Report

	final.contigs
# contigs (>= 0 bp)	248
# contigs (>= 1000 bp)	125
# contigs (>= 5000 bp)	96
# contigs (>= 10000 bp)	80
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4600560
Total length (>= 1000 bp)	4556256
Total length (>= 5000 bp)	4490129
Total length (>= 10000 bp)	4368049
Total length (>= 25000 bp)	4030828
Total length (>= 50000 bp)	2995237
# contigs	141
Largest contig	238358
Total length	4566737
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	75638
NG50	75638
N75	41453
NG75	40948
L50	19
LG50	19
L75	40
LG75	41
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	44276
# local misassemblies	2
# unaligned contigs	0 + 2 part
Unaligned length	122
Genome fraction (%)	98.215
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.39
# indels per 100 kbp	0.07
Largest alignment	238358
NA50	75638
NGA50	75638
NA75	41453
NGA75	40948
LA50	19
LGA50	19
LA75	40
LGA75	41

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

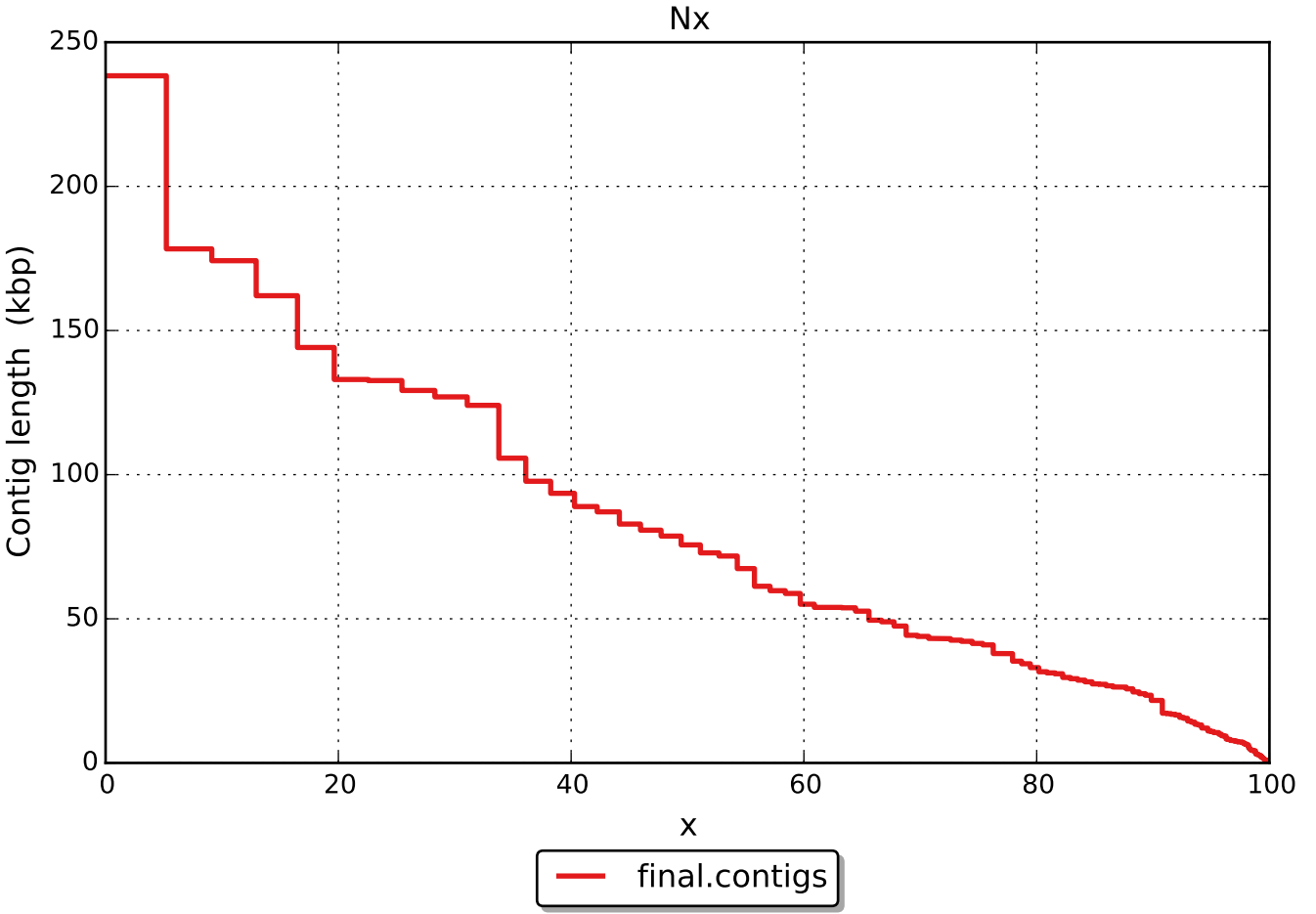
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	44276
# local misassemblies	2
# mismatches	337
# indels	3
# short indels	2
# long indels	1
Indels length	87

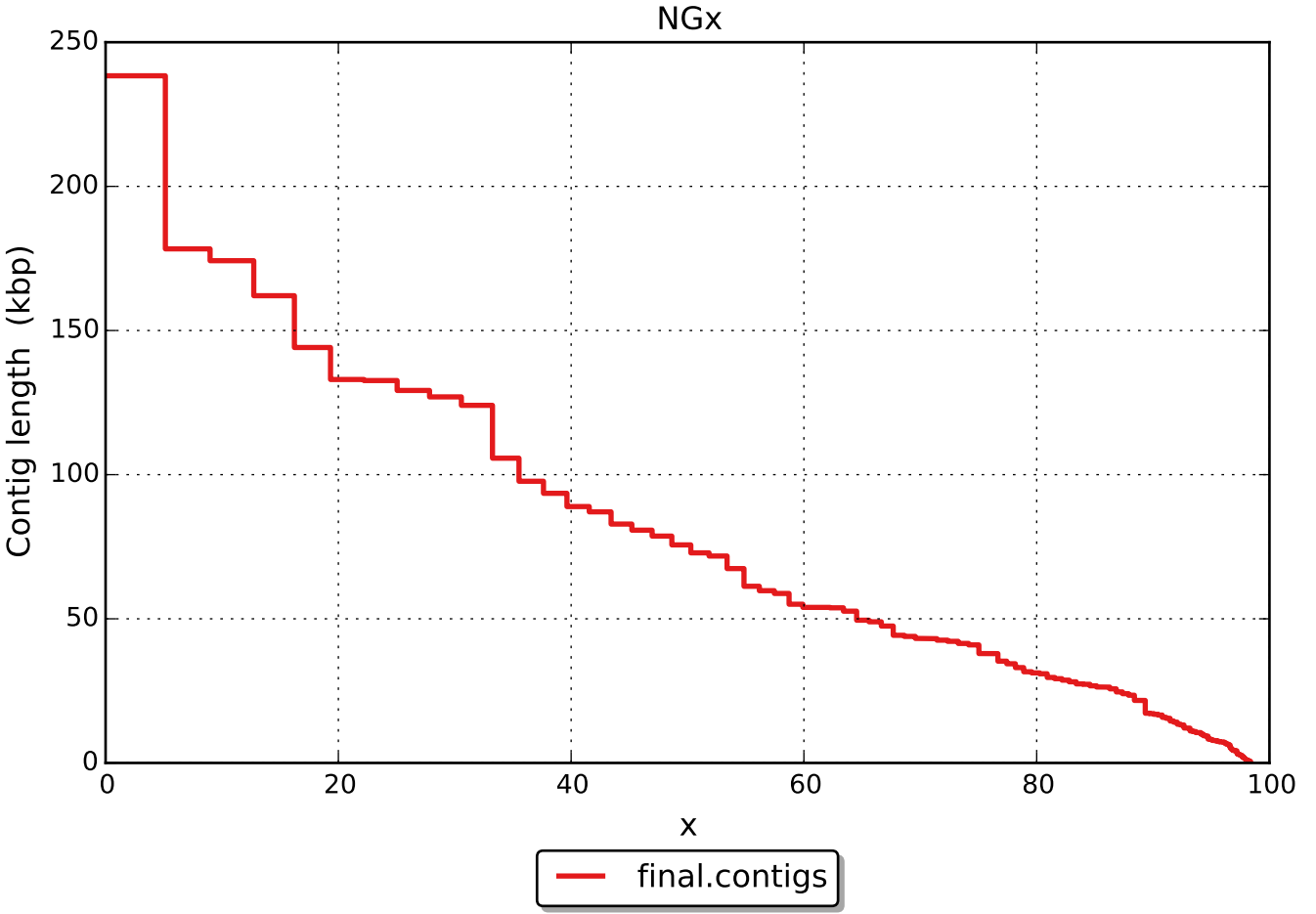
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

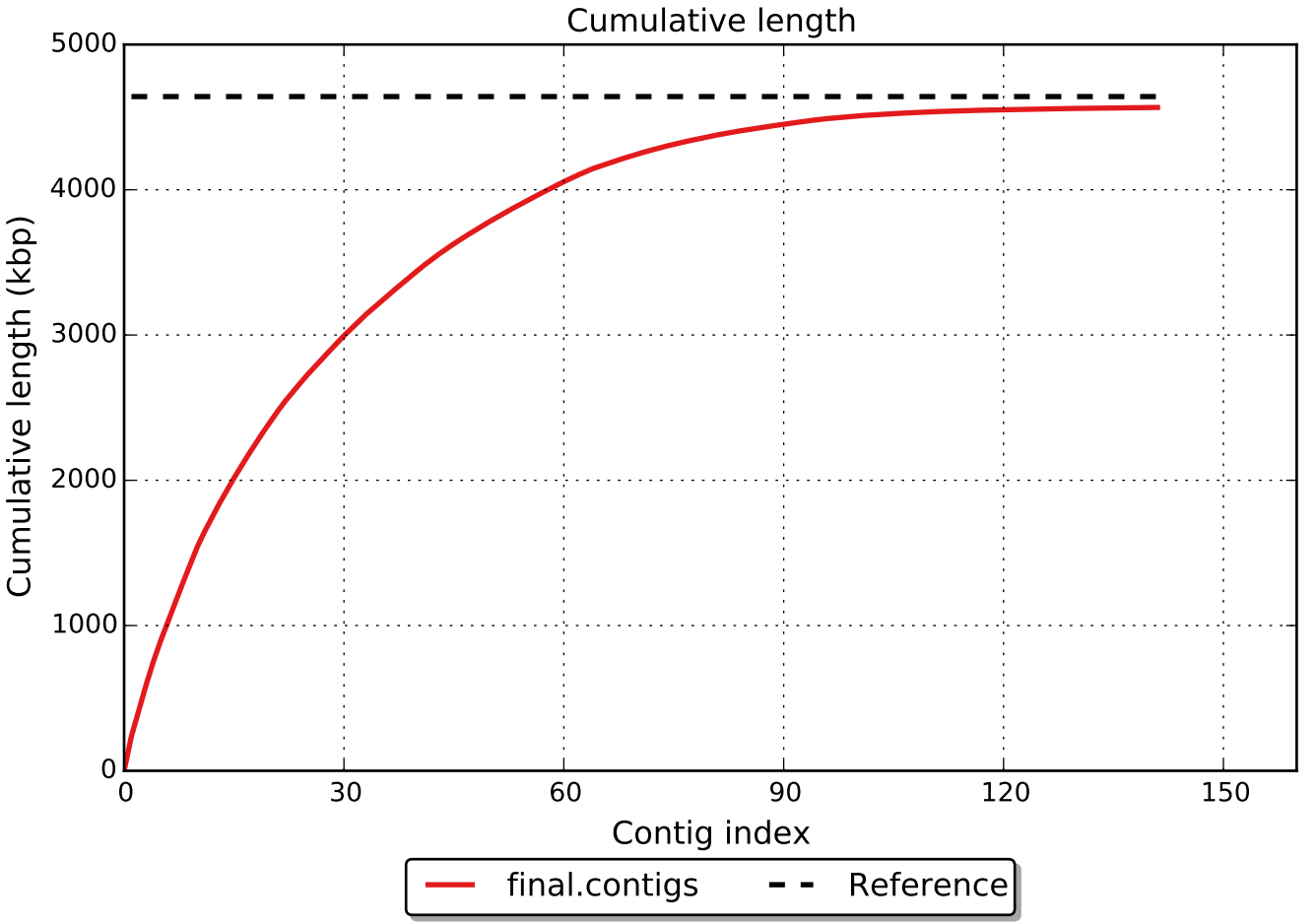
Unaligned report

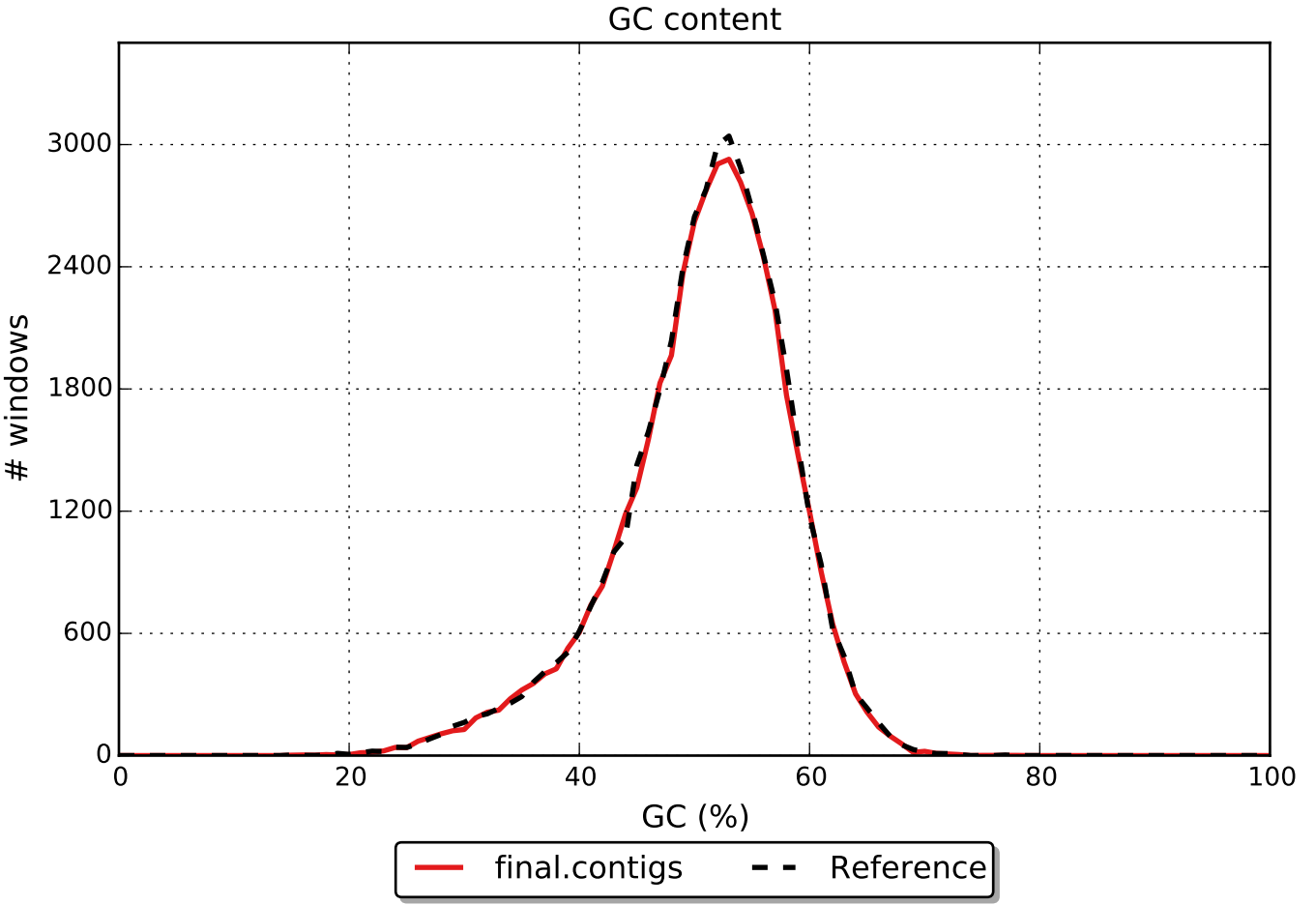
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	122
# N's	0

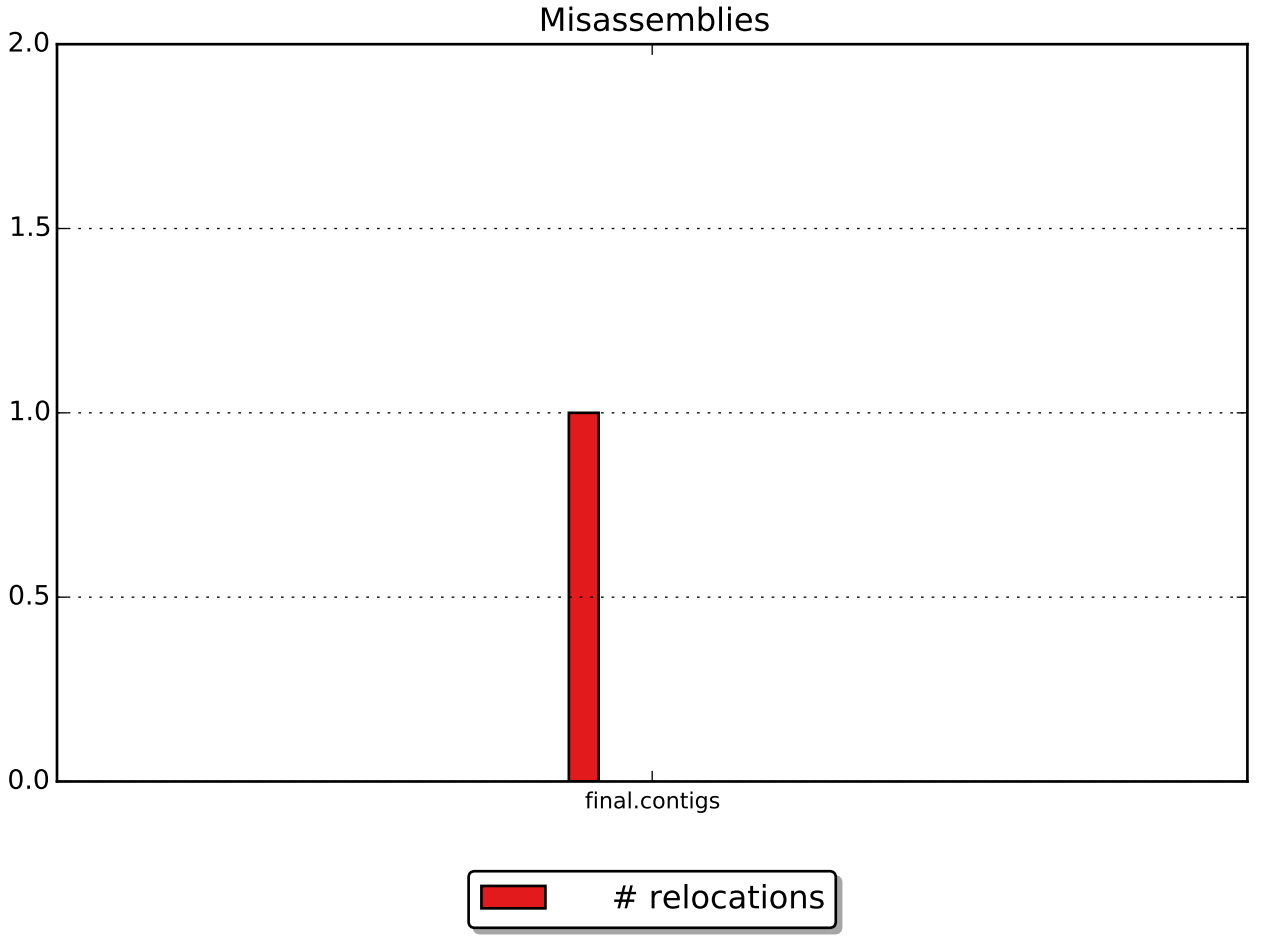
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

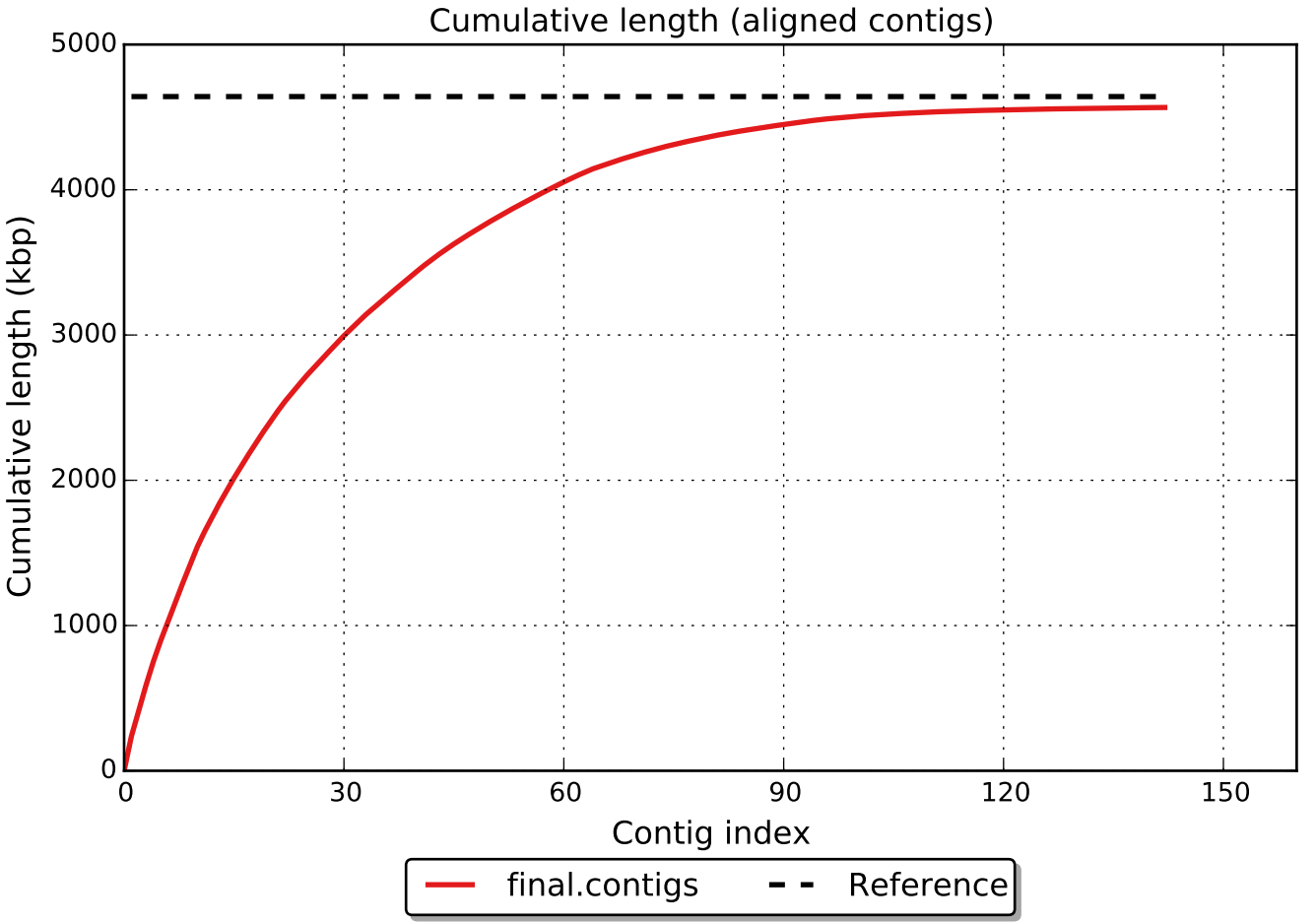

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

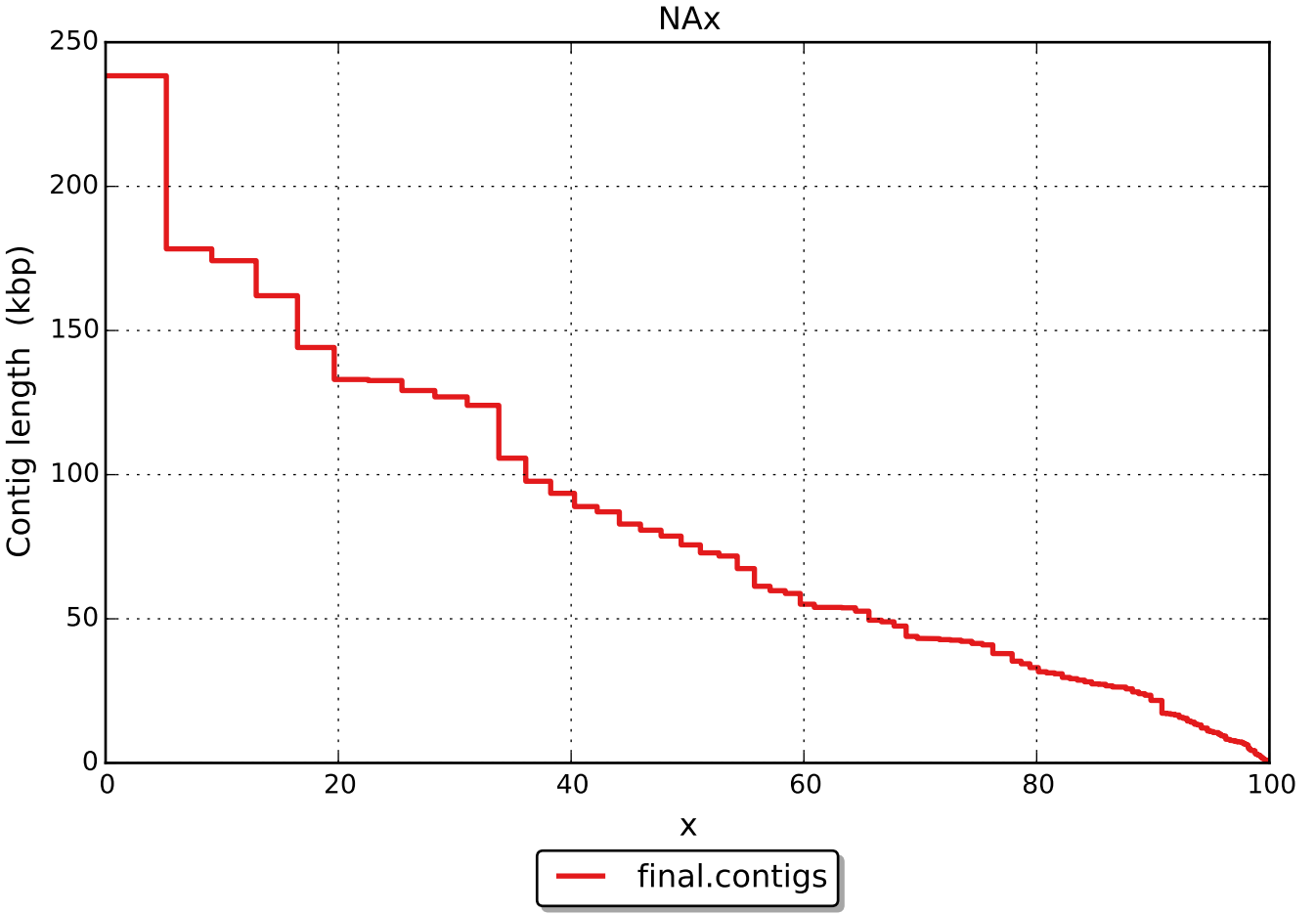

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

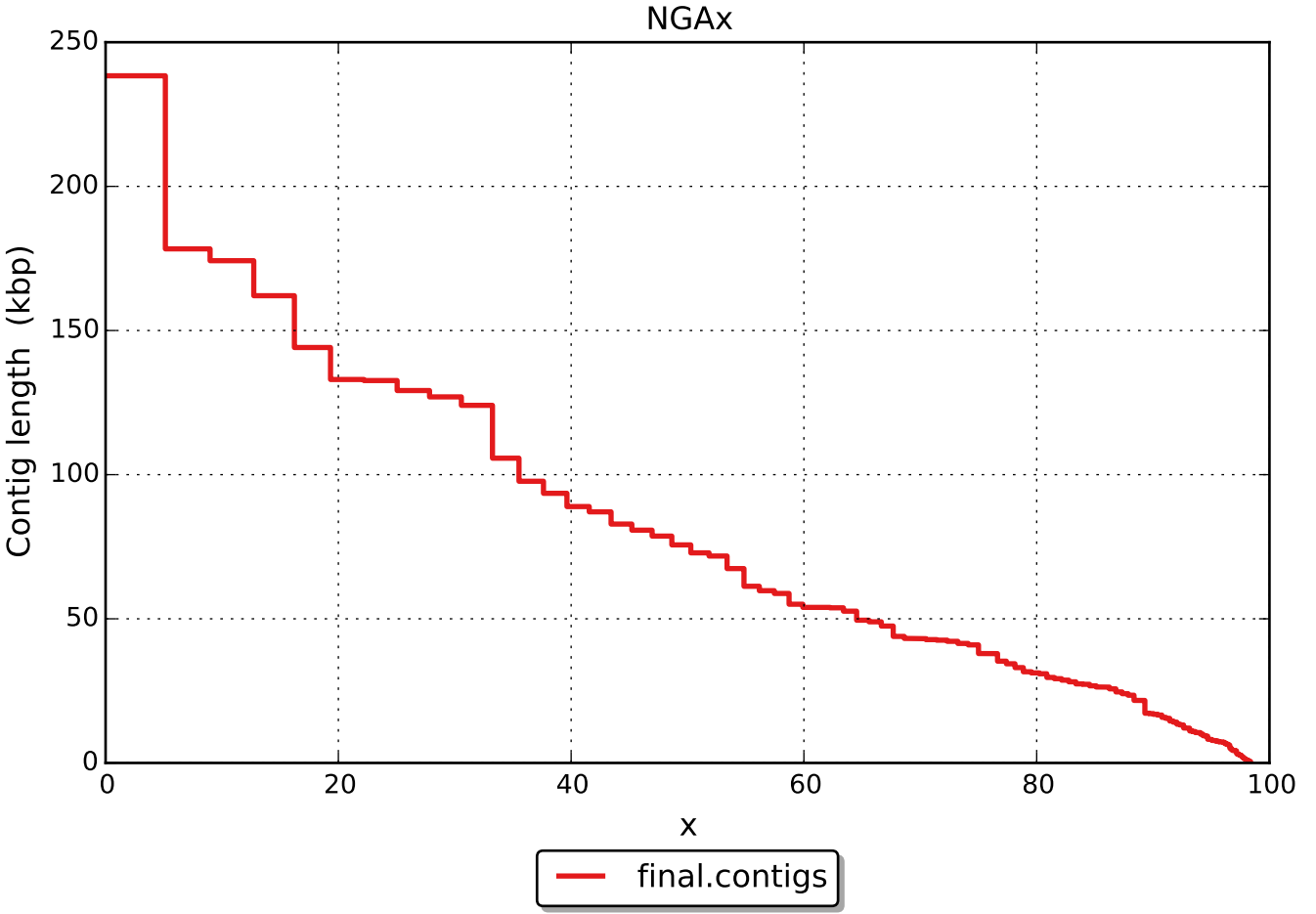

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


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


Misassemblies
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
30
60
90
120
150
Contig index
final.contigs
Reference


NAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs