

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

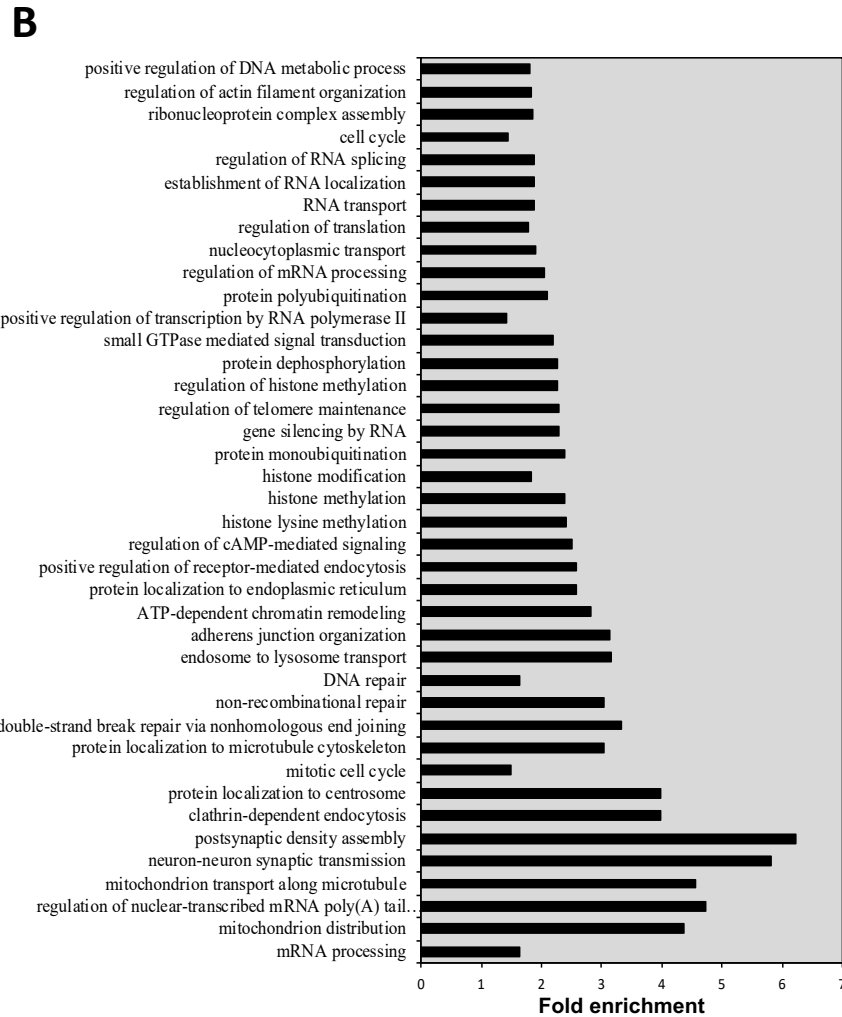
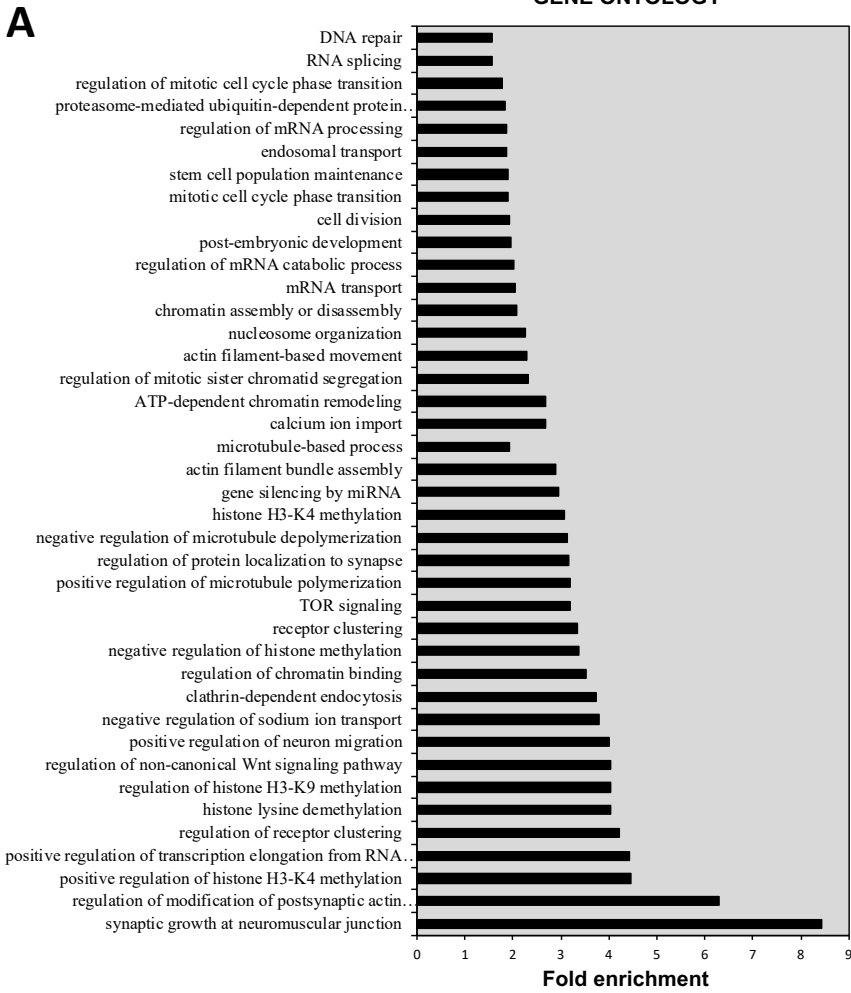


Figure S2. Gene ontology (GO) enrichment analysis of host genes. (A) The Top 40 GO annotations in CB1^{-/-} SPZ up-regulated circRNAs. **(B)** The Top 40 GO annotations in CB1^{-/-} SPZ down-regulated circRNAs.

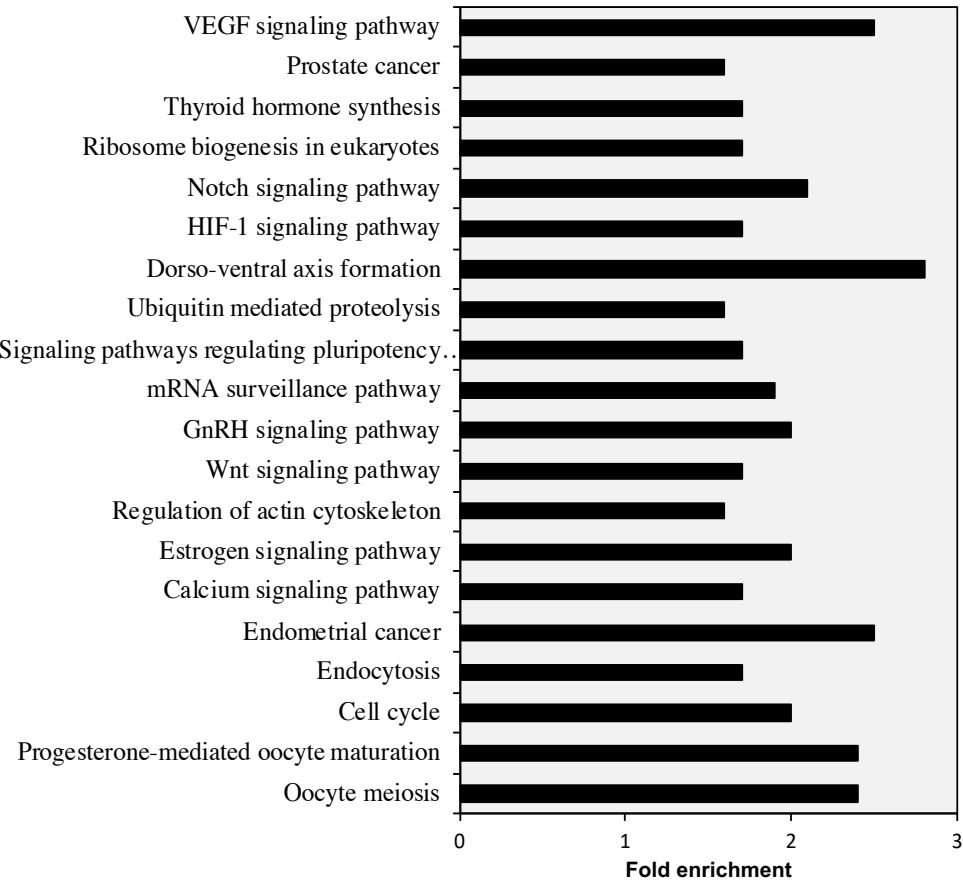
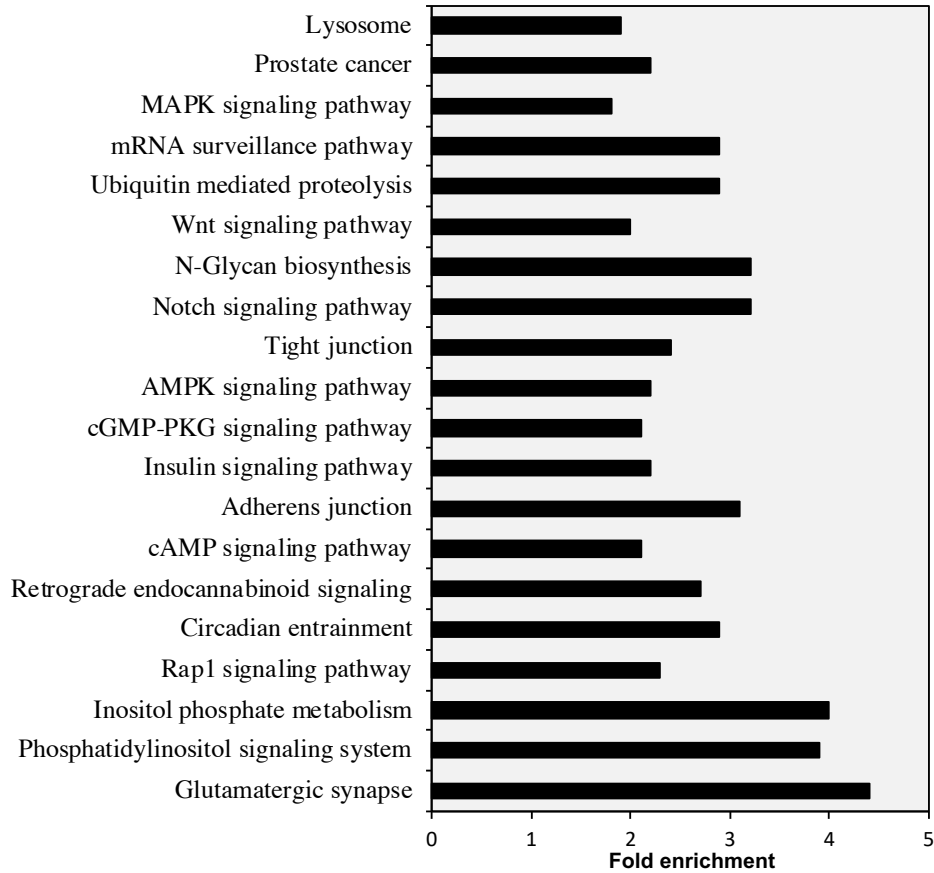
A**KEGG PATHWAY****B**

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.