## Report

	final.contigs
# contigs (>= 0 bp)	252
# contigs (>= 1000 bp)	115
# contigs (>= 5000 bp)	91
# contigs (>= 10000 bp)	82
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	32
Total length ( $>= 0 bp$ )	4603311
Total length (>= 1000 bp)	4553543
Total length (>= 5000 bp)	4498722
Total length (>= 10000 bp)	4431525
Total length (>= 25000 bp)	4014870
Total length (>= 50000 bp)	3229822
# contigs	133
Largest contig	193070
Total length	4565076
Reference length	4641652
N50	78692
N75	37774
L50	18
L75	37
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.068
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.76
# indels per 100 kbp	0.37
Largest alignment	193070
NA50	78692
NA75	37774
LA50	18
LA75	37

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	403
# indels	17
# short indels	11
# long indels	6
Indels length	96

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

	final.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

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).









