Report

	final.contigs
# contigs (>= 0 bp)	563
# contigs (>= 1000 bp)	225
Total length (>= 0 bp)	736895
Total length (>= 1000 bp)	510290
# contigs	563
Largest contig	9129
Total length	736895
Reference length	641799
GC (%)	26.33
Reference GC (%)	26.30
N50	1740
NG50	2107
N75	844
NG75	1098
L50	118
LG50	93
L75	272
LG75	198
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	9065
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.209
Duplication ratio	1.219
# N's per 100 kbp	0.00
# mismatches per 100 kbp	828.27
# indels per 100 kbp	0.33
Largest alignment	9129
NA50	1725
NGA50	2106
NA75	837
NGA75	1092
LA50	119
LGA50	93
LA75	273
LGA75	199

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

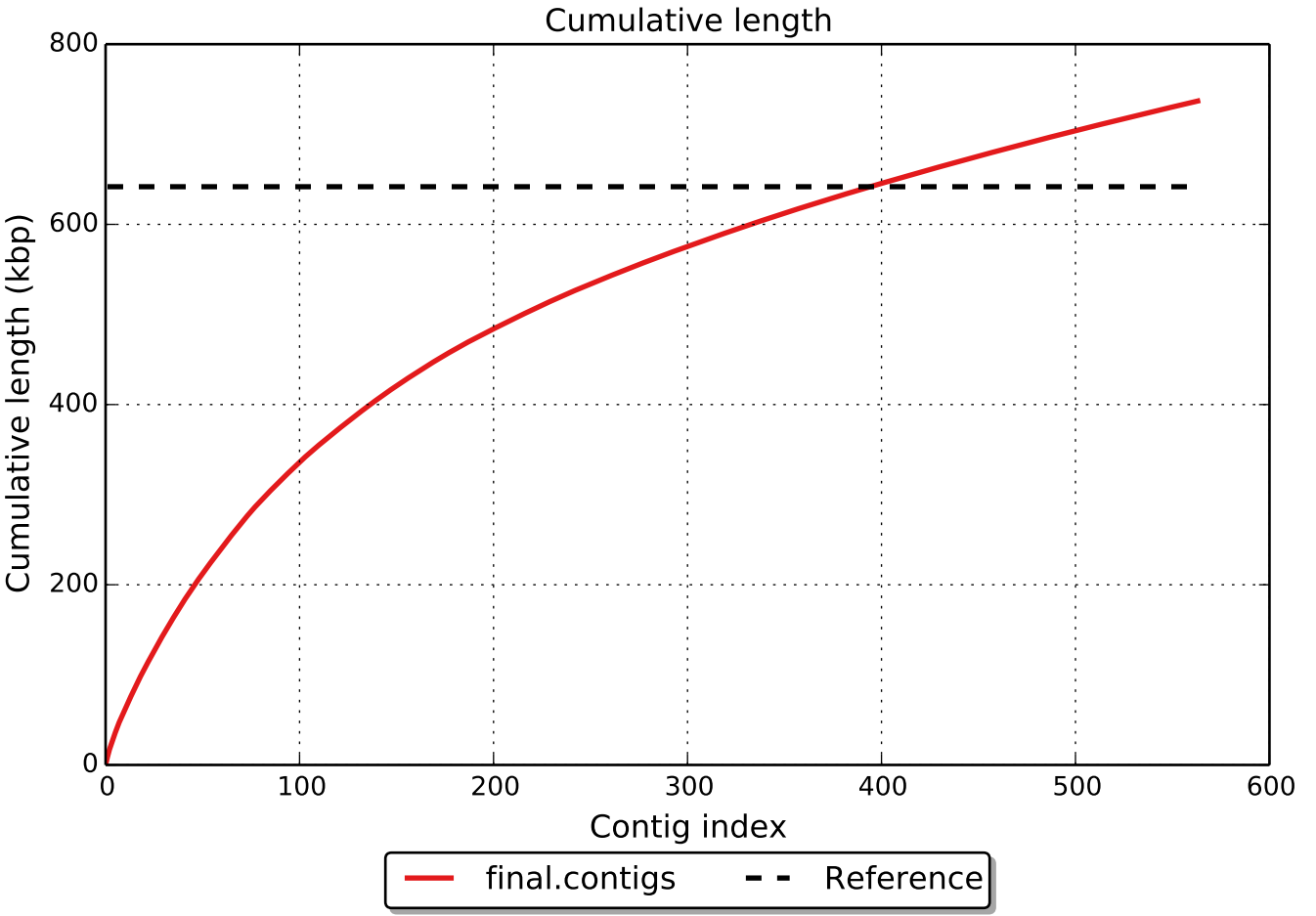
	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	9065
# local misassemblies	0
# mismatches	5008
# indels	2
# short indels	2
# long indels	0
Indels length	2

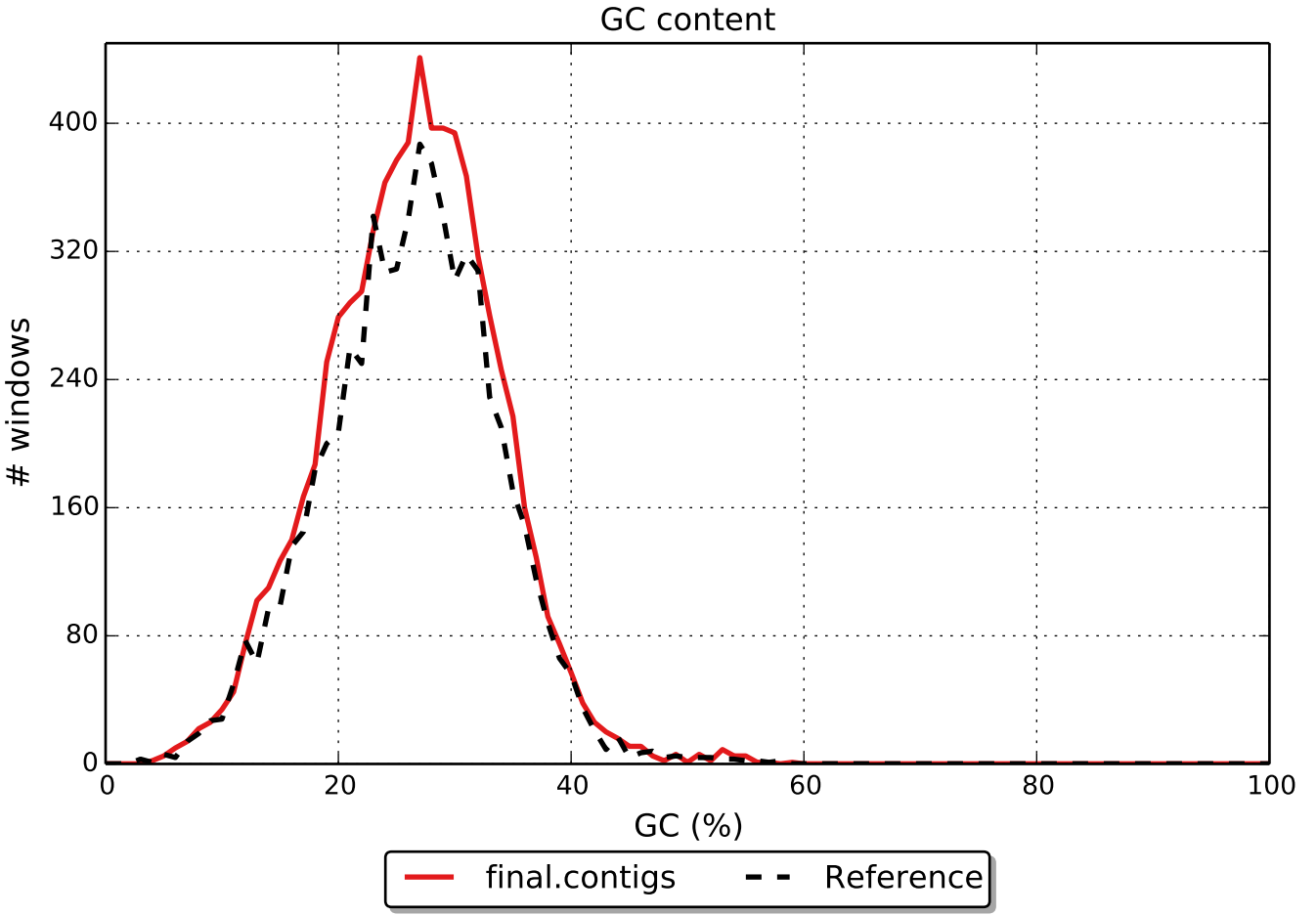
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

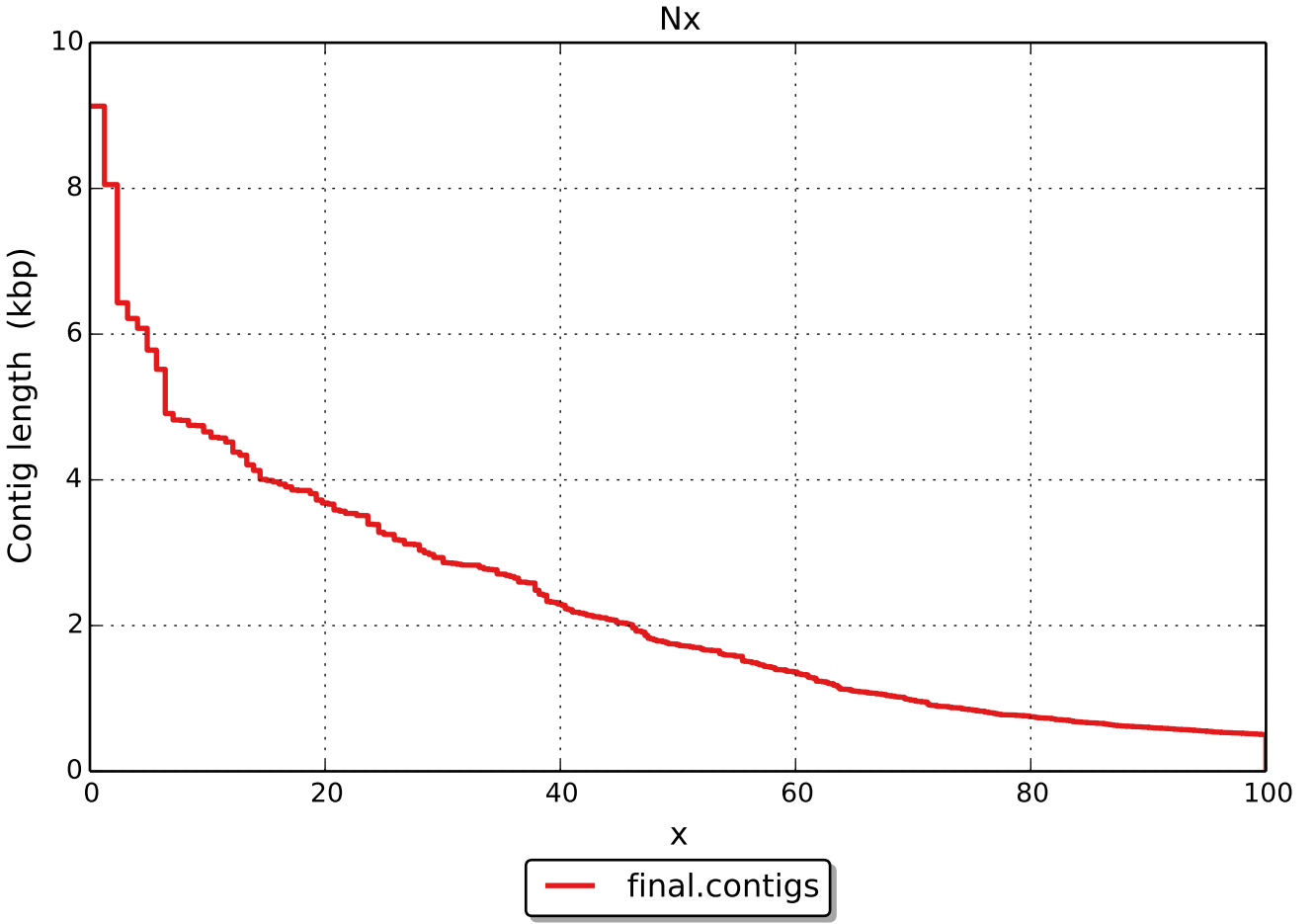
Unaligned report

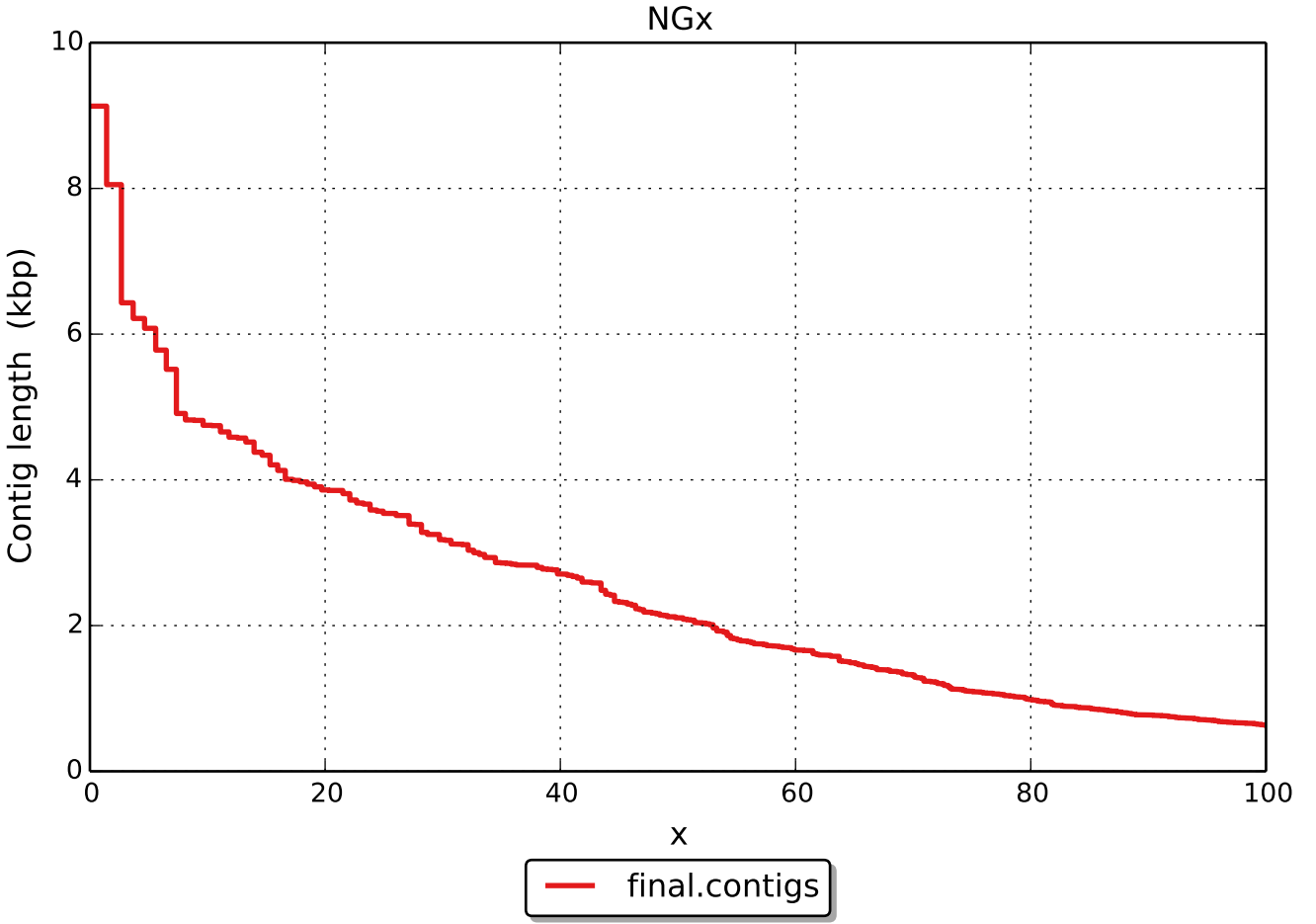
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

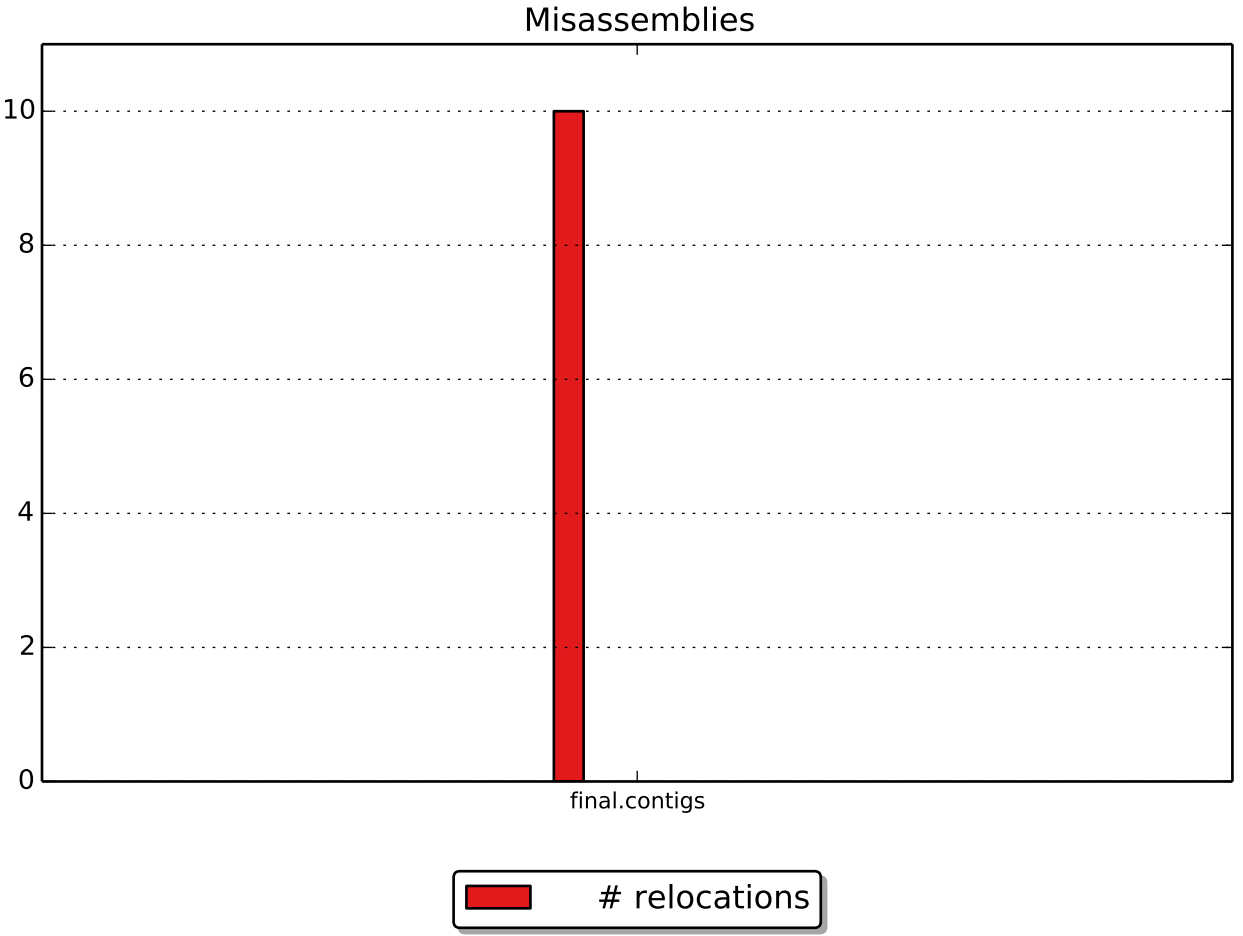
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

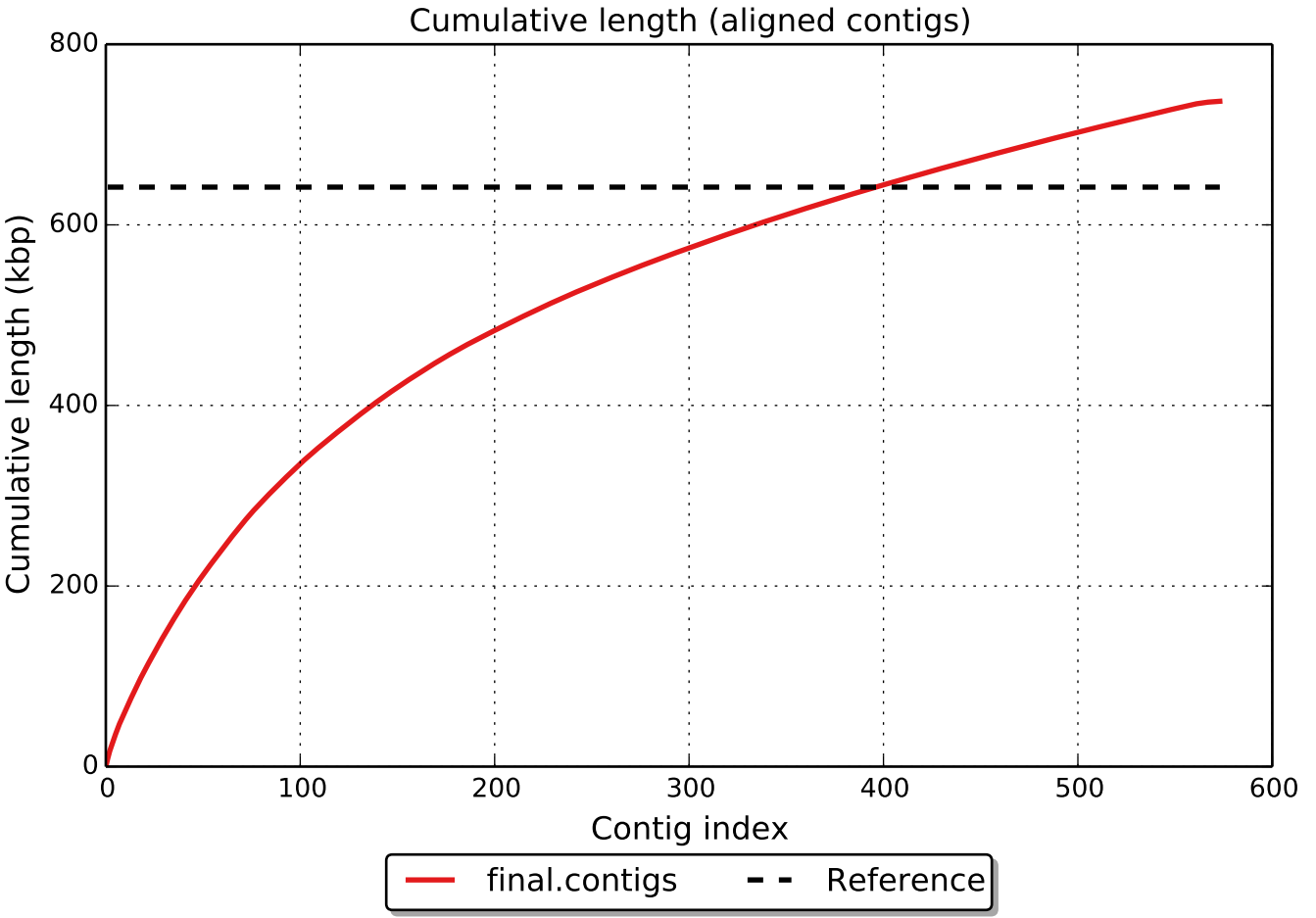

Cumulative length
Cumulative length (kbp)
800
600
400
200
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

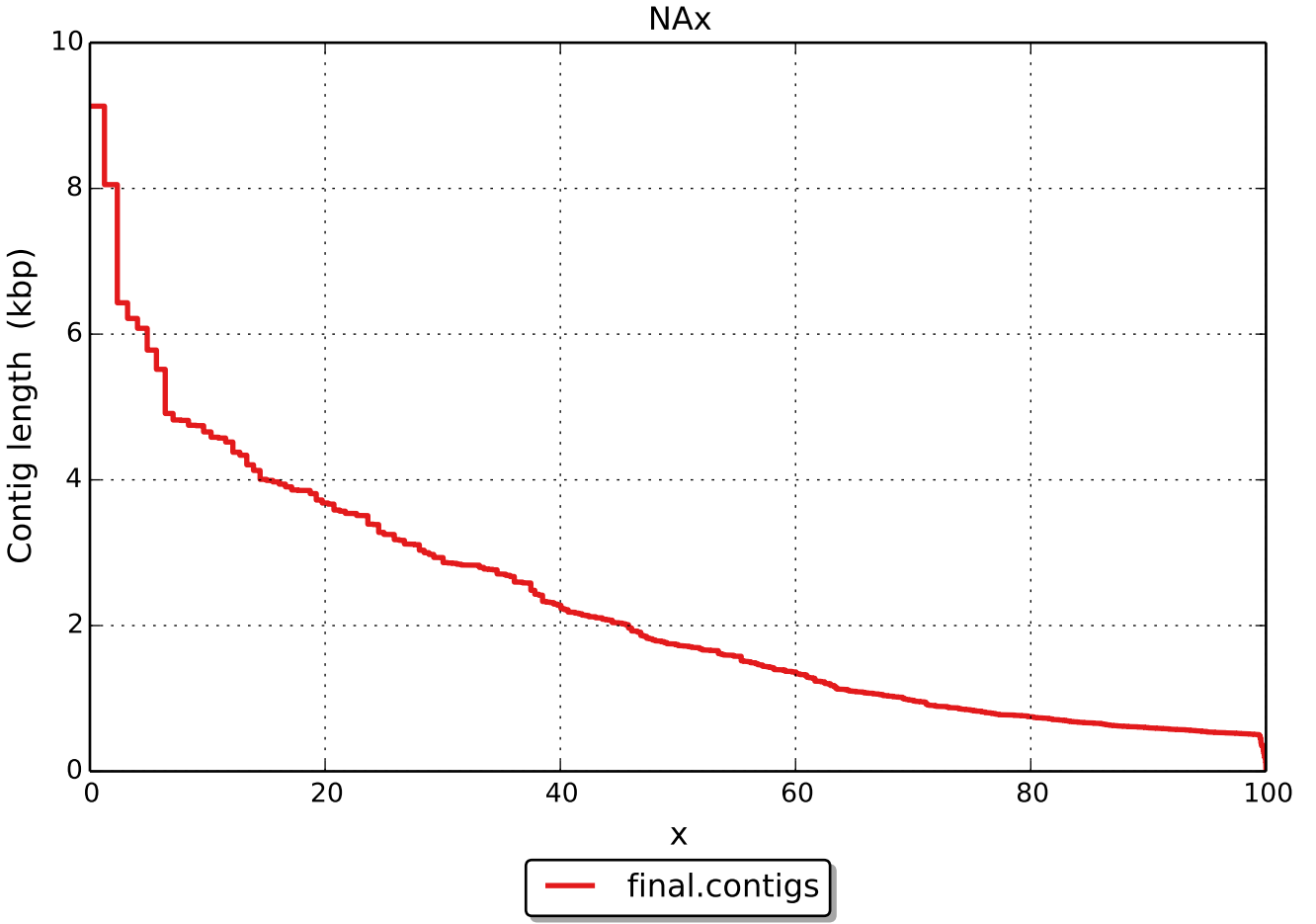

GC content
windows
GC (%)
0
80
160
240
320
400
0
20
40
60
80
100
final.contigs
Reference

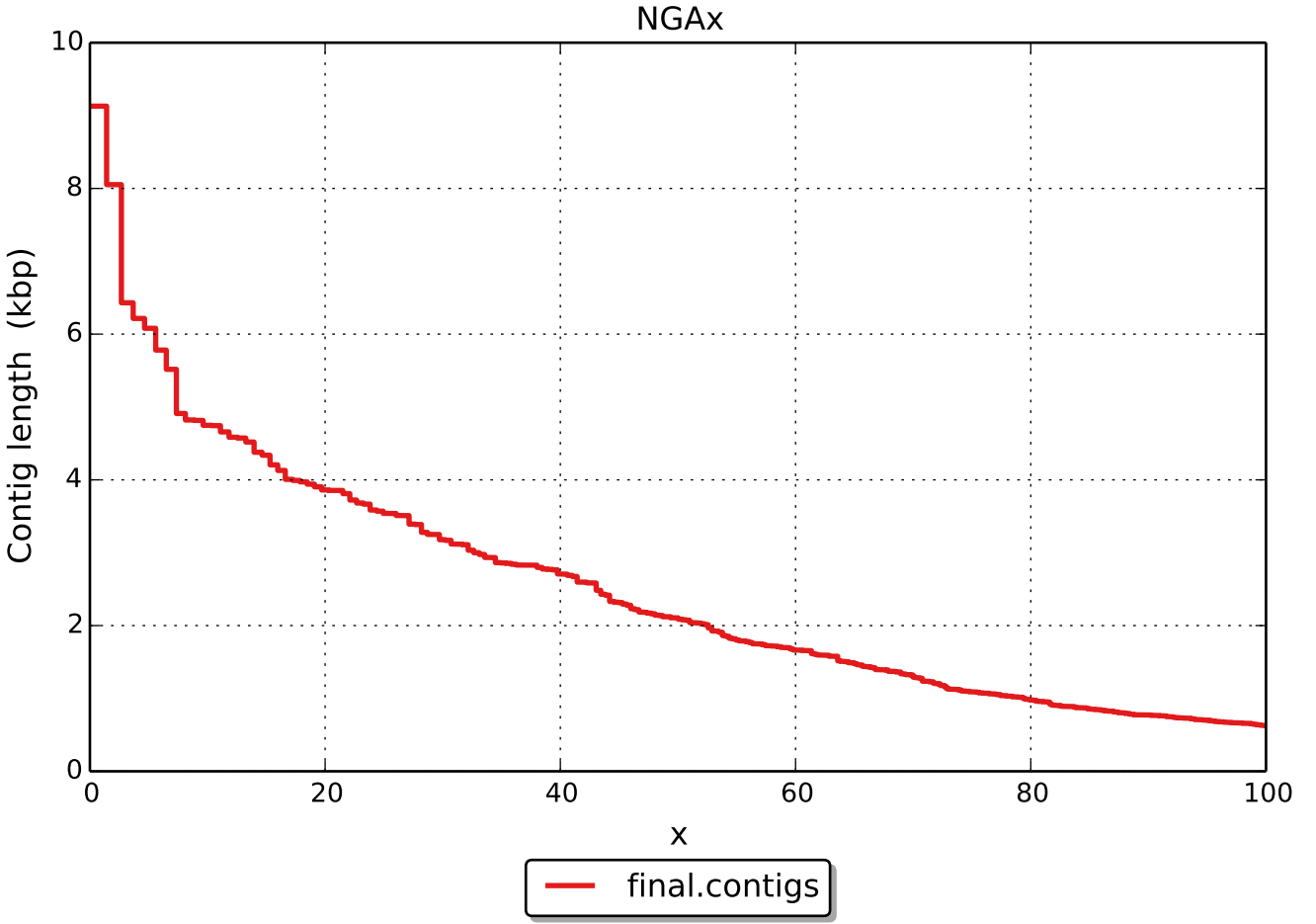

Nx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
10
8
6
4
2
0
final.contigs
relocations


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


NAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs