

Report

	final.contigs
# contigs (≥ 0 bp)	8478
# contigs (≥ 1000 bp)	1780
# contigs (≥ 5000 bp)	63
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	6861032
Total length (≥ 1000 bp)	3904323
Total length (≥ 5000 bp)	396789
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3727
Largest contig	9194
Total length	5216997
Reference length	9714864
N50	1865
N75	998
L50	839
L75	1789
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.303
Duplication ratio	1.061
# N's per 100 kbp	0.00
# mismatches per 100 kbp	588.82
# indels per 100 kbp	0.23
Largest alignment	9194
NA50	1865
NA75	998
LA50	839
LA75	1789

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	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	2
# mismatches	49368
# indels	19
# short indels	19
# long indels	0
Indels length	25

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	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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