Report

	final.contigs
# contigs (>= 0 bp)	136
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4572774
Total length (>= 1000 bp)	4555229
Total length (>= 5000 bp)	4499621
Total length (>= 10000 bp)	4448450
Total length (>= 25000 bp)	4253085
Total length (>= 50000 bp)	3544631
# contigs	110
Largest contig	327142
Total length	4563914
Reference length	4641652
N50	112683
N75	54949
L50	14
L75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.273
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.43
# indels per 100 kbp	10.02
Largest alignment	327142
NA50	112683
NA75	54949
LA50	14
LA75	29

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	10
# mismatches	2711
# indels	457
# short indels	452
# long indels	5
Indels length	737

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).









