Report

	final.contigs
# contigs (>= 0 bp)	507
# contigs (>= 1000 bp)	478
Total length (>= 0 bp)	3744104
Total length (>= 1000 bp)	3721380
# contigs	507
Largest contig	40013
Total length	3744104
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.27
N50	12018
NG50	18214
N75	6586
NG75	14480
L50	103
LG50	40
L75	207
LG75	69
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	28614
# local misassemblies	0
# unaligned contigs	179 + 80 part
Unaligned length	1749084
Genome fraction (%)	99.870
Duplication ratio	1.055
# N's per 100 kbp	0.00
# mismatches per 100 kbp	64.91
# indels per 100 kbp	0.58
Largest alignment	40013
NA50	2025
NGA50	13586
NGA75	7962
LA50	190
LGA50	47
LGA75	91

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

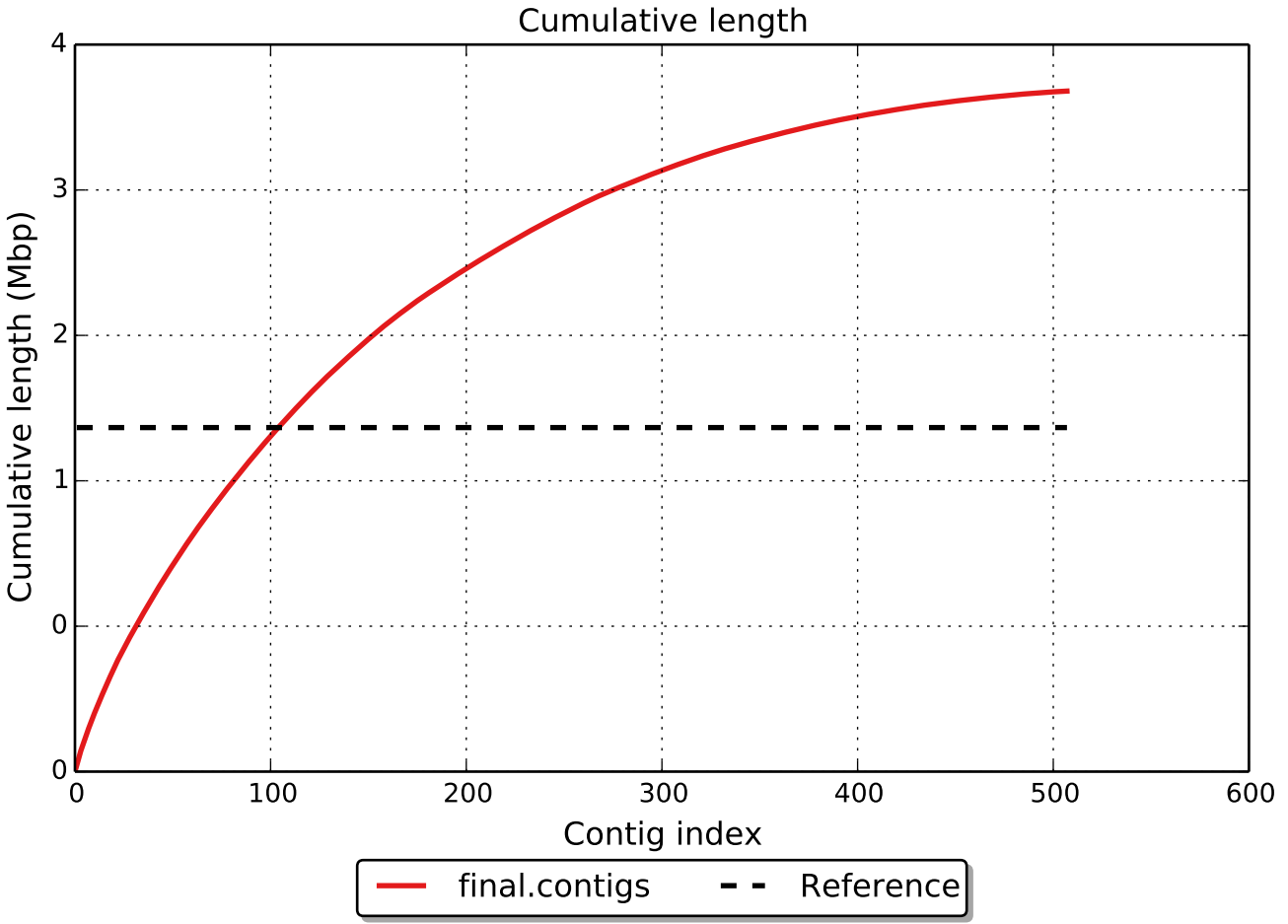
	final.contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	1
# possibly misassembled contigs	9
# misassembled contigs	2
Misassembled contigs length	28614
# local misassemblies	0
# mismatches	1227
# indels	11
# short indels	5
# long indels	6
Indels length	73

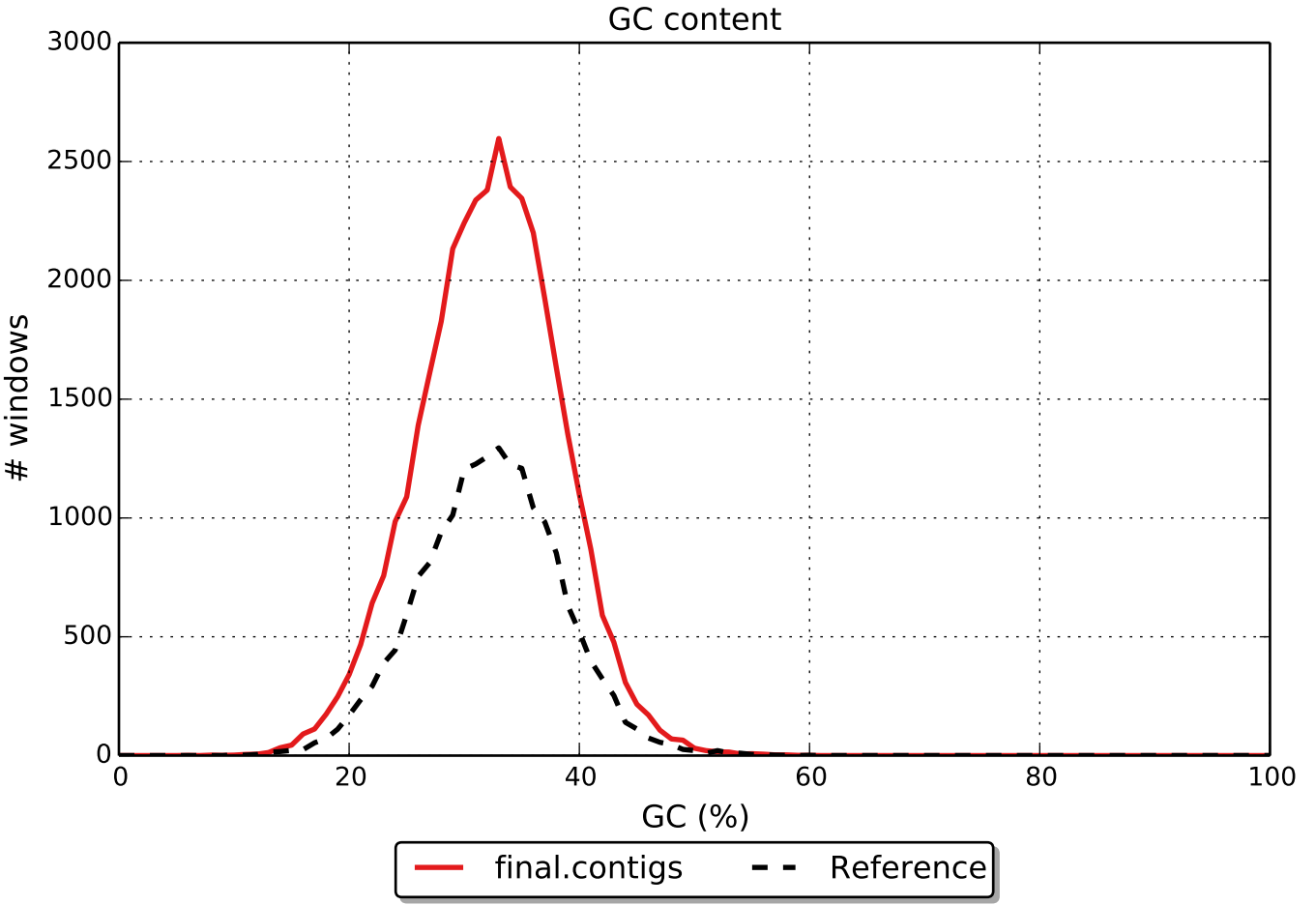
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

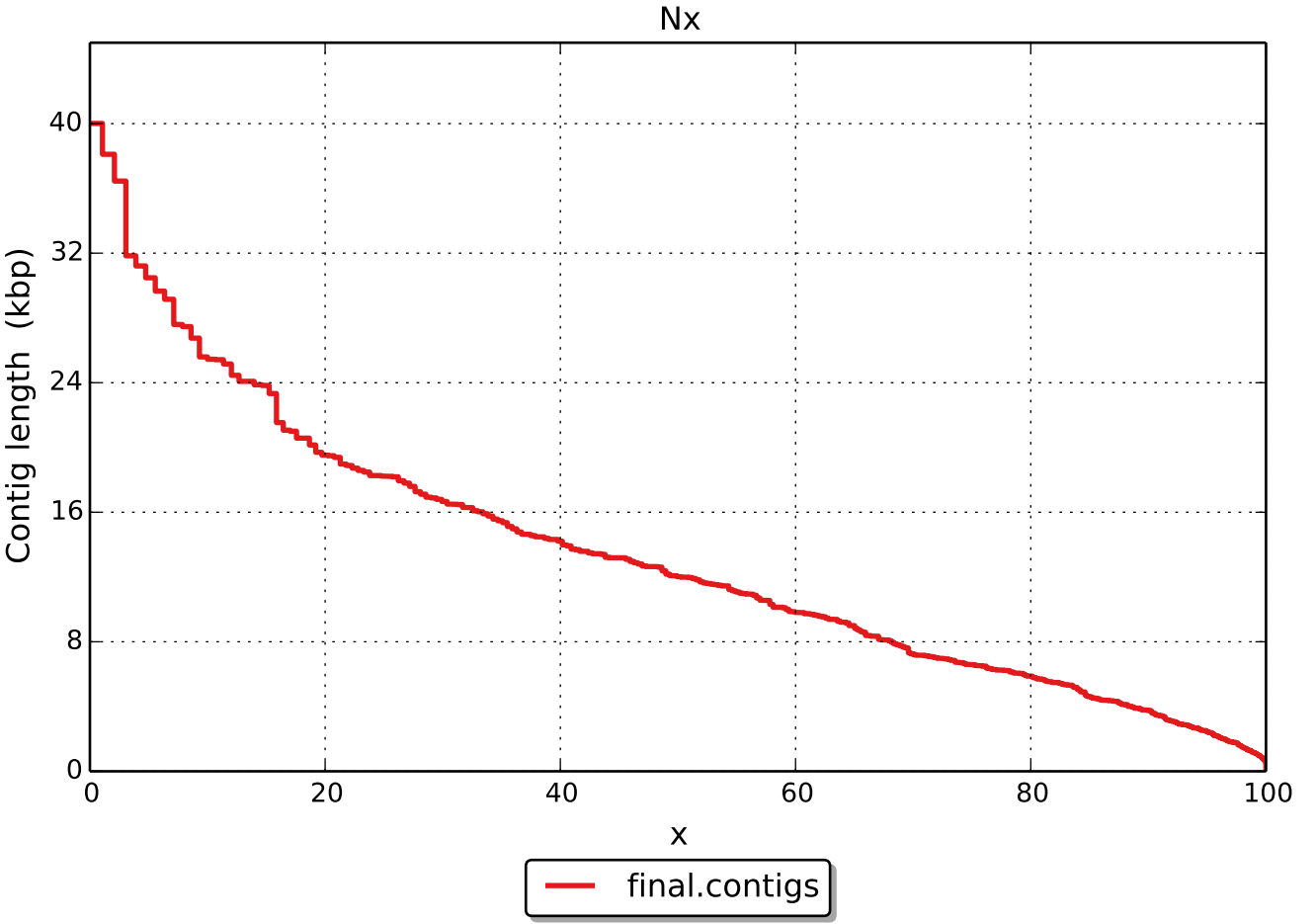
Unaligned report

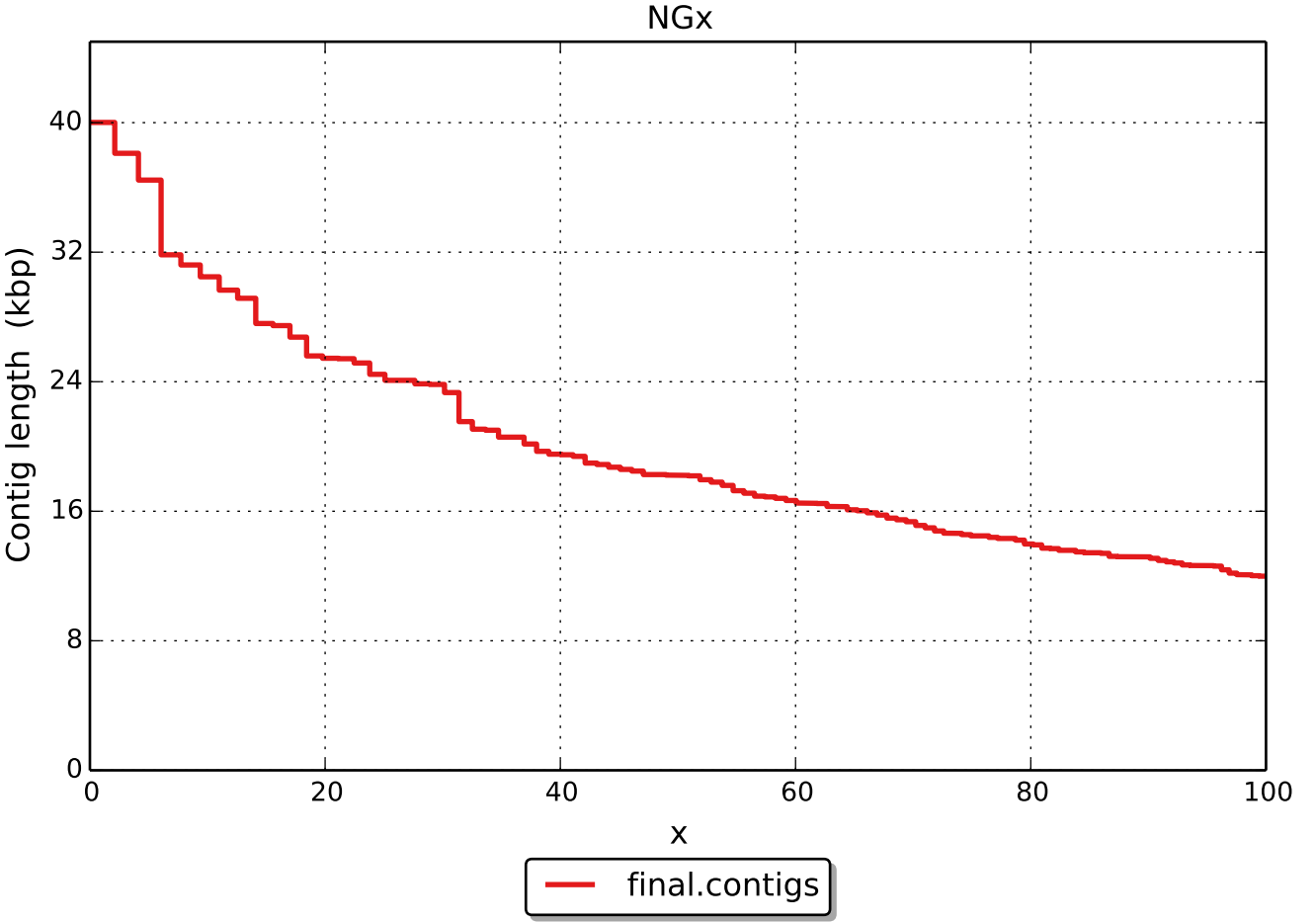
	final.contigs
# fully unaligned contigs	179
Fully unaligned length	1199989
# partially unaligned contigs	80
# with misassembly	5
# both parts are significant	7
Partially unaligned length	549095
# N's	0

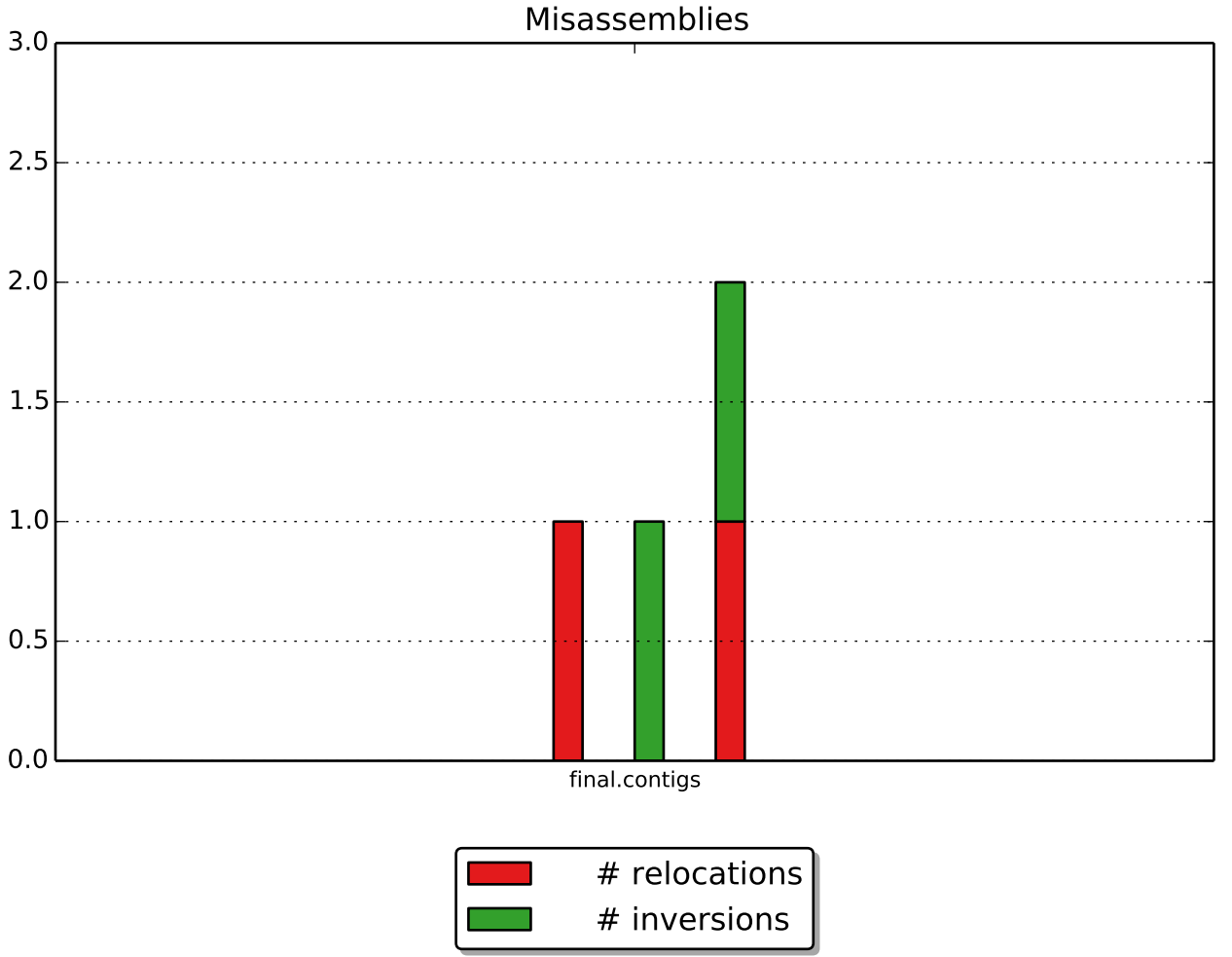
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

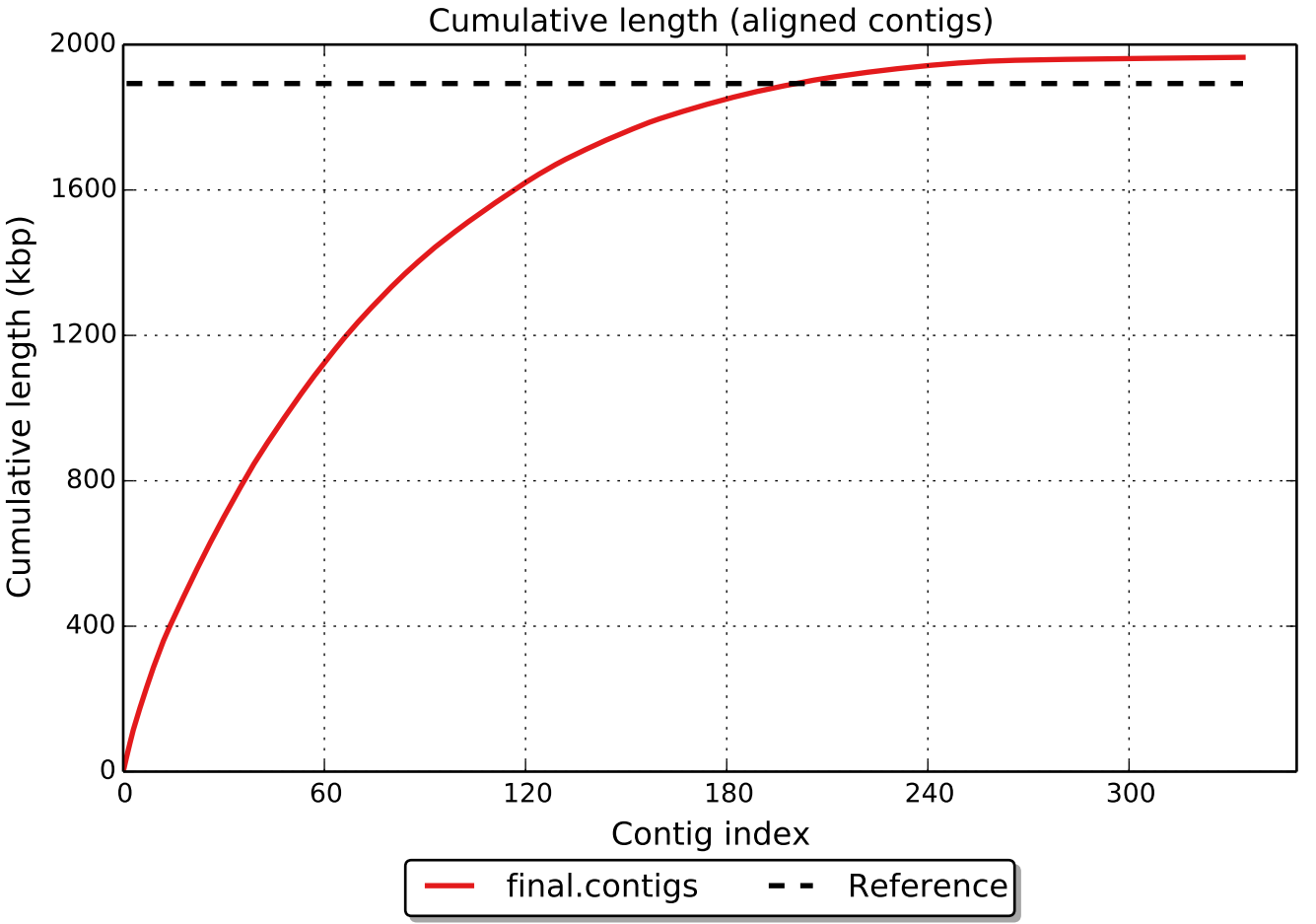

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

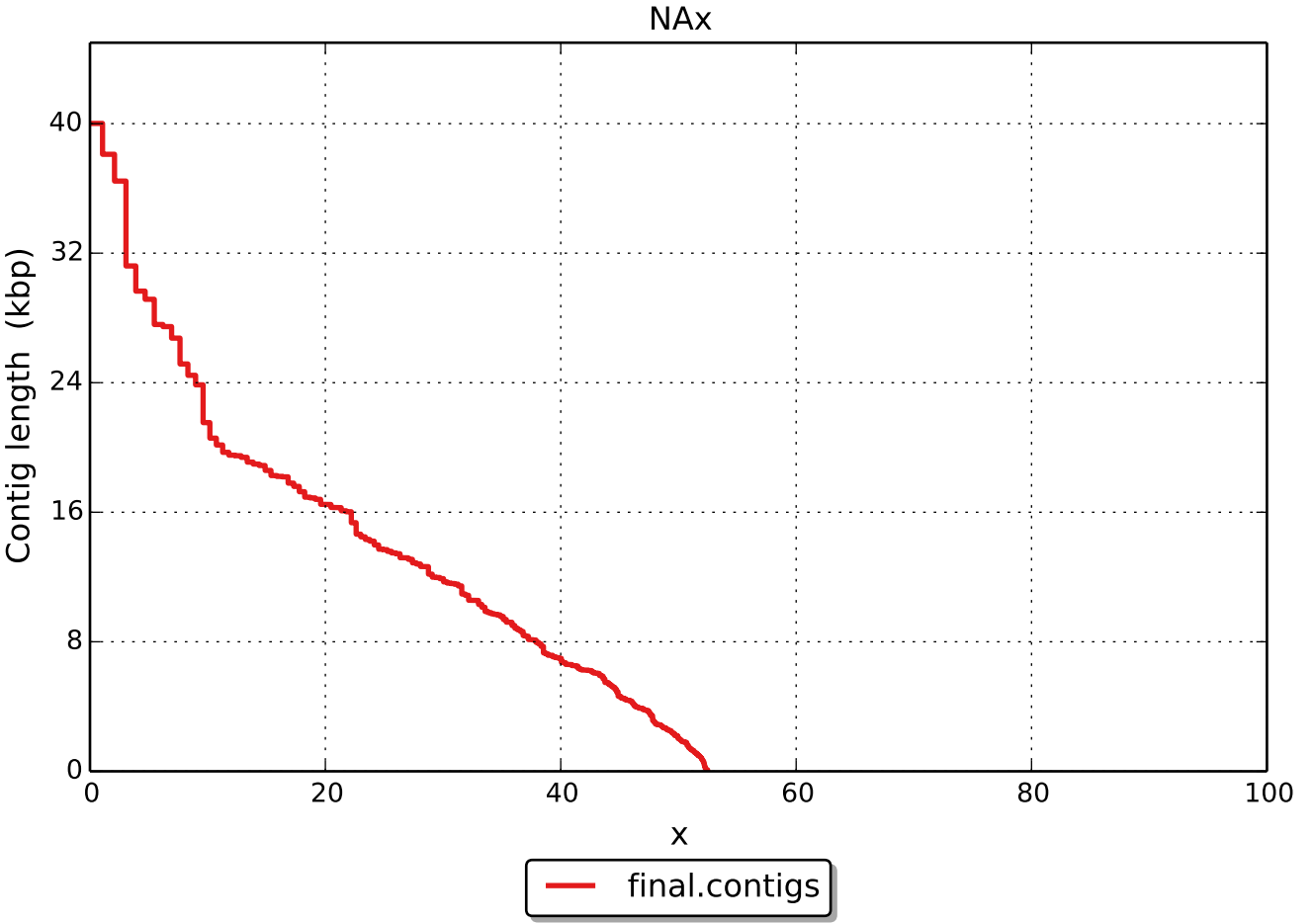

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

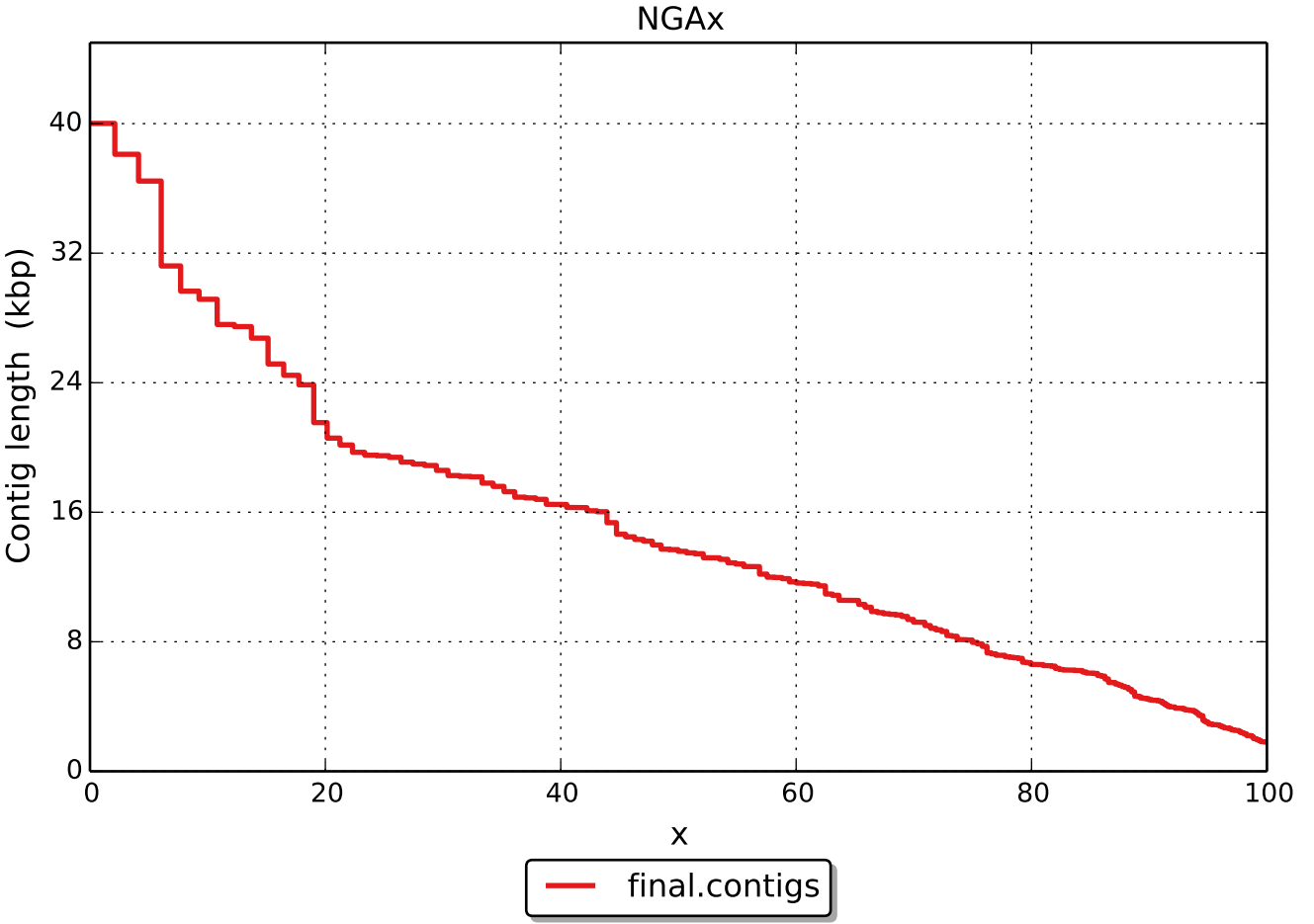

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


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


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
60
120
180
240
300
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)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs