Report

	final.contigs
# contigs (>= 0 bp)	6687
# contigs (>= 1000 bp)	3791
Total length (>= 0 bp)	11153269
Total length (>= 1000 bp)	9572714
# contigs	5317
Largest contig	12275
Total length	10689776
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	2681
NG50	2616
N75	1591
NG75	1509
L50	1270
LG50	1321
L75	2563
LG75	2693
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.413
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	25.38
# indels per 100 kbp	0.06
Largest alignment	12275
NA50	2681
NGA50	2615
NA75	1591
NGA75	1509
LA50	1271
LGA50	1322
LA75	2564
LGA75	2694

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

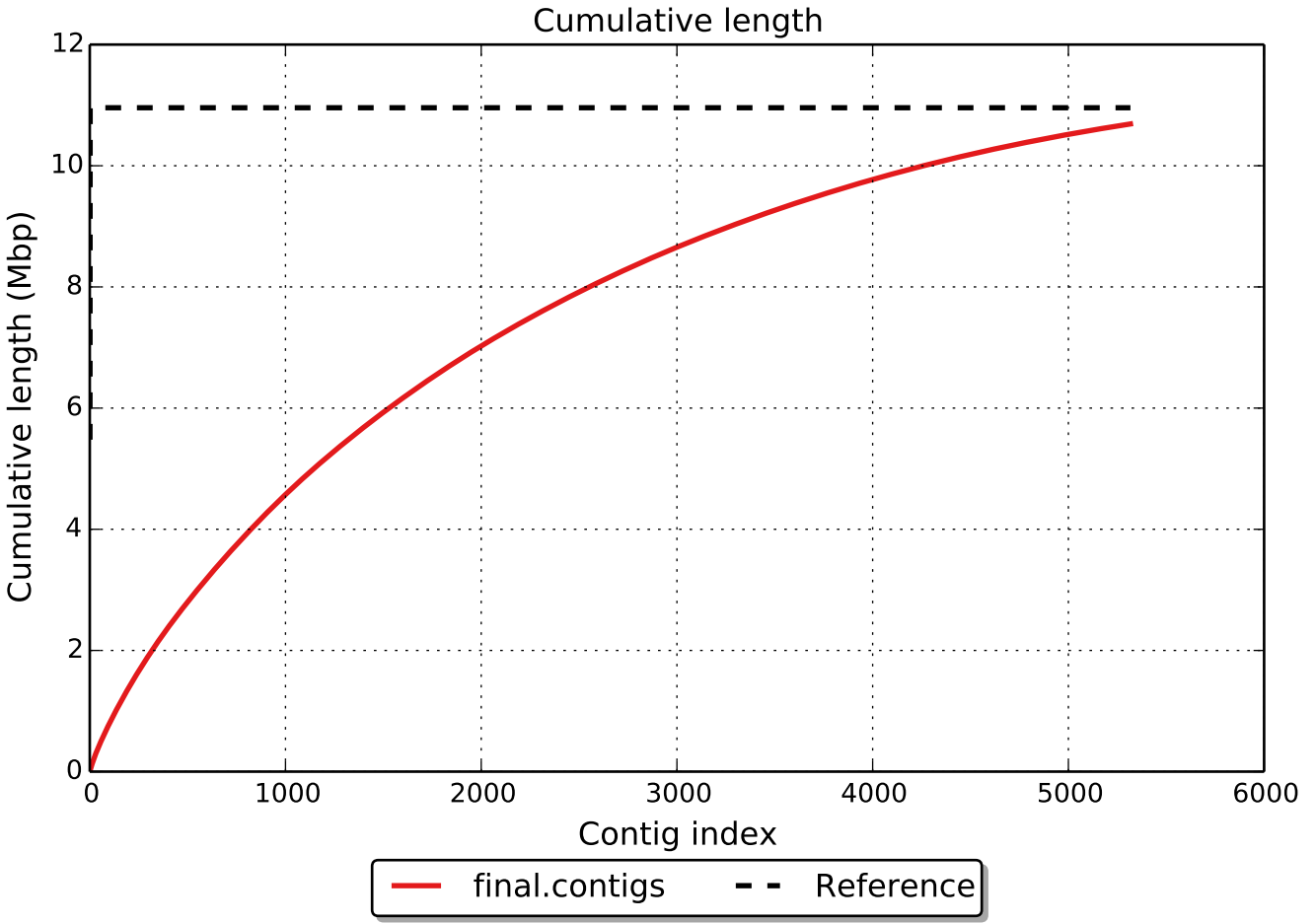
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# mismatches	2626
# indels	6
# short indels	3
# long indels	3
Indels length	42

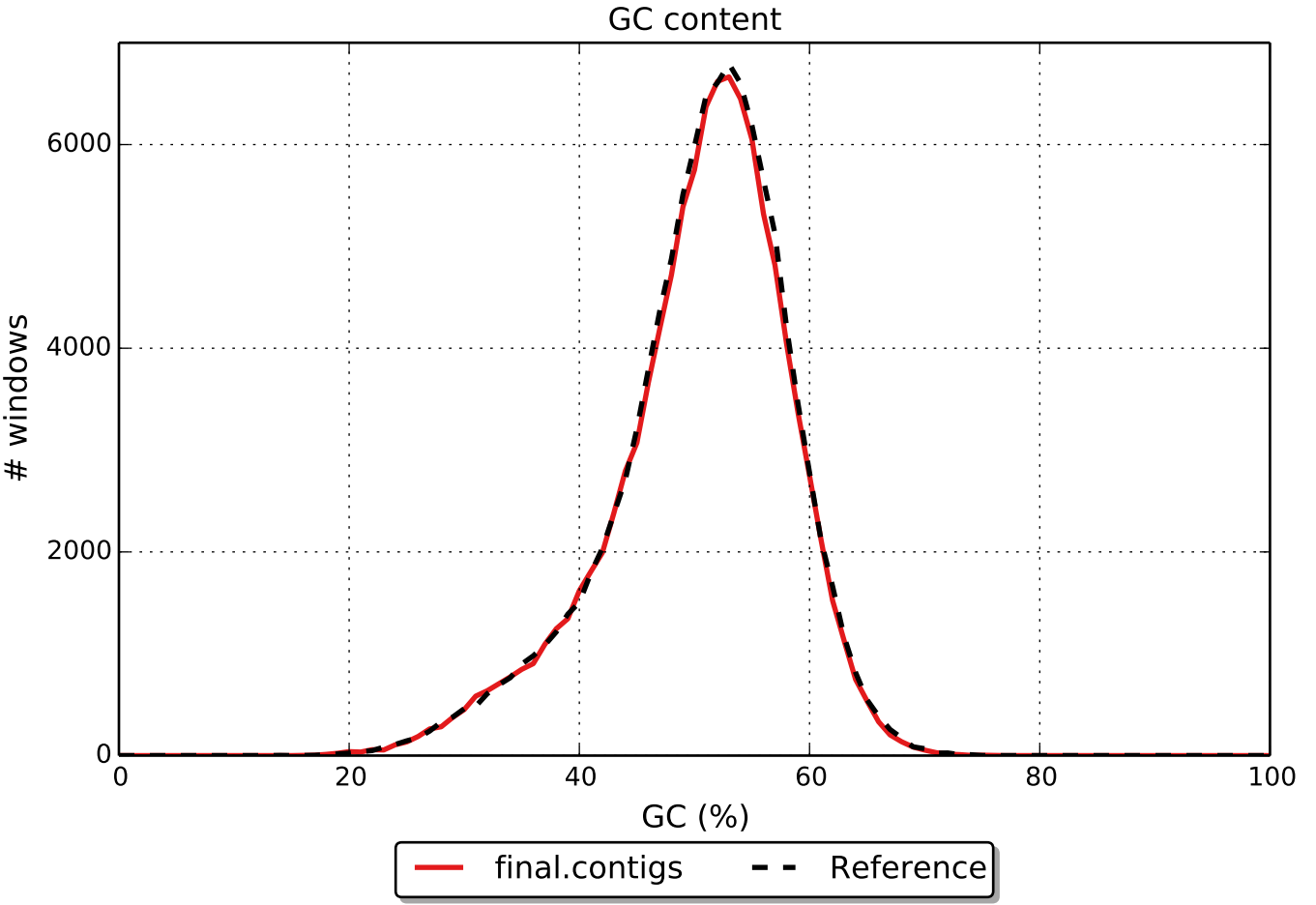
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

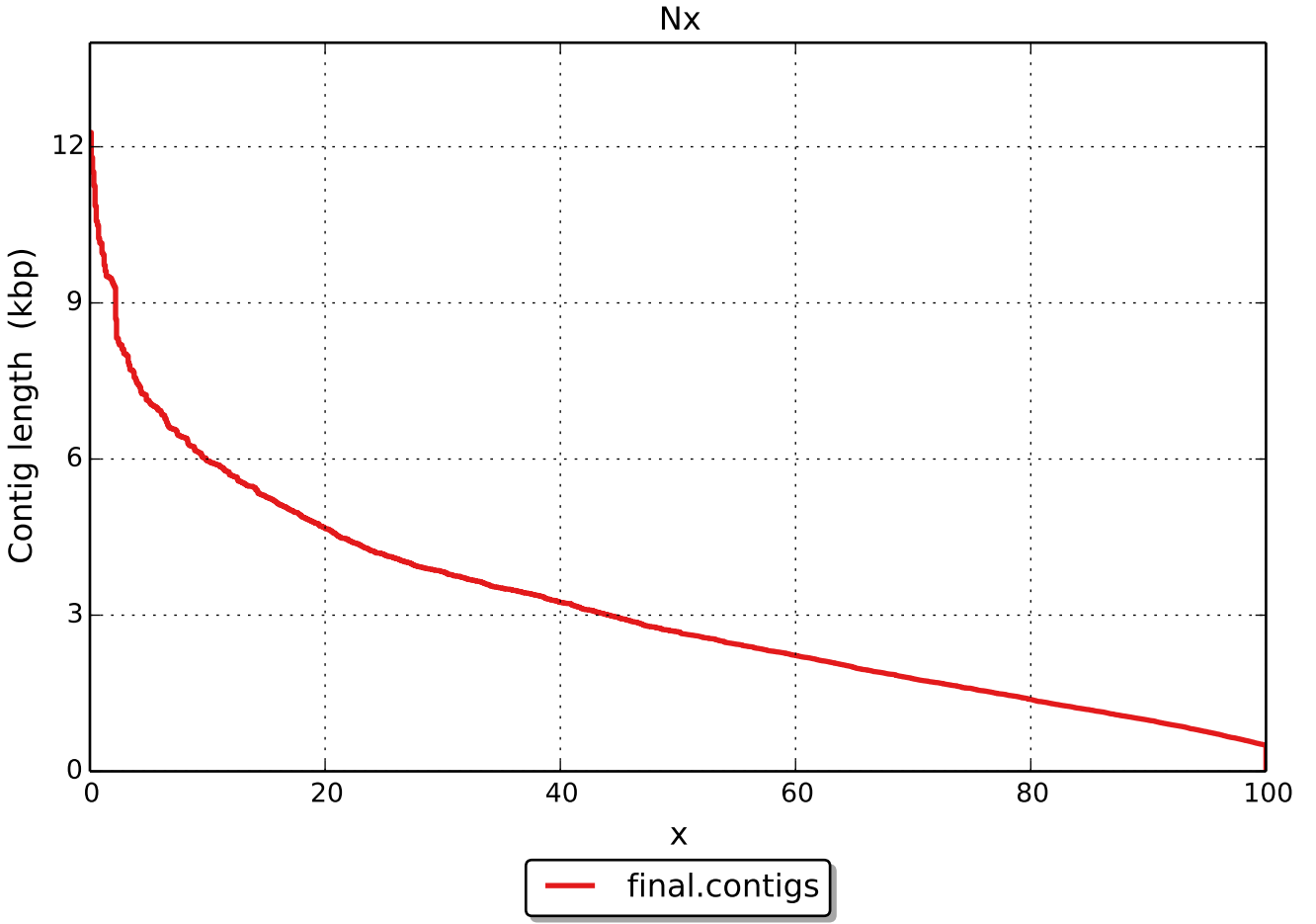
Unaligned report

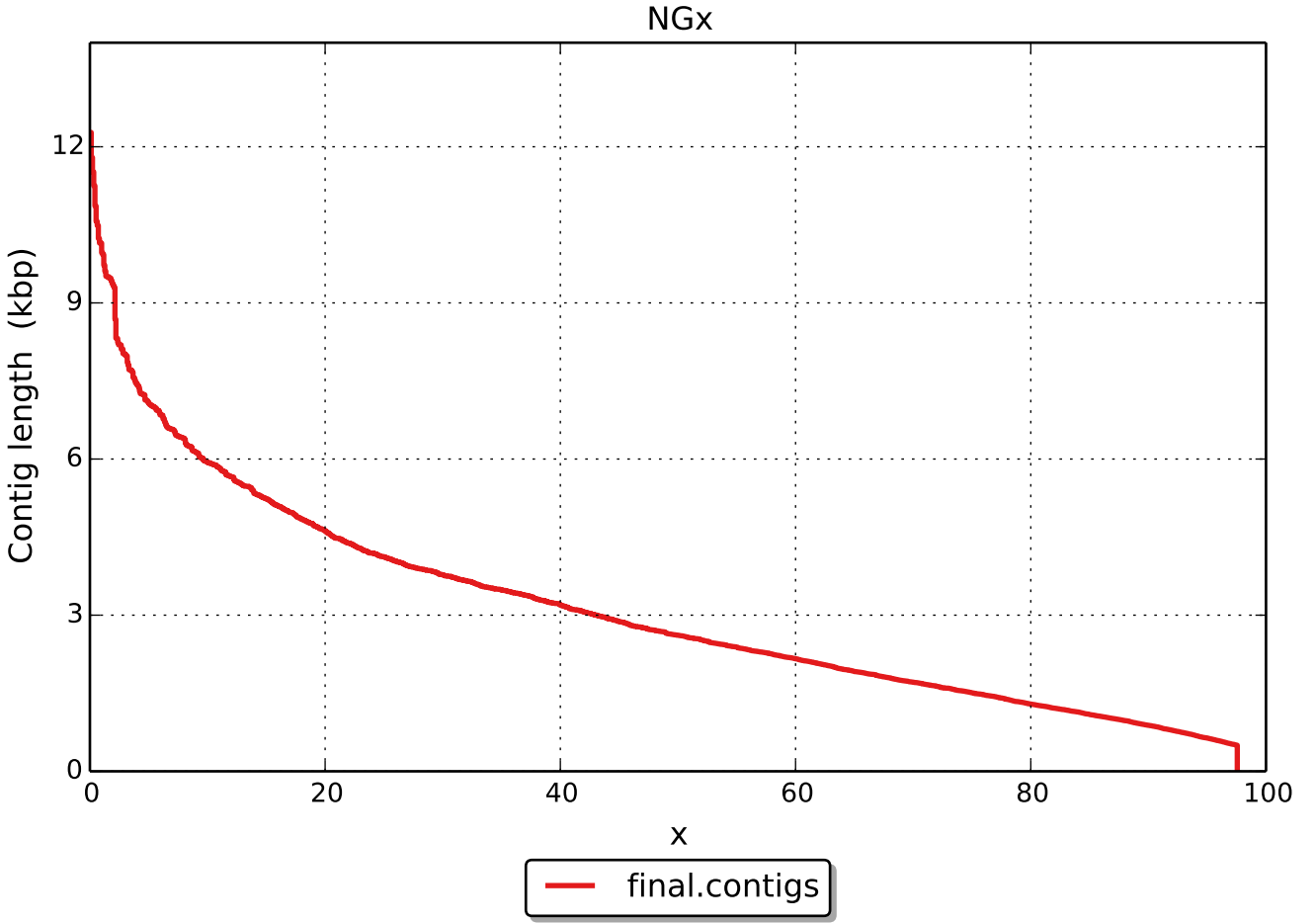
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

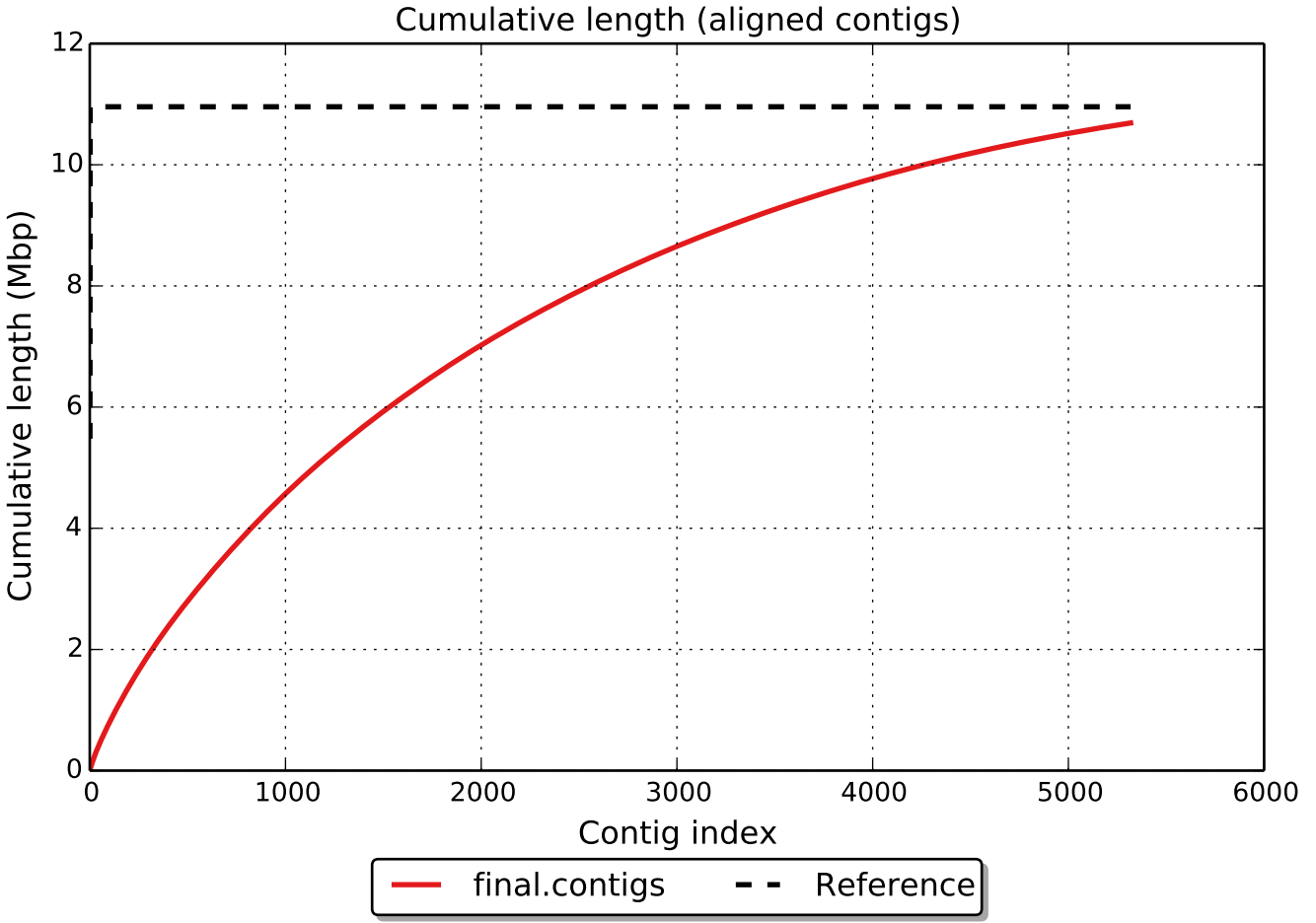

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
1000
2000
3000
4000
5000
6000
final.contigs
Reference

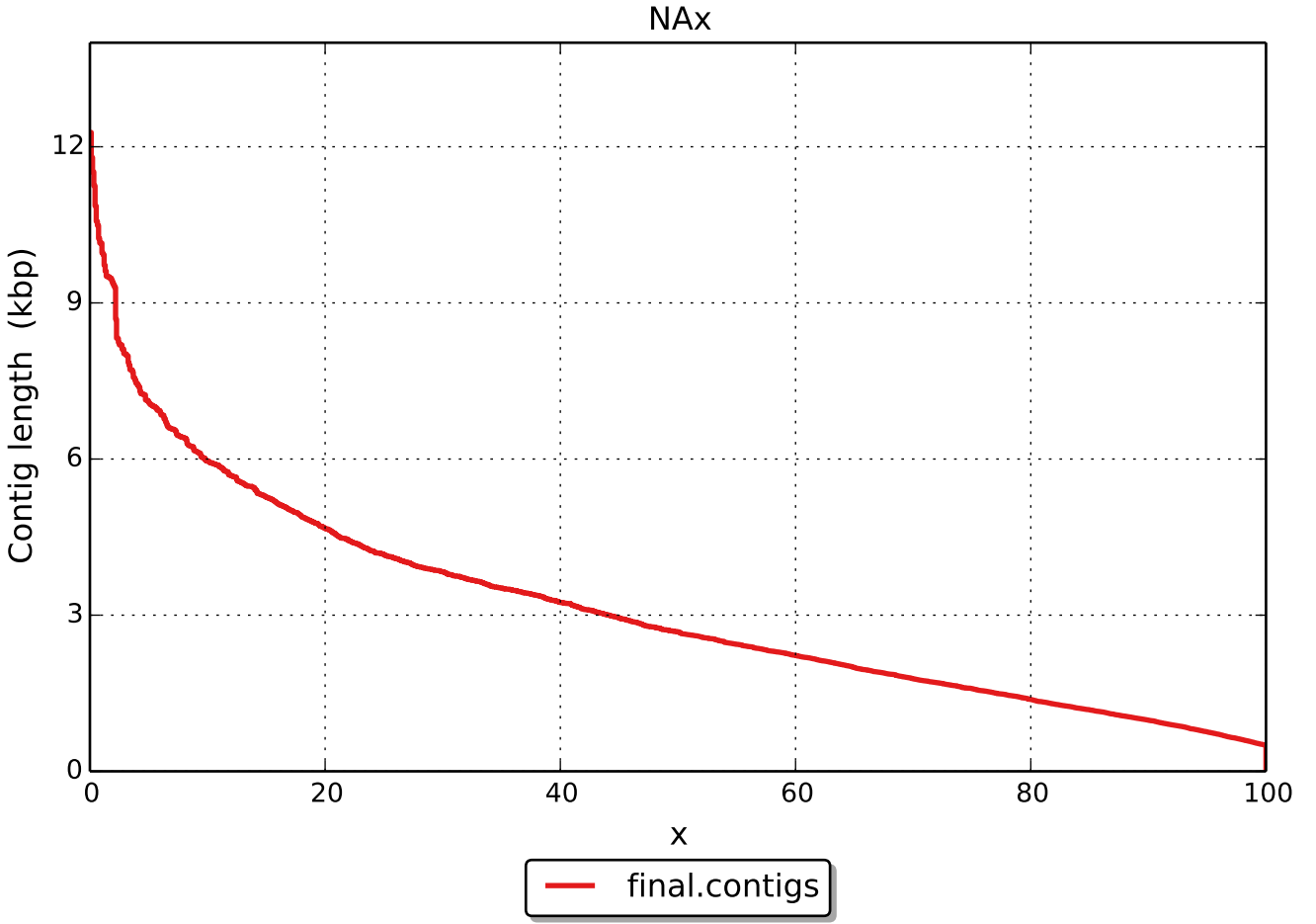

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

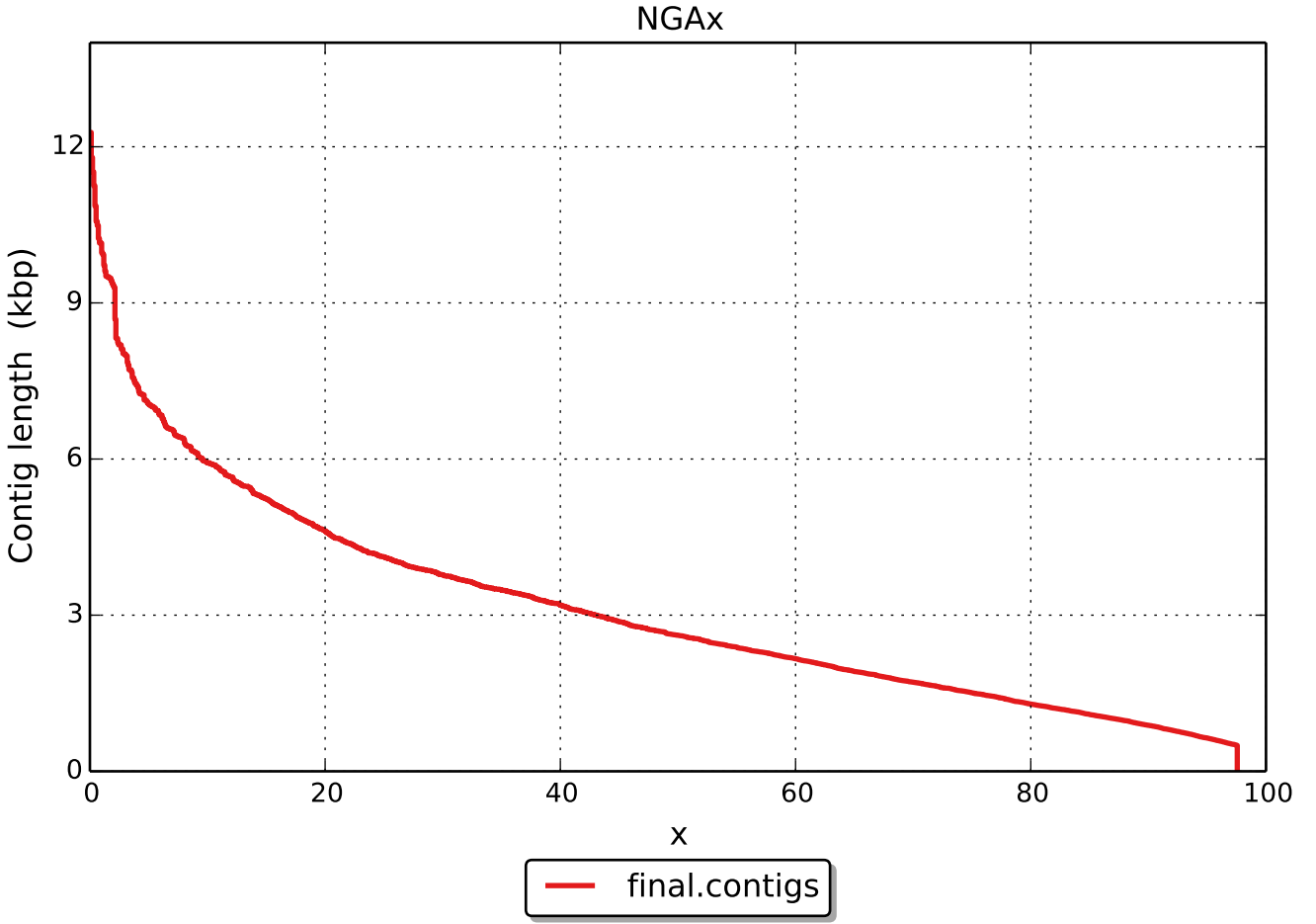

Nx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
12
9
6
3
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)
Contig index
0
2
4
6
8
10
12
0
1000
2000
3000
4000
5000
6000
final.contigs
Reference


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


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