Report

	final.contigs
# contigs (>= 0 bp)	391
# contigs (>= 1000 bp)	290
Total length (>= 0 bp)	1258487
Total length (>= 1000 bp)	1197042
# contigs	359
Largest contig	17058
Total length	1247089
Reference length	1231960
GC (%)	25.36
Reference GC (%)	25.34
N50	5168
NG50	5168
N75	2997
NG75	3025
L50	76
LG50	75
L75	153
LG75	149
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.760
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.67
# indels per 100 kbp	0.33
Largest alignment	17058
NA50	5168
NGA50	5168
NA75	2997
NGA75	3025
LA50	76
LGA50	75
LA75	153
LGA75	149

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

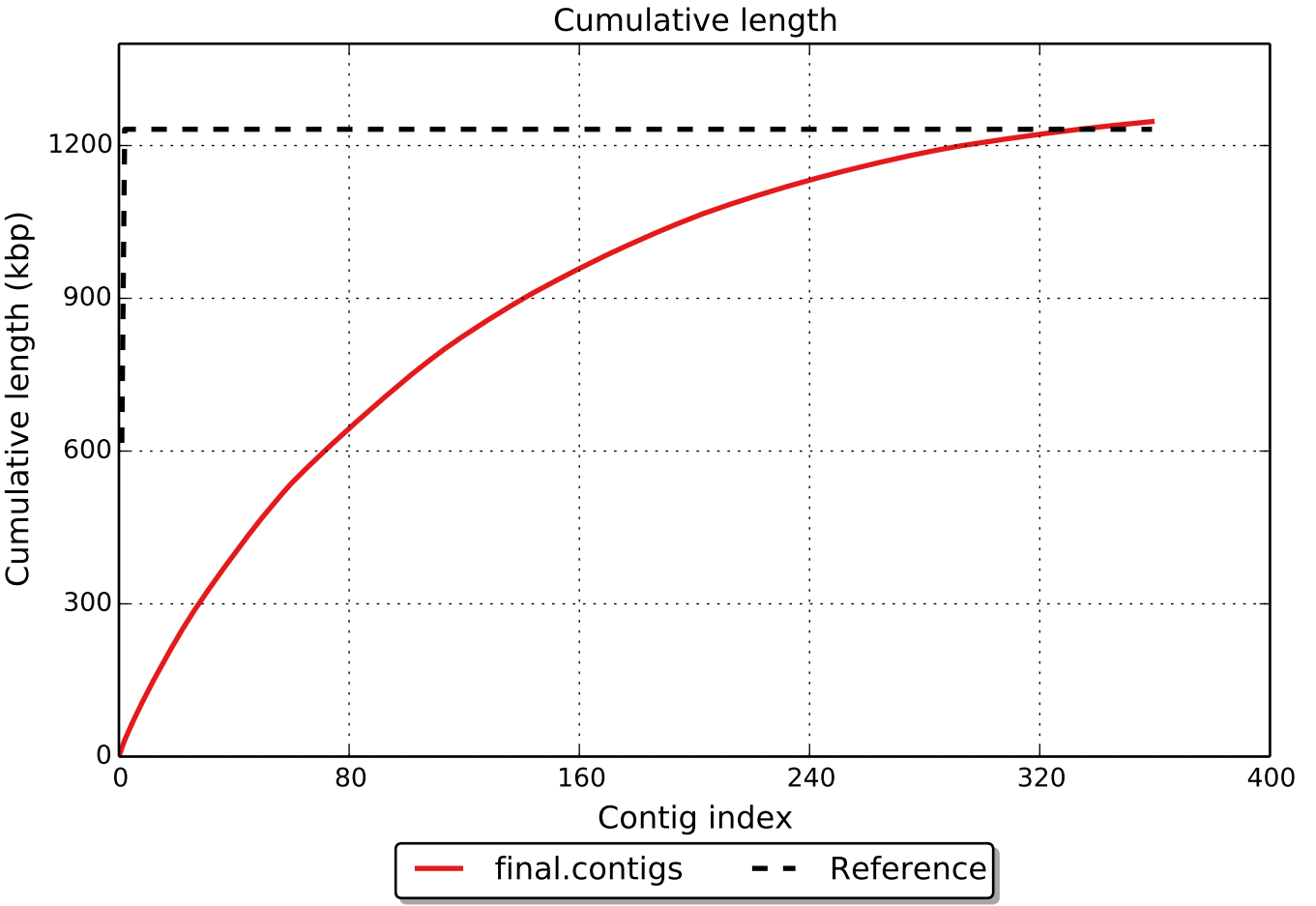
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	361
# indels	4
# short indels	4
# long indels	0
Indels length	4

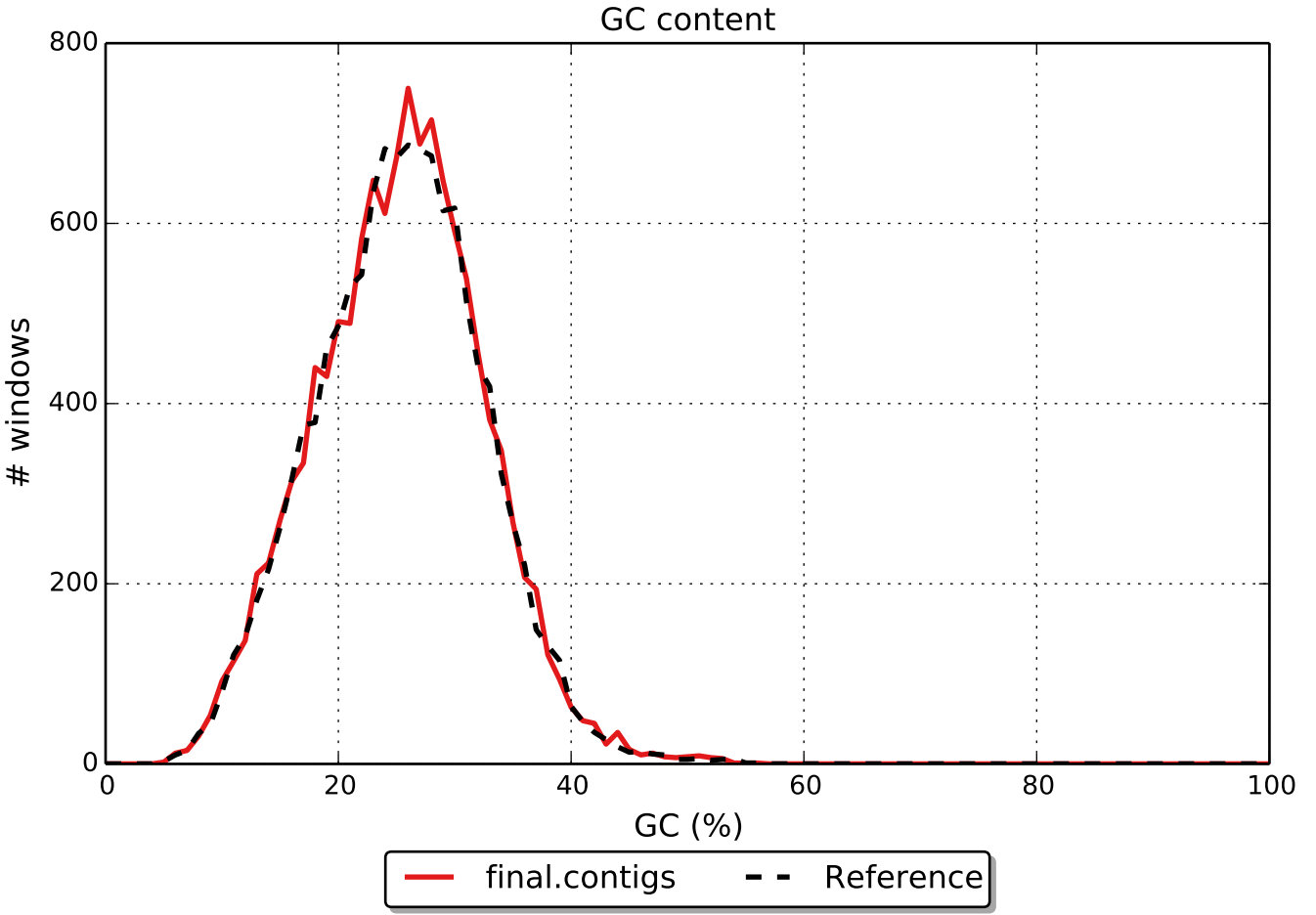
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

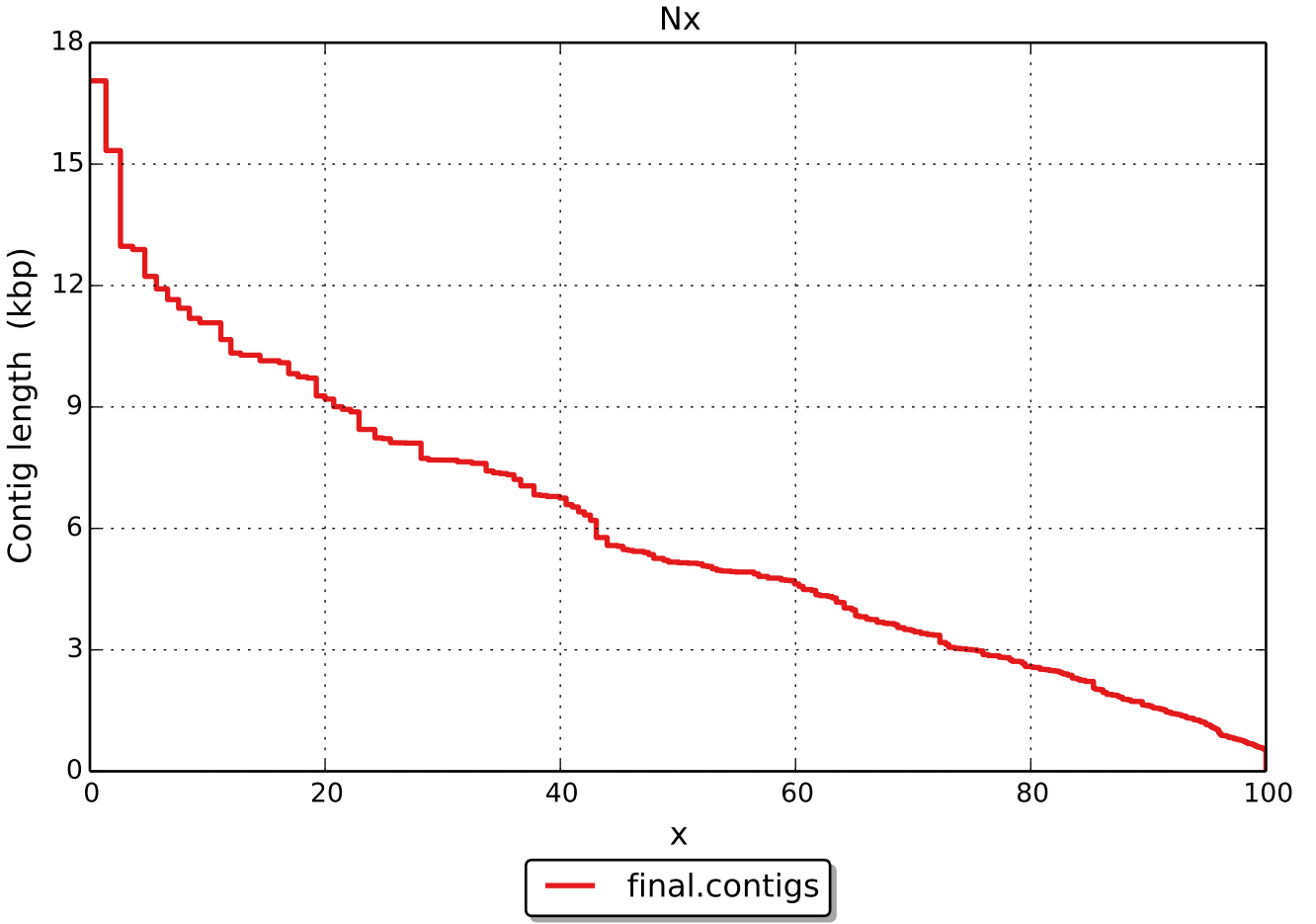
Unaligned report

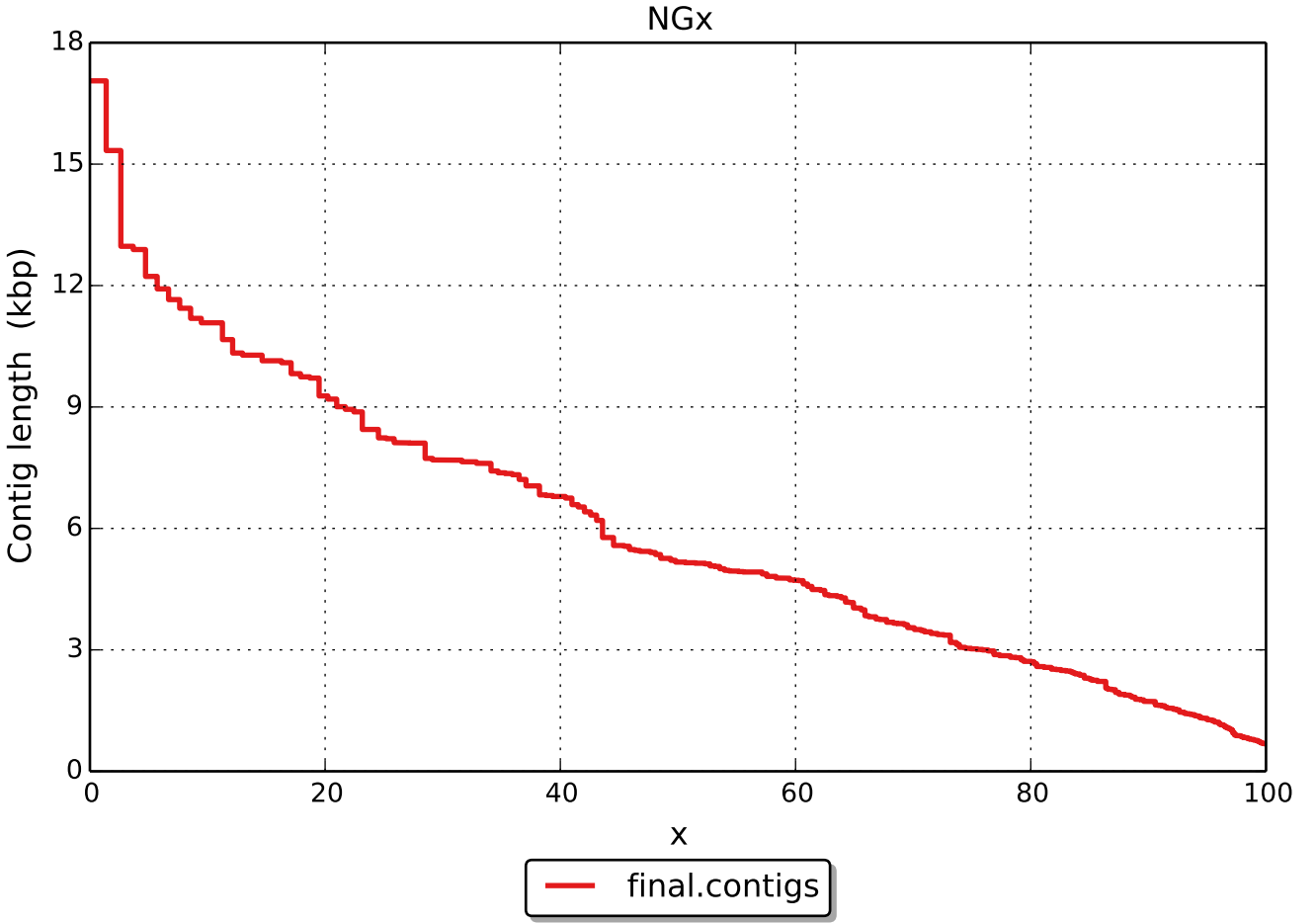
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

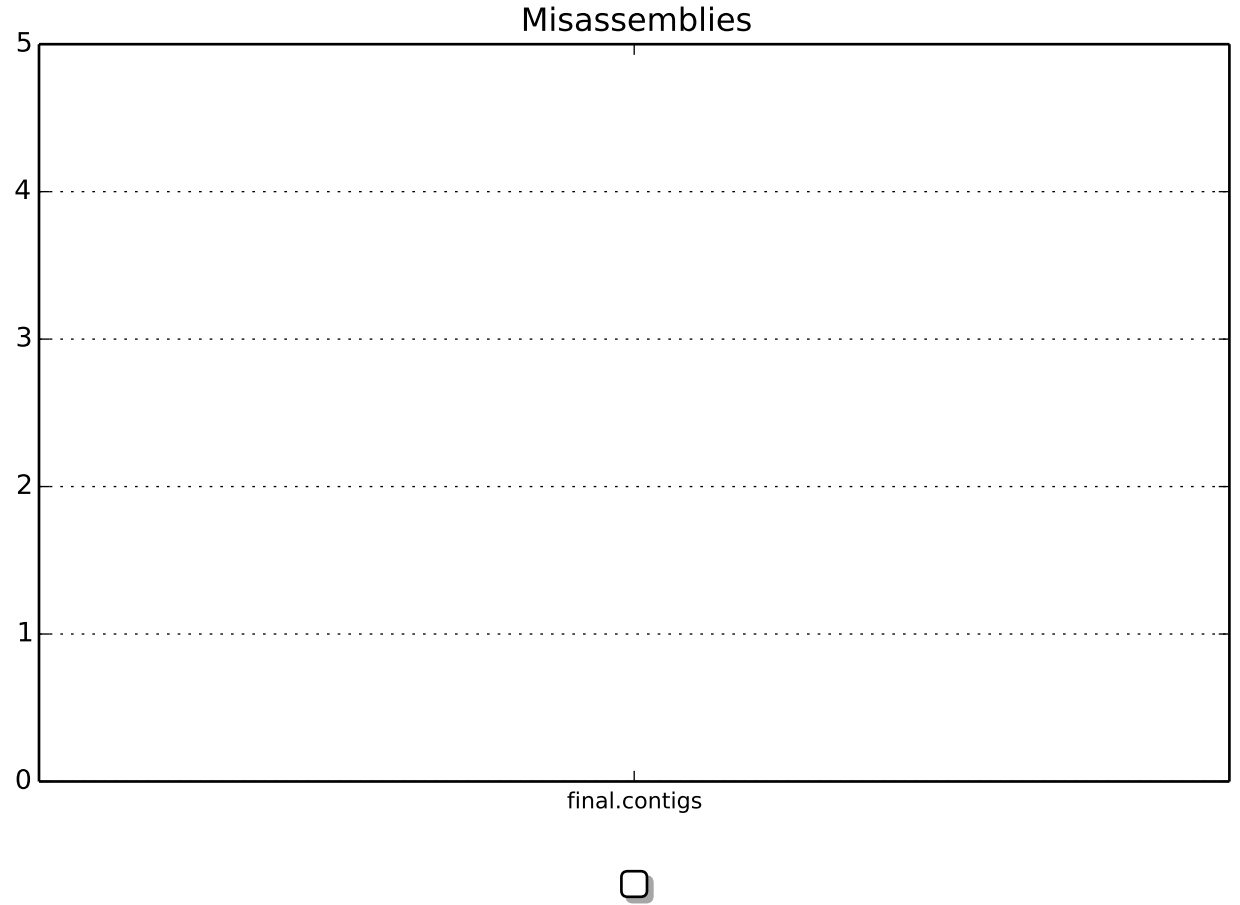
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

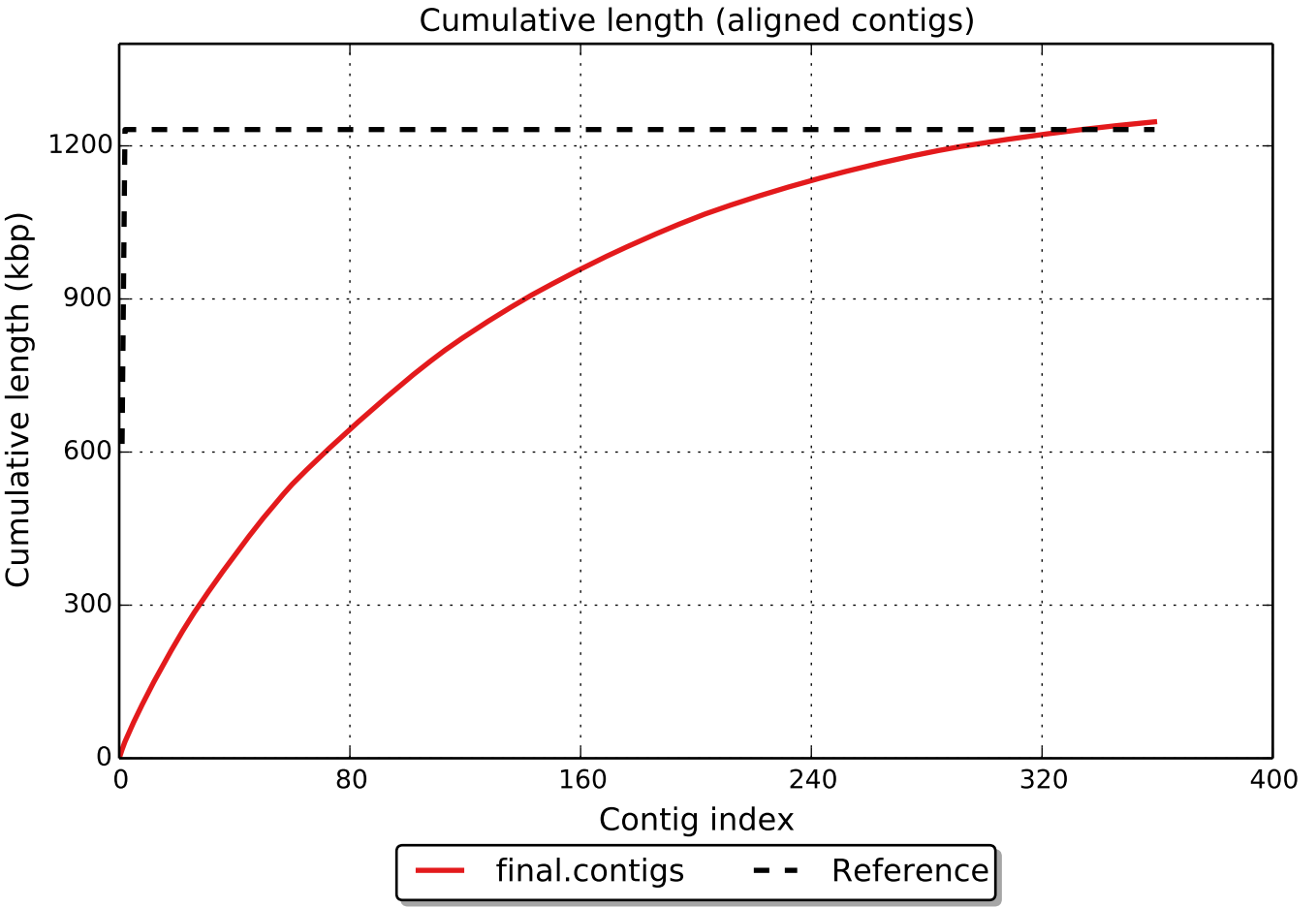

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
80
160
240
320
400
Contig index
final.contigs
Reference

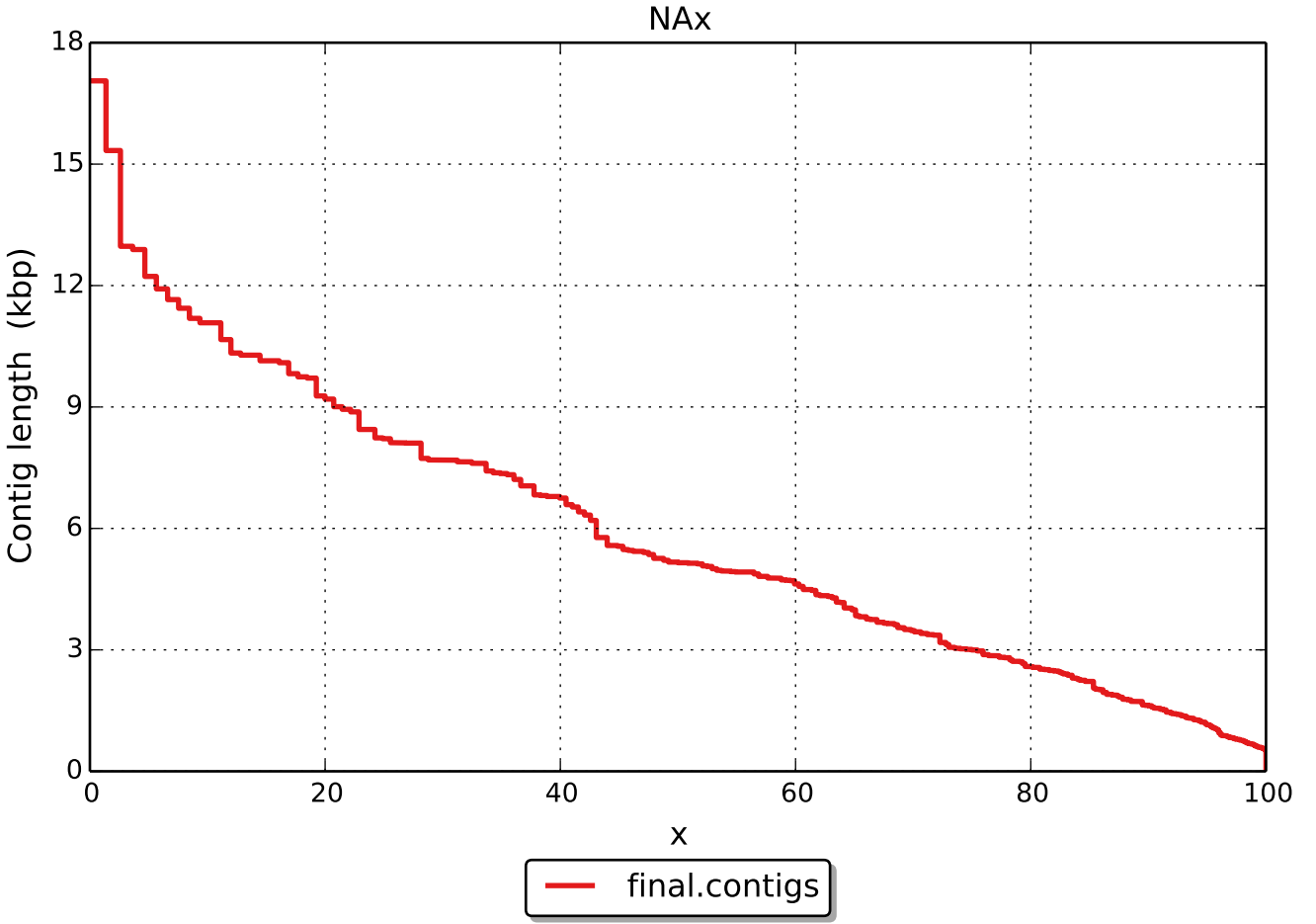

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

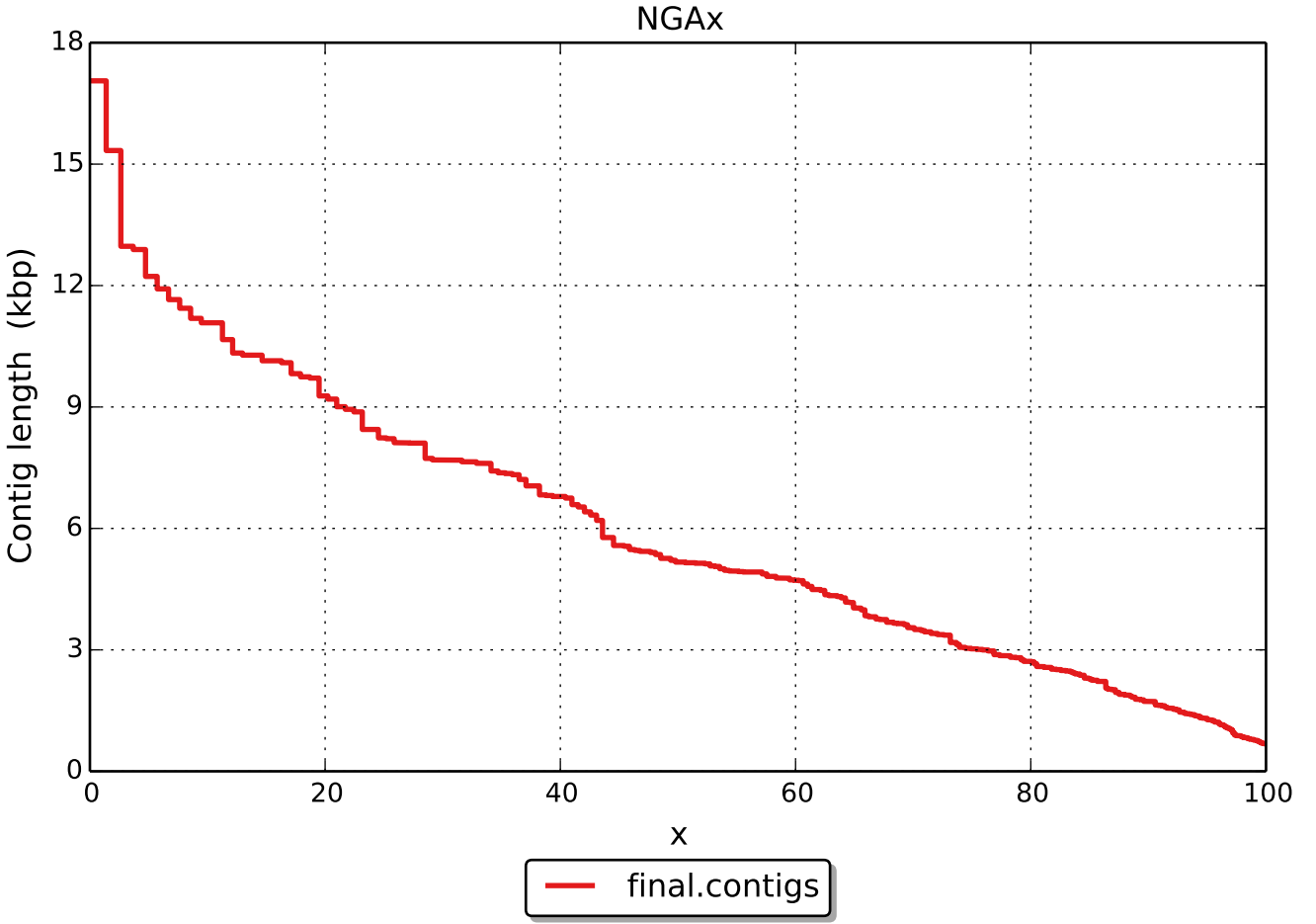

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
18
15
12
9
6
3
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)
1200
900
600
300
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs