

## COMPLETENESS ASSESSMENT RESULTS:

Total number of core genes queried	954
Number of core genes detected	
Complete	750 (78.62%)
Complete + Partial	859 (90.04%)
Number of missing core genes	95 (9.96%)
Average number of orthologs per core genes	1.38
% of detected core genes that have more than 1 ortholog	23.47
Scores in BUSCO format	C:78.6%[S:60.2%,D:18.4%],F:11.4%,M:10.0%

## LENGTH STATISTICS AND COMPOSITION:

Number of sequences	234123
Total length (nt)	115167979
Longest sequence (nt)	30058
Shortest sequence (nt)	188
Mean sequence length (nt)	492
Median sequence length (nt)	333
N50 sequence length (nt)	565
L50 sequence count	52502
Number of sequences > 1K (nt)	20150 (8.6% of total number)
Number of sequences > 10K (nt)	18 (0.0% of total number)
Number of sequences > 100K (nt)	0 (0.0% of total number)
Number of sequences > 1M (nt)	0 (0.0% of total number)
Number of sequences > 10M (nt)	0 (0.0% of total number)
	A: 27.53
	T: 27.89
	G: 22.11
Base composition (%)	C: 22.47
	N: 0.00
	Other: 0.00
Number of gaps (>=5 N's)	
GC-content (%)	44.58
Number of non-ACGTN (nt)	0