Report

	final.contigs
# contigs (>= 0 bp)	2069
# contigs (>= 1000 bp)	1359
Total length (>= 0 bp)	10971998
Total length (>= 1000 bp)	10675367
# contigs	1554
Largest contig	47562
Total length	10813259
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.49
N50	11845
NG50	11545
N75	6579
NG75	6193
L50	276
LG50	288
L75	574
LG75	607
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	101981
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.880
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.34
# indels per 100 kbp	0.12
Largest alignment	47562
NA50	11793
NGA50	11487
NA75	6578
NGA75	6174
LA50	277
LGA50	289
LA75	577
LGA75	610

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

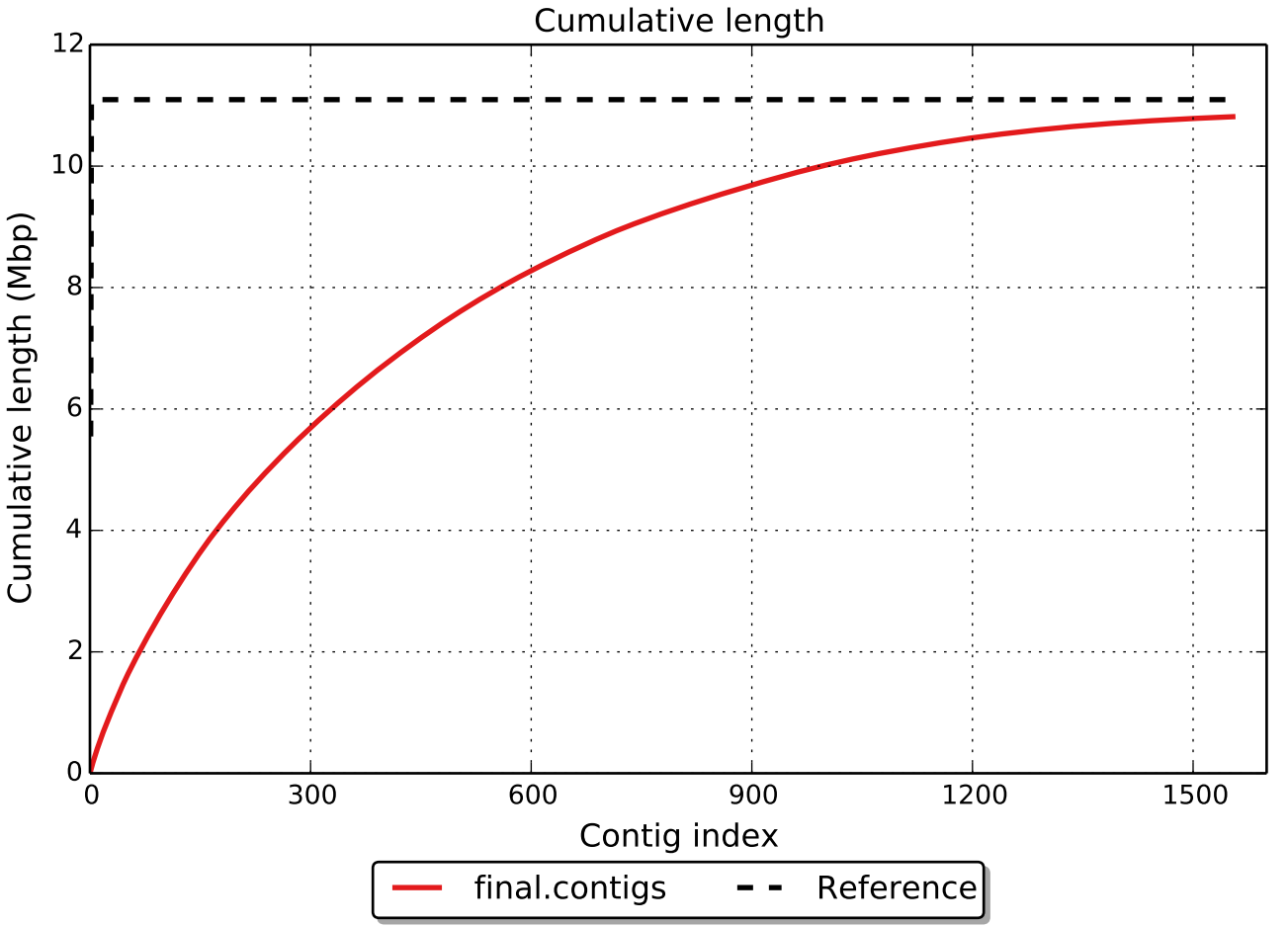
	final.contigs
# misassemblies	4
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	101981
# local misassemblies	3
# mismatches	3015
# indels	13
# short indels	12
# long indels	1
Indels length	18

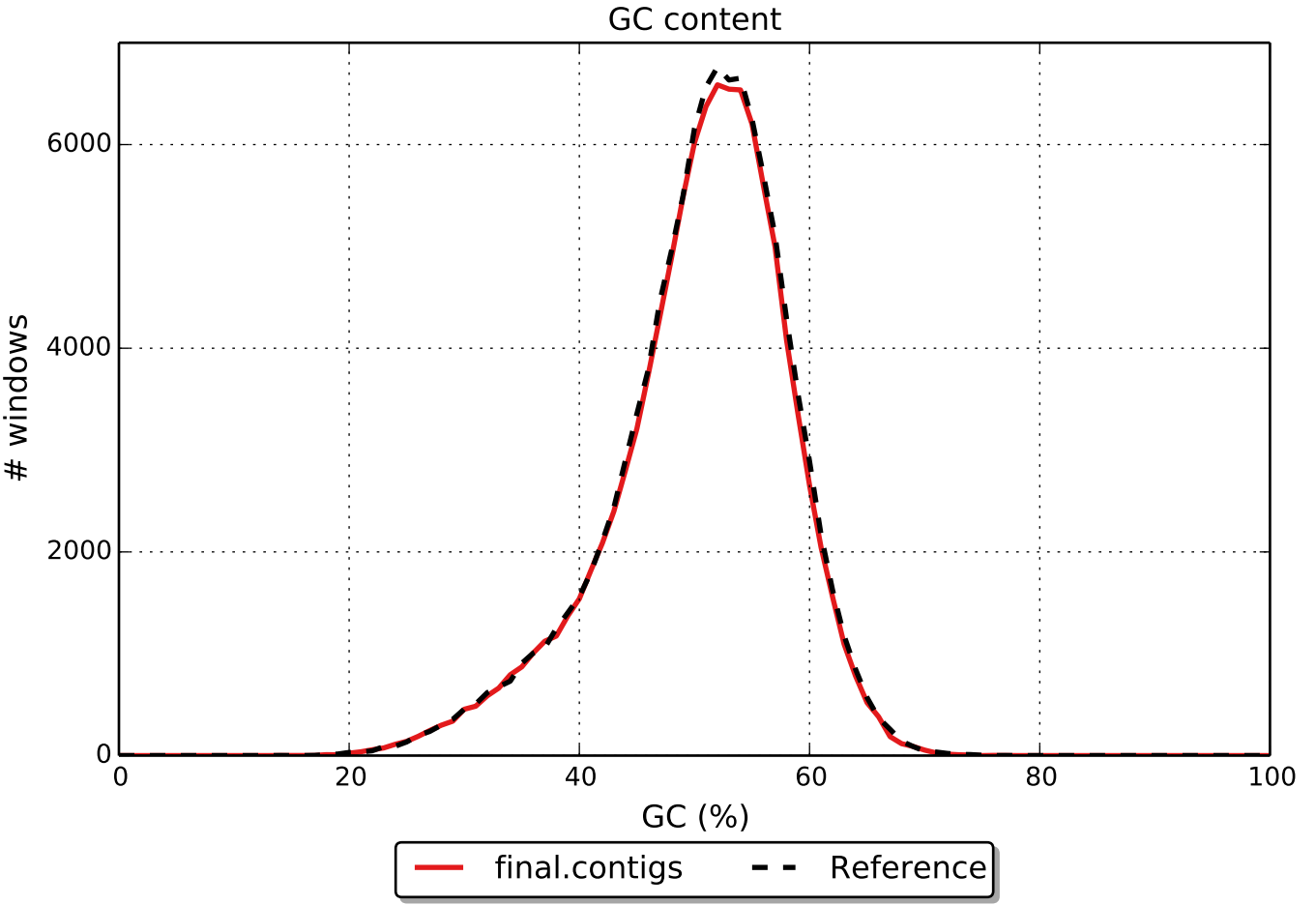
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

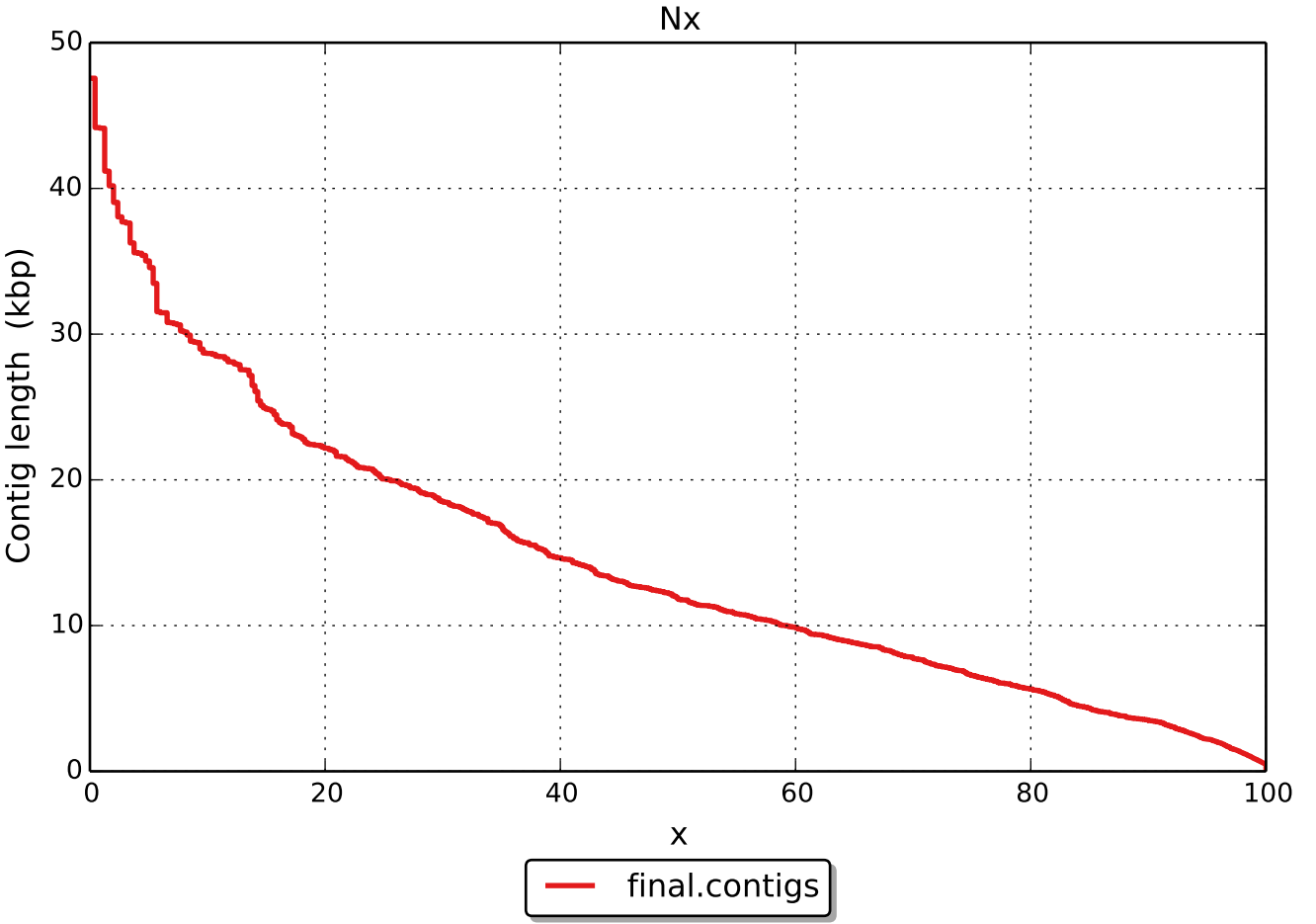
Unaligned report

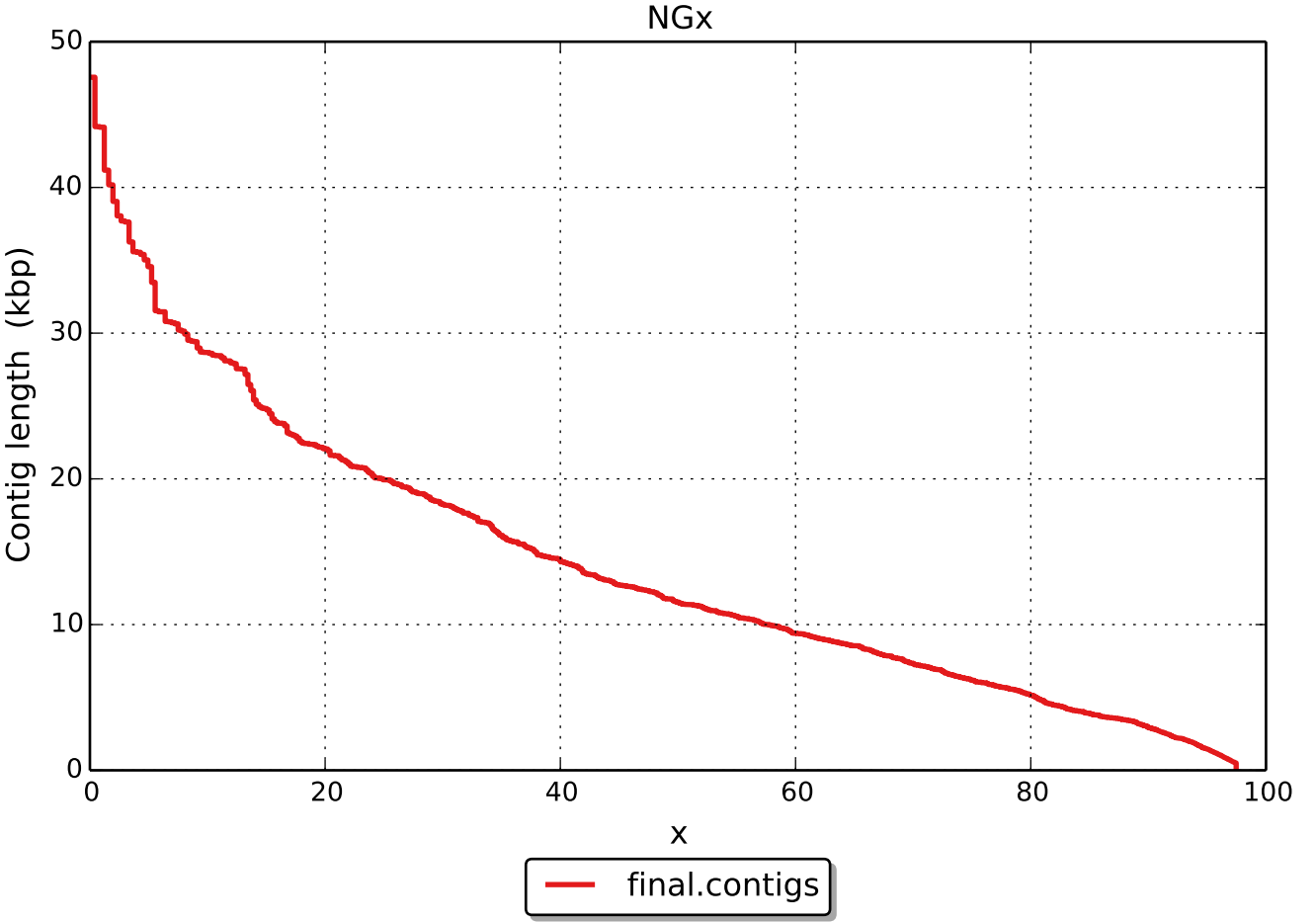
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

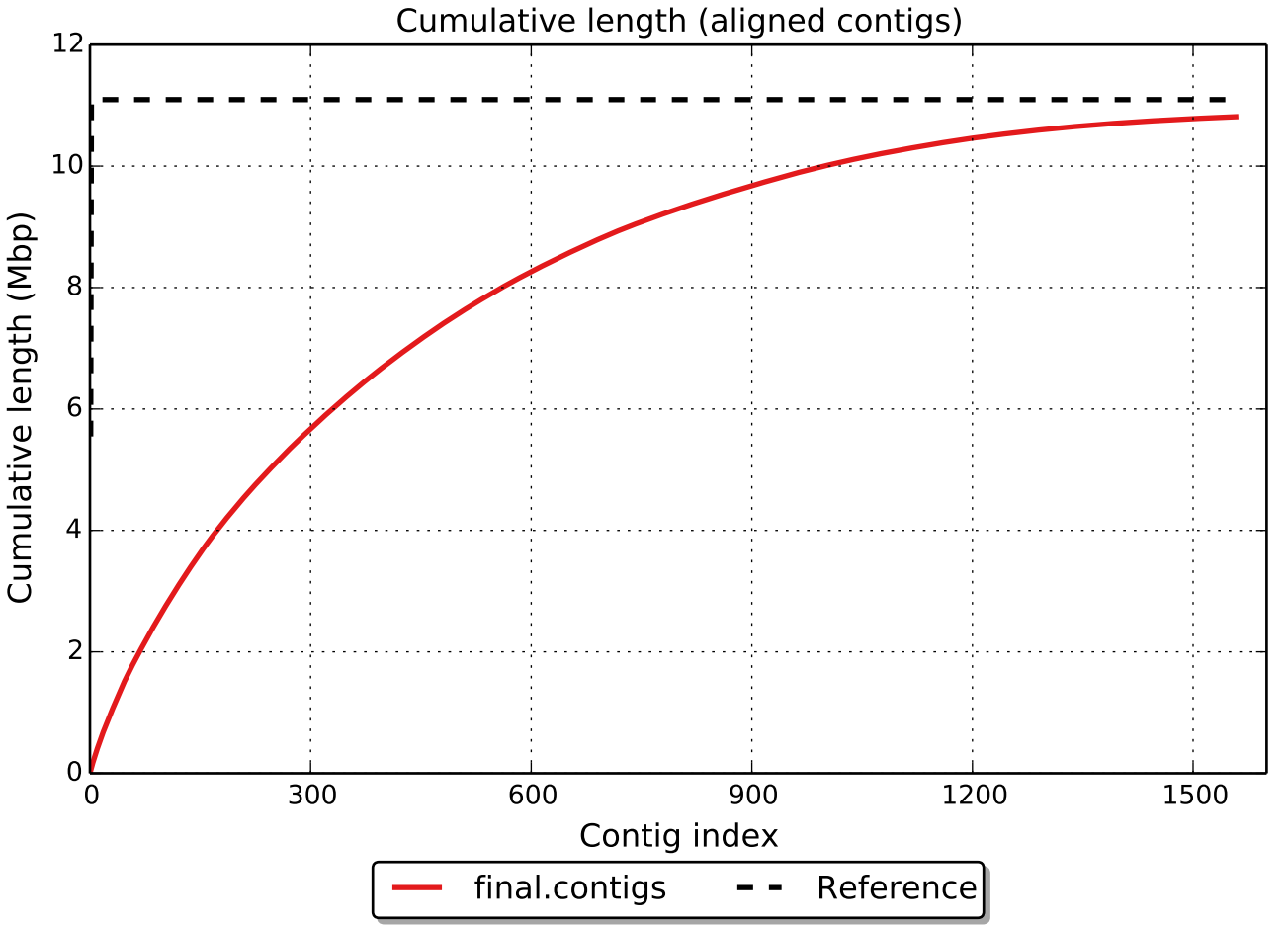

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
300
600
900
1200
1500
Contig index
final.contigs
Reference

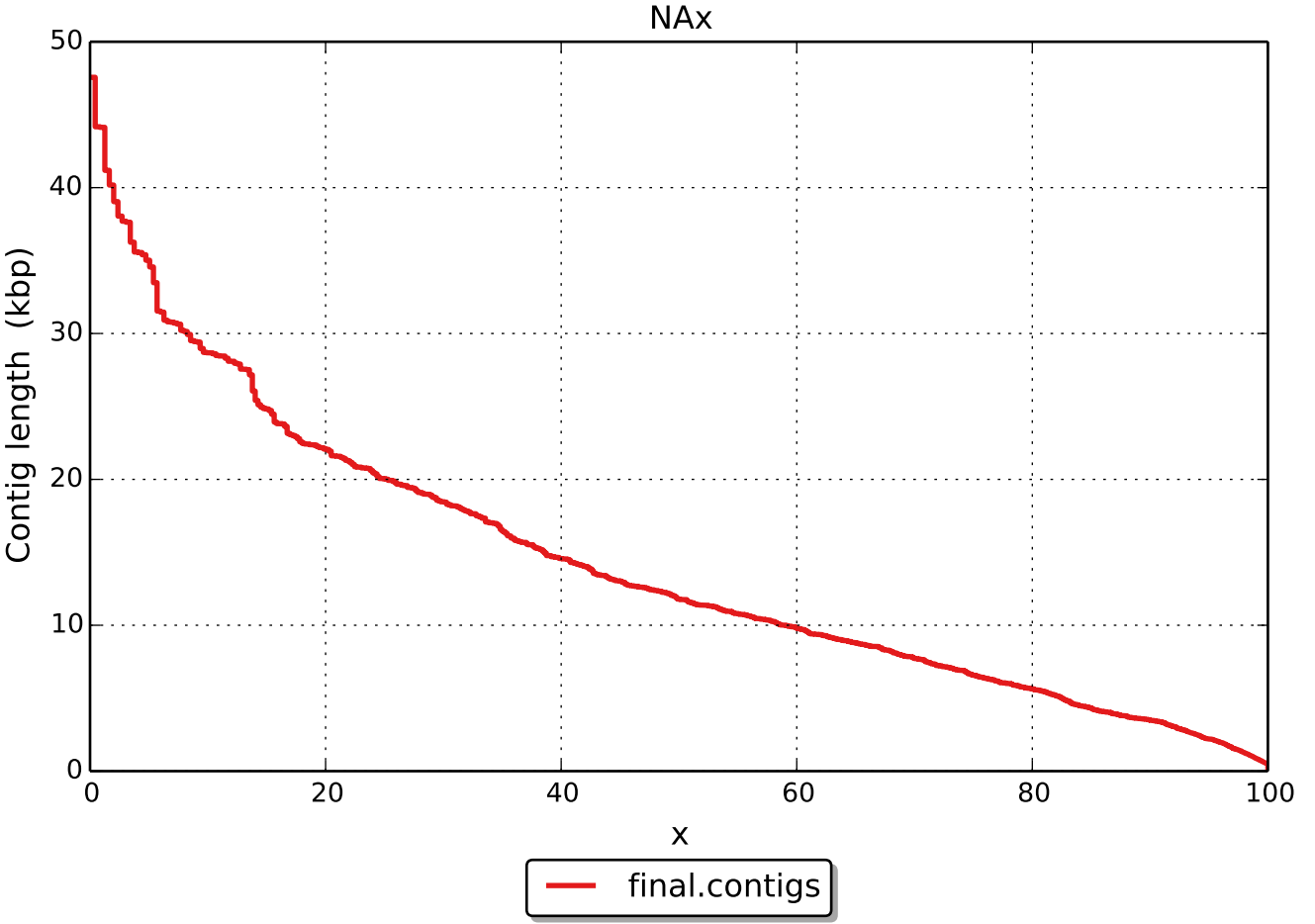

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

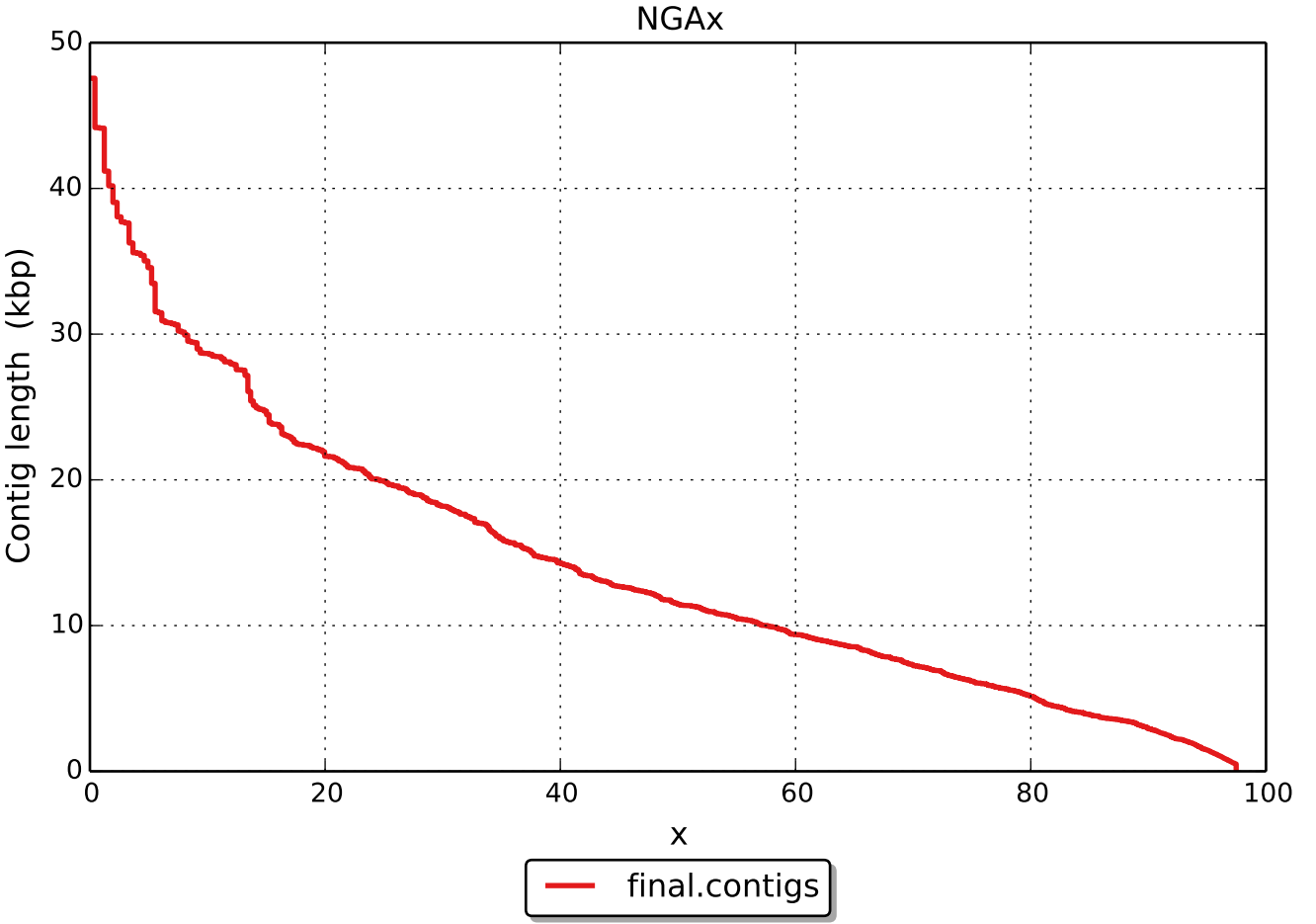

Nx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs

Misassemblies
5
4
3
2
1
0
final.contigs
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
300
600
900
1200
1500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs