

Figures:

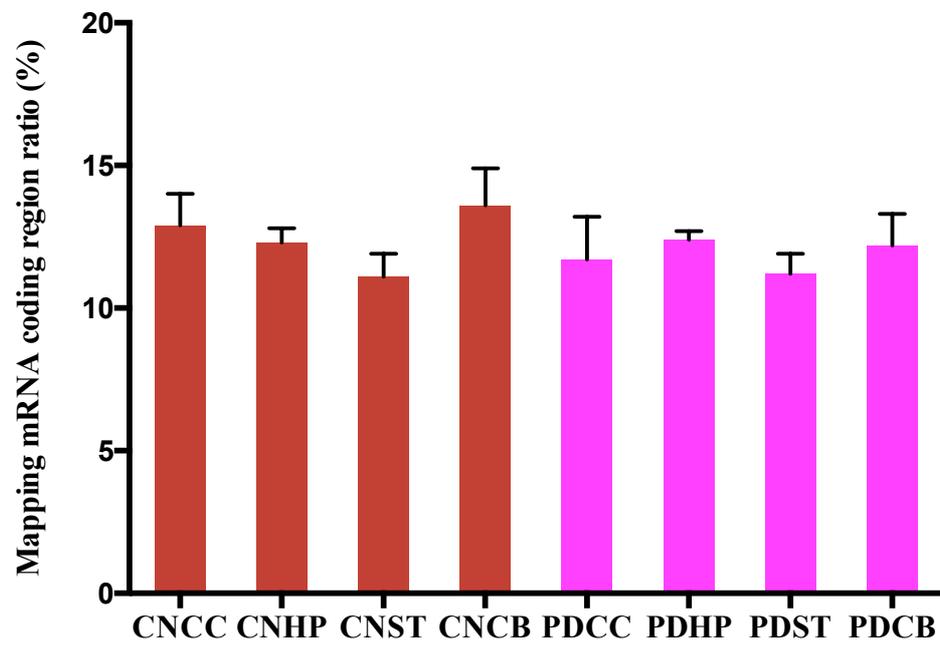


Figure S1. Mapping coding region distribution. Shows the ratio of reads mapped to the coding region in all samples.

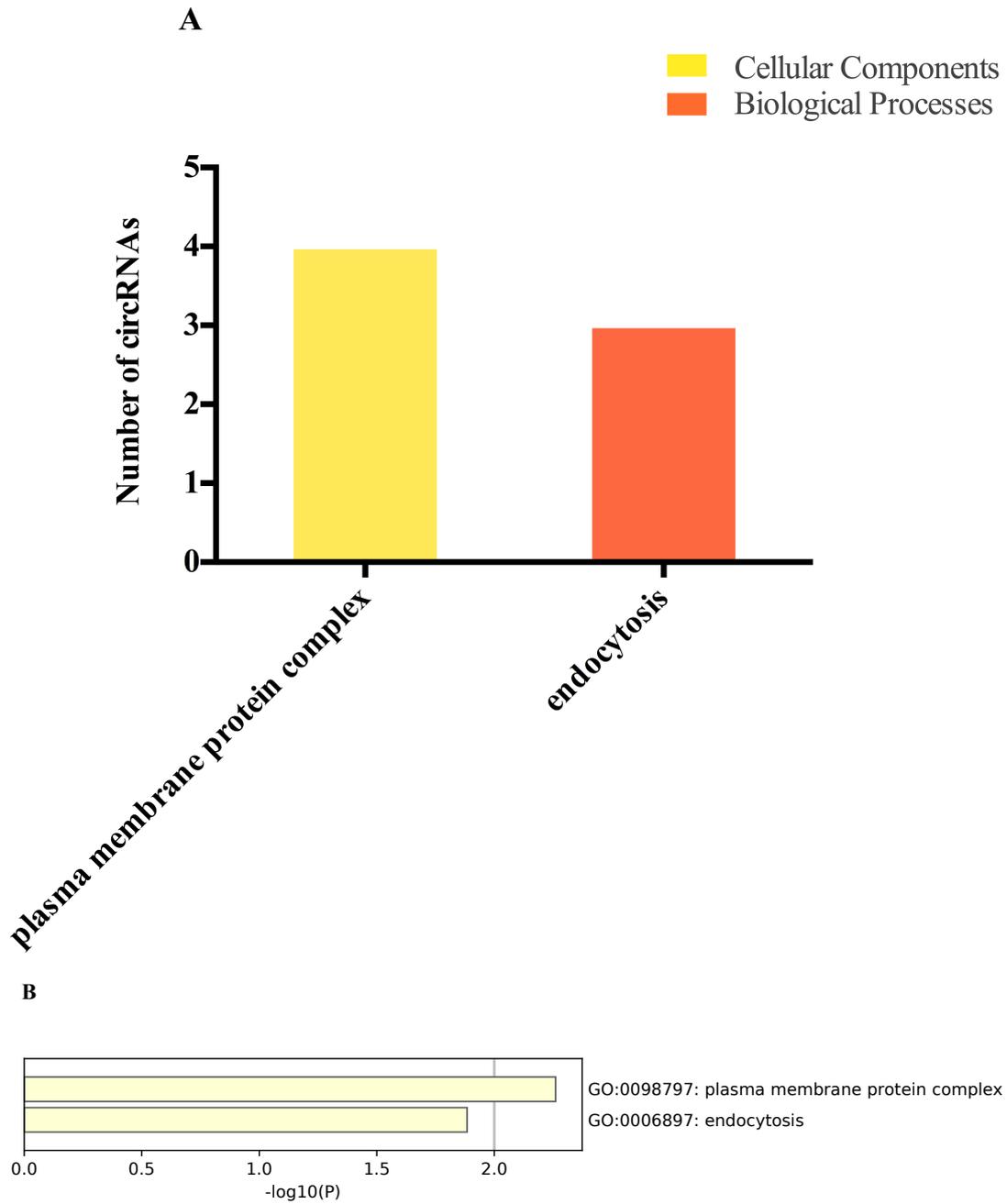
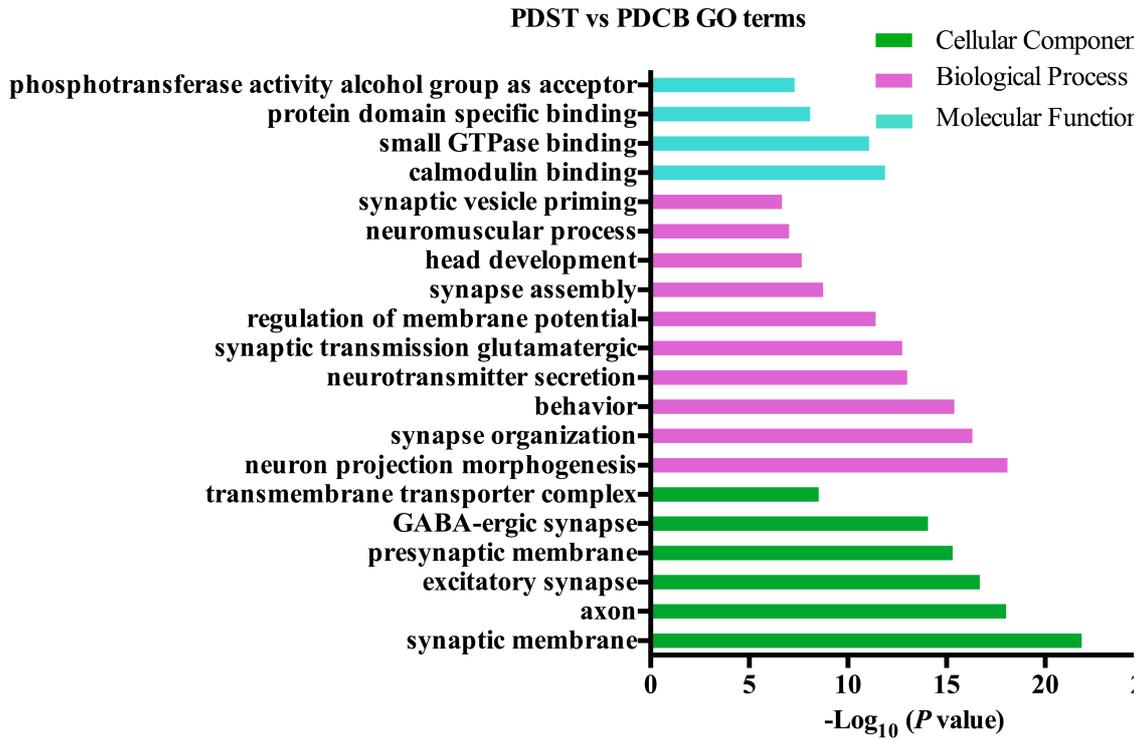
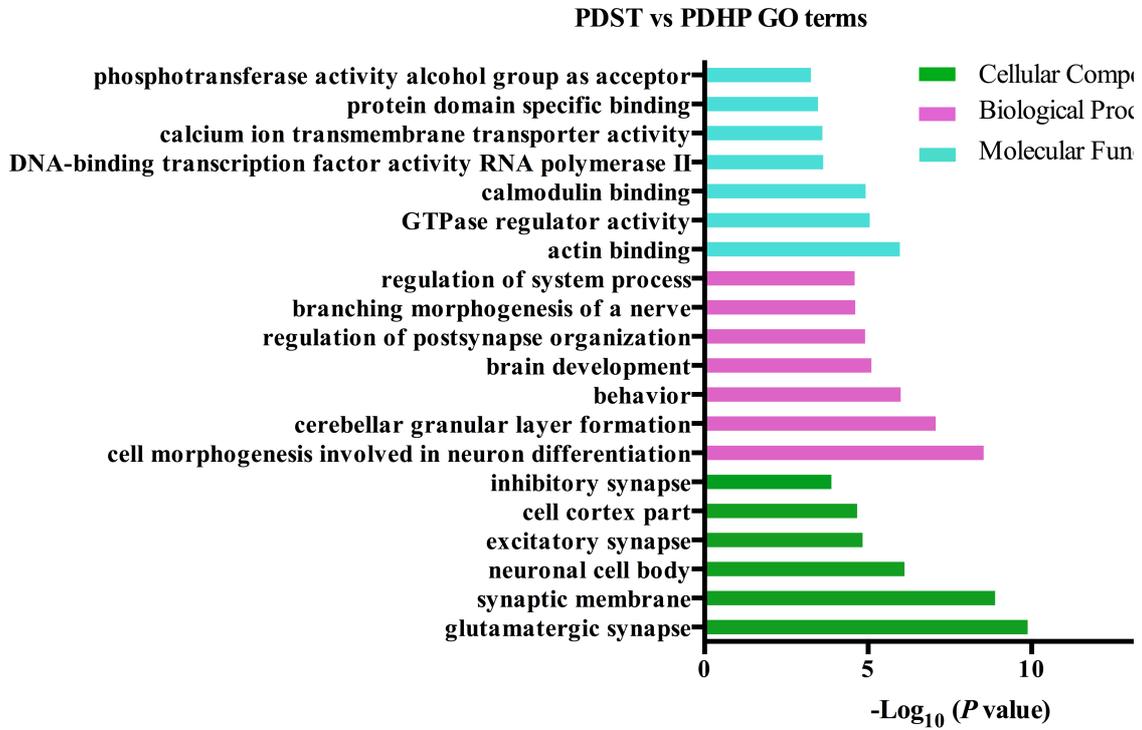


Figure. S2. GO analyses of the DE-circRNAs parental genes in the CC regions. (A) GO function classification of all DE-circRNAs in the CC region. (B) Bar chart of the all DE-circRNAs clusters in CC region.

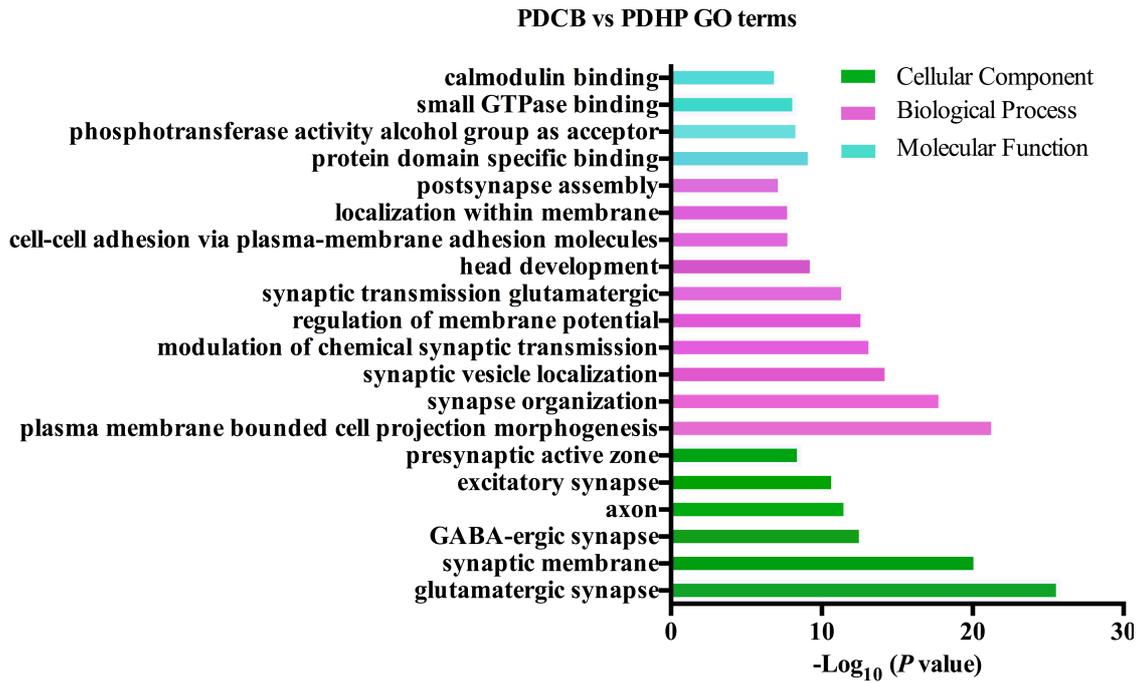
A



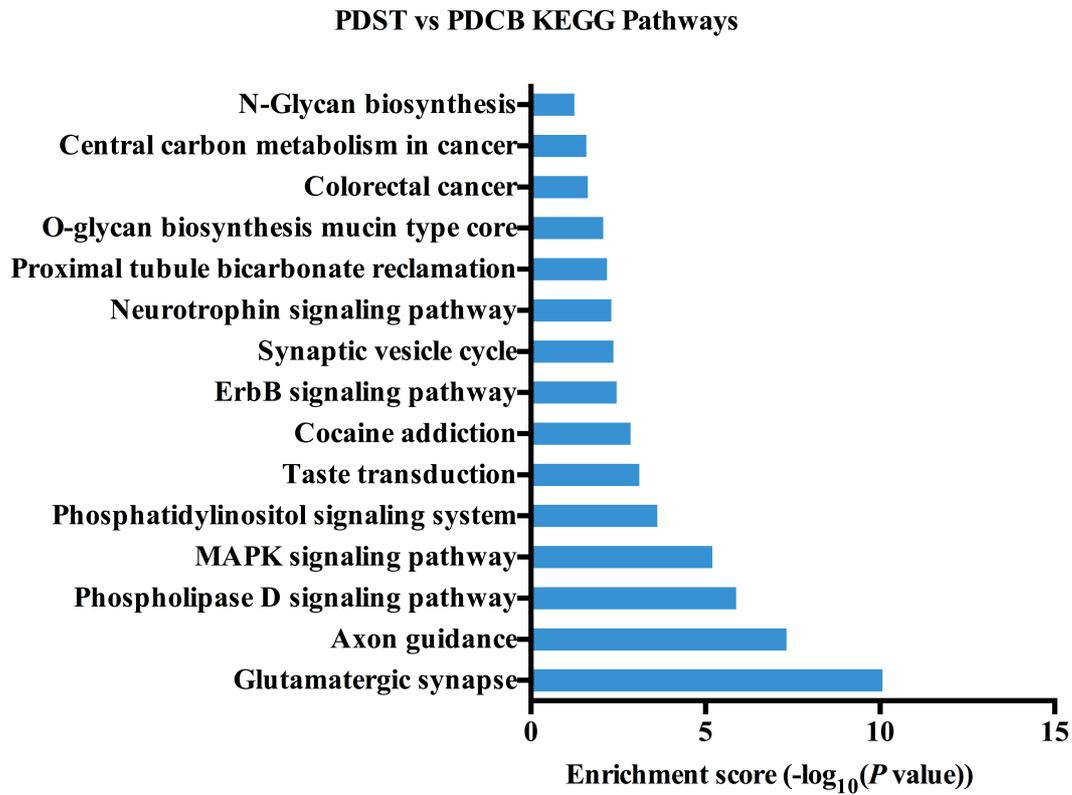
B



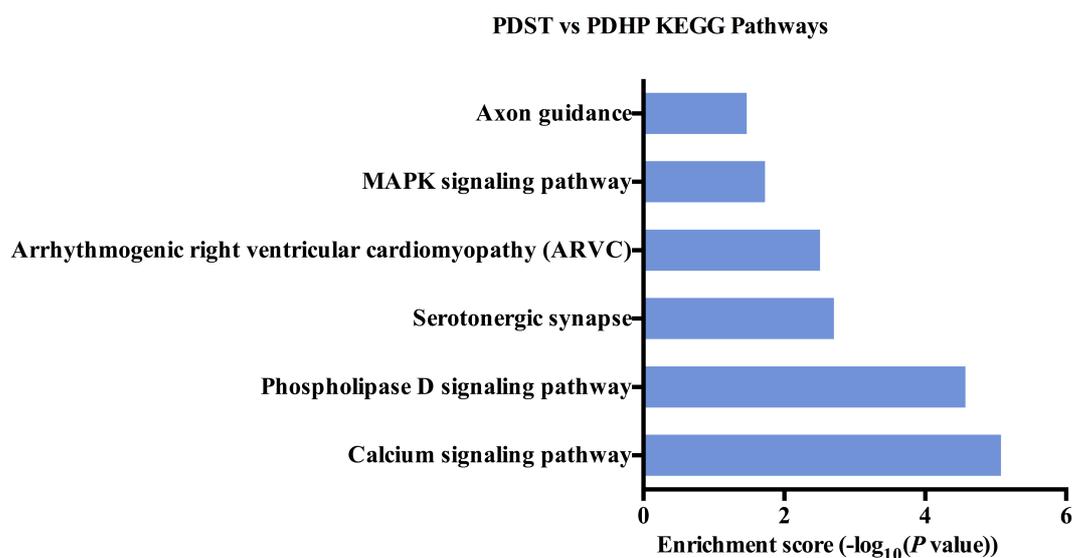
C



D



E



F

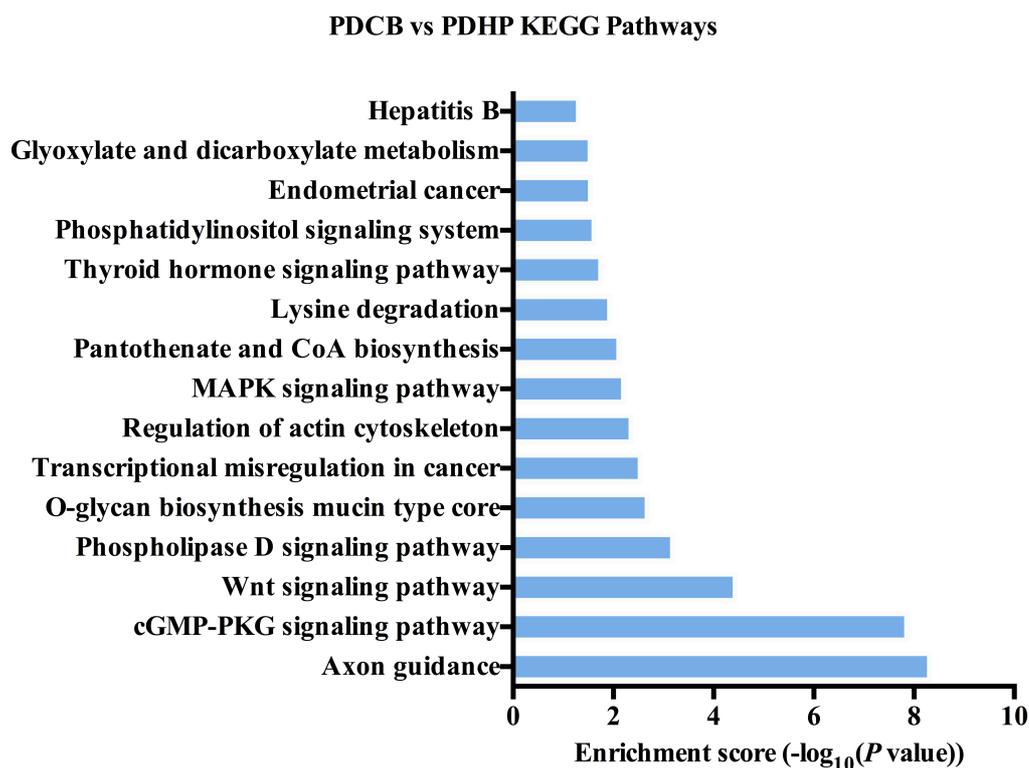


Figure S3. GO and KEGG analysis of differentially expressed circRNA host genes. (A) GO analysis was performed for the DE-circRNAs on PDST vs PDCB. (B) GO analysis was performed for the DE-circRNAs on PDST vs PDHP. (C) GO analysis was performed for the DE-circRNAs on PDCB vs PDHP. (D) KEGG analysis of the pathways of the differential circRNA parental genes on PDST vs PDCB. (E) KEGG analysis of the pathways of the differential circRNA parental genes on PDST vs PDHP. (F) KEGG analysis of the pathways of the differential circRNA parental genes on PDCB vs PDHP.

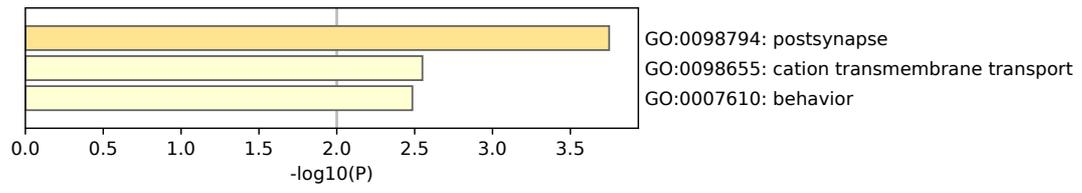


Figure. S4. GO analyses of the co-expressed DE-circRNAs parental genes in the PDST vs PDCB, PDST vs PDHP and PDCB vs PDHP groups.