Report

	final.contigs
# contigs (>= 0 bp)	8495
# contigs (>= 1000 bp)	4117
Total length (>= 0 bp)	11256110
Total length (>= 1000 bp)	8821425
# contigs	6518
Largest contig	9231
Total length	10574542
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	2018
NG50	1946
N75	1243
NG75	1136
L50	1659
LG50	1790
L75	3320
LG75	3649
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.510
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.43
# indels per 100 kbp	0.16
Largest alignment	9231
NA50	2018
NGA50	1946
NA75	1243
NGA75	1136
LA50	1659
LGA50	1790
LA75	3320
LGA75	3649

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).
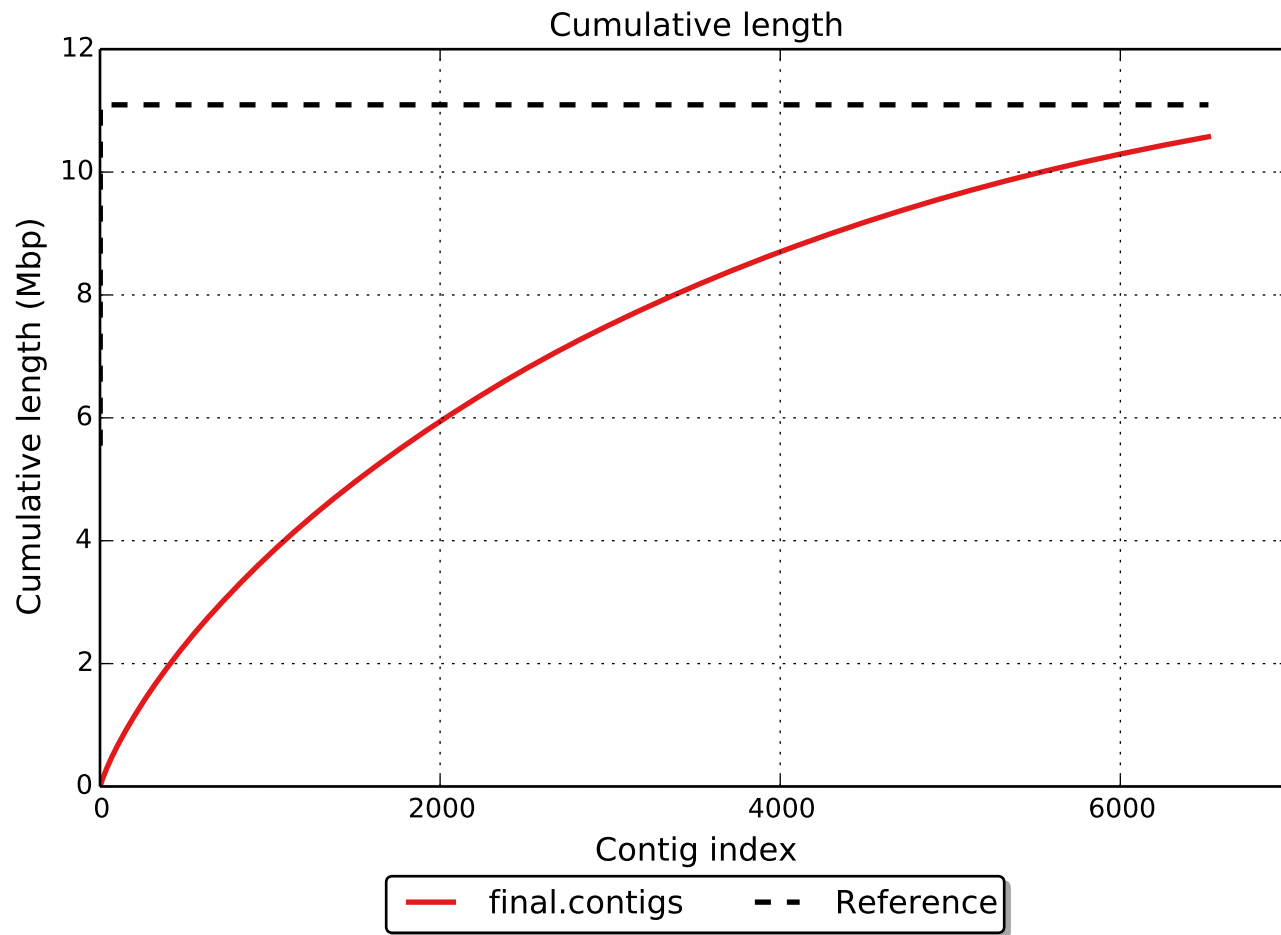
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# mismatches	5381
# indels	16
# short indels	14
# long indels	2
Indels length	27

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).

Cumulative length

Cumulative length (Mbp) vs Contig index

Legend: final.contigs, Reference

GC content

windows

GC (%)

final.contigs — — Reference

Misassemblies

Cumulative length (aligned contigs)