

# Report

	contigs
# contigs ( $\geq 0$ bp)	3043
# contigs ( $\geq 1000$ bp)	1028
# contigs ( $\geq 5000$ bp)	286
# contigs ( $\geq 10000$ bp)	66
# contigs ( $\geq 25000$ bp)	4
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	5149723
Total length ( $\geq 1000$ bp)	4344635
Total length ( $\geq 5000$ bp)	2472077
Total length ( $\geq 10000$ bp)	934010
Total length ( $\geq 25000$ bp)	125579
Total length ( $\geq 50000$ bp)	0
# contigs	1308
Largest contig	36999
Total length	4534934
Reference length	9283304
N50	5672
N75	3054
L50	248
L75	522
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9660
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	48.617
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	804.57
# indels per 100 kbp	0.73
Largest alignment	36999
NA50	5672
NA75	3054
LA50	248
LA75	522

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

	contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9660
# local misassemblies	3
# mismatches	36312
# indels	33
# short indels	33
# long indels	0
Indels length	41

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## Unaligned report

	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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