Report

	final.contigs
# contigs (>= 1000 bp)	150
# contigs (>= 5000 bp)	130
# contigs (>= 10000 bp)	109
# contigs (>= 25000 bp)	73
# contigs (>= 50000 bp)	33
Total length (>= 1000 bp)	4868129
Total length (>= 5000 bp)	4811579
Total length (>= 10000 bp)	4654625
Total length (>= 25000 bp)	4084167
Total length (>= 50000 bp)	2708933
# contigs	153
Largest contig	160557
Total length	4870317
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	56364
NG50	56364
N75	29888
NG75	29901
L50	28
LG50	28
L75	58
LG75	57
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.998
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	160557
NA50	56364
NGA50	56364
NA75	29888
NGA75	29901
LA50	28
LGA50	28
LA75	58
LGA75	57

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

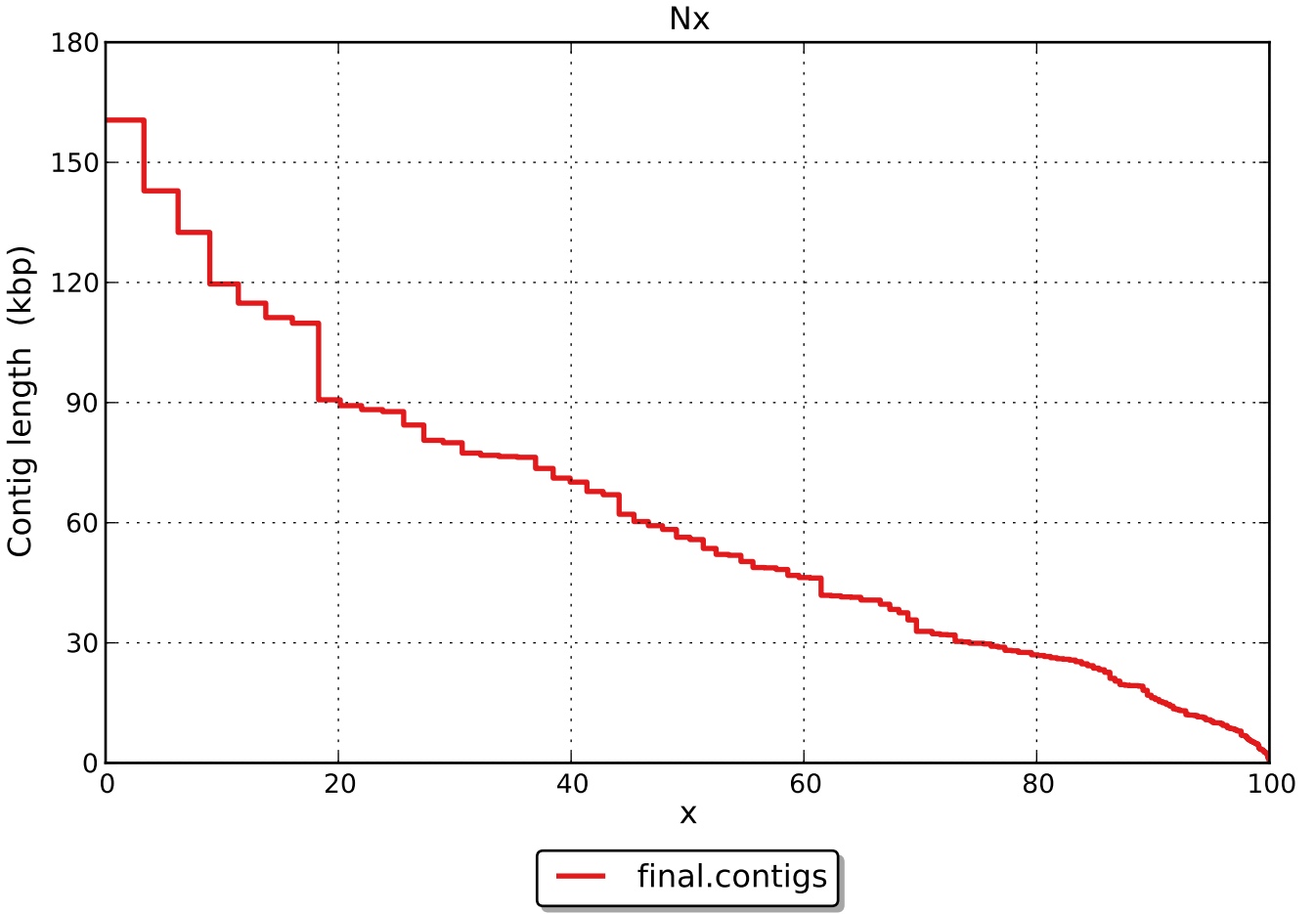
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

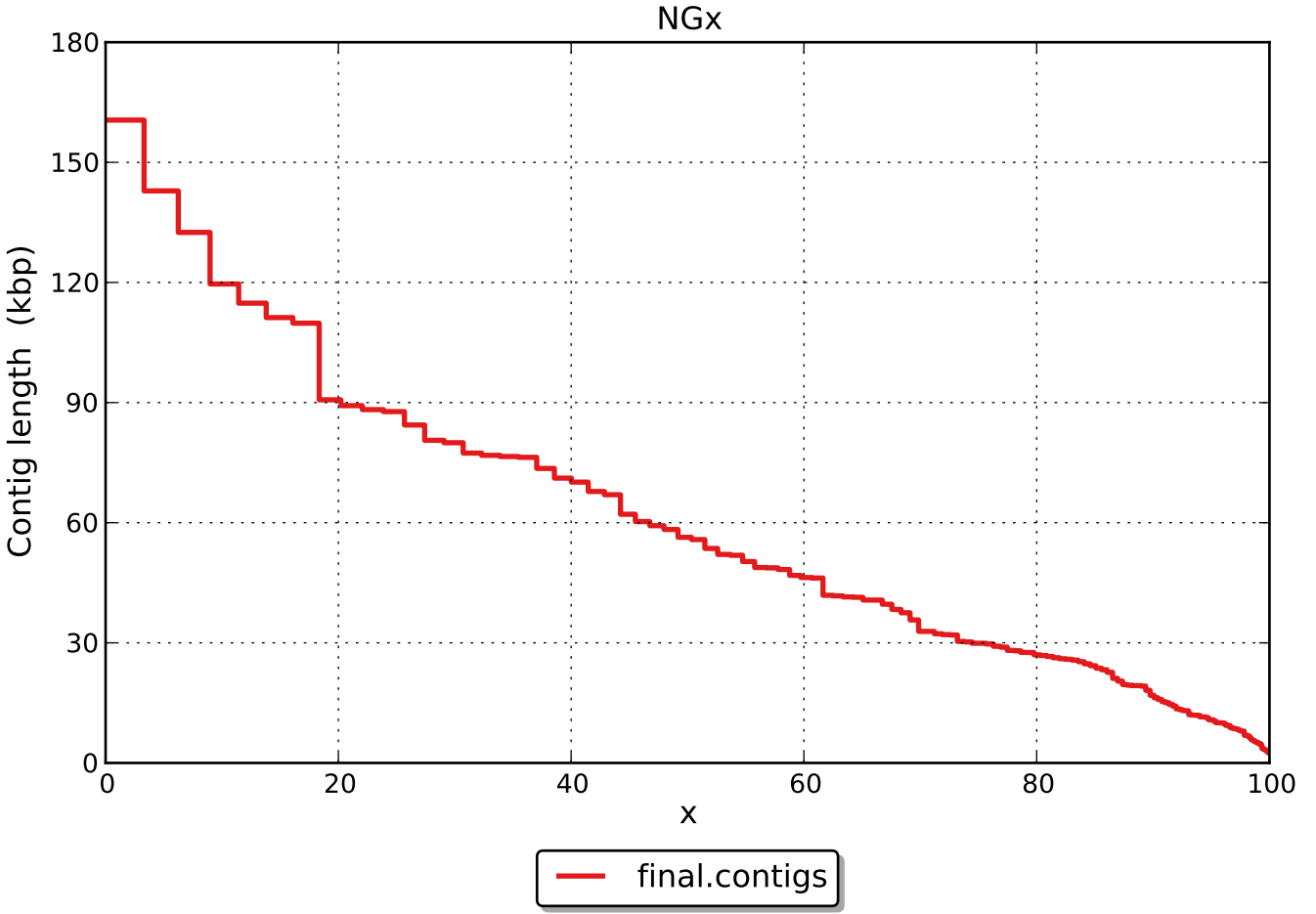
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

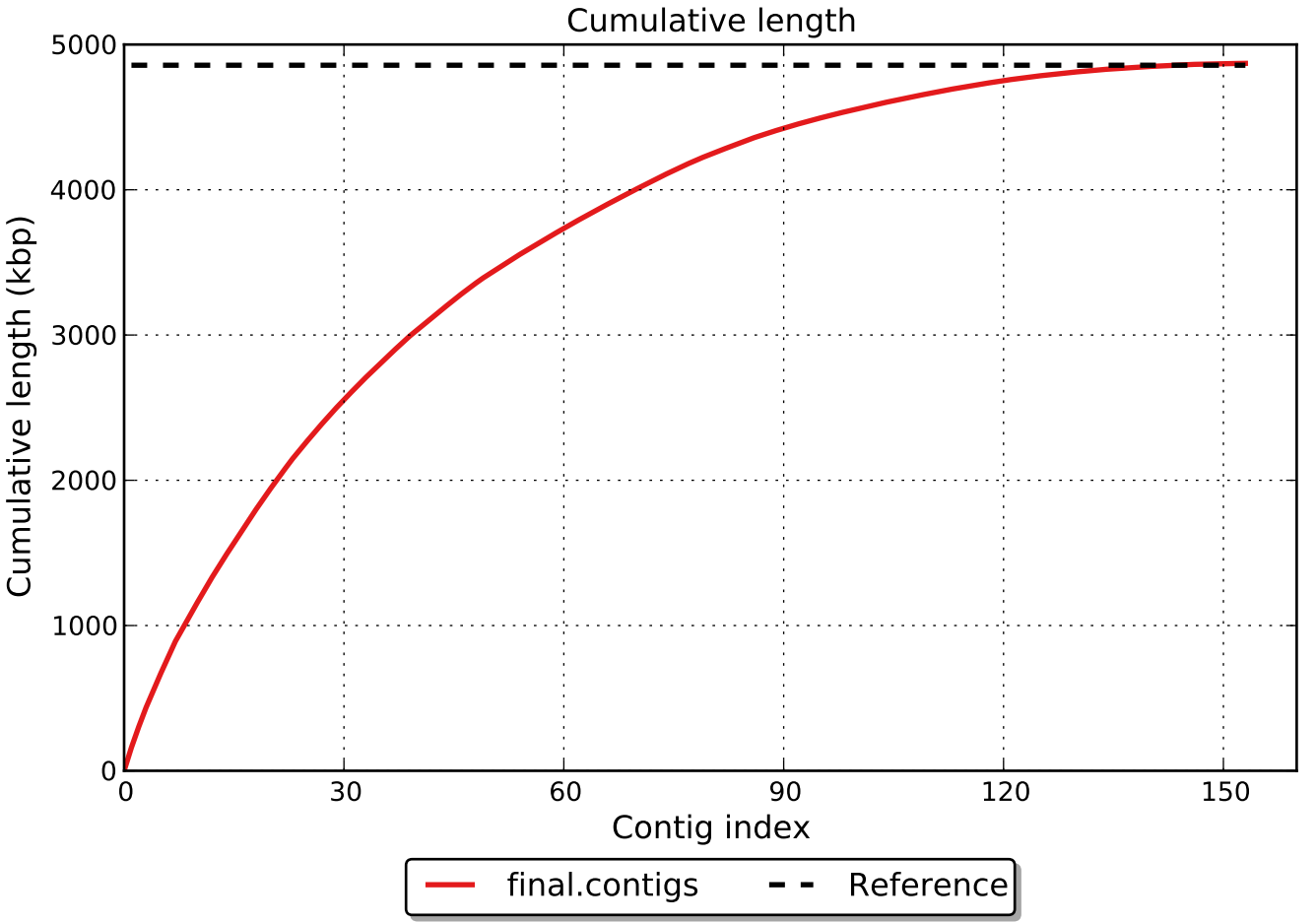
Unaligned report

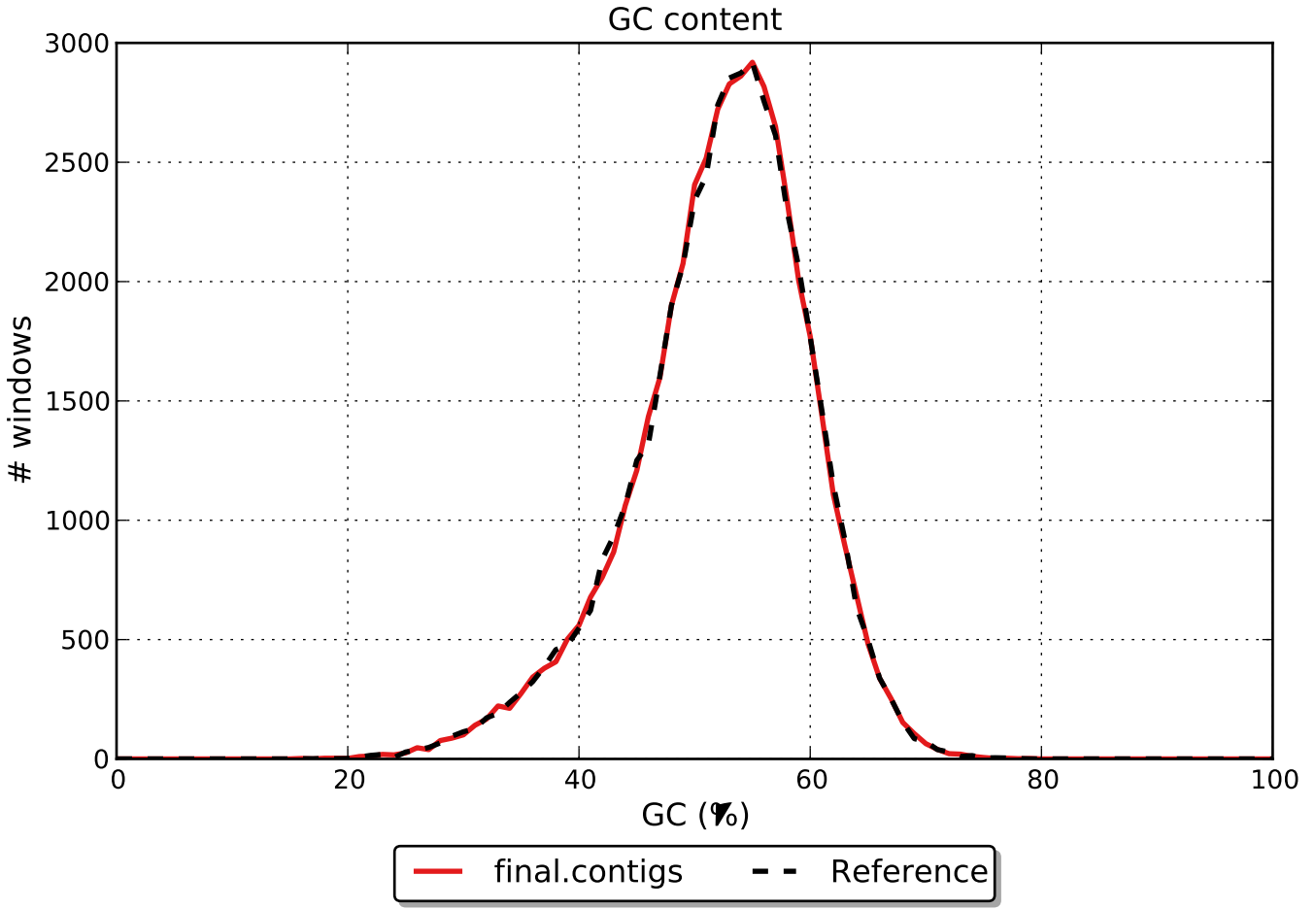
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

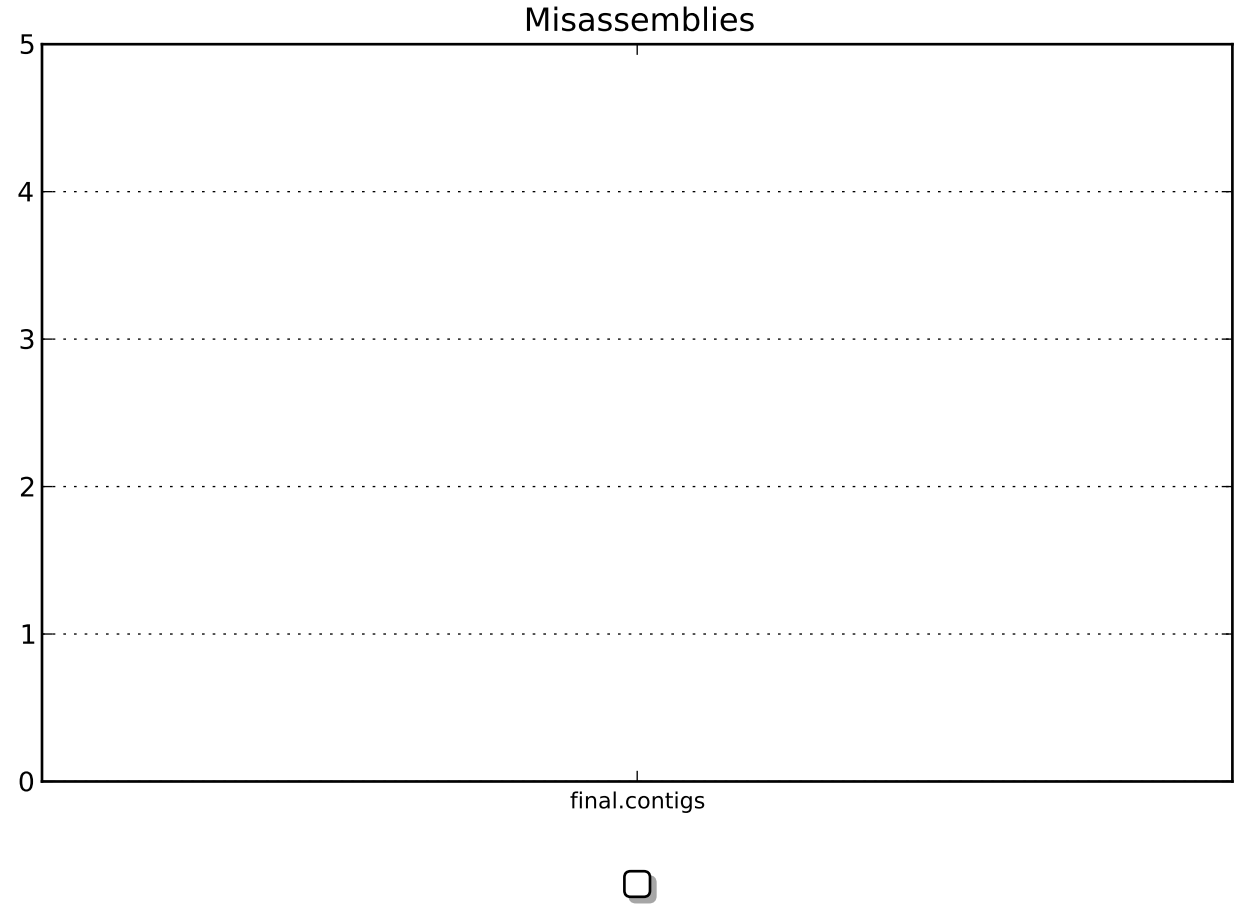
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

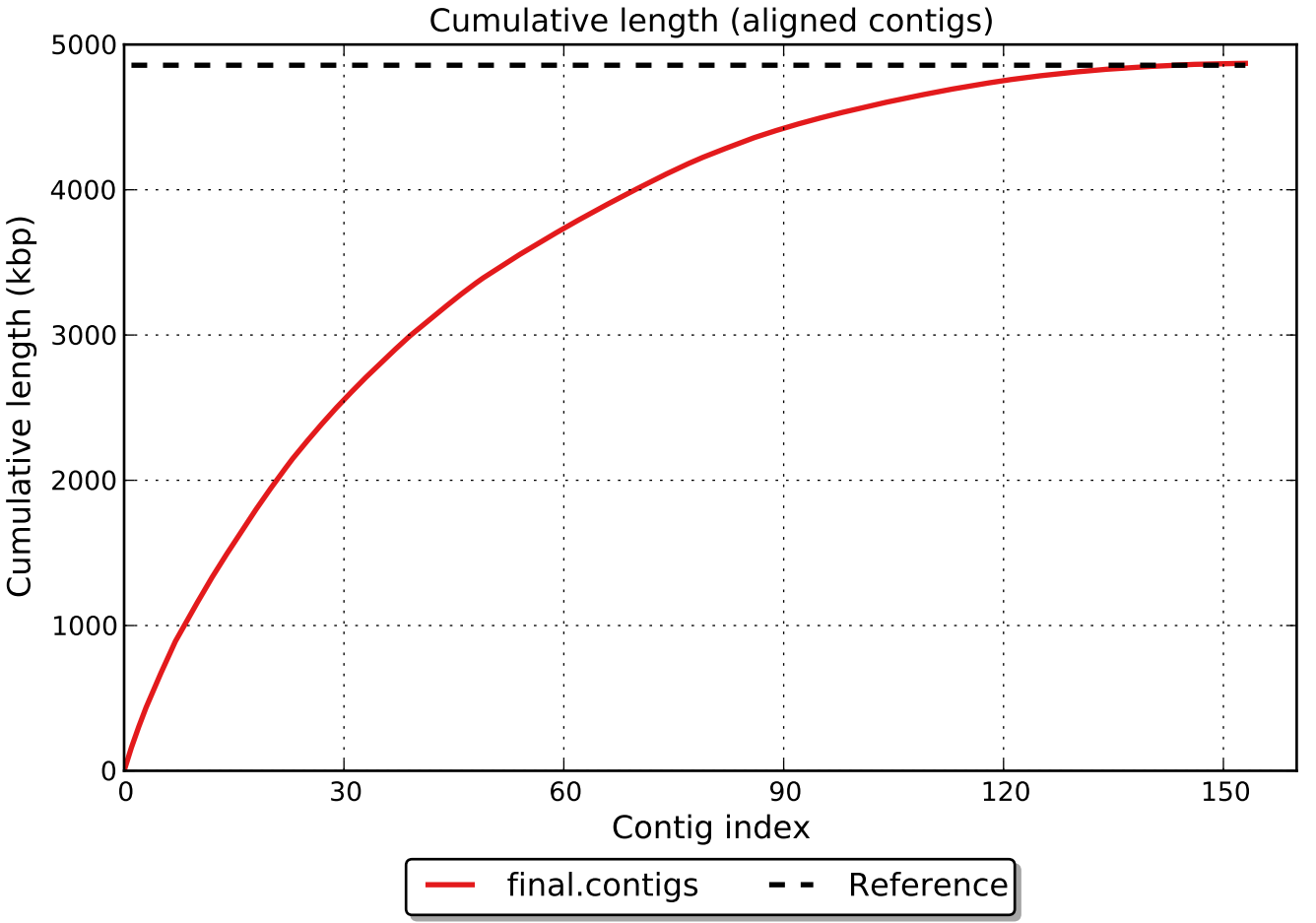

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

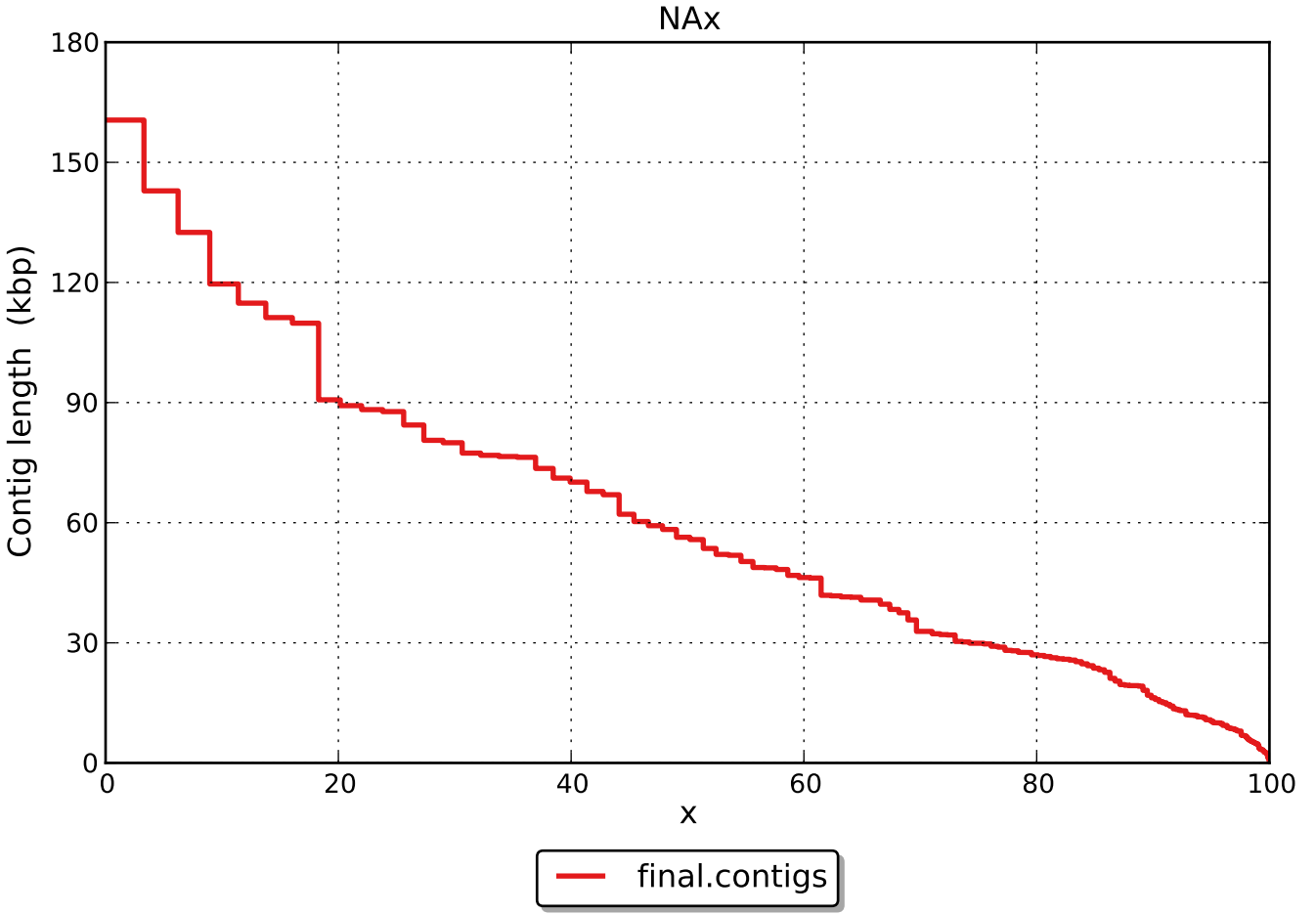

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

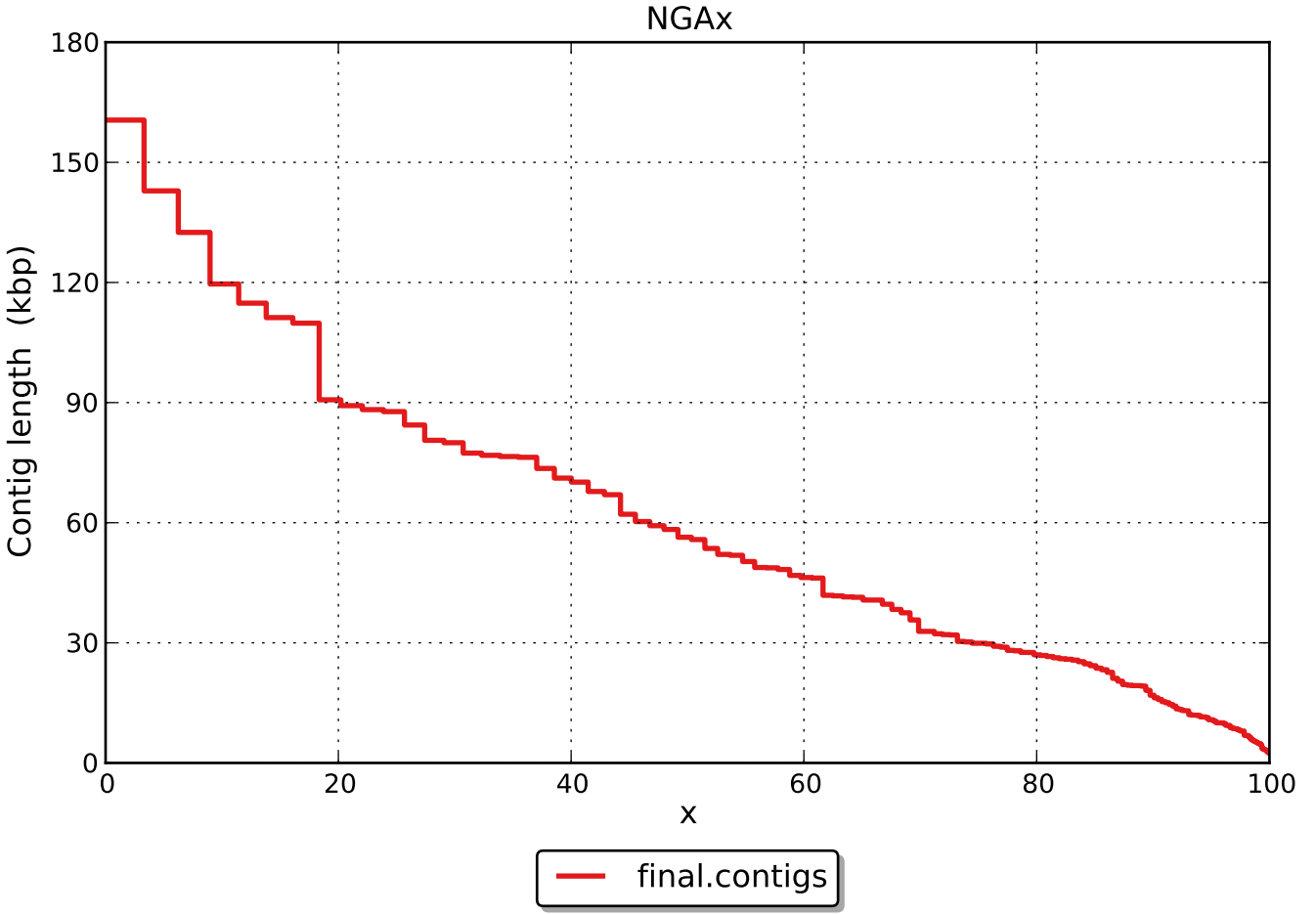

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
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
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