Report

	final.contigs
# contigs (>= 1000 bp)	409
# contigs (>= 5000 bp)	278
# contigs (>= 10000 bp)	180
# contigs (>= 25000 bp)	37
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	4814459
Total length (>= 5000 bp)	4454823
Total length (>= 10000 bp)	3728761
Total length (>= 25000 bp)	1385398
Total length (>= 50000 bp)	199824
# contigs	453
Largest contig	74919
Total length	4846610
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	18511
NG50	18511
N75	10564
NG75	10518
L50	86
LG50	86
L75	171
LG75	172
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.659
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.85
# indels per 100 kbp	0.02
Largest alignment	74919
NA50	18511
NGA50	18511
NA75	10564
NGA75	10518
LA50	86
LGA50	86
LA75	171
LGA75	172

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

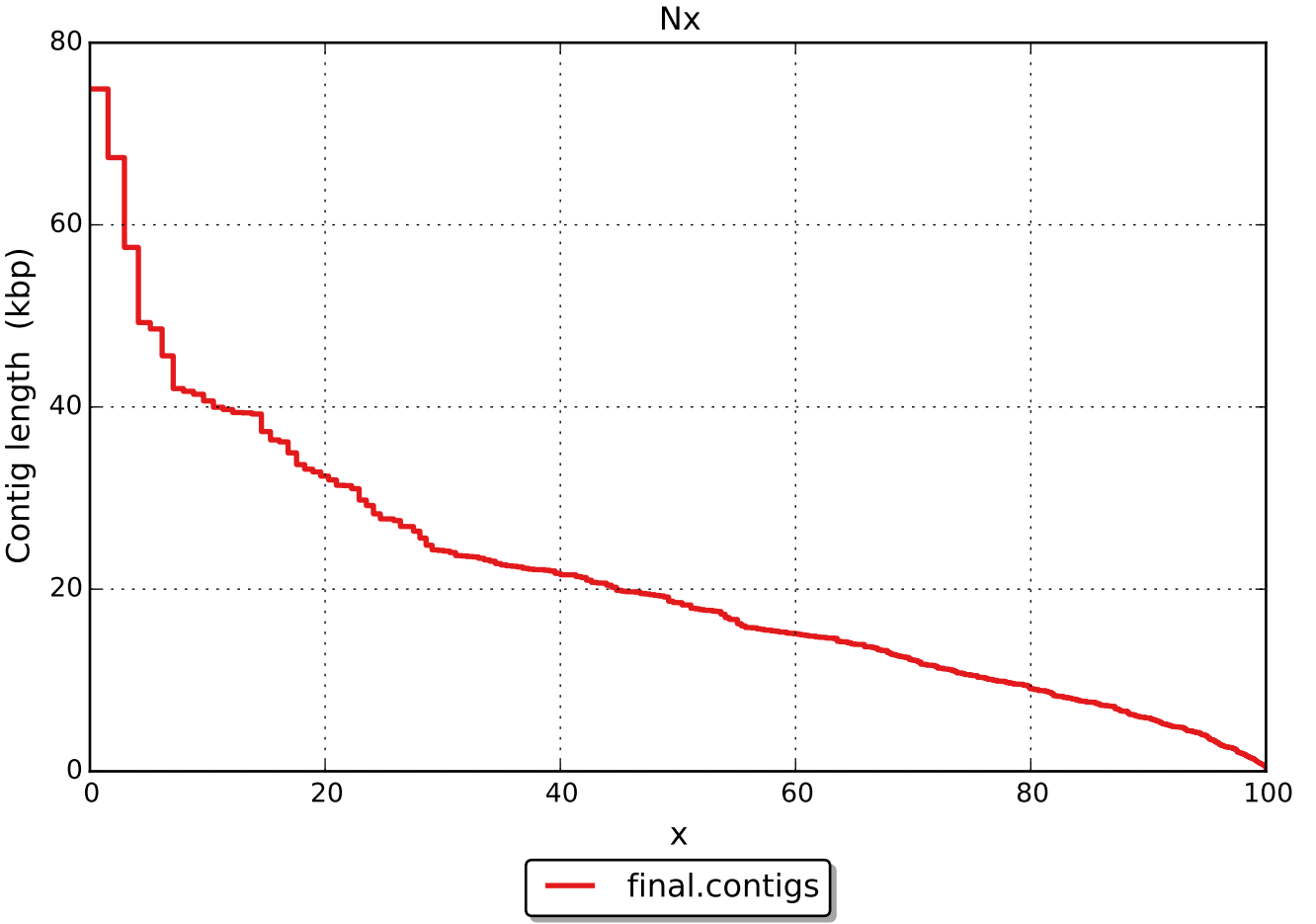
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1670
# indels	1
# short indels	1
# long indels	0
Indels length	1

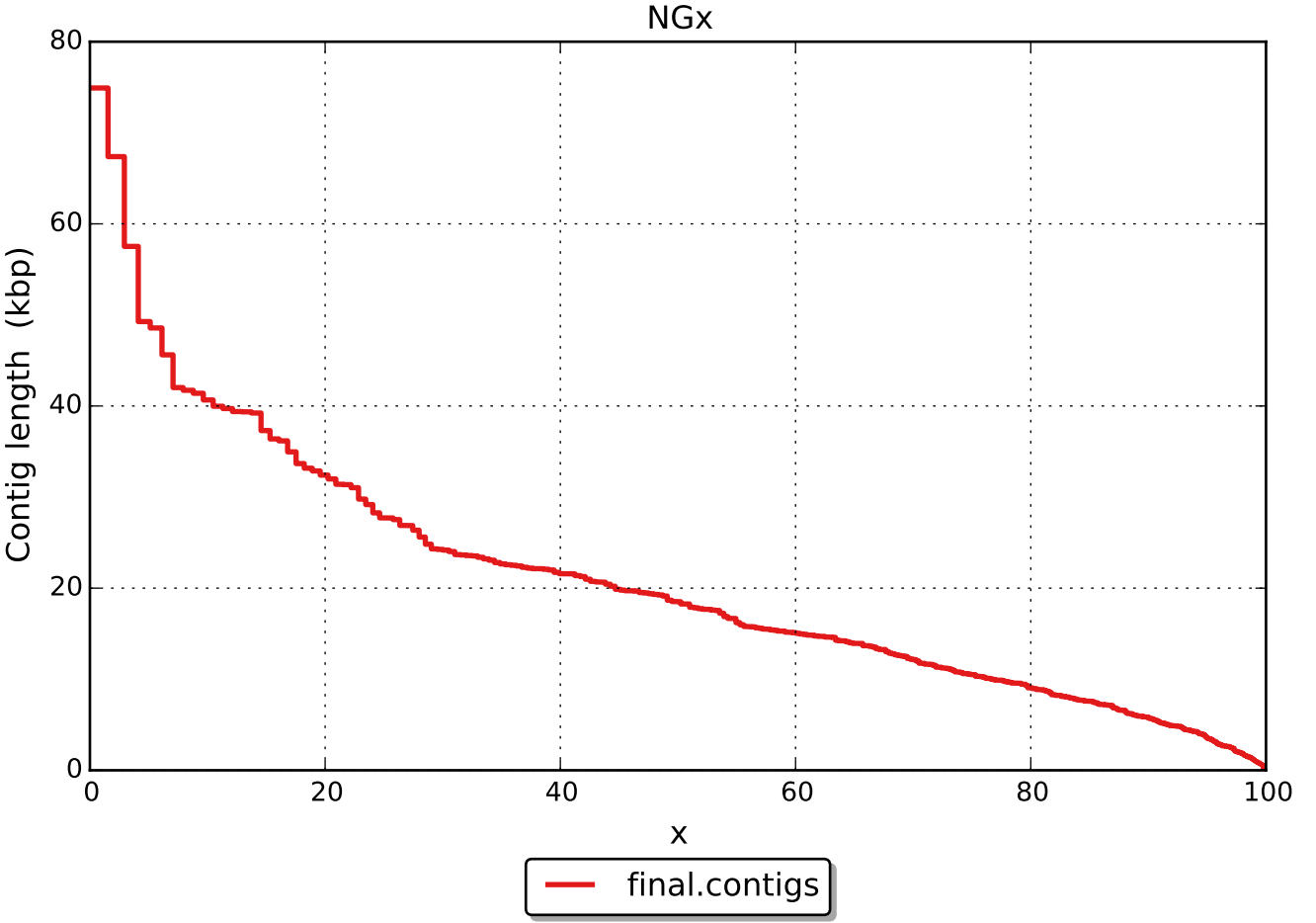
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

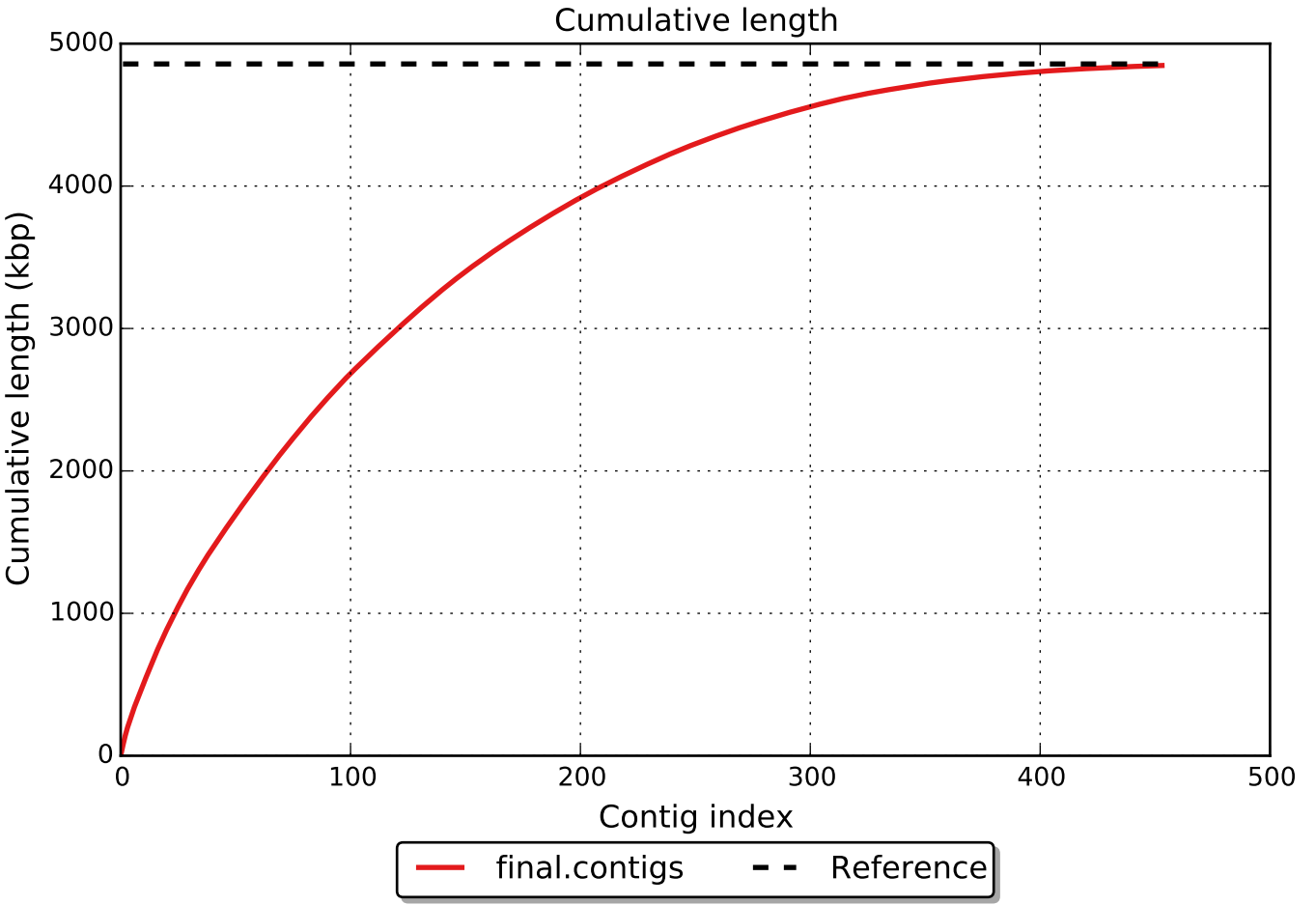
Unaligned report

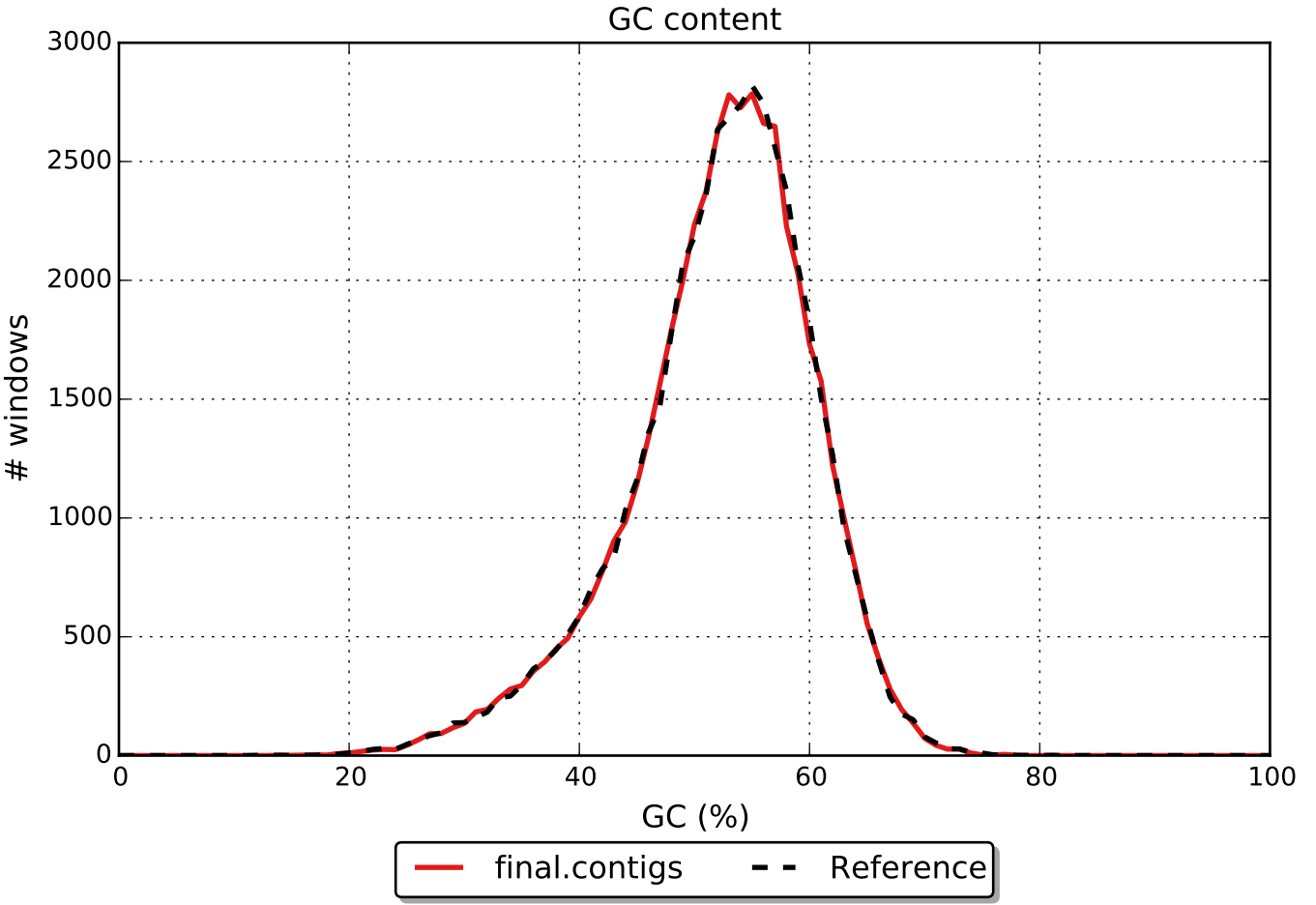
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

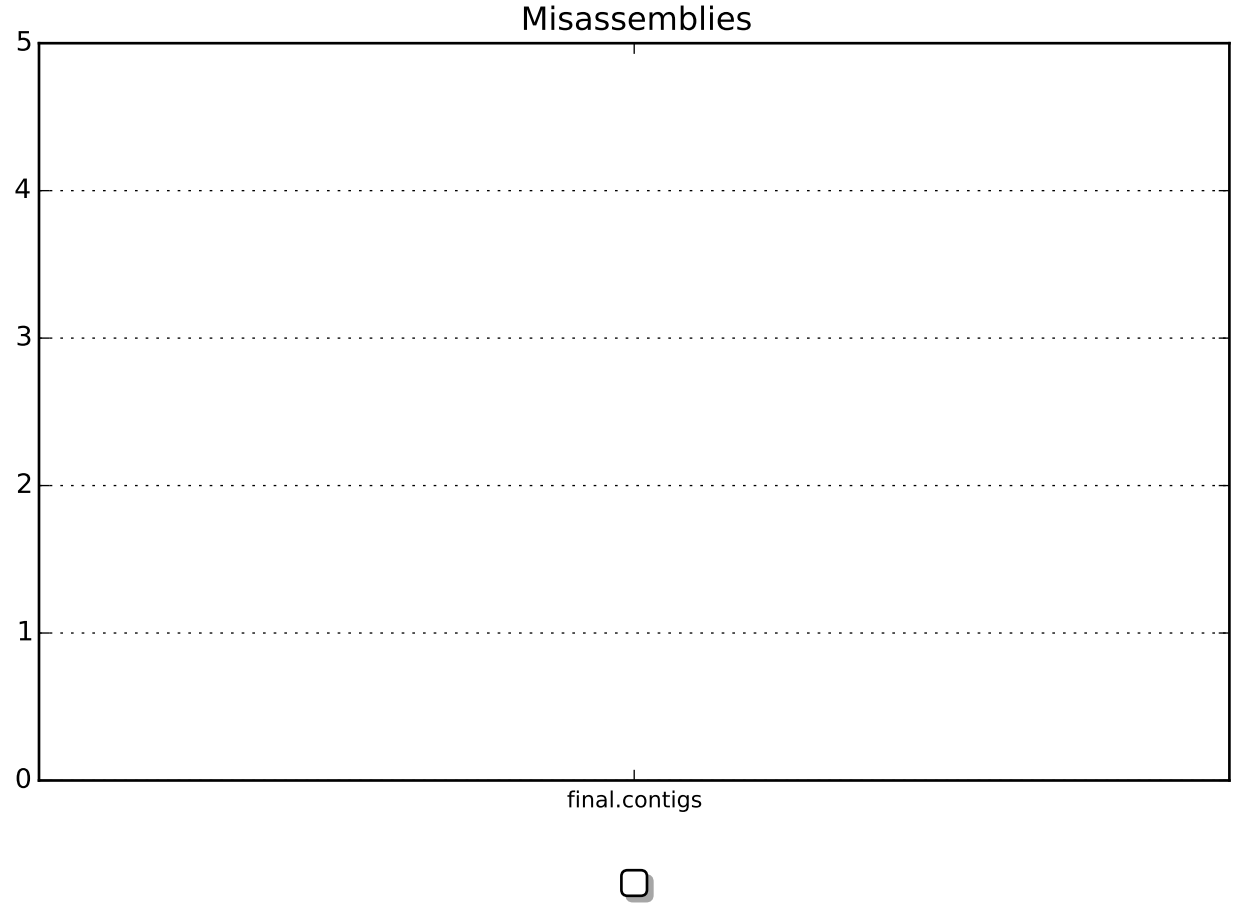
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

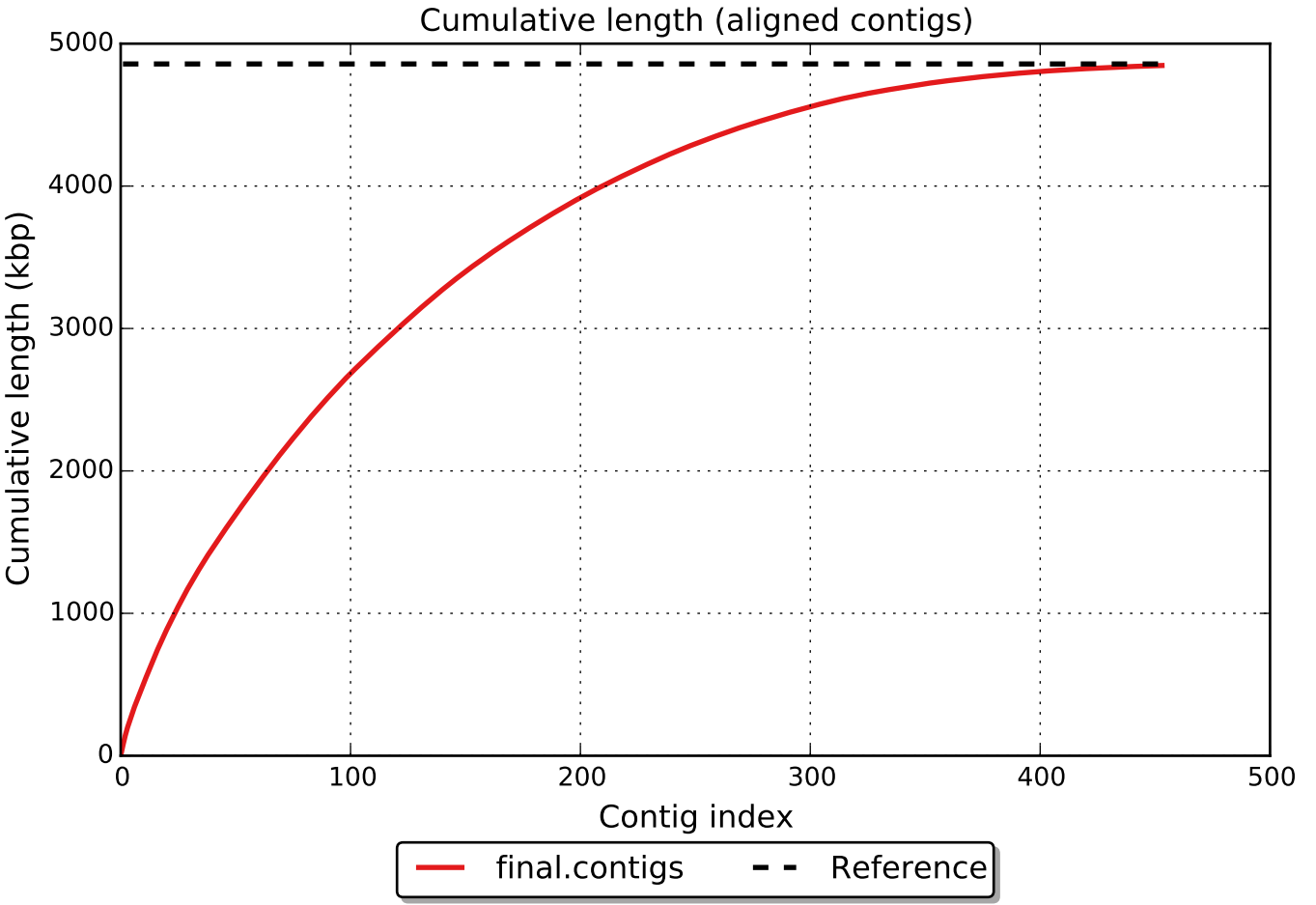

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

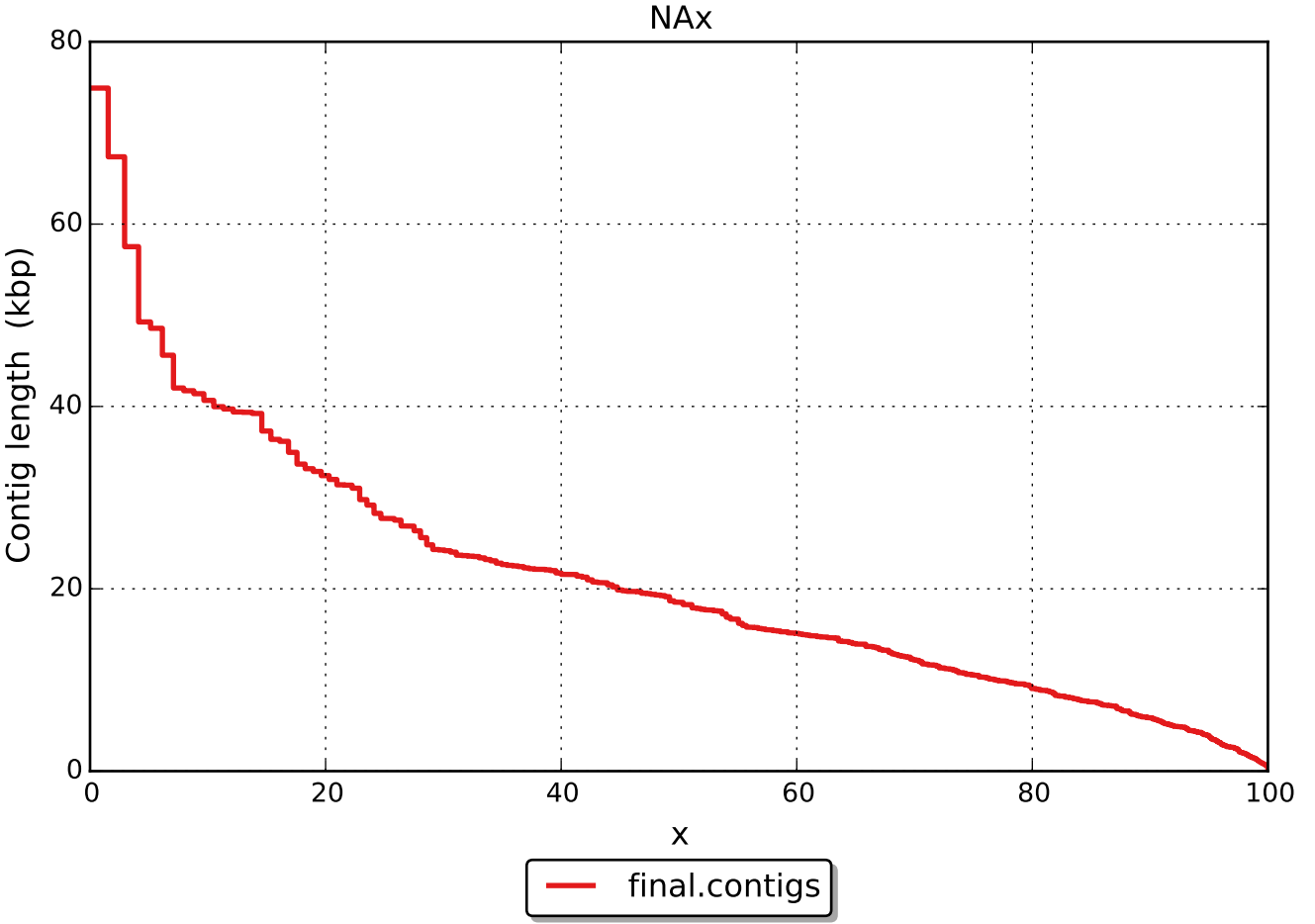

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

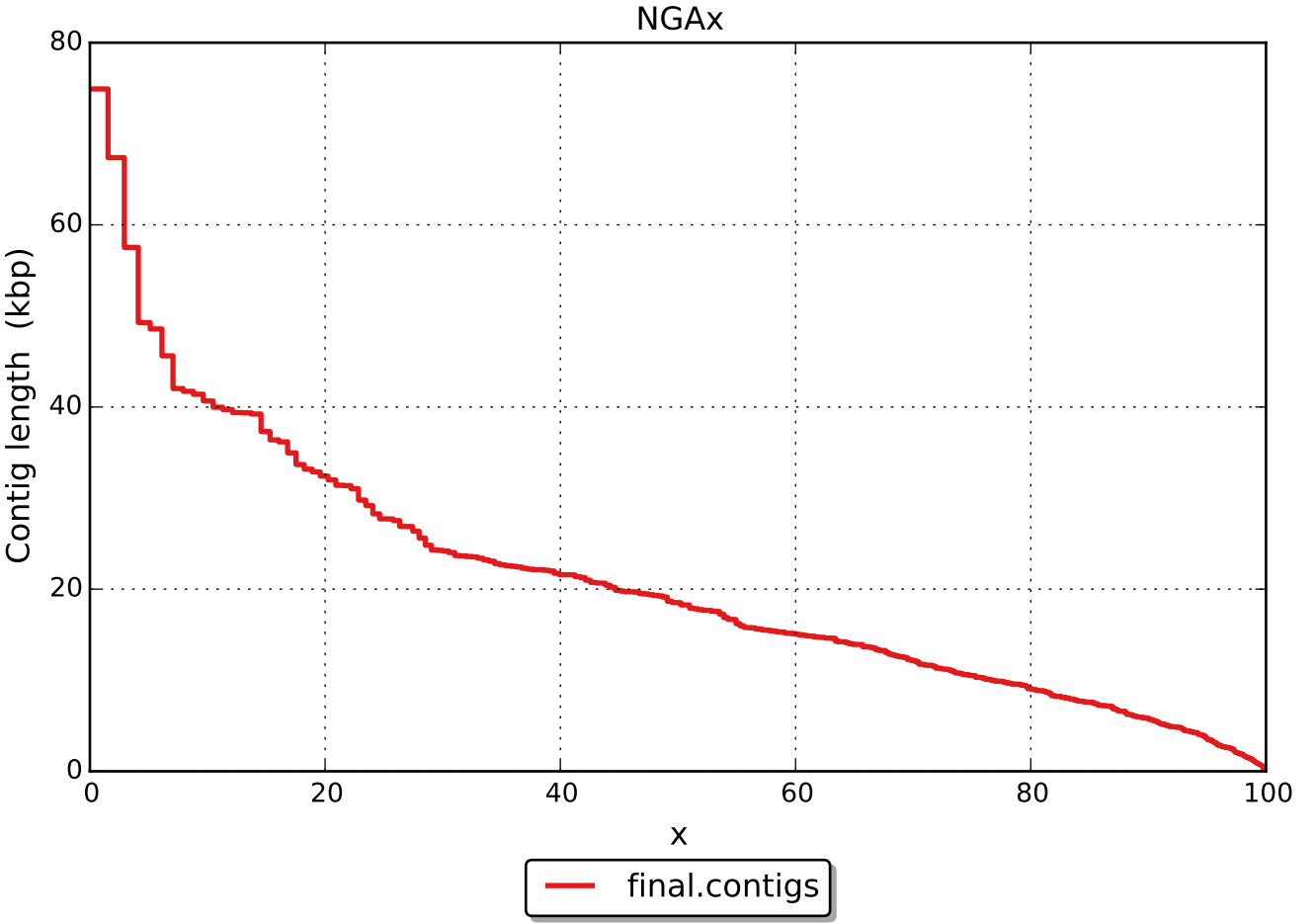

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


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
100
200
300
400
500
Contig index
final.contigs
Reference


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


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