Report

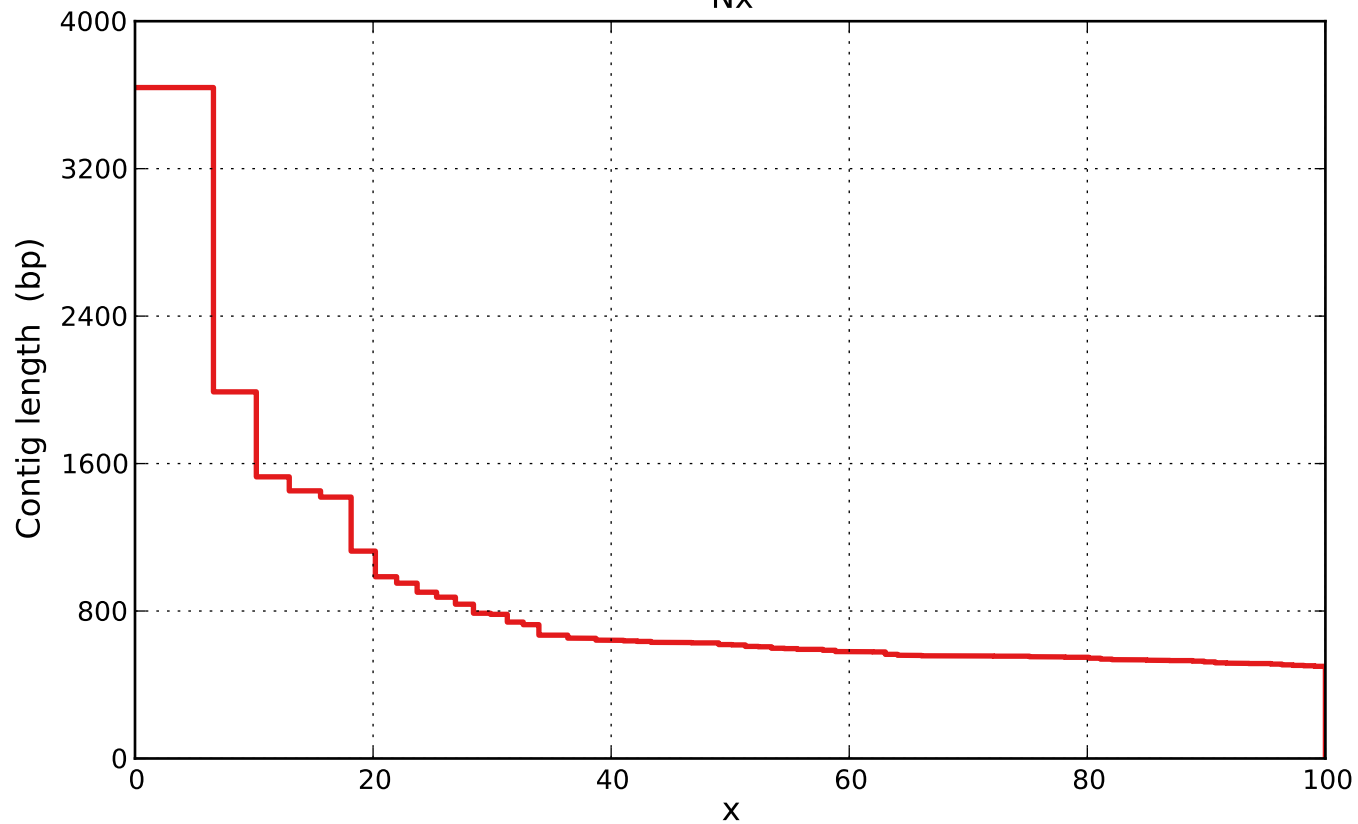|	final.contigs
# contigs (>= 0 bp)	464
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	201954
Total length (>= 1000 bp)	11152
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	79
Largest contig	3640
Total length	55228
Reference length	4641652
N50	618
N75	555
L50	29
L75	53
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	2438
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	42
Genome fraction (%)	1.189
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	308.11
# indels per 100 kbp	9.06
Largest alignment	3640
NA50	616
NA75	552
LA50	30
LA75	54

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	2438
# local misassemblies	0
# mismatches	170
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	42
# N's	0

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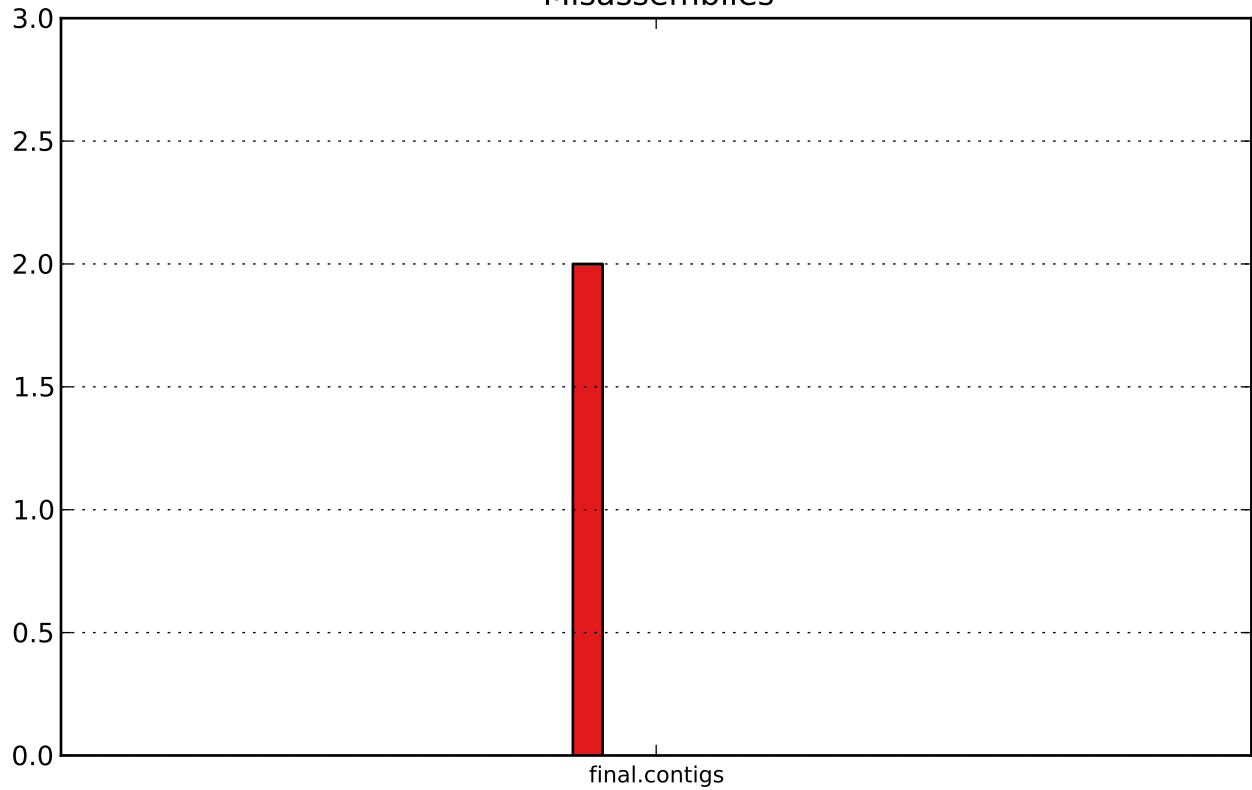(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length
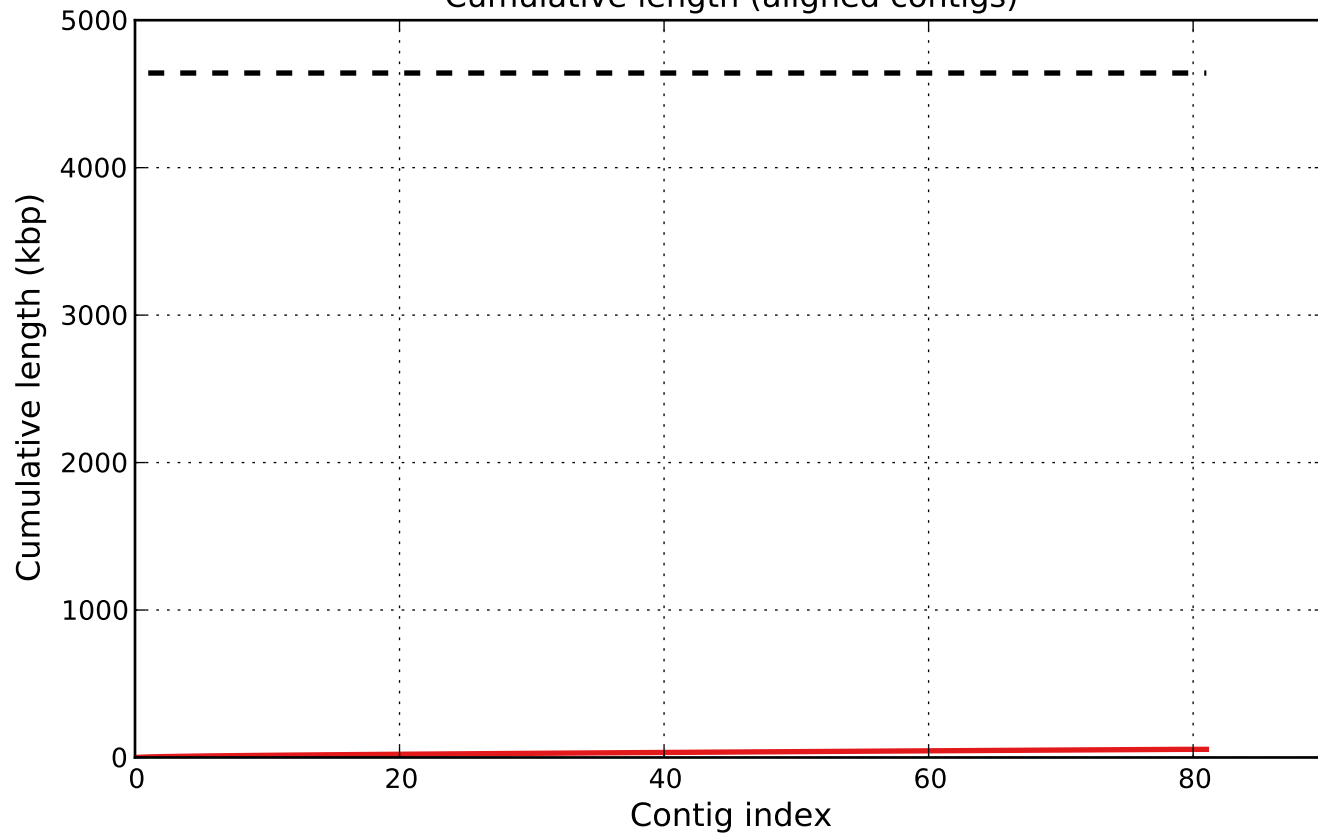
Cumulative length (kbp)

Contig index
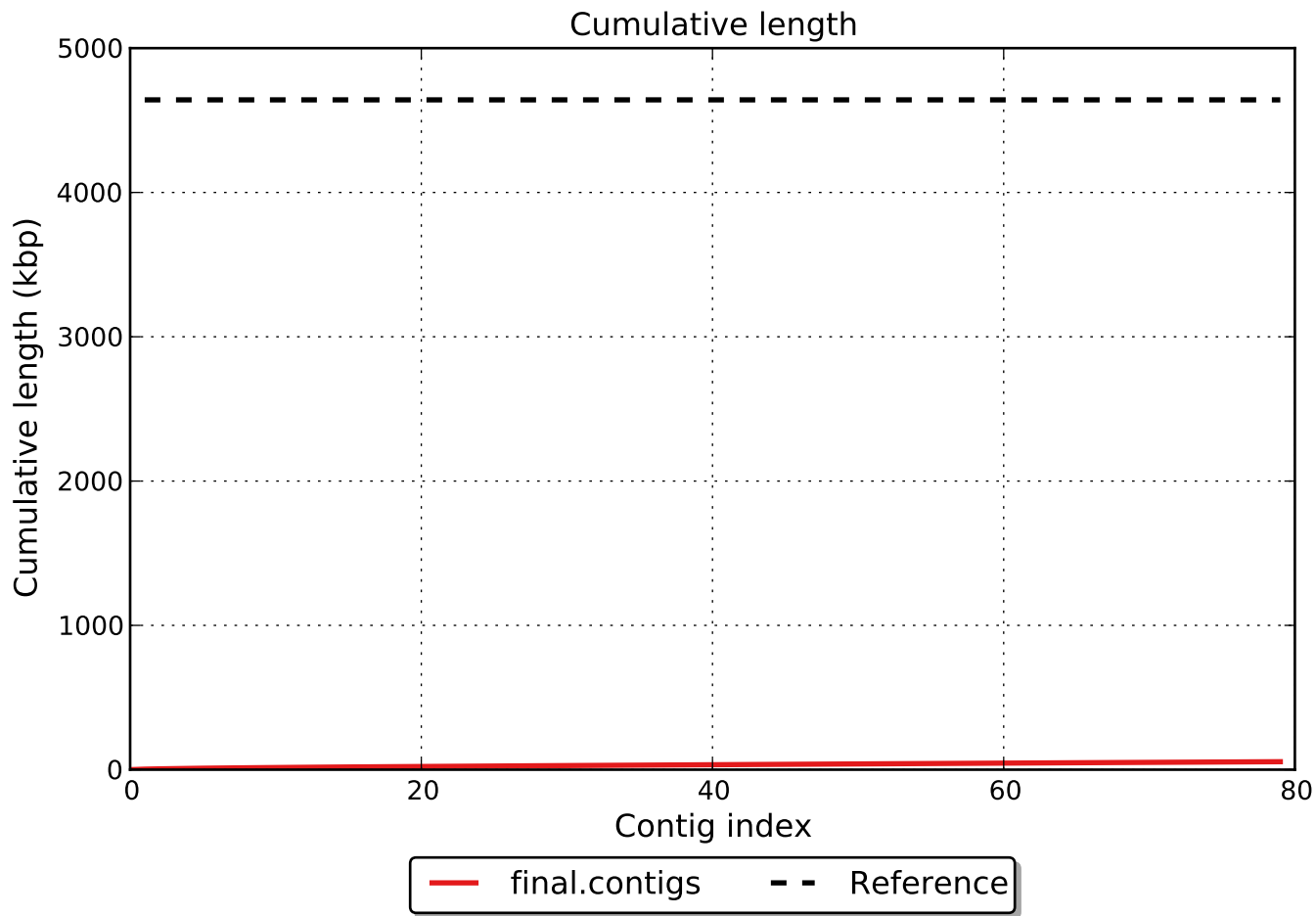
final.contigs — — Reference

Misassemblies

Cumulative length (aligned contigs)