

Genome Assembly Statistics

	BUSCO									
	Contigs (n)	Scaffolds (n)	Ungapped Size (Gbp)	Gapped Size (Gbp)	Ambiguous Bases (%)	Contig N50 (kbp)	Scaffold N50 (kbp)	Largest Contig (kbp)	Largest Scaffold (kbp)	Complete Genes (%)
Short-Read Assembly	3,860,052	3,860,072	1.9	1.9	0.0	1.89	1.89	54	54	67.7
Scaffolding and Gap Filling ¹	3,662,748	3,458,610	2.2	2.7	19.2	5.42	103.51	232	1,489	94.0
Length Filtering ²	436,743	232,605	1.6	2.1	24.6	11.29	164.61	232	1,489	94.0
Gap Filling and Polishing ³	407,409	232,605	1.6	2.1	24.4	13.11	164.10	235	1,484	94.7

¹ With ONT long reads $^2 \leq 500\text{bp}$

³ With Illumina short reads