Report

	final.contigs
# contigs (>= 0 bp)	1136
# contigs (>= 1000 bp)	367
Total length (>= 0 bp)	1081000
Total length (>= 1000 bp)	539349
# contigs	1136
Largest contig	4410
Total length	1081000
Reference length	615980
GC (%)	25.41
Reference GC (%)	25.35
N50	999
NG50	1397
N75	716
NG75	1099
L50	369
LG50	169
L75	690
LG75	293
# misassemblies	15
# misassembled contigs	15
Misassembled contigs length	12970
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	451
Genome fraction (%)	90.044
Duplication ratio	1.948
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1149.01
# indels per 100 kbp	0.36
Largest alignment	4410
NA50	835
NGA50	1200
NA75	567
NGA75	929
LA50	424
LGA50	187
LA75	817
LGA75	334

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

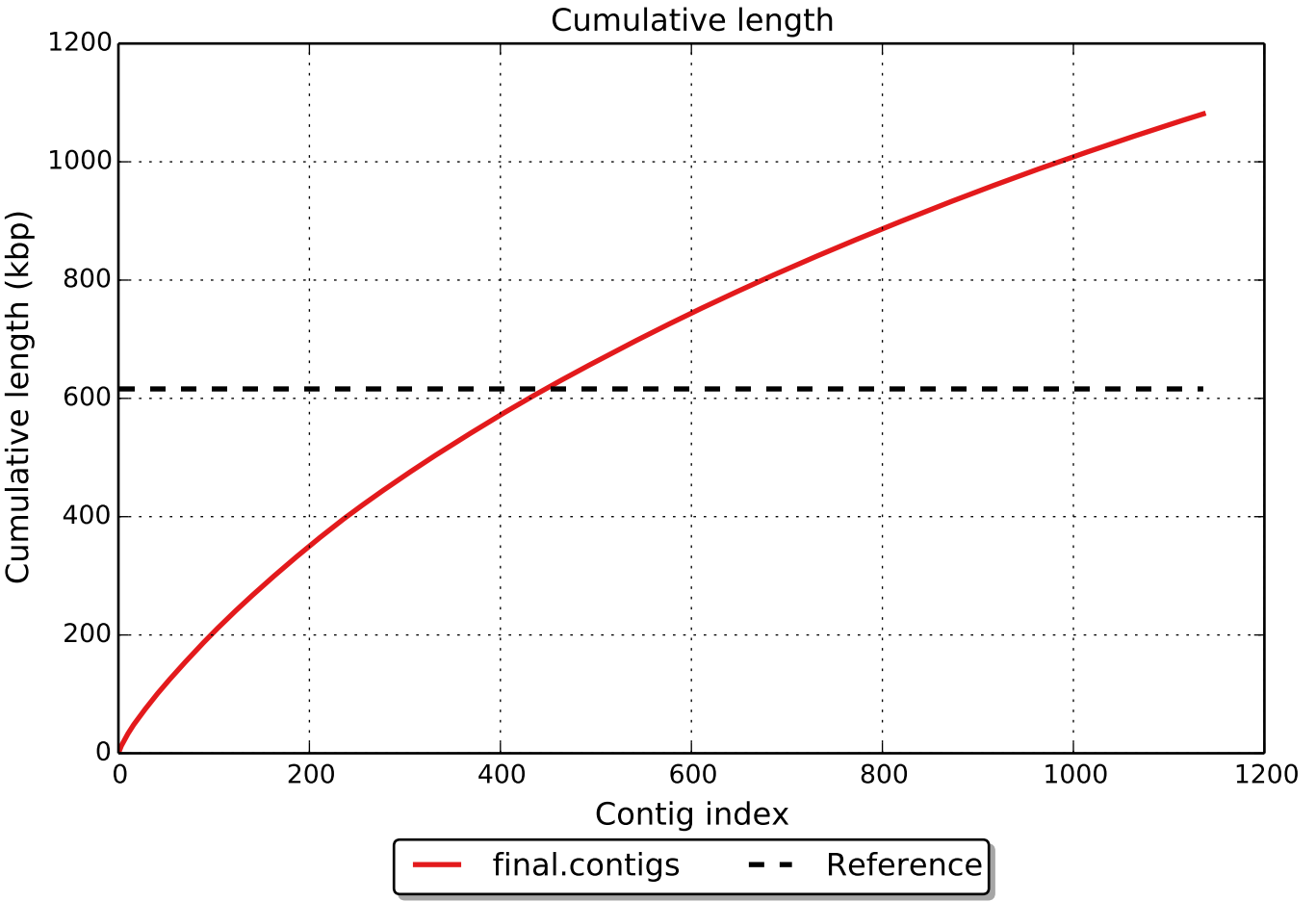
	final.contigs
# misassemblies	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	15
Misassembled contigs length	12970
# local misassemblies	0
# mismatches	6373
# indels	2
# short indels	2
# long indels	0
Indels length	2

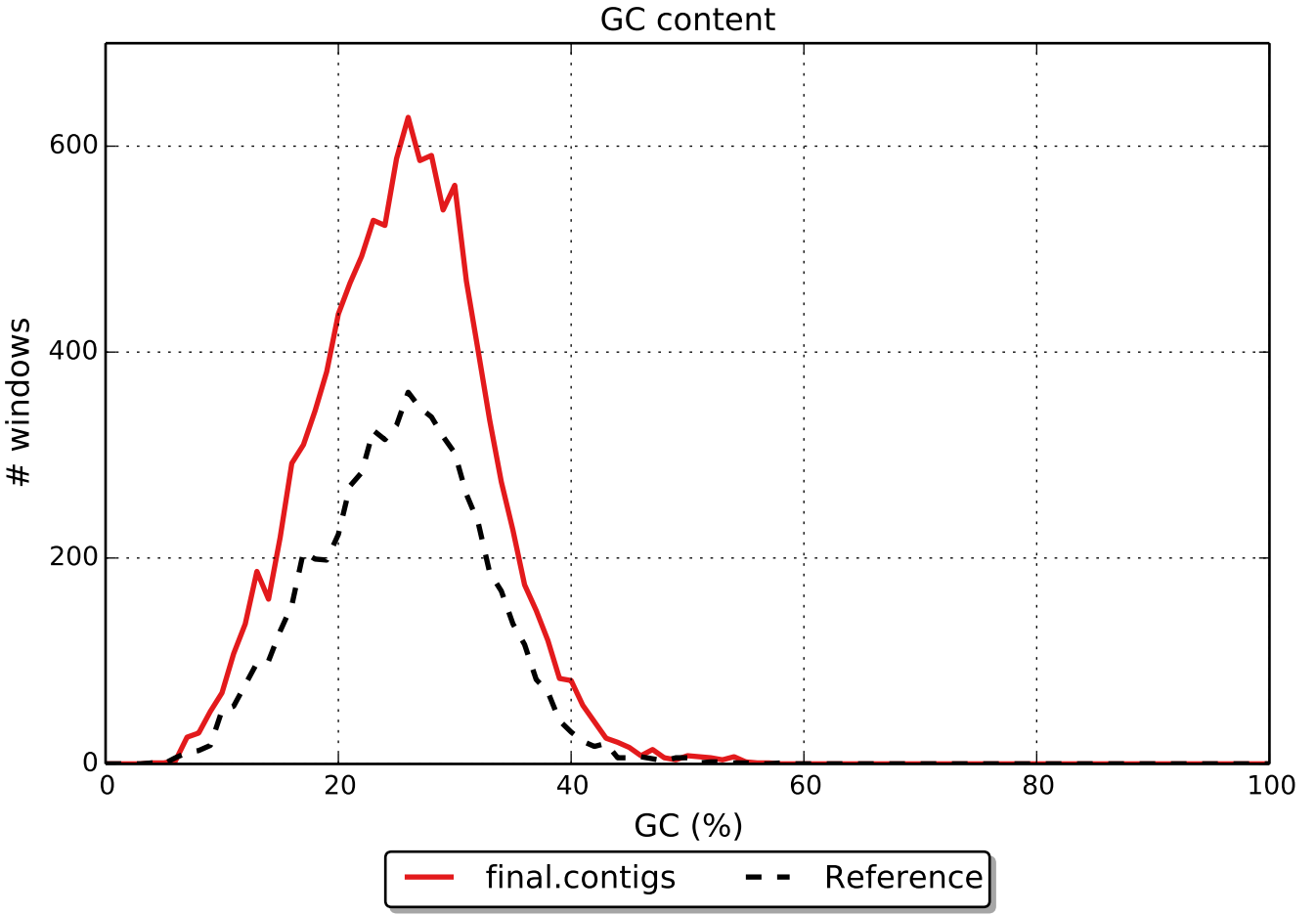
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

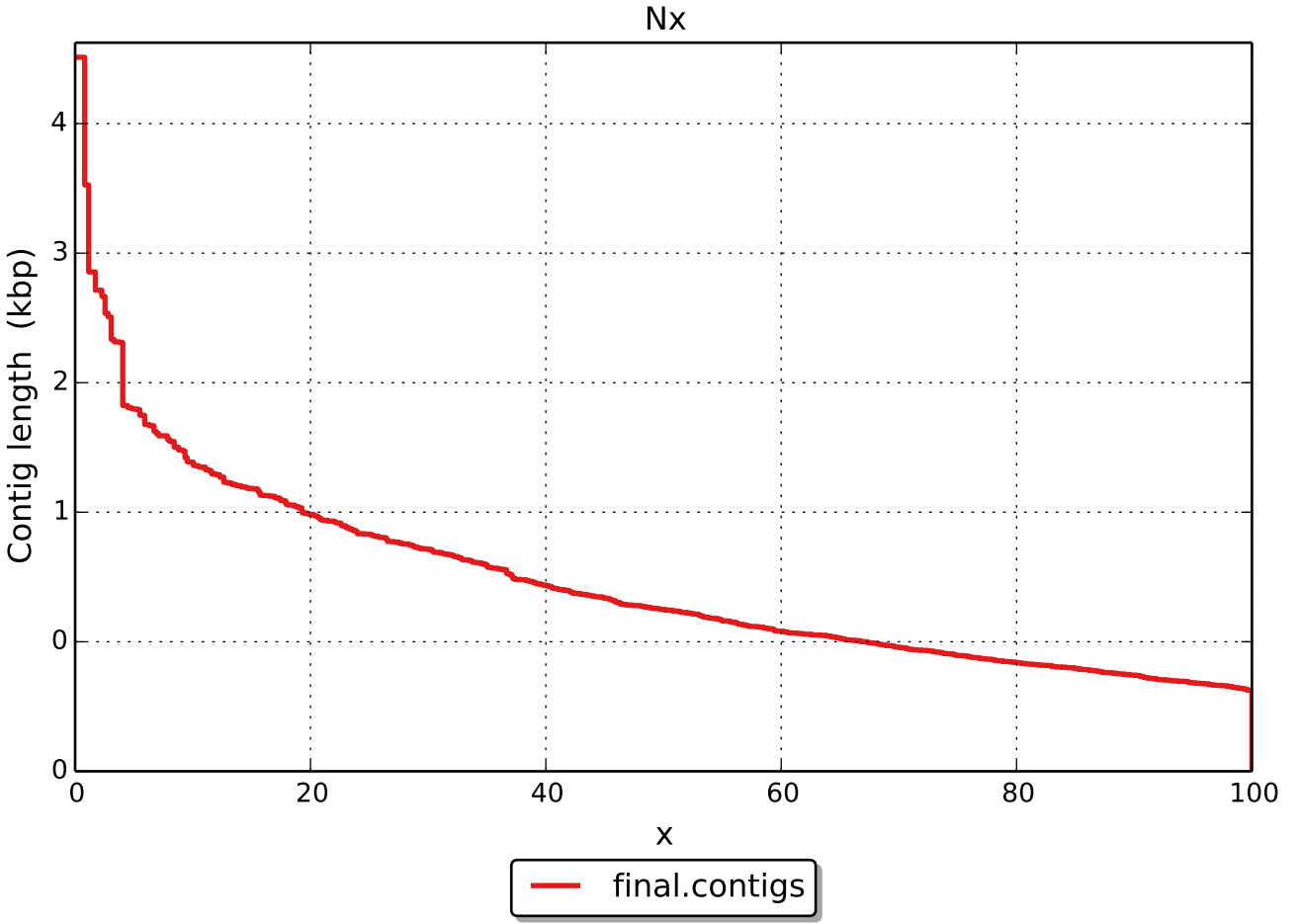
Unaligned report

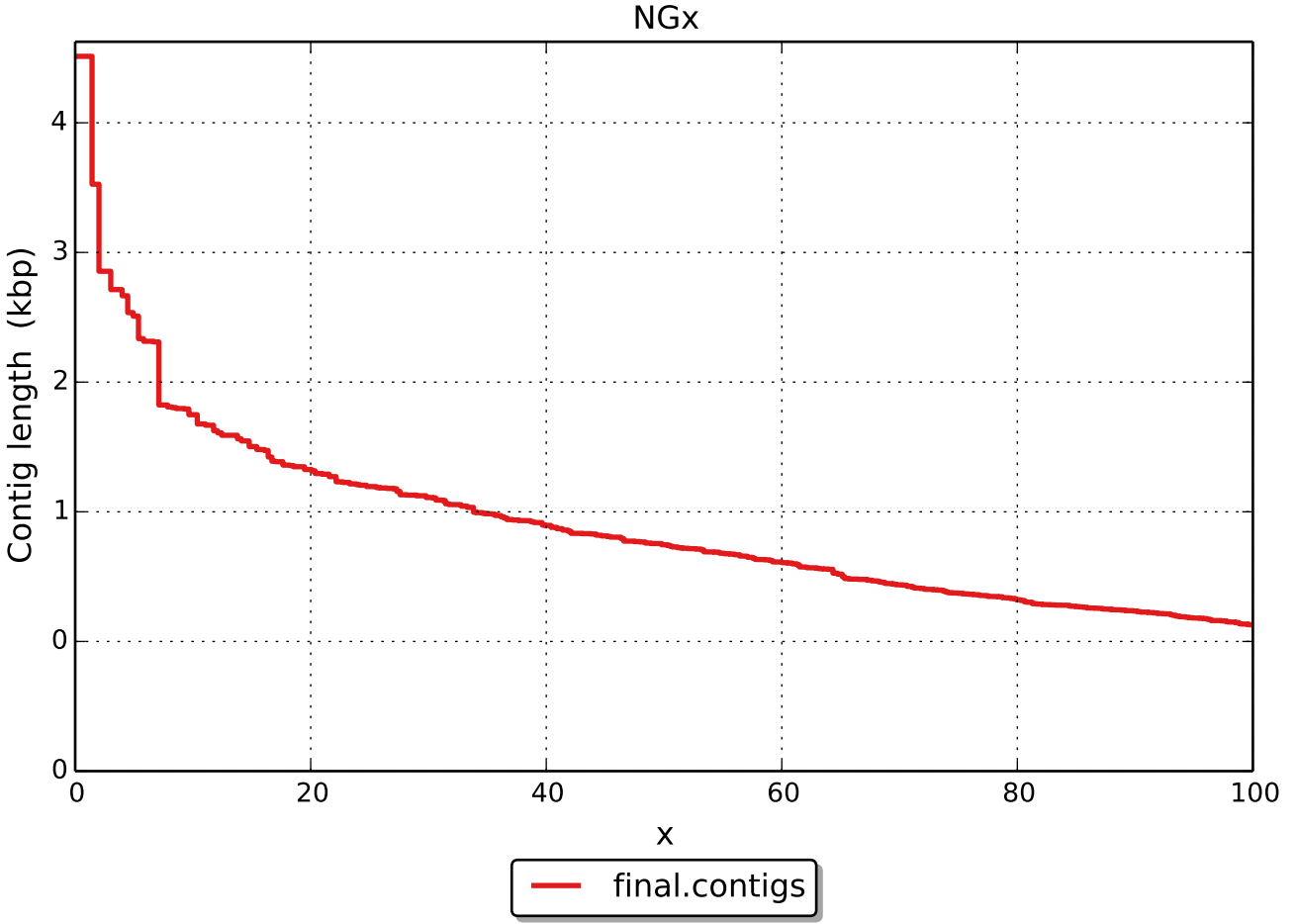
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	451
# N's	0

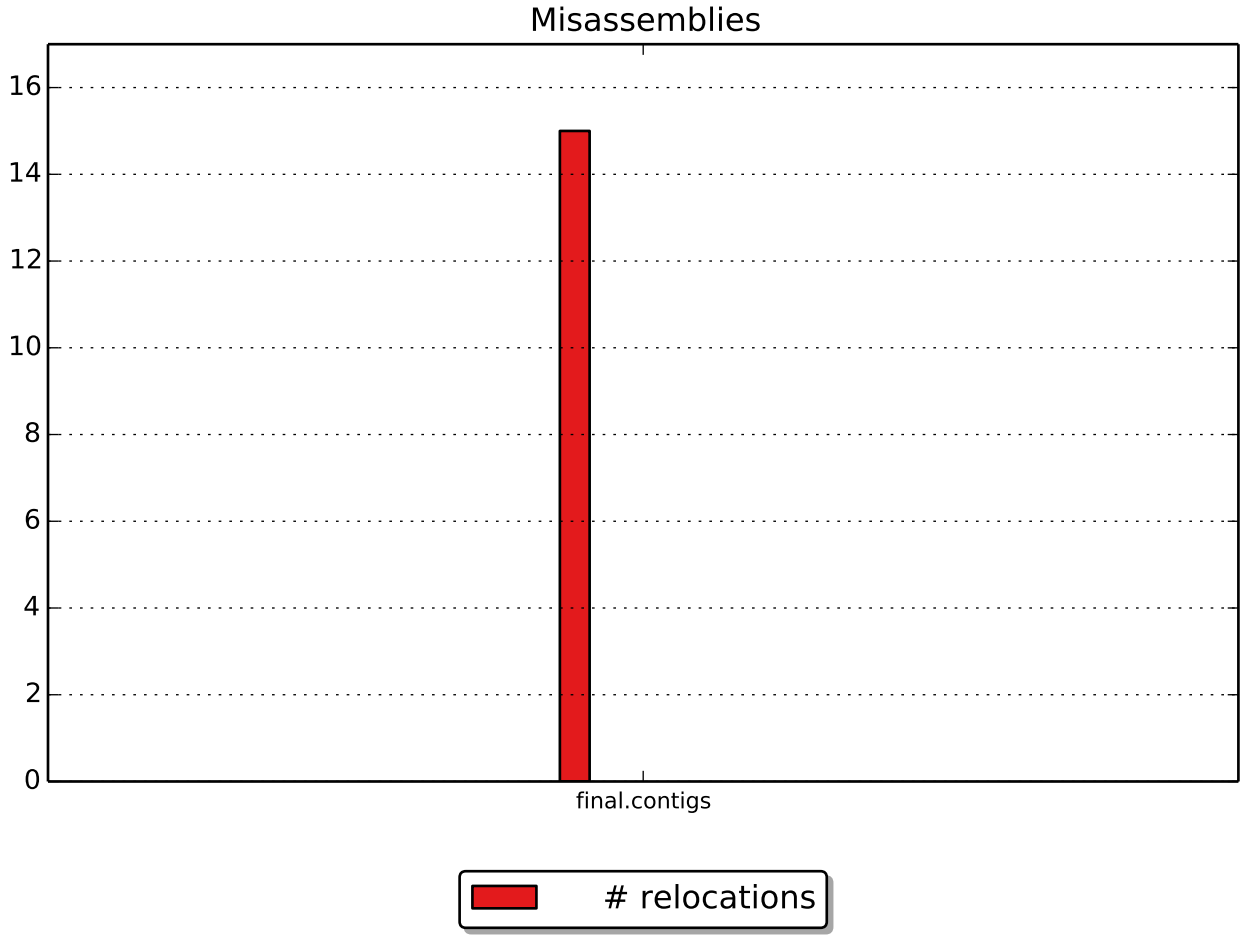
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

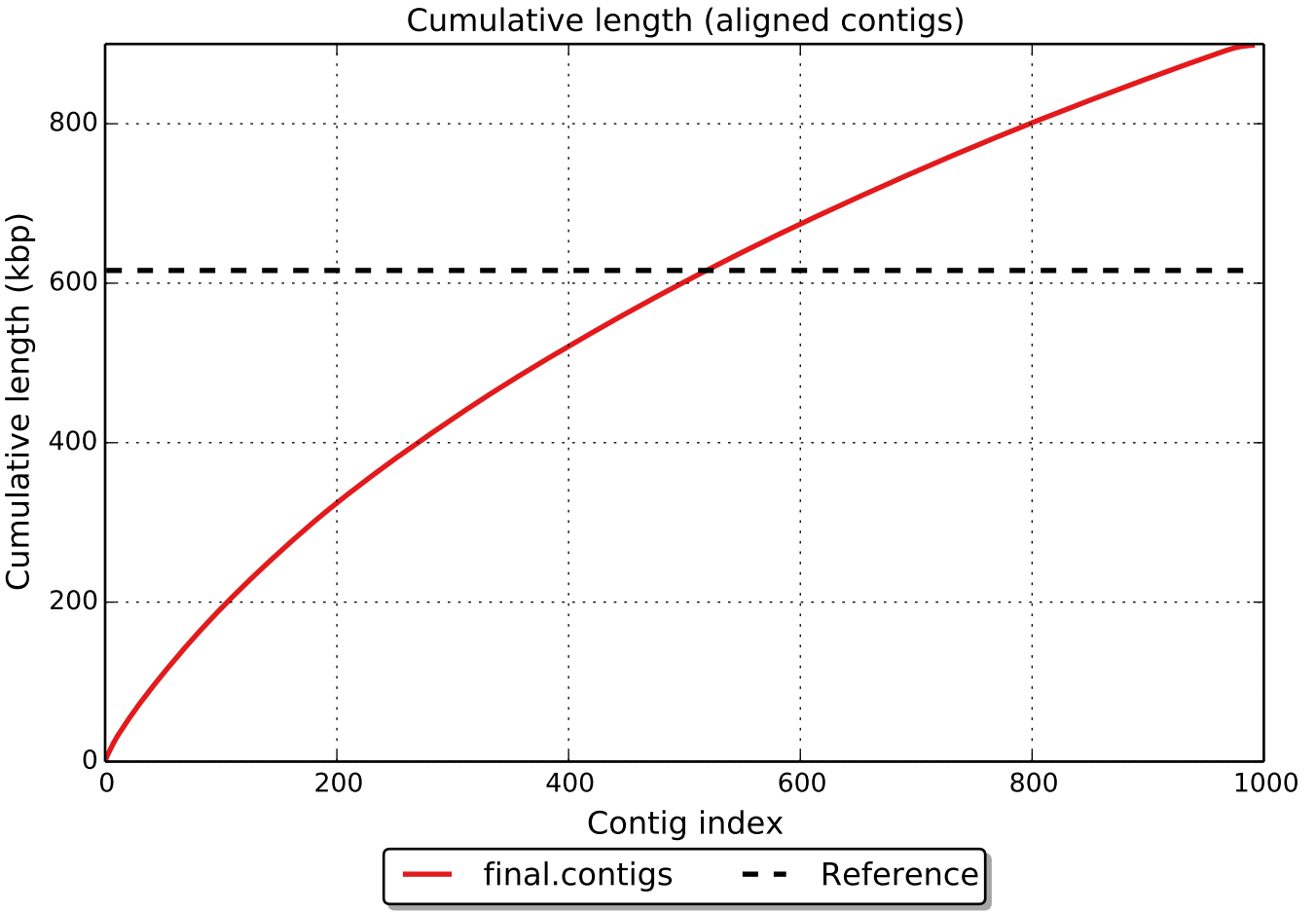

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

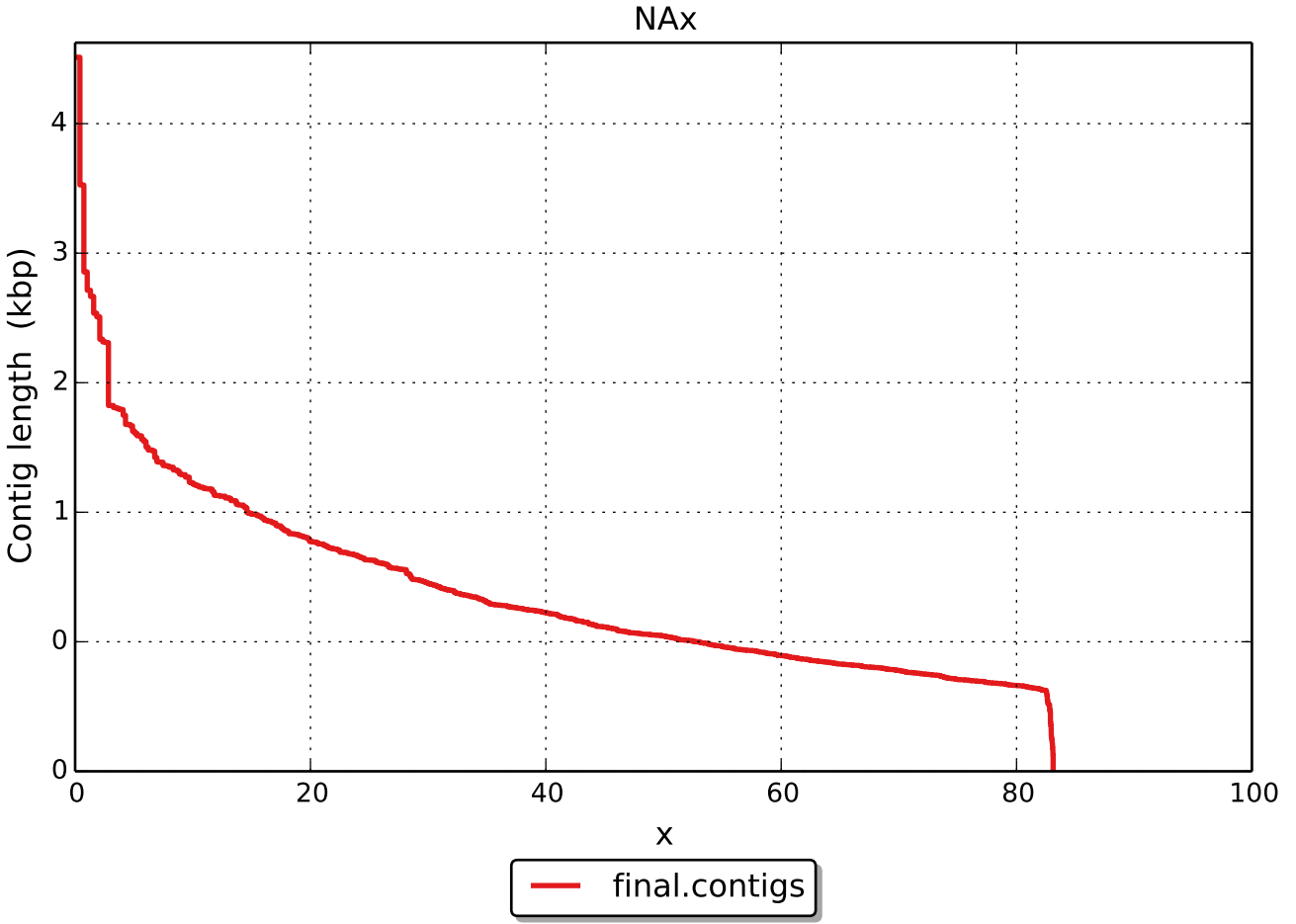

GC content
windows
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

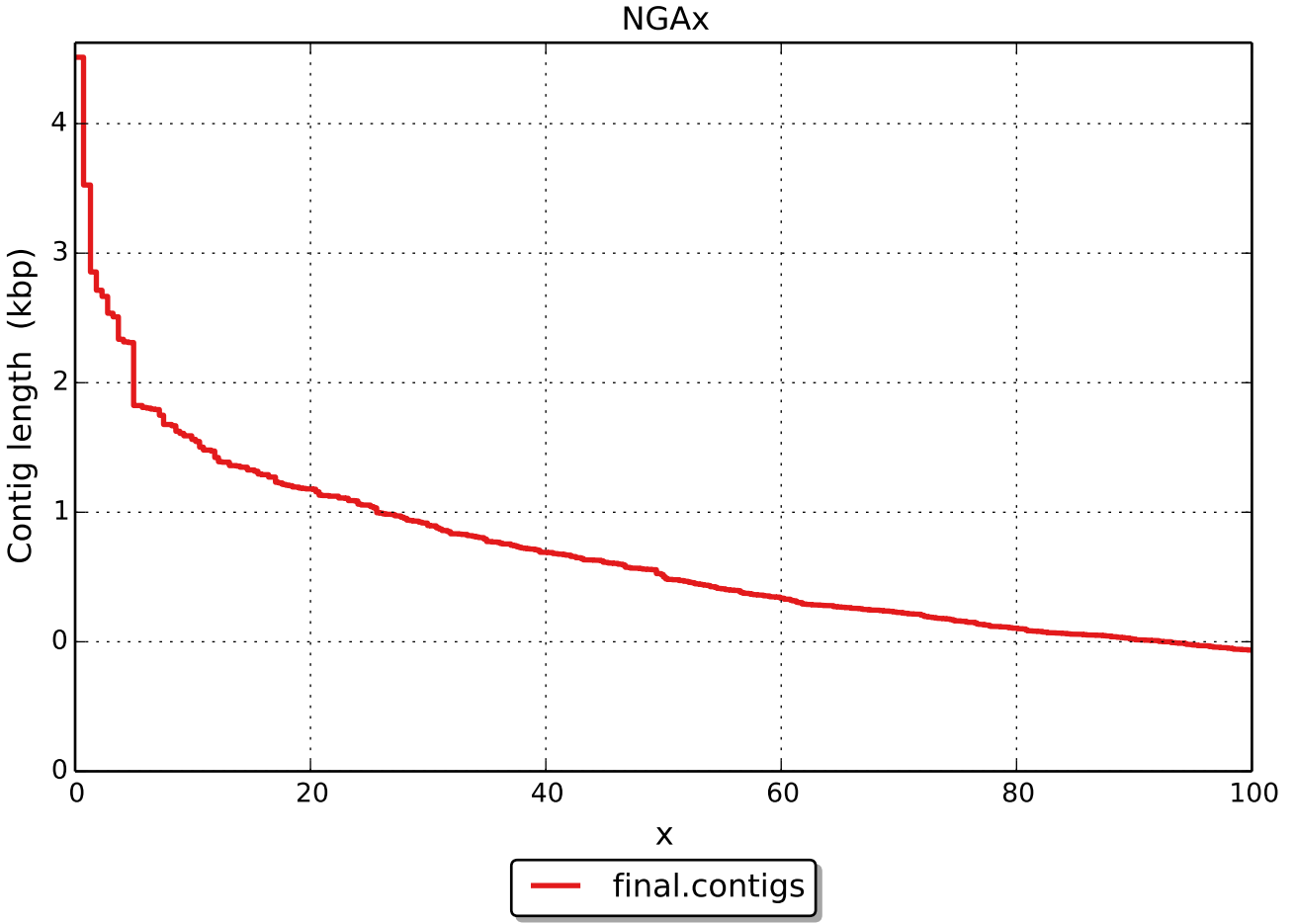

Nx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
16
14
12
10
8
6
4
2
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
200
400
600
800
0
200
400
600
800
1000
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