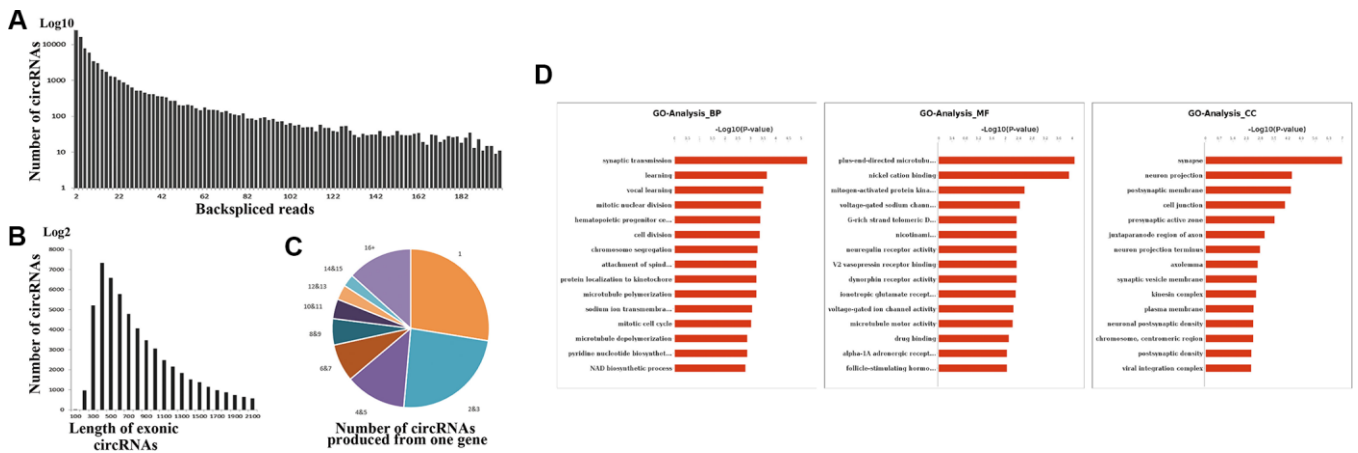
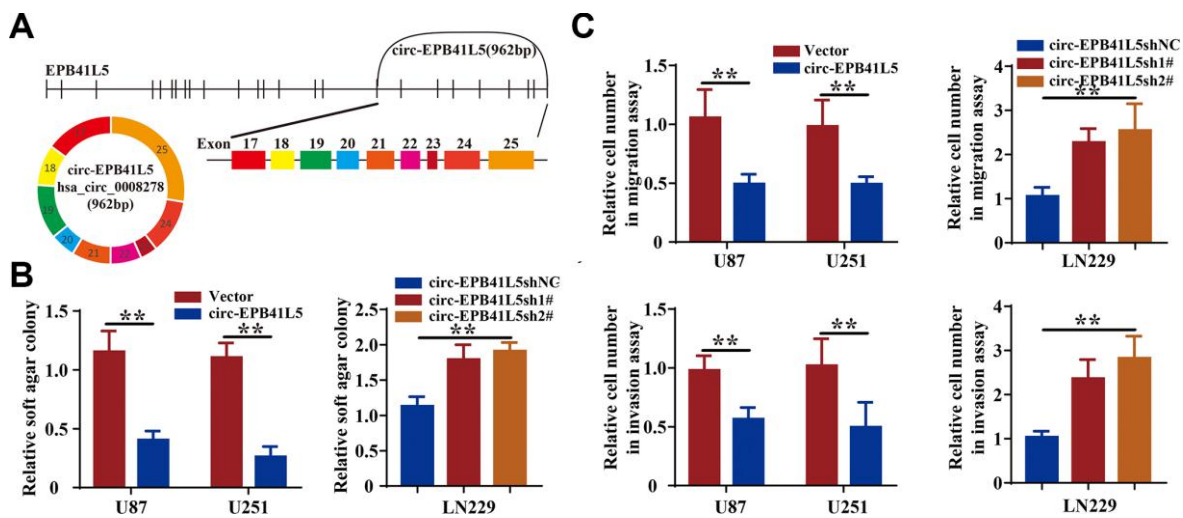


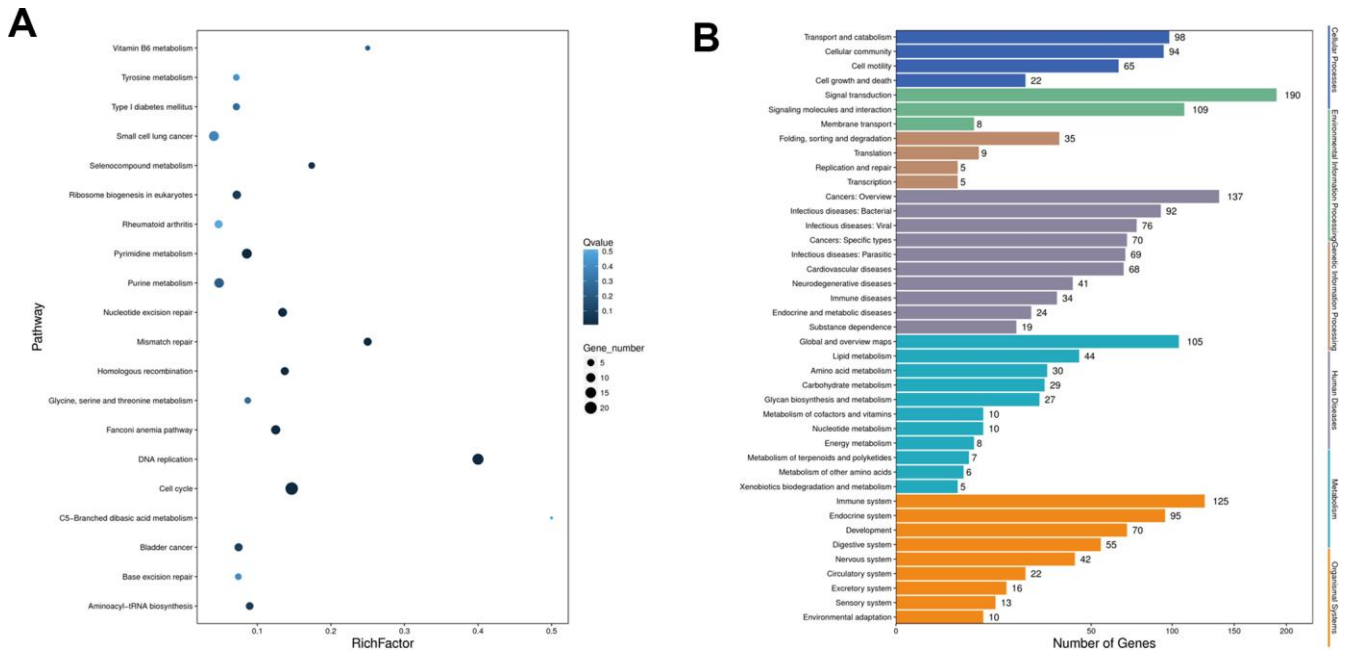
## SUPPLEMENTARY FIGURES



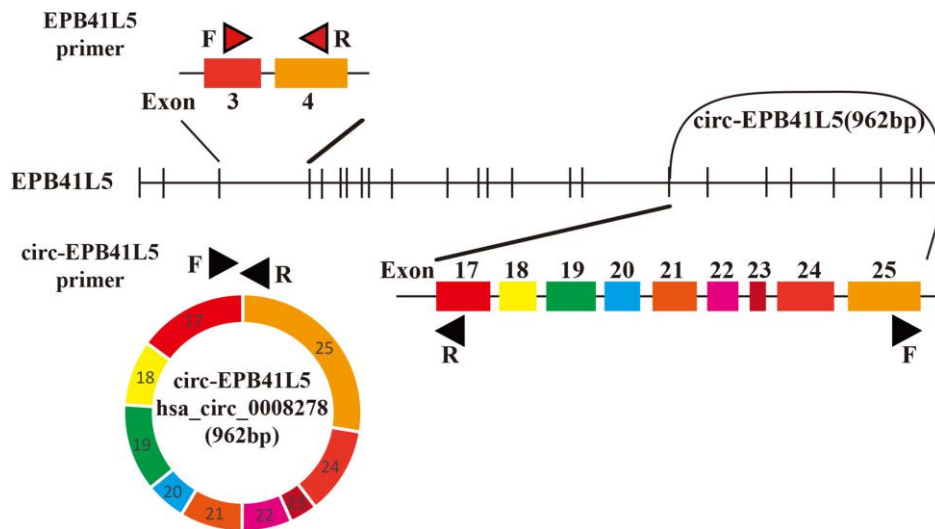
**Supplementary Figure 1.** (A) The back spliced reads and the corresponding number of circRNAs. (B) The length distribution for exonic circRNAs. (C) The number of circRNAs generated from one host gene. (D) GO analysis of the host gene of dysregulated circRNAs.



**Supplementary Figure 2.** (A) Schematic representation of circ-EPB41L5. (B) Quantification of Colony formation rates (C) Quantification of relative migration or invasion.



**Supplementary Figure 3. (A)** KEGG analysis of down-regulated genes. **(B)** Pathway enrichment analysis of up-regulated genes.



**Supplementary Figure 4. The sketch of primers of circ-EPB41L5 and EPB41L5 mRNA.** Red arrows represent primers amplifying genome region of EPB41L5 which does not contain circ-EPB41L5 sequence. Black arrows represent divergent primers, which are used to amplify the genome region of circPTK2 containing the back splice junction site.