

Report

	final.contigs
# contigs (>= 0 bp)	13358
# contigs (>= 1000 bp)	2857
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9837472
Total length (>= 1000 bp)	4287712
Total length (>= 5000 bp)	16888
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7947
Largest contig	5936
Total length	7897681
Reference length	9283304
N50	1061
N75	758
L50	2528
L75	4744
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1094
# local misassemblies	4
# unaligned contigs	0 + 2 part
Unaligned length	77
Genome fraction (%)	80.817
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	133.18
# indels per 100 kbp	0.17
Largest alignment	5936
NA50	1060
NA75	757
LA50	2528
LA75	4745

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	1094
# local misassemblies	4
# mismatches	9992
# indels	13
# short indels	13
# long indels	0
Indels length	14

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	77
# N's	0

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).









