Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	6580
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	785
Largest contig	1226
Total length	443269
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.79
N50	547
N75	517
L50	359
L75	567
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	2168
# local misassemblies	3
# unaligned contigs	0 + 4 part
Unaligned length	822
Genome fraction (%)	9.136
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1579.79
# indels per 100 kbp	0.24
Largest alignment	1226
NA50	546
NGA50	-
NA75	516
LA50	359
LA75	568

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

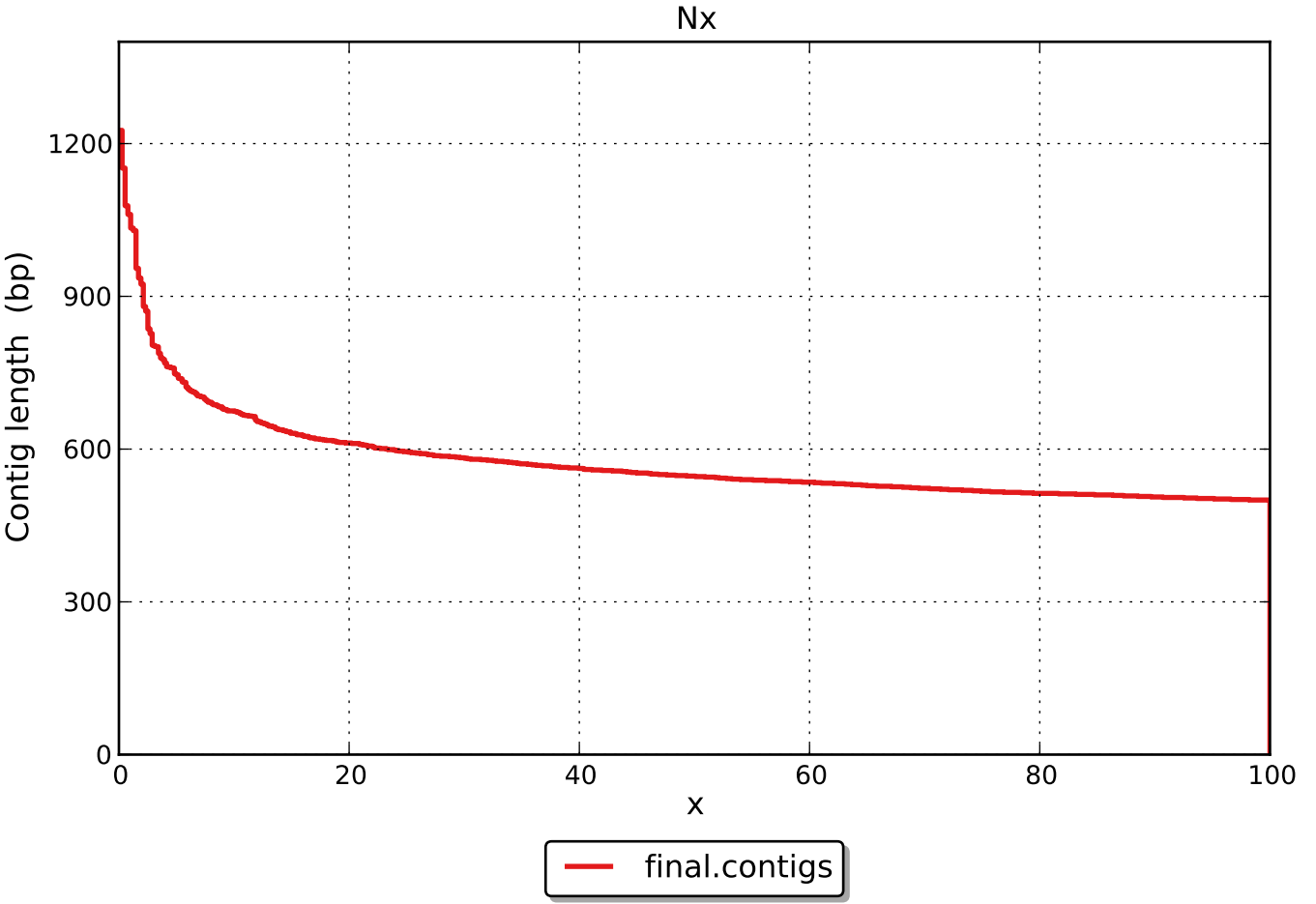
	final.contigs
# misassemblies	4
# relocations	0
# translocations	0
# inversions	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	2168
# local misassemblies	3
# mismatches	6699
# indels	1
# short indels	1
# long indels	0
Indels length	1

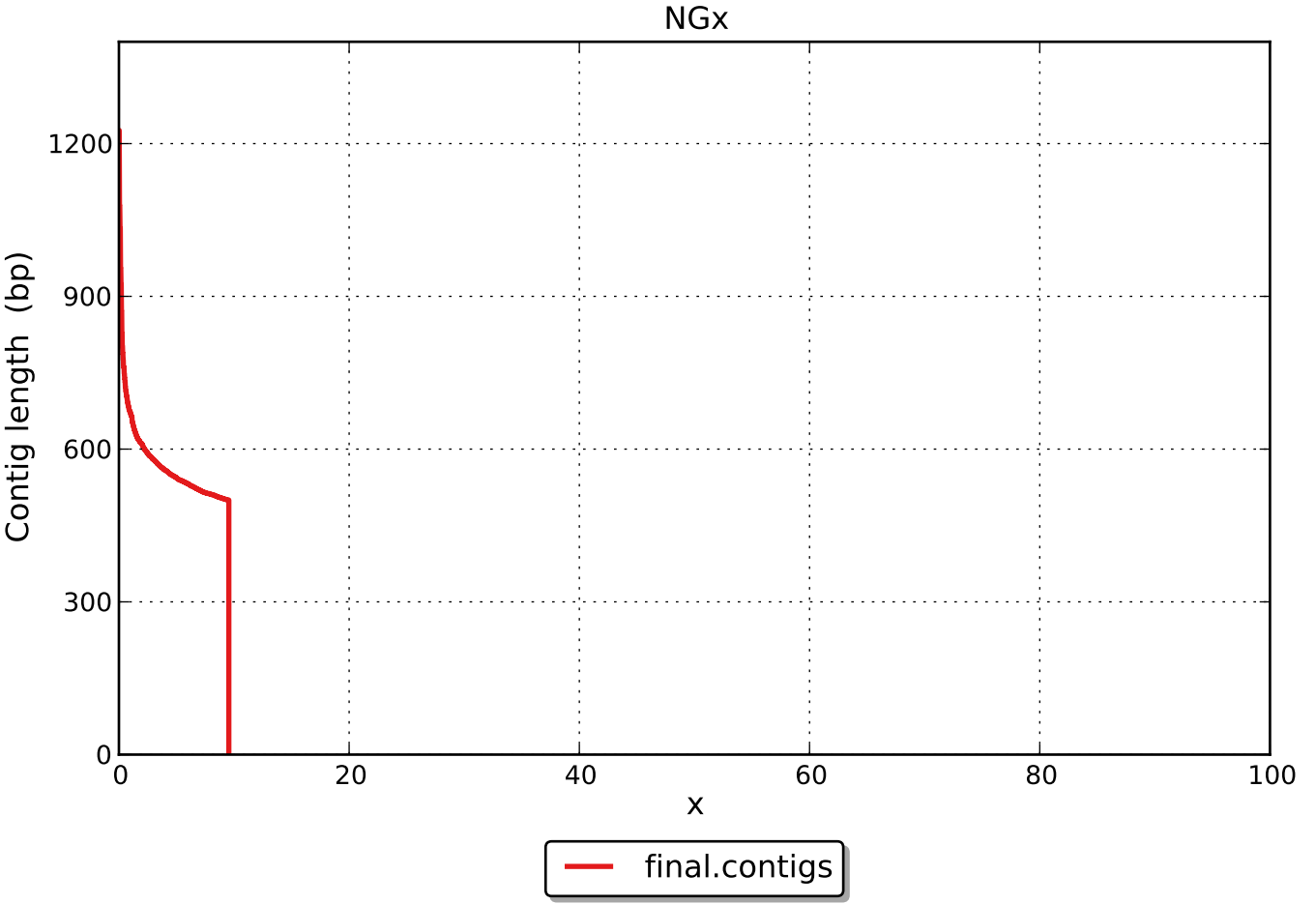
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

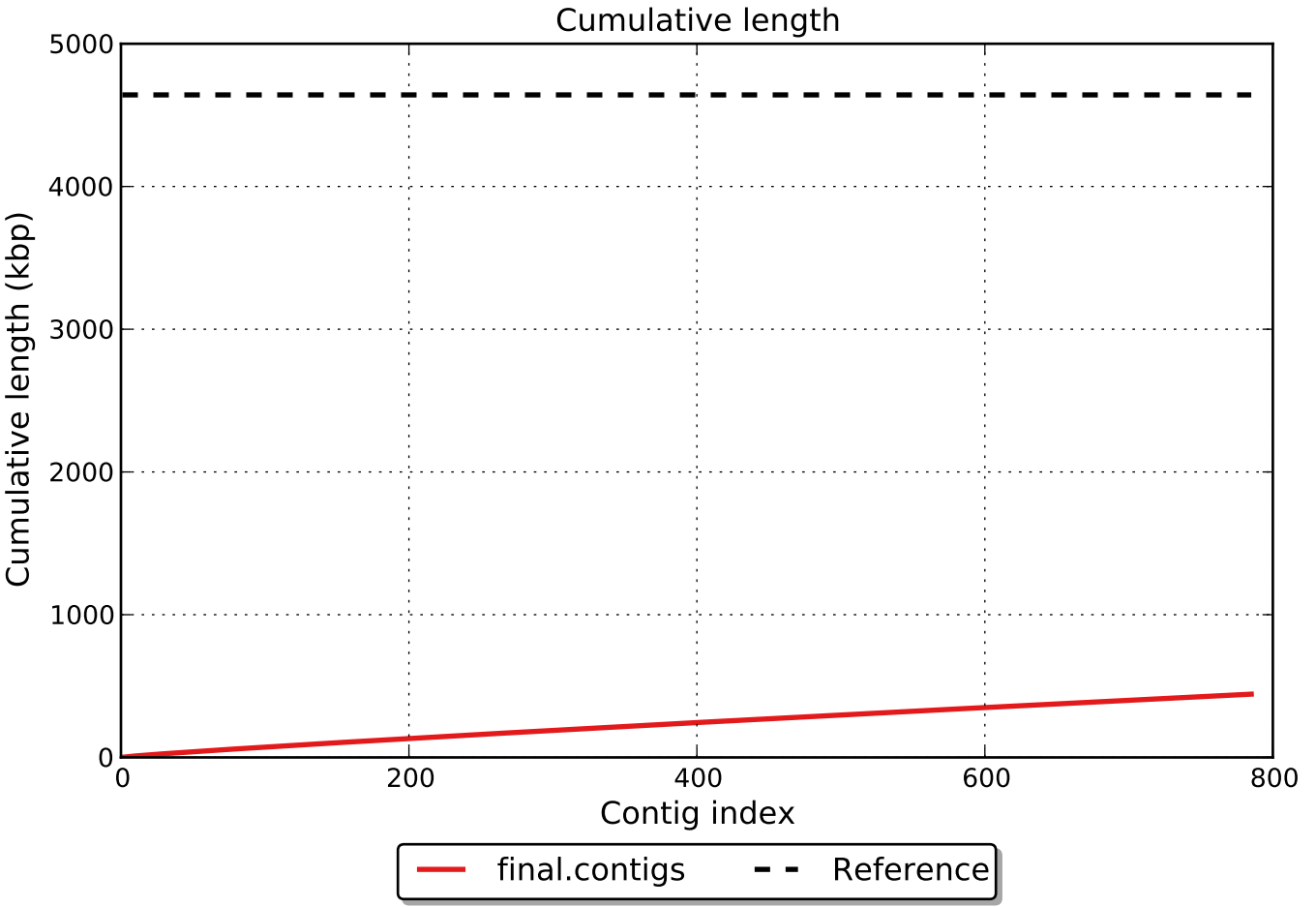
Unaligned report

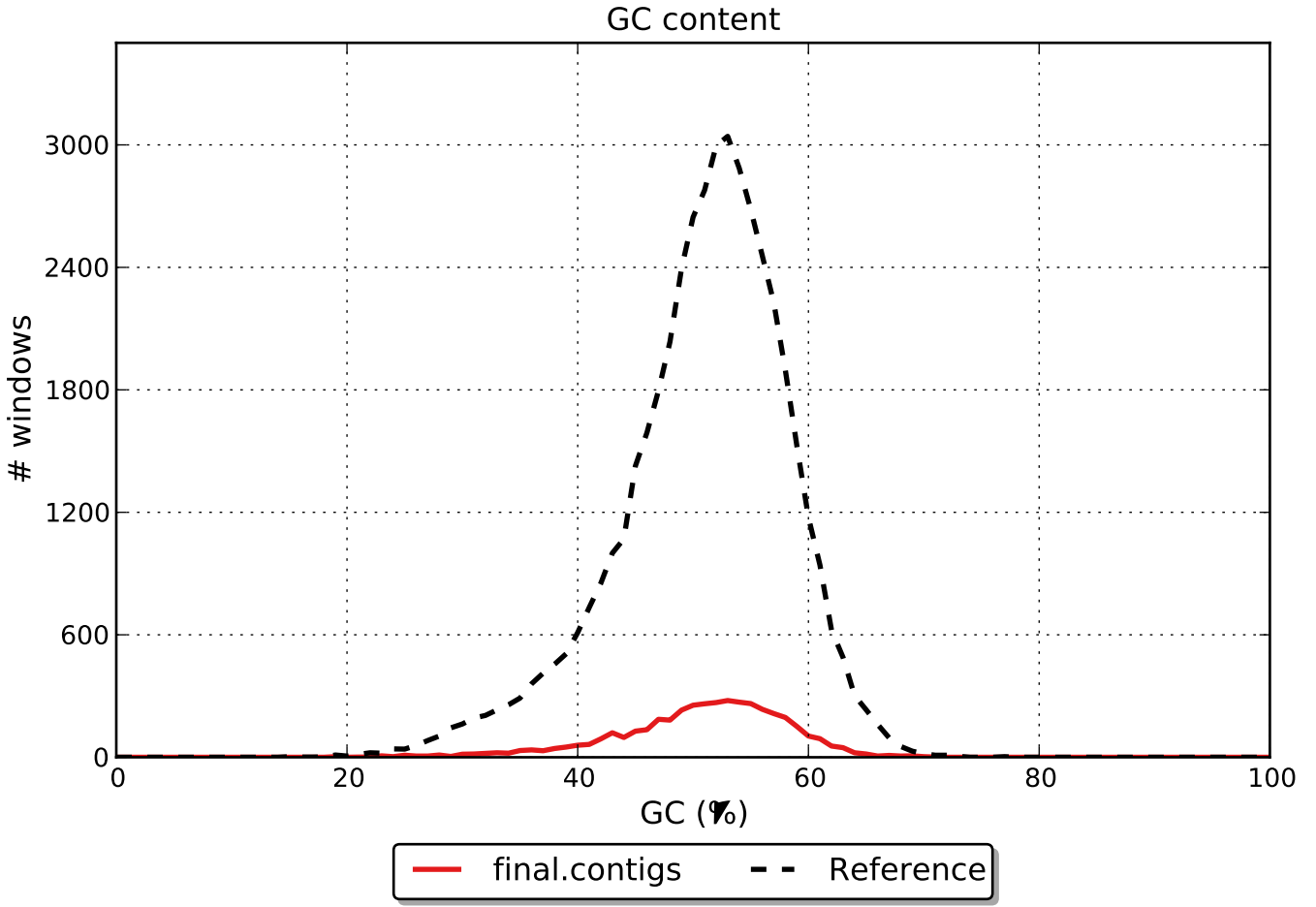
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	822
# N's	0

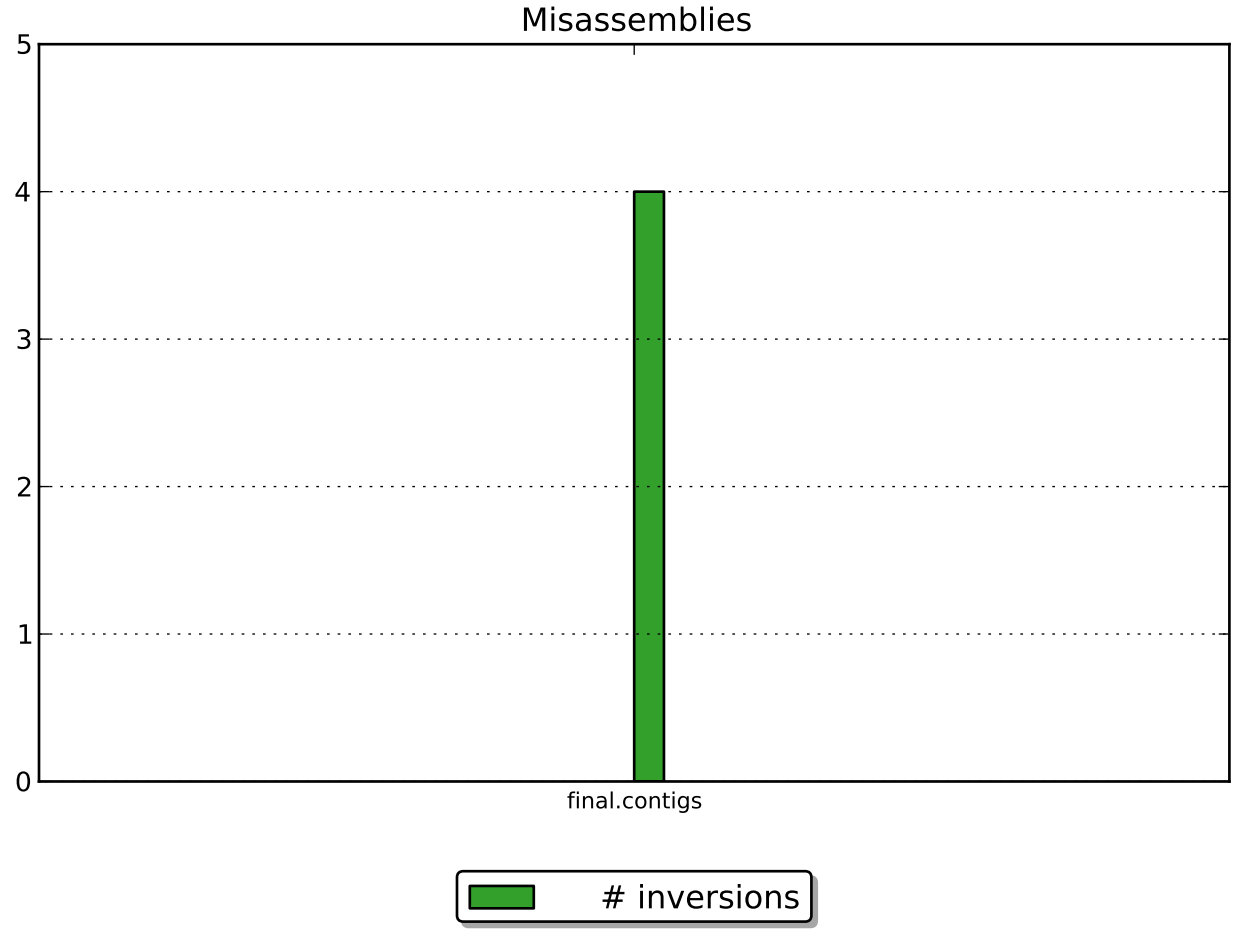
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

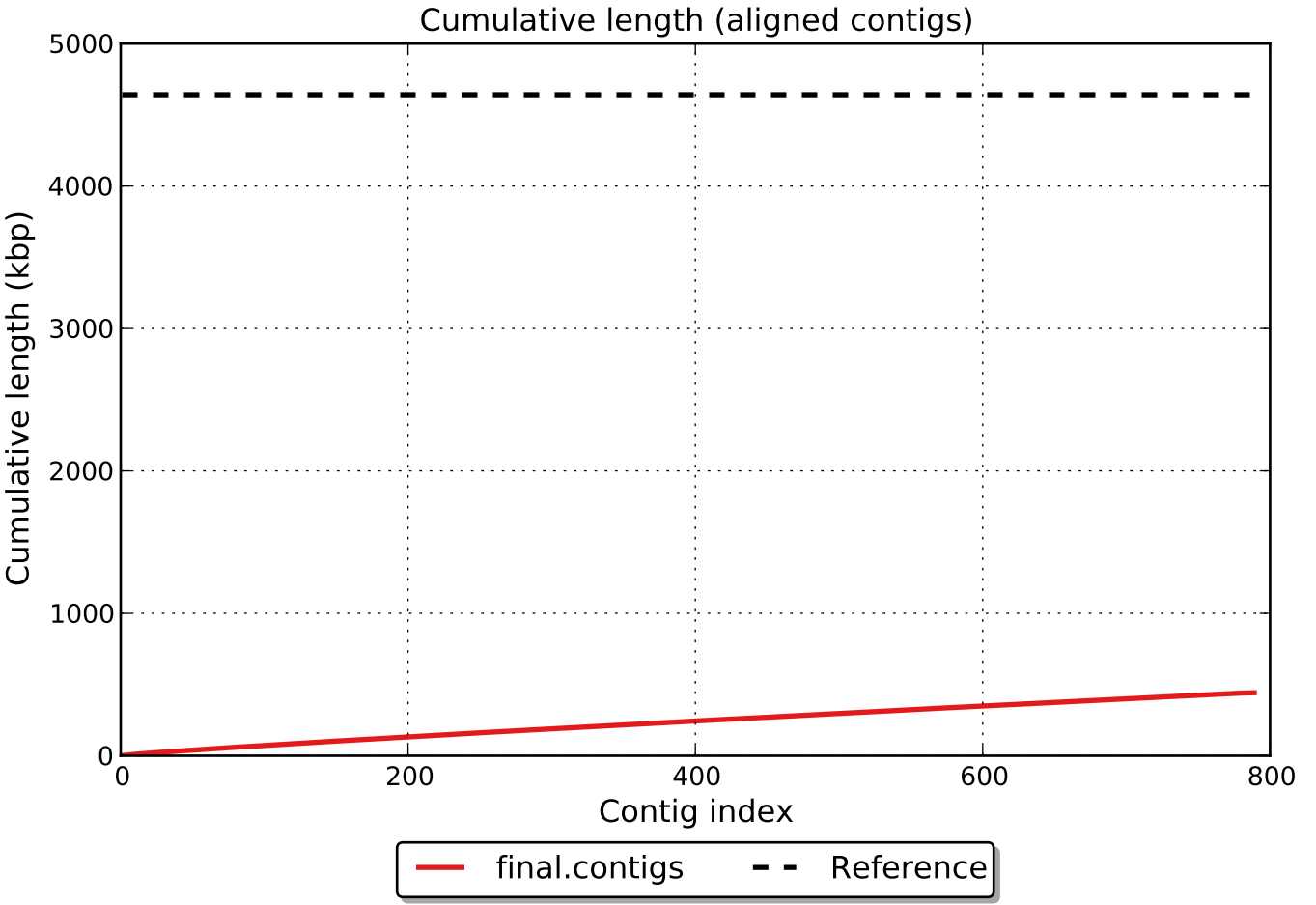

Nx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs

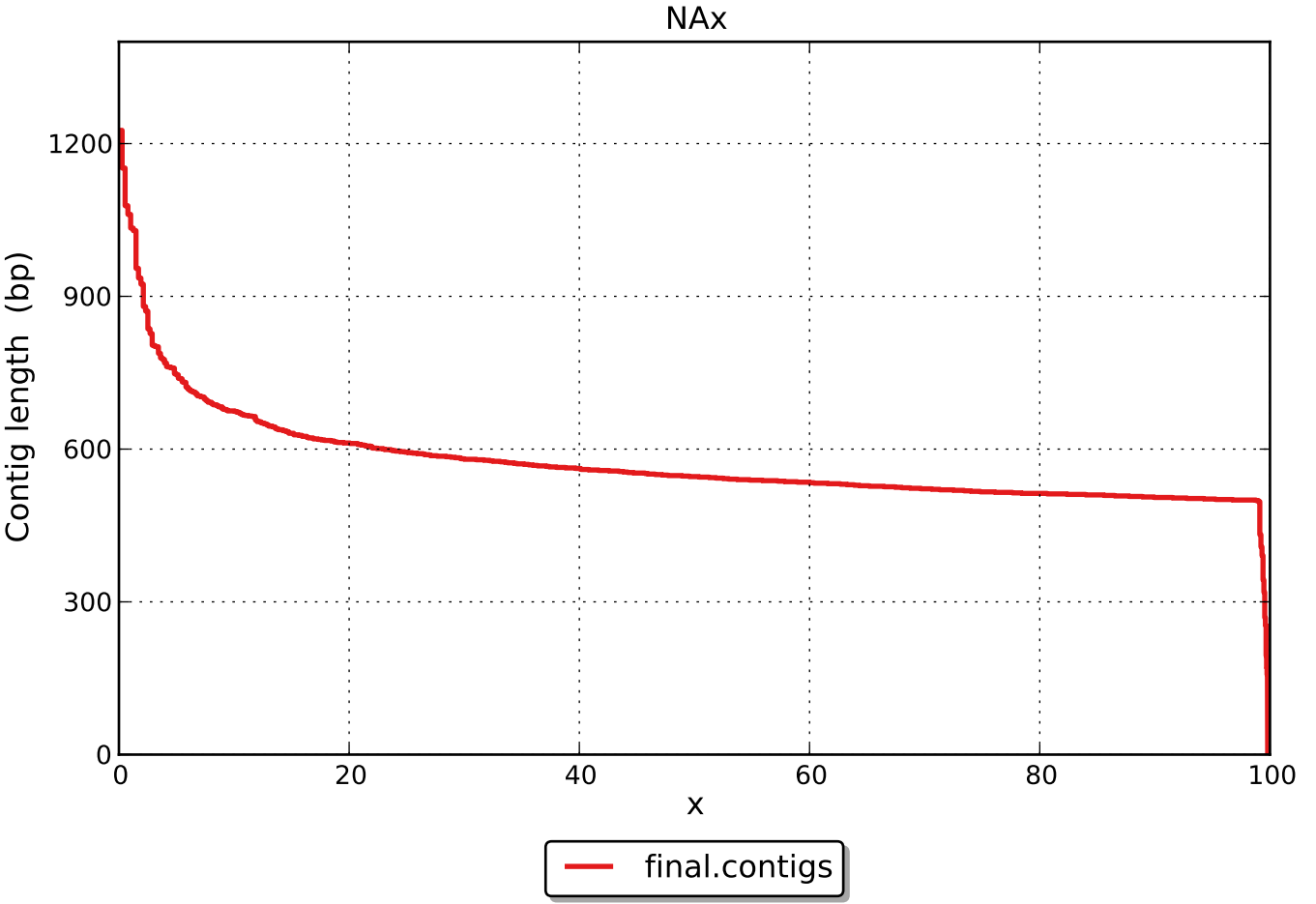

NGx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs

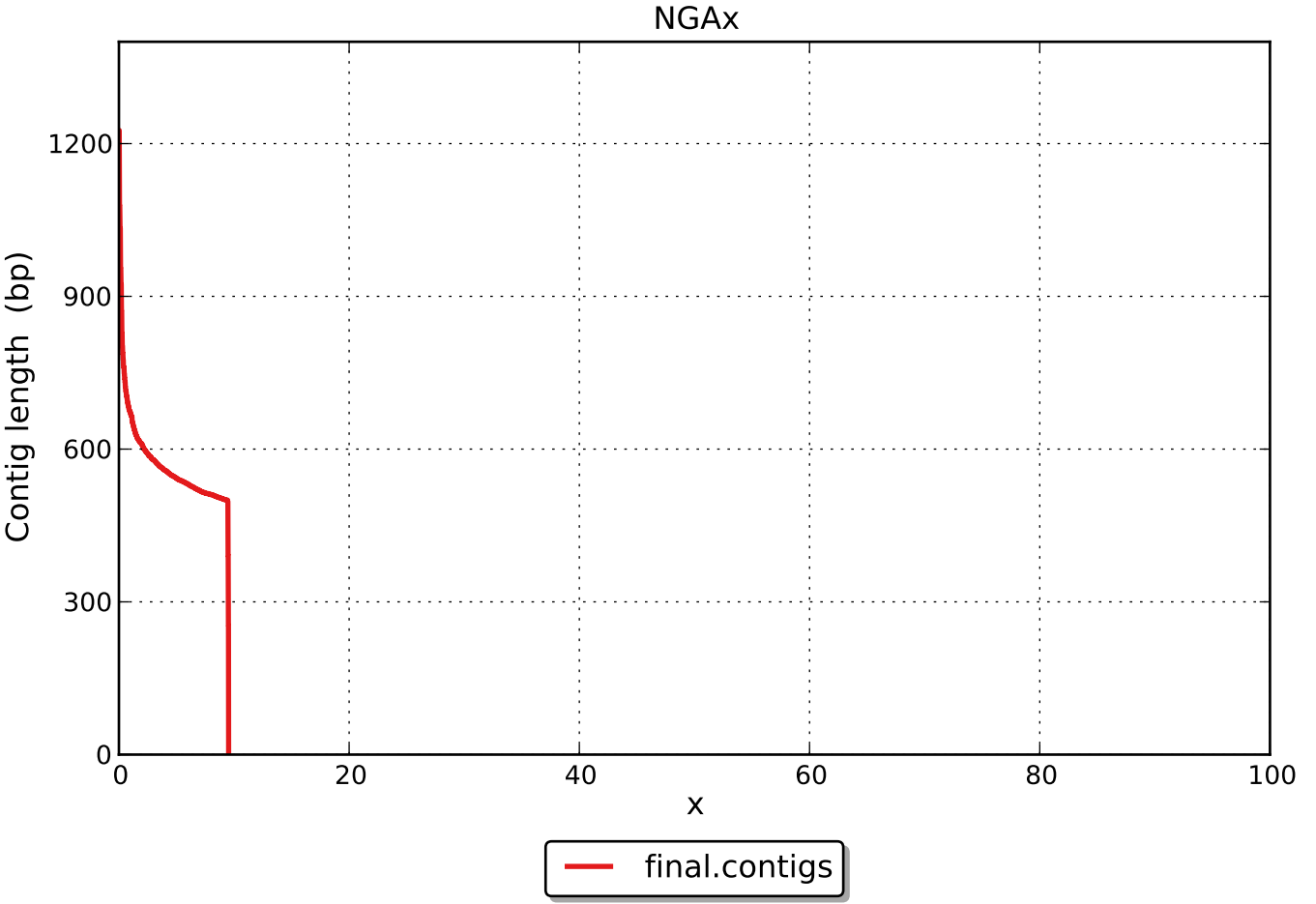

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
final.contigs
Reference


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
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
final.contigs
Reference


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


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