

Figure S1. Length distribution of 454 raw reads

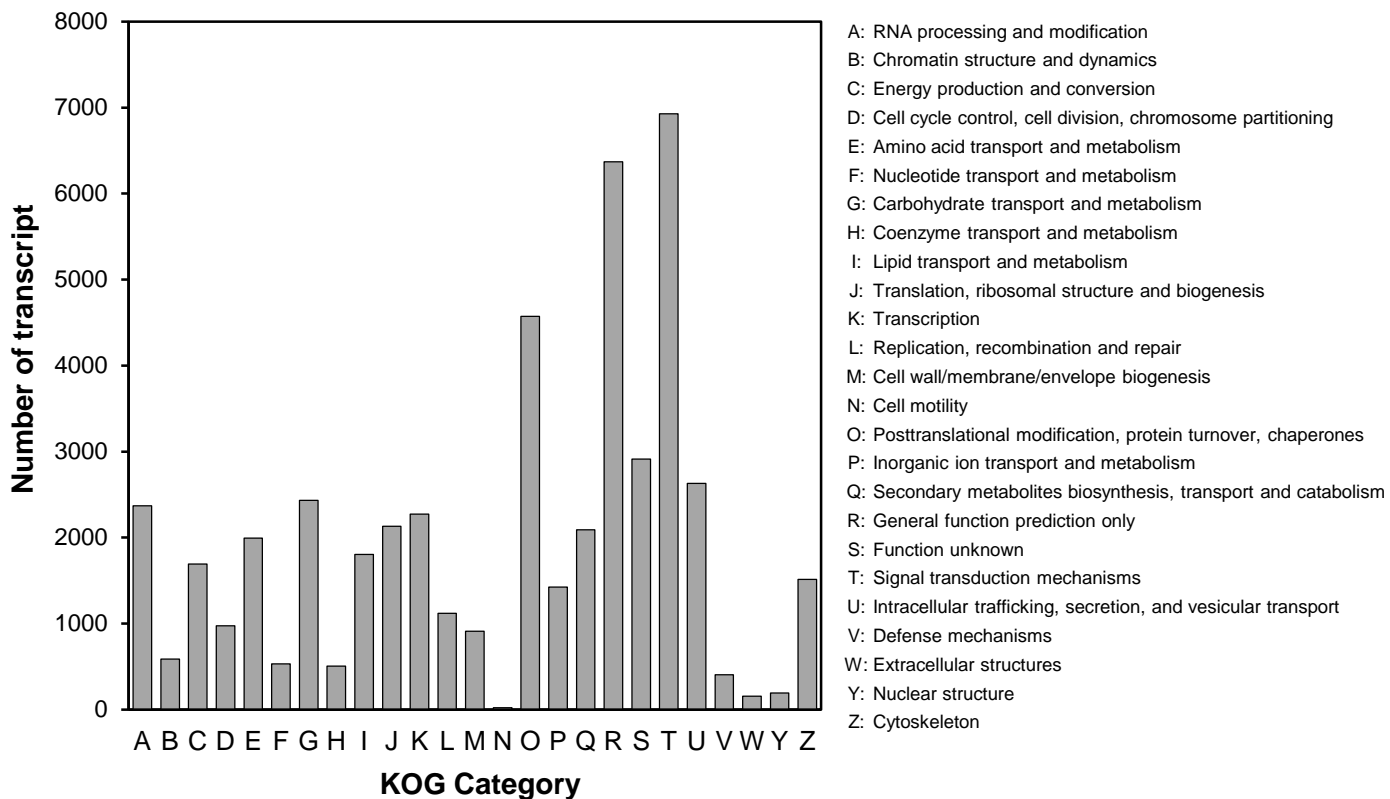


Figure S2. Eukaryotic Orthologous Groups (KOG) classification with translated peptides from *P. minus* combined assembly.

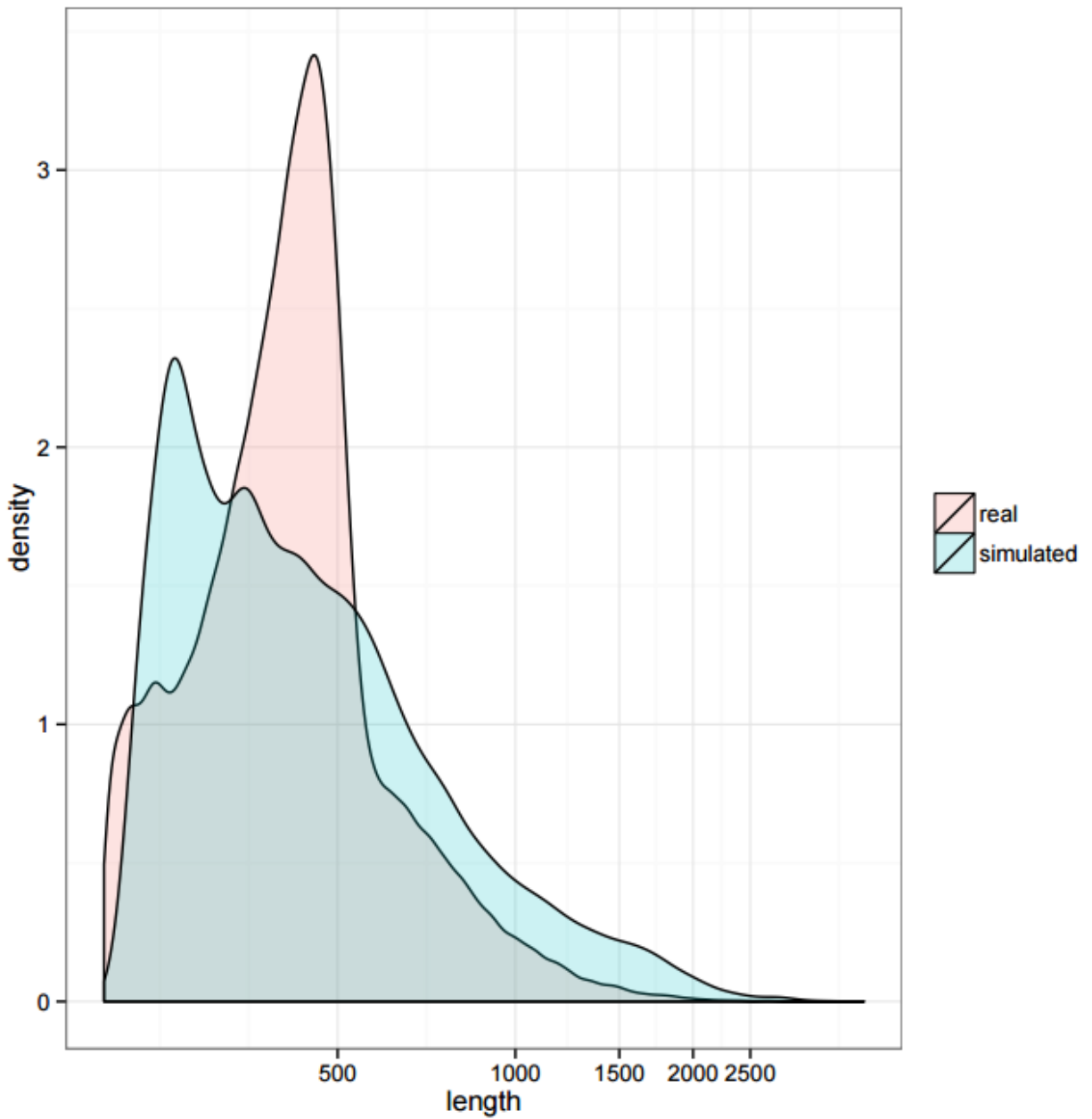


Figure S3. Length distribution of transcripts assembled using actual 454 reads through iAssembler pipeline (real) compared to simulated Illumina reads from assembled root transcriptome through Trinity pipeline