Report

	final.contigs
# contigs (>= 0 bp)	71
# contigs (>= 1000 bp)	67
Total length (>= 0 bp)	1237309
Total length (>= 1000 bp)	1235477
# contigs	69
Largest contig	70492
Total length	1236567
Reference length	1231960
GC (%)	25.34
Reference GC (%)	25.34
N50	28564
NG50	28564
N75	17290
NG75	17290
L50	14
LG50	14
L75	29
LG75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.940
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	70492
NA50	28564
NGA50	28564
NA75	17290
NGA75	17290
LA50	14
LGA50	14
LA75	29
LGA75	29

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

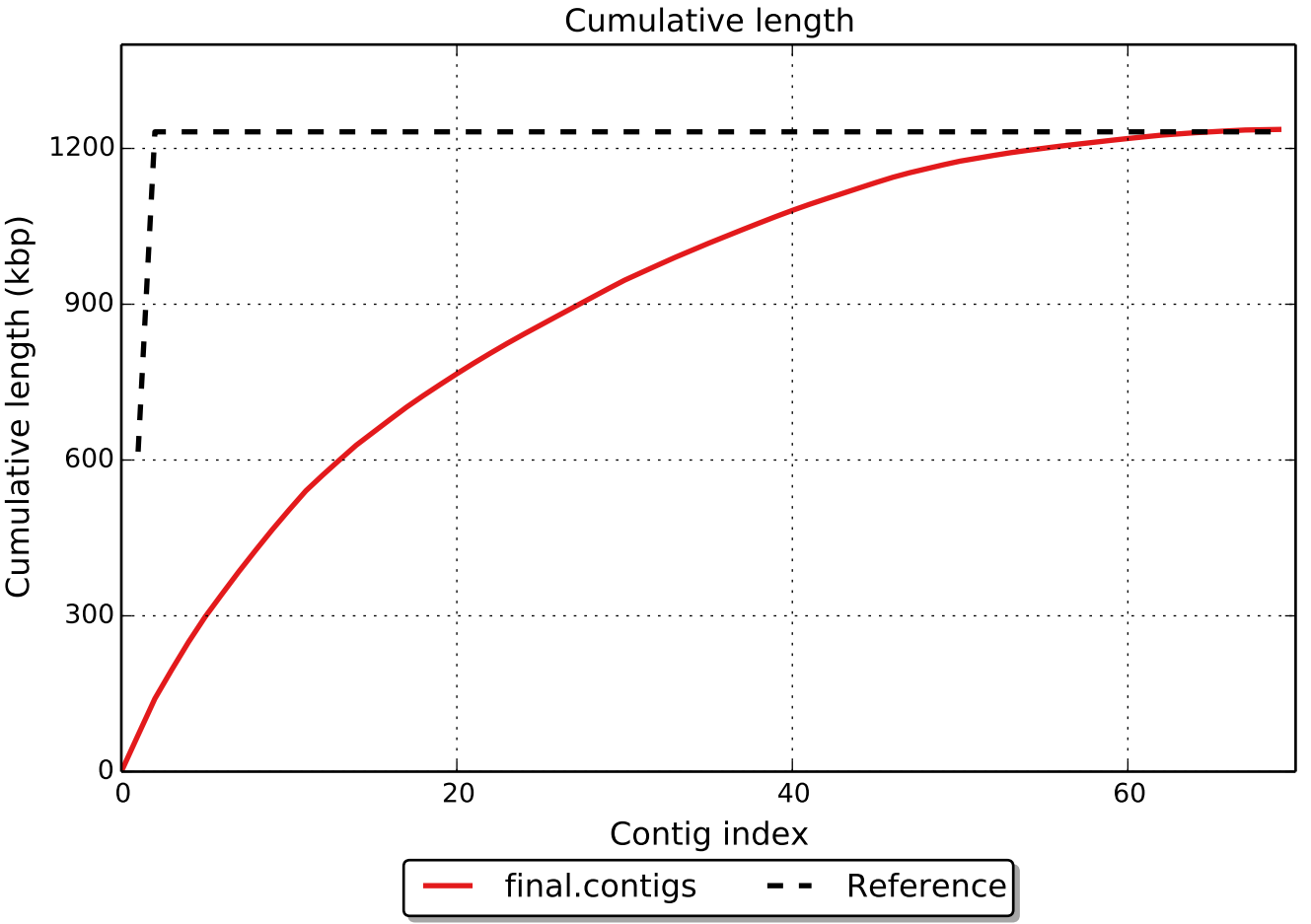
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

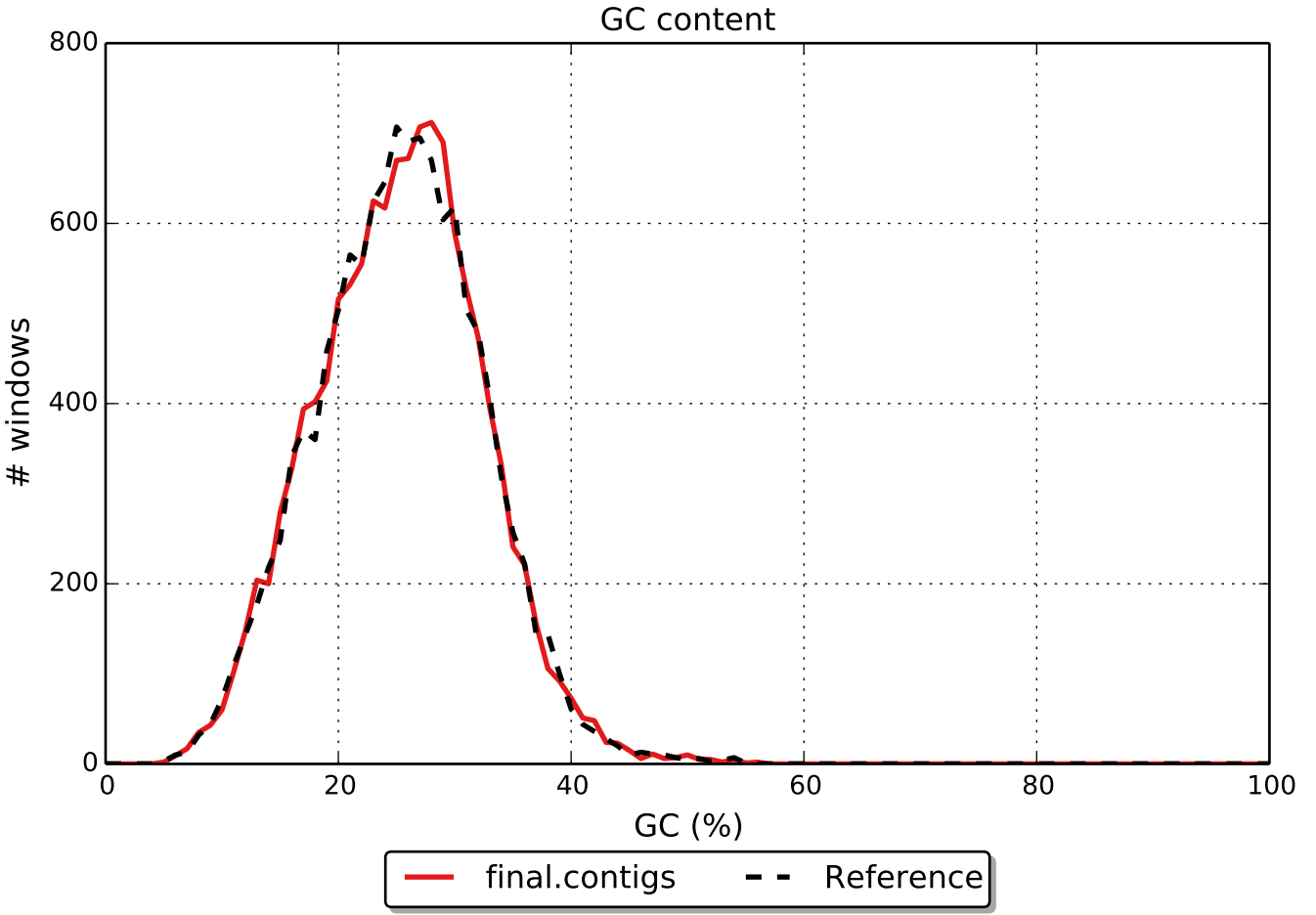
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

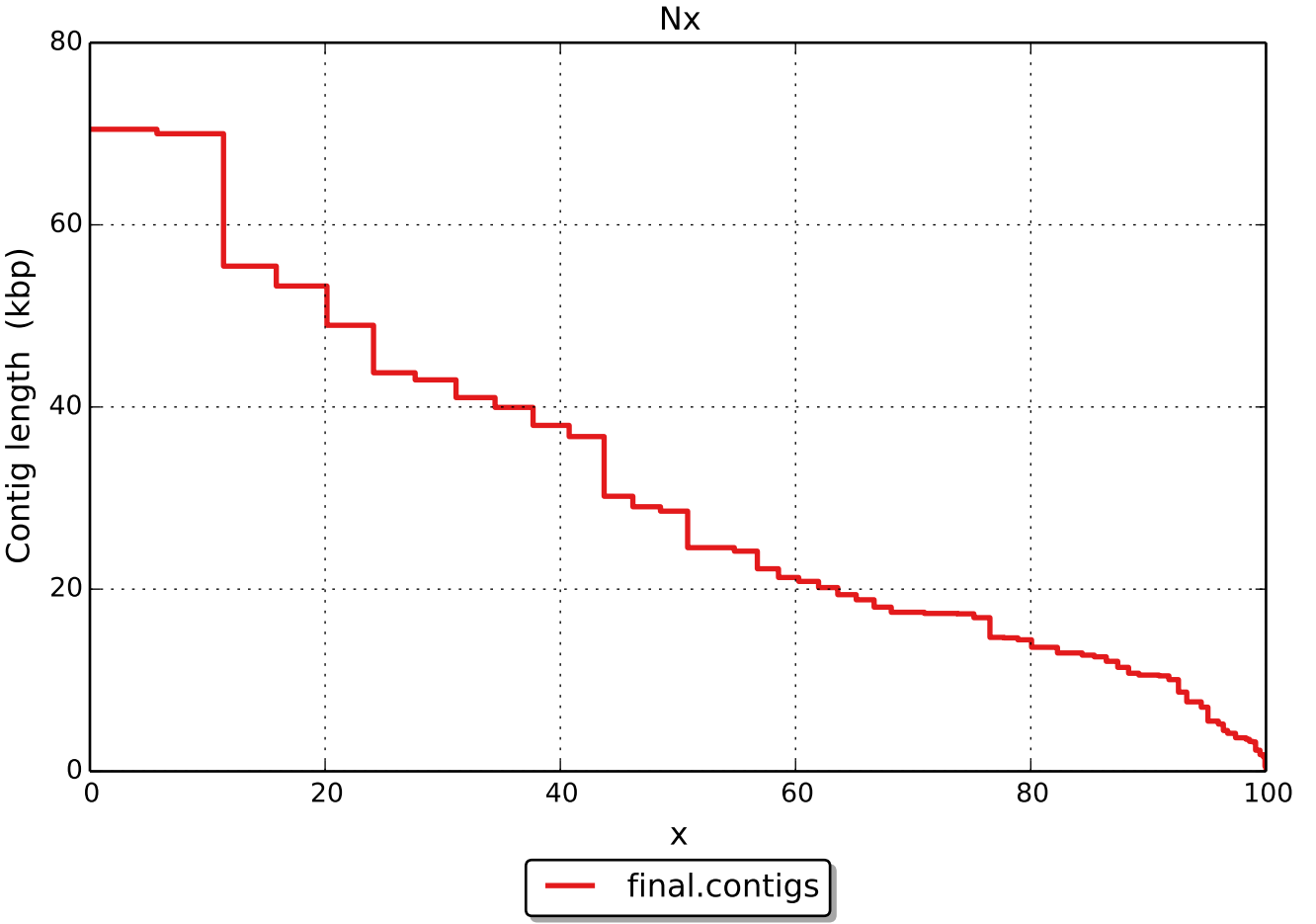
Unaligned report

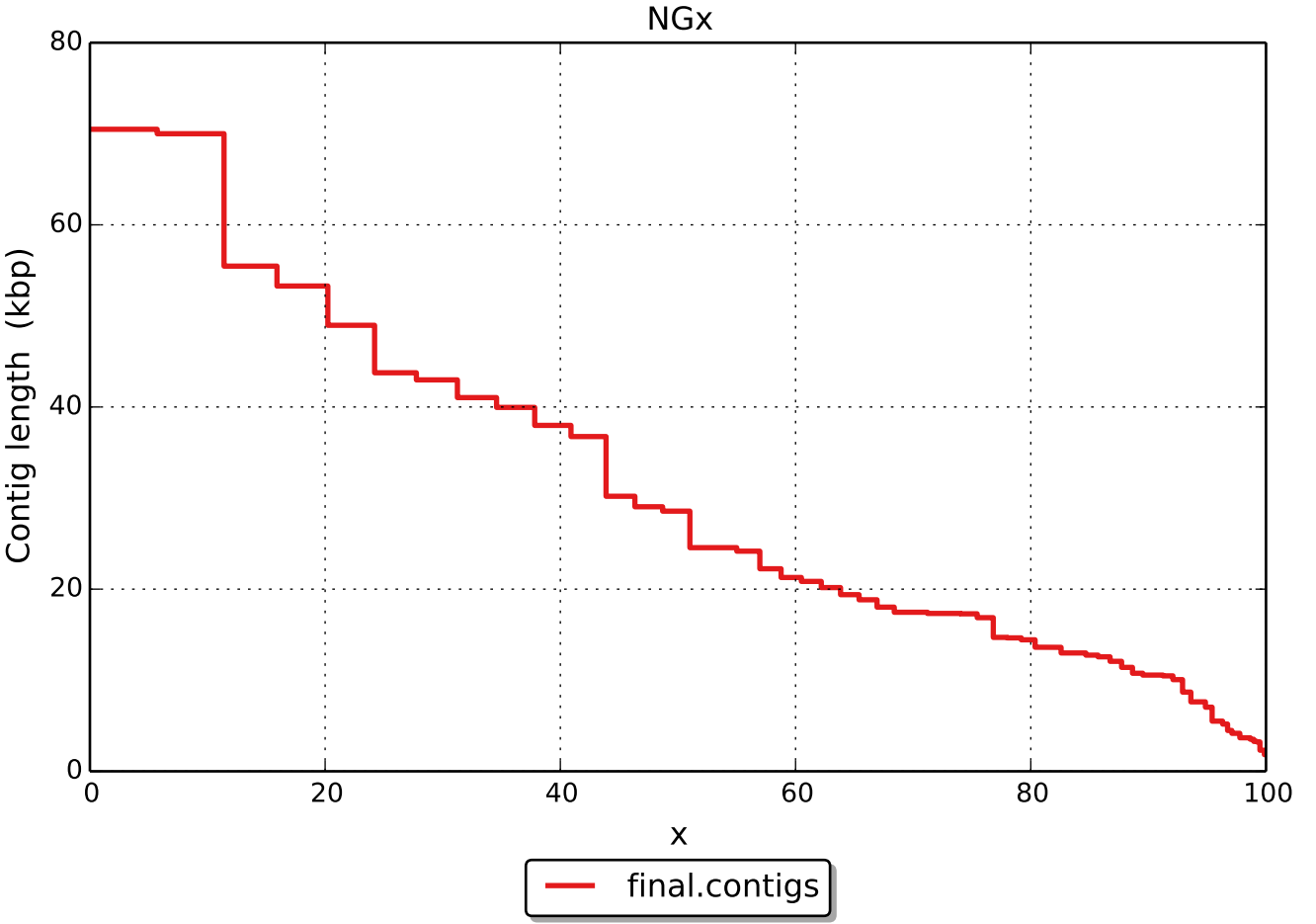
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

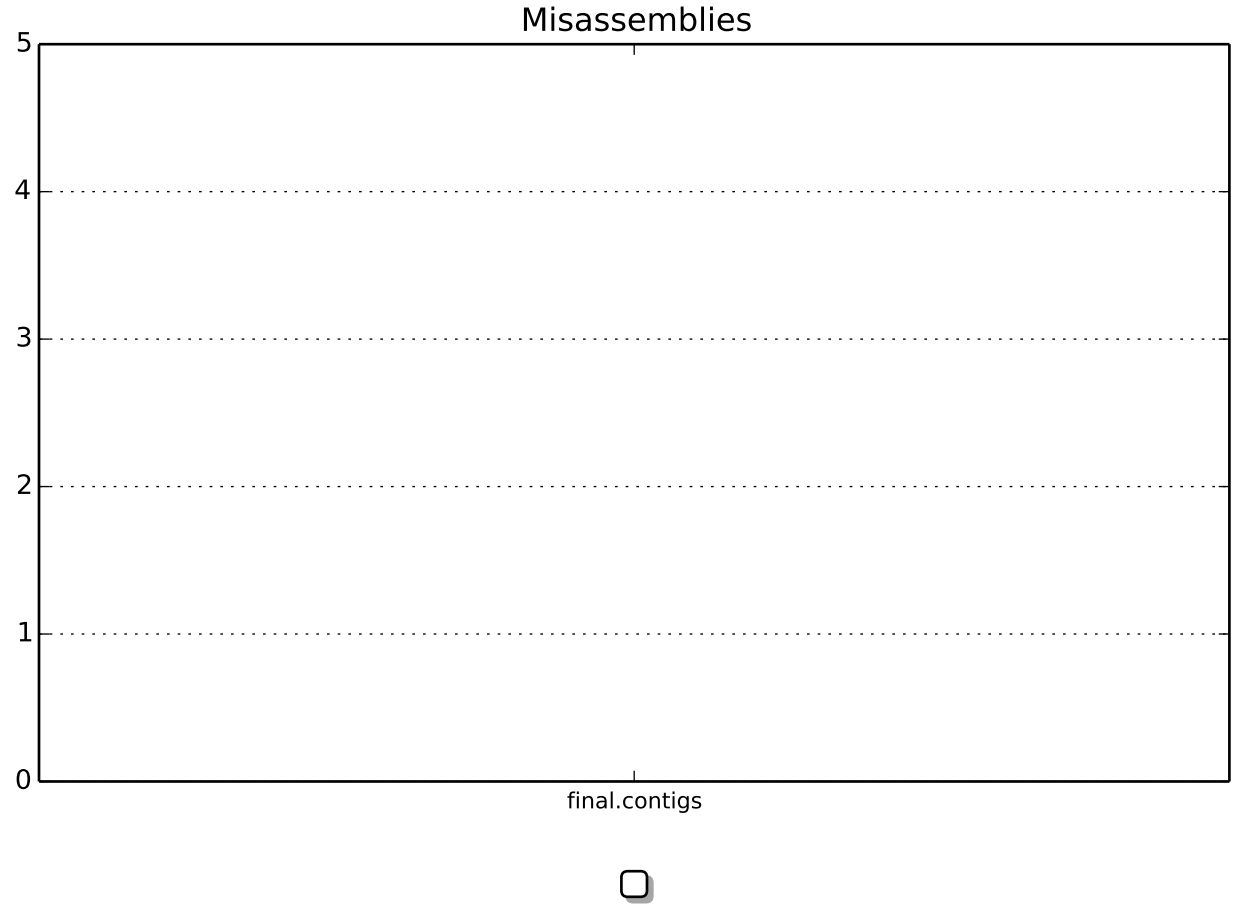
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

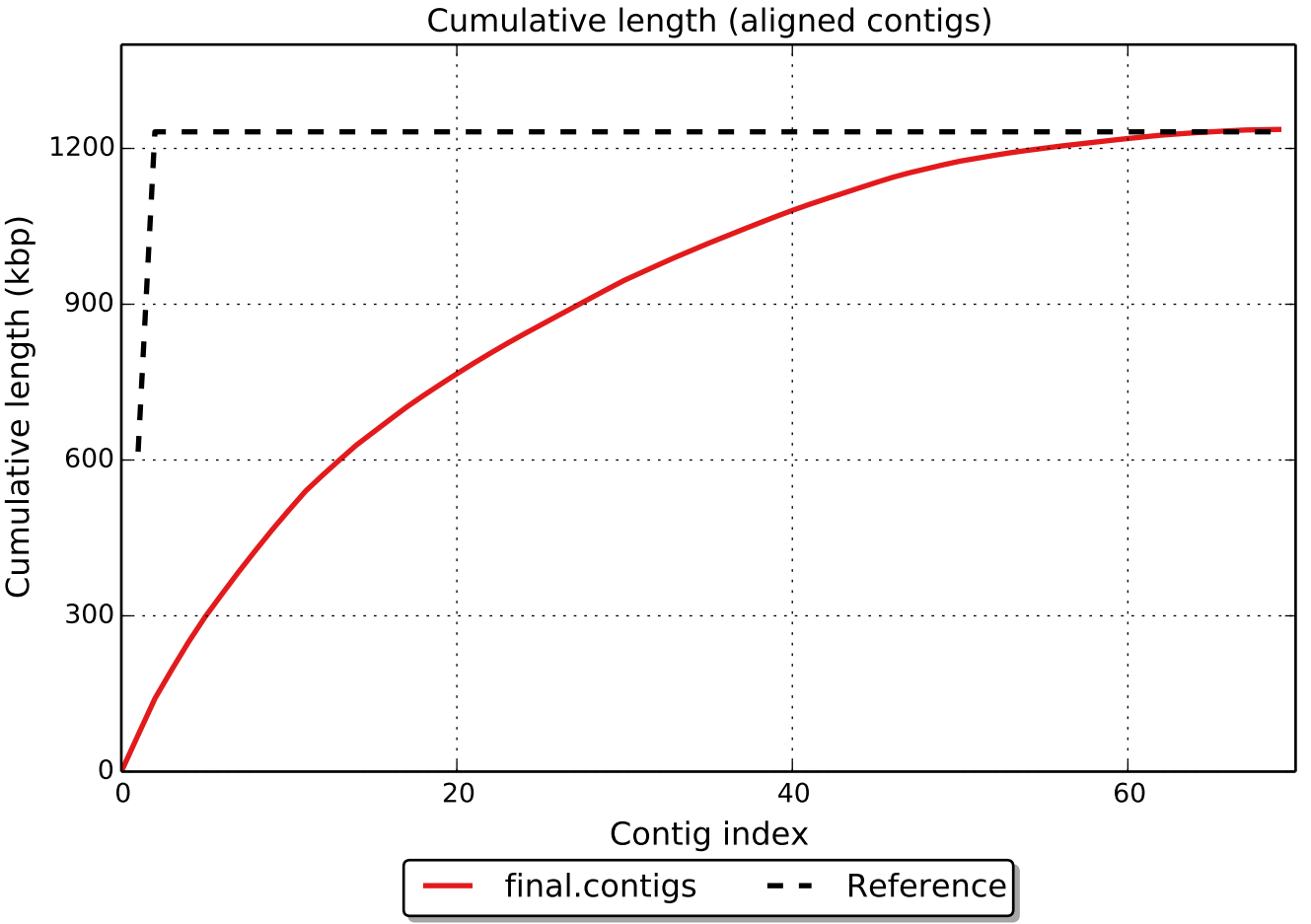

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
20
40
60
Contig index
final.contigs
Reference

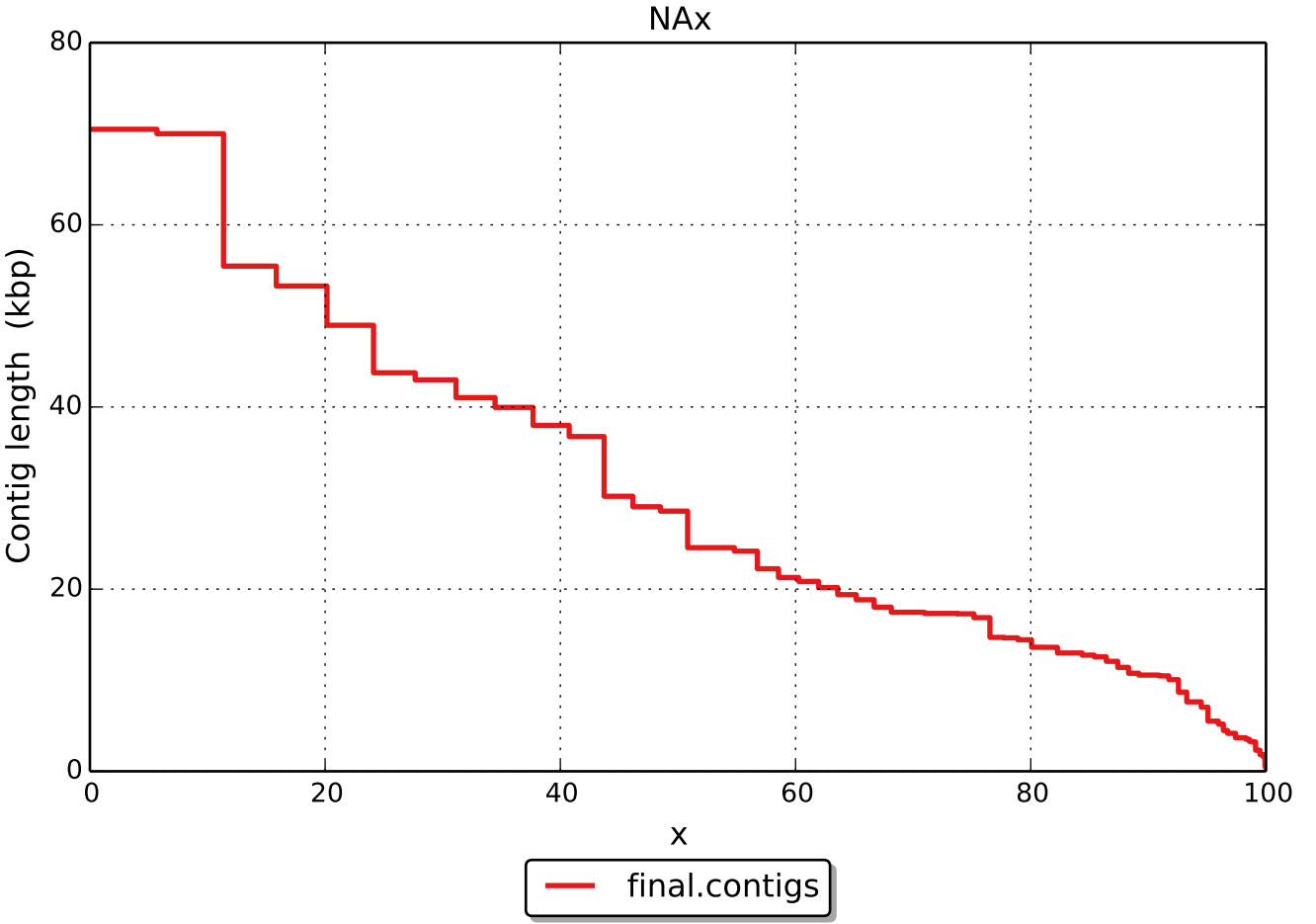

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

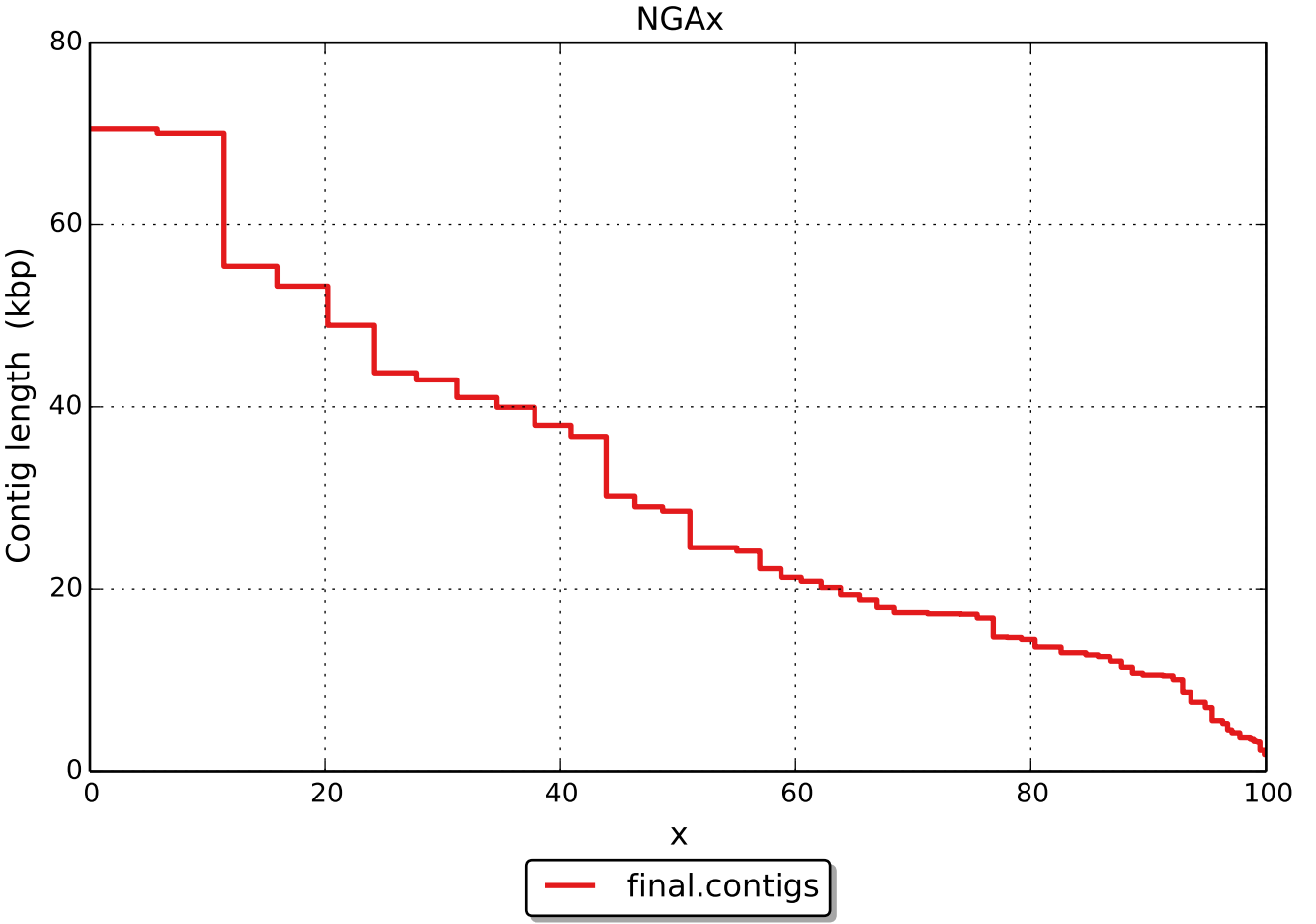

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


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


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