Report

	final.contigs
# contigs (>= 0 bp)	1079
# contigs (>= 1000 bp)	408
Total length (>= 0 bp)	1119941
Total length (>= 1000 bp)	641890
# contigs	1079
Largest contig	4490
Total length	1119941
Reference length	641799
GC (%)	26.35
Reference GC (%)	26.30
N50	1130
NG50	1585
N75	781
NG75	1235
L50	331
LG50	148
L75	635
LG75	264
# misassemblies	21
# misassembled contigs	21
Misassembled contigs length	29556
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	299
Genome fraction (%)	91.543
Duplication ratio	1.906
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1412.38
# indels per 100 kbp	1.02
Largest alignment	4490
NA50	1107
NGA50	1579
NA75	776
NGA75	1225
LA50	336
LGA50	150
LA75	642
LGA75	268

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

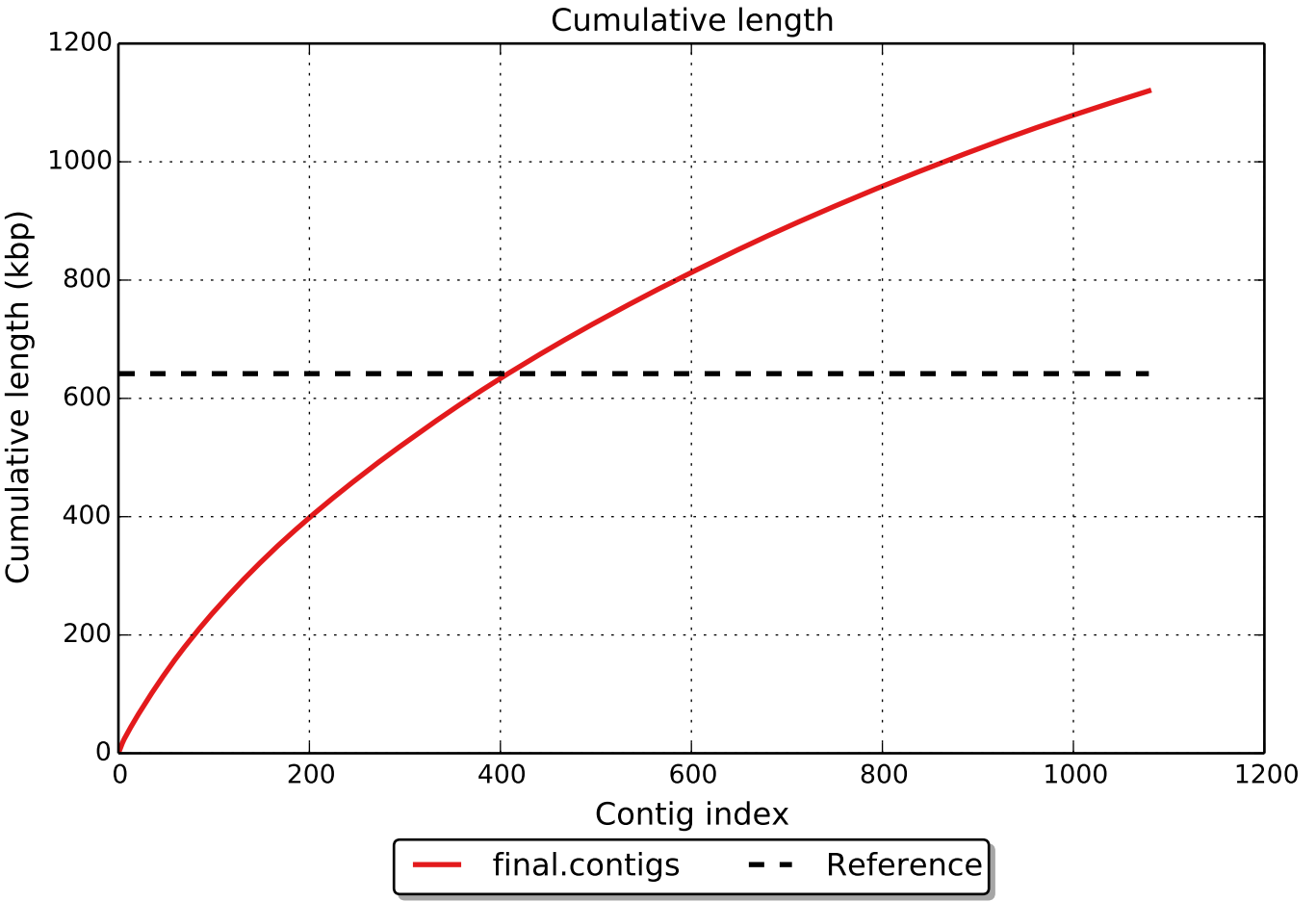
	final.contigs
# misassemblies	21
# relocations	20
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	21
Misassembled contigs length	29556
# local misassemblies	0
# mismatches	8298
# indels	6
# short indels	6
# long indels	0
Indels length	6

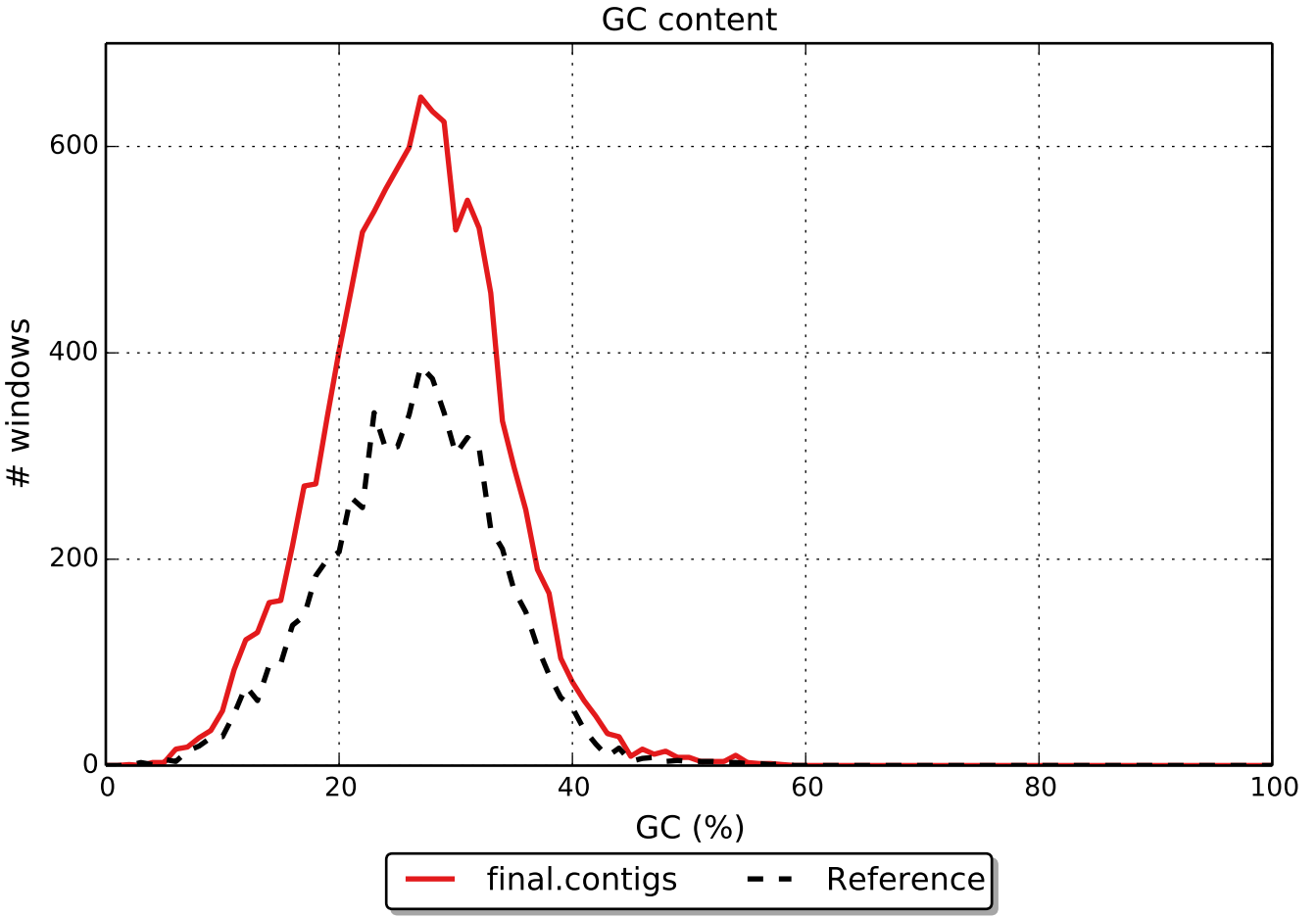
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

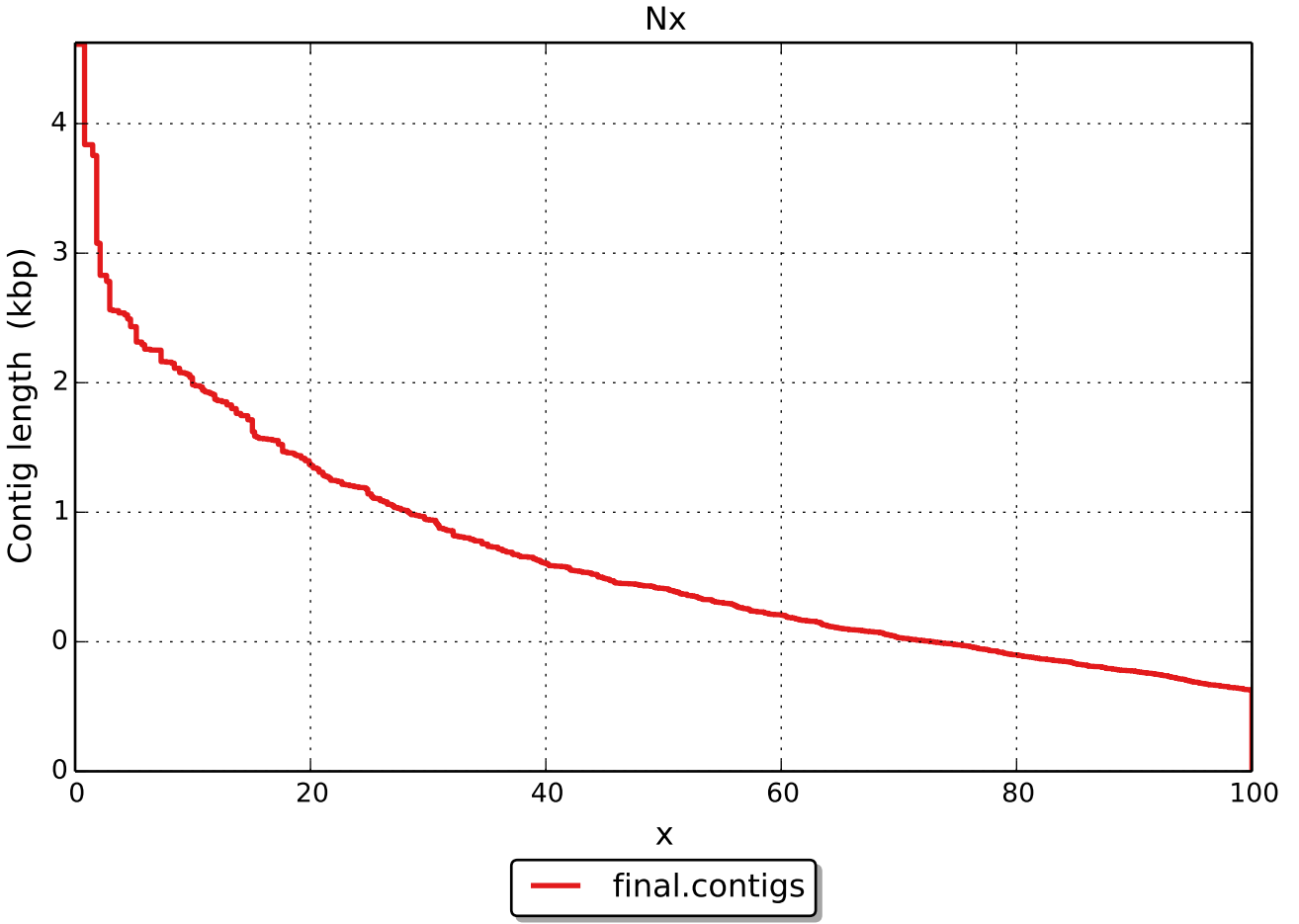
Unaligned report

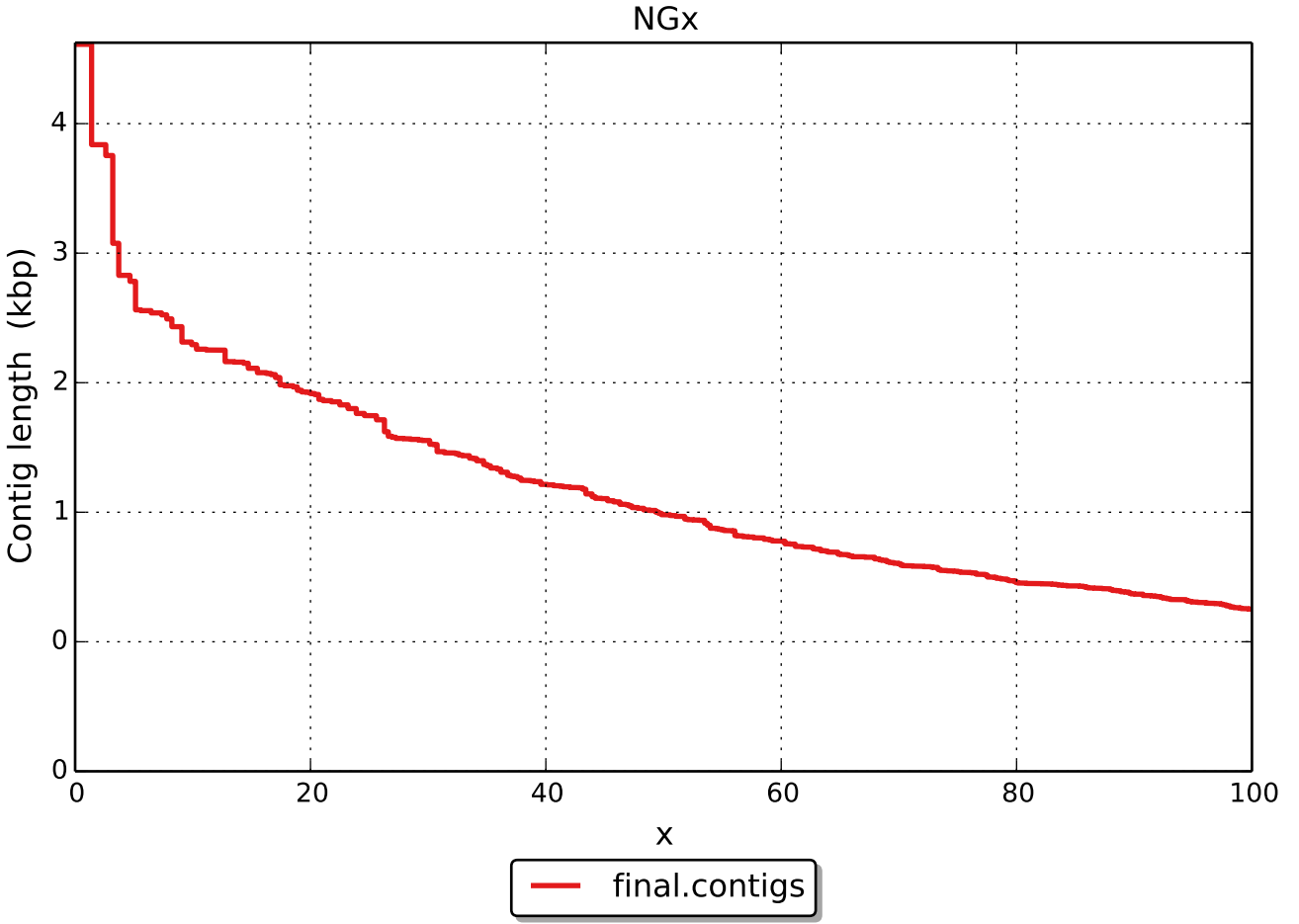
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	299
# N's	0

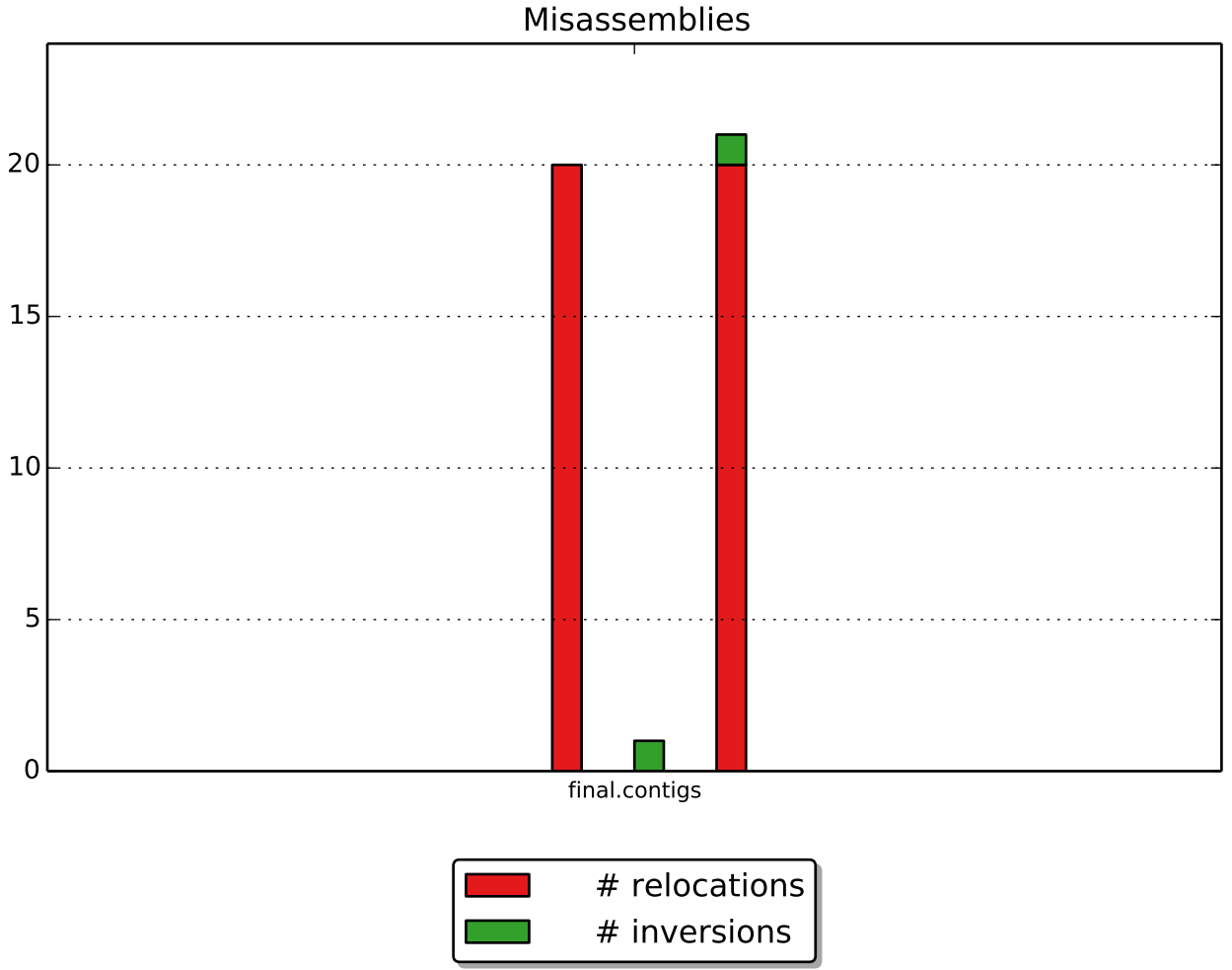
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

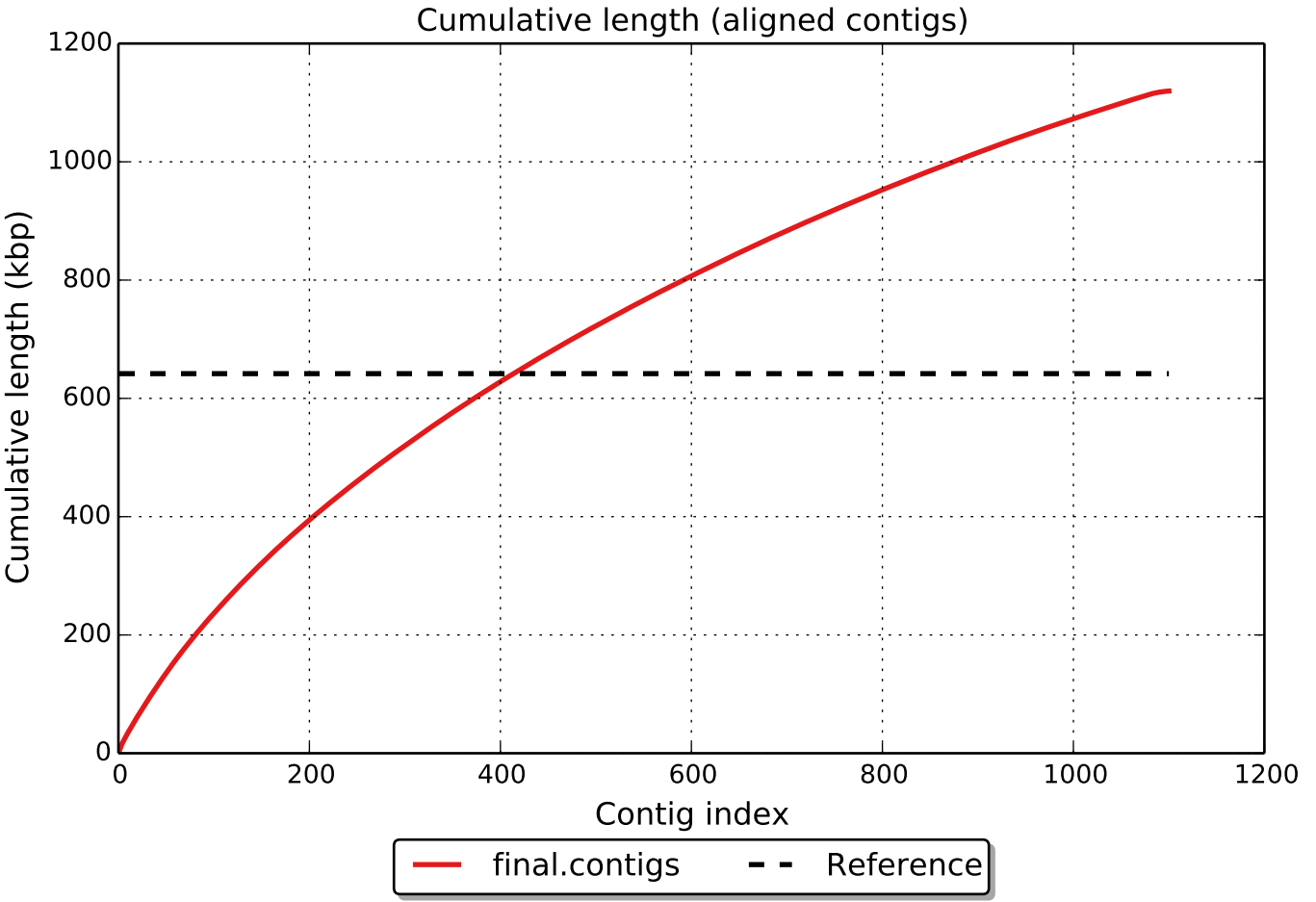

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

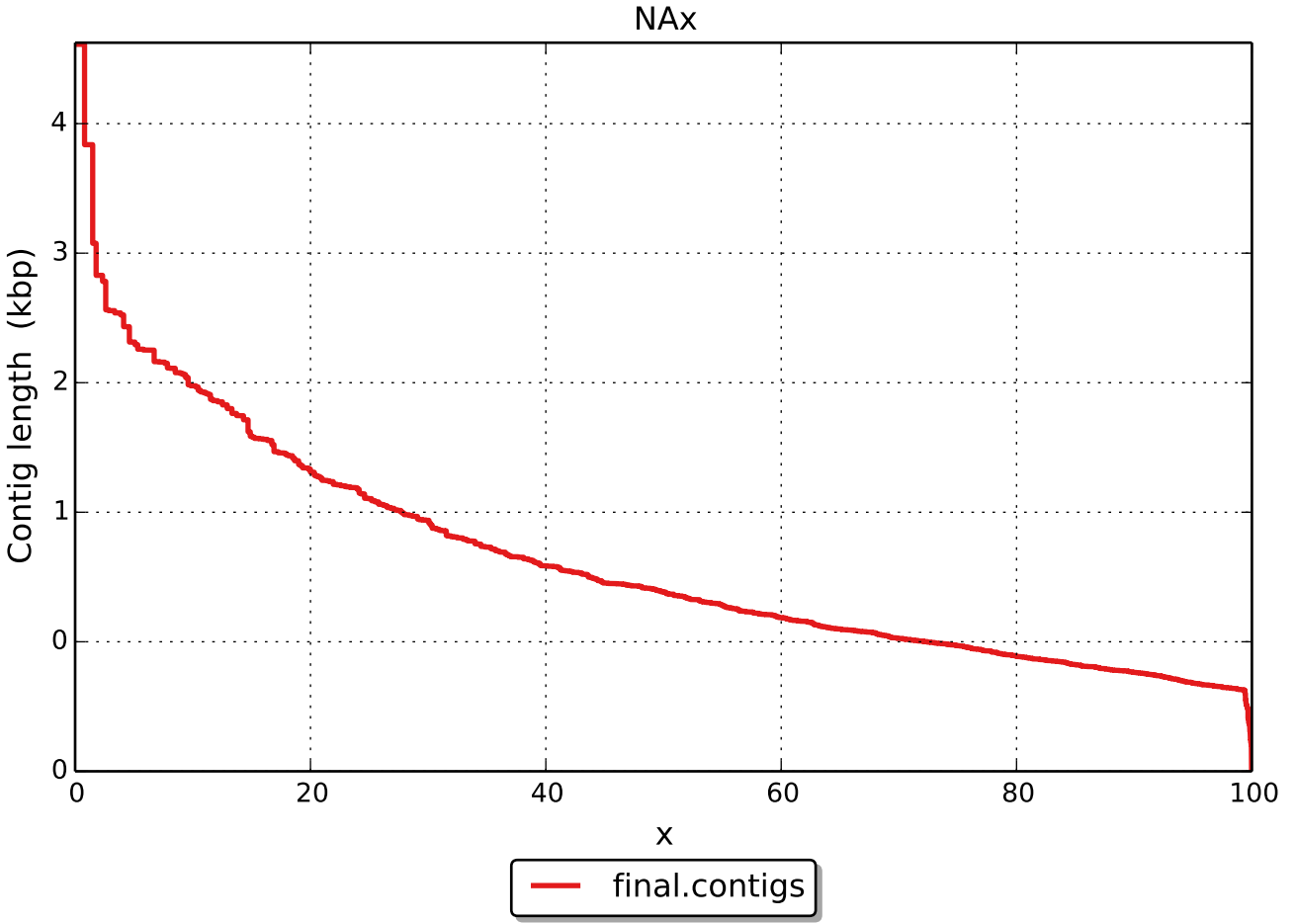

GC content
windows
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

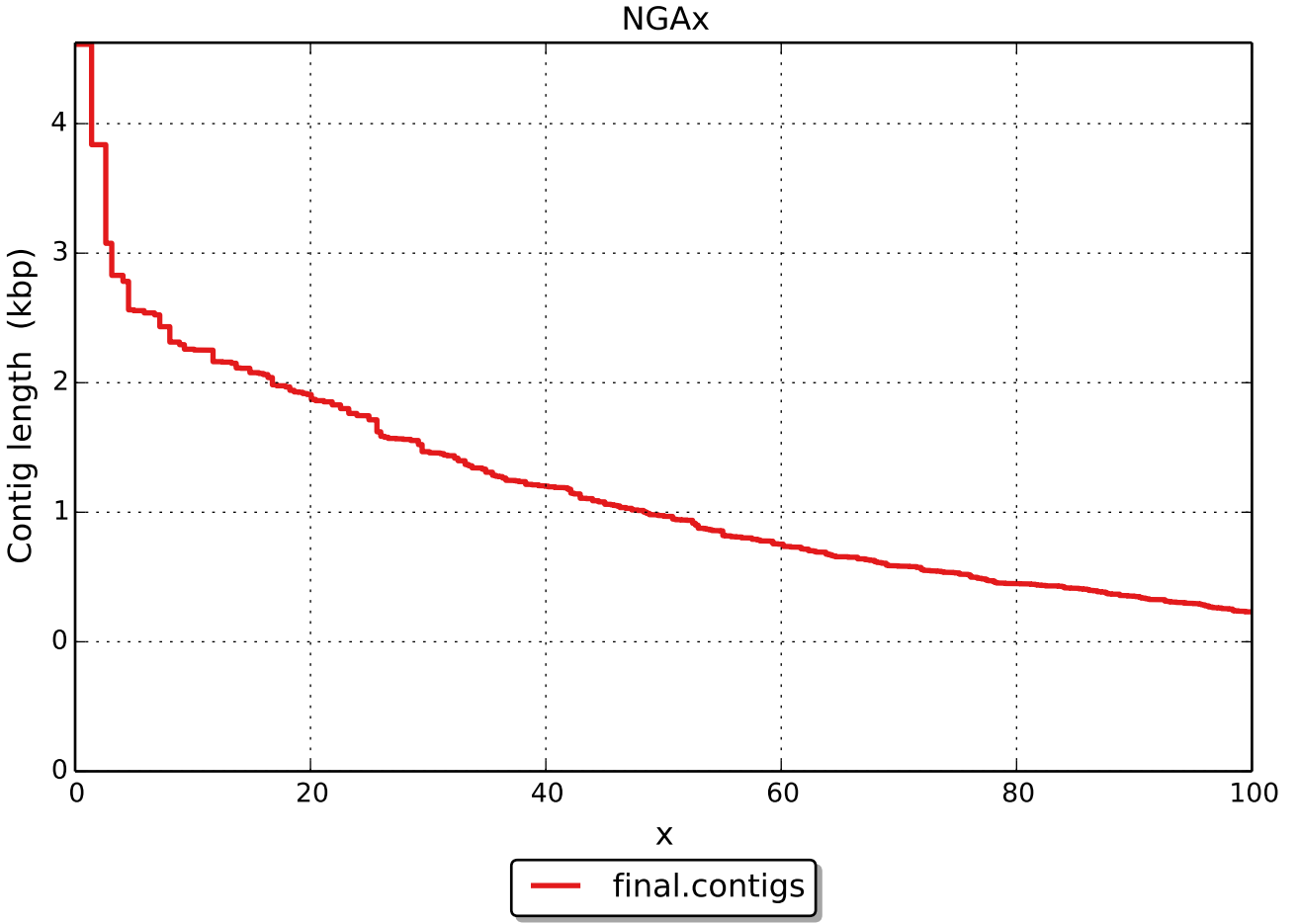

Nx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
20
15
10
5
0
final.contigs
relocations
inversions


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


NAx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs