Report

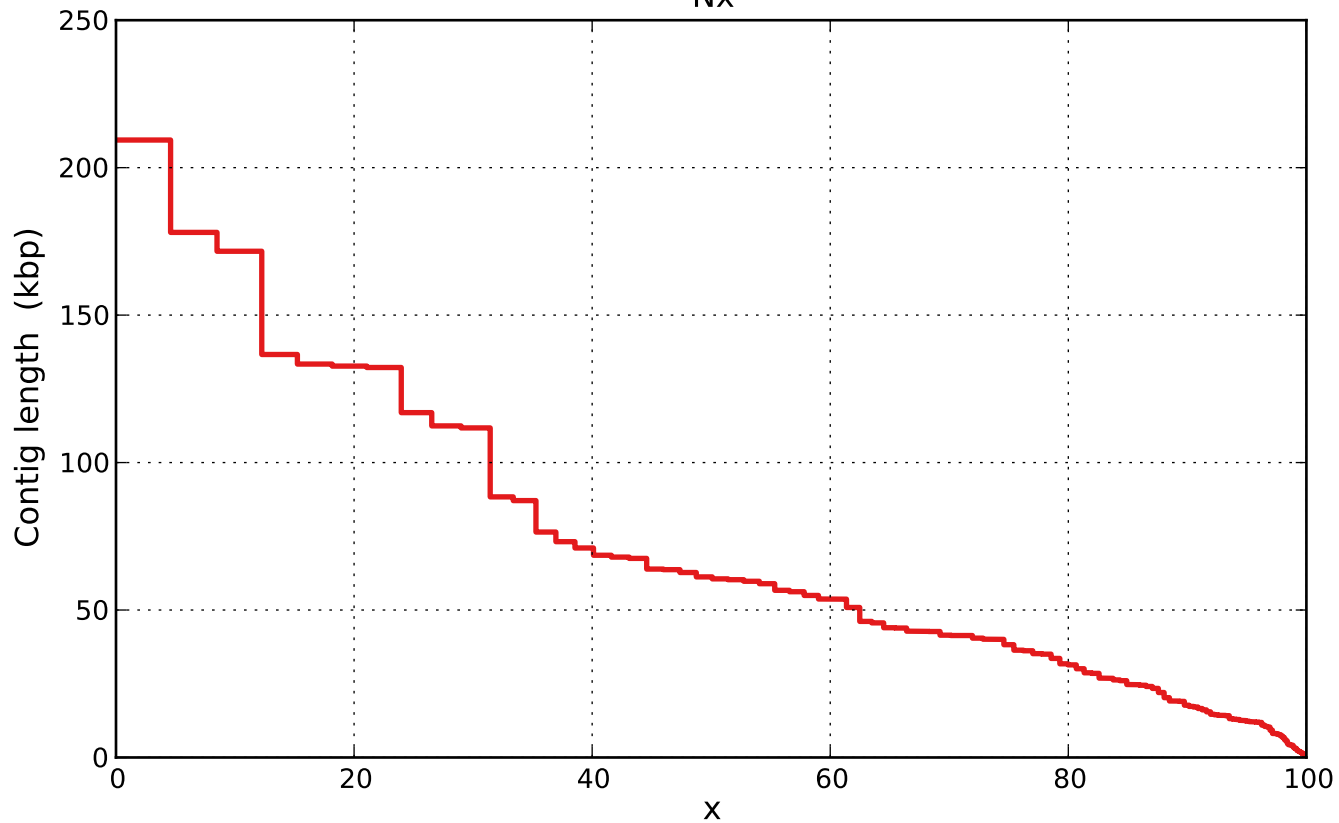|	final.contigs
# contigs (>= 0 bp)	161
# contigs (>= 1000 bp)	132
# contigs (>= 5000 bp)	103
# contigs (>= 10000 bp)	94
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4571933
Total length (>= 1000 bp)	4559753
Total length (>= 5000 bp)	4492726
Total length (>= 10000 bp)	4425935
Total length (>= 25000 bp)	3876408
Total length (>= 50000 bp)	2852455
# contigs	141
Largest contig	209367
Total length	4565463
Reference length	4641652
N50	61232
N75	38244
L50	22
L75	46
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	63121
# local misassemblies	12
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.231
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	67.20
# indels per 100 kbp	9.80
Largest alignment	209367
NA50	61232
NA75	38244
LA50	22
LA75	46

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	63121
# local misassemblies	12
# mismatches	3064
# indels	447
# short indels	446
# long indels	1
Indels length	637

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).
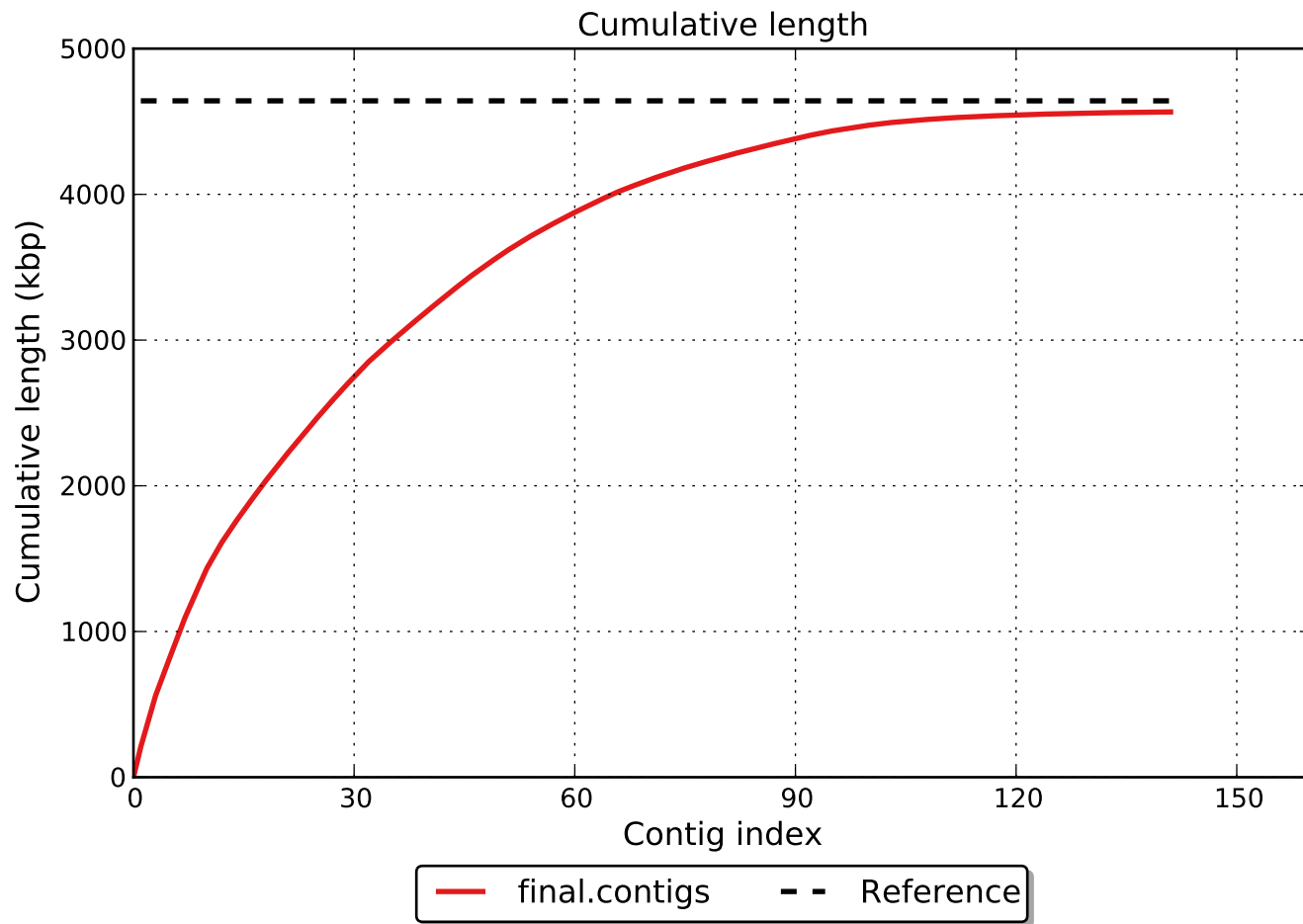
Unaligned report

	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).
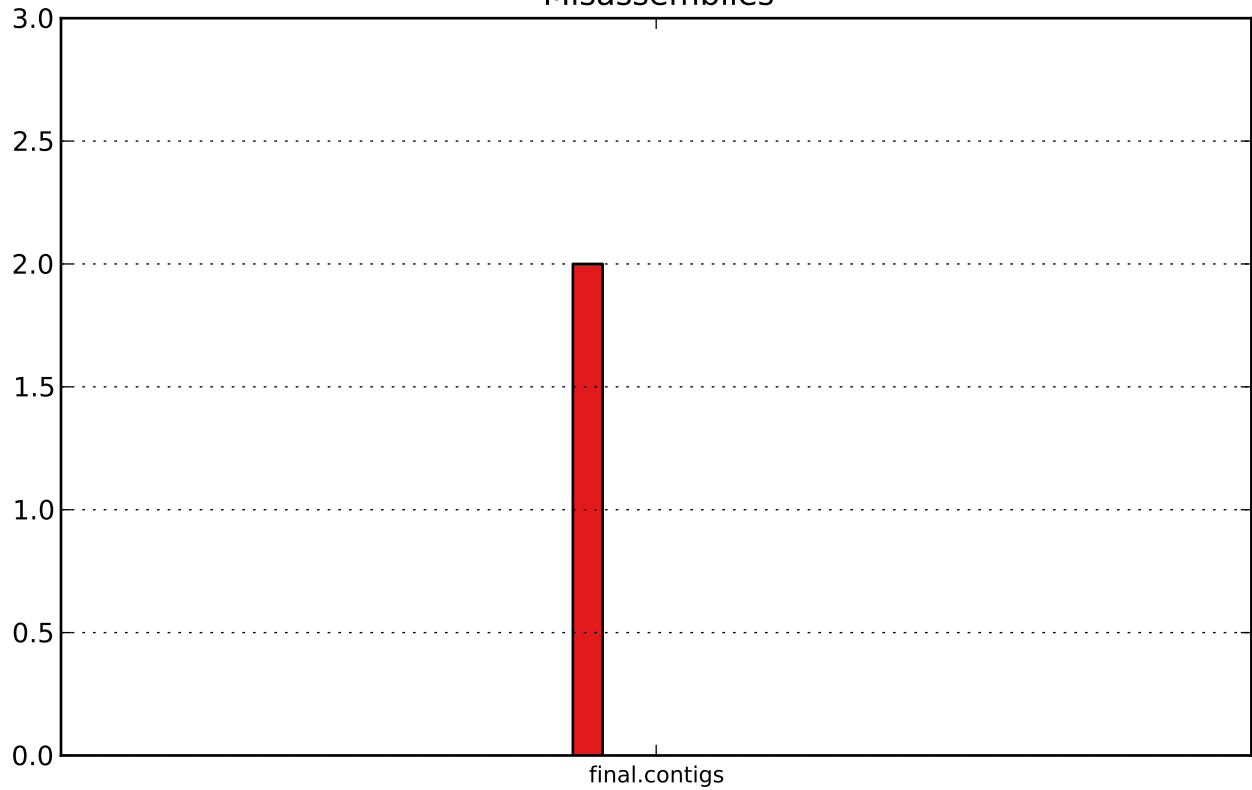
Nx

Cumulative length
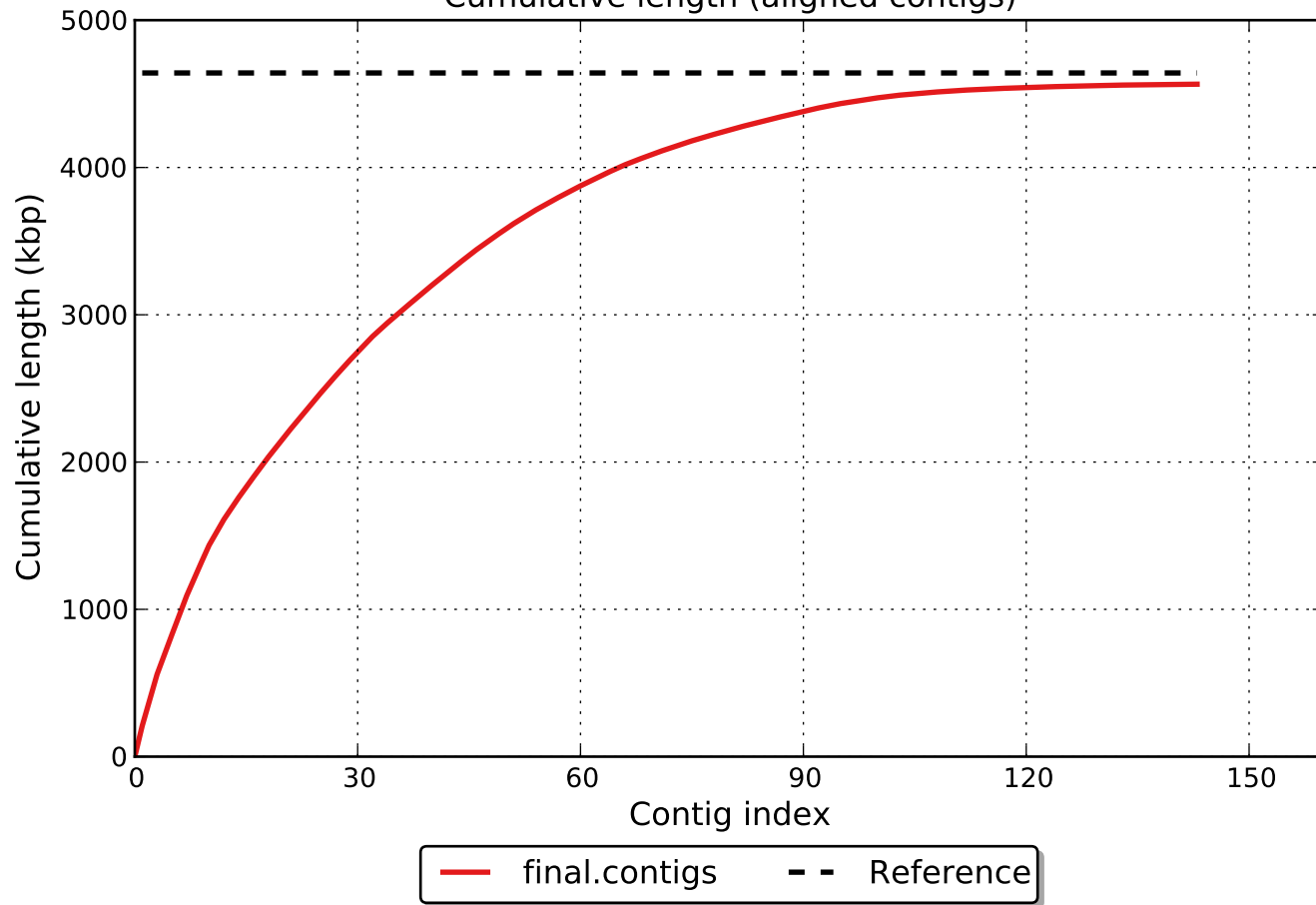
Cumulative length (aligned contigs)

NAx