Report

	final.contigs
# contigs (>= 1000 bp)	212
# contigs (>= 5000 bp)	161
# contigs (>= 10000 bp)	134
# contigs (>= 25000 bp)	62
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4791897
Total length (>= 5000 bp)	4648522
Total length (>= 10000 bp)	4448060
Total length (>= 25000 bp)	3271305
Total length (>= 50000 bp)	2054723
# contigs	238
Largest contig	137613
Total length	4810531
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	42013
NG50	41846
N75	20553
NG75	20438
L50	35
LG50	36
L75	77
LG75	79
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.708
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.21
# indels per 100 kbp	0.00
Largest alignment	137613
NA50	42013
NGA50	41846
NA75	20553
NGA75	20438
LA50	35
LGA50	36
LA75	77
LGA75	79

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

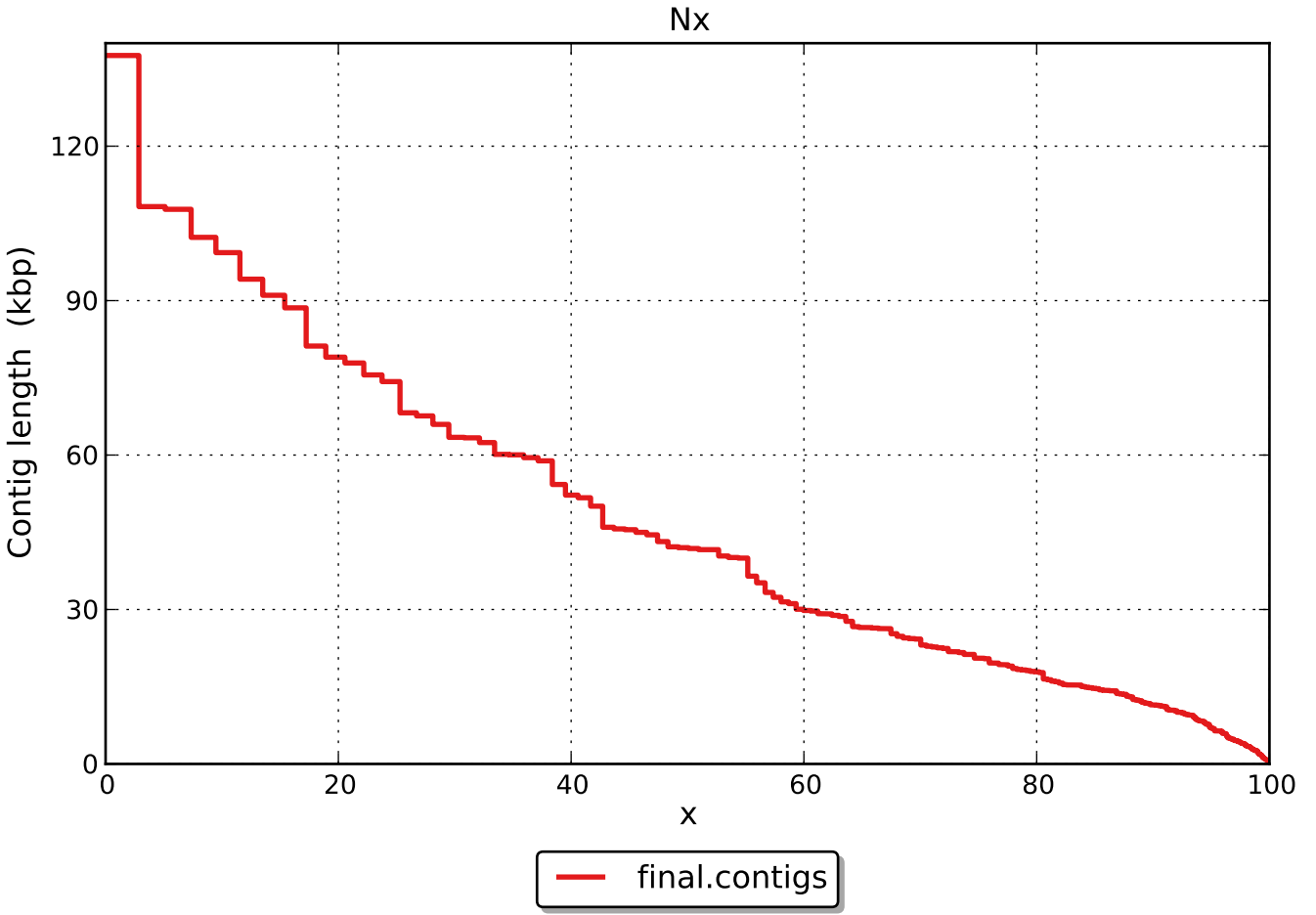
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	58
# indels	0
# short indels	0
# long indels	0
Indels length	0

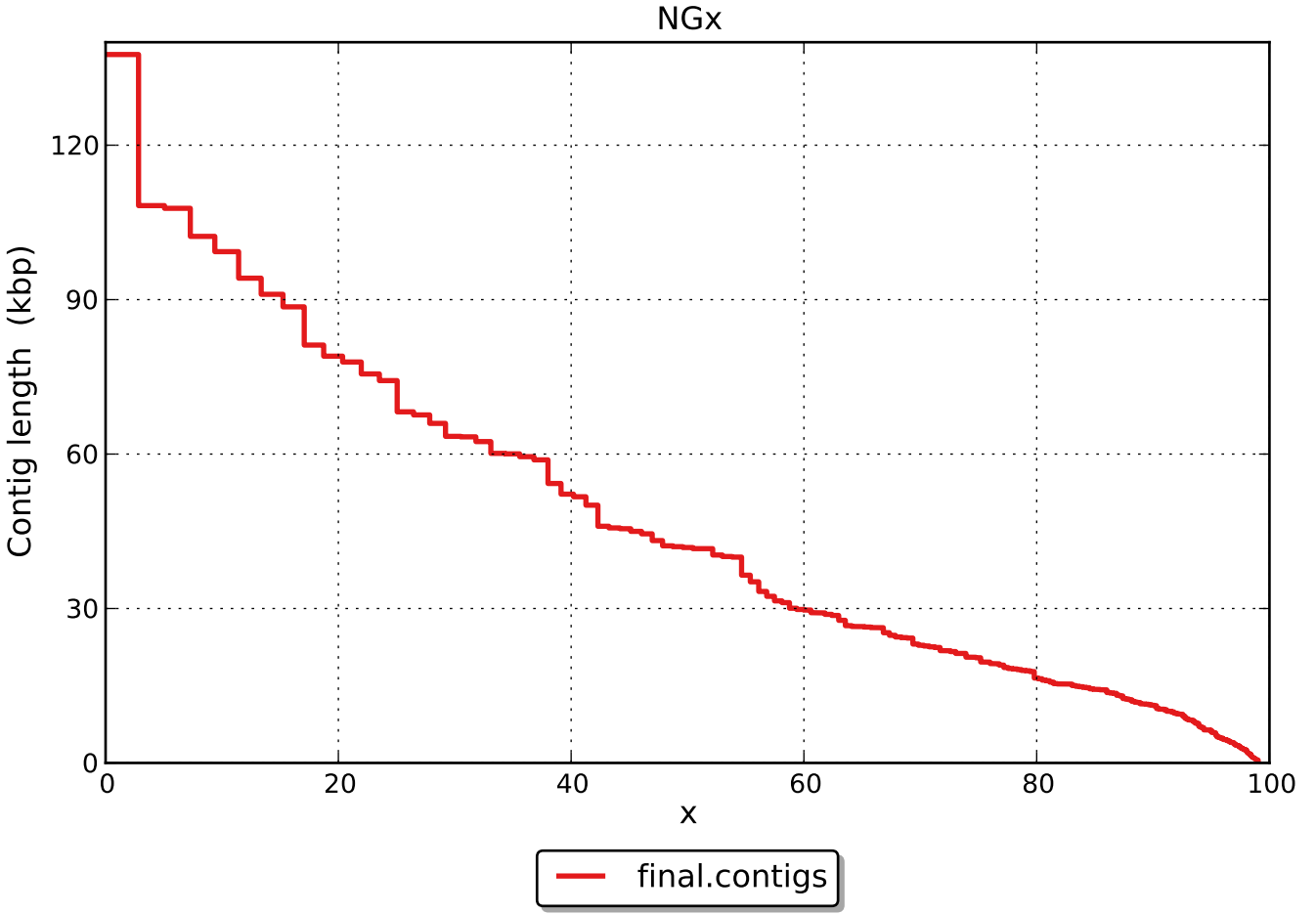
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

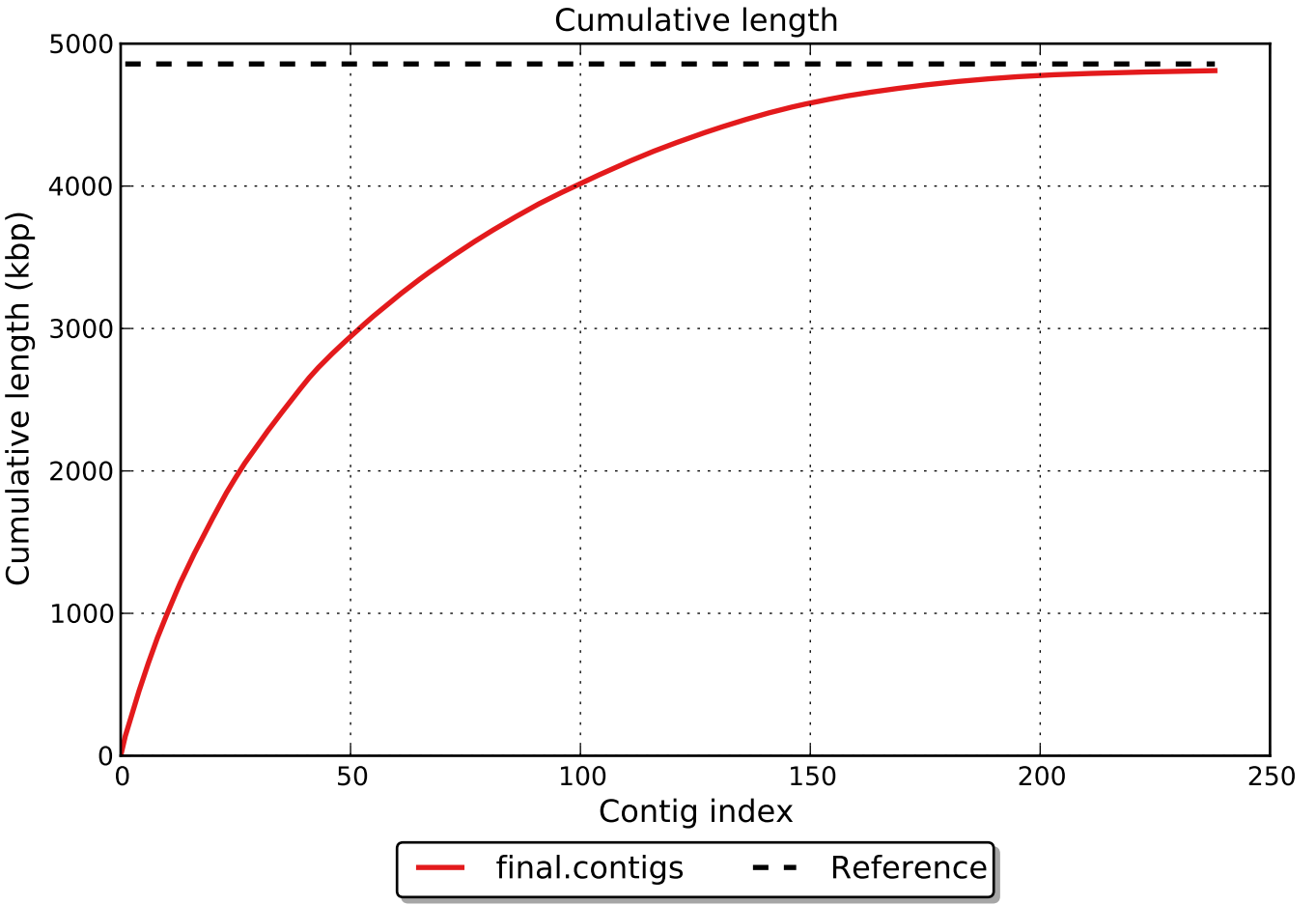
Unaligned report

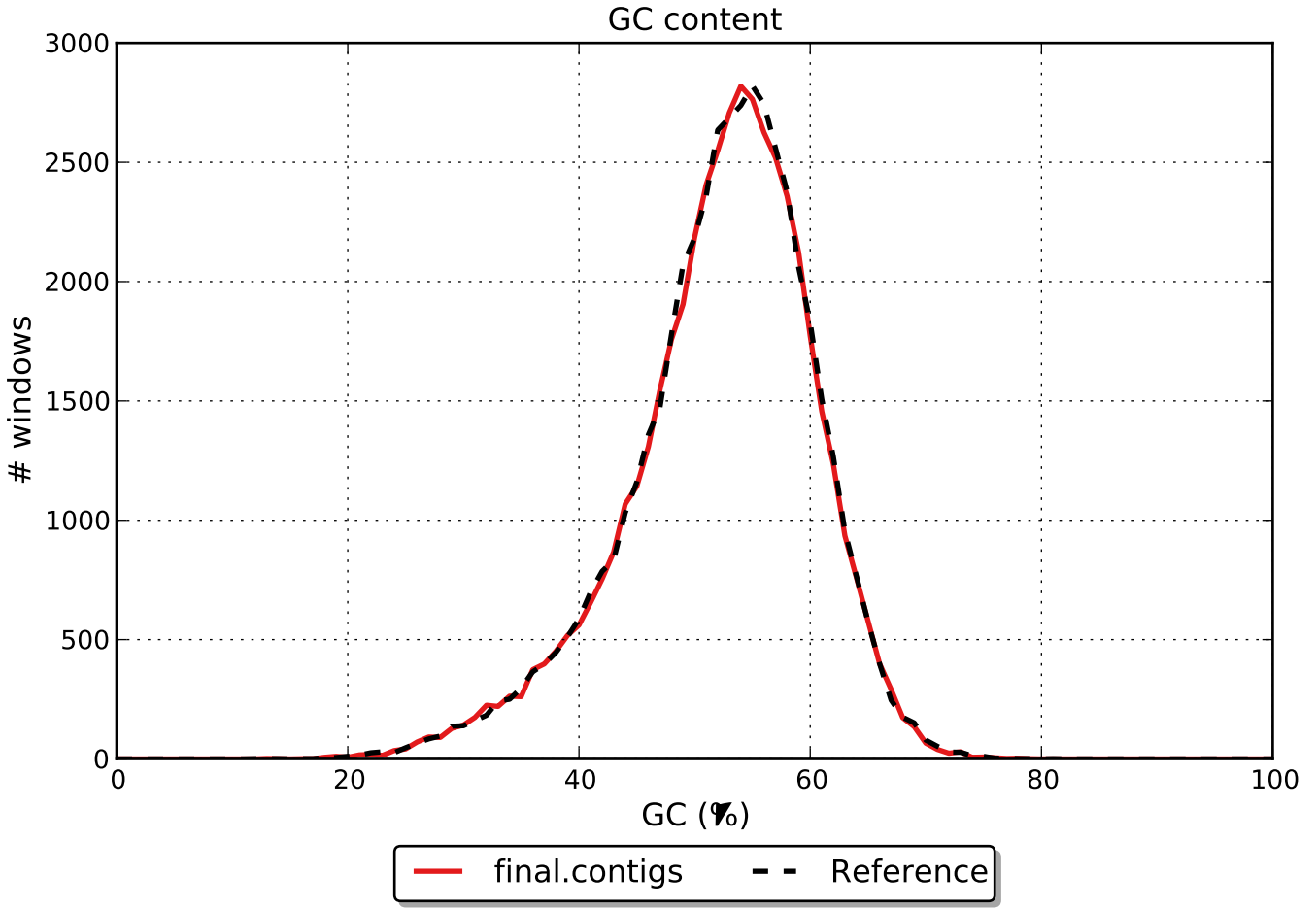
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

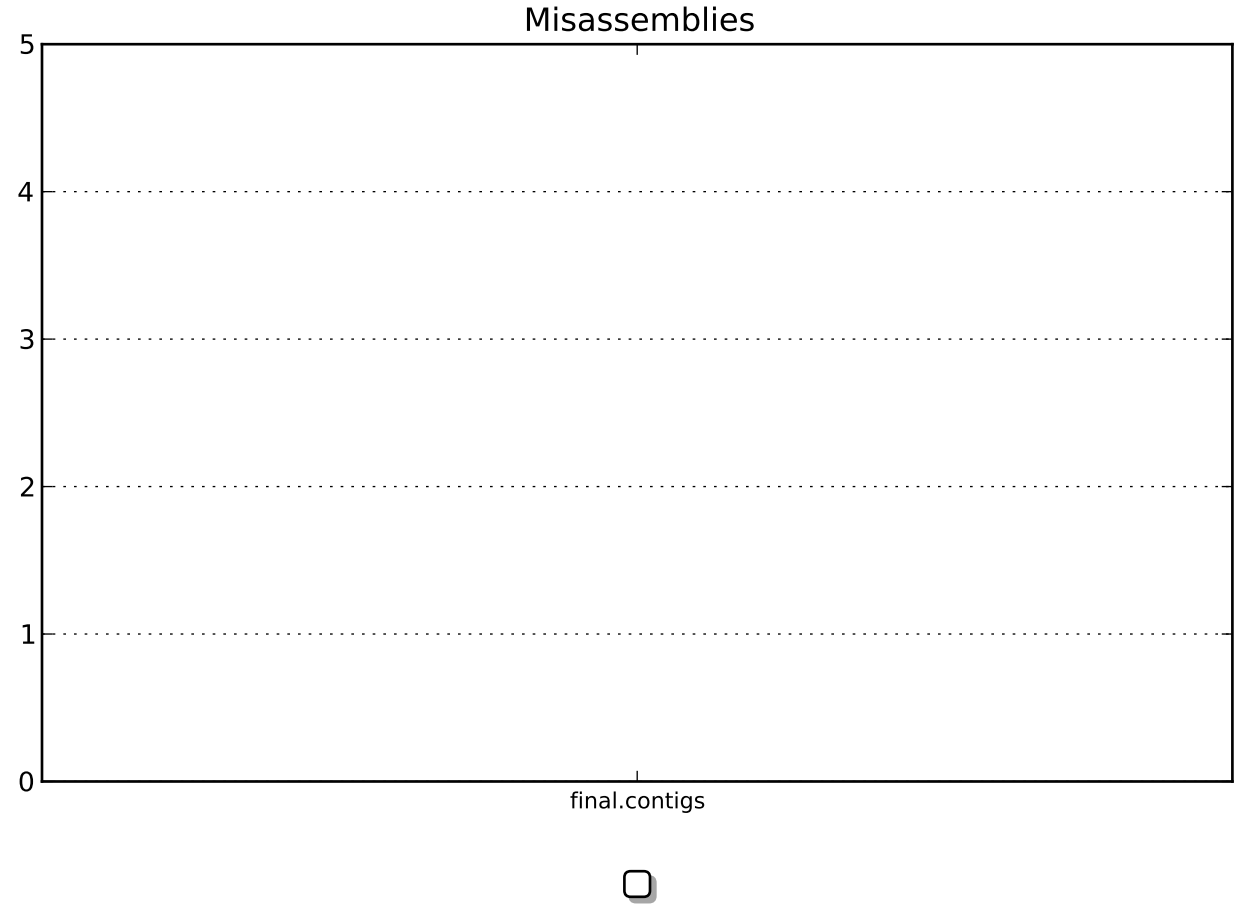
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

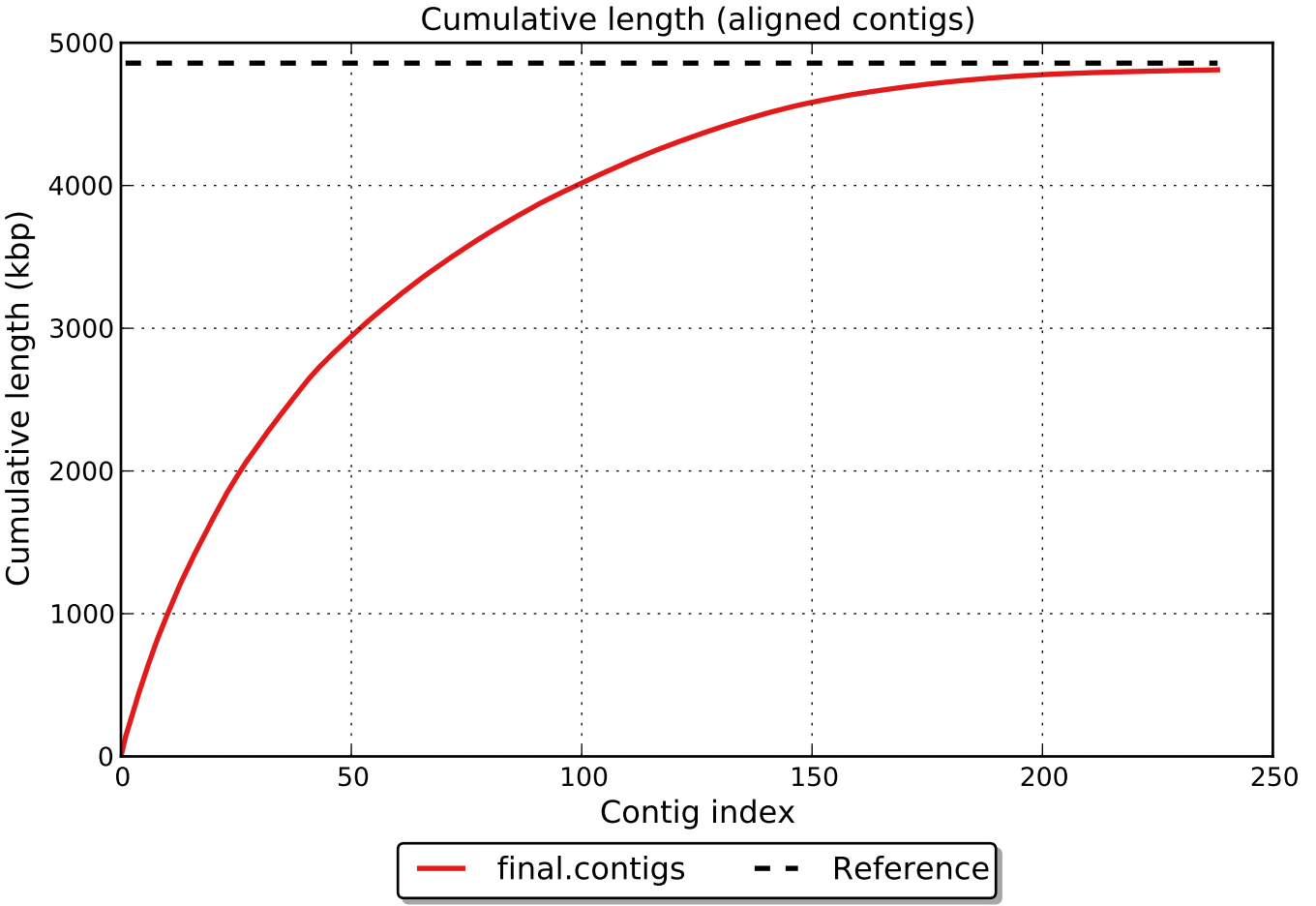

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

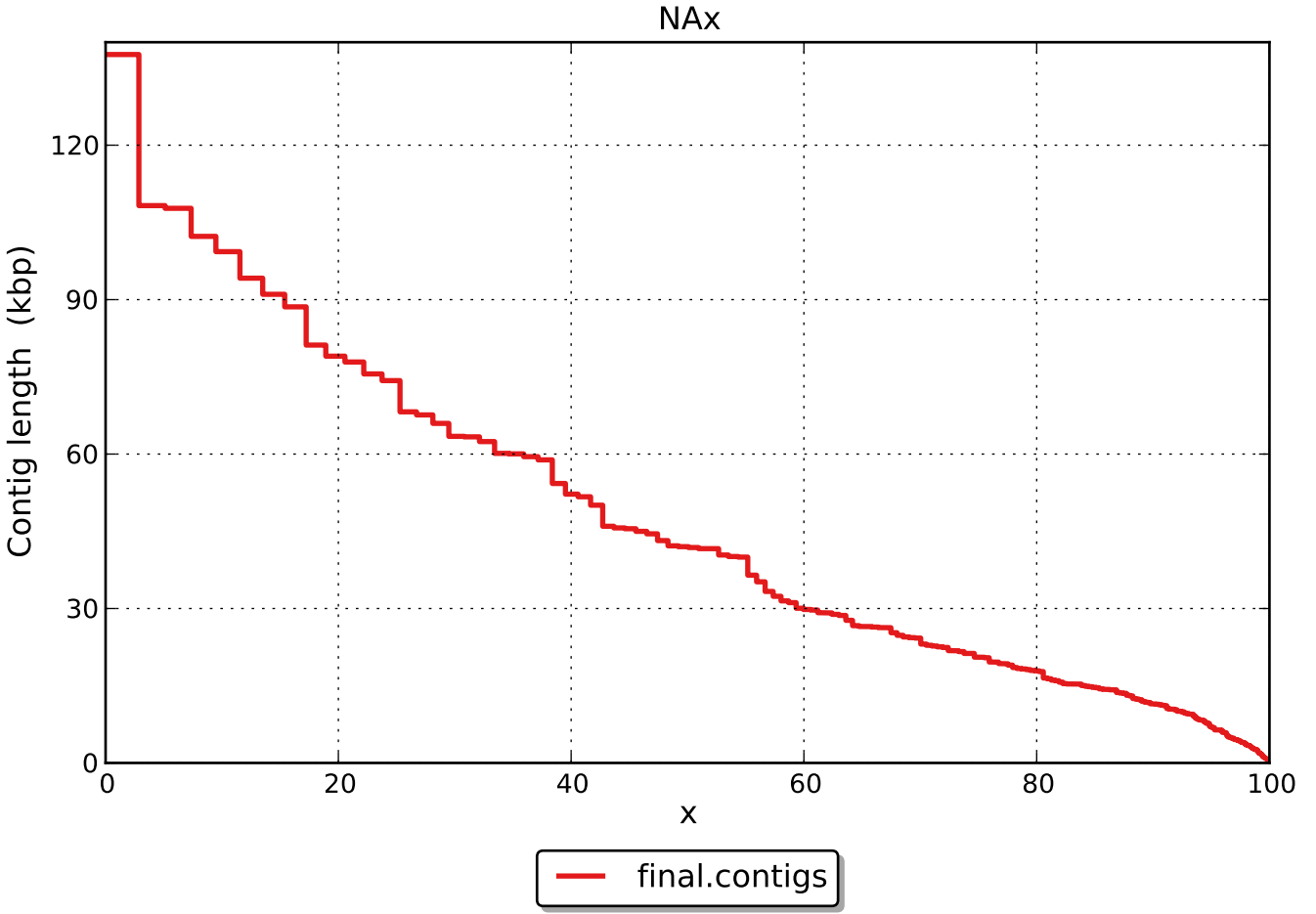

NGx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

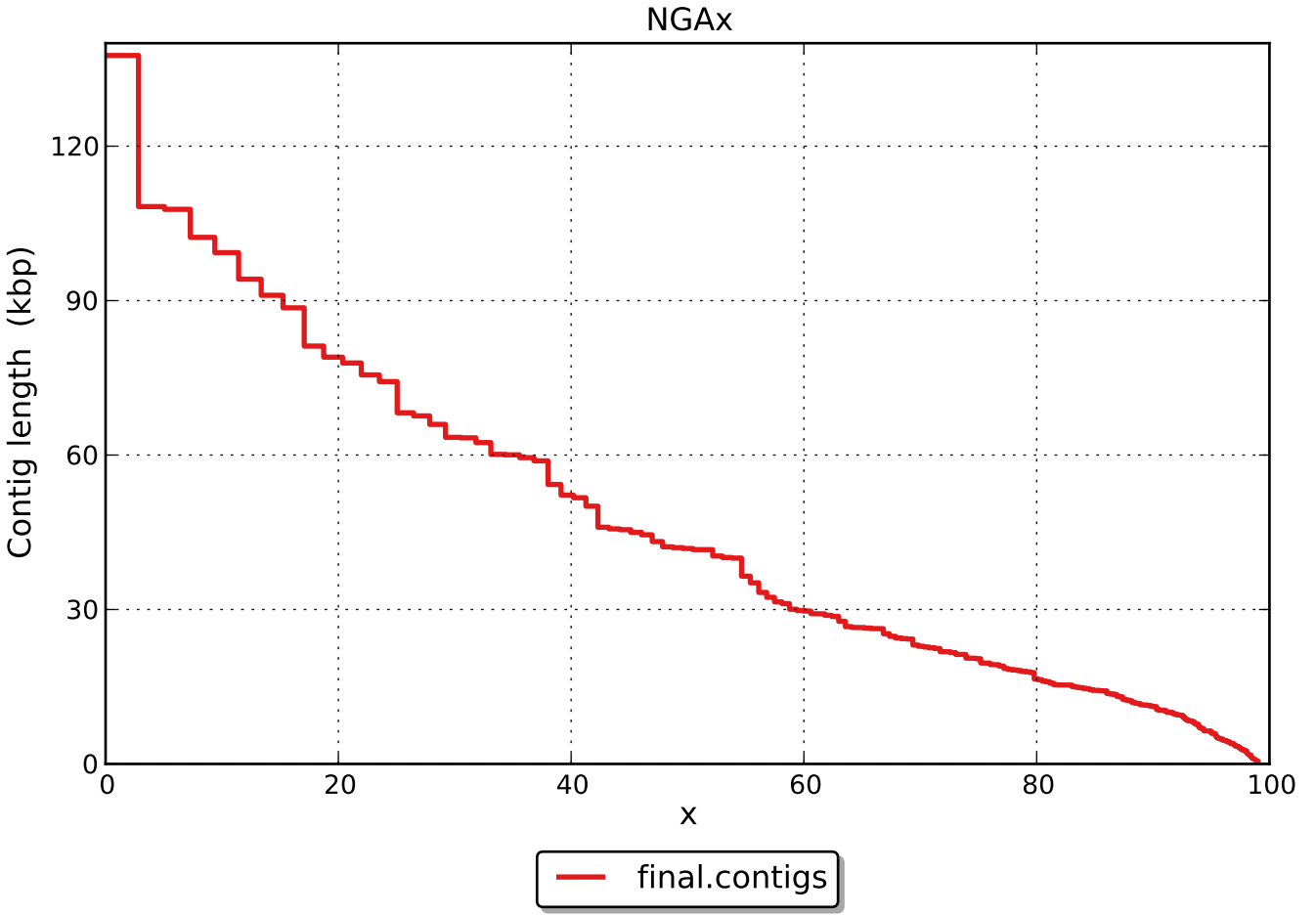

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
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
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs