Genome Assembly Statistics

	Contigs (n)	Scaffolds (n)	Ungapped Size (Gbp)	Gapped Size (Gbp)	Ambiguous Bases (%)	Contig N50 (kbp)	Scaffold N50 (kbp)	Largest Contig (kbp)	Largest Scaffold (kbp)
Short-Read Assembly	3,860,052	3,860,072	1.9	1.9	0.0	1.89	1.89	53	53
Scaffolding and Gap Filling[1]	3,662,748	3,458,610	2.2	2.7	19.2	5.42	103.51	232	1,489
Length Filtering[2]	436,743	232,605	1.6	2.1	24.6	11.29	164.61	232	1,489
Gap Filling and Polishing[3]	407,409	232,605	1.6	2.1	24.4	13.11	164.10	235	1,484

[1] With ONT long reads

[2] ≤ 500bp

[3] With Illumina short reads