Report

	final.contigs
# contigs (>= 1000 bp)	1699
# contigs (>= 5000 bp)	86
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3915920
Total length (>= 5000 bp)	533575
Total length (>= 10000 bp)	21899
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2566
Largest contig	11062
Total length	4554188
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	2261
NG50	2235
N75	1387
NG75	1333
L50	637
LG50	656
L75	1278
LG75	1326
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.900
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.31
# indels per 100 kbp	0.00
Largest alignment	11062
NA50	2261
NGA50	2235
NA75	1387
NGA75	1333
LA50	637
LGA50	656
LA75	1278
LGA75	1326

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

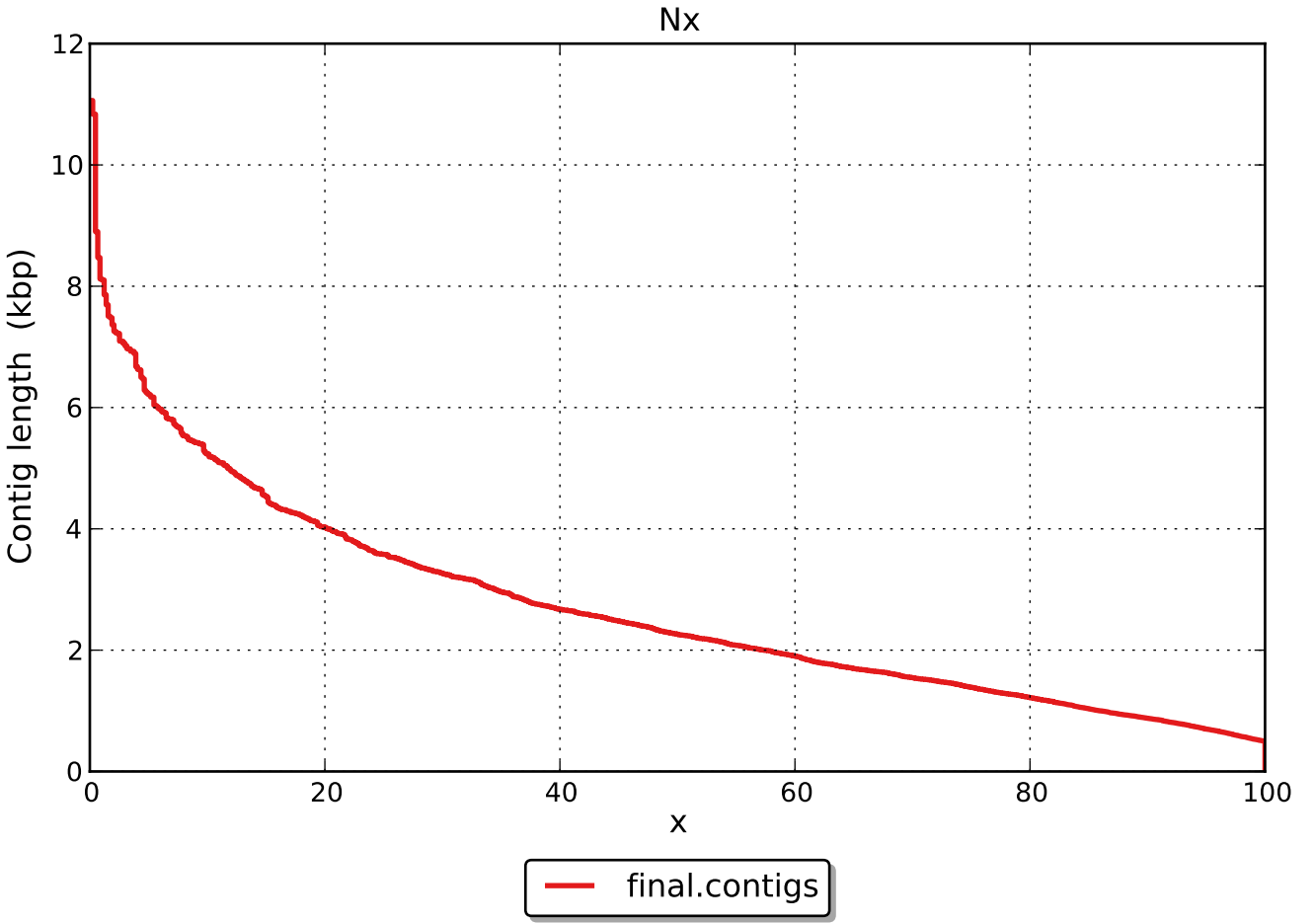
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	278
# indels	0
# short indels	0
# long indels	0
Indels length	0

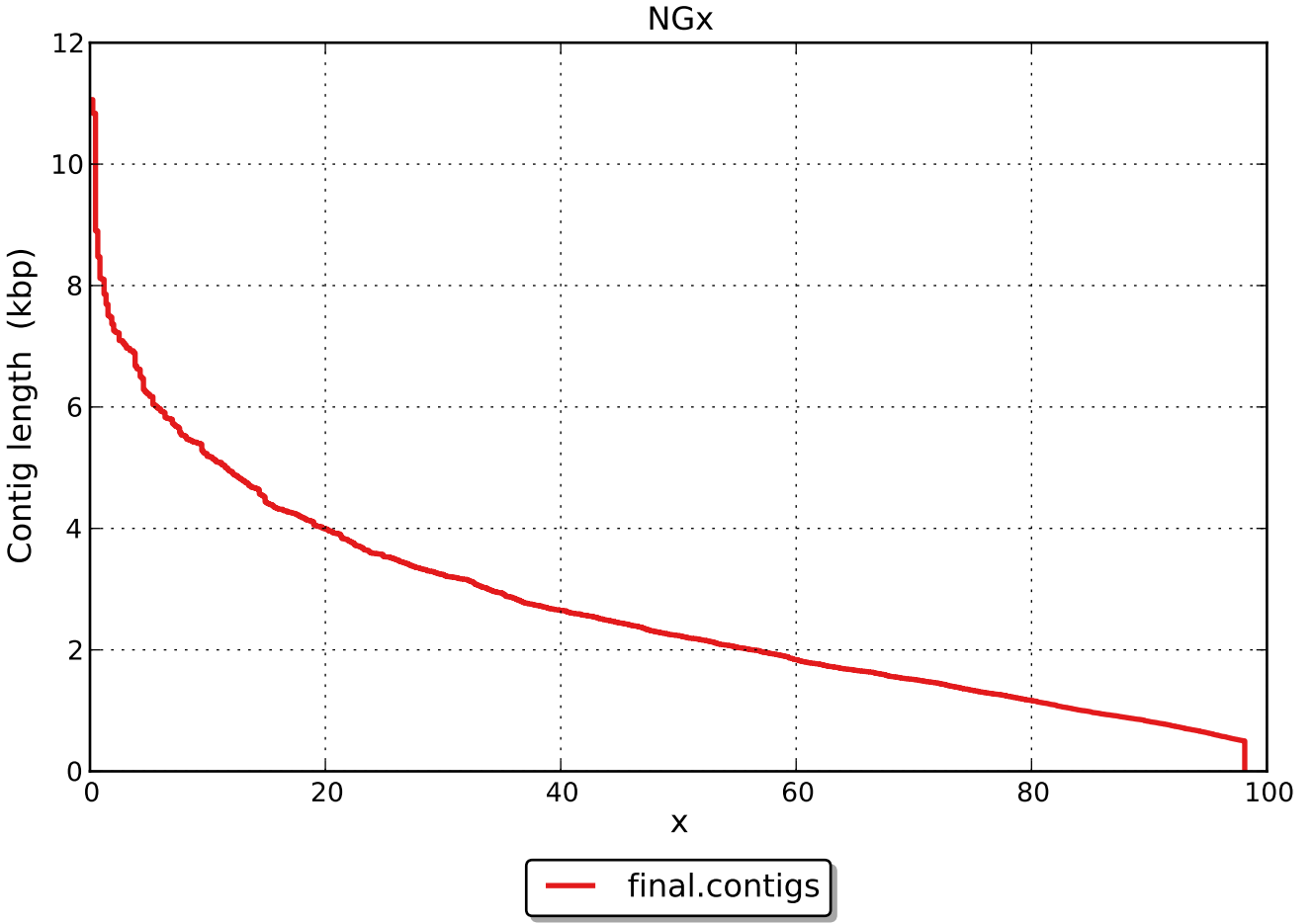
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

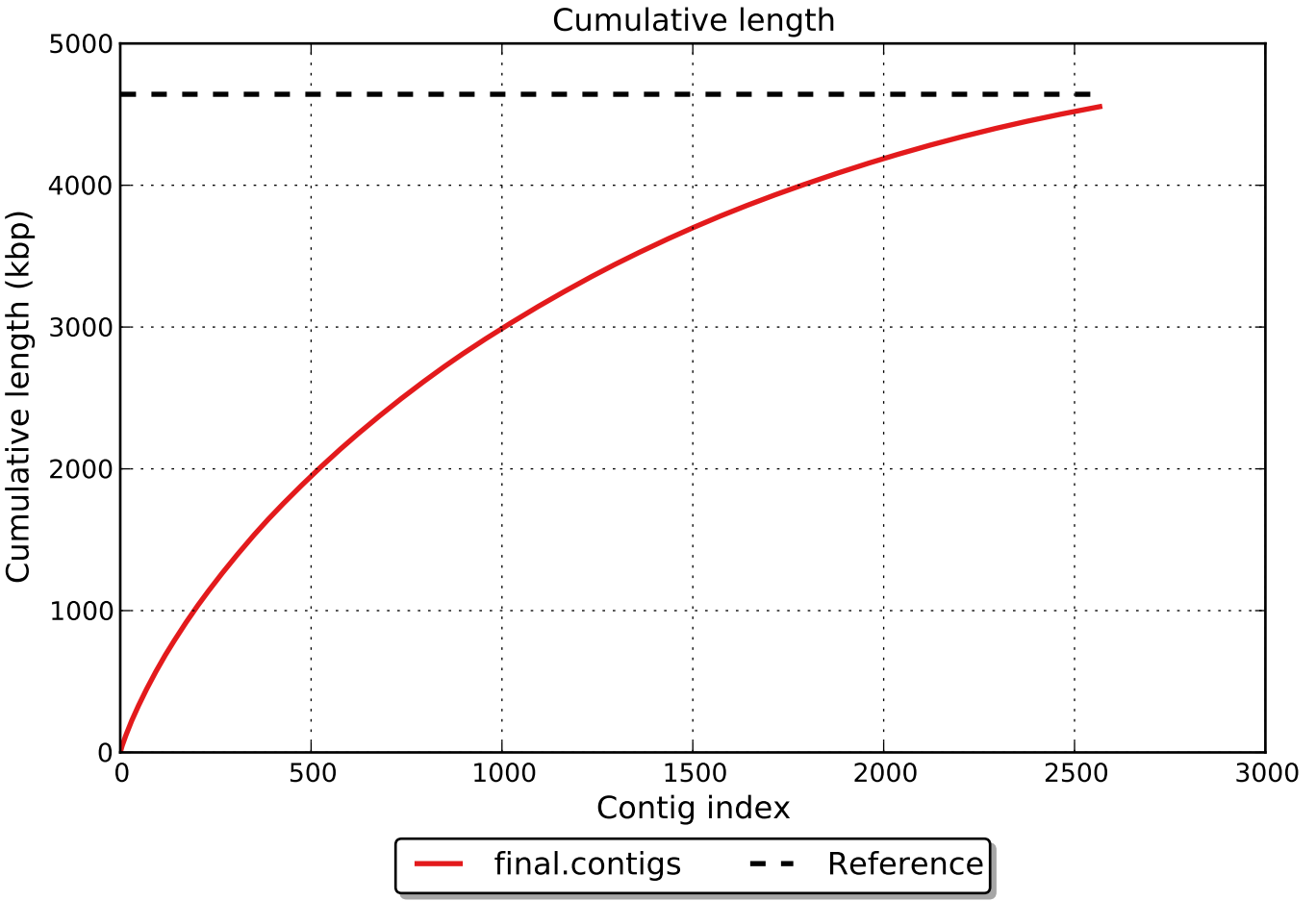
Unaligned report

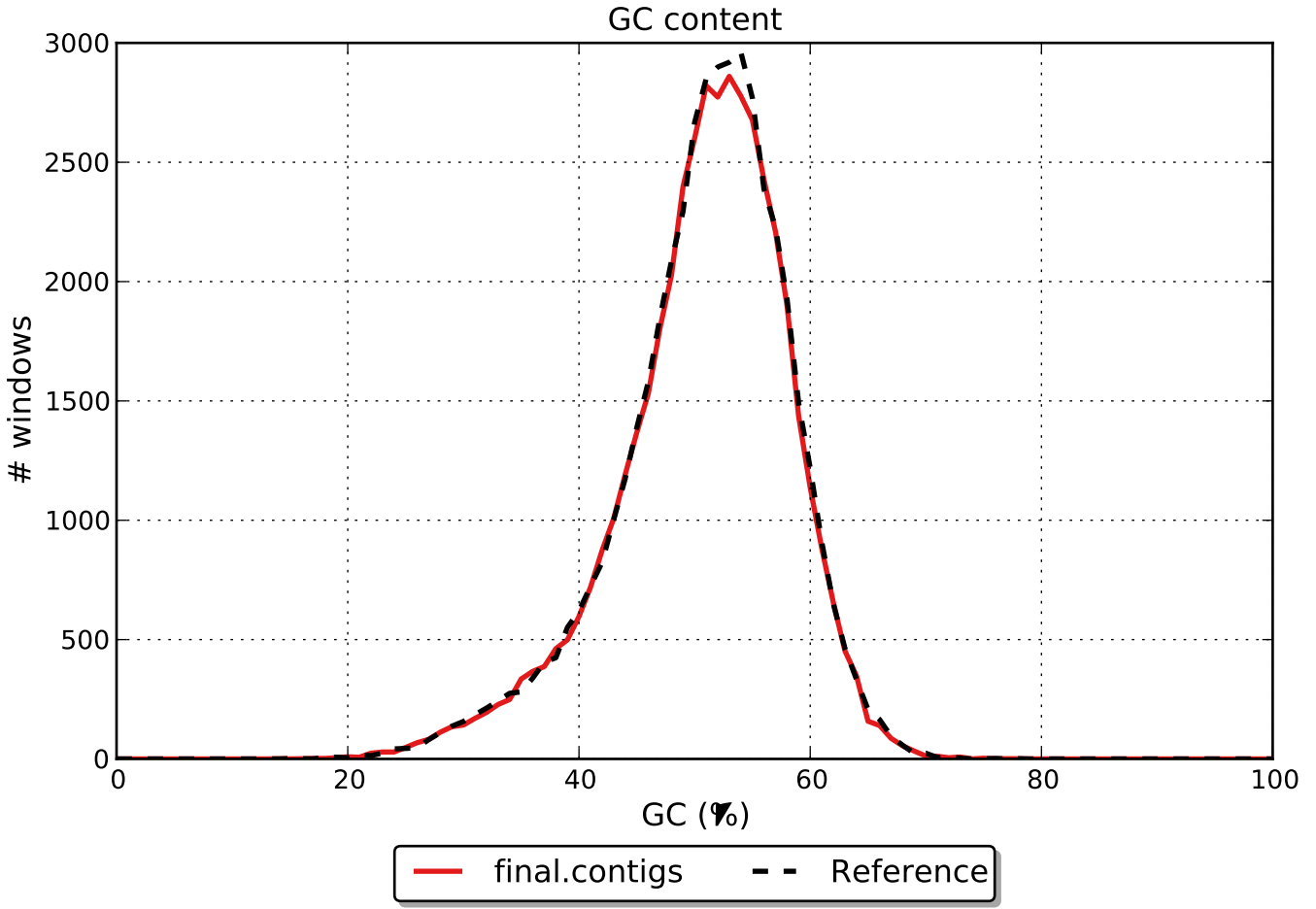
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

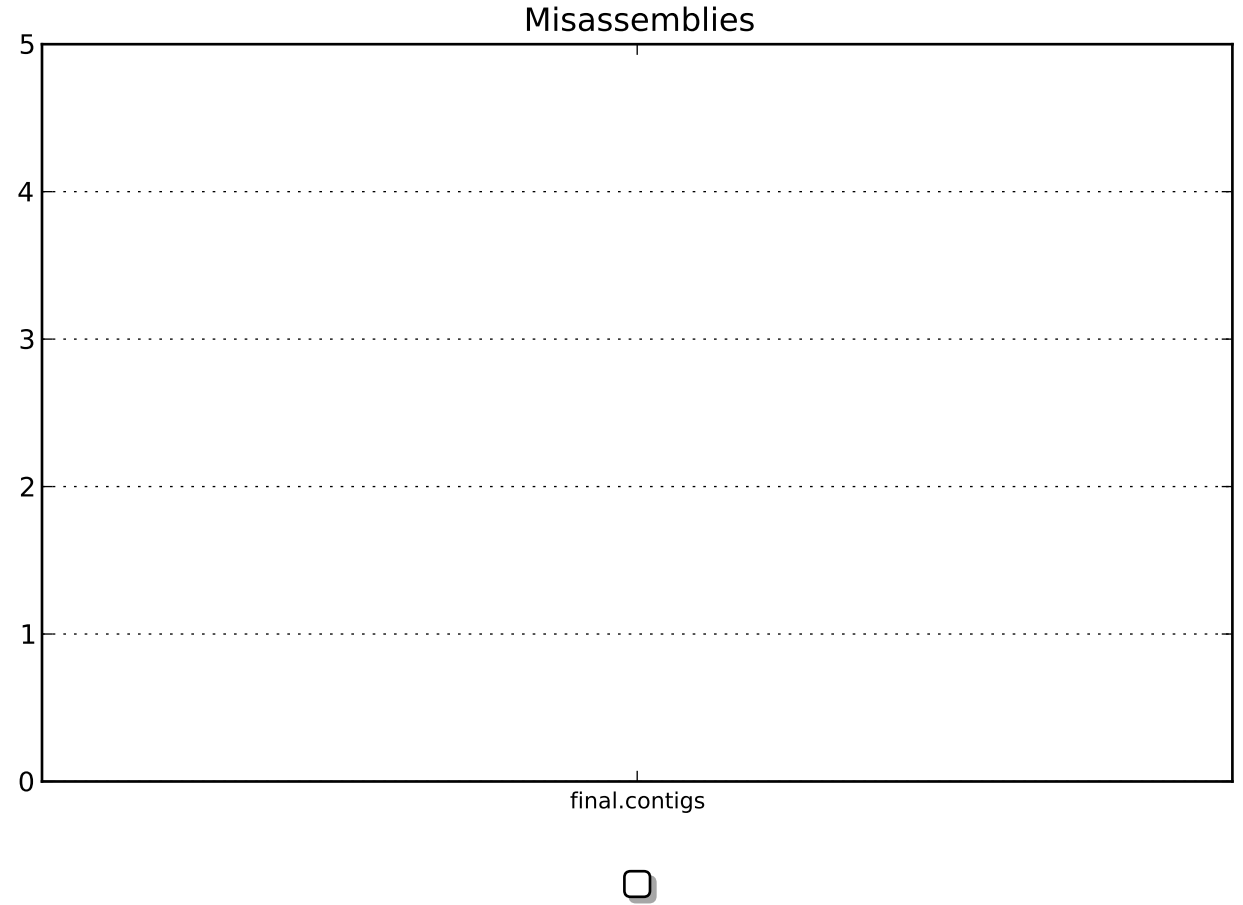
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

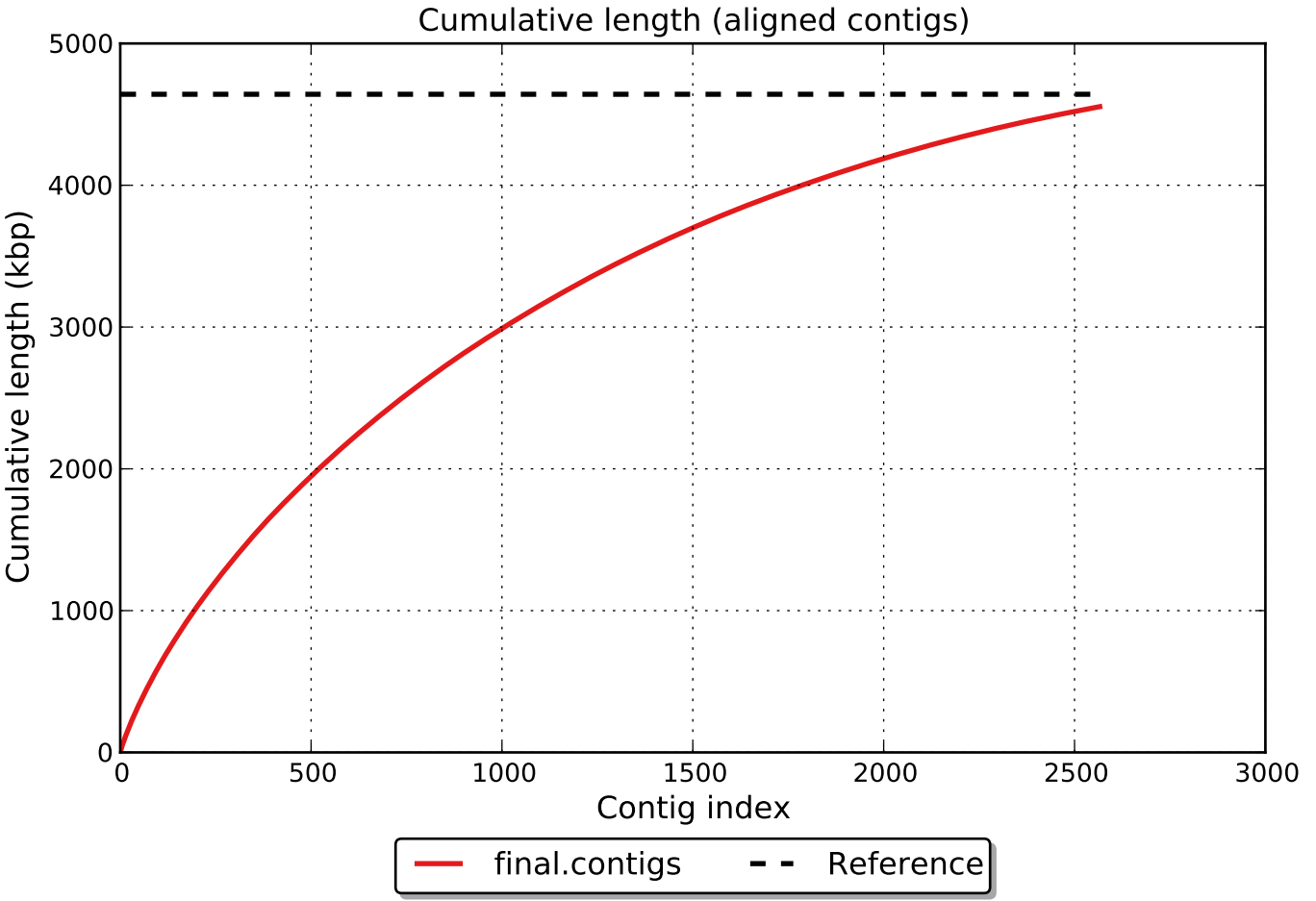

Nx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs

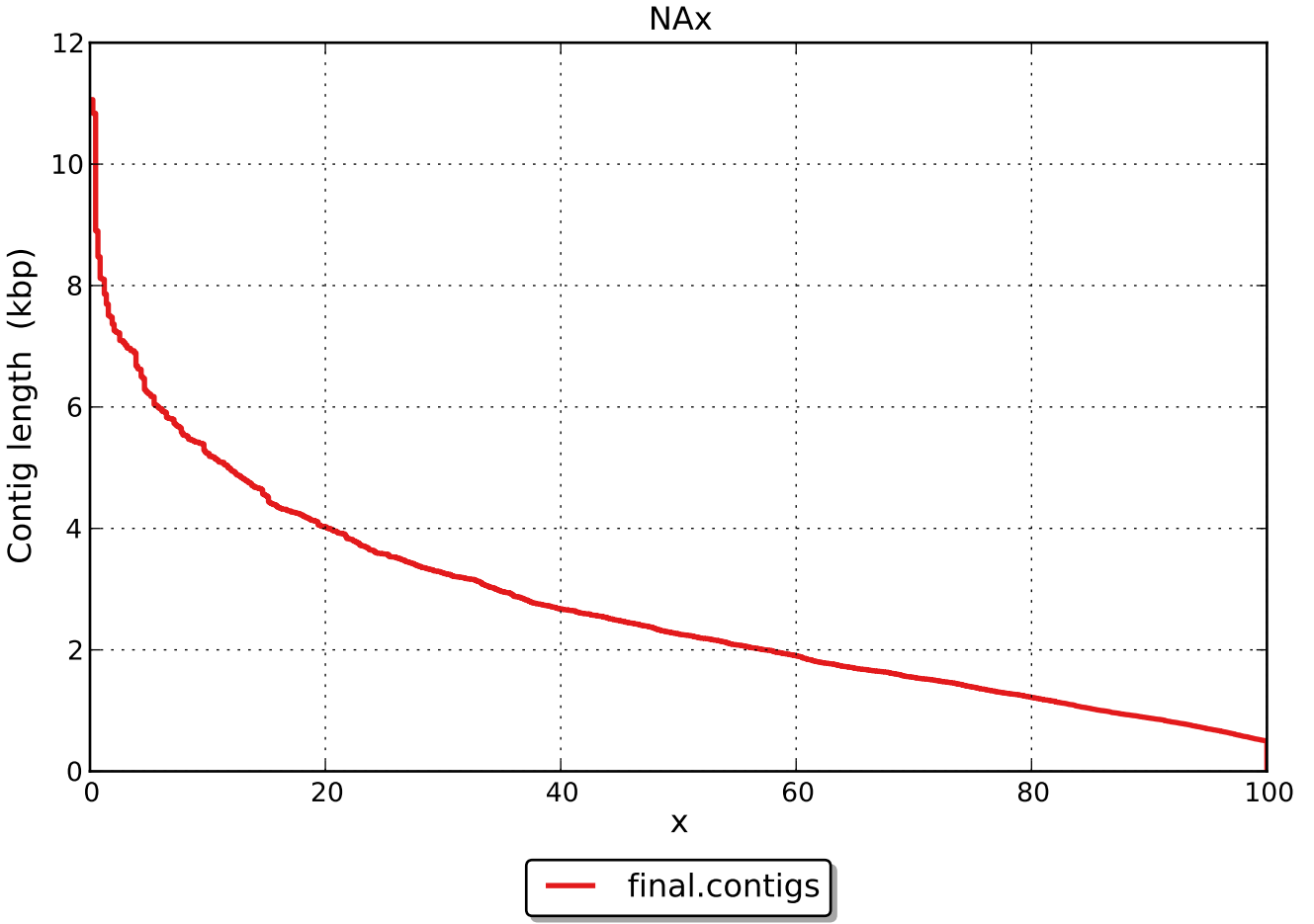

NGx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs

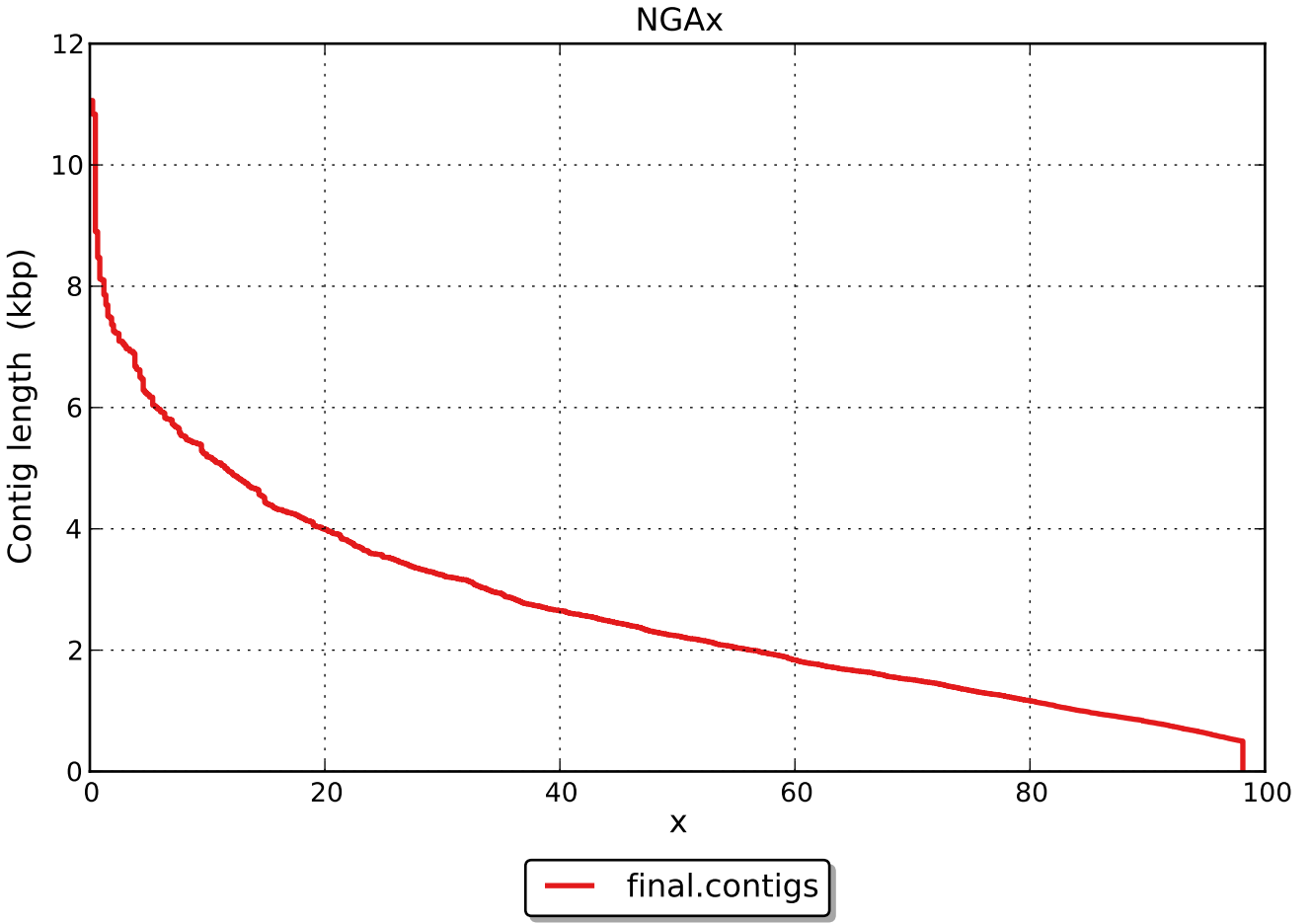

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
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
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


NGAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs