Report

	final.contigs
# contigs (>= 0 bp)	8511
# contigs (>= 1000 bp)	4094
Total length (>= 0 bp)	11195088
Total length (>= 1000 bp)	8731046
# contigs	6541
Largest contig	10098
Total length	10518594
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	2007
NG50	1939
N75	1241
NG75	1143
L50	1681
LG50	1792
L75	3338
LG75	3615
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.038
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.41
# indels per 100 kbp	0.12
Largest alignment	10098
NA50	2007
NGA50	1939
NA75	1241
NGA75	1142
LA50	1681
LGA50	1792
LA75	3338
LGA75	3615

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

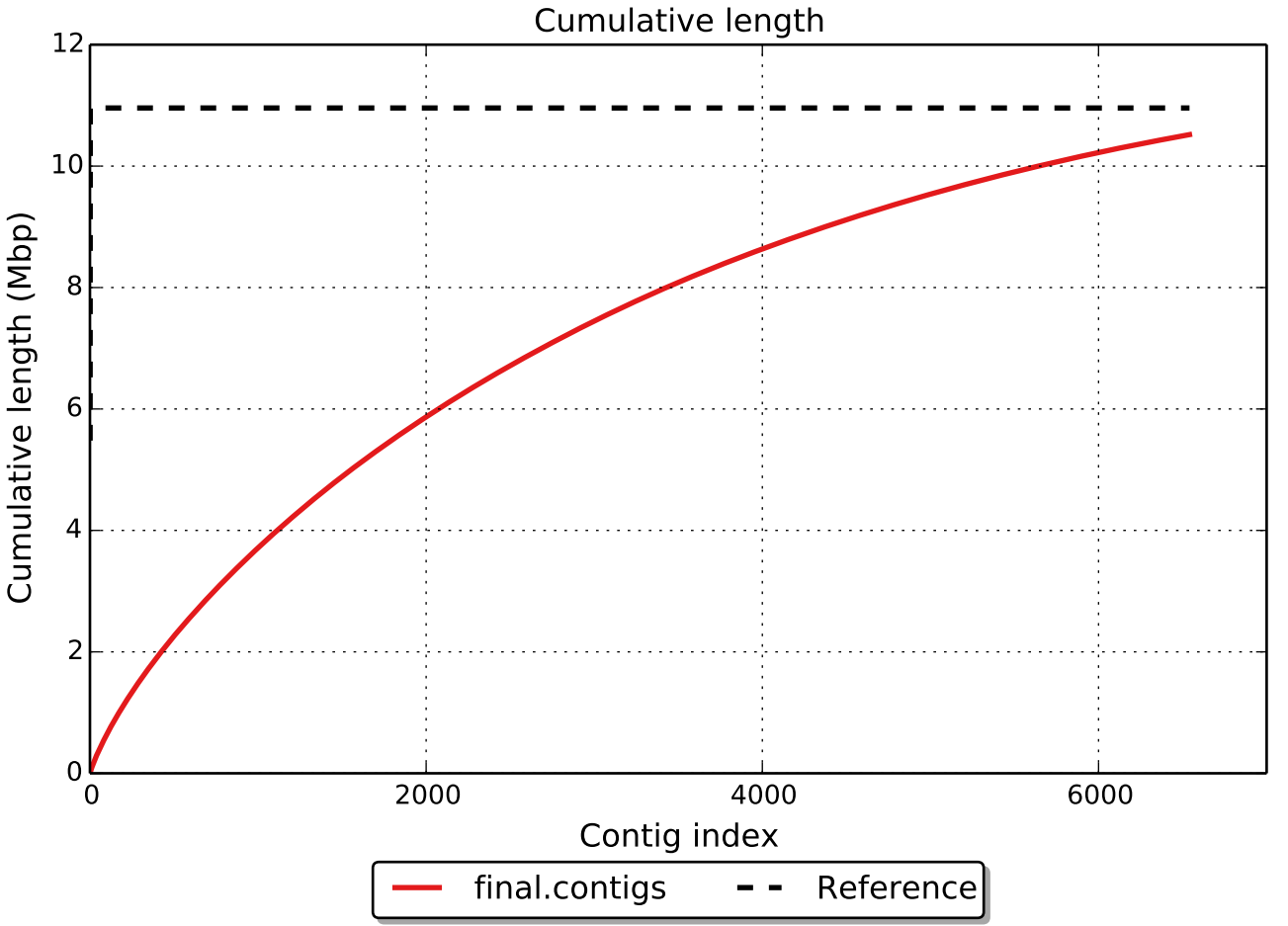
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	2
# mismatches	4731
# indels	12
# short indels	12
# long indels	0
Indels length	21

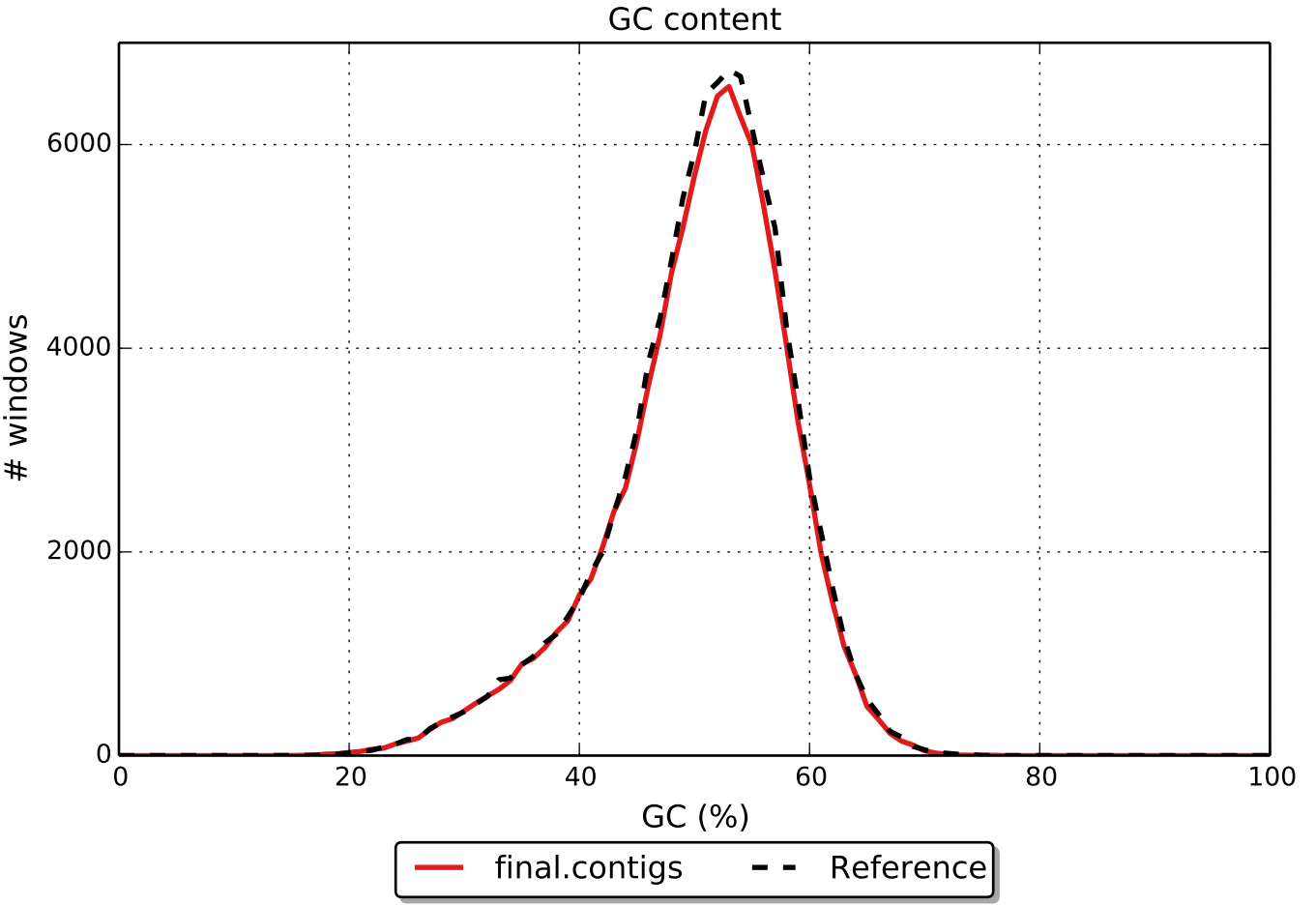
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

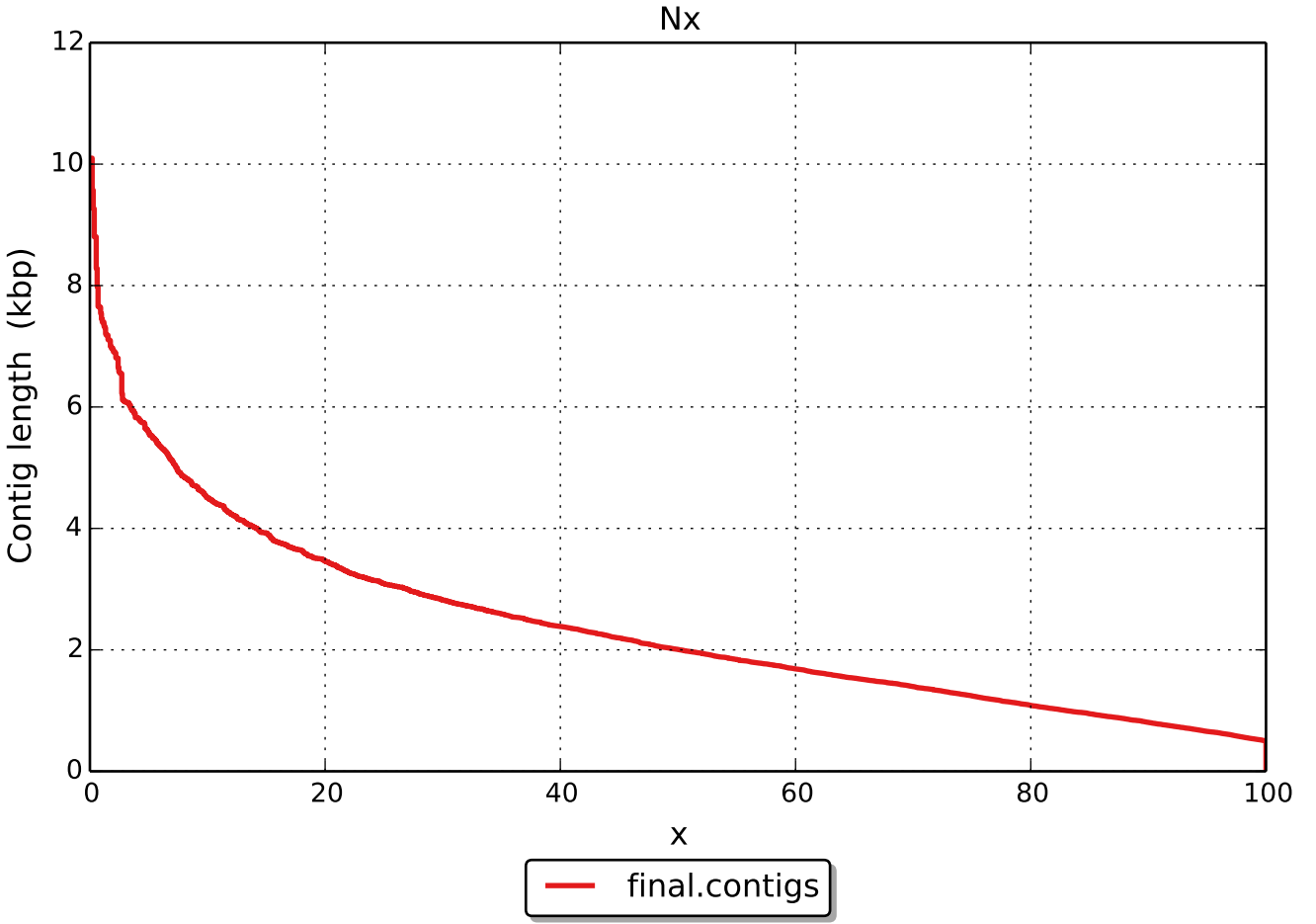
Unaligned report

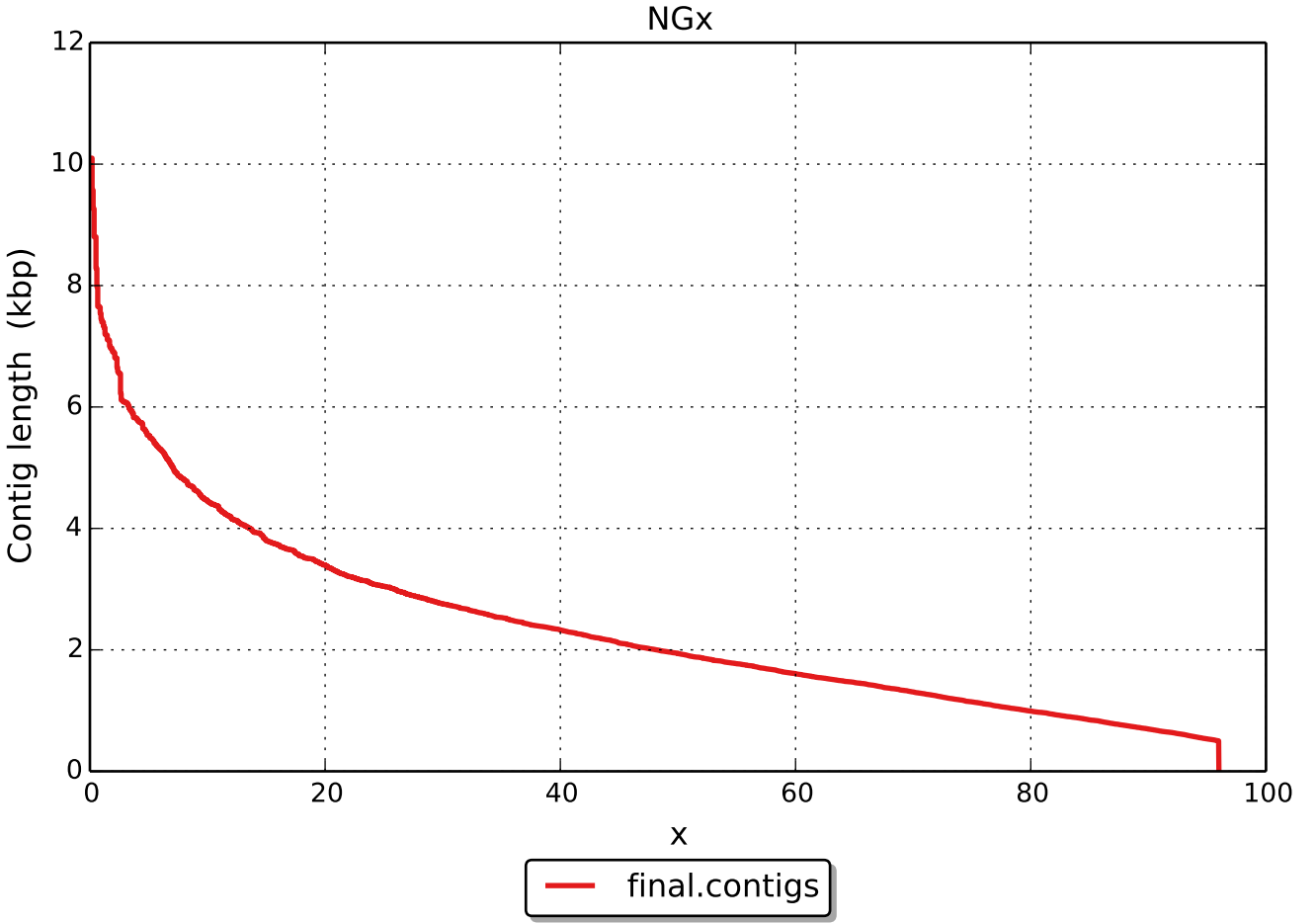
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

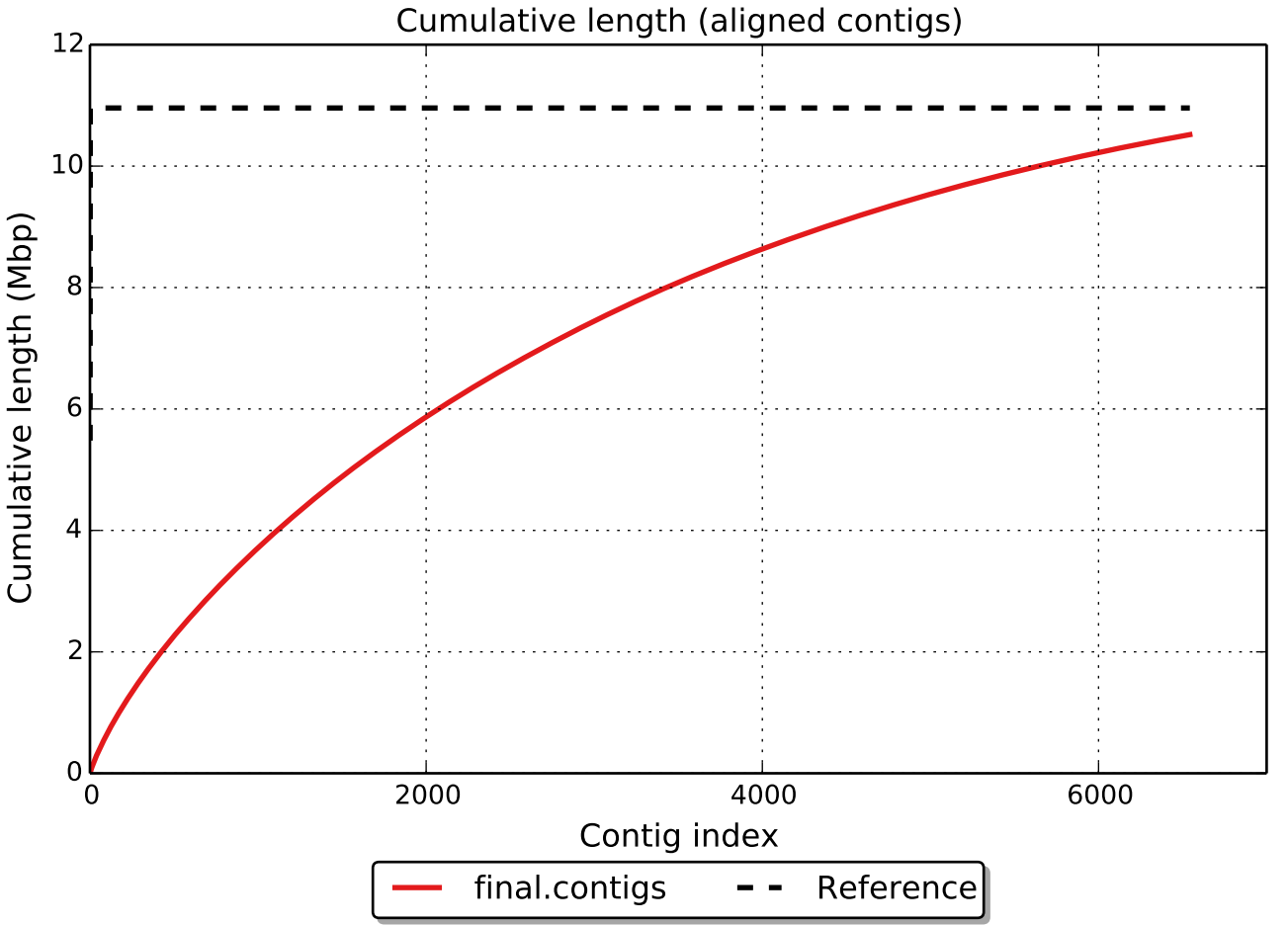

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
2000
4000
6000
Contig index
final.contigs
Reference

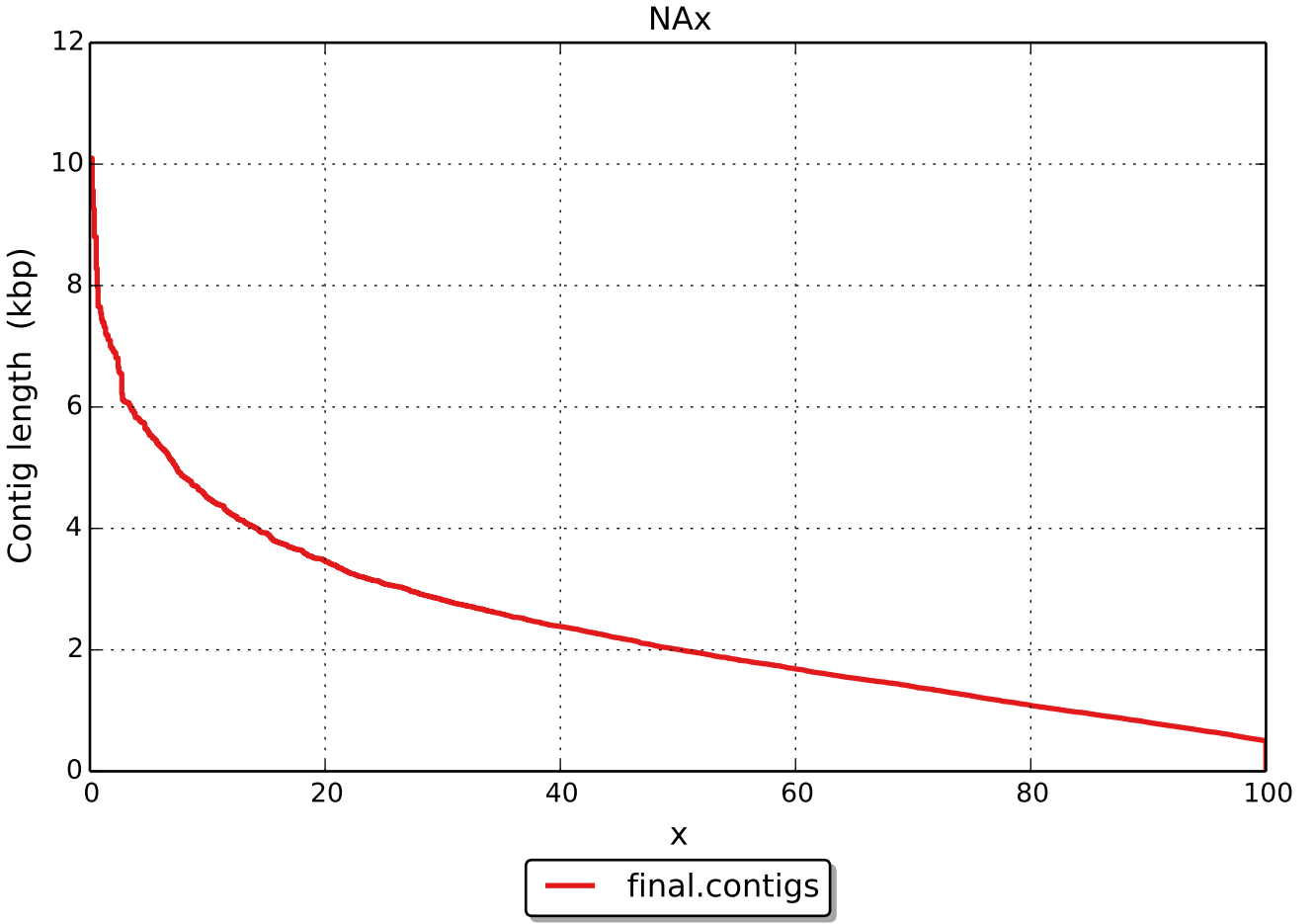

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

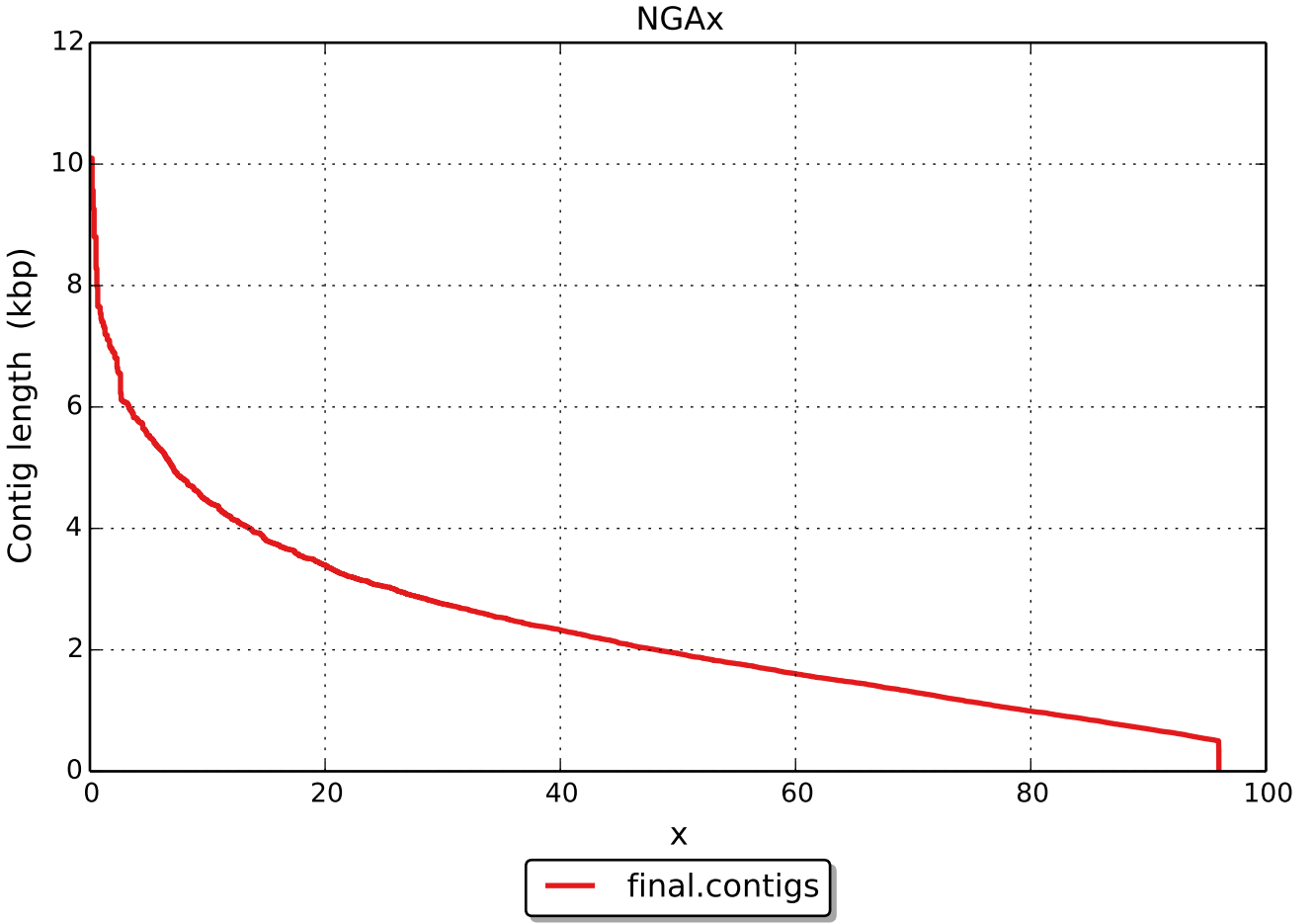

Nx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs

Misassemblies
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
2000
4000
6000
final.contigs
Reference


NAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs