Report

	final.contigs
# contigs (>= 1000 bp)	136
# contigs (>= 5000 bp)	111
# contigs (>= 10000 bp)	98
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4547414
Total length (>= 5000 bp)	4479948
Total length (>= 10000 bp)	4379149
Total length (>= 25000 bp)	3733533
Total length (>= 50000 bp)	2766902
# contigs	153
Largest contig	229997
Total length	4559533
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	58023
NG50	58023
N75	31670
NG75	31157
L50	24
LG50	24
L75	48
LG75	50
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.087
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.70
# indels per 100 kbp	0.07
Largest alignment	229997
NA50	58023
NGA50	58023
NA75	31670
NGA75	31157
LA50	24
LGA50	24
LA75	48
LGA75	50

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

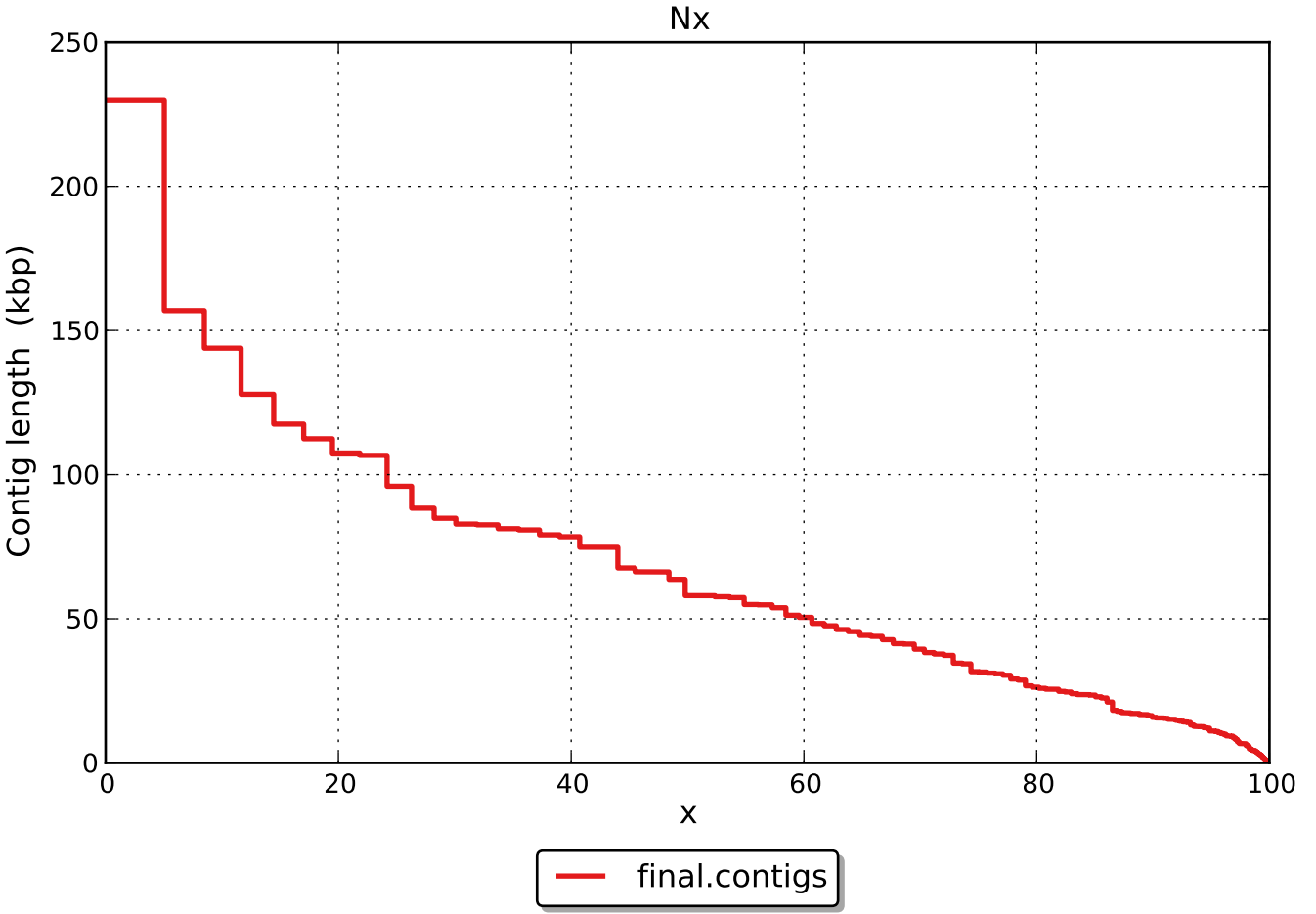
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	123
# indels	3
# short indels	3
# long indels	0
Indels length	3

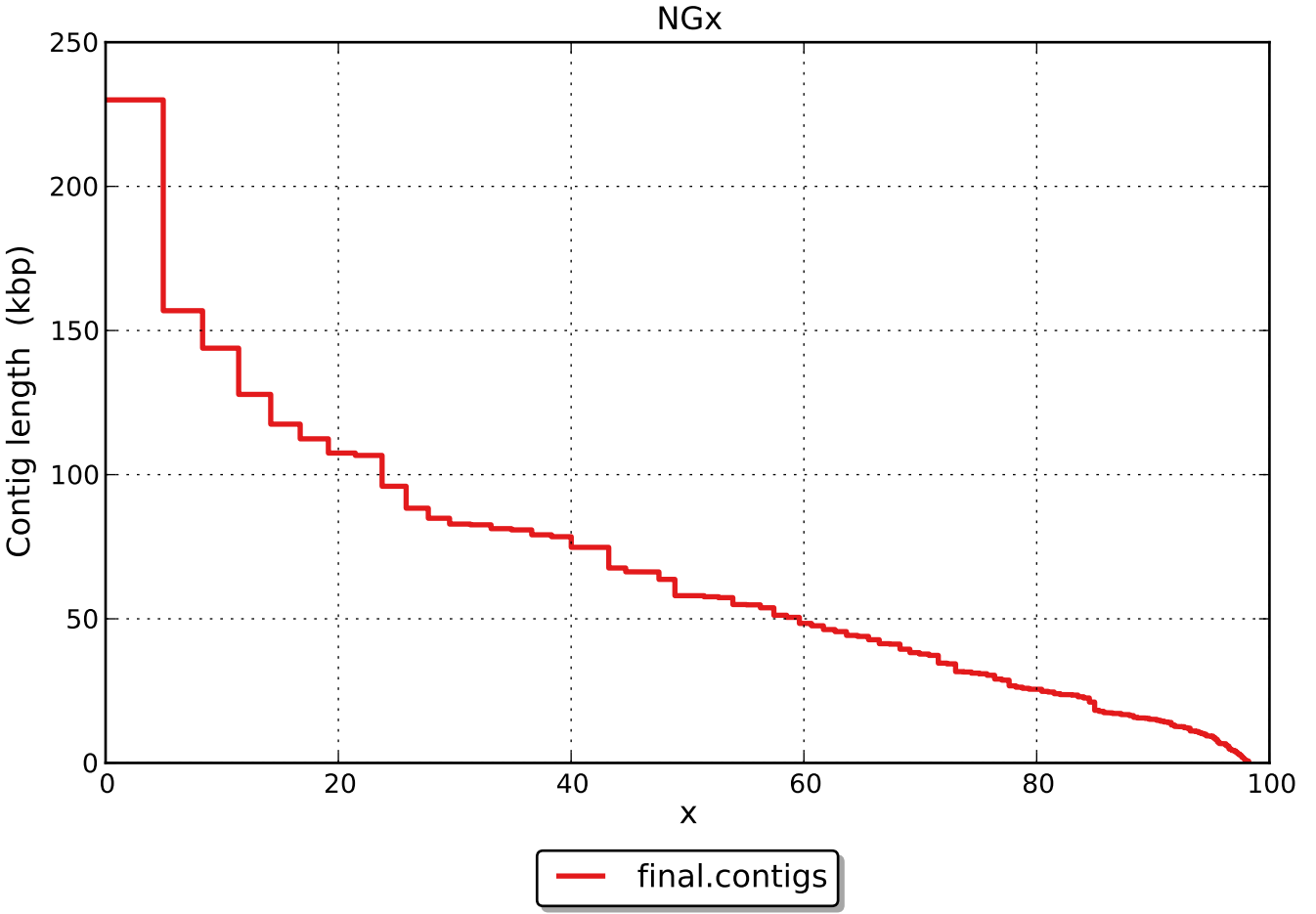
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

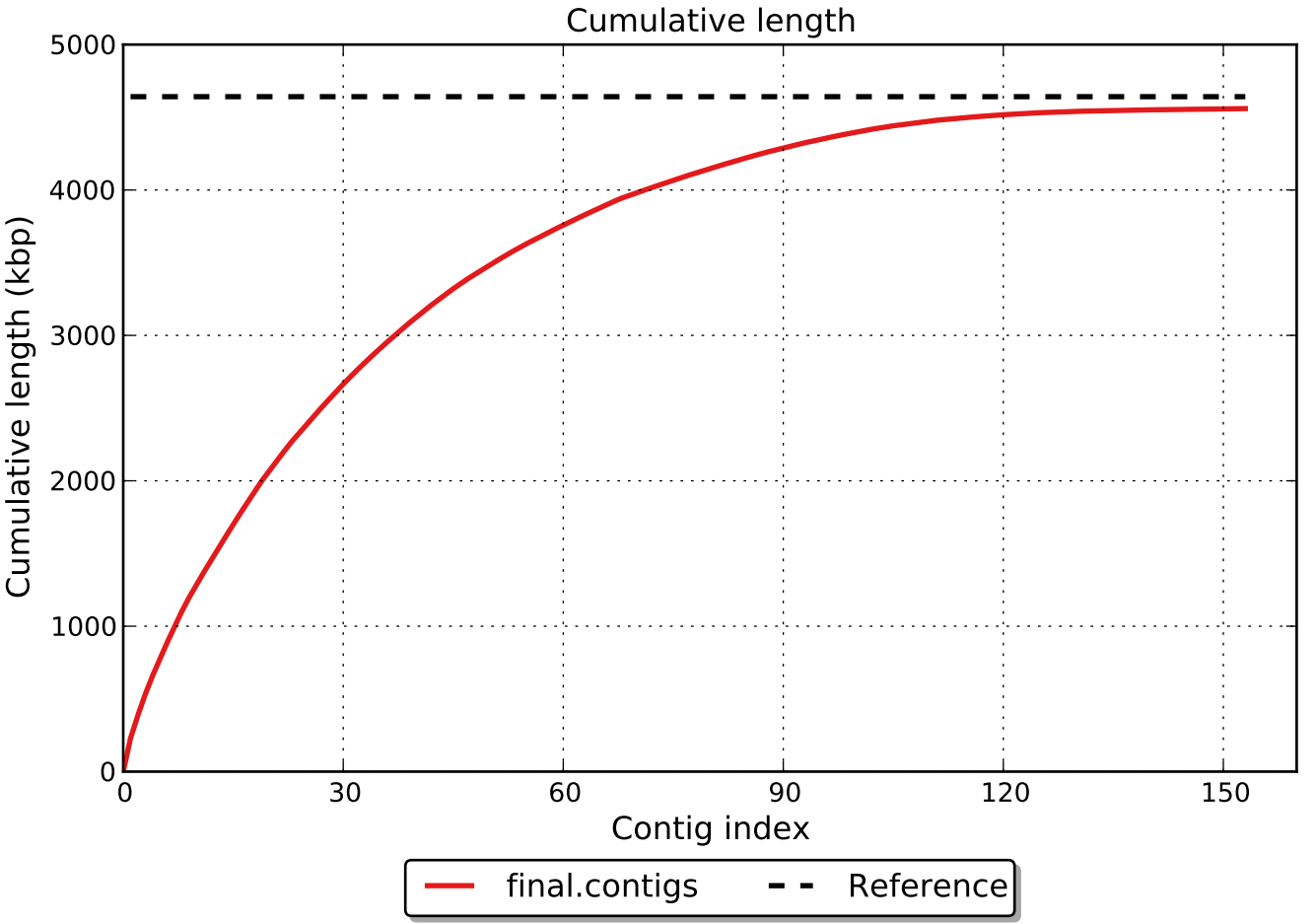
Unaligned report

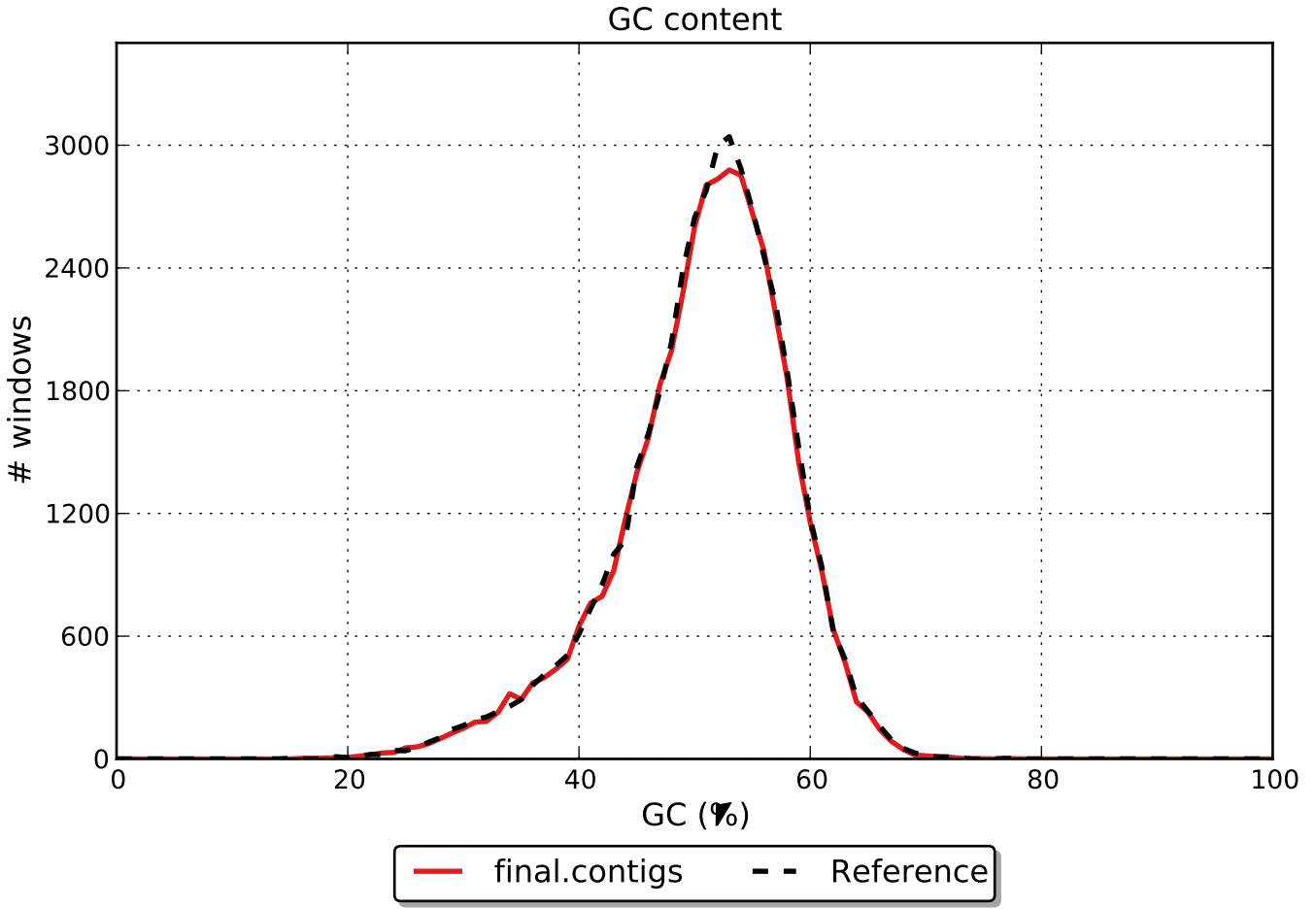
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

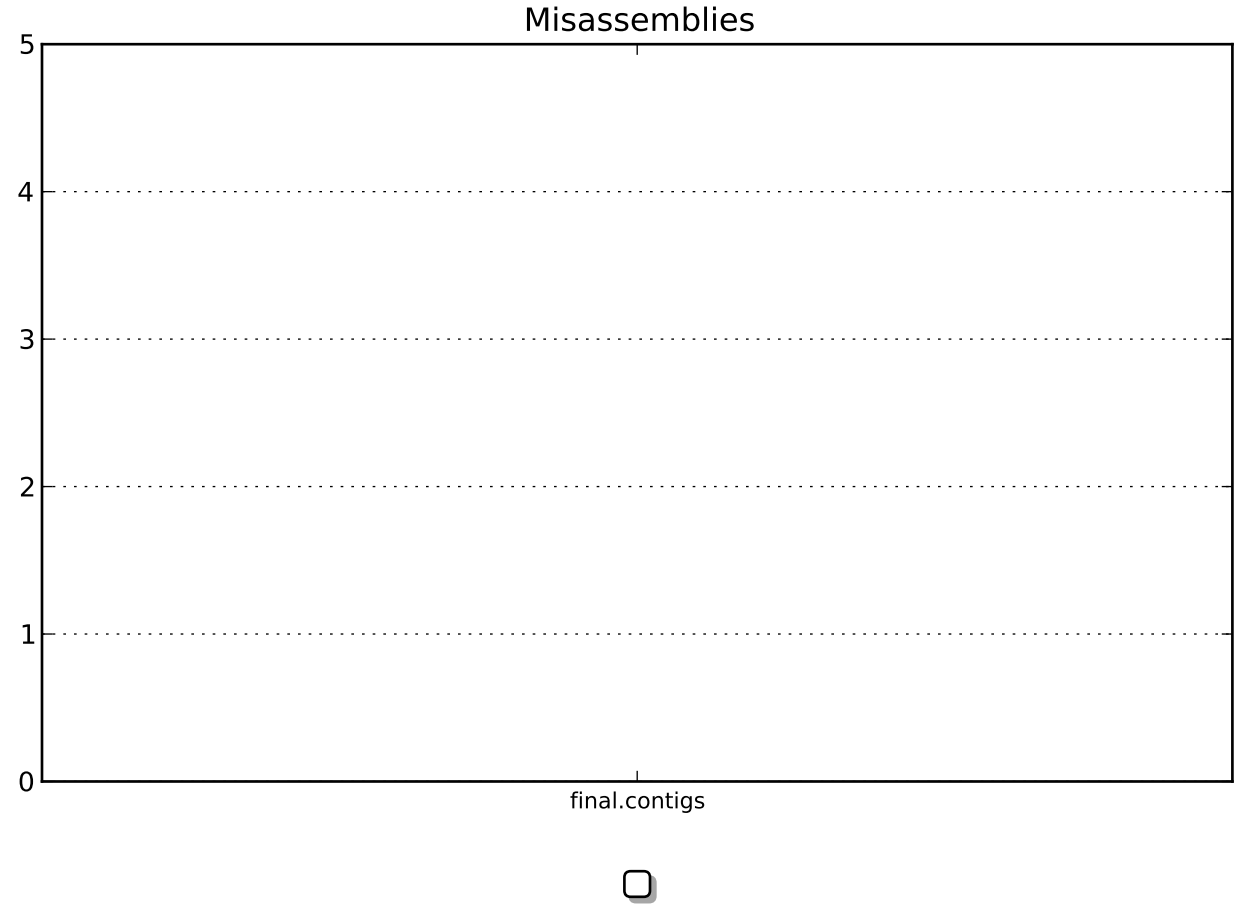
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

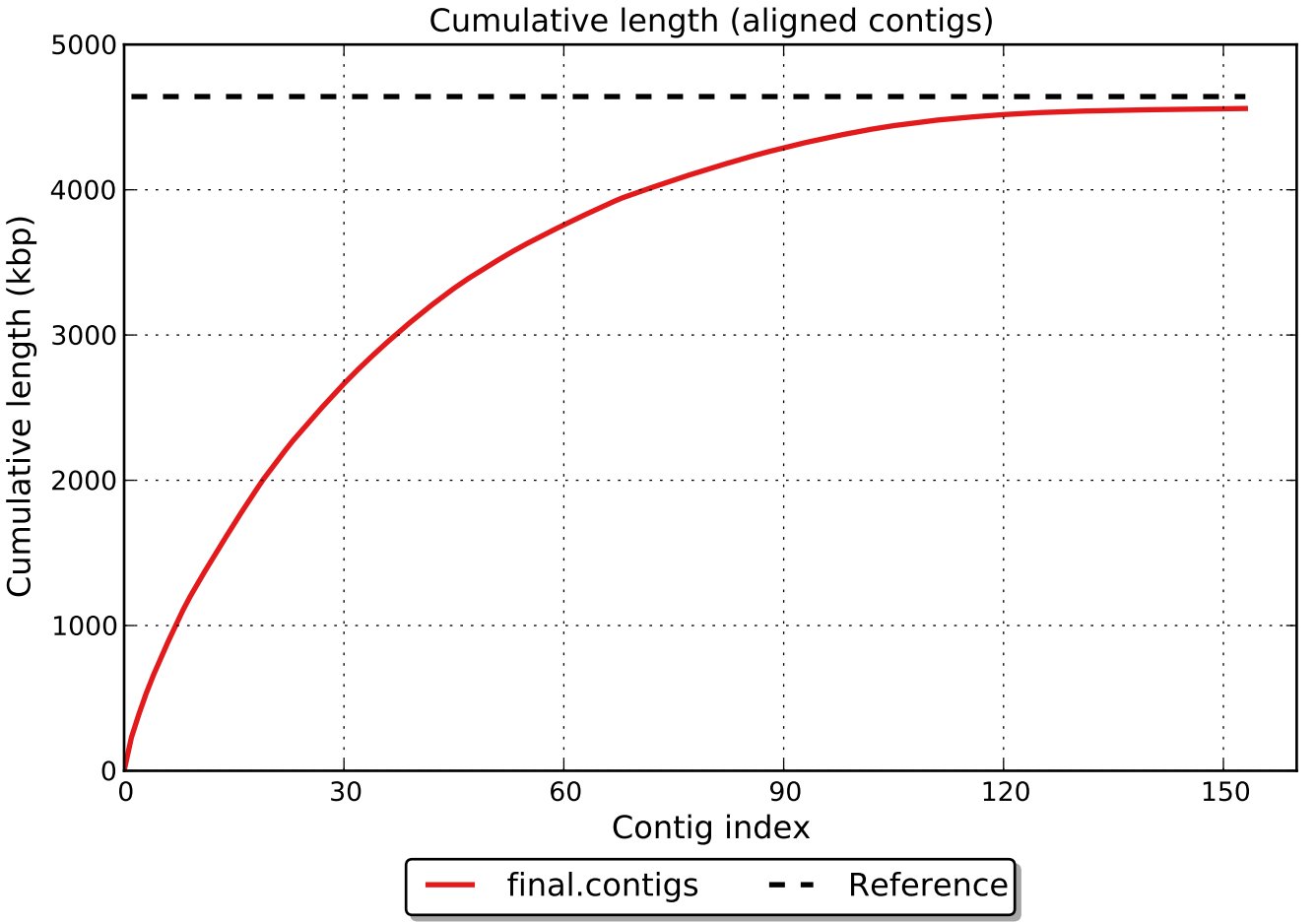

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

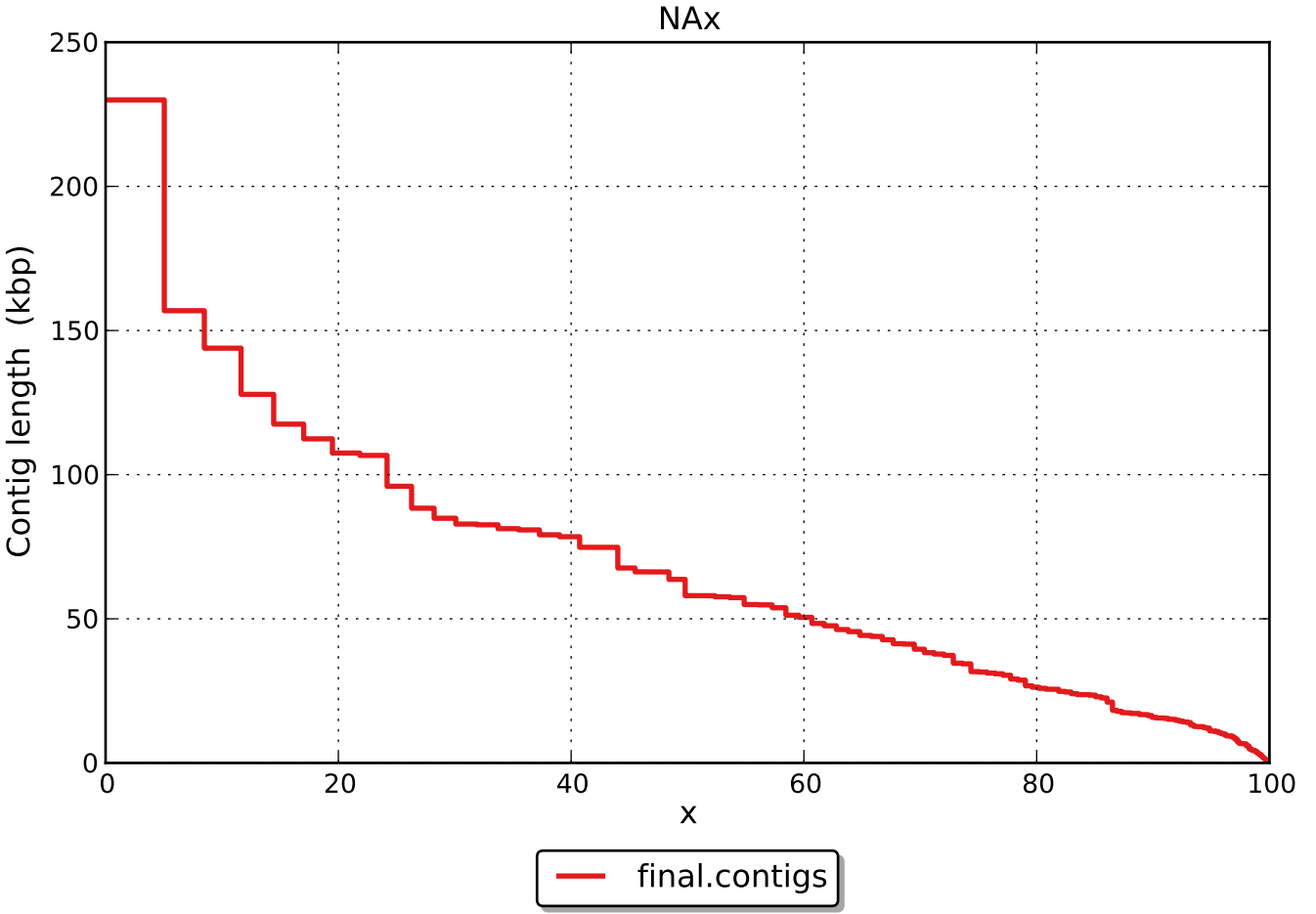

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

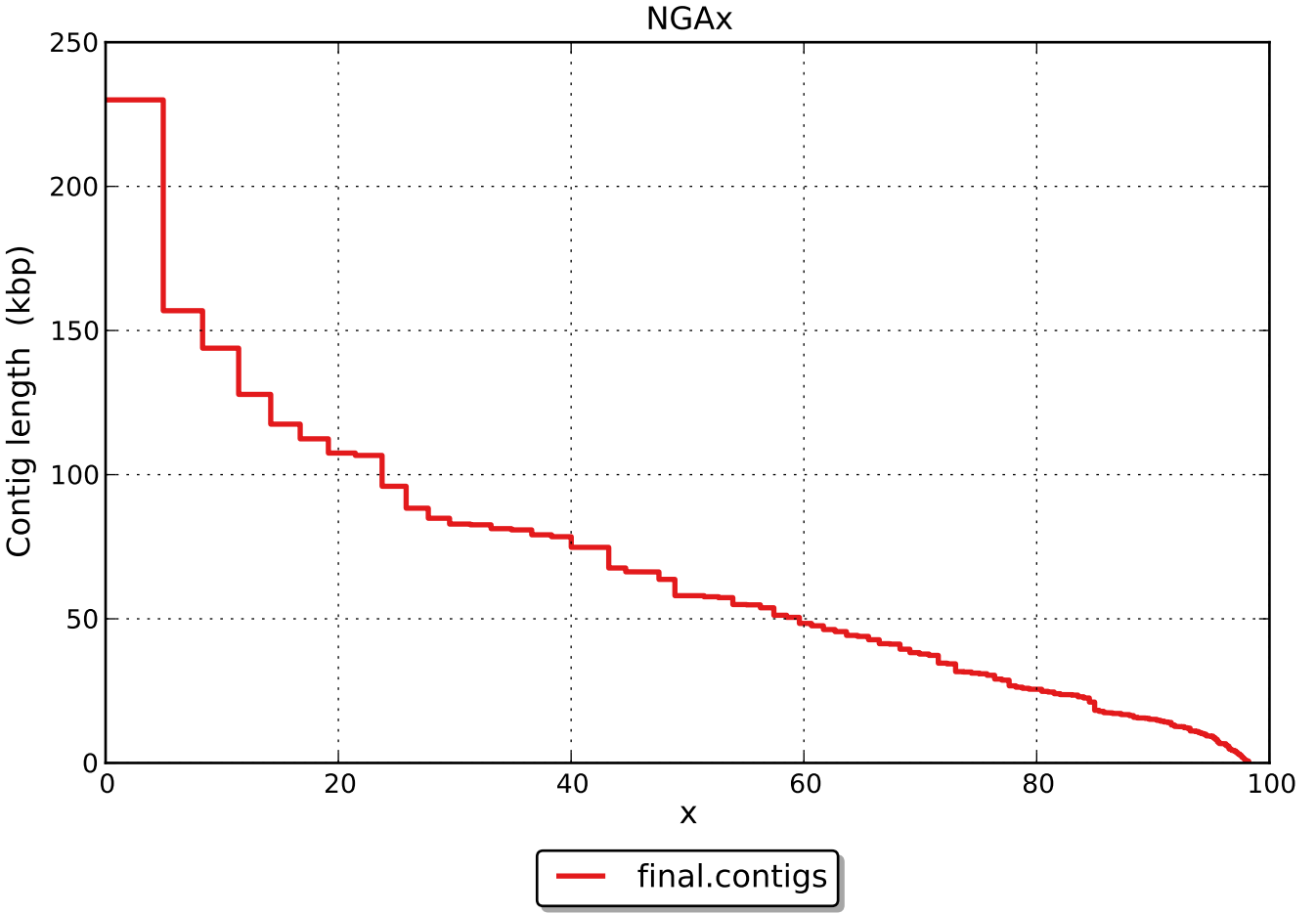

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
30
60
90
120
150
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


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
Contig length (kbp)
250
200
150
100
50
0
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