Report

	final.contigs
# contigs (>= 1000 bp)	132
# contigs (>= 5000 bp)	103
# contigs (>= 10000 bp)	94
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	32
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
GC (%)	50.74
Reference GC (%)	50.79
N50	61232
NG50	60564
N75	38244
NG75	36187
L50	22
LG50	23
L75	46
LG75	48
# 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
NGA50	60564
NA75	38244
NGA75	36187
LA50	22
LGA50	23
LA75	46
LGA75	48

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

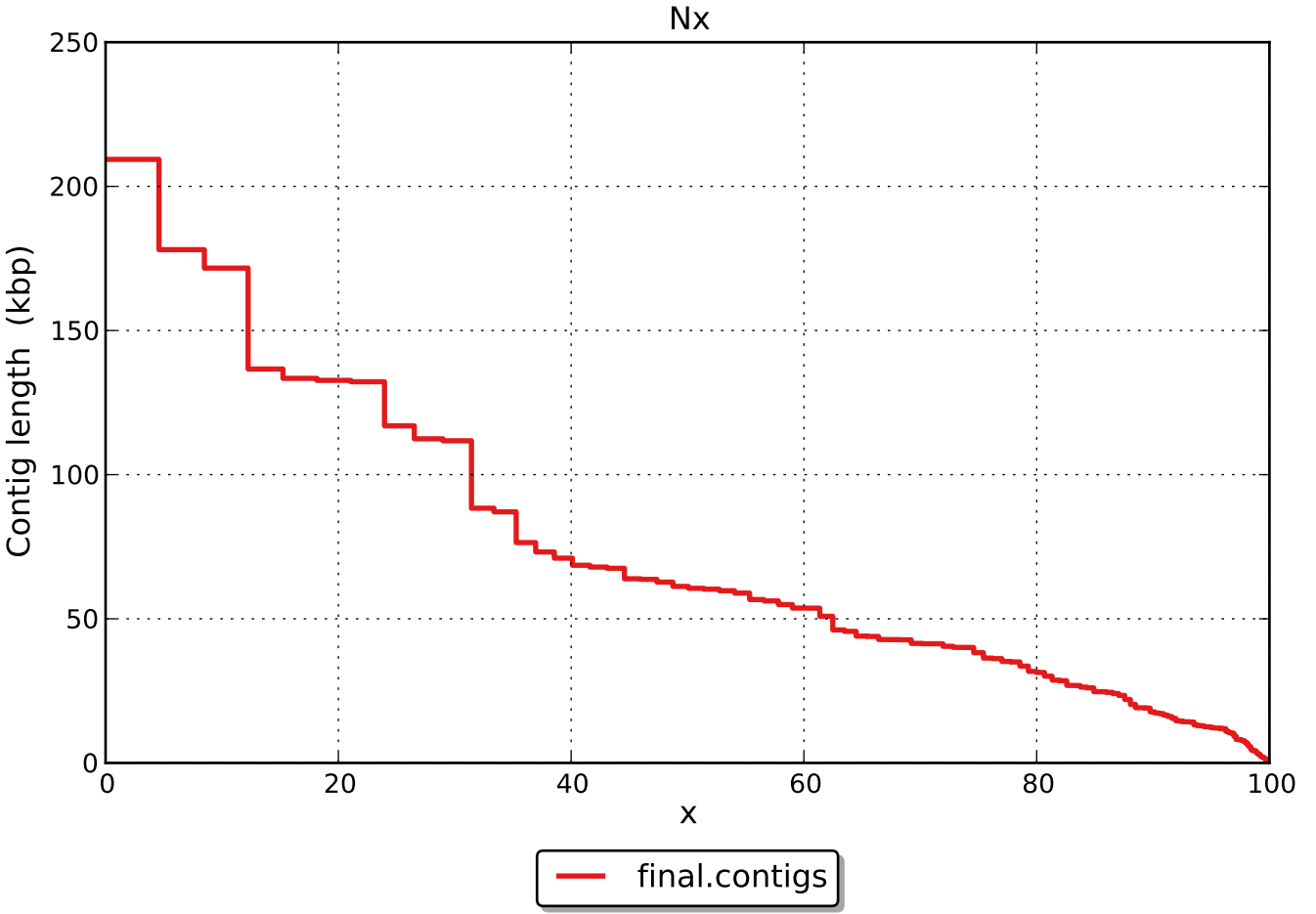
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	63121
# local misassemblies	12
# mismatches	3064
# indels	447
# short indels	446
# long indels	1
Indels length	637

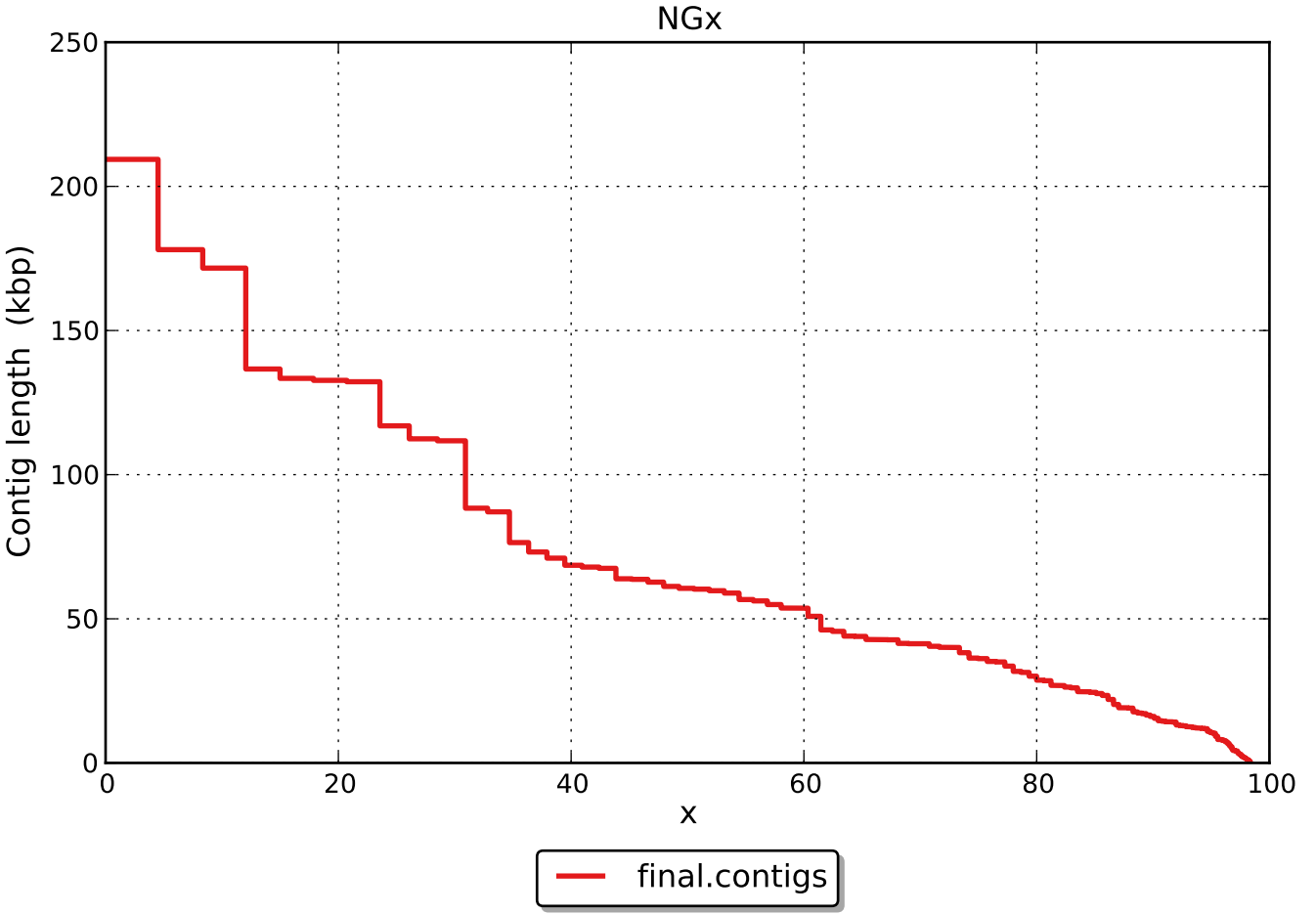
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

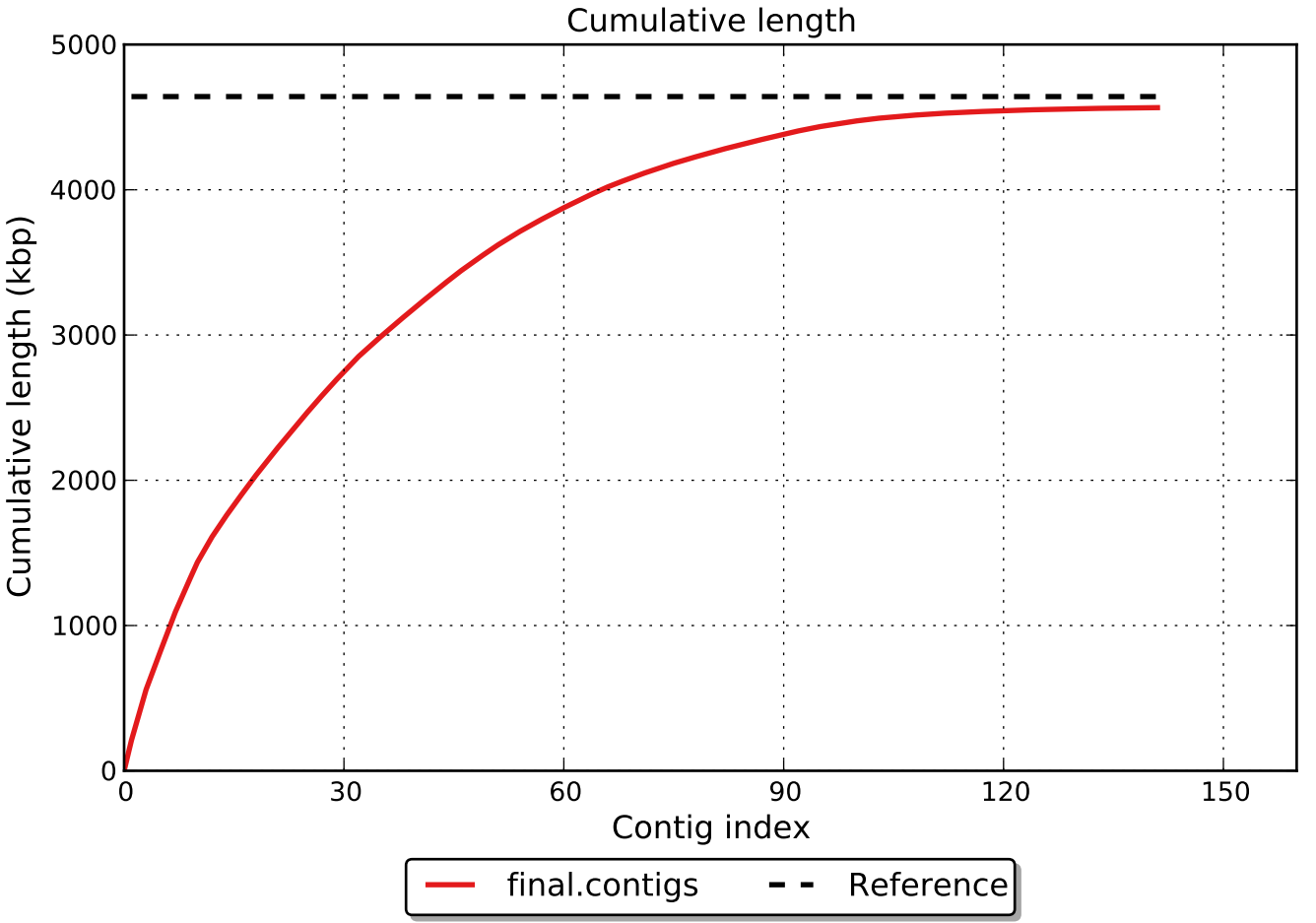
Unaligned report

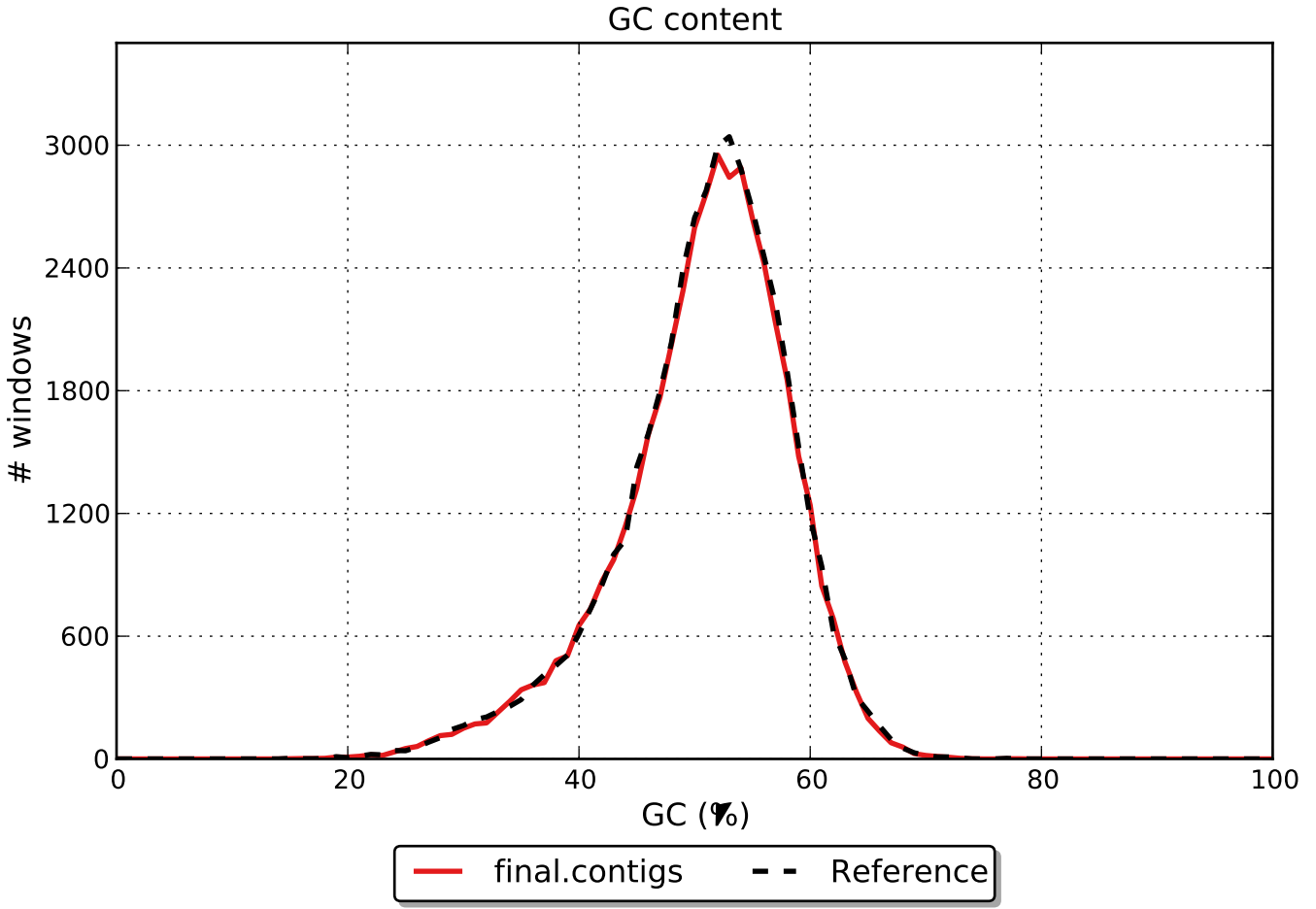
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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).

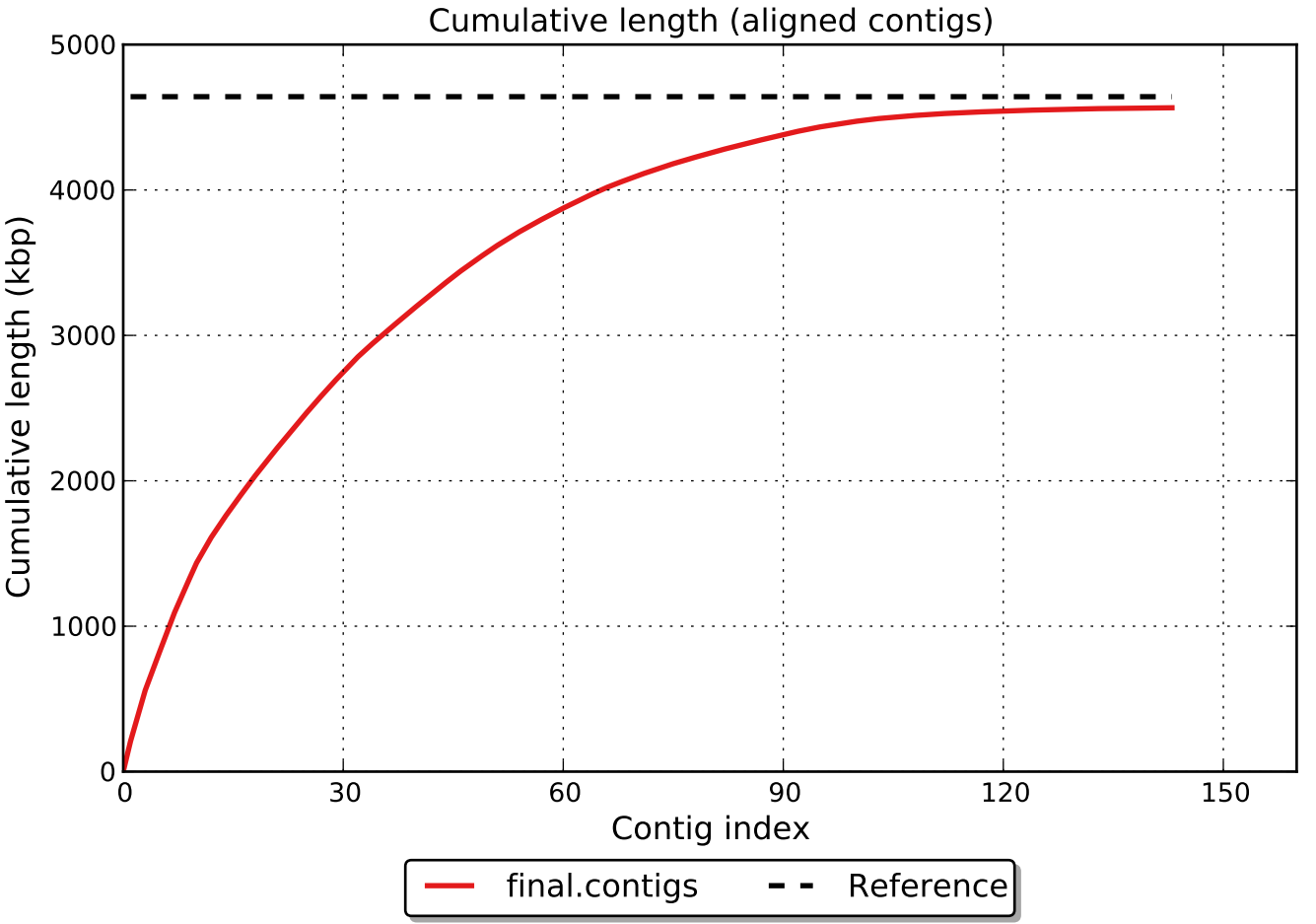

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

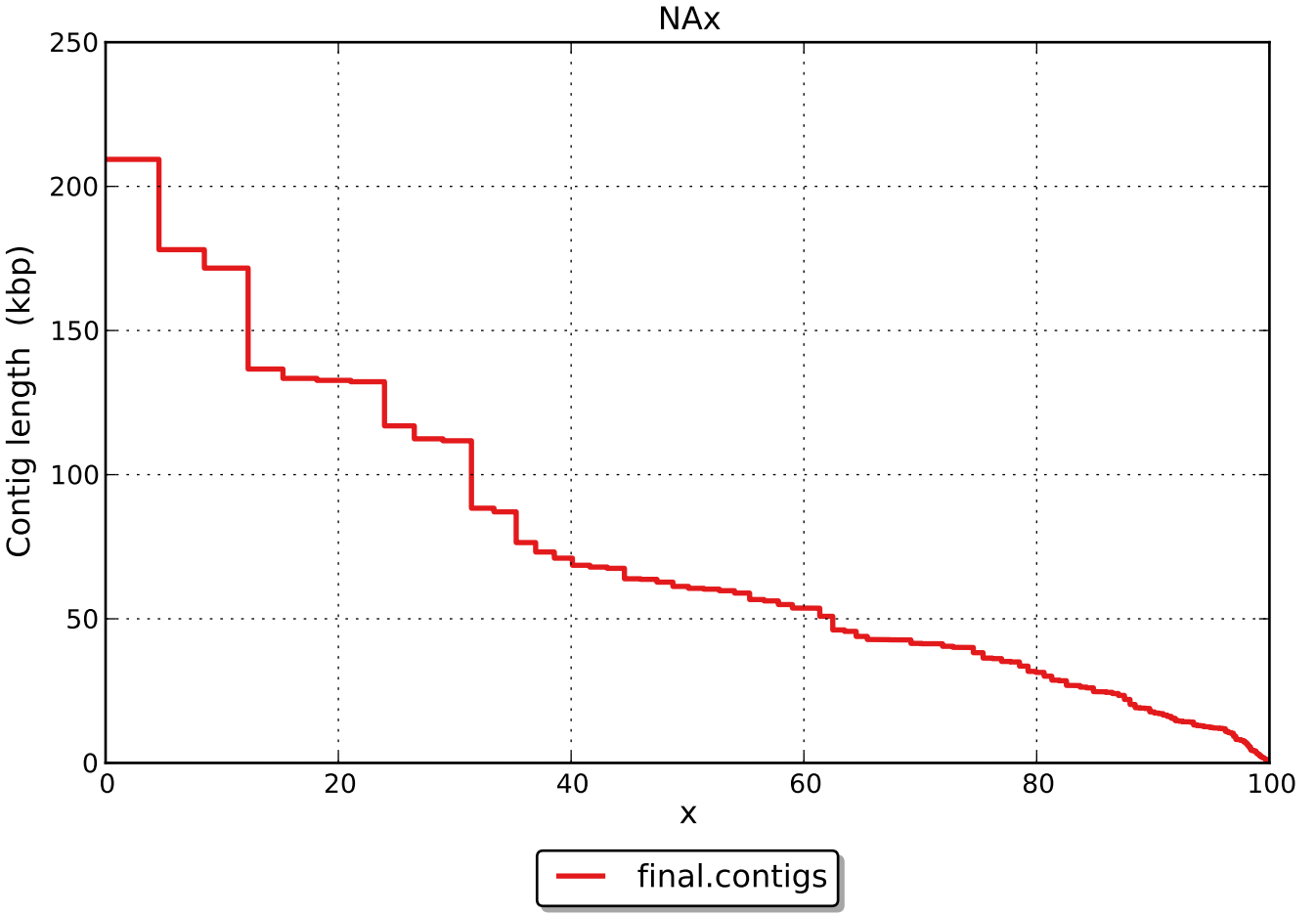

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

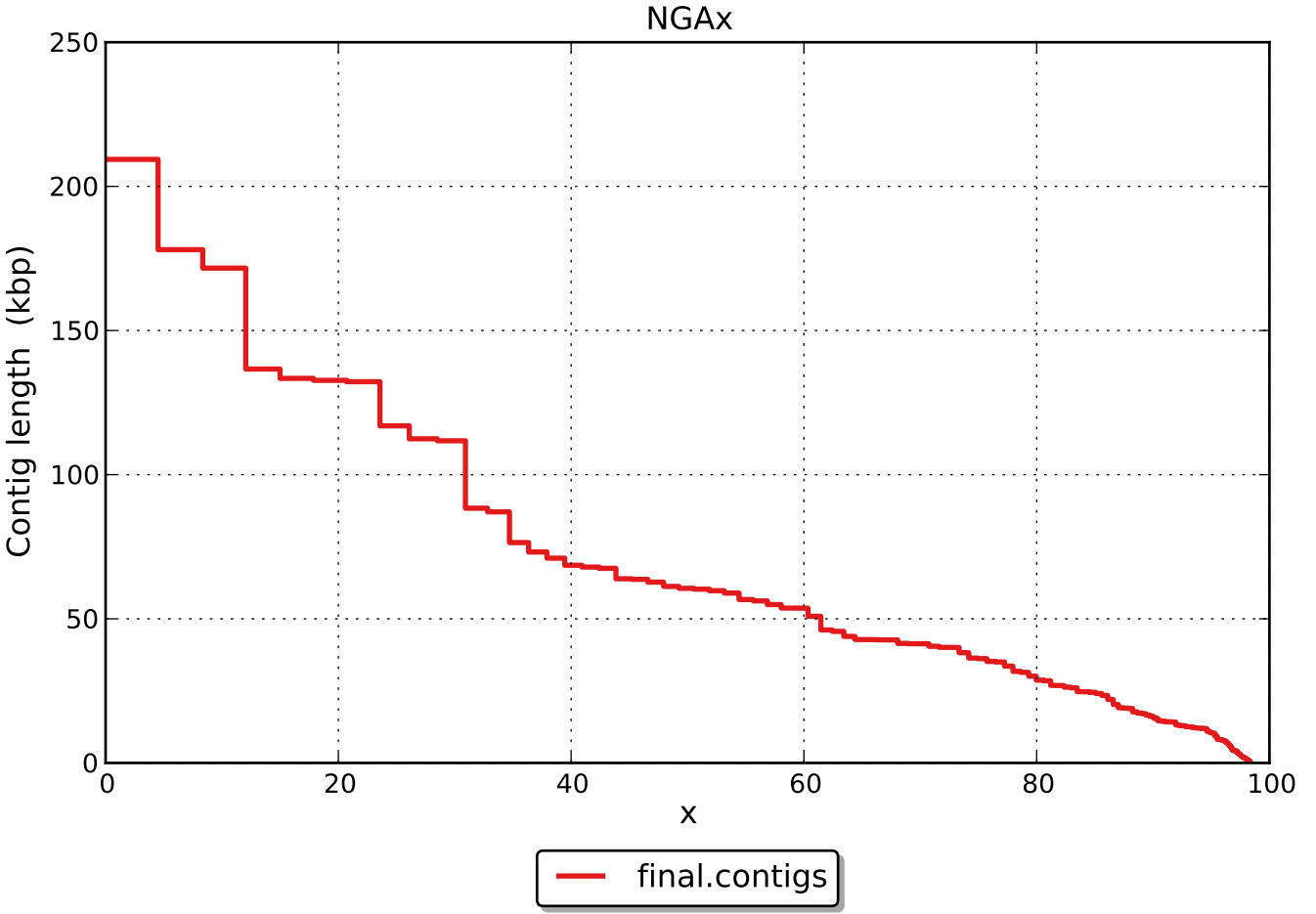

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


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

Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


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


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