Report

	final.contigs
# contigs (>= 0 bp)	237
# contigs (>= 1000 bp)	197
Total length (>= 0 bp)	1249401
Total length (>= 1000 bp)	1228106
# contigs	214
Largest contig	36991
Total length	1241819
Reference length	1231960
GC (%)	25.35
Reference GC (%)	25.34
N50	9198
NG50	9274
N75	5022
NG75	5047
L50	42
LG50	41
L75	86
LG75	85
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	26043
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.354
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.40
# indels per 100 kbp	0.00
Largest alignment	36991
NA50	9198
NGA50	9198
NA75	5022
NGA75	5047
LA50	42
LGA50	42
LA75	87
LGA75	85

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

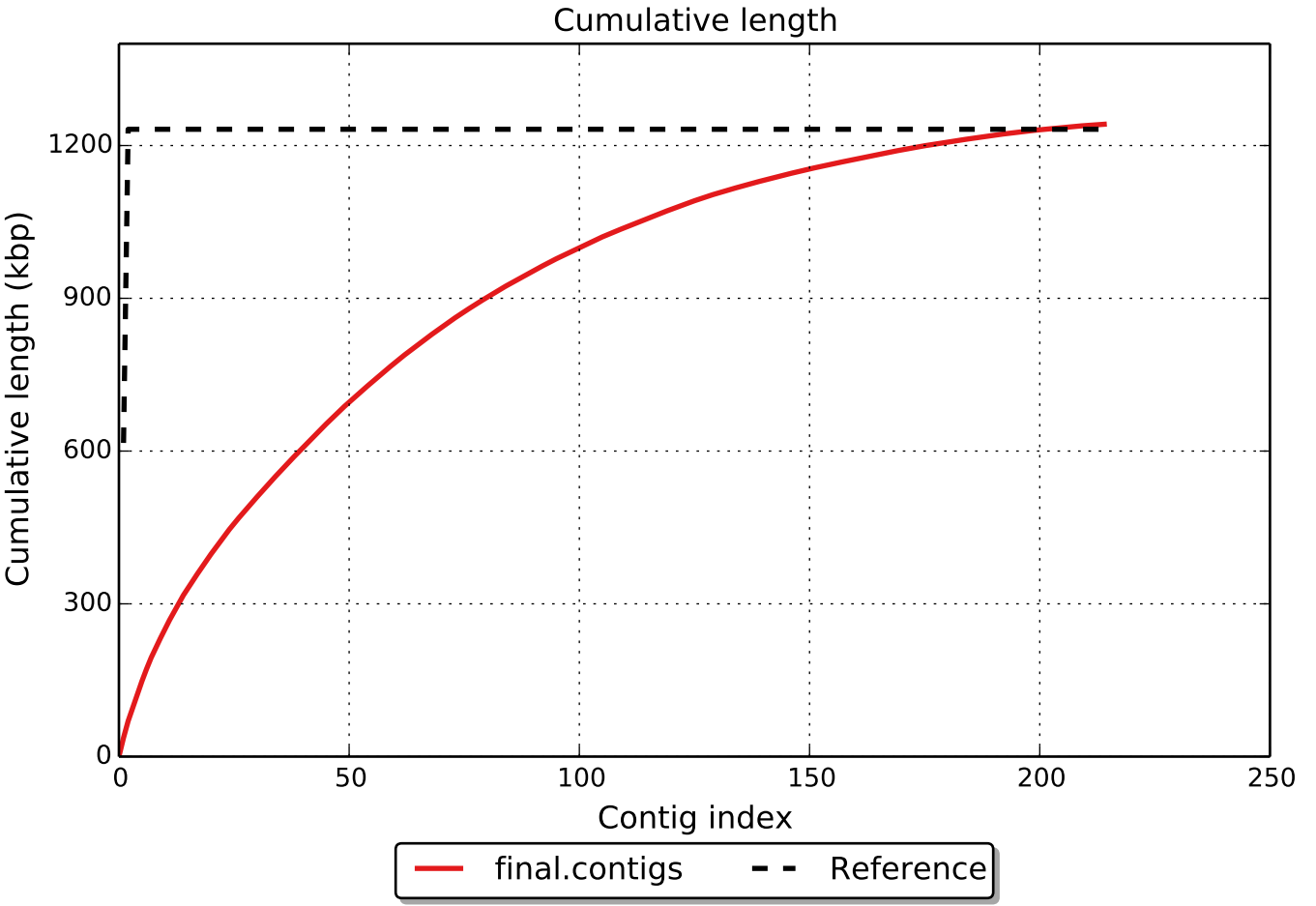
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	26043
# local misassemblies	0
# mismatches	17
# indels	0
# short indels	0
# long indels	0
Indels length	0

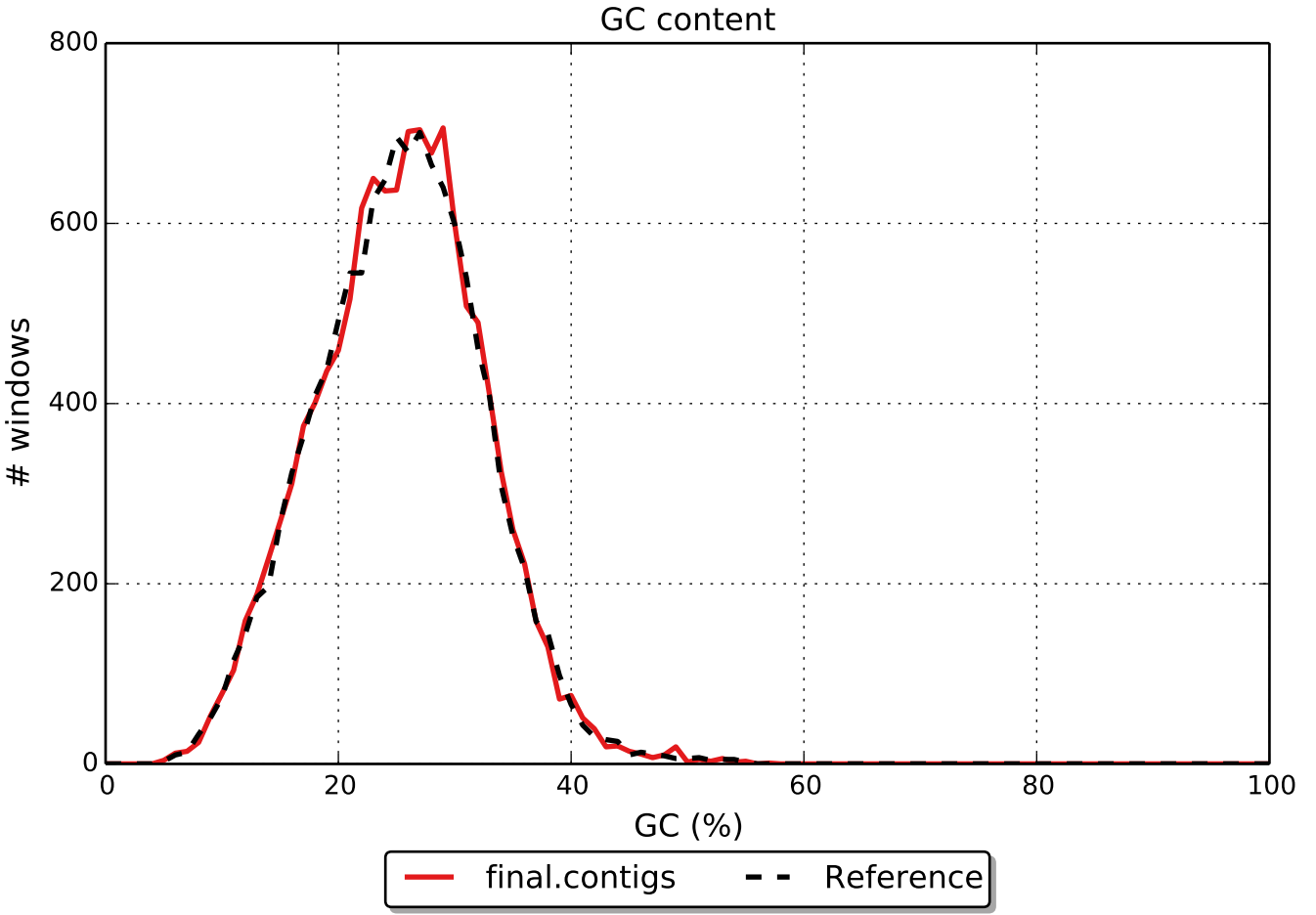
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

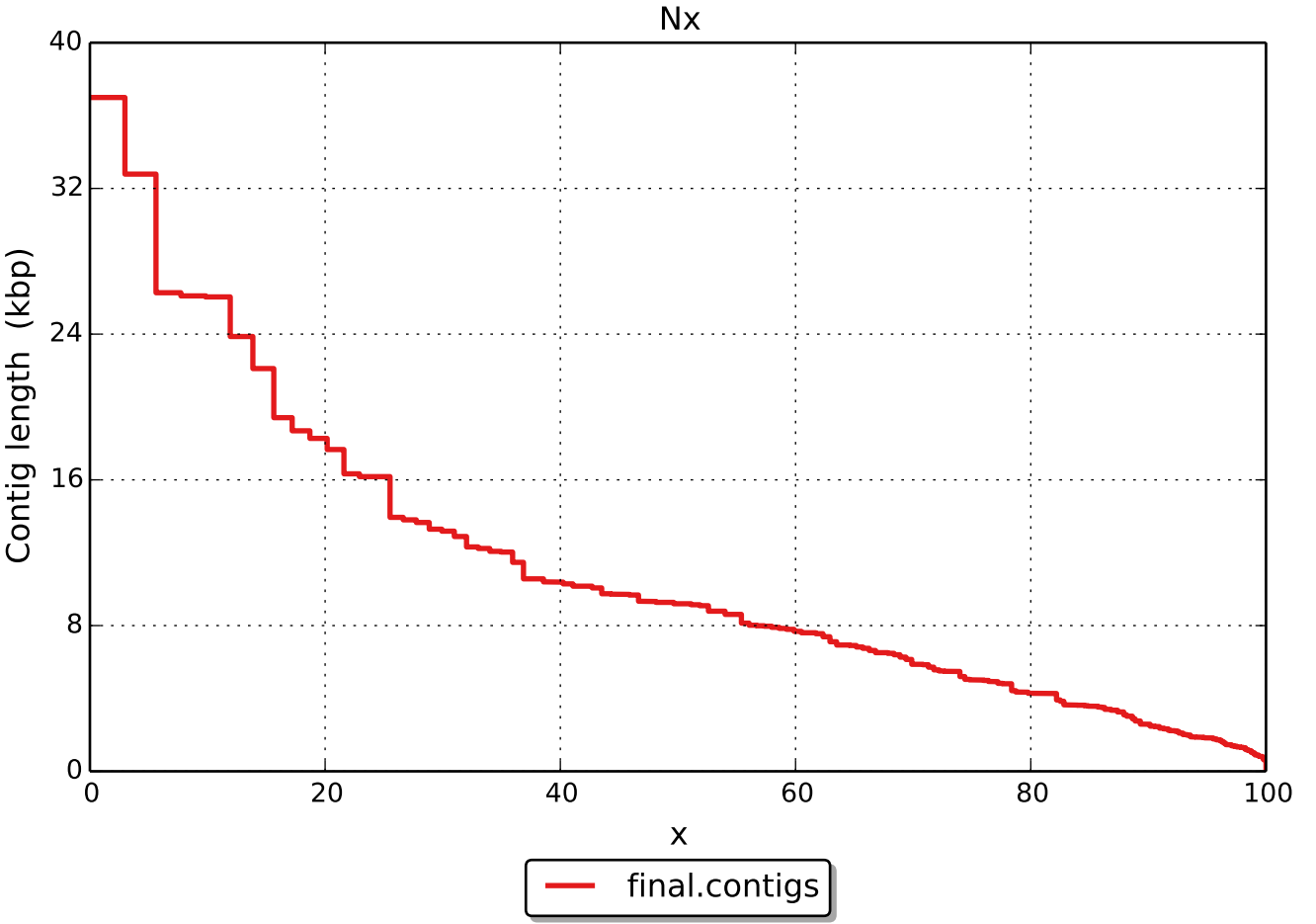
Unaligned report

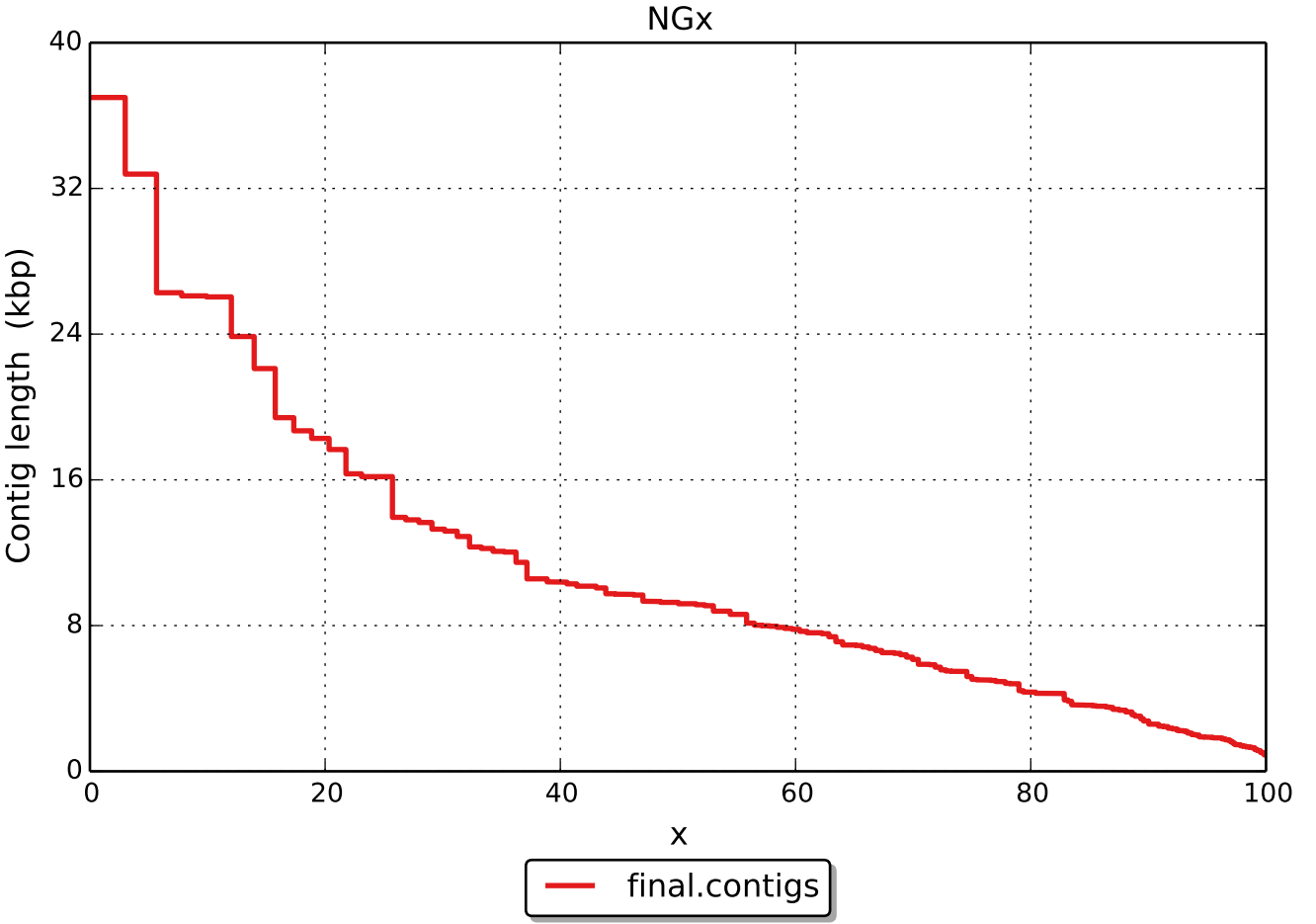
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

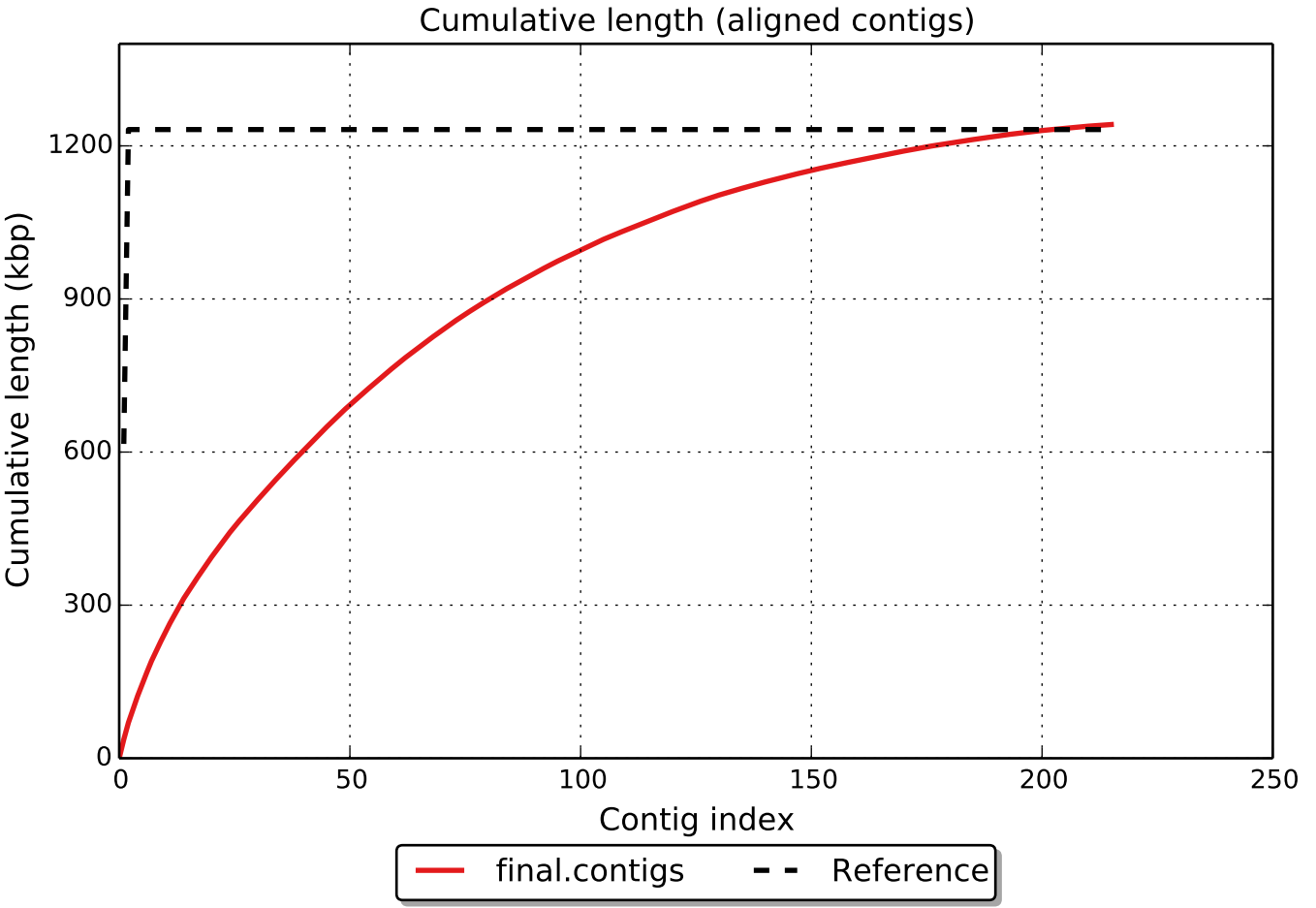

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
50
100
150
200
250
Contig index
final.contigs
Reference

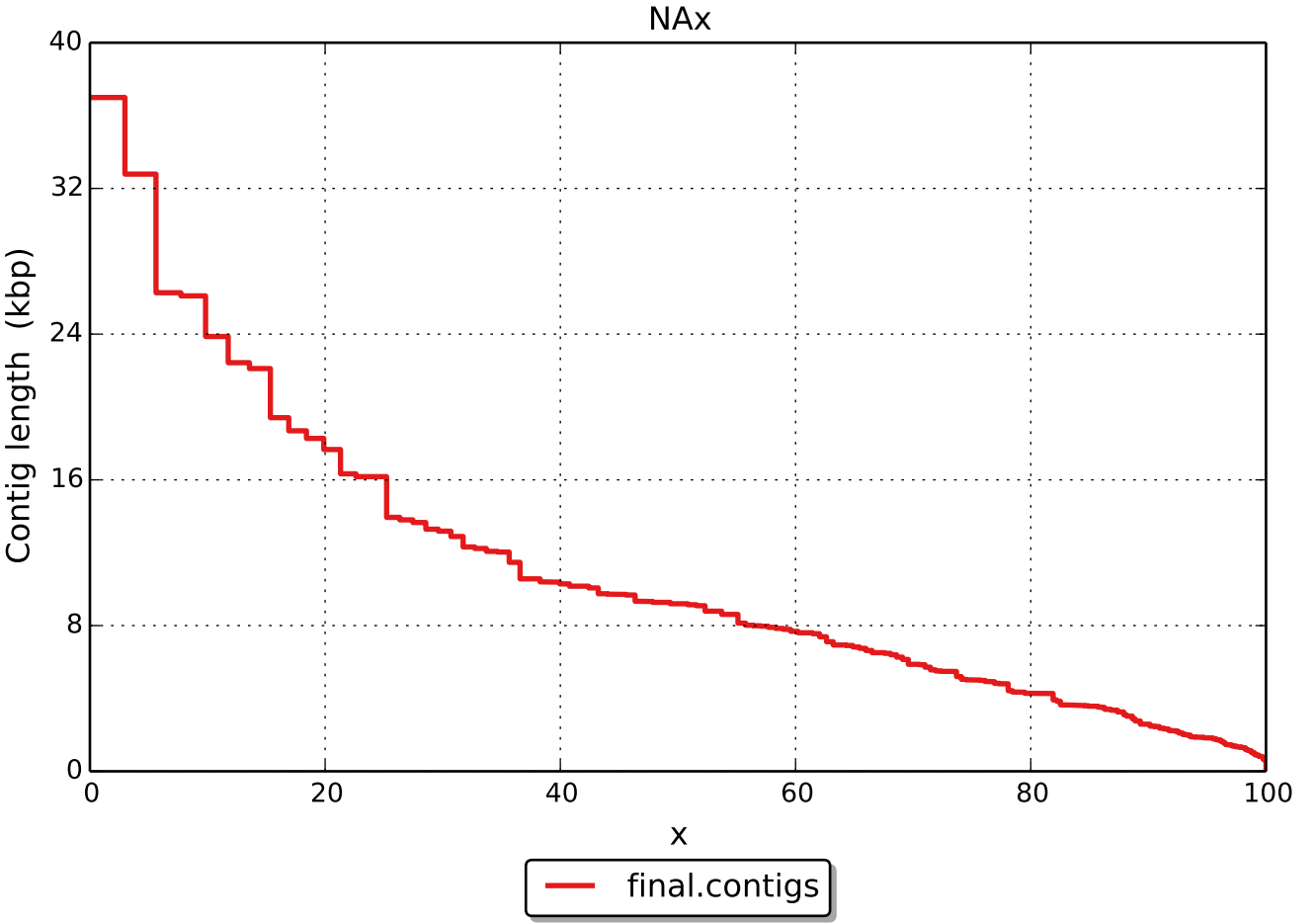

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

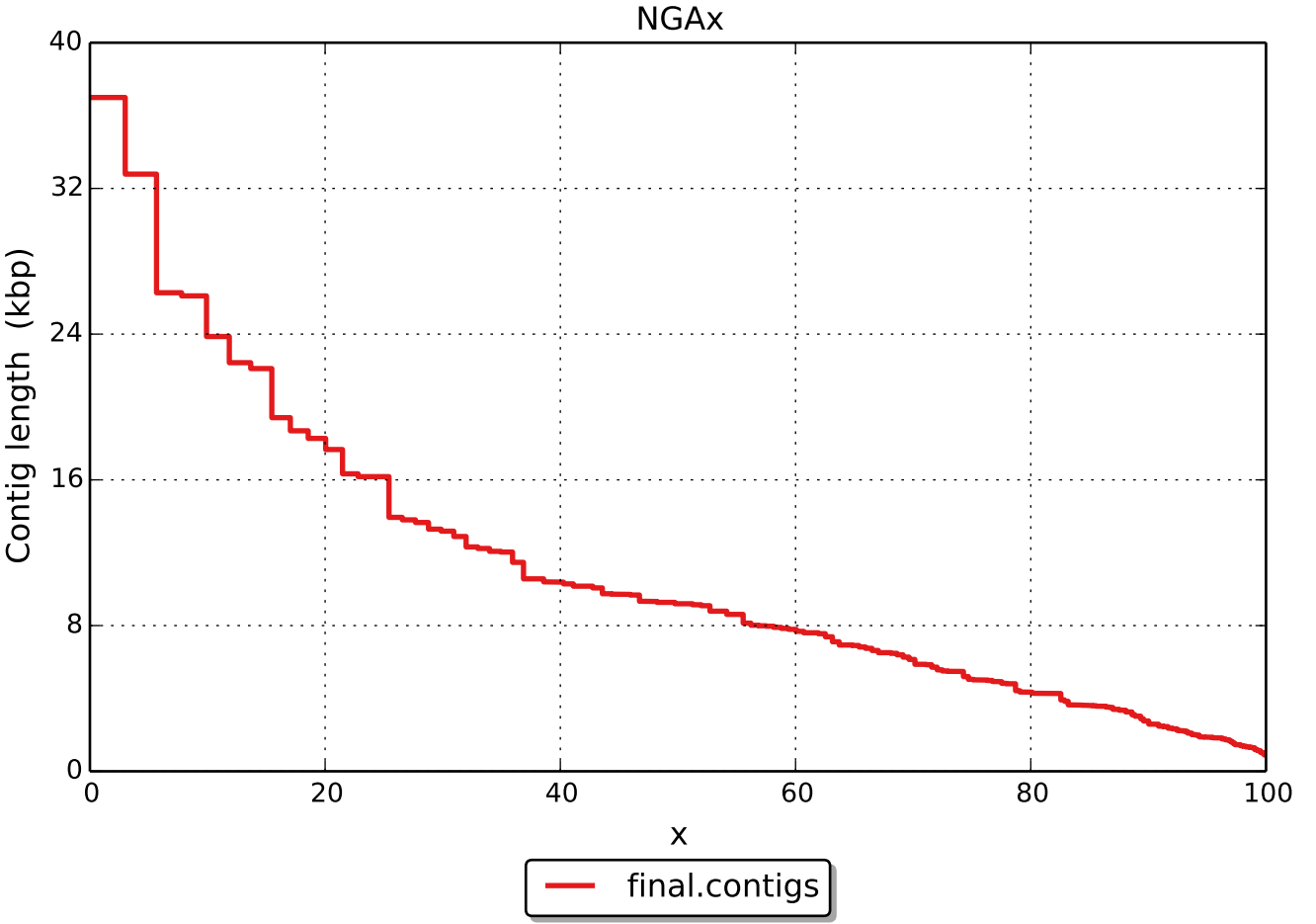

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


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

Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
interspecies translocations


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