Report

	final.contigs
# contigs (>= 1000 bp)	1150
# contigs (>= 5000 bp)	321
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4694542
Total length (>= 5000 bp)	2551920
Total length (>= 10000 bp)	819183
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1380
Largest contig	18922
Total length	4860075
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	5198
NG50	5206
N75	3025
NG75	3042
L50	298
LG50	297
L75	603
LG75	602
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.068
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.18
# indels per 100 kbp	0.00
Largest alignment	18922
NA50	5198
NGA50	5206
NA75	3025
NGA75	3042
LA50	298
LGA50	297
LA75	603
LGA75	602

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

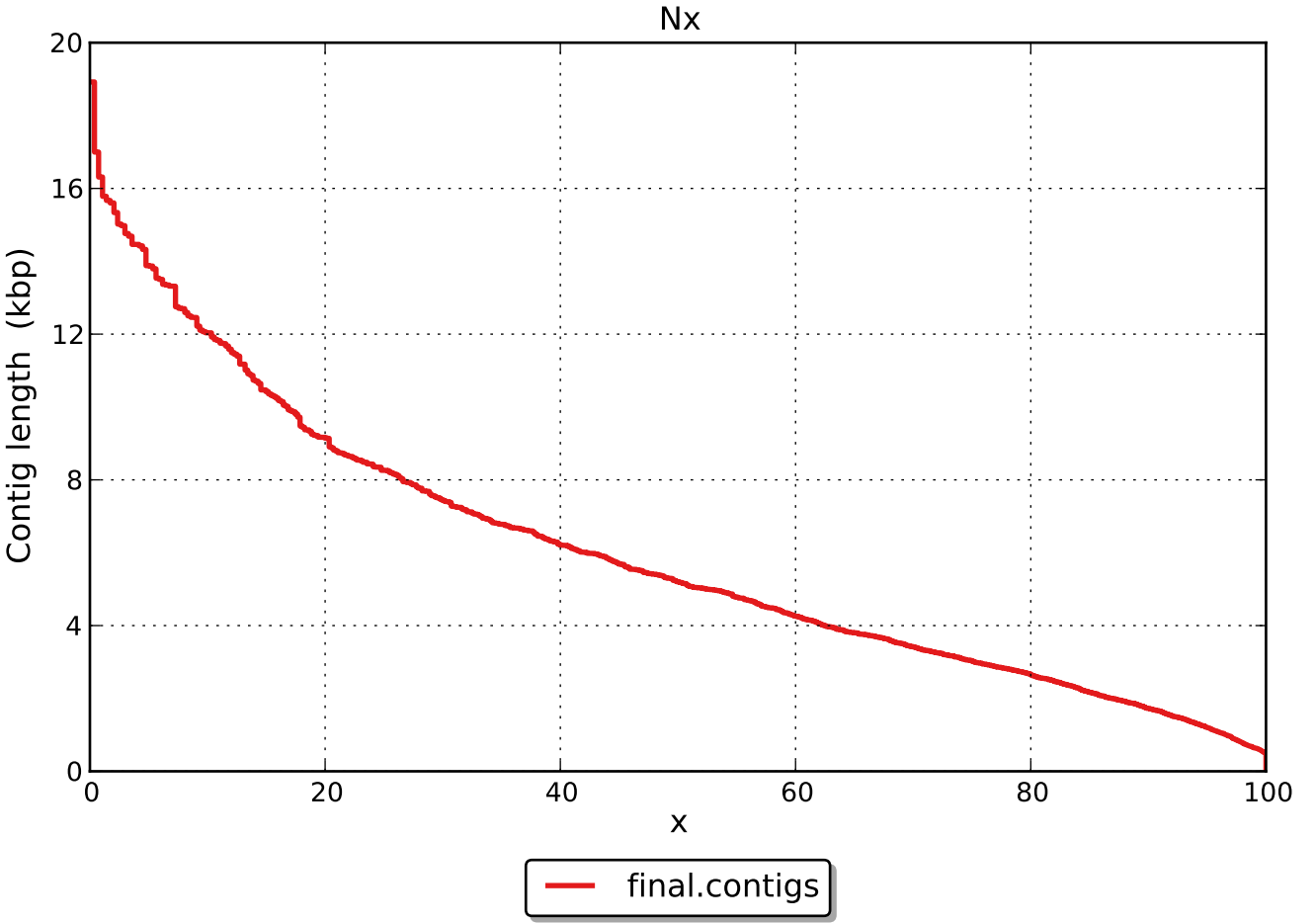
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	56
# indels	0
# short indels	0
# long indels	0
Indels length	0

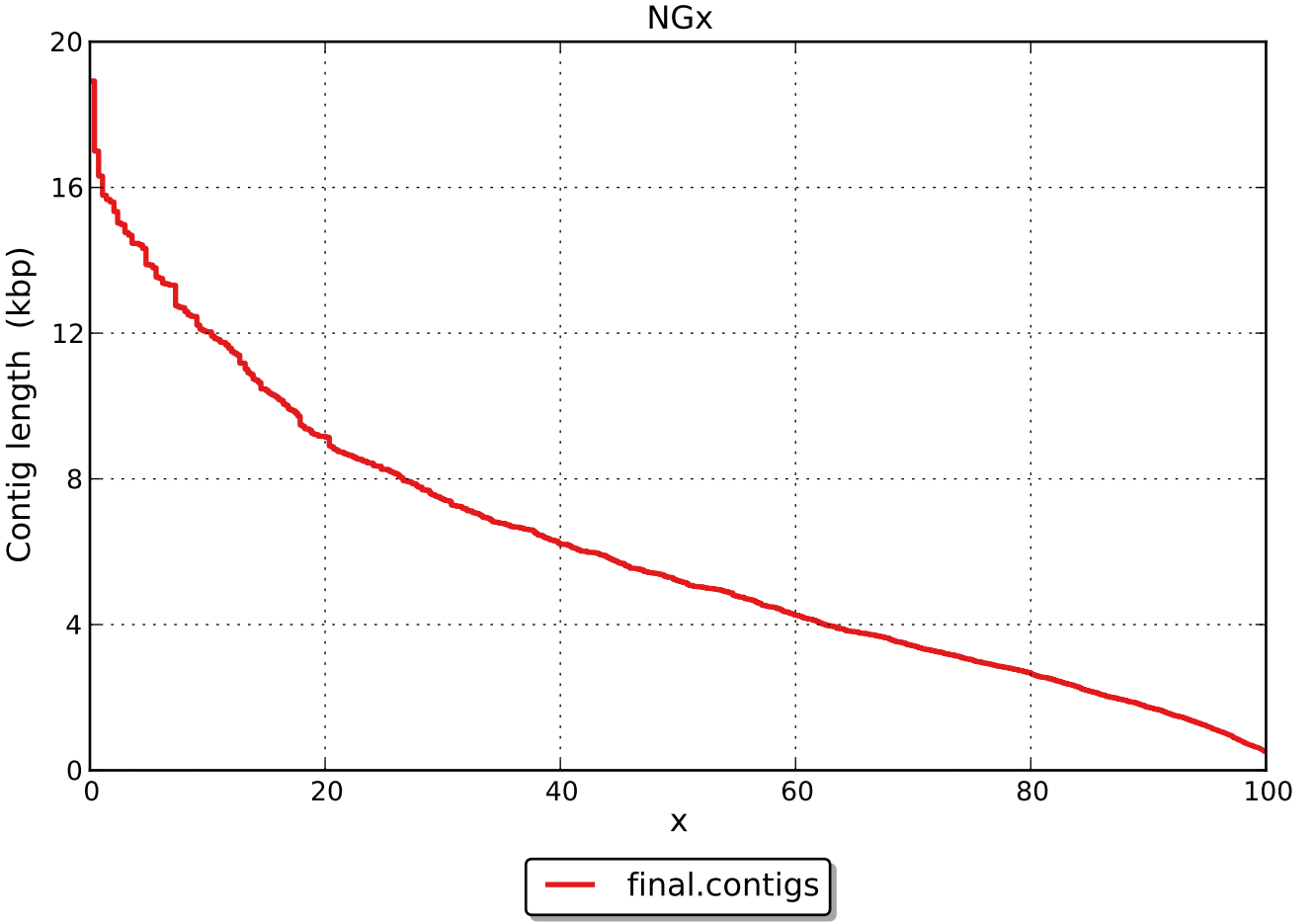
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

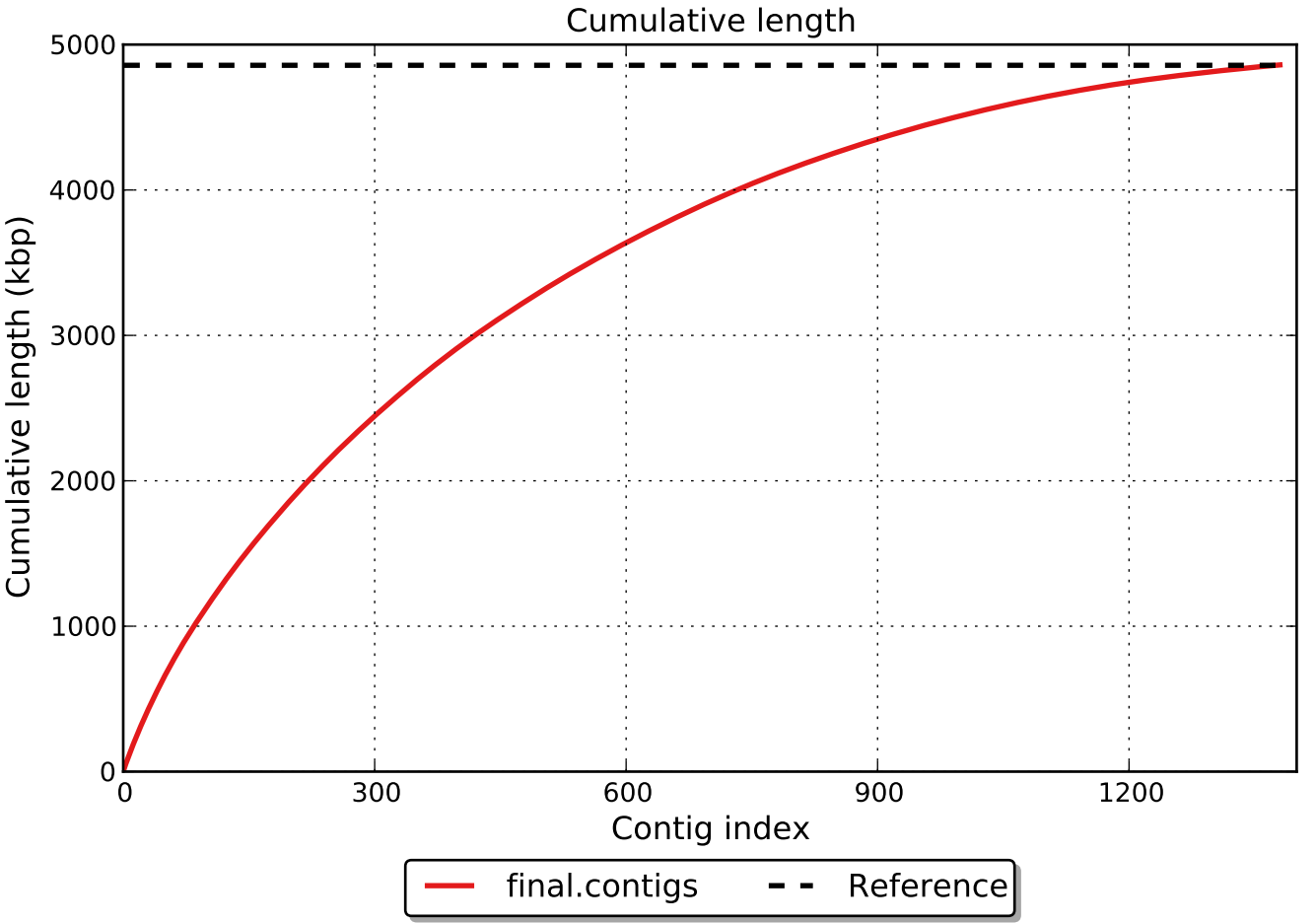
Unaligned report

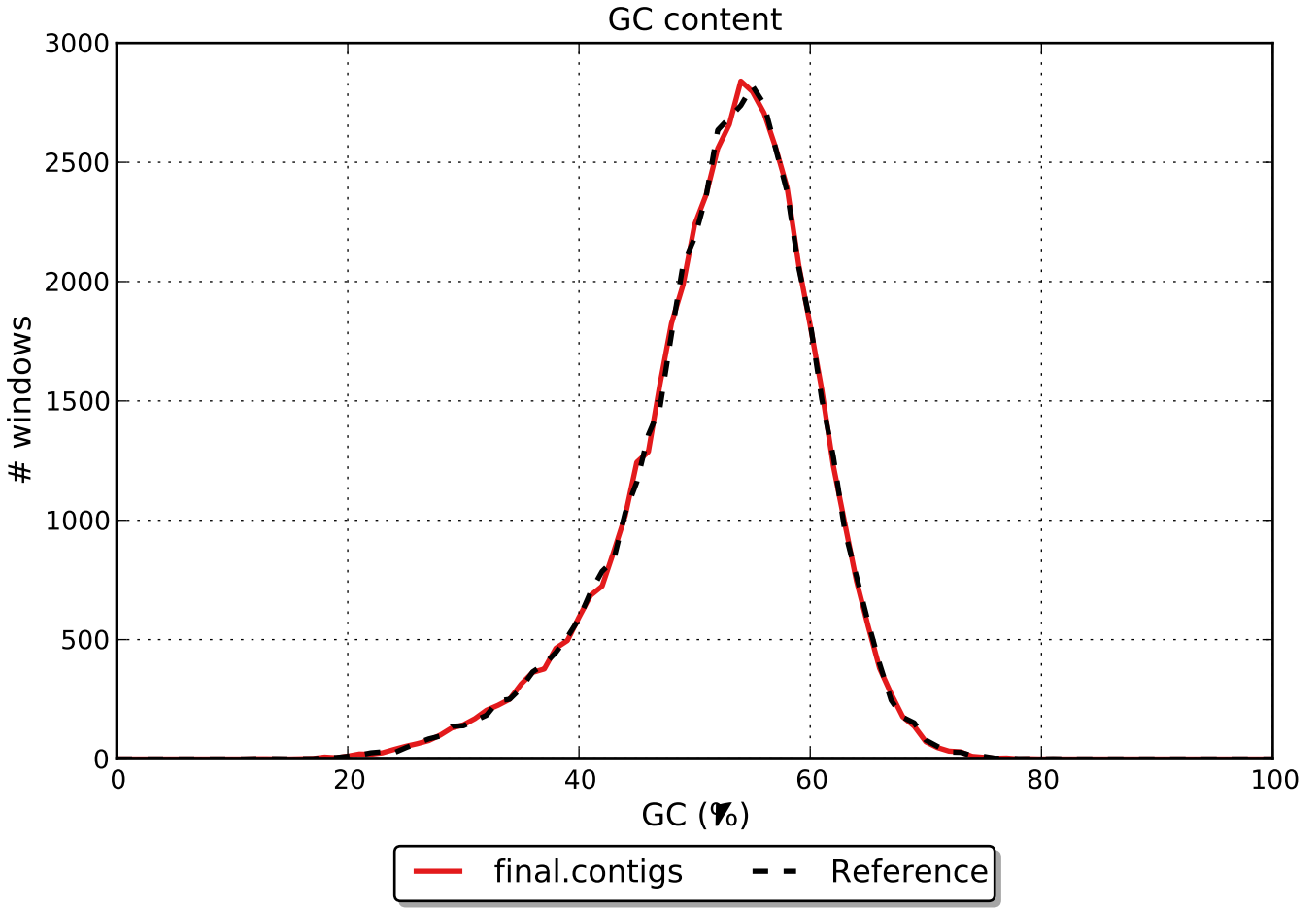
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

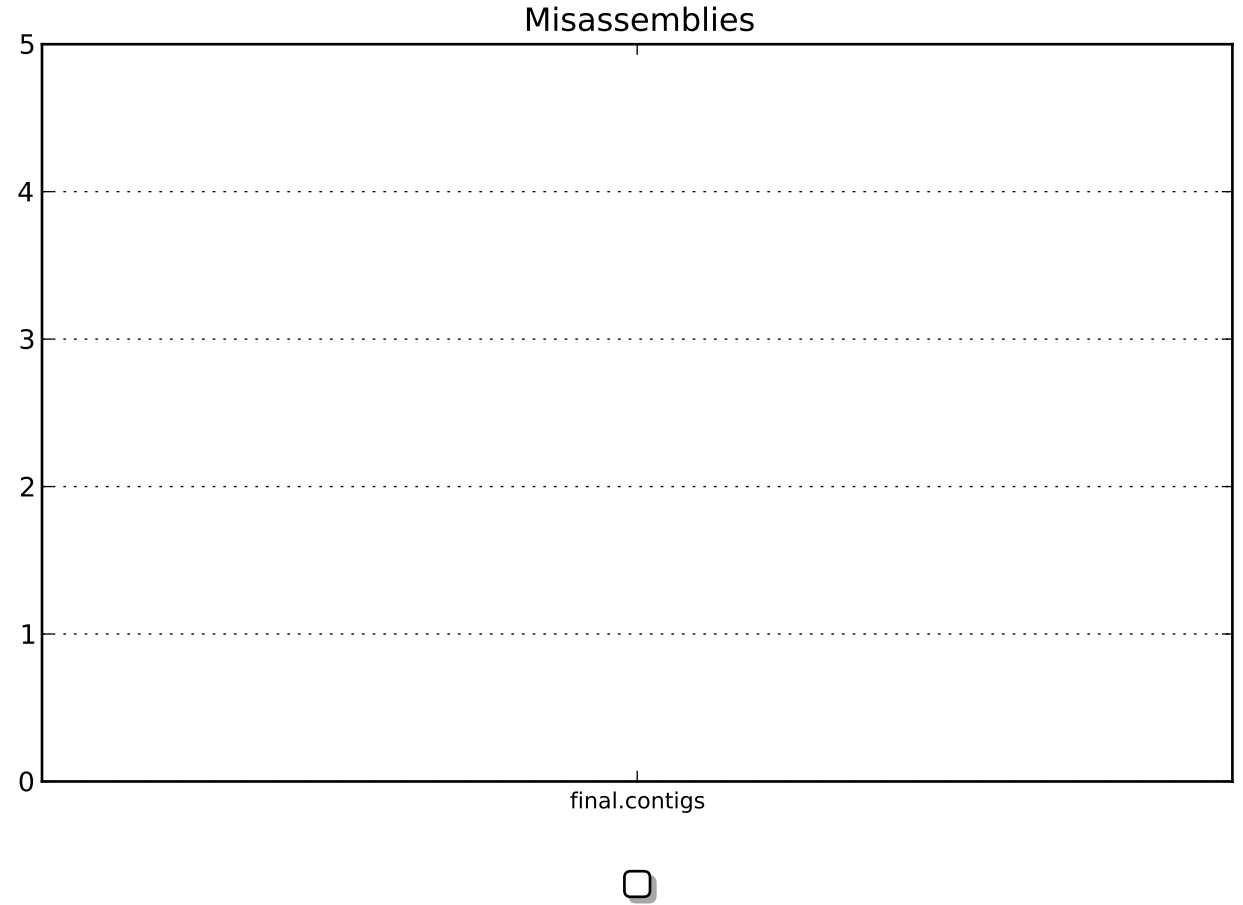
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

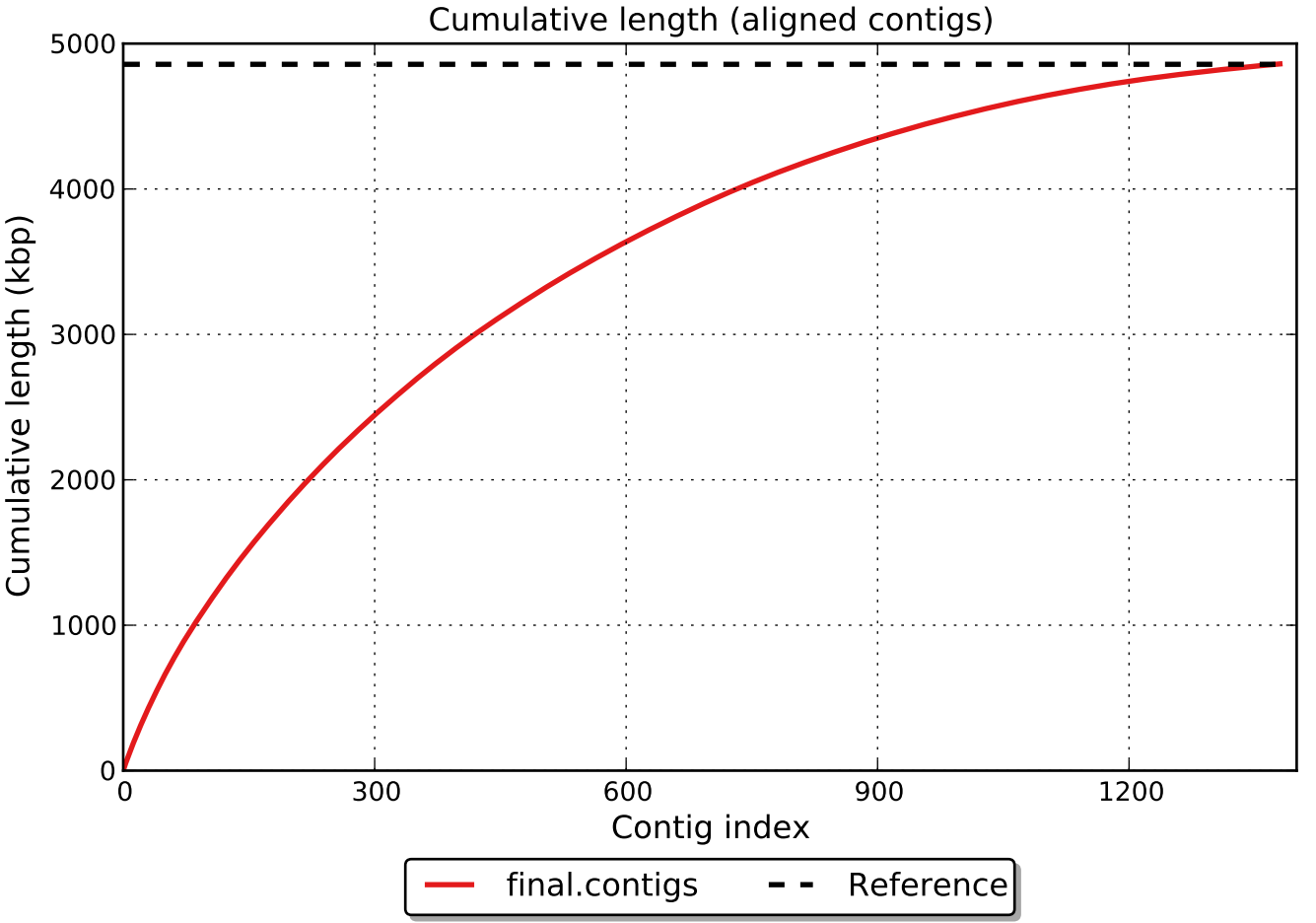

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

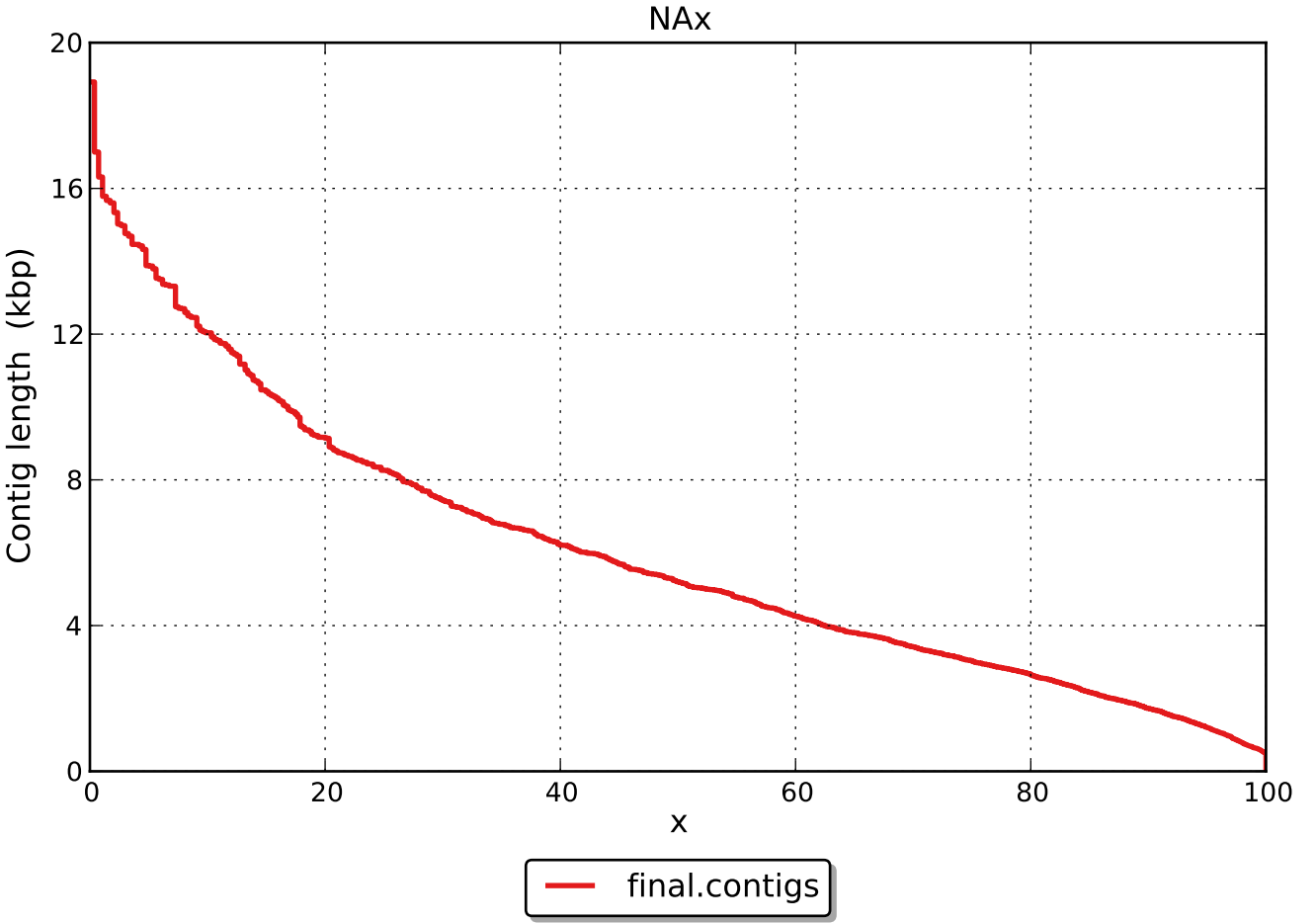

NGx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

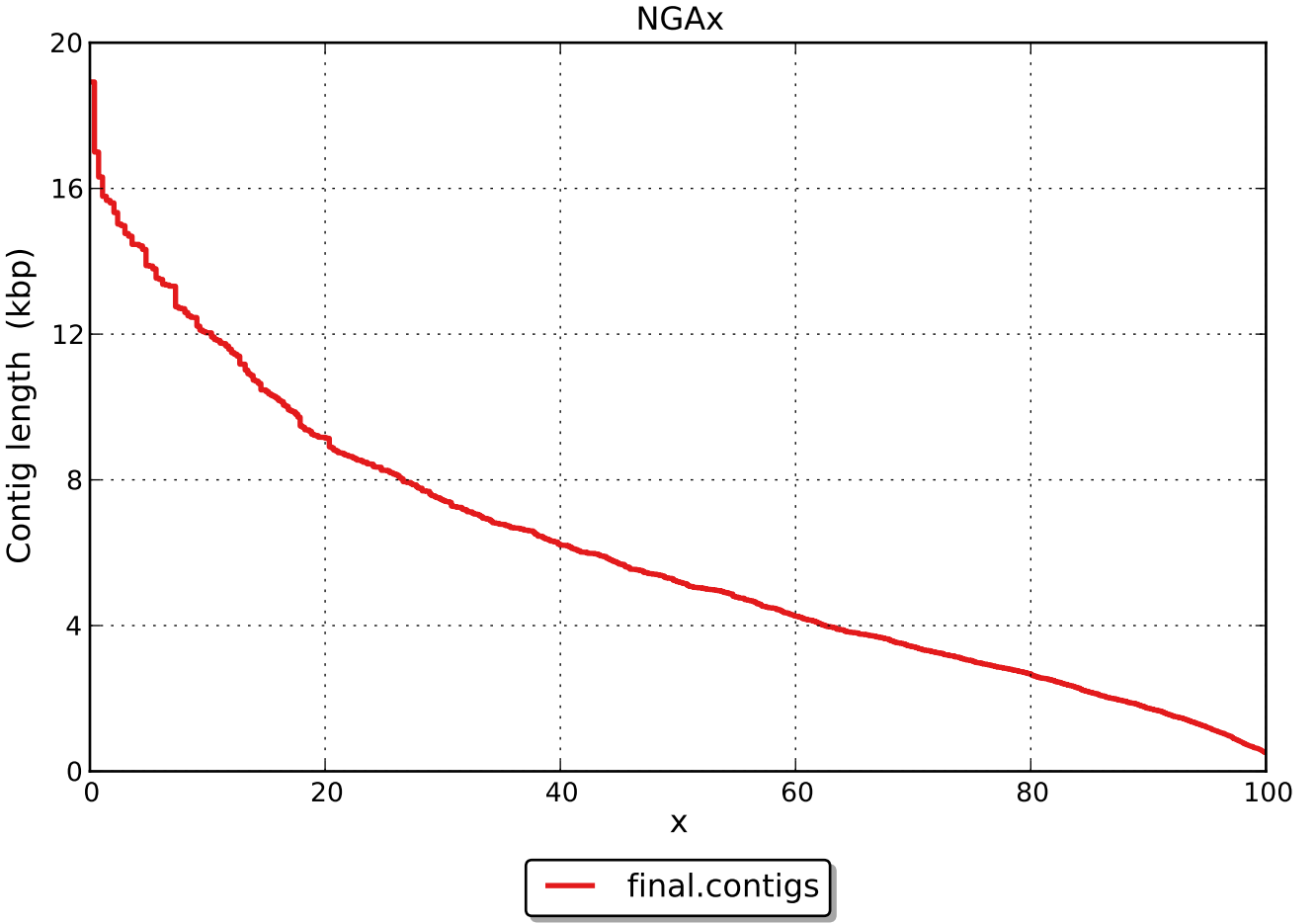

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
final.contigs
Reference


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
300
600
900
1200
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs