Report

	final.contigs
# contigs (>= 1000 bp)	223
# contigs (>= 5000 bp)	182
# contigs (>= 10000 bp)	139
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	21
Total length (>= 1000 bp)	4652256
Total length (>= 5000 bp)	4525703
Total length (>= 10000 bp)	4195118
Total length (>= 25000 bp)	2985022
Total length (>= 50000 bp)	1399011
# contigs	233
Largest contig	107366
Total length	4660155
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	34788
NG50	34788
N75	19366
NG75	19389
L50	44
LG50	44
L75	90
LG75	89
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.980
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	107366
NA50	34788
NGA50	34788
NA75	19366
NGA75	19389
LA50	44
LGA50	44
LA75	90
LGA75	89

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

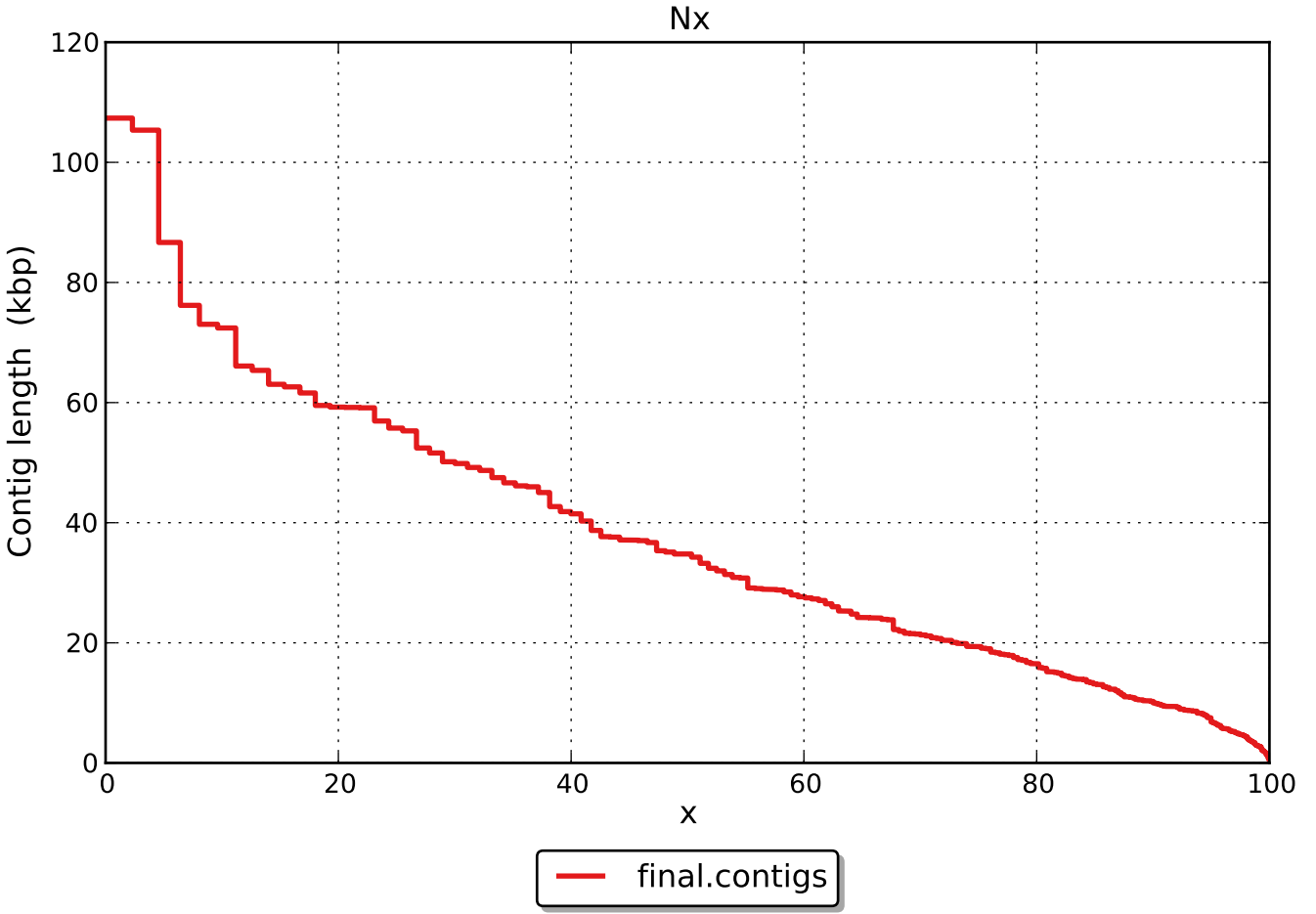
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

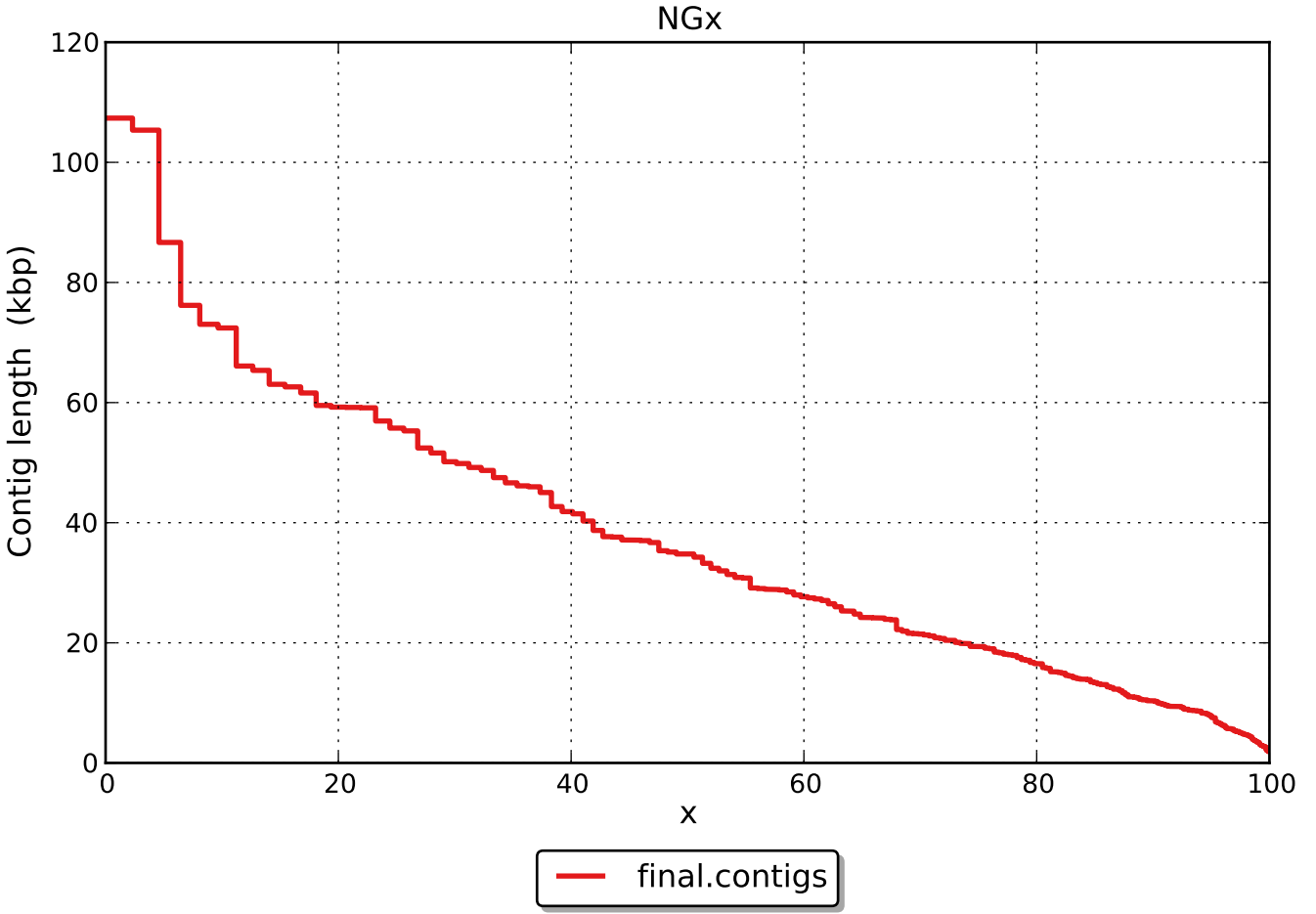
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

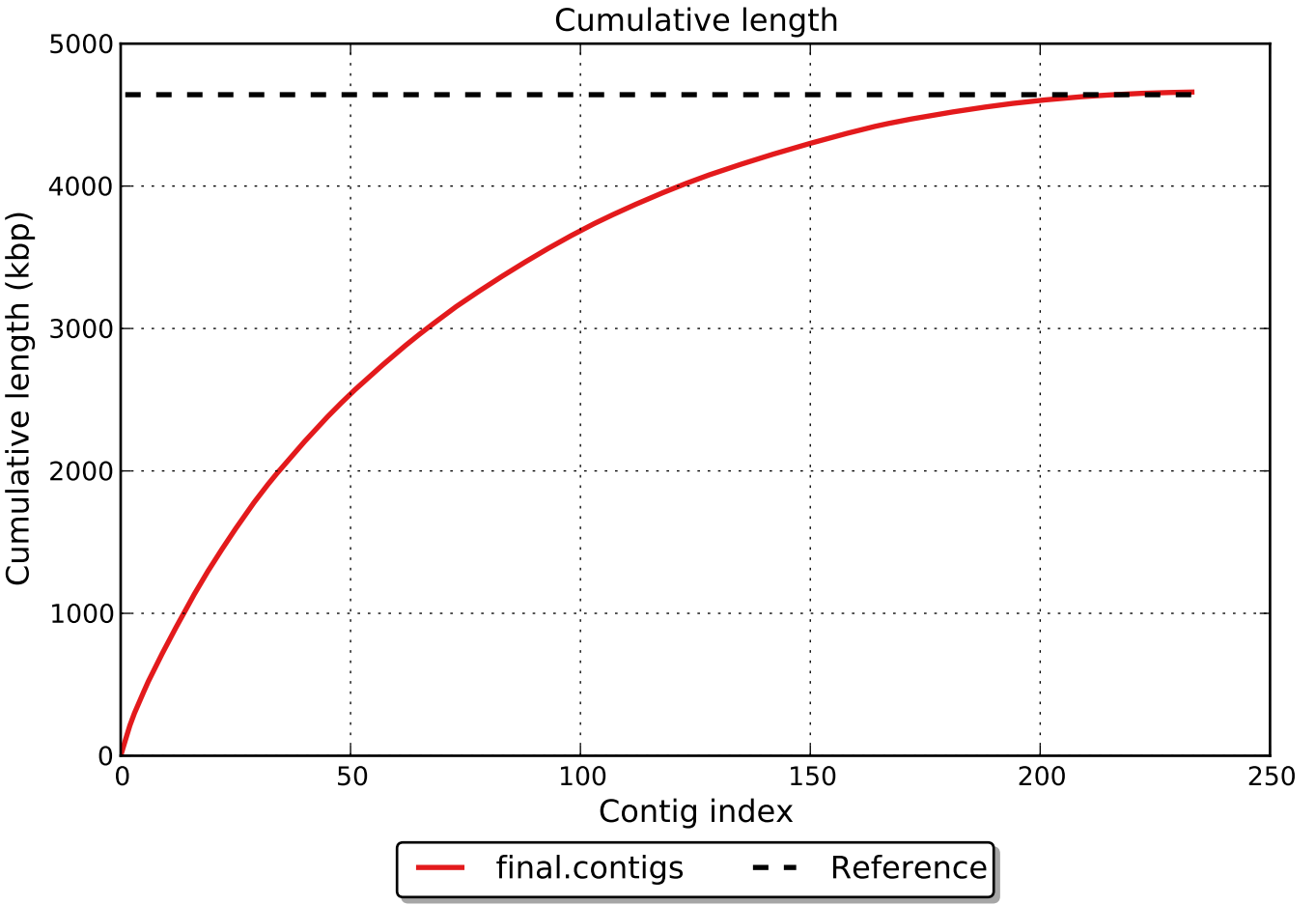
Unaligned report

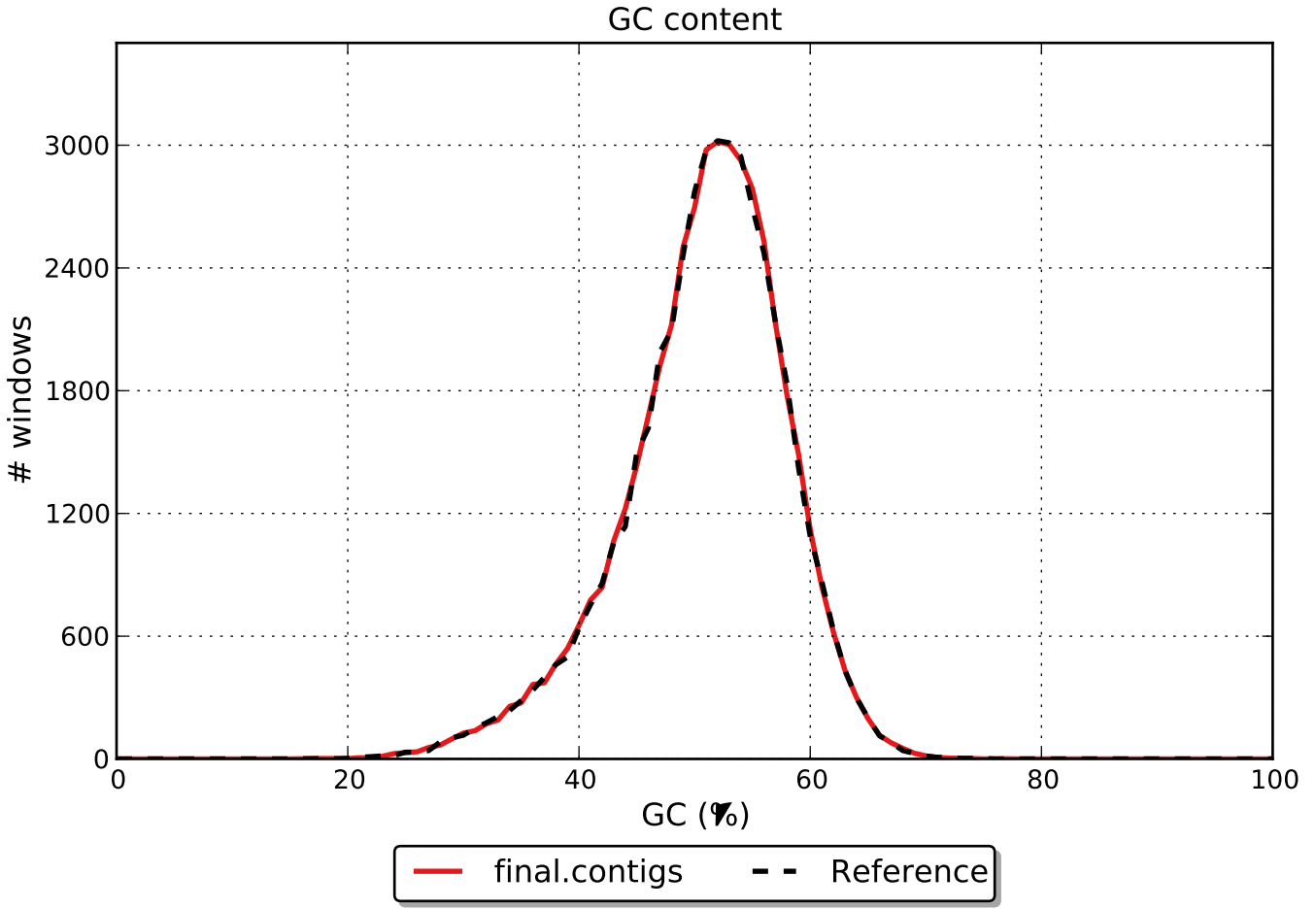
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

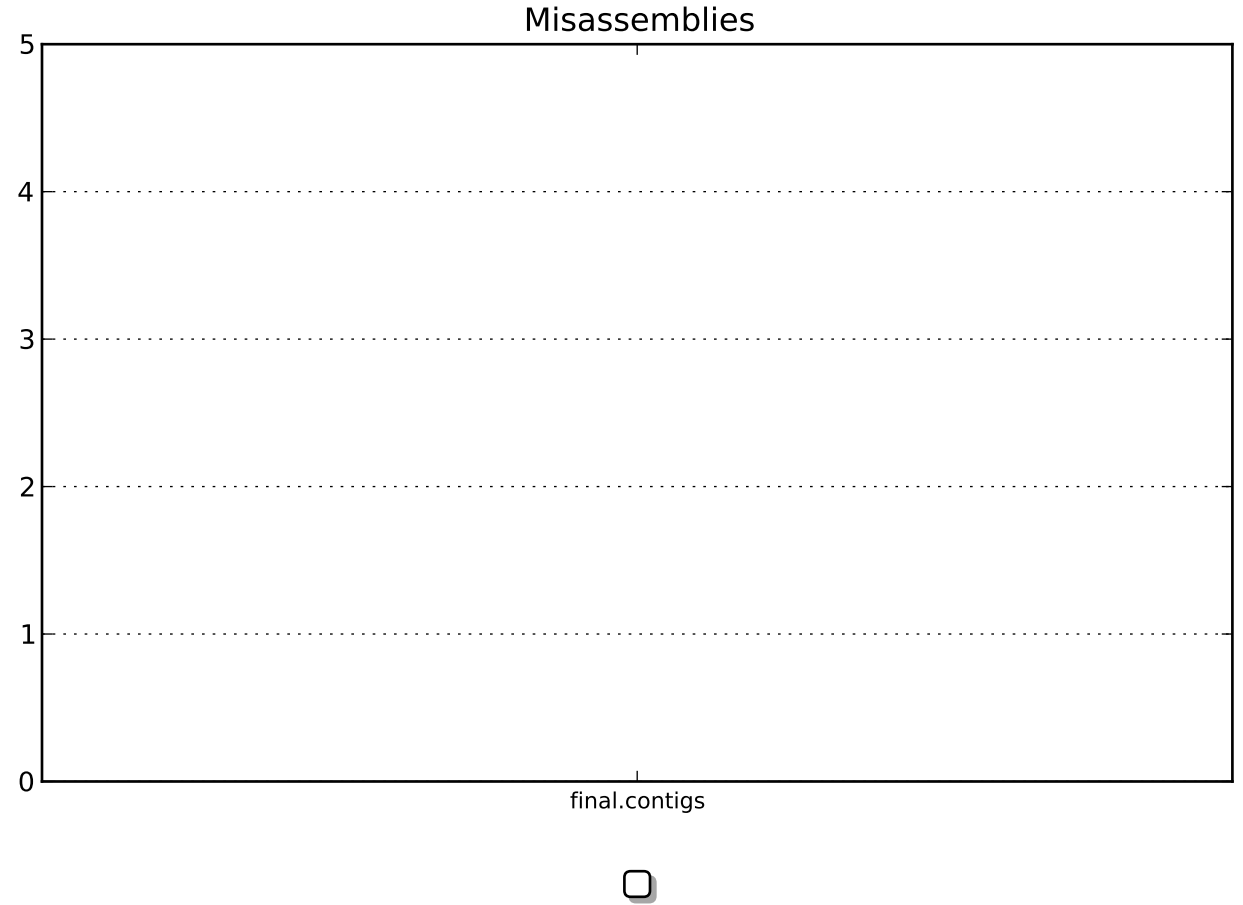
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

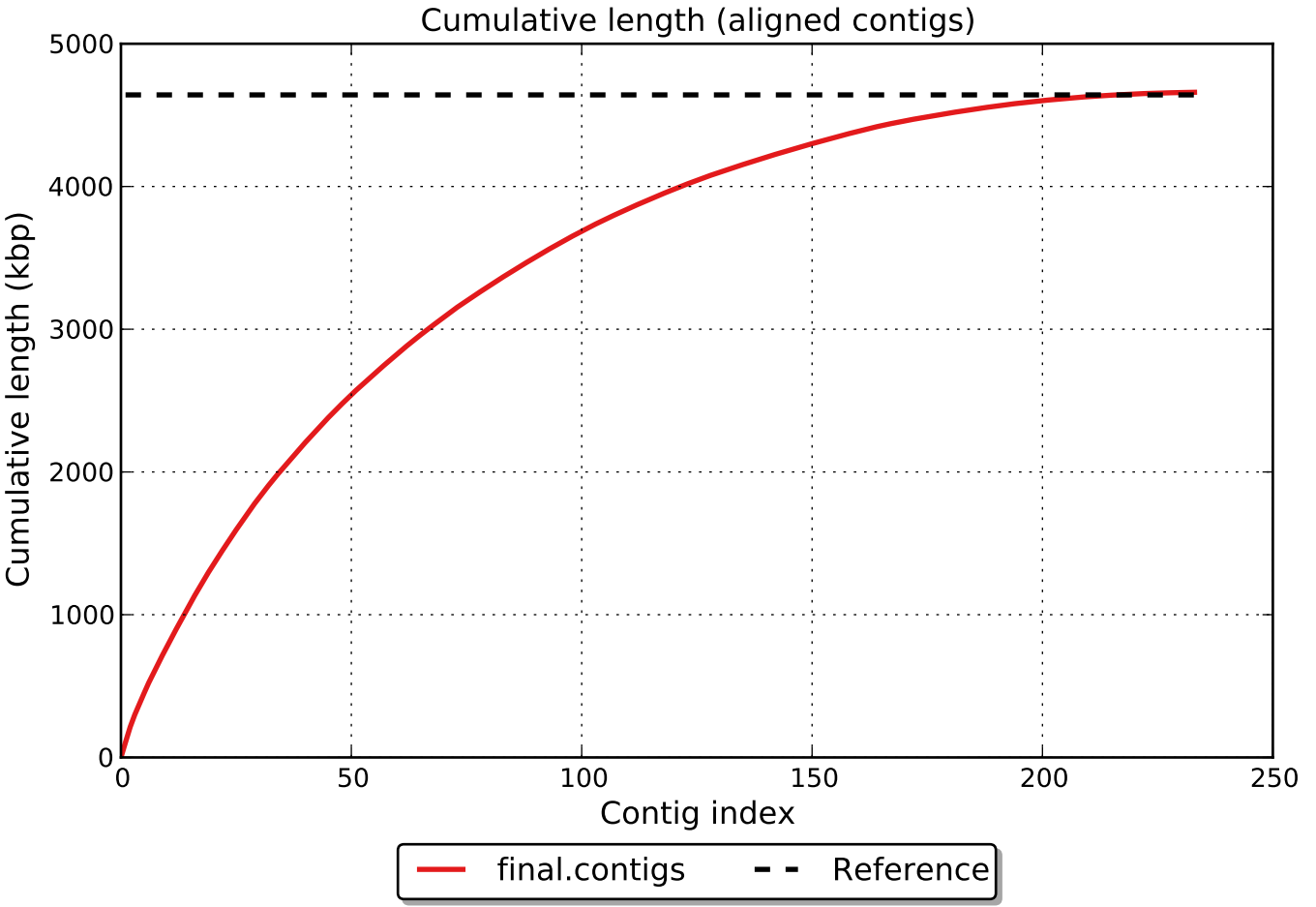

Nx
Contig length (kbp)
x
0
20
40
60
80
100
120
final.contigs

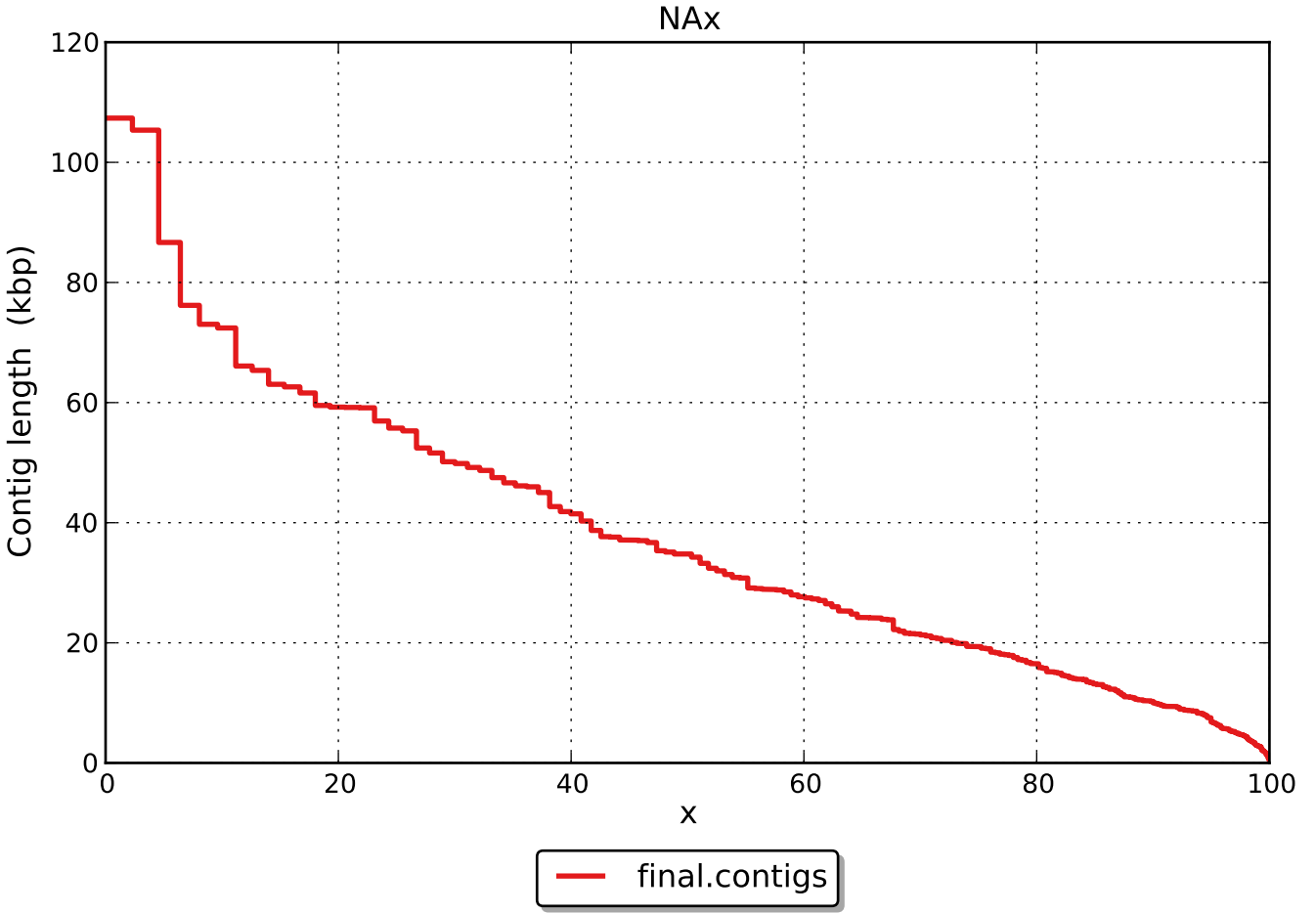

NGx
Contig length (kbp)
x
0
20
40
60
80
100
120
final.contigs

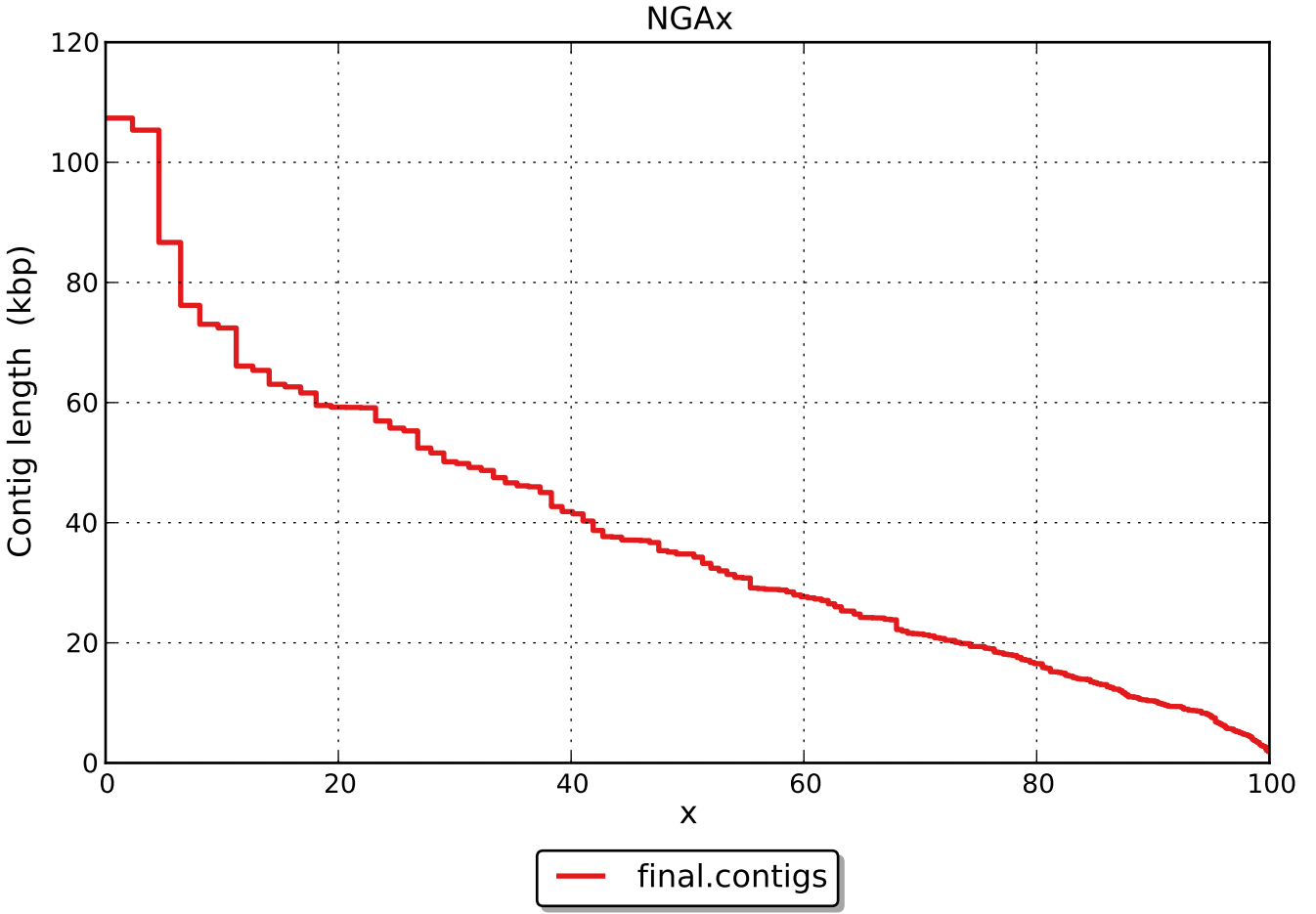

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
final.contigs
Reference


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


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