Report

	final conting
# contigs (>= 1000 bp)	final.contigs 1574
# contigs (>= 1000 bp) # contigs (>= 5000 bp)	190
# contigs (>= 3000 bp) # contigs (>= 10000 bp)	190
# contigs (>= 25000 bp)	0
# contigs (>= 2000 bp) # contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4497384
Total length (>= 5000 bp)	1309968
Total length (>= 10000 bp)	168998
Total length (>= 25000 bp)	100990
Total length (>= 50000 bp)	0
# contigs	2086
Largest contig	16780
Total length	4869768
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	3197
NG50	3199
N75	1890
NG75	1901
L50	478
LG50	476
L75	968
LG75	963
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.747
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	47.26
# indels per 100 kbp	0.02
Largest alignment	16780
NA50	3197
NGA50	3199
NA75	1886
NGA75	1895
LA50	478
LGA50	476
LA75	969
LGA75	964

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
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# mismatches	2221
# 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).















