Report

	final.contigs
# contigs (>= 0 bp)	399
# contigs (>= 1000 bp)	291
Total length (>= 0 bp)	1803953
Total length (>= 1000 bp)	1733229
# contigs	399
Largest contig	25589
Total length	1803953
Reference length	1892775
GC (%)	32.29
Reference GC (%)	32.26
N50	8216
NG50	8004
N75	4398
NG75	4033
L50	65
LG50	70
L75	138
LG75	153
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	4797
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.202
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	529.11
# indels per 100 kbp	0.17
Largest alignment	25589
NA50	8216
NGA50	8004
NA75	4398
NGA75	4033
LA50	65
LGA50	70
LA75	138
LGA75	153

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

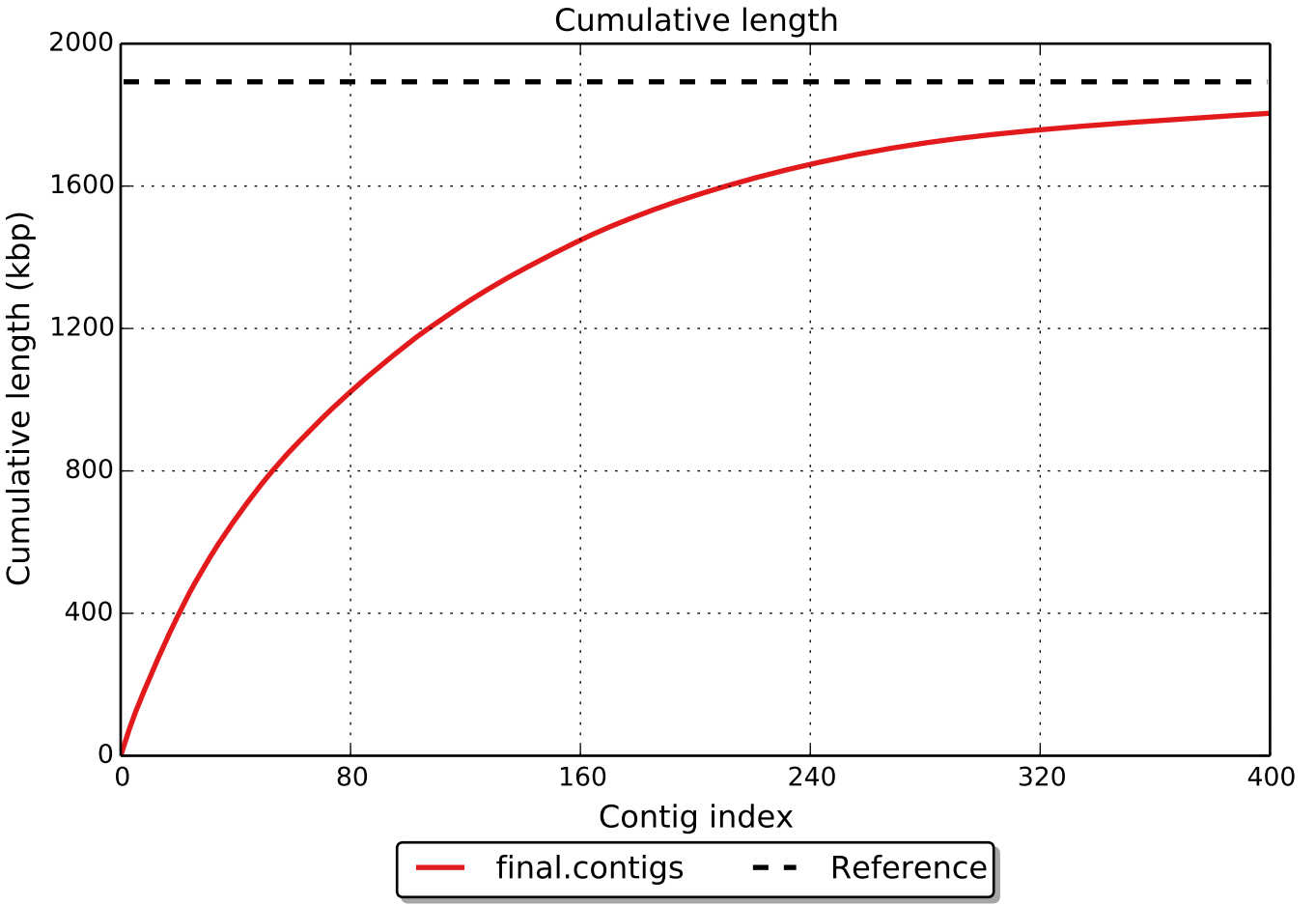
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	4797
# local misassemblies	0
# mismatches	9334
# indels	3
# short indels	2
# long indels	1
Indels length	82

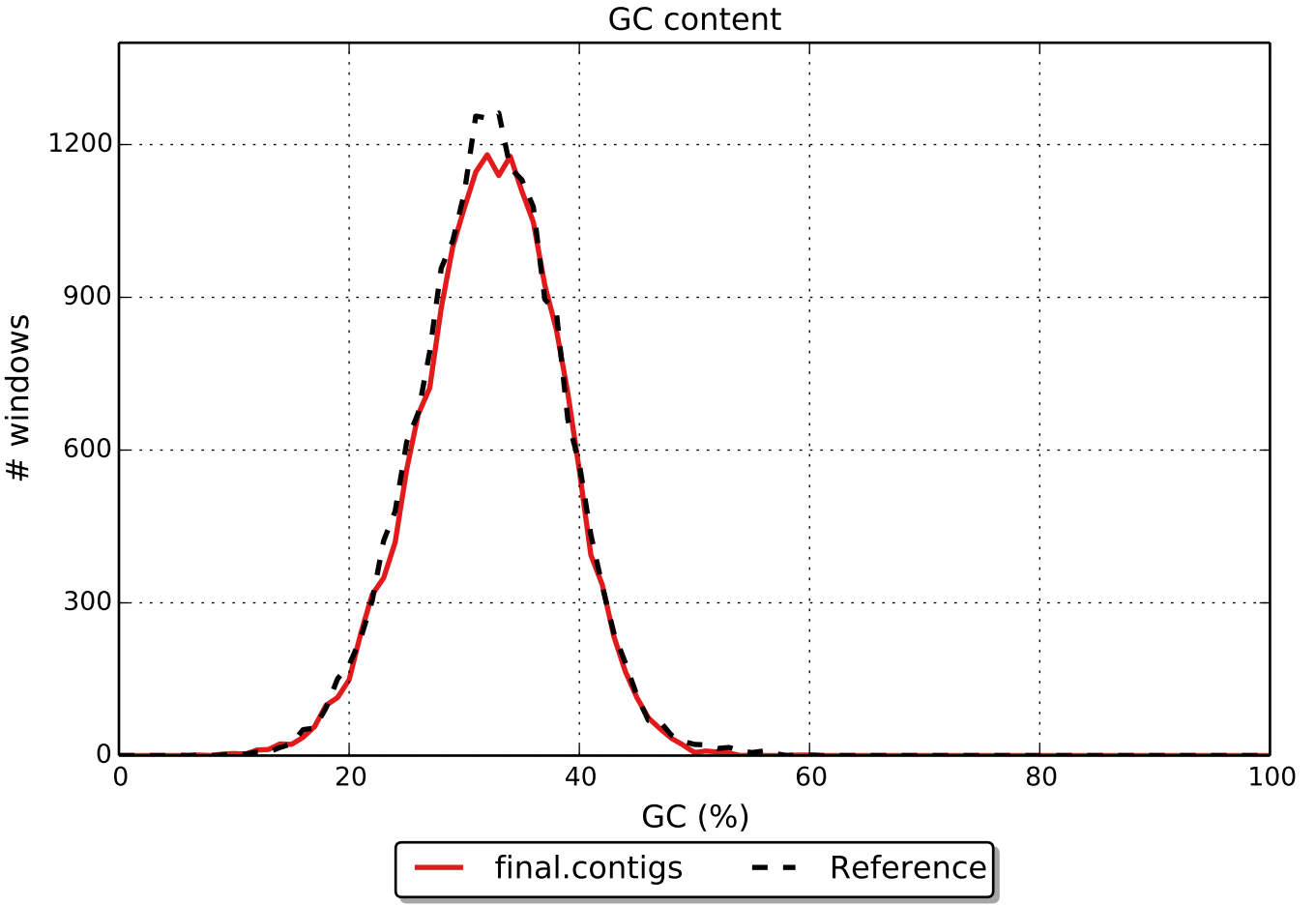
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

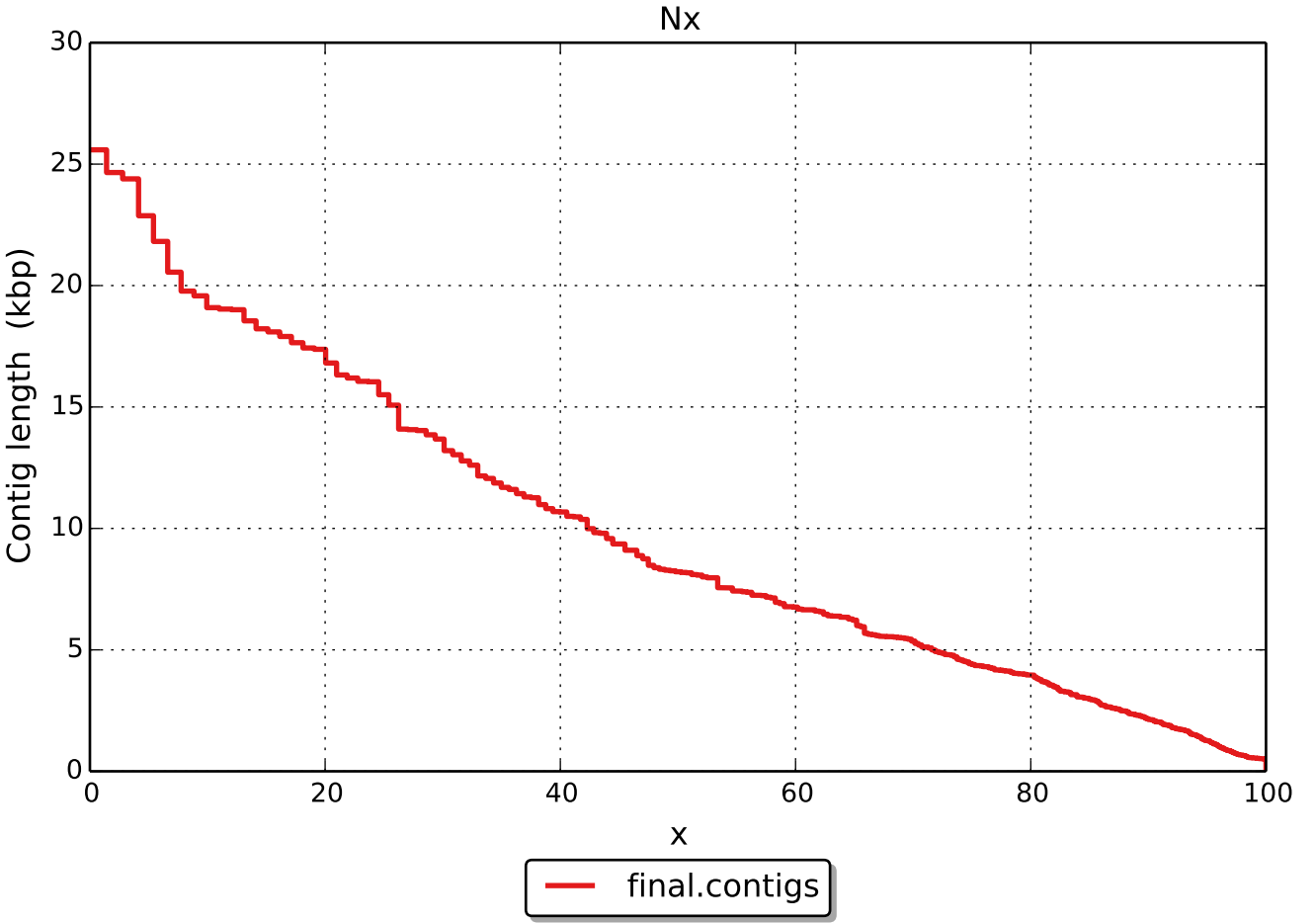
Unaligned report

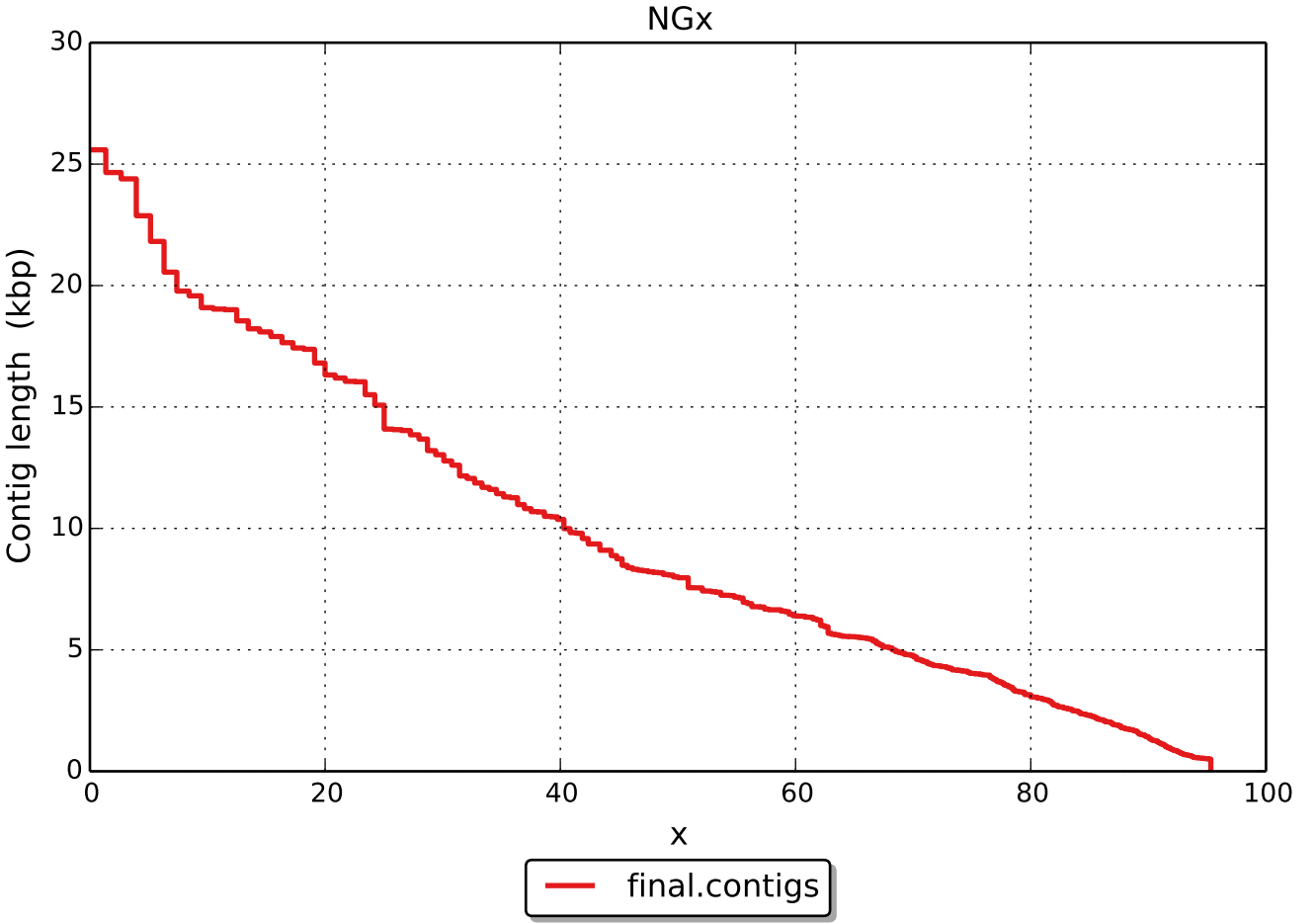
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

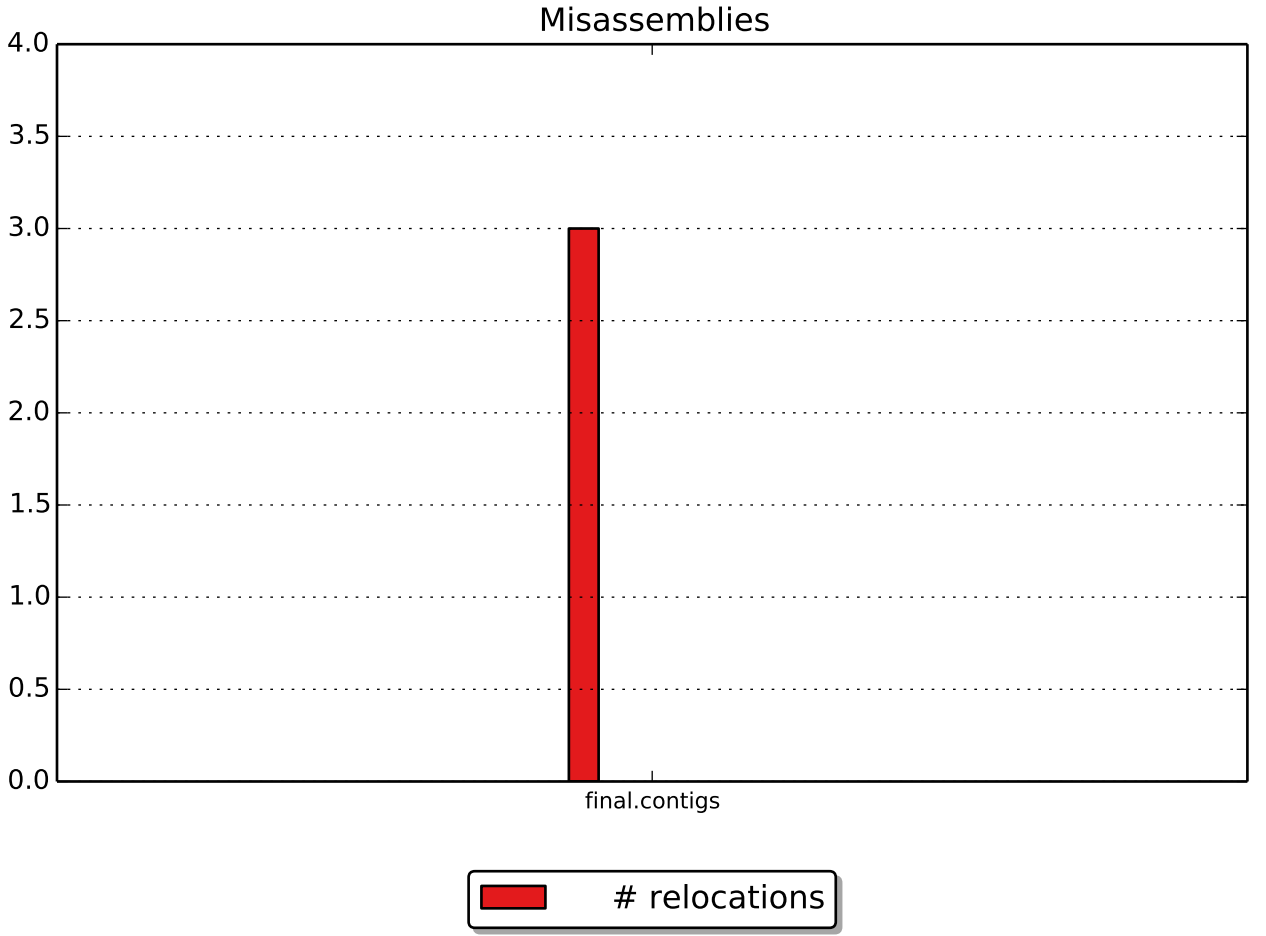
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

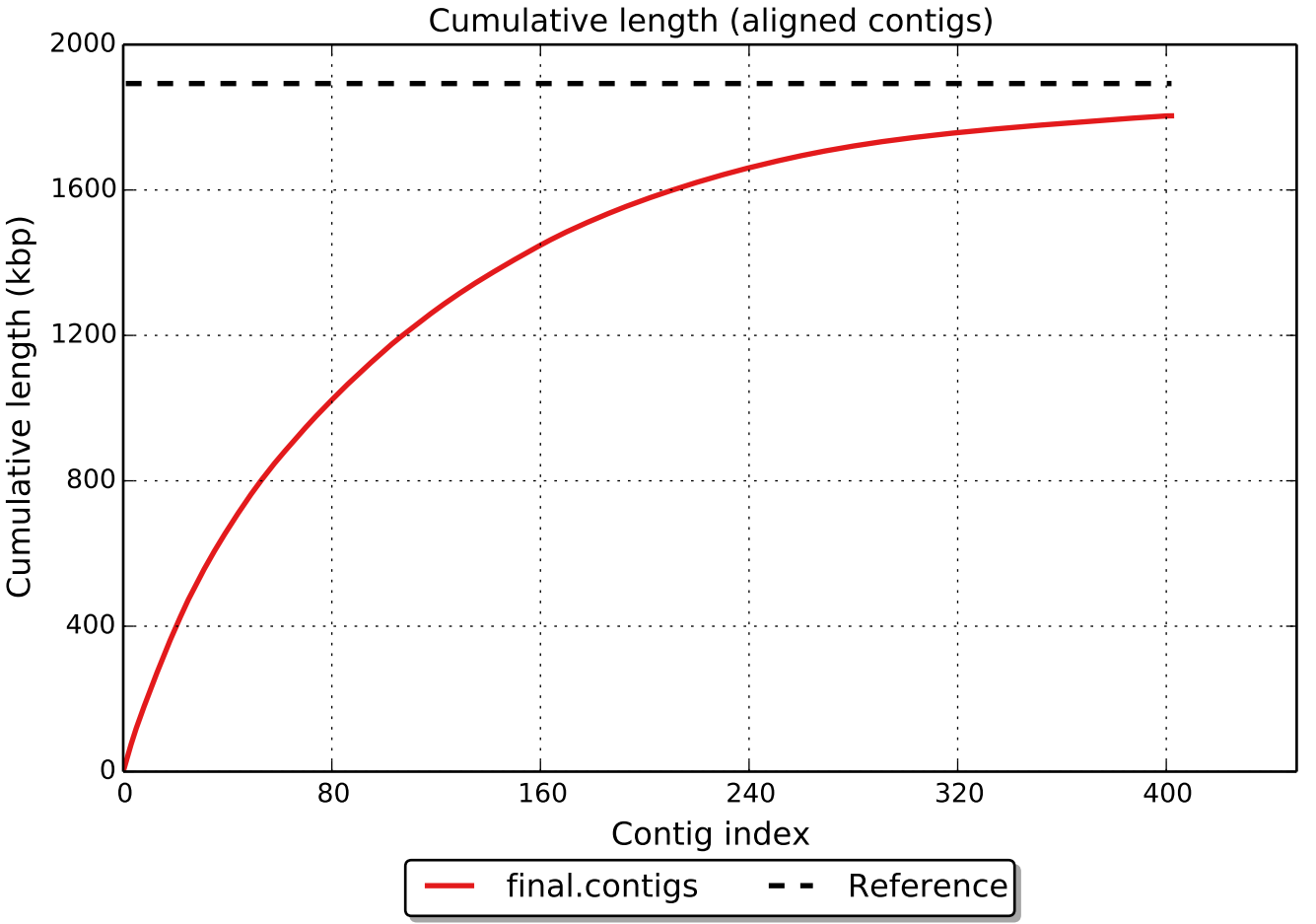

Cumulative length
2000
1600
1200
800
400
0
Cumulative length (kbp)
0
80
160
240
320
400
Contig index
final.contigs
Reference

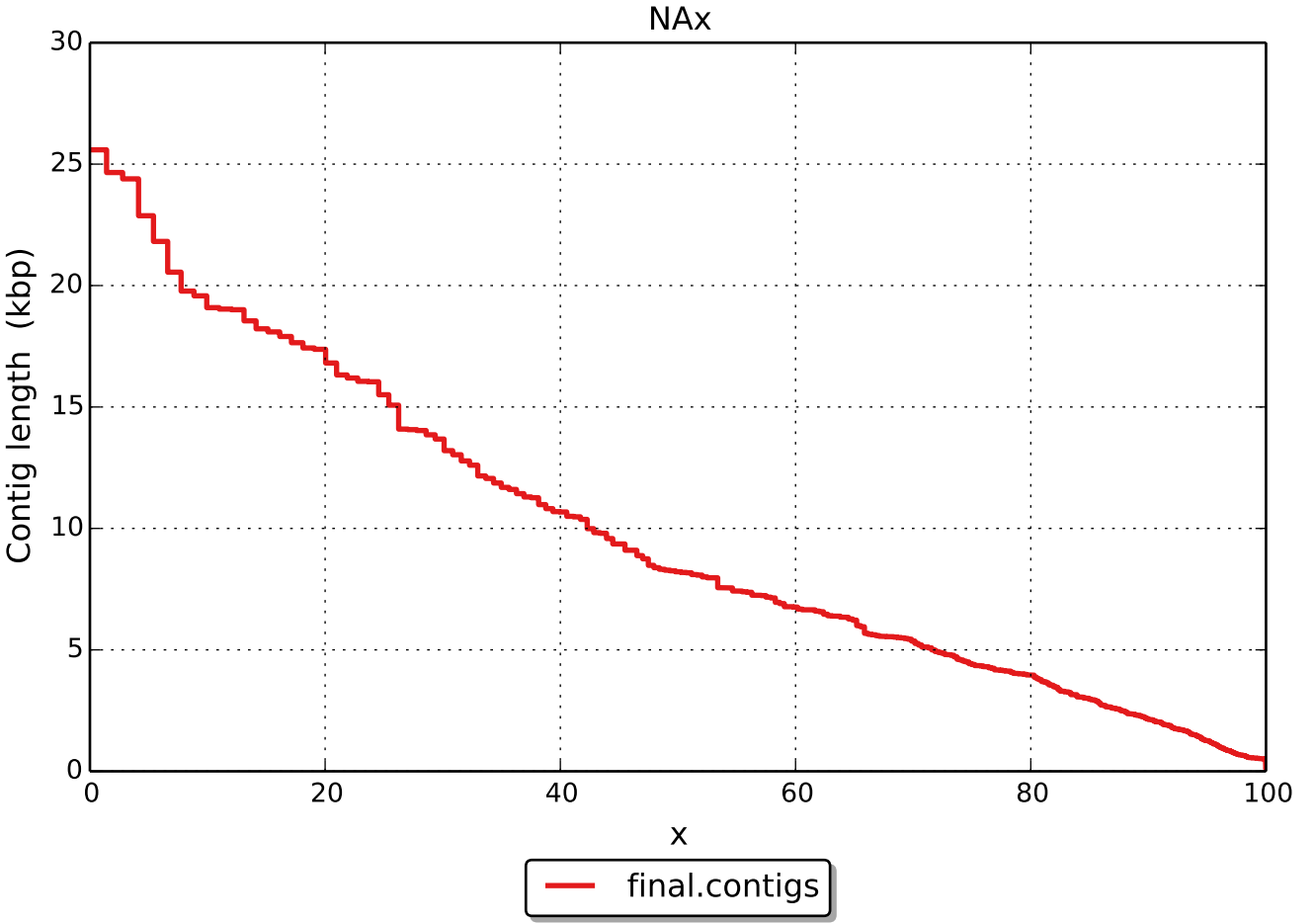

GC content
windows
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

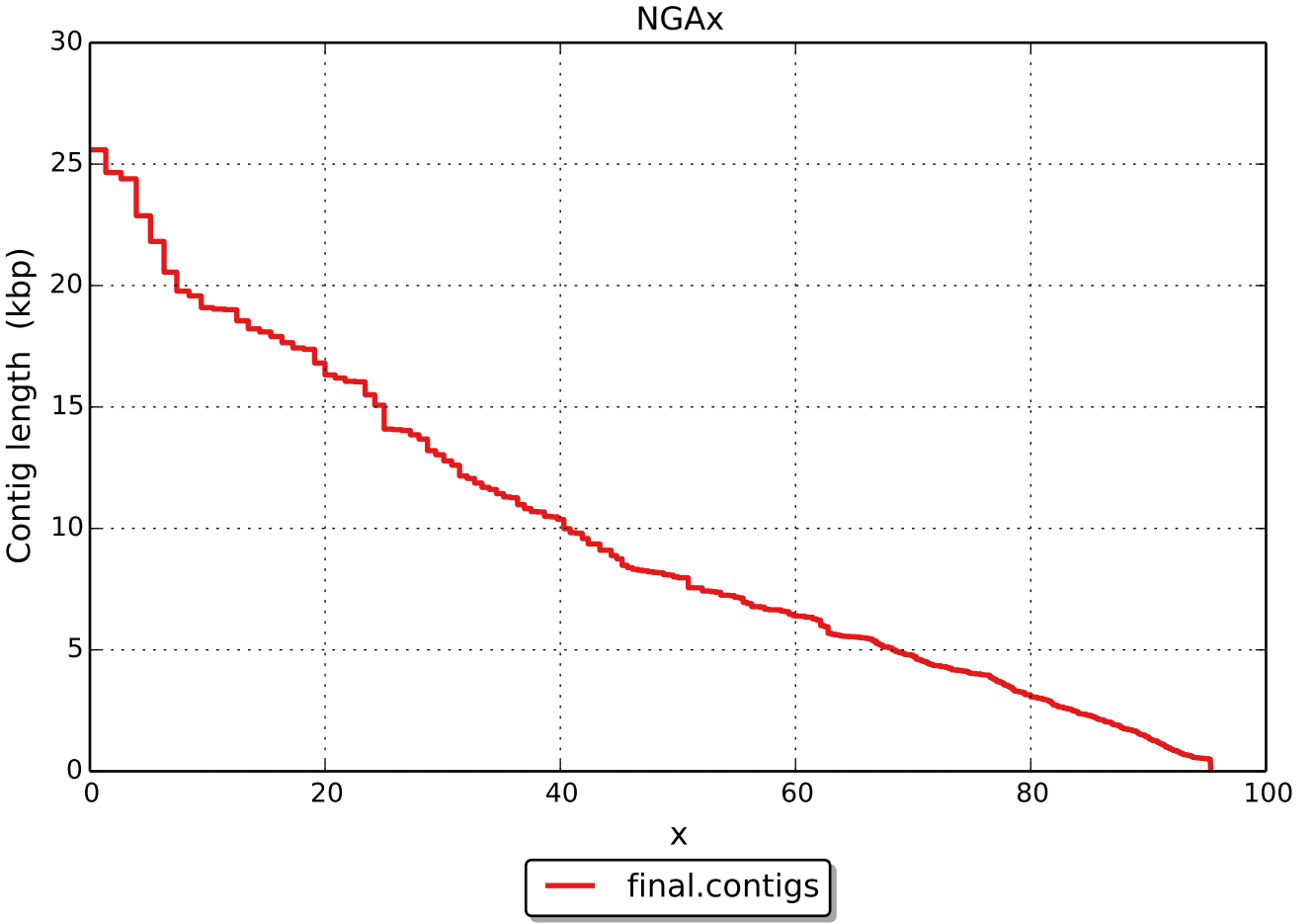

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs