Report

	final.contigs
# contigs (>= 1000 bp)	1502
# contigs (>= 5000 bp) # contigs (>= 5000 bp)	176
# contigs (>= 10000 bp) # contigs (>= 10000 bp)	170
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4281844
Total length (>= 5000 bp)	1217547
Total length (>= 10000 bp)	231167
Total length (>= 25000 bp)	231107
Total length (>= 50000 bp)	0
# contigs	1979
Largest contig	14635
Total length	4636011
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	3166
NG50	
N75	3161 1899
NG75	
	1894
L50	457
LG50	458
L75	932
LG75	934
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	58
Genome fraction (%)	96.243
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	53.03
# indels per 100 kbp	0.25
Largest alignment	14635
NA50	3166
NGA50	3161
NA75	1899
NGA75	1894
LA50	457
LGA50	458
LA75	932
LGA75	934

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	2369
# indels	11
# short indels	11
# long indels	0
Indels length	11

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	58
# 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).















