Report

	final.contigs
# contigs (>= 0 bp)	394
# contigs (>= 1000 bp)	272
# contigs (>= 5000 bp)	193
# contigs (>= 10000 bp)	146
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	4630903
Total length (>= 1000 bp)	4582994
Total length (>= 5000 bp)	4350294
Total length (>= 10000 bp)	3982556
Total length (>= 25000 bp)	2567638
Total length (>= 50000 bp)	1039192
# contigs	297
Largest contig	92325
Total length	4599538
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	28183
NG50	28023
N75	15909
NG75	15650
L50	50
LG50	51
L75	103
LG75	105
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	44151
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	63
Genome fraction (%)	98.234
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.91
# indels per 100 kbp	0.07
Largest alignment	92325
NA50	28183
NGA50	28023
NA75	15909
NGA75	15650
LA50	50
LGA50	51
LA75	103
LGA75	105

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

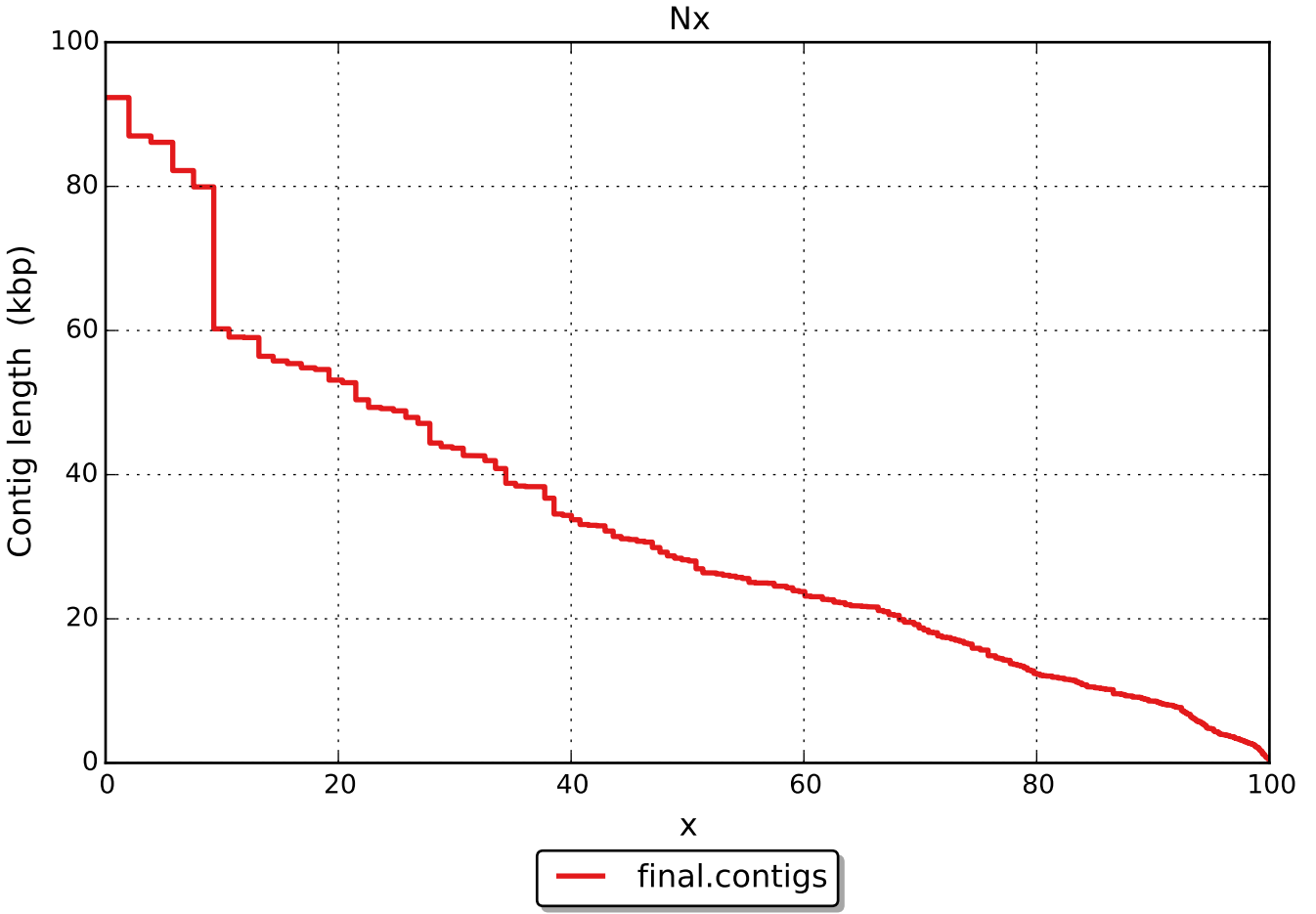
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	44151
# local misassemblies	6
# mismatches	1546
# indels	3
# short indels	3
# long indels	0
Indels length	3

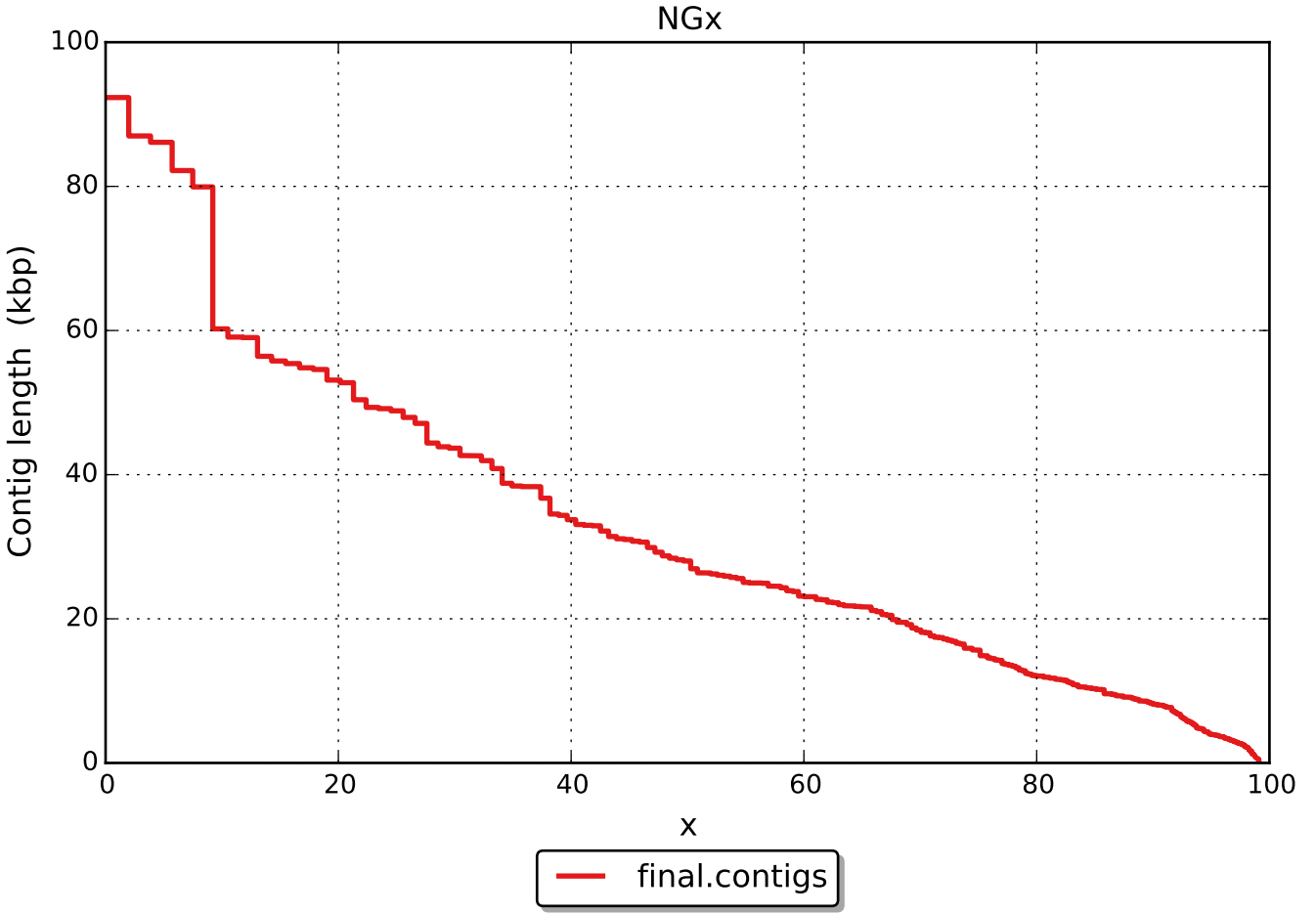
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

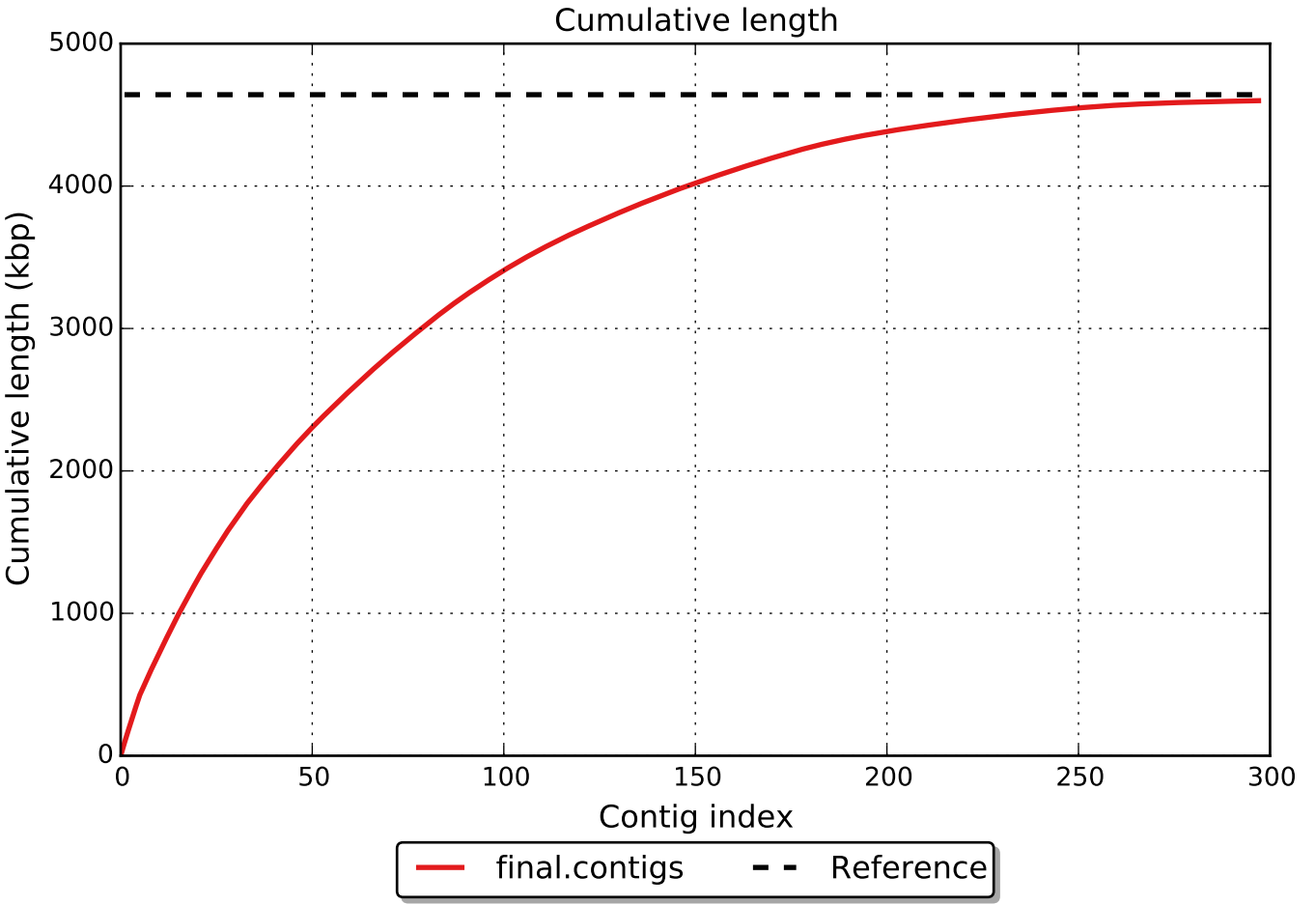
Unaligned report

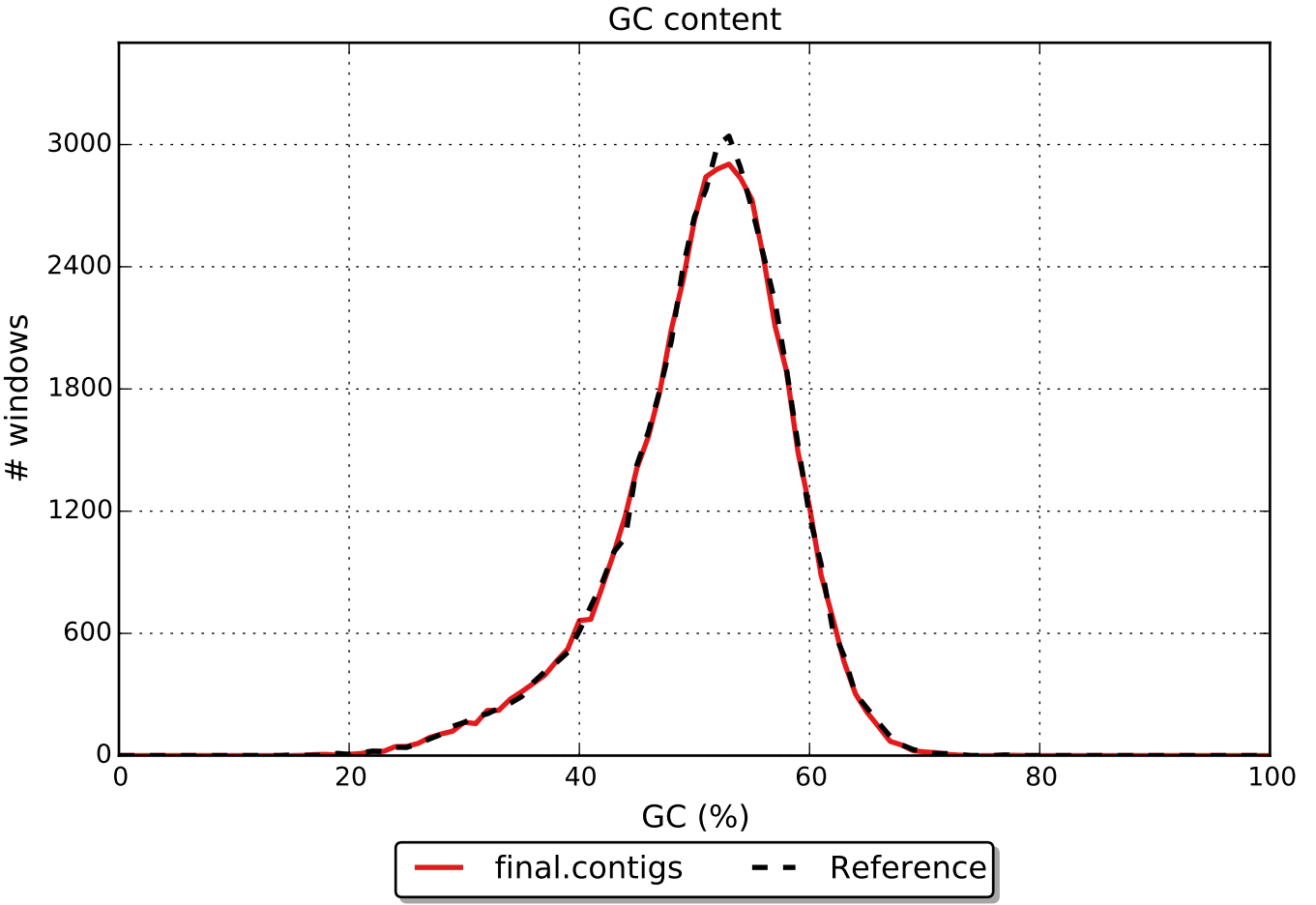
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	63
# N's	0

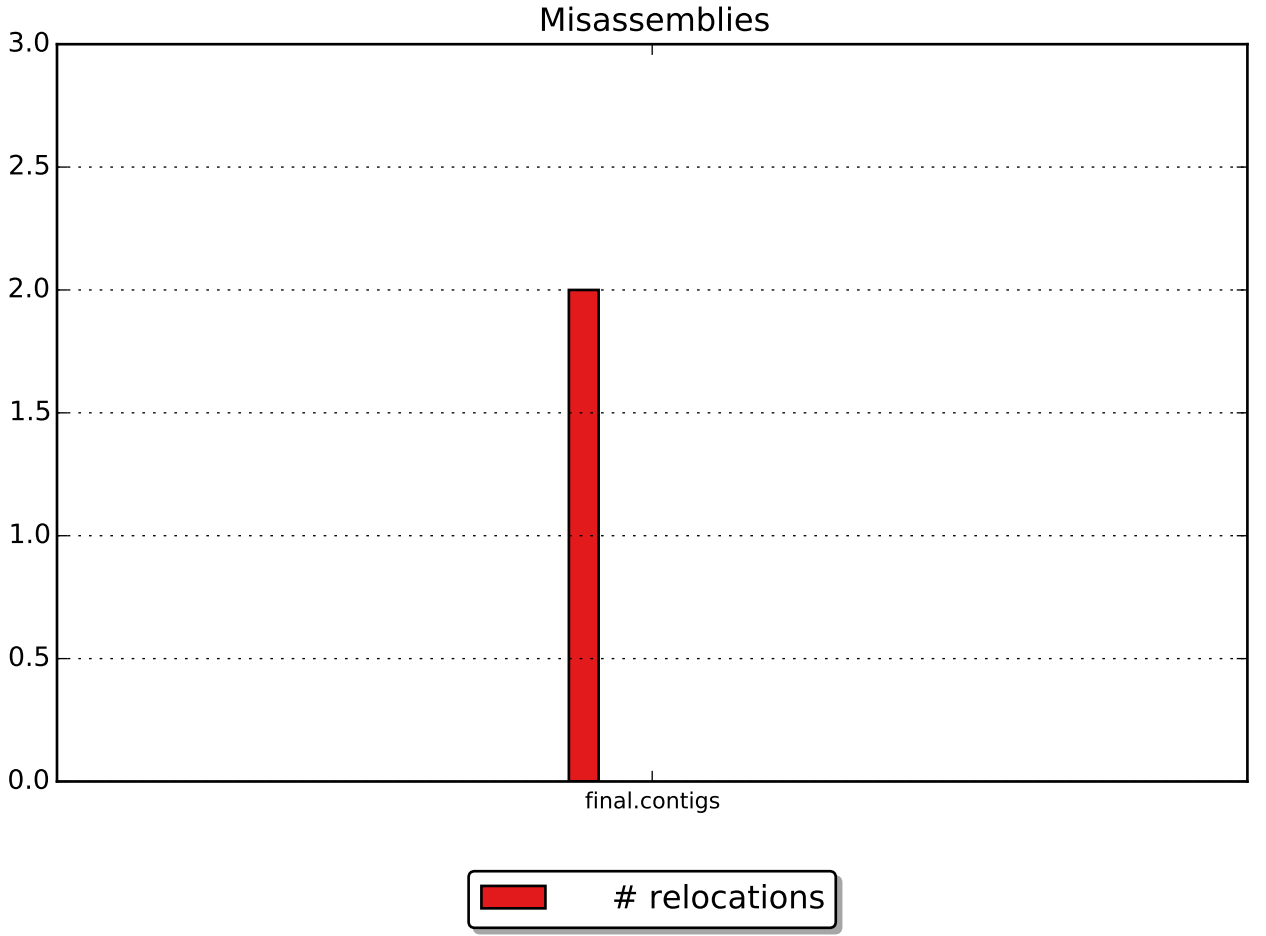
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

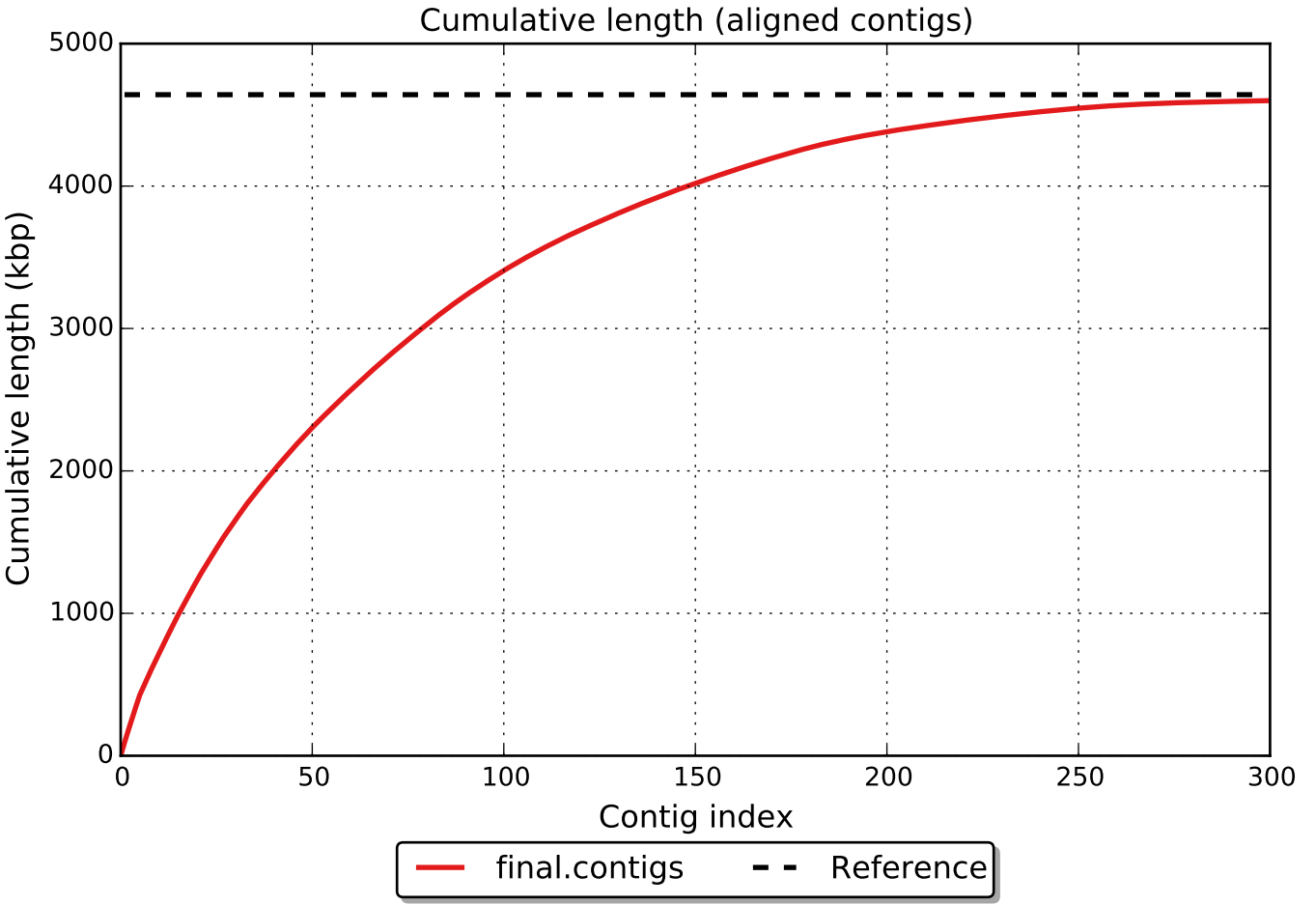

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

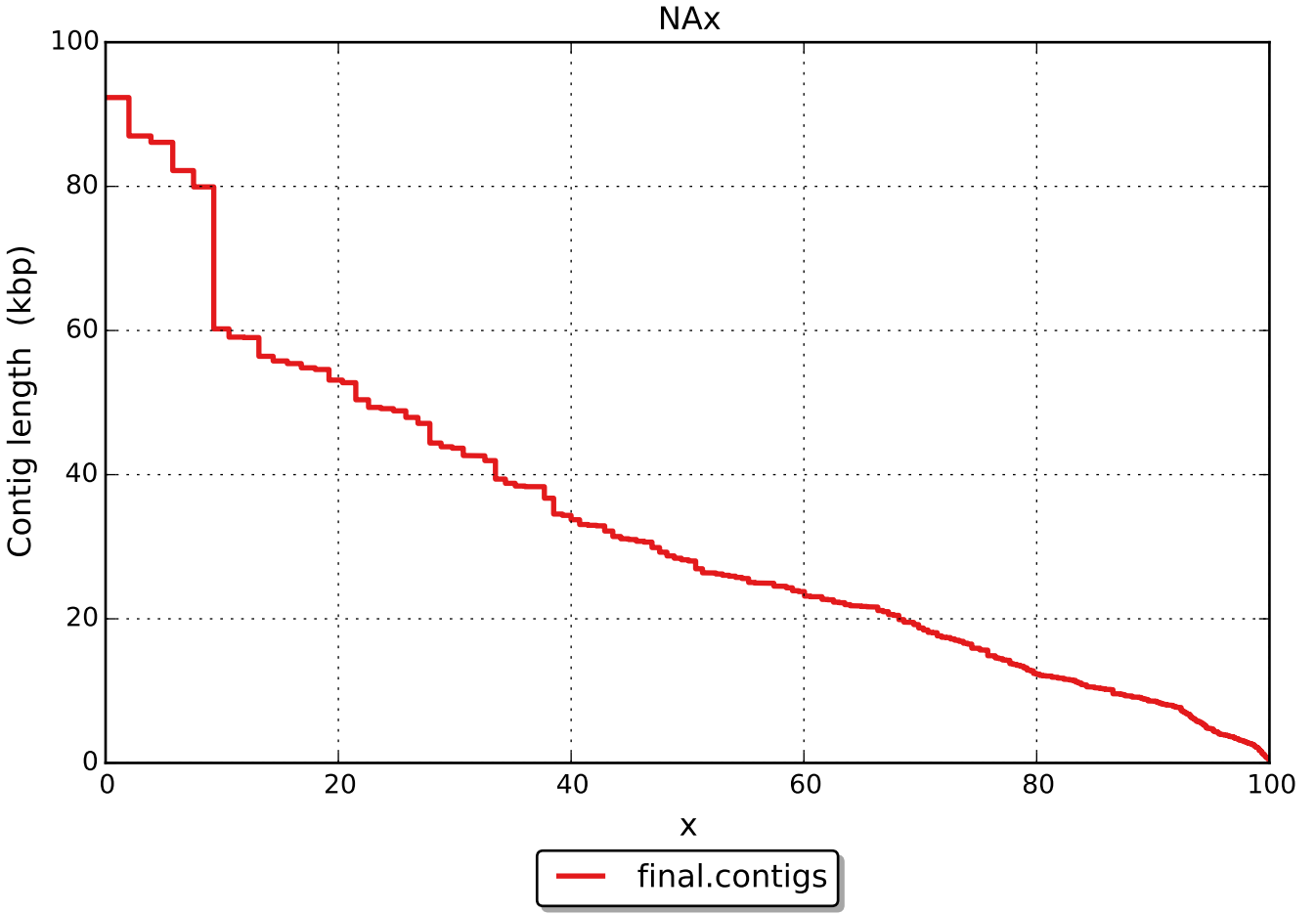

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

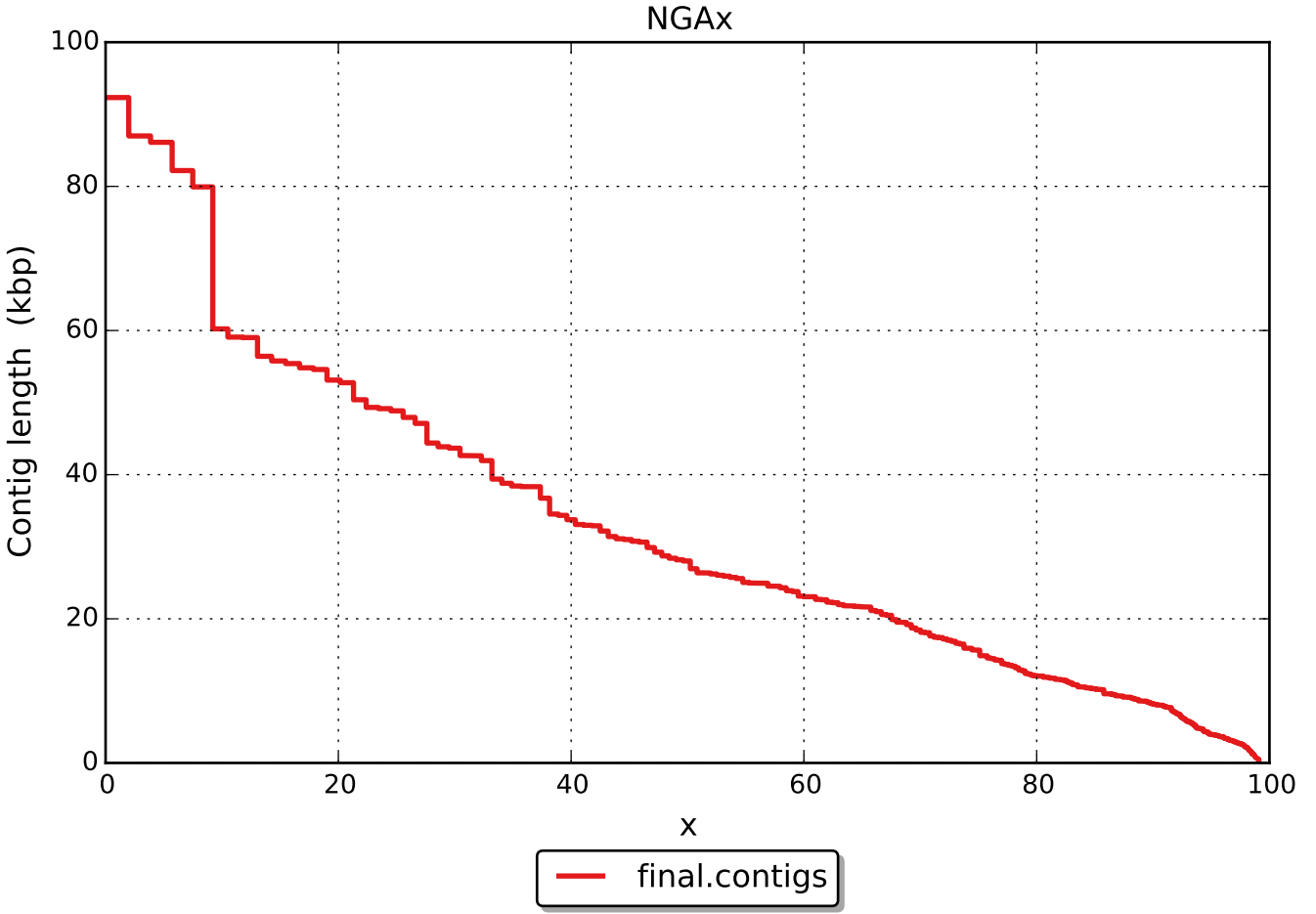

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
final.contigs
Reference


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


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