Report

	final.contigs
# contigs (>= 0 bp)	4149
# contigs (>= 1000 bp)	2673
Total length (>= 0 bp)	11099271
Total length (>= 1000 bp)	10347323
# contigs	3340
Largest contig	23946
Total length	10839537
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	4983
NG50	4866
N75	2792
NG75	2590
L50	689
LG50	714
L75	1411
LG75	1483
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2818
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.373
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.44
# indels per 100 kbp	0.24
Largest alignment	23946
NA50	4983
NGA50	4866
NA75	2790
NGA75	2590
LA50	689
LGA50	714
LA75	1411
LGA75	1483

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

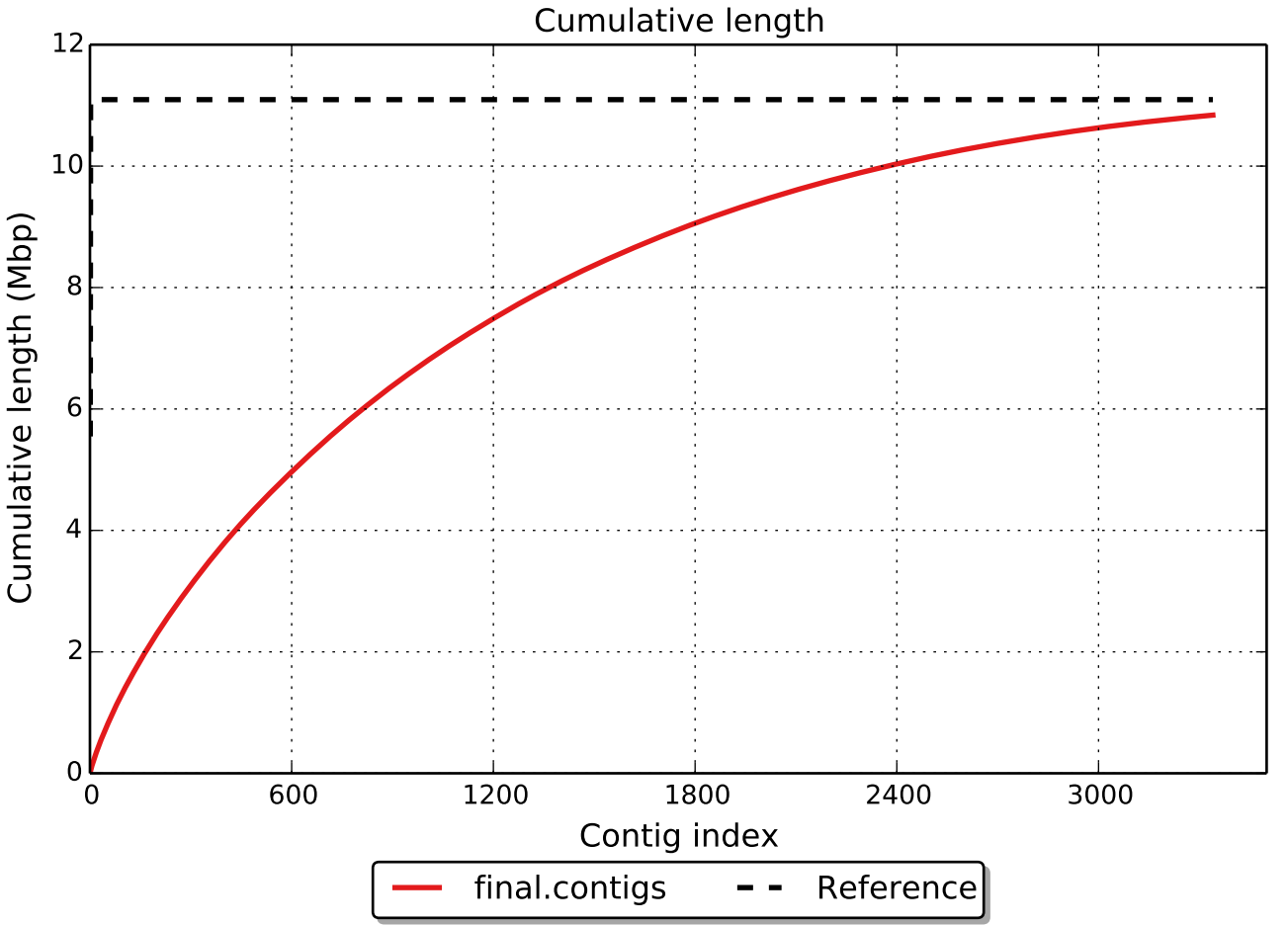
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2818
# local misassemblies	0
# mismatches	4003
# indels	26
# short indels	25
# long indels	1
Indels length	31

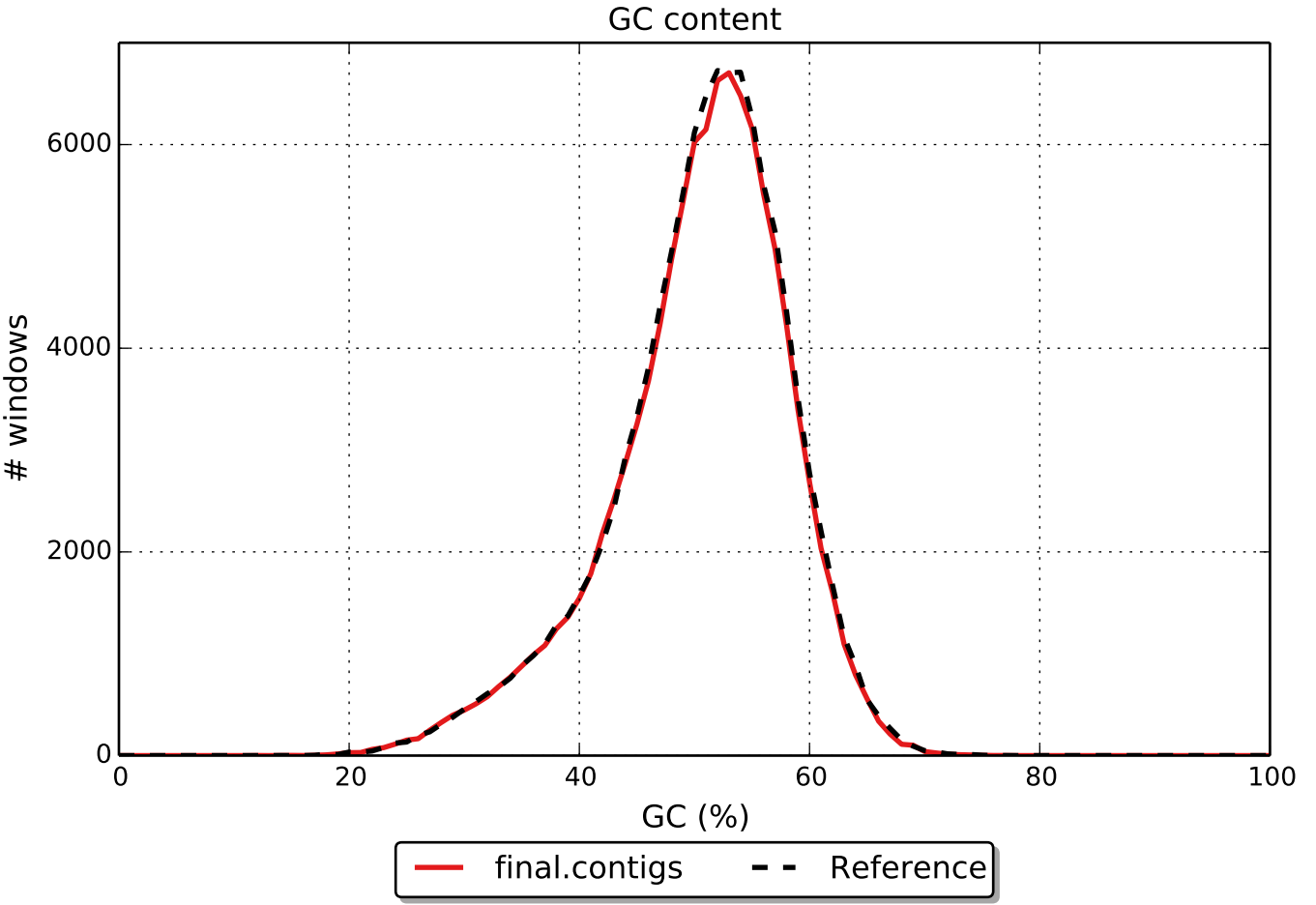
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

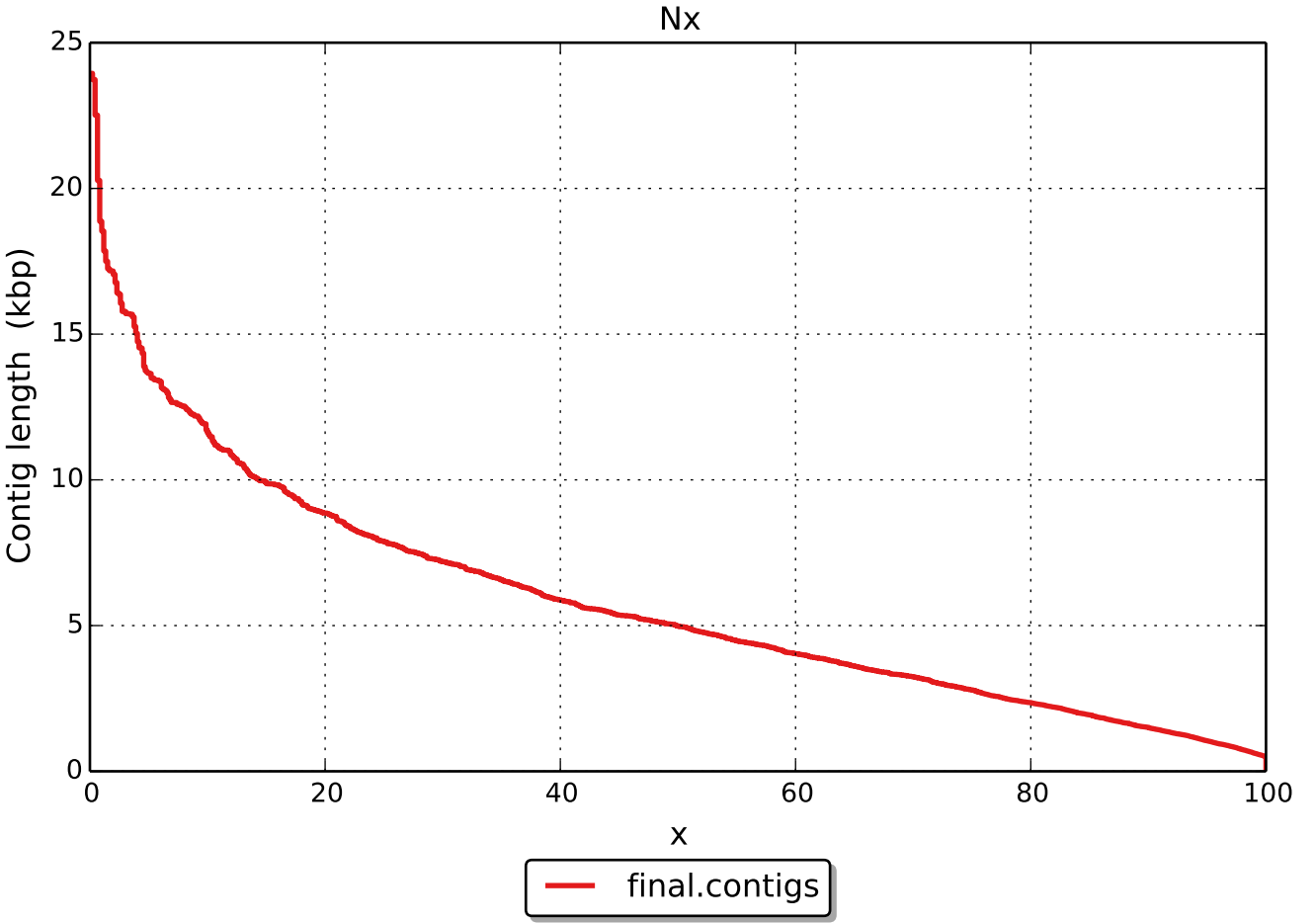
Unaligned report

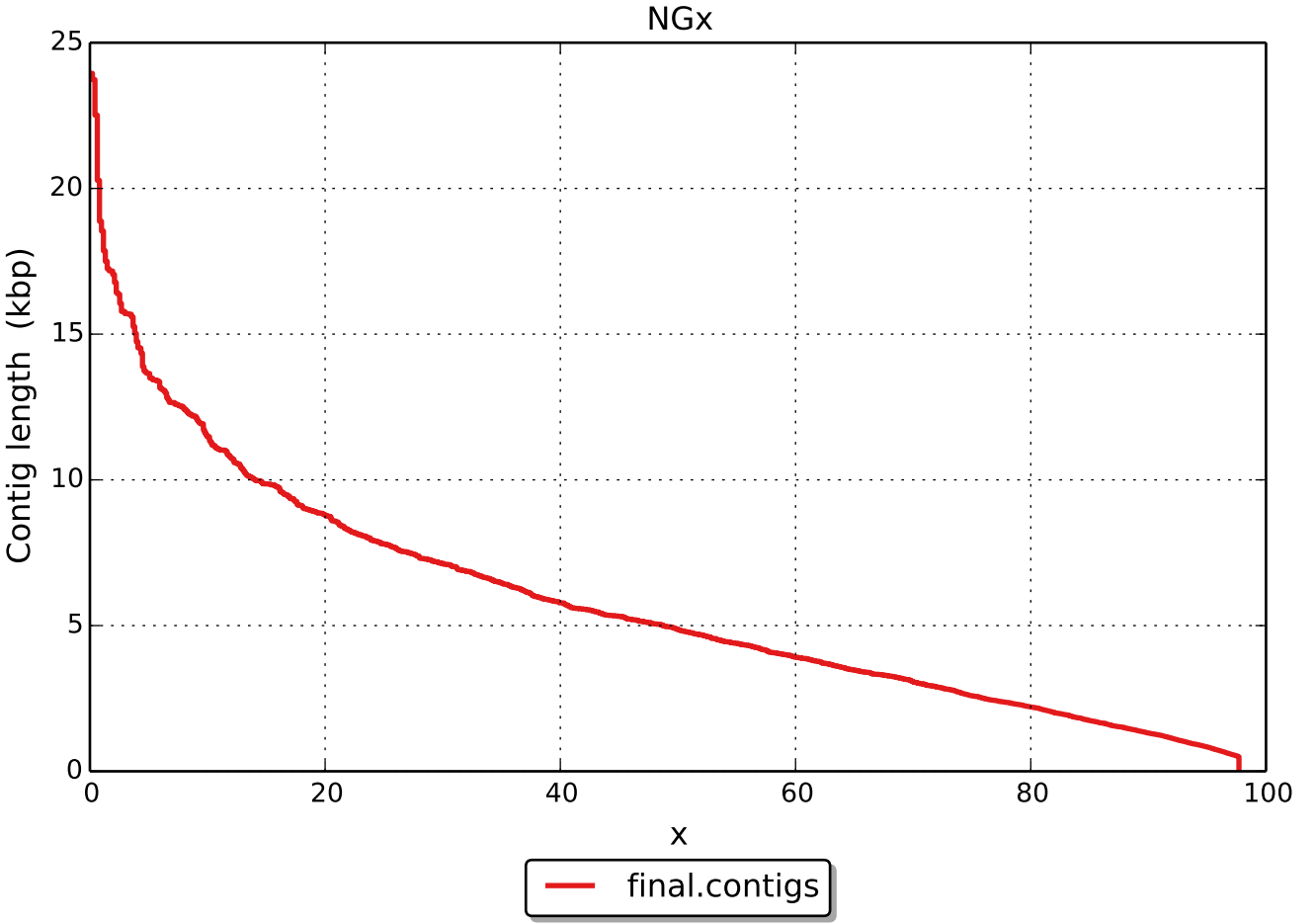
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

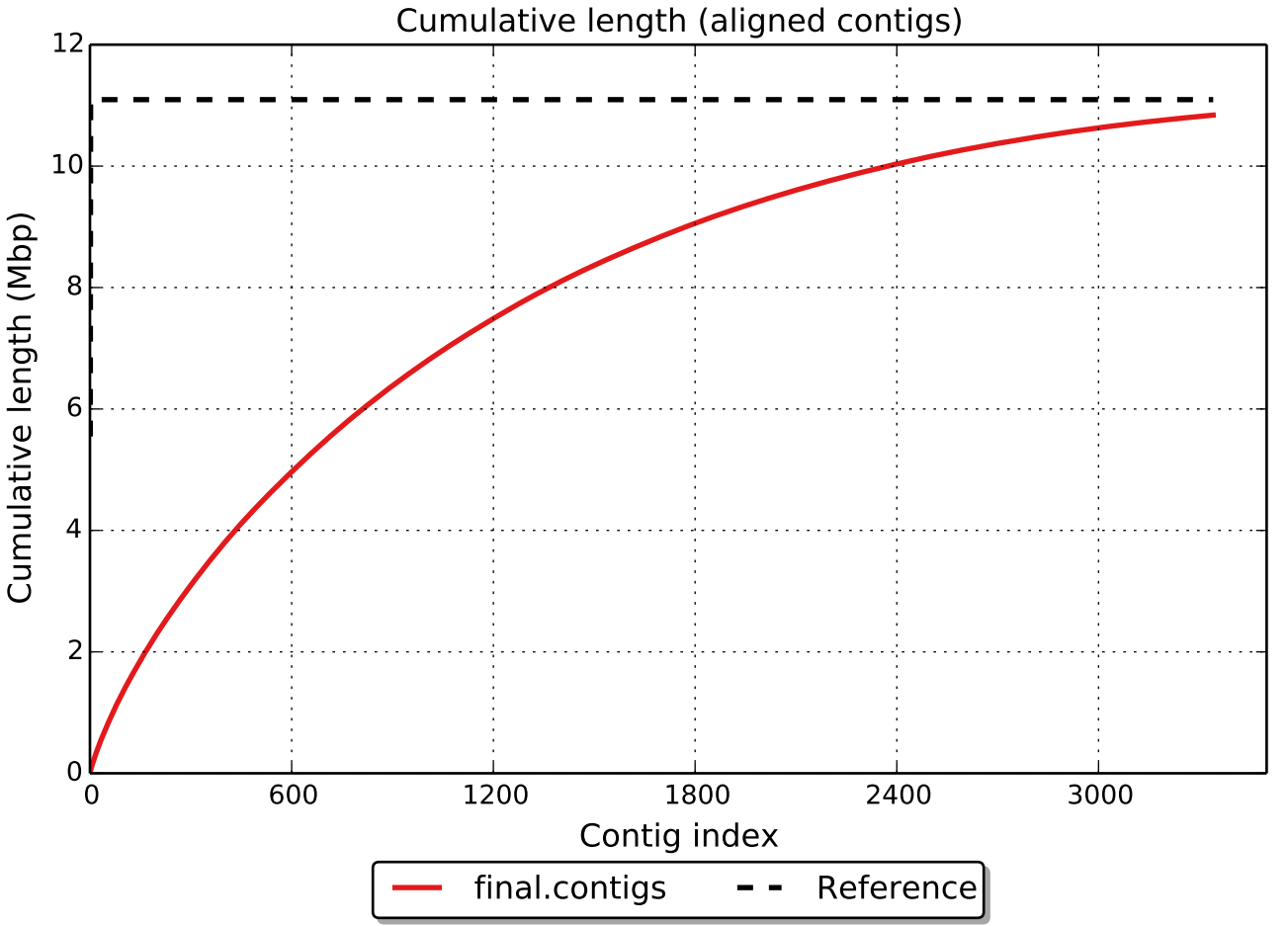

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference

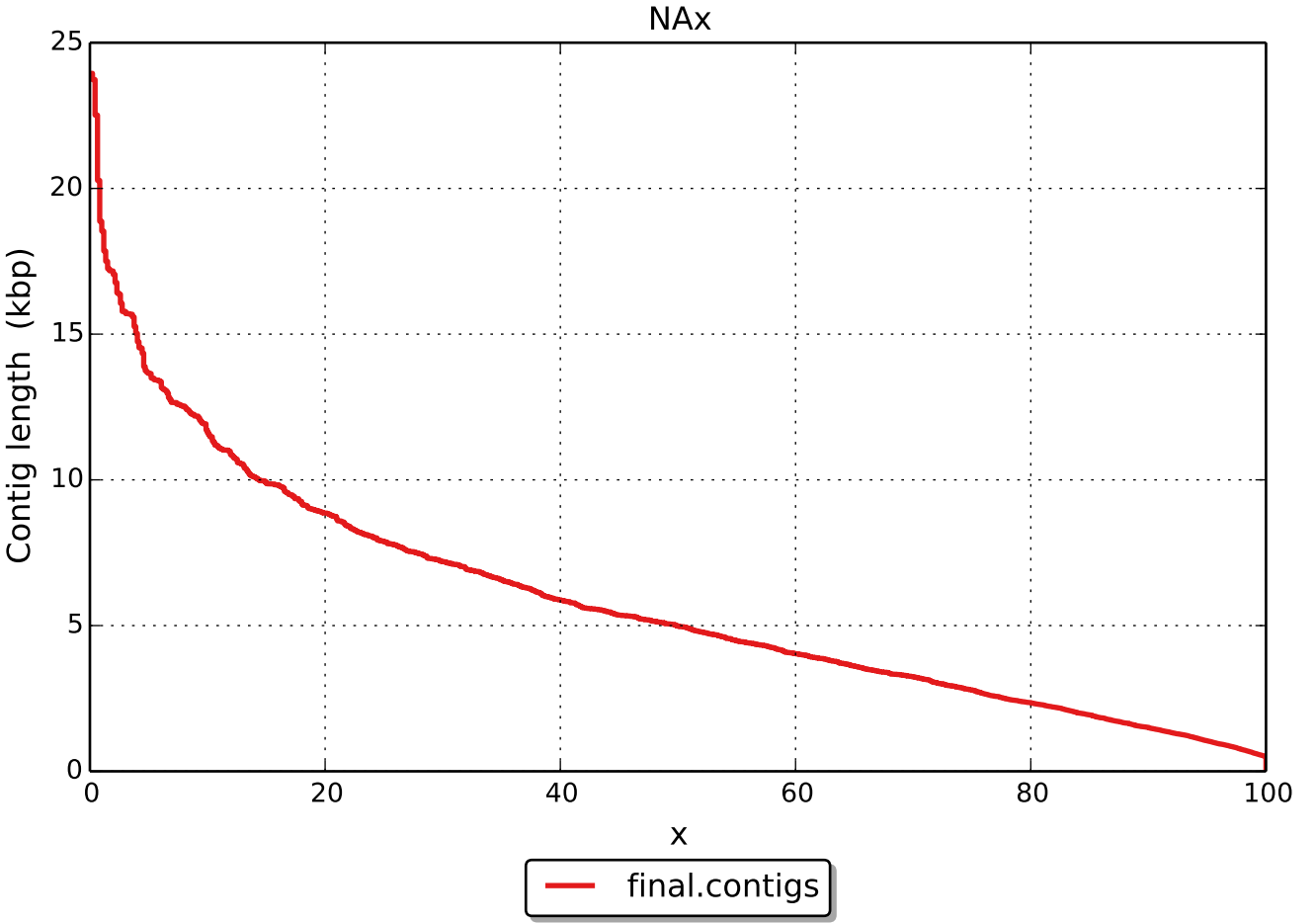

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

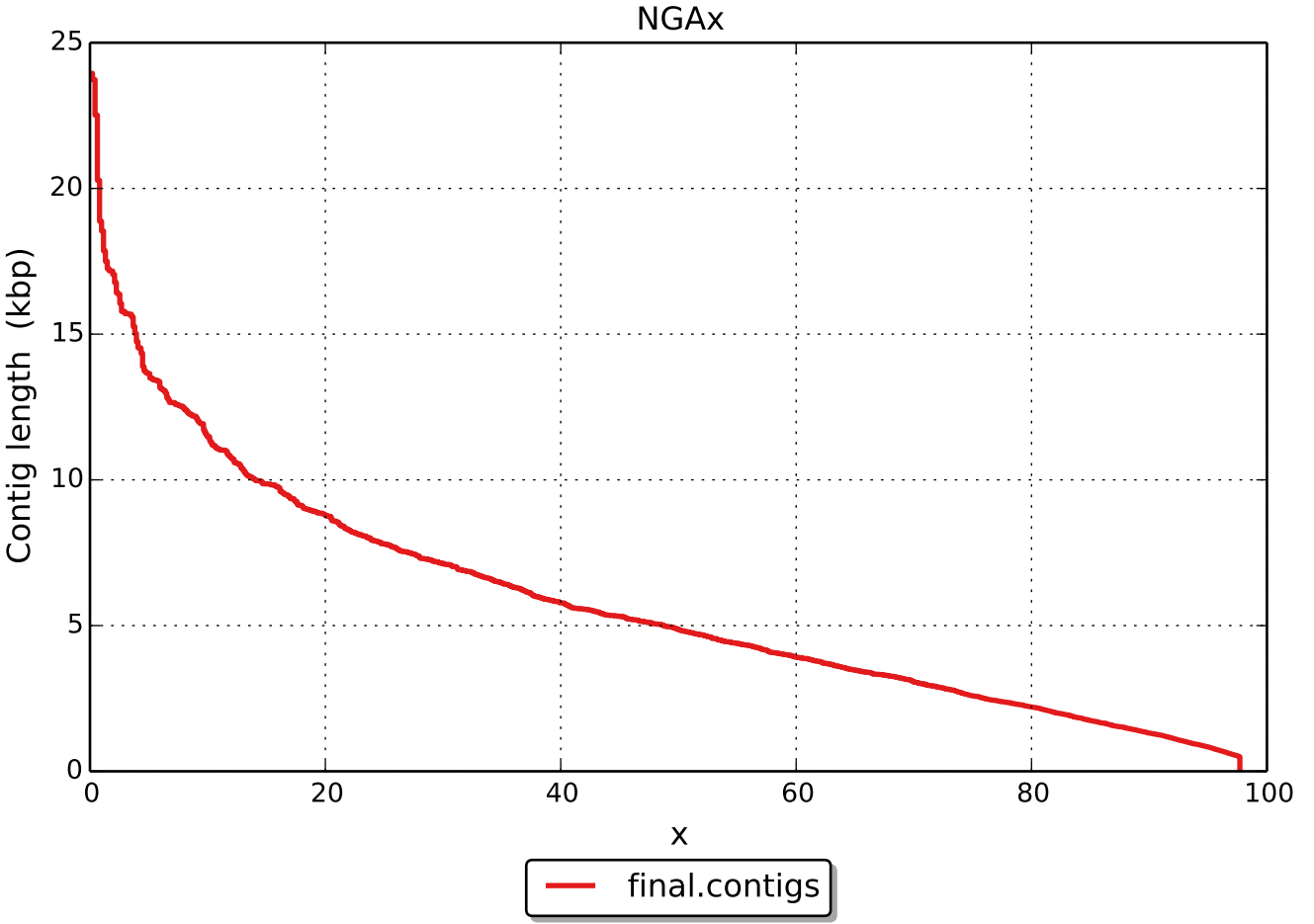

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
25
20
15
10
5
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 (Mbp)
0
2
4
6
8
10
12
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs