Report

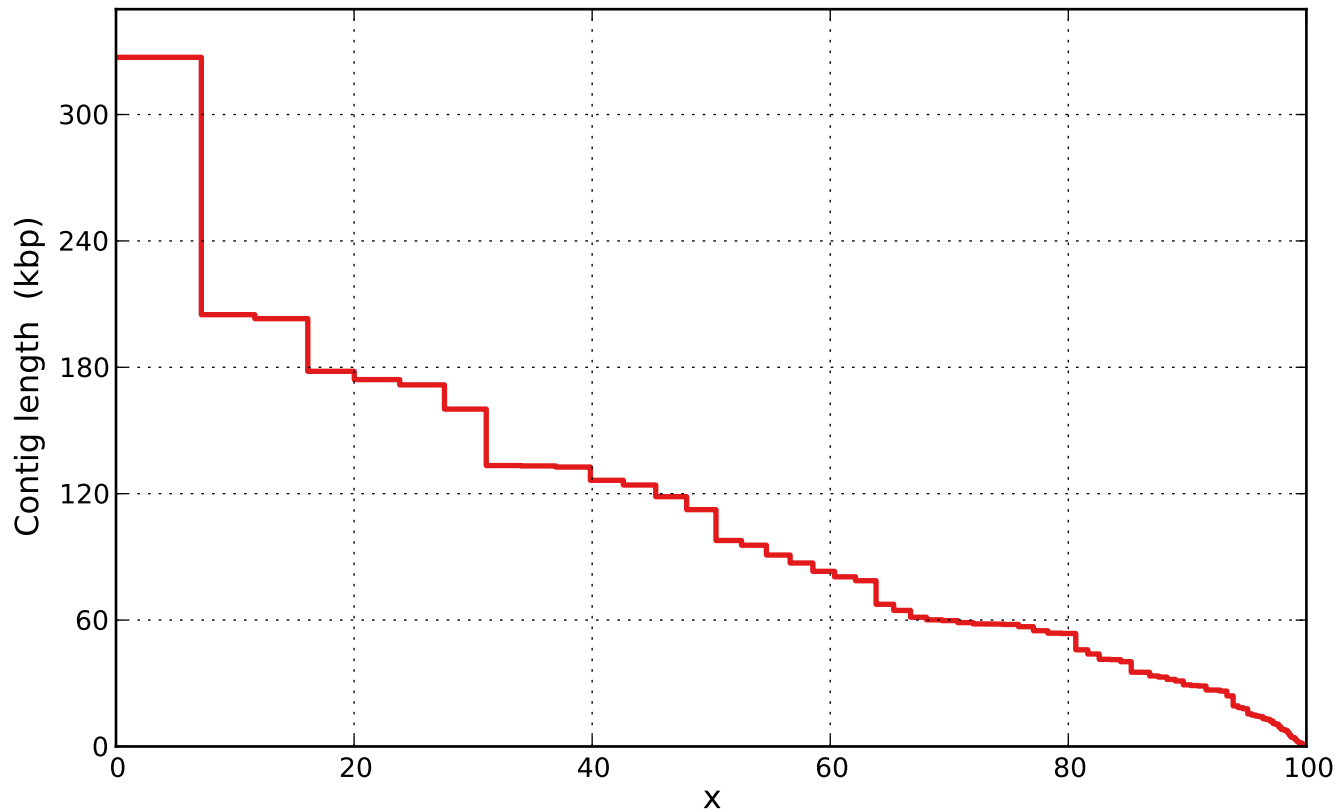|	final.contigs
# contigs (>= 0 bp)	127
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4569703
Total length (>= 1000 bp)	4555837
Total length (>= 5000 bp)	4502124
Total length (>= 10000 bp)	4456744
Total length (>= 25000 bp)	4258489
Total length (>= 50000 bp)	3679265
# contigs	107
Largest contig	327154
Total length	4563292
Reference length	4641652
N50	112427
N75	57924
L50	14
L75	30
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45889
# local misassemblies	11
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.251
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.86
# indels per 100 kbp	9.89
Largest alignment	327154
NA50	112427
NA75	57924
LA50	14
LA75	30

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45889
# local misassemblies	11
# mismatches	2730
# indels	451
# short indels	450
# long indels	1
Indels length	712

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
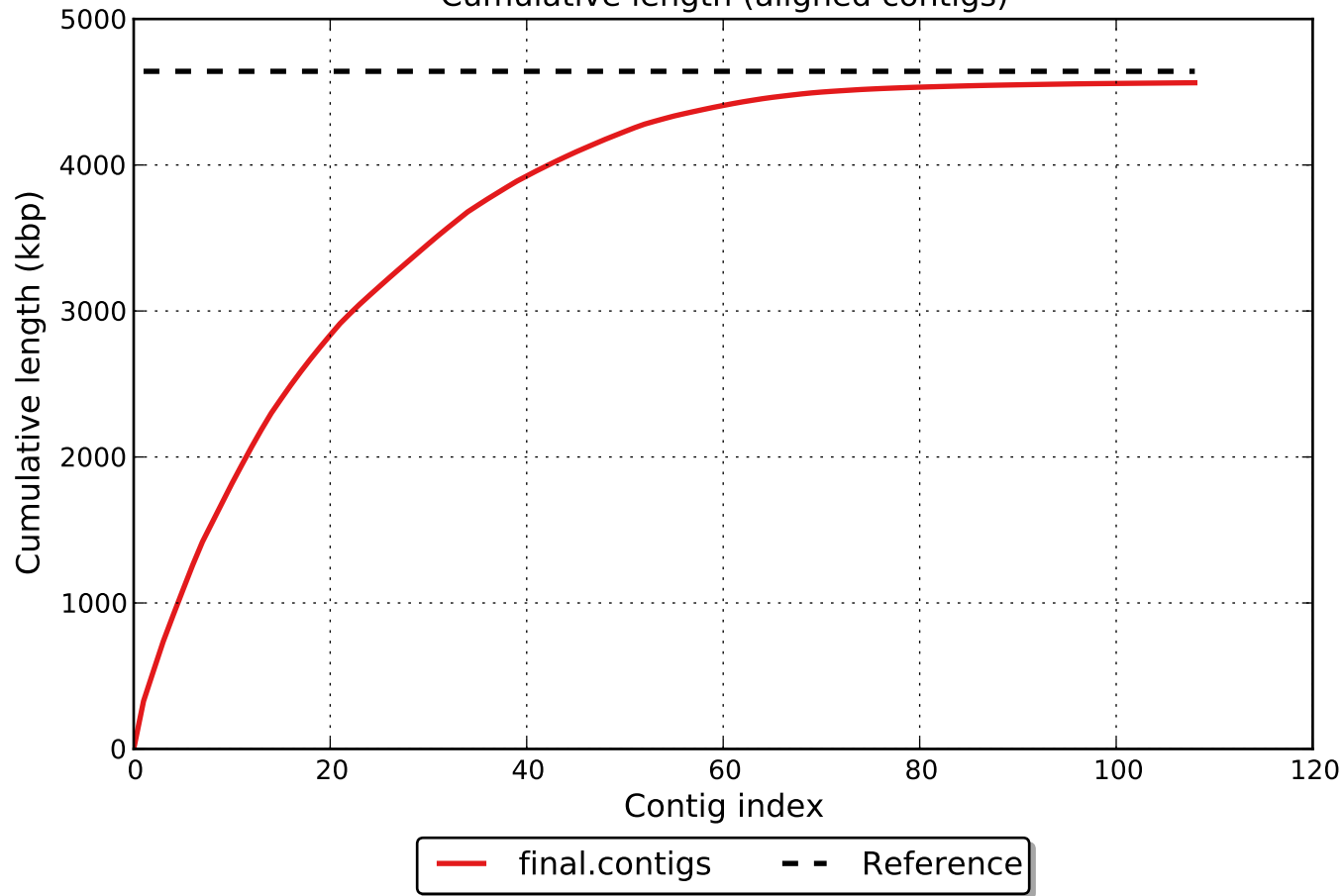(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

Misassemblies
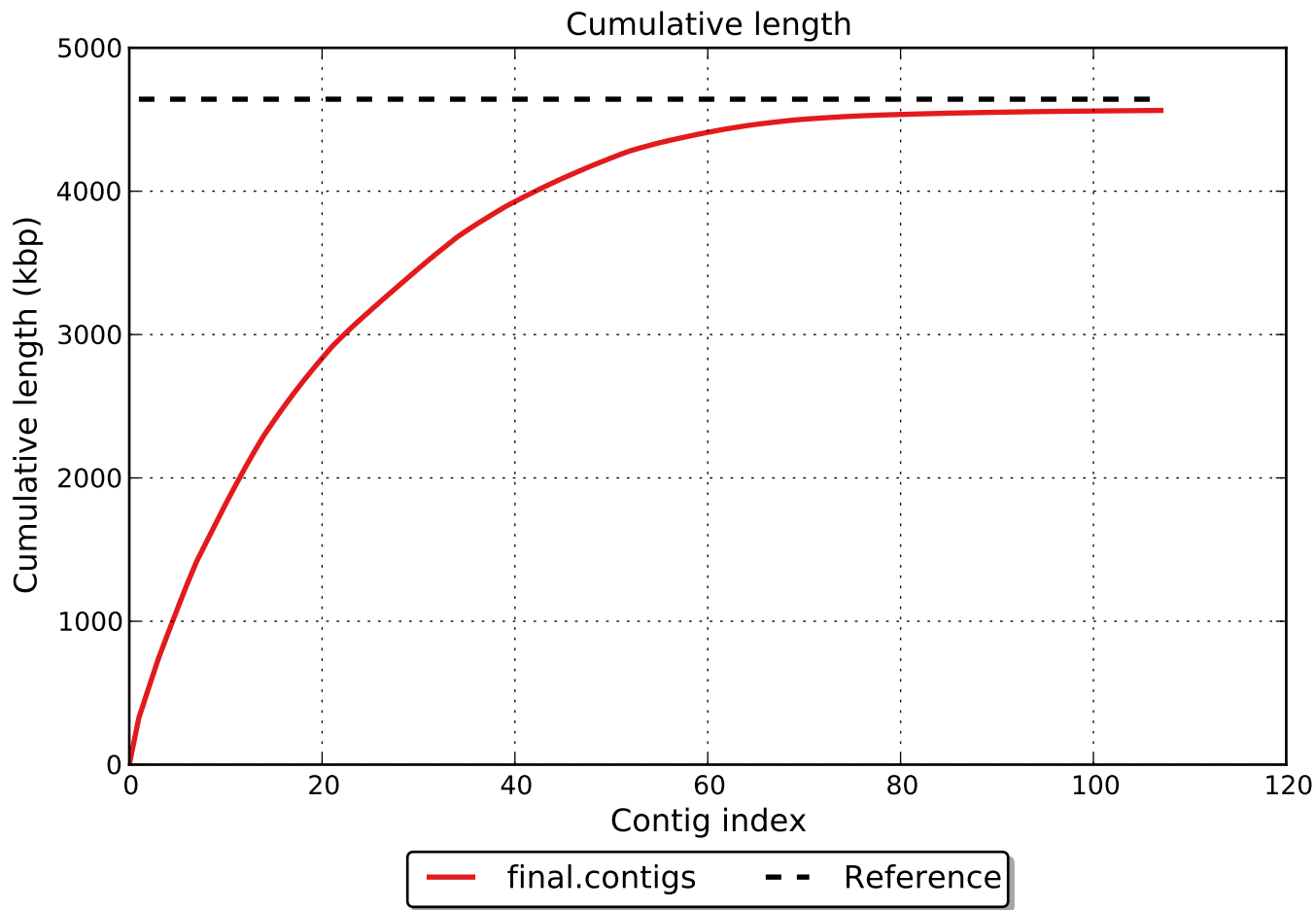
Cumulative length (aligned contigs)