Report

	final.contigs
# contigs (>= 0 bp)	185
# contigs (>= 1000 bp)	180
Total length (>= 0 bp)	5694387
Total length (>= 1000 bp)	5691004
# contigs	185
Largest contig	194428
Total length	5694387
Reference length	5478683
GC (%)	50.56
Reference GC (%)	50.50
N50	53310
NG50	55863
N75	29375
NG75	31554
L50	32
LG50	30
L75	68
LG75	63
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	182916
Genome fraction (%)	99.996
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.19
# indels per 100 kbp	0.07
Largest alignment	165821
NA50	48266
NGA50	50788
NA75	25862
NGA75	28247
LA50	35
LGA50	33
LA75	75
LGA75	69

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

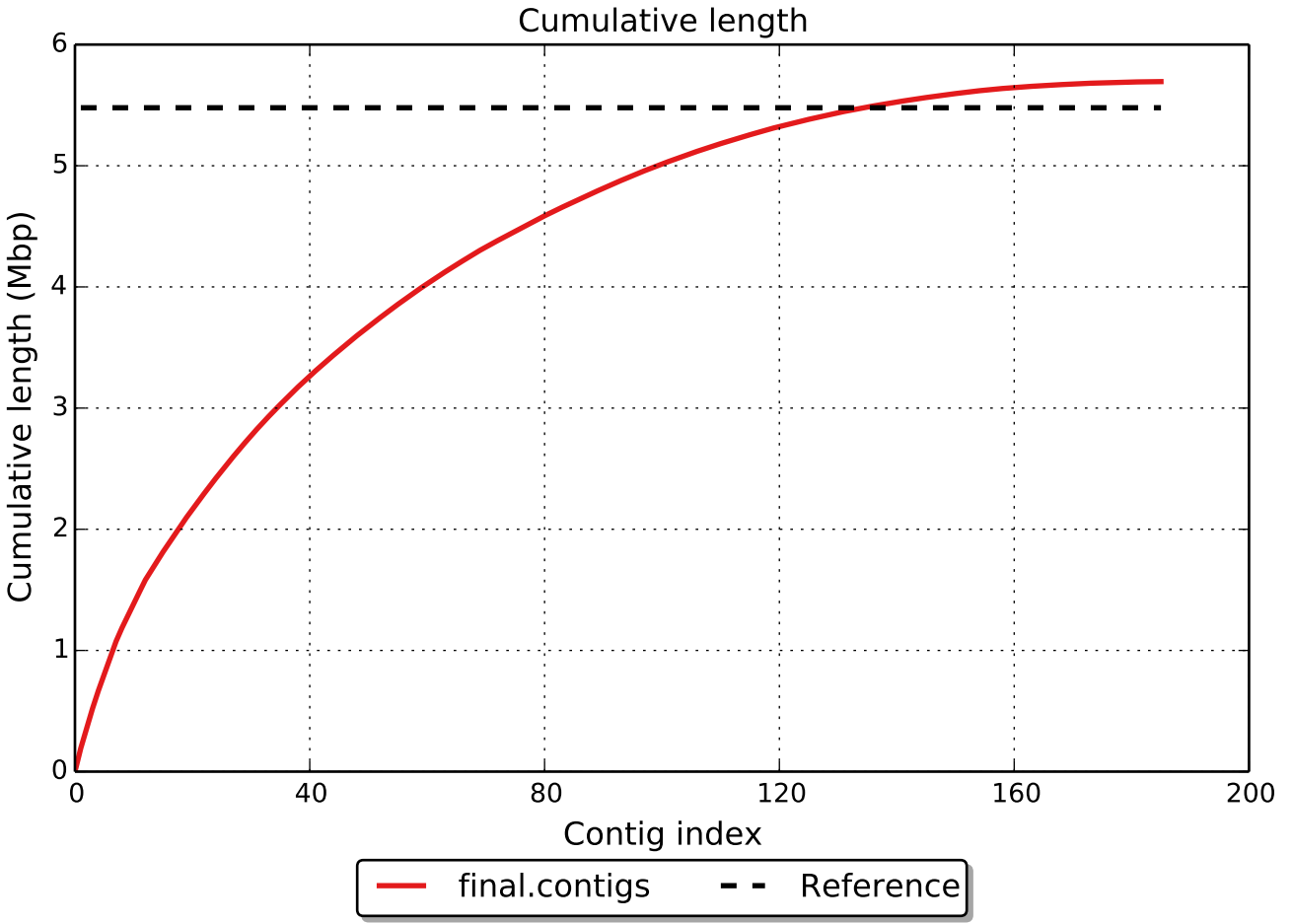
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	832
# indels	4
# short indels	4
# long indels	0
Indels length	4

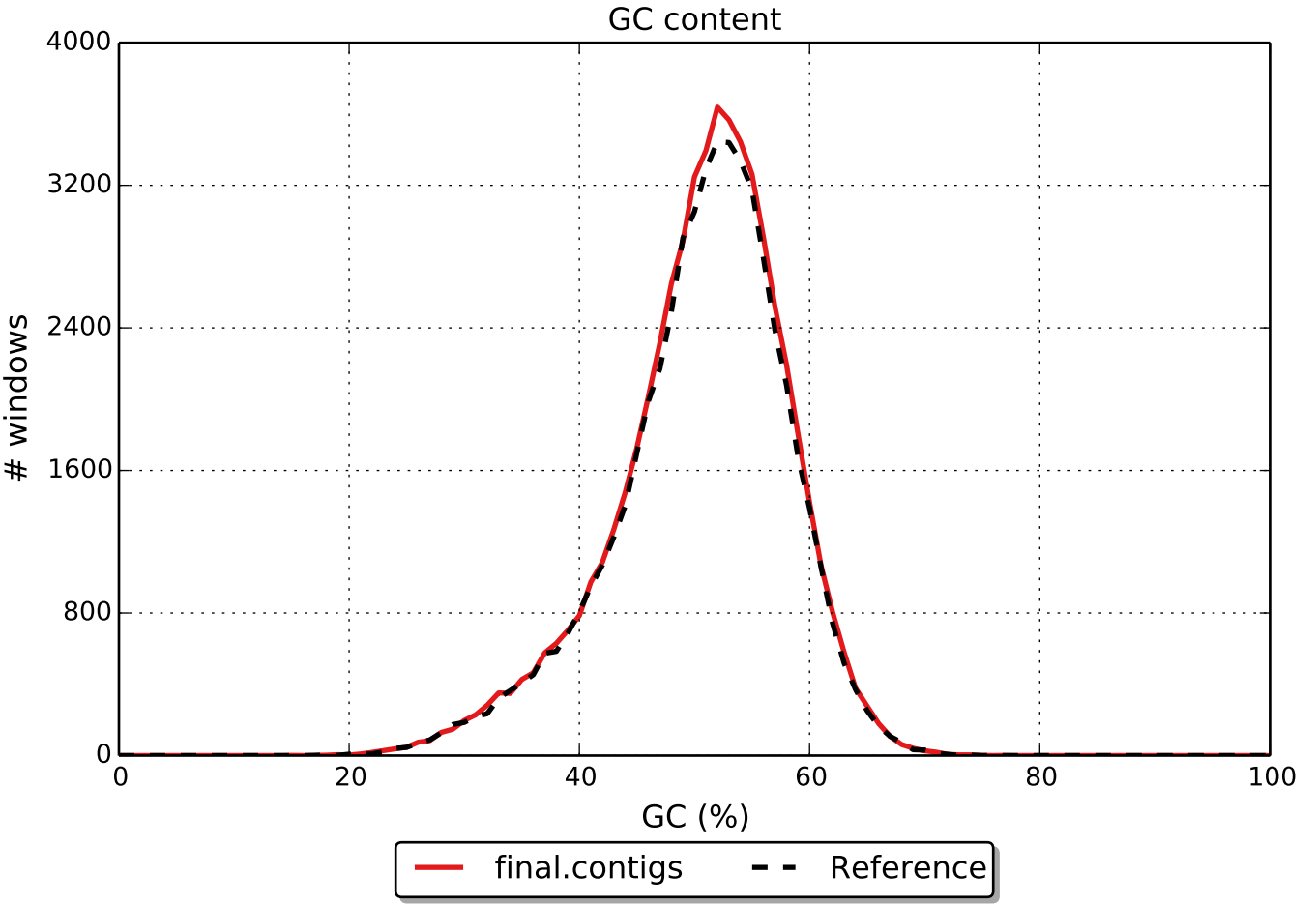
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

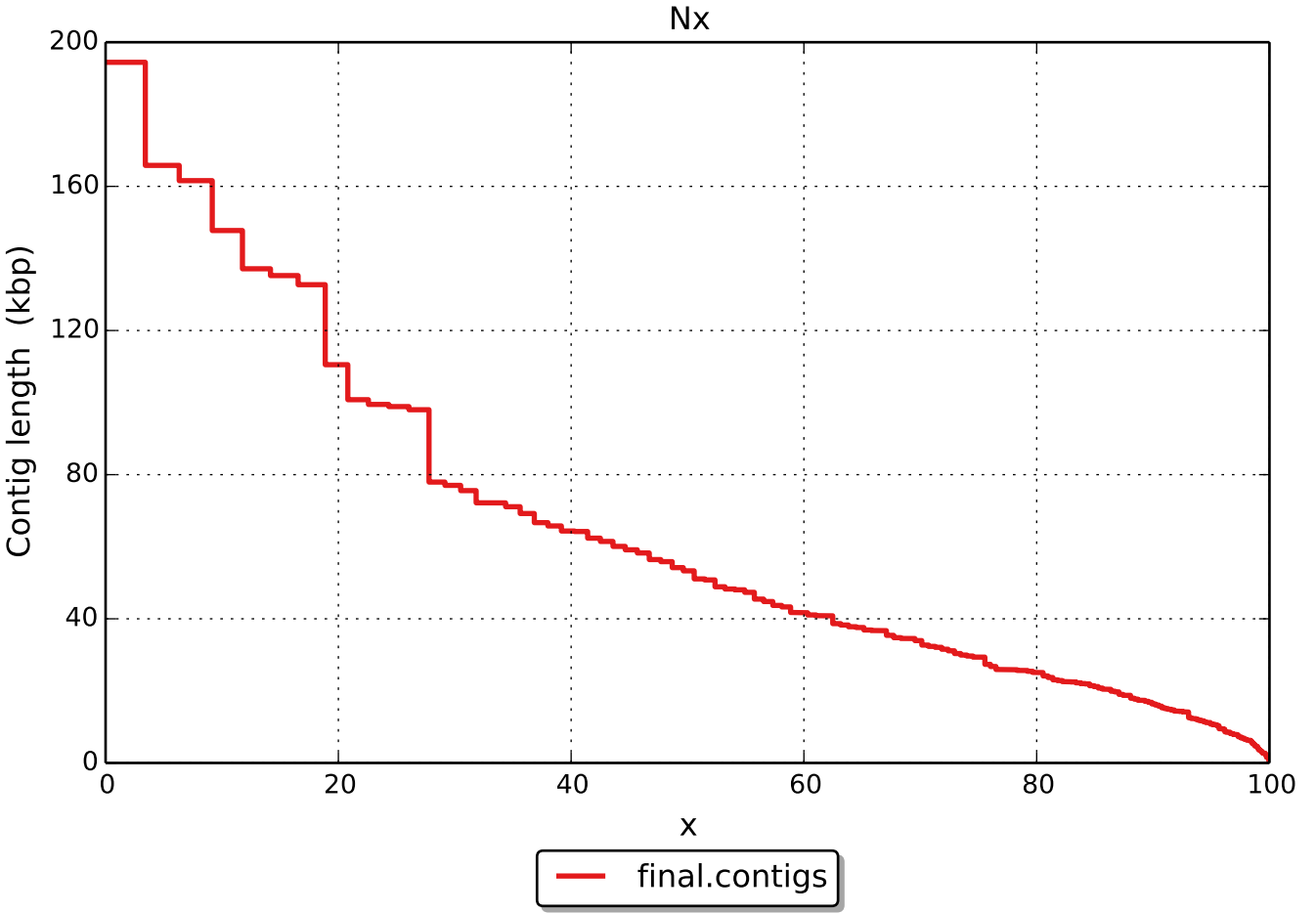
Unaligned report

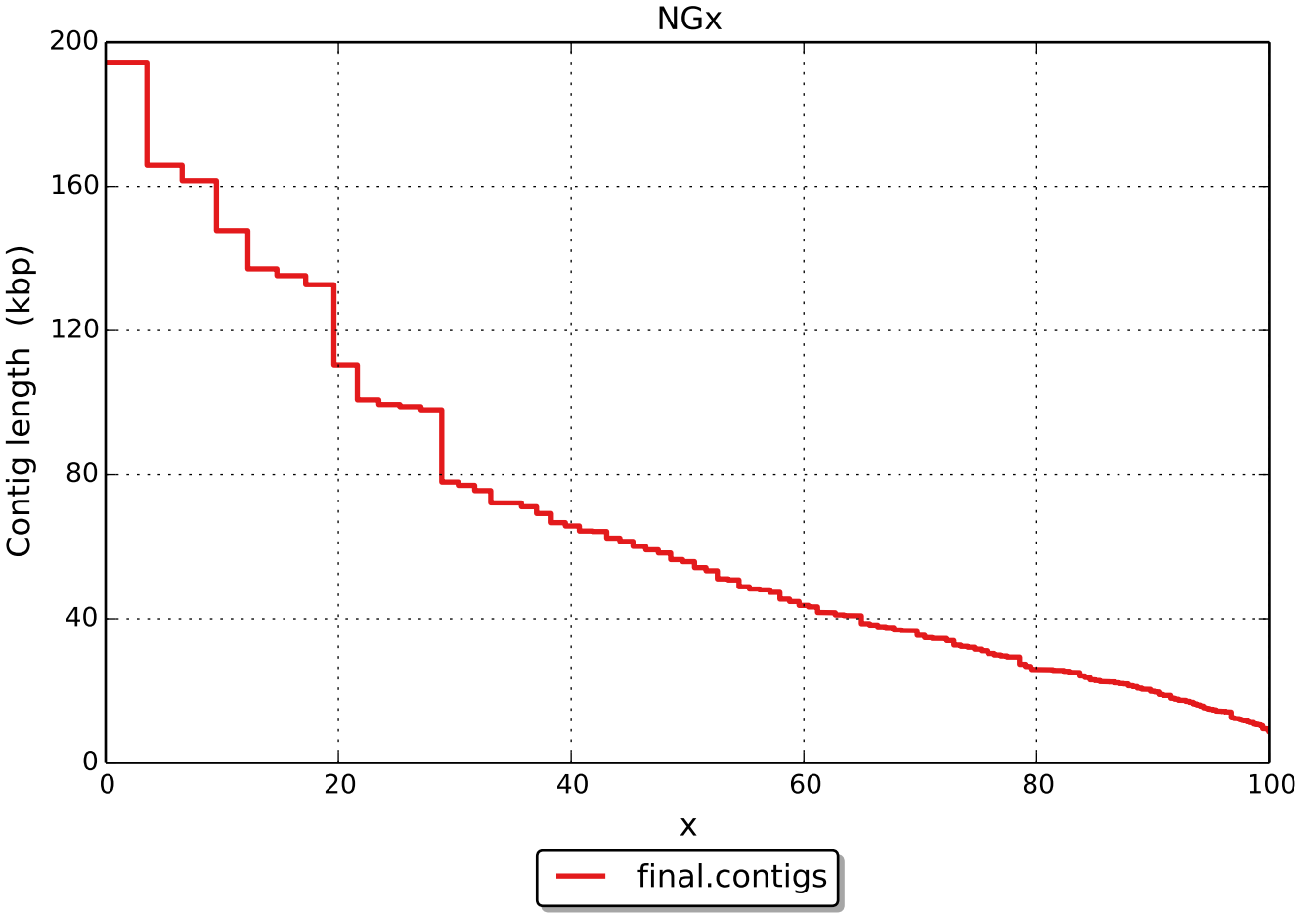
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	182916
# N's	0

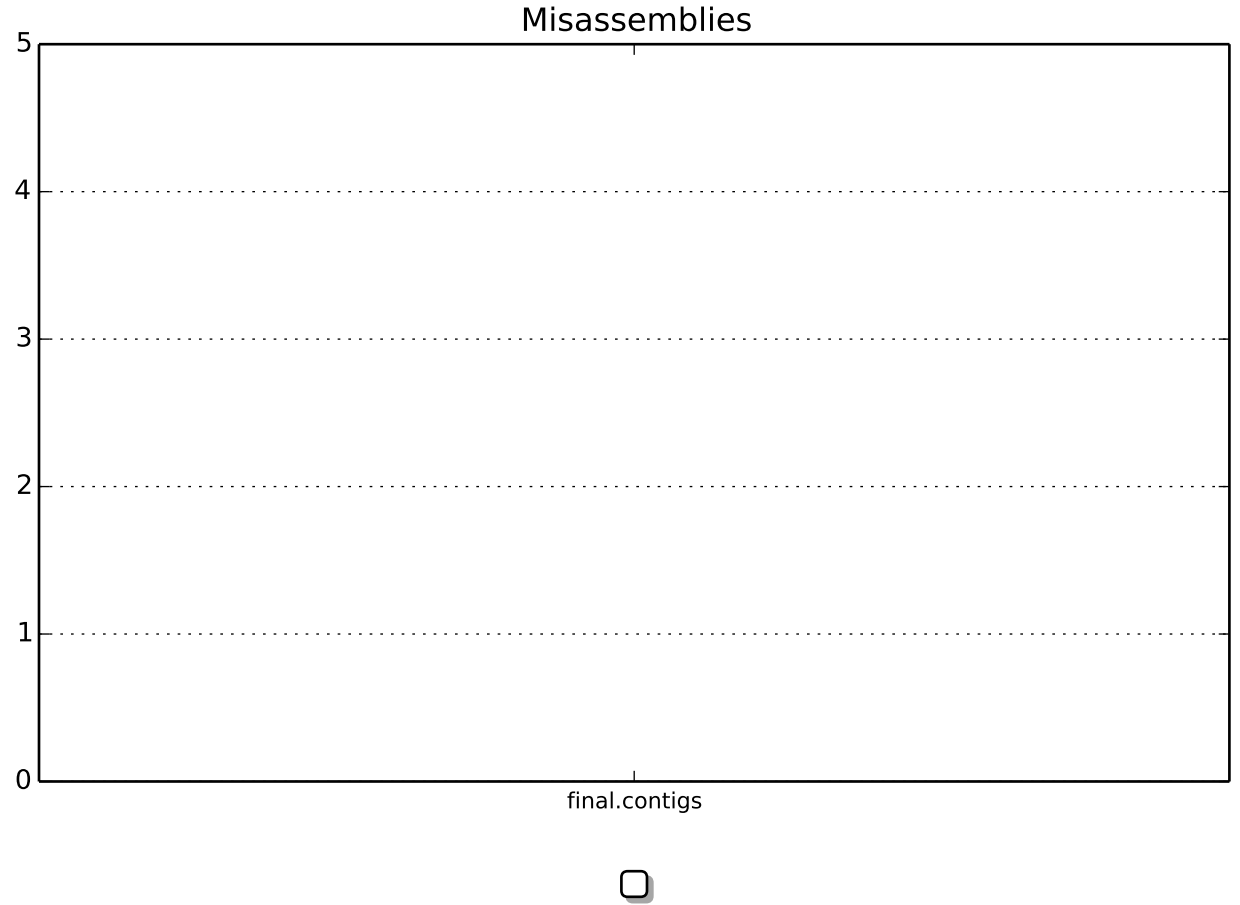
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

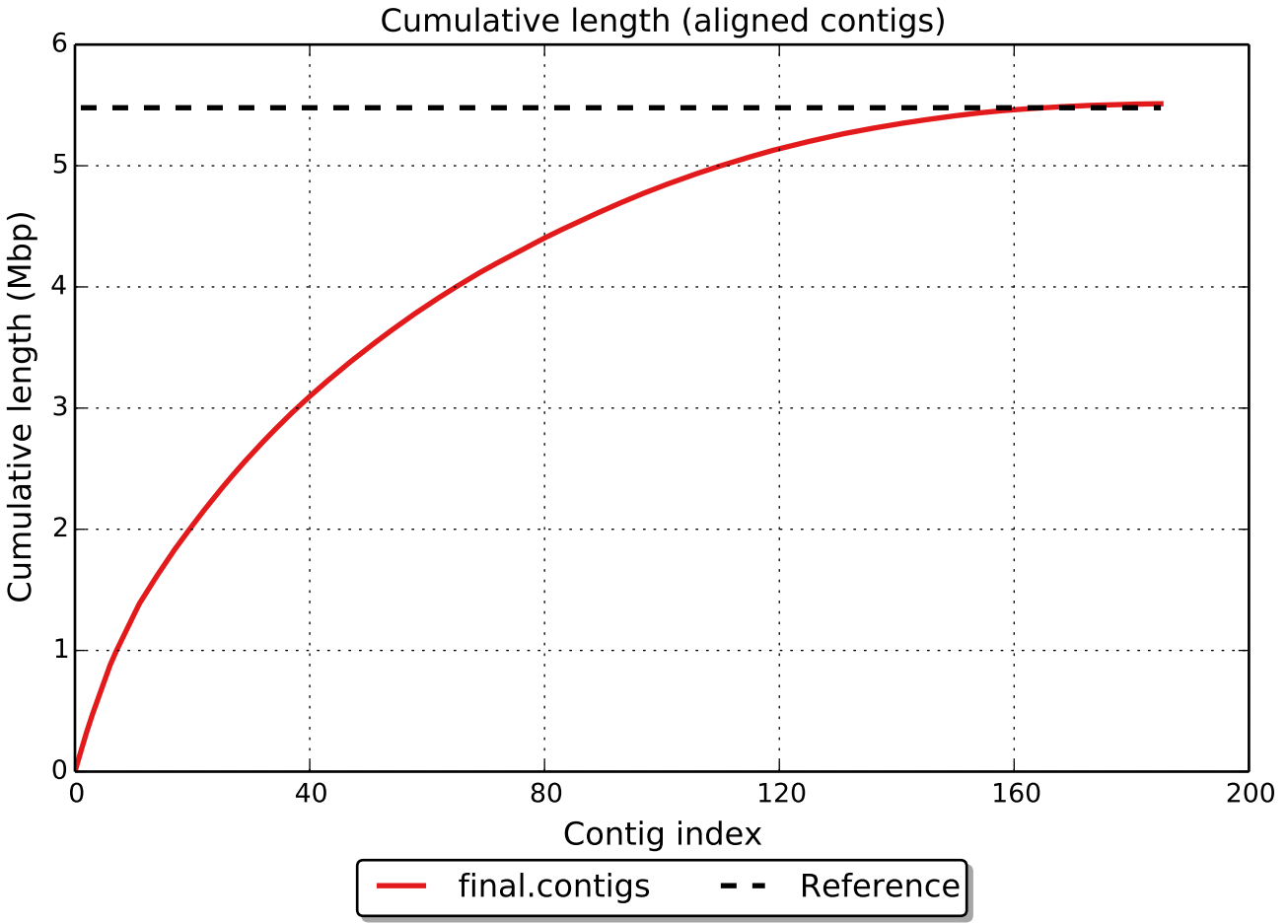

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
40
80
120
160
200
Contig index
final.contigs
Reference

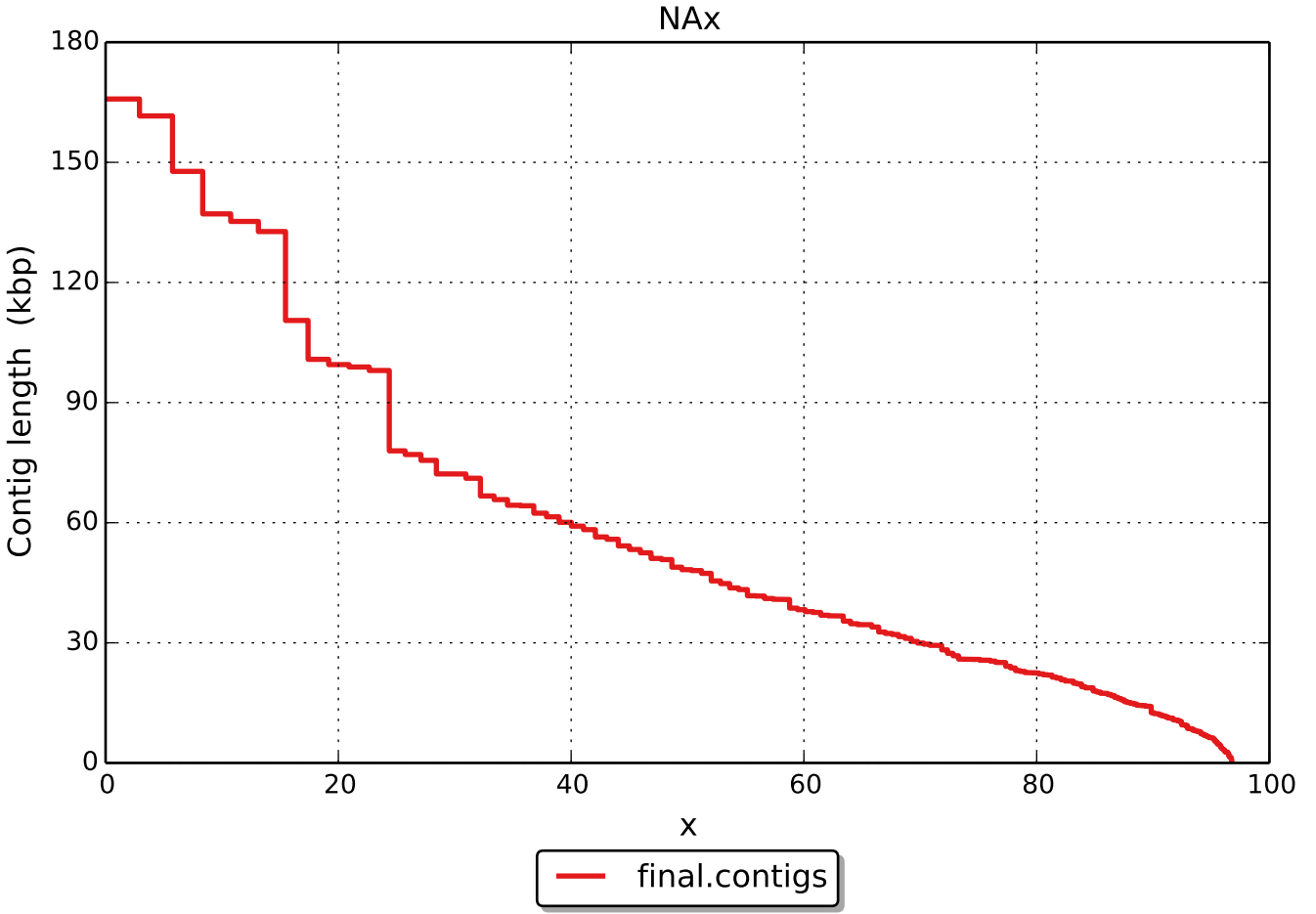

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

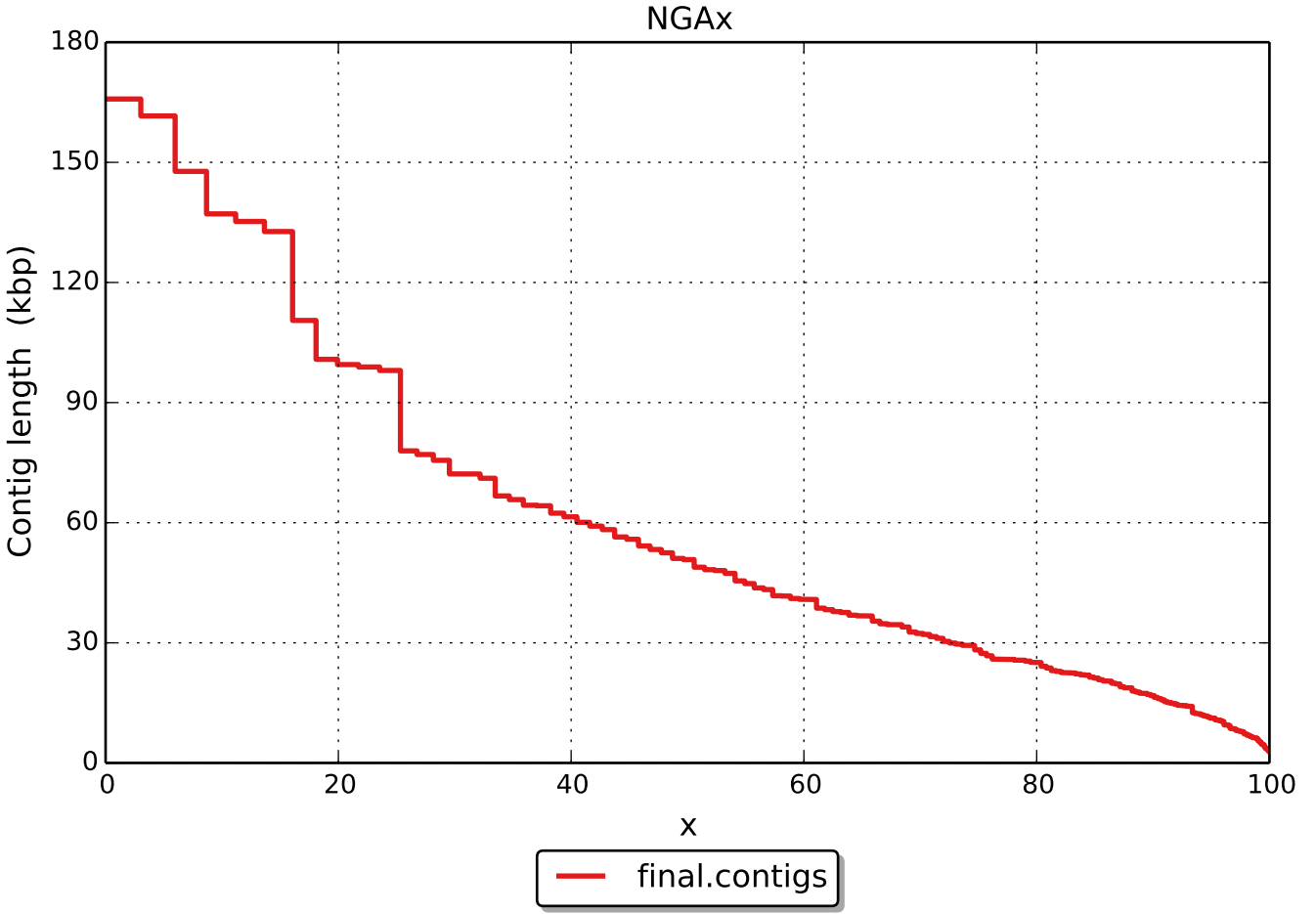

Nx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
200
160
120
80
40
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
180
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs


NGAx
180
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs