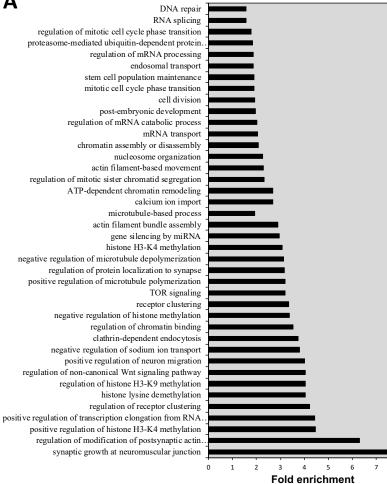


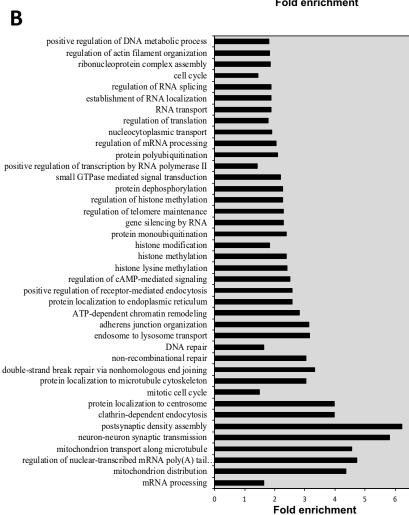
Supplementary Figure S1

Figure S1. Functional clustering of DE-circRNAs in CB1^{-/-} **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

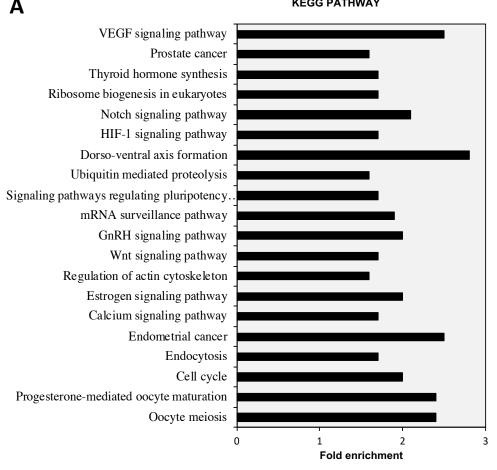


B



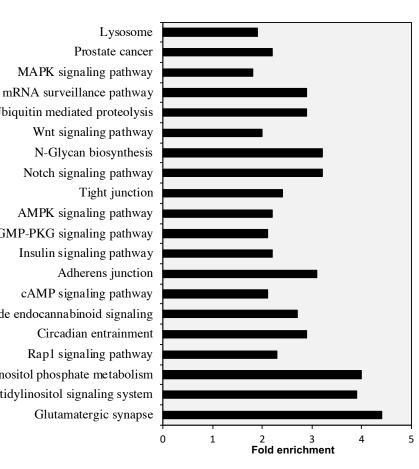
Supplementary Figure S2

Figure S2. Gene ontology (GO) enrichment analysis of host genes. **(A)** The Top 40 GO annotations in CB1^{-/-} SPZ up-regulated circRNAs. **(B)** The Top 40 GO annotations in CB1^{-/-} 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^{-/-} SPZ up-regulated circRNAs. **(B)** The Top 20 KEGG signaling pathway annotations in CB1^{-/-} SPZ down-regulated circRNAs.