Report

	final.contigs
# contigs (>= 0 bp)	152
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4574960
Total length (>= 1000 bp)	4551877
Total length (>= 5000 bp)	4497397
Total length (>= 10000 bp)	4454018
Total length (>= 25000 bp)	4174547
Total length (>= 50000 bp)	3607181
# contigs	113
Largest contig	249259
Total length	4562633
Reference length	4641652
N50	105838
N75	56775
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 (%)	98.241
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.87
# indels per 100 kbp	8.93
Largest alignment	249259
NA50	105838
NA75	56775
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	2639
# indels	407
# short indels	406
# long indels	1
Indels length	680

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).









