

Supplementary Materials:

Figure s. 1

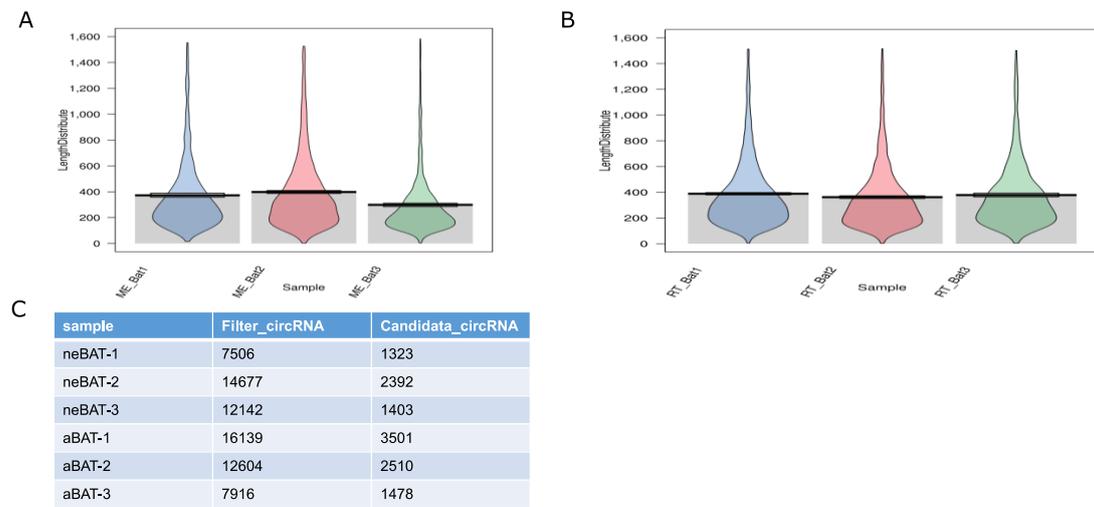


Figure s. 1. CircRNA analysis of aBATs and neBATs. (A and B) The length of most exonic circRNAs was < 1,500 nucleotides (nt), and the median length was about 400 nt. (C) Filtered circRNAs and candidate circRNAs in neBATs and aBATs.

Figure s. 2

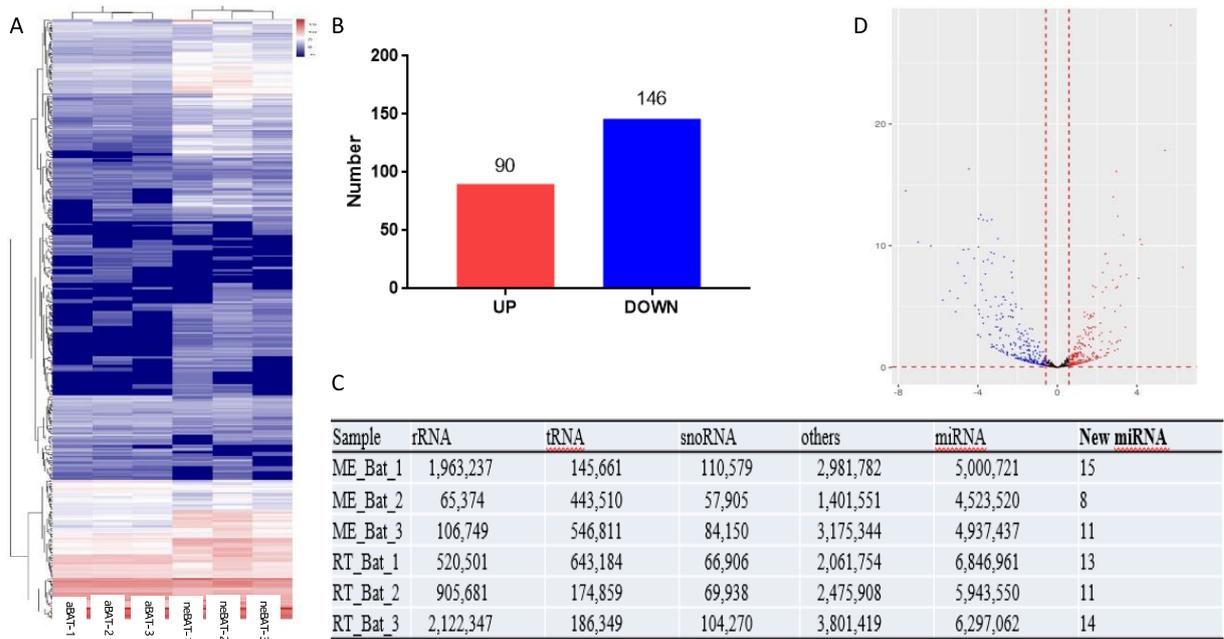


Figure s. 2

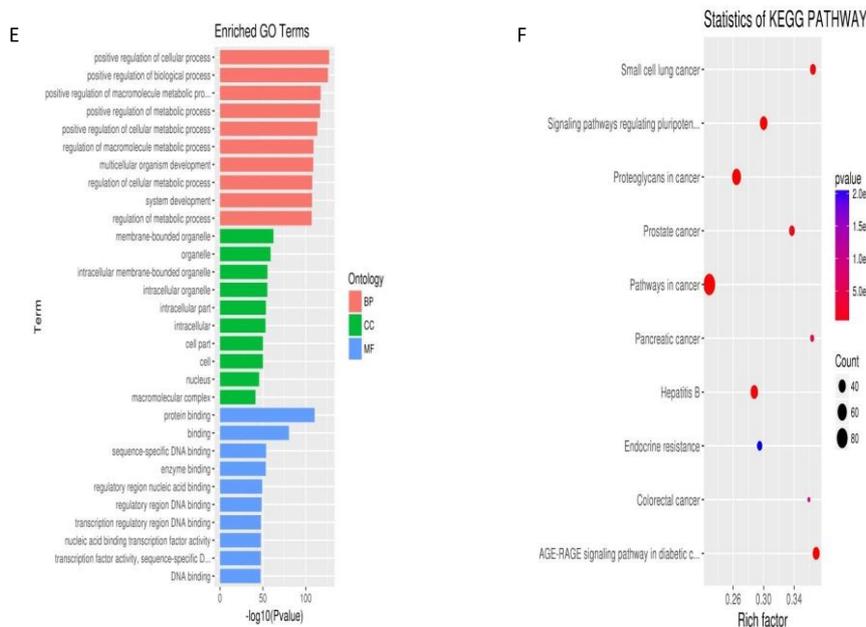


Figure s. 2. MicroRNA analysis of aBATs and neBATs (A) Heat map showing the differences in microRNAs between neBATs and aBATs. (B) Number of upregulated and downregulated microRNAs in neBATs and aBATs. (C) sRNA statistics in neBATs and aBATs. (D) Volcano plot of microRNAs. The volcano plots show significance on the y-axis ($-\log_{10}$, p-value) against the gene expression ratio (\log_2 , fold change in neBATs vs. aBATs), and the FDR cutoff < 0.05 is indicated. (E) GO categories of differentially expressed microRNAs. (F) KEGG analysis of differentially expressed microRNAs. The number and p-value of differentially expressed microRNAs in each pathway.

Figure s. 3

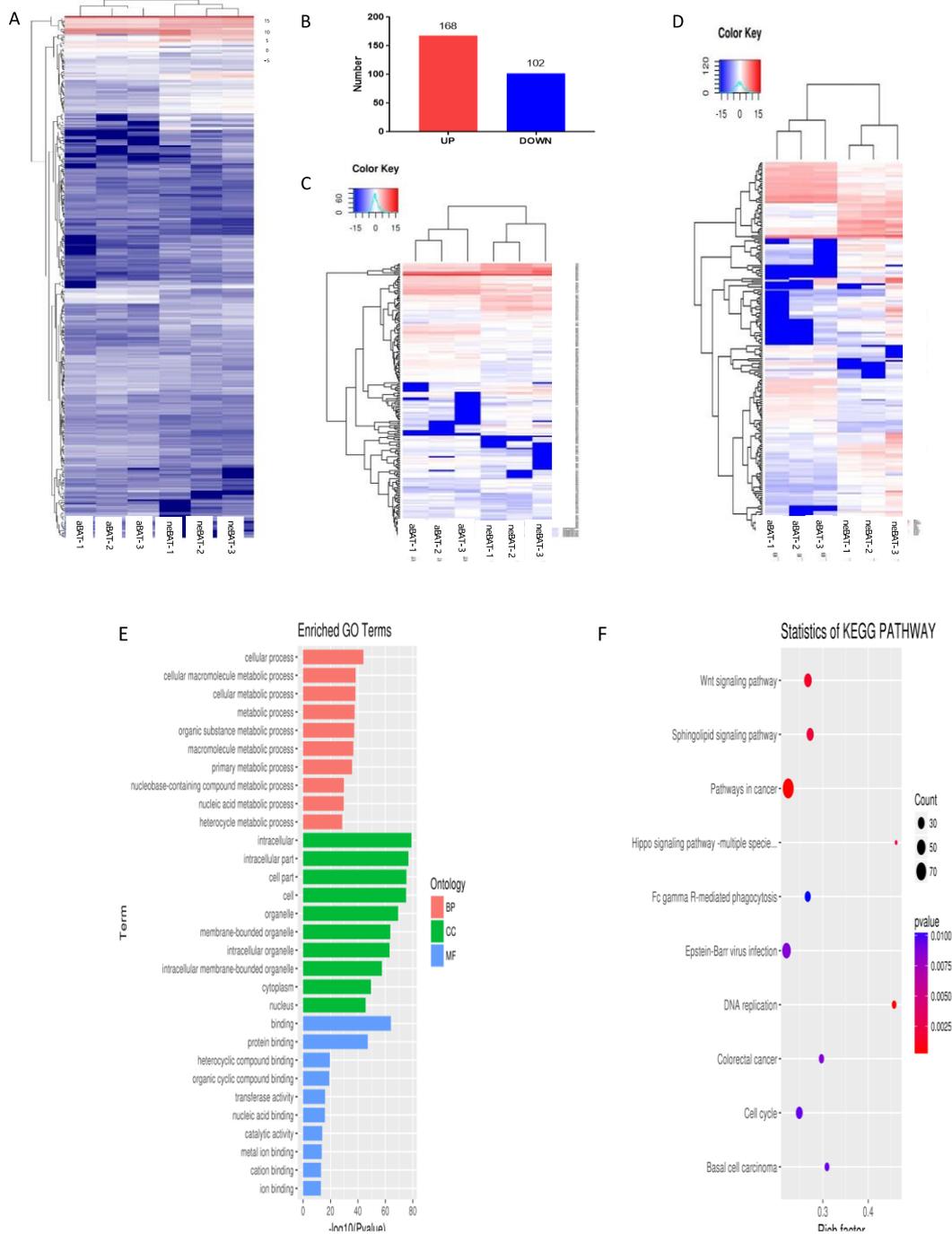


Figure s. 3. LncRNA analysis of aBATs and neBATs. (A) Heat map showing the differences in LncRNAs between neBATs and aBATs. (B) Number of upregulated and downregulated LncRNAs in neBATs and aBATs. (C) Heat map showing expression profiles of the top 200 differentially expressed LncRNAs. (D) Heat map showing expression profiles of the top 200 differentially expressed mRNAs. (E) GO categories for differentially expressed LncRNAs. (F) KEGG pathway analysis of differentially expressed LncRNAs. The number and p-value of differentially expressed LncRNAs.