

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	13358
# contigs ( $\geq 1000$ bp)	2857
# contigs ( $\geq 5000$ bp)	3
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9837472
Total length ( $\geq 1000$ bp)	4287712
Total length ( $\geq 5000$ bp)	16888
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ 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 (%)	83.221
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	175.75
# indels per 100 kbp	0.13
Largest alignment	5936
NA50	1060
NA75	757
LA50	2528
LA75	4745

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	1094
# local misassemblies	4
# mismatches	13578
# indels	10
# short indels	10
# long indels	0
Indels length	11

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).

## 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

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