Report

	final.contigs
# contigs (>= 0 bp)	1522
# contigs (>= 1000 bp)	972
# contigs (>= 5000 bp)	611
# contigs (>= 10000 bp)	341
# contigs (>= 25000 bp)	75
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	9898128
Total length (>= 1000 bp)	9689284
Total length (>= 5000 bp)	8654826
Total length (>= 10000 bp)	6702975
Total length (>= 25000 bp)	2578929
Total length (>= 50000 bp)	252781
# contigs	1043
Largest contig	78529
Total length	9741997
Reference length	9714864
N50	15372
N75	8556
L50	193
L75	407
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	12230
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.406
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.84
# indels per 100 kbp	0.01
Largest alignment	78529
NA50	15372
NA75	8556
LA50	193
LA75	407

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	12230
# local misassemblies	1
# mismatches	1337
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)