Report

	final.contigs
# contigs (>= 0 bp)	453
# contigs (>= 1000 bp)	356
Total length (>= 0 bp)	1246532
Total length (>= 1000 bp)	1175224
# contigs	453
Largest contig	17588
Total length	1246532
Reference length	615980
GC (%)	25.38
Reference GC (%)	25.32
N50	3892
NG50	6191
N75	2341
NG75	5112
L50	100
LG50	35
L75	203
LG75	63
# misassemblies	36
# misassembled contigs	29
Misassembled contigs length	146916
# local misassemblies	0
# unaligned contigs	19 + 7 part
Unaligned length	62568
Genome fraction (%)	98.800
Duplication ratio	1.945
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1551.96
# indels per 100 kbp	2.96
Largest alignment	14027
NA50	3392
NGA50	5356
NA75	1866
NGA75	4204
LA50	116
LGA50	41
LA75	237
LGA75	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).

Misassemblies report

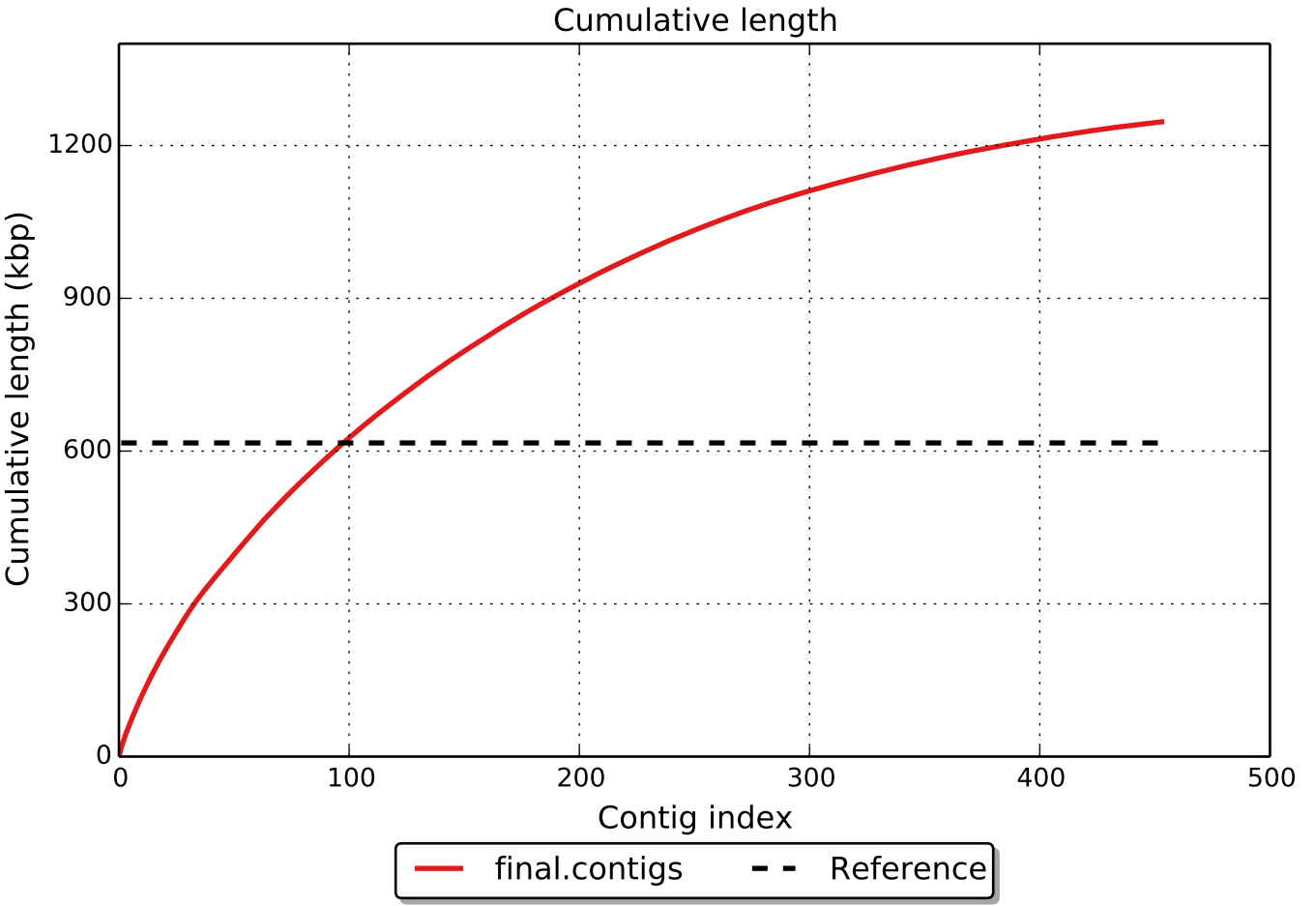
	final.contigs
# misassemblies	36
# relocations	35
# translocations	0
# inversions	1
# possibly misassembled contigs	8
# misassembled contigs	29
Misassembled contigs length	146916
# local misassemblies	0
# mismatches	9445
# indels	18
# short indels	18
# long indels	0
Indels length	18

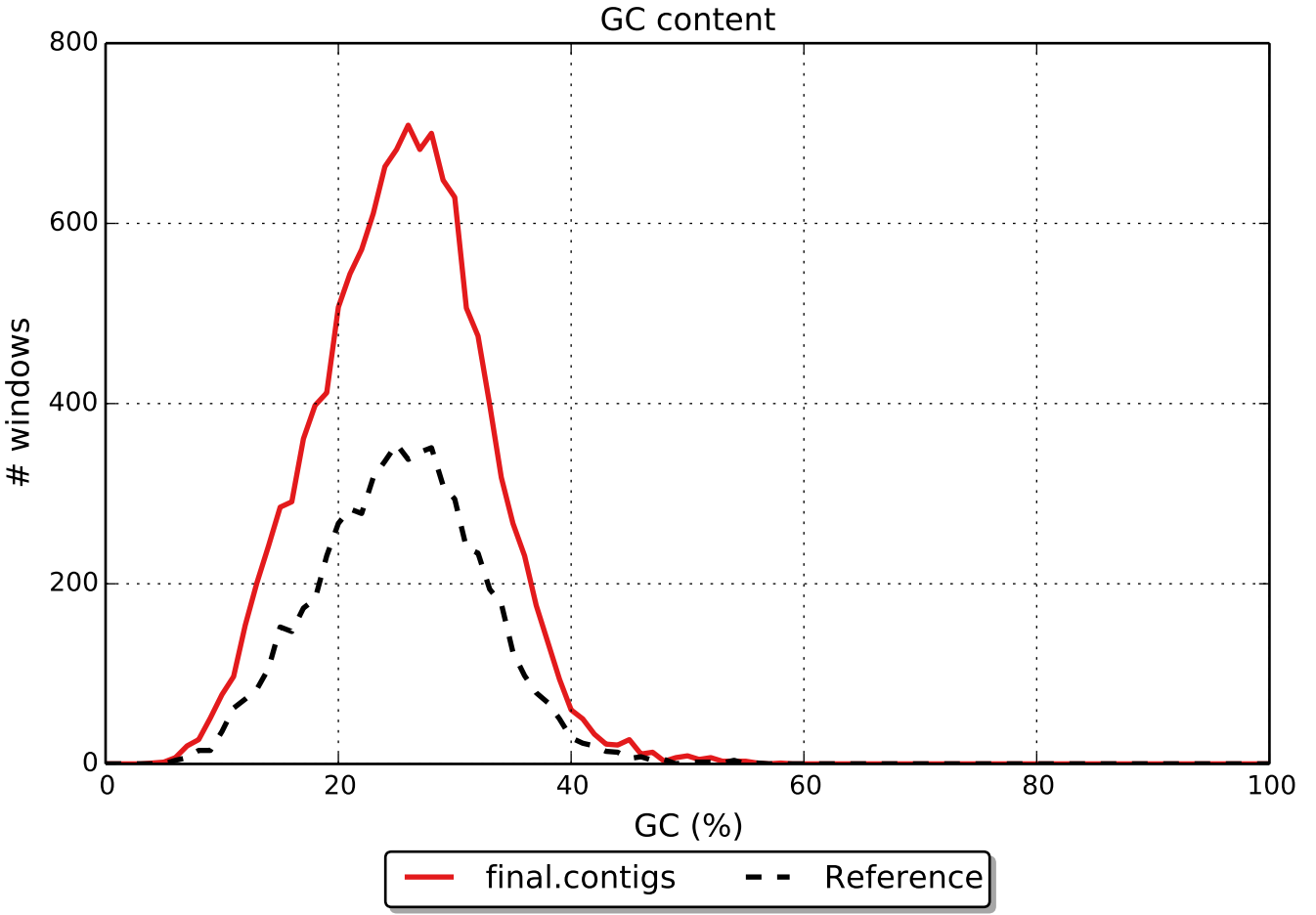
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

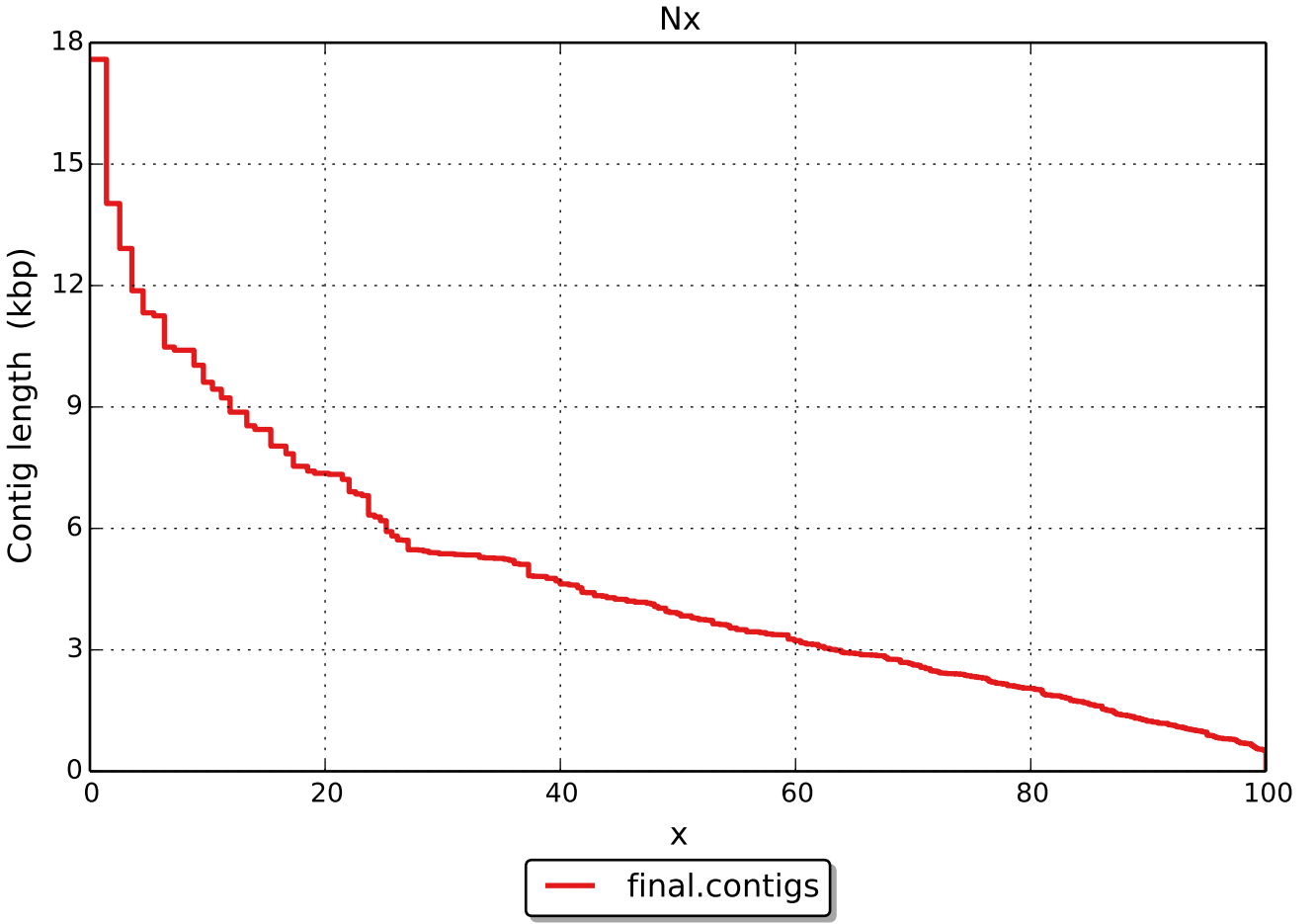
Unaligned report

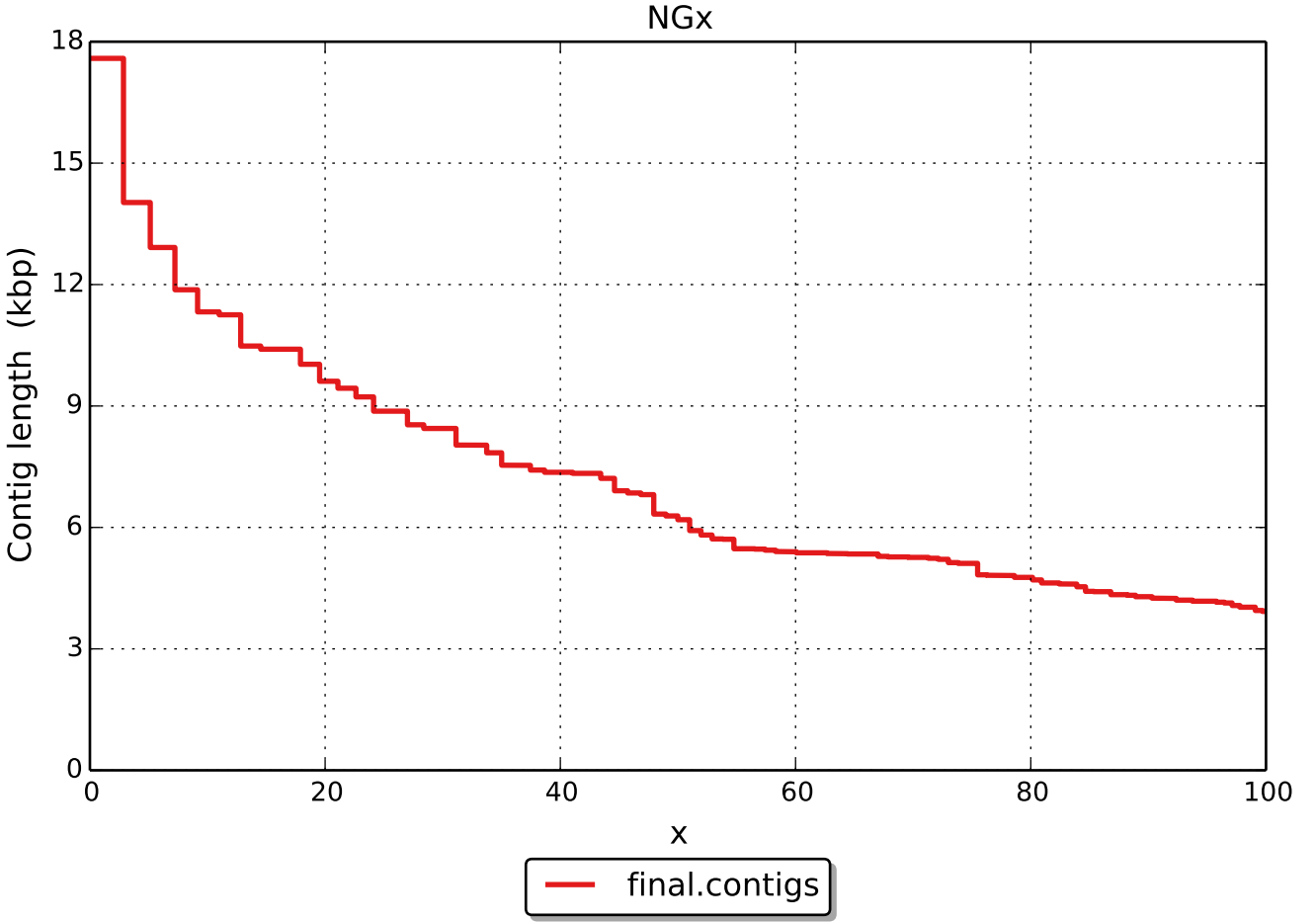
	final.contigs
# fully unaligned contigs	19
Fully unaligned length	42543
# partially unaligned contigs	7
# with misassembly	1
# both parts are significant	6
Partially unaligned length	20025
# N's	0

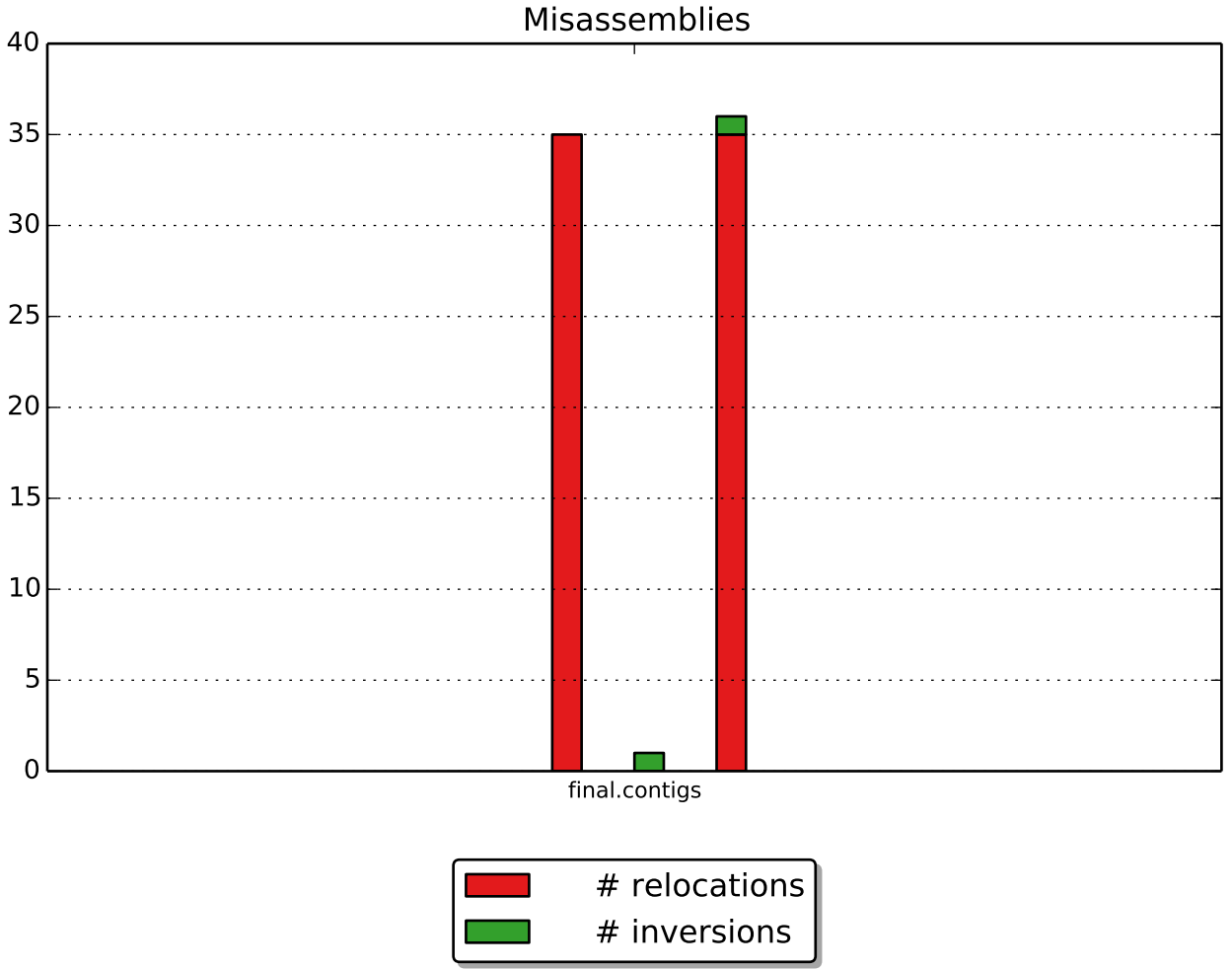
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

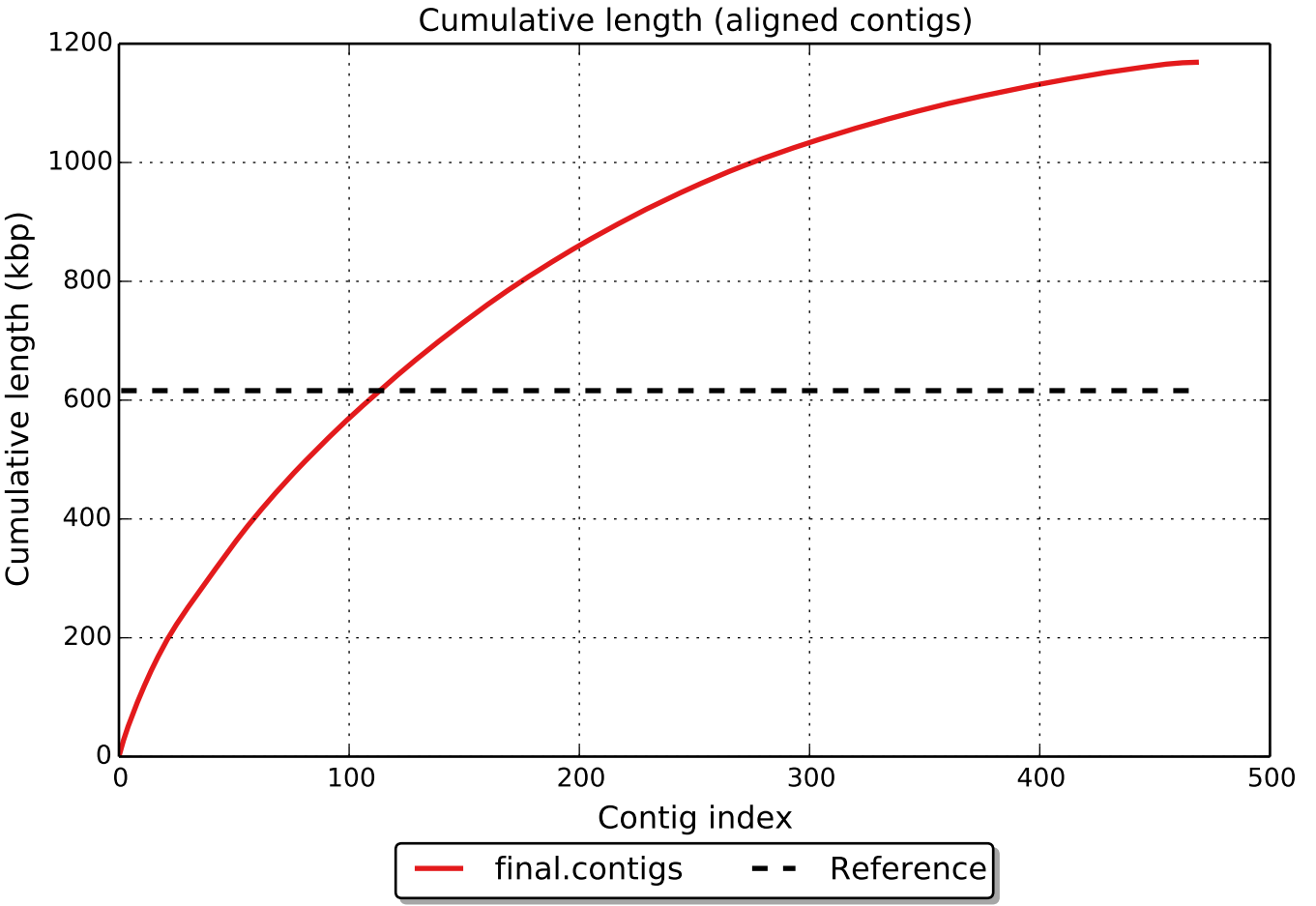

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
100
200
300
400
500
Contig index
final.contigs
Reference

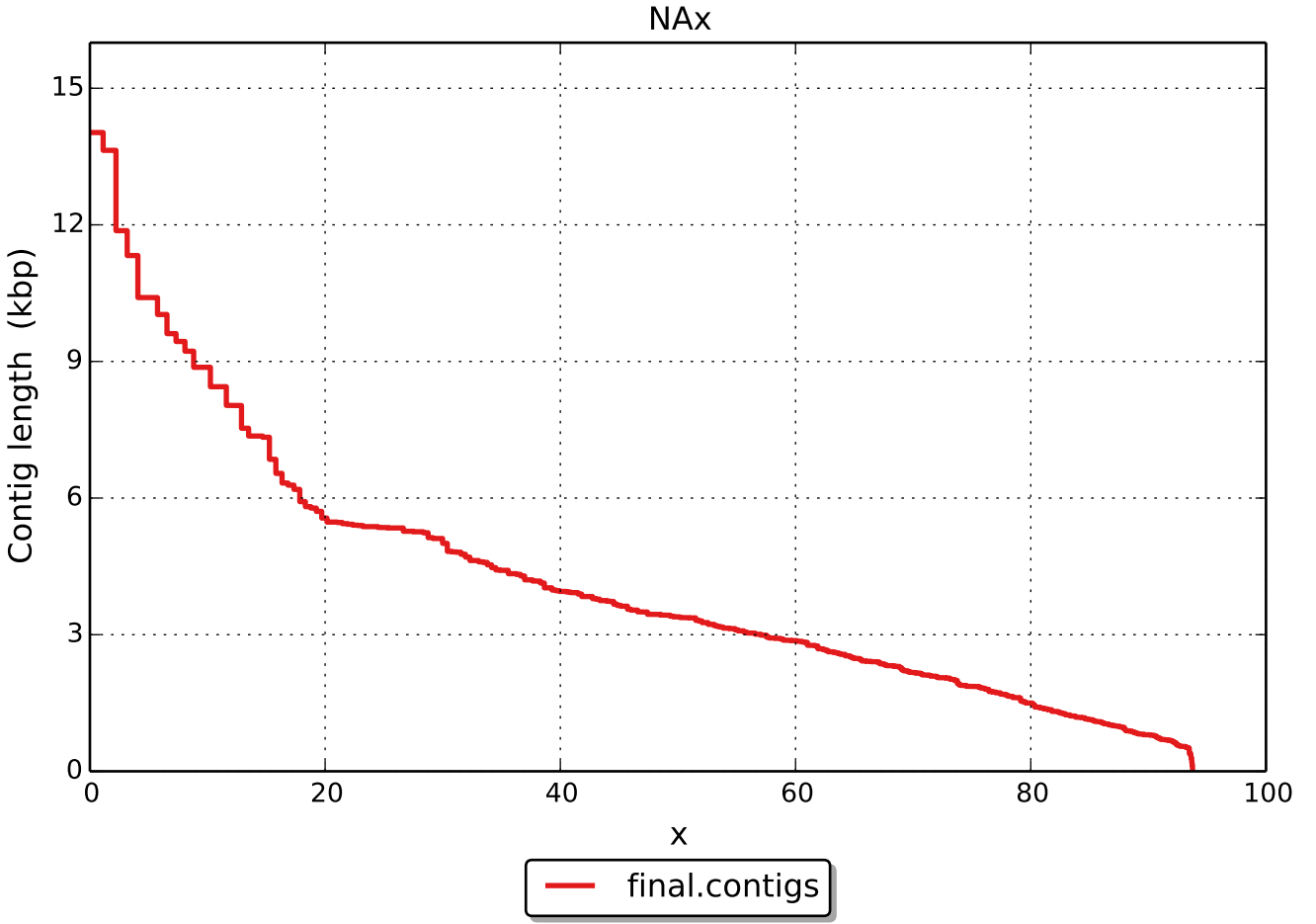

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

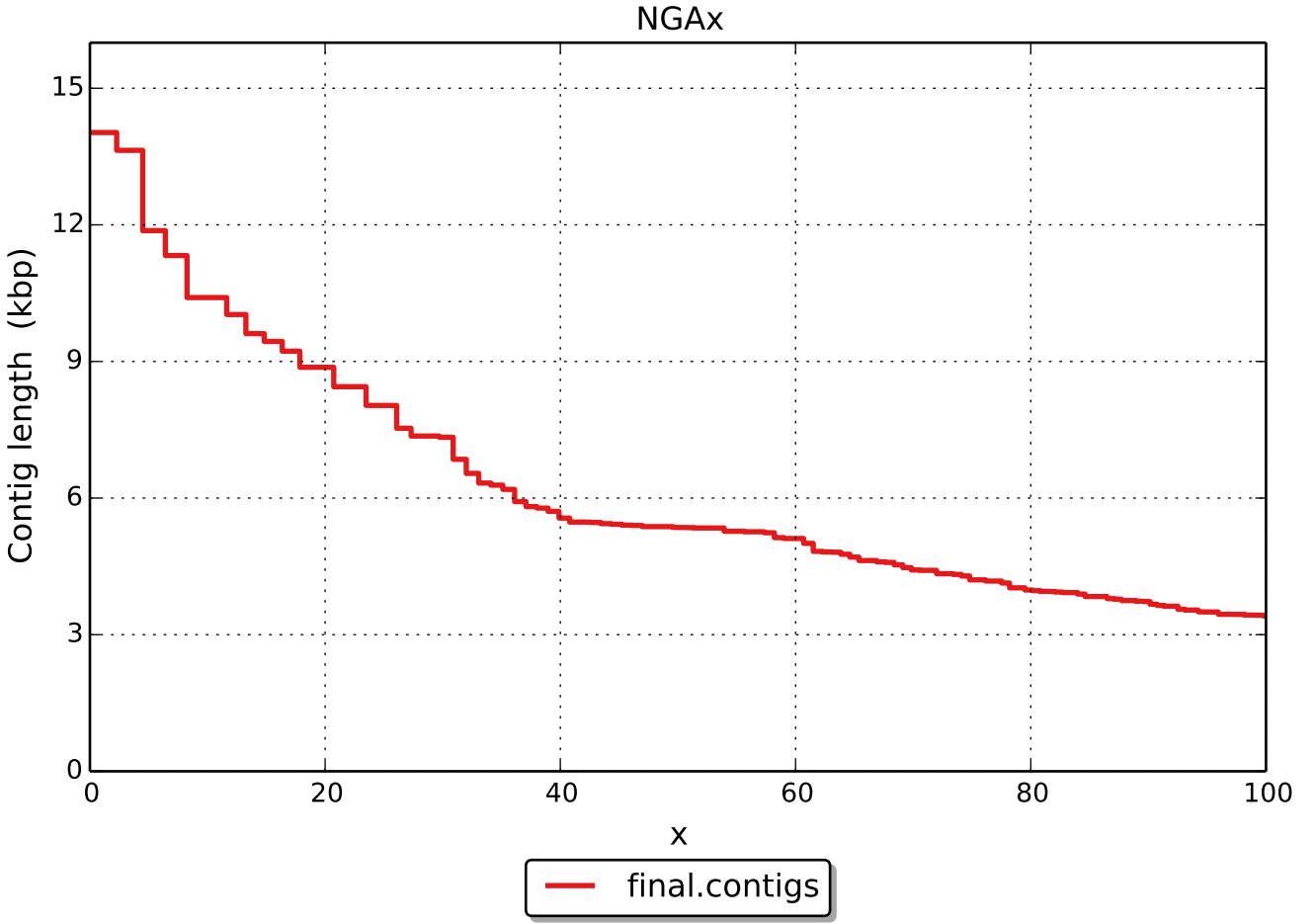

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
40
35
30
25
20
15
10
5
0
final.contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
1200
1000
800
600
400
200
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


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


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