Report

	final.contigs
# contigs (>= 0 bp)	1433
# contigs (>= 1000 bp)	843
Total length (>= 0 bp)	10926316
Total length (>= 1000 bp)	10700074
# contigs	976
Largest contig	83434
Total length	10789178
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	20236
NG50	19557
N75	11059
NG75	10461
L50	168
LG50	175
L75	346
LG75	367
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	48702
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.641
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.58
# indels per 100 kbp	0.07
Largest alignment	83434
NA50	20236
NGA50	19550
NA75	11056
NGA75	10401
LA50	168
LGA50	176
LA75	347
LGA75	368

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

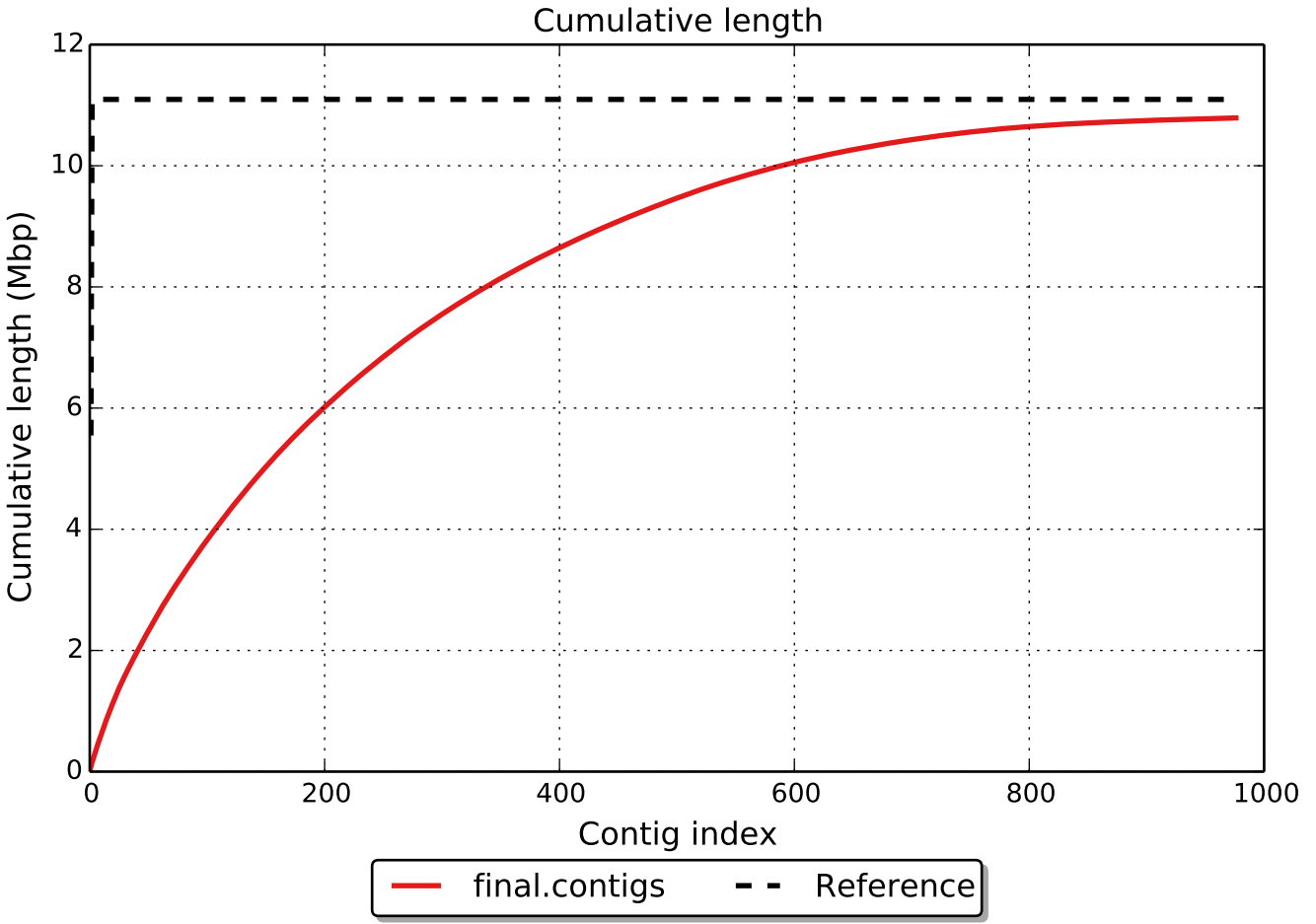
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	48702
# local misassemblies	2
# mismatches	598
# indels	8
# short indels	6
# long indels	2
Indels length	74

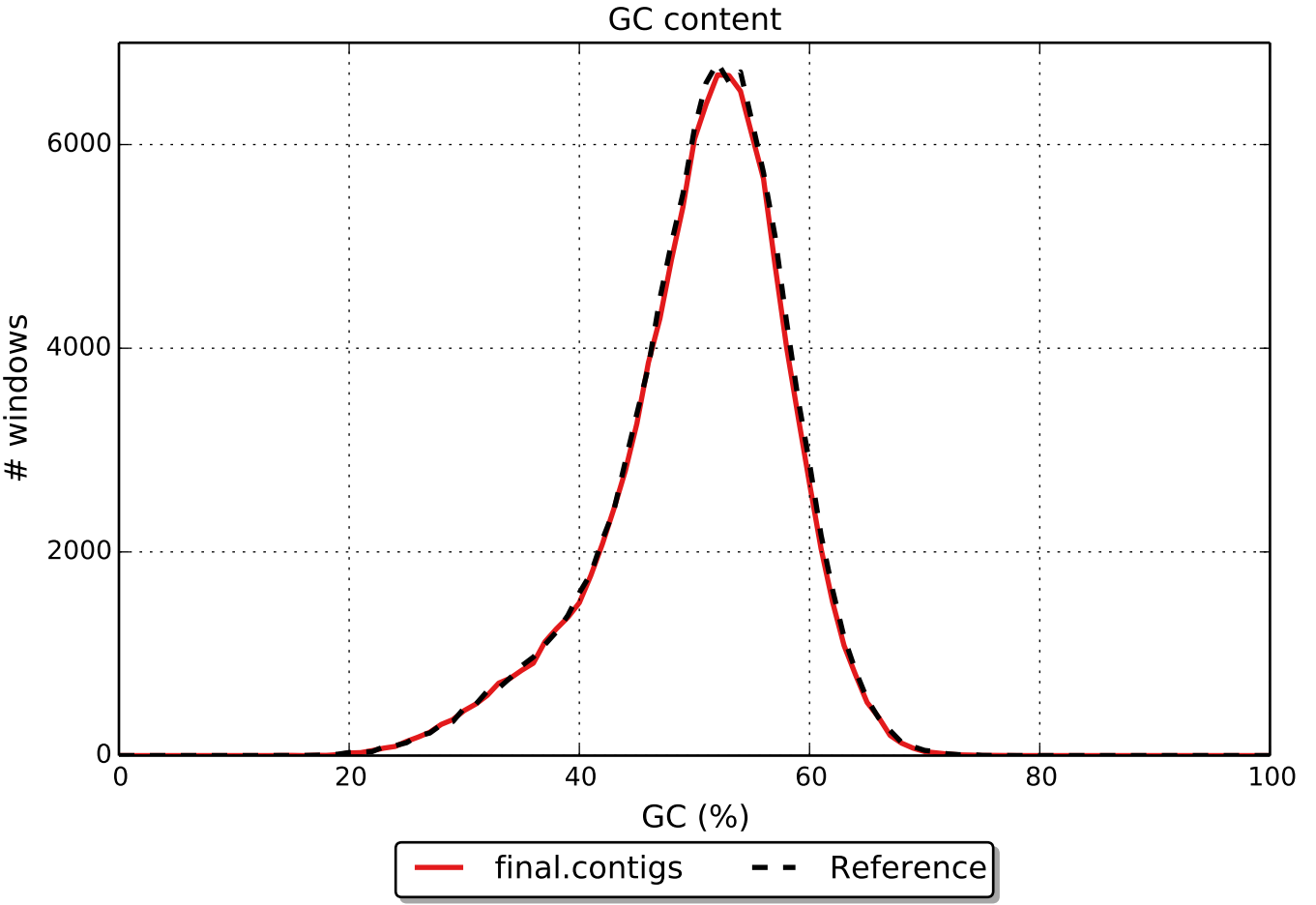
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

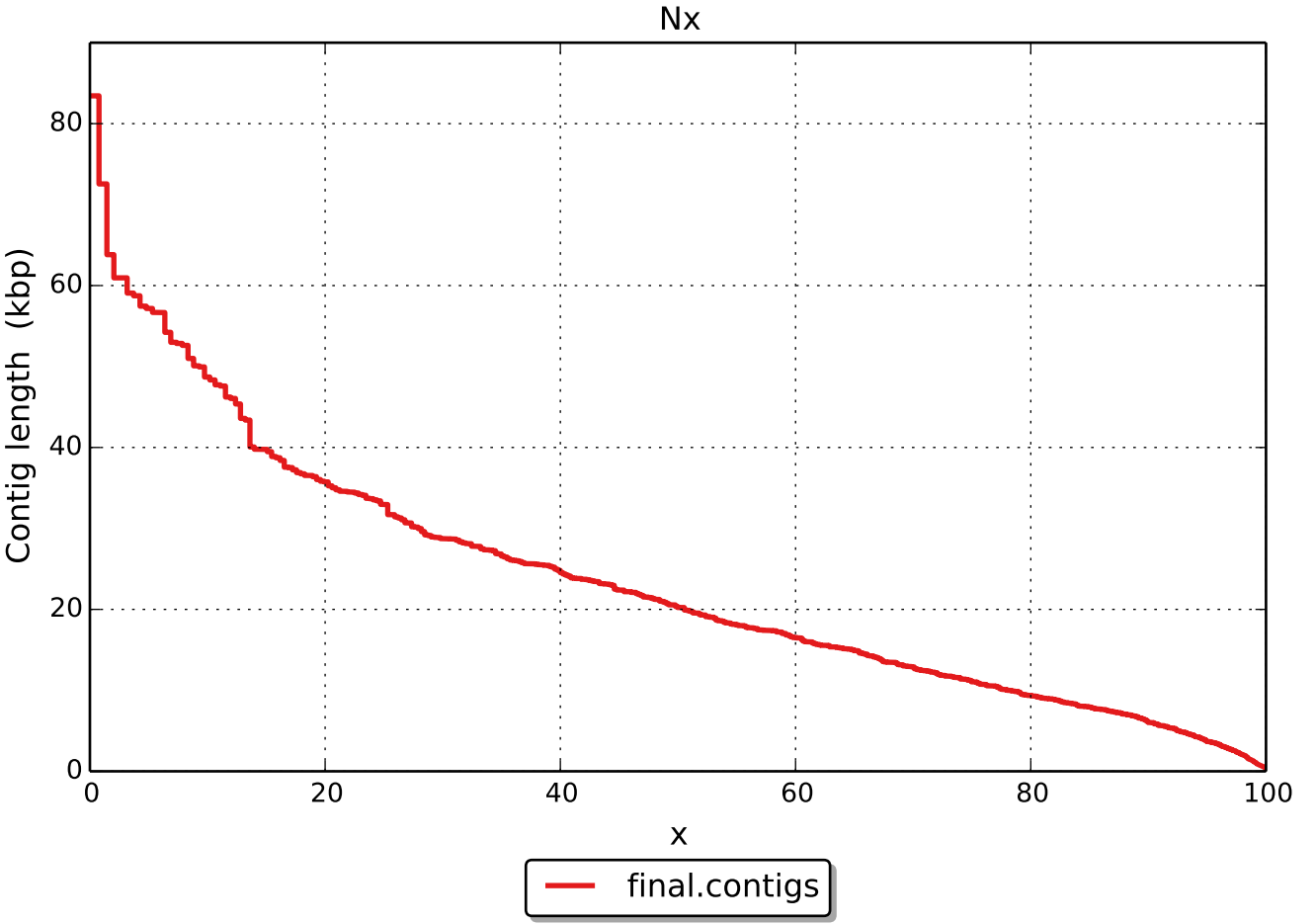
Unaligned report

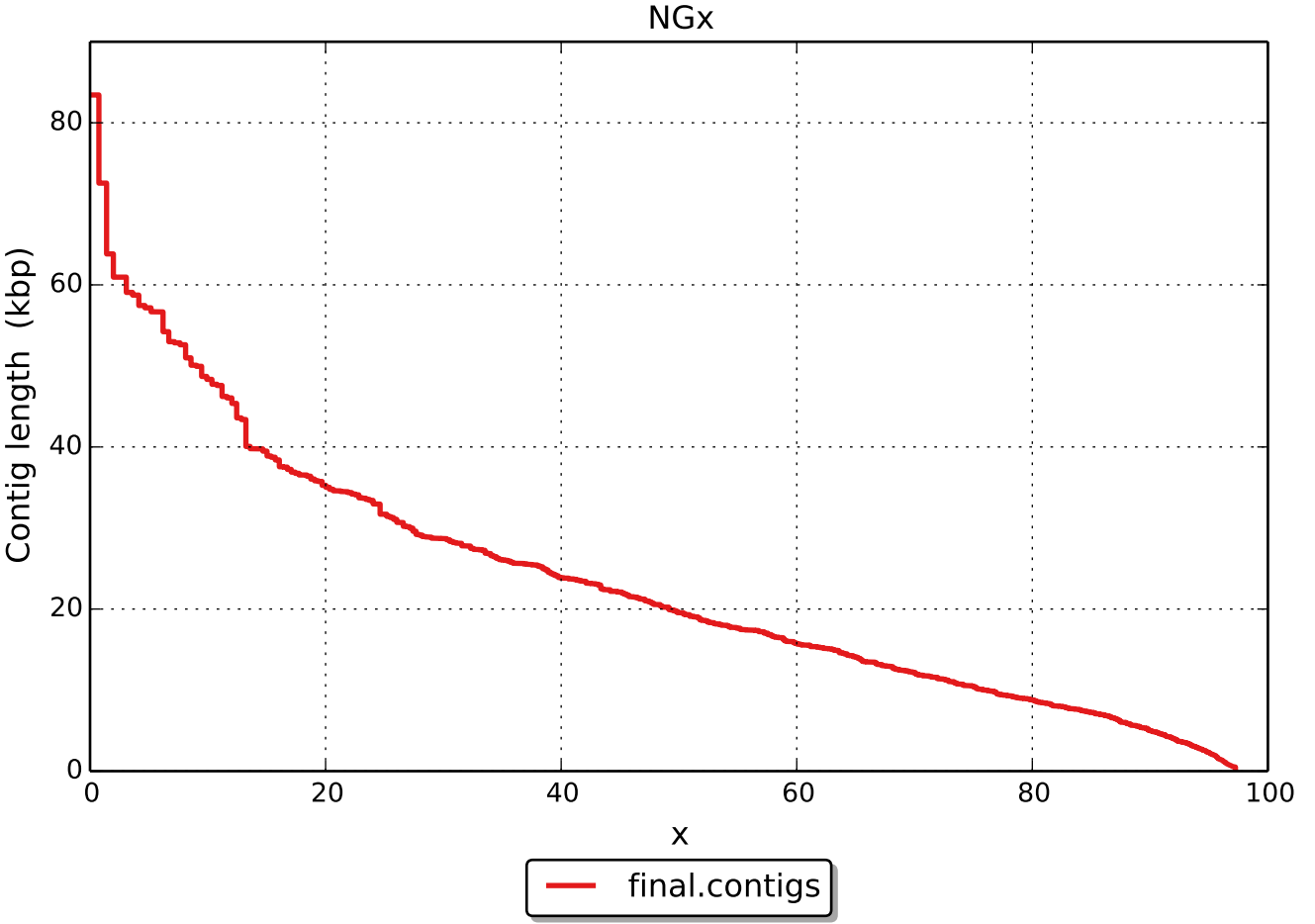
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

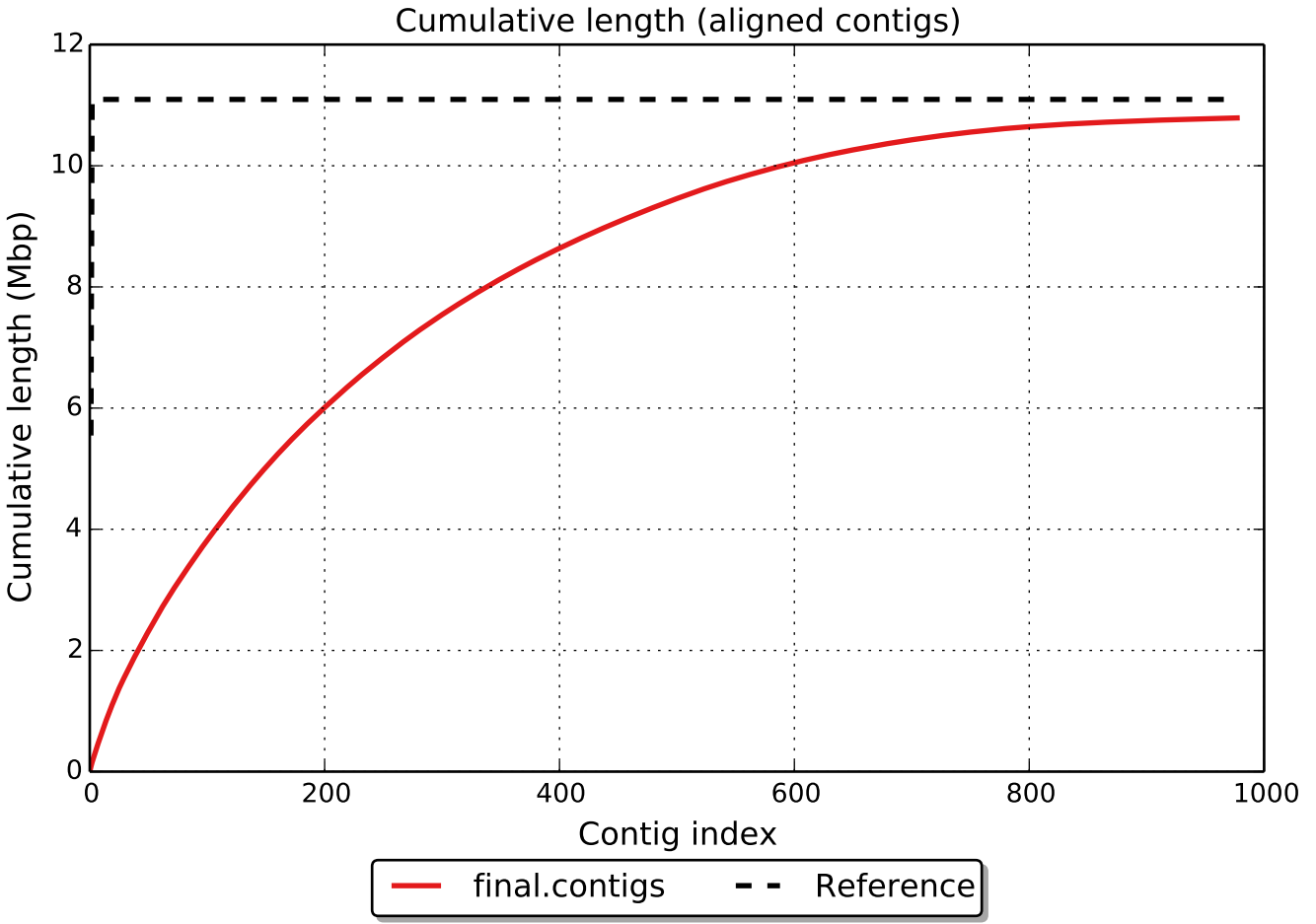

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
200
400
600
800
1000
final.contigs
Reference

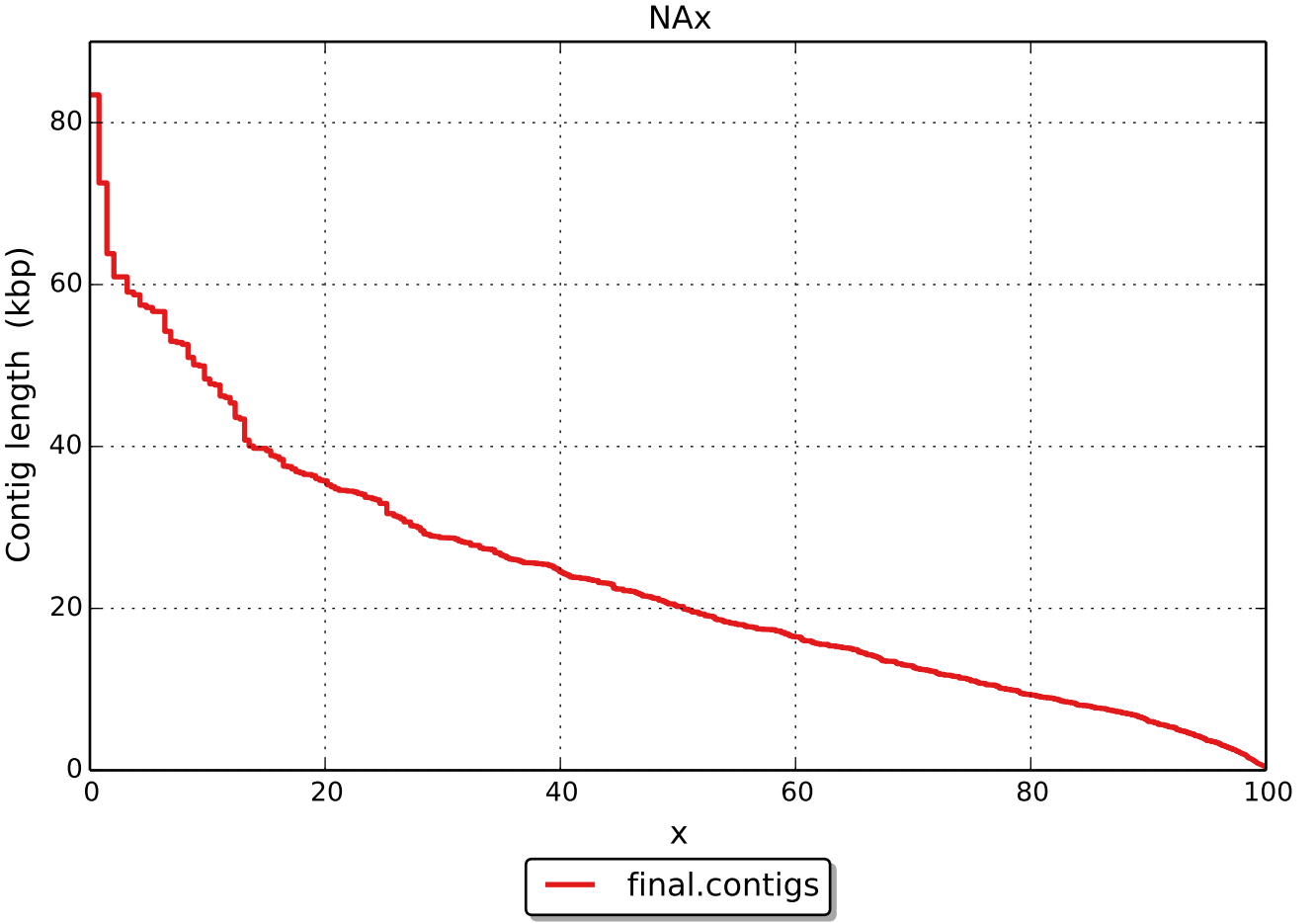

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

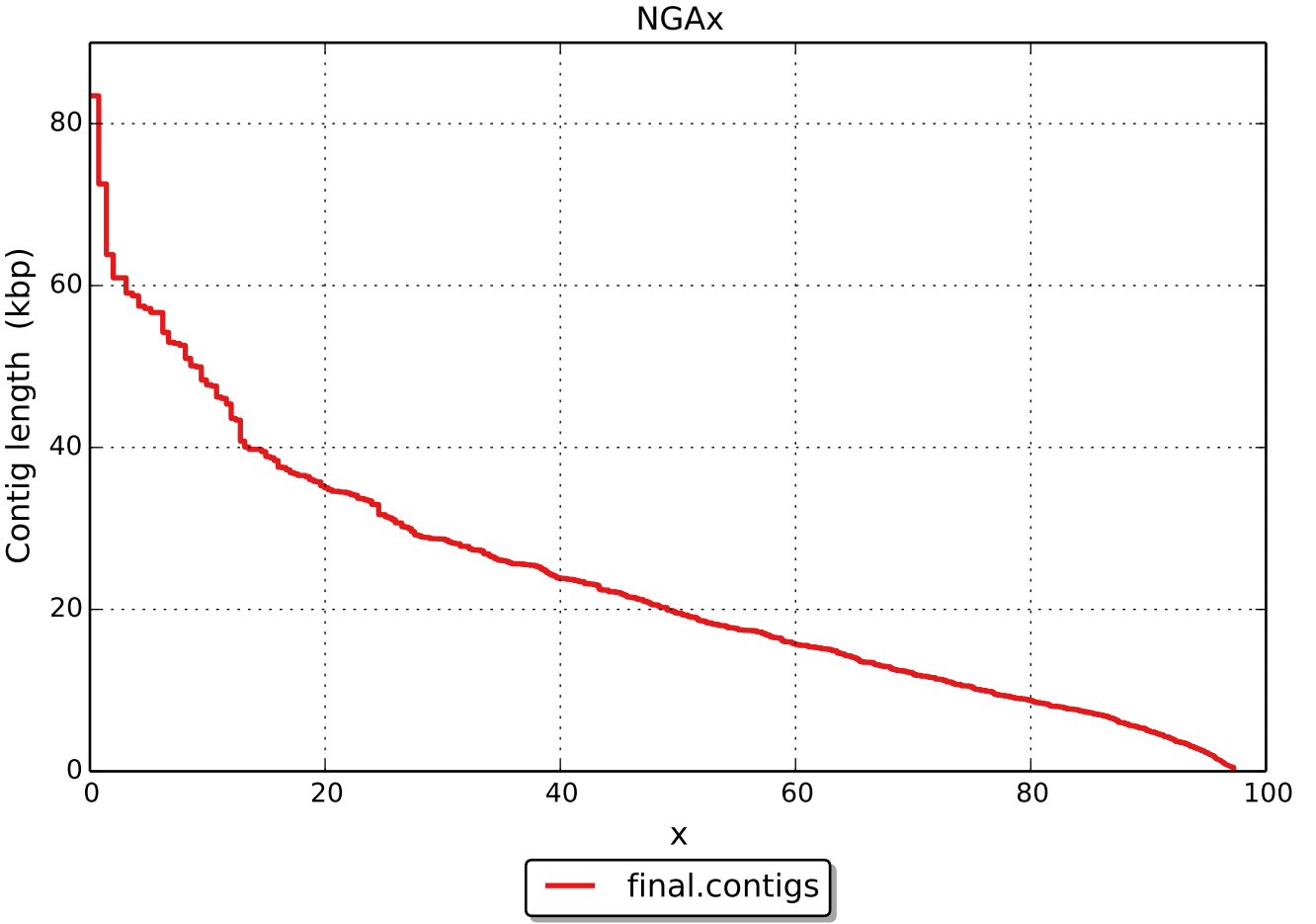

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
20
40
60
80
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 (Mbp)
Contig index
0
2
4
6
8
10
12
0
200
400
600
800
1000
final.contigs
Reference


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


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