Report

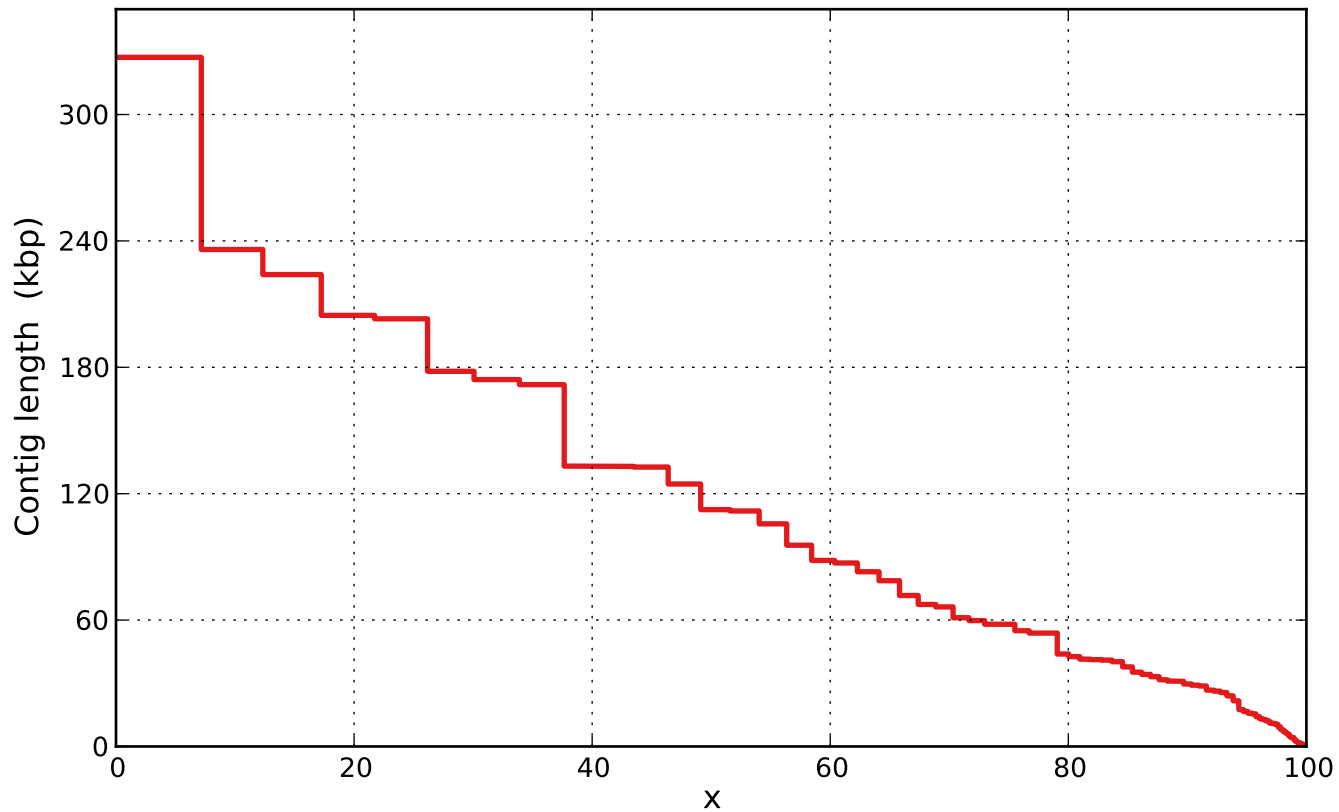|	final.contigs
# contigs (>= 0 bp)	131
# contigs (>= 1000 bp)	93
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4571833
Total length (>= 1000 bp)	4553503
Total length (>= 5000 bp)	4499364
Total length (>= 10000 bp)	4455804
Total length (>= 25000 bp)	4260057
Total length (>= 50000 bp)	3609437
# contigs	109
Largest contig	327151
Total length	4564765
Reference length	4641652
N50	112430
N75	58008
L50	13
L75	27
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	14
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.276
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.78
# indels per 100 kbp	0.15
Largest alignment	327151
NA50	112430
NA75	58008
LA50	13
LA75	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).

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	14
# mismatches	127
# indels	7
# short indels	6
# long indels	1
Indels length	92

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).
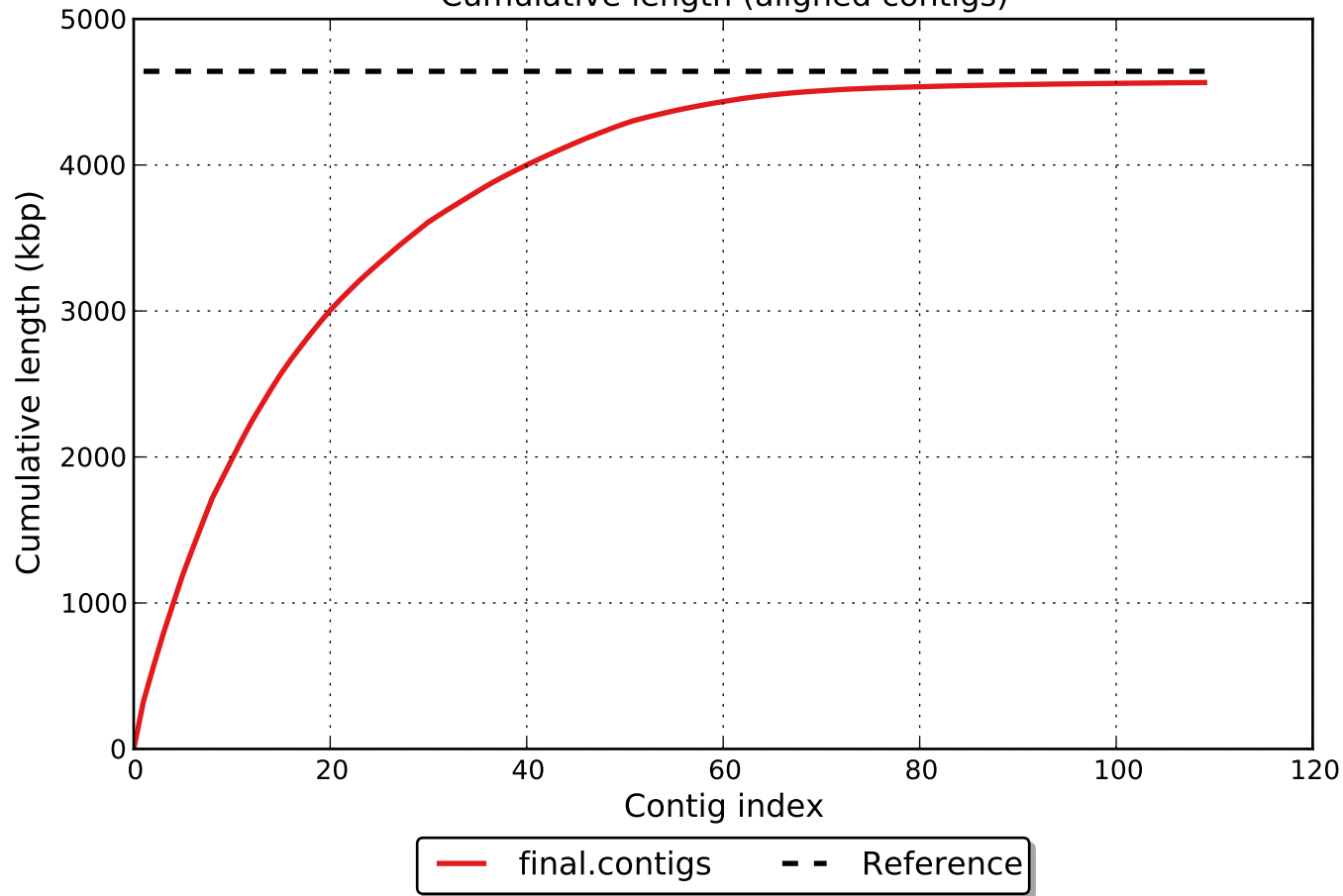
Cumulative length

Misassemblies

final.contigs
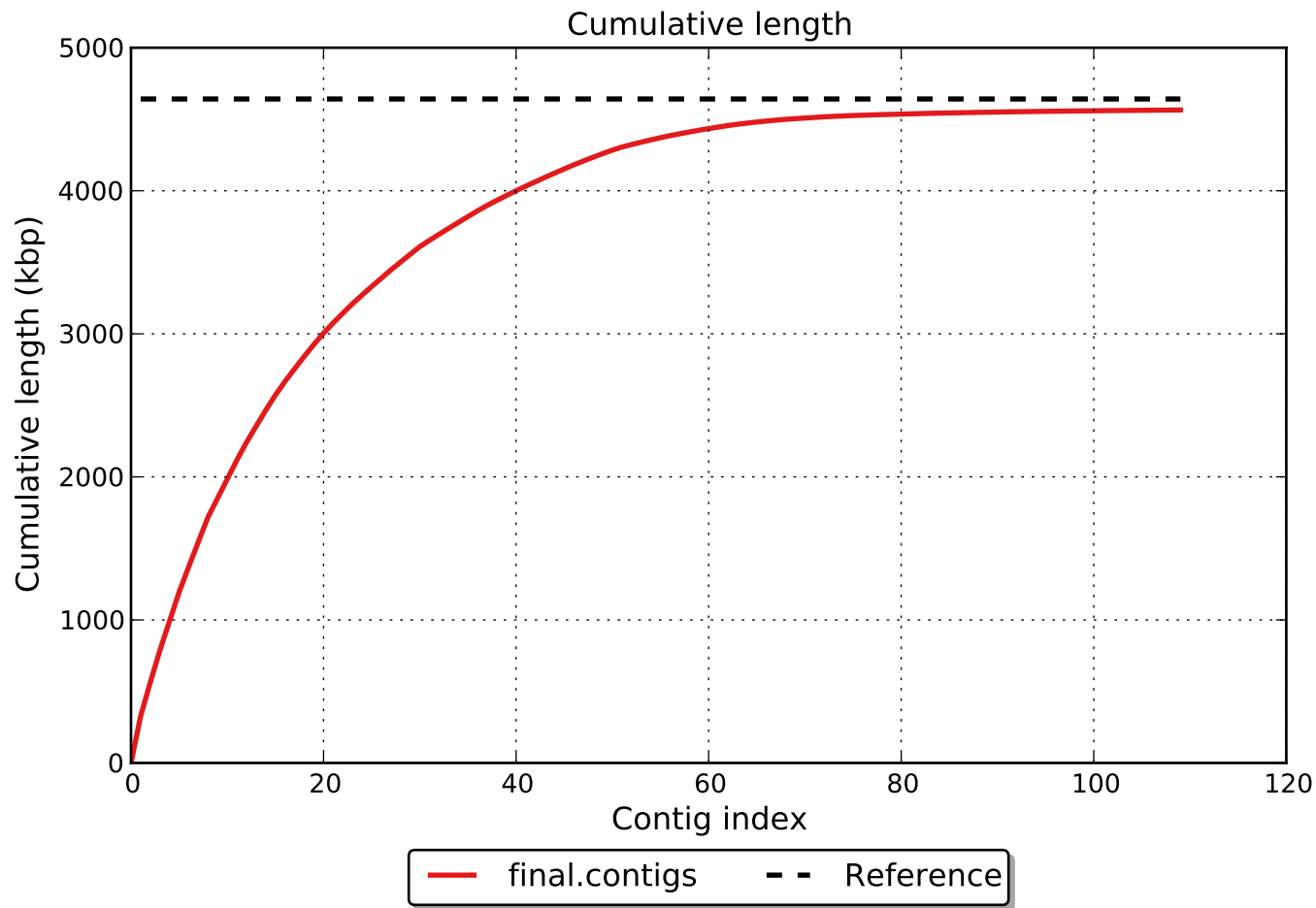
Cumulative length (aligned contigs)