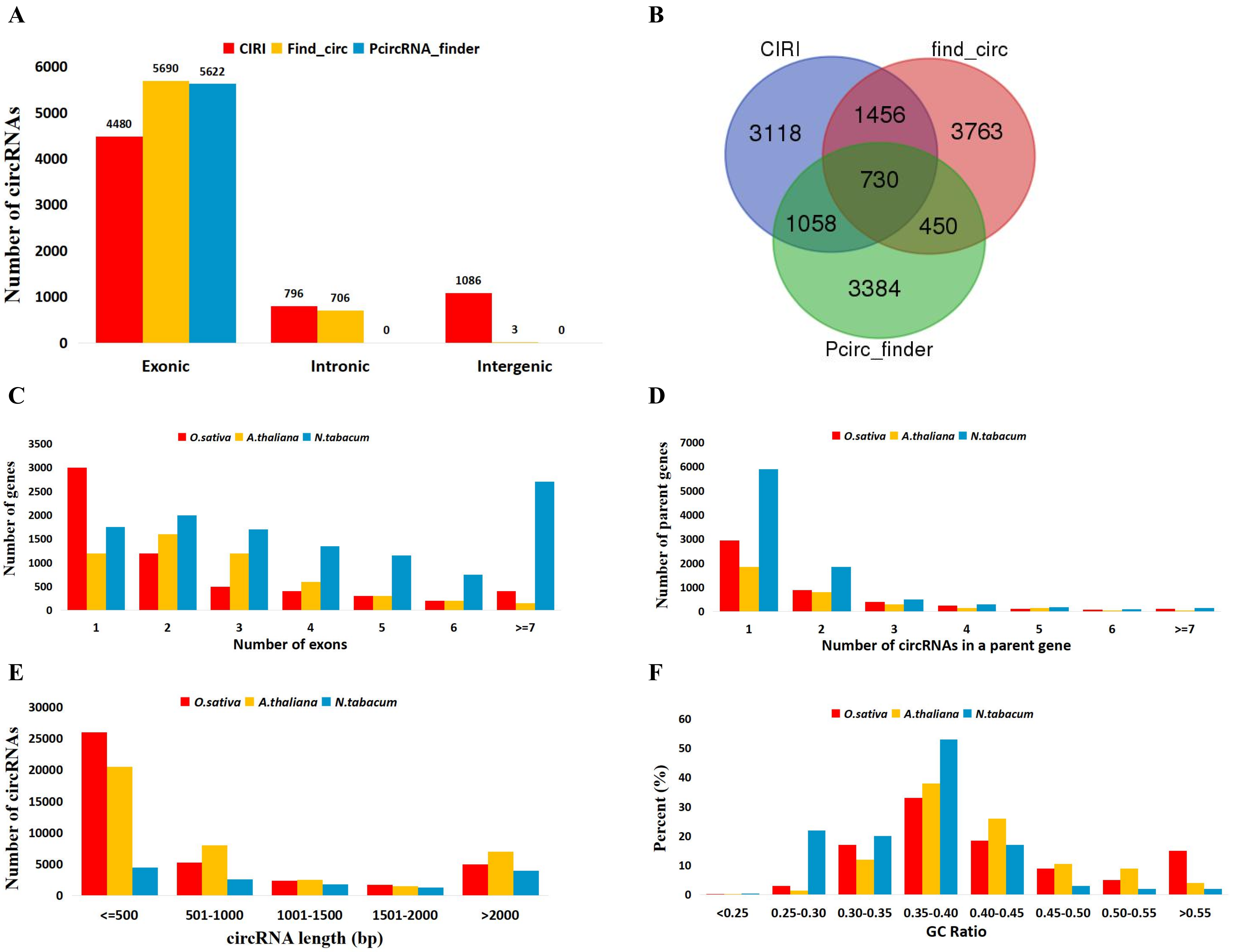

Fig. S3. Genome-wide identification of circRNAs in tobacco. (**A**) Number of different types of circRNAs identified in this study. (**B**) Number of circRNAs identified by different methods in tobacco. (**C**) Number of exonic circRNAs that contained different number of exons derived from parental genes in plants. (**D**) Number of parent genes that generated different number of circRNAs in plants. (**E**) Distribution of length of circRNAs in plants. (**F**) Distribution of GC ratio of circRNAs in plants.