Report

	final.contigs
# contigs (>= 0 bp)	2106
# contigs (>= 1000 bp)	1685
Total length (>= 0 bp)	5567268
Total length (>= 1000 bp)	5256978
# contigs	2106
Largest contig	19900
Total length	5567268
Reference length	5478683
GC (%)	50.48
Reference GC (%)	50.49
N50	3628
NG50	3677
N75	2141
NG75	2211
L50	478
LG50	466
L75	969
LG75	939
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9427
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	116
Genome fraction (%)	98.263
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	38.32
# indels per 100 kbp	0.00
Largest alignment	19900
NA50	3625
NGA50	3677
NA75	2139
NGA75	2208
LA50	479
LGA50	466
LA75	970
LGA75	940

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).
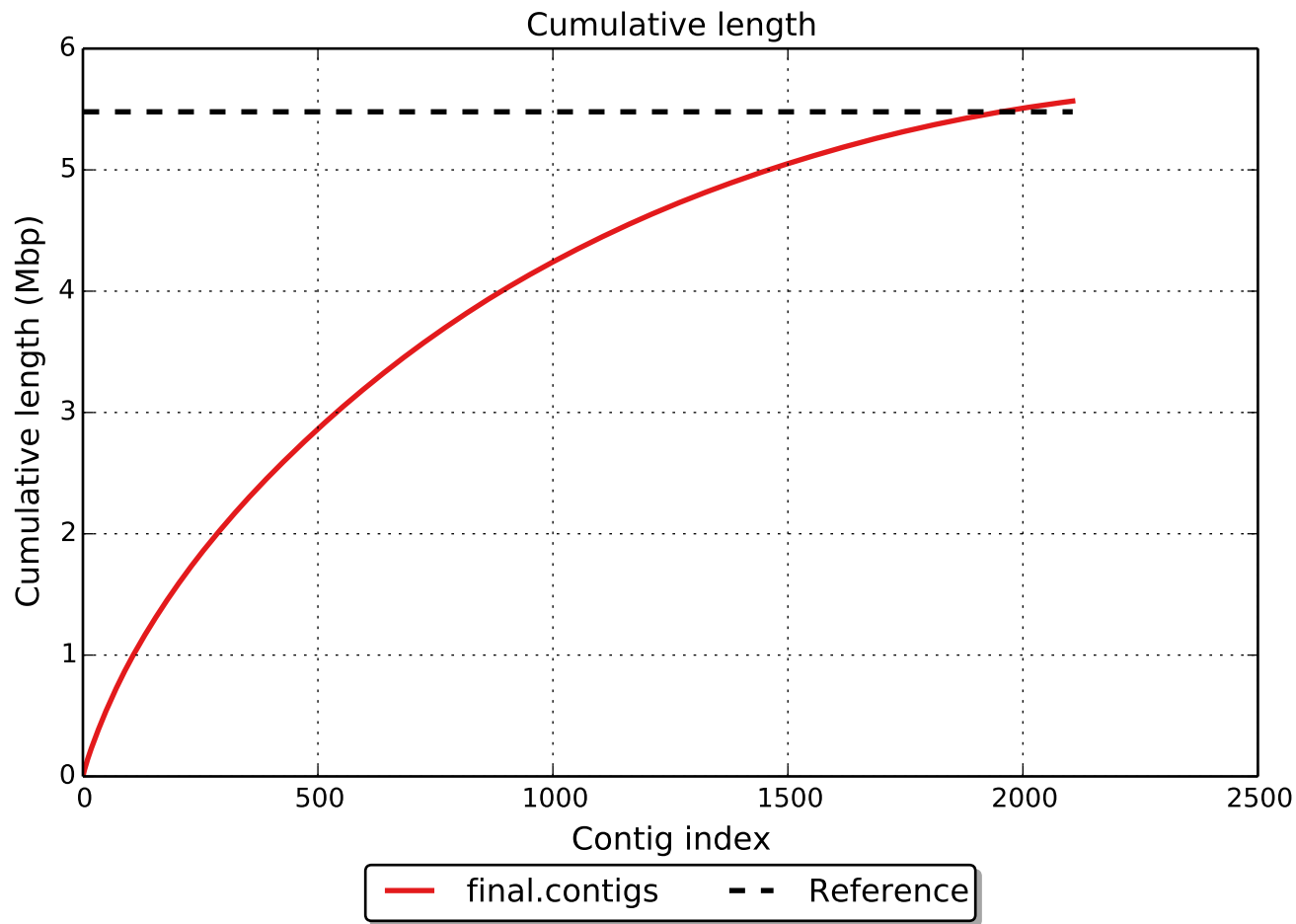
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9427
# local misassemblies	0
# mismatches	2063
# 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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	116
# 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

GC content

windows vs GC (%)

final.contigs — Reference

Nx

Contig length (kbp)

x

final.contigs

Misassemblies

relocations

Cumulative length (aligned contigs)