Report

	final.contigs
# contigs (>= 0 bp)	153
# contigs (>= 1000 bp)	145
Total length (>= 0 bp)	1240083
Total length (>= 1000 bp)	1234563
# contigs	153
Largest contig	38663
Total length	1240083
Reference length	615980
GC (%)	25.35
Reference GC (%)	25.34
N50	12232
NG50	18849
N75	8270
NG75	15409
L50	34
LG50	13
L75	65
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	765
# local misassemblies	0
# unaligned contigs	67 + 5 part
Unaligned length	610586
Genome fraction (%)	99.732
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.60
# indels per 100 kbp	0.00
Largest alignment	30414
NA50	1314
NGA50	12571
NGA75	8839
LA50	73
LGA50	16
LGA75	31

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

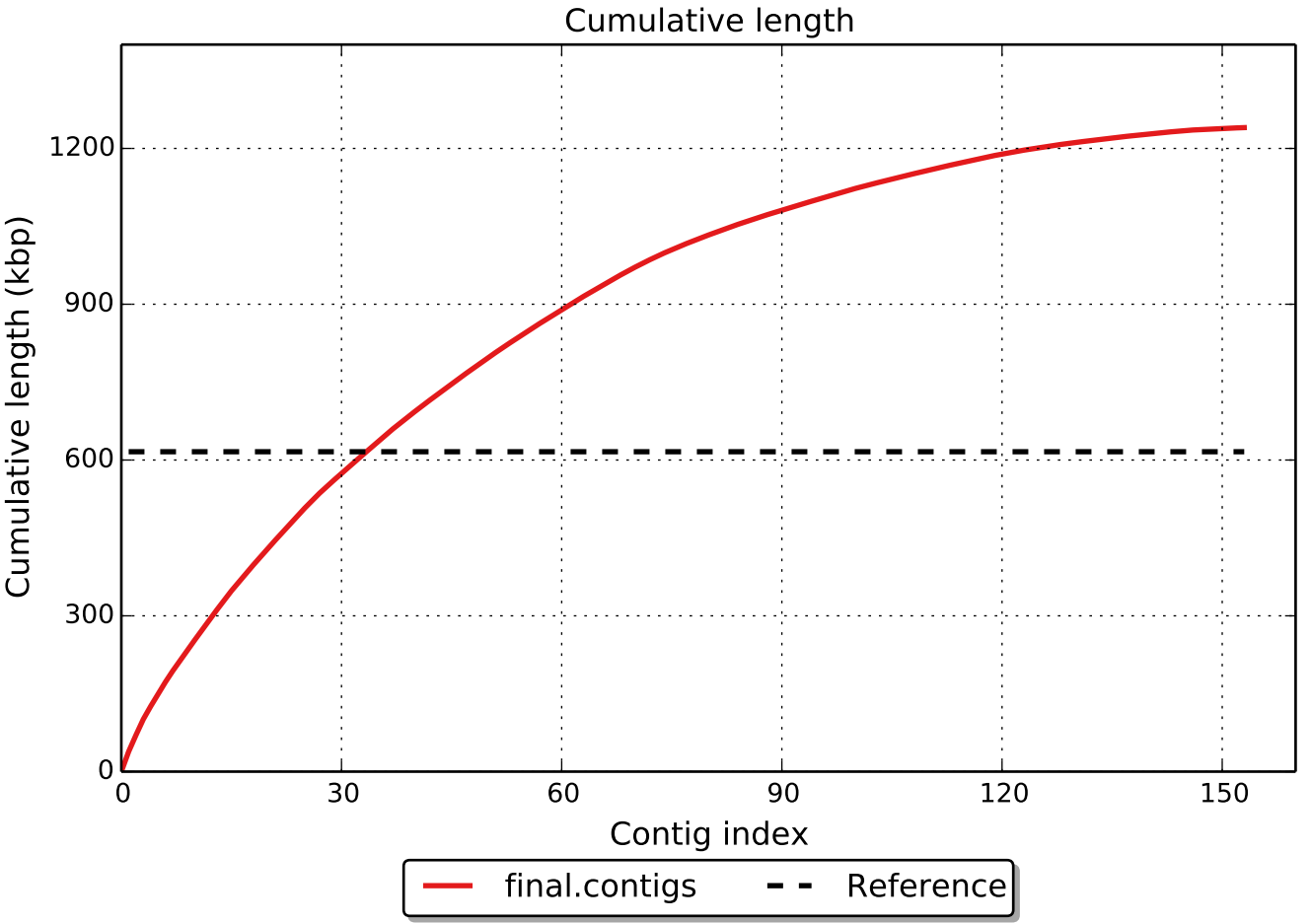
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	765
# local misassemblies	0
# mismatches	231
# indels	0
# short indels	0
# long indels	0
Indels length	0

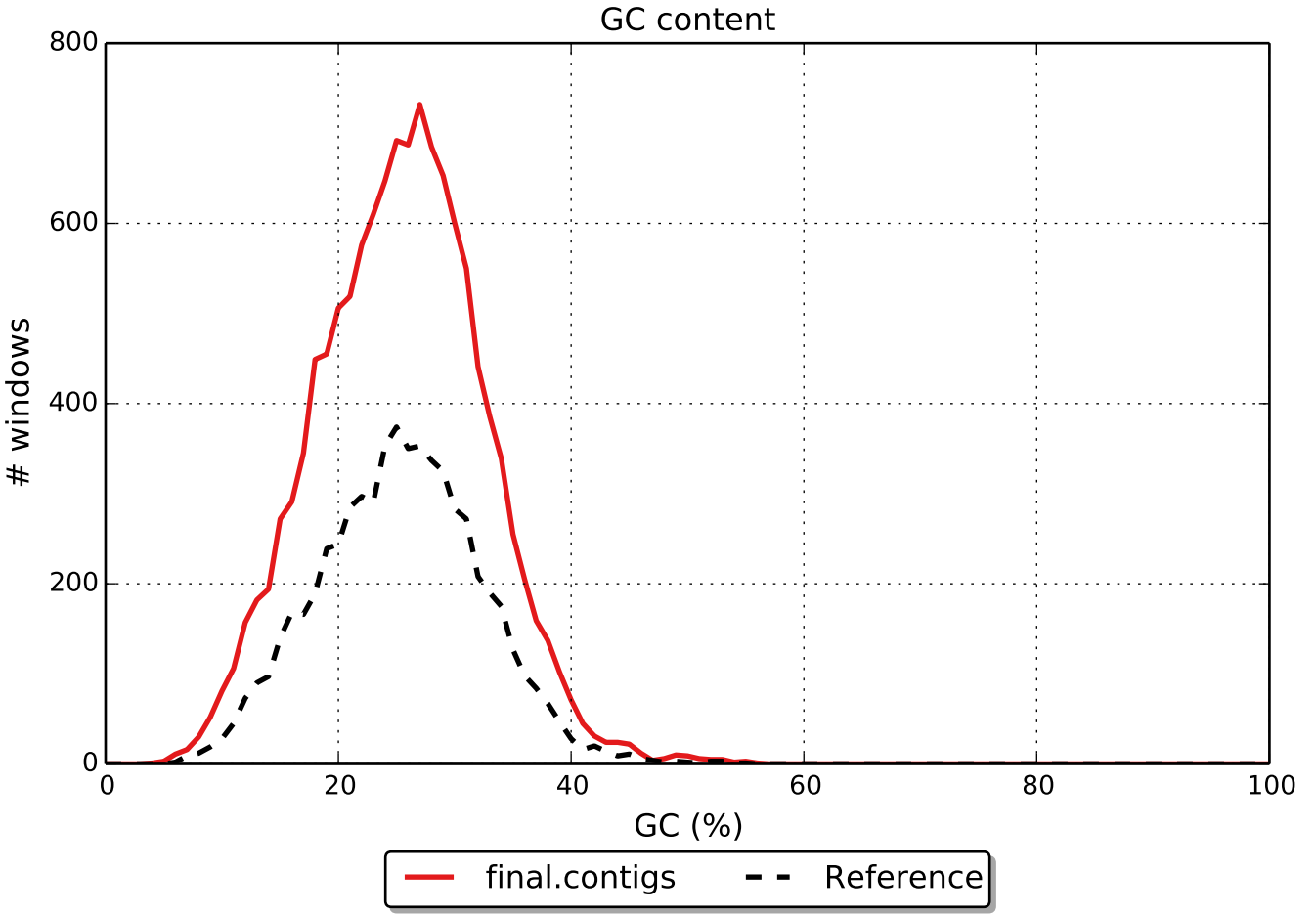
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

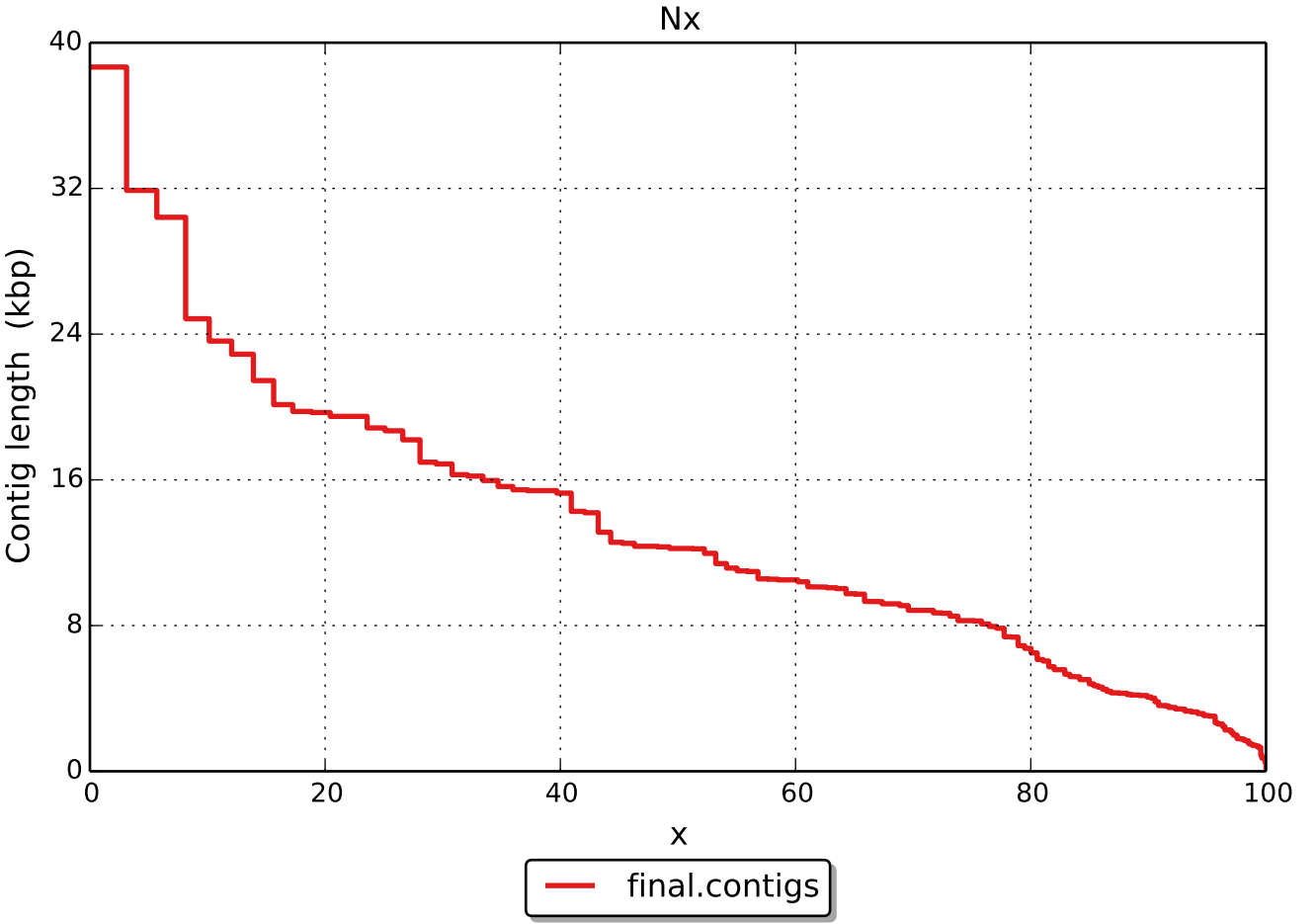
Unaligned report

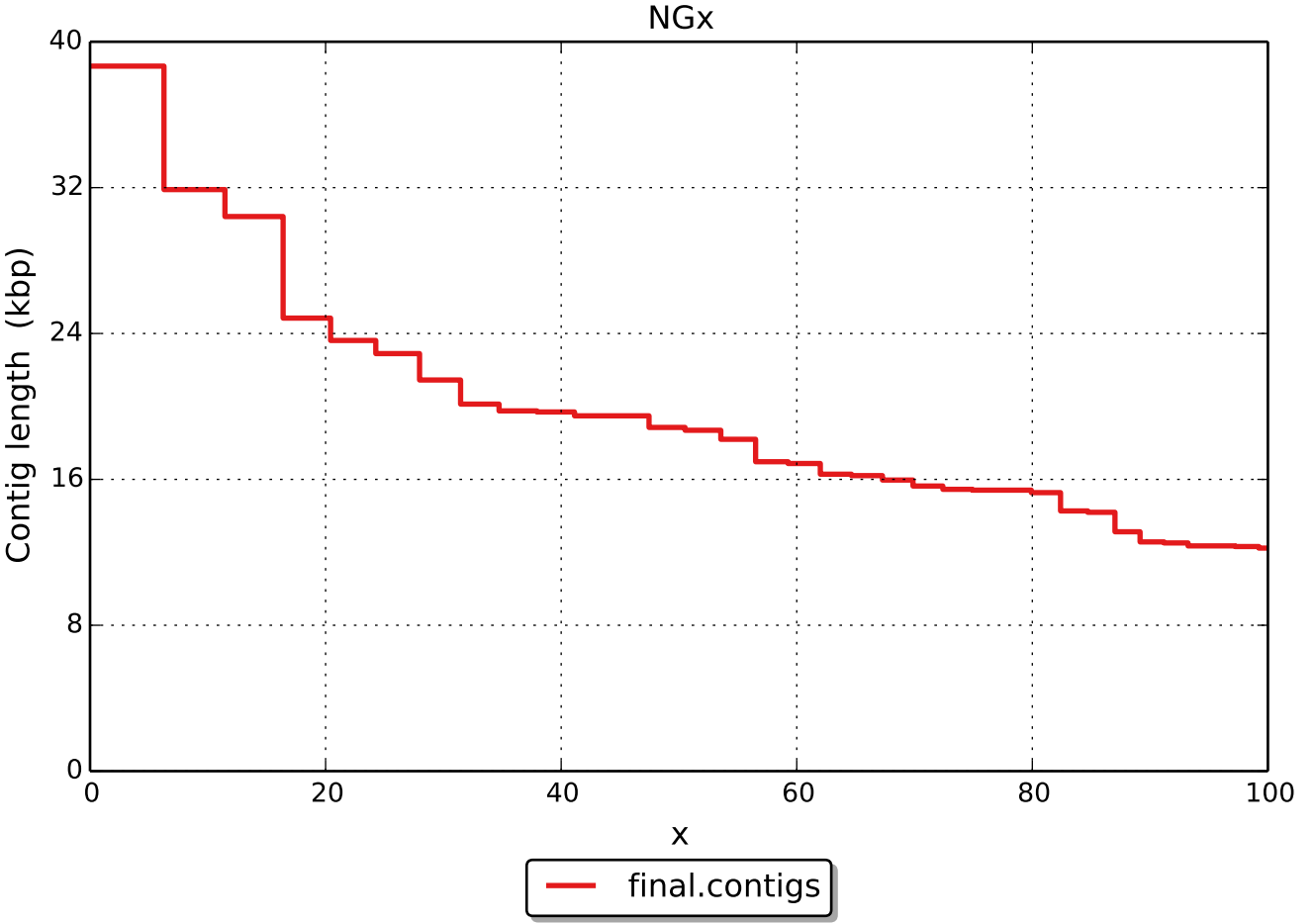
	final.contigs
# fully unaligned contigs	67
Fully unaligned length	593553
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	2
Partially unaligned length	17033
# N's	0

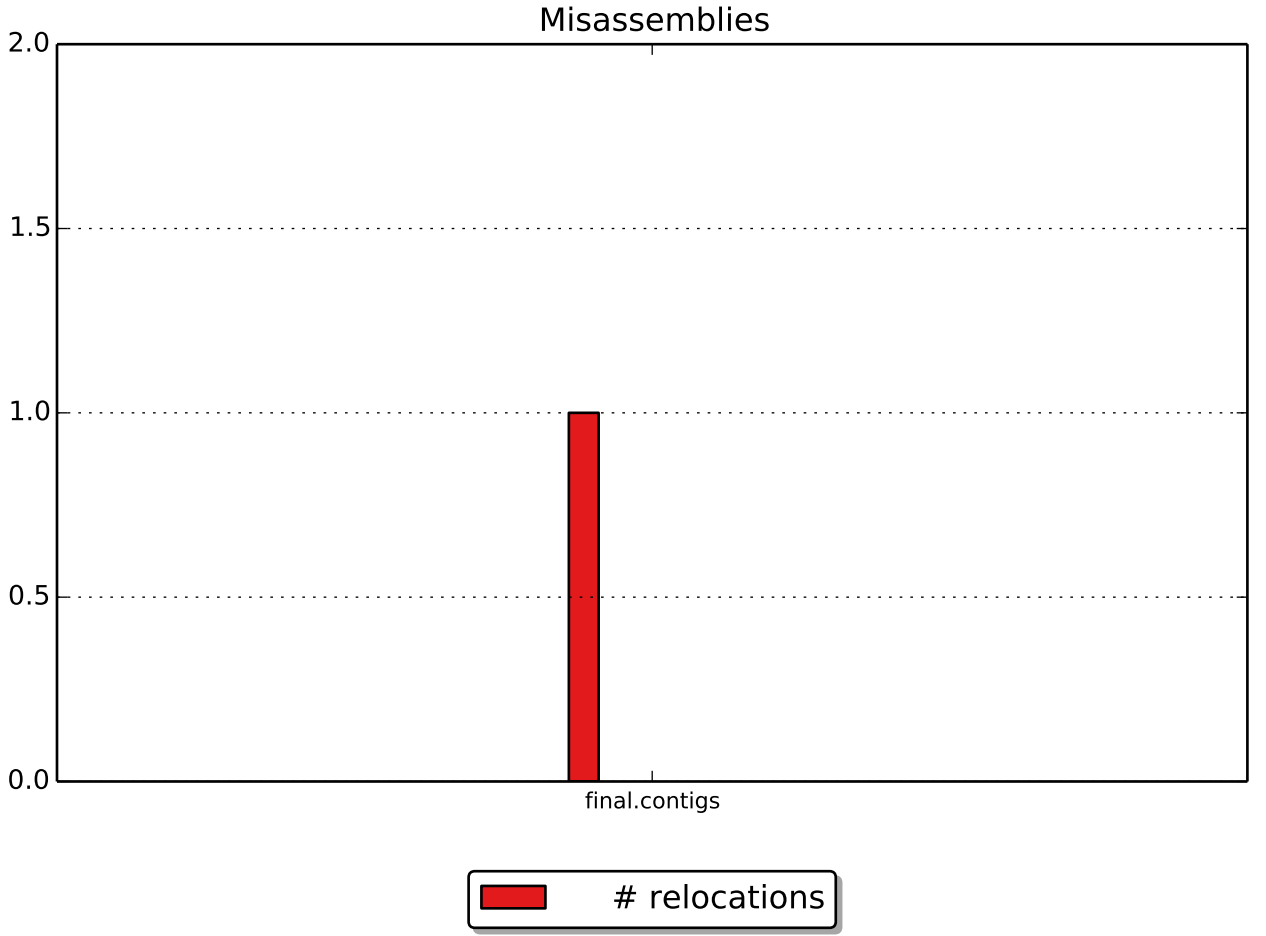
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

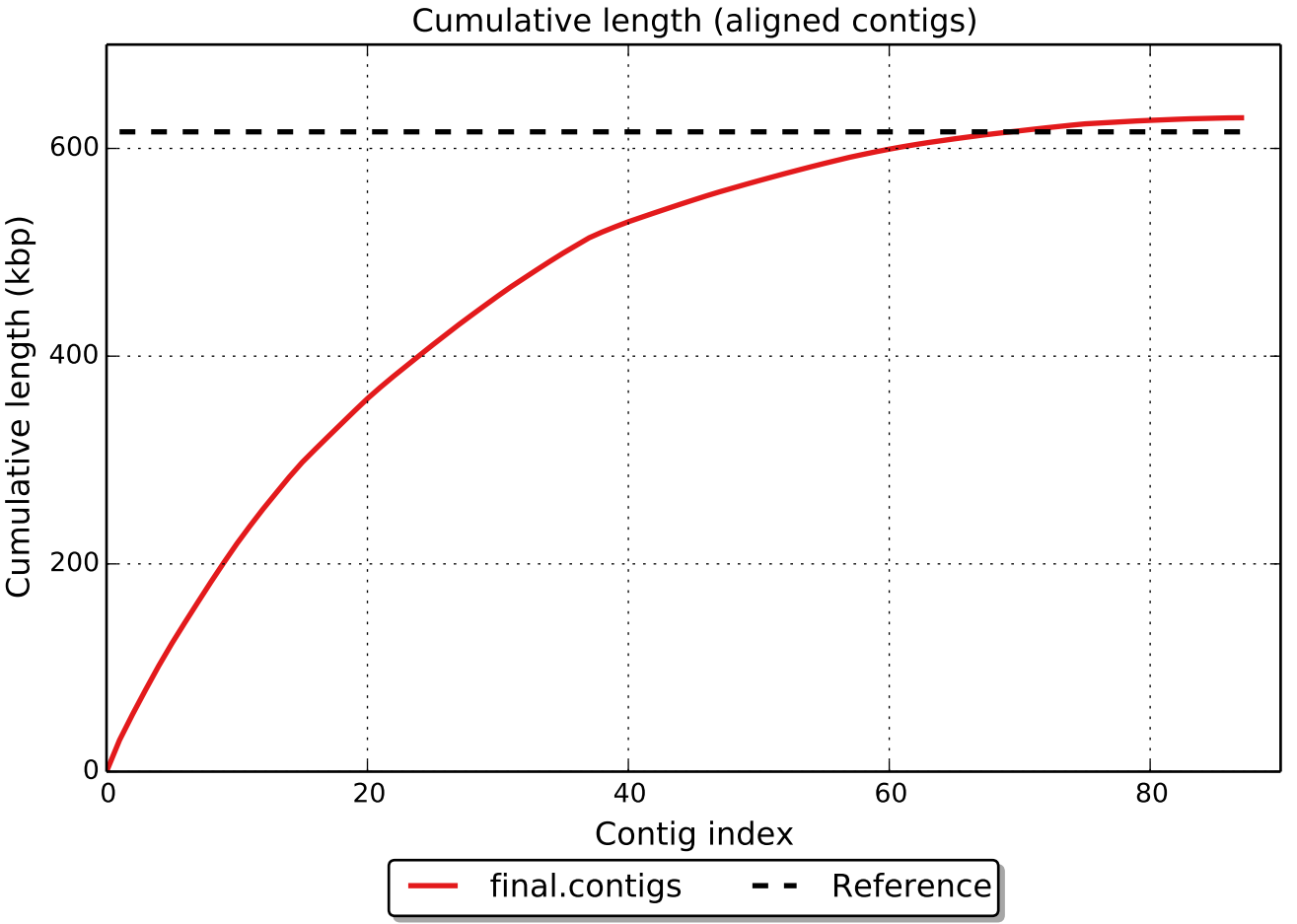

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
30
60
90
120
150
Contig index
final.contigs
Reference

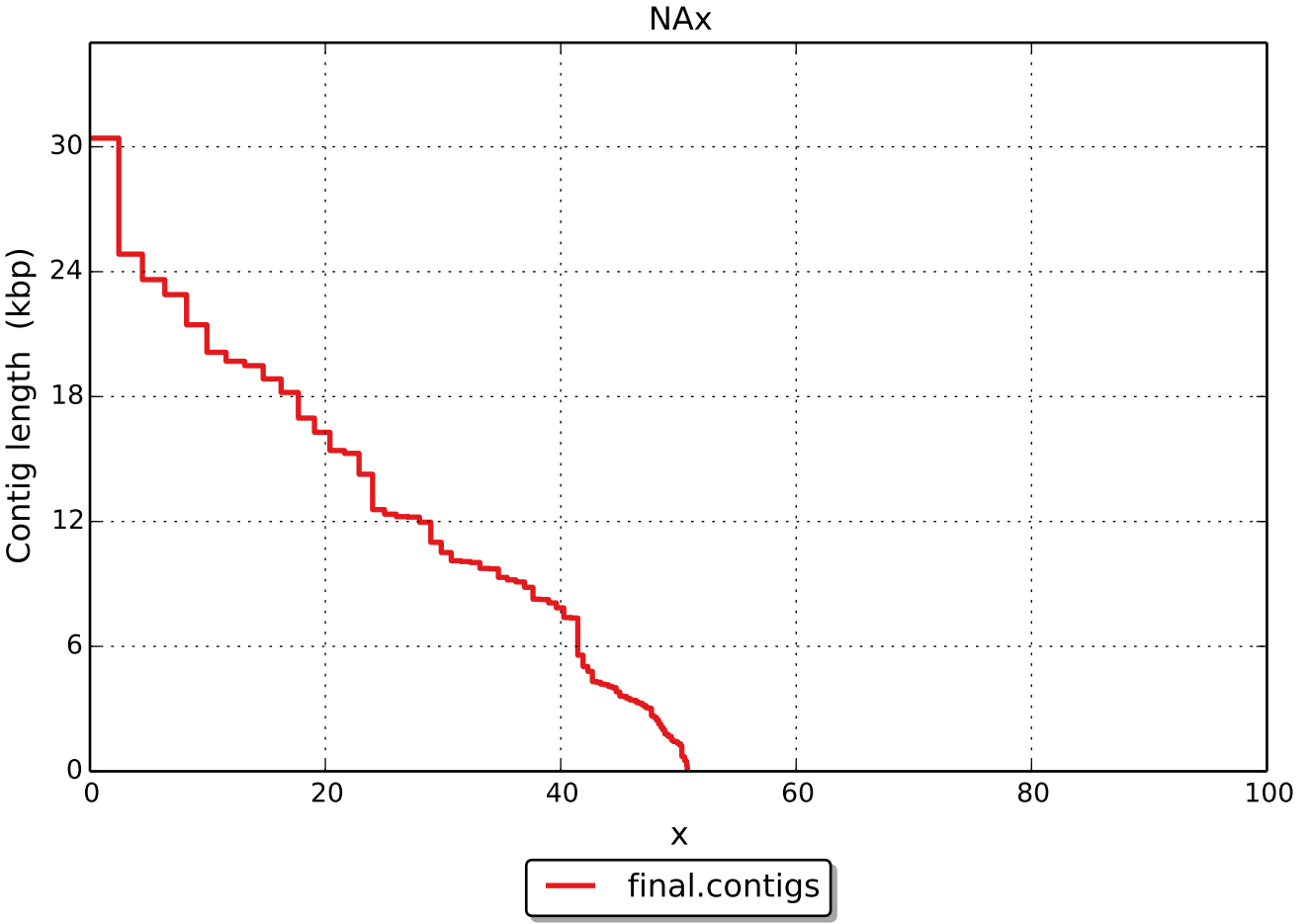

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

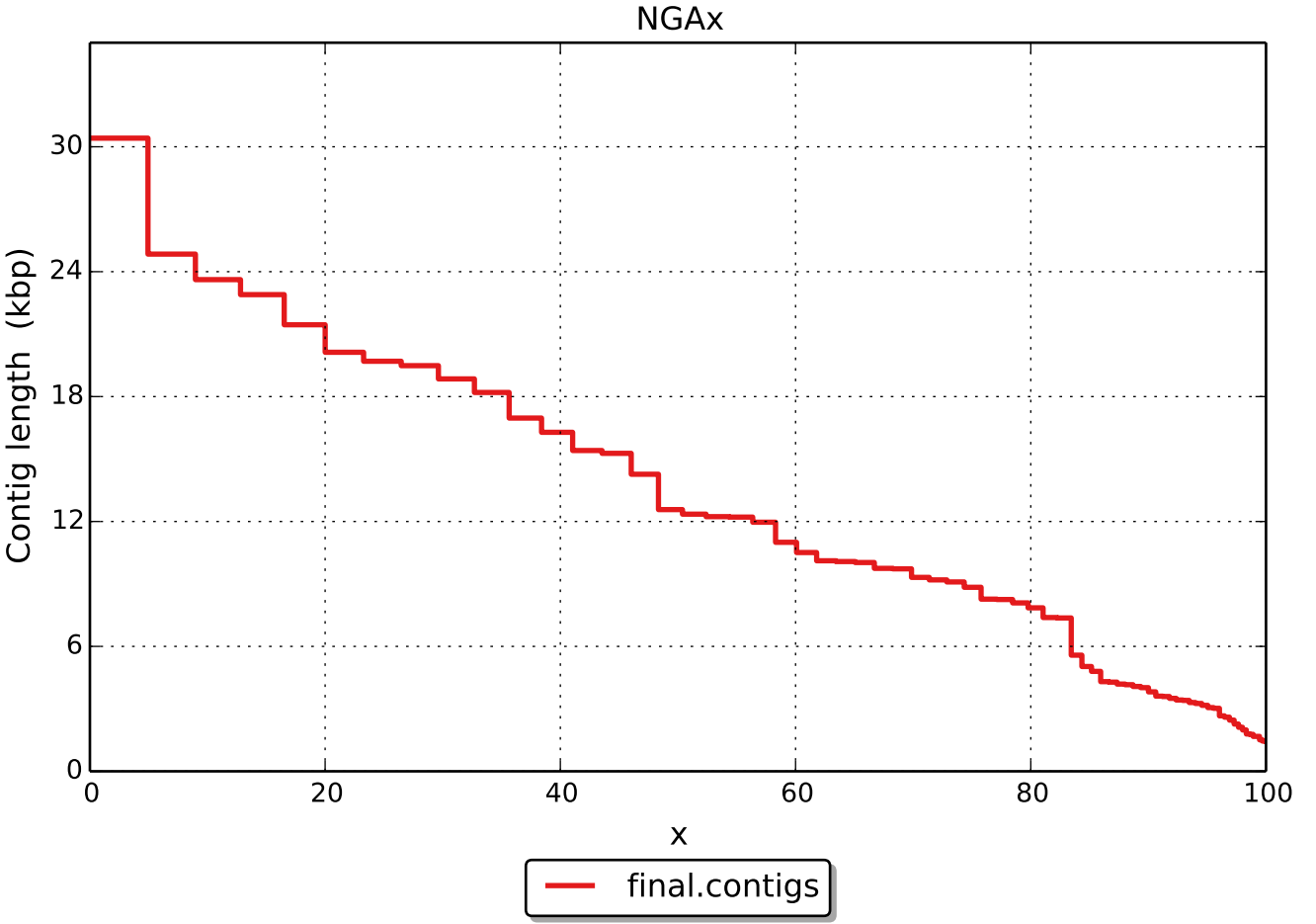

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
200
400
600
0
20
40
60
80
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs