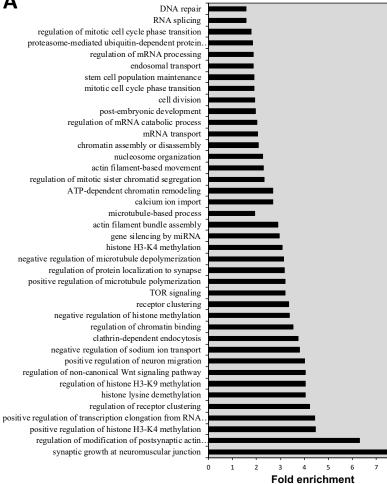


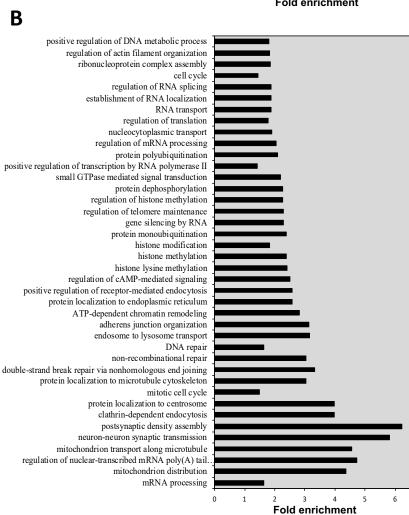
## **Supplementary Figure S1**

**Figure S1. Functional clustering of DE-circRNAs in CB1**<sup>-/-</sup> **compared to WT SPZ**. **(A)** Two circRNAs whose host genes are members of the same gene family but located on different chromosomes show tethering activity toward the same miRNA as target. **(B)** Four circRNAs whose host genes are located on different chromosomes, tether the same miRNA. **(C)** The same circRNA shows tethering activity toward a family of miRNA isoforms. Networks were built using Cytoscape. Ovoid and rectangular symbols represent circRNAs and miRNAs, respectively. The arrow indicates the tethering activity of circRNAs toward miRNAs.

## GENE ONTOLOGY

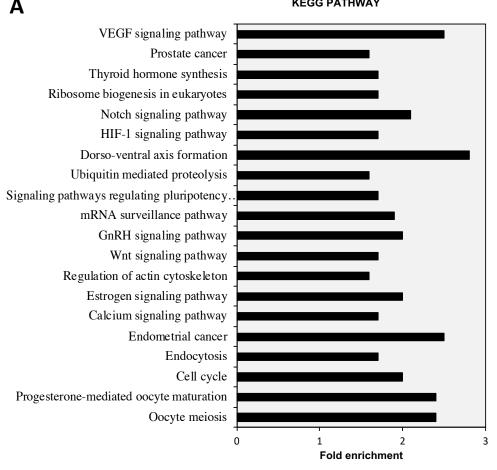


B



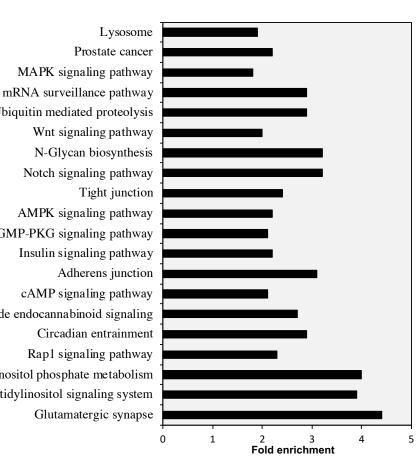
## **Supplementary Figure S2**

**Figure S2. Gene ontology (GO) enrichment analysis of host genes**. **(A)** The Top 40 GO annotations in CB1<sup>-/-</sup> SPZ up-regulated circRNAs. **(B)** The Top 40 GO annotations in CB1<sup>-/-</sup> SPZ down-regulated circRNAs.



В

Ubiquitin mediated proteolysis Wnt signaling pathway N-Glycan biosynthesis Notch signaling pathway Tight junction AMPK signaling pathway cGMP-PKG signaling pathway Insulin signaling pathway Adherens junction cAMP signaling pathway Retrograde endocannabinoid signaling Circadian entrainment Rap1 signaling pathway Inositol phosphate metabolism Phosphatidylinositol signaling system Glutamatergic synapse



Supplementary Figure S3

**Figure S3. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway annotation of host genes**. **(A)** The Top 20 KEGG signaling pathway annotations in CB1<sup>-/-</sup> SPZ up-regulated circRNAs. **(B)** The Top 20 KEGG signaling pathway annotations in CB1<sup>-/-</sup> SPZ down-regulated circRNAs.