

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2185
# contigs ( $\geq 1000$ bp)	1413
# contigs ( $\geq 5000$ bp)	681
# contigs ( $\geq 10000$ bp)	279
# contigs ( $\geq 25000$ bp)	18
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9512188
Total length ( $\geq 1000$ bp)	9171609
Total length ( $\geq 5000$ bp)	7176112
Total length ( $\geq 10000$ bp)	4326038
Total length ( $\geq 25000$ bp)	536830
Total length ( $\geq 50000$ bp)	0
# contigs	1606
Largest contig	44678
Total length	9323107
Reference length	9283304
N50	9453
N75	5326
L50	314
L75	646
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3970
# local misassemblies	2
# unaligned contigs	1 + 1 part
Unaligned length	739
Genome fraction (%)	98.960
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17.35
# indels per 100 kbp	0.03
Largest alignment	44678
NA50	9453
NA75	5326
LA50	314
LA75	646

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  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	3970
# local misassemblies	2
# mismatches	1594
# indels	3
# short indels	3
# long indels	0
Indels length	3

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## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	507
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	232
# N's	0

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