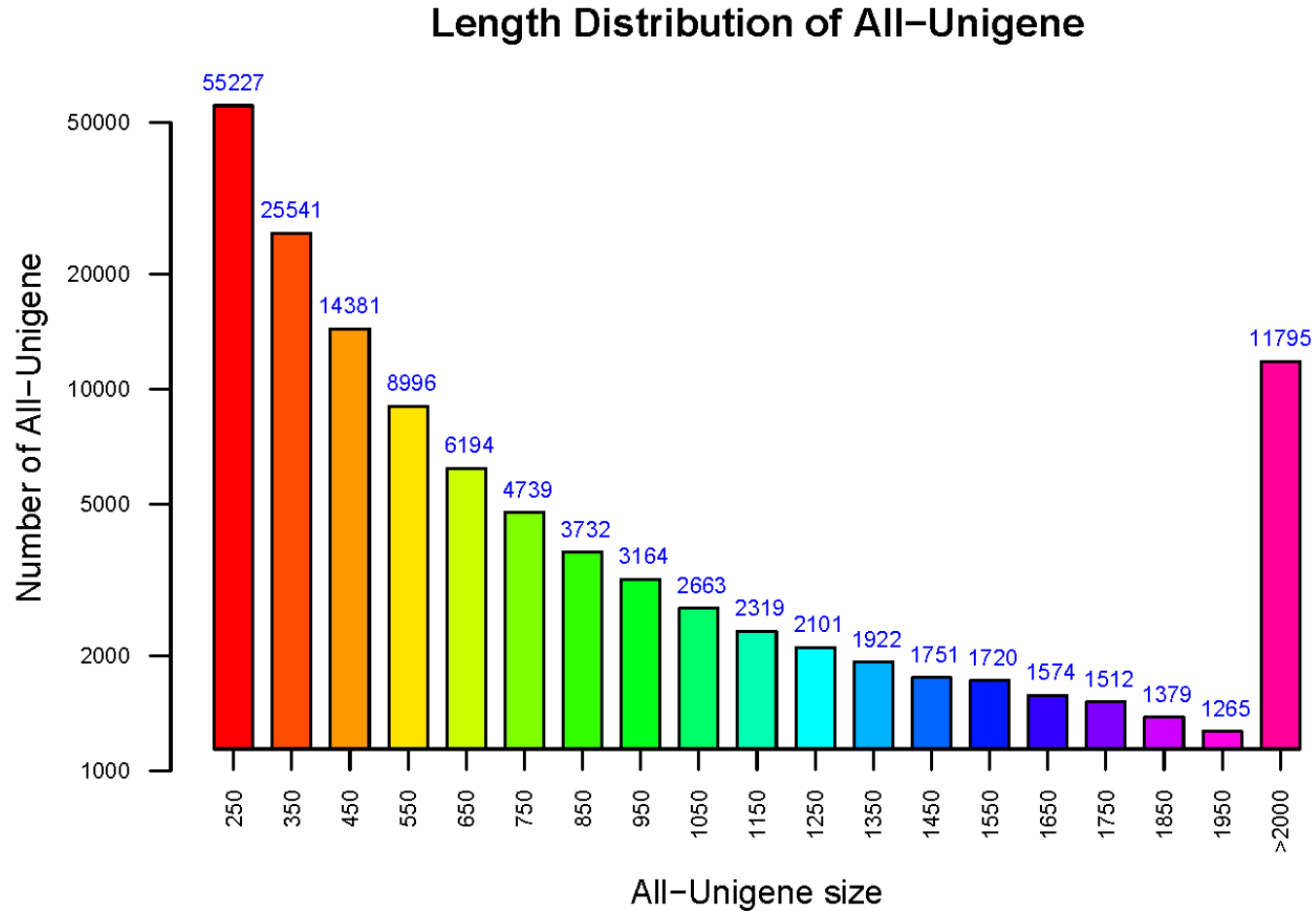
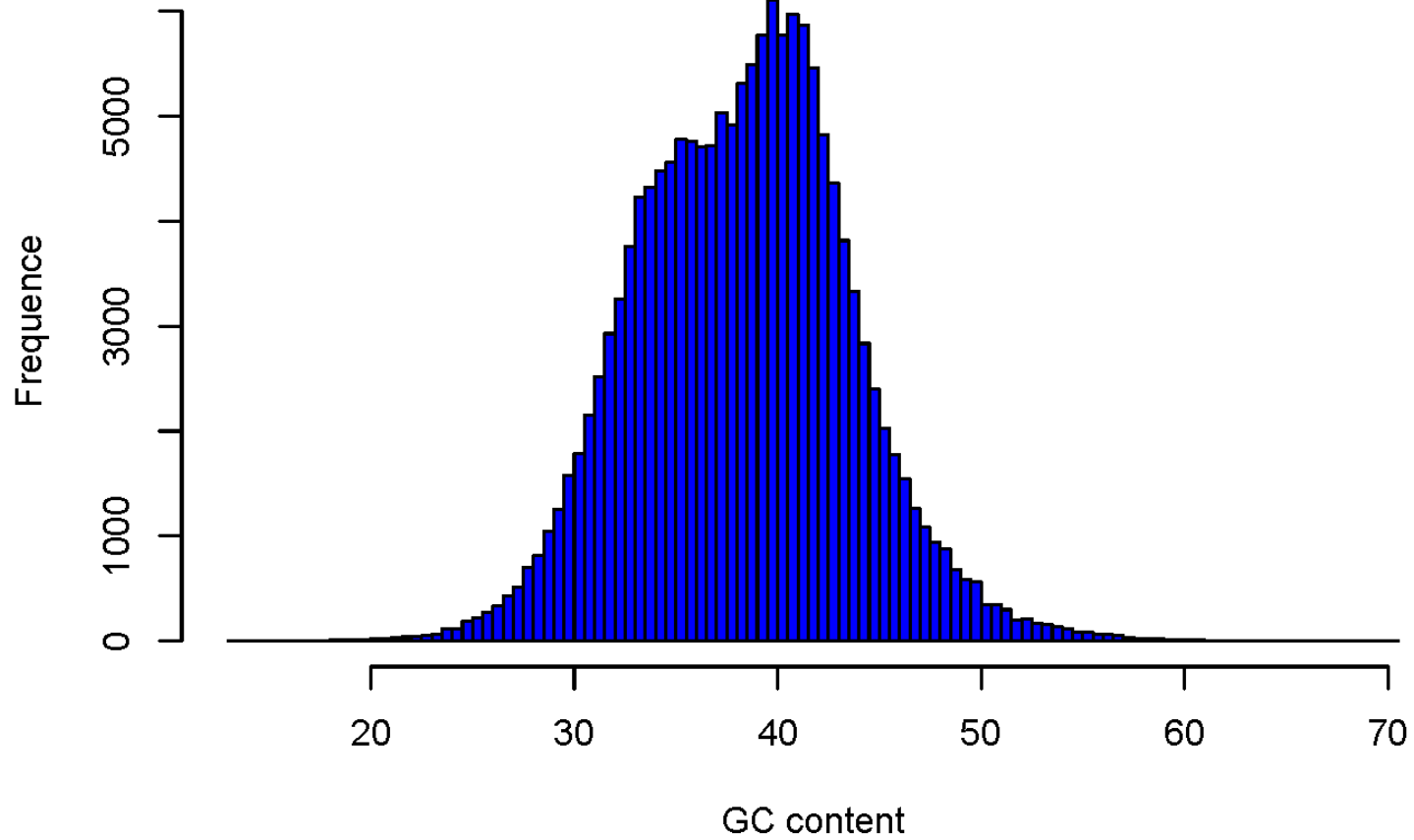


Additional file 1. Summary of *de novo* assembled mRNA-seq transcriptome data



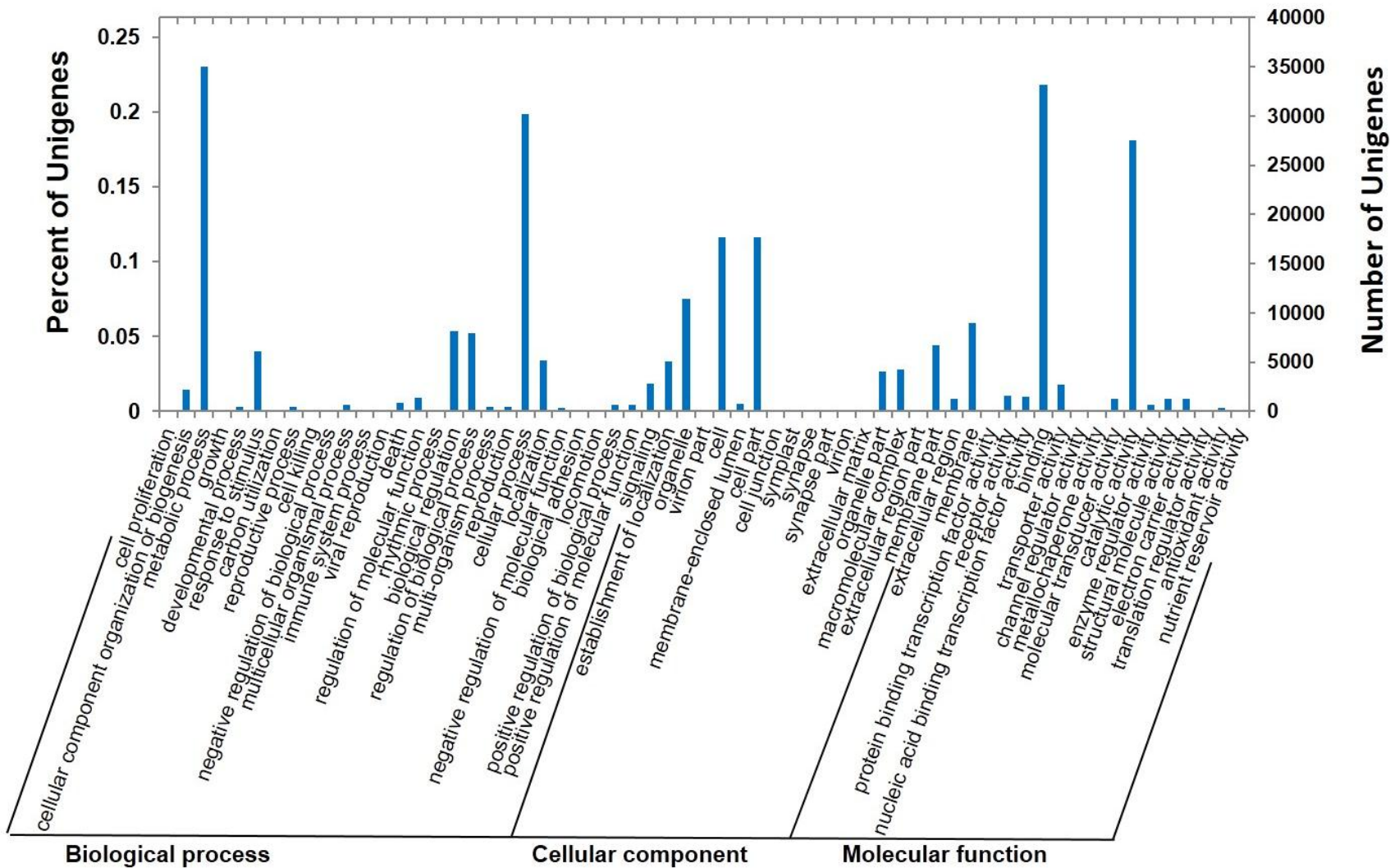
A. Mapping of the length distribution of all-unigene

GC Content Frequency Distribution



B. GC content of all unigenes

Comparison of GO classification



C. Functional classifications of GO annotated unigenes