Report

	final.contigs
# contigs (>= 0 bp)	234
# contigs (>= 1000 bp)	196
Total length (>= 0 bp)	1301715
Total length (>= 1000 bp)	1278850
# contigs	216
Largest contig	37441
Total length	1294222
Reference length	1283598
GC (%)	26.31
Reference GC (%)	26.30
N50	8699
NG50	8699
N75	5707
NG75	5724
L50	49
LG50	49
L75	96
LG75	94
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.624
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.70
# indels per 100 kbp	0.00
Largest alignment	37441
NA50	8699
NGA50	8699
NA75	5707
NGA75	5724
LA50	49
LGA50	49
LA75	96
LGA75	94

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

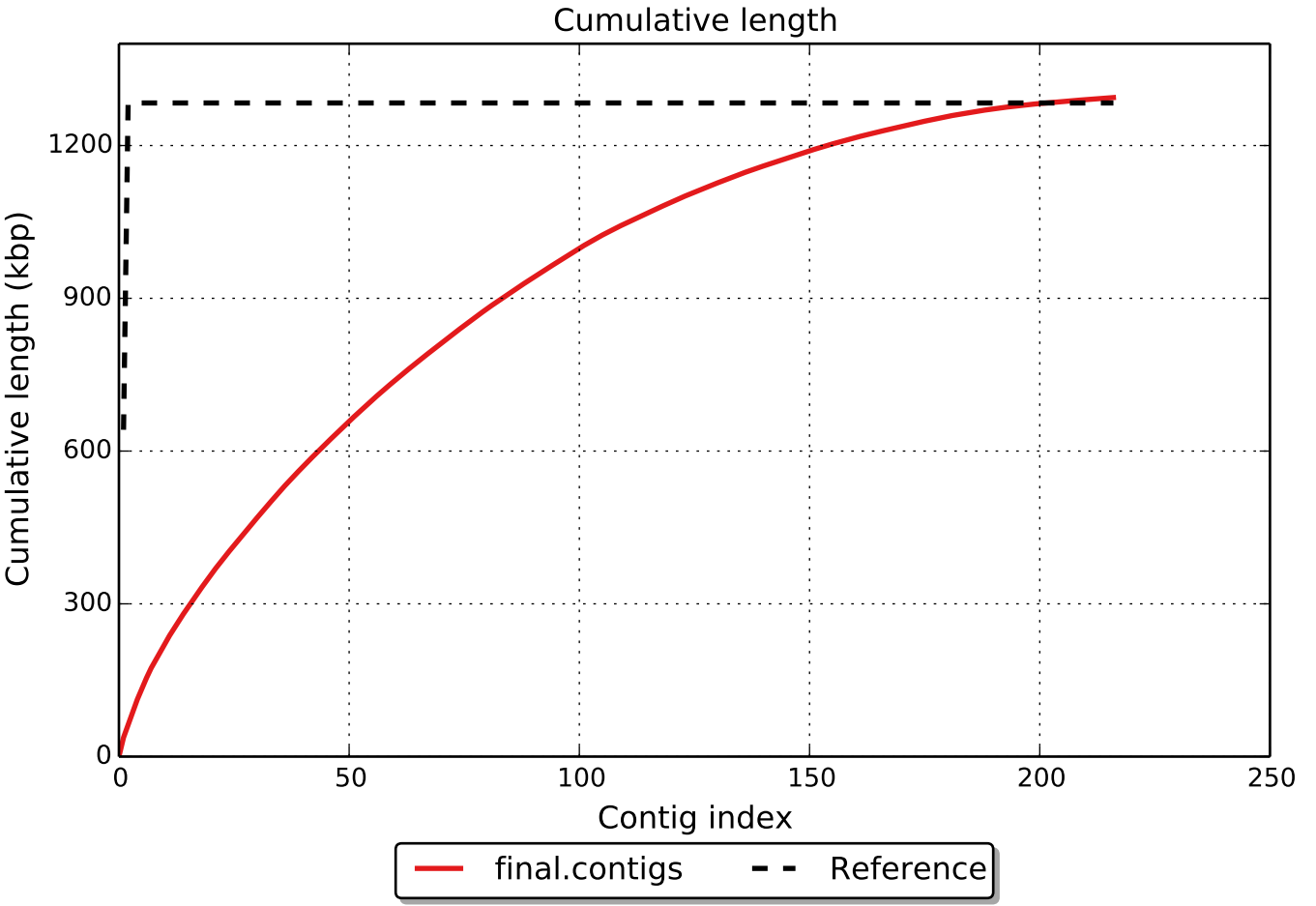
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9
# indels	0
# short indels	0
# long indels	0
Indels length	0

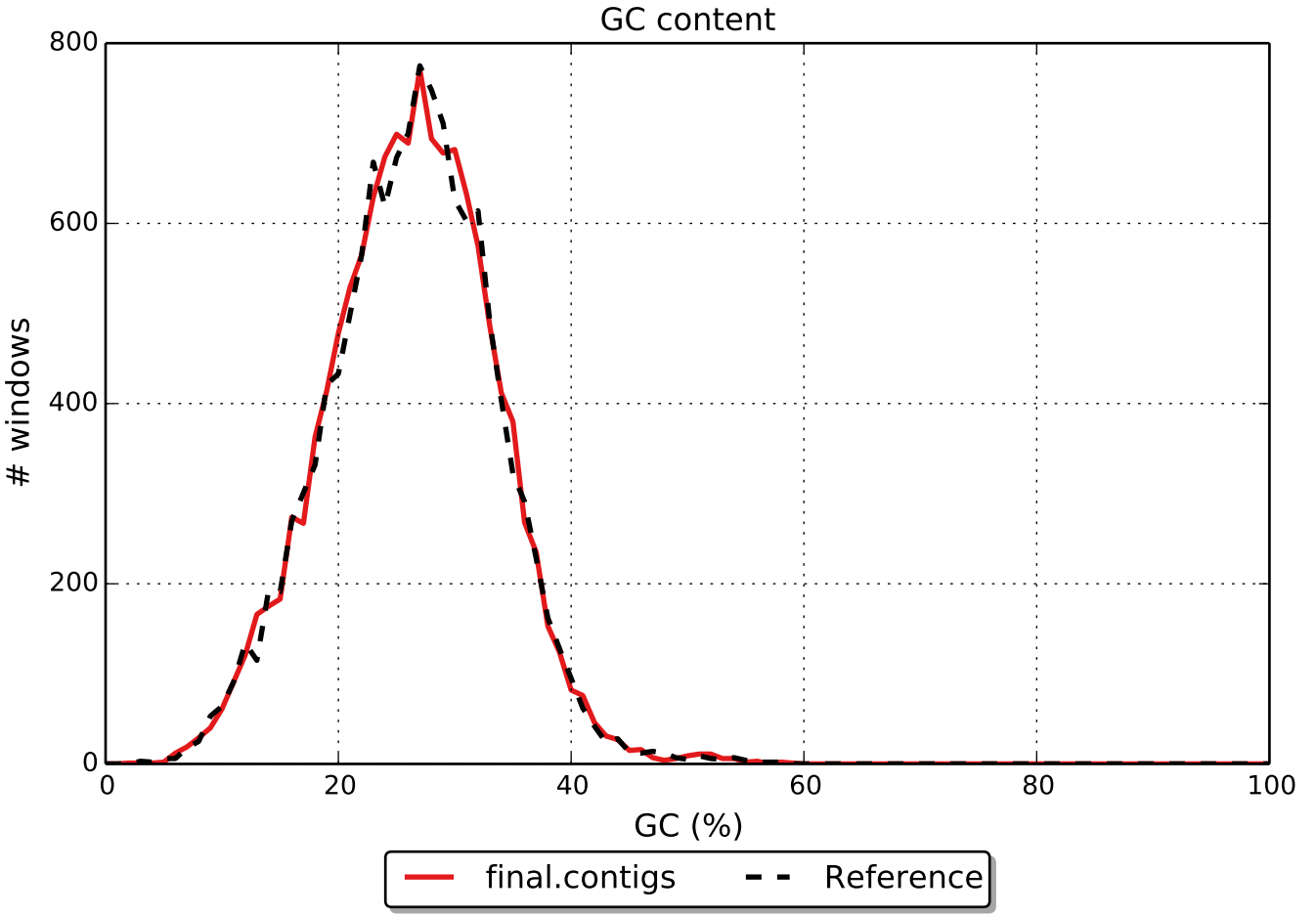
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

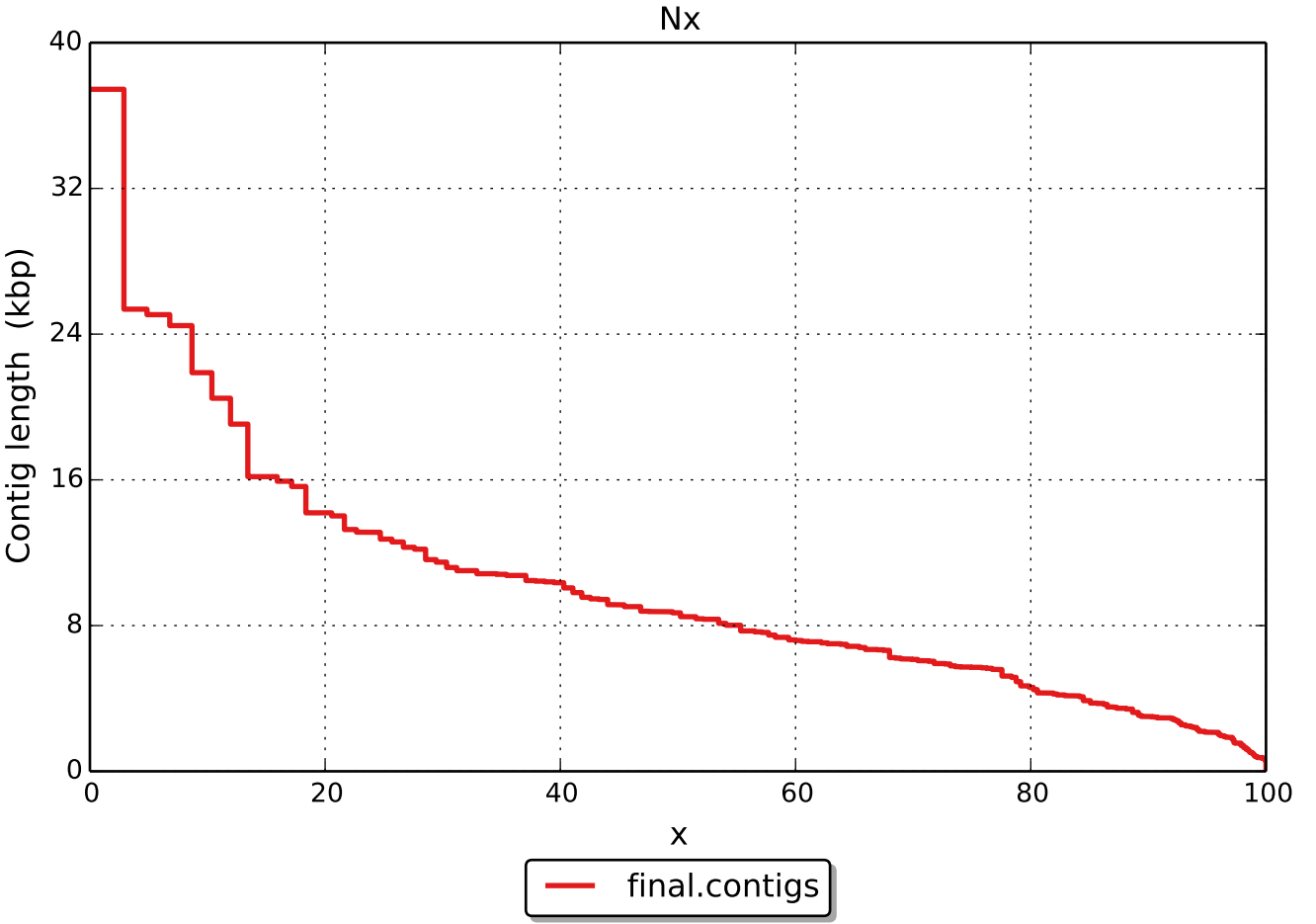
Unaligned report

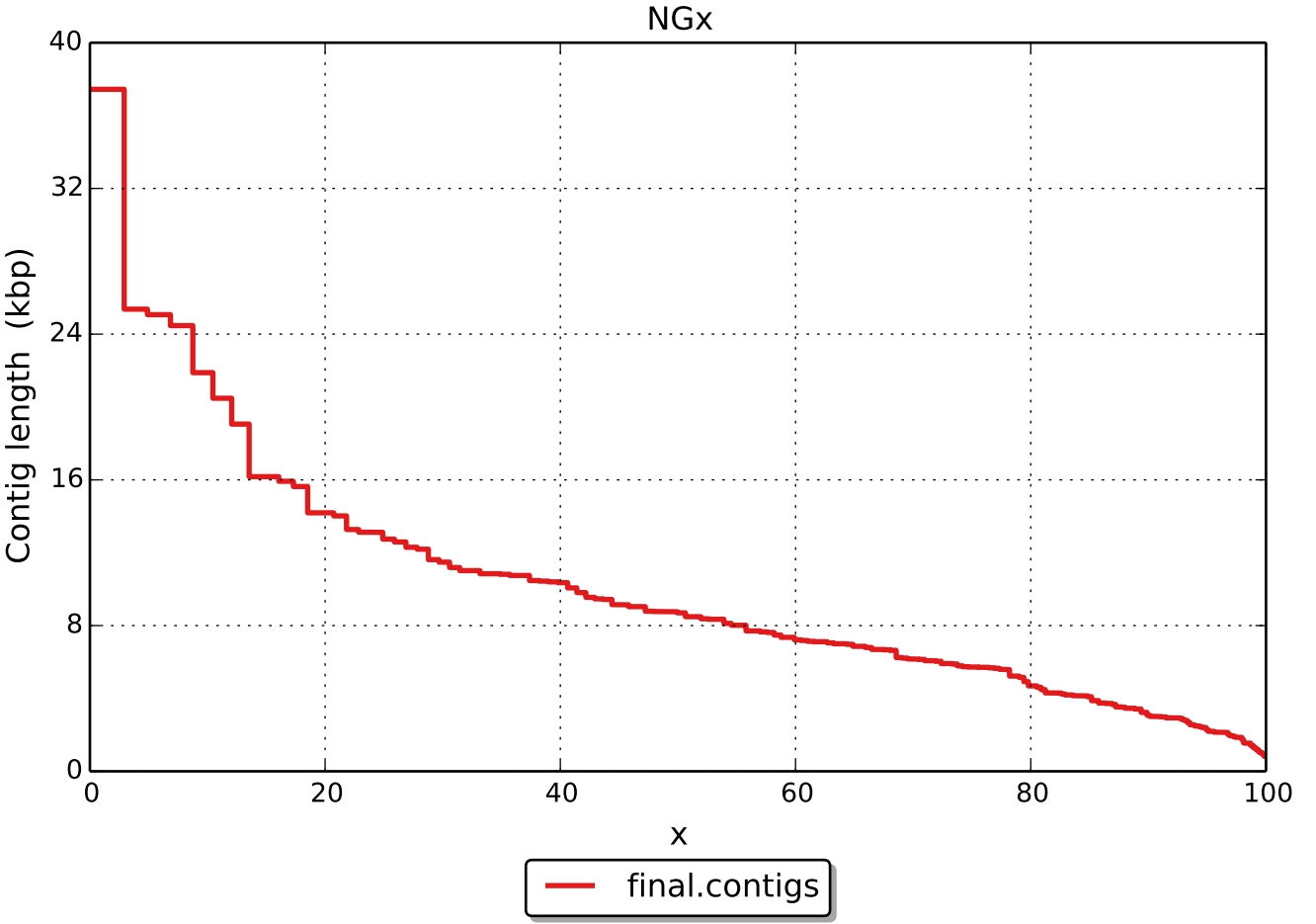
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

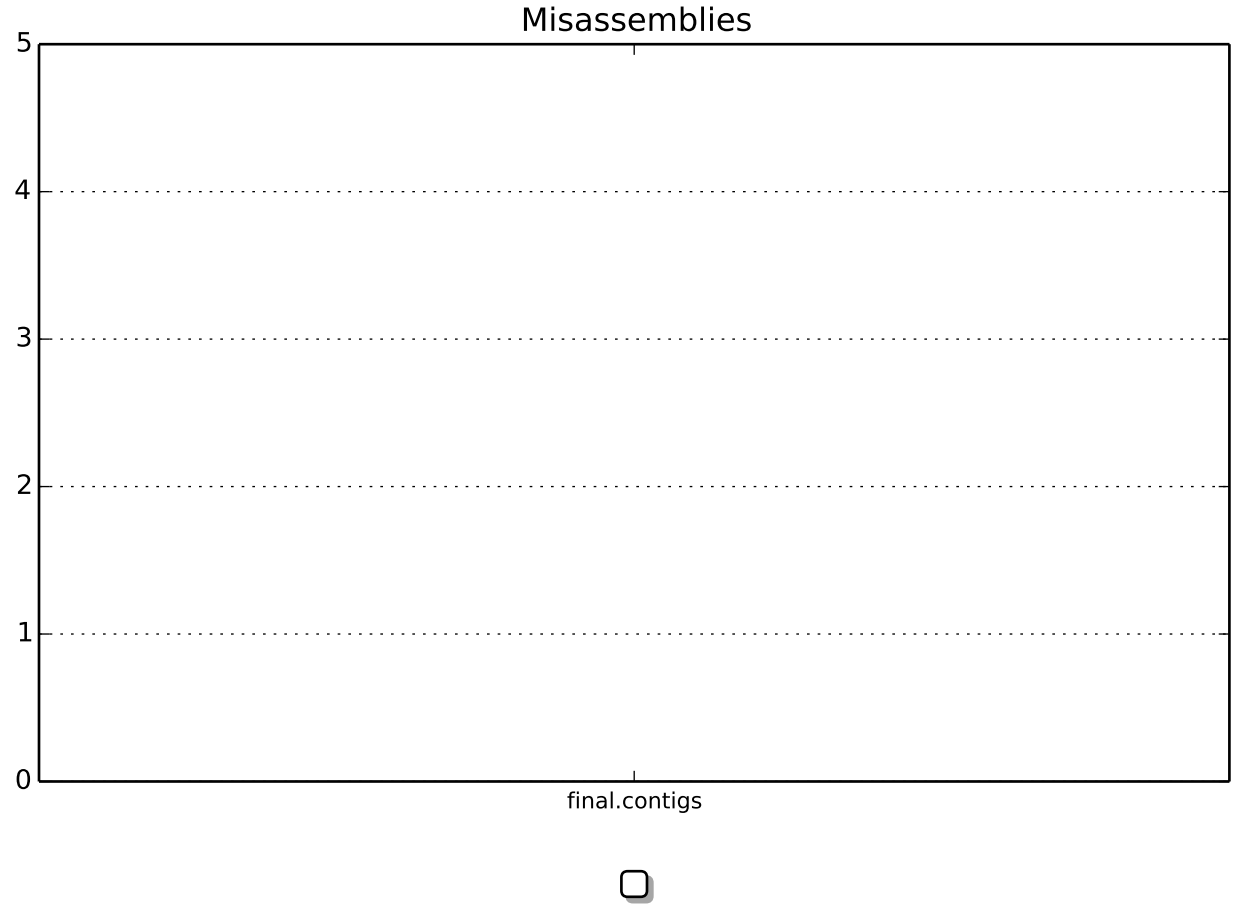
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

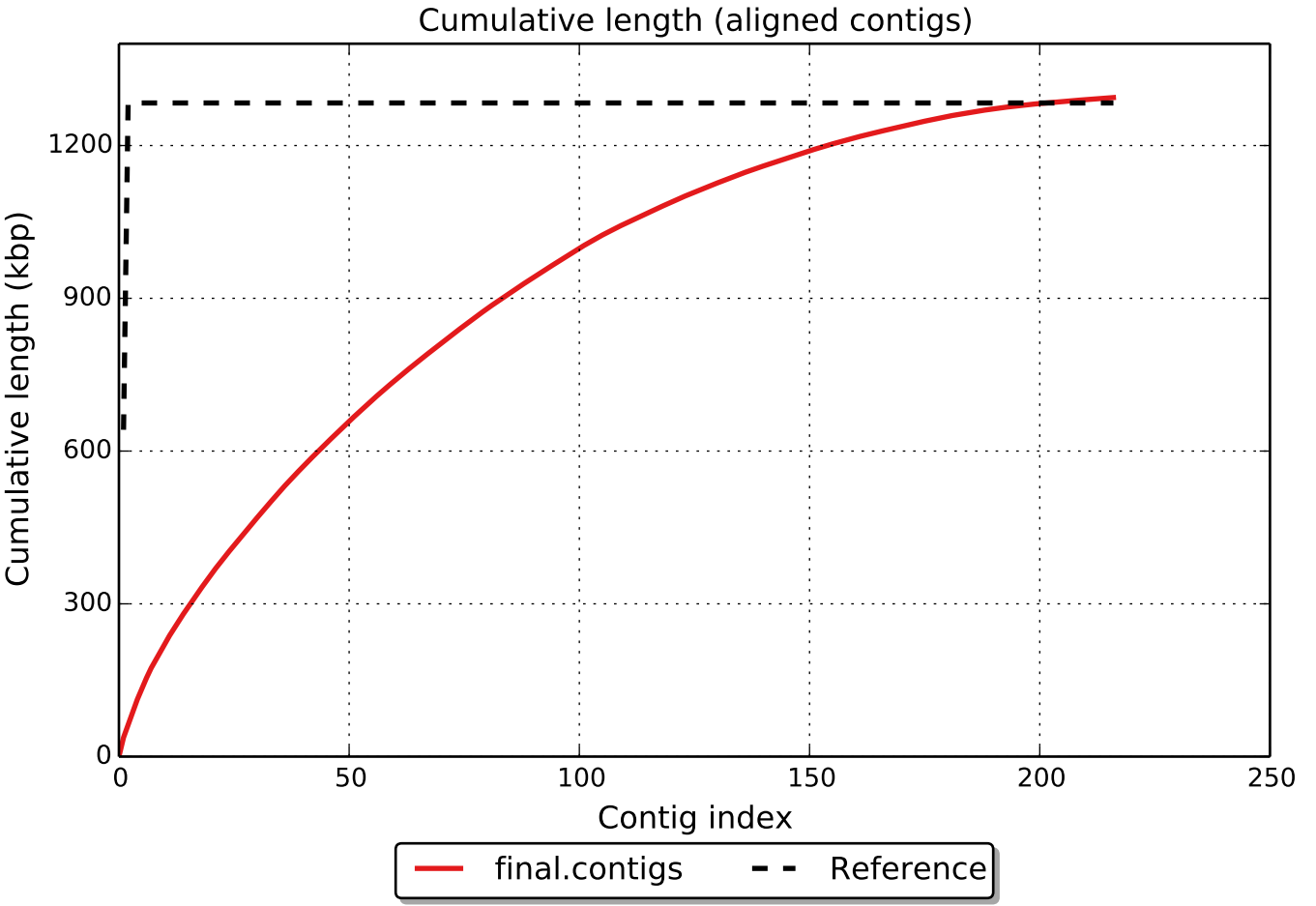

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
50
100
150
200
250
Contig index
final.contigs
Reference

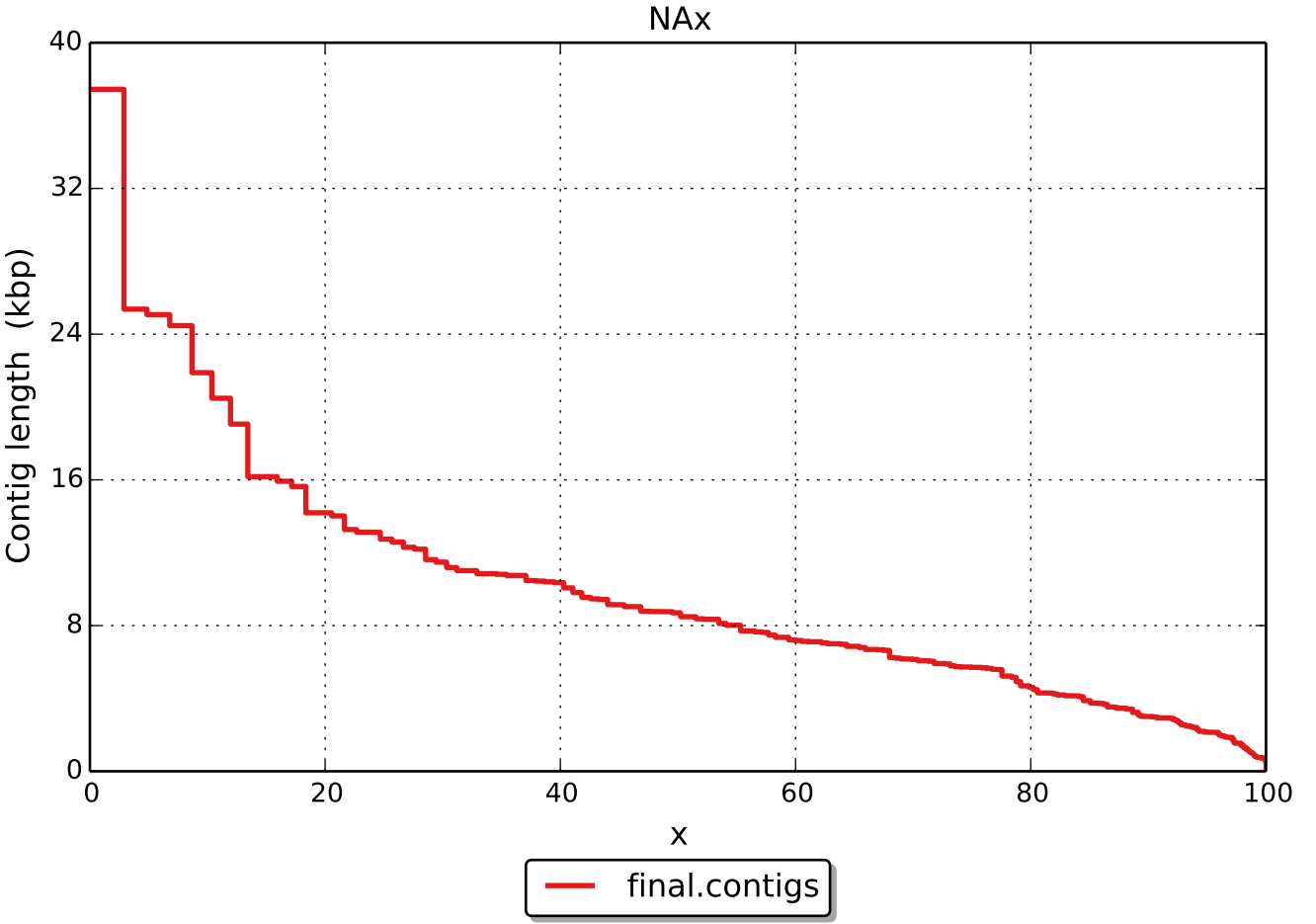

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

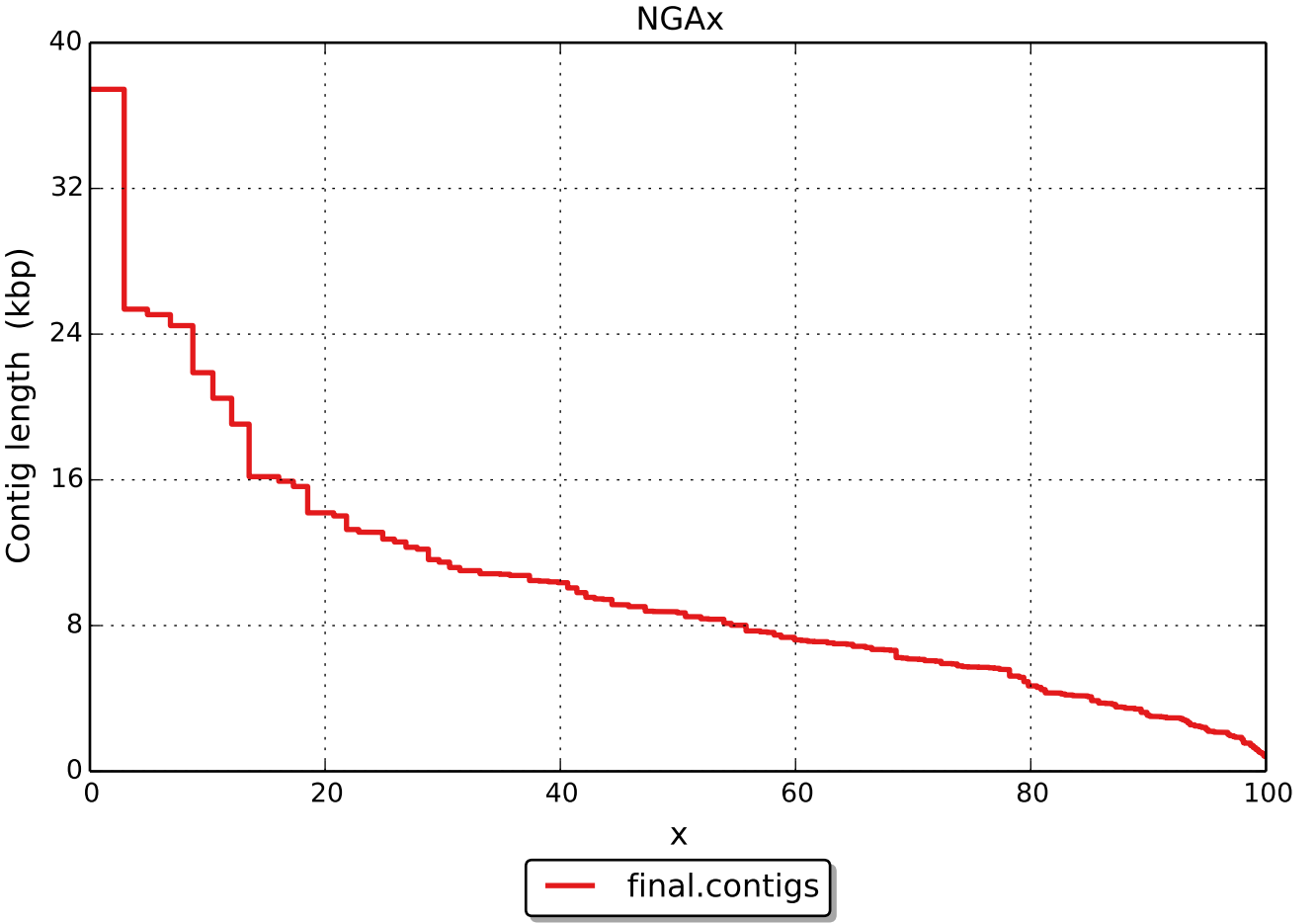

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
40
32
24
16
8
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 (kbp)
0
300
600
900
1200
0
50
100
150
200
250
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs