

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1522
# contigs ( $\geq 1000$ bp)	972
# contigs ( $\geq 5000$ bp)	611
# contigs ( $\geq 10000$ bp)	341
# contigs ( $\geq 25000$ bp)	75
# contigs ( $\geq 50000$ bp)	4
Total length ( $\geq 0$ bp)	9898128
Total length ( $\geq 1000$ bp)	9689284
Total length ( $\geq 5000$ bp)	8654826
Total length ( $\geq 10000$ bp)	6702975
Total length ( $\geq 25000$ bp)	2578929
Total length ( $\geq 50000$ bp)	252781
# contigs	1043
Largest contig	78529
Total length	9741997
Reference length	9714864
N50	15372
N75	8556
L50	193
L75	407
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	12230
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.251
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.87
# indels per 100 kbp	0.01
Largest alignment	78529
NA50	15372
NA75	8556
LA50	193
LA75	407

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	12230
# local misassemblies	1
# mismatches	1241
# indels	1
# short indels	1
# long indels	0
Indels length	1

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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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