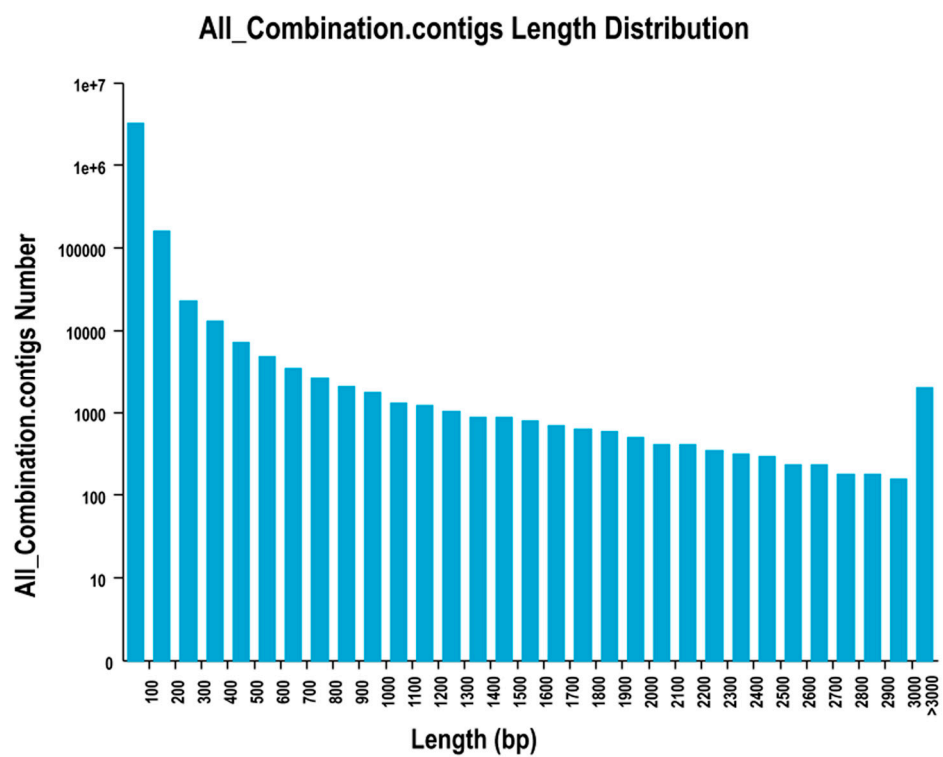
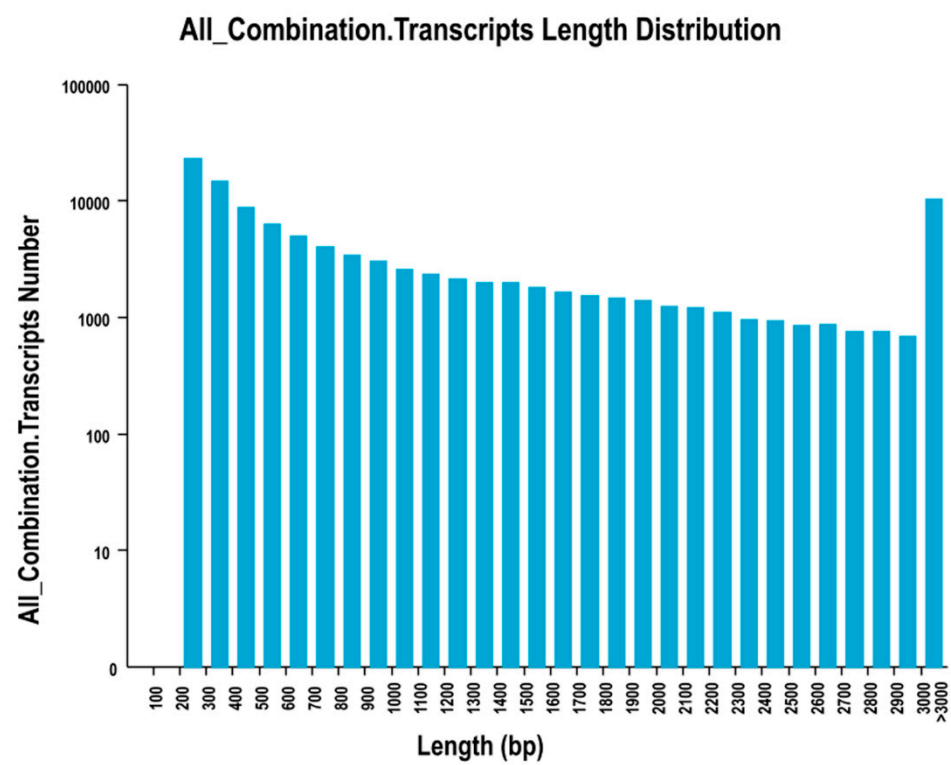


Supplementary Information



(A)



(B)

Figure S1. *Cont.*

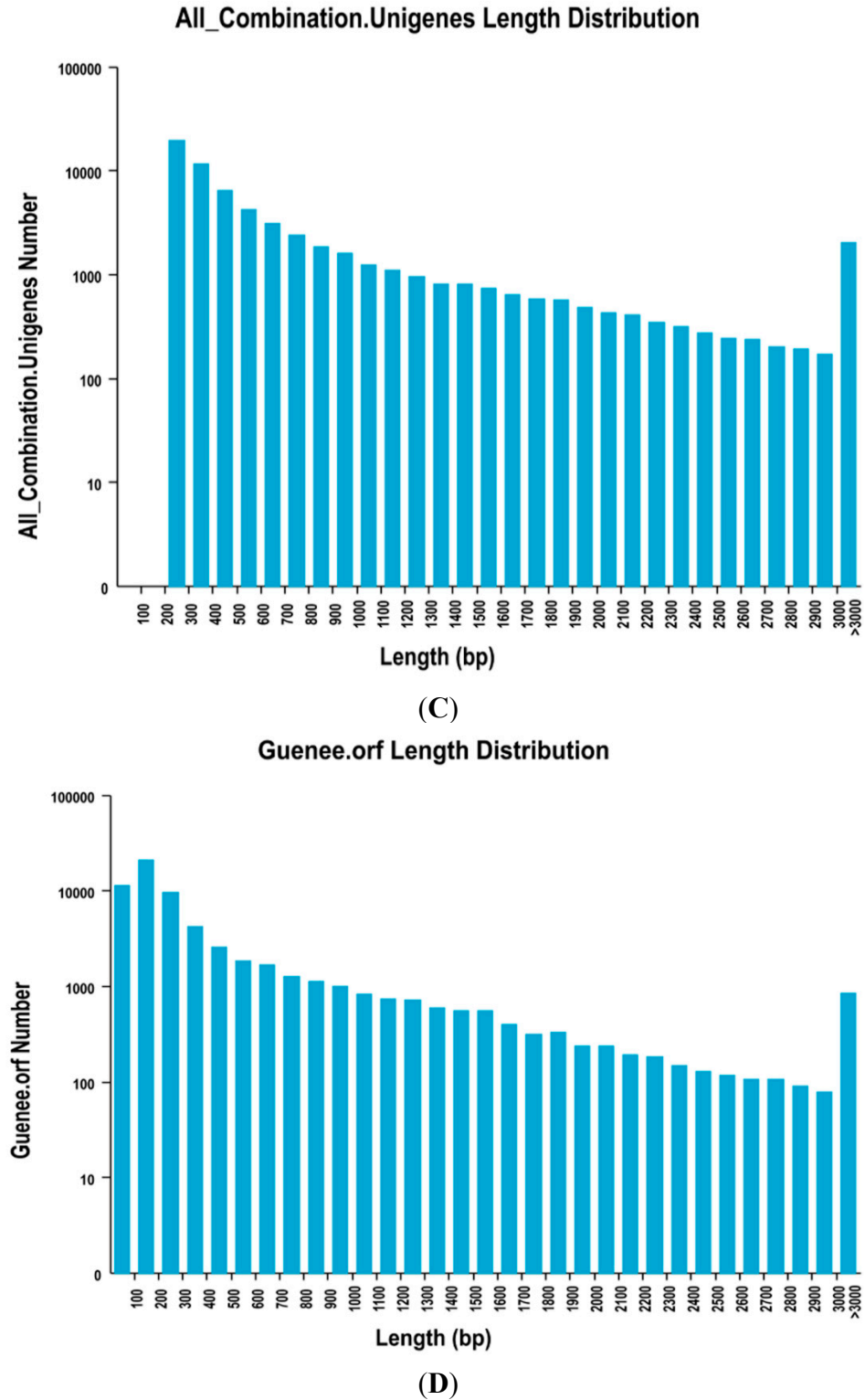


Figure S1. All contigs, transcripts and unigenes distribution of the *C. medinalis* transcriptome sequencing. (A) Length distribution of the contigs obtained from do novo assembly of high-quality clean reads; (B) Length distribution of the transcripts produced from further assembly of contigs; (C) Size distribution of the unigenes produced from further clustering of transcripts; (D) Length distribution of the opening reading frame (ORF). The x-axis indicates the length distribution from different range. The y-axis indicates the number of unigenes.