Report

	final.contigs
# contigs (>= 0 bp)	437
# contigs (>= 1000 bp)	129
# contigs (>= 5000 bp)	104
# contigs (>= 10000 bp)	92
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4650409
Total length (>= 1000 bp)	4548228
Total length (>= 5000 bp)	4489034
Total length (>= 10000 bp)	4400897
Total length (>= 25000 bp)	3916029
Total length (>= 50000 bp)	2849208
# contigs	141
Largest contig	203098
Total length	4555926
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	61722
NG50	60955
N75	34115
NG75	32765
L50	22
LG50	23
L75	46
LG75	48
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	656
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.038
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.01
# indels per 100 kbp	0.07
Largest alignment	203098
NA50	61722
NGA50	60955
NA75	34115
NGA75	32765
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

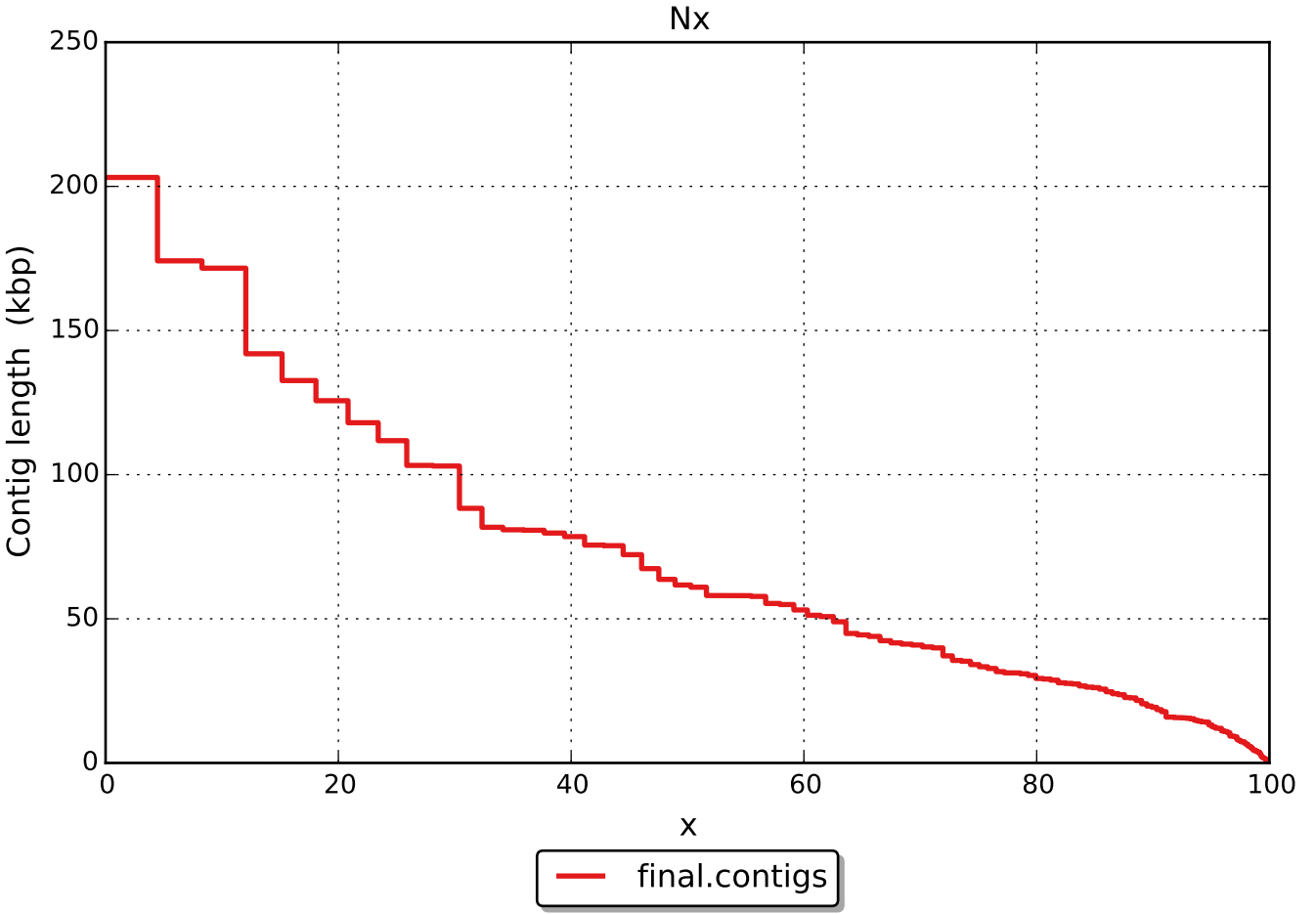
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	656
# local misassemblies	1
# mismatches	137
# indels	3
# short indels	3
# long indels	0
Indels length	3

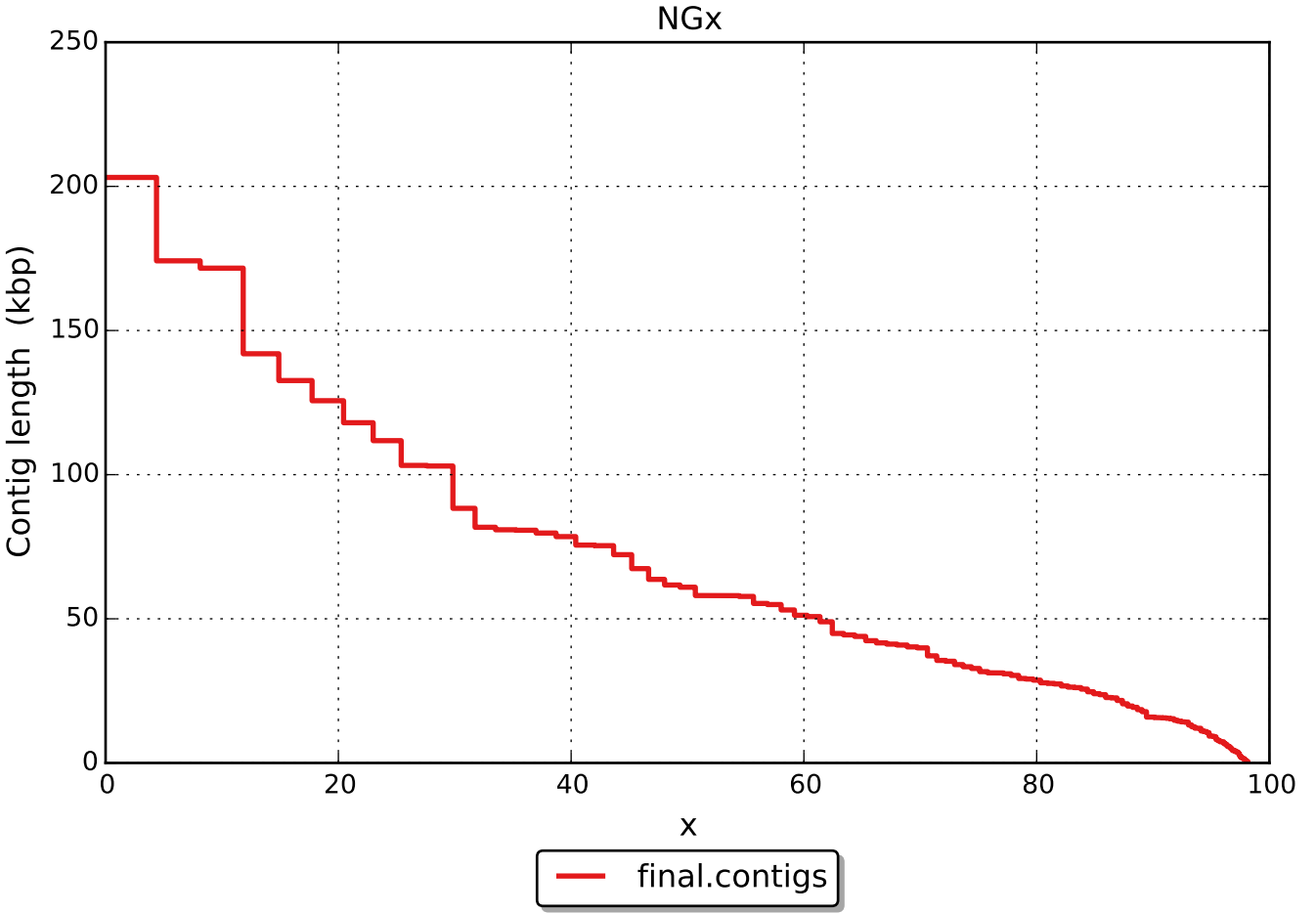
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

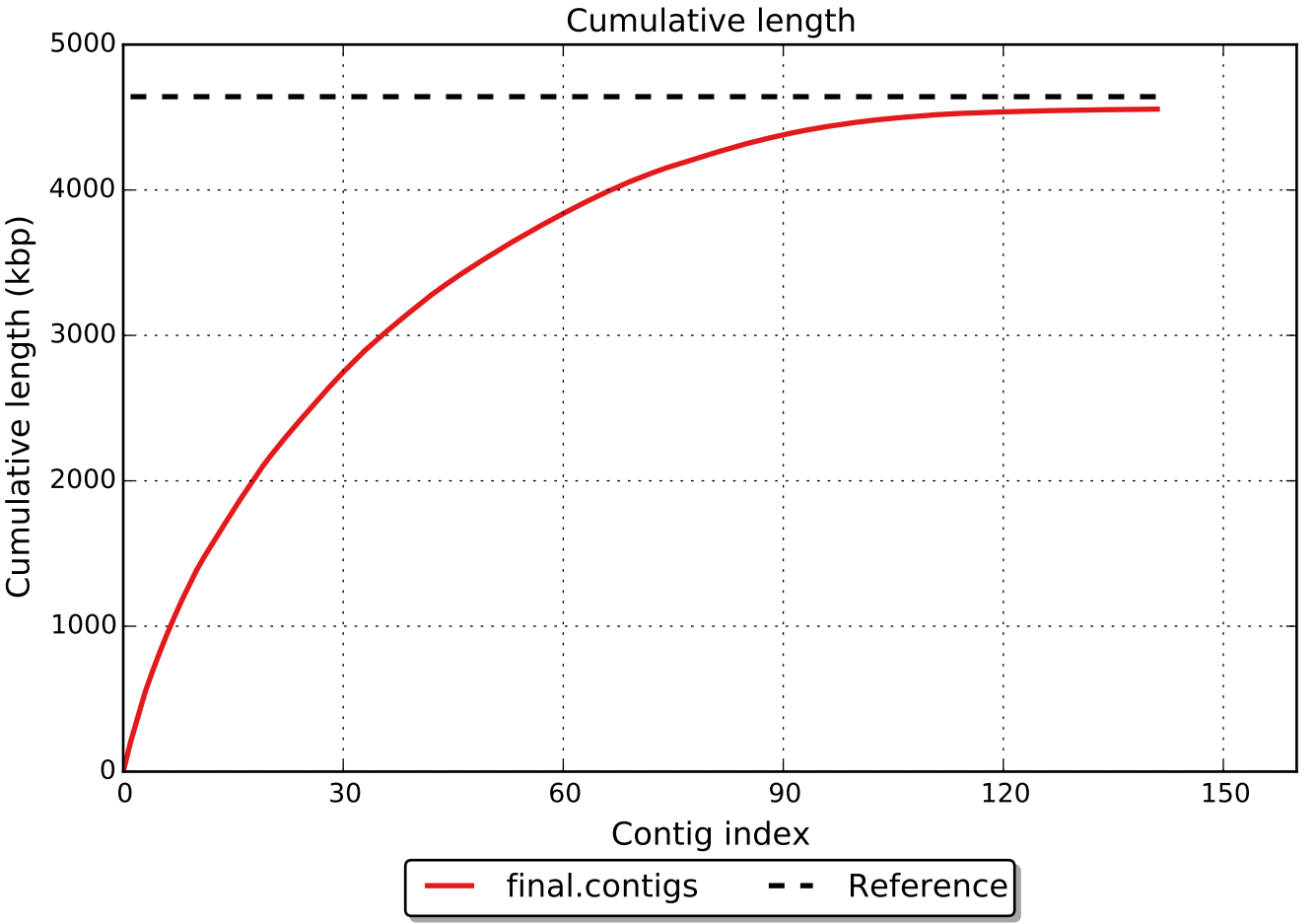
Unaligned report

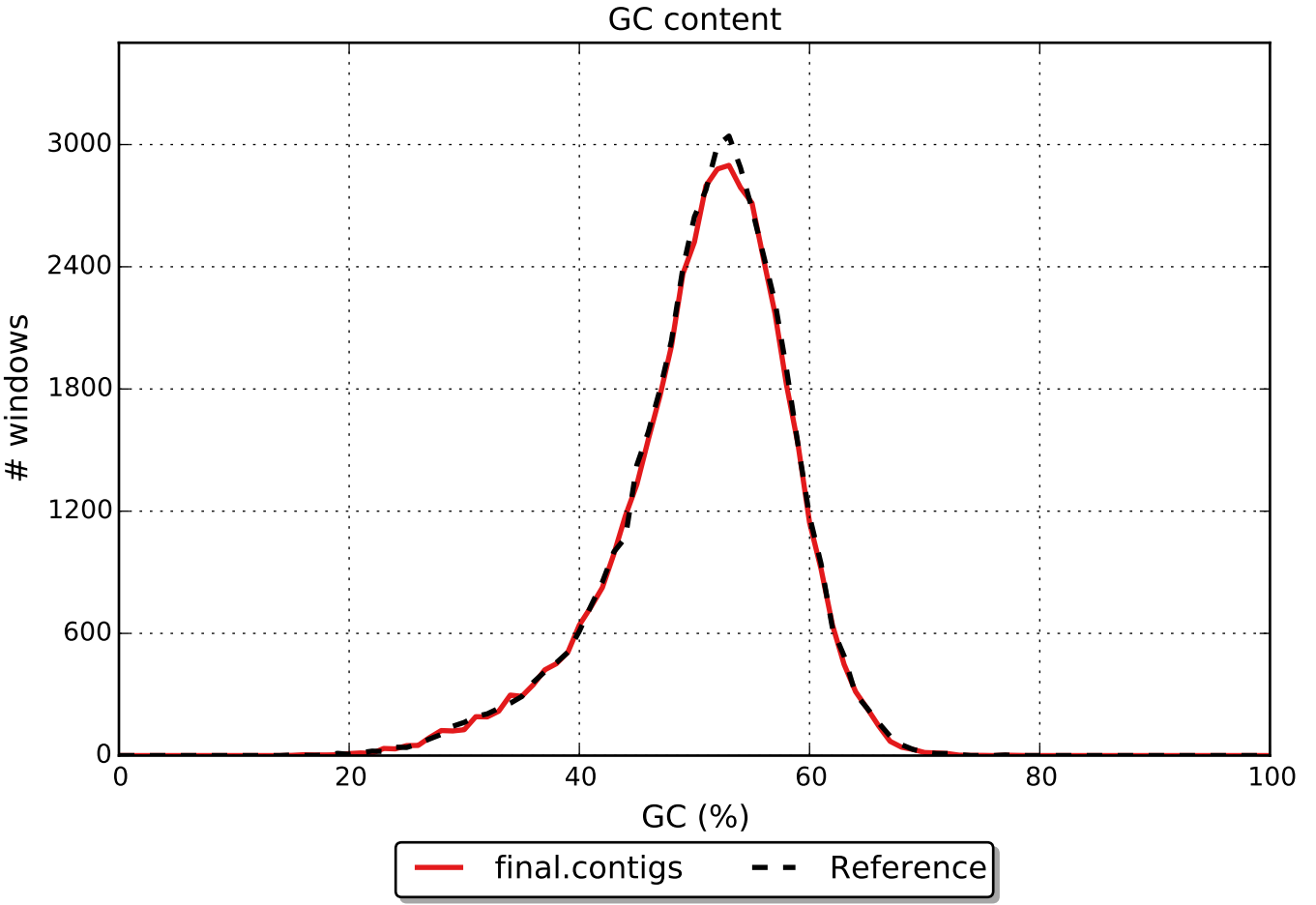
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

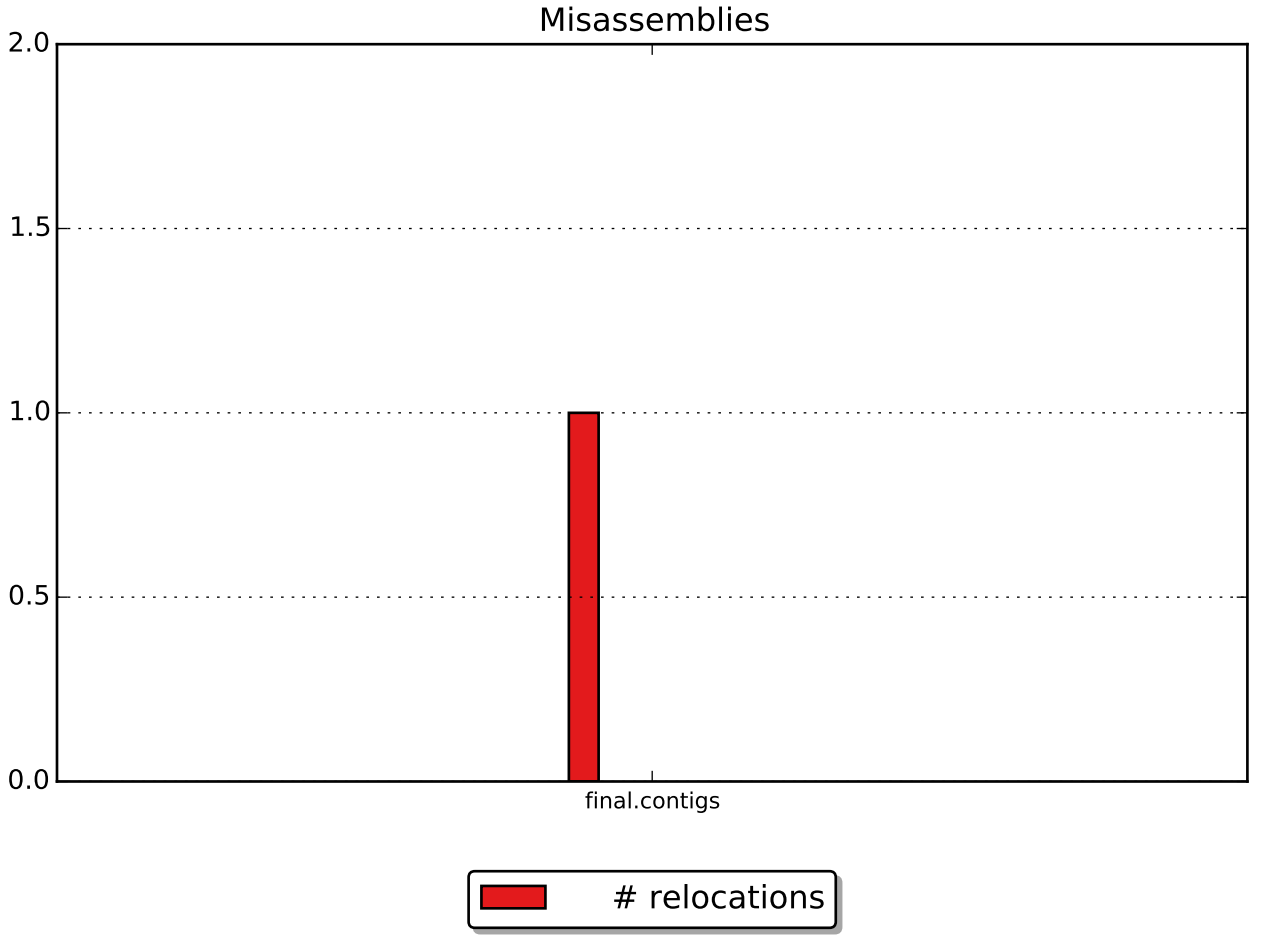
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

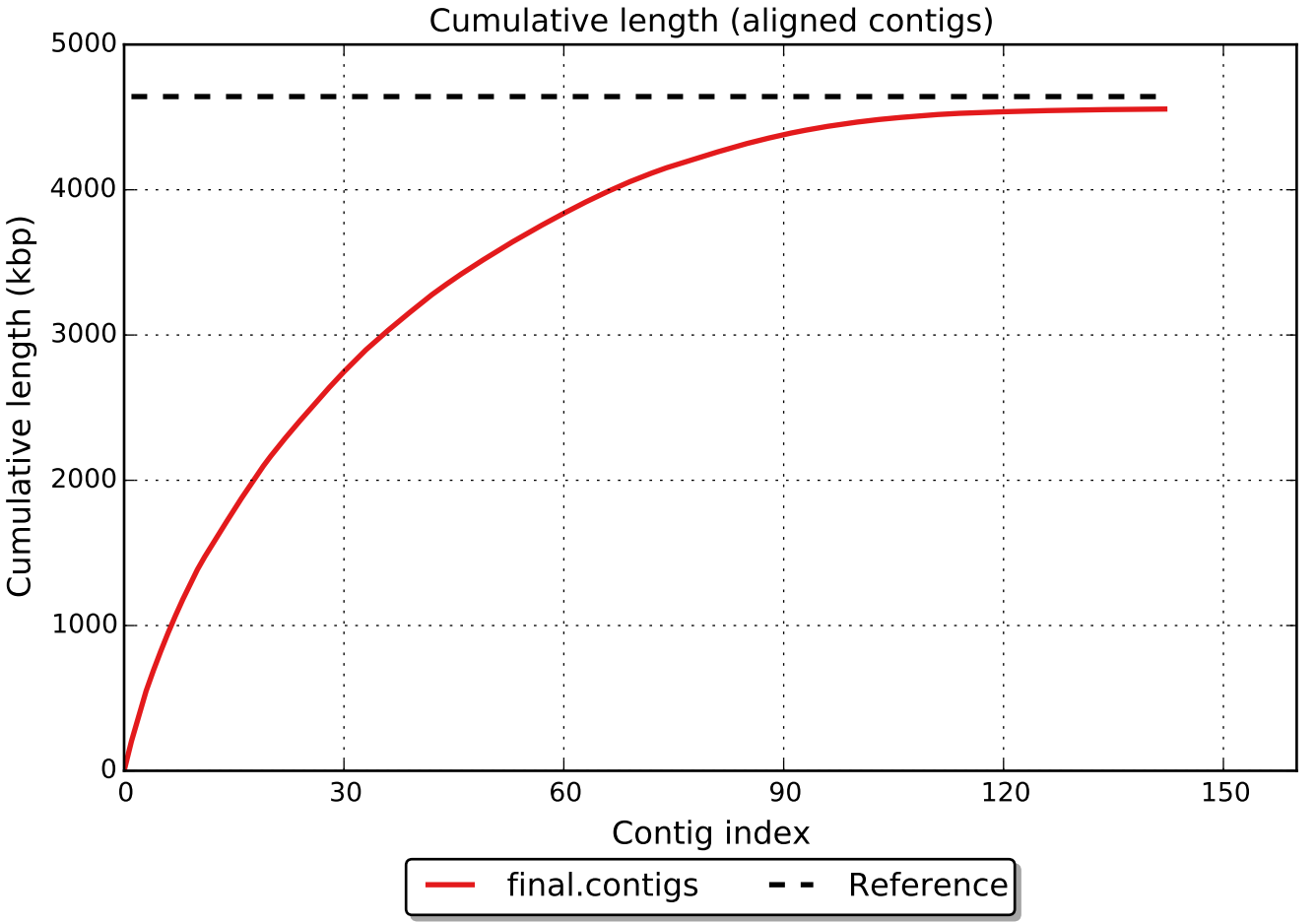

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

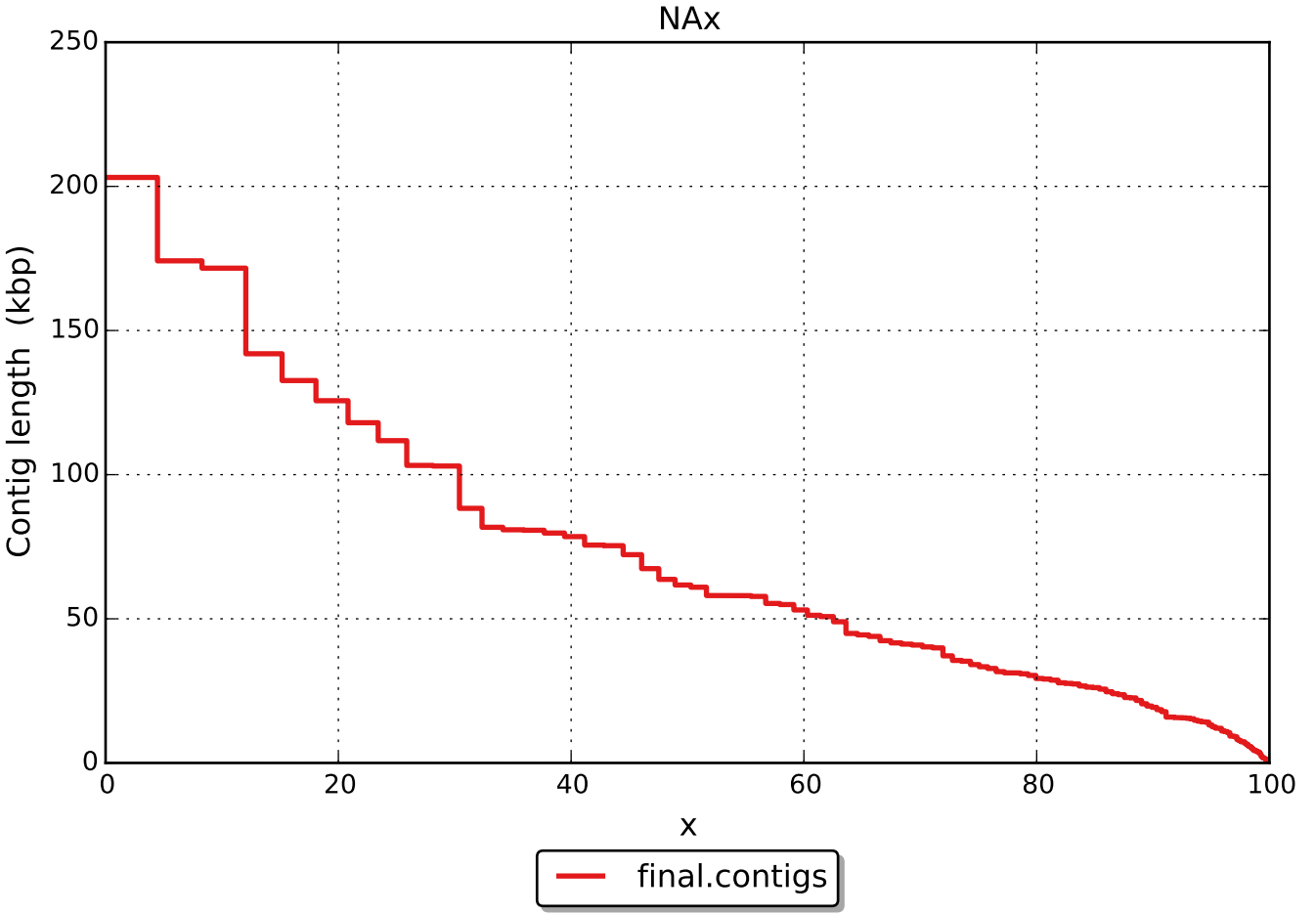

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

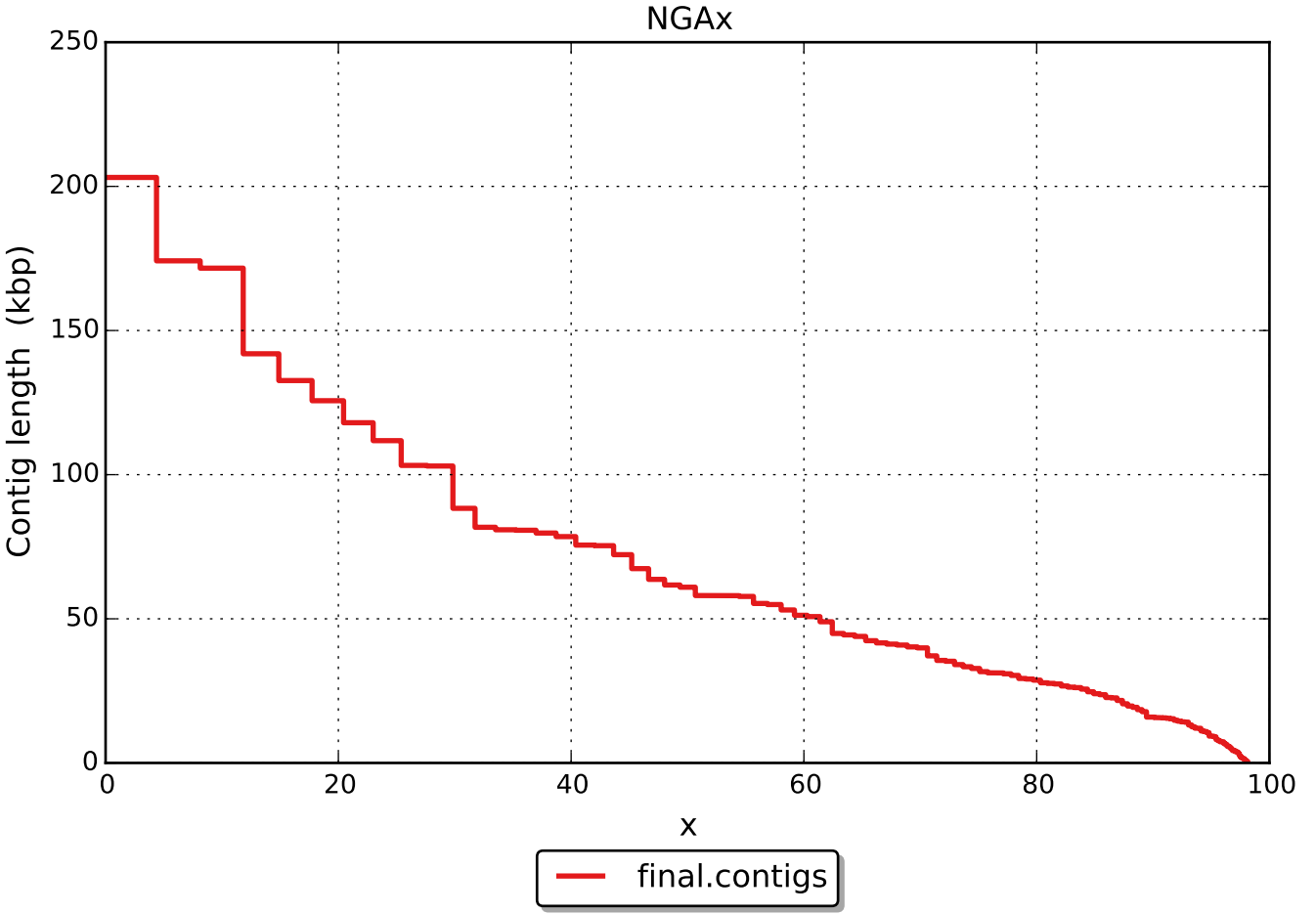

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


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


Misassemblies
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
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