Report

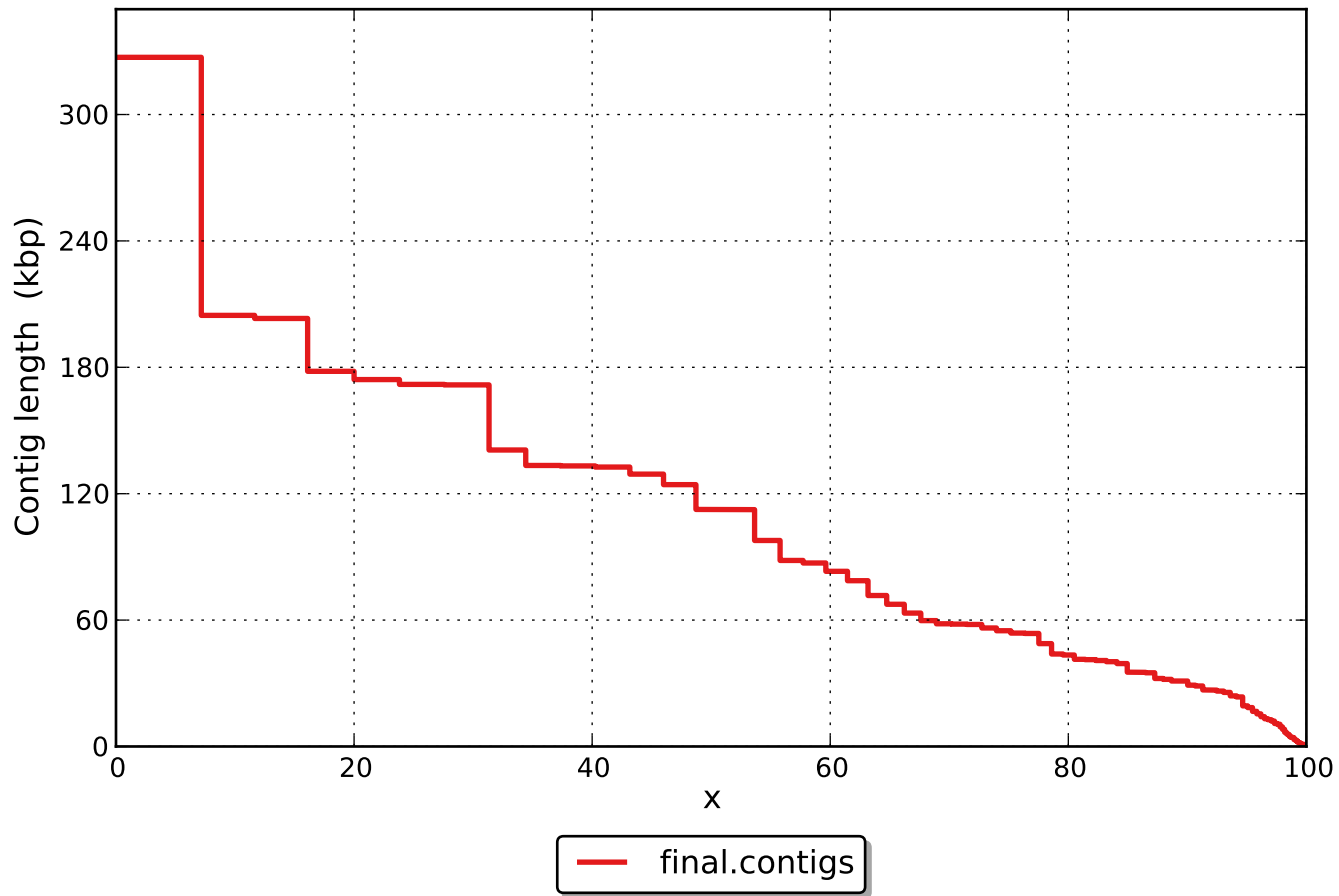|	final.contigs
# contigs (>= 0 bp)	131
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4572717
Total length (>= 1000 bp)	4556211
Total length (>= 5000 bp)	4500478
Total length (>= 10000 bp)	4464670
Total length (>= 25000 bp)	4273726
Total length (>= 50000 bp)	3539504
# contigs	109
Largest contig	327149
Total length	4565727
Reference length	4641652
N50	112525
N75	54942
L50	14
L75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.314
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.36
# indels per 100 kbp	9.97
Largest alignment	327149
NA50	112525
NA75	54942
LA50	14
LA75	29

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# mismatches	2663
# indels	455
# short indels	455
# long indels	0
Indels length	623

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).
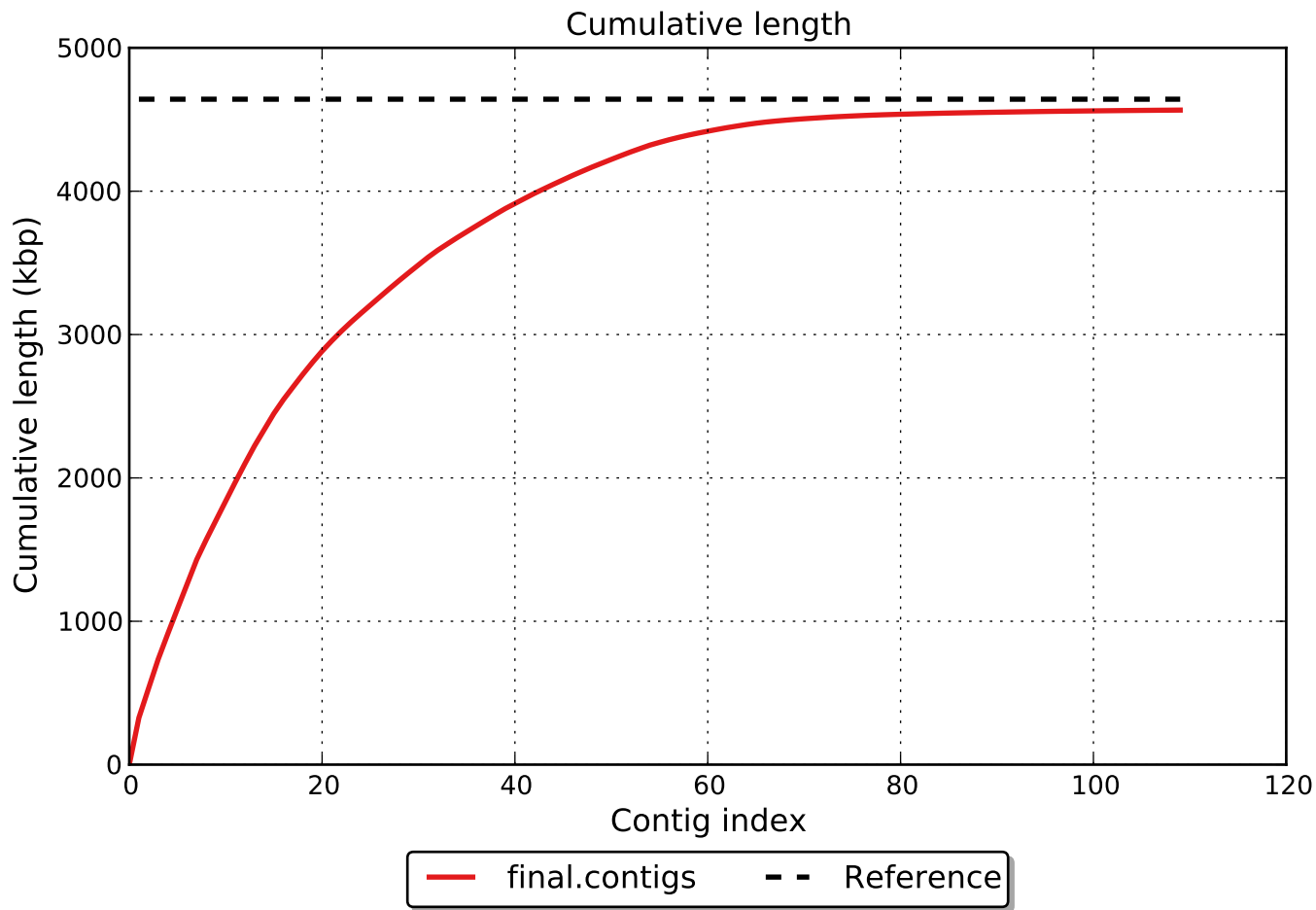
Unaligned report

	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	53
# N's	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
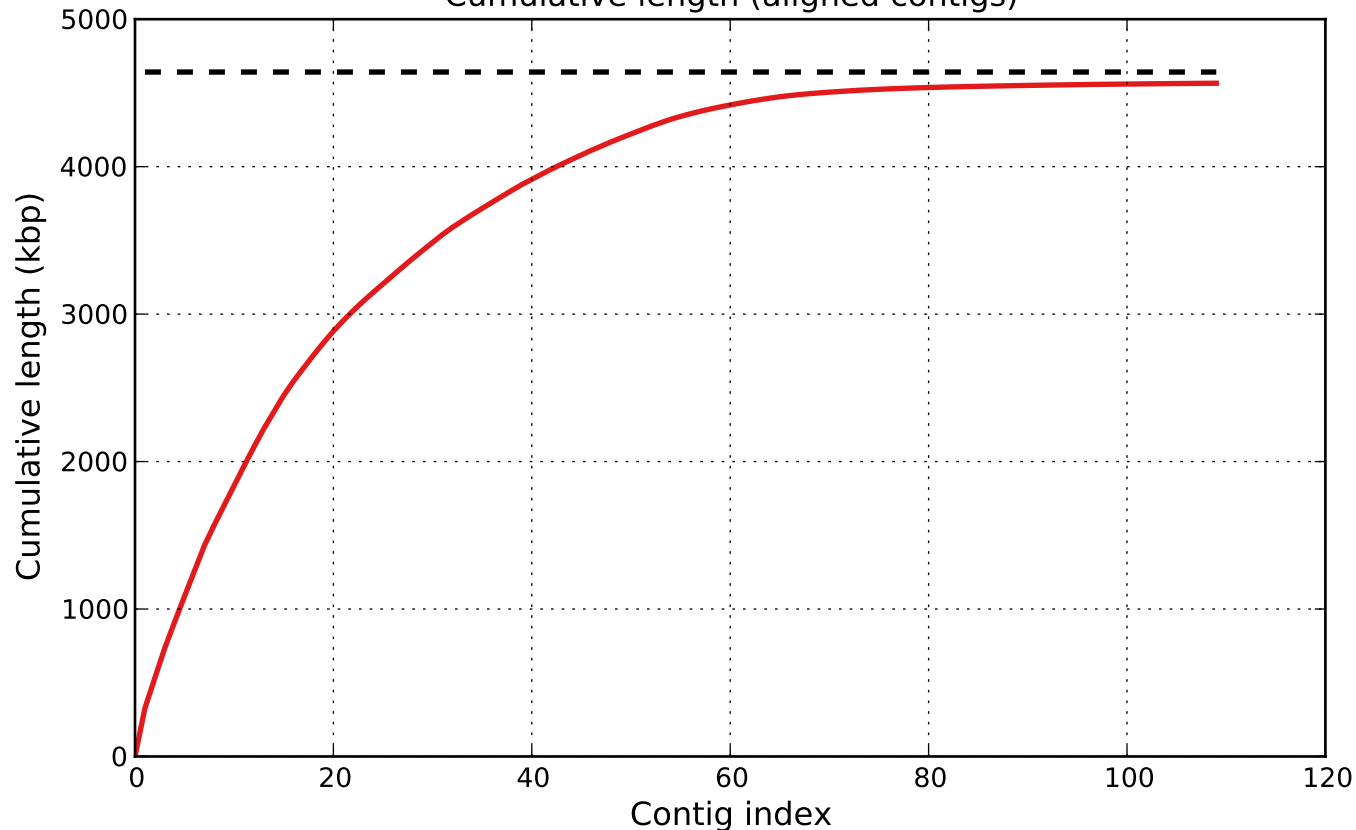(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)