Report

	scaffolds
# contigs (>= 0 bp)	104
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length ($>= 0 \text{ bp}$)	4566207
Total length (>= 1000 bp)	4558404
Total length (>= 5000 bp)	4513119
Total length (>= 10000 bp)	4489168
Total length (>= 25000 bp)	4398036
Total length (>= 50000 bp)	3914279
# contigs	77
Largest contig	327064
Total length	4561971
Reference length	4641652
N50	133023
N75	87064
L50	11
L75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.227
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.75
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	133023
NA75	87064
LA50	11
LA75	21
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All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	171
# indels	18
# short indels	18
# long indels	0
Indels length	25

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).









