Report

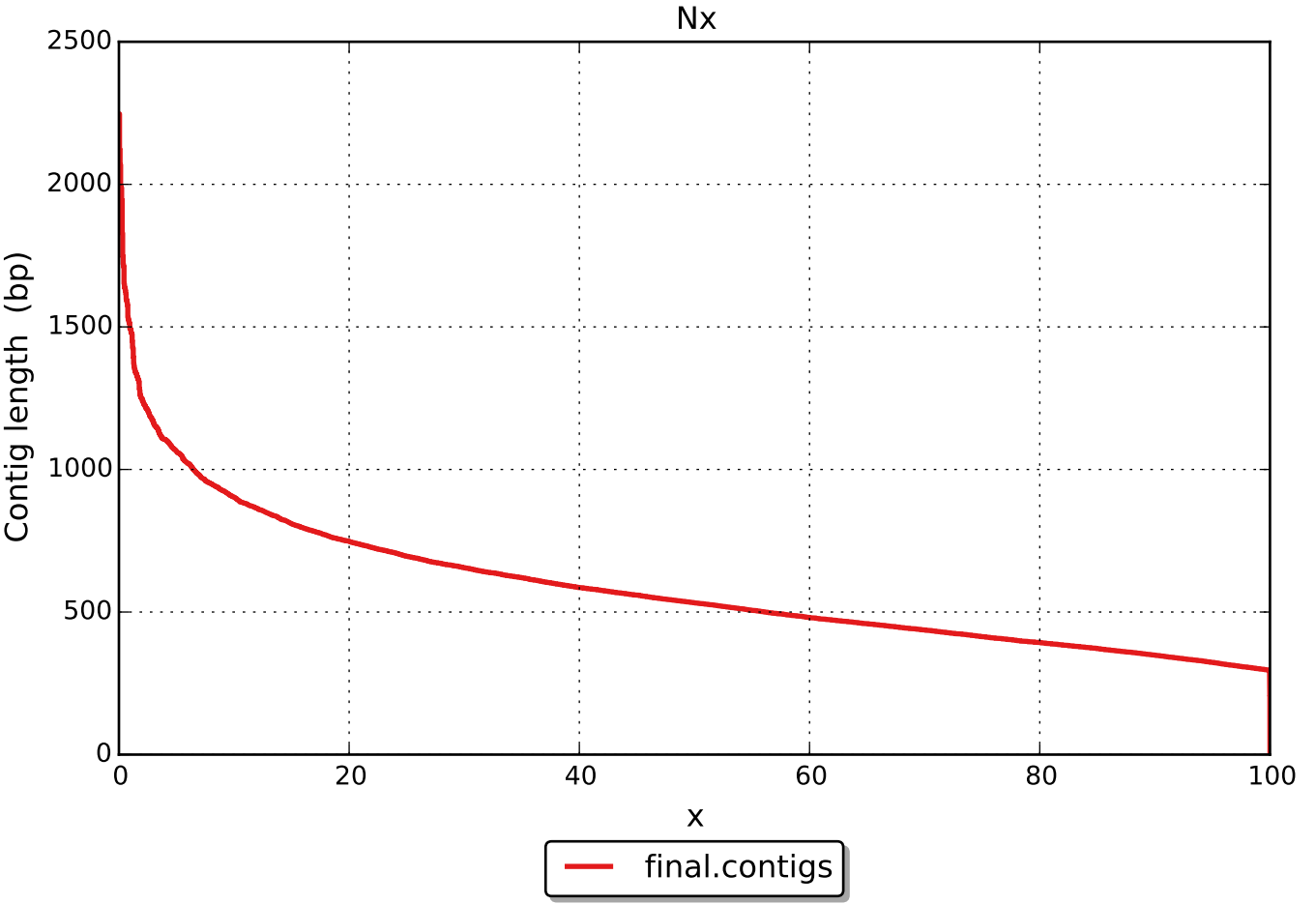
	final.contigs
# contigs (>= 0 bp)	8502
# contigs (>= 1000 bp)	237
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4390792
Total length (>= 1000 bp)	284621
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8502
Largest contig	2247
Total length	4390792
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	532
NG50	518
N75	414
NG75	395
L50	3066
LG50	3305
L75	5408
LG75	5873
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	8385 + 8 part
Unaligned length	4329500
Genome fraction (%)	1.320
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	692.15
# indels per 100 kbp	3.26
Largest alignment	1711
NGA50	-

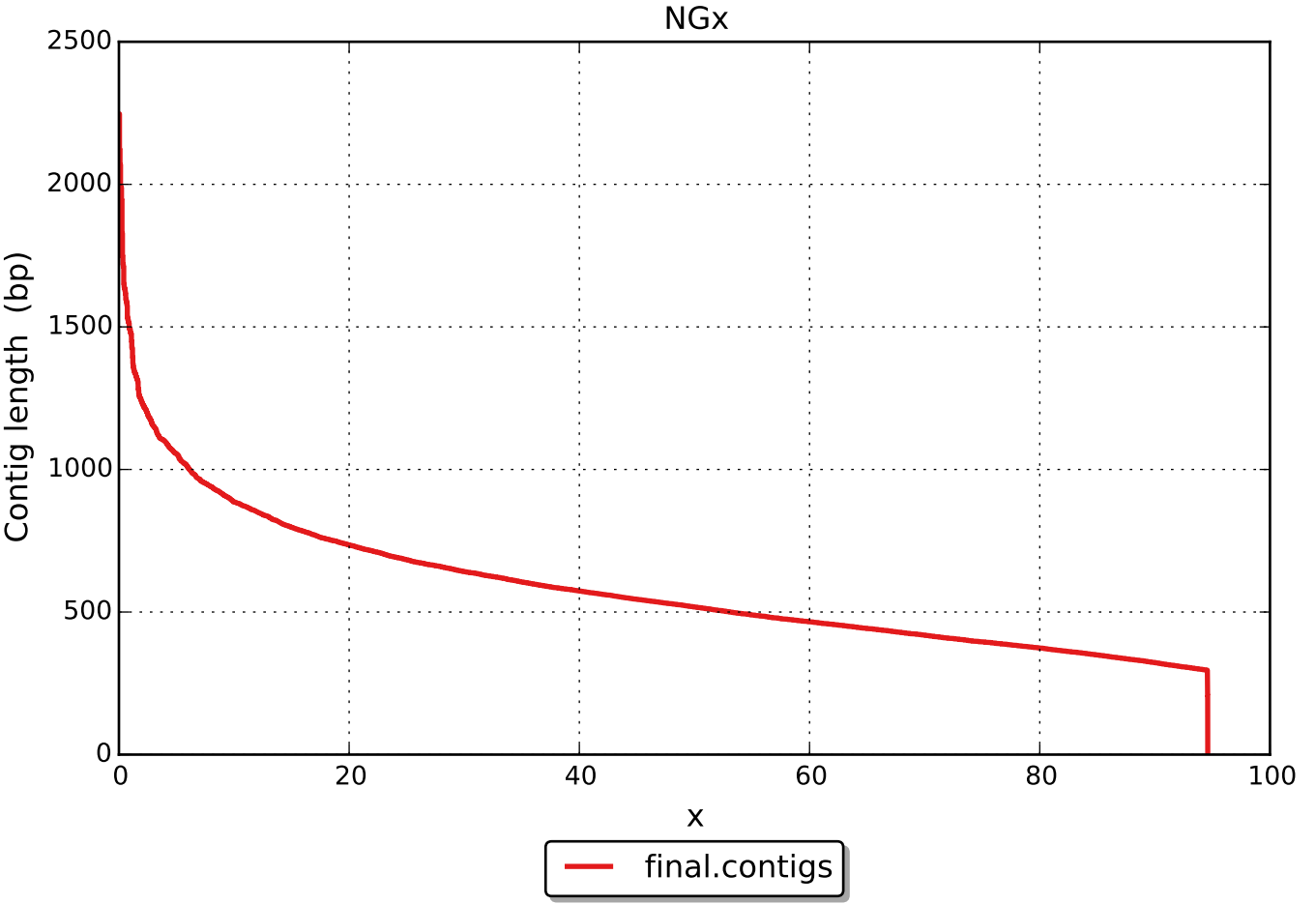
Misassemblies report

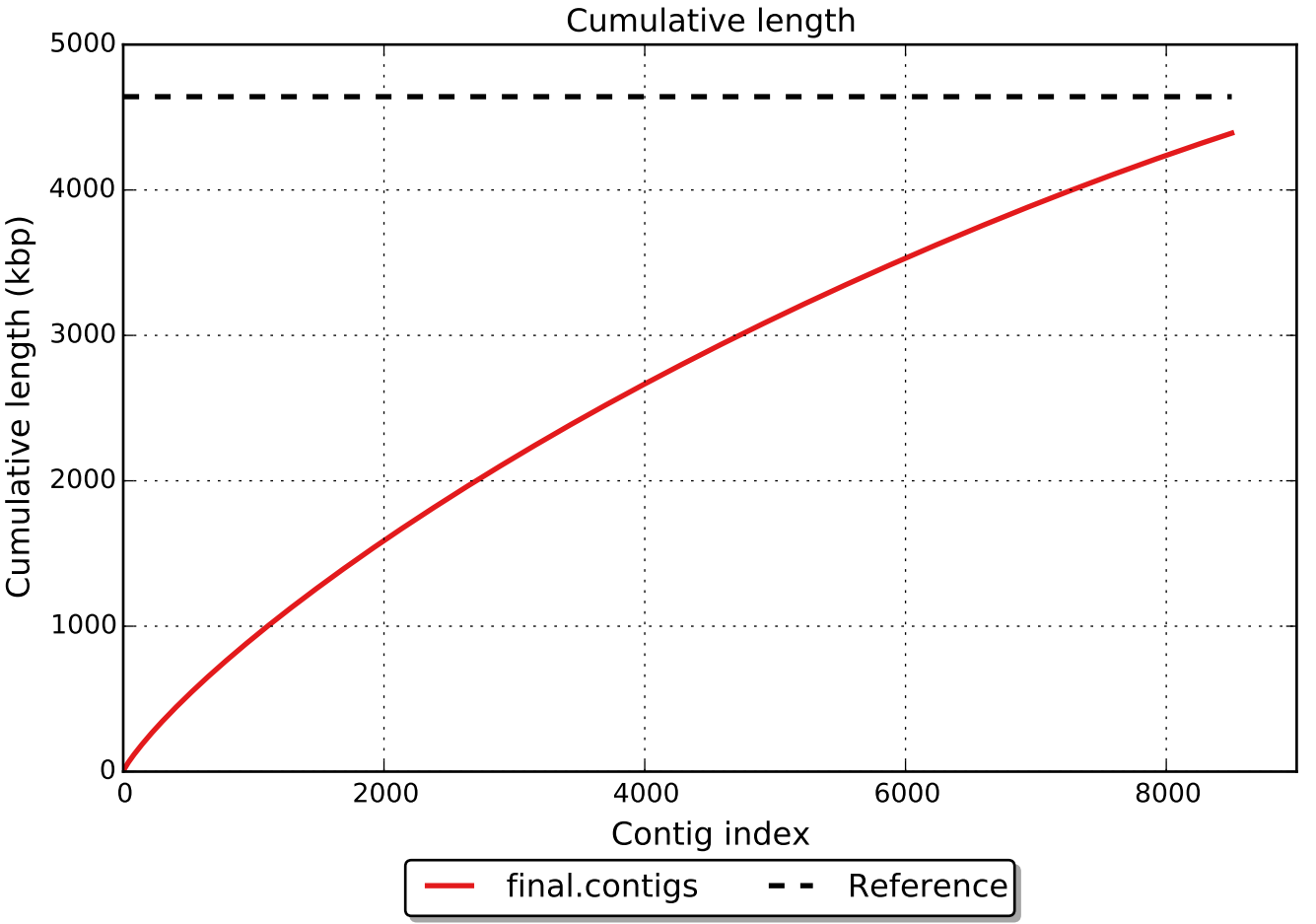
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	424
# indels	2
# short indels	2
# long indels	0
Indels length	2

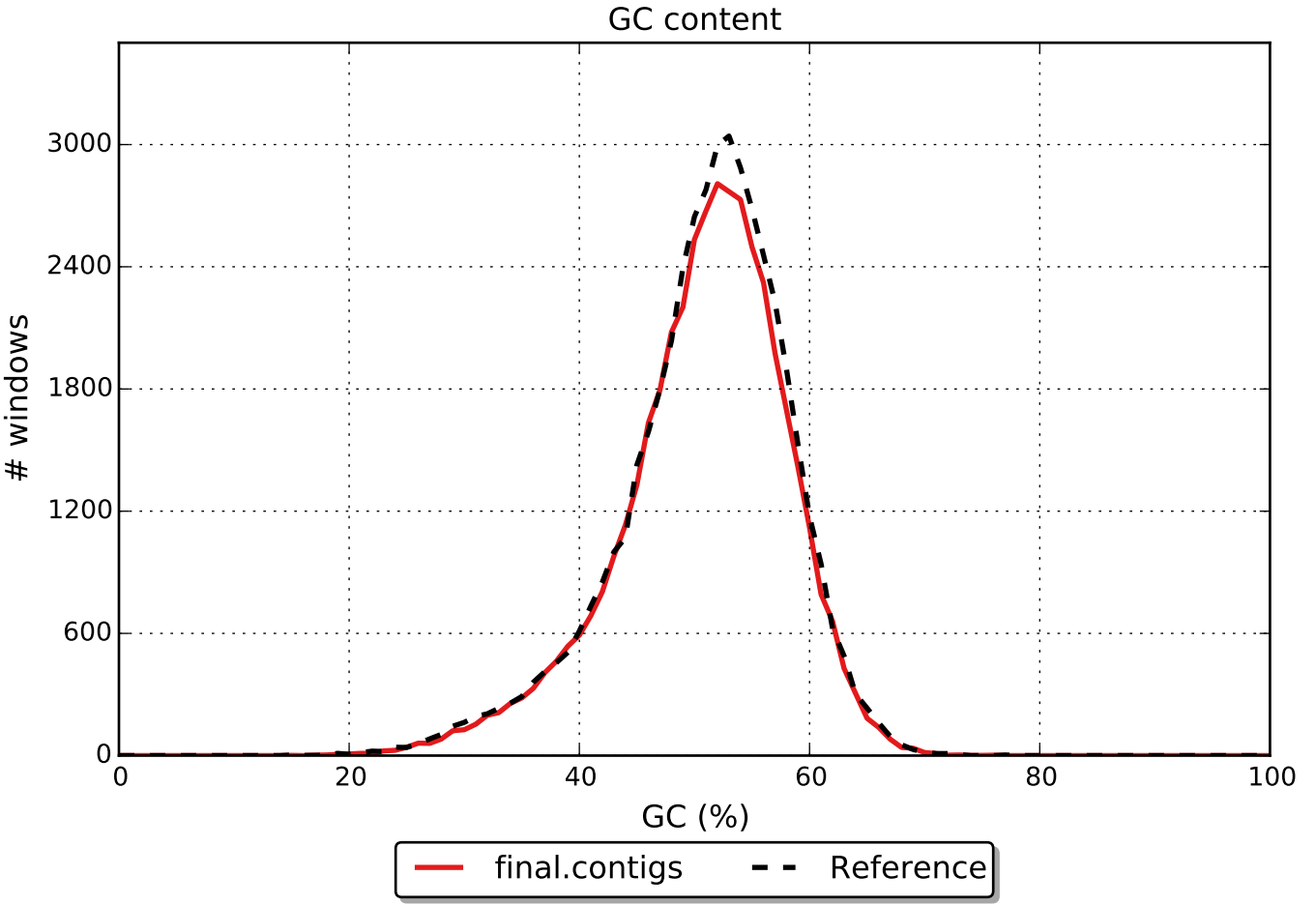
Unaligned report

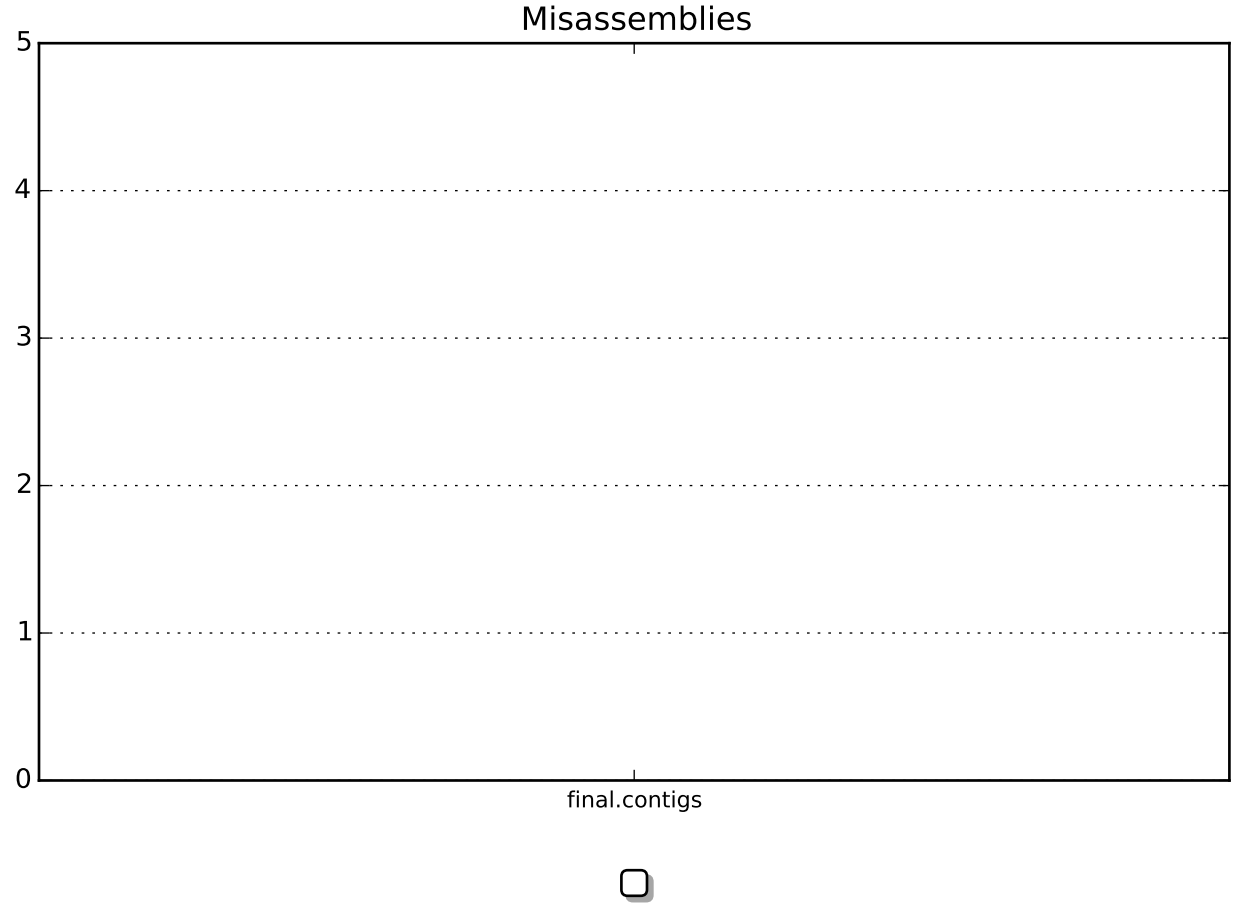
	final.contigs
# fully unaligned contigs	8385
Fully unaligned length	4327037
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	8
Partially unaligned length	2463
# N's	0

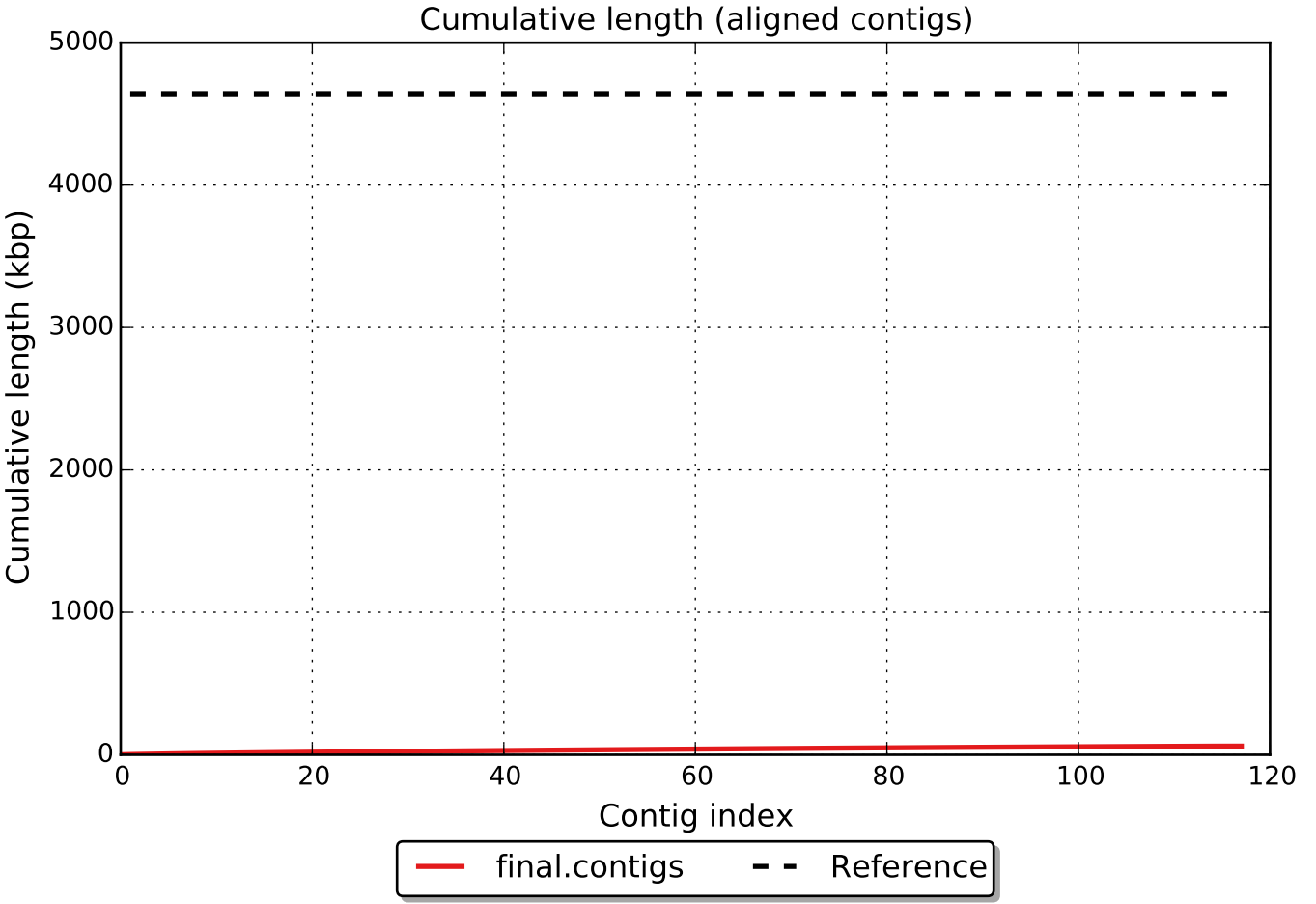

Nx
2500
2000
1500
1000
500
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

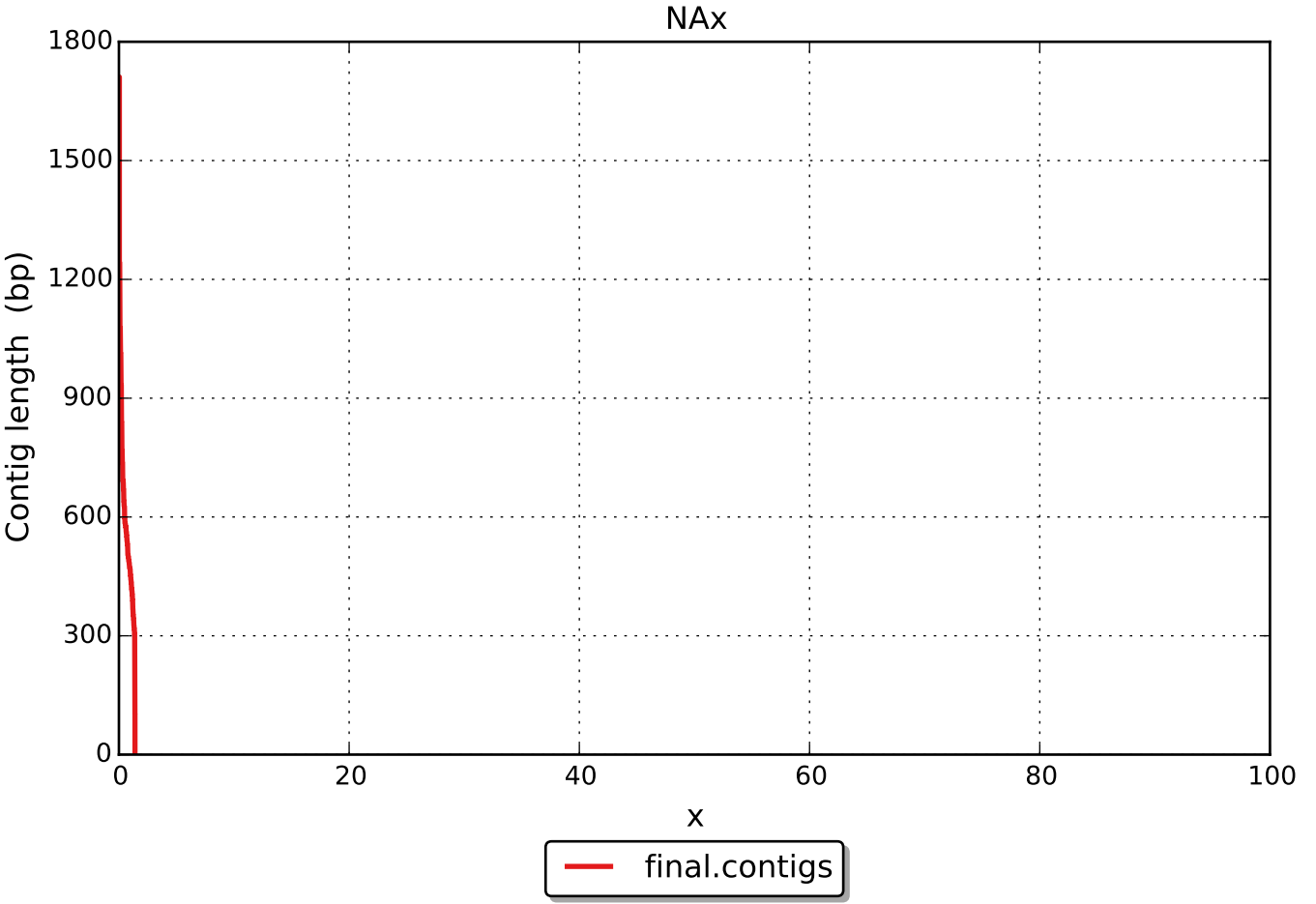

NGx
2500
2000
1500
1000
500
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

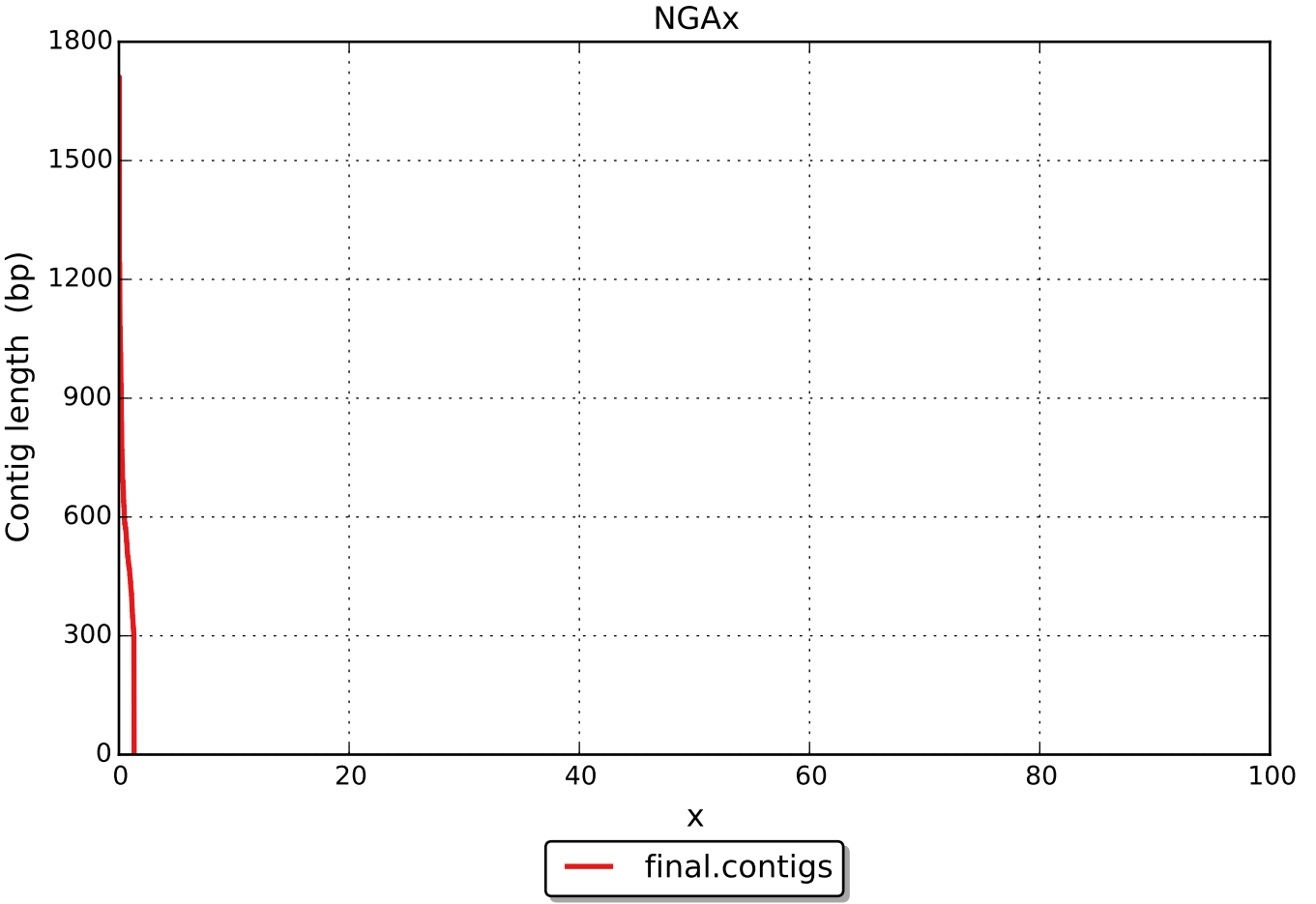

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
2000
4000
6000
8000
Contig index
final.contigs
Reference


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)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
final.contigs
Reference


NAx
1800
1500
1200
900
600
300
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
1800
1500
1200
900
600
300
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs