

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1740
# contigs ( $\geq 1000$ bp)	1386
# contigs ( $\geq 5000$ bp)	697
# contigs ( $\geq 10000$ bp)	262
# contigs ( $\geq 25000$ bp)	27
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9352212
Total length ( $\geq 1000$ bp)	9168181
Total length ( $\geq 5000$ bp)	7270597
Total length ( $\geq 10000$ bp)	4156298
Total length ( $\geq 25000$ bp)	792121
Total length ( $\geq 50000$ bp)	0
# contigs	1555
Largest contig	45348
Total length	9292963
Reference length	9283304
N50	9319
N75	5443
L50	313
L75	640
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.952
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.14
# indels per 100 kbp	0.00
Largest alignment	45348
NA50	9319
NA75	5443
LA50	313
LA75	640

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	15101
# local misassemblies	0
# mismatches	105
# indels	0
# short indels	0
# long indels	0
Indels length	0

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## 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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