Report

	final.contigs
# contigs (>= 0 bp)	559
# contigs (>= 1000 bp)	423
Total length (>= 0 bp)	1233504
Total length (>= 1000 bp)	1134938
# contigs	559
Largest contig	11592
Total length	1233504
Reference length	615980
GC (%)	25.33
Reference GC (%)	25.35
N50	2927
NG50	4649
N75	1746
NG75	3663
L50	137
LG50	52
L75	269
LG75	89
# misassemblies	37
# misassembled contigs	36
Misassembled contigs length	136834
# local misassemblies	0
# unaligned contigs	3 + 3 part
Unaligned length	8122
Genome fraction (%)	98.151
Duplication ratio	2.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1814.62
# indels per 100 kbp	3.97
Largest alignment	11592
NA50	2814
NGA50	4289
NA75	1609
NGA75	3297
LA50	147
LGA50	55
LA75	289
LGA75	96

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

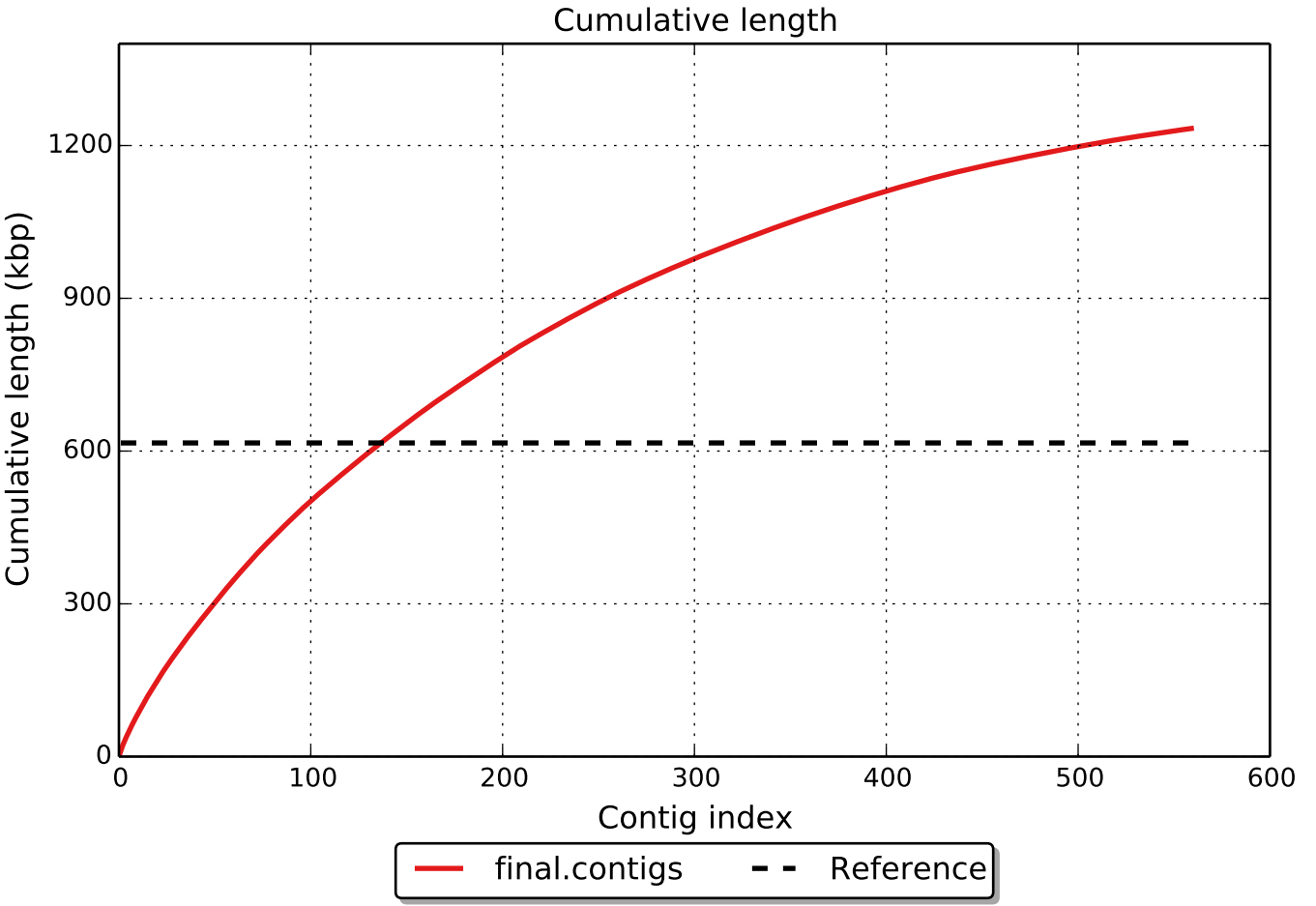
	final.contigs
# misassemblies	37
# relocations	37
# translocations	0
# inversions	0
# possibly misassembled contigs	5
# misassembled contigs	36
Misassembled contigs length	136834
# local misassemblies	0
# mismatches	10971
# indels	24
# short indels	24
# long indels	0
Indels length	24

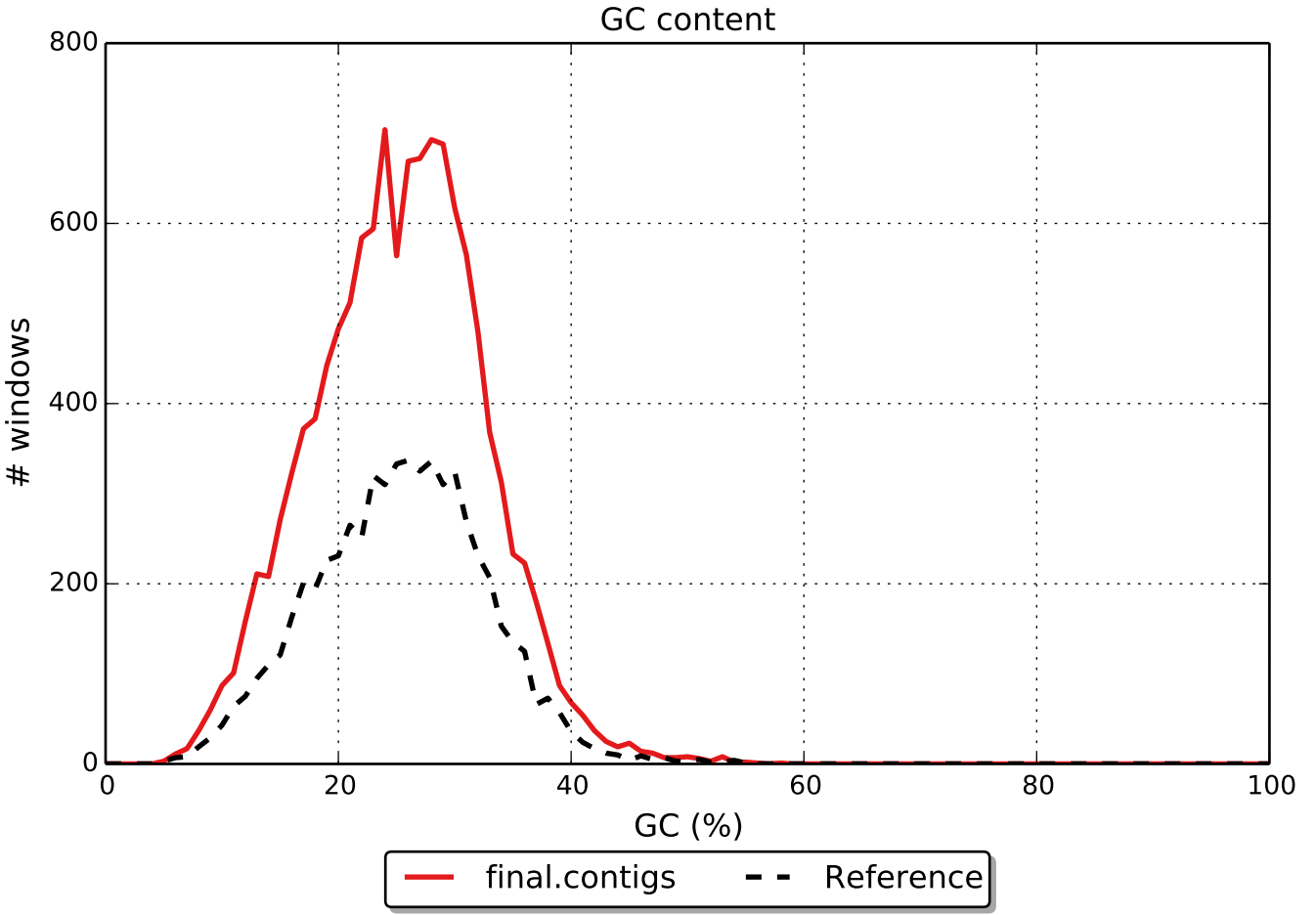
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

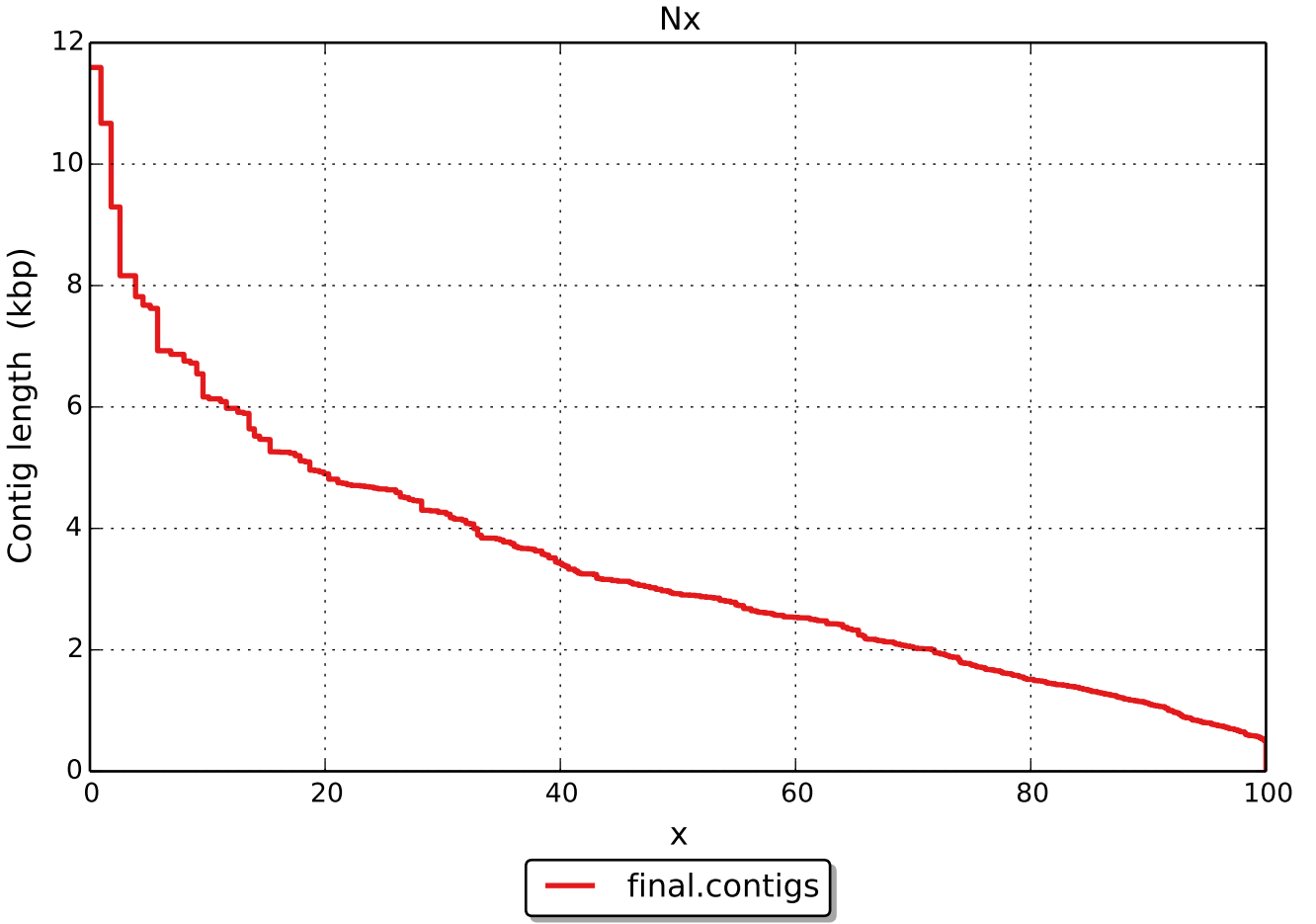
Unaligned report

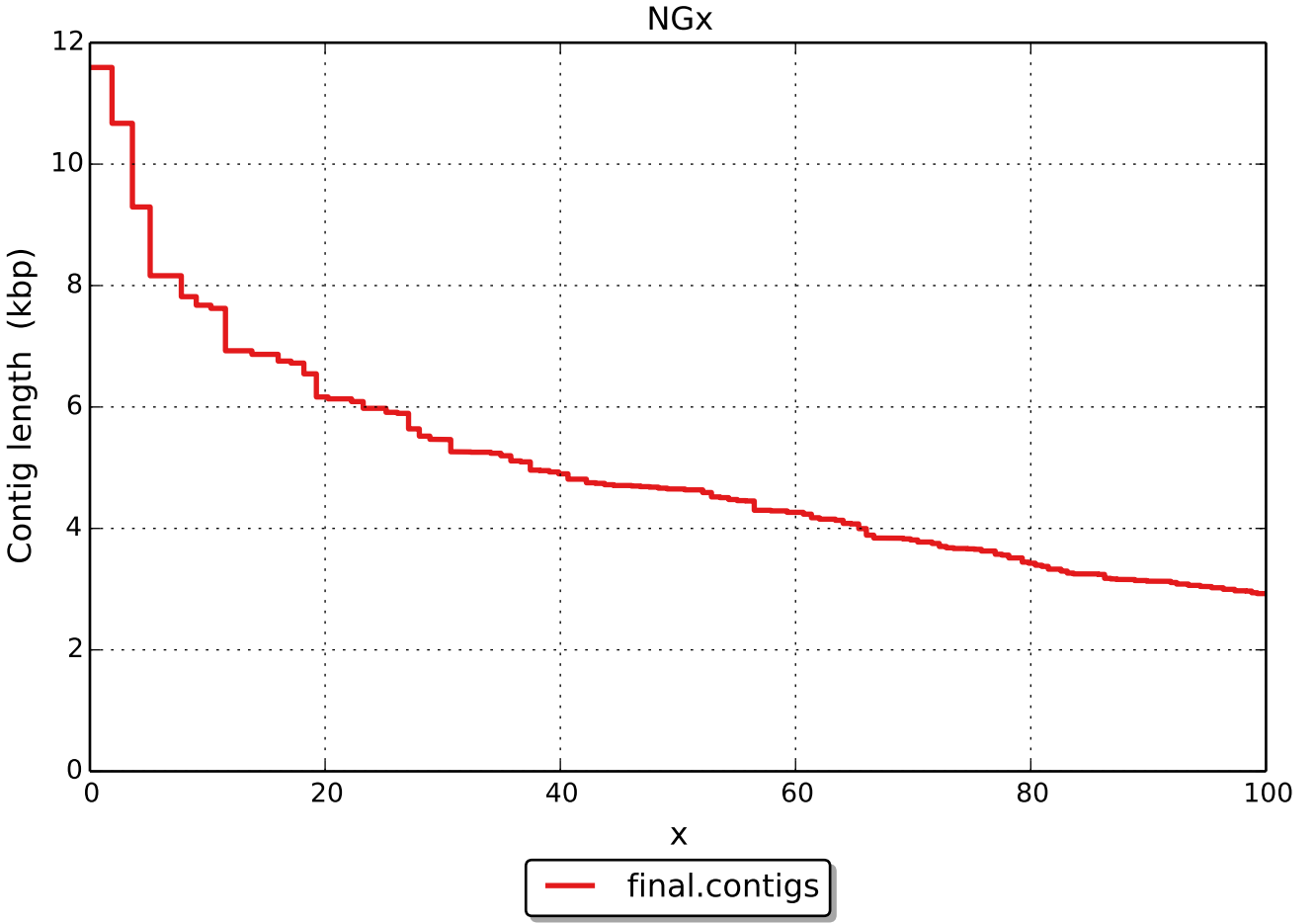
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	5495
# partially unaligned contigs	3
# with misassembly	1
# both parts are significant	2
Partially unaligned length	2627
# N's	0

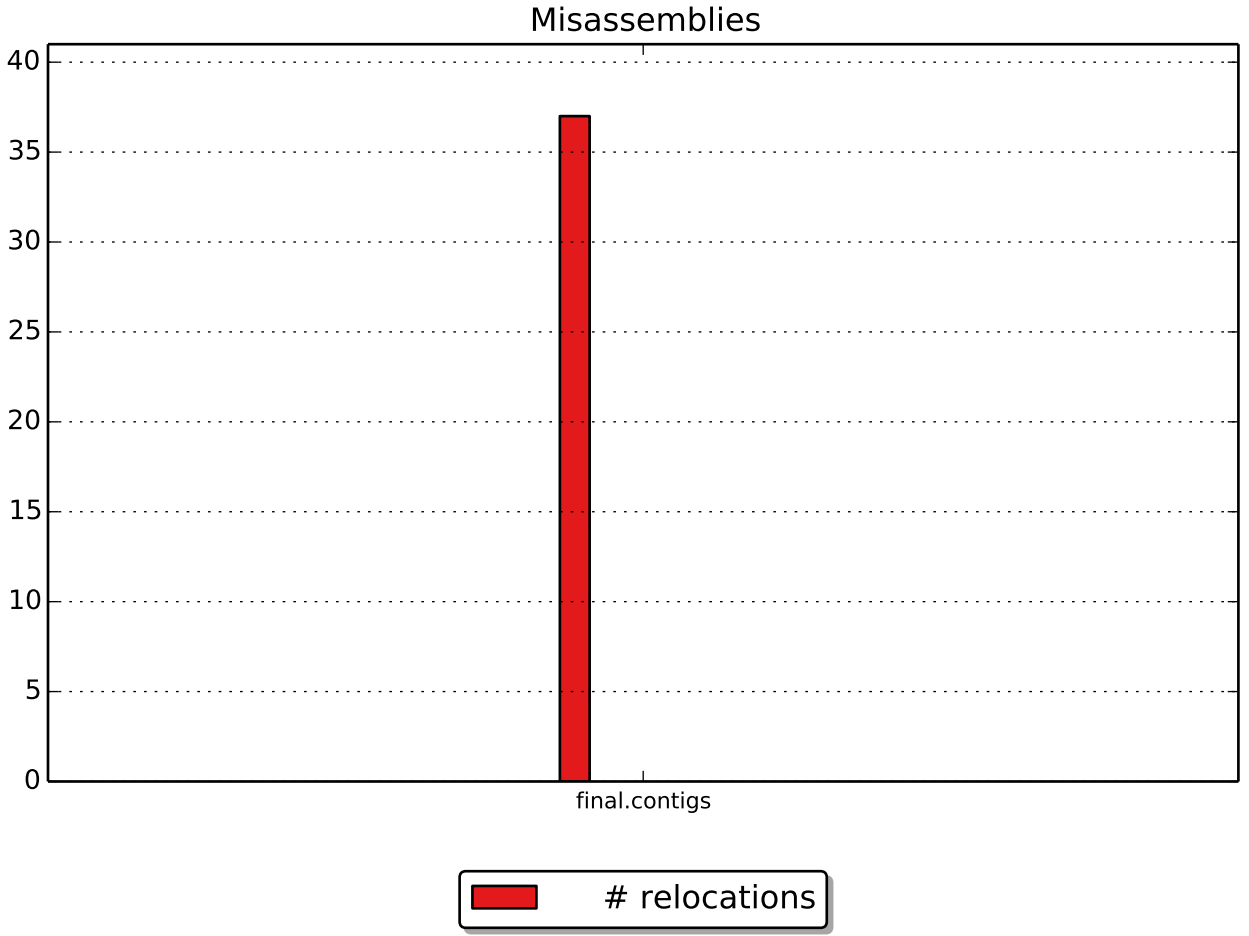
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

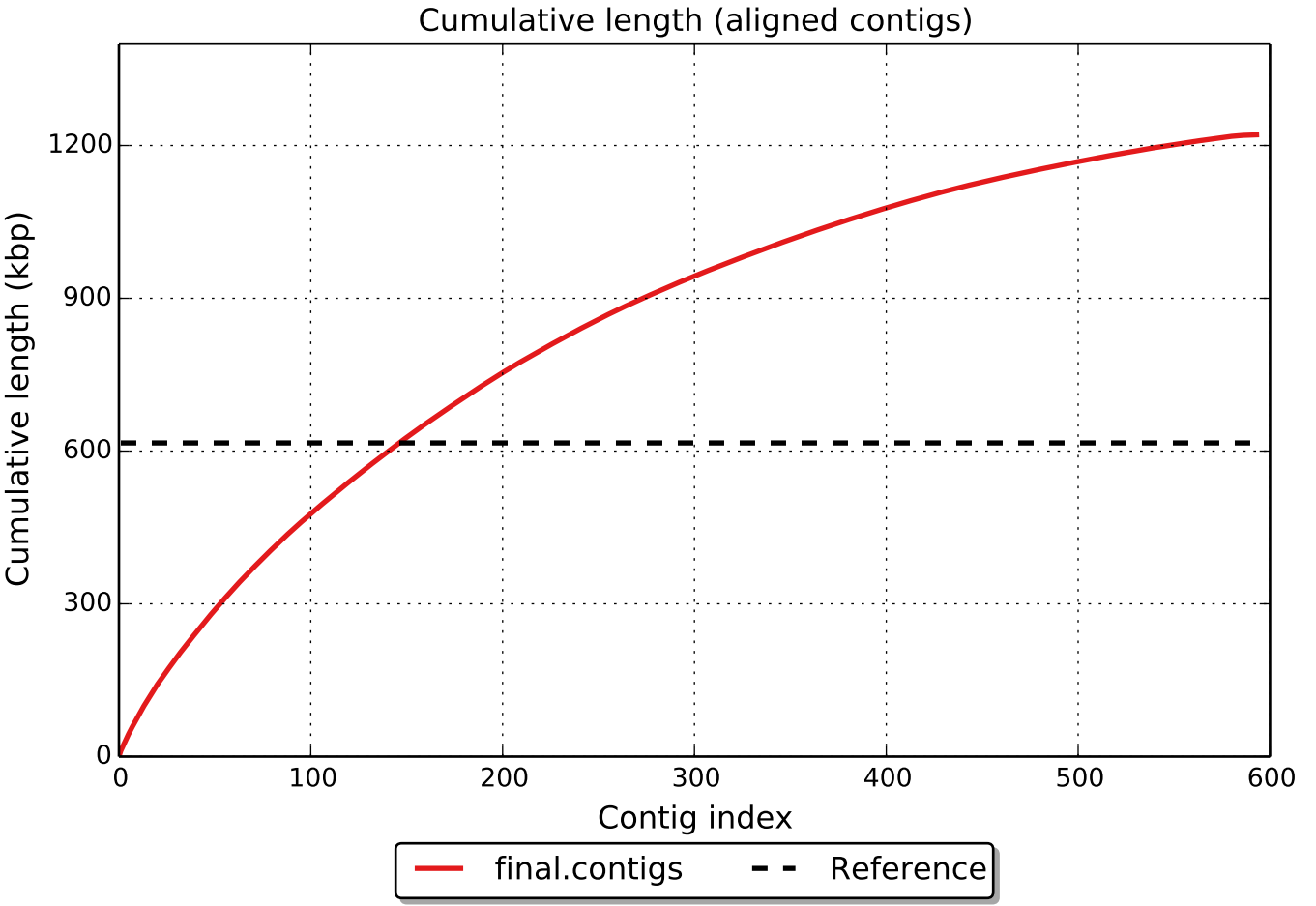

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

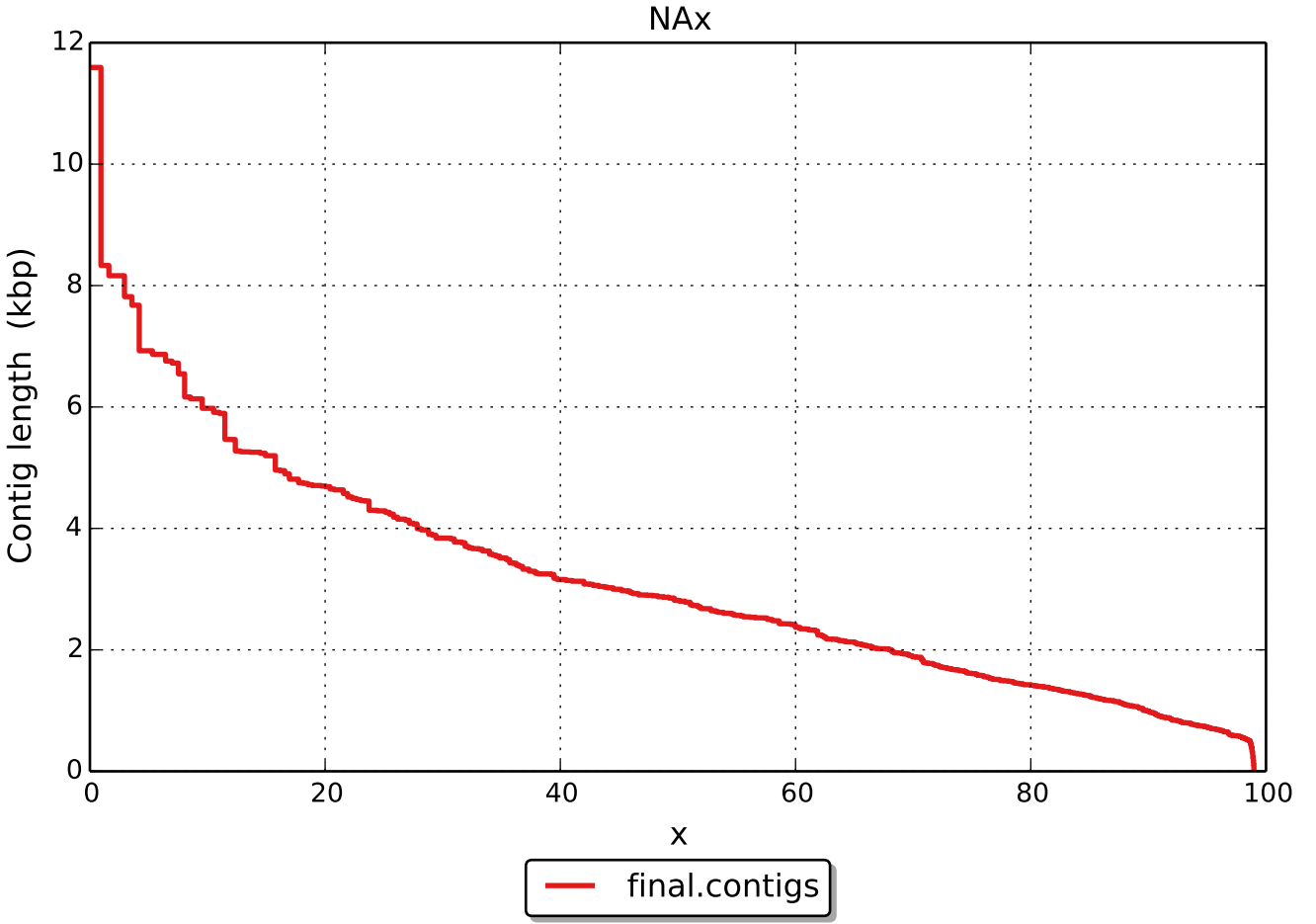

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

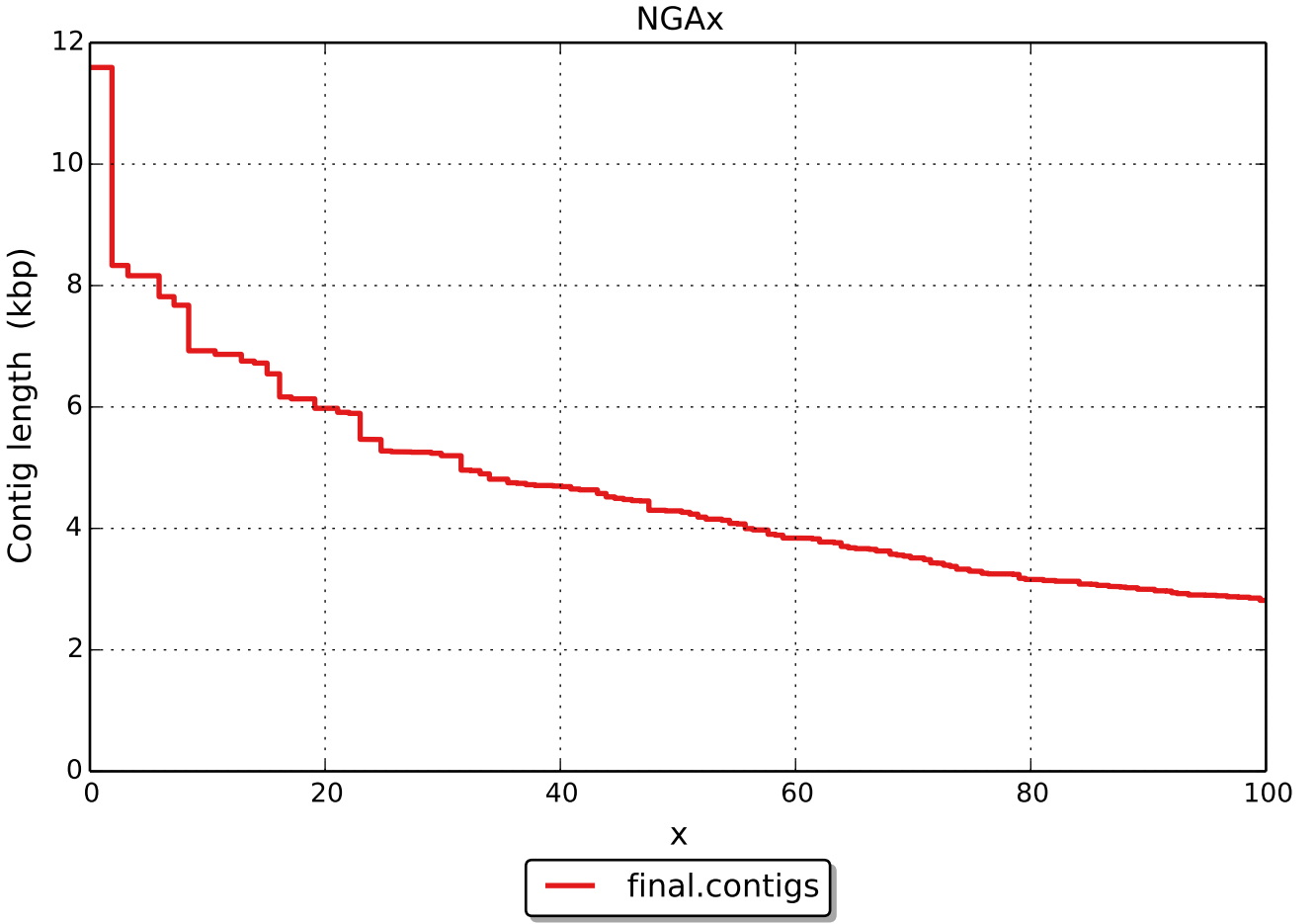

Nx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


Misassemblies
40
35
30
25
20
15
10
5
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
1200
900
600
300
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs