Report

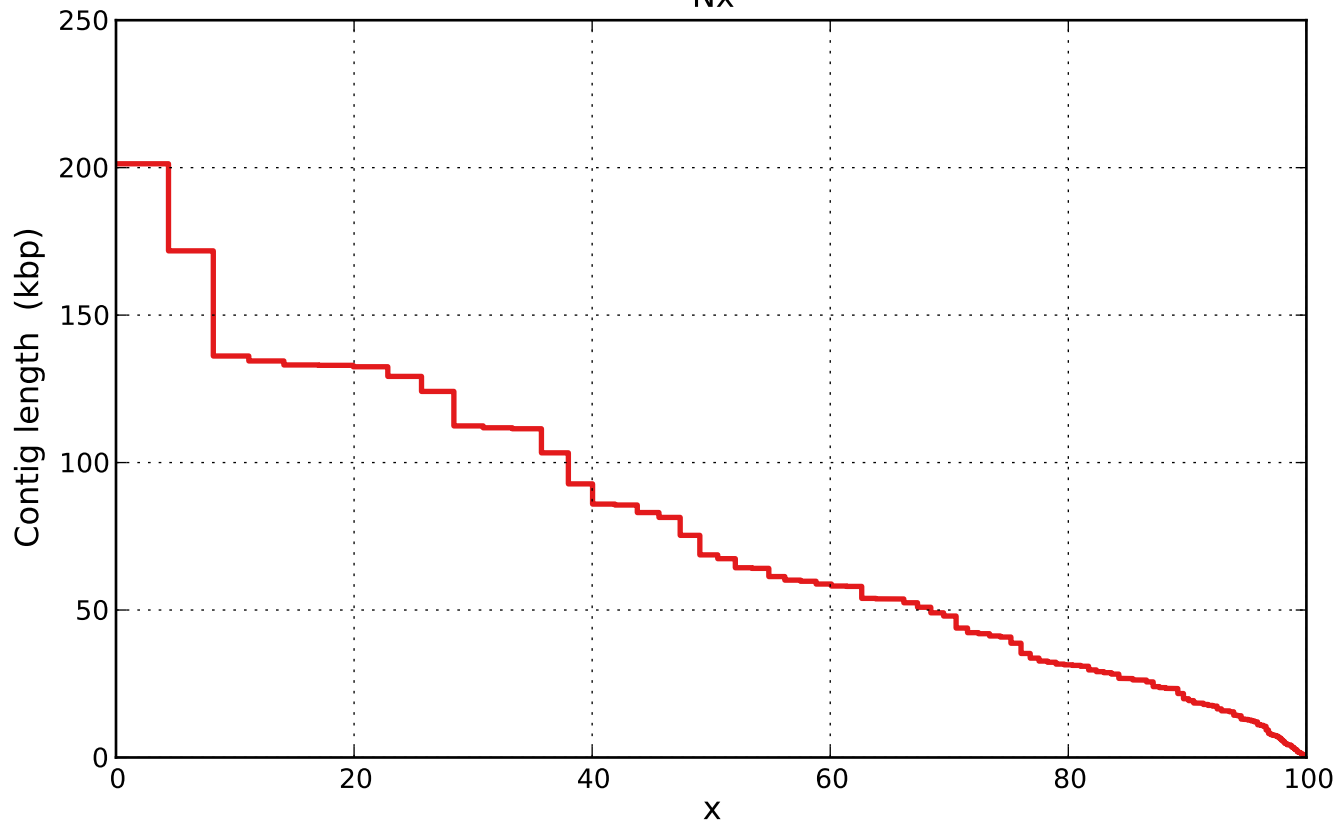|	final.contigs
# contigs (>= 0 bp)	178
# contigs (>= 1000 bp)	125
# contigs (>= 5000 bp)	95
# contigs (>= 10000 bp)	85
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4576101
Total length (>= 1000 bp)	4553641
Total length (>= 5000 bp)	4481300
Total length (>= 10000 bp)	4409854
Total length (>= 25000 bp)	3976911
Total length (>= 50000 bp)	3124256
# contigs	141
Largest contig	201313
Total length	4564449
Reference length	4641652
N50	68696
N75	40833
L50	20
L75	41
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.262
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.99
# indels per 100 kbp	10.09
Largest alignment	201313
NA50	68696
NA75	40833
LA50	20
LA75	41

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	8
# mismatches	2645
# indels	460
# short indels	454
# long indels	6
Indels length	793

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).
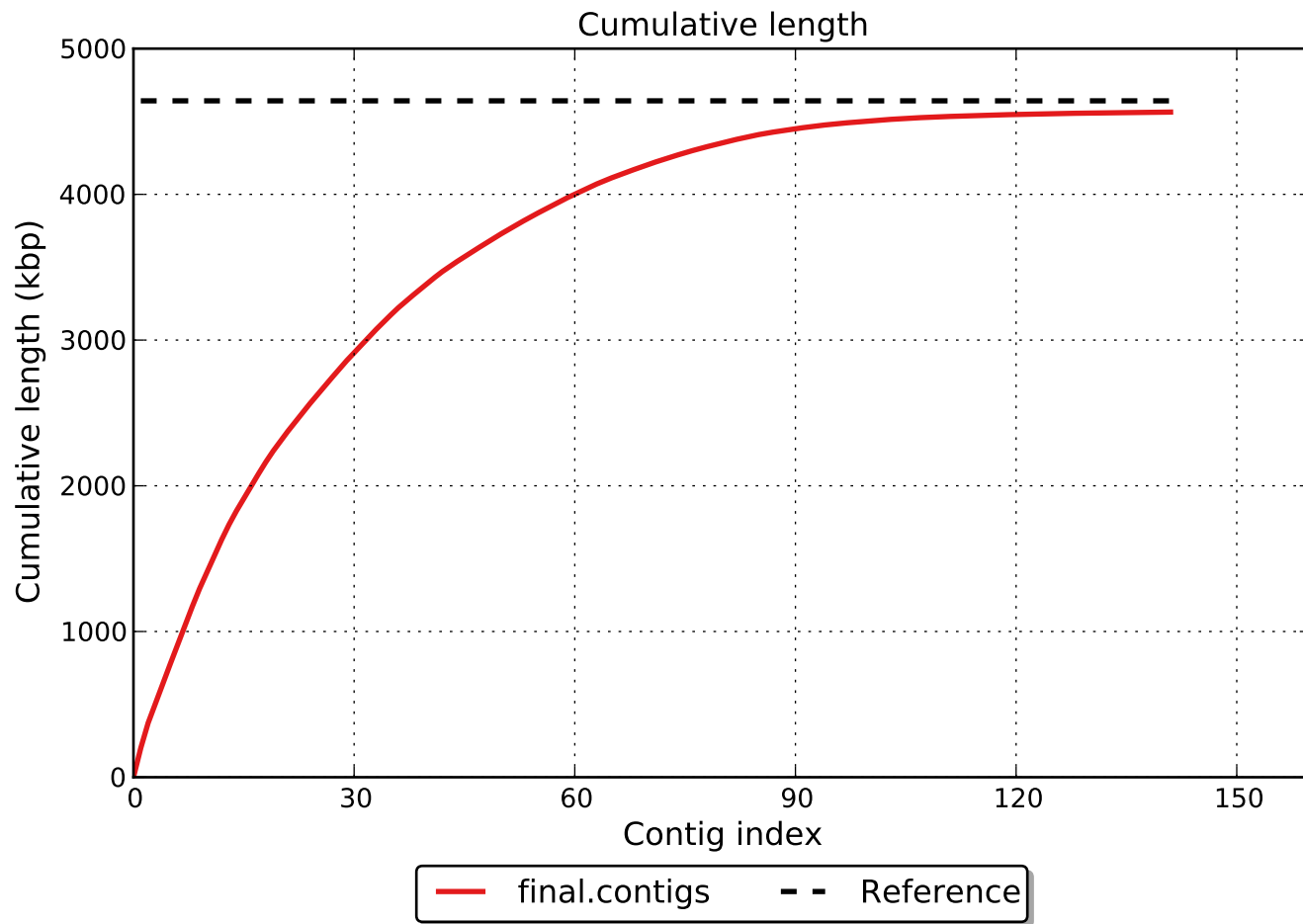
Unaligned report

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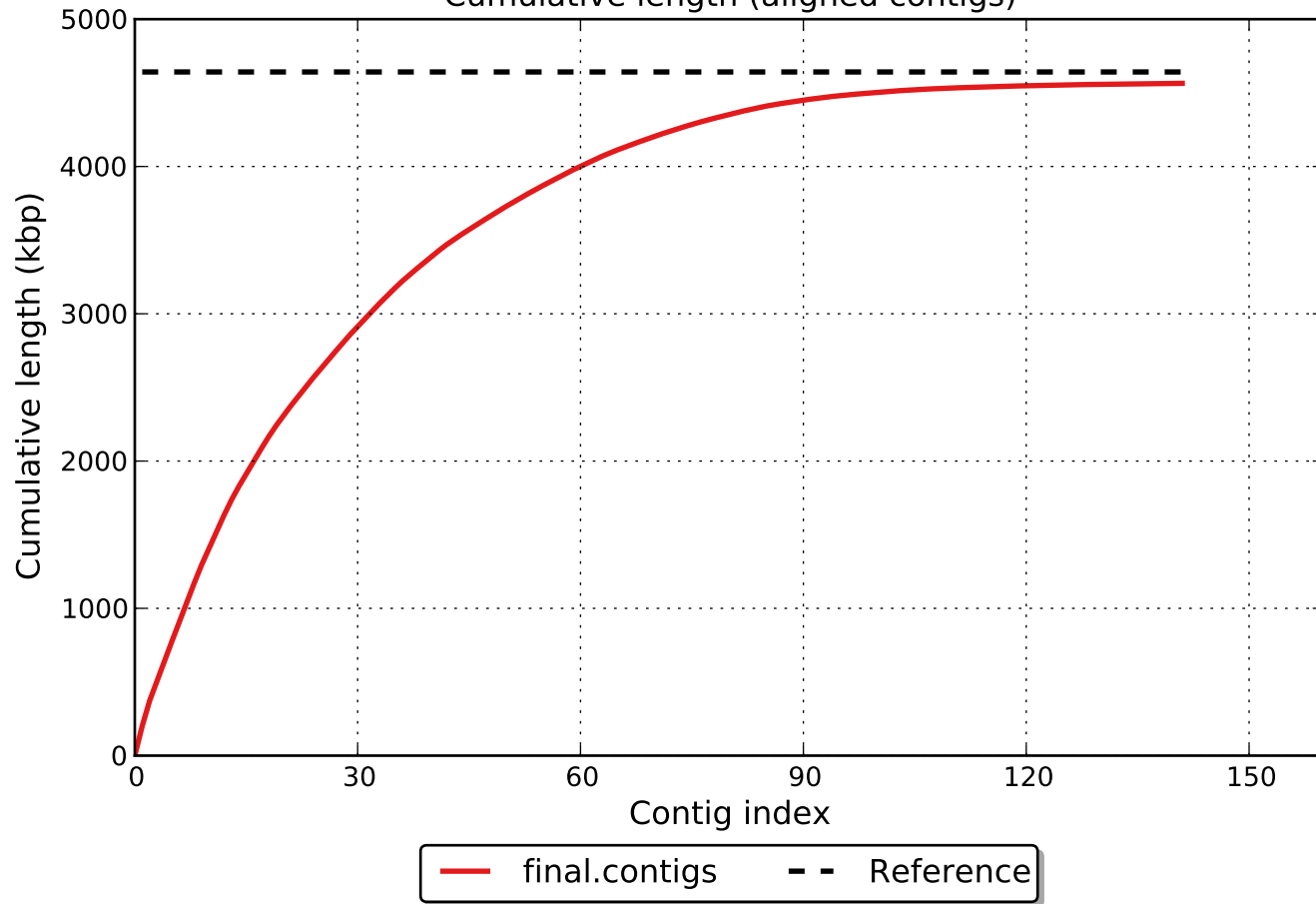(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)