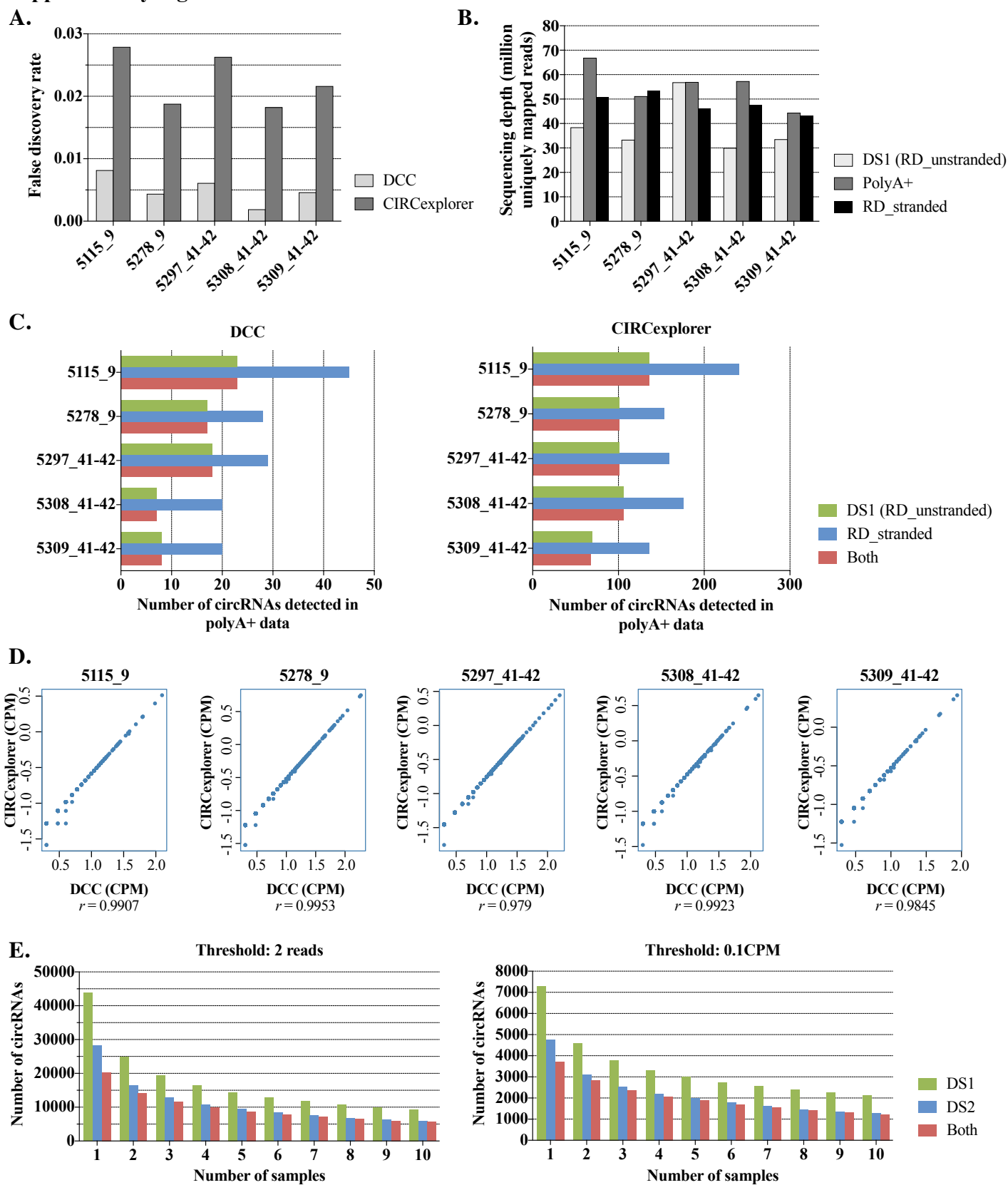


## Supplementary Figure 2



**Supplementary Figure 2. Benchmarking of circRNA expression data.** (A) Barplots of false positive rates defined as the % of circRNAs detected in each DS1 sample that were also detected in polyA+ data from the same sample, normalized for the sequencing depth. (B) Barplots of sequencing depth (millions of uniquely mapped reads) for DS1 libraries, as well as RNA-seq data generated in the present study (polyA+ and RD\_stranded). RD: ribo-depleted. (C) Barplots of the number of circRNAs detected in polyA+ libraries (i.e. false-positives) for DS1 data, ribo-depleted stranded data, as well as those common between both types of data. RD: ribo-depleted. *Left*: DCC, *Right*: CIRCexplorer. (D) Scatterplots of normalized circRNA expression levels (CPM: counts per million) quantified by DCC and CIRCexplorer.  $r$ : Pearson correlation coefficient. (E) circRNA detection using DCC across various expression thresholds. Number of circRNAs detected by using a threshold of either 2 back-splice junction reads (left), or 0.1 CPM (right), in a minimum of 1 to 10 independent samples