Report

	final.contigs
# contigs (>= 0 bp)	136
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4567976
Total length (>= 1000 bp)	4549180
Total length (>= 5000 bp)	4508520
Total length (>= 10000 bp)	4469795
Total length (>= 25000 bp)	4253771
Total length (>= 50000 bp)	3595787
# contigs	104
Largest contig	209435
Total length	4557558
Reference length	4641652
N50	95681
N75	56609
L50	15
L75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.146
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.93
# indels per 100 kbp	9.44
Largest alignment	209435
NA50	95681
NA75	56609
LA50	15
LA75	31

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	9
# mismatches	2639
# indels	430
# short indels	430
# long indels	0
Indels length	596

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).









