Report

	final.contigs
# contigs (>= 0 bp)	1207
# contigs (>= 1000 bp)	388
Total length (>= 0 bp)	1140341
Total length (>= 1000 bp)	562066
# contigs	1207
Largest contig	2937
Total length	1140341
Reference length	641799
GC (%)	26.36
Reference GC (%)	26.30
N50	993
NG50	1354
N75	720
NG75	1102
L50	397
LG50	182
L75	736
LG75	311
# misassemblies	17
# misassembled contigs	17
Misassembled contigs length	20480
# local misassemblies	0
# unaligned contigs	0 + 4 part
Unaligned length	1235
Genome fraction (%)	89.397
Duplication ratio	1.985
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1327.93
# indels per 100 kbp	0.70
Largest alignment	2937
NA50	916
NGA50	1280
NA75	644
NGA75	1014
LA50	425
LGA50	192
LA75	797
LGA75	333

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

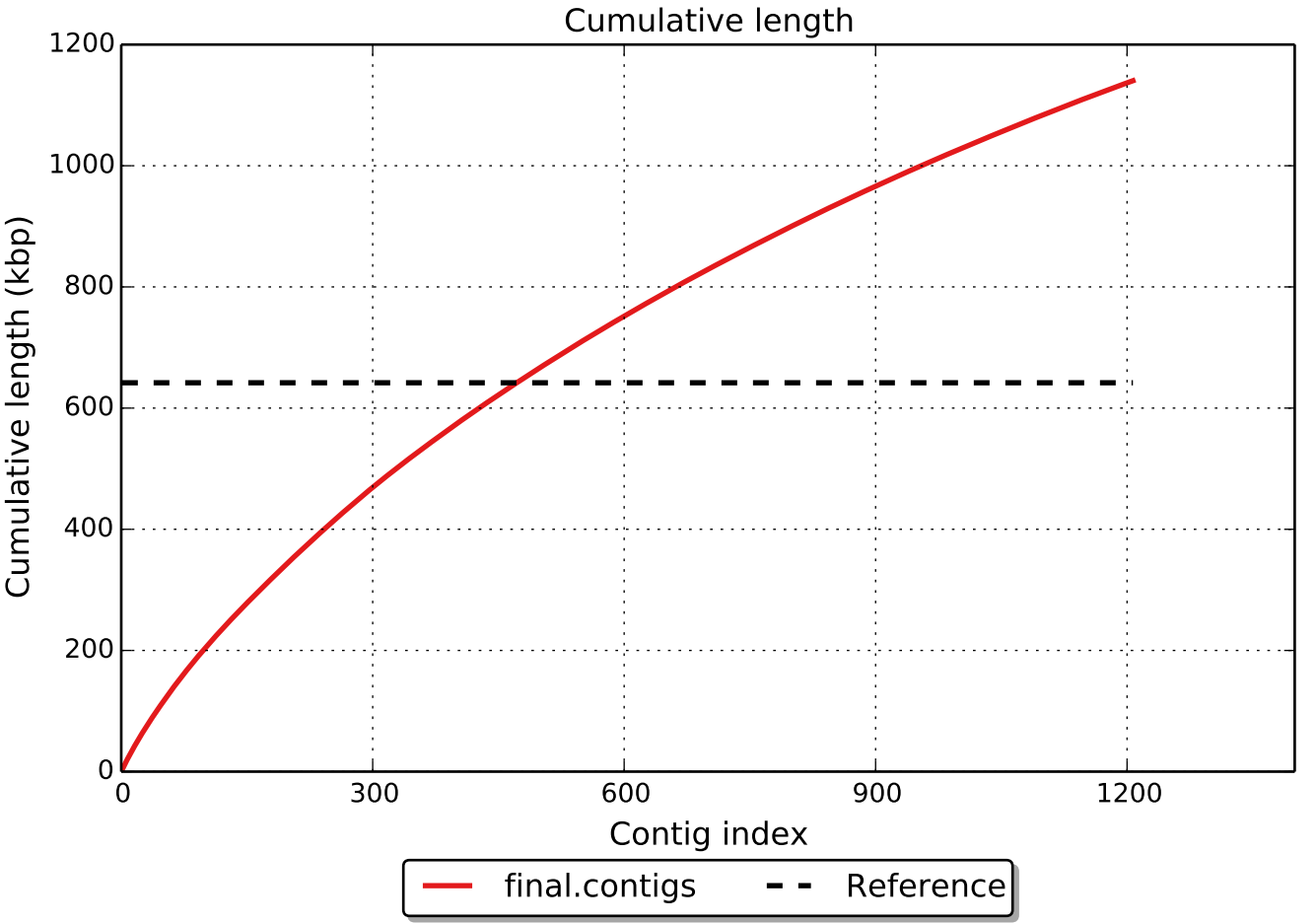
	final.contigs
# misassemblies	17
# relocations	17
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	17
Misassembled contigs length	20480
# local misassemblies	0
# mismatches	7619
# indels	4
# short indels	4
# long indels	0
Indels length	4

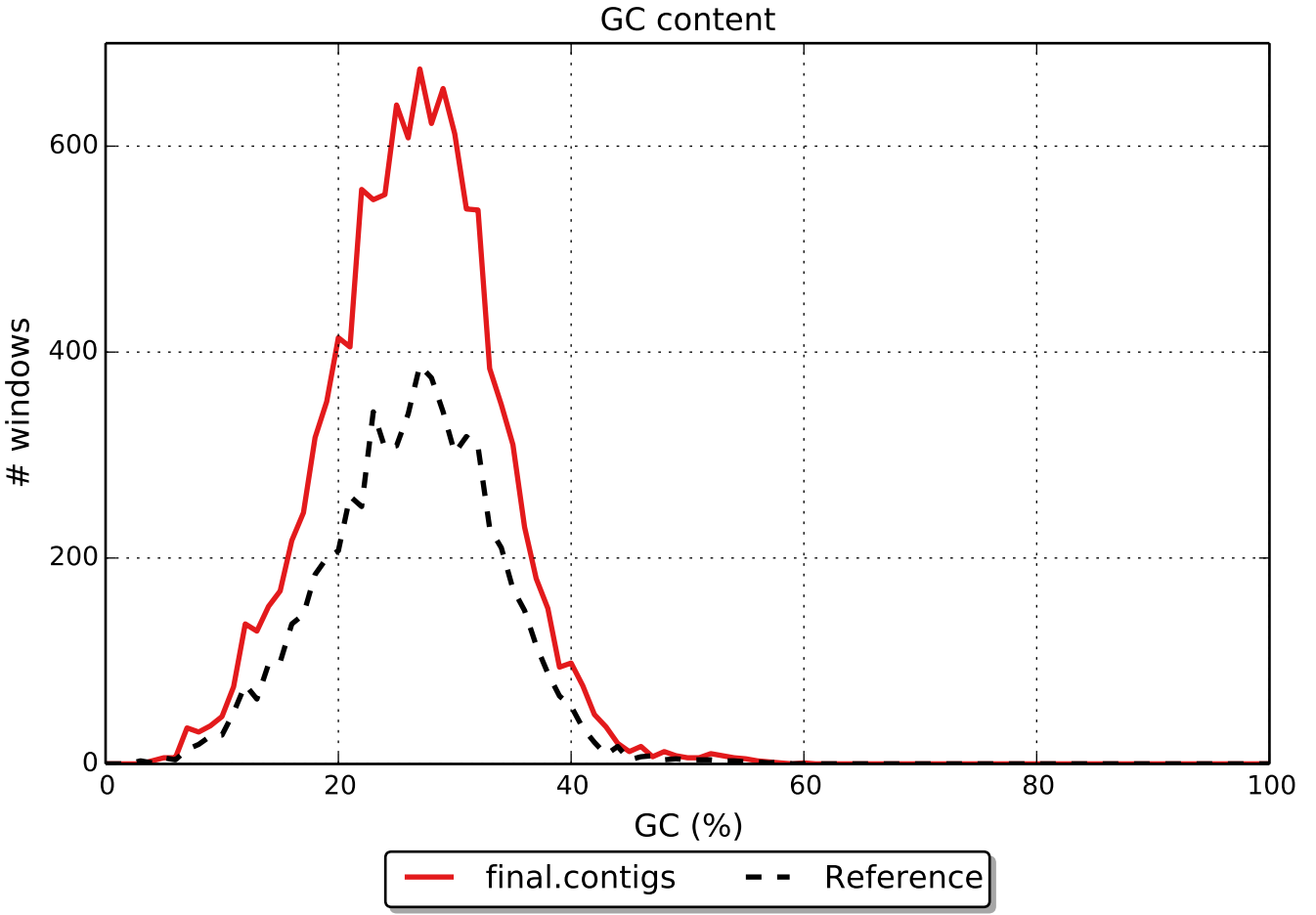
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

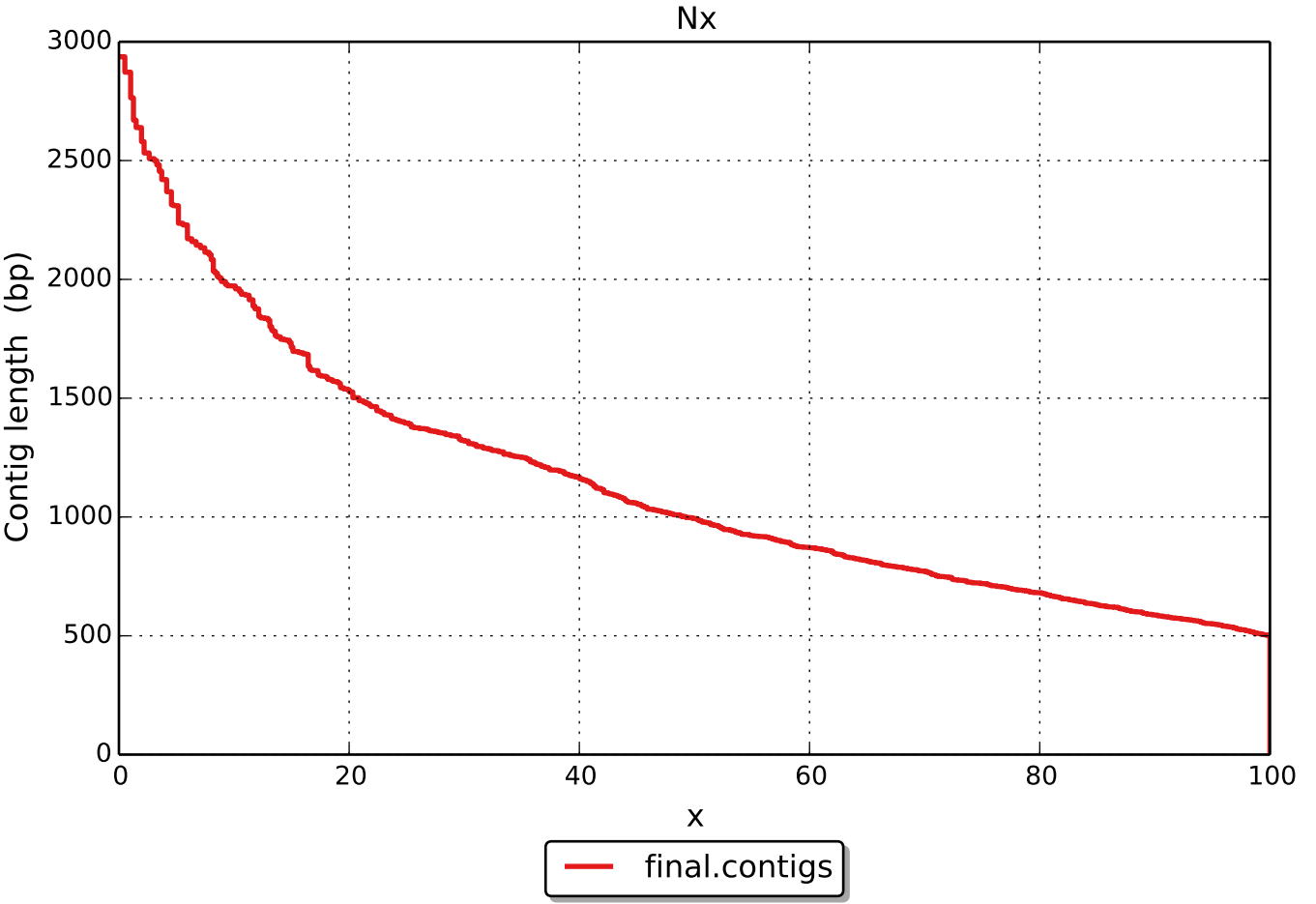
Unaligned report

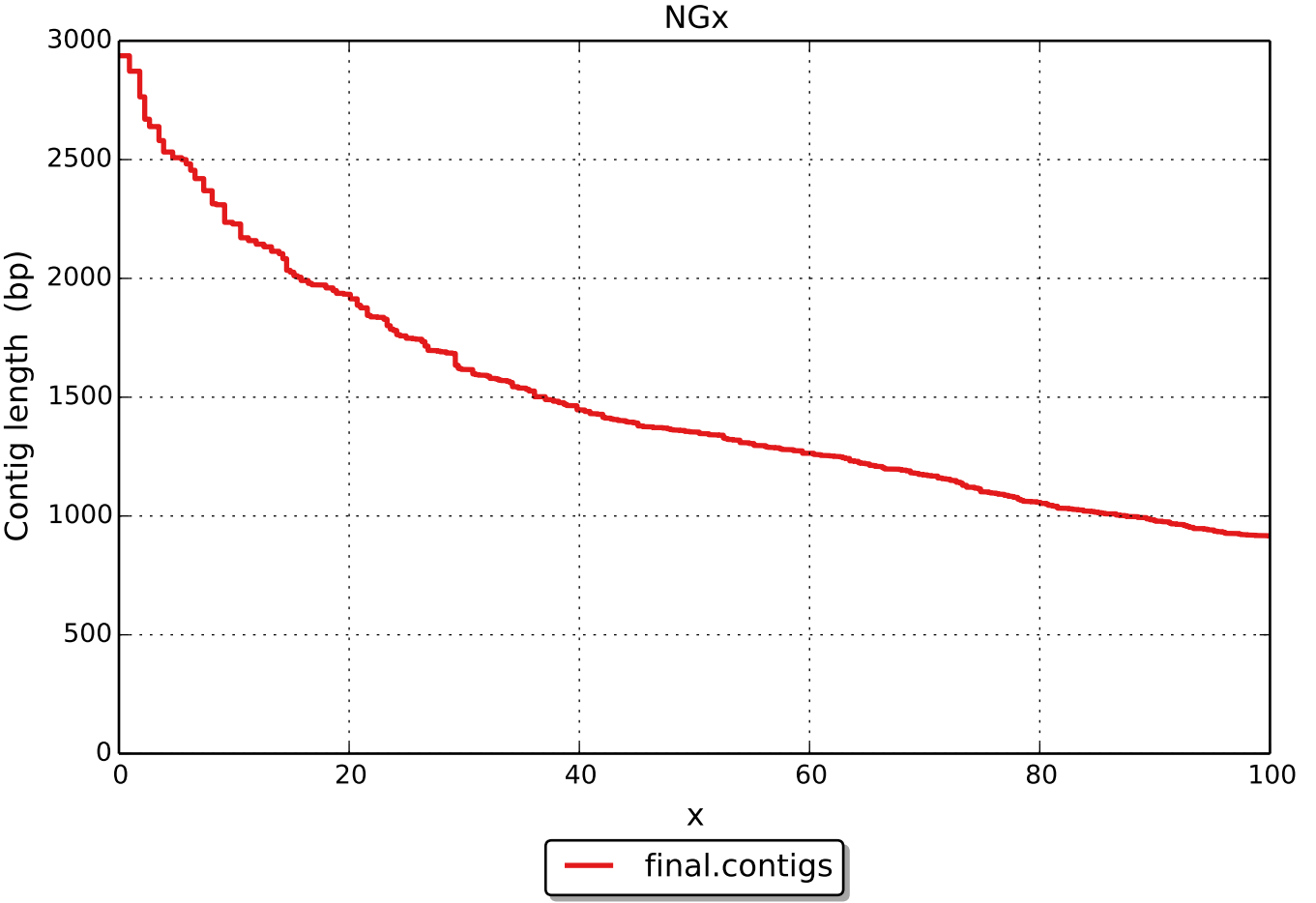
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1235
# N's	0

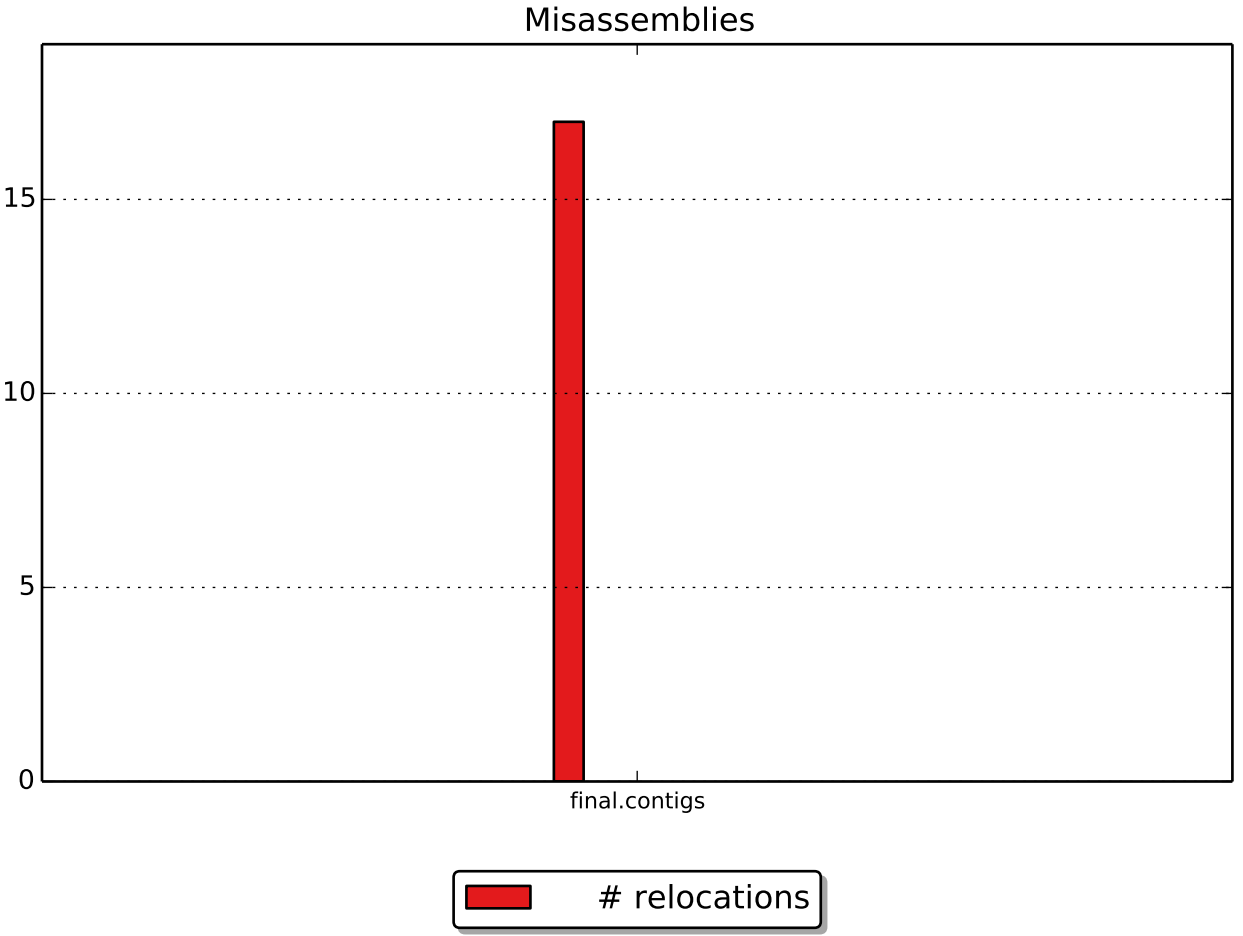
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

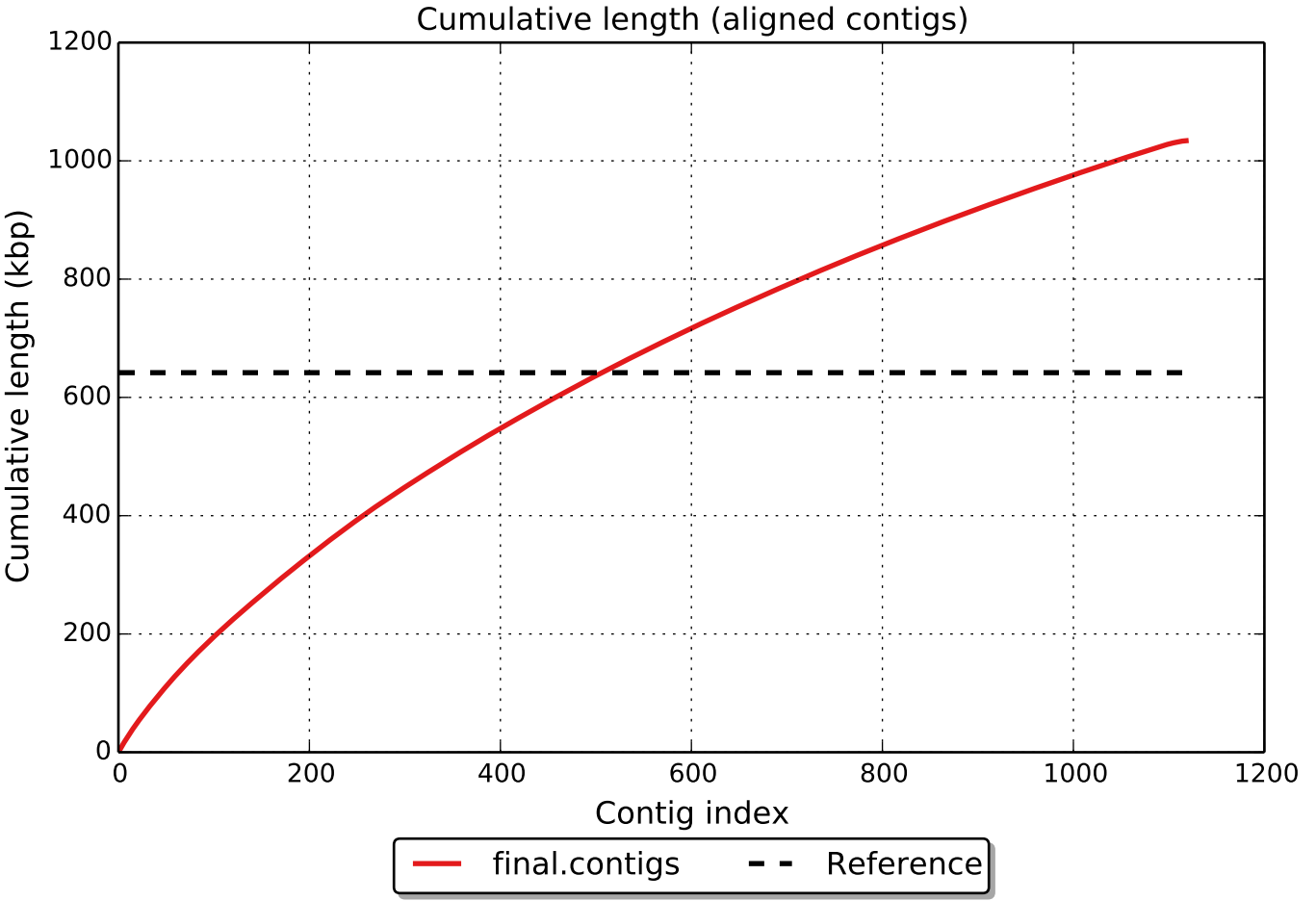

Cumulative length
Cumulative length (kbp)
1200
1000
800
600
400
200
0
0
300
600
900
1200
Contig index
final.contigs
Reference

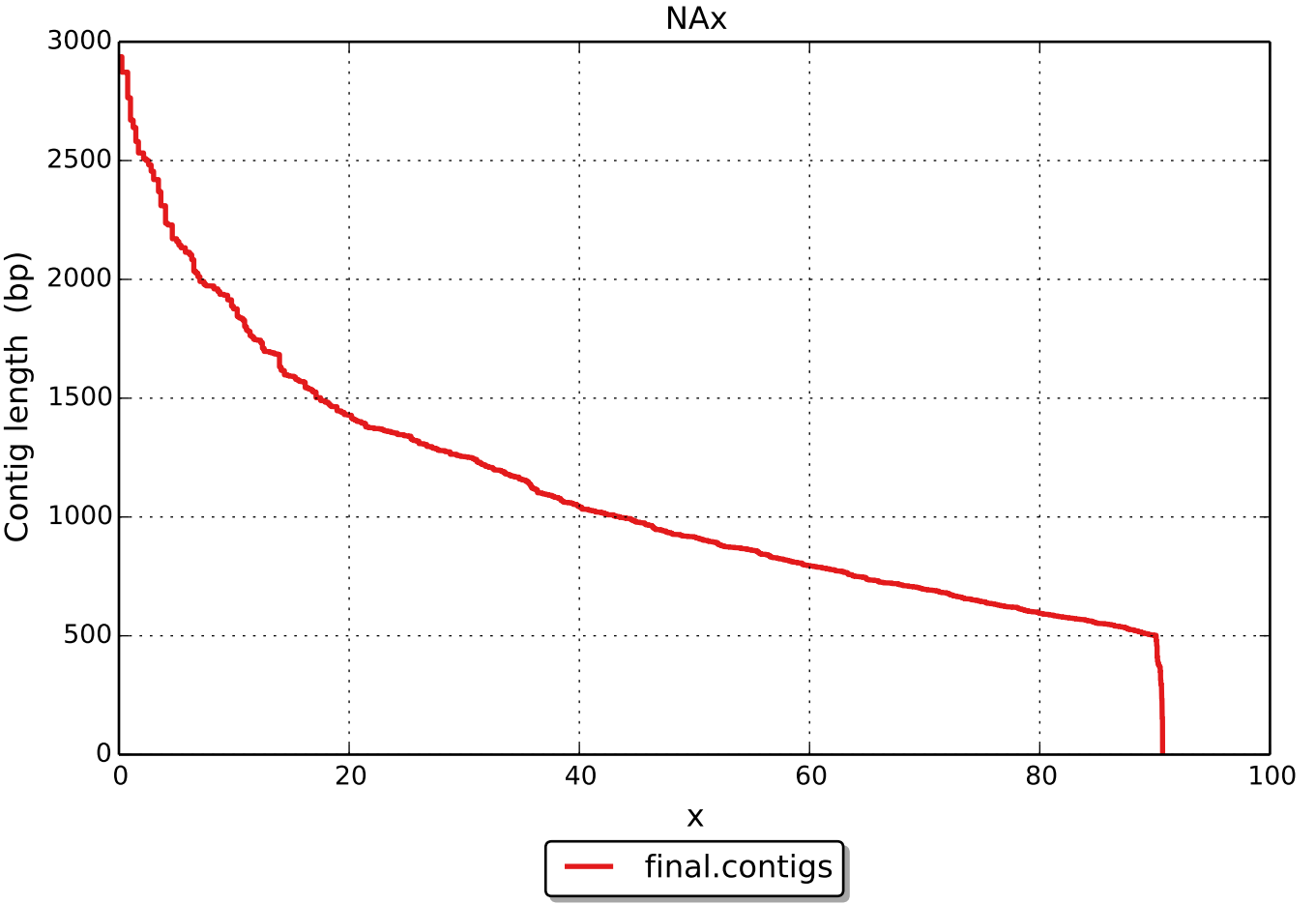

GC content
windows
GC (%)
0
200
400
600
0
20
40
60
80
100
final.contigs
Reference

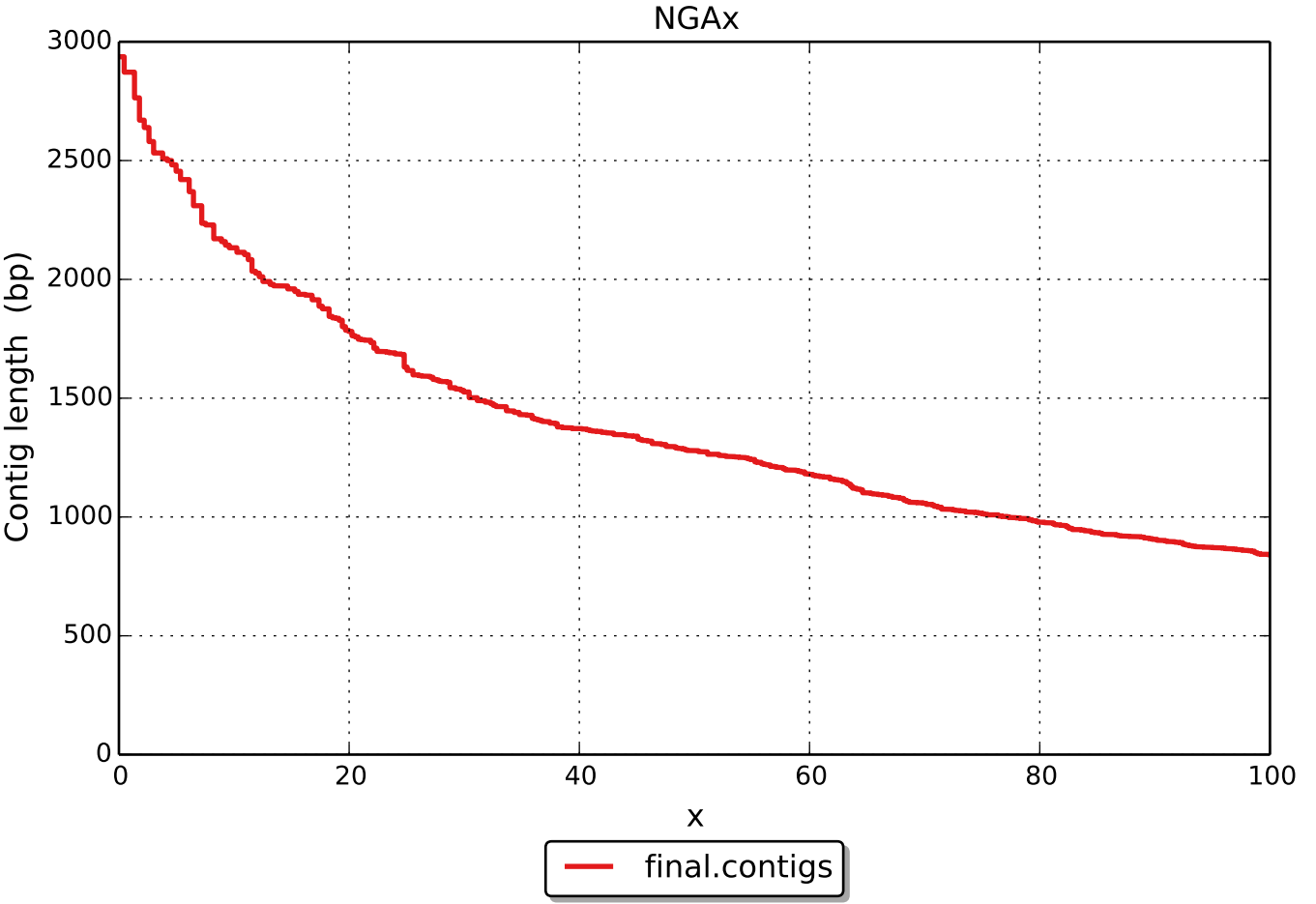

Nx
3000
2500
2000
1500
1000
500
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
15
10
5
0
final.contigs
relocations


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


NAx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs