Report

	final.contigs
# contigs (>= 1000 bp)	321
# contigs (>= 5000 bp)	229
# contigs (>= 10000 bp)	167
# contigs (>= 25000 bp)	58
# contigs (>= 50000 bp)	7
Total length (>= 1000 bp)	4596099
Total length (>= 5000 bp)	4328383
Total length (>= 10000 bp)	3874021
Total length (>= 25000 bp)	2147732
Total length (>= 50000 bp)	449374
# contigs	341
Largest contig	94484
Total length	4609297
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	23507
NG50	23419
N75	12945
NG75	12755
L50	65
LG50	66
L75	131
LG75	133
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	23372
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.306
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	50.60
# indels per 100 kbp	0.09
Largest alignment	94484
NA50	23507
NGA50	23419
NA75	12945
NGA75	12755
LA50	65
LGA50	66
LA75	131
LGA75	133

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

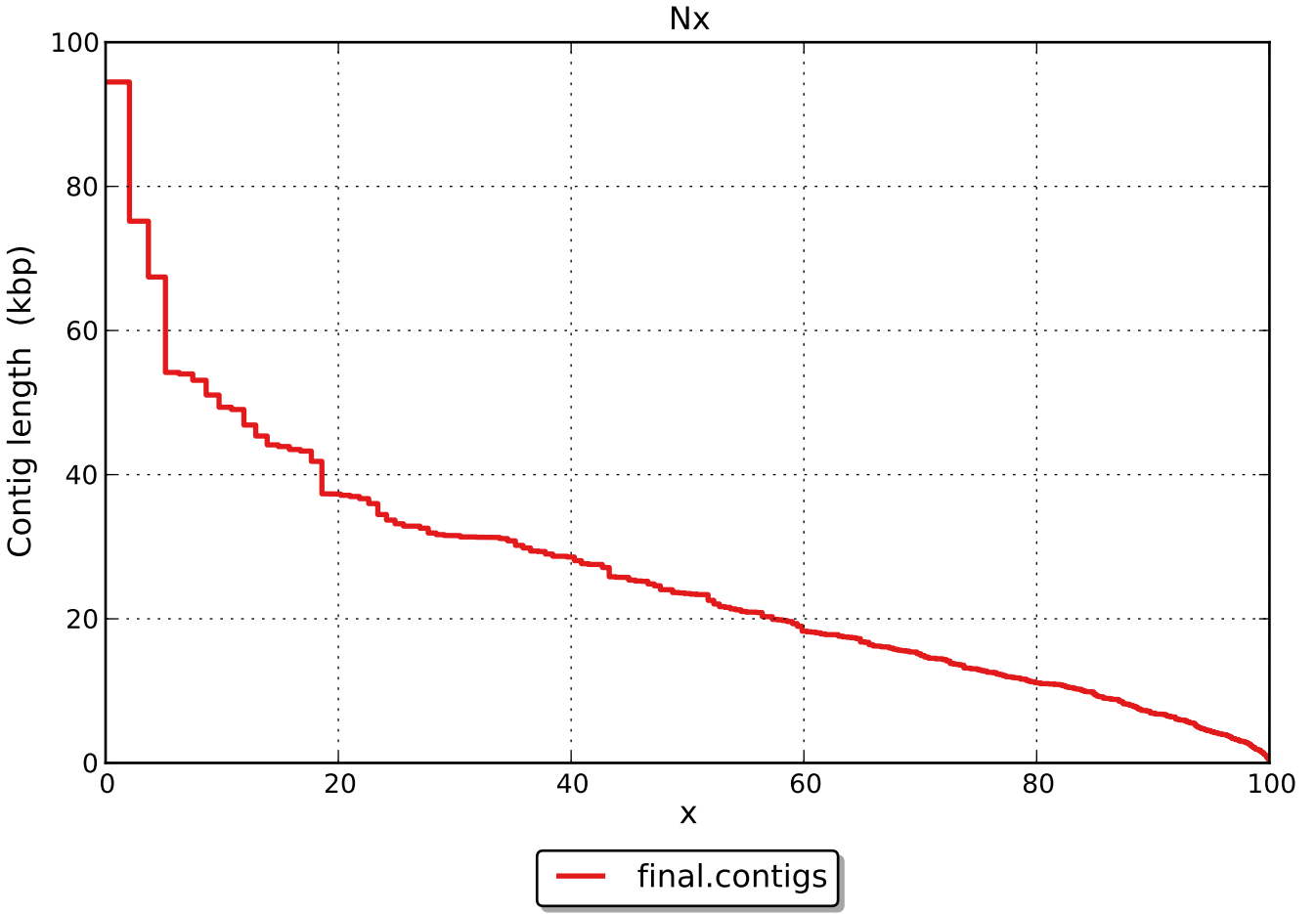
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	23372
# local misassemblies	9
# mismatches	2309
# indels	4
# short indels	4
# long indels	0
Indels length	4

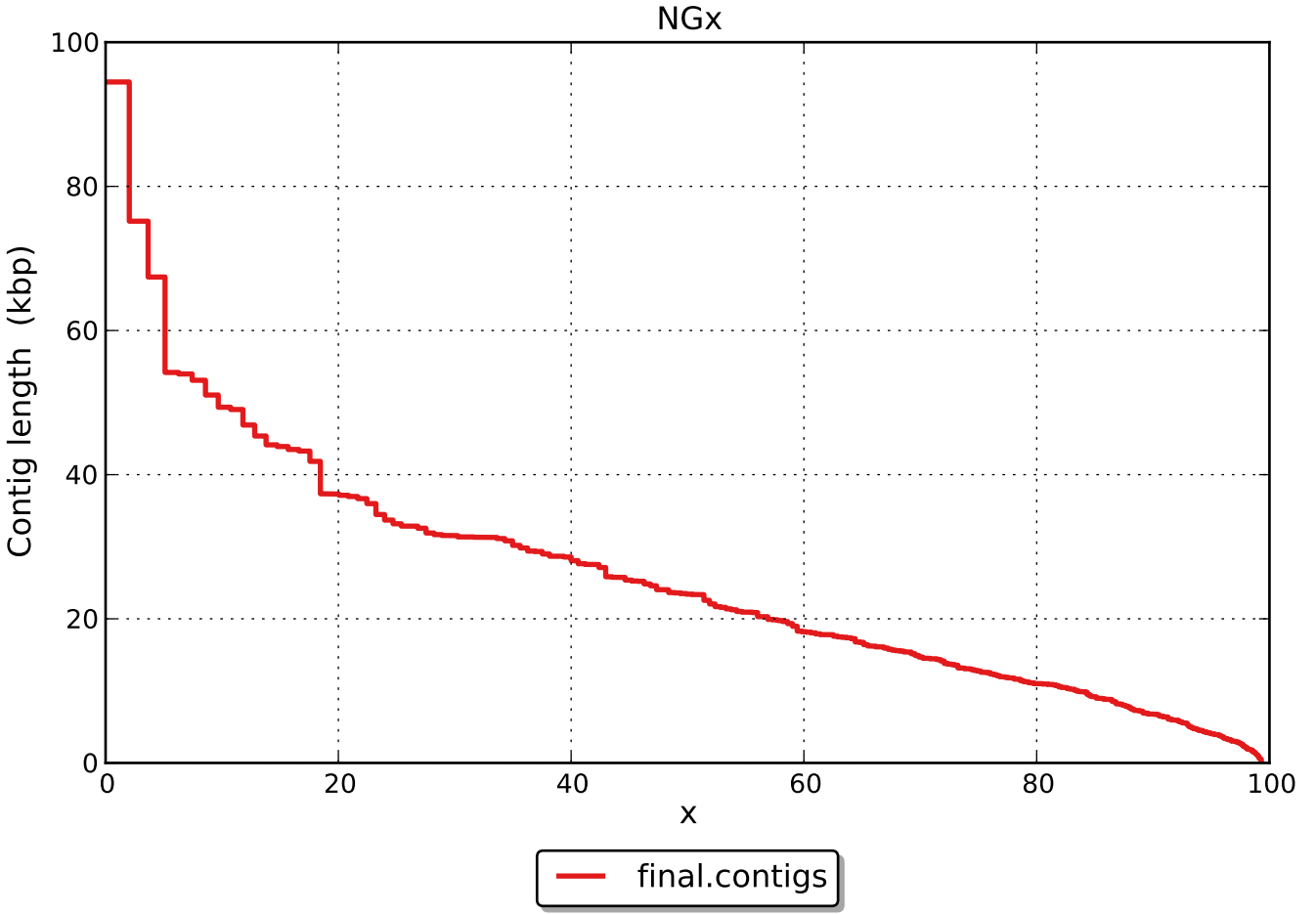
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

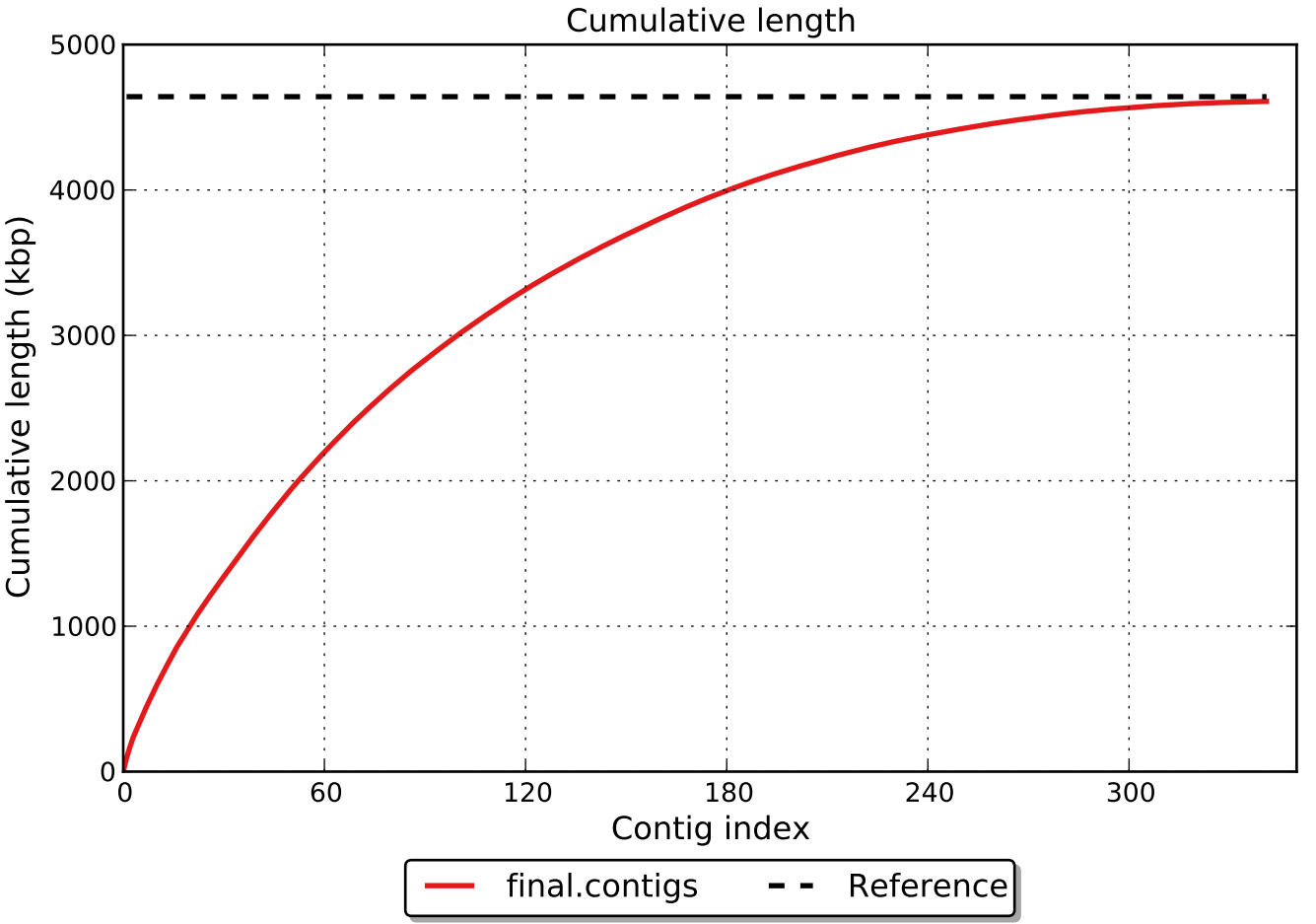
Unaligned report

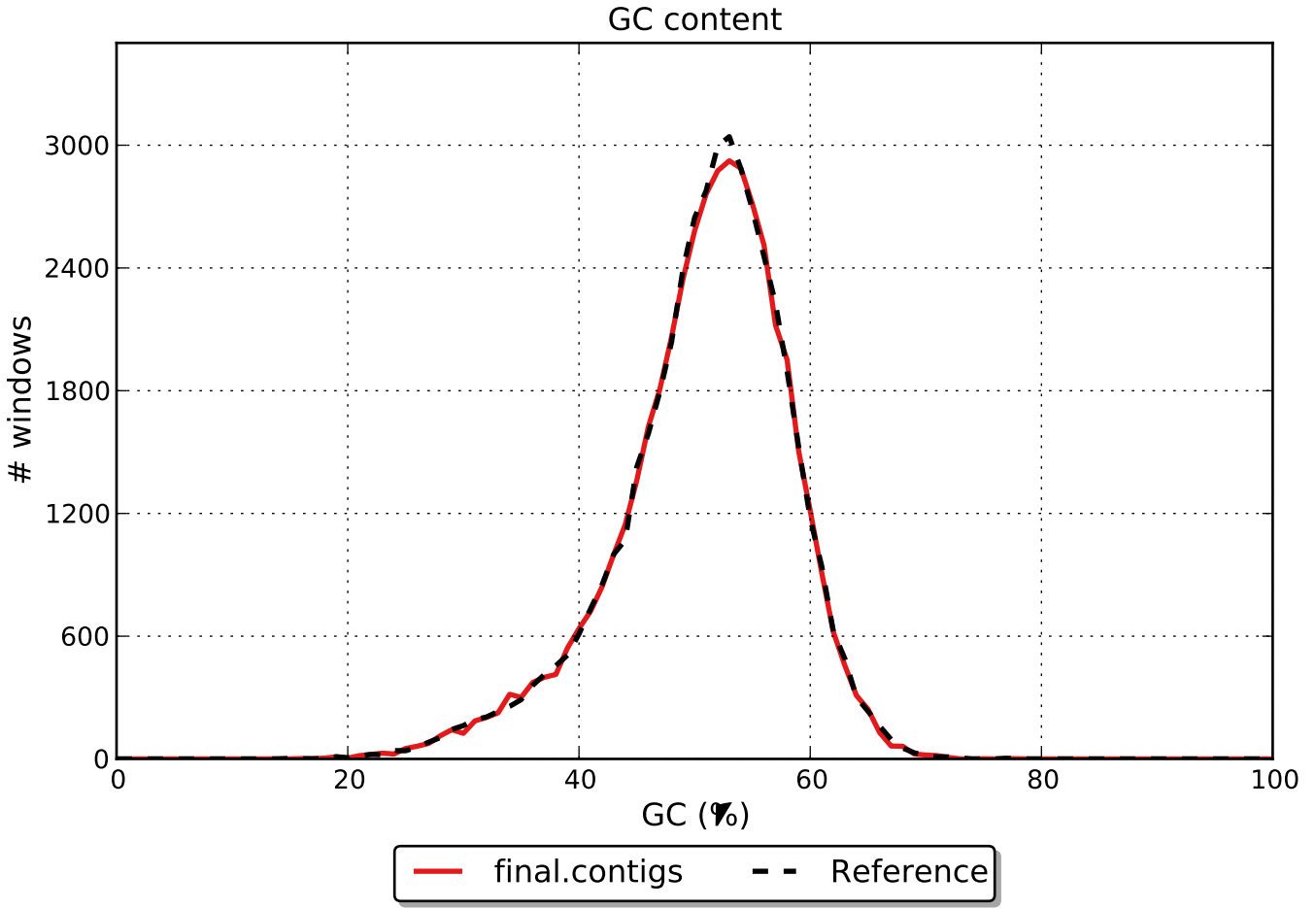
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

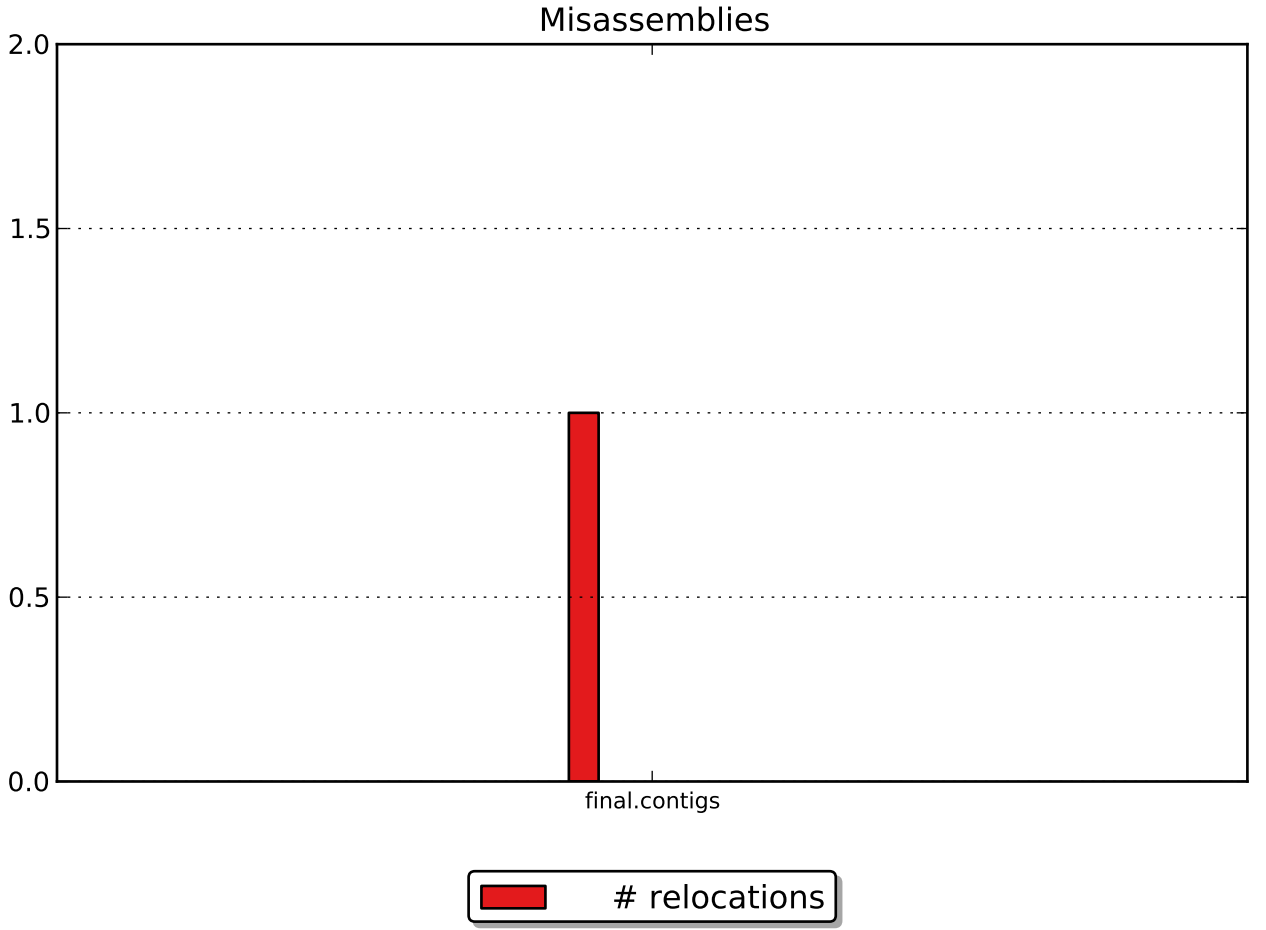
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

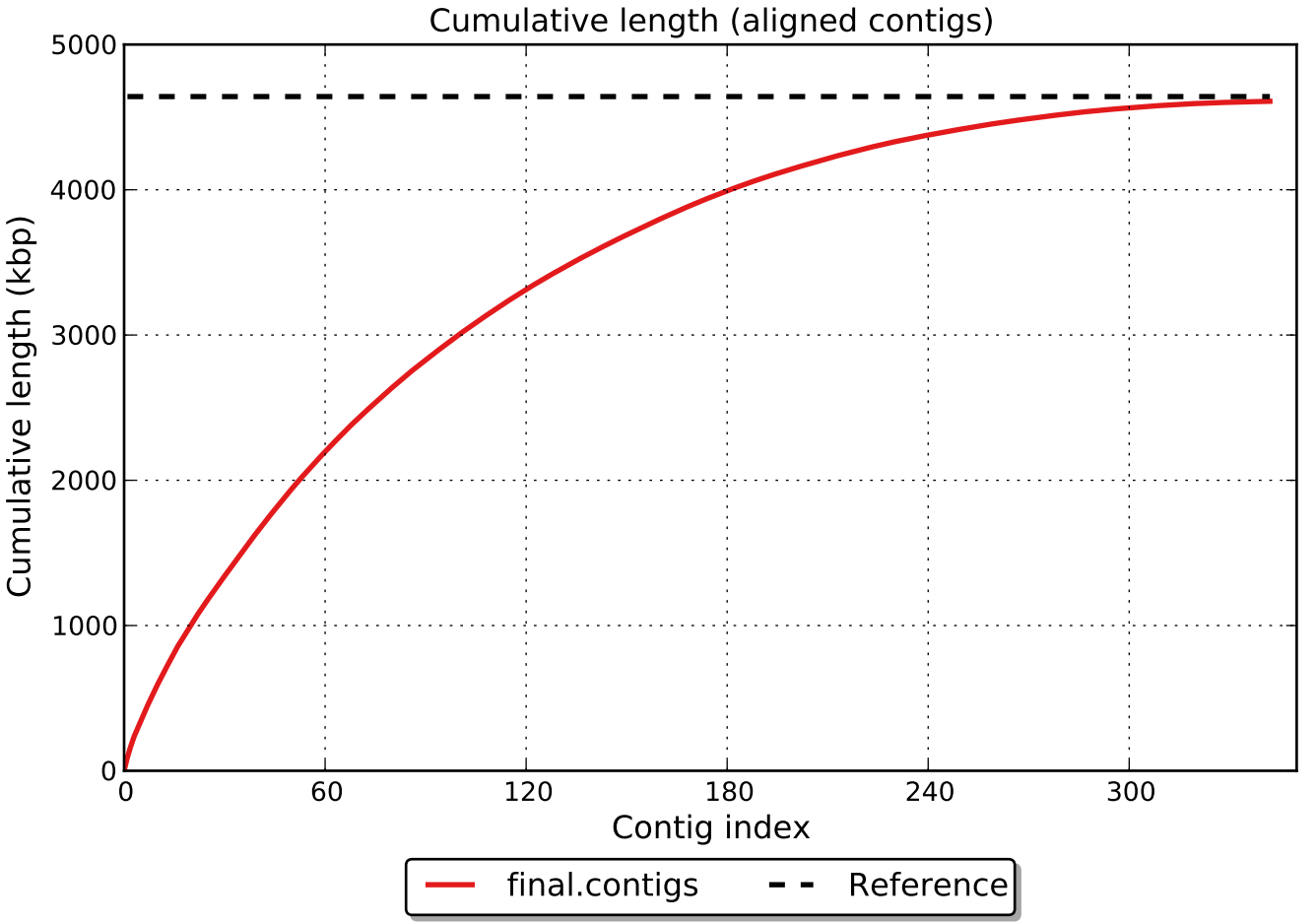

Nx
Contig length (kbp)
x
0
20
40
60
80
100
final.contigs

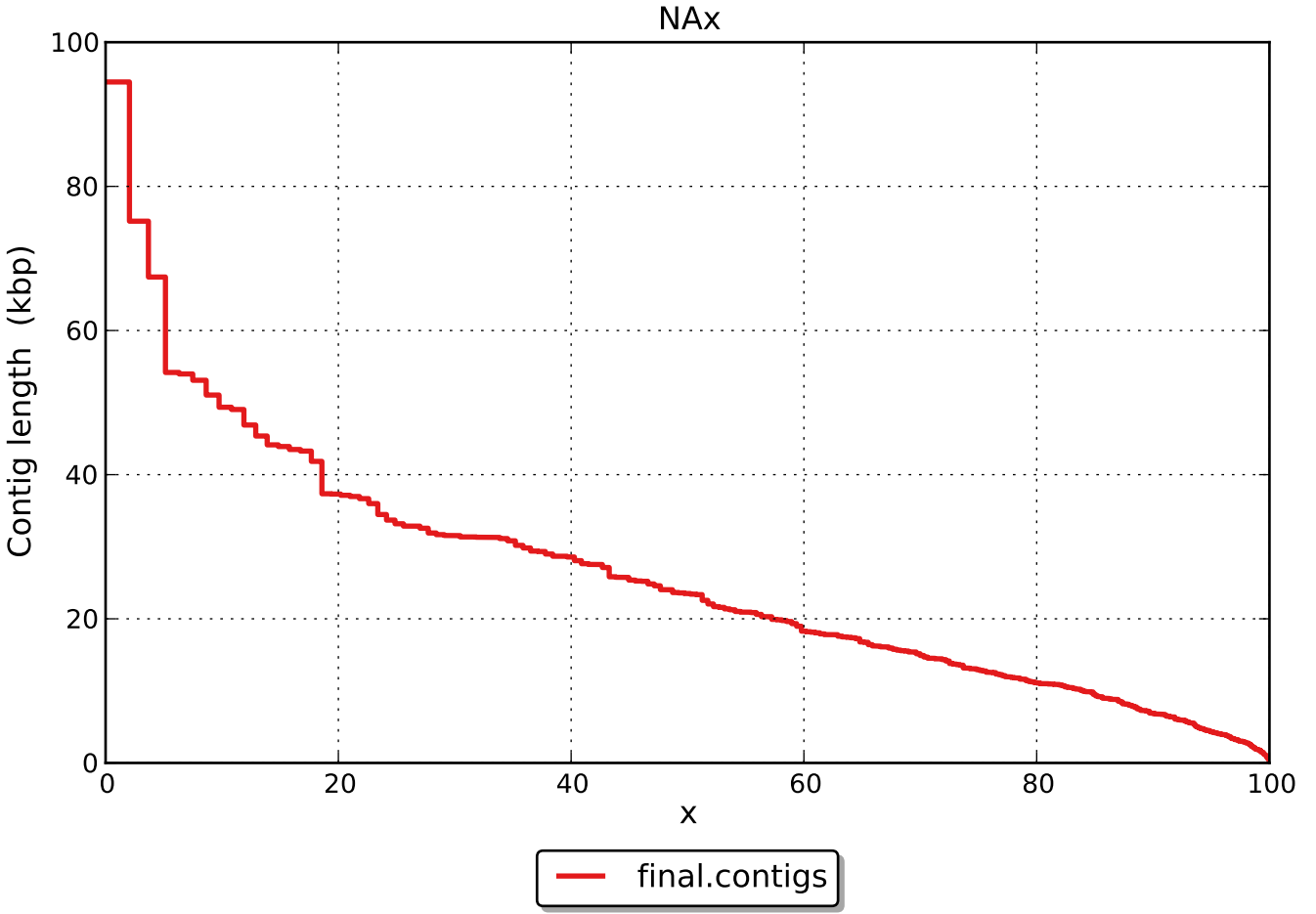

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

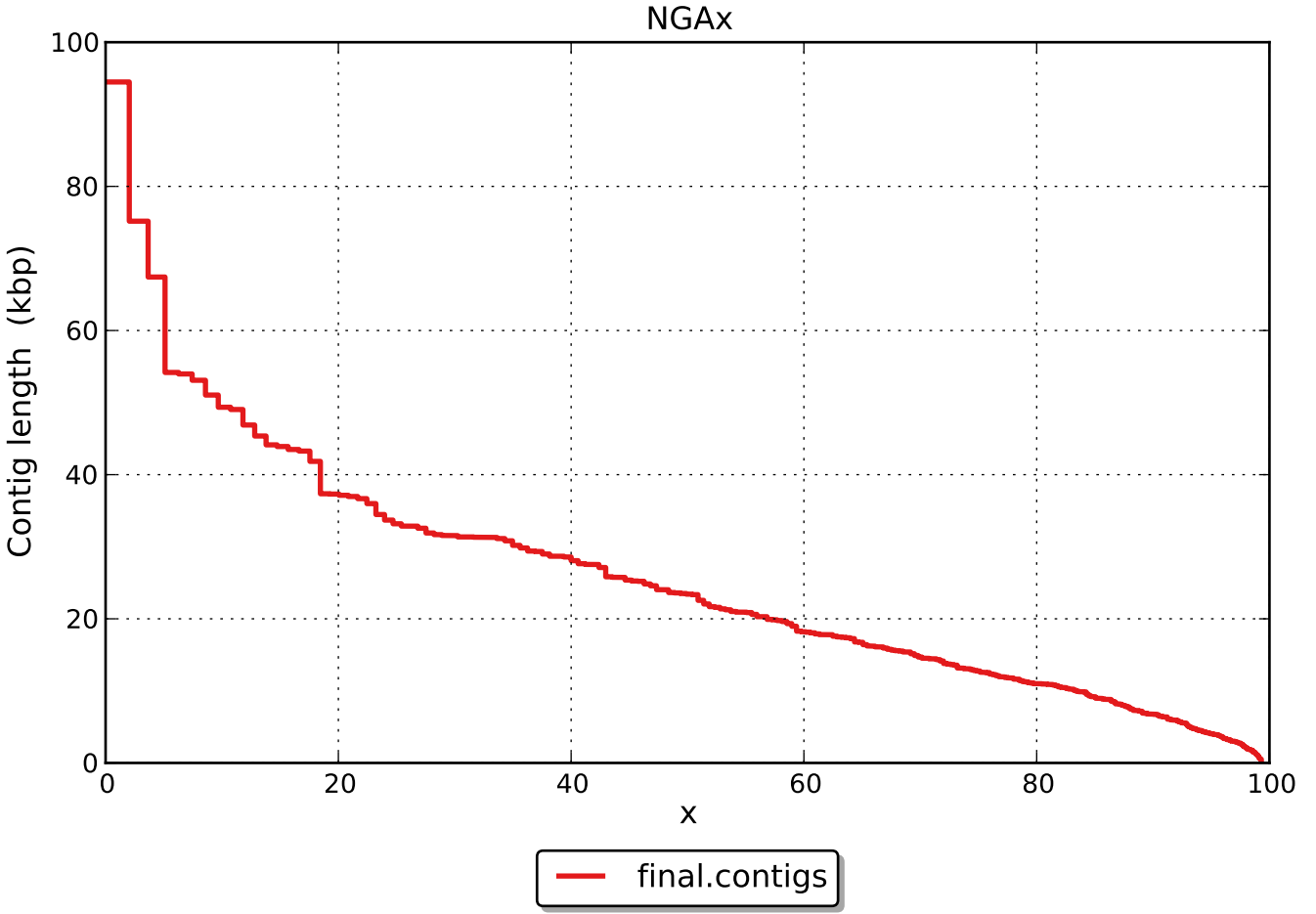

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
final.contigs
Reference


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


Misassemblies
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
60
120
180
240
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