Report

	final.contigs
# contigs (>= 0 bp)	286
# contigs (>= 1000 bp)	280
Total length (>= 0 bp)	5641366
Total length (>= 1000 bp)	5636753
# contigs	286
Largest contig	100879
Total length	5641366
Reference length	5547323
GC (%)	50.47
Reference GC (%)	50.49
N50	32809
NG50	33211
N75	18062
NG75	18514
L50	56
LG50	55
L75	116
LG75	112
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	62258
Genome fraction (%)	99.983
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.60
# indels per 100 kbp	0.00
Largest alignment	100879
NA50	31067
NGA50	32169
NA75	17658
NGA75	18231
LA50	58
LGA50	57
LA75	119
LGA75	115

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

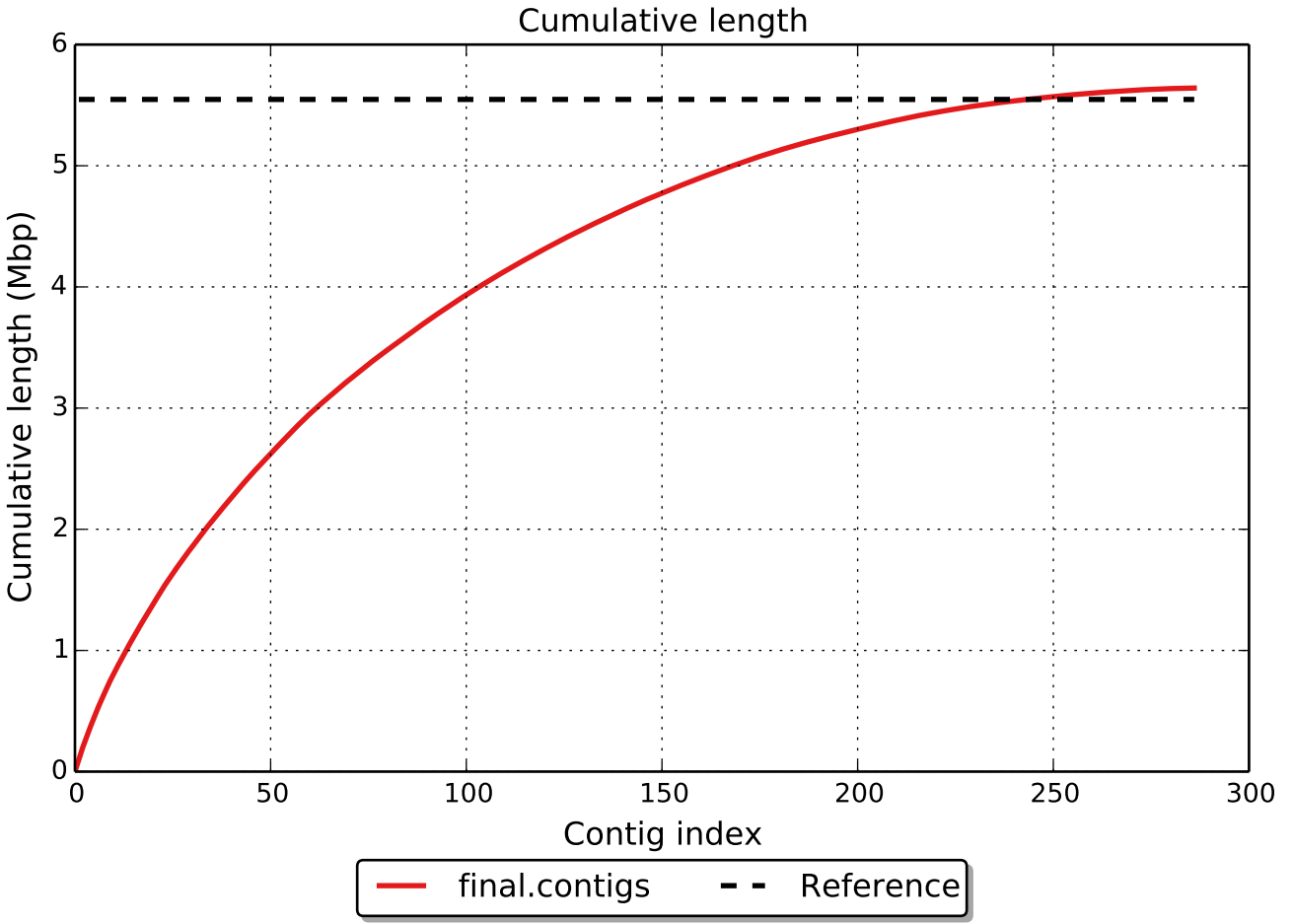
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	144
# indels	0
# short indels	0
# long indels	0
Indels length	0

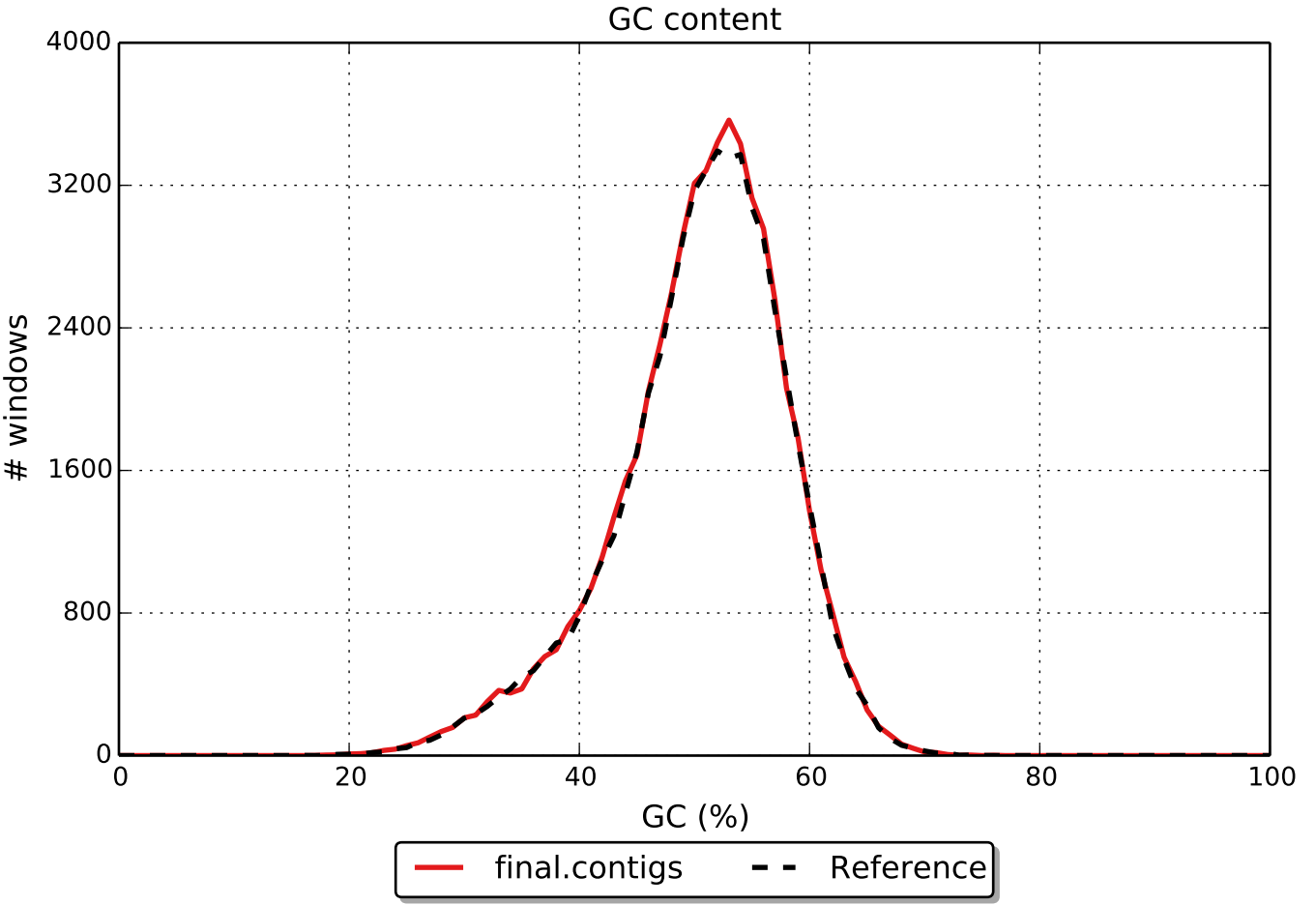
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

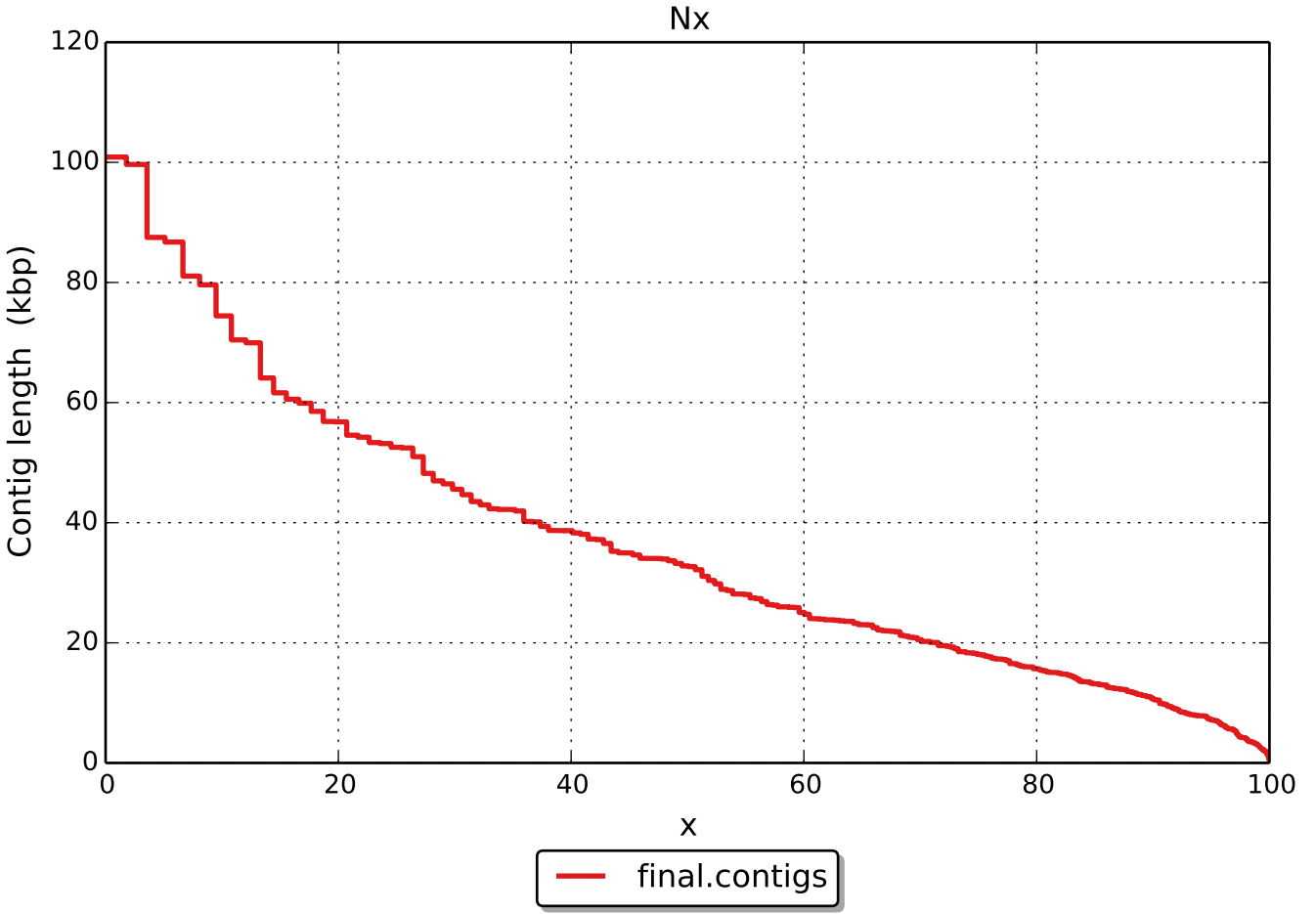
Unaligned report

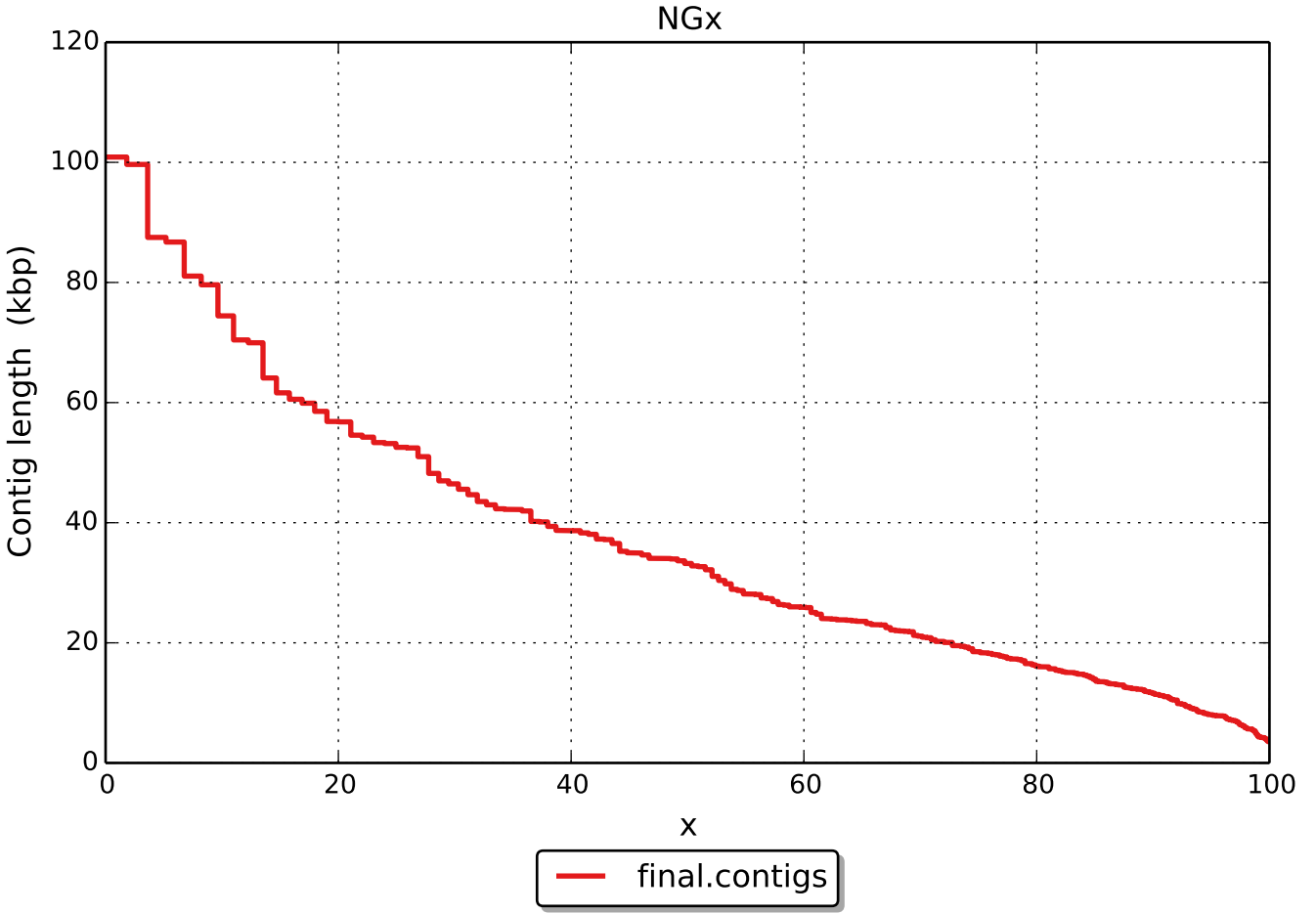
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	3
Partially unaligned length	62258
# N's	0

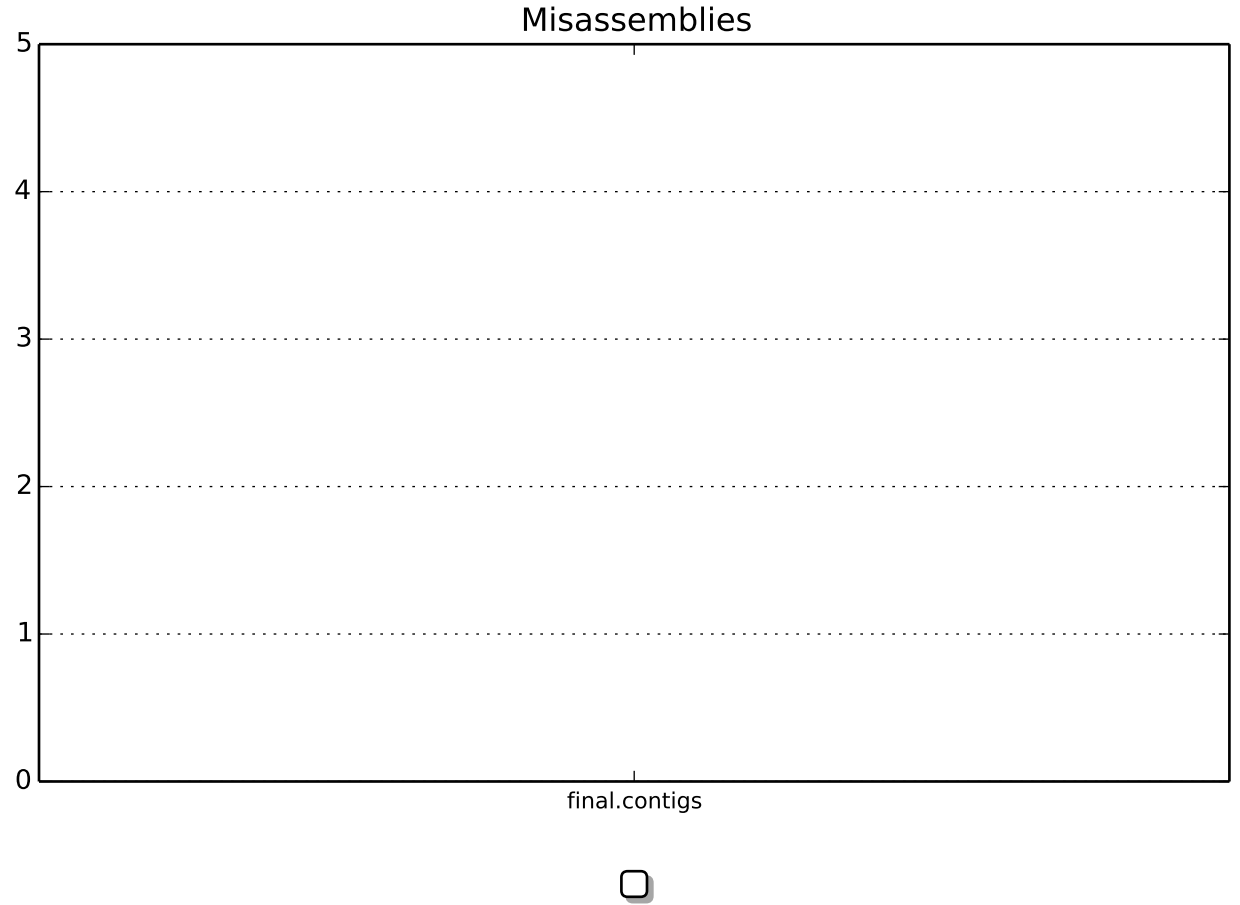
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

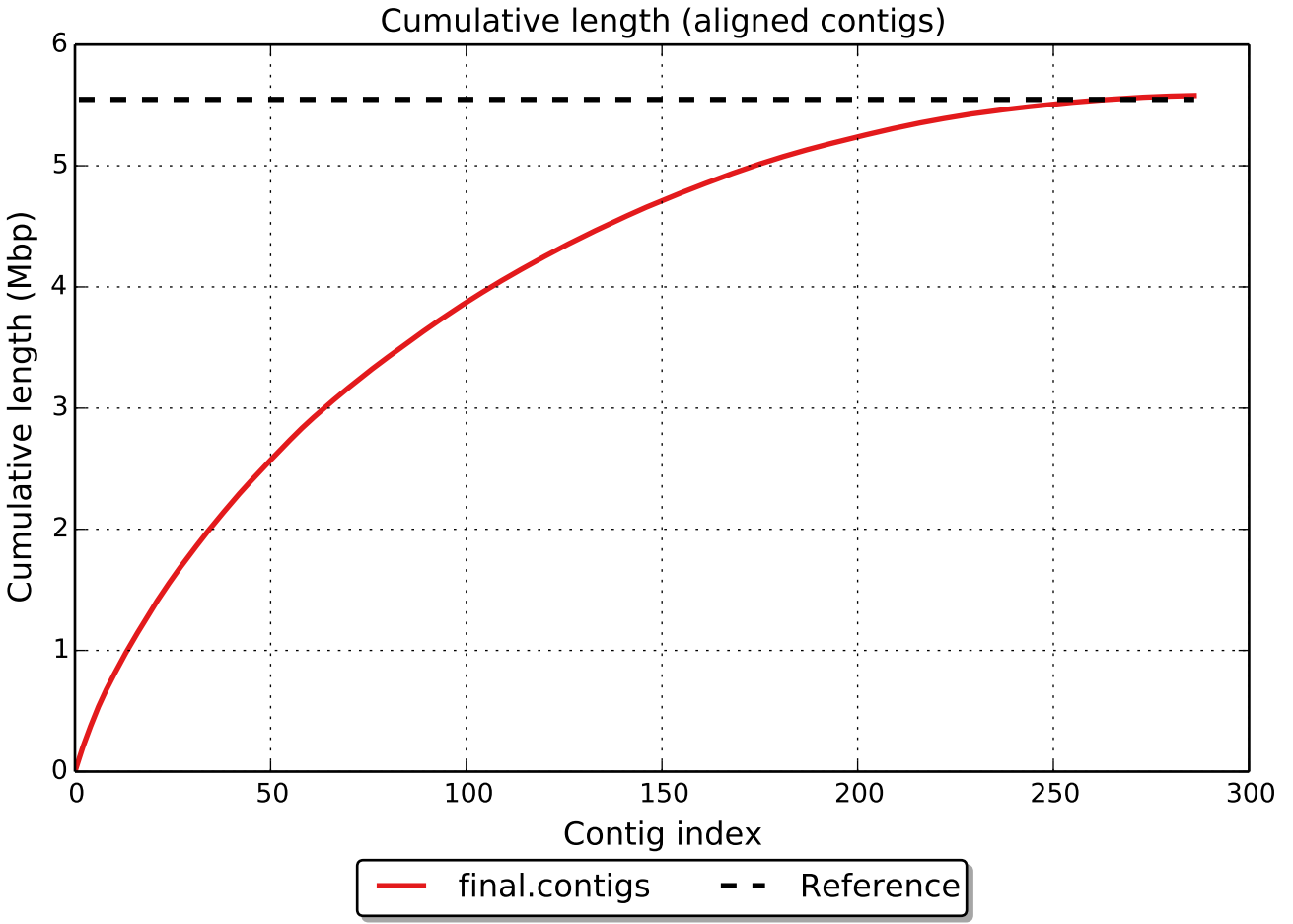

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
50
100
150
200
250
300
Contig index
final.contigs
Reference

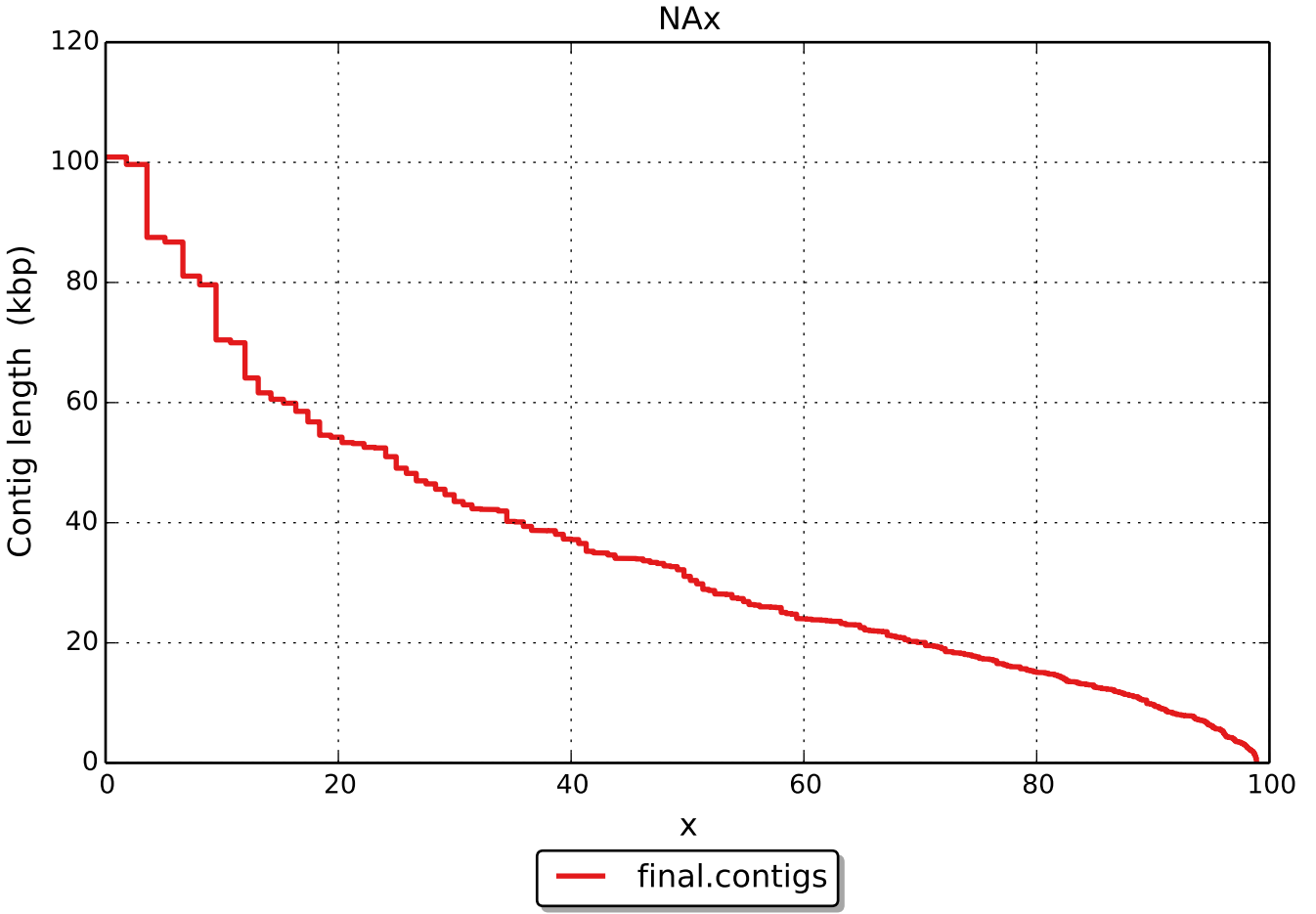

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

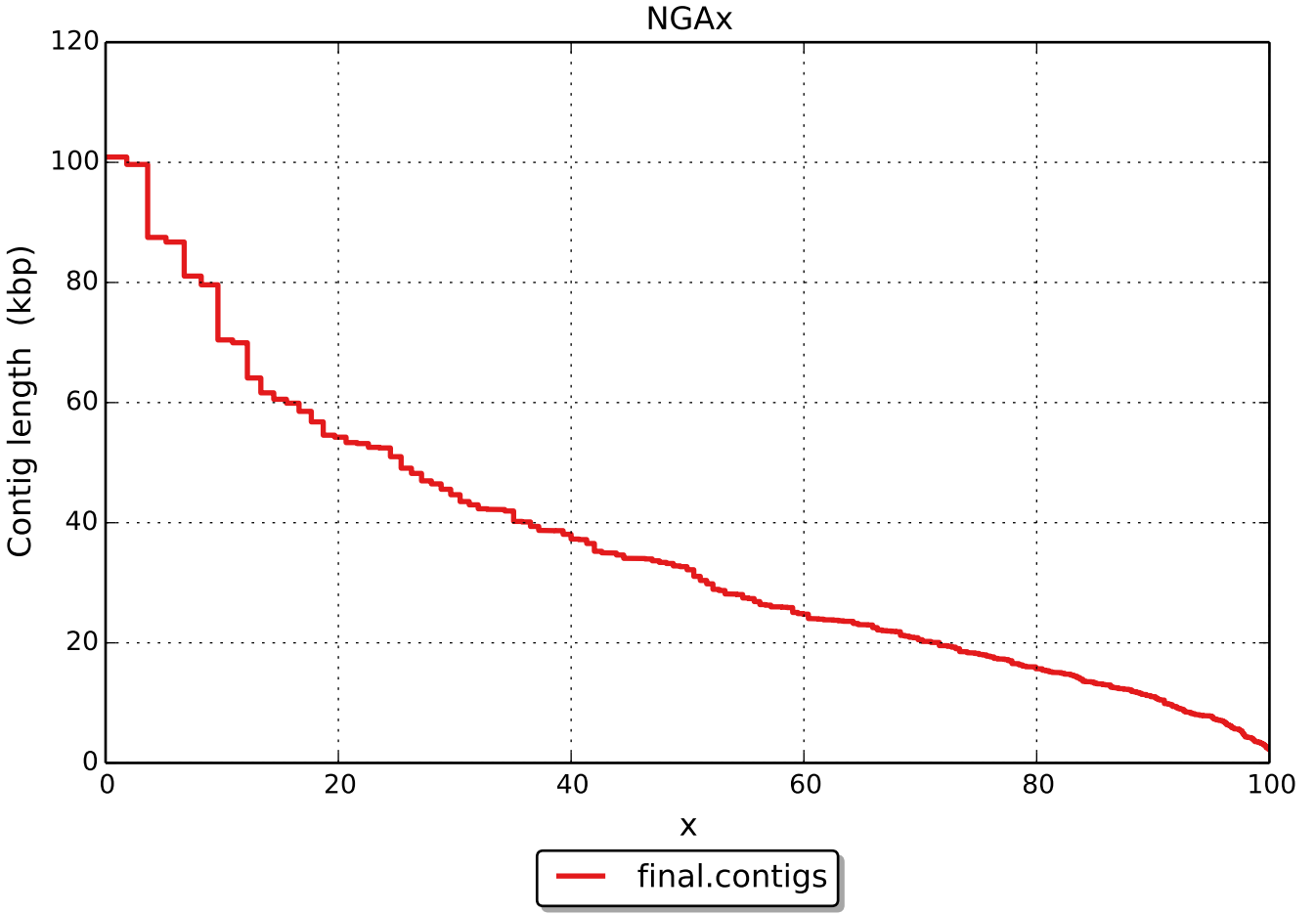

Nx
Contig length (kbp)
120
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


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


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