

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	10015
# contigs ( $\geq 1000$ bp)	3621
# contigs ( $\geq 5000$ bp)	34
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	10040043
Total length ( $\geq 1000$ bp)	6609169
Total length ( $\geq 5000$ bp)	206120
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	6795
Largest contig	8916
Total length	8911858
Reference length	9283304
N50	1531
N75	982
L50	1889
L75	3697
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	3
# unaligned contigs	1 + 0 part
Unaligned length	515
Genome fraction (%)	91.981
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.43
# indels per 100 kbp	0.08
Largest alignment	8916
NA50	1529
NA75	982
LA50	1889
LA75	3698

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	3
# mismatches	7380
# indels	7
# short indels	7
# long indels	0
Indels length	7

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## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	515
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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