

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	2532
# contigs ( $\geq 1000$ bp)	539
# contigs ( $\geq 5000$ bp)	269
# contigs ( $\geq 10000$ bp)	149
# contigs ( $\geq 25000$ bp)	36
# contigs ( $\geq 50000$ bp)	1
Total length ( $\geq 0$ bp)	5279867
Total length ( $\geq 1000$ bp)	4490880
Total length ( $\geq 5000$ bp)	3899587
Total length ( $\geq 10000$ bp)	3011827
Total length ( $\geq 25000$ bp)	1258049
Total length ( $\geq 50000$ bp)	61819
# contigs	803
Largest contig	61819
Total length	4669416
Reference length	9283304
N50	14917
N75	7346
L50	94
L75	206
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	19577
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	48.447
Duplication ratio	1.038
# N's per 100 kbp	3250.24
# mismatches per 100 kbp	948.33
# indels per 100 kbp	9.69
Largest alignment	59611
NA50	13558
NA75	6662
LA50	101
LA75	227

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

	scaffolds
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	103
# misassembled contigs	1
Misassembled contigs length	19577
# local misassemblies	4
# mismatches	42651
# indels	436
# short indels	35
# long indels	401
Indels length	22083

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## Unaligned report

	scaffolds
# 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	151767

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