Report

	final.contigs
# contigs (>= 0 bp)	950
# contigs (>= 1000 bp)	451
Total length (>= 0 bp)	1143011
Total length (>= 1000 bp)	780191
# contigs	950
Largest contig	8192
Total length	1143011
Reference length	615980
GC (%)	25.44
Reference GC (%)	25.35
N50	1356
NG50	1998
N75	888
NG75	1629
L50	271
LG50	113
L75	533
LG75	198
# misassemblies	27
# misassembled contigs	27
Misassembled contigs length	48365
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	920
Genome fraction (%)	92.952
Duplication ratio	1.995
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1562.61
# indels per 100 kbp	0.87
Largest alignment	8192
NA50	1333
NGA50	1966
NA75	872
NGA75	1599
LA50	276
LGA50	115
LA75	544
LGA75	201

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

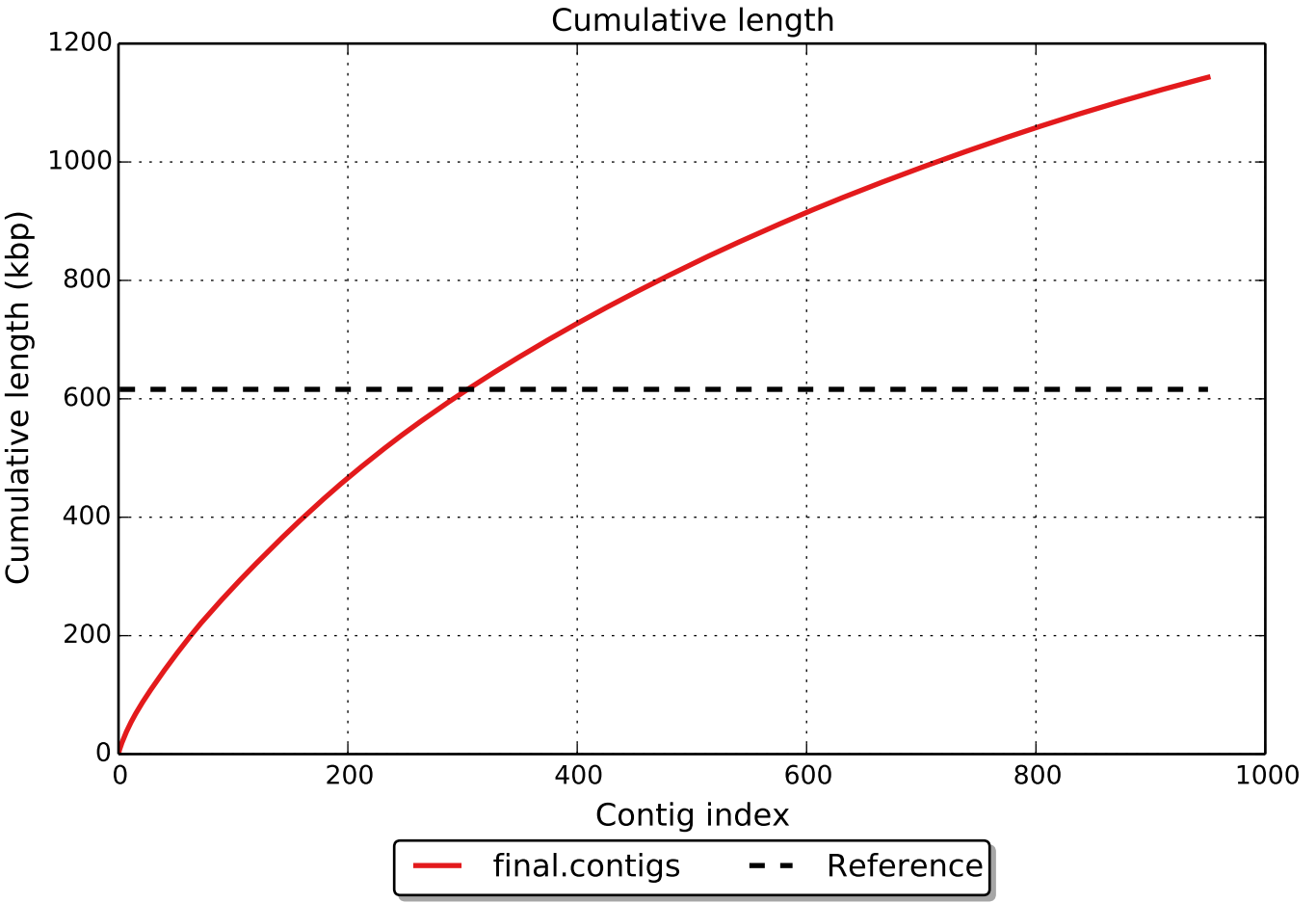
	final.contigs
# misassemblies	27
# relocations	27
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	27
Misassembled contigs length	48365
# local misassemblies	0
# mismatches	8947
# indels	5
# short indels	5
# long indels	0
Indels length	5

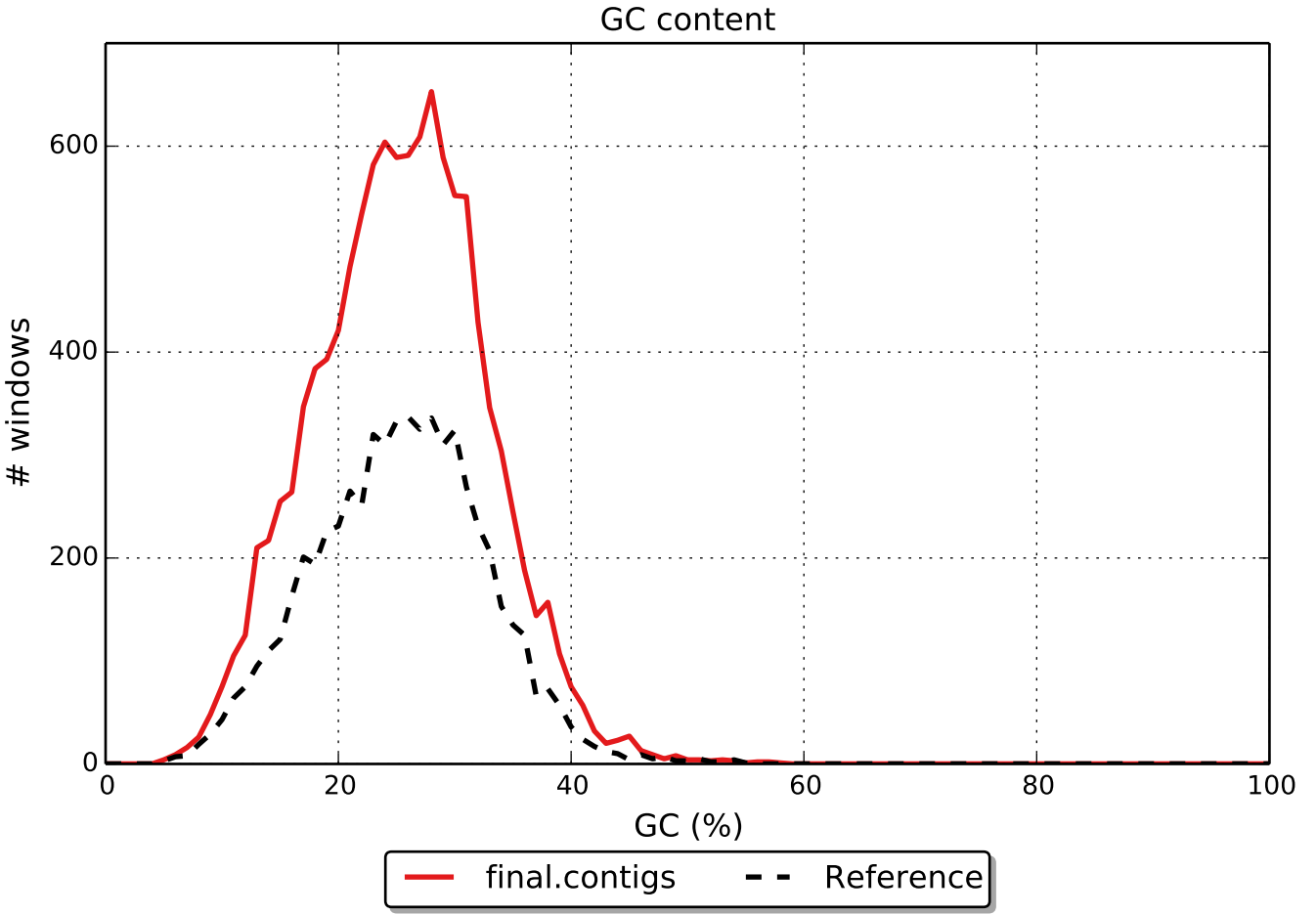
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

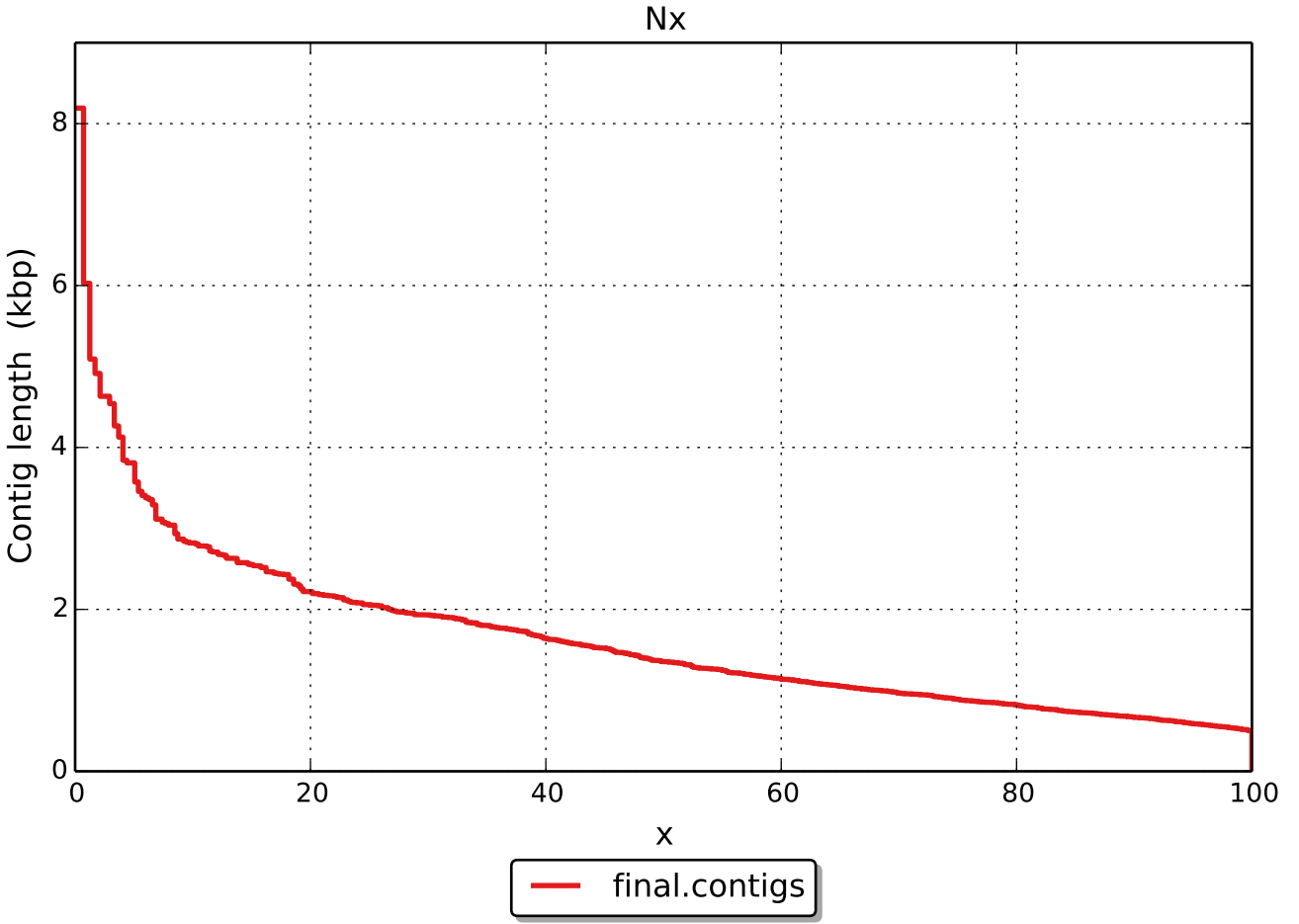
Unaligned report

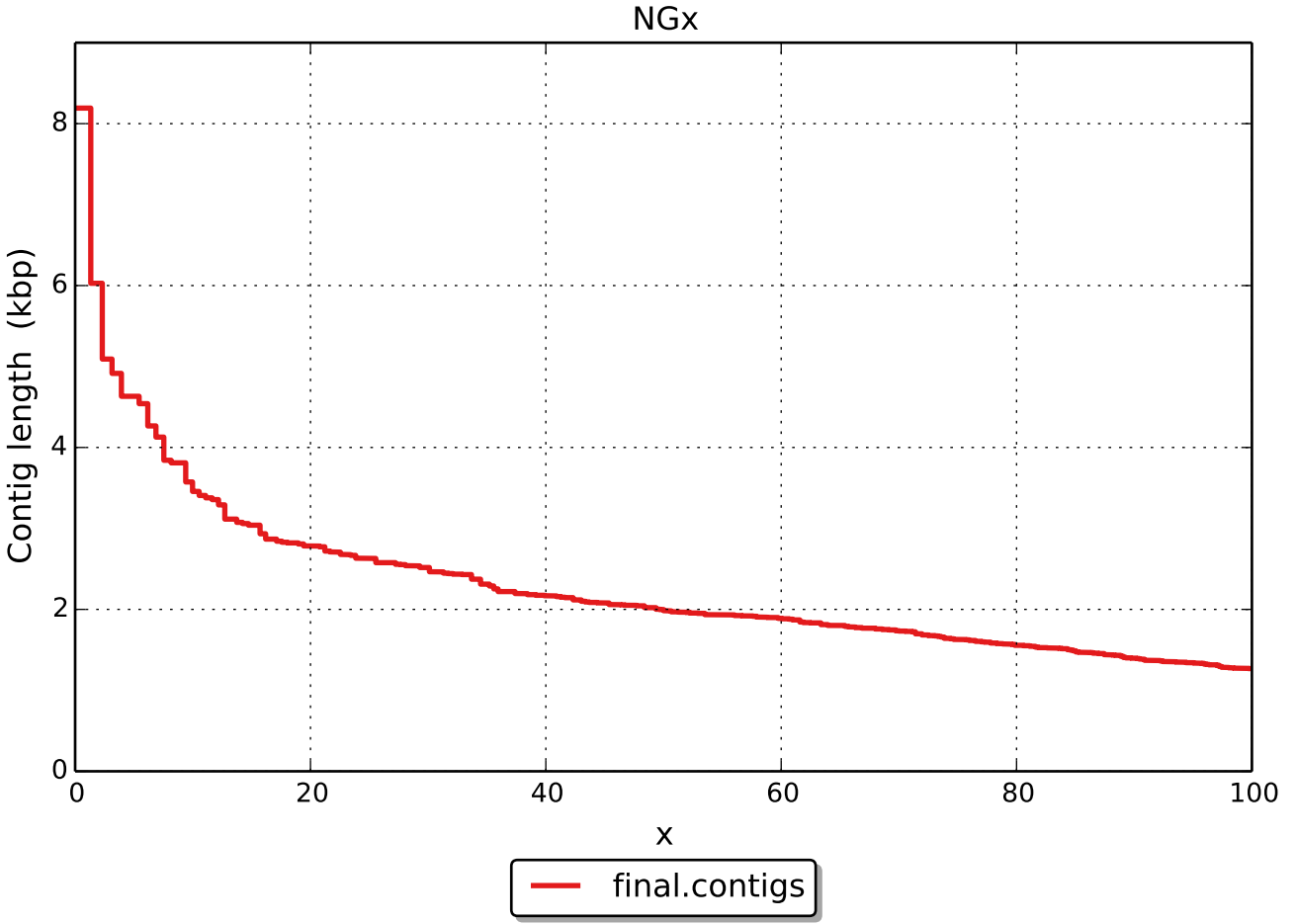
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	920
# N's	0

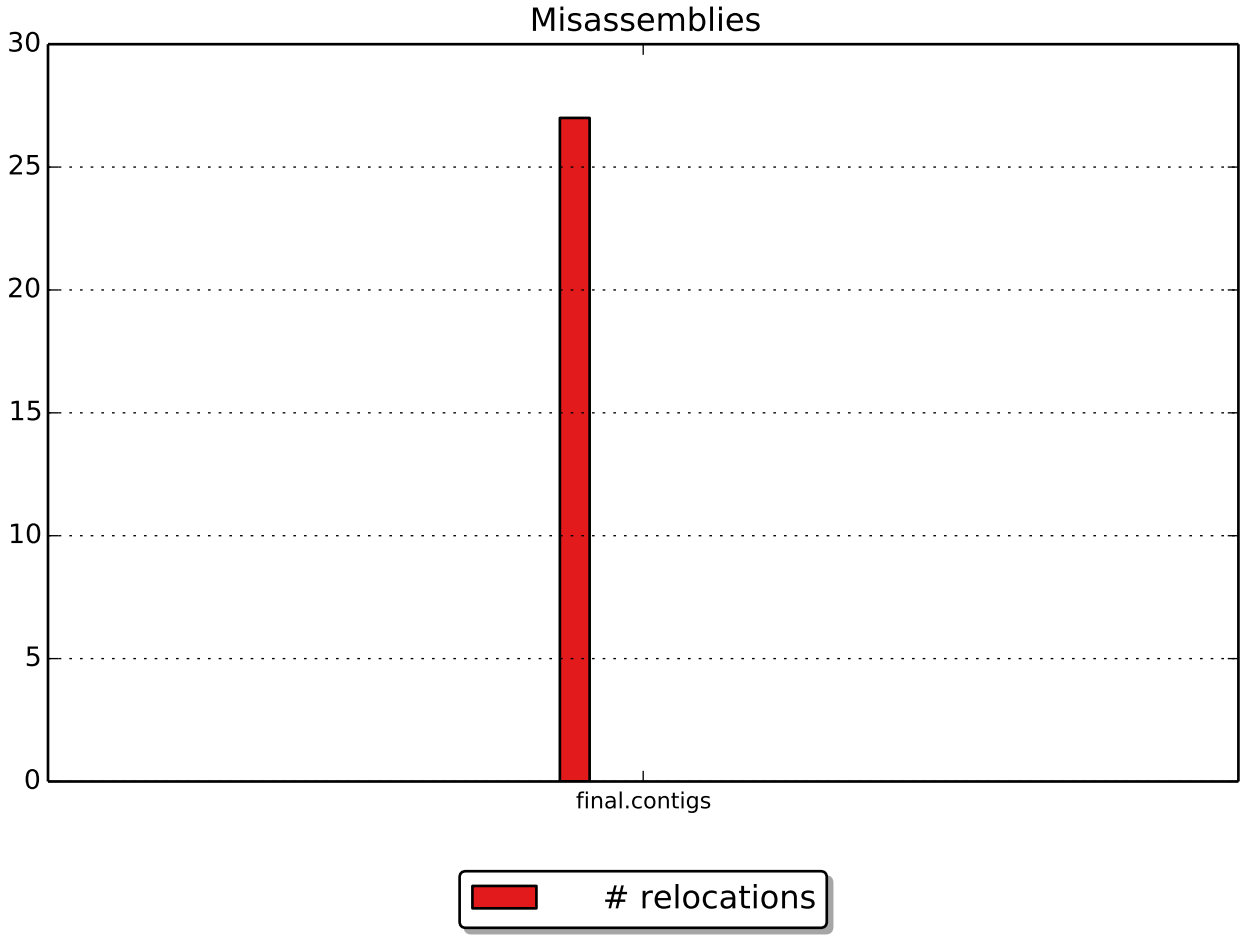
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

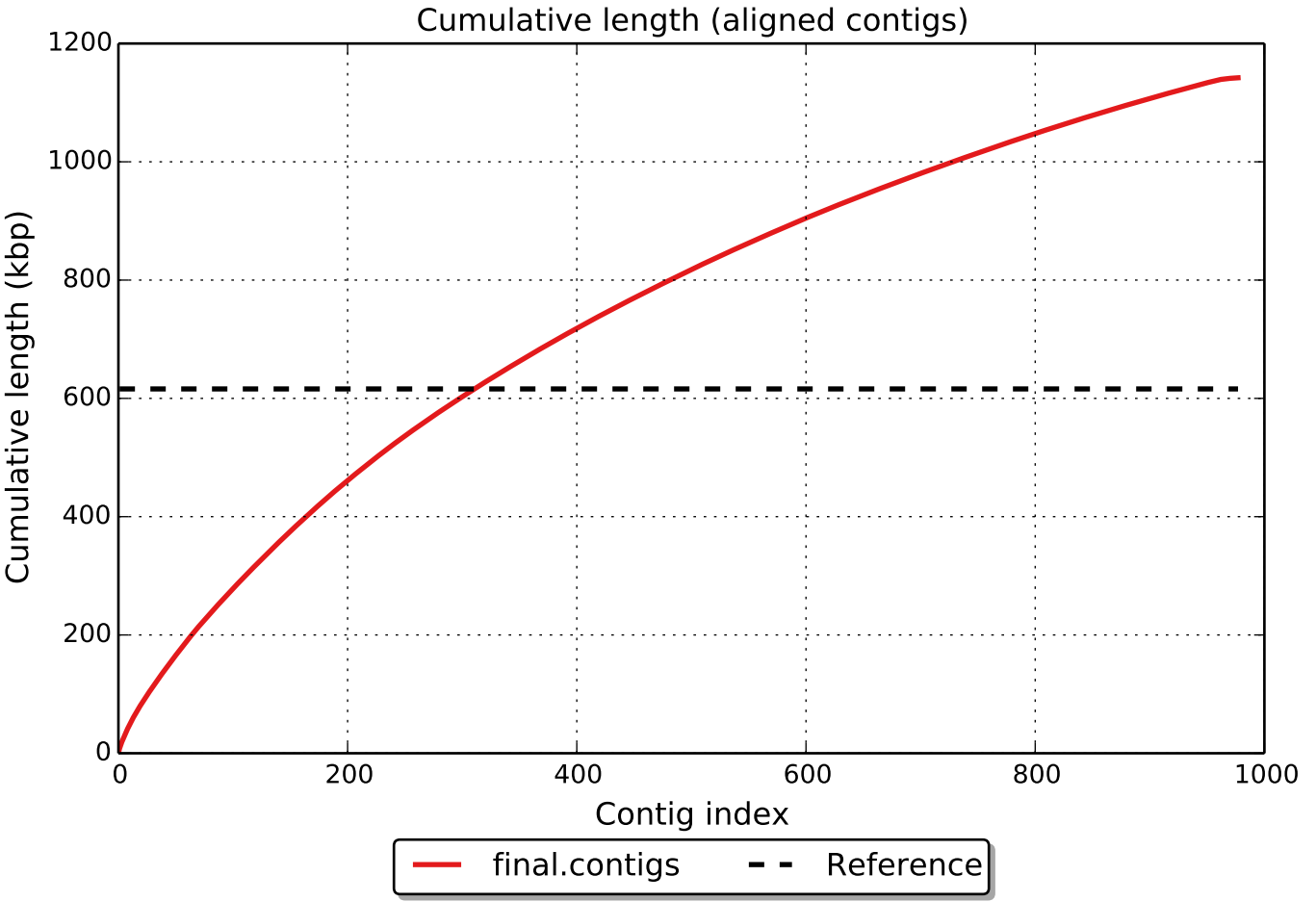

Cumulative length
Cumulative length (kbp)
1200
1000
800
600
400
200
0
0
200
400
600
800
1000
Contig index
final.contigs
Reference

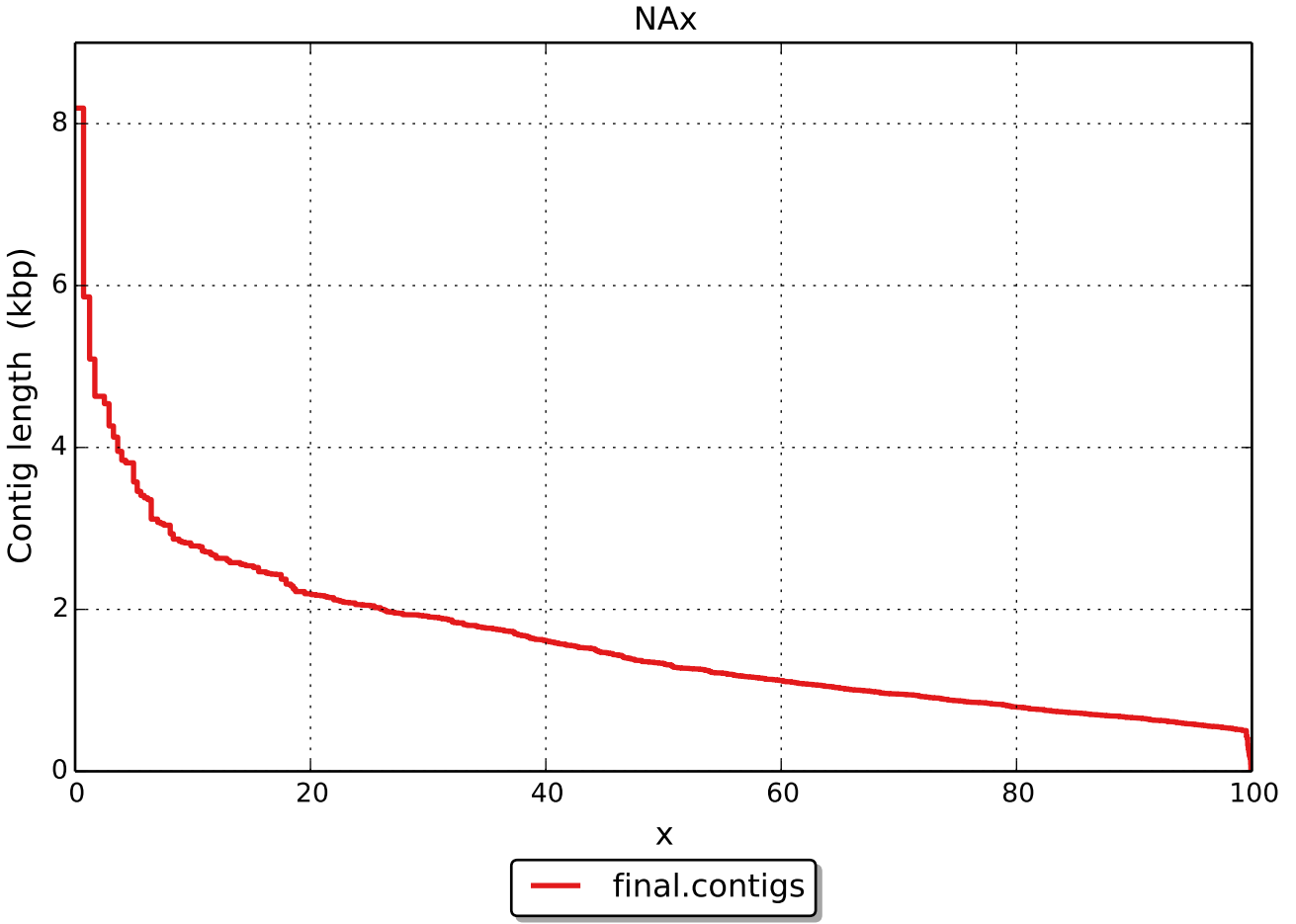

GC content
windows
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

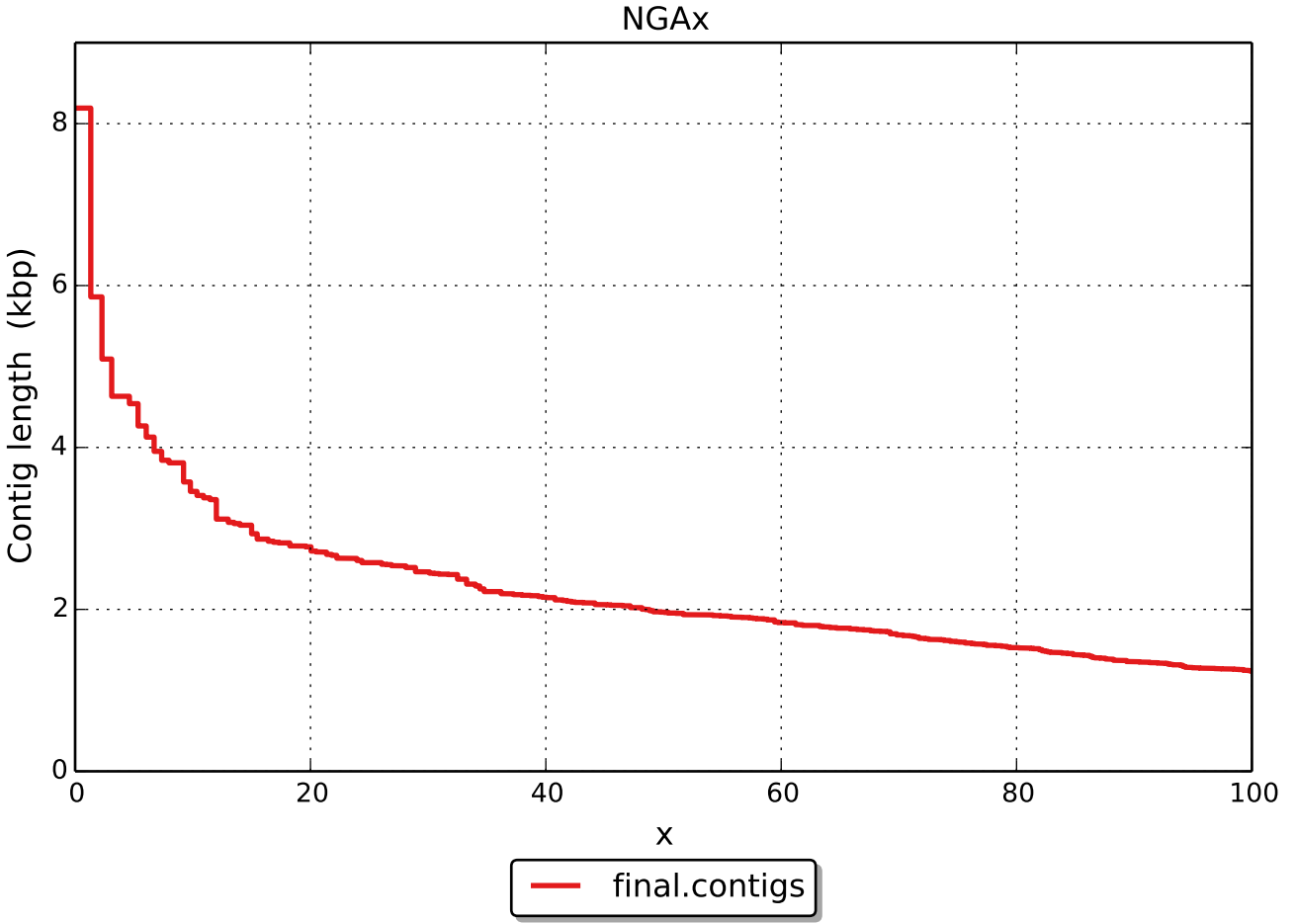

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


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


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


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs