## Report

	final.contigs
# contigs (>= 1000 bp)	1131
# contigs (>= 5000 bp)	335
# contigs (>= 10000 bp)	69
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4730647
Total length (>= 5000 bp)	2717092
Total length (>= 10000 bp)	905164
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1334
Largest contig	20845
Total length	4883186
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	5525
NG50	5529
N75	3101
NG75	3135
L50	283
LG50	281
L75	573
LG75	567
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	360
Genome fraction (%)	98.095
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.75
# indels per 100 kbp	0.04
Largest alignment	20845
NA50	5525
NGA50	5529
NA75	3101
NGA75	3135
LA50	283
LGA50	281
LA75	573
LGA75	567

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	1
# mismatches	1513
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	360
# 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).















