Report

	final.contigs
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4556211
Total length (>= 5000 bp)	4500478
Total length (>= 10000 bp)	4464670
Total length (>= 25000 bp)	4273726
Total length (>= 50000 bp)	3539504
# contigs	109
Largest contig	327149
Total length	4565727
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	112525
NG50	112525
N75	54942
NG75	53828
L50	14
LG50	14
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.314
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.36
# indels per 100 kbp	9.97
Largest alignment	327149
NA50	112525
NGA50	112525
NA75	54942
NGA75	53828
LA50	14
LGA50	14
LA75	29
LGA75	30

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

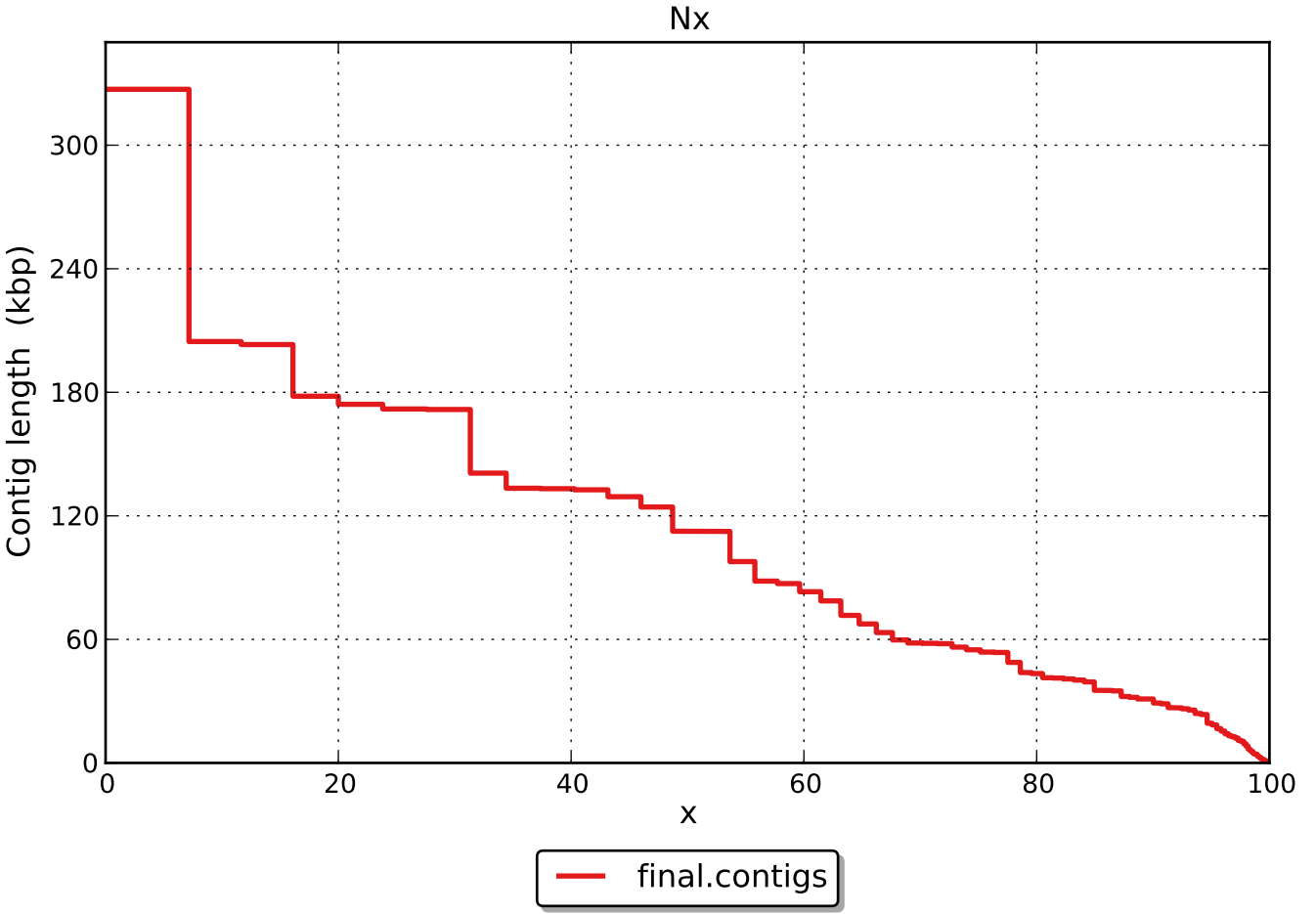
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# mismatches	2663
# indels	455
# short indels	455
# long indels	0
Indels length	623

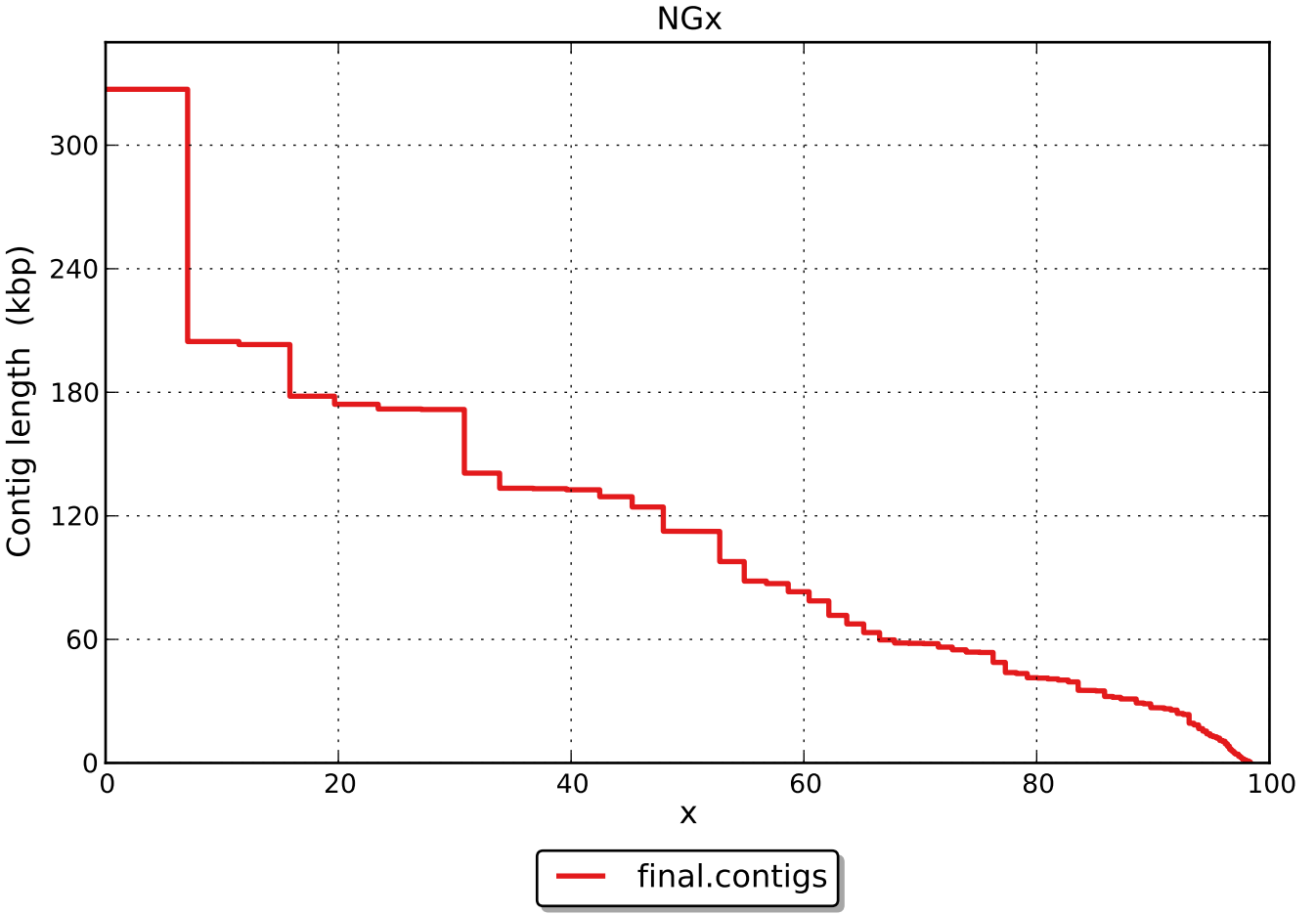
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

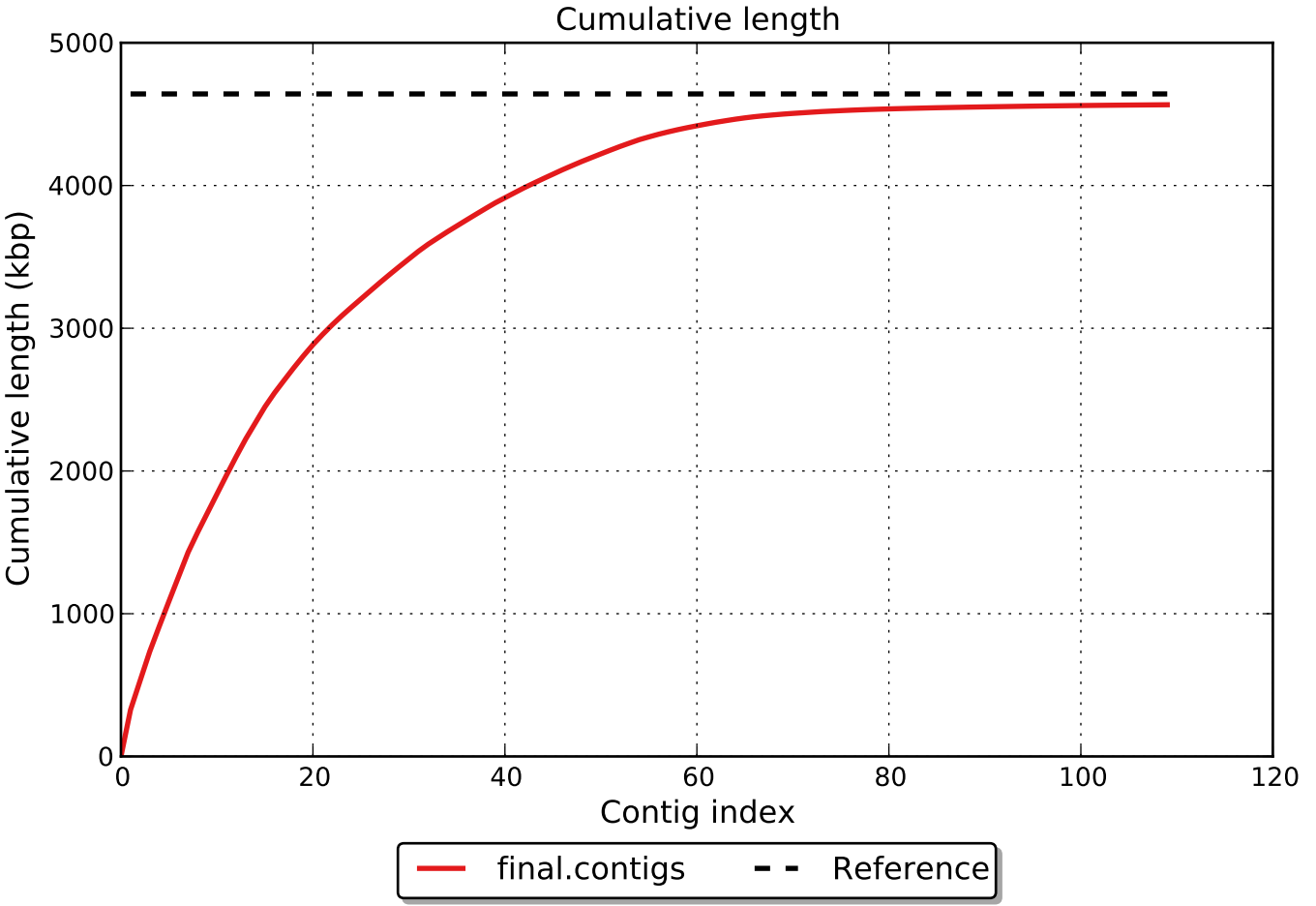
Unaligned report

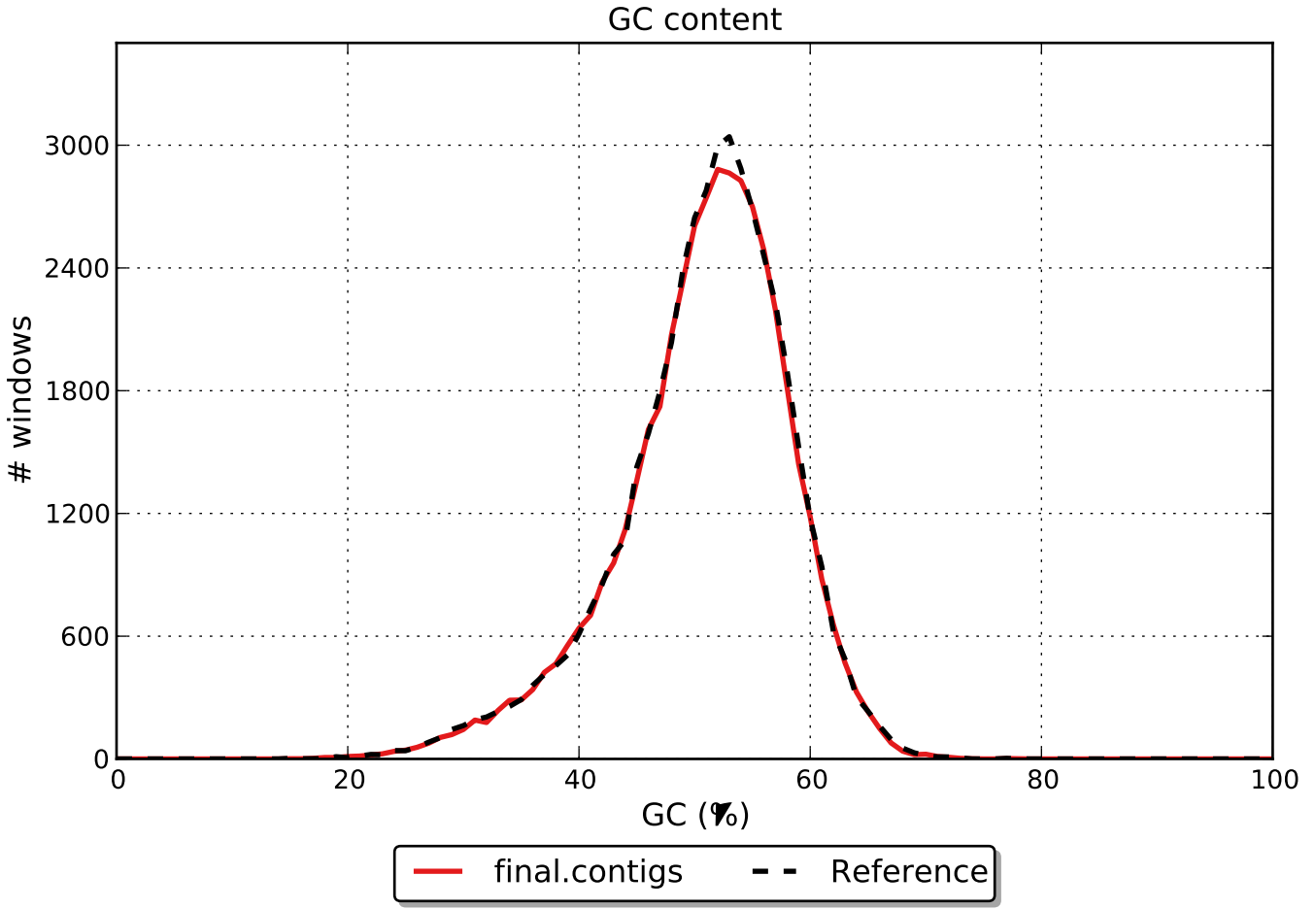
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

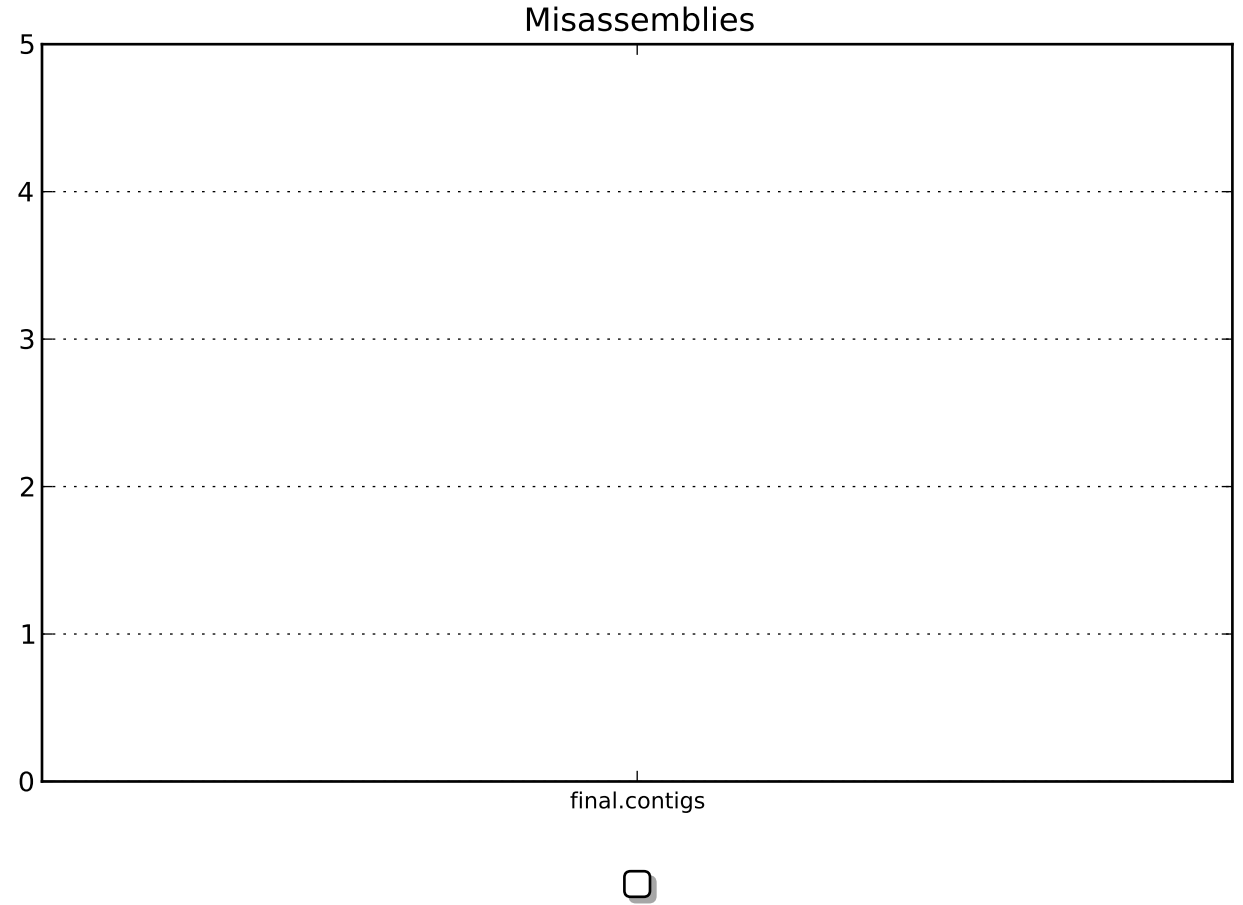
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

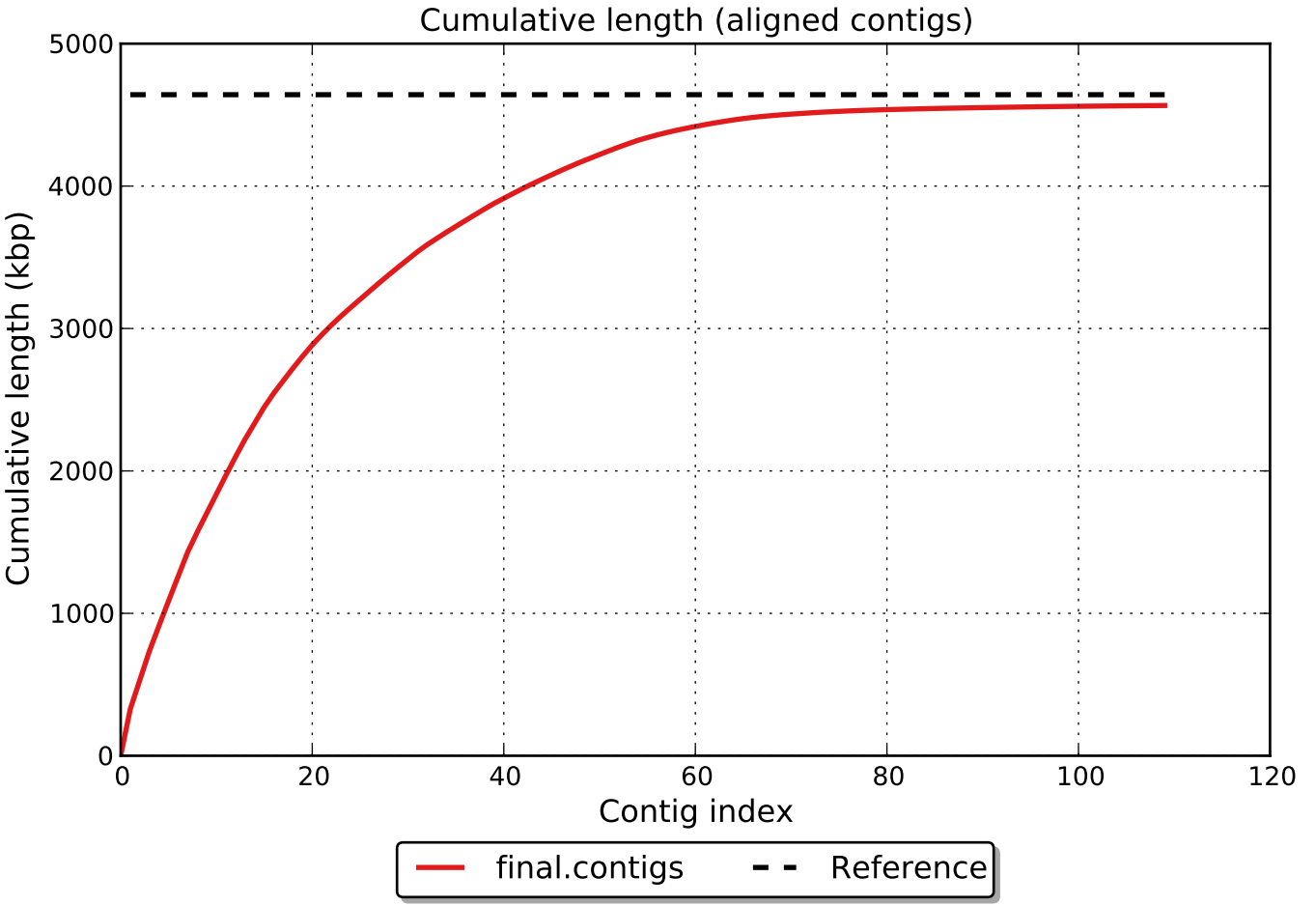

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

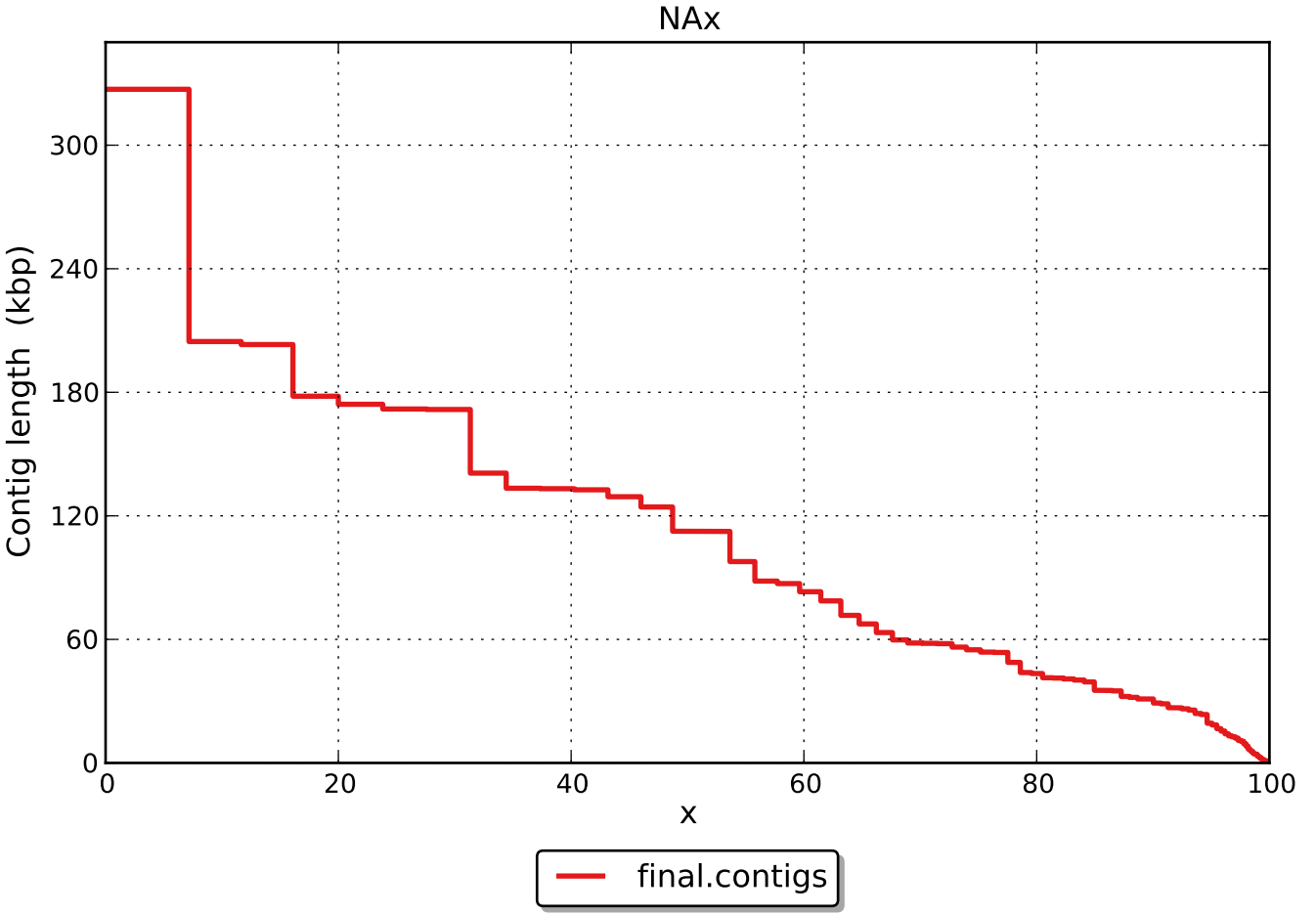

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

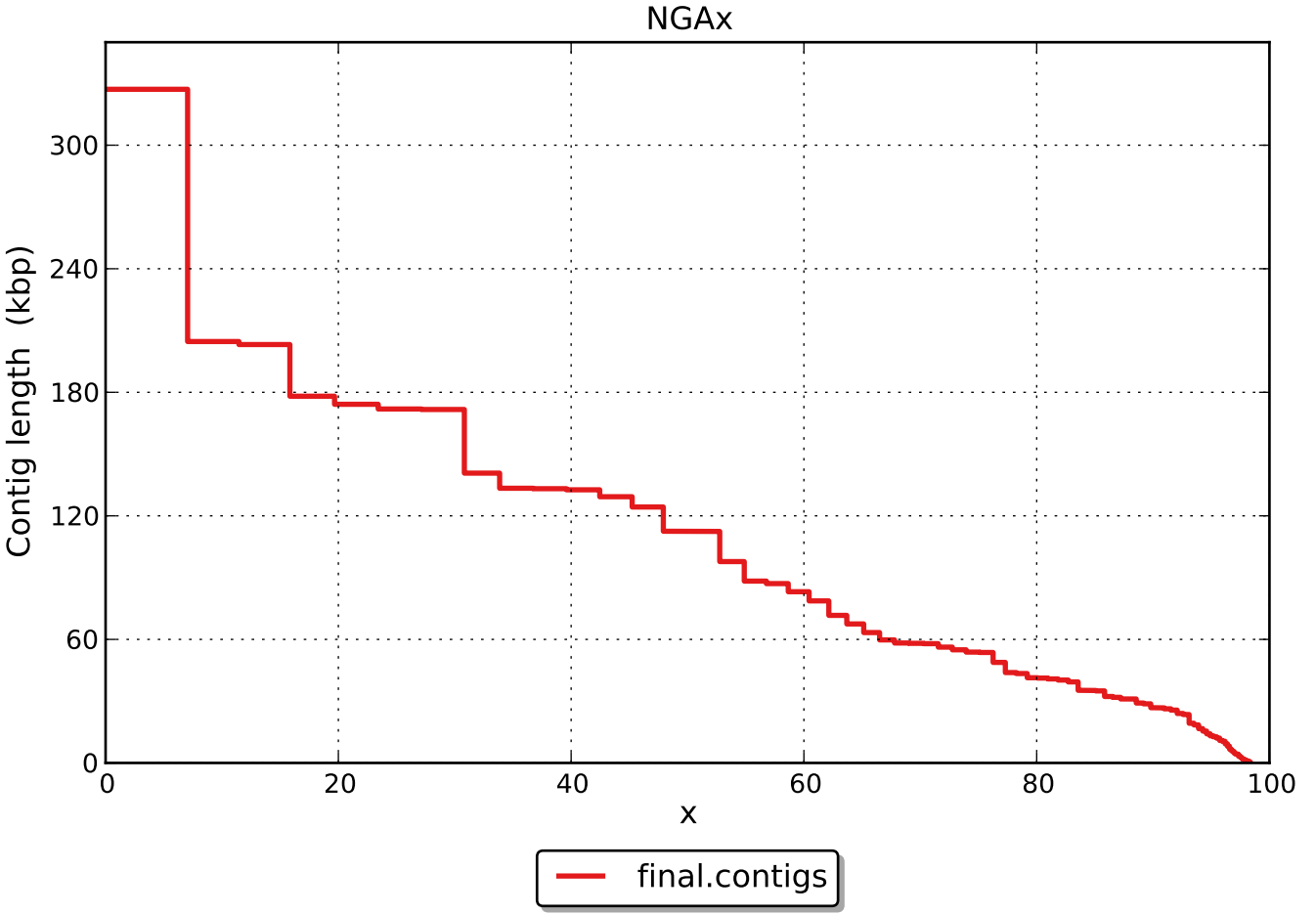

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
final.contigs
Reference


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
20
40
60
80
100
120
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs