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	3595
Largest contig	2247
Total length	2468572
Reference length	4641652
GC (%)	50.66
Reference GC (%)	50.79
N50	669
NG50	518
N75	575
L50	1446
LG50	3305
L75	2444
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	3542 + 6 part
Unaligned length	2432438
Genome fraction (%)	0.778
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	728.03
# indels per 100 kbp	5.54
Largest alignment	1711
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

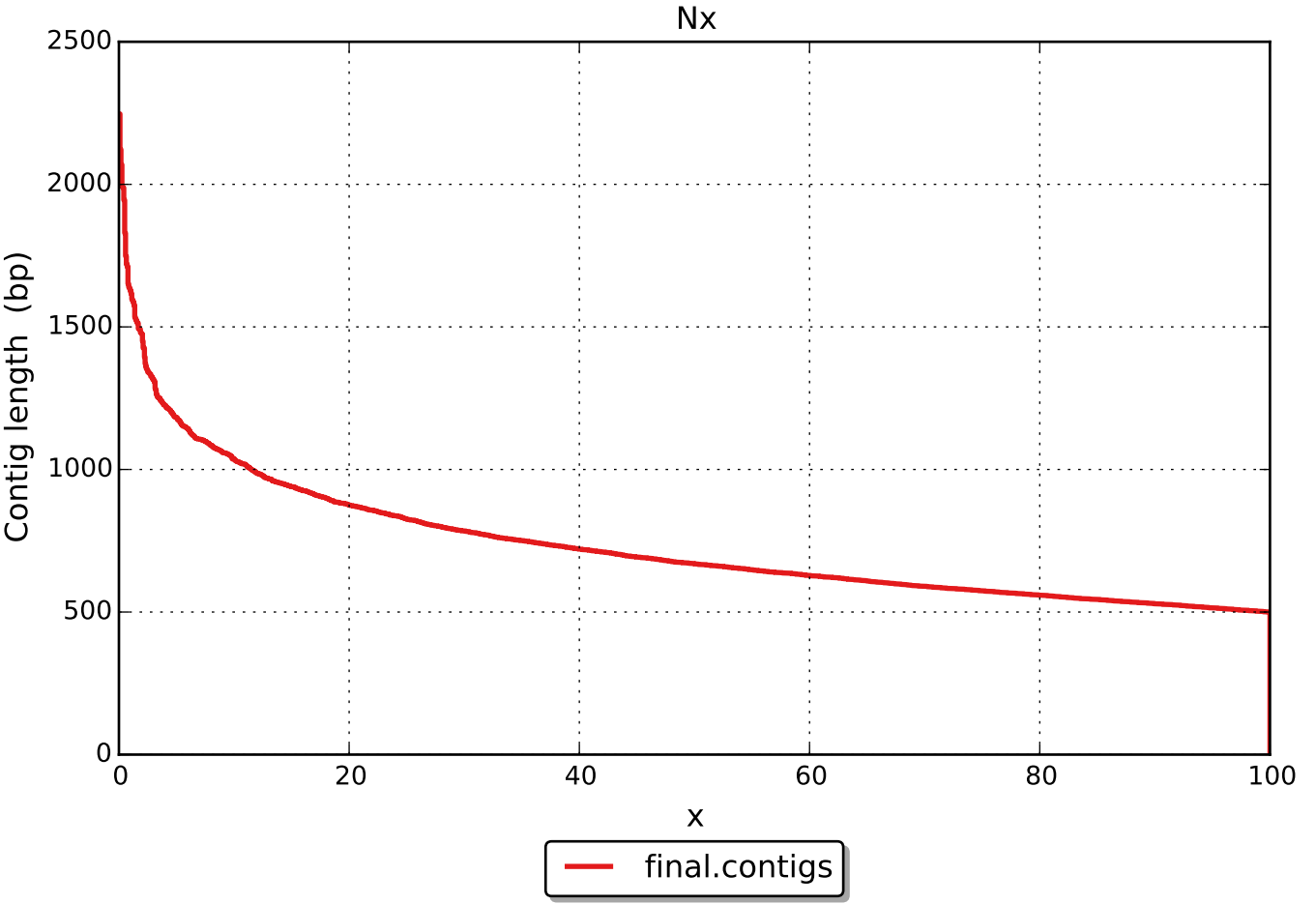
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	263
# indels	2
# short indels	2
# long indels	0
Indels length	2

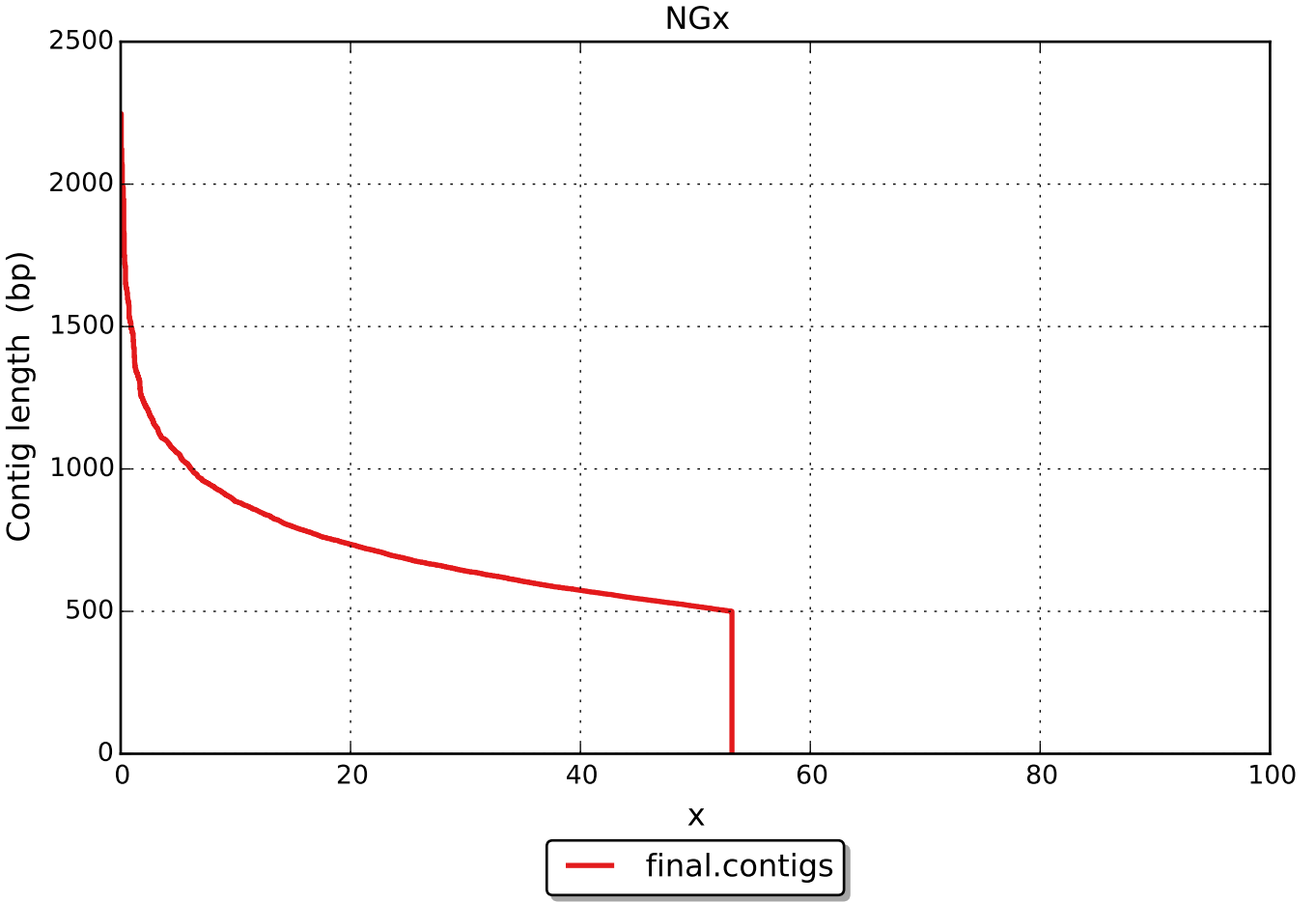
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

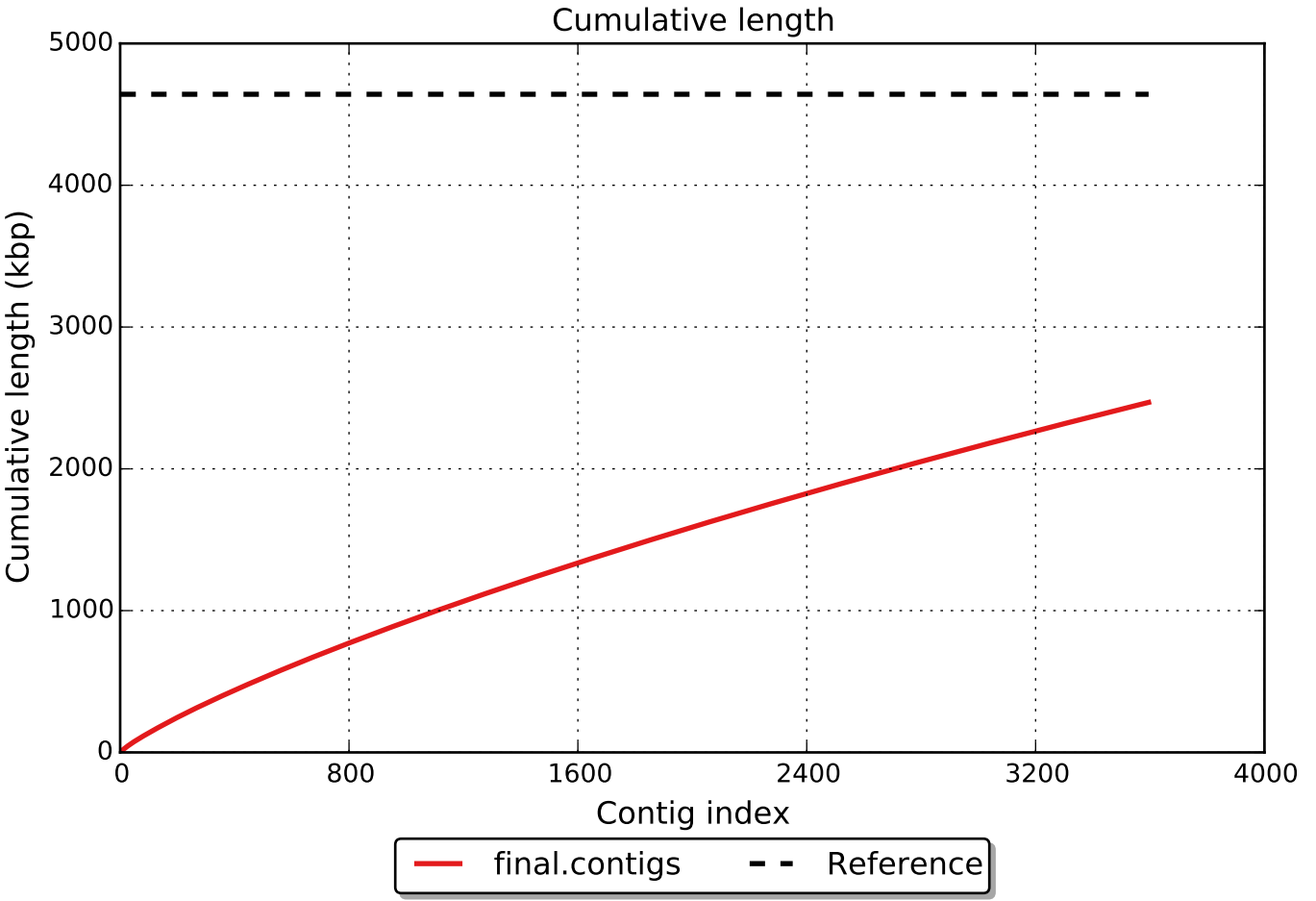
Unaligned report

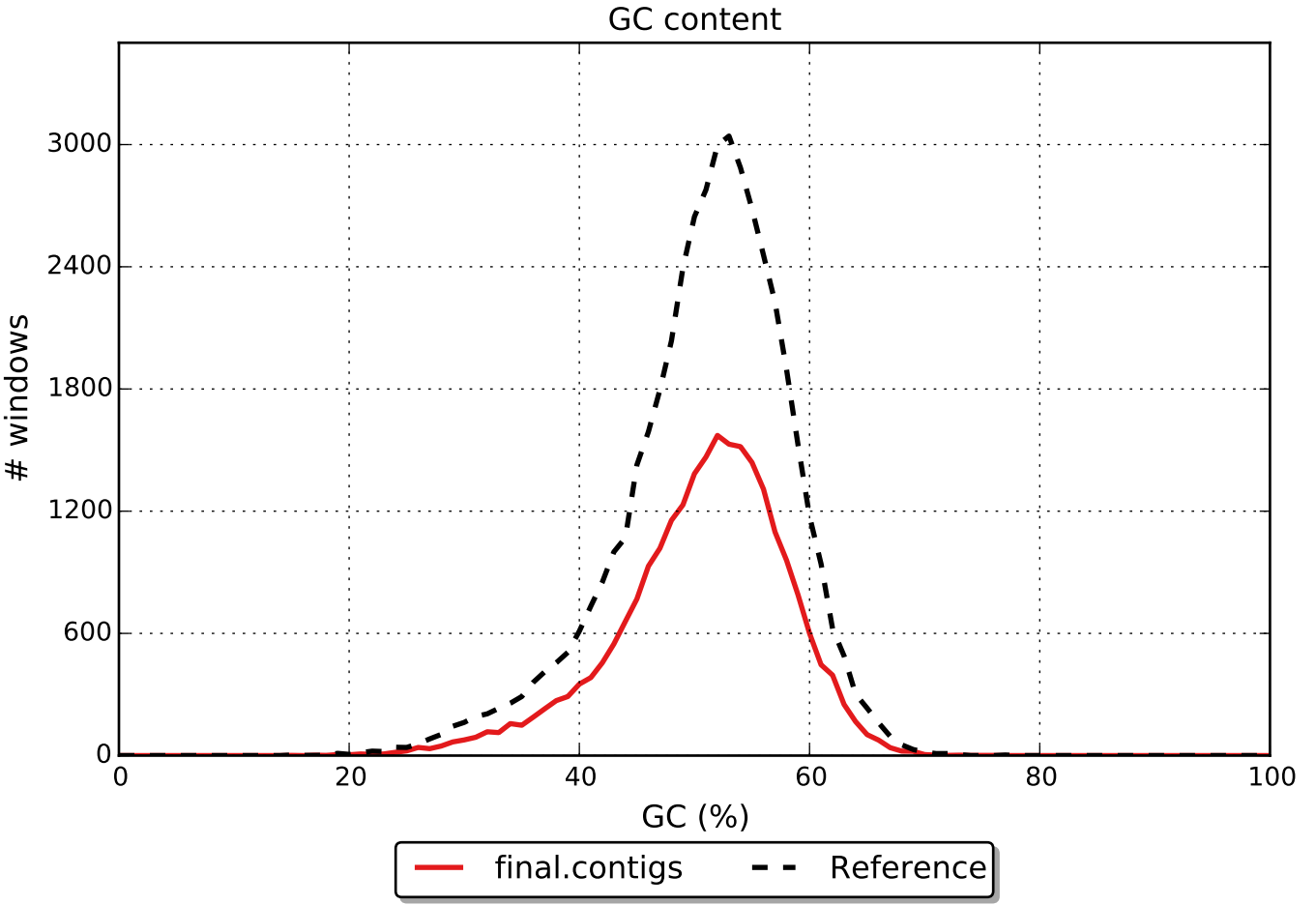
	final.contigs
# fully unaligned contigs	3542
Fully unaligned length	2430252
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2186
# N's	0

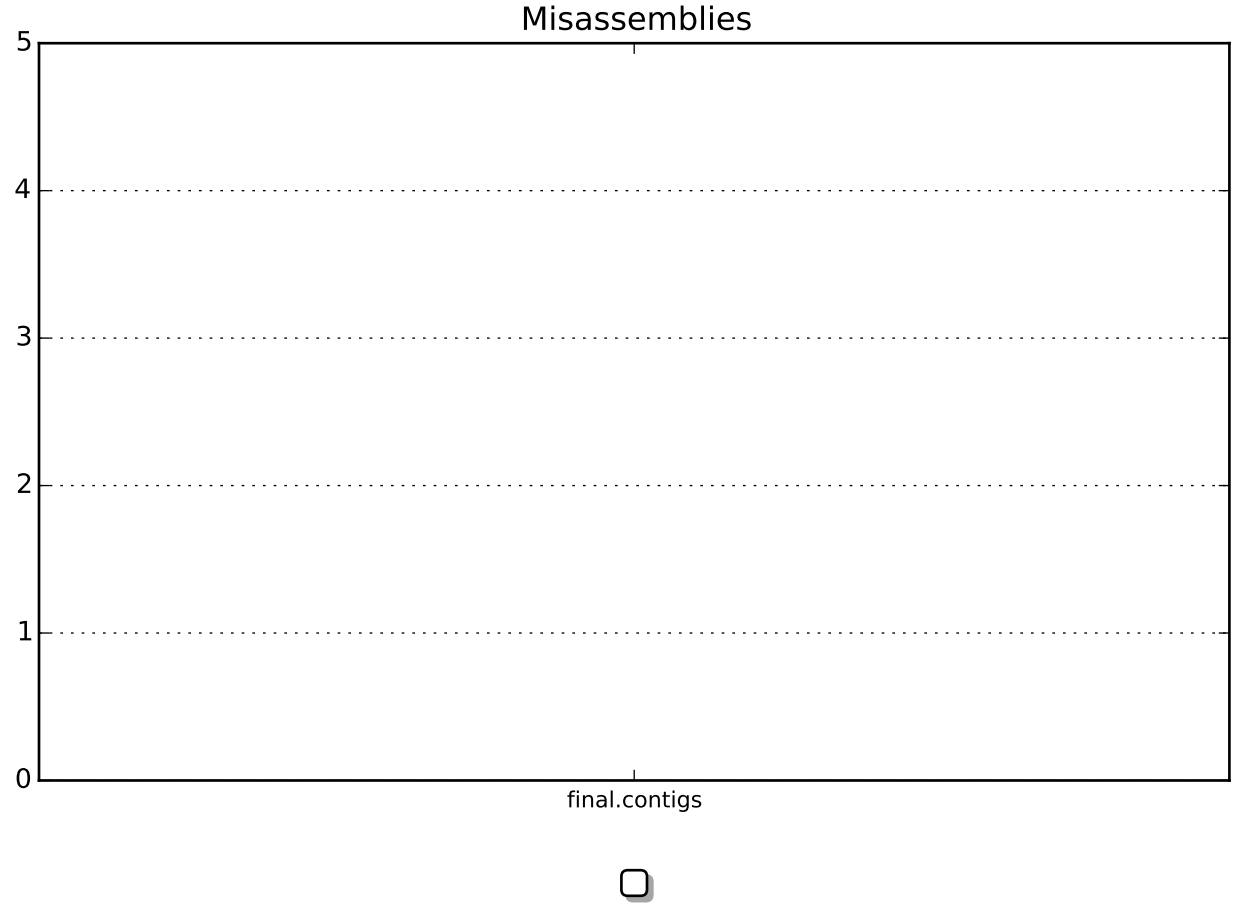
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

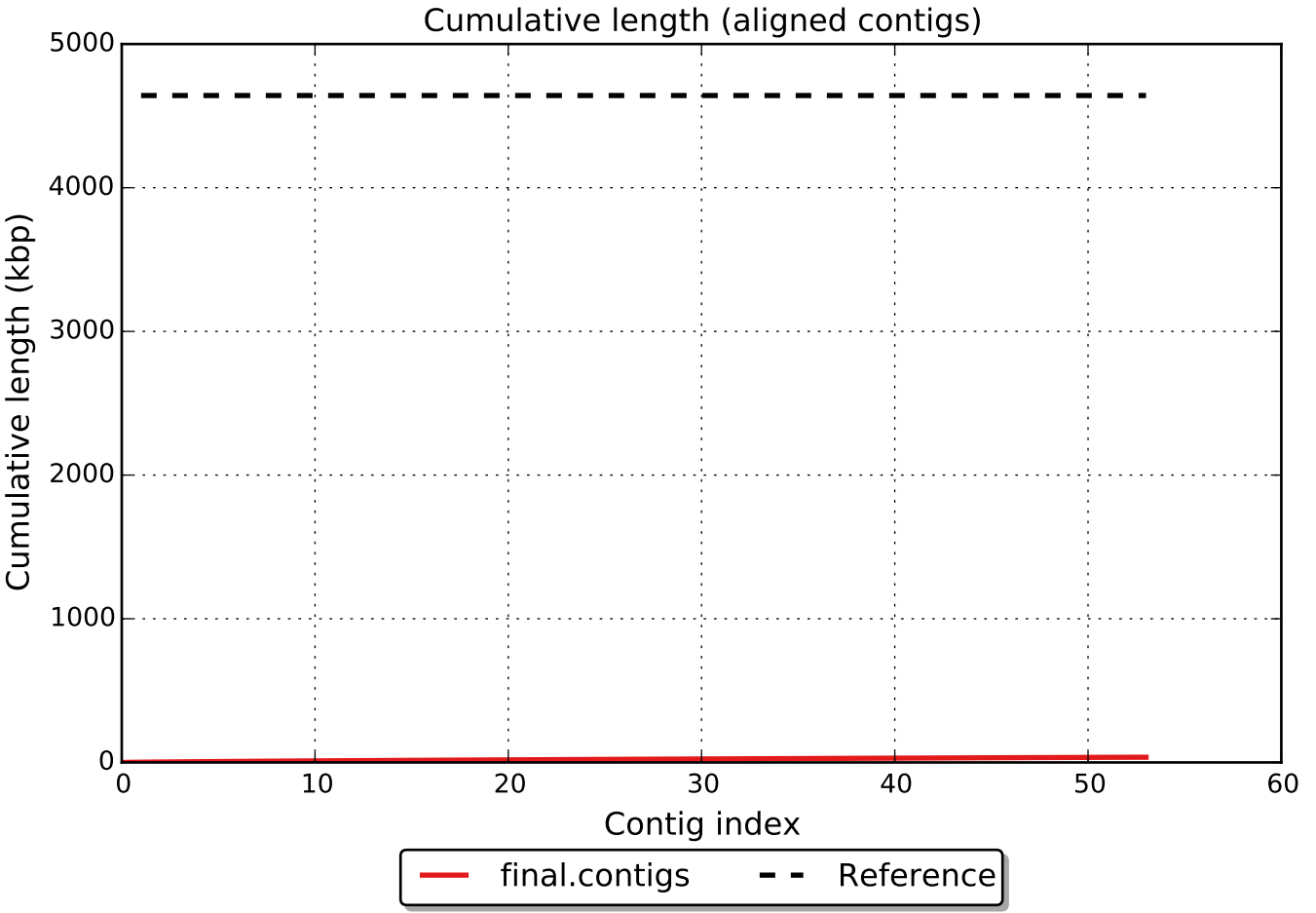

Nx
2500
2000
1500
1000
500
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

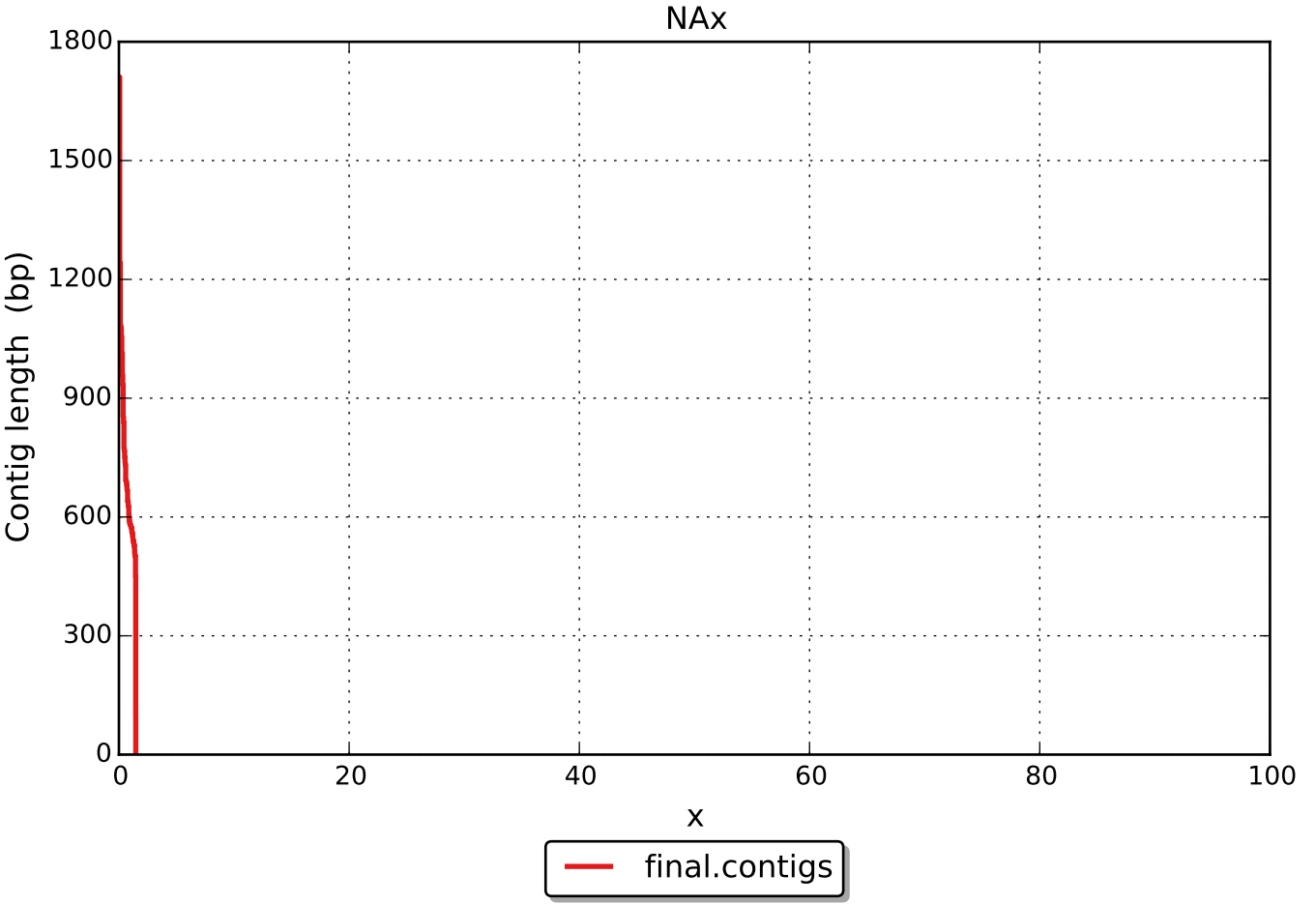

NGx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs

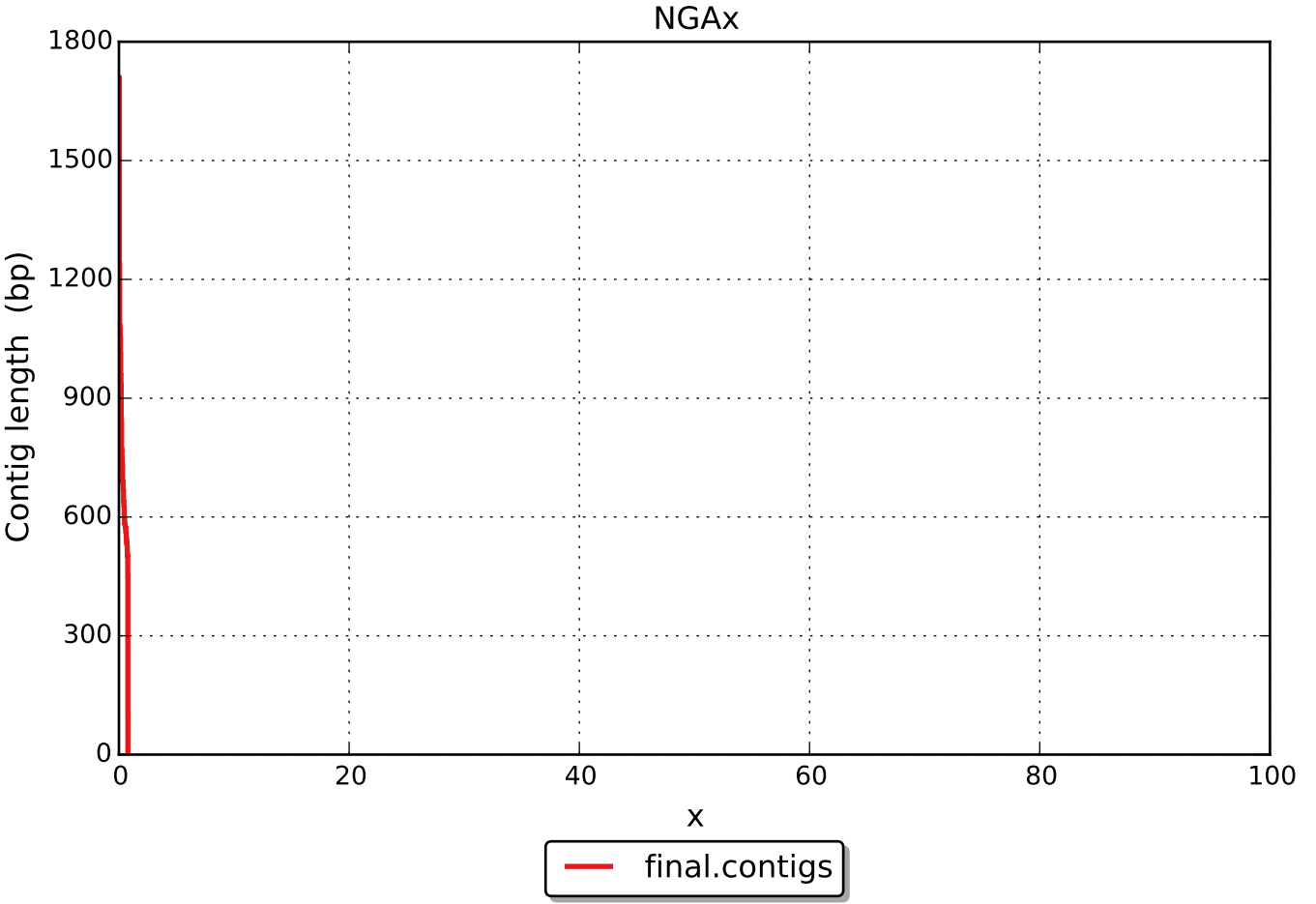

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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
10
20
30
40
50
60
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
Contig length (bp)
1800
1500
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs