Report

	final.contigs
# contigs (>= 1000 bp)	93
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4553503
Total length (>= 5000 bp)	4499364
Total length (>= 10000 bp)	4455804
Total length (>= 25000 bp)	4260057
Total length (>= 50000 bp)	3609437
# contigs	109
Largest contig	327151
Total length	4564765
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	112430
NG50	112430
N75	58008
NG75	54946
L50	13
LG50	13
L75	27
LG75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	14
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.276
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.78
# indels per 100 kbp	0.15
Largest alignment	327151
NA50	112430
NGA50	112430
NA75	58008
NGA75	54946
LA50	13
LGA50	13
LA75	27
LGA75	28

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

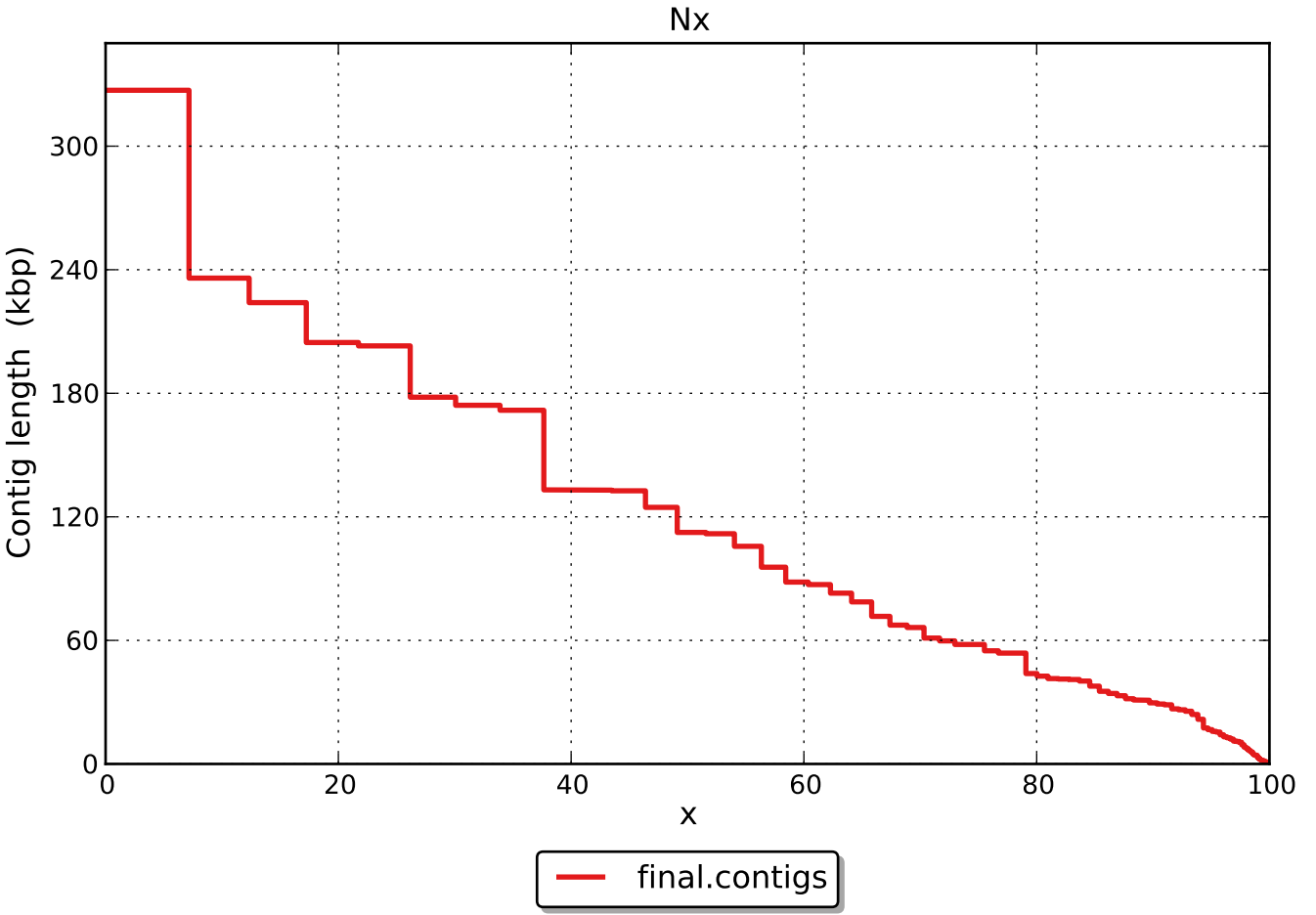
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	14
# mismatches	127
# indels	7
# short indels	6
# long indels	1
Indels length	92

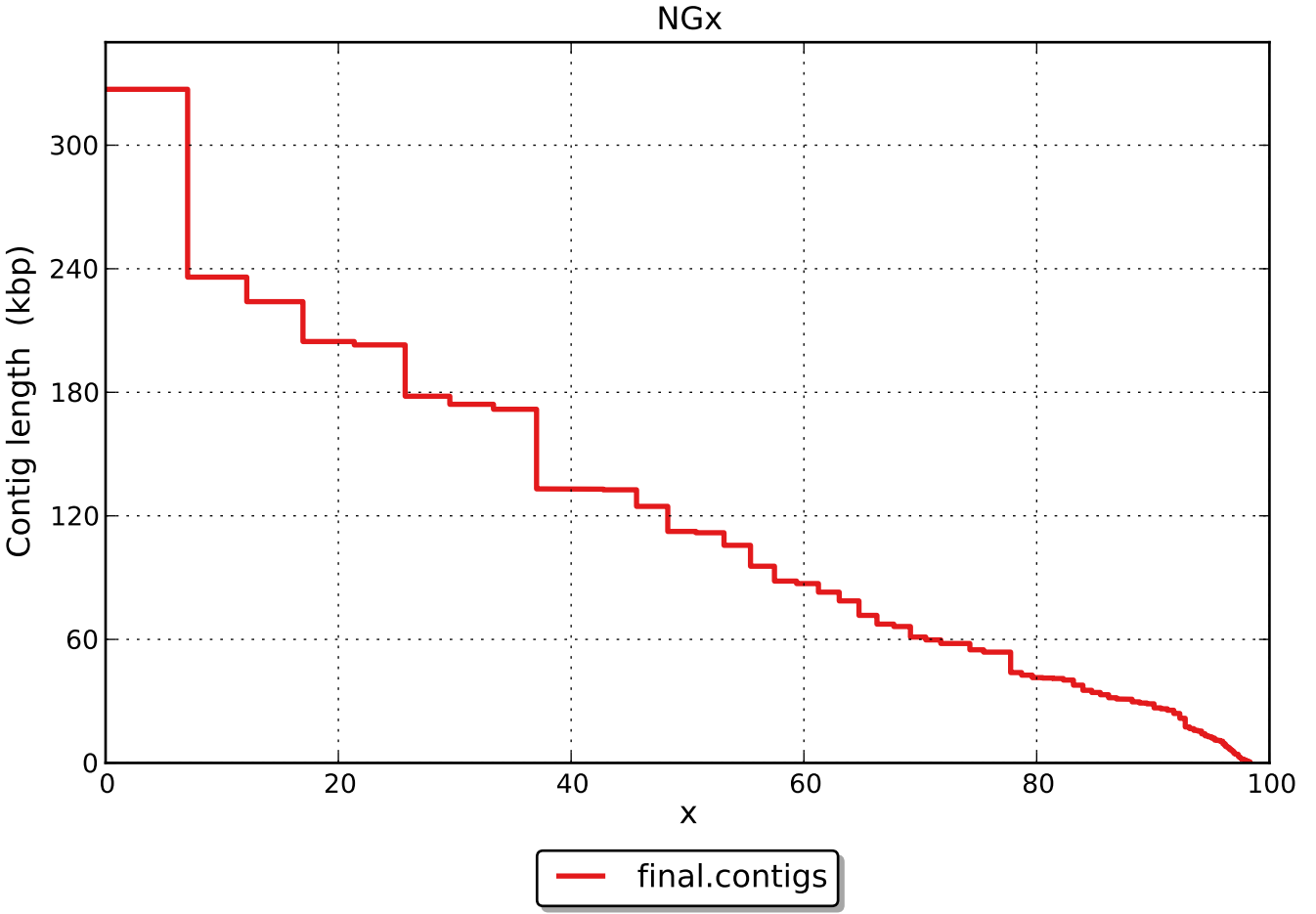
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

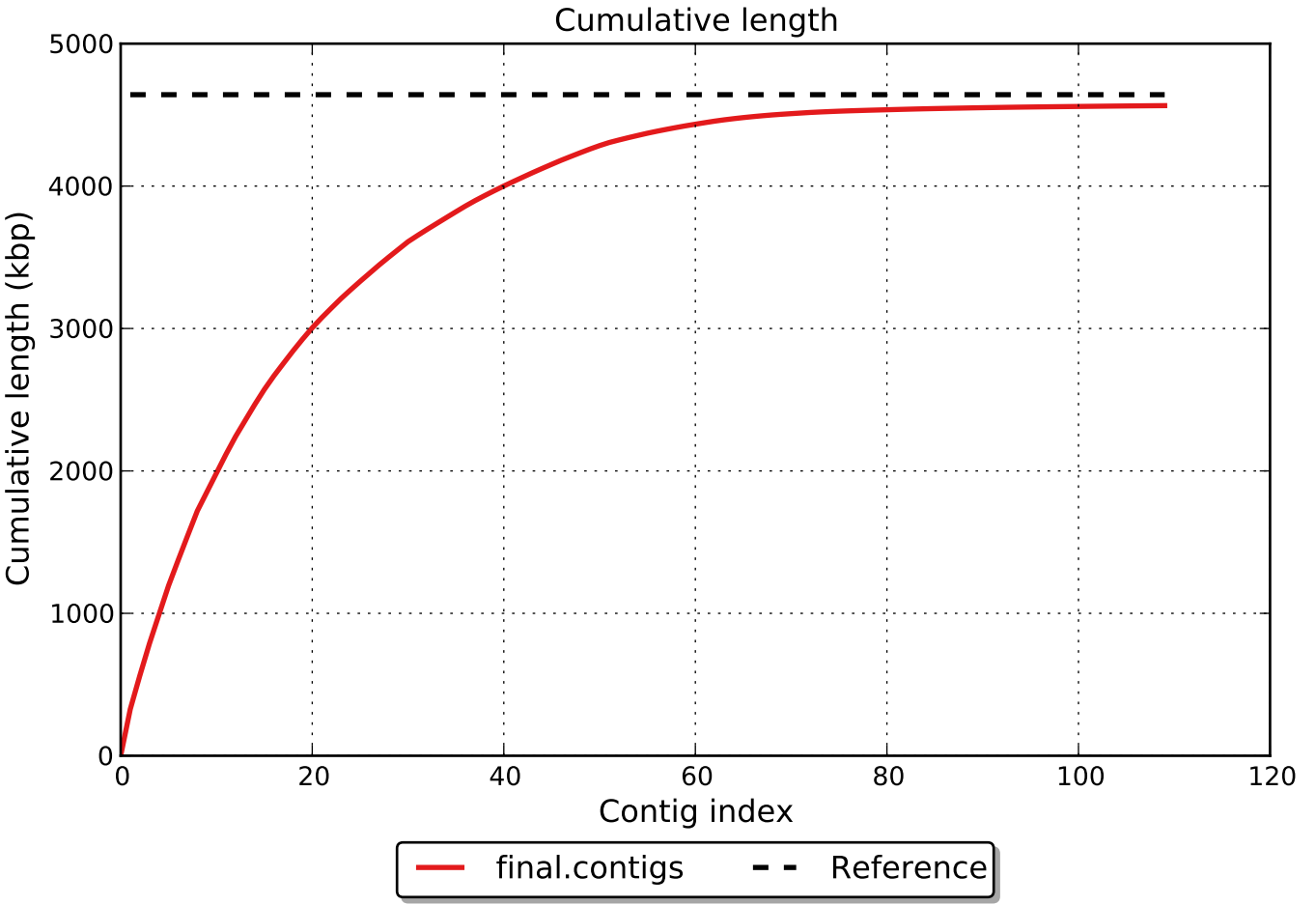
Unaligned report

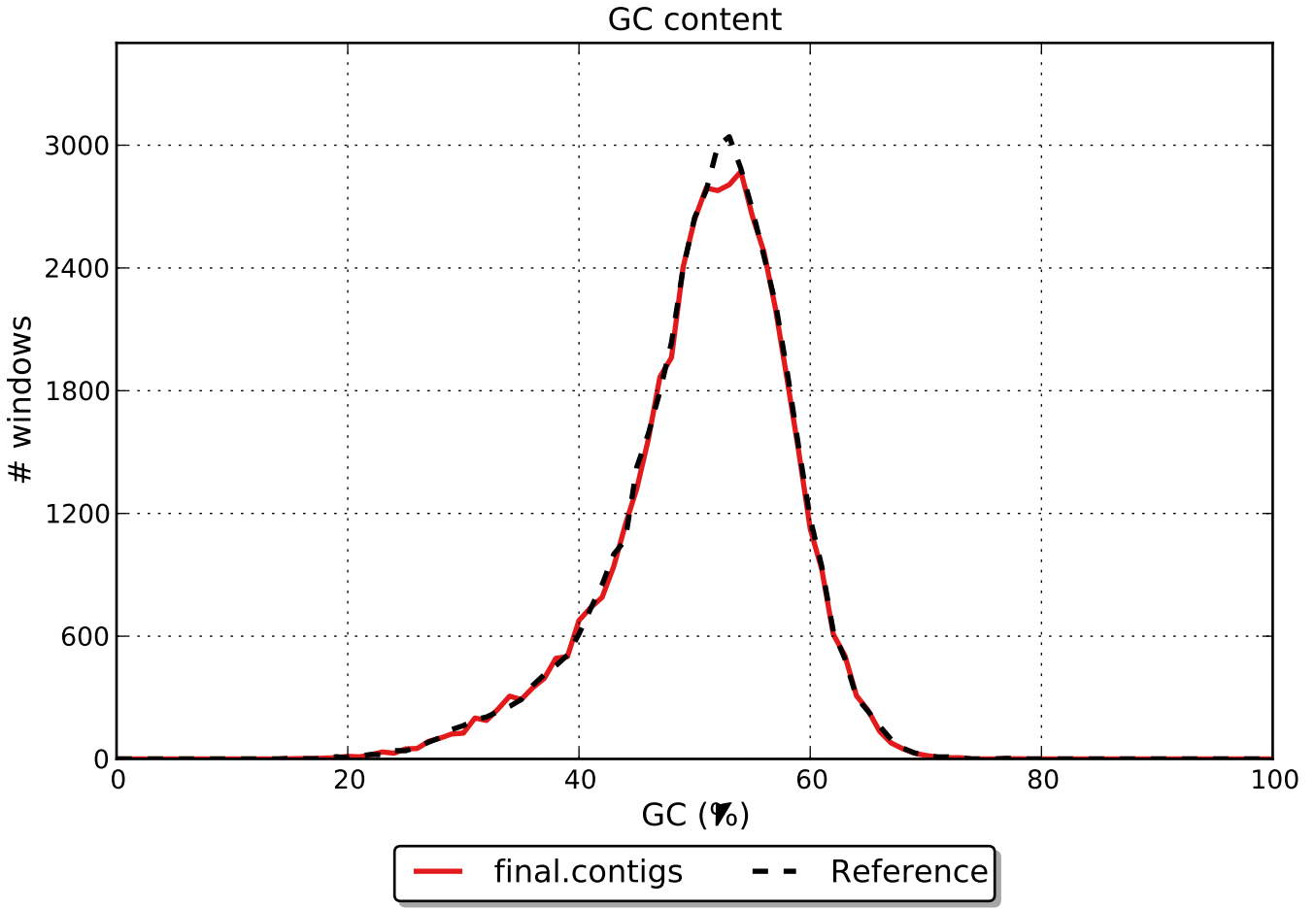
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

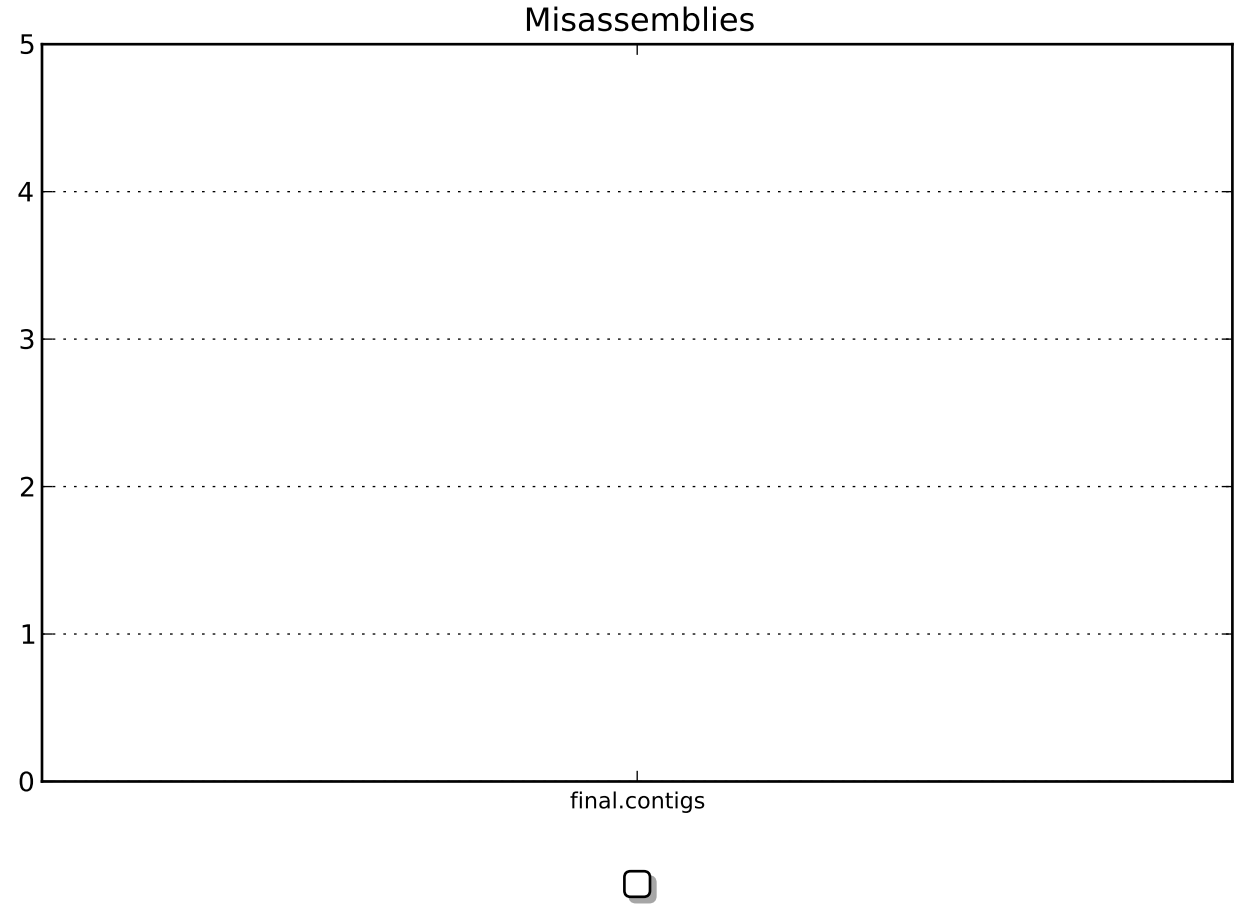
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

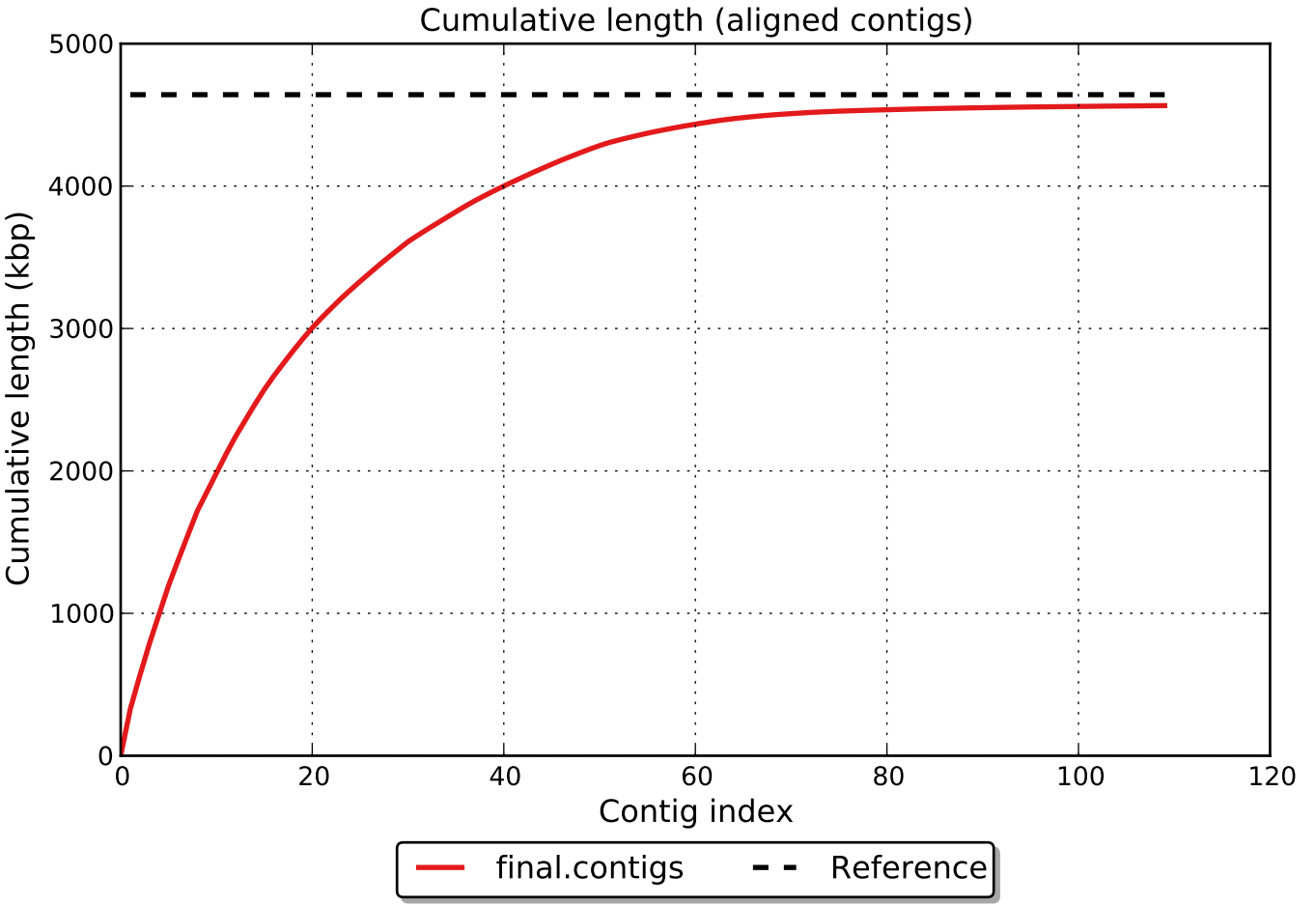

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

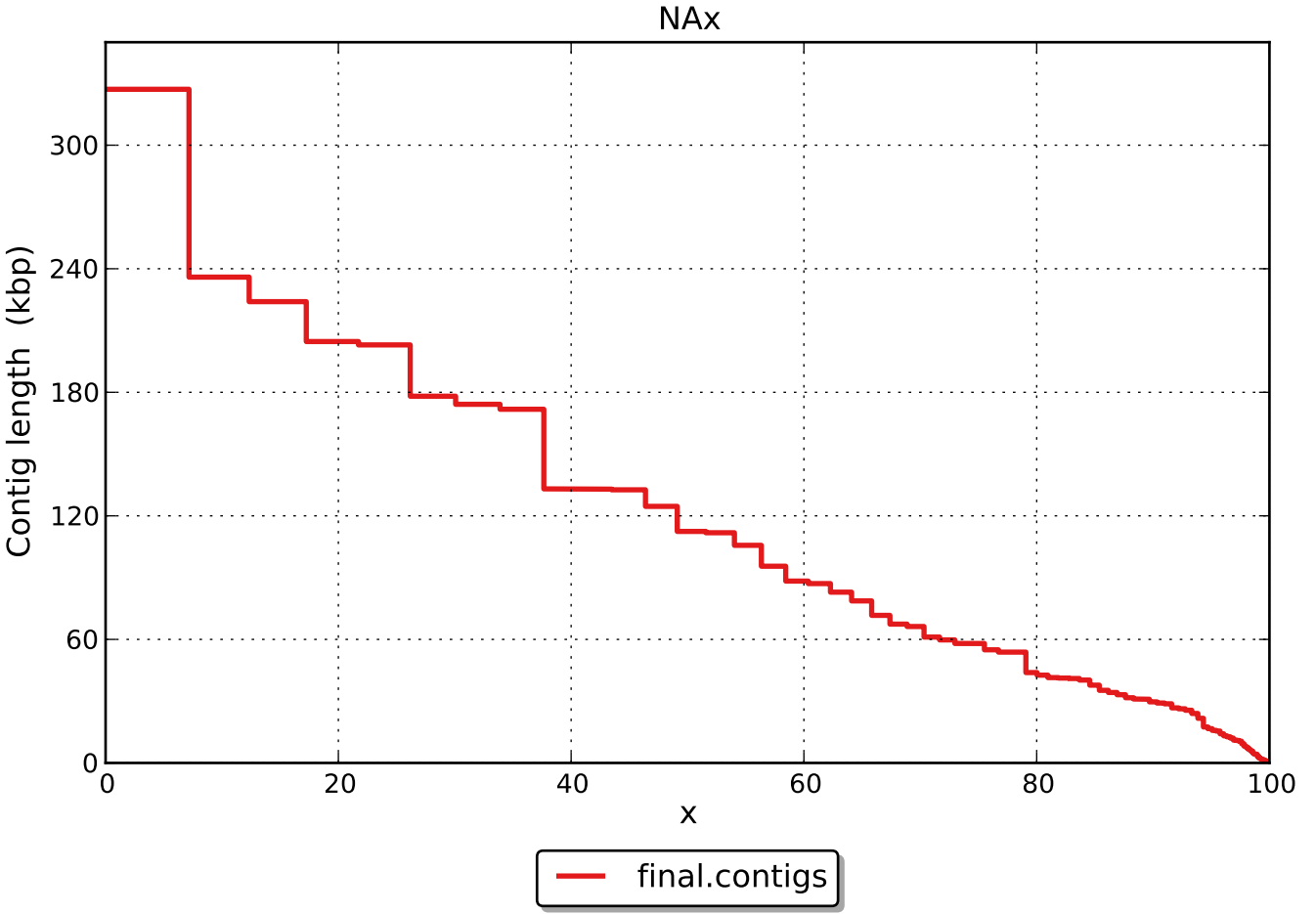

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

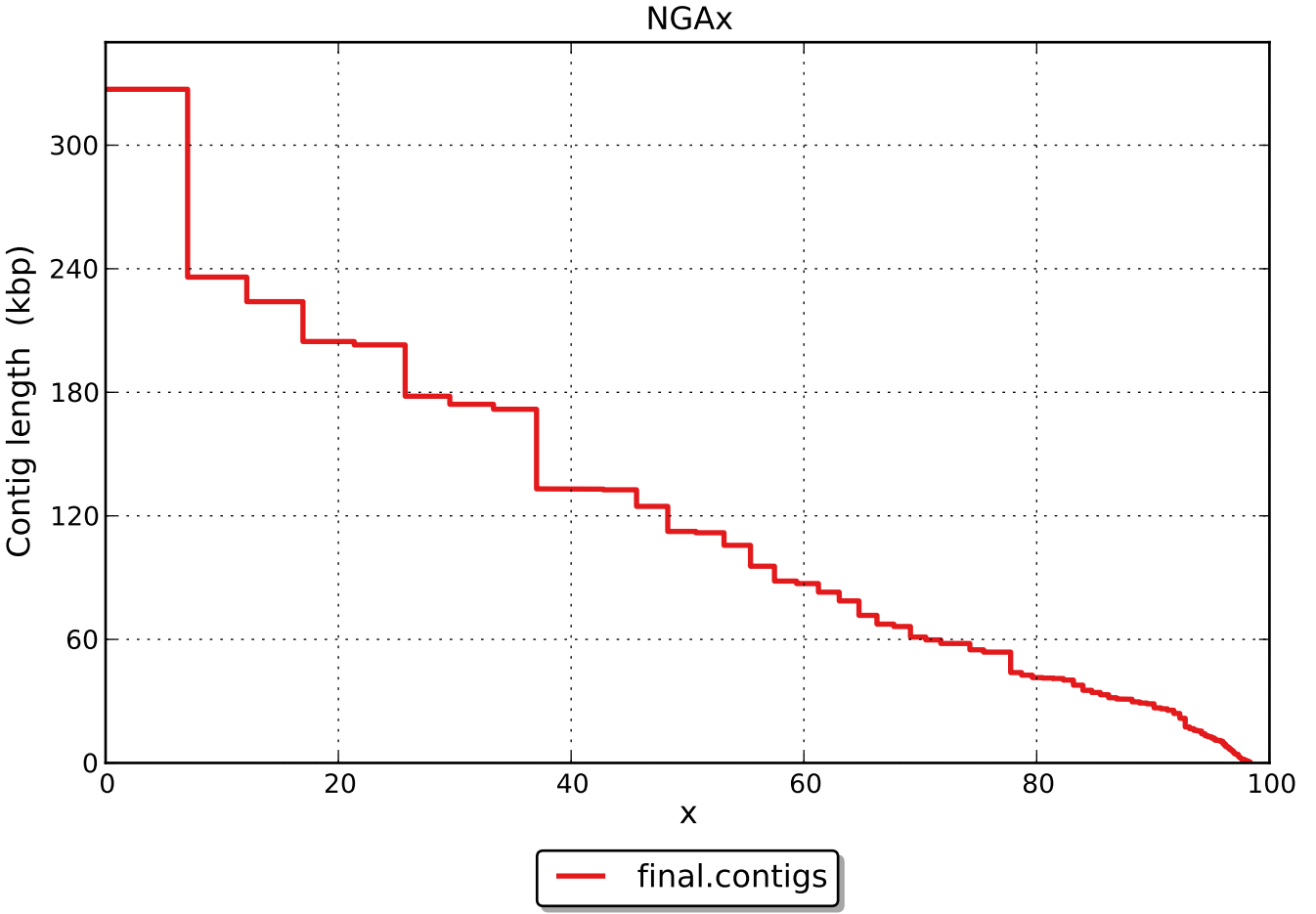

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
final.contigs
Reference


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