Report

	final.contigs
# contigs (>= 0 bp)	1101
# contigs (>= 1000 bp)	351
Total length (>= 0 bp)	1035241
Total length (>= 1000 bp)	503853
# contigs	1101
Largest contig	2937
Total length	1035241
Reference length	641799
GC (%)	26.39
Reference GC (%)	26.30
N50	984
NG50	1288
N75	720
NG75	1021
L50	365
LG50	190
L75	674
LG75	329
# 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	1.802
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1323.23
# indels per 100 kbp	0.70
Largest alignment	2937
NA50	976
NGA50	1280
NA75	714
NGA75	1014
LA50	369
LGA50	192
LA75	681
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

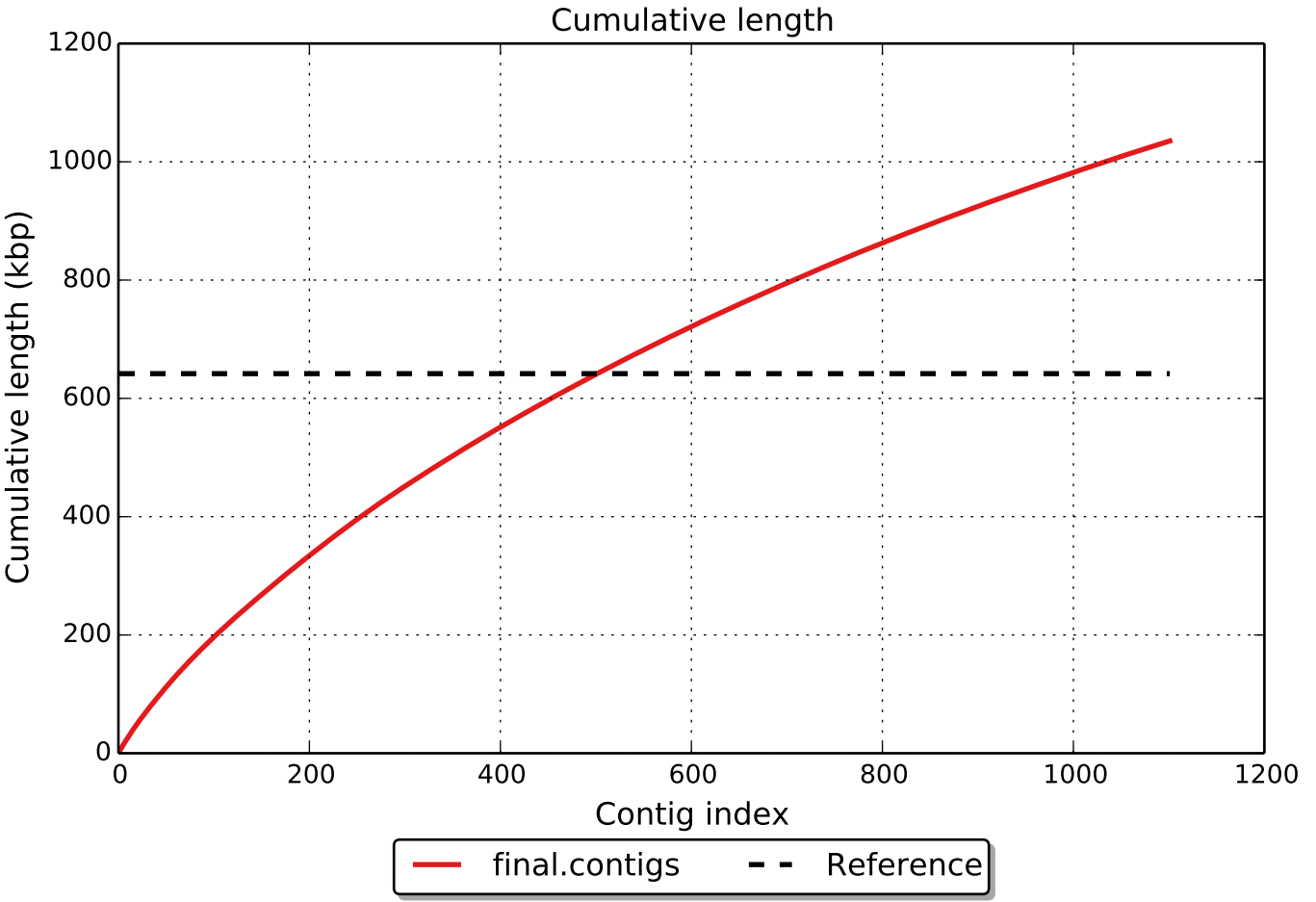
	final.contigs
# misassemblies	17
# relocations	17
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	17
Misassembled contigs length	20480
# local misassemblies	0
# mismatches	7592
# indels	4
# short indels	4
# long indels	0
Indels length	4

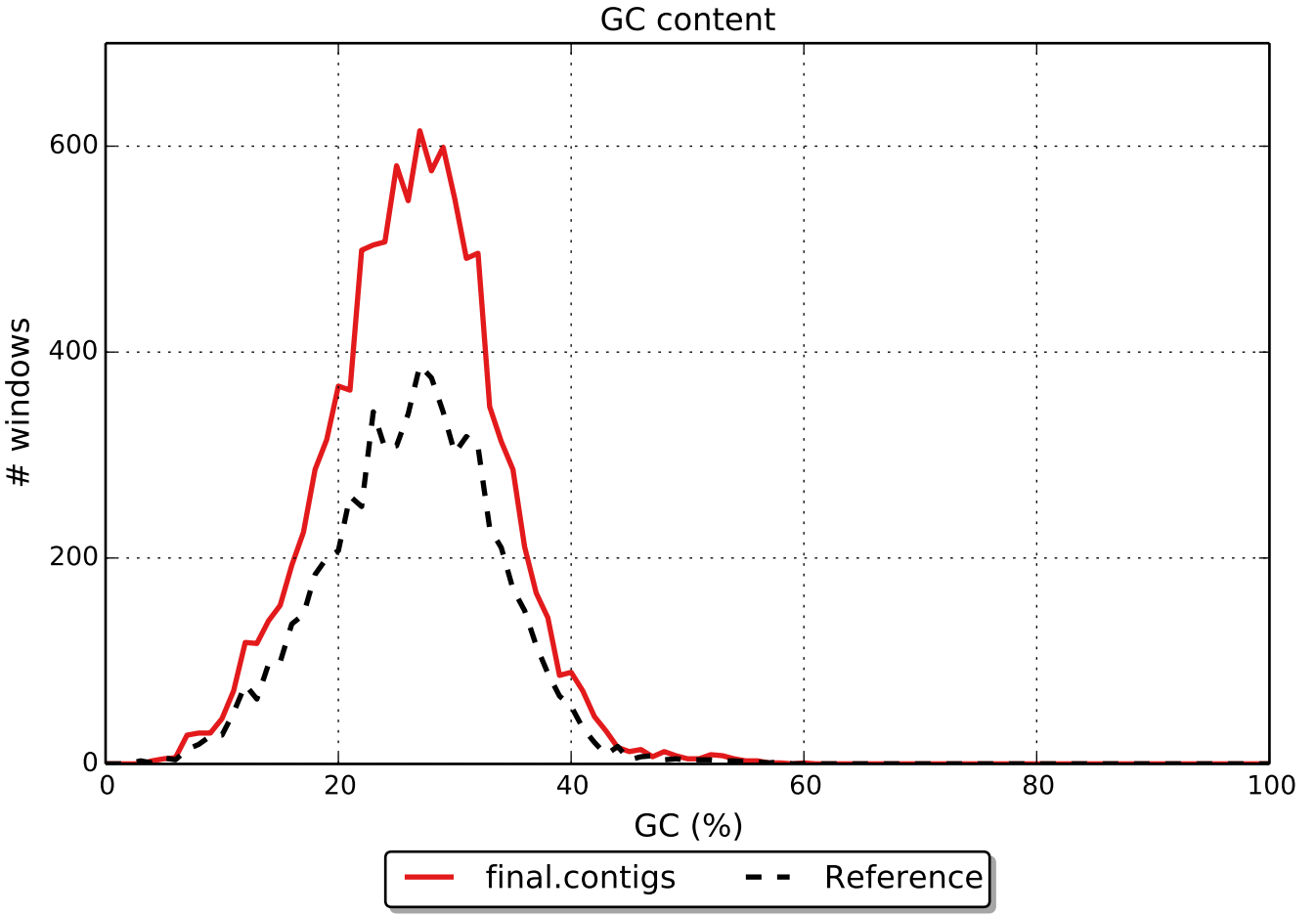
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

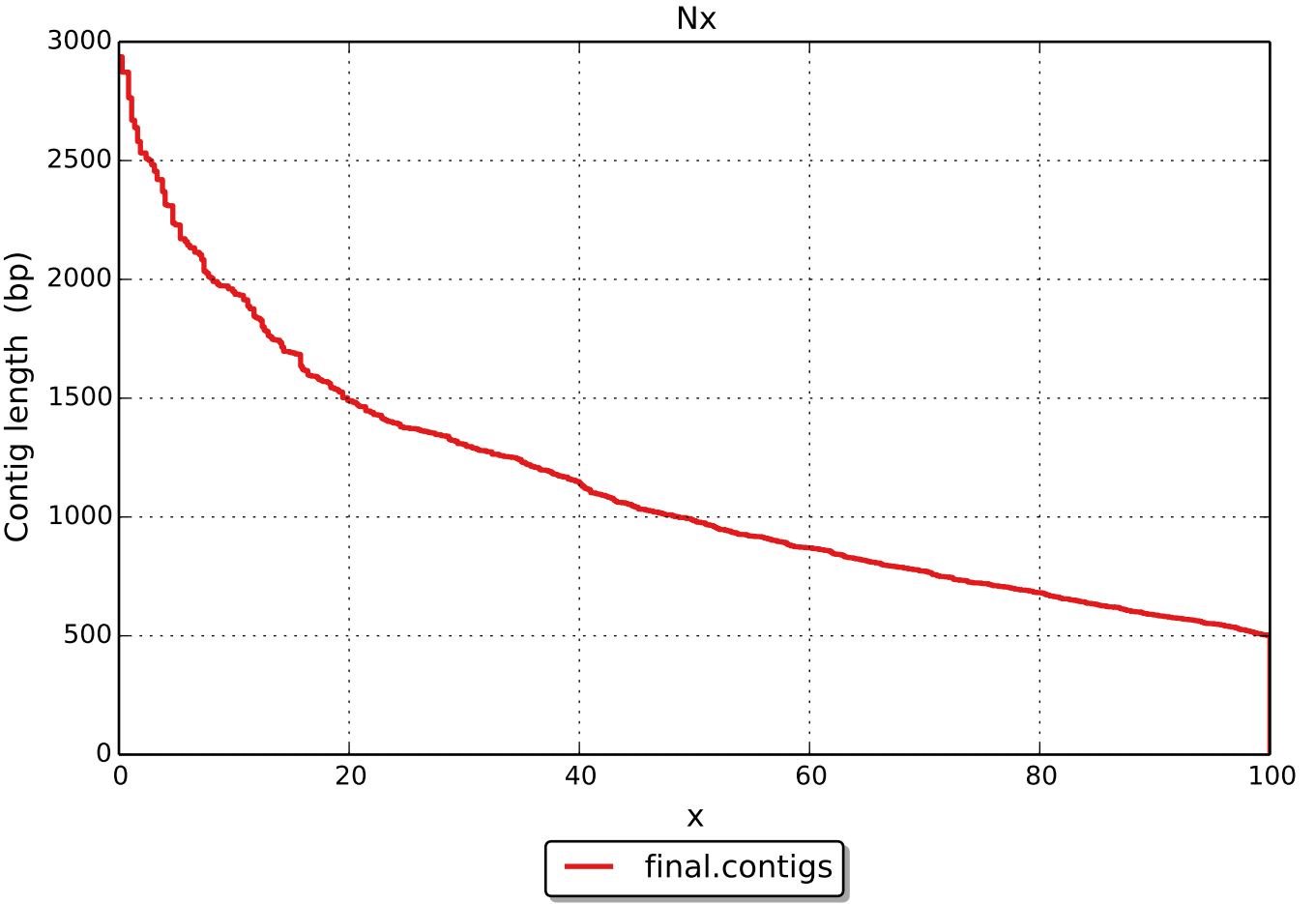
Unaligned report

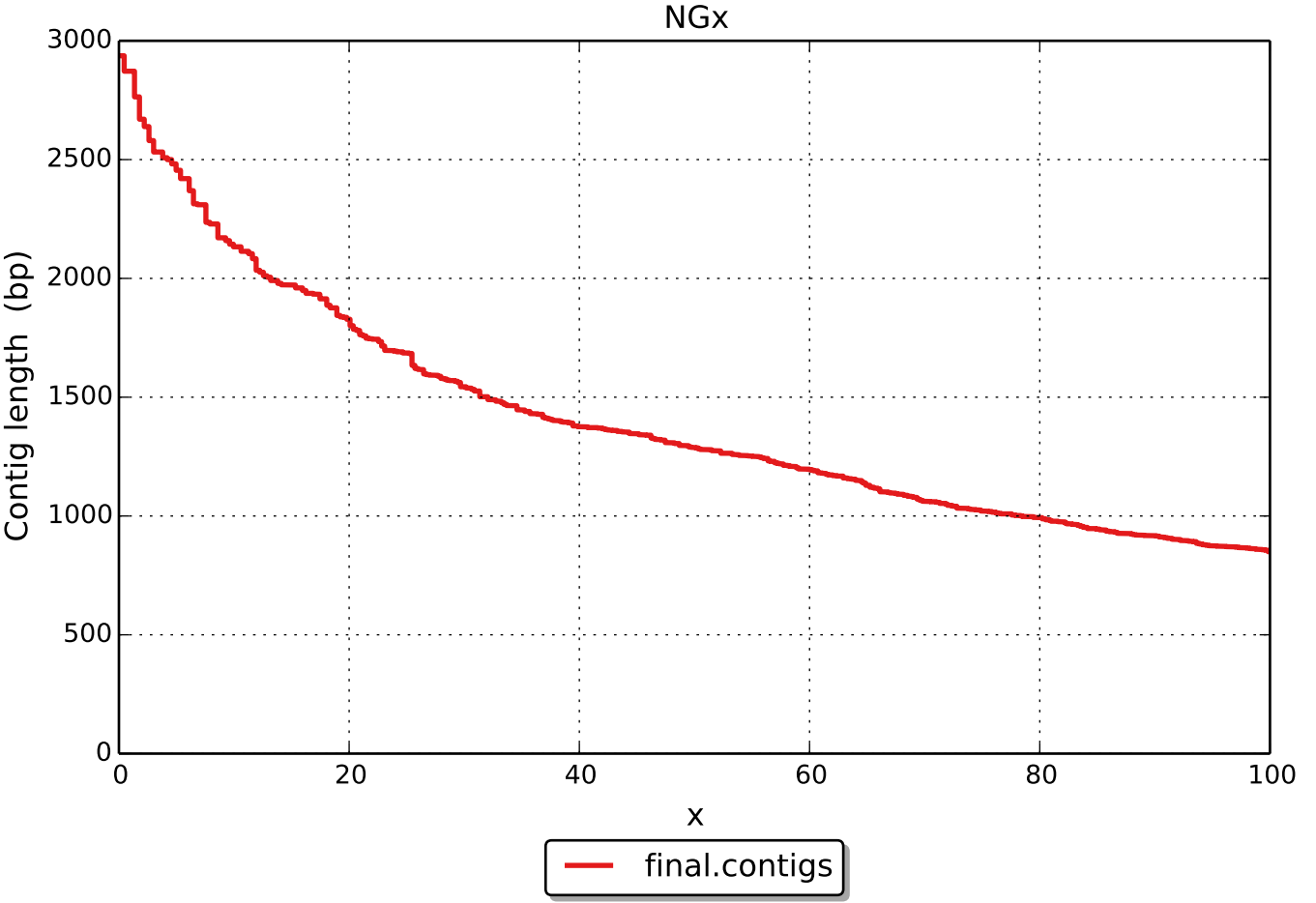
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1235
# N's	0

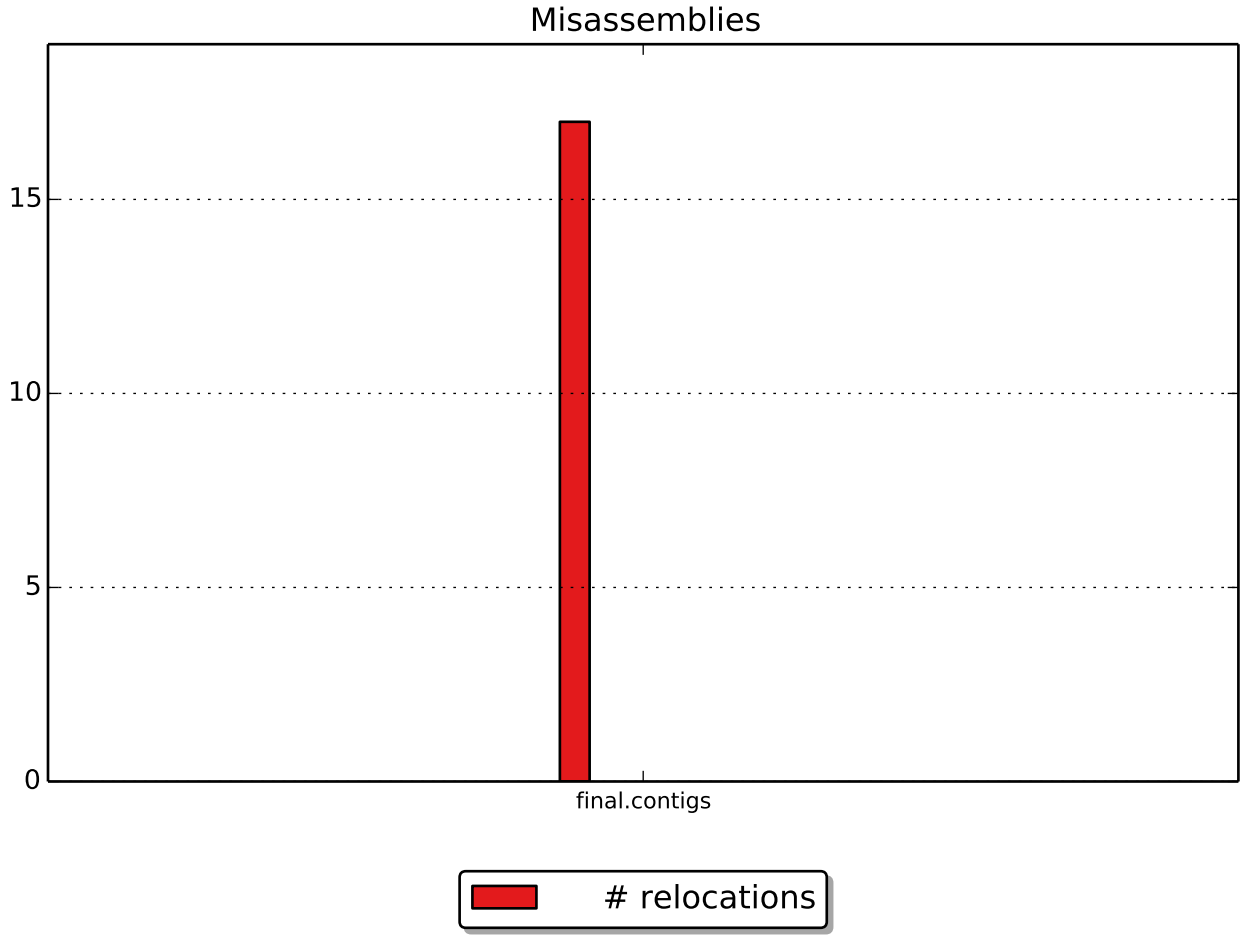
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

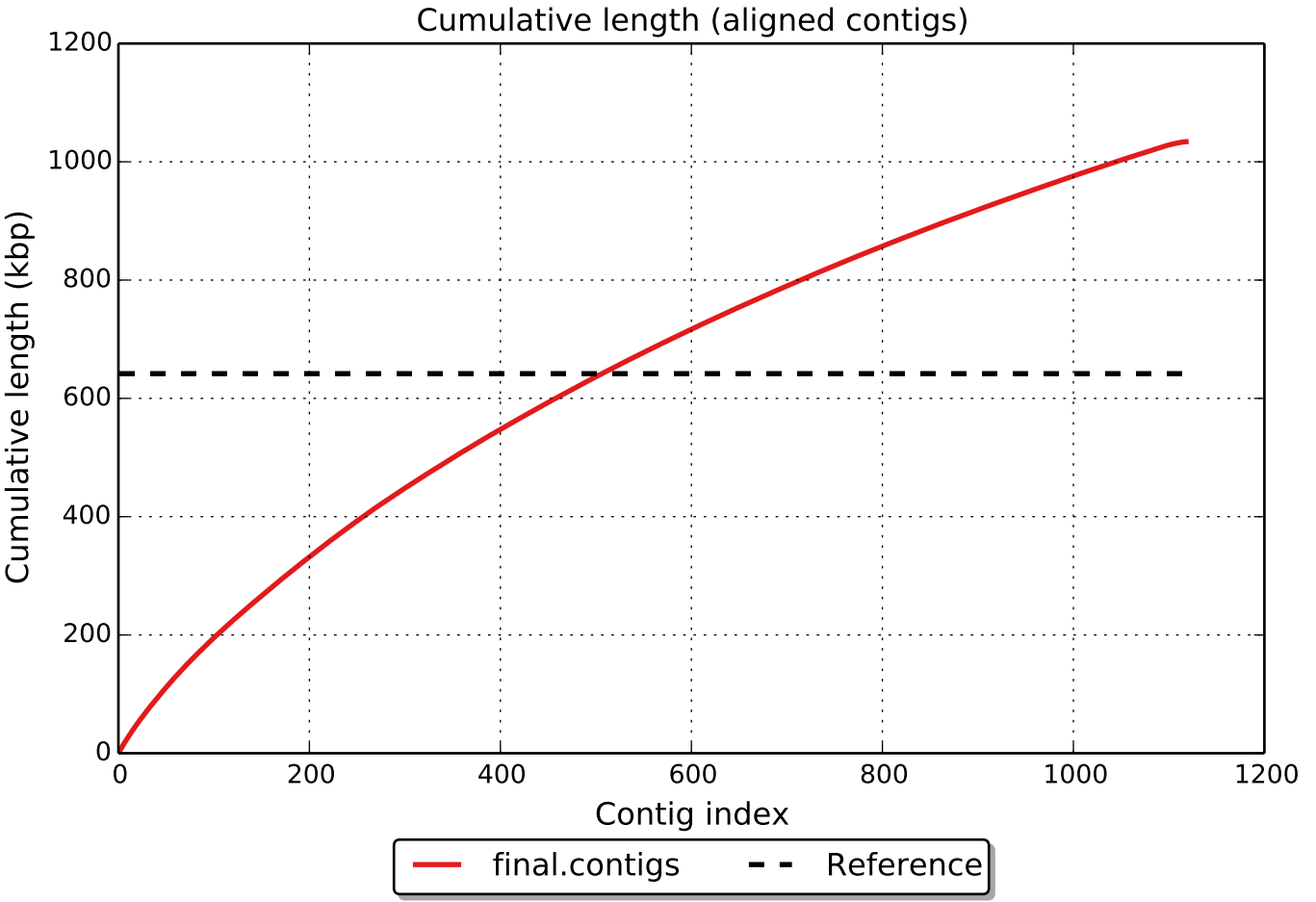

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

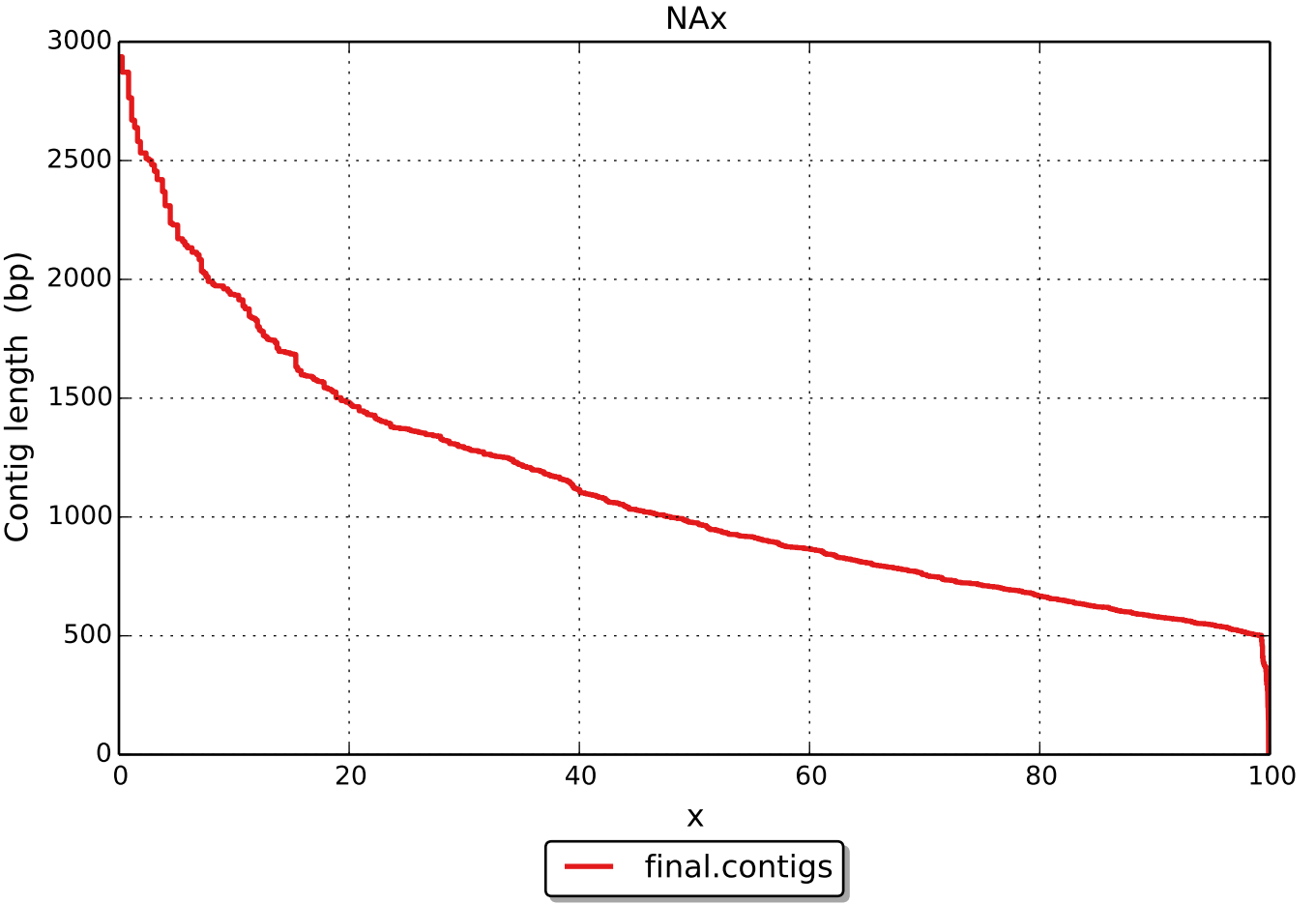

GC content
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

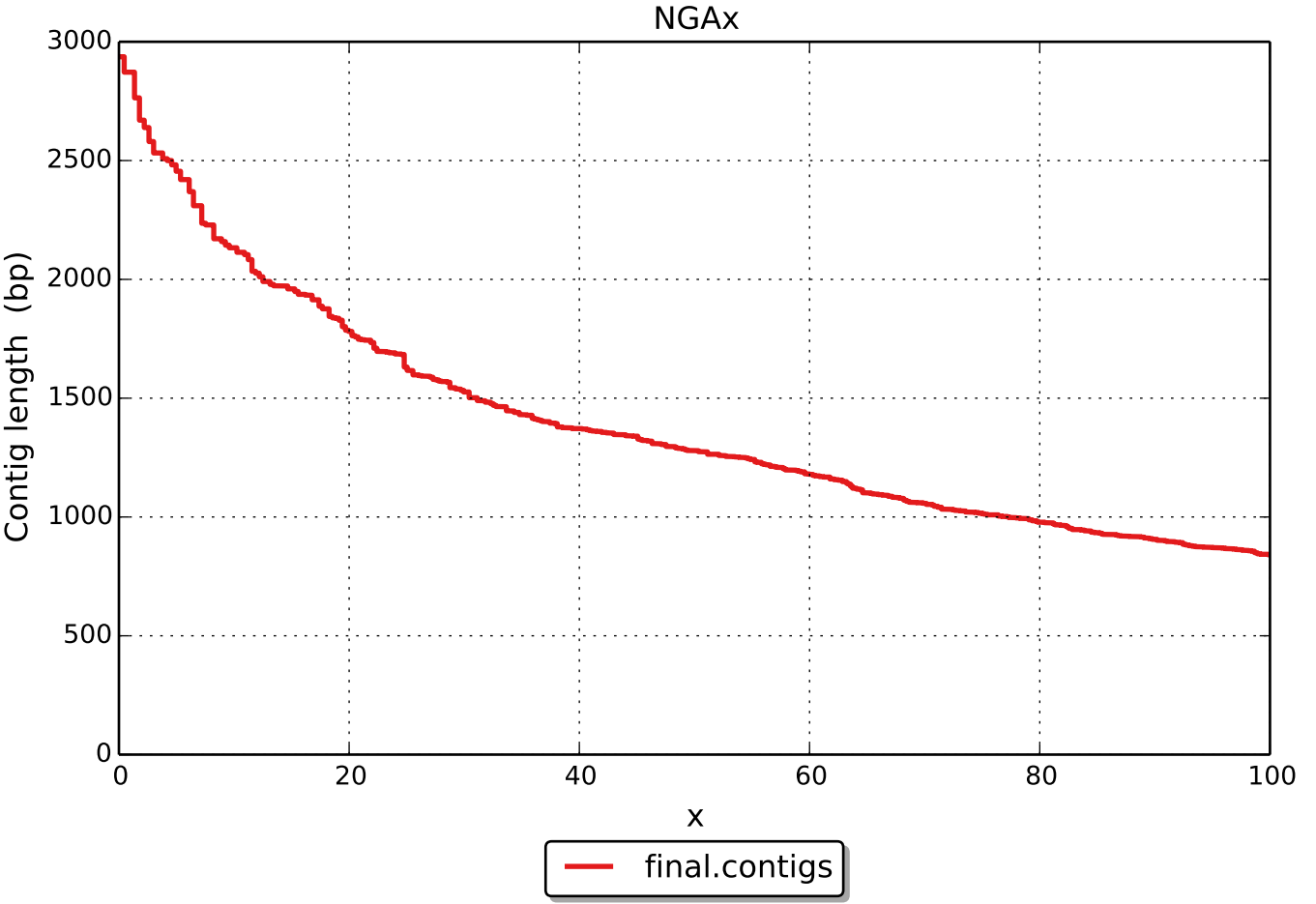

Nx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs


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