Report

	final.contigs
# contigs (>= 0 bp)	265
# contigs (>= 1000 bp)	256
Total length (>= 0 bp)	5552797
Total length (>= 1000 bp)	5547050
# contigs	265
Largest contig	129092
Total length	5552797
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	36352
NG50	36631
N75	20748
NG75	20980
L50	51
LG50	50
L75	100
LG75	98
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	28513
Genome fraction (%)	99.980
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.68
# indels per 100 kbp	0.04
Largest alignment	129092
NA50	34939
NGA50	35348
NA75	20207
NGA75	20855
LA50	51
LGA50	50
LA75	102
LGA75	99

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

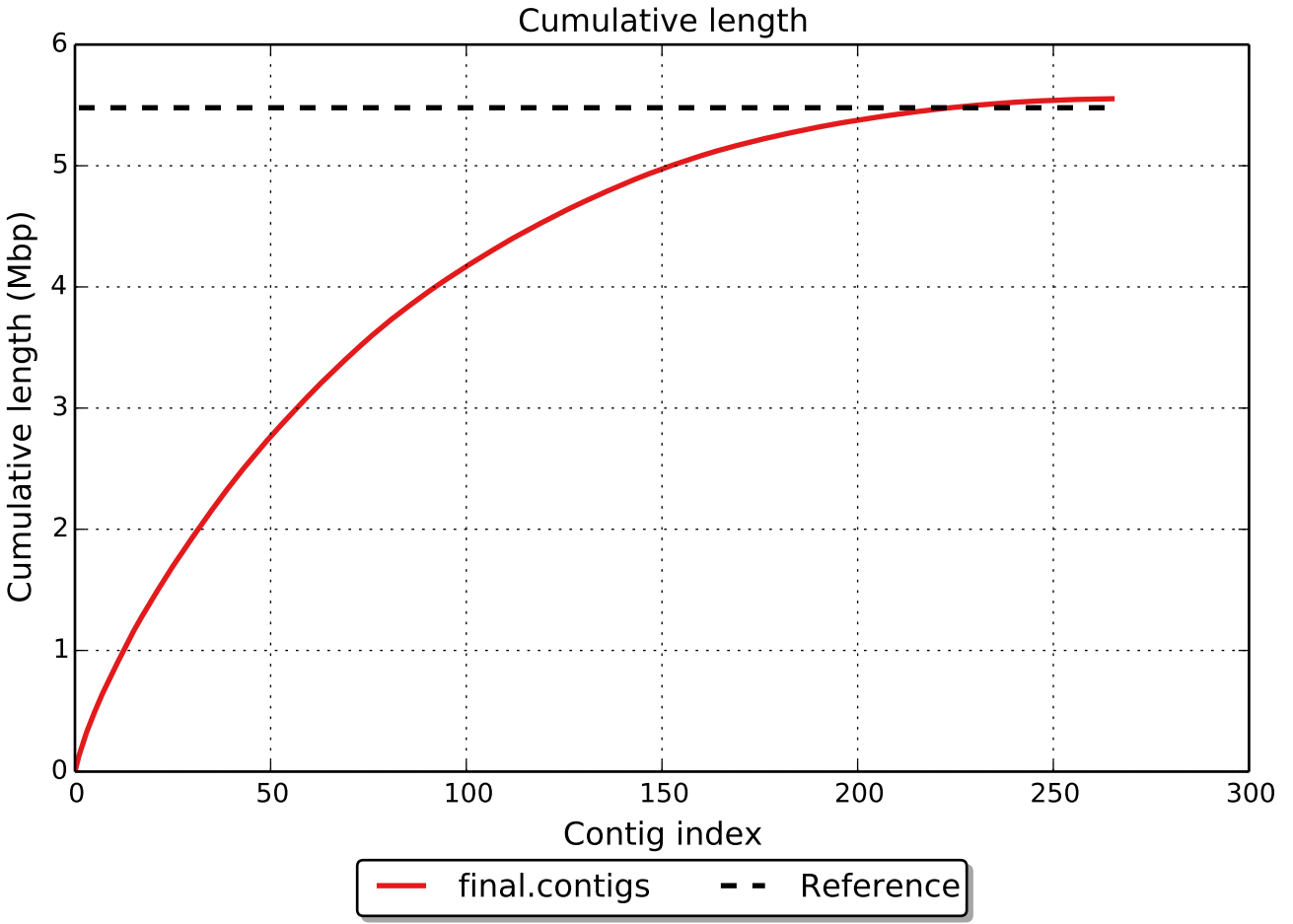
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1352
# indels	2
# short indels	2
# long indels	0
Indels length	2

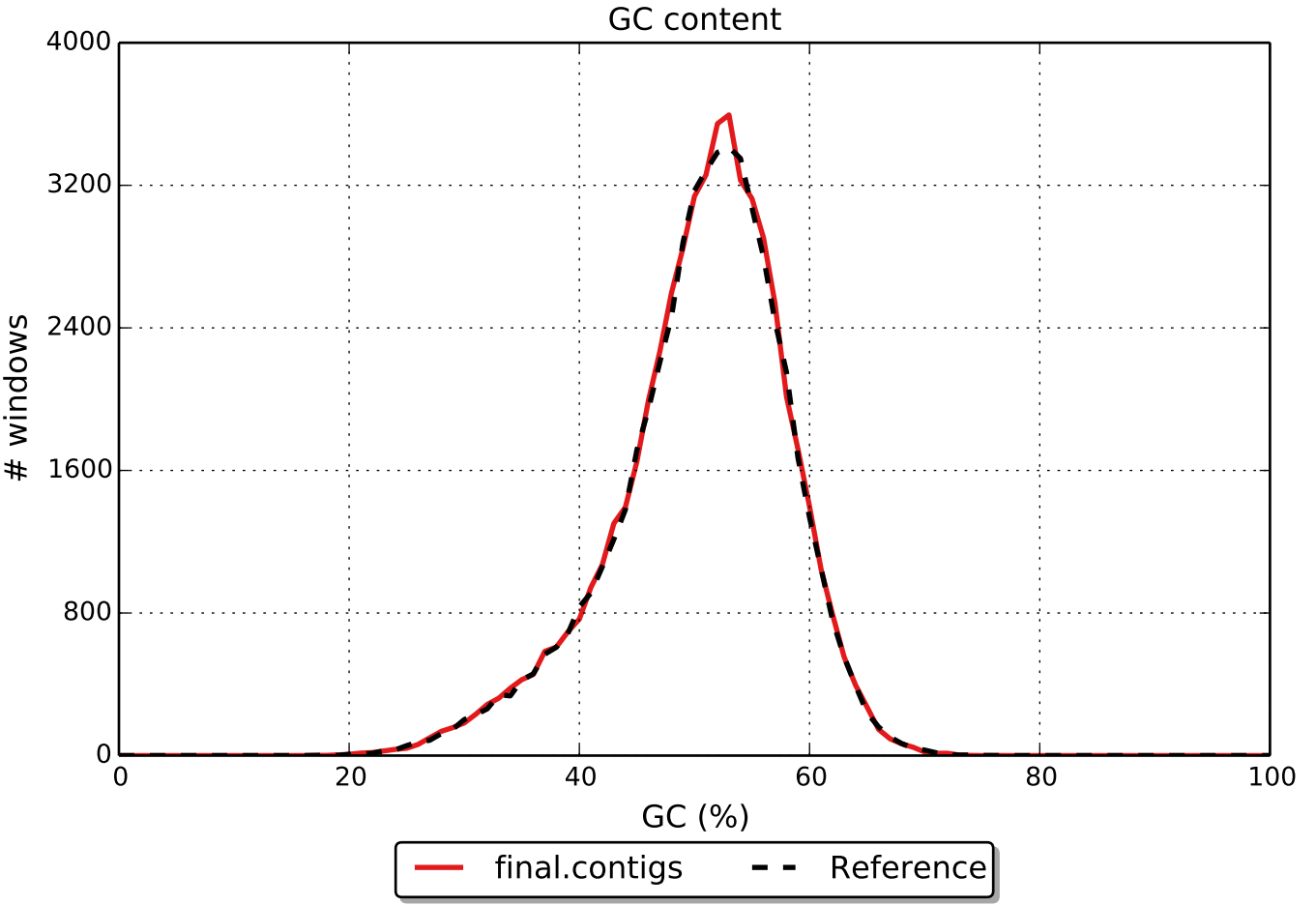
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

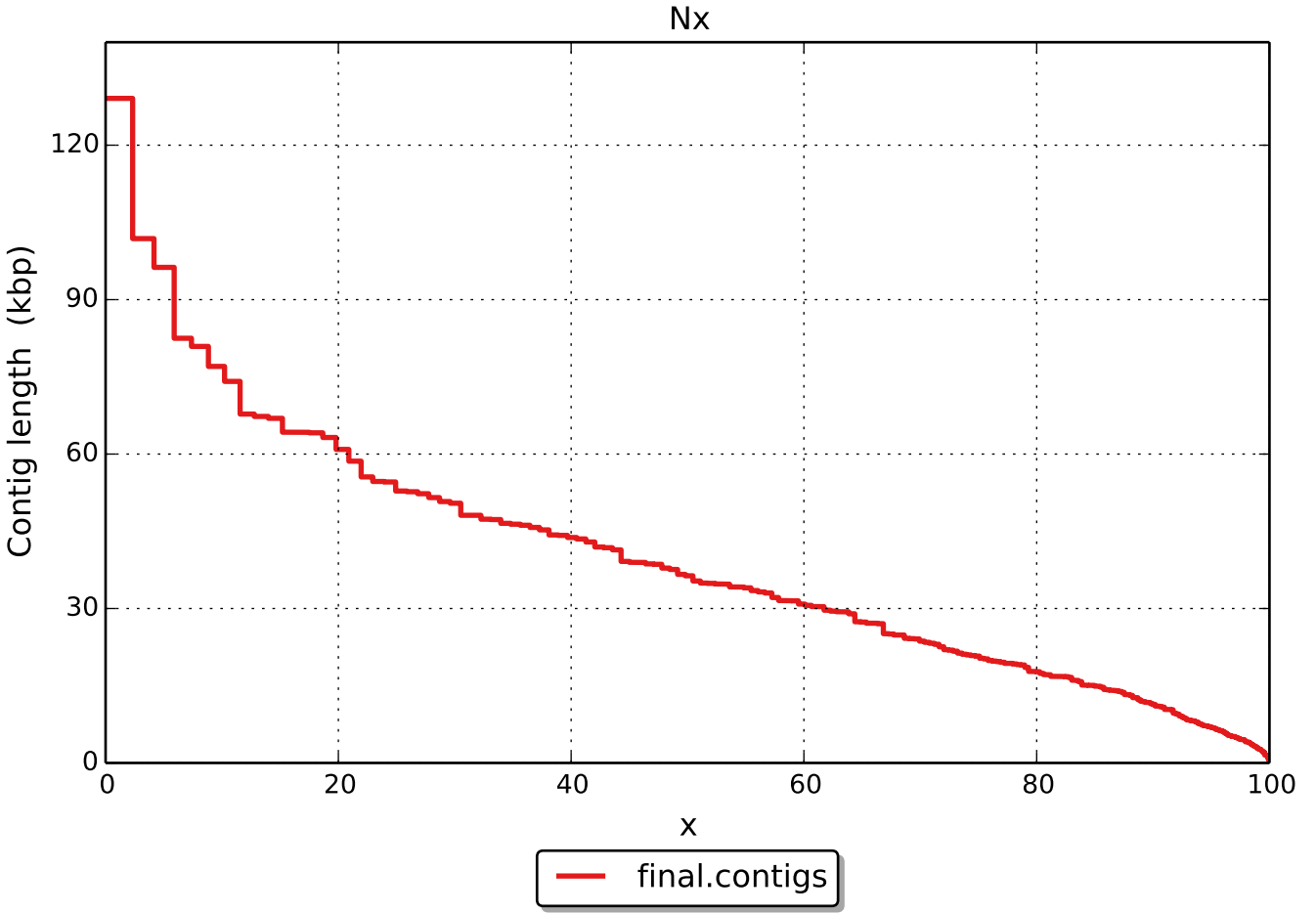
Unaligned report

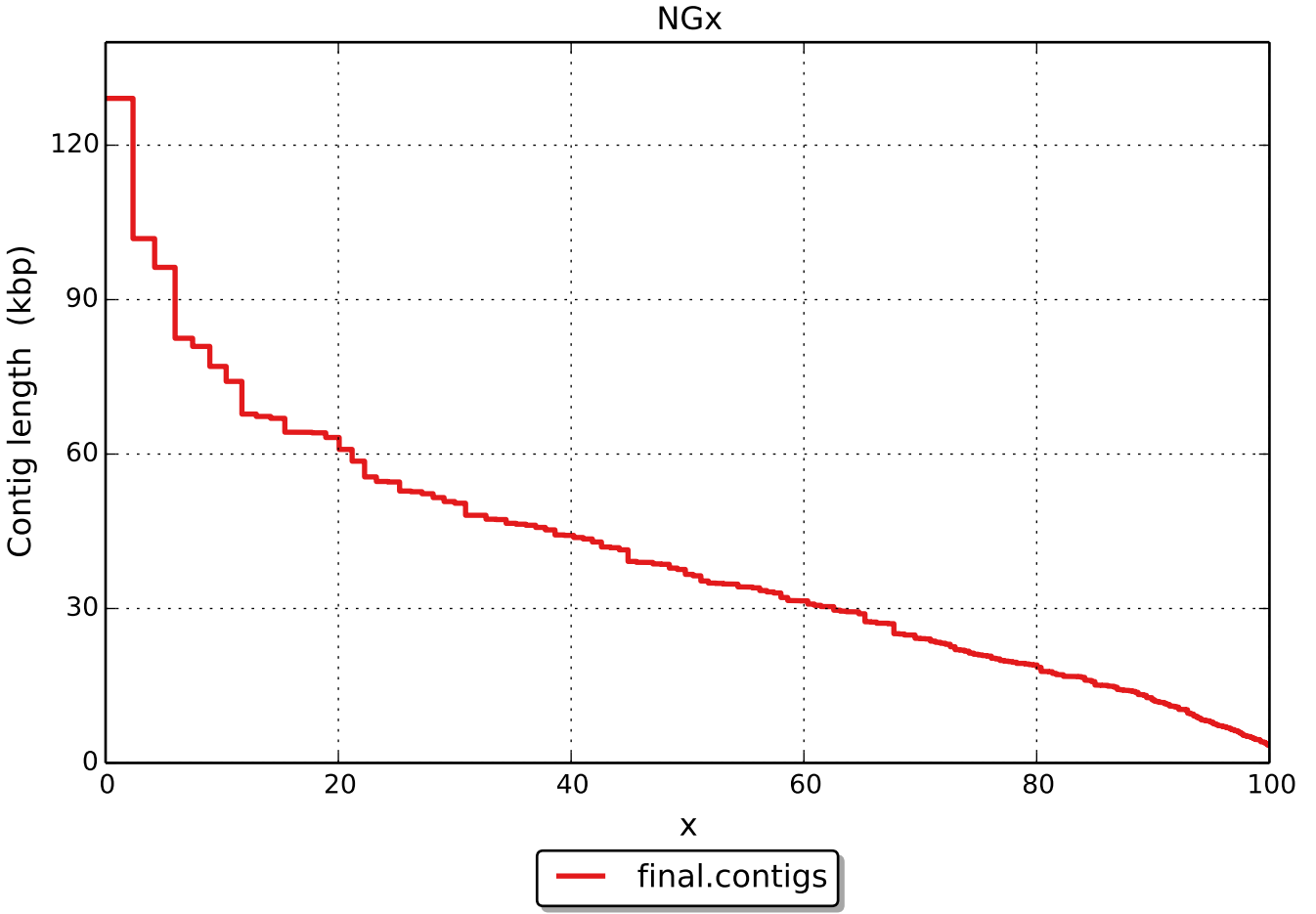
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	28513
# N's	0

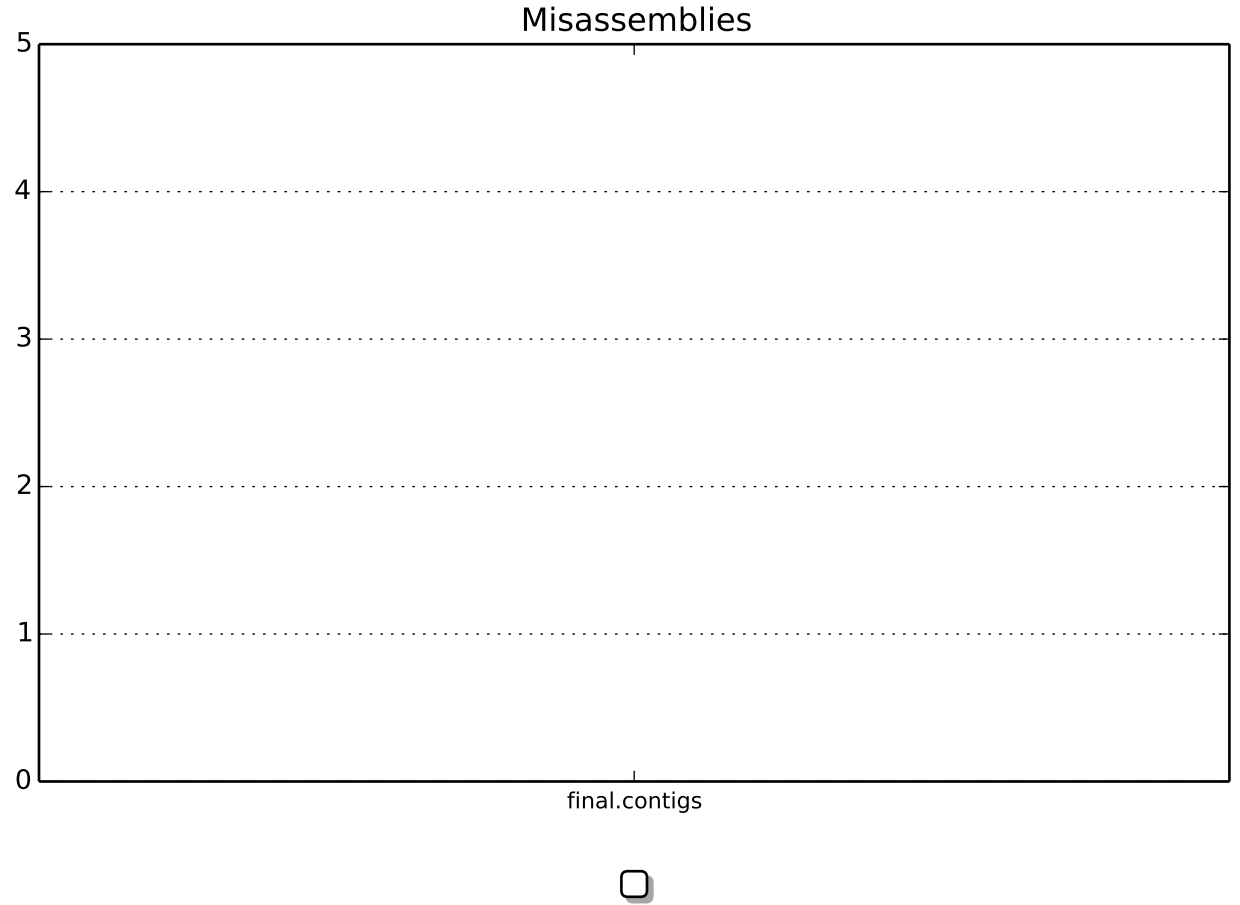
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

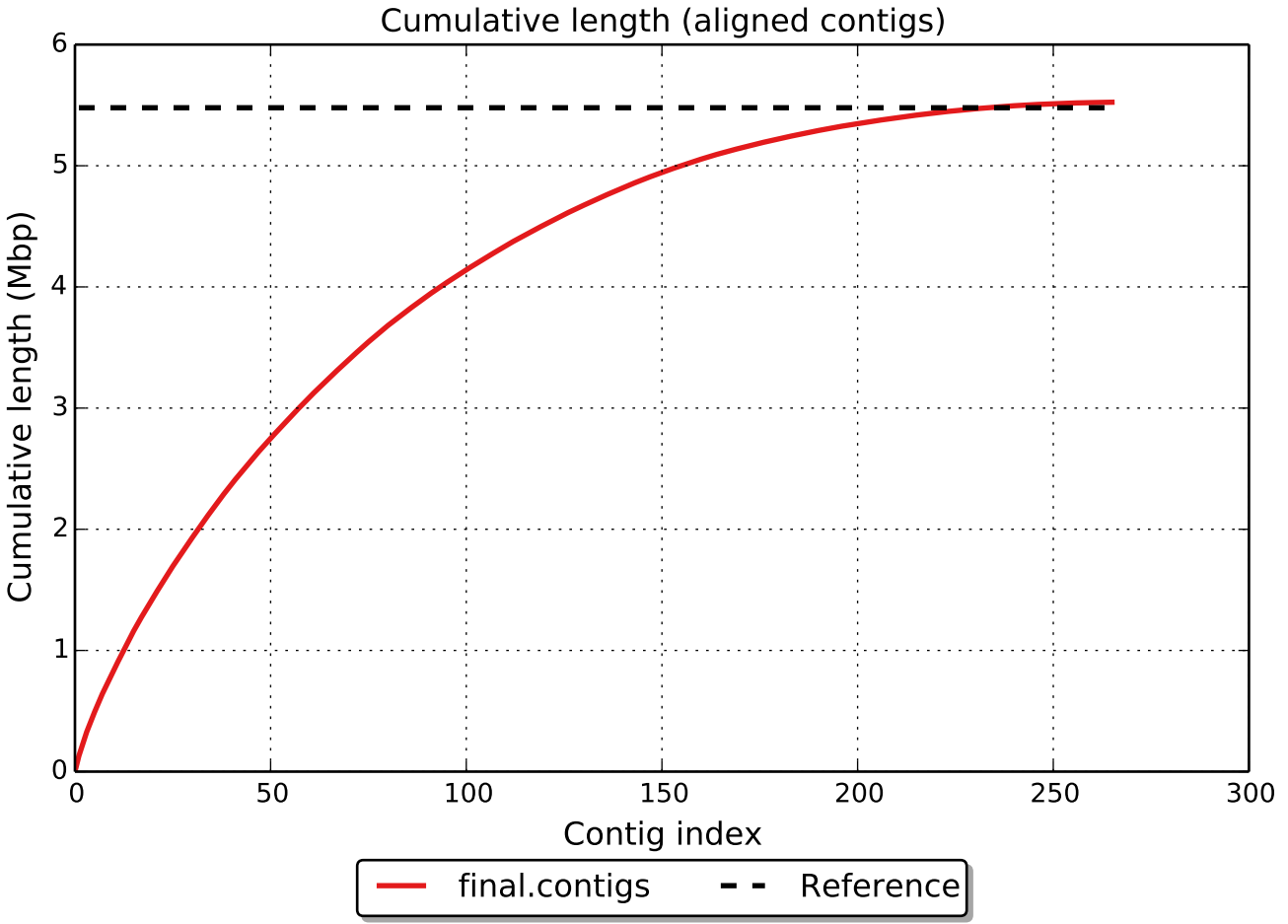

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
50
100
150
200
250
300
Contig index
final.contigs
Reference

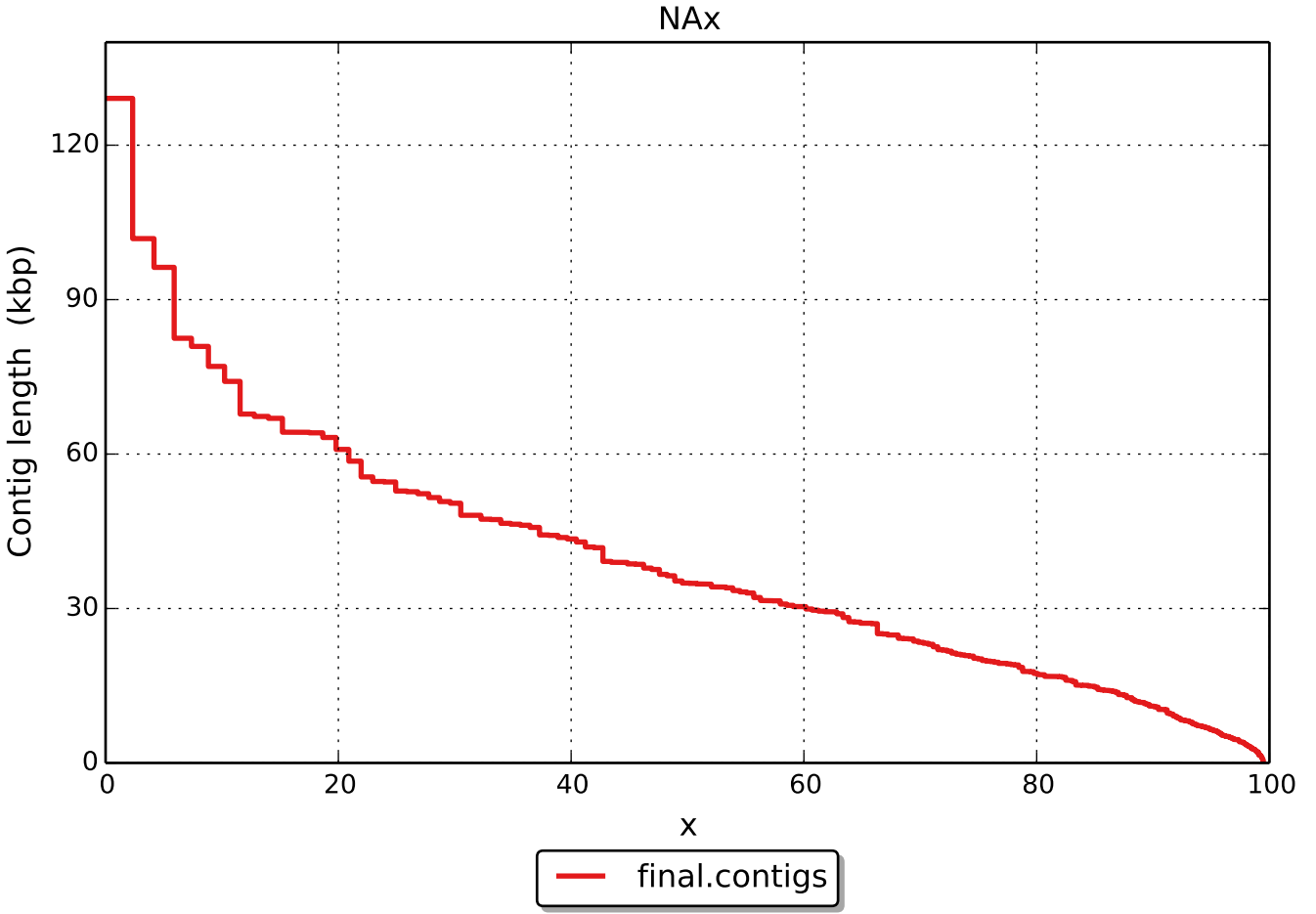

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

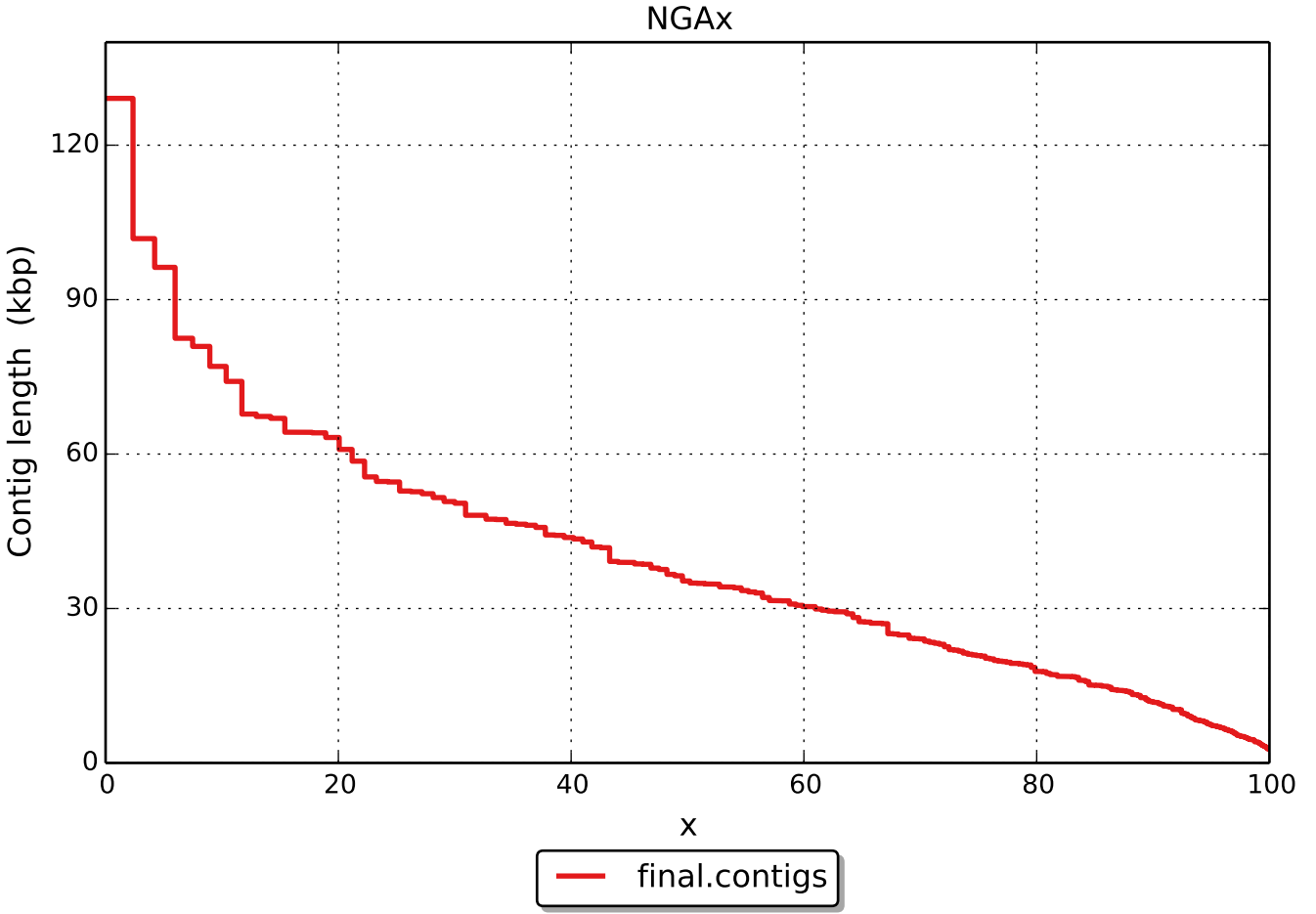

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
120
90
60
30
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 (Mbp)
Contig index
0
1
2
3
4
5
6
0
50
100
150
200
250
300
final.contigs
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs