## Report

	final.contigs
# contigs (>= 1000 bp)	1896
# contigs (>= 5000 bp)	41
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3932559
Total length (>= 5000 bp)	240581
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3006
Largest contig	9054
Total length	4752551
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	1956
NG50	1919
N75	1209
NG75	1164
L50	795
LG50	822
L75	1562
LG75	1628
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.795
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.67
# indels per 100 kbp	0.00
Largest alignment	9054
NA50	1956
NGA50	1919
NA75	1209
NGA75	1164
LA50	795
LGA50	822
LA75	1562
LGA75	1628

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2673
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## 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).















