

## 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	14
# misassembled contigs	14
Misassembled contigs length	147002
# local misassemblies	7
# unaligned contigs	65 + 15 part
Unaligned length	40071
Genome fraction (%)	47.233
Duplication ratio	1.056
# N's per 100 kbp	3250.24
# mismatches per 100 kbp	1062.10
# indels per 100 kbp	9.94
Largest alignment	59611
NA50	13549
NA75	6511
LA50	102
LA75	228

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	14
# relocations	13
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	103
# misassembled contigs	14
Misassembled contigs length	147002
# local misassemblies	7
# mismatches	46571
# indels	436
# short indels	36
# long indels	400
Indels length	22029

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## Unaligned report

	scaffolds
# fully unaligned contigs	65
Fully unaligned length	37563
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2508
# N's	151767

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