Transcriptome statistics	
Raw number of contigs	211,840
Total number of filtered contigs	40,130
Percent GC	47.61
Contigs N50 (bp)	2,664
Total assembled bases	67,152,264
Median contig length (bp)	1,151
Average contig length (bp)	1,673.37
Annotation	
Contig with match against nt (e-value 10-4)	34,969 (87.14%)
Contig with match against Uniprot-Swissprot (e-value 10-3)	27,801 (69.28%)
Contig with GO identifier annotation	26,630 (66.36%)
Percent BUSCO completedness (metazoa_od10)	93.6