## Report

	final.contigs
# contigs (>= 1000 bp)	1947
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3540570
Total length (>= 5000 bp)	99232
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3627
Largest contig	6648
Total length	4757920
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	1524
NG50	1502
N75	985
NG75	954
L50	1008
LG50	1041
L75	1976
LG75	2053
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	59
Genome fraction (%)	93.021
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	82.26
# indels per 100 kbp	0.02
Largest alignment	6648
NA50	1524
NGA50	1502
NA75	985
NGA75	954
LA50	1008
LGA50	1041
LA75	1976
LGA75	2053

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	1359
# local misassemblies	0
# mismatches	3717
# indels	1
# short indels	1
# long indels	0
Indels length	5

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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	59
# 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).















