Report

	final.contigs
# contigs (>= 0 bp)	111
# contigs (>= 1000 bp)	105
Total length (>= 0 bp)	1240062
Total length (>= 1000 bp)	1235606
# contigs	111
Largest contig	48138
Total length	1240062
Reference length	615980
GC (%)	25.34
Reference GC (%)	25.35
N50	17367
NG50	31370
N75	10805
NG75	21276
L50	23
LG50	8
L75	46
LG75	14
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	49 + 4 part
Unaligned length	618050
Genome fraction (%)	99.943
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.74
# indels per 100 kbp	0.00
Largest alignment	44541
NA50	723
NGA50	17462
NGA75	11002
LA50	57
LGA50	11
LGA75	23

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

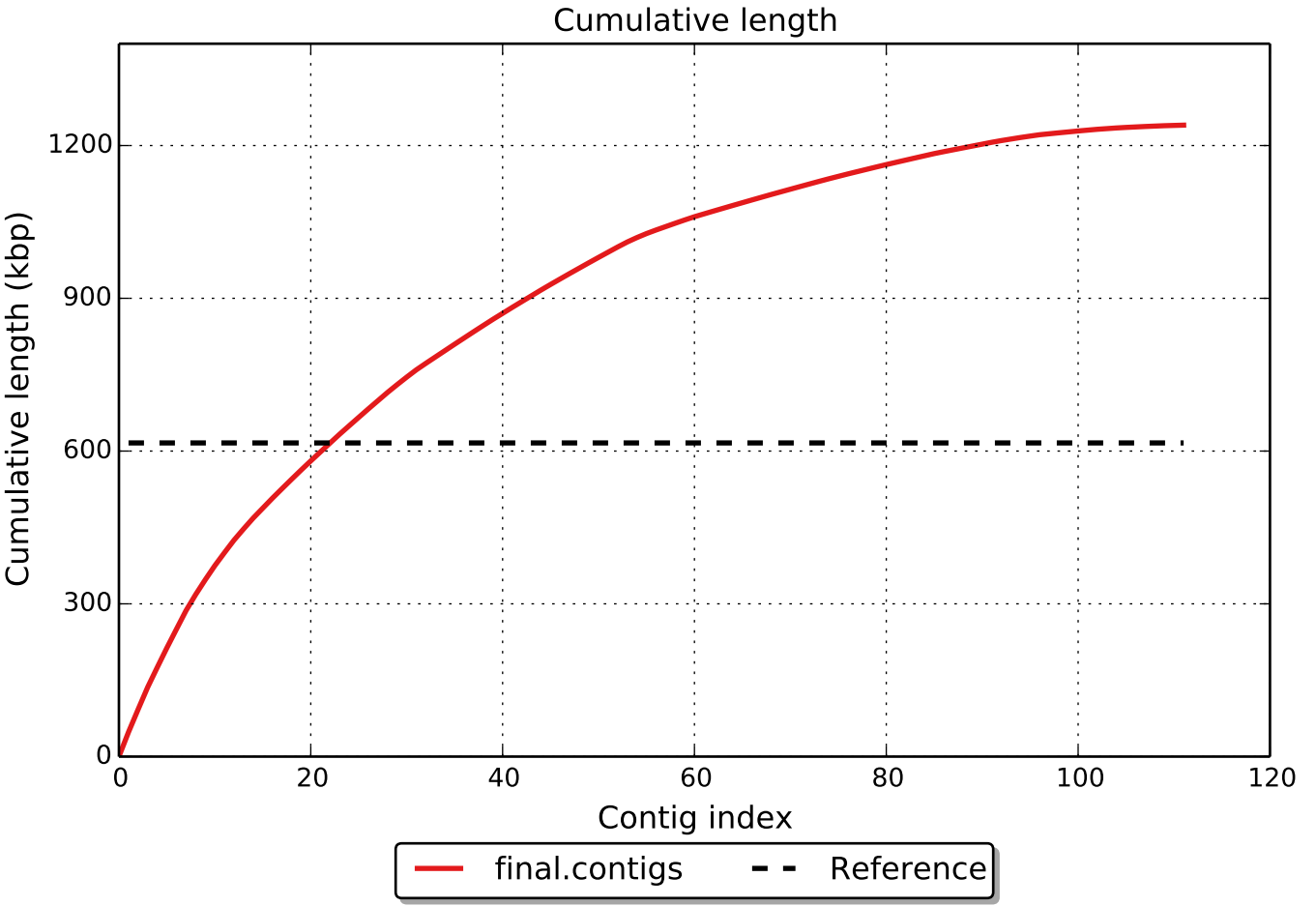
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	23
# indels	0
# short indels	0
# long indels	0
Indels length	0

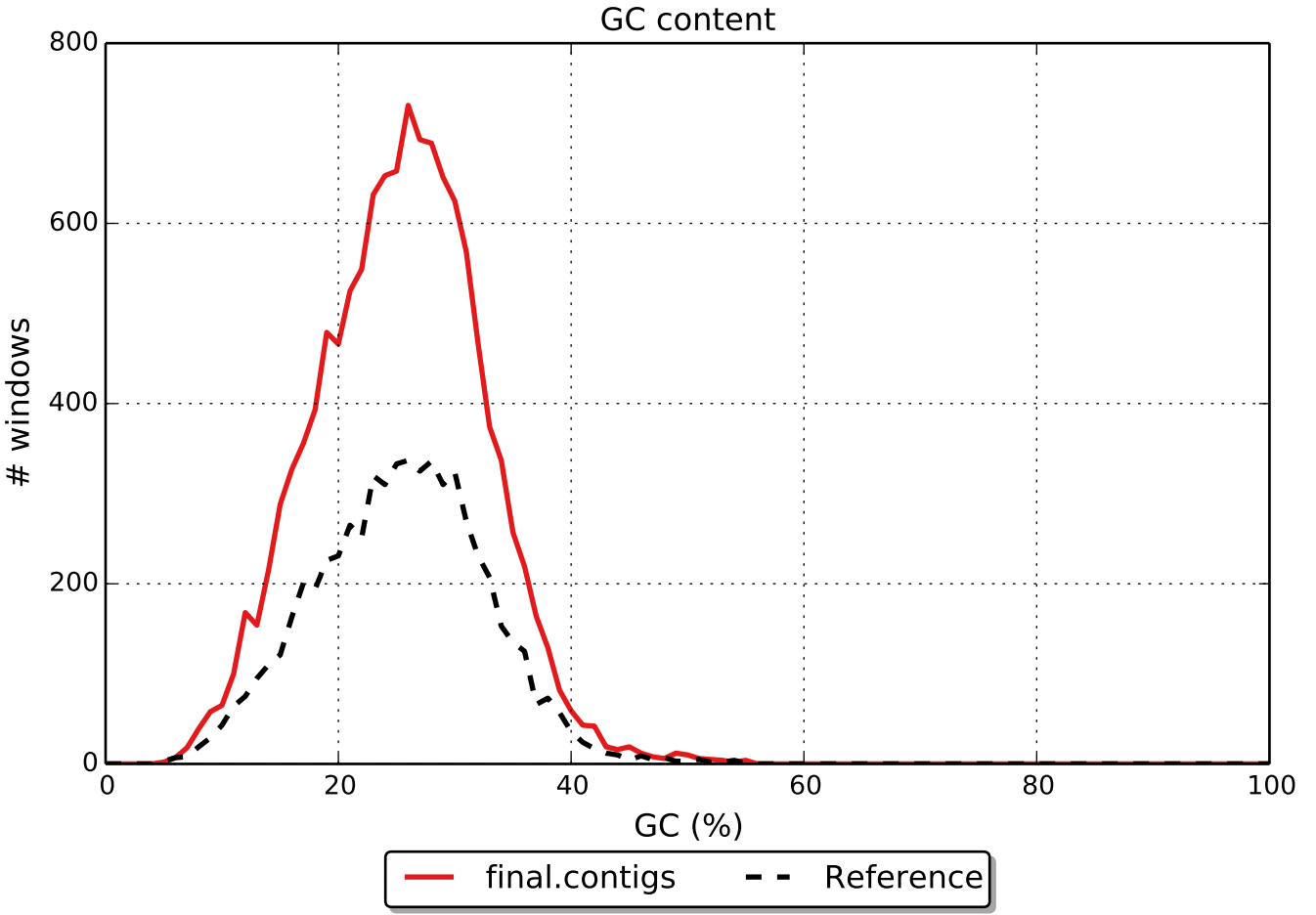
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

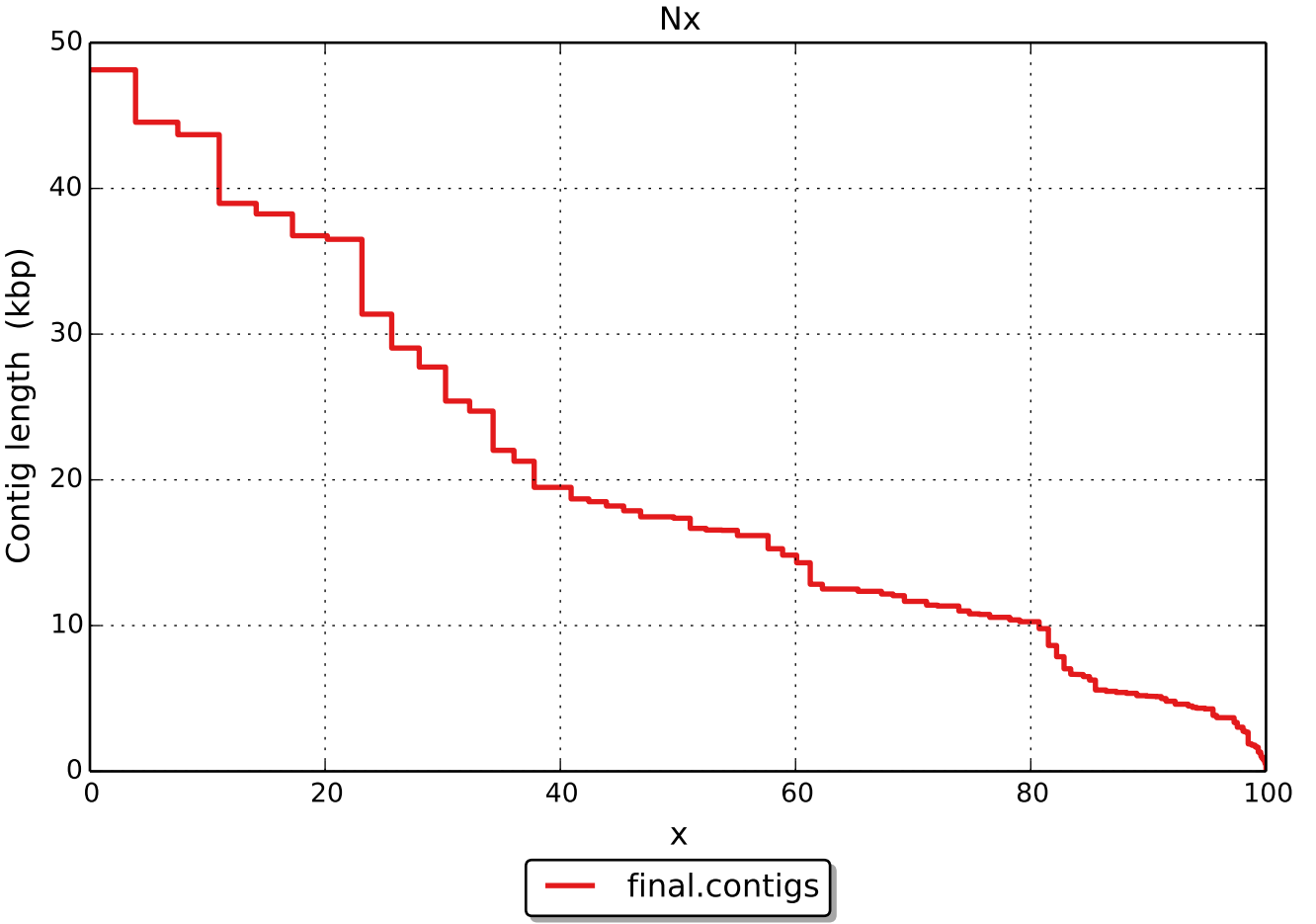
Unaligned report

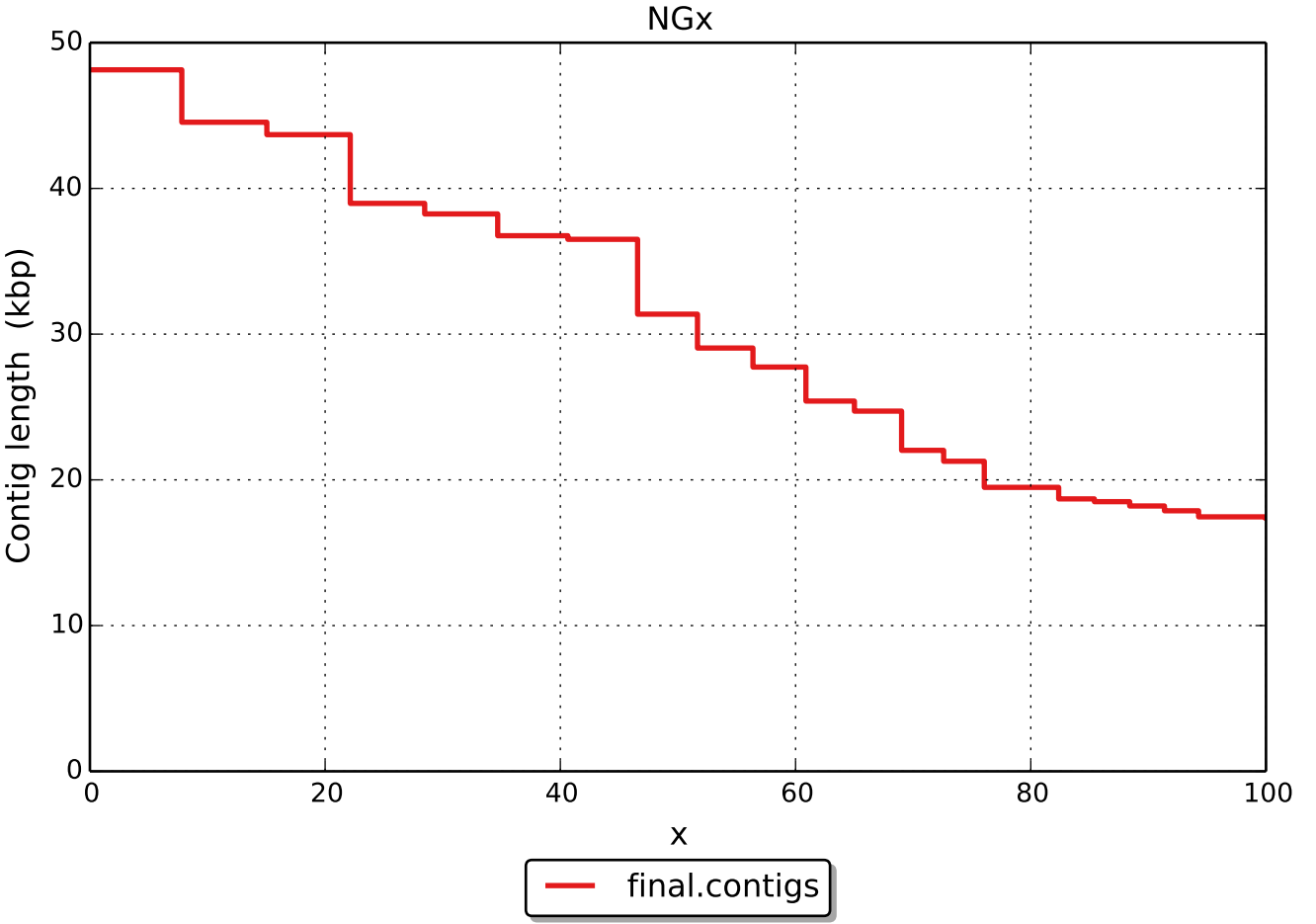
	final.contigs
# fully unaligned contigs	49
Fully unaligned length	566230
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	1
Partially unaligned length	51820
# N's	0

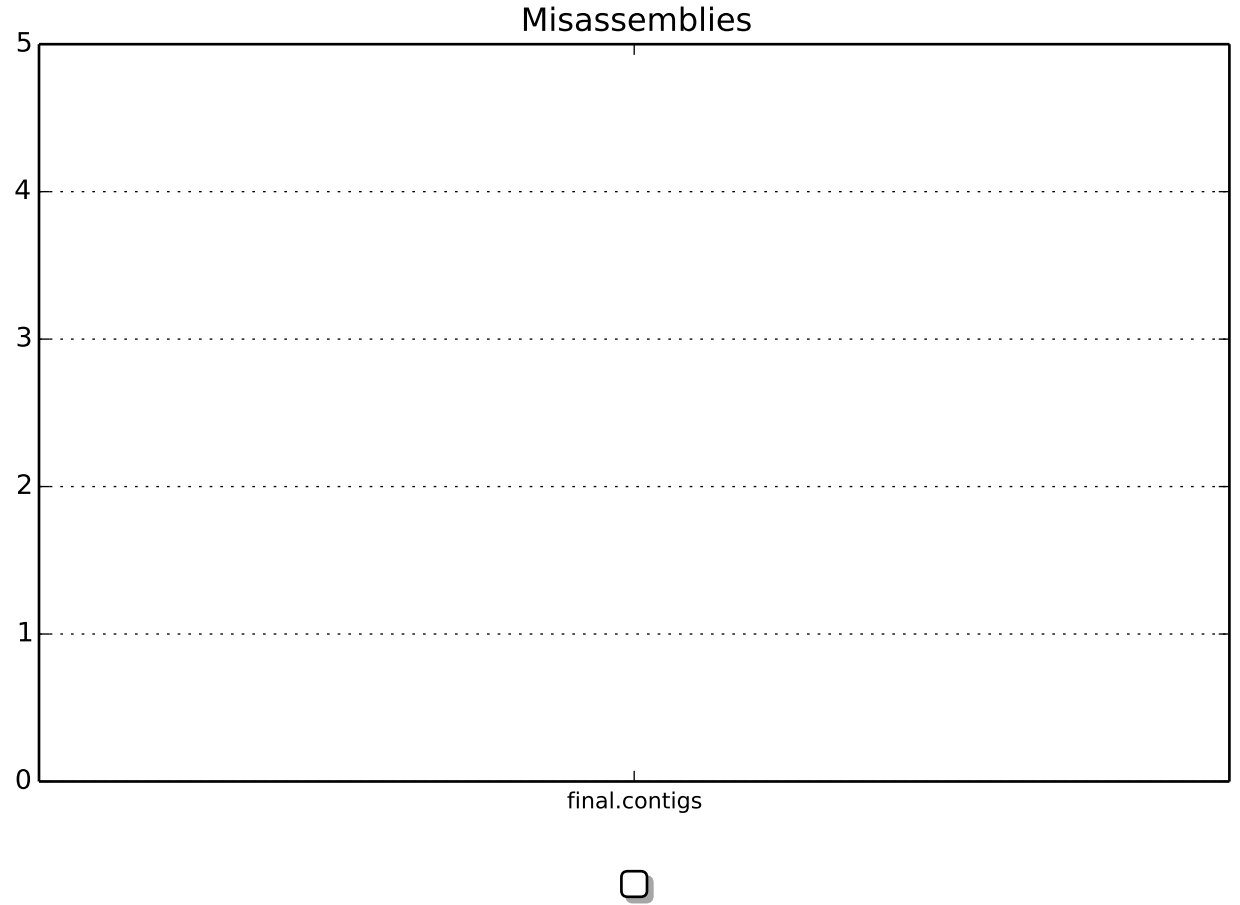
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

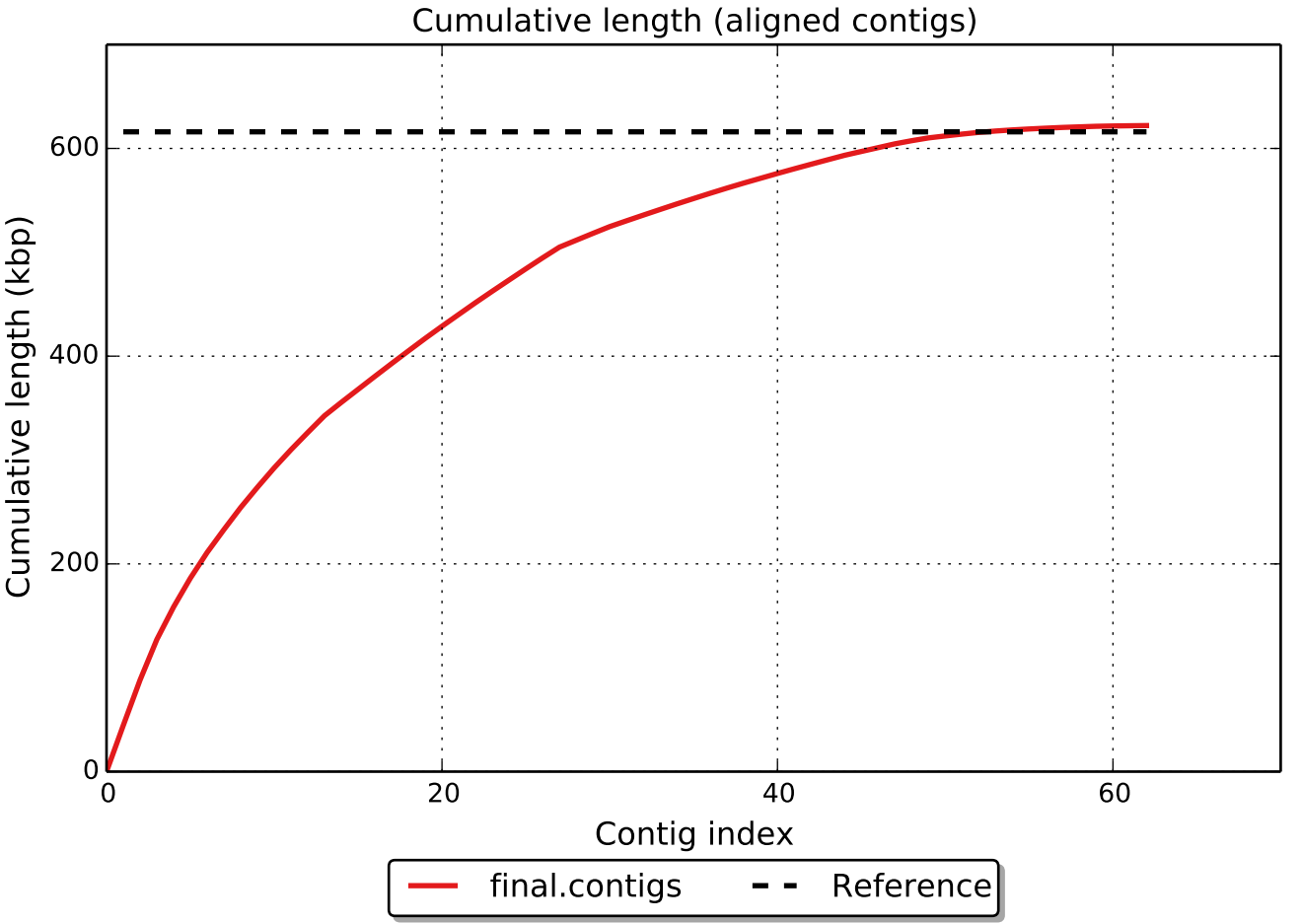

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
20
40
60
80
100
120
Contig index
final.contigs
Reference

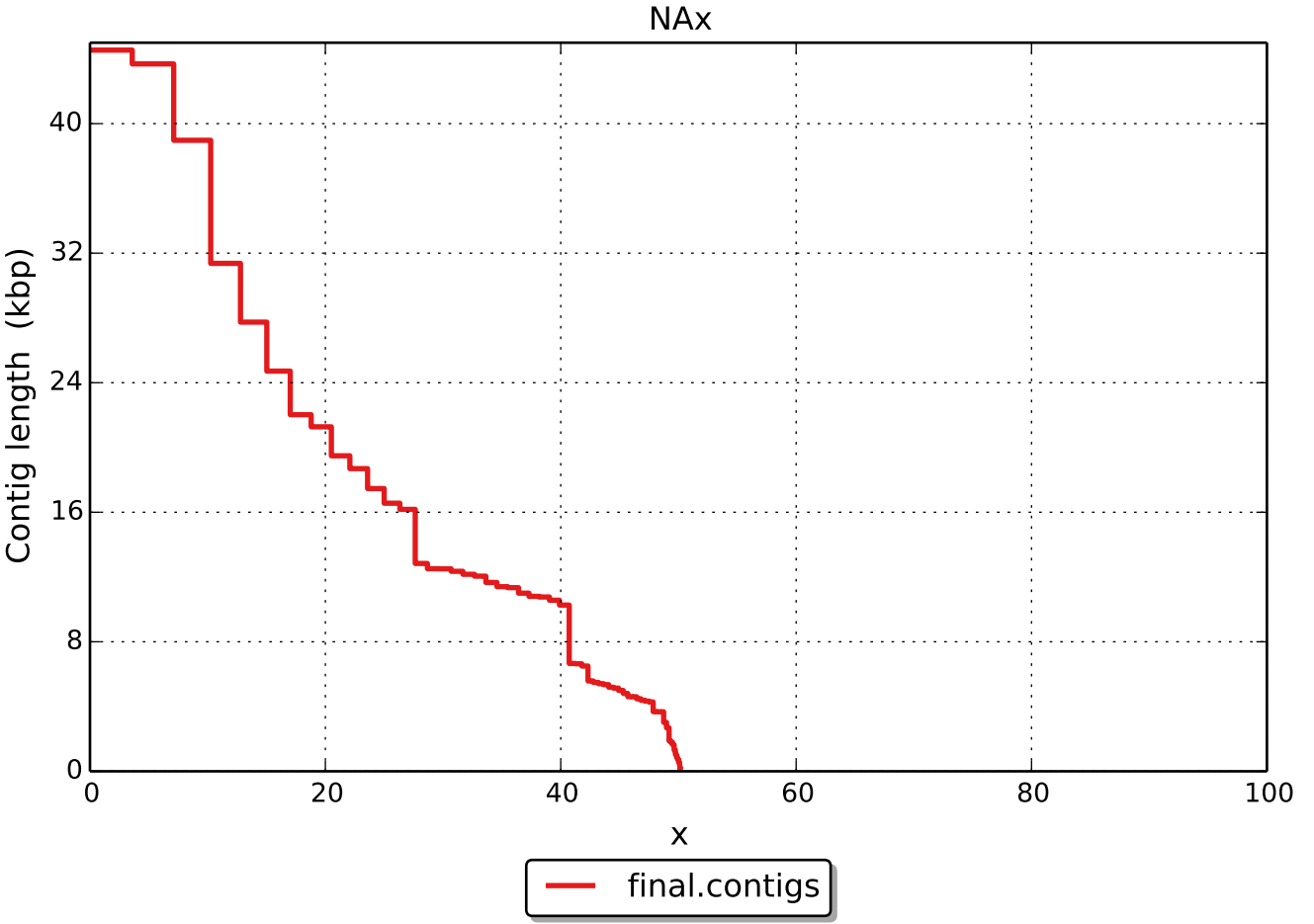

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

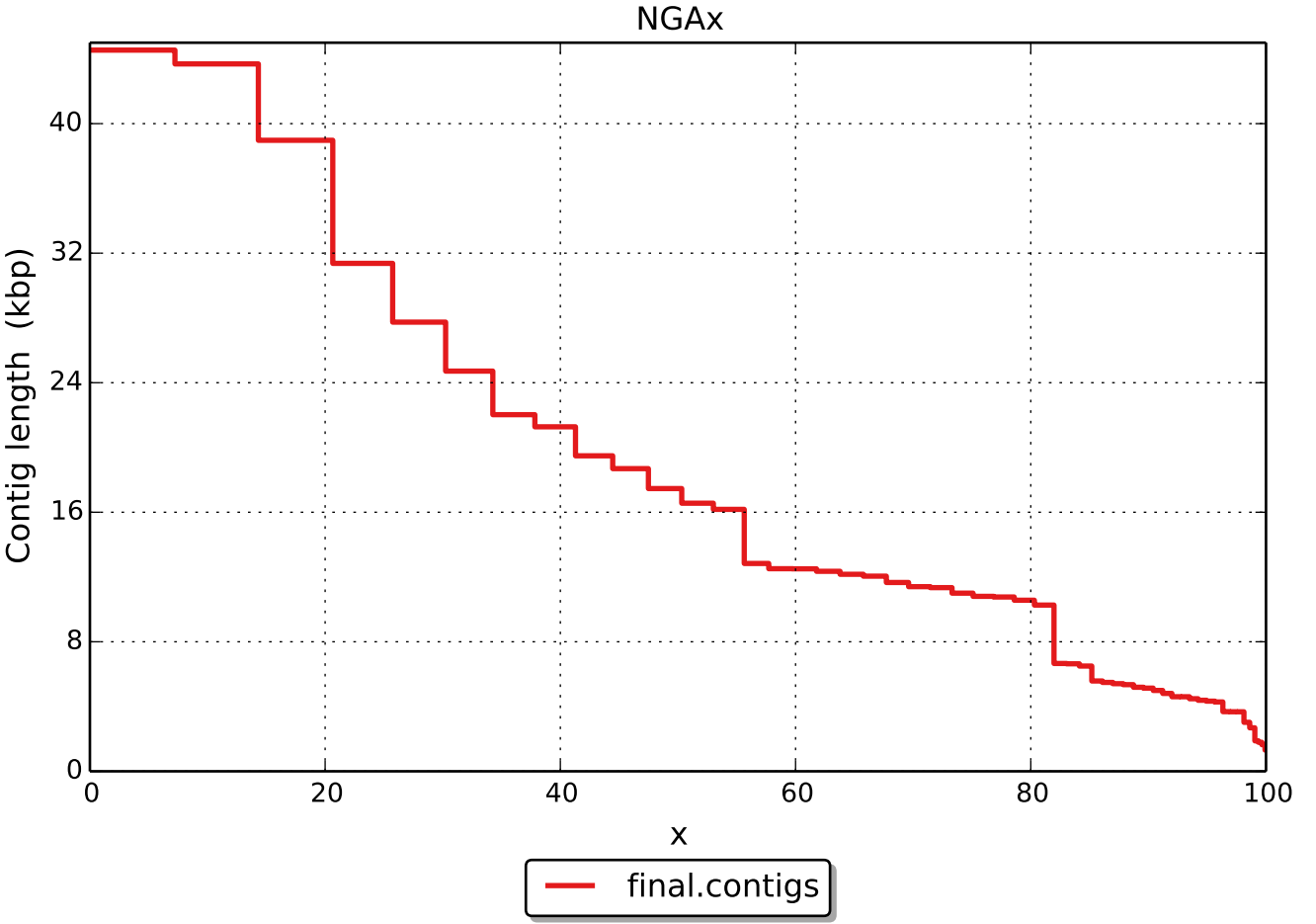

Nx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
200
400
600
0
20
40
60
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
8
16
24
32
40
0
20
40
60
80
100
x
final.contigs