Report

	final.contigs
# contigs (>= 0 bp)	2139
# contigs (>= 1000 bp)	1578
Total length (>= 0 bp)	5205037
Total length (>= 1000 bp)	4794559
# contigs	2139
Largest contig	16656
Total length	5205037
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	3485
NG50	3294
N75	1969
NG75	1690
L50	468
LG50	519
L75	957
LG75	1097
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.880
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	51.30
# indels per 100 kbp	0.30
Largest alignment	16656
NA50	3485
NGA50	3294
NA75	1967
NGA75	1689
LA50	468
LGA50	519
LA75	957
LGA75	1098

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).
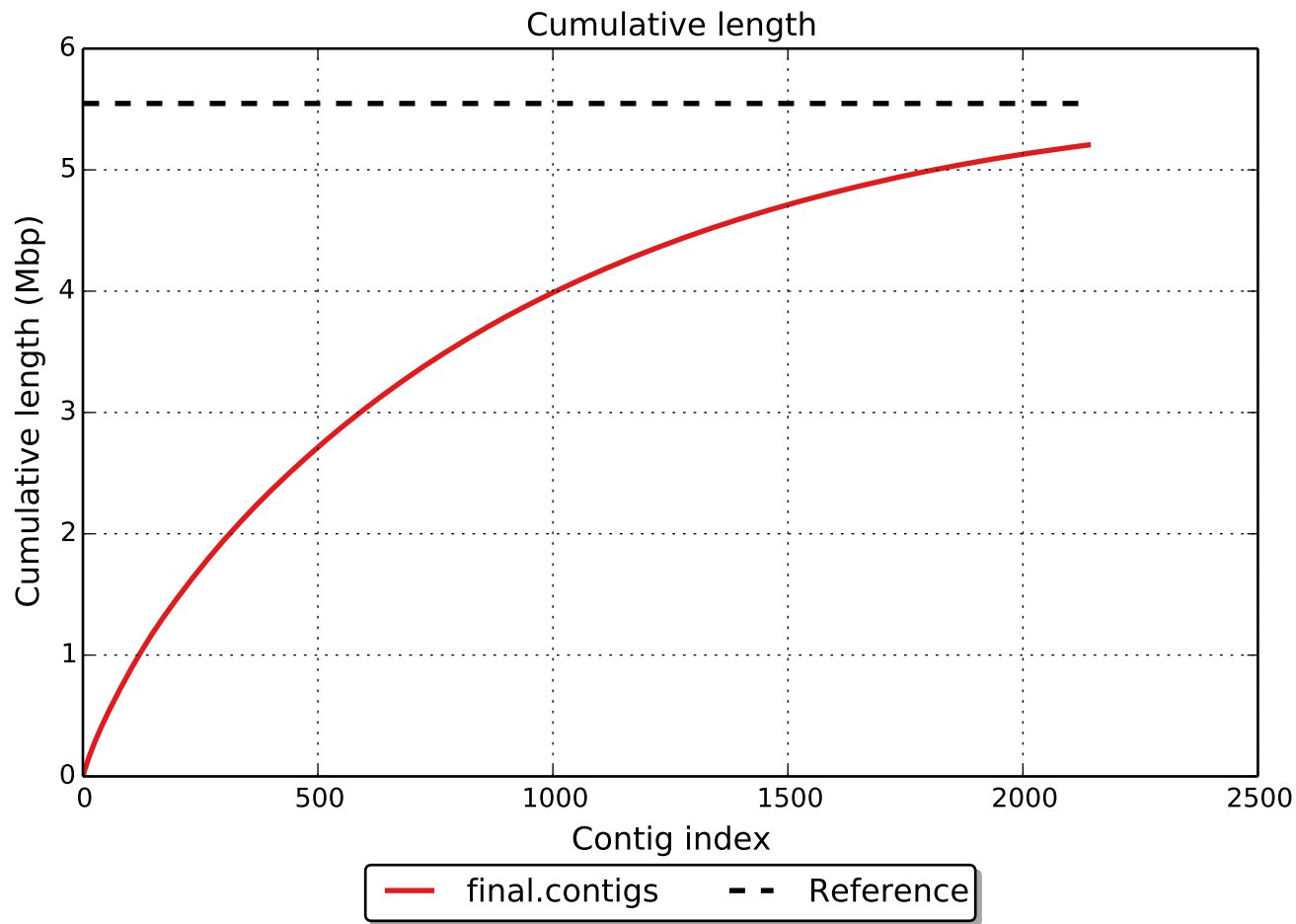
Misassemblies report

	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# mismatches	2586
# indels	15
# short indels	12
# long indels	3
Indels length	57

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

Nx

Misassemblies

4.0

3.5

3.0

2.5

2.0

1.5

1.0

0.5

0.0

final.contigs

relocations

Cumulative length (aligned contigs)

NAx