Report

	final.contigs
# contigs (>= 0 bp)	1754
# contigs (>= 1000 bp)	1401
Total length (>= 0 bp)	5269424
Total length (>= 1000 bp)	5014301
# contigs	1754
Largest contig	20525
Total length	5269424
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	4412
NG50	4221
N75	2512
NG75	2294
L50	369
LG50	393
L75	756
LG75	821
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	26942
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	9710
Genome fraction (%)	93.541
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.91
# indels per 100 kbp	0.14
Largest alignment	20525
NA50	4397
NGA50	4205
NA75	2502
NGA75	2284
LA50	372
LGA50	397
LA75	763
LGA75	828

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).
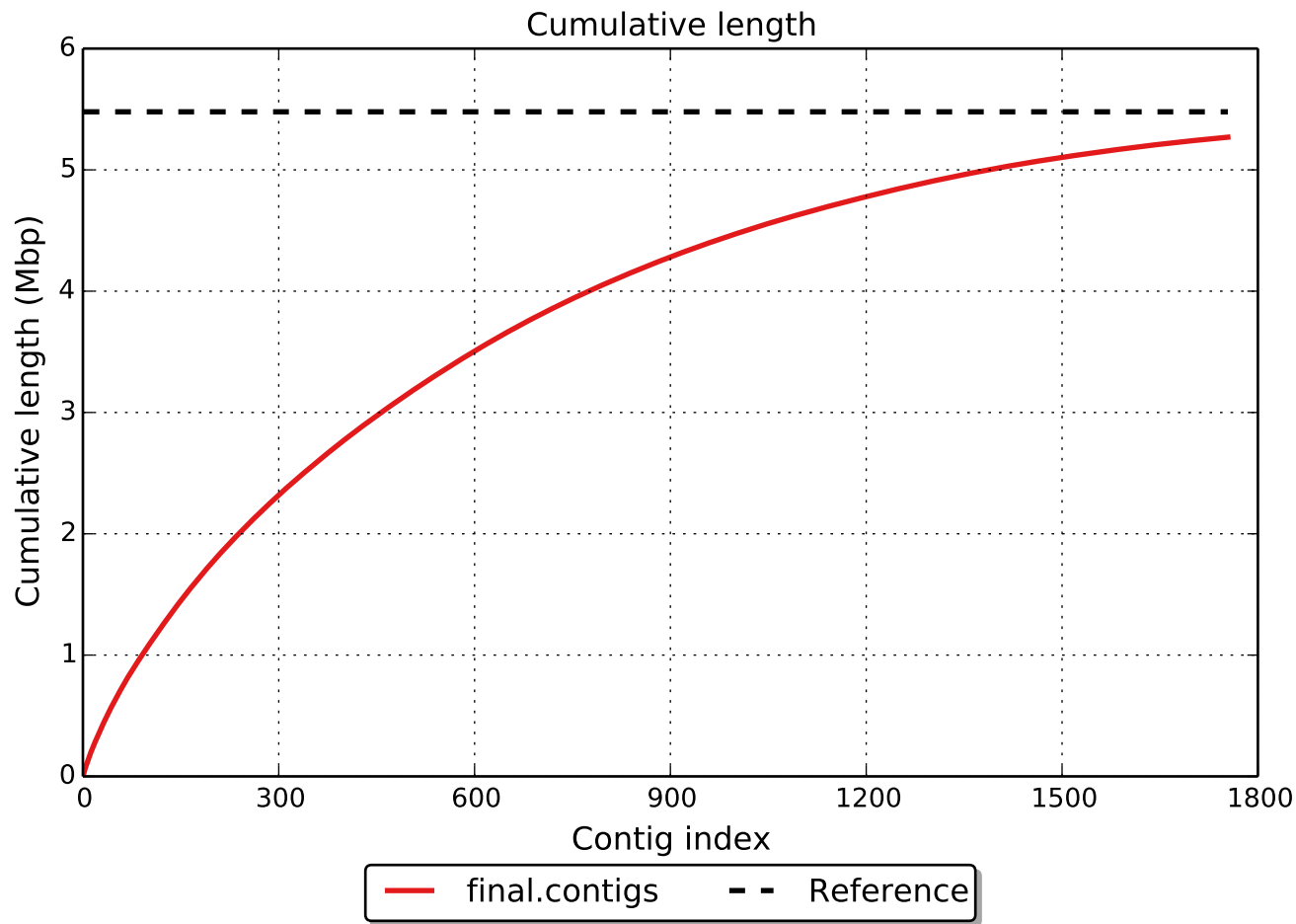
Misassemblies report

	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	4
Misassembled contigs length	26942
# local misassemblies	1
# mismatches	1533
# indels	7
# short indels	6
# long indels	1
Indels length	14

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	2
Partially unaligned length	9710
# 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

GC (%)

final.contigs   - - - Reference

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)