Report

	final.contigs
# contigs (>= 1000 bp)	125
# contigs (>= 5000 bp)	95
# contigs (>= 10000 bp)	85
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	34
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
GC (%)	50.75
Reference GC (%)	50.79
N50	68696
NG50	67410
N75	40833
NG75	35269
L50	20
LG50	21
L75	41
LG75	43
# 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
NGA50	67410
NA75	40833
NGA75	35269
LA50	20
LGA50	21
LA75	41
LGA75	43

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

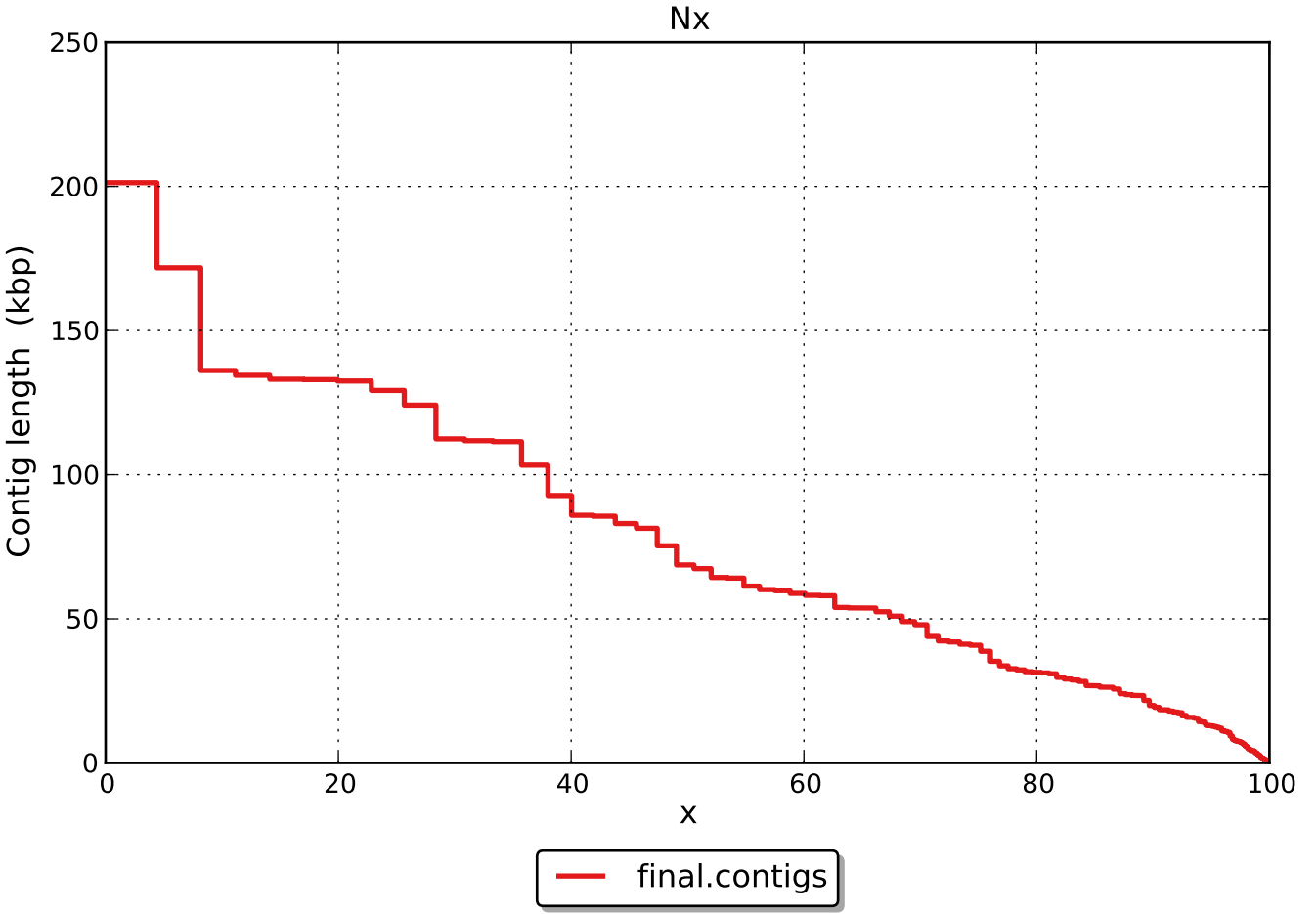
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# mismatches	2645
# indels	460
# short indels	454
# long indels	6
Indels length	793

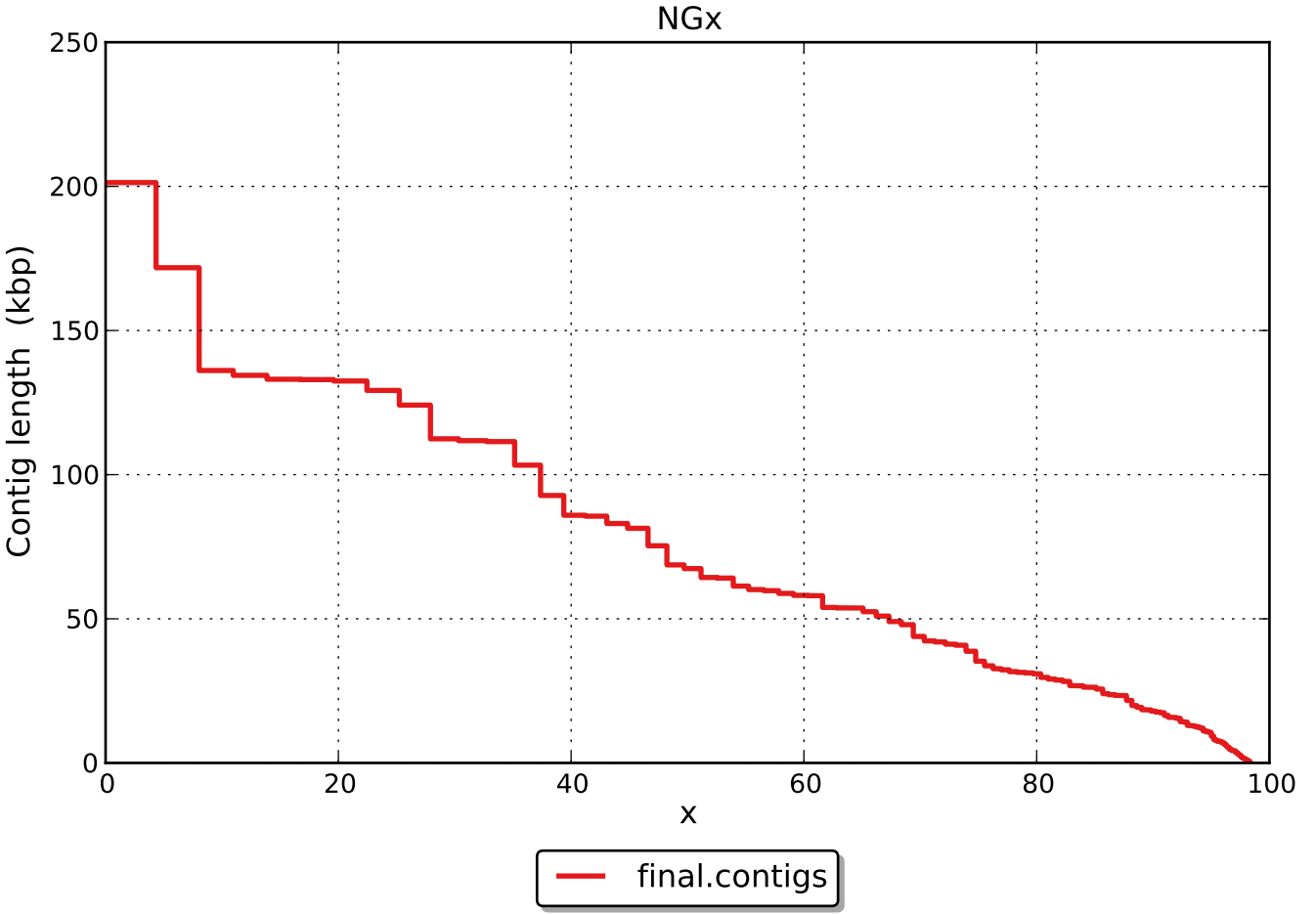
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

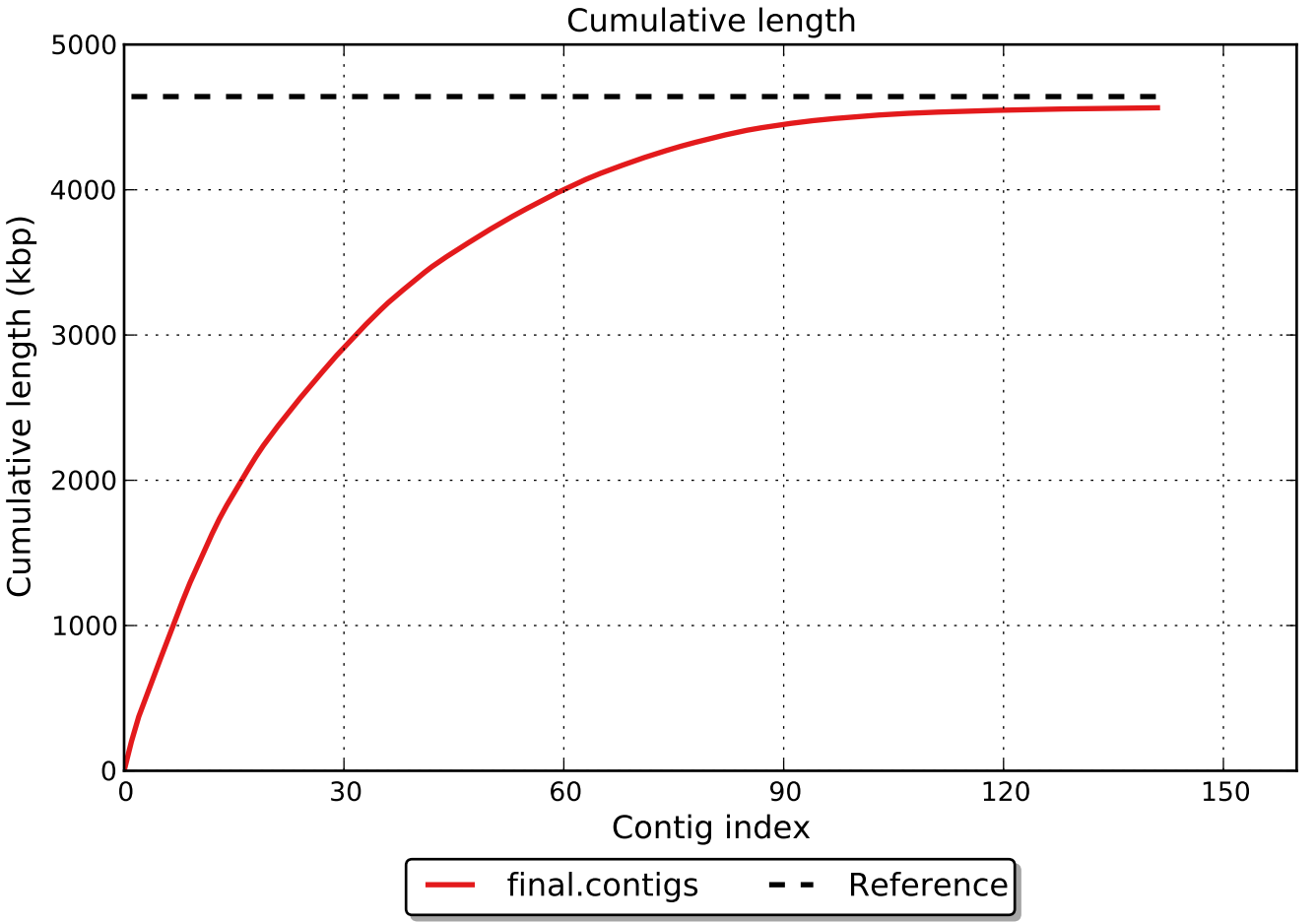
Unaligned report

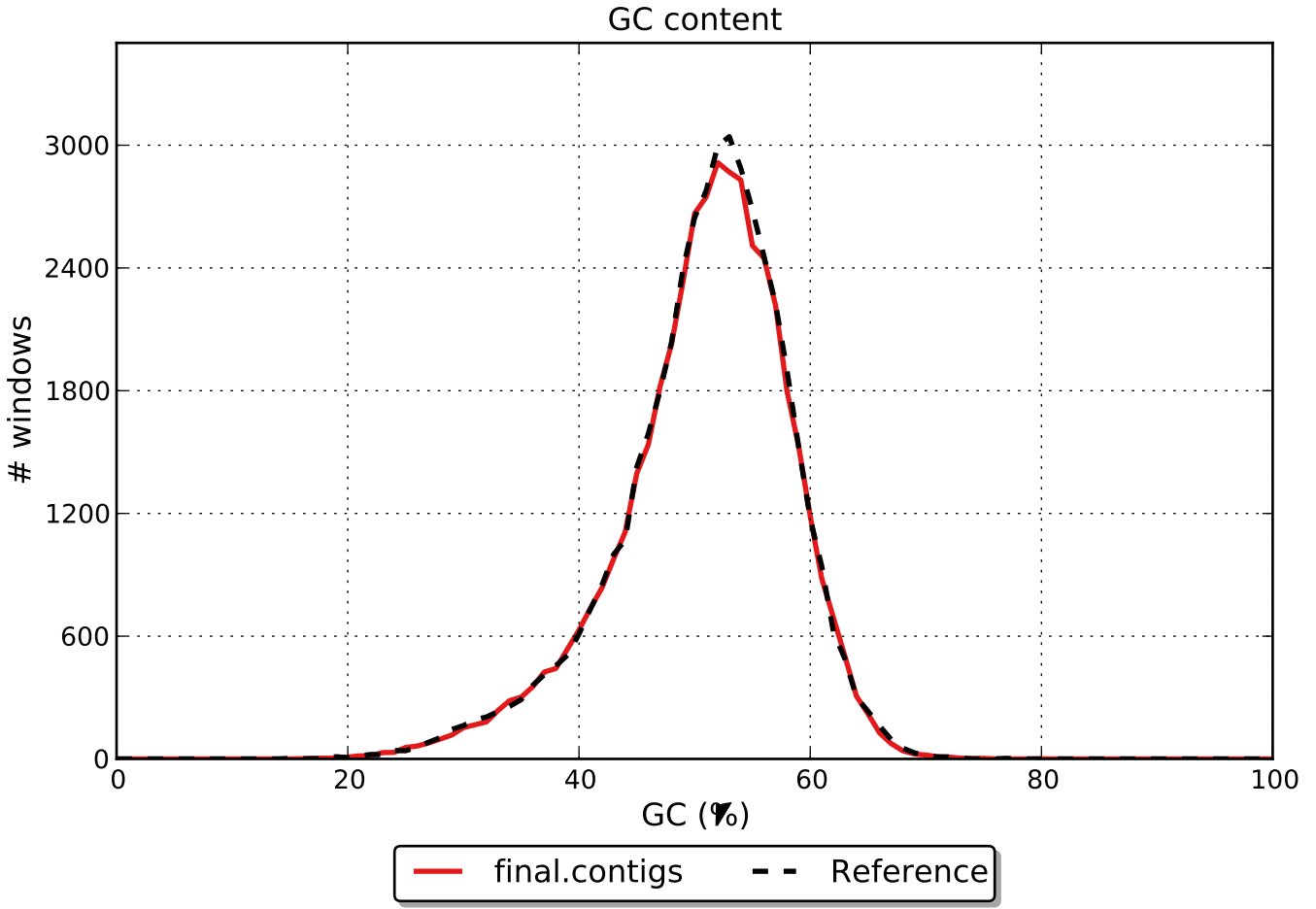
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

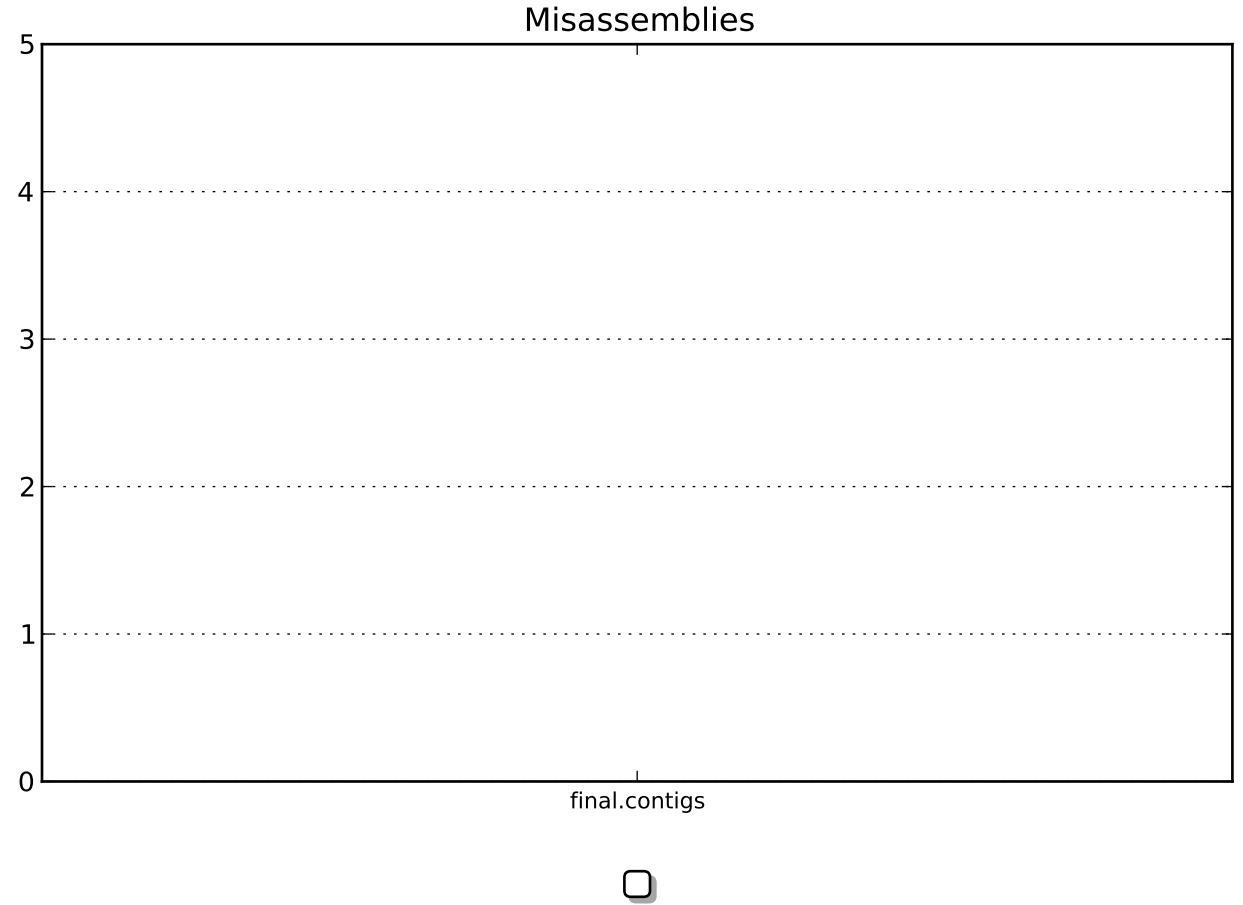
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

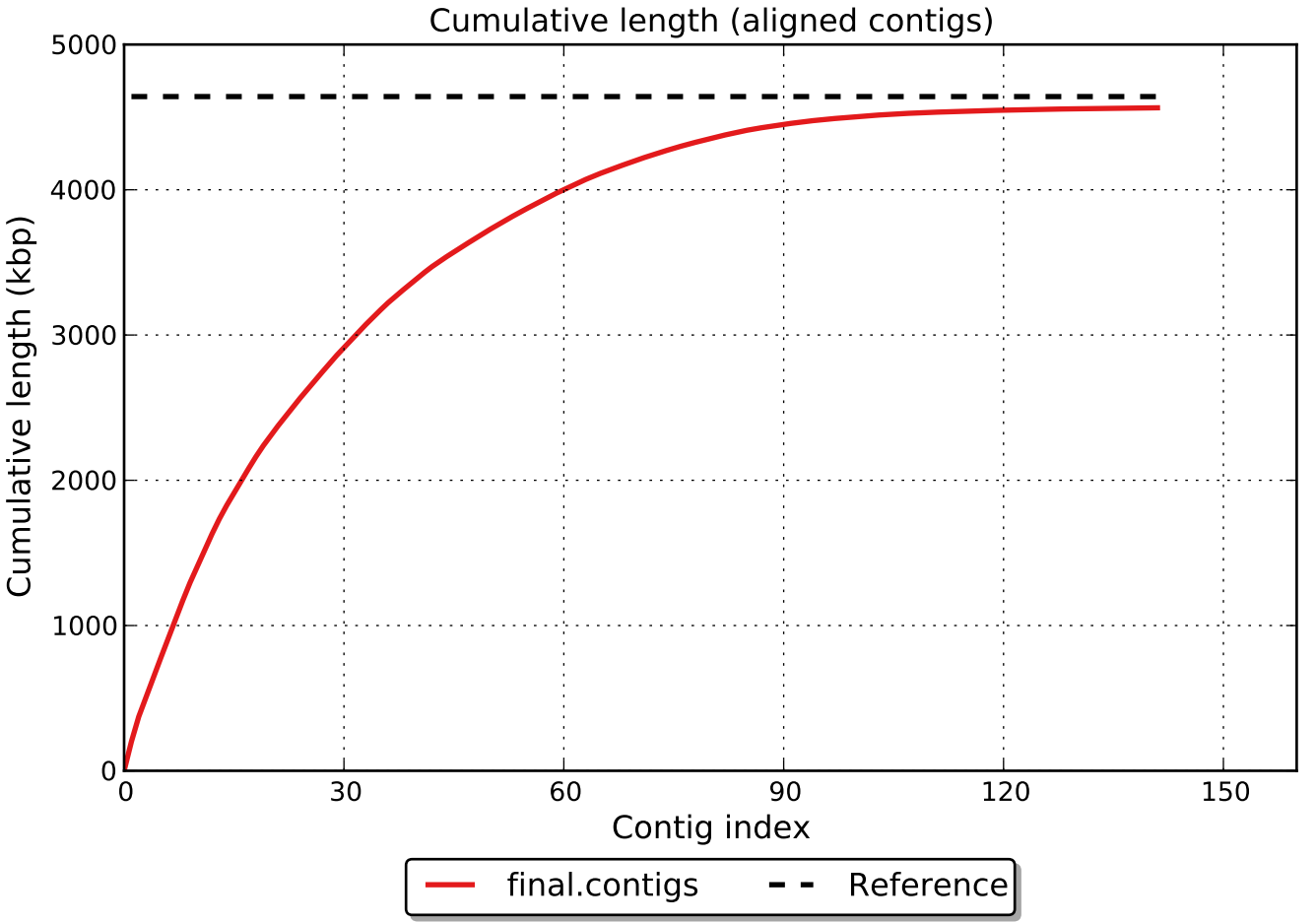

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

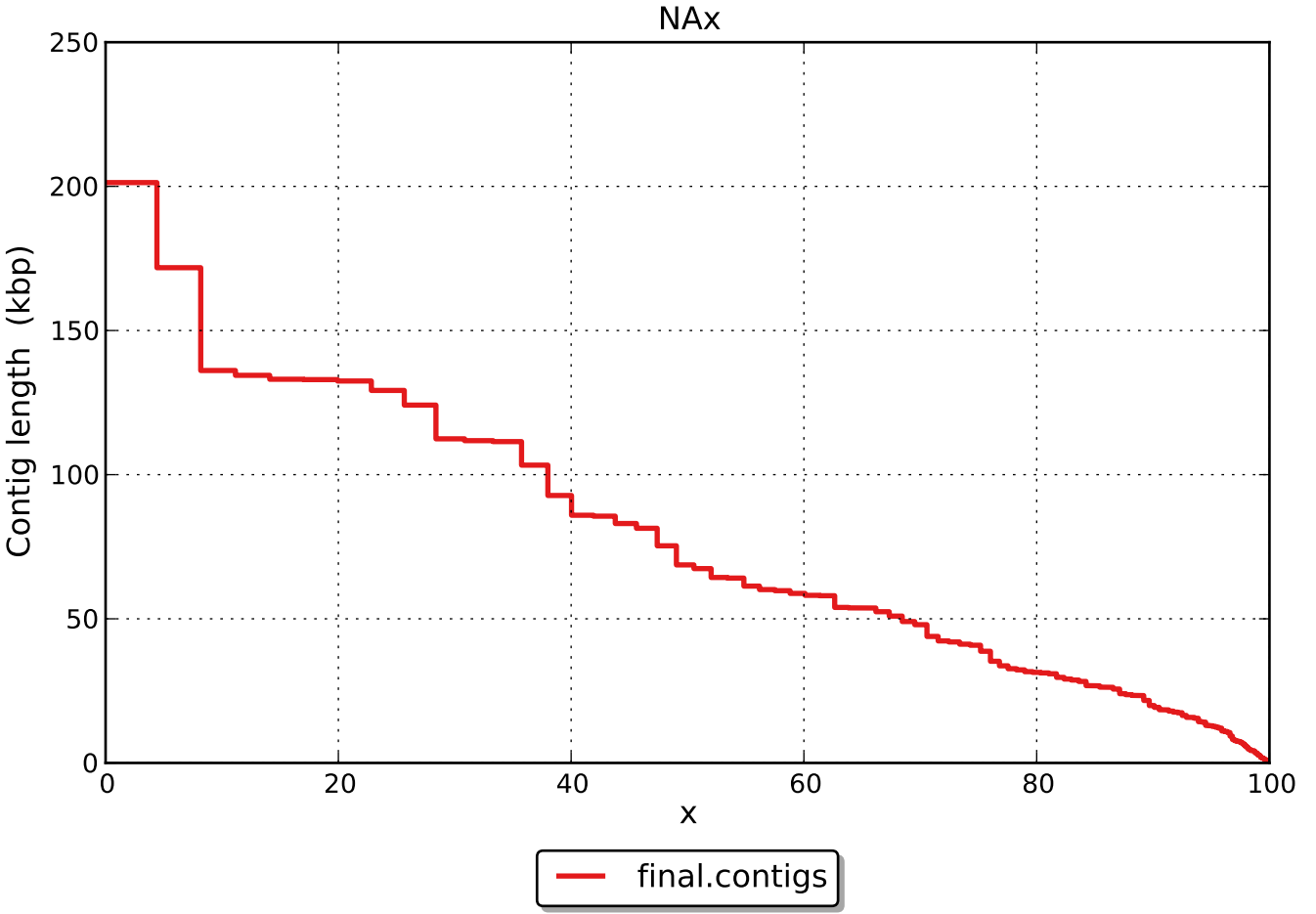

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

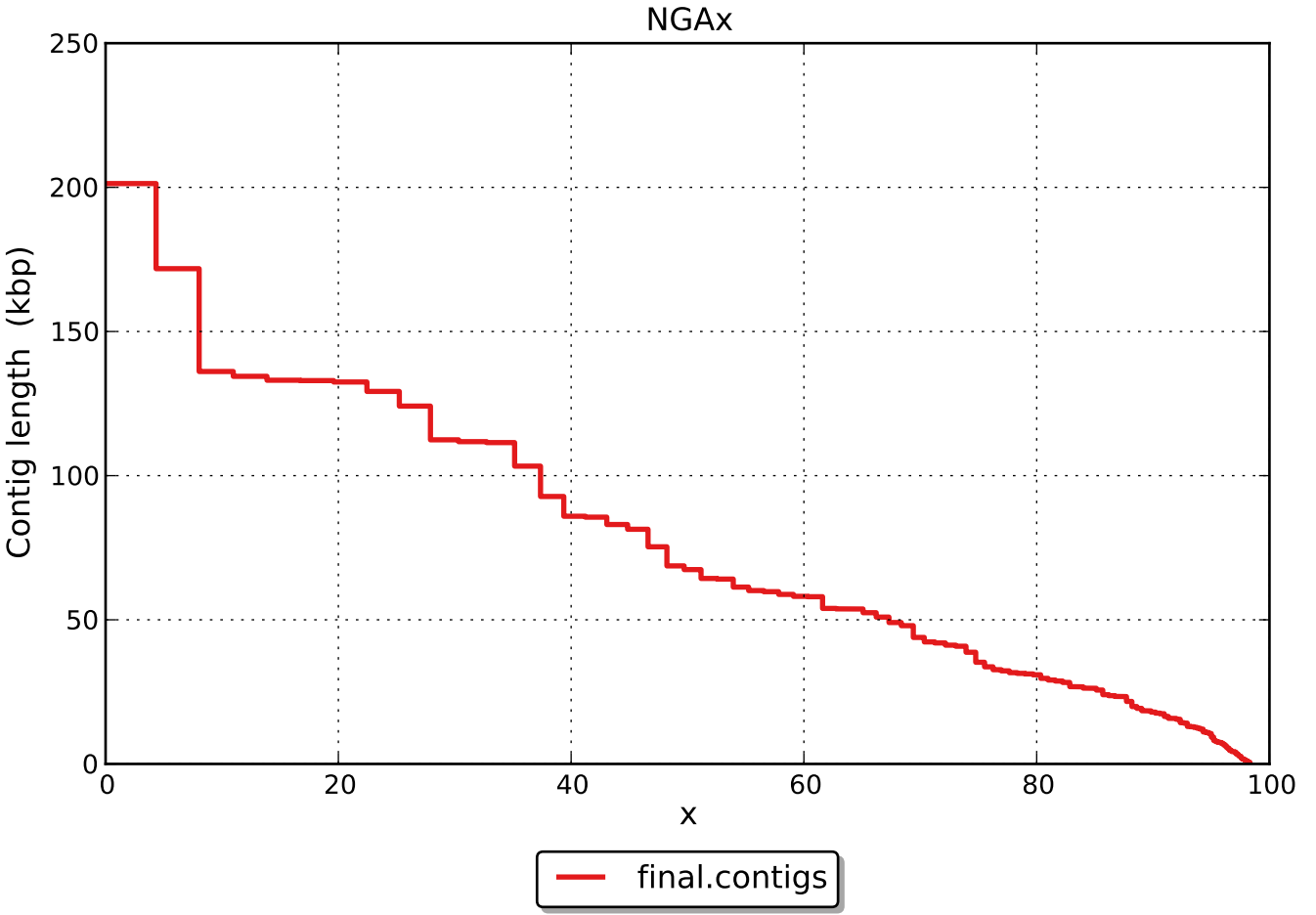

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


NAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs


NGAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs