Report

	final.contigs
# contigs (>= 0 bp)	2185
# contigs (>= 1000 bp)	1413
# contigs (>= 5000 bp)	681
# contigs (>= 10000 bp)	279
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9512188
Total length (>= 1000 bp)	9171609
Total length (>= 5000 bp)	7176112
Total length (>= 10000 bp)	4326038
Total length (>= 25000 bp)	536830
Total length (>= 50000 bp)	0
# contigs	1606
Largest contig	44678
Total length	9323107
Reference length	9283304
N50	9453
N75	5326
L50	314
L75	646
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3970
# local misassemblies	2
# unaligned contigs	1 + 1 part
Unaligned length	739
Genome fraction (%)	98.872
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.90
# indels per 100 kbp	0.07
Largest alignment	44678
NA50	9453
NA75	5326
LA50	314
LA75	646

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3970
# local misassemblies	2
# mismatches	1551
# indels	6
# short indels	6
# long indels	0
Indels length	6

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	1
Fully unaligned length	507
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	232
# 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).

Cumulative length

Cumulative length (aligned contigs)