Report

	final.contigs
# contigs (>= 0 bp)	4395
# contigs (>= 1000 bp)	2723
# contigs (>= 5000 bp)	539
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10178553
Total length (>= 1000 bp)	9361070
Total length (>= 5000 bp)	3986906
Total length (>= 10000 bp)	769951
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3376
Largest contig	21956
Total length	9835064
Reference length	9714864
N50	4089
N75	2448
L50	746
L75	1518
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3170
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.335
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.11
# indels per 100 kbp	0.01
Largest alignment	21956
NA50	4089
NA75	2448
LA50	746
LA75	1518

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	3170
# local misassemblies	1
# mismatches	2972
# 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

relocations