Report

	final.contigs
# contigs (>= 0 bp)	1519
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	609335
Total length (>= 1000 bp)	3352
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	197
Largest contig	1195
Total length	115161
Reference length	4641652
GC (%)	51.00
Reference GC (%)	50.79
N50	565
N75	523
L50	88
L75	141
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	195 + 2 part
Unaligned length	113203
Genome fraction (%)	0.042
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	766.09
# indels per 100 kbp	0.00
Largest alignment	1050
NGA50	-

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

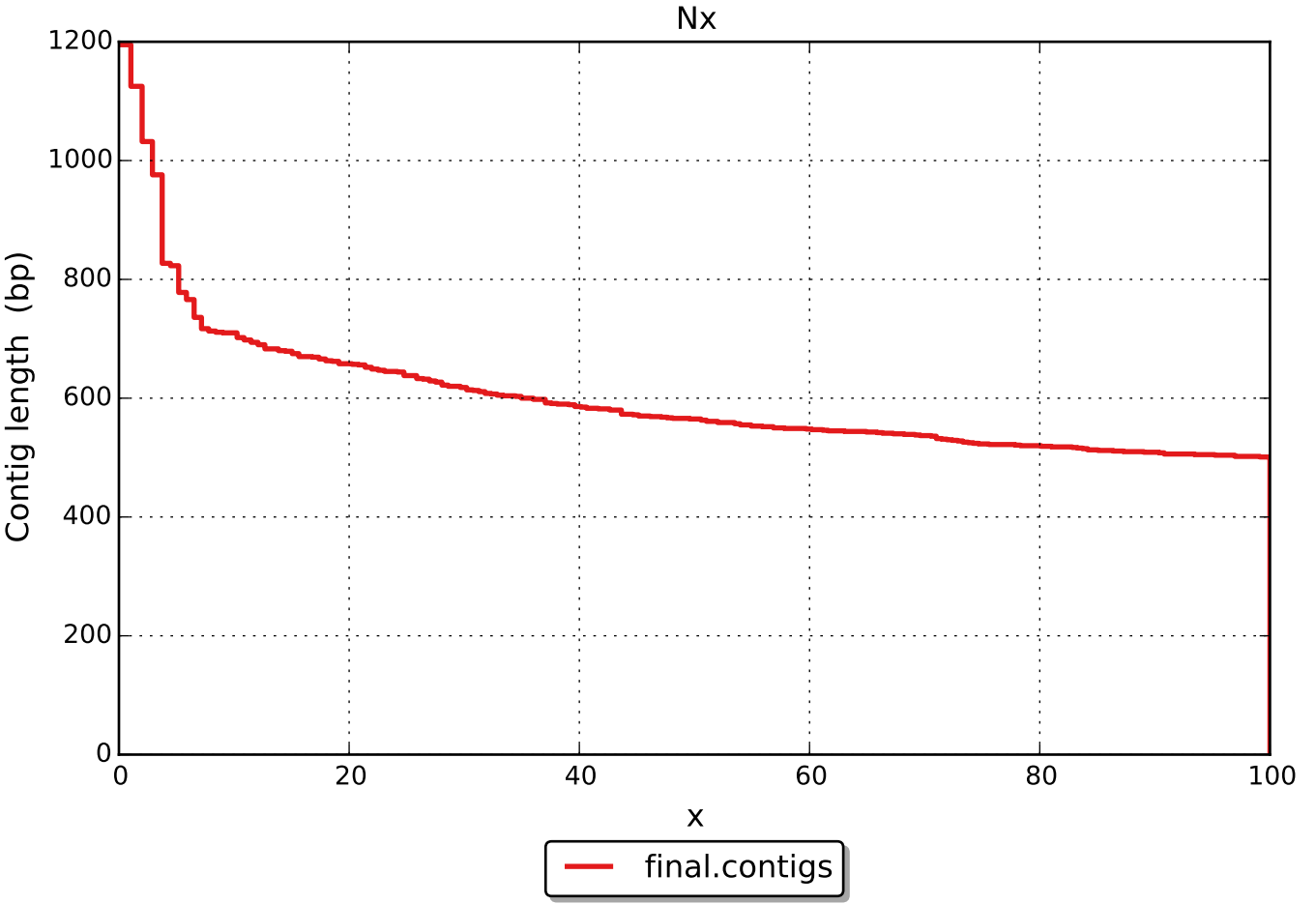
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	15
# indels	0
# short indels	0
# long indels	0
Indels length	0

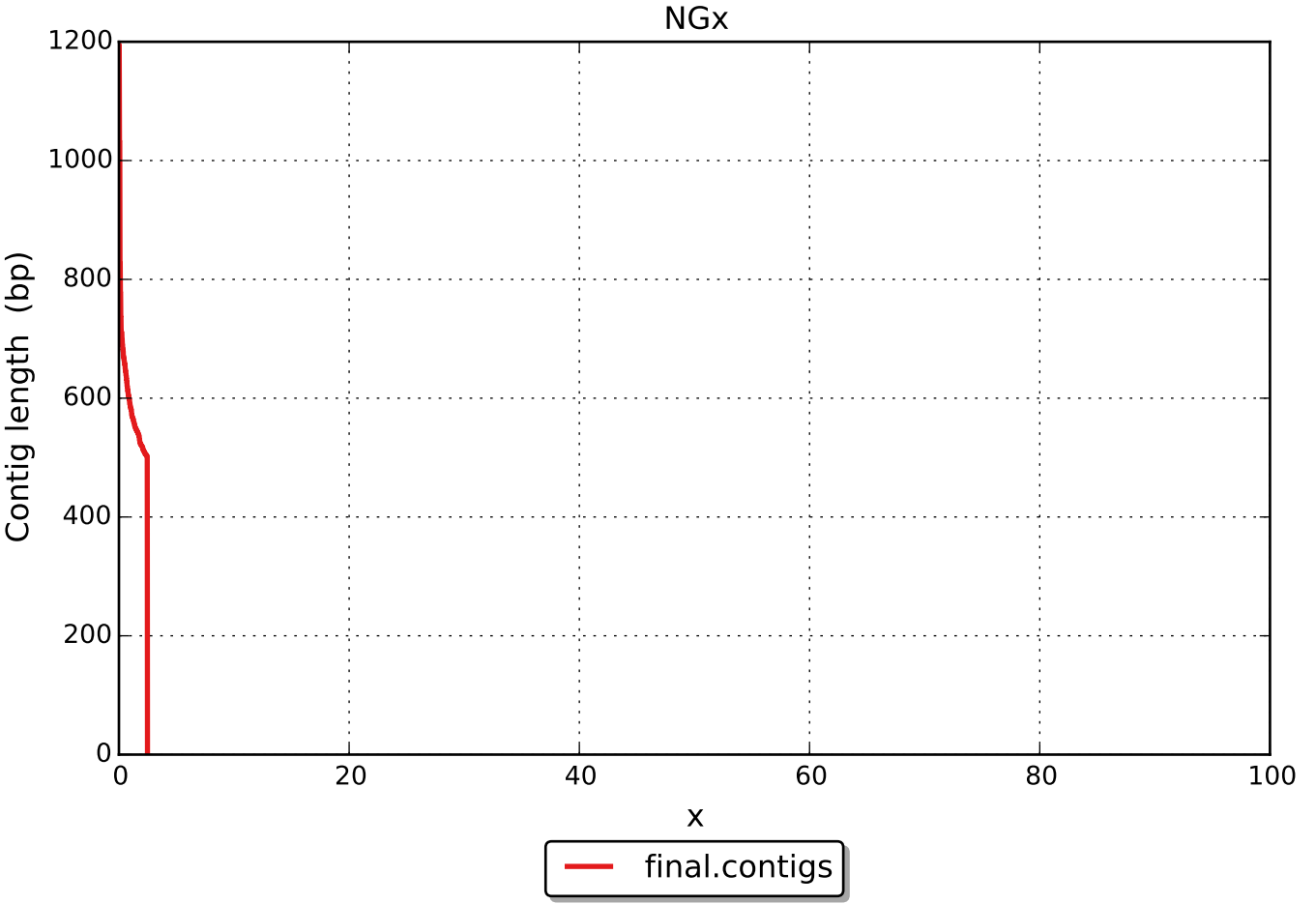
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

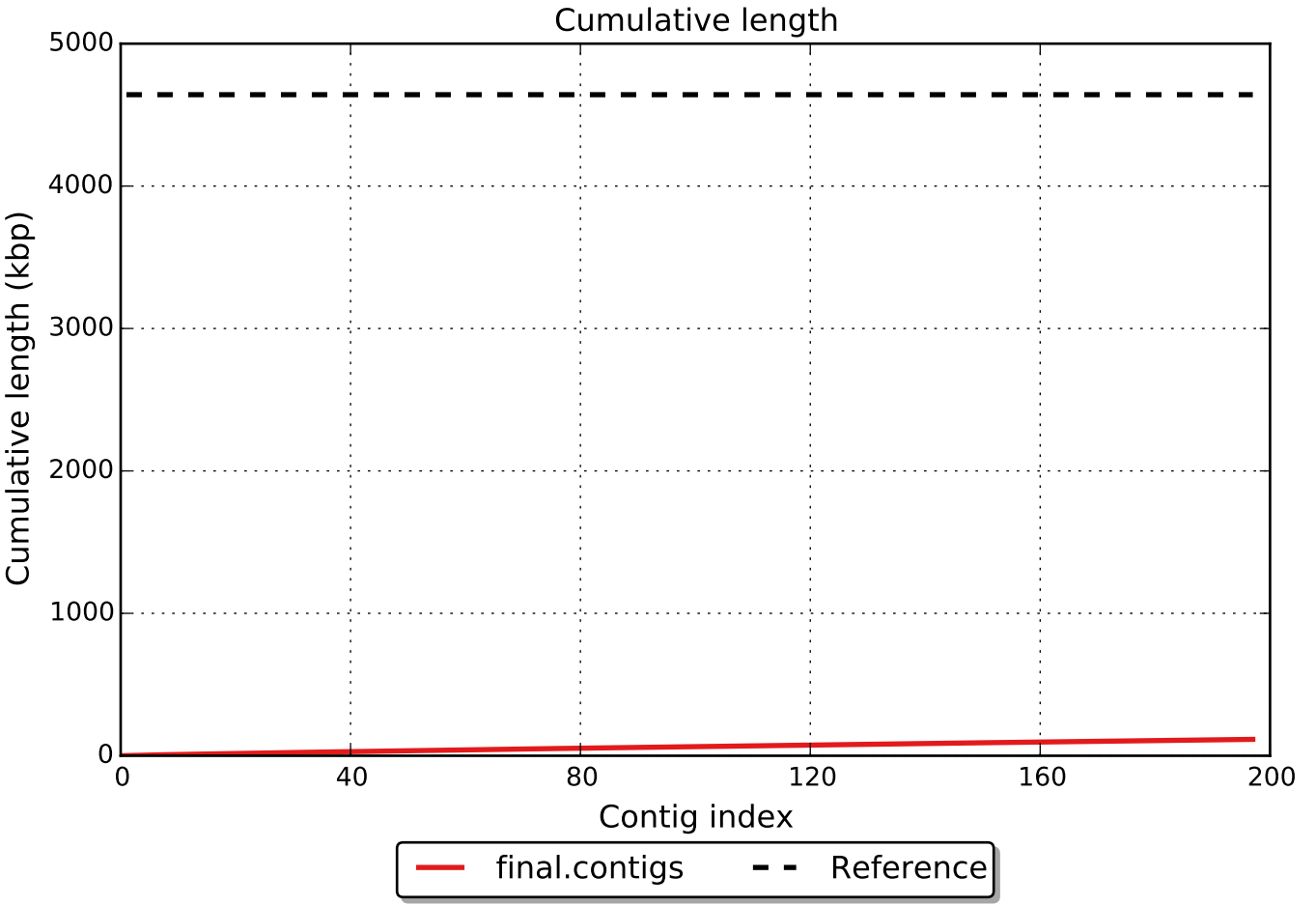
Unaligned report

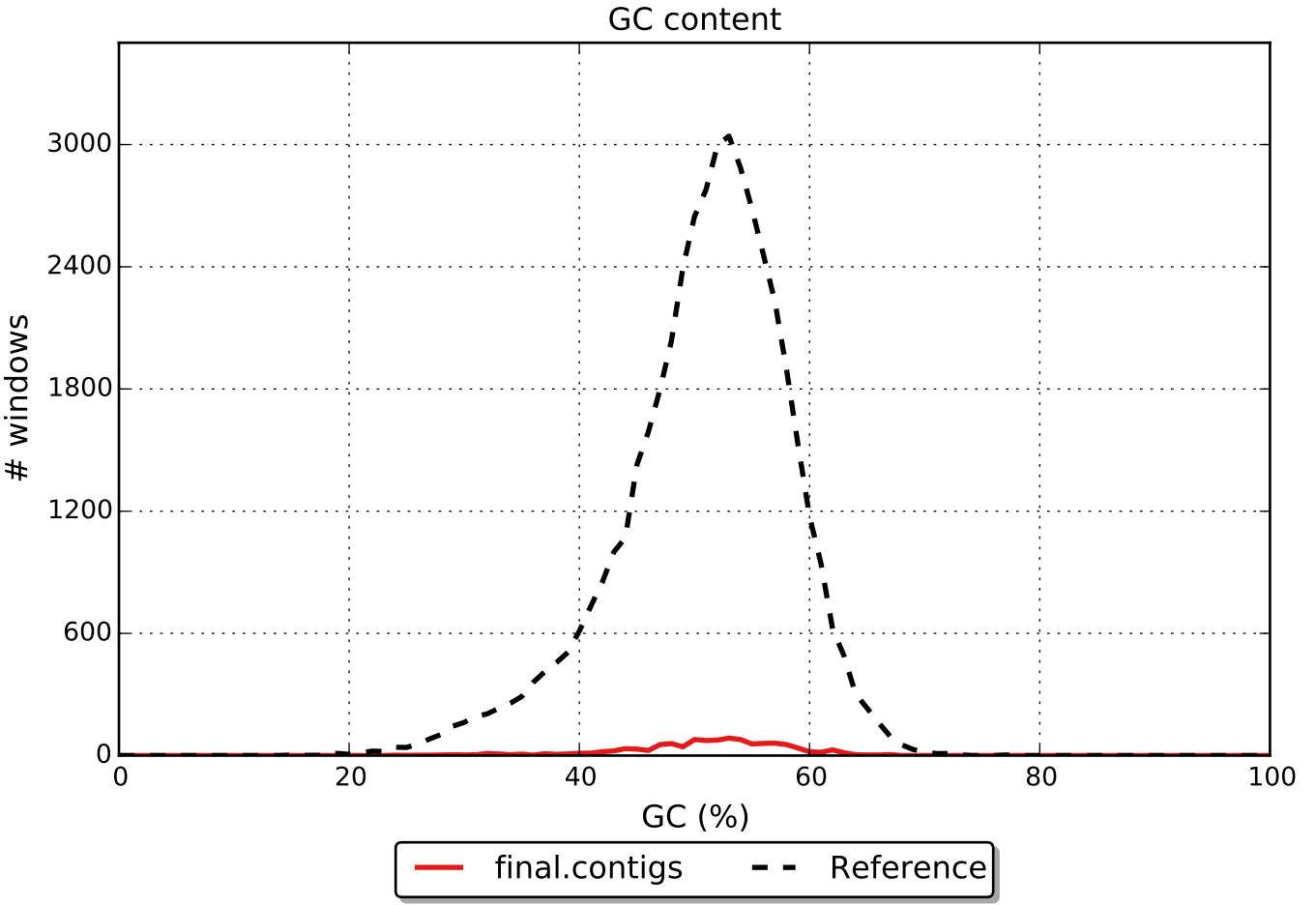
	final.contigs
# fully unaligned contigs	195
Fully unaligned length	113004
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	199
# N's	0

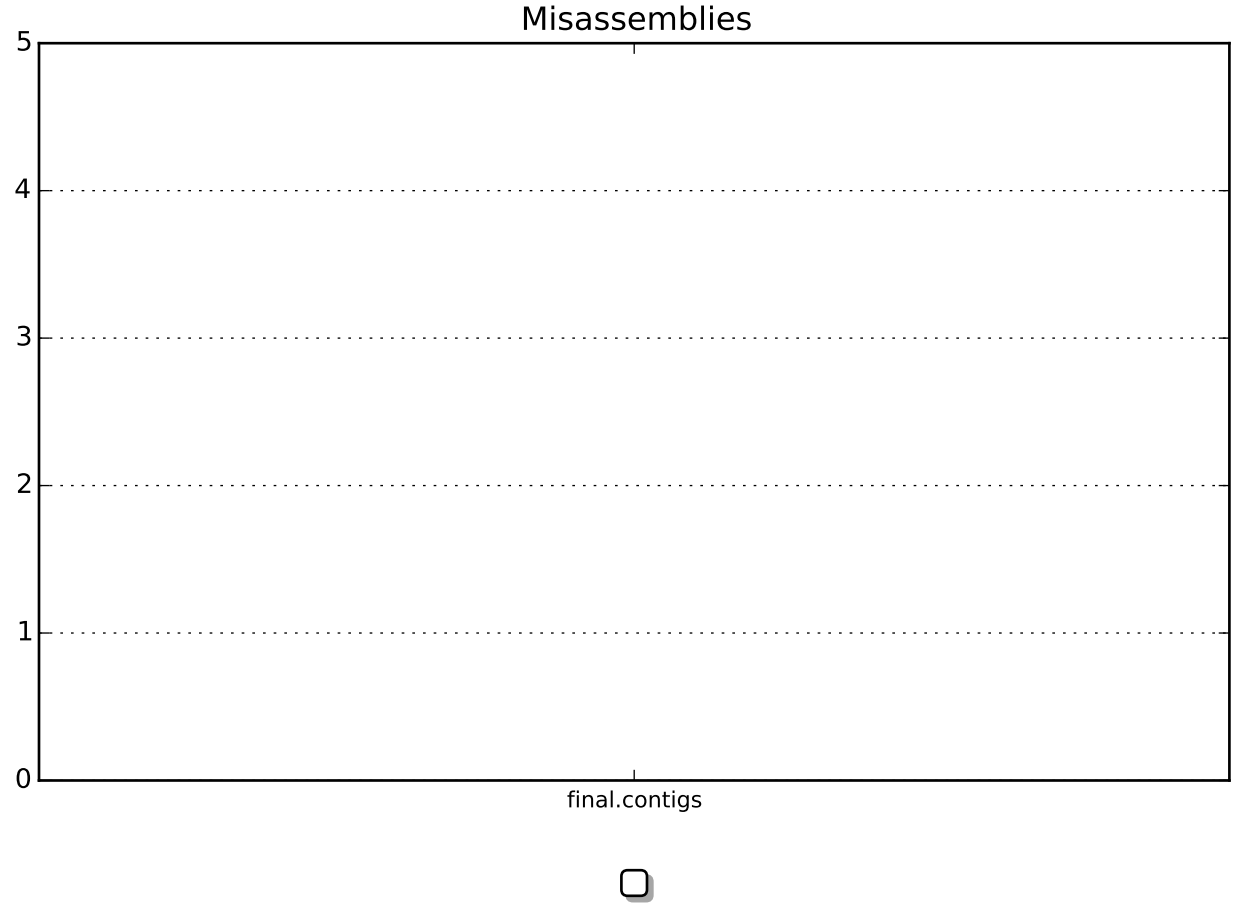
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

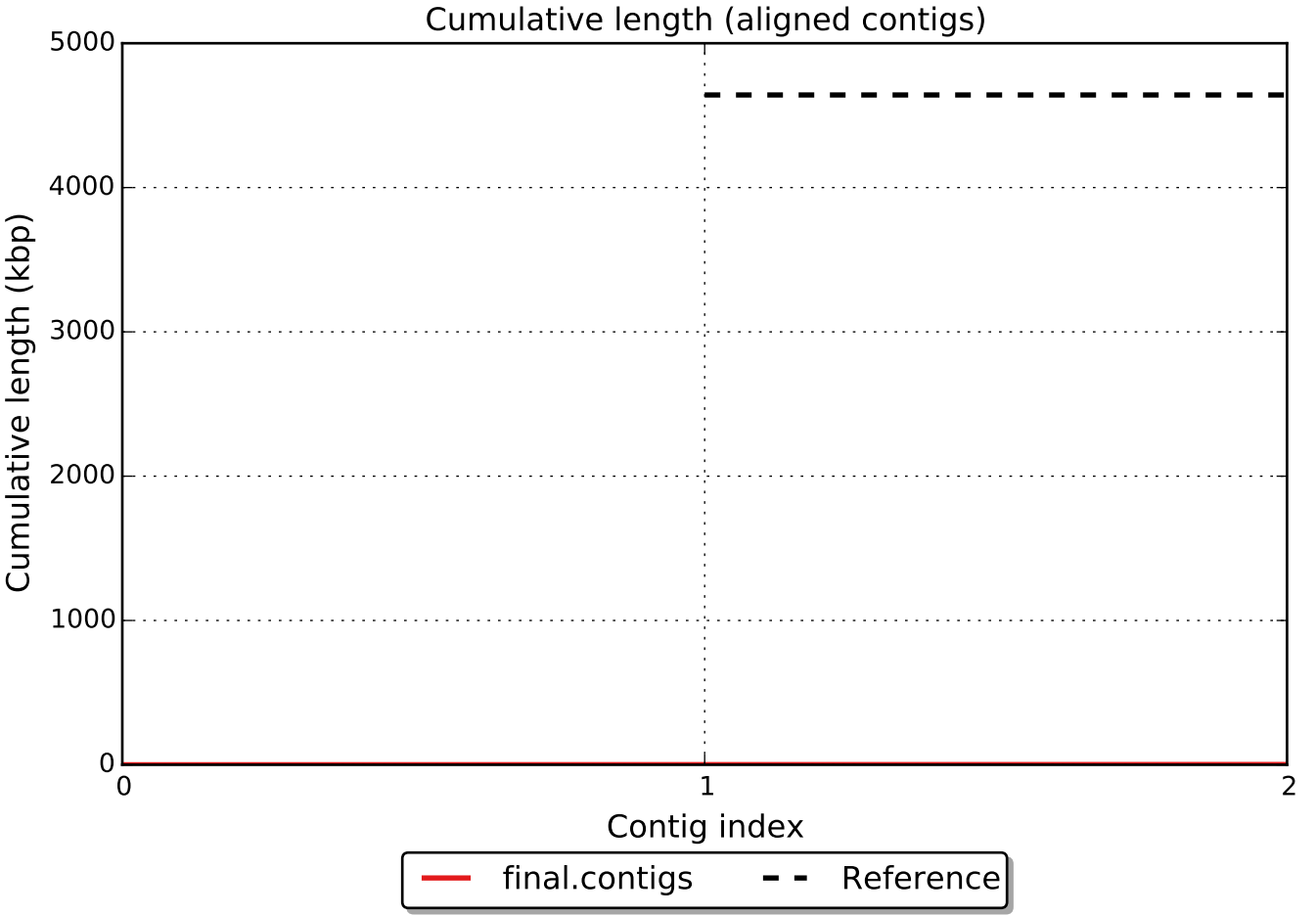

Nx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs

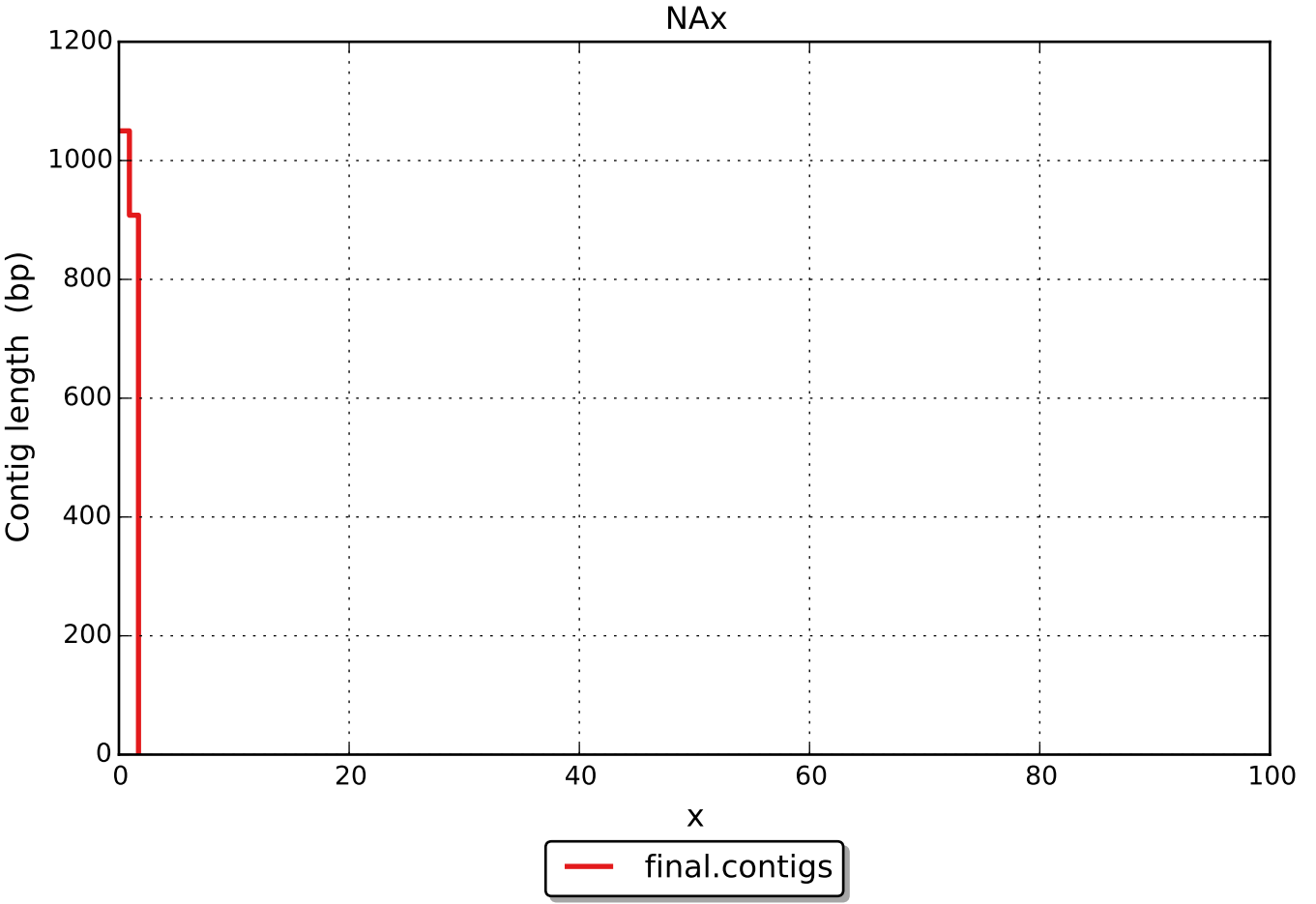

NGx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs

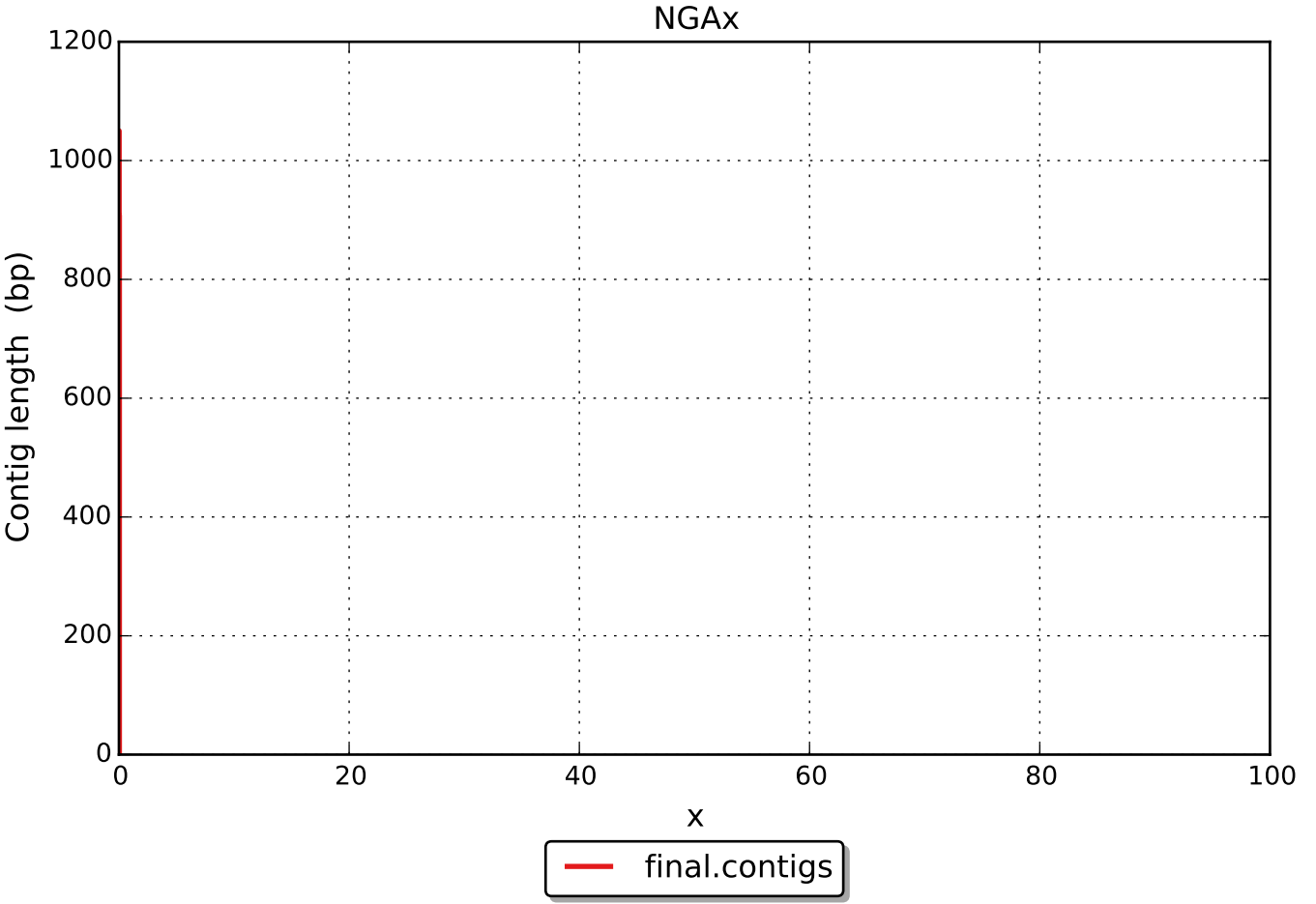

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
40
80
120
160
200
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
1
2
Contig index
final.contigs
Reference


NAx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs