Report

	final.contigs
# contigs (>= 0 bp)	340
# contigs (>= 1000 bp)	258
Total length (>= 0 bp)	3729744
Total length (>= 1000 bp)	3701411
# contigs	269
Largest contig	58143
Total length	3709443
Reference length	3785550
GC (%)	32.26
Reference GC (%)	32.26
N50	21298
NG50	21287
N75	12857
NG75	12583
L50	59
LG50	60
L75	113
LG75	118
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.394
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.95
# indels per 100 kbp	0.00
Largest alignment	58143
NA50	21298
NGA50	21287
NA75	12857
NGA75	12583
LA50	59
LGA50	60
LA75	113
LGA75	118

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

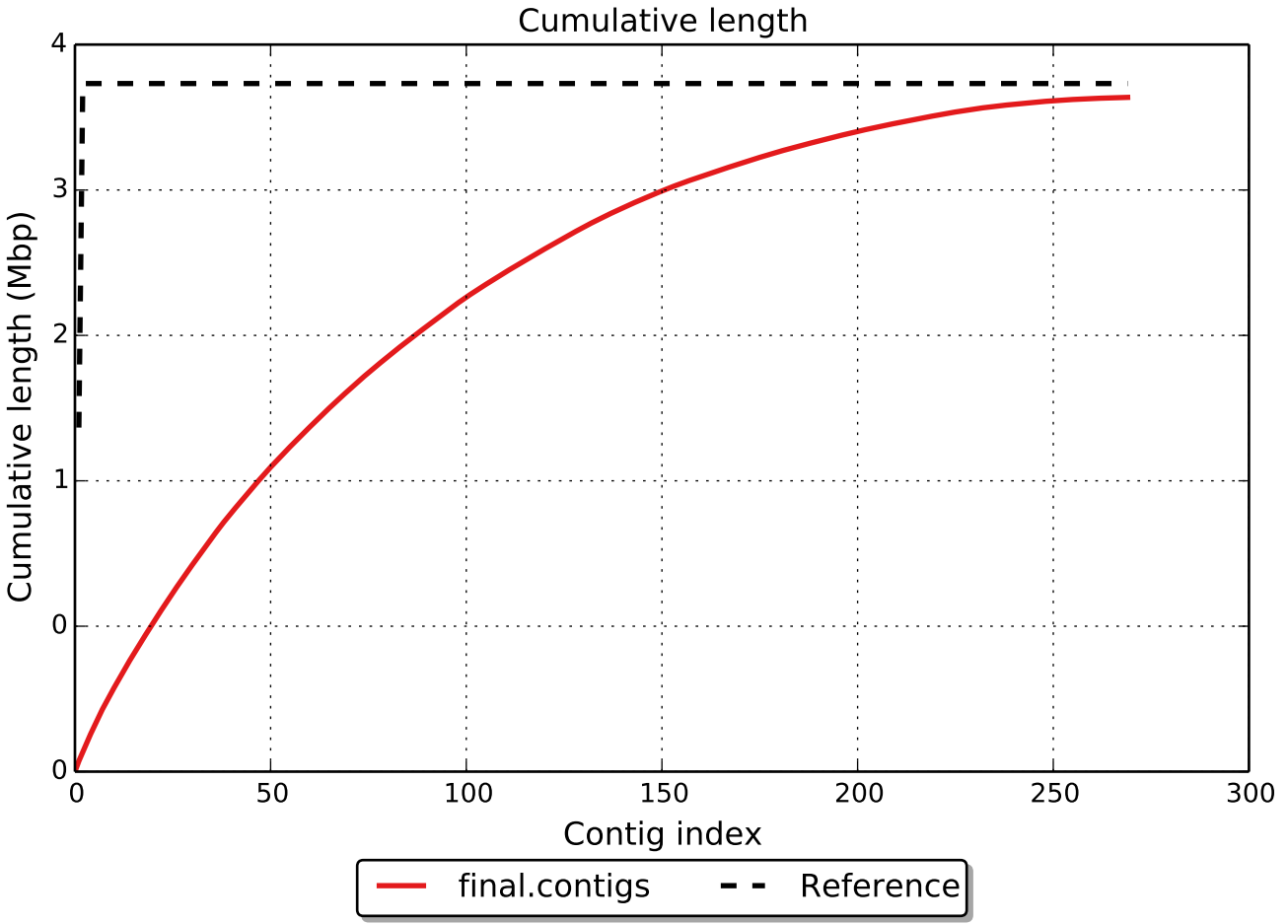
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	557
# indels	0
# short indels	0
# long indels	0
Indels length	0

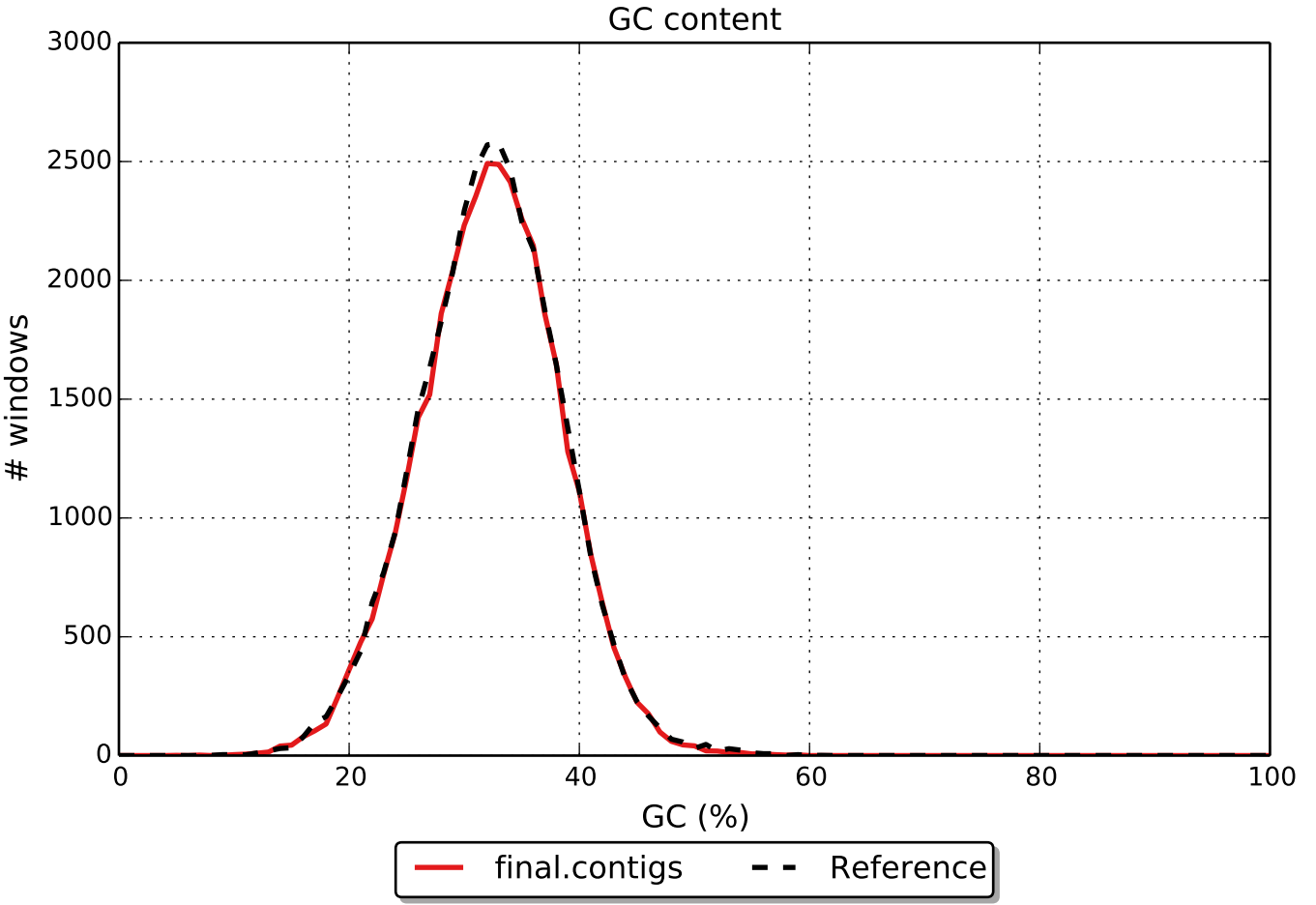
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

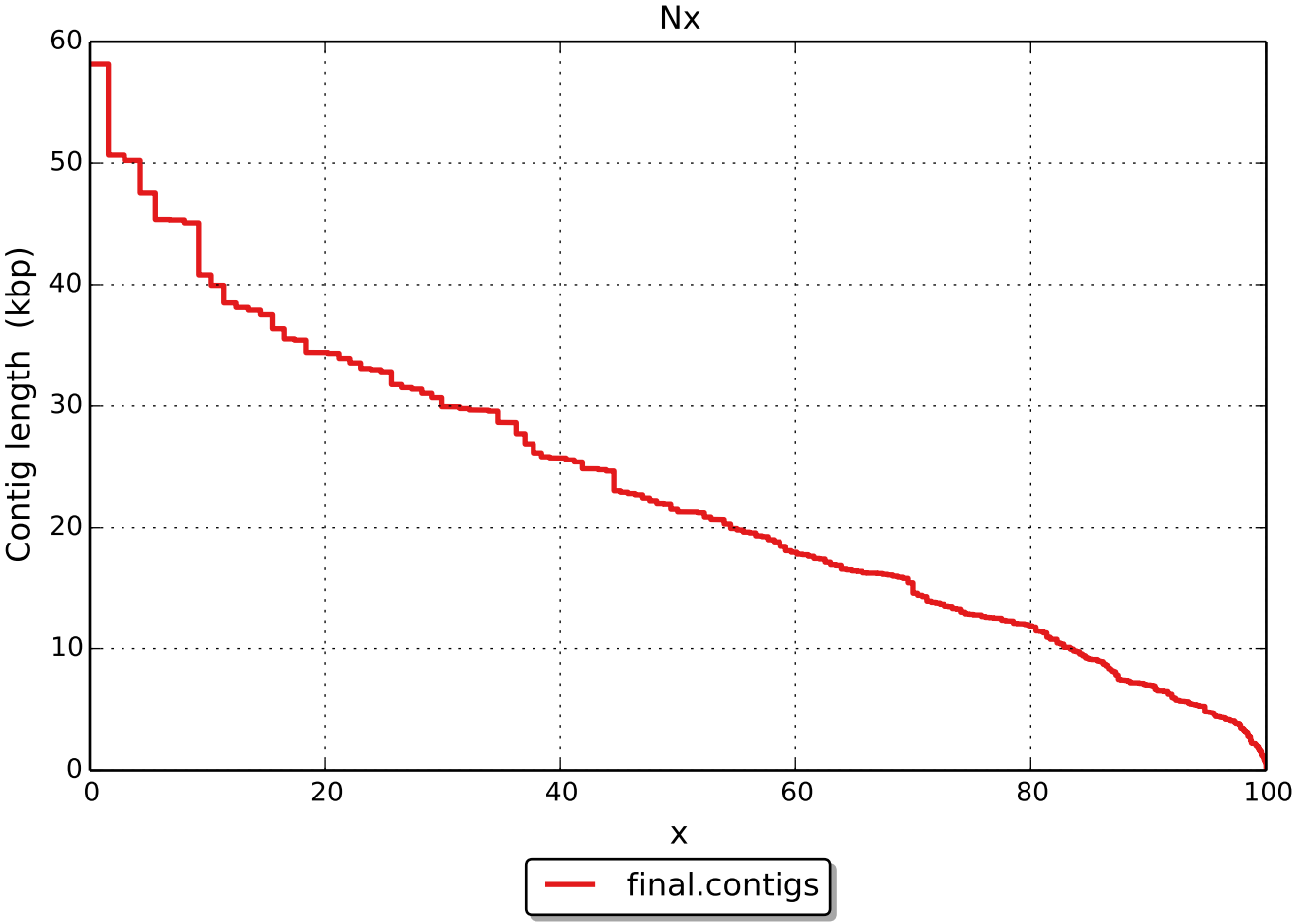
Unaligned report

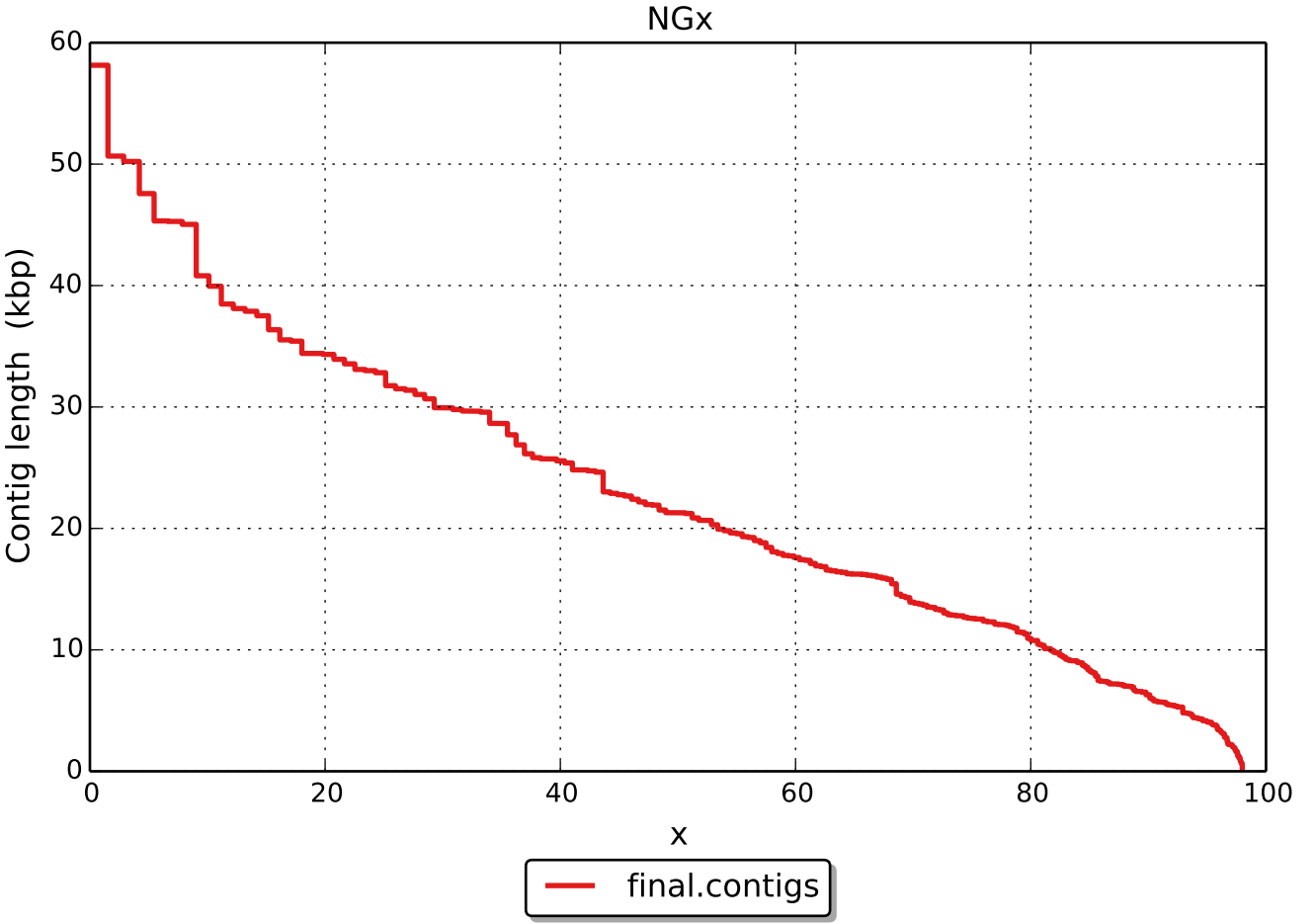
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

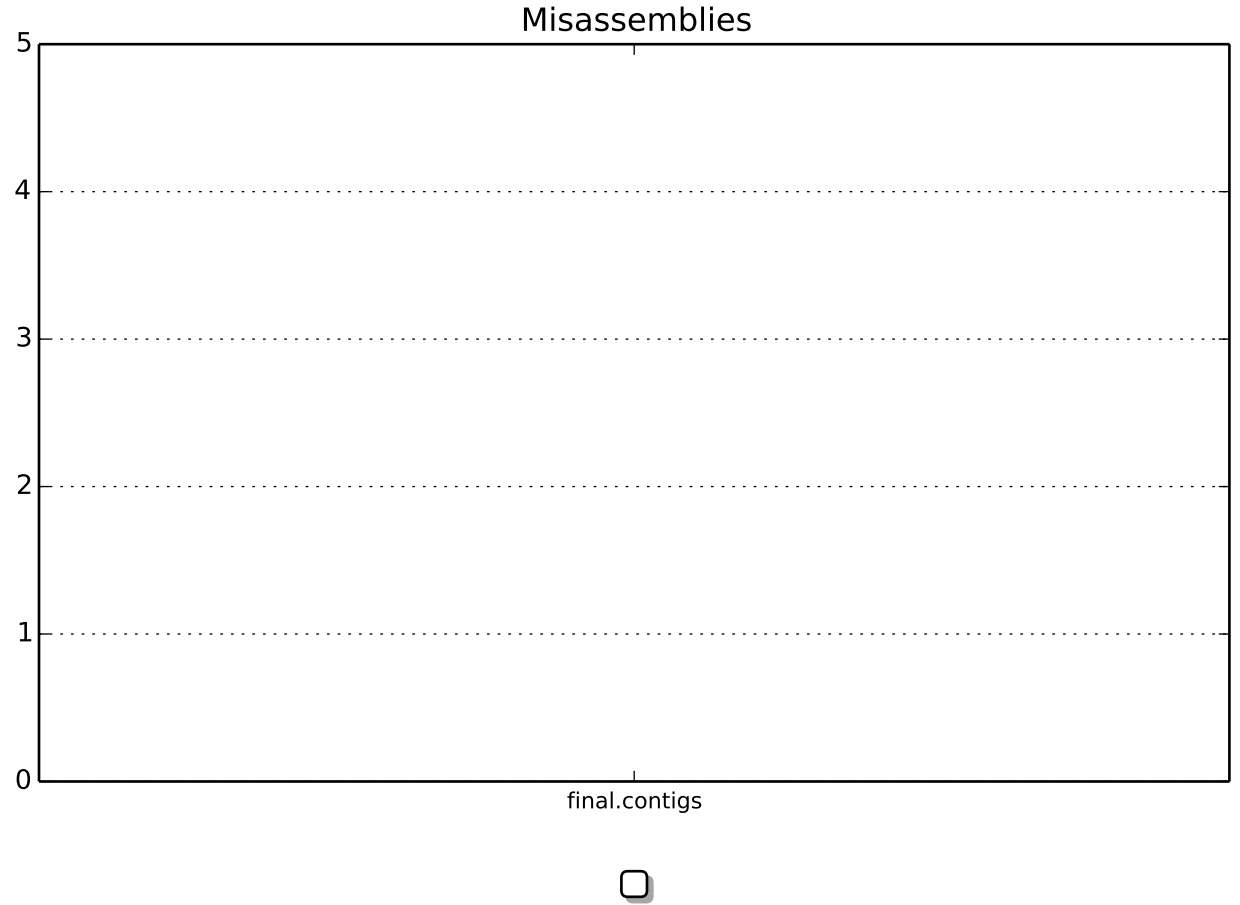
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

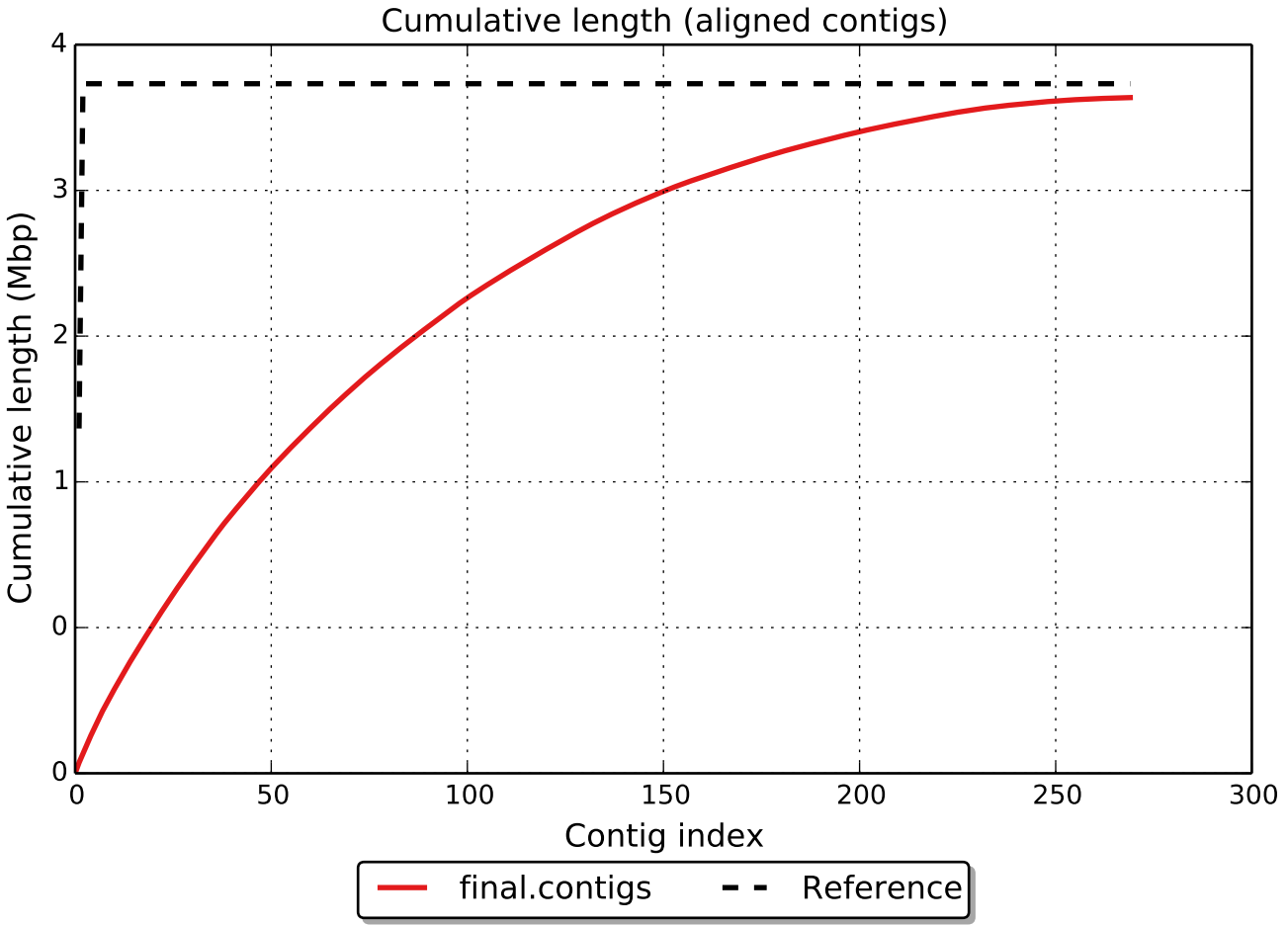

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
50
100
150
200
250
300
final.contigs
Reference

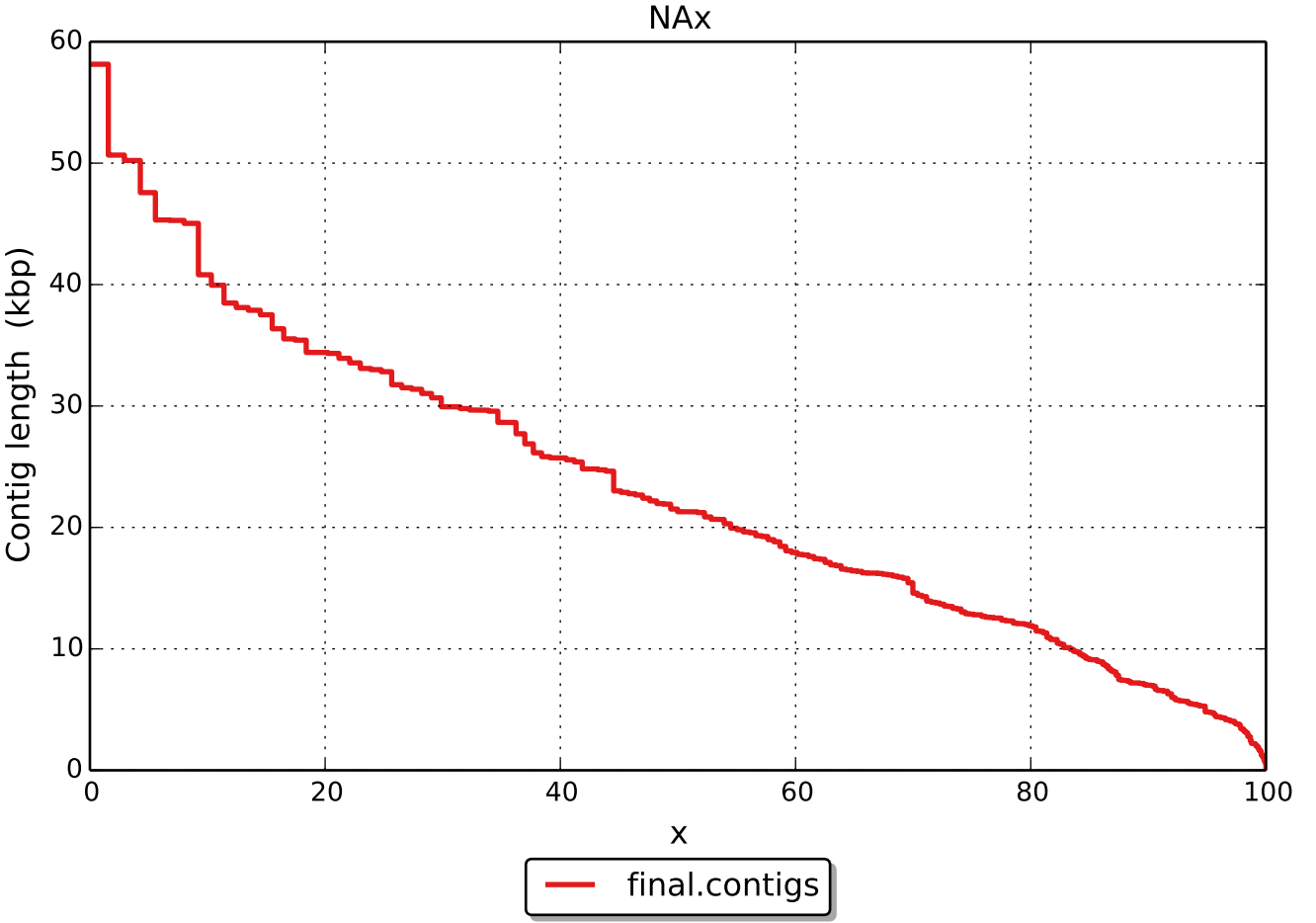

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

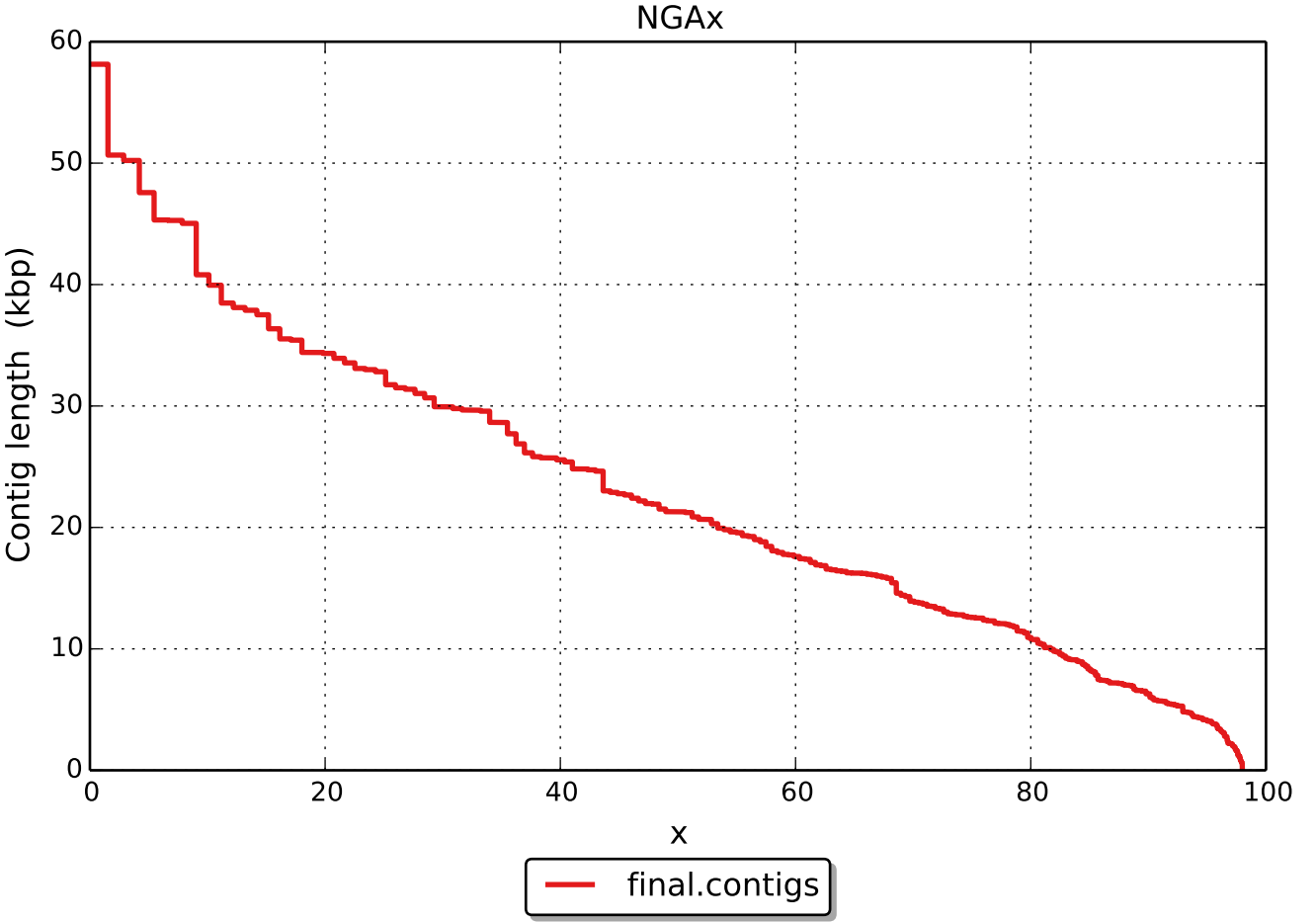

Nx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
10
20
30
40
50
60
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
0
50
100
150
200
250
300
final.contigs
Reference


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs