

Report

	final.contigs
# contigs (≥ 0 bp)	1855
# contigs (≥ 1000 bp)	1172
# contigs (≥ 5000 bp)	657
# contigs (≥ 10000 bp)	313
# contigs (≥ 25000 bp)	35
# contigs (≥ 50000 bp)	1
Total length (≥ 0 bp)	9481088
Total length (≥ 1000 bp)	9209664
Total length (≥ 5000 bp)	7805100
Total length (≥ 10000 bp)	5335038
Total length (≥ 25000 bp)	1077390
Total length (≥ 50000 bp)	51384
# contigs	1287
Largest contig	51384
Total length	9296959
Reference length	9283304
N50	11772
N75	6689
L50	250
L75	514
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29999
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	138
Genome fraction (%)	98.949
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.02
# indels per 100 kbp	0.07
Largest alignment	51384
NA50	11772
NA75	6689
LA50	250
LA75	514

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	29999
# local misassemblies	2
# mismatches	2115
# indels	6
# short indels	6
# long indels	0
Indels length	6

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	138
# N's	0

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