Report

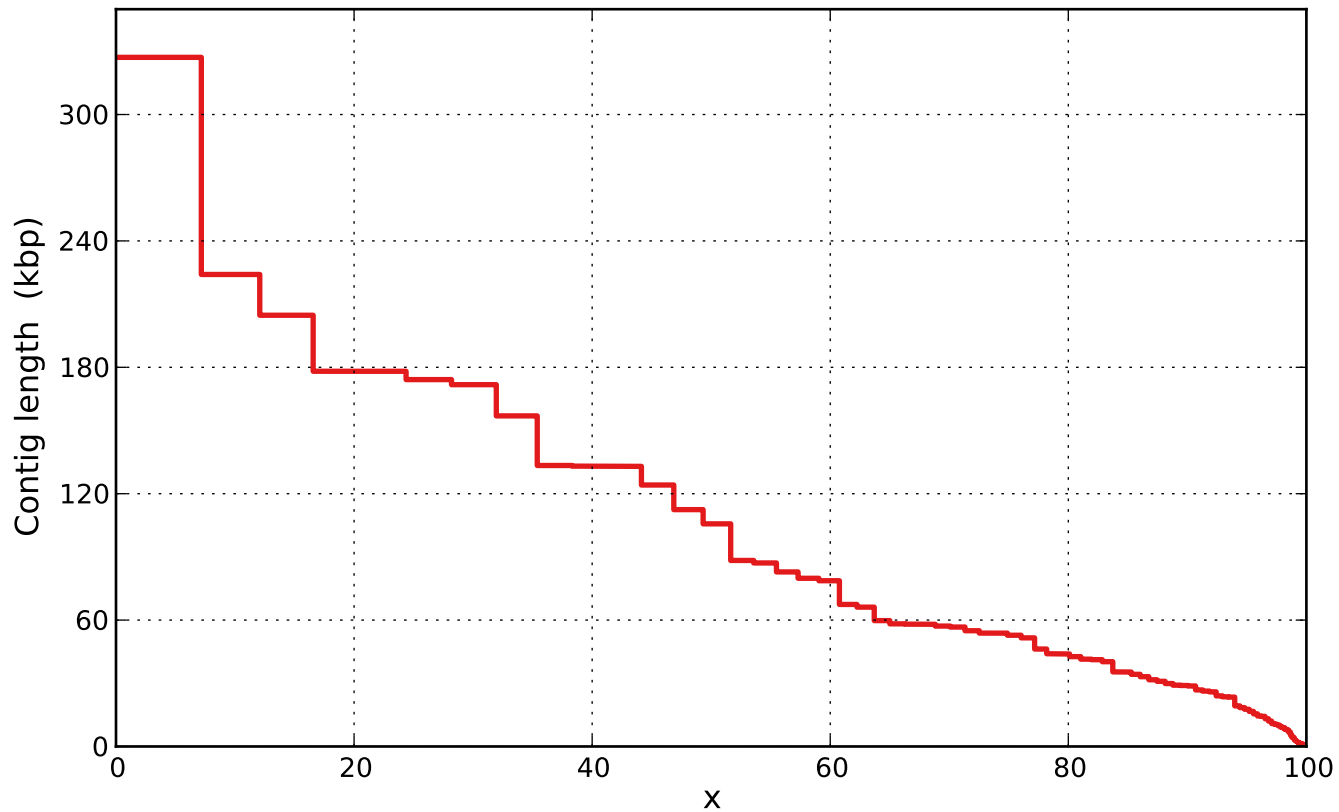|	final.contigs
# contigs (>= 0 bp)	146
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4575088
Total length (>= 1000 bp)	4553175
Total length (>= 5000 bp)	4508428
Total length (>= 10000 bp)	4462114
Total length (>= 25000 bp)	4218044
Total length (>= 50000 bp)	3521899
# contigs	111
Largest contig	327137
Total length	4563905
Reference length	4641652
N50	105688
N75	52804
L50	14
L75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 3 part
Unaligned length	153
Genome fraction (%)	98.270
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.84
# indels per 100 kbp	9.27
Largest alignment	327137
NA50	105688
NA75	52804
LA50	14
LA75	31

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	12
# mismatches	2684
# indels	423
# short indels	422
# long indels	1
Indels length	660

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	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	153
# 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).
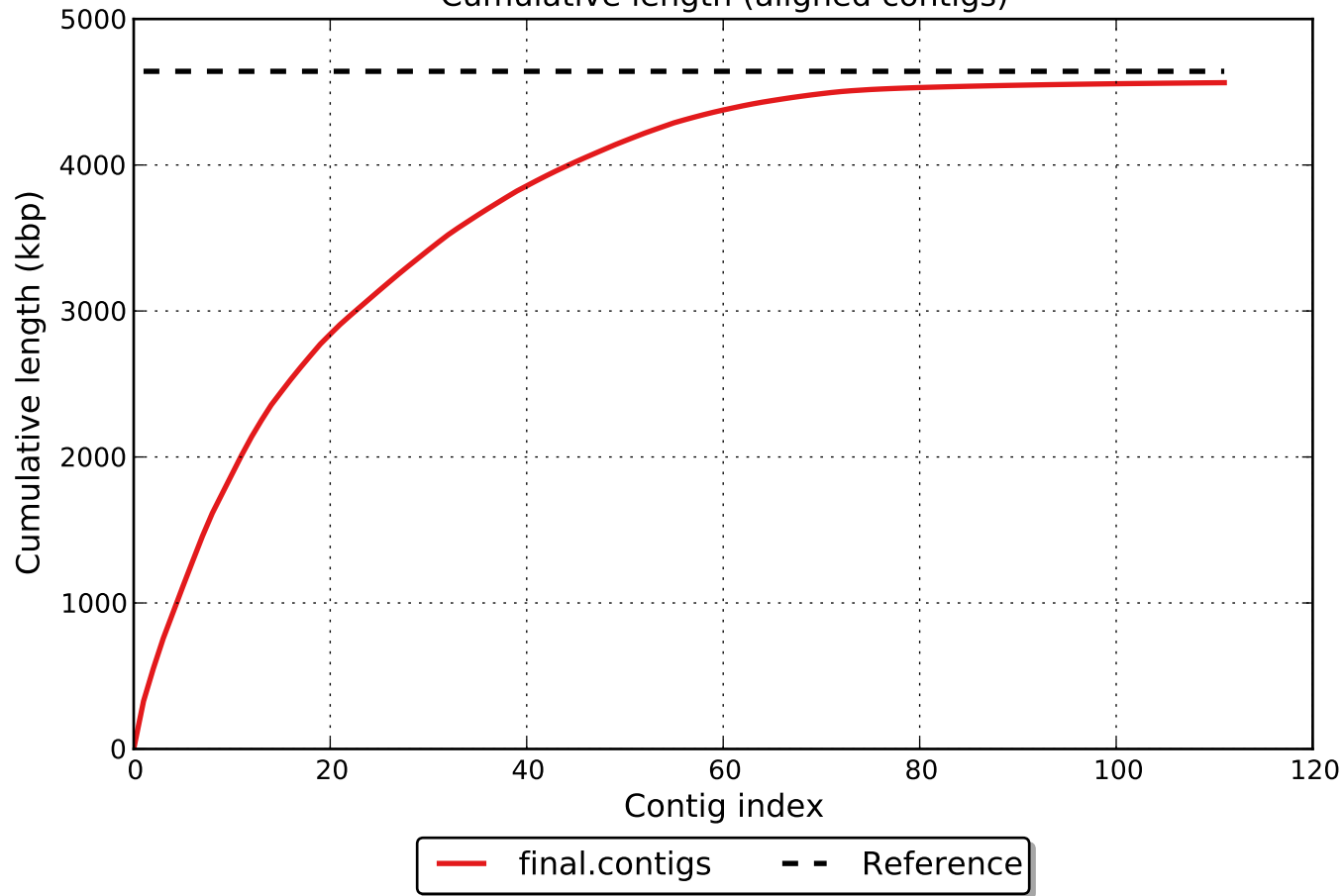
Cumulative length

Misassemblies

final.contigs
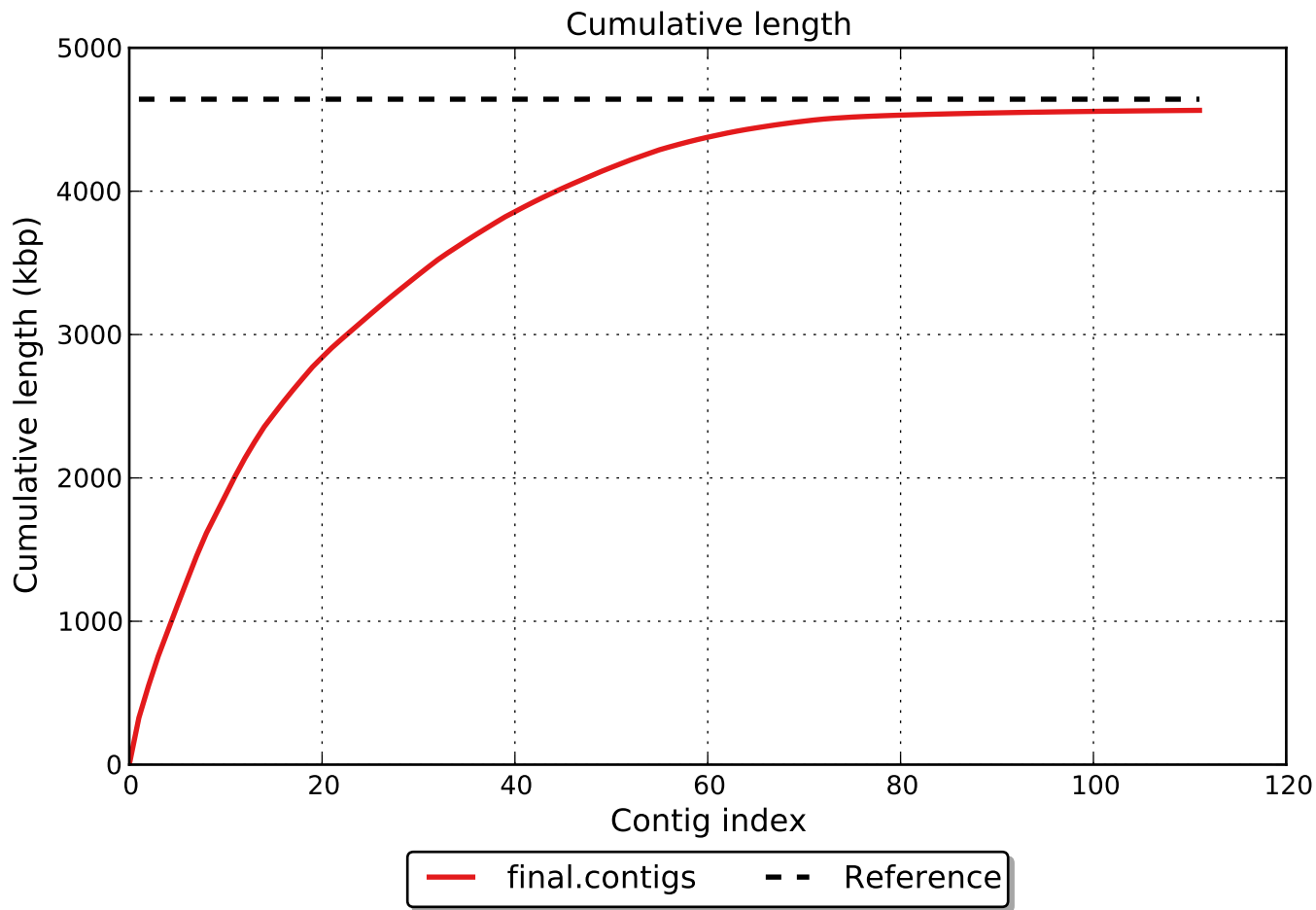
Cumulative length (aligned contigs)