Report

	final.contigs
# contigs (>= 0 bp)	1643
# contigs (>= 1000 bp)	1196
Total length (>= 0 bp)	3707914
Total length (>= 1000 bp)	3380572
# contigs	1643
Largest contig	18614
Total length	3707914
Reference length	1892775
GC (%)	32.24
Reference GC (%)	32.25
N50	3240
NG50	5393
N75	1709
NG75	4091
L50	352
LG50	129
L75	746
LG75	232
# misassemblies	79
# misassembled contigs	72
Misassembled contigs length	273081
# local misassemblies	0
# unaligned contigs	40 + 38 part
Unaligned length	162628
Genome fraction (%)	98.697
Duplication ratio	1.898
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1519.02
# indels per 100 kbp	1.55
Largest alignment	15203
NA50	2876
NGA50	4794
NA75	1490
NGA75	3761
LA50	384
LGA50	139
LA75	833
LGA75	251

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

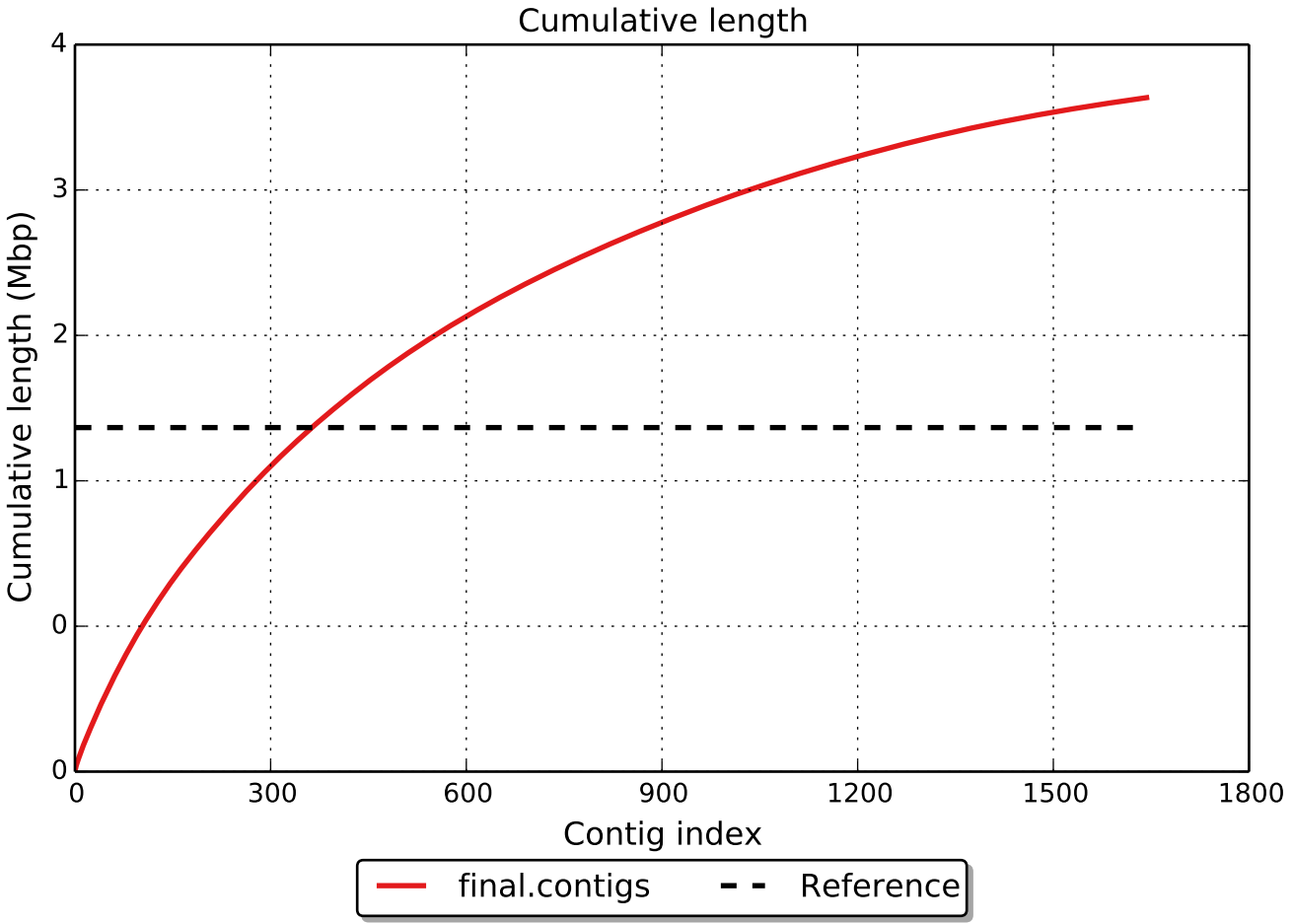
	final.contigs
# misassemblies	79
# relocations	78
# translocations	0
# inversions	1
# possibly misassembled contigs	15
# misassembled contigs	72
Misassembled contigs length	273081
# local misassemblies	0
# mismatches	28377
# indels	29
# short indels	29
# long indels	0
Indels length	29

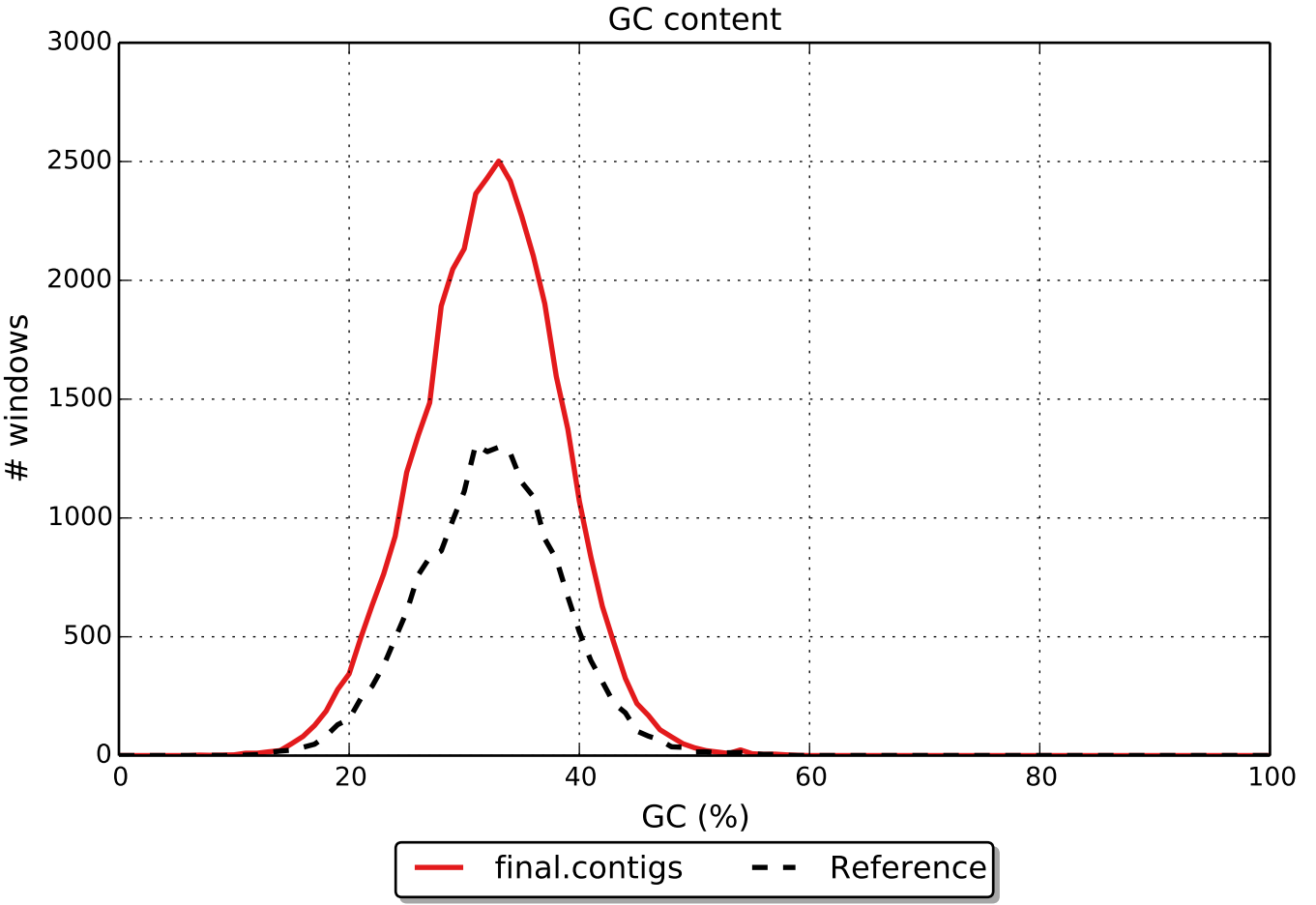
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

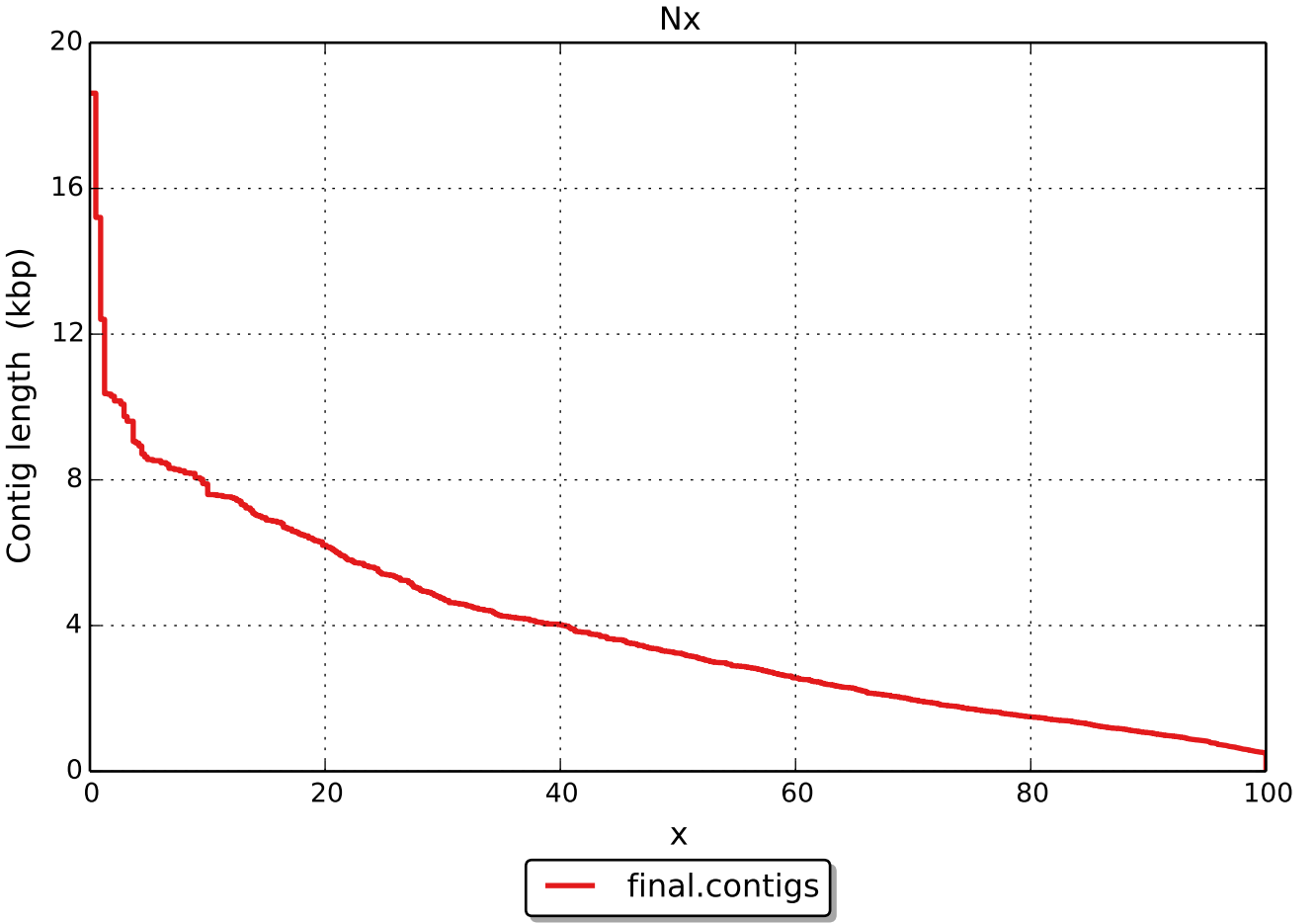
Unaligned report

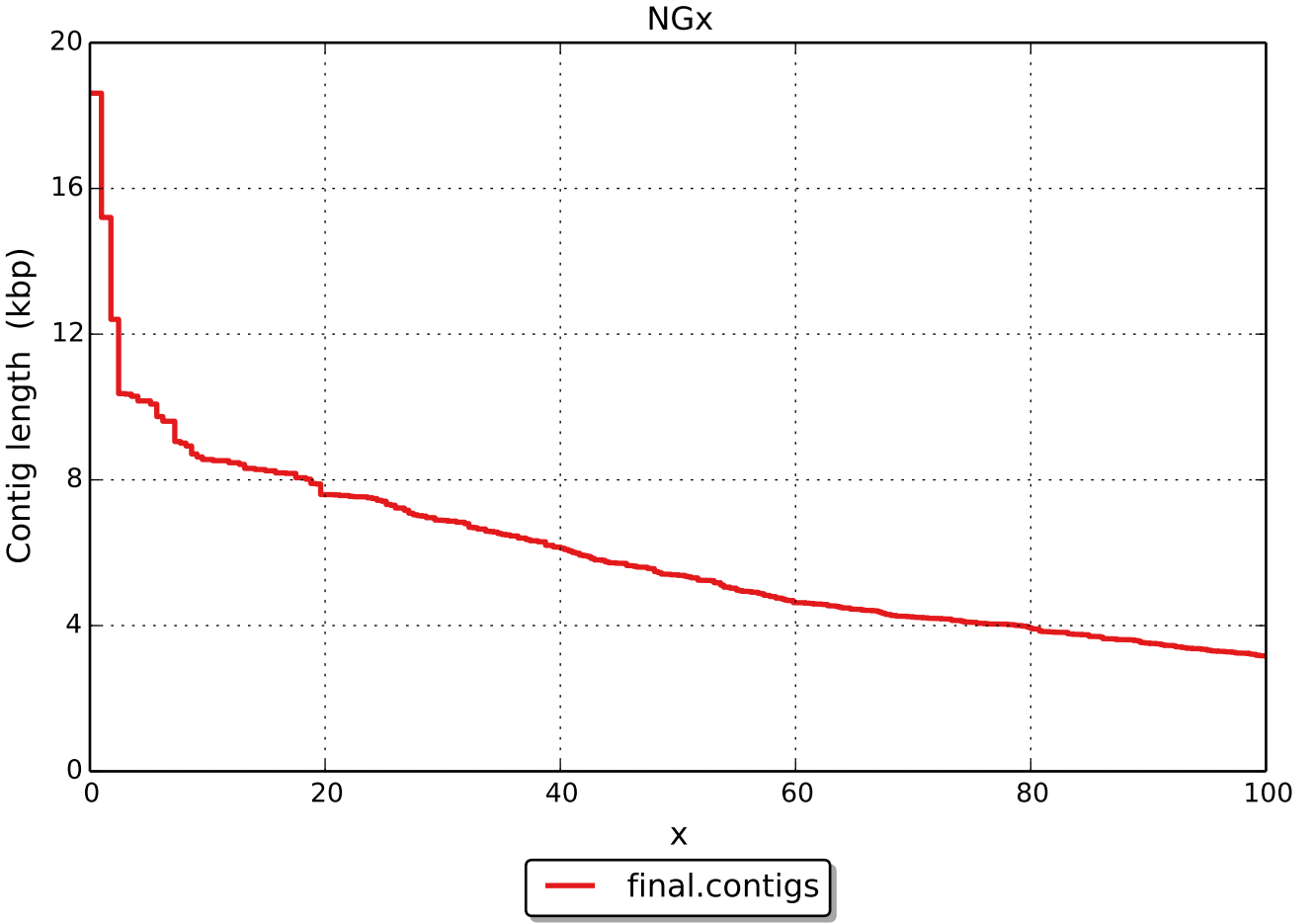
	final.contigs
# fully unaligned contigs	40
Fully unaligned length	98713
# partially unaligned contigs	38
# with misassembly	2
# both parts are significant	13
Partially unaligned length	63915
# N's	0

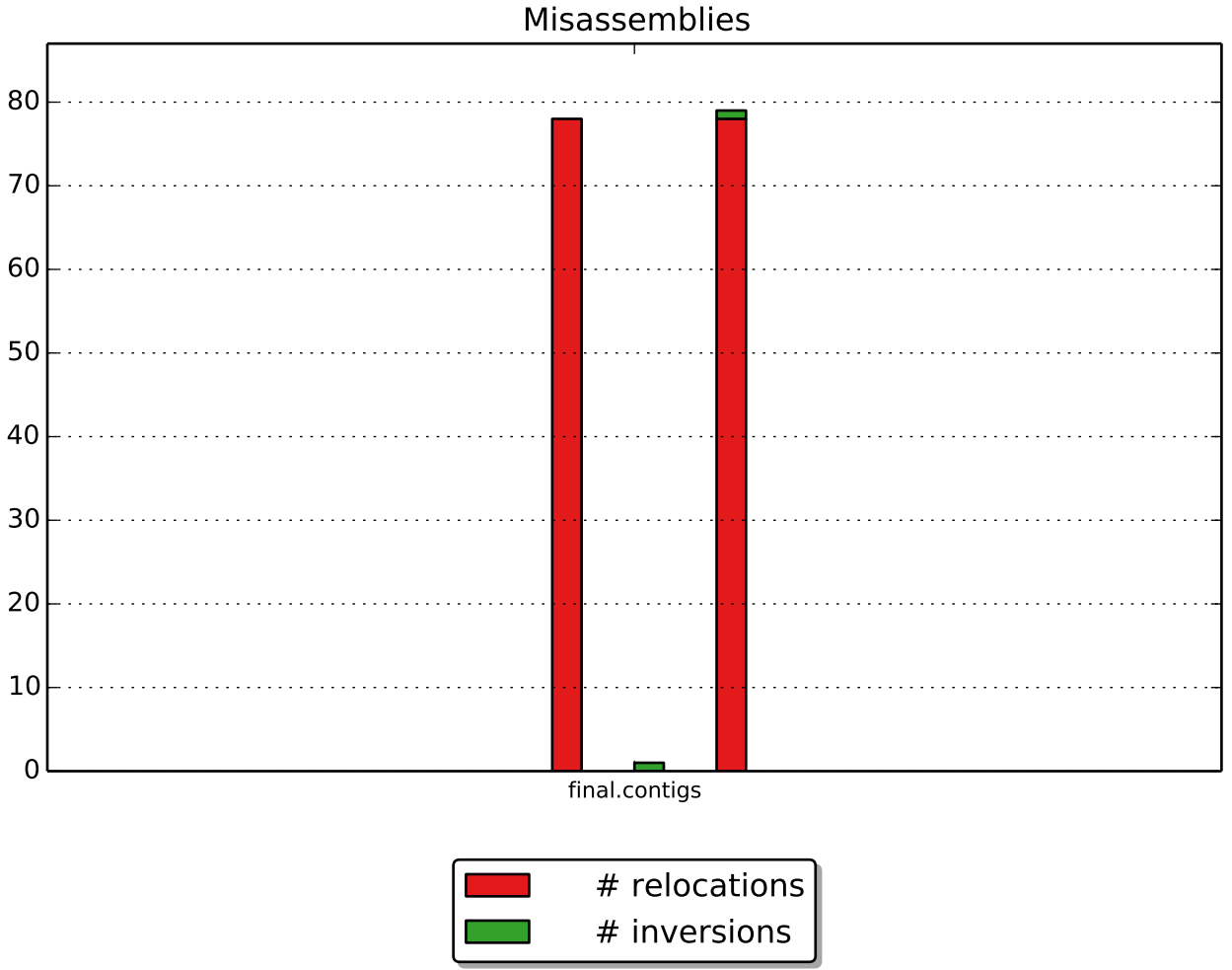
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

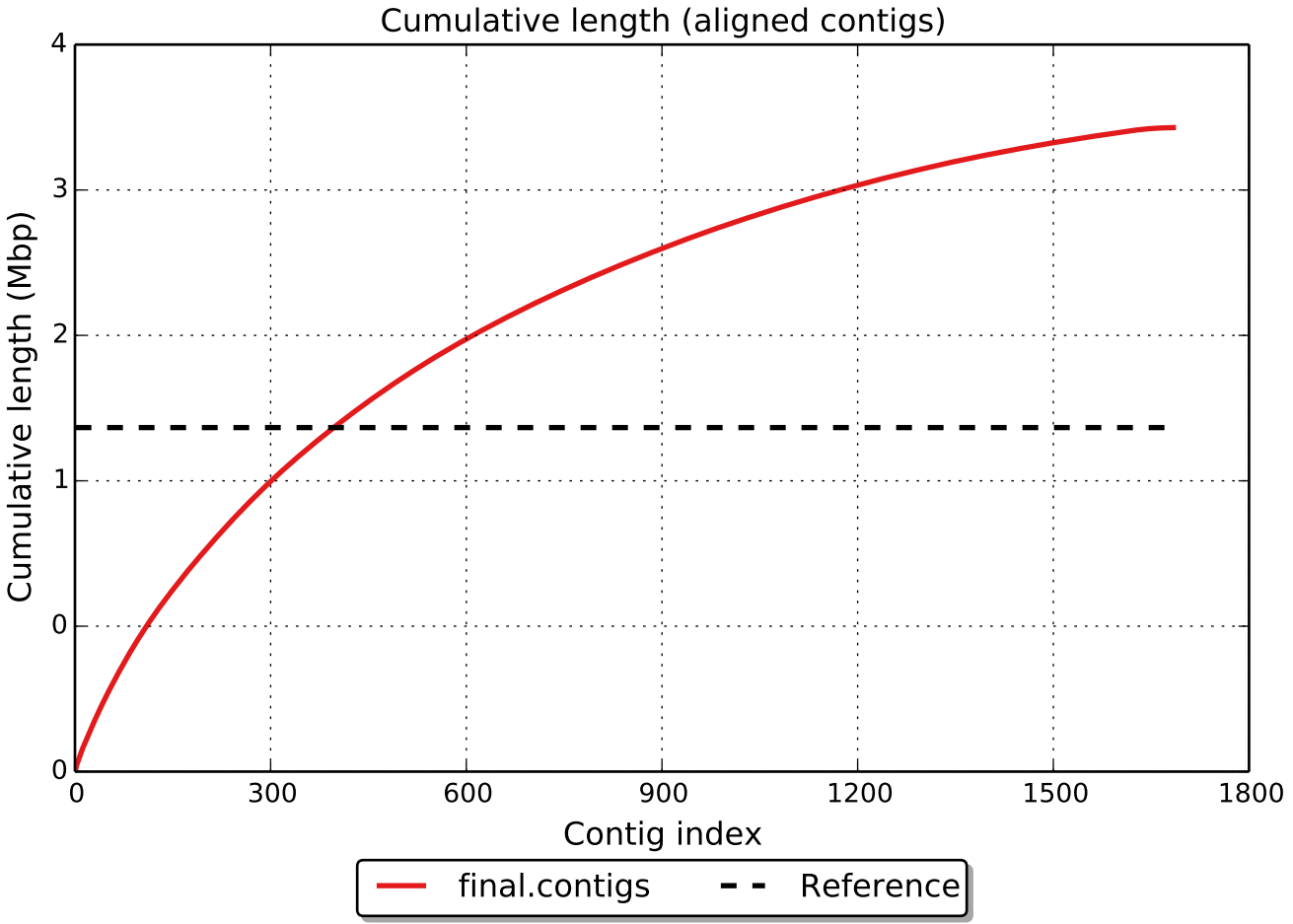

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference

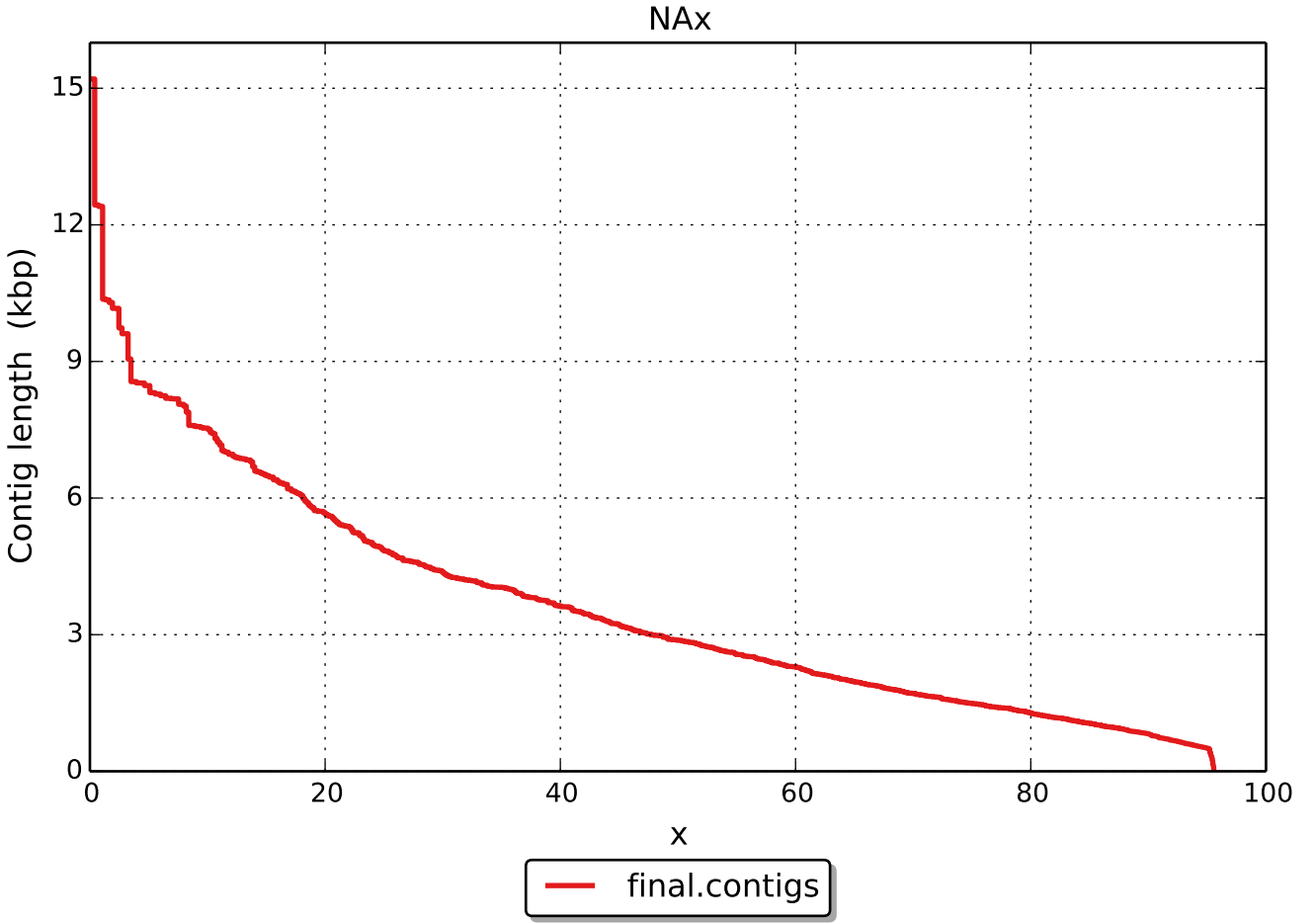

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

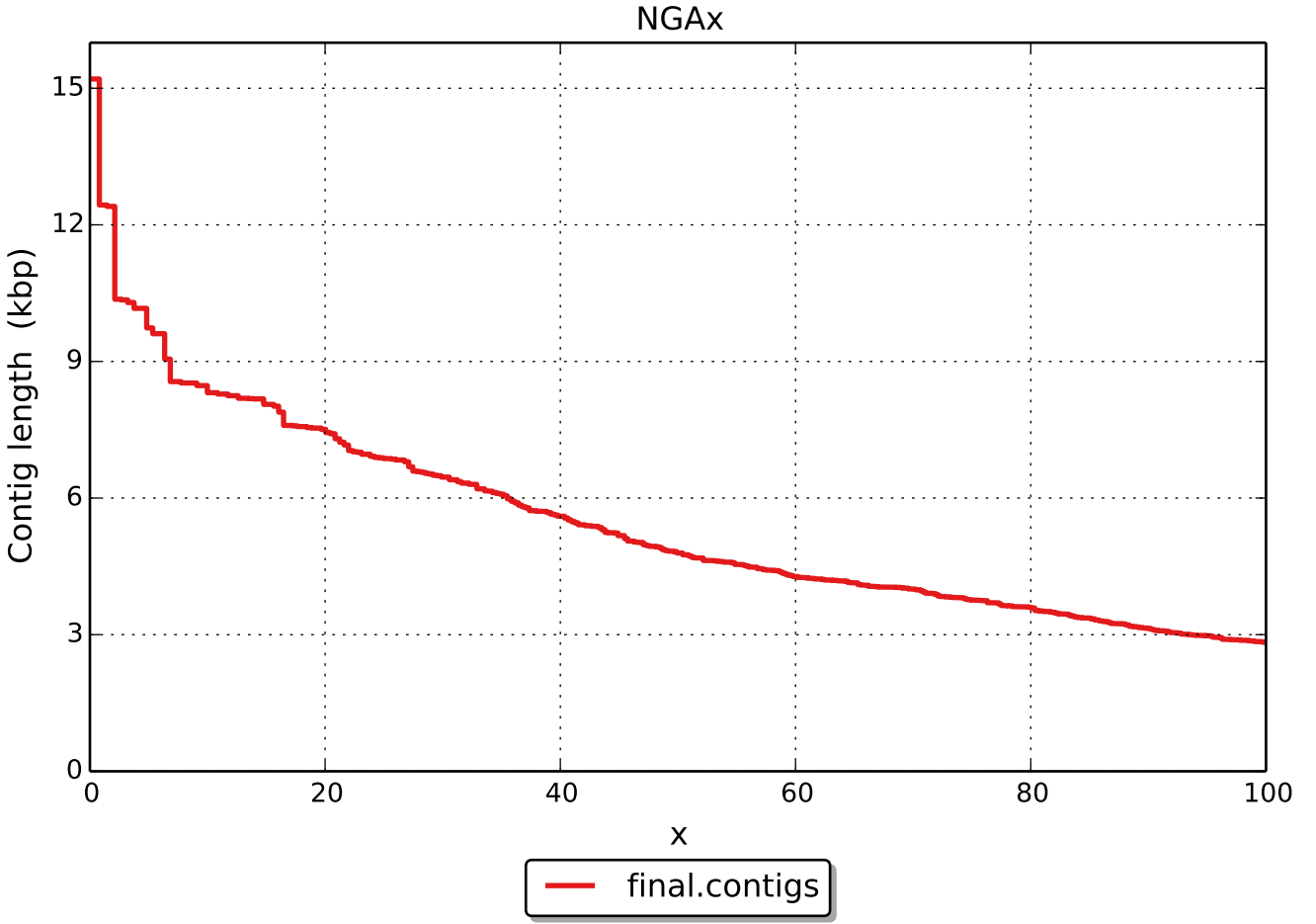

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
80
70
60
50
40
30
20
10
0
final.contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
300
600
900
1200
1500
1800
final.contigs
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs