Report

	final.contigs
# contigs (>= 0 bp)	279
# contigs (>= 1000 bp)	270
Total length (>= 0 bp)	3709906
Total length (>= 1000 bp)	3703431
# contigs	279
Largest contig	74321
Total length	3709906
Reference length	1892775
GC (%)	32.27
Reference GC (%)	32.28
N50	21538
NG50	33551
N75	12583
NG75	26655
L50	56
LG50	22
L75	111
LG75	38
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	116 + 54 part
Unaligned length	1799836
Genome fraction (%)	99.972
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.42
# indels per 100 kbp	0.00
Largest alignment	63635
NA50	4008
NGA50	27696
NGA75	18440
LA50	90
LGA50	25
LGA75	46

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

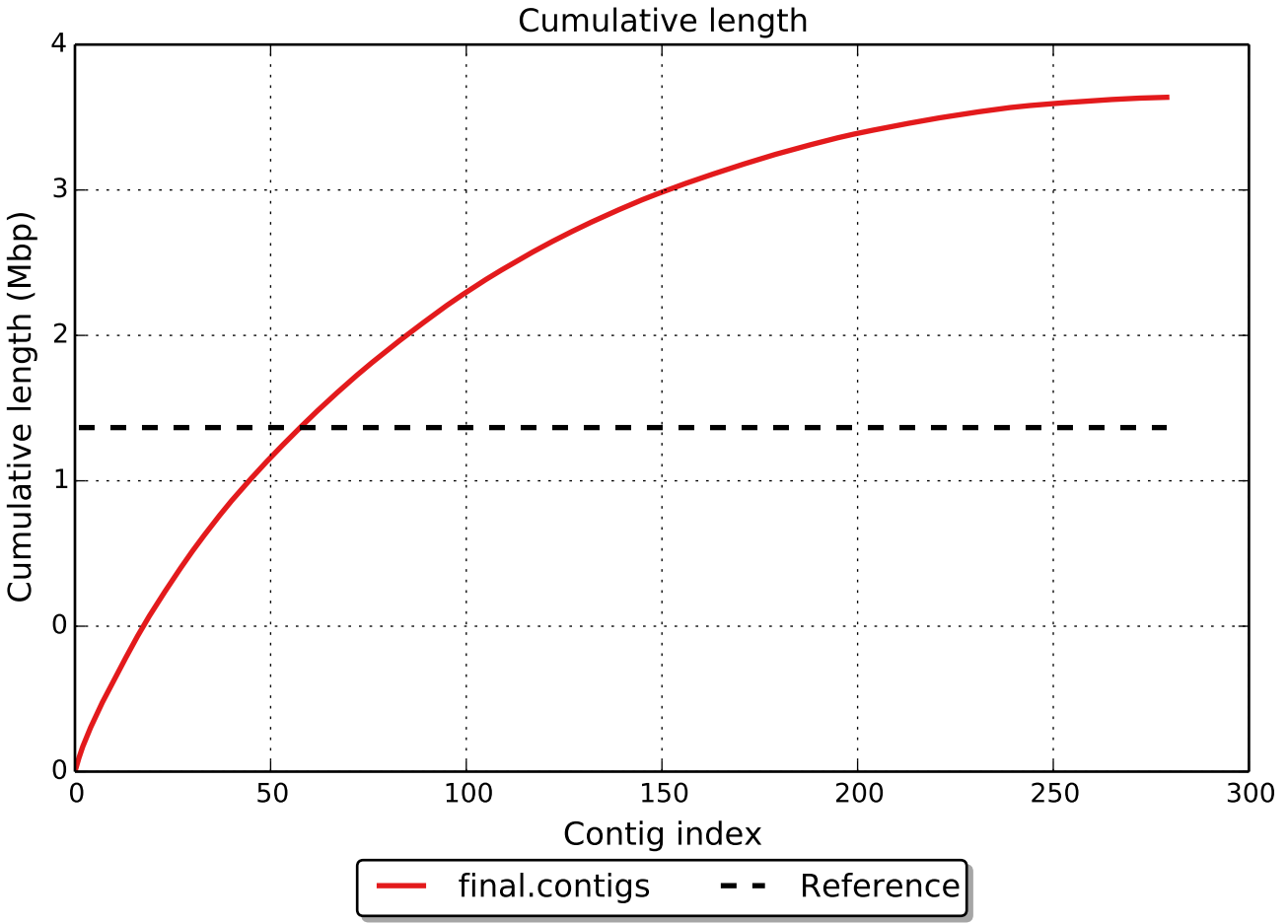
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8
# indels	0
# short indels	0
# long indels	0
Indels length	0

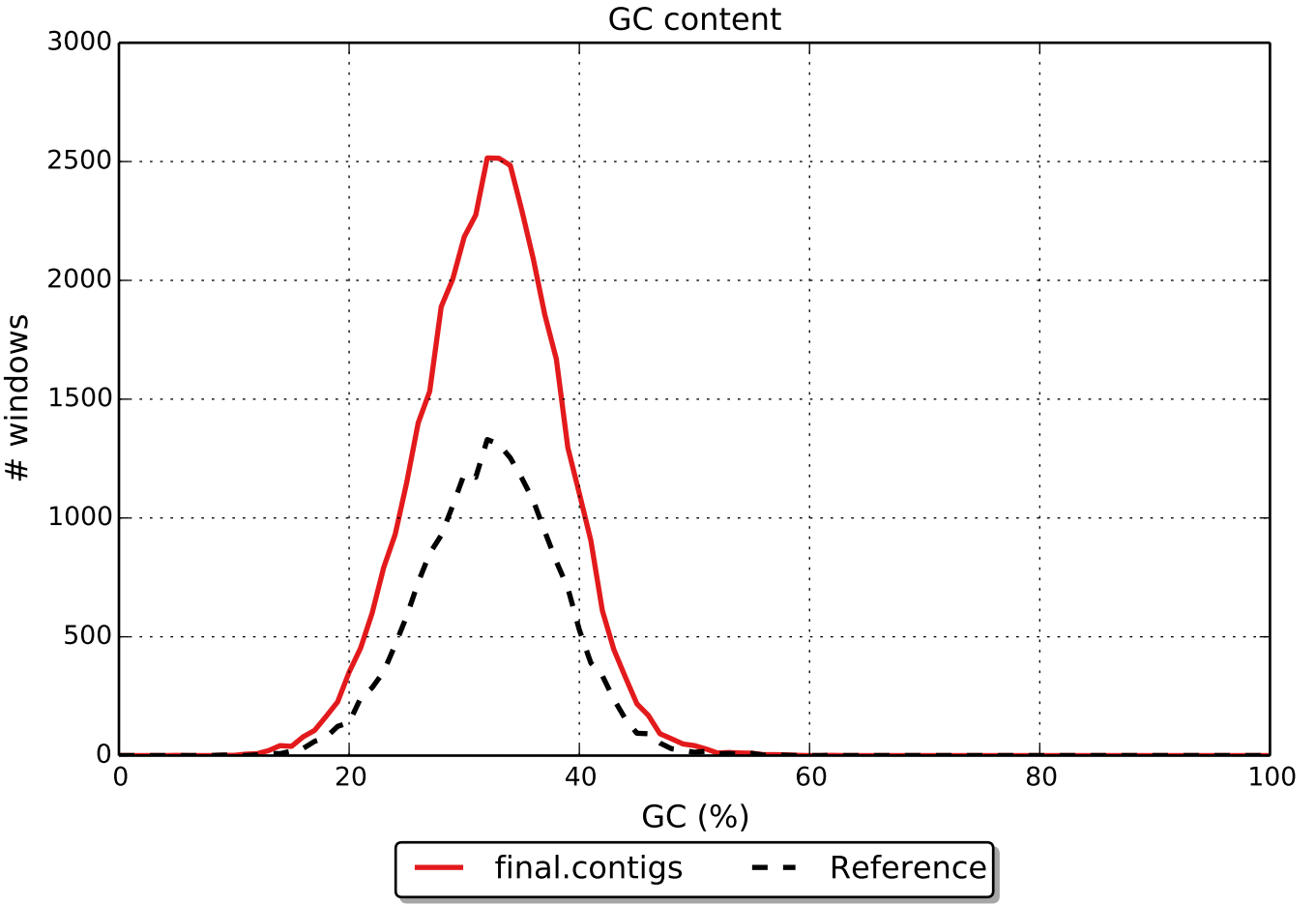
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

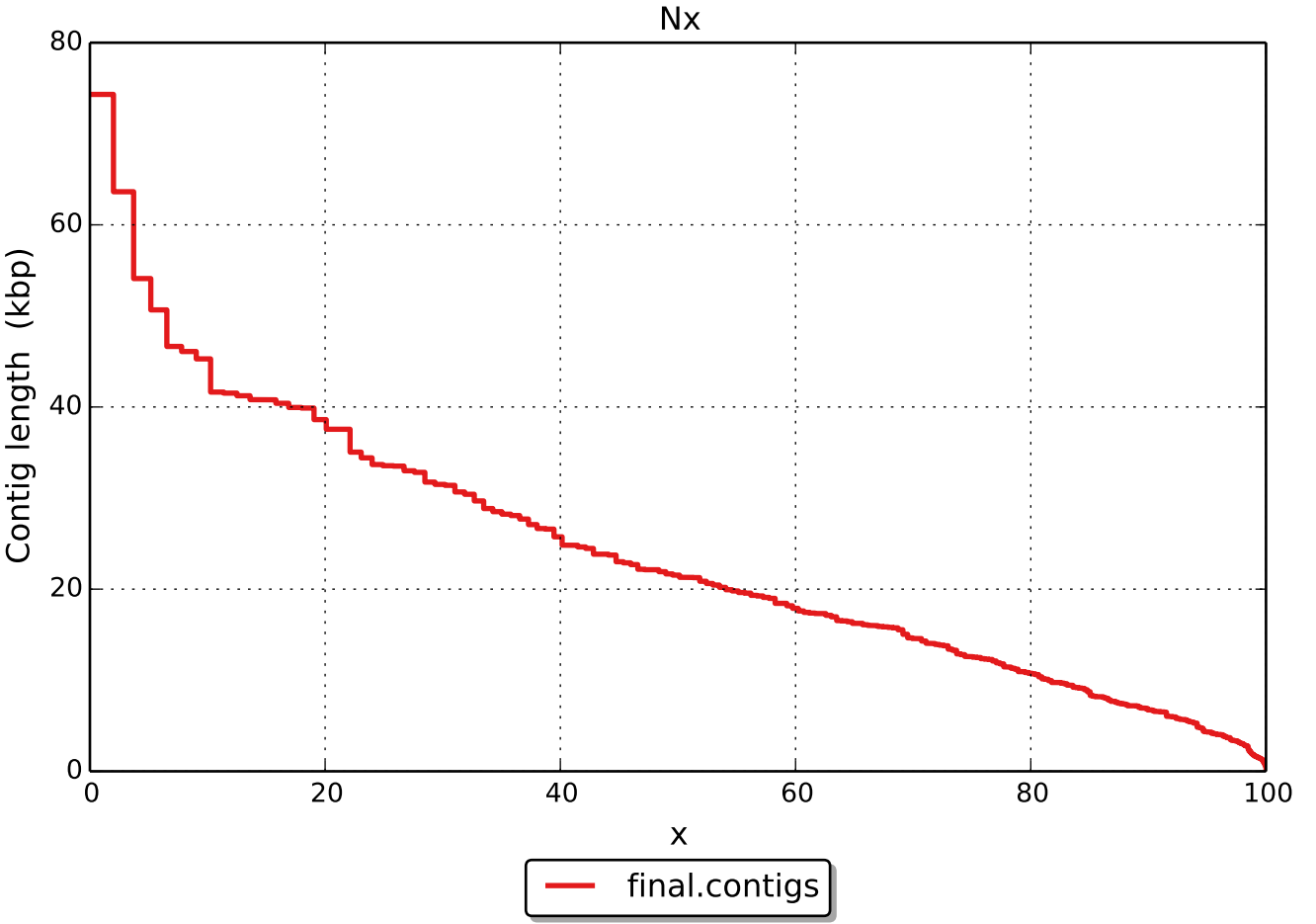
Unaligned report

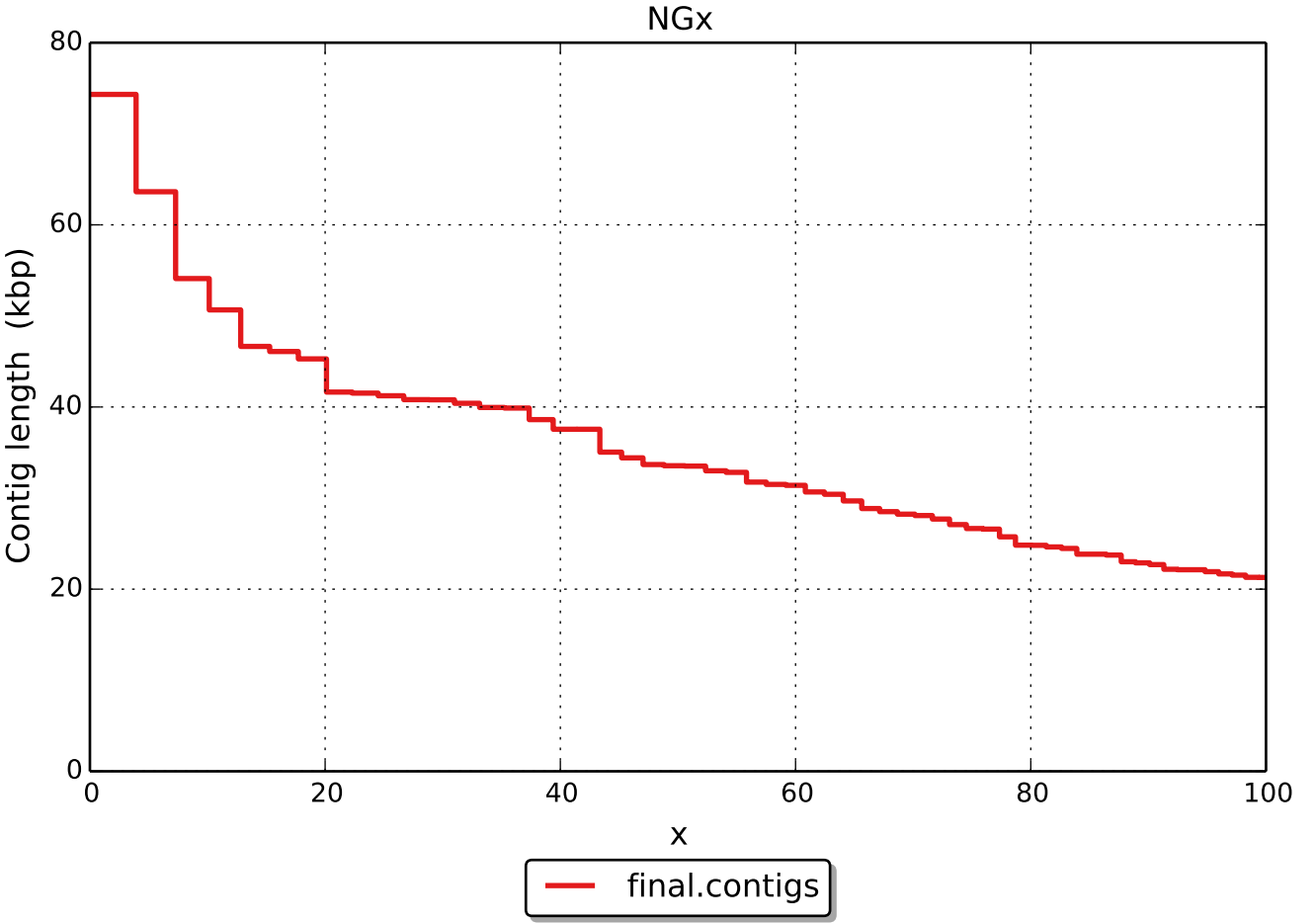
	final.contigs
# fully unaligned contigs	116
Fully unaligned length	1126186
# partially unaligned contigs	54
# with misassembly	7
# both parts are significant	0
Partially unaligned length	673650
# N's	0

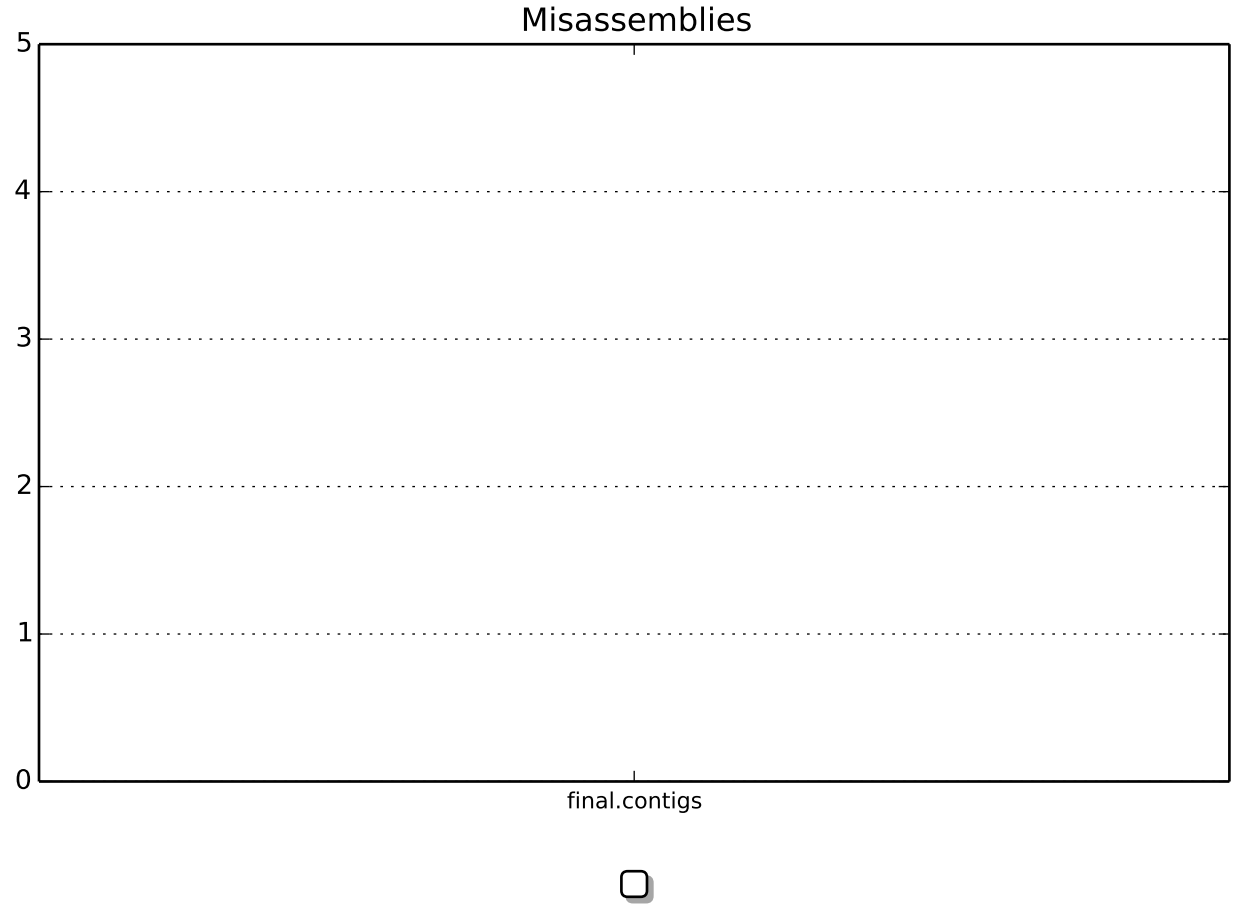
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

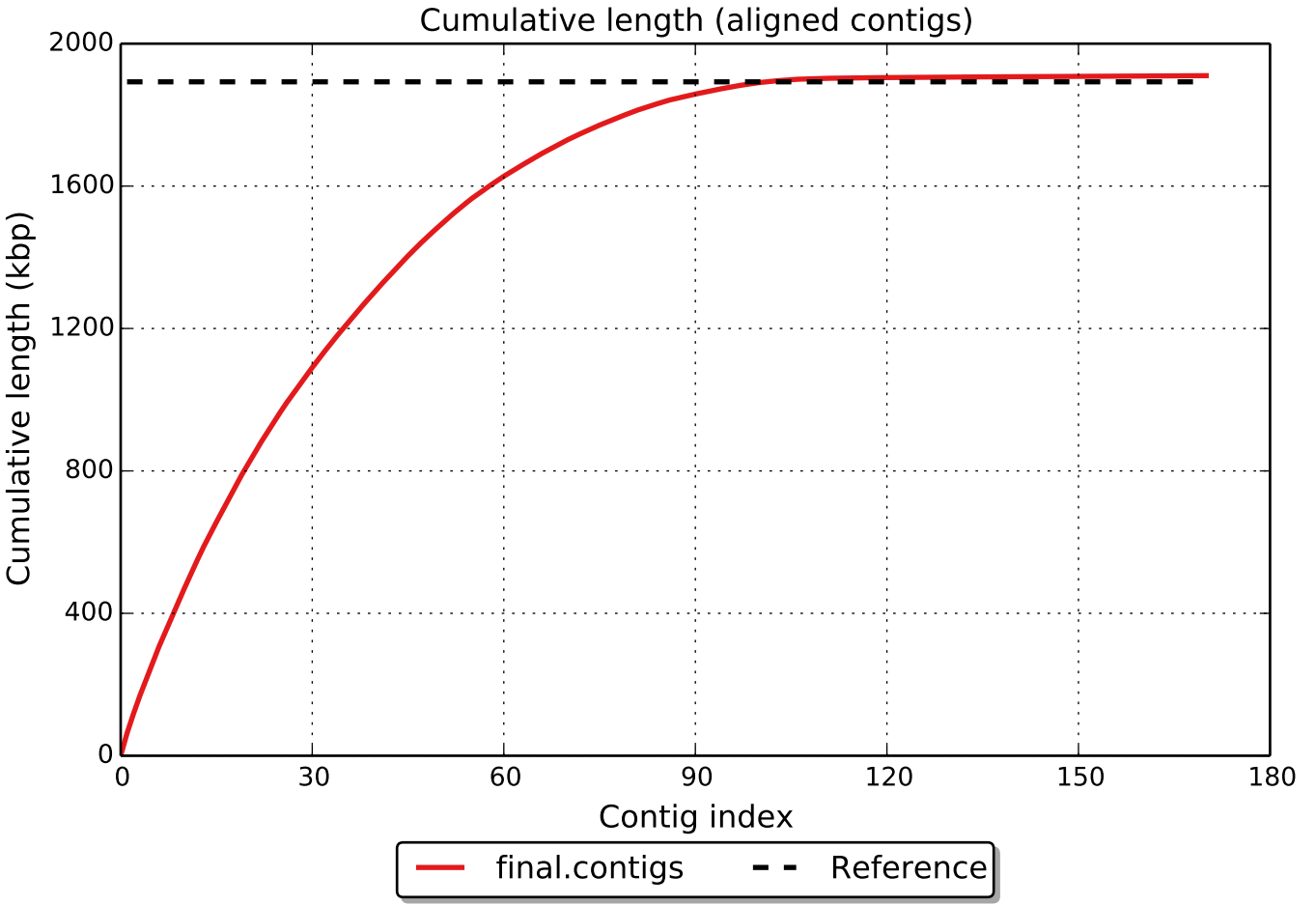

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
0
50
100
150
200
250
300
Contig index
final.contigs
Reference

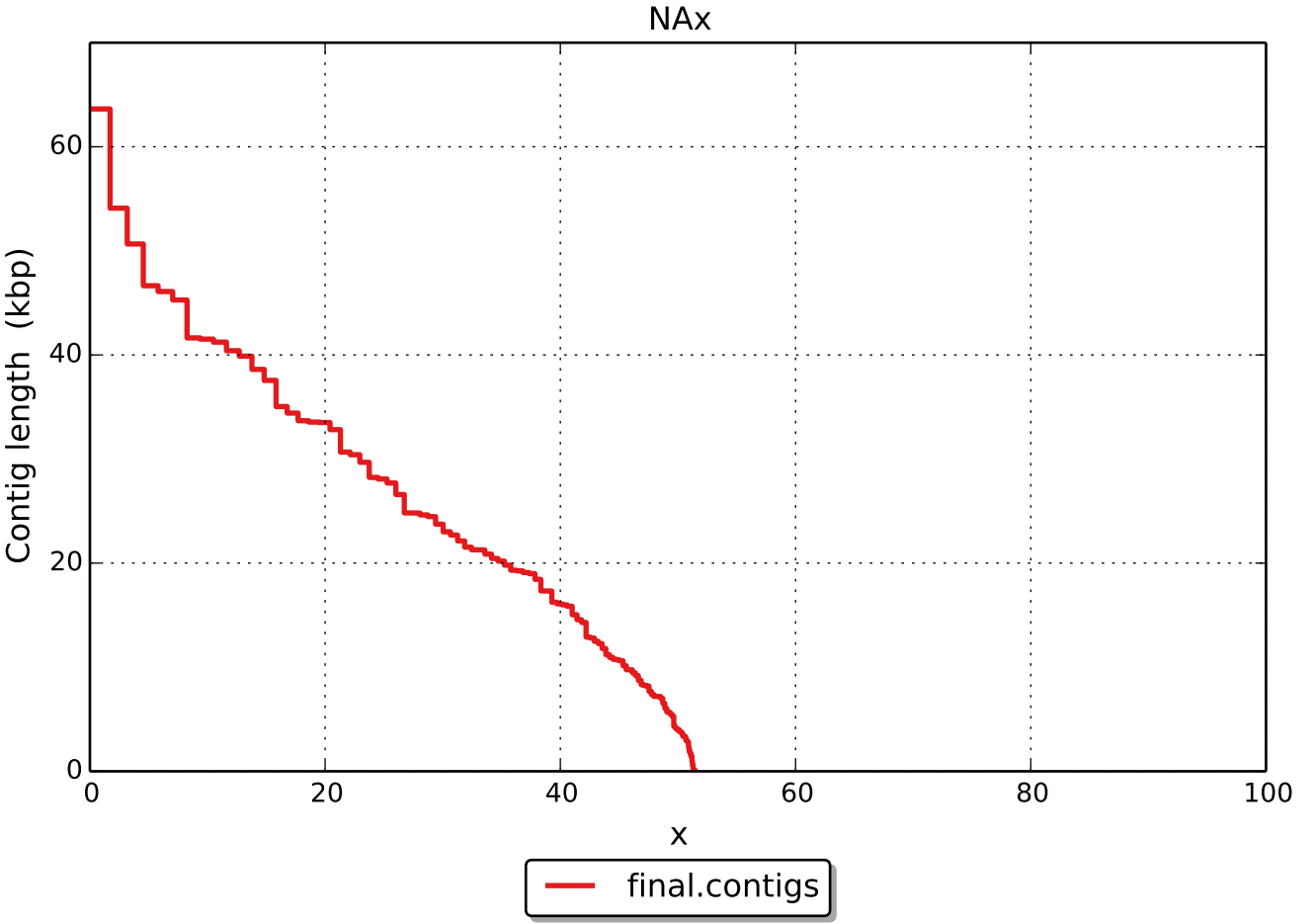

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

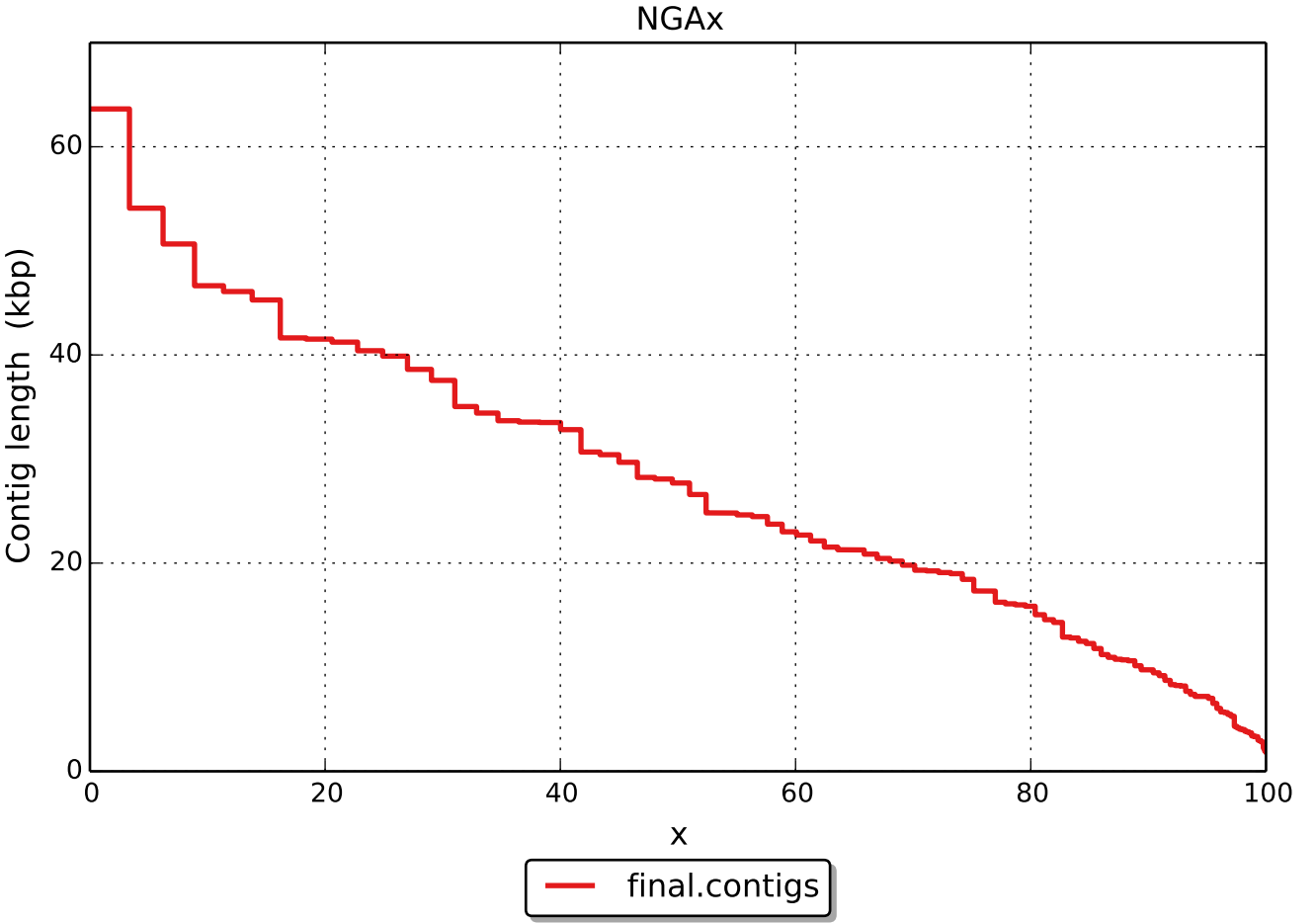

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
30
60
90
120
150
180
Contig index
final.contigs
Reference


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


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