## Report

	final.contigs
# contigs (>= 1000 bp)	1947
# contigs (>= 5000 bp)	27
# contigs (>= 10000 bp)	0
# contigs (>= 10000 bp)  # contigs (>= 25000 bp)	0
# contigs (>= 25000 bp) # contigs (>= 50000 bp)	0
	3772411
Total length (>= 1000 bp)	158891
Total length (>= 5000 bp)	
Total length (>= 10000 bp)  Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	
Largest contig	3310
	8552
Total length	4767855
Reference length	4857432
GC (%)	52.24
Reference GC (%)	52.23
N50	1731
NG50	1697
N75	1091
NG75	1058
L50	893
LG50	919
L75	1759
LG75	1822
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.424
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.74
# indels per 100 kbp	0.00
Largest alignment	8552
NA50	1731
NGA50	1697
NA75	1091
NGA75	1058
LA50	893
LGA50	919
LA75	1759
LGA75	1822

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	630
# 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).















