Report

	final.contigs
# contigs (>= 0 bp)	3263
# contigs (>= 1000 bp)	2173
Total length (>= 0 bp)	11052617
Total length (>= 1000 bp)	10545119
# contigs	2571
Largest contig	30455
Total length	10834958
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	6653
NG50	6530
N75	3624
NG75	3494
L50	508
LG50	527
L75	1061
LG75	1116
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	33243
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.867
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.01
# indels per 100 kbp	0.21
Largest alignment	30455
NA50	6653
NGA50	6526
NA75	3616
NGA75	3489
LA50	508
LGA50	528
LA75	1062
LGA75	1117

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

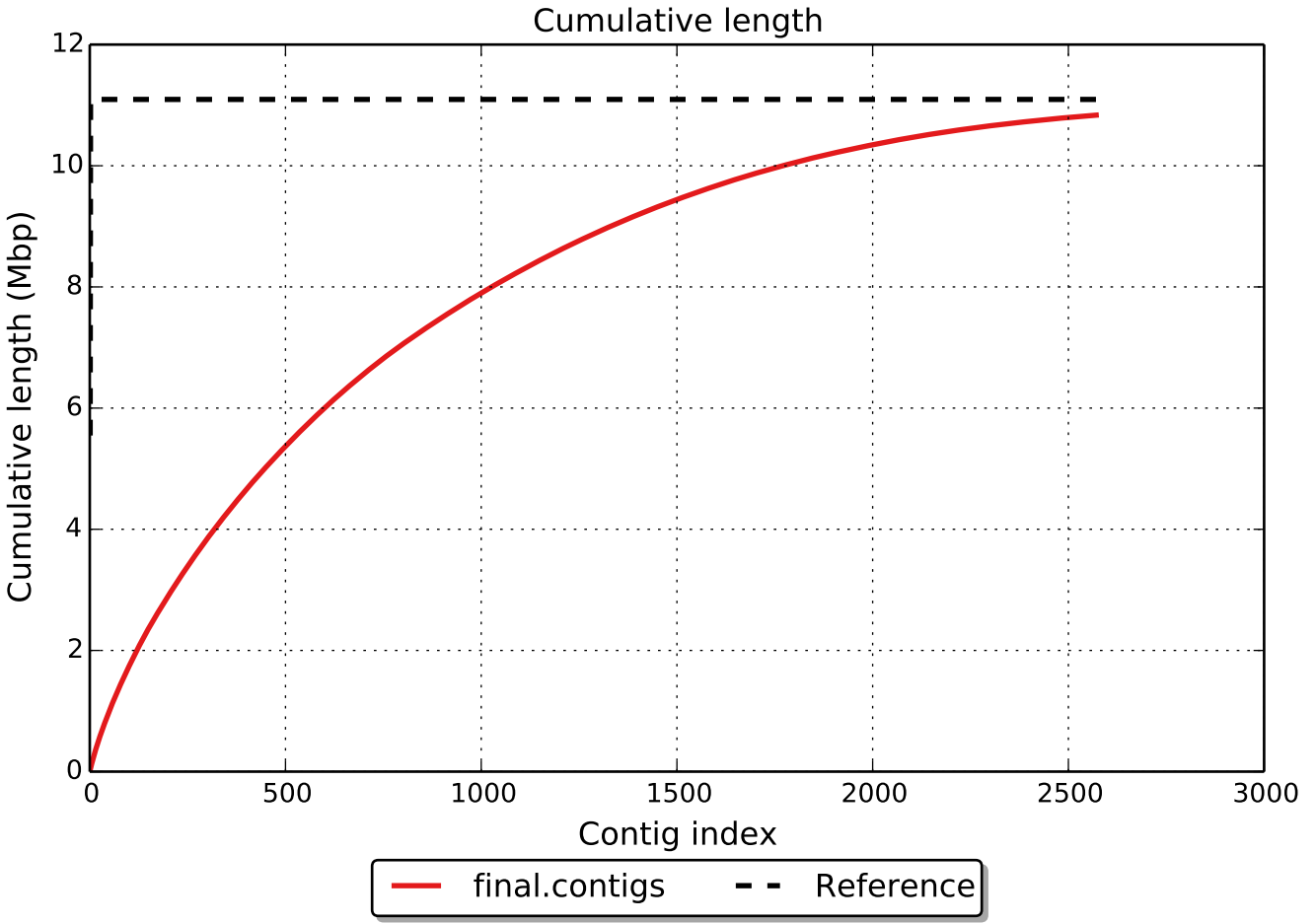
	final.contigs
# misassemblies	3
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	3
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	33243
# local misassemblies	4
# mismatches	1703
# indels	22
# short indels	18
# long indels	4
Indels length	143

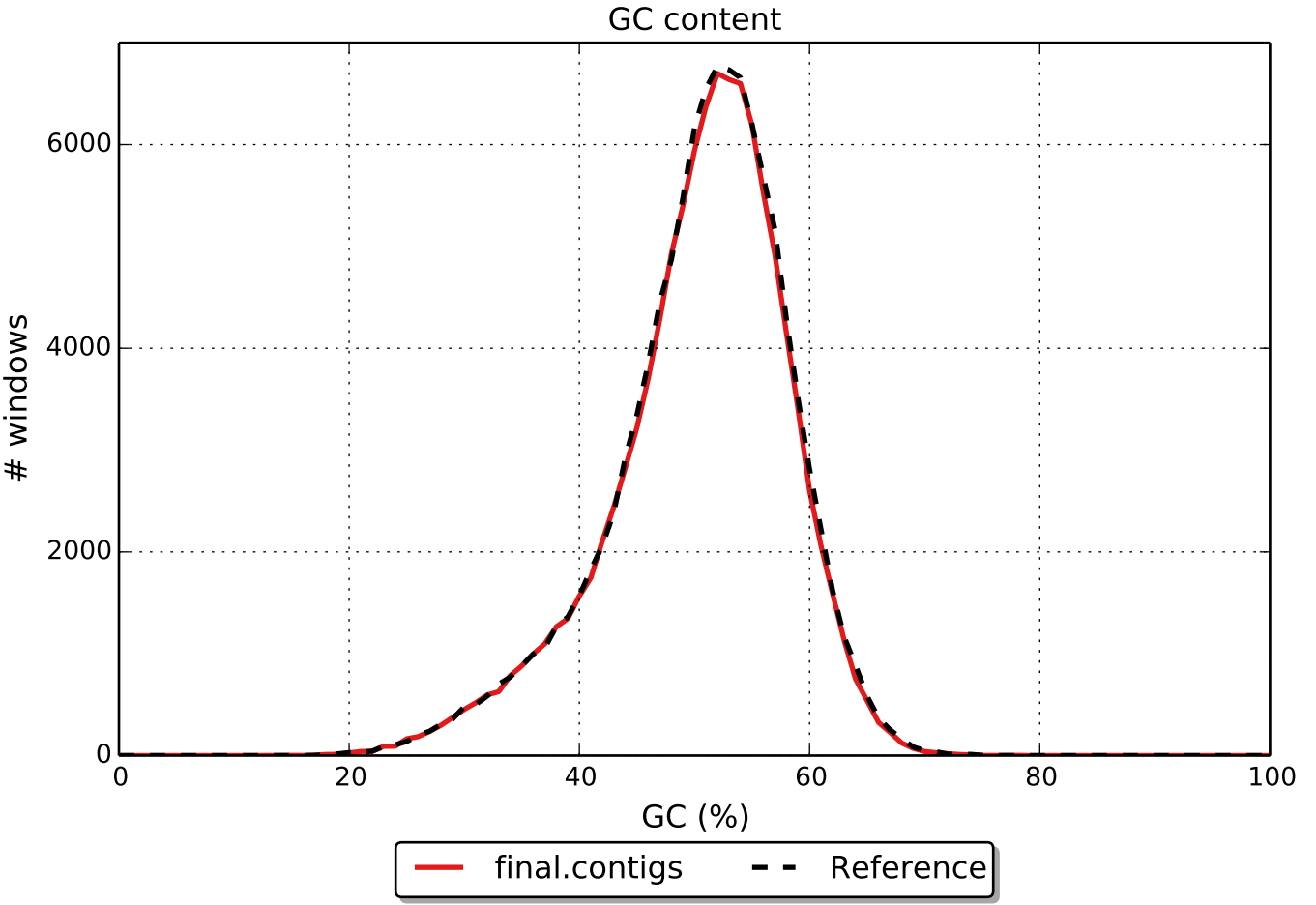
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

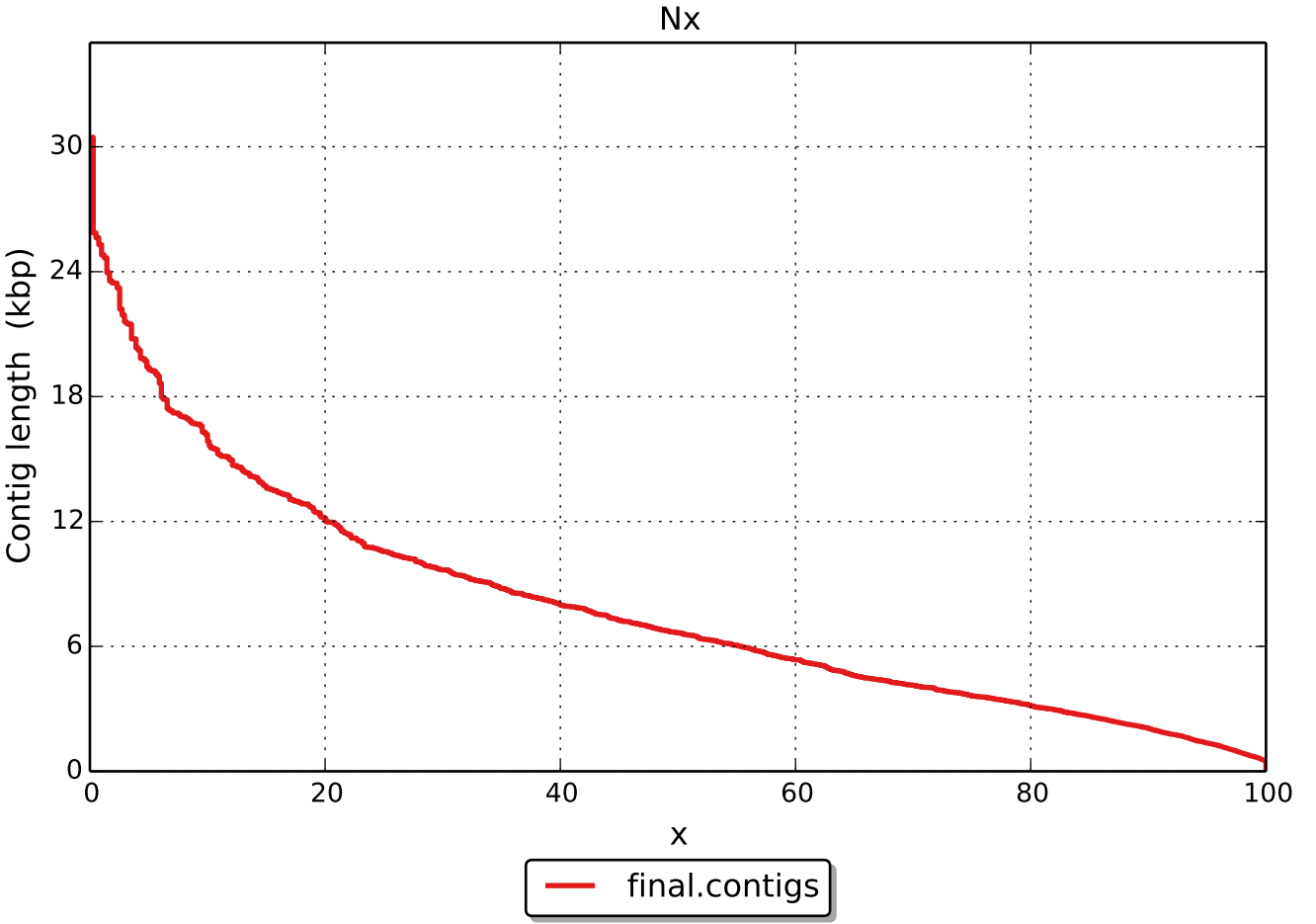
Unaligned report

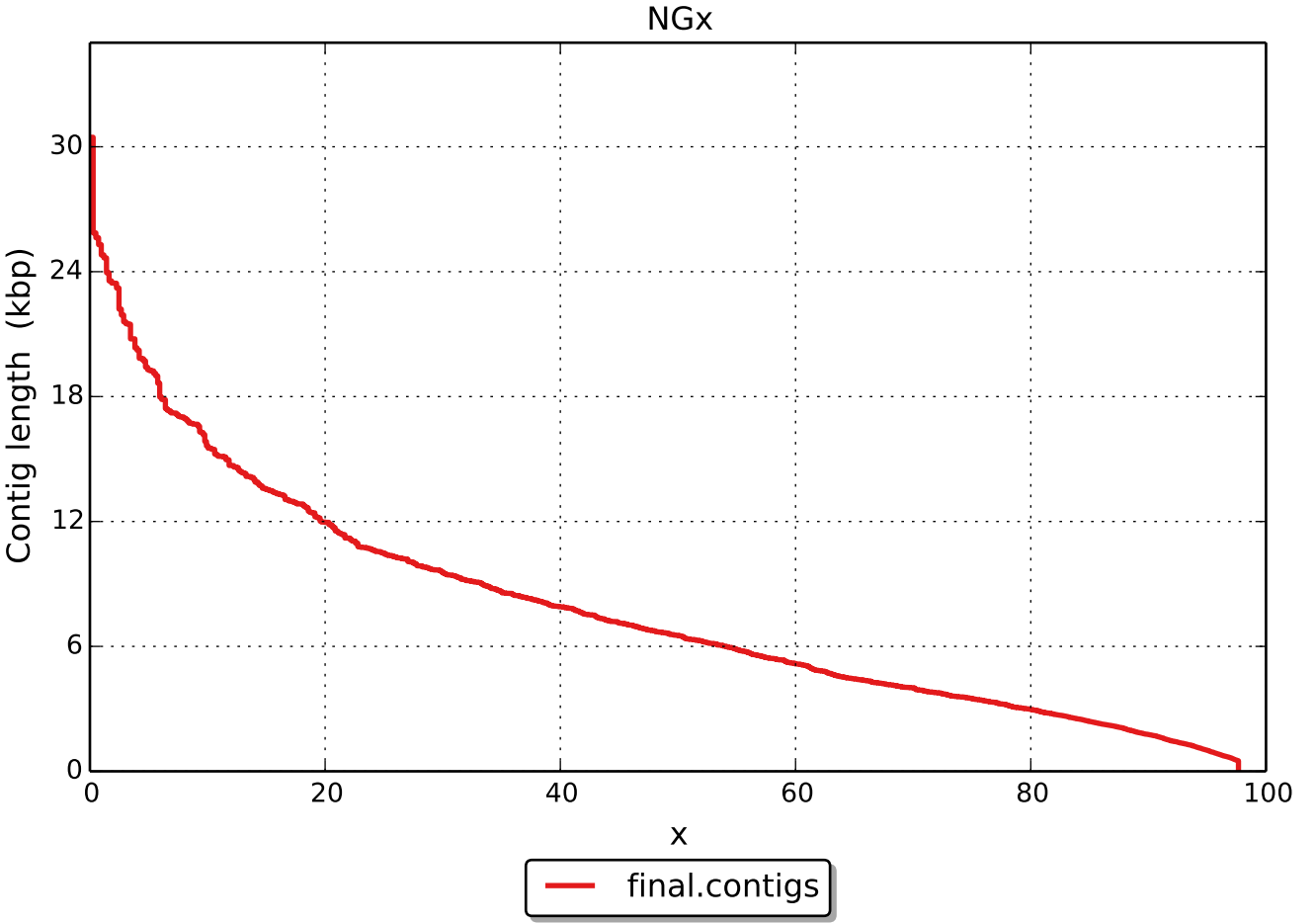
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

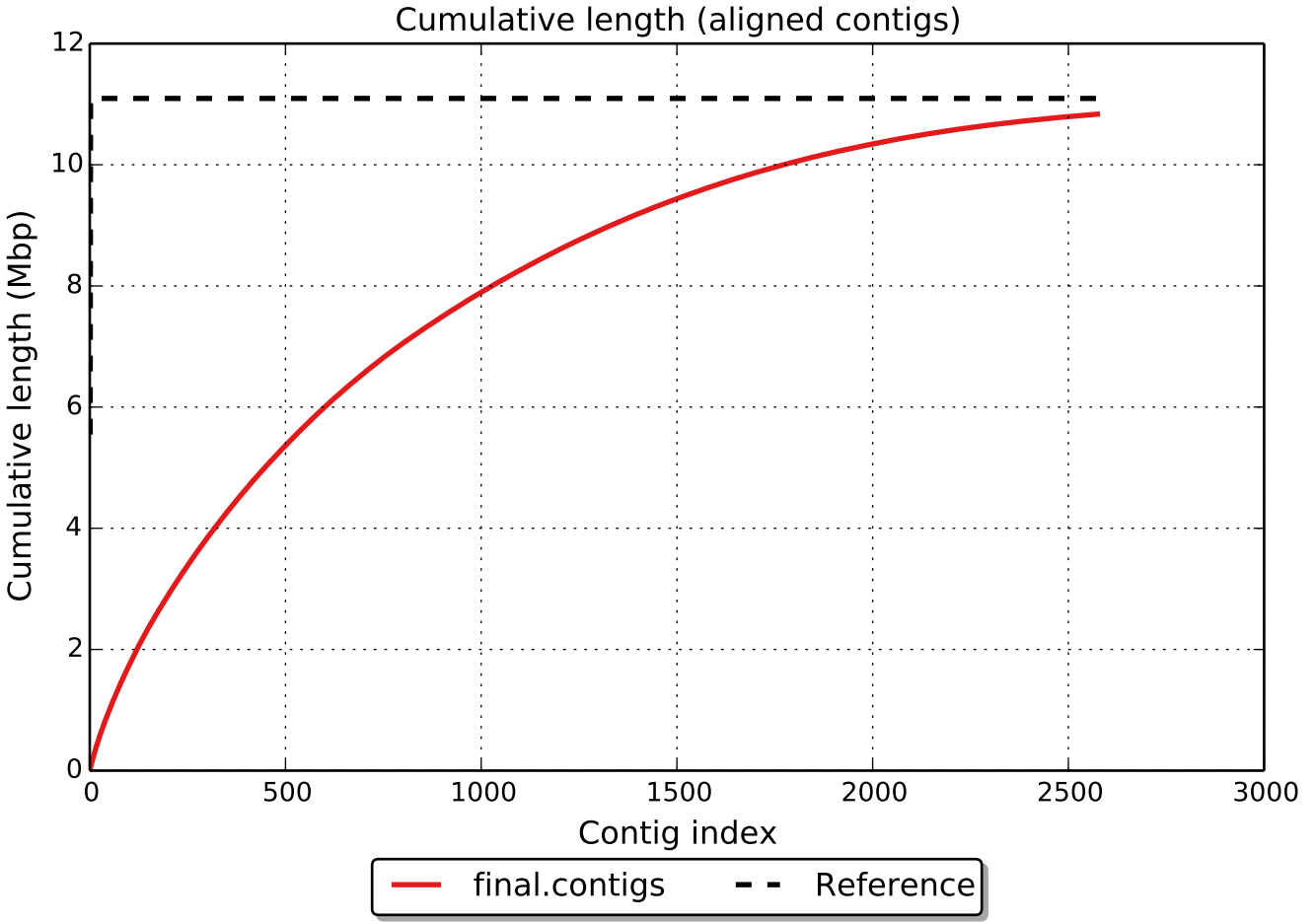

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
500
1000
1500
2000
2500
3000
final.contigs
Reference

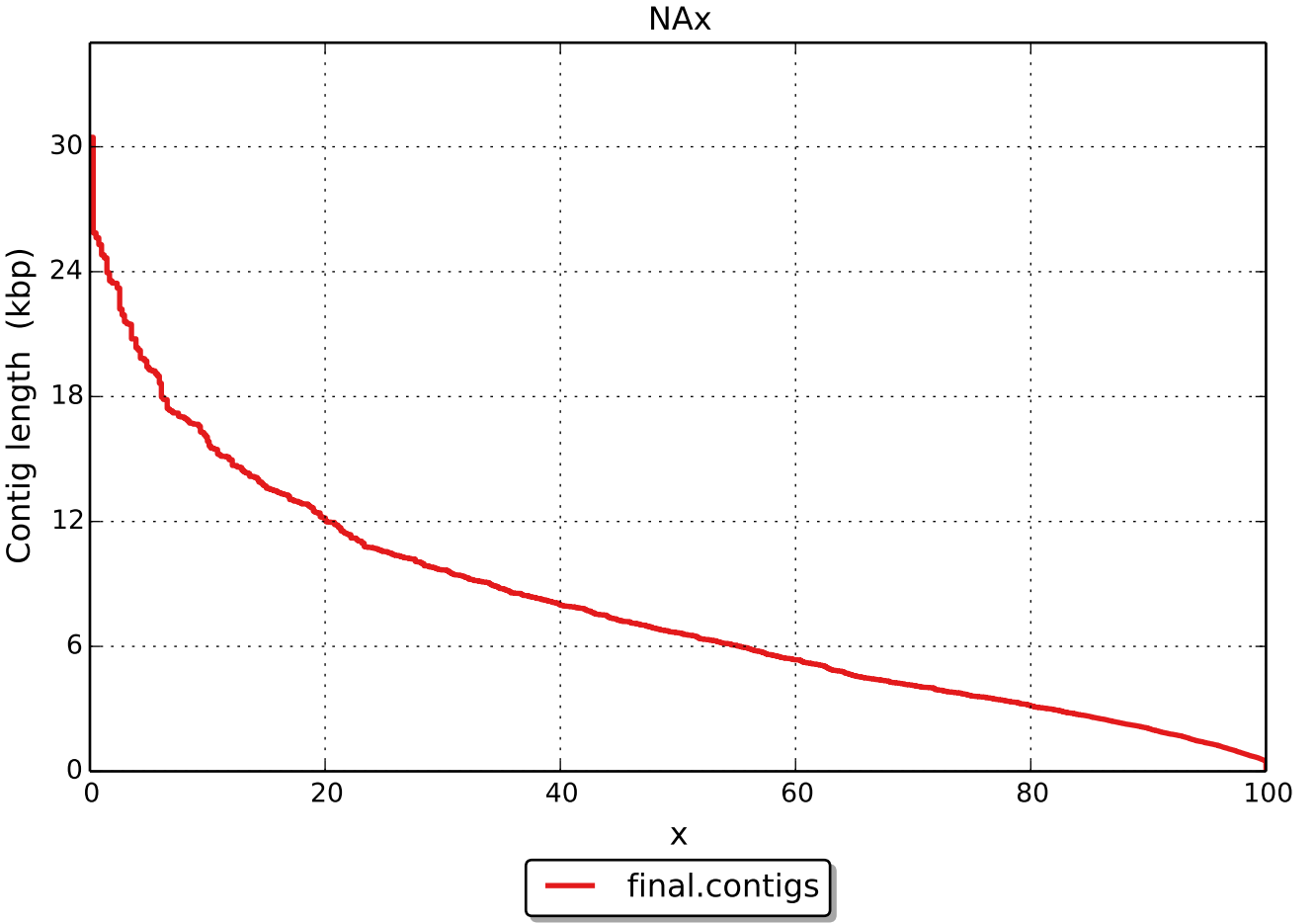

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

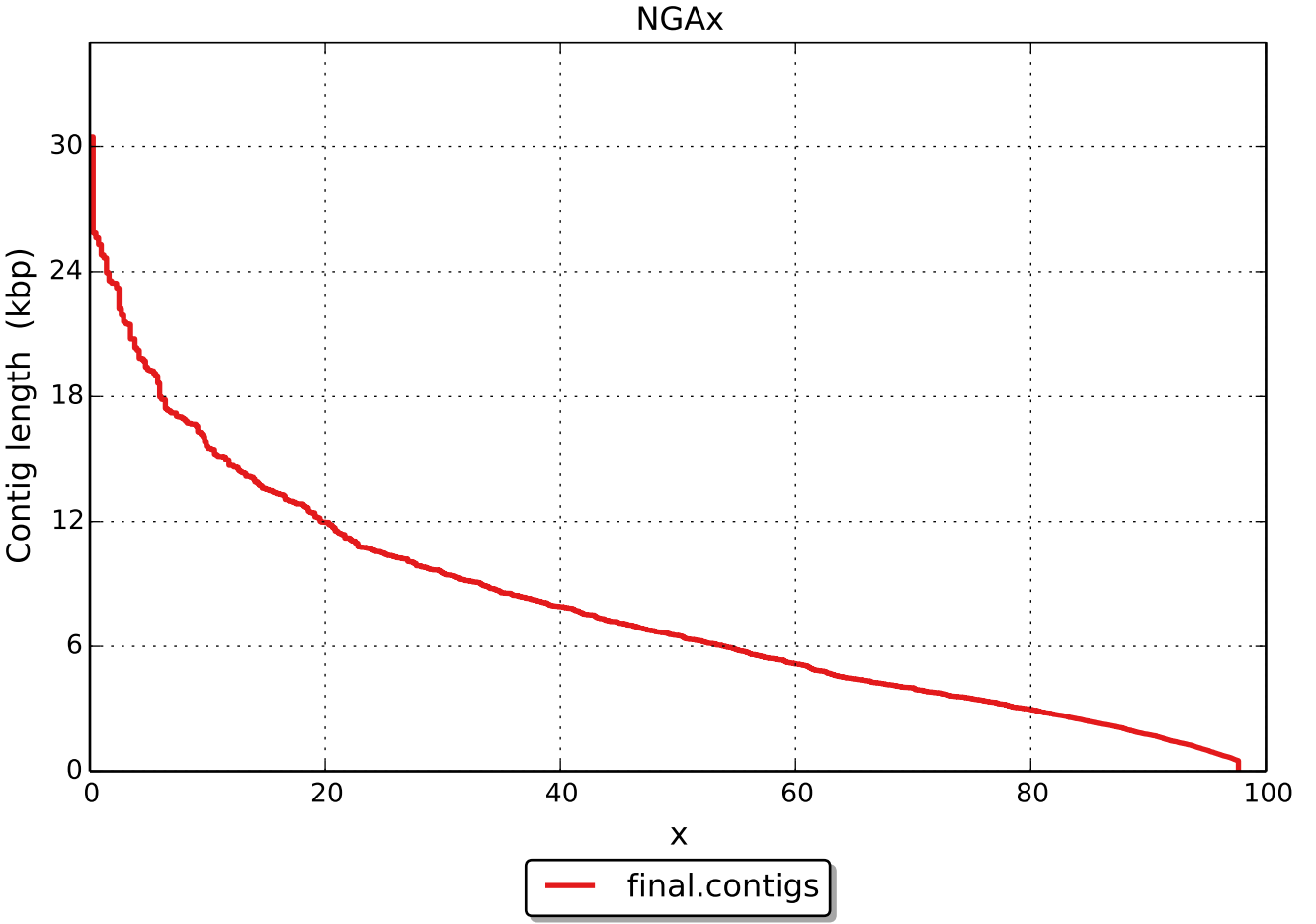

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

Misassemblies
4.0
3.5
3.0
2.5
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
500
1000
1500
2000
2500
3000
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs