Report

	final.contigs
# contigs (>= 0 bp)	466
# contigs (>= 1000 bp)	344
Total length (>= 0 bp)	1312972
Total length (>= 1000 bp)	1239024
# contigs	425
Largest contig	13166
Total length	1297290
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.30
N50	4334
NG50	4342
N75	2499
NG75	2602
L50	98
LG50	96
L75	192
LG75	188
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6898
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.249
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.26
# indels per 100 kbp	0.00
Largest alignment	13166
NA50	4310
NGA50	4334
NA75	2499
NGA75	2588
LA50	98
LGA50	97
LA75	193
LGA75	189

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

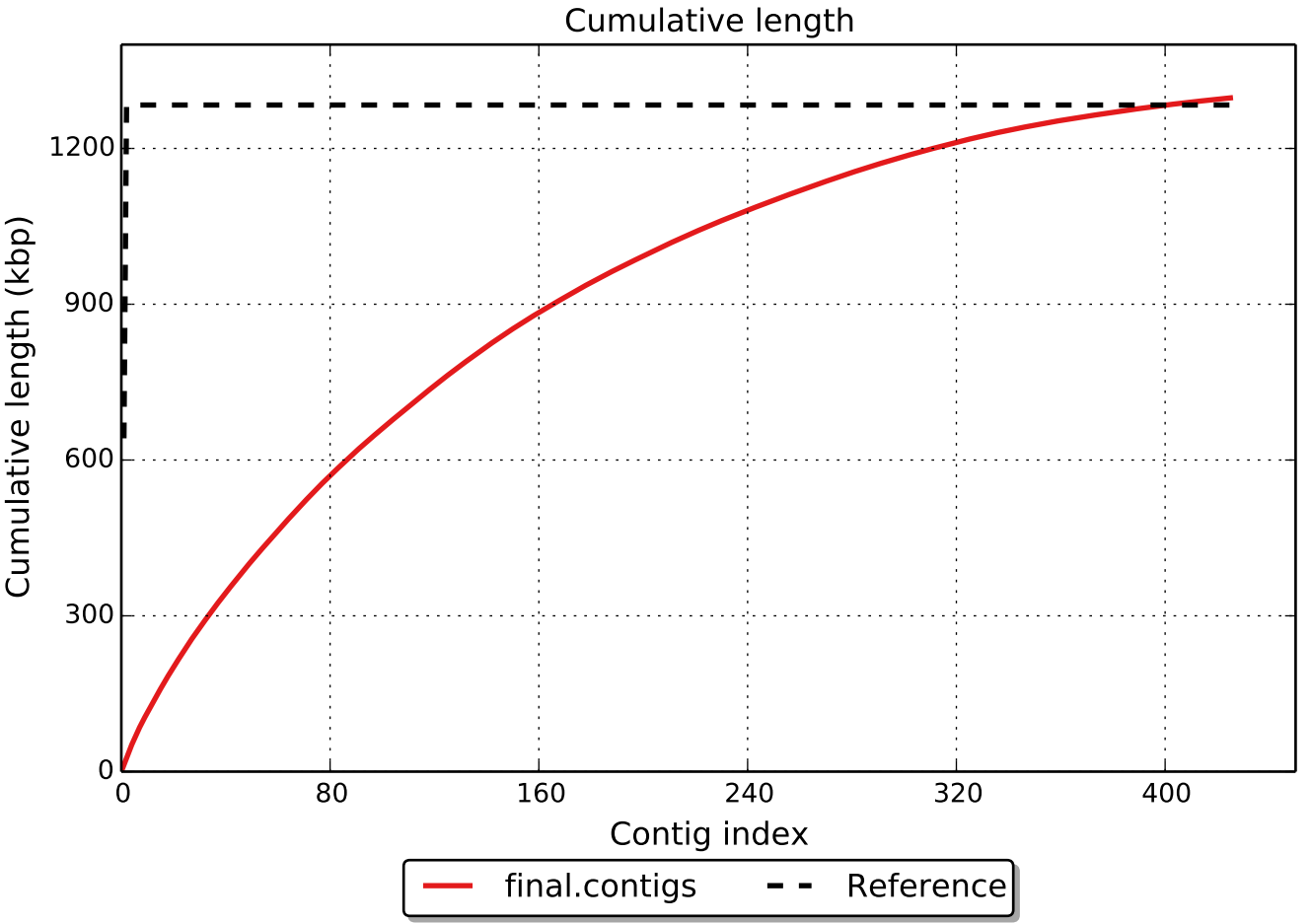
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	6898
# local misassemblies	0
# mismatches	432
# indels	0
# short indels	0
# long indels	0
Indels length	0

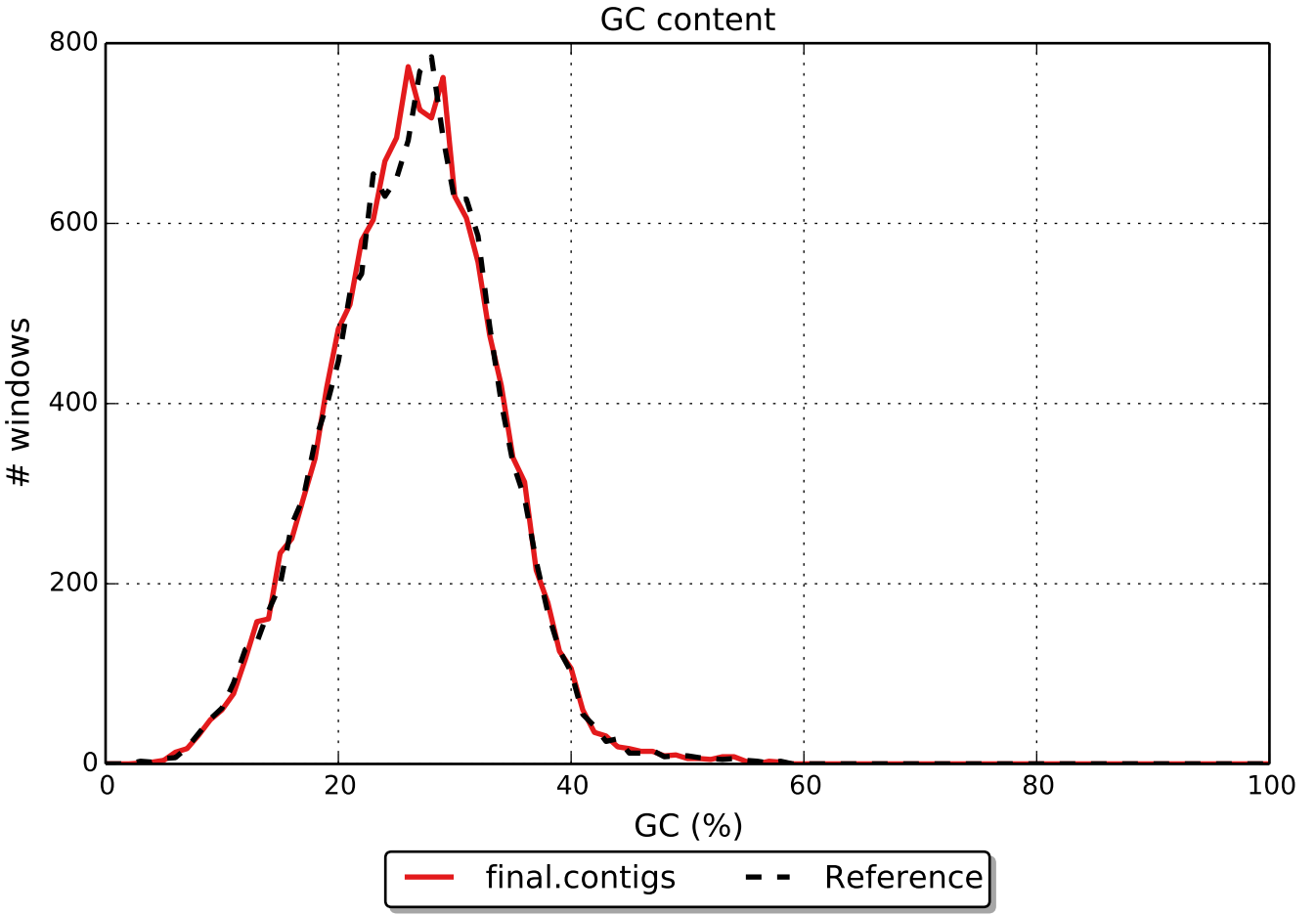
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

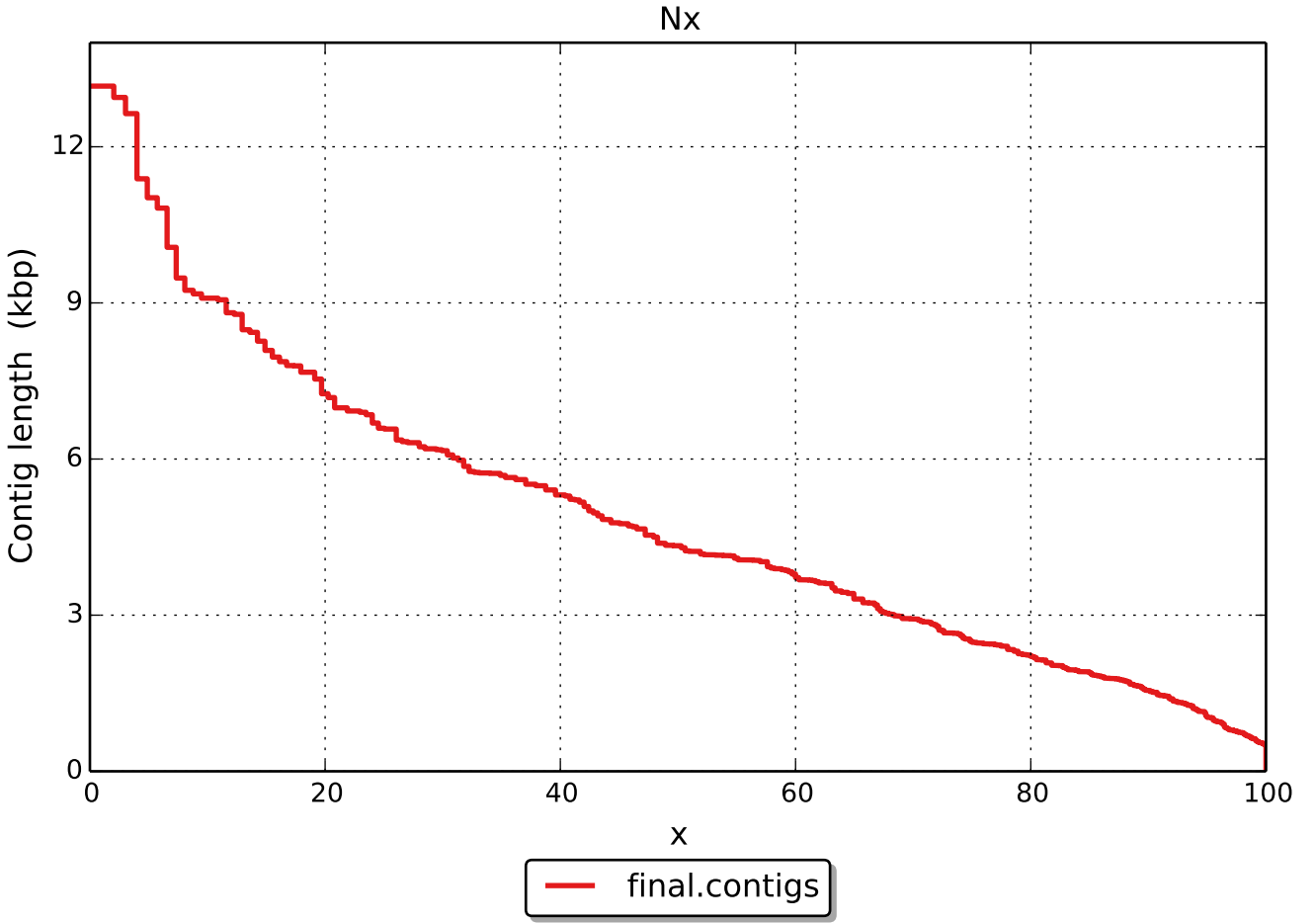
Unaligned report

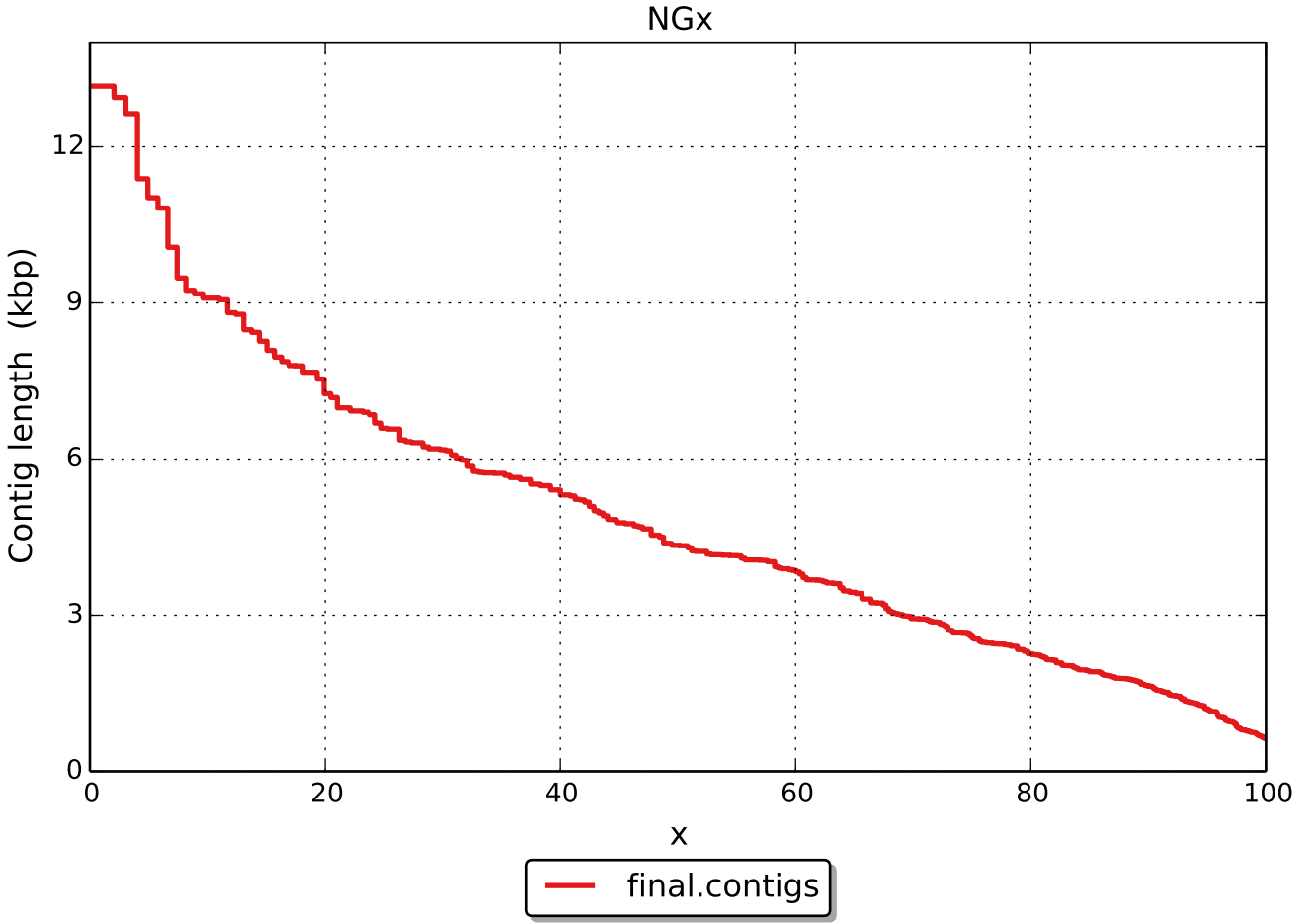
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

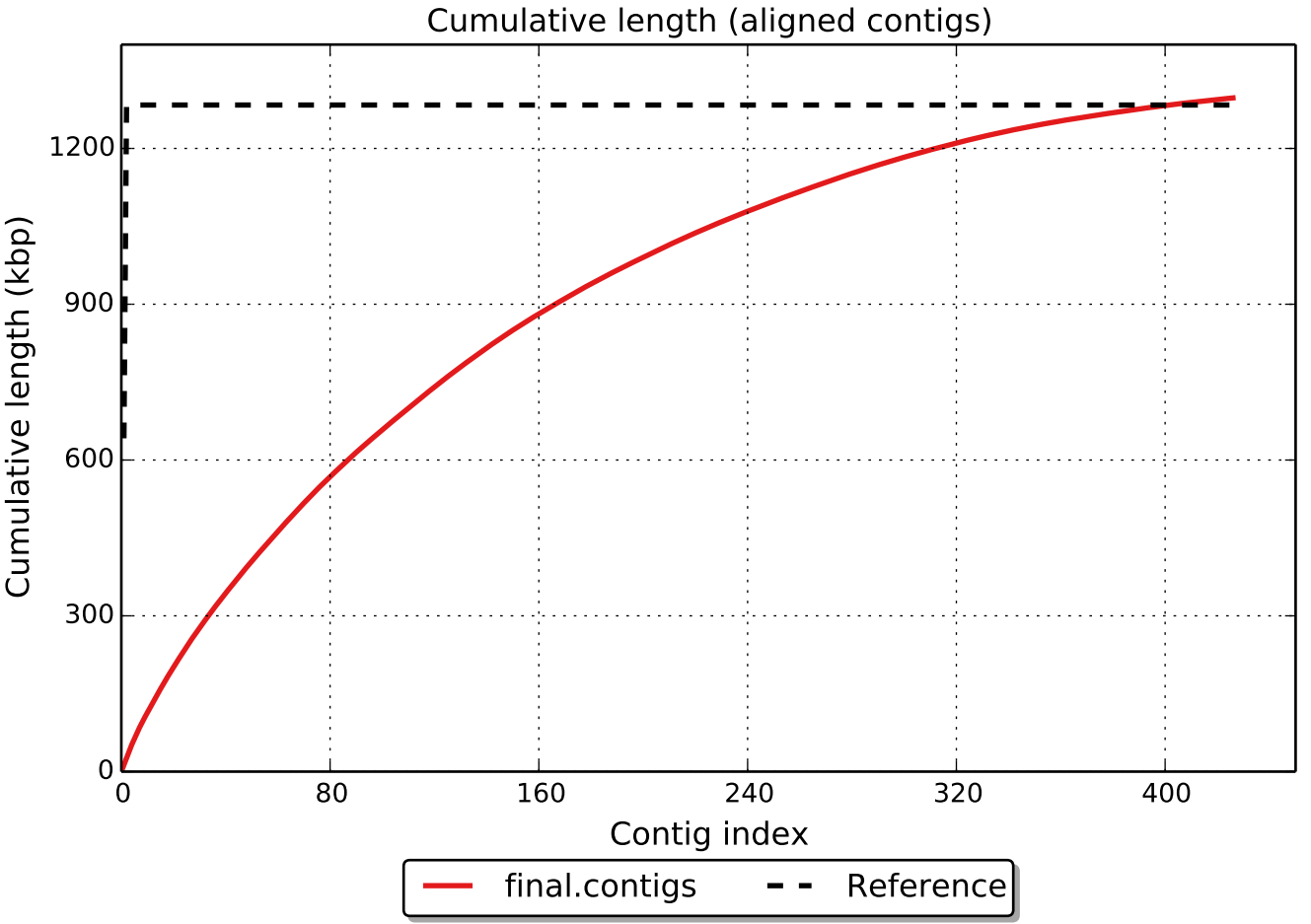

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
80
160
240
320
400
Contig index
final.contigs
Reference

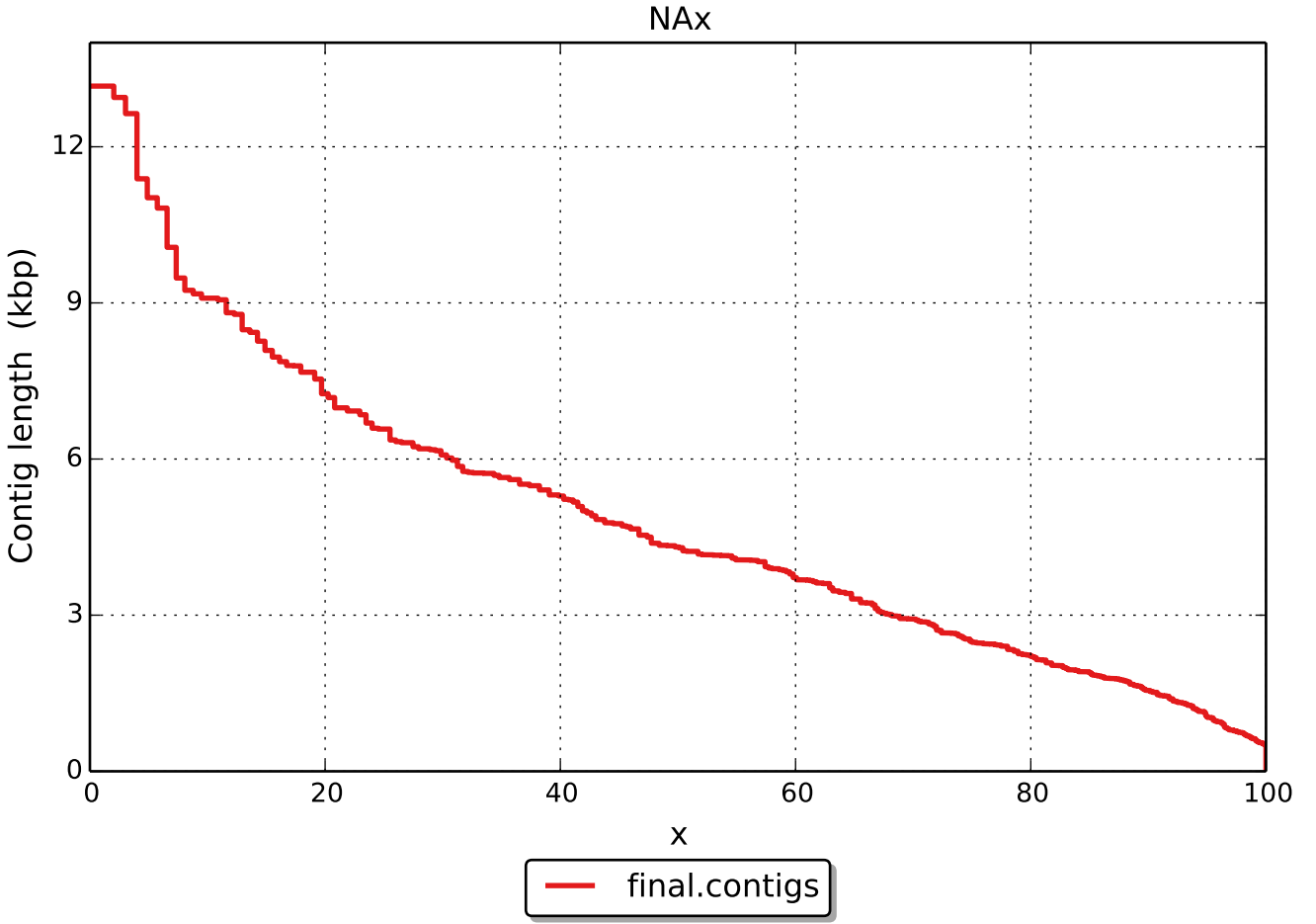

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

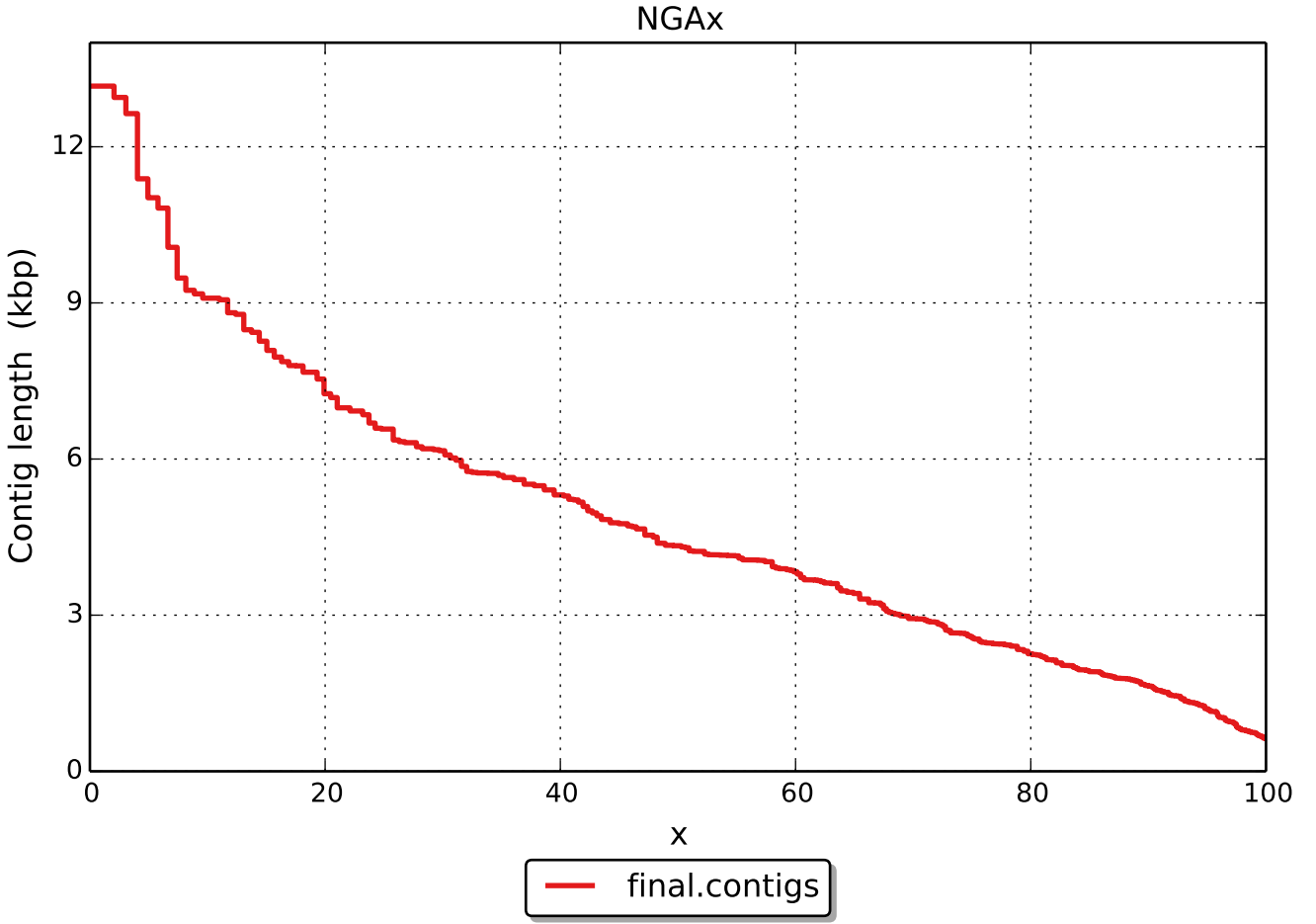

Nx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
3
6
9
12
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)
1200
900
600
300
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs