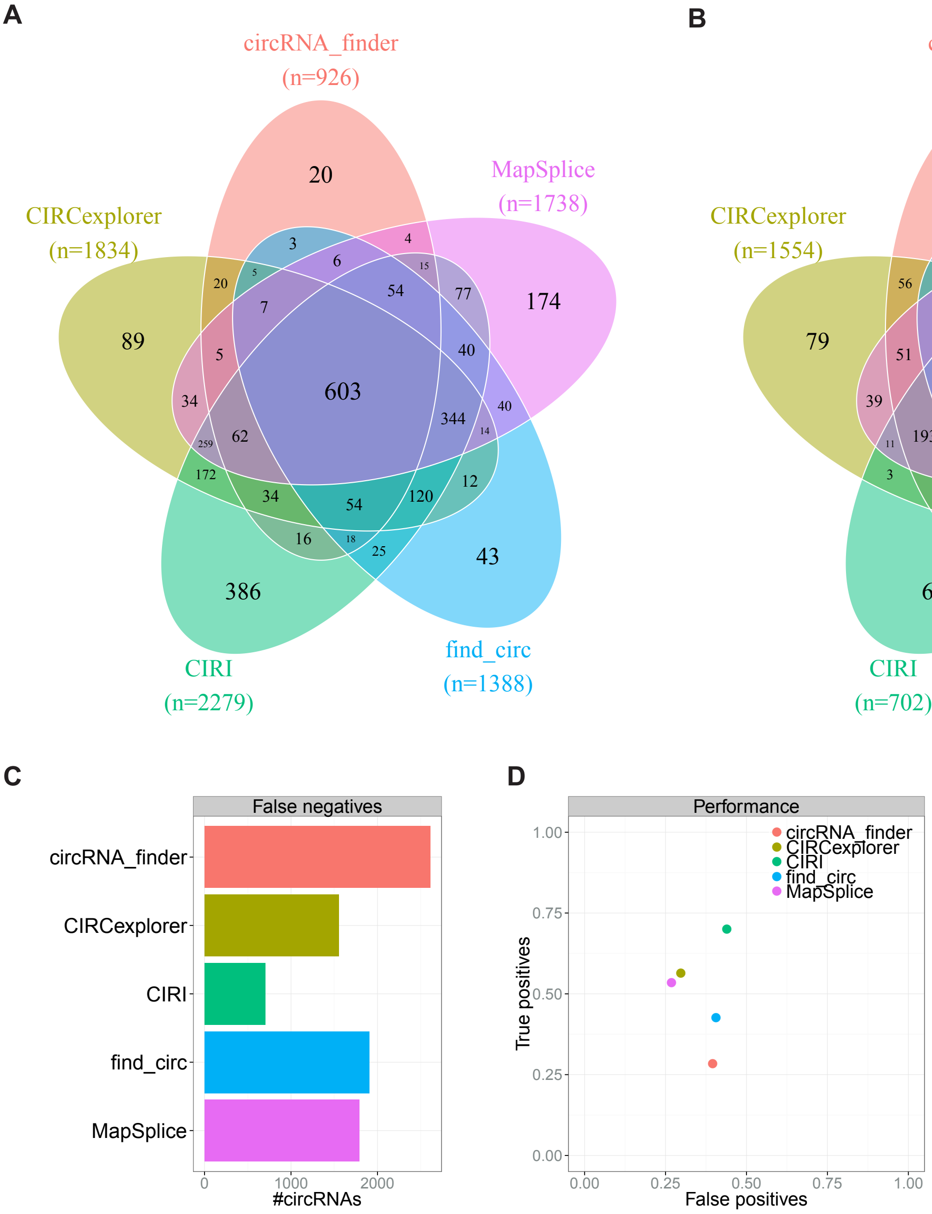
Supplementary Figure 1



Supplementary Figure 1: True positives and false negatives. A+B) Venn diagram depicting the overlap of RNAse R resistant circRNAs between the 5 different prediction algorithms (A), or the overlap of false negatives (i.e. circRNAs missed by the individual algorithms) based on the collective group of all RNAse R resistant circRNA predicted at least once using all algorithms (B). **C)** Barplot showing number of false positives calculated as the total number of RNAse R resistant circRNA (n=3251) subtracted by true positive circRNAs predicted by the individual algorithms. **D)** The overall performance of the algorithms depicted as the true positive by false positive rate. The true positive rate is calculated as the fraction of RNAse R resistant circRNAs relative to the total number of circRNAs for each algorithm. The false positive rate is calculated as 1-sensitivity, where sensitivity is defined as the fraction of true positives predicted by individual algorithms relative to the total number of RNAse R resistant circRNAs found collectively by all algorithms.