Report

	final.contigs
# contigs (>= 0 bp)	69
# contigs (>= 1000 bp)	69
Total length (>= 0 bp)	1237426
Total length (>= 1000 bp)	1237426
# contigs	69
Largest contig	108160
Total length	1237426
Reference length	1231960
GC (%)	25.35
Reference GC (%)	25.35
N50	30198
NG50	30198
N75	15327
NG75	15327
L50	13
LG50	13
L75	28
LG75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.994
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.08
# indels per 100 kbp	0.00
Largest alignment	108160
NA50	30198
NGA50	30198
NA75	15327
NGA75	15327
LA50	13
LGA50	13
LA75	28
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

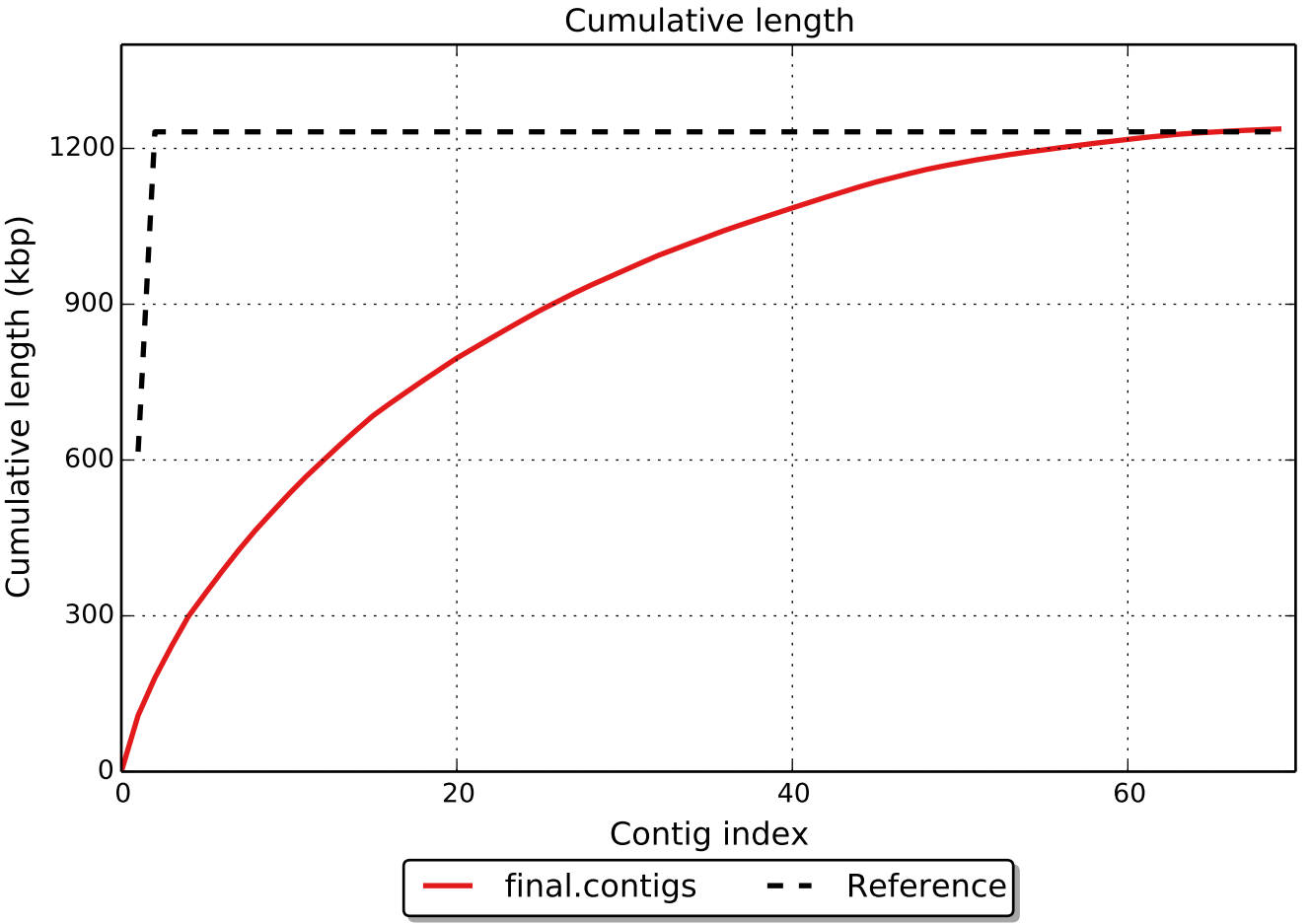
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1
# indels	0
# short indels	0
# long indels	0
Indels length	0

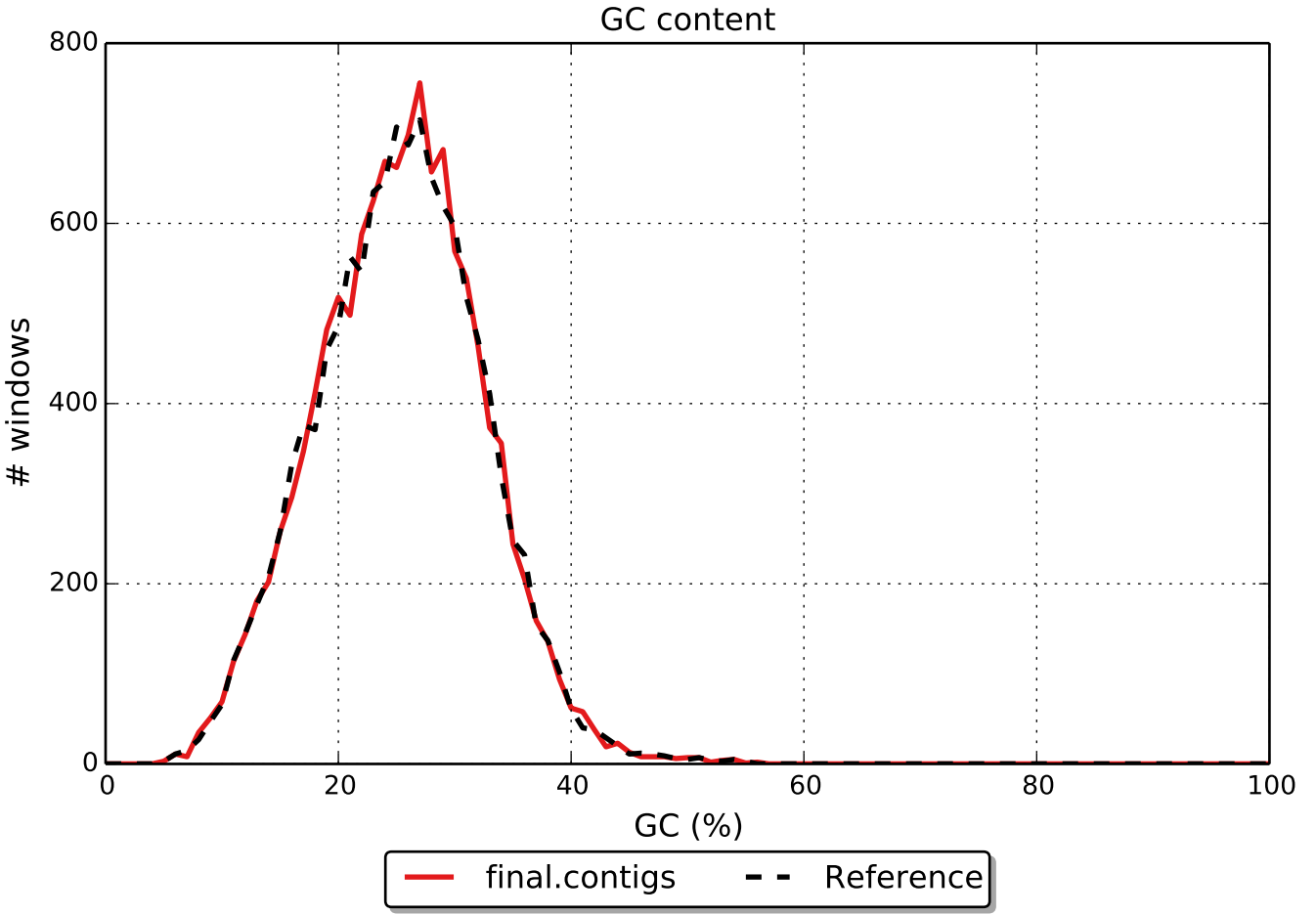
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

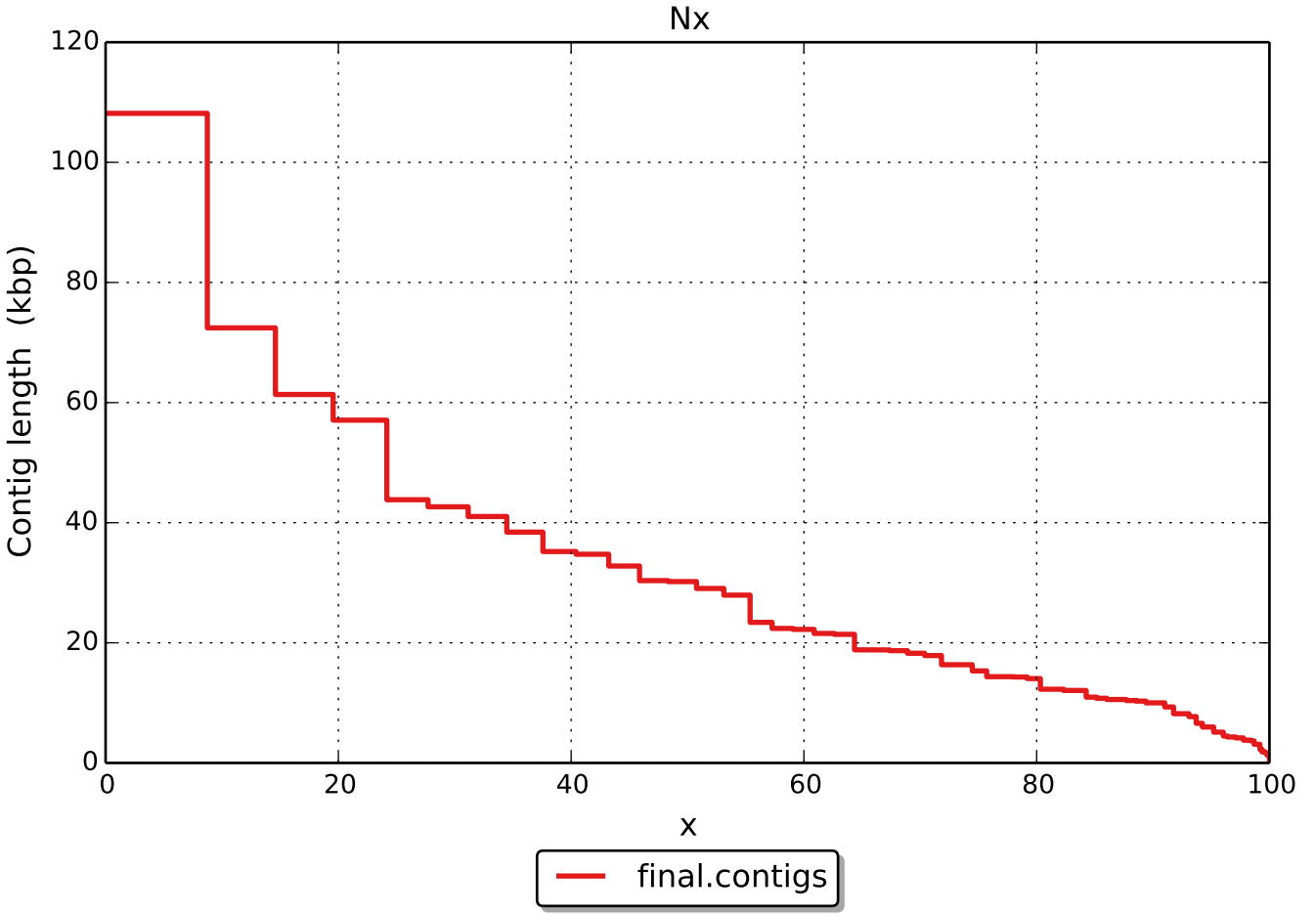
Unaligned report

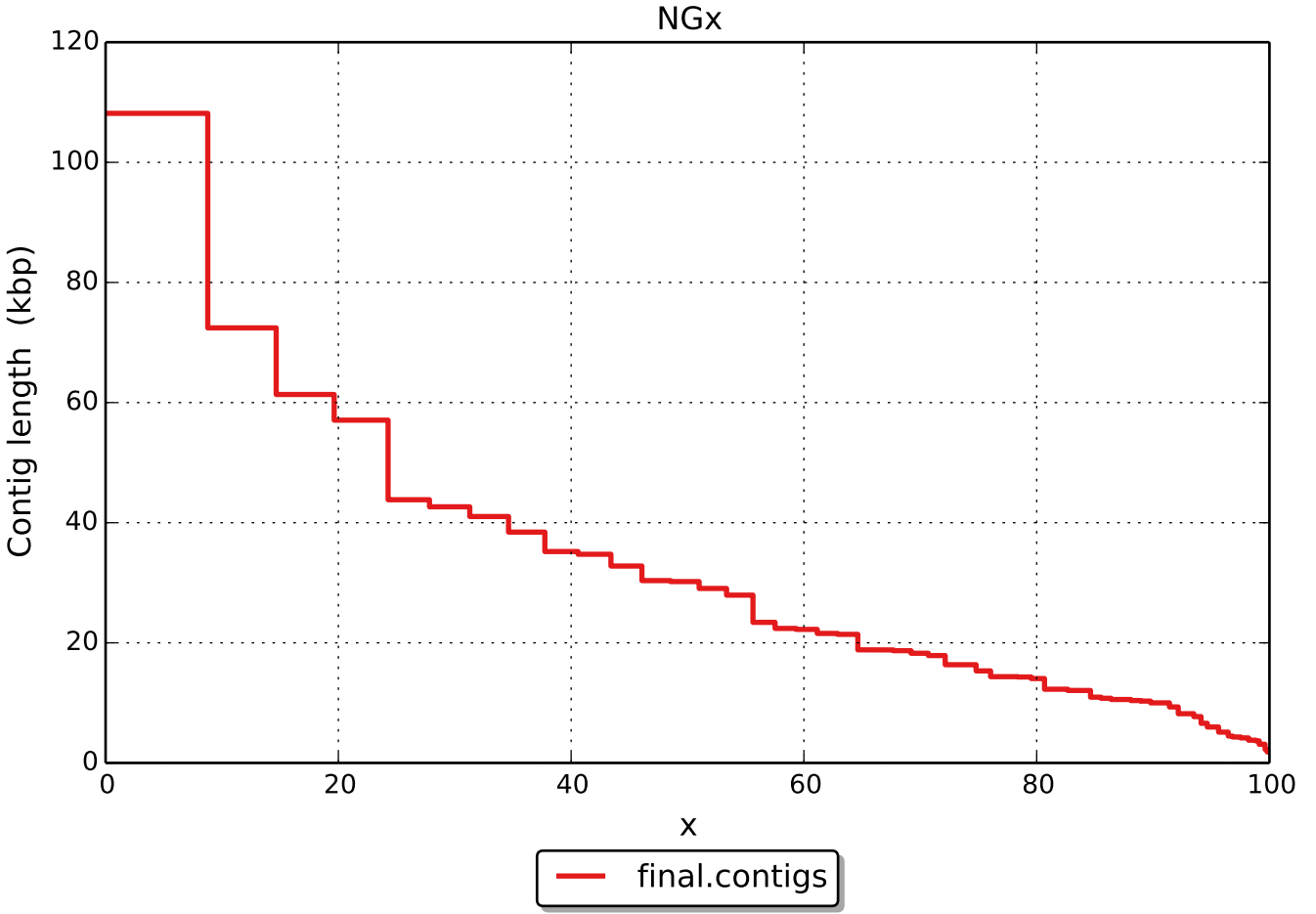
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

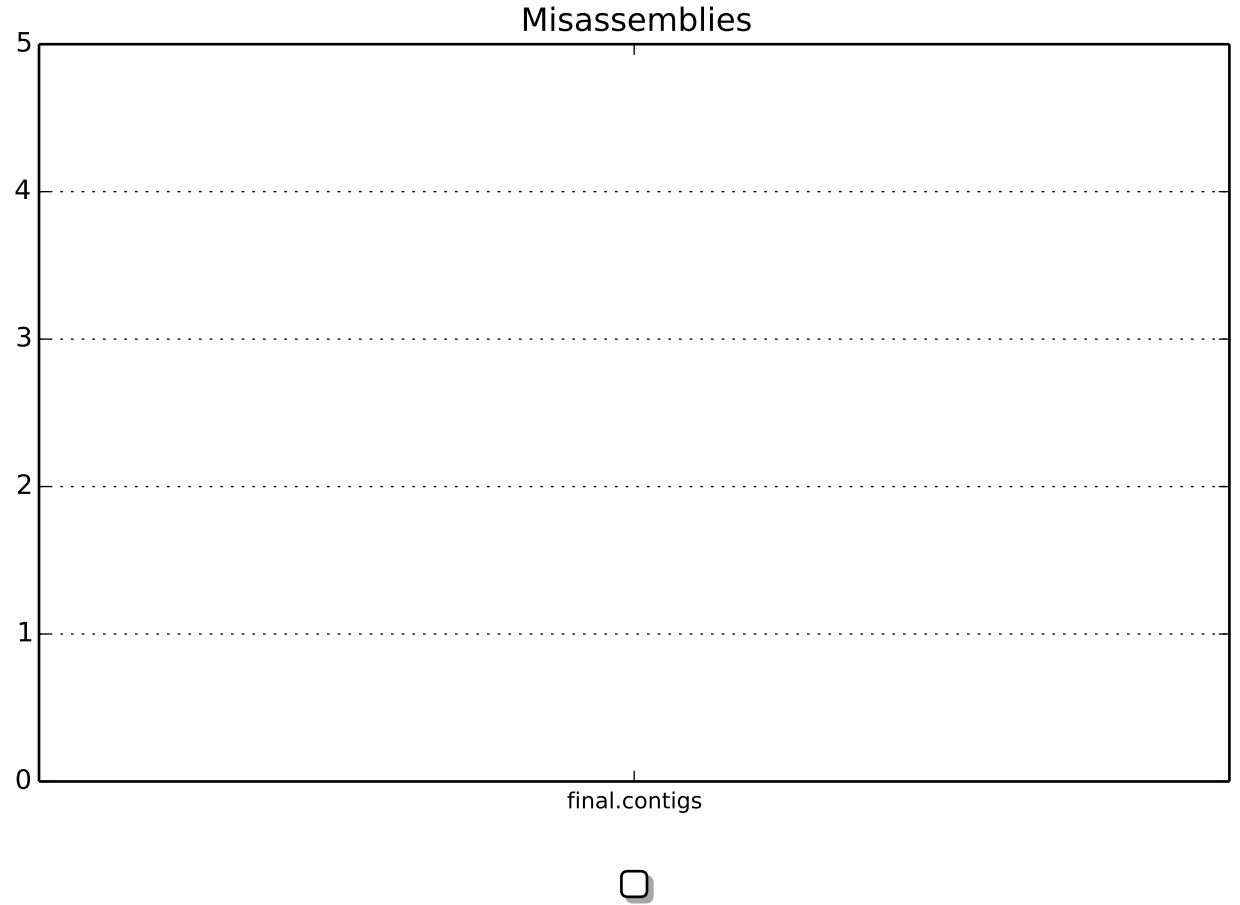
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

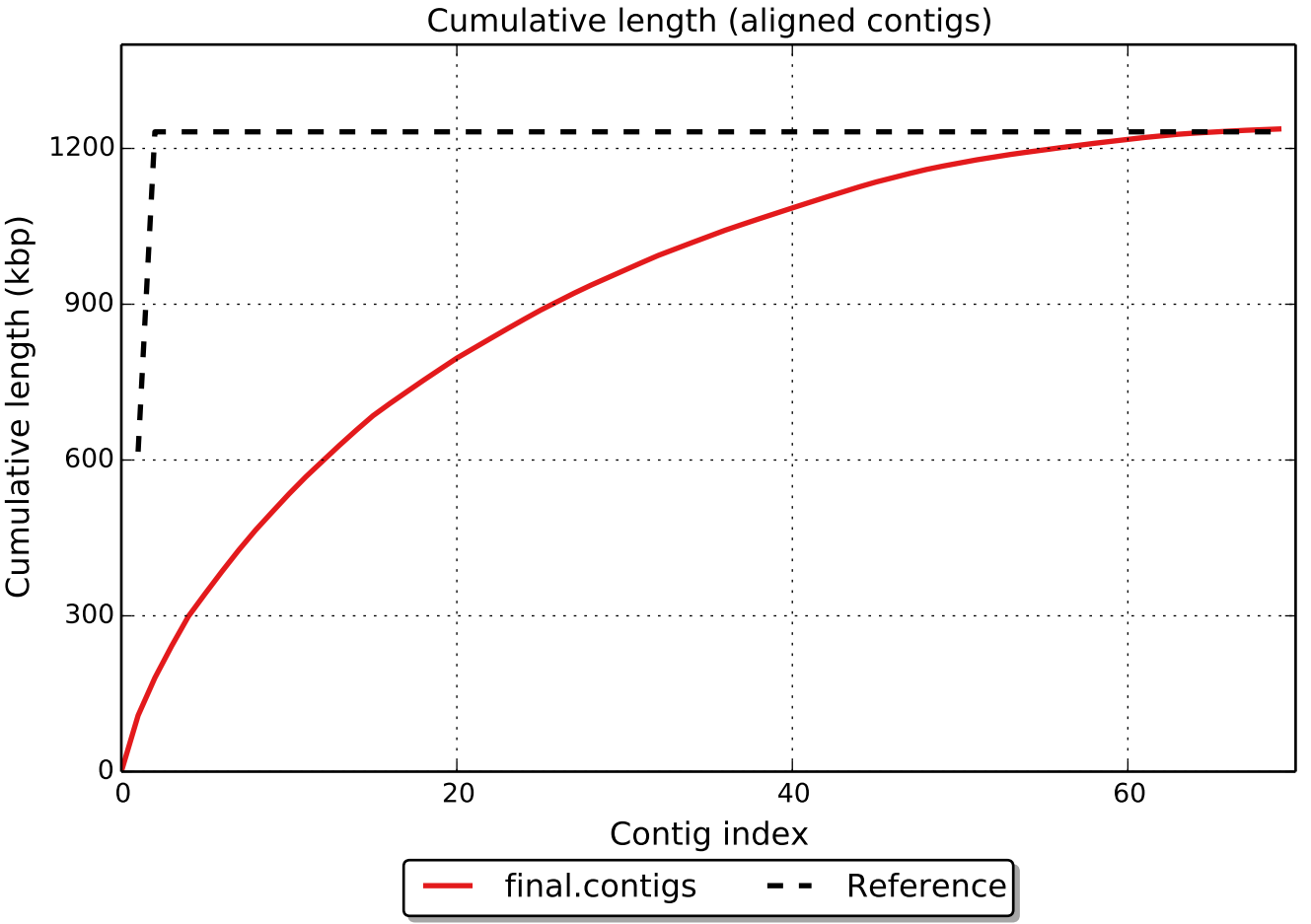

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
20
40
60
Contig index
final.contigs
Reference

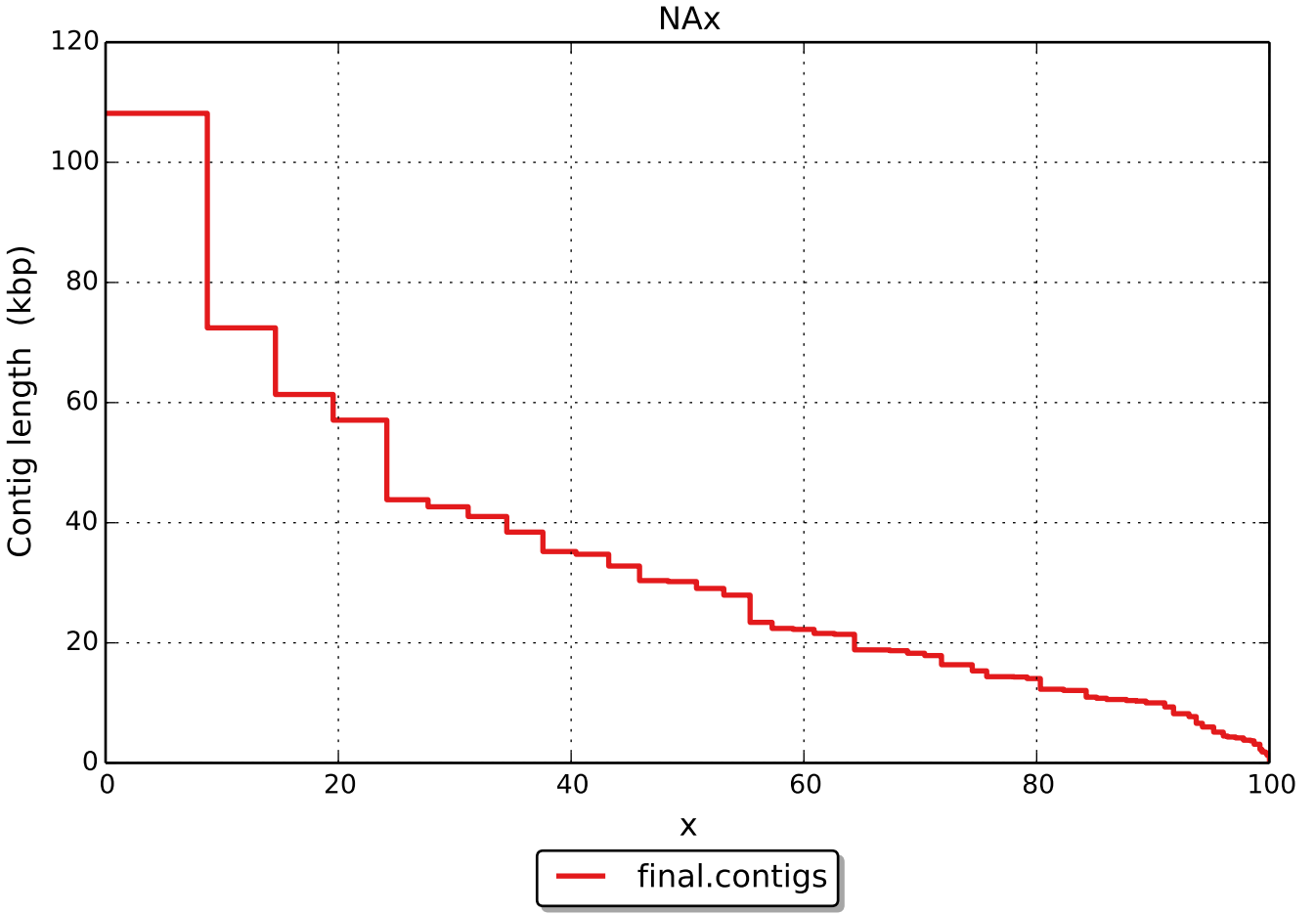

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

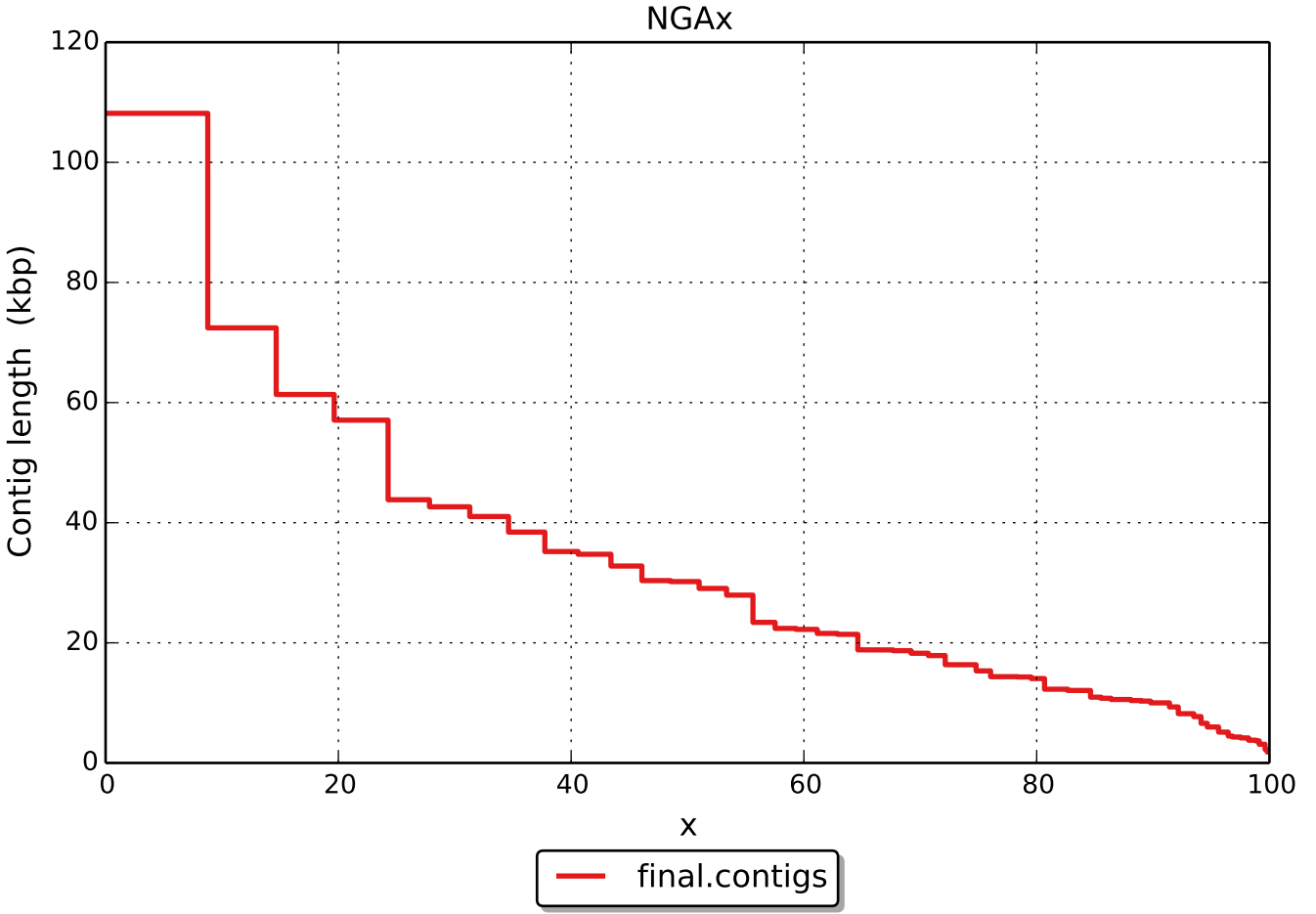

Nx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs


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


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


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