Report

	final.contigs
# contigs (>= 0 bp)	189
# contigs (>= 1000 bp)	184
Total length (>= 0 bp)	5562479
Total length (>= 1000 bp)	5558739
# contigs	189
Largest contig	134607
Total length	5562479
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	46051
NG50	46051
N75	28622
NG75	28622
L50	38
LG50	38
L75	77
LG75	77
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.985
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	134607
NA50	46051
NGA50	46051
NA75	28622
NGA75	28622
LA50	38
LGA50	38
LA75	77
LGA75	77

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

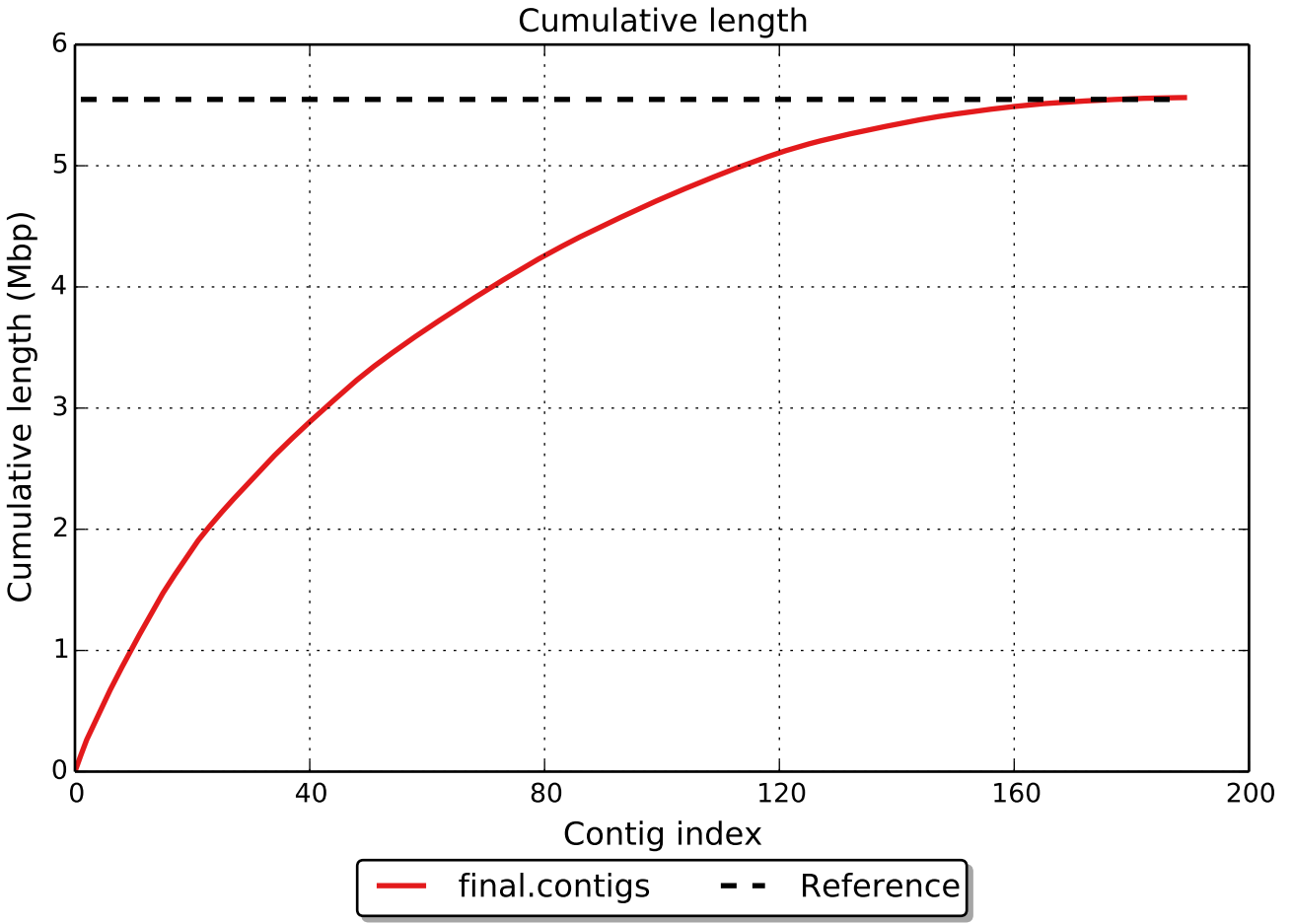
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

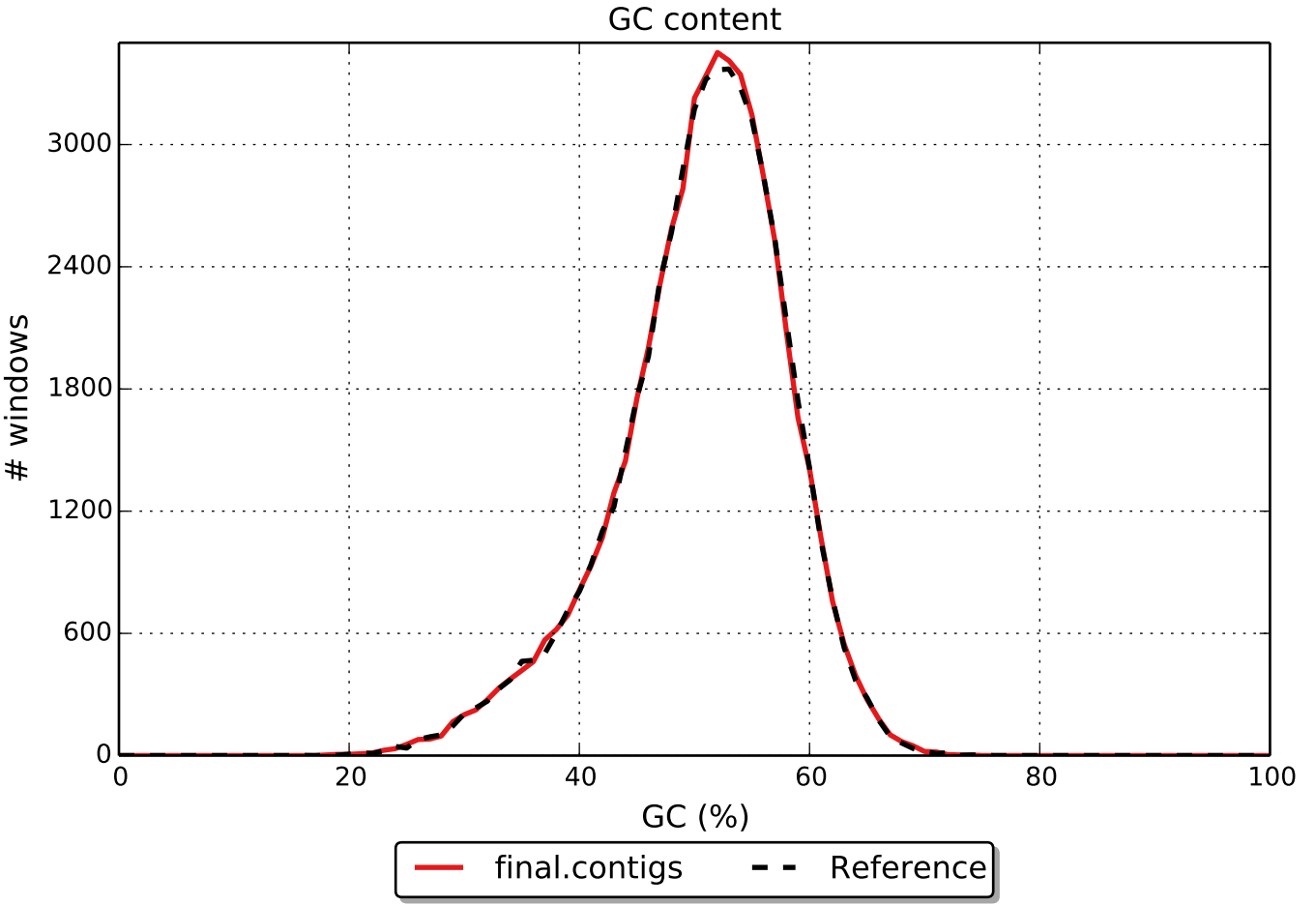
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

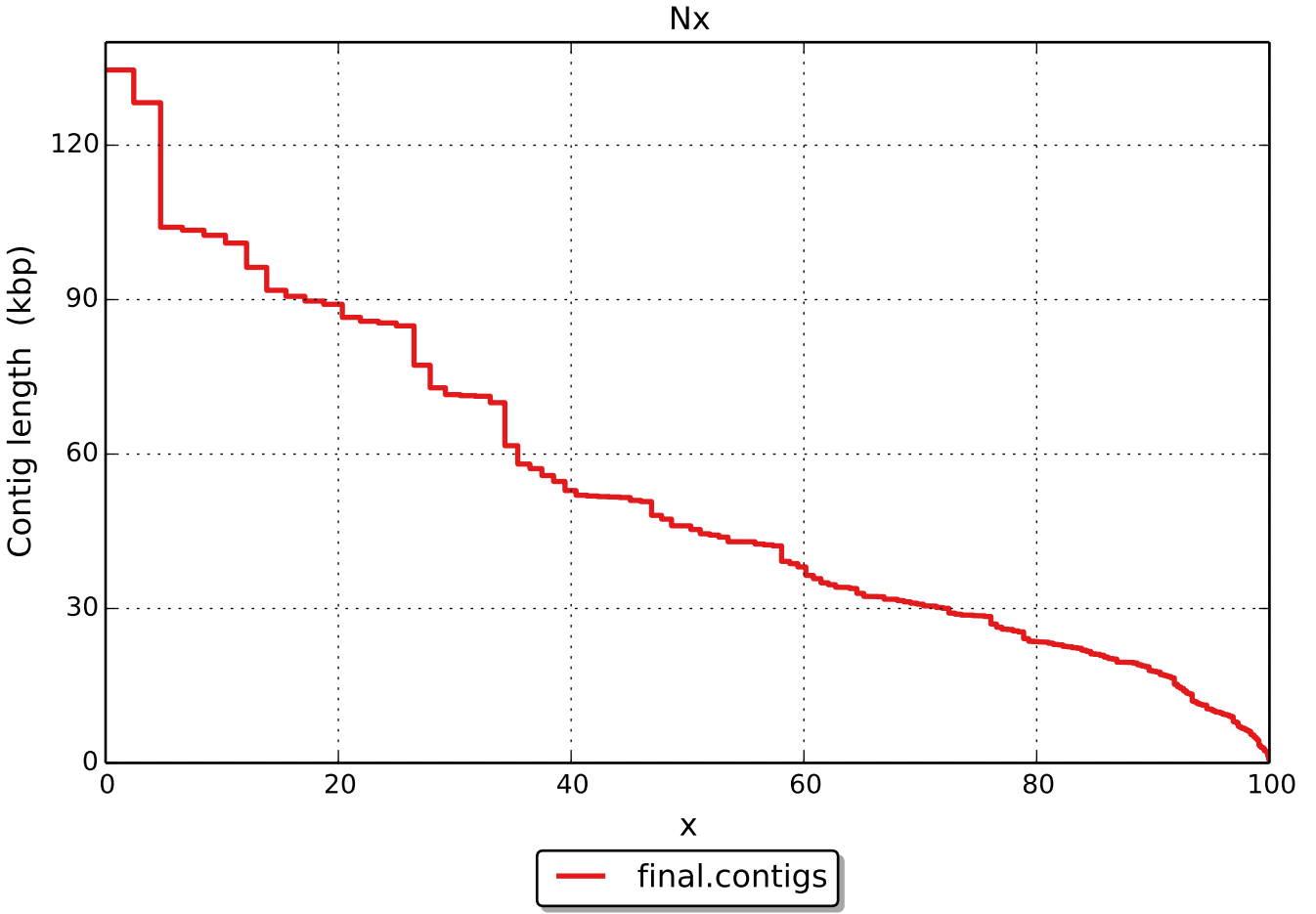
Unaligned report

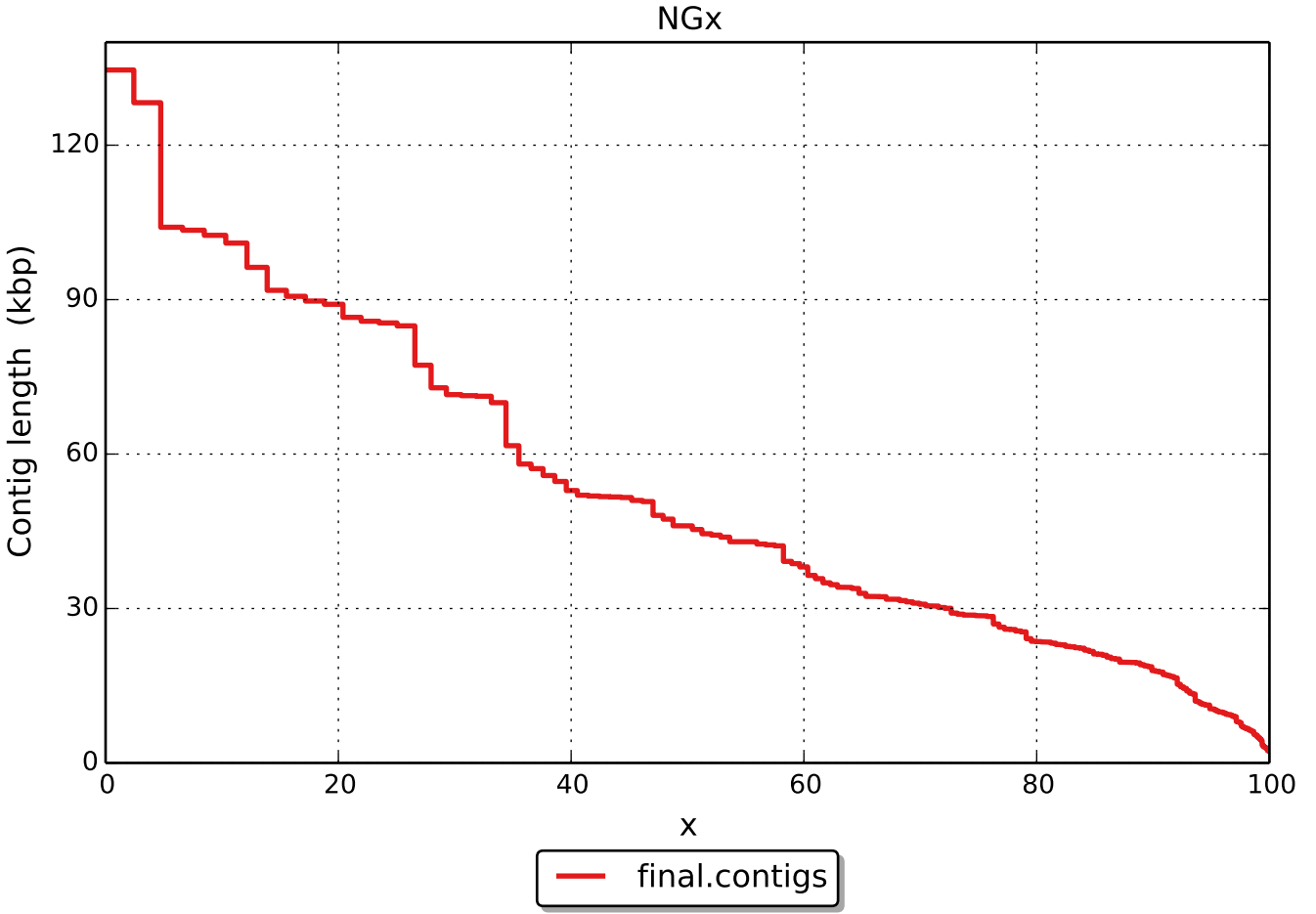
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

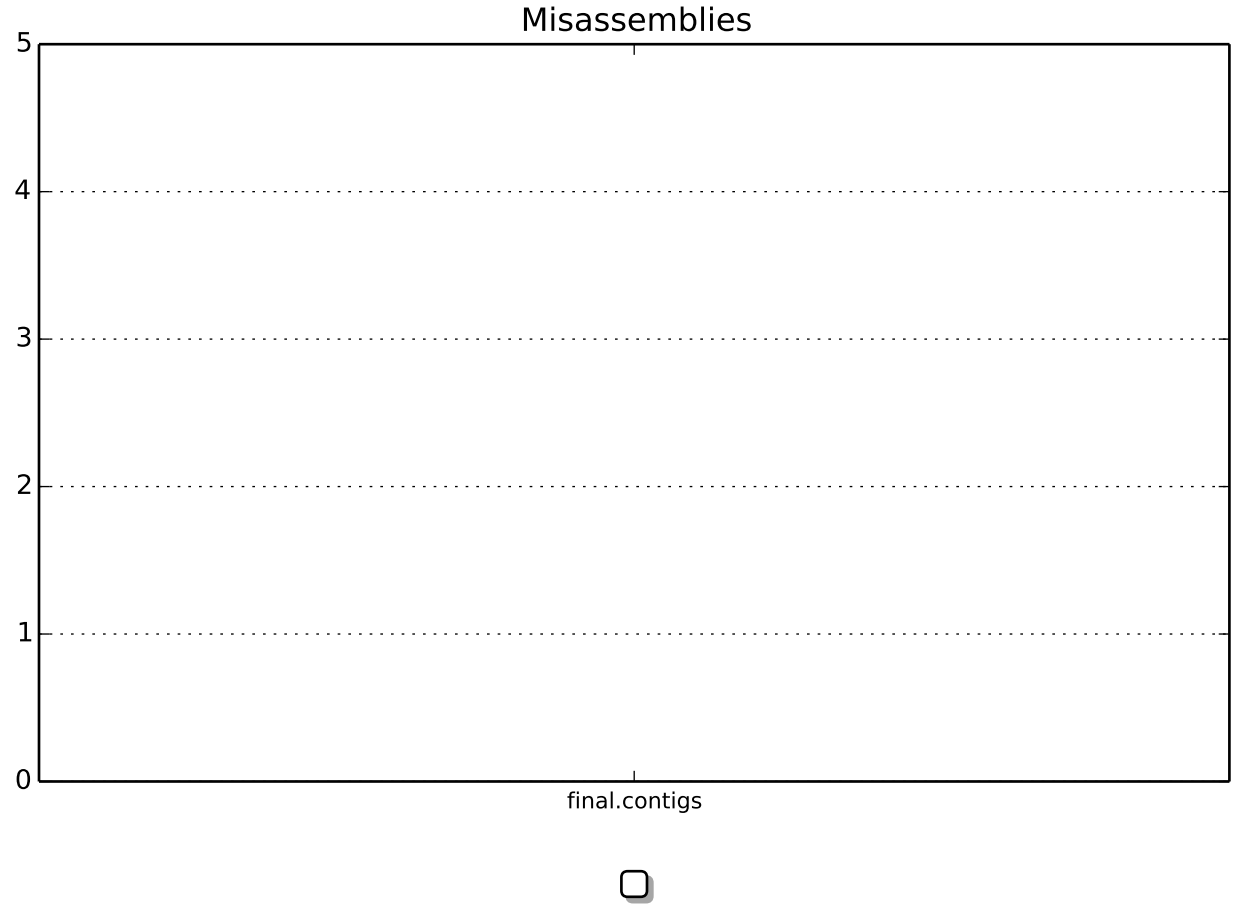
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

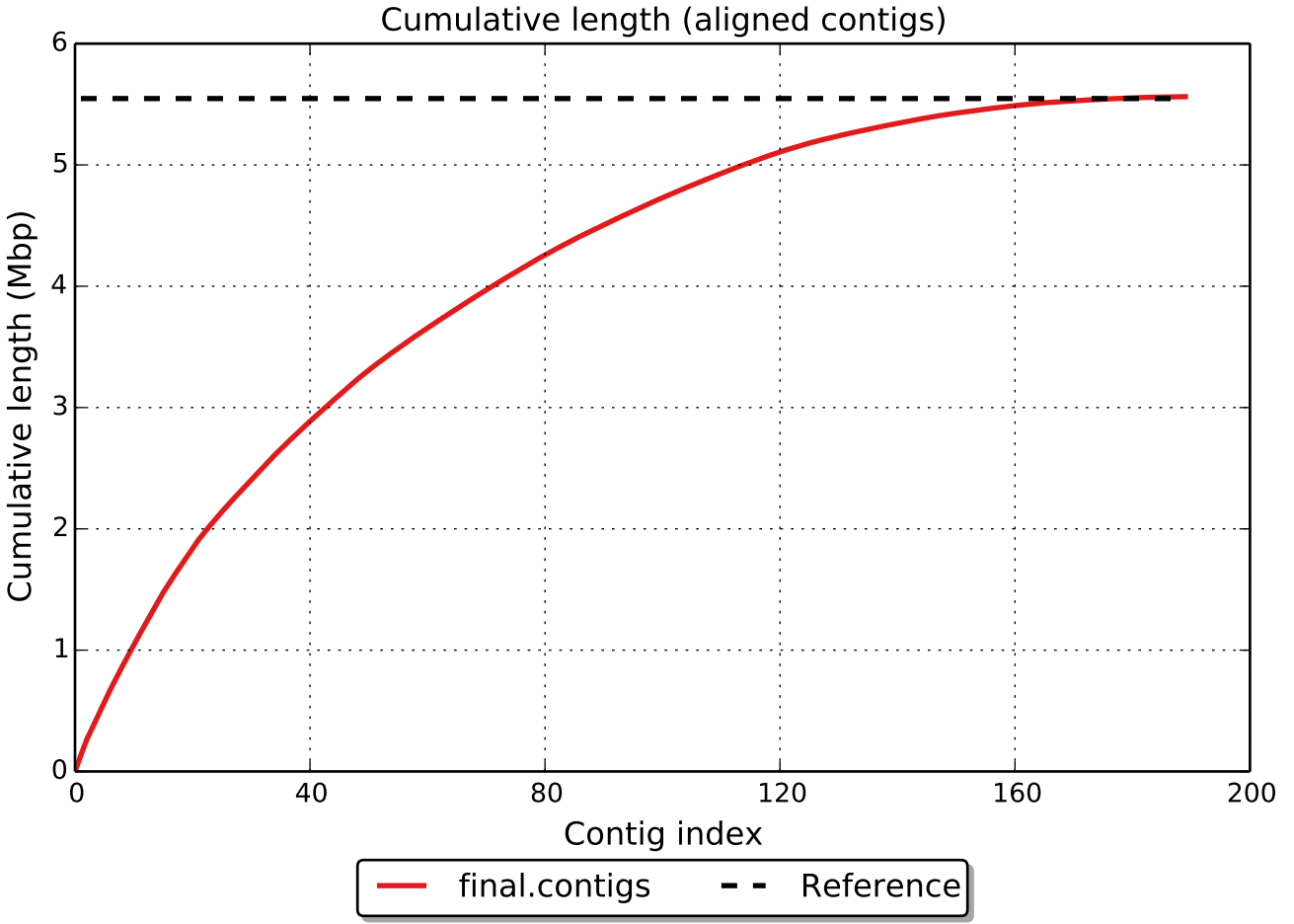

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
40
80
120
160
200
Contig index
final.contigs
Reference

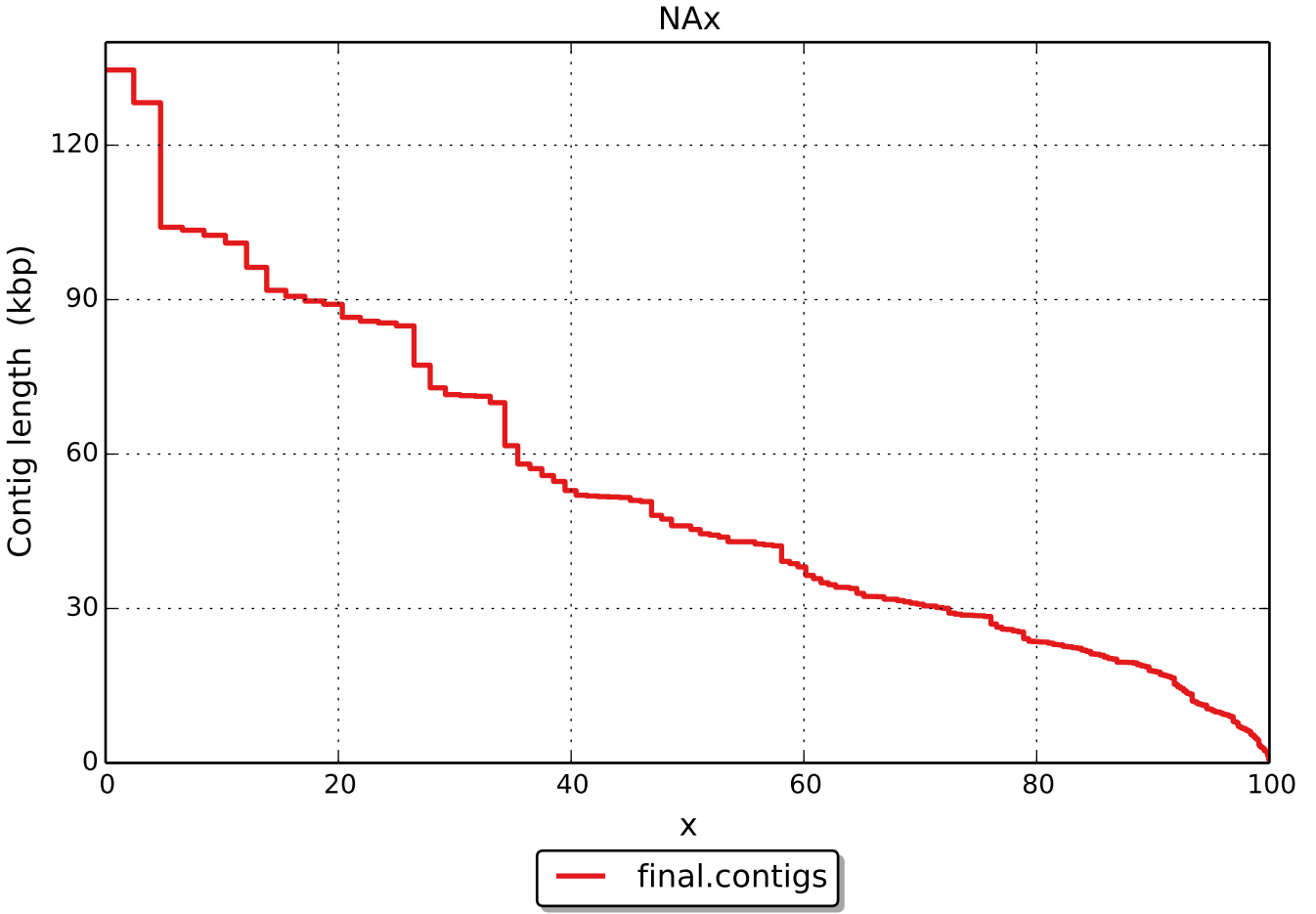

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

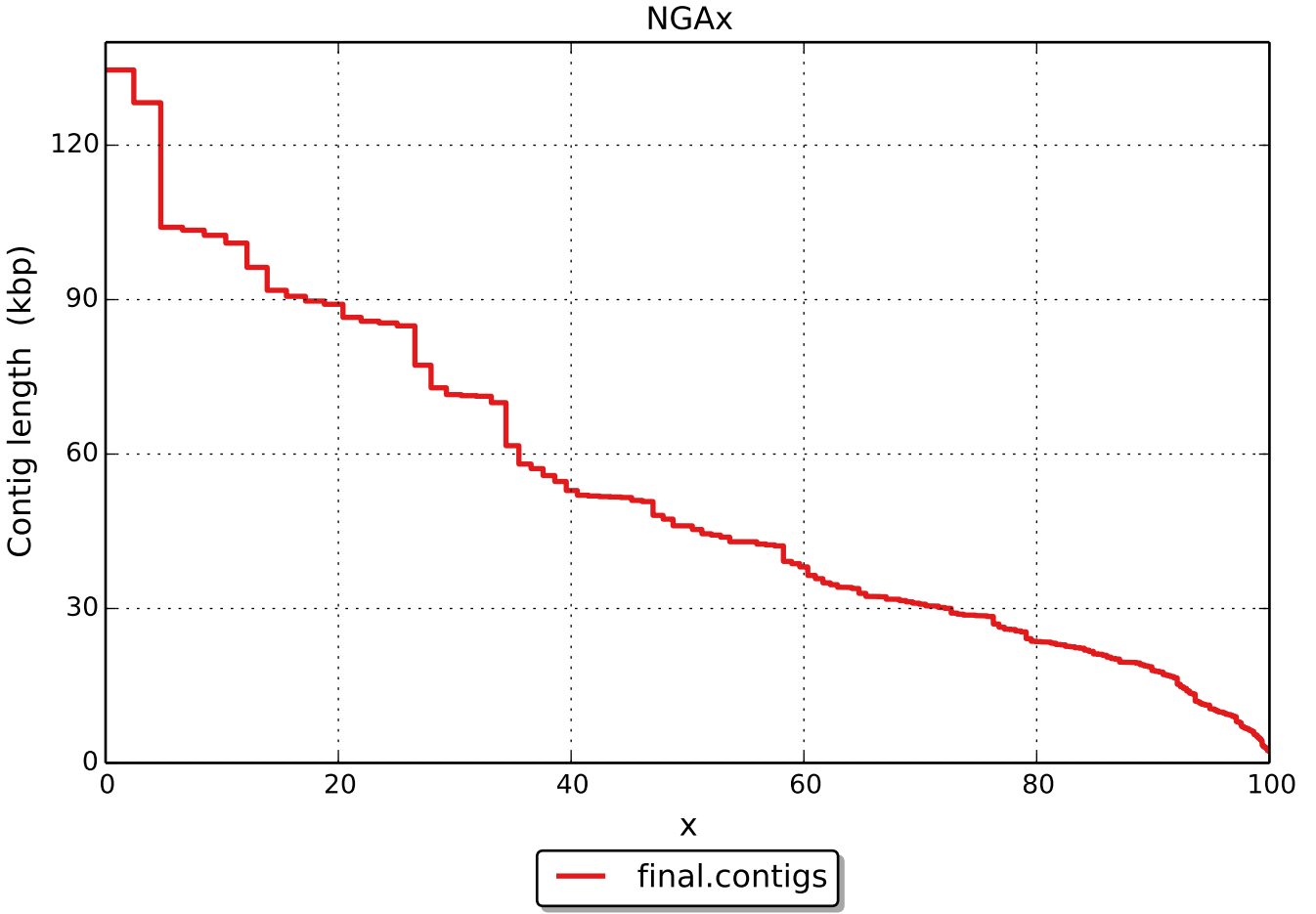

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


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)
0
1
2
3
4
5
6
0
40
80
120
160
200
Contig index
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