Report

	final.contigs
# contigs (>= 0 bp)	1320
# contigs (>= 1000 bp)	1061
Total length (>= 0 bp)	3763428
Total length (>= 1000 bp)	3569583
# contigs	1320
Largest contig	15927
Total length	3763428
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.26
N50	4207
NG50	6647
N75	2277
NG75	5175
L50	285
LG50	103
L75	587
LG75	184
# misassemblies	56
# misassembled contigs	53
Misassembled contigs length	216160
# local misassemblies	0
# unaligned contigs	99 + 72 part
Unaligned length	513008
Genome fraction (%)	99.328
Duplication ratio	1.729
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1356.82
# indels per 100 kbp	1.49
Largest alignment	15927
NA50	3230
NGA50	5553
NA75	1320
NGA75	4241
LA50	340
LGA50	116
LA75	792
LGA75	215

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

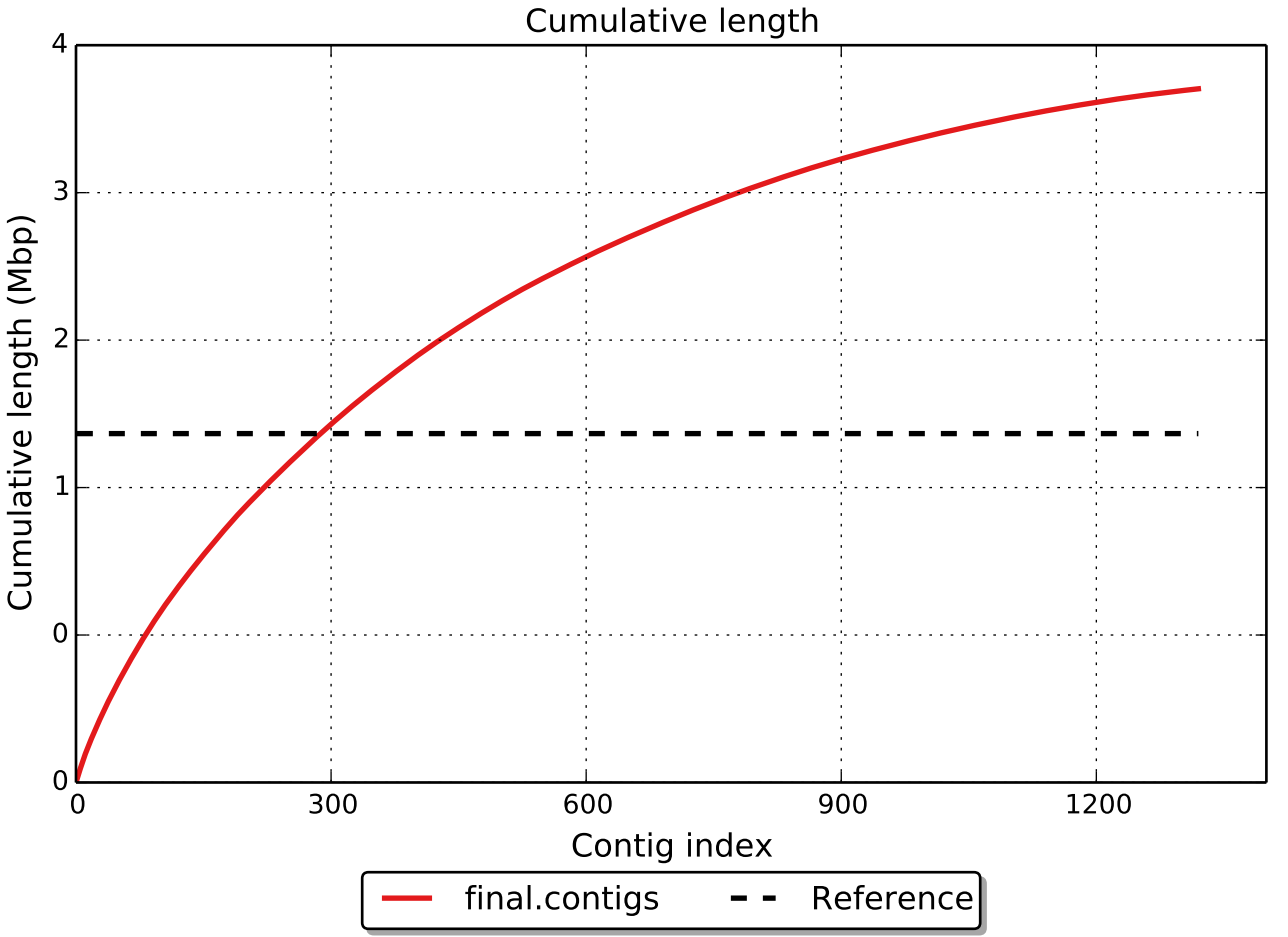
	final.contigs
# misassemblies	56
# relocations	53
# translocations	0
# inversions	3
# possibly misassembled contigs	46
# misassembled contigs	53
Misassembled contigs length	216160
# local misassemblies	0
# mismatches	25509
# indels	28
# short indels	28
# long indels	0
Indels length	28

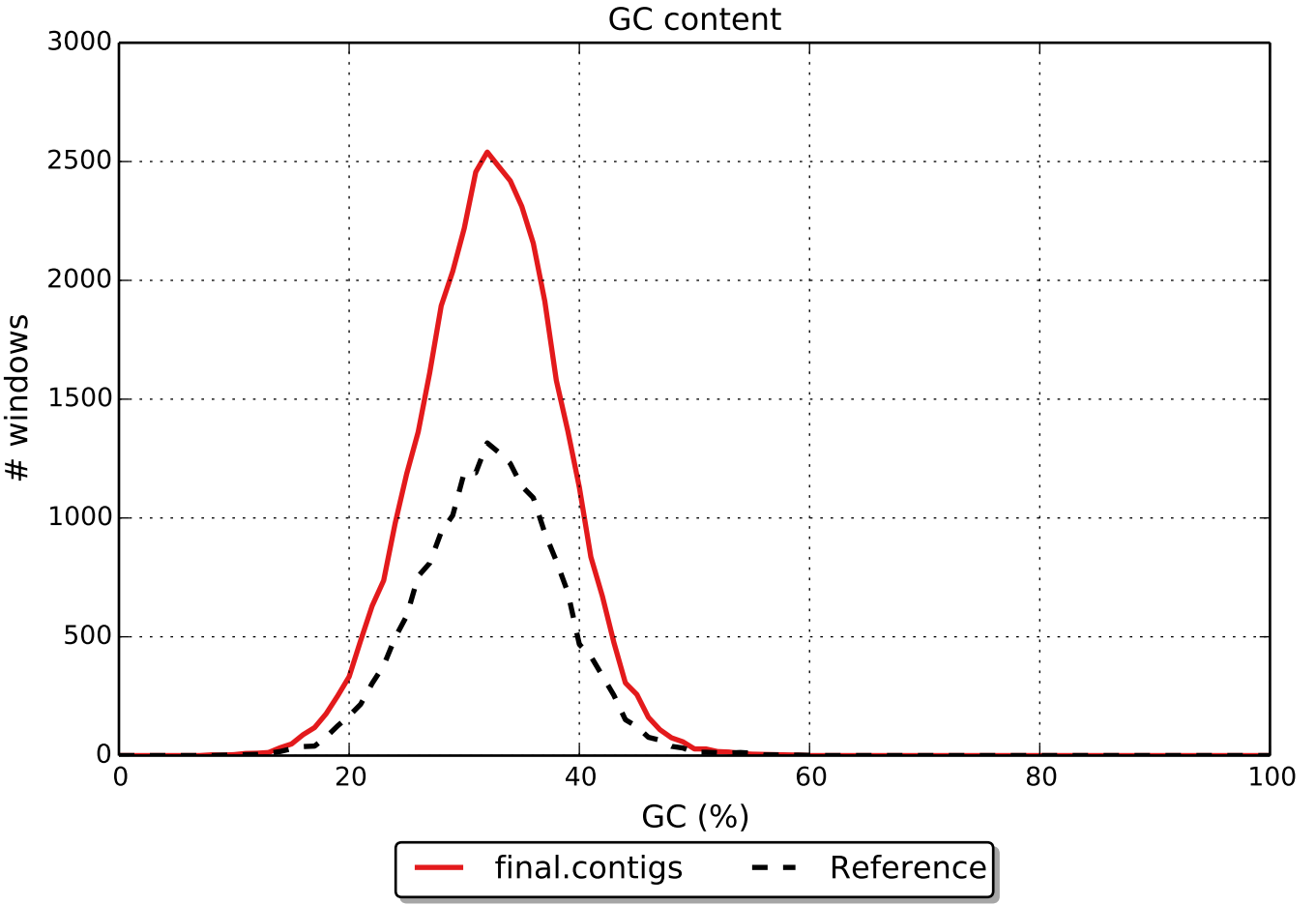
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

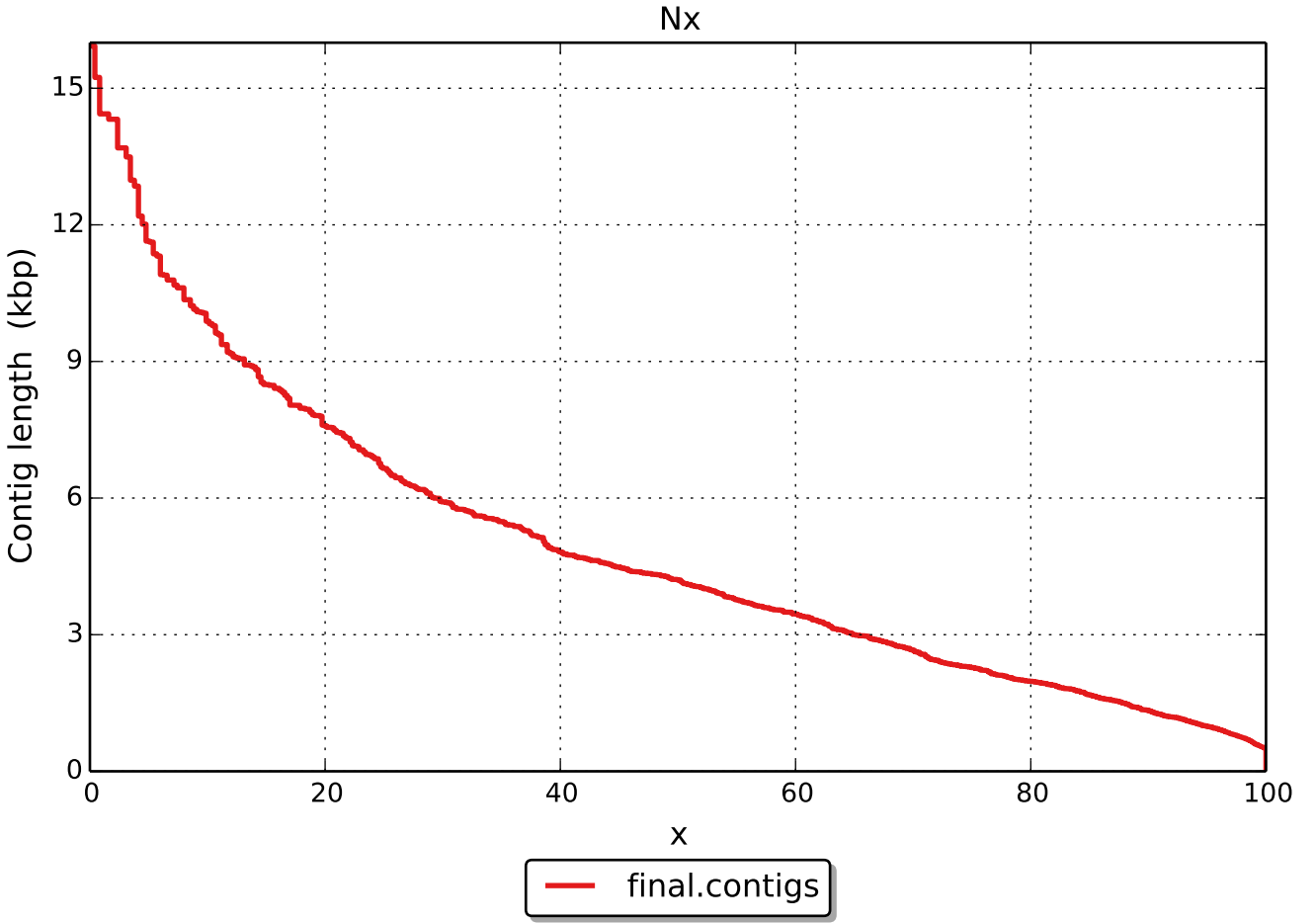
Unaligned report

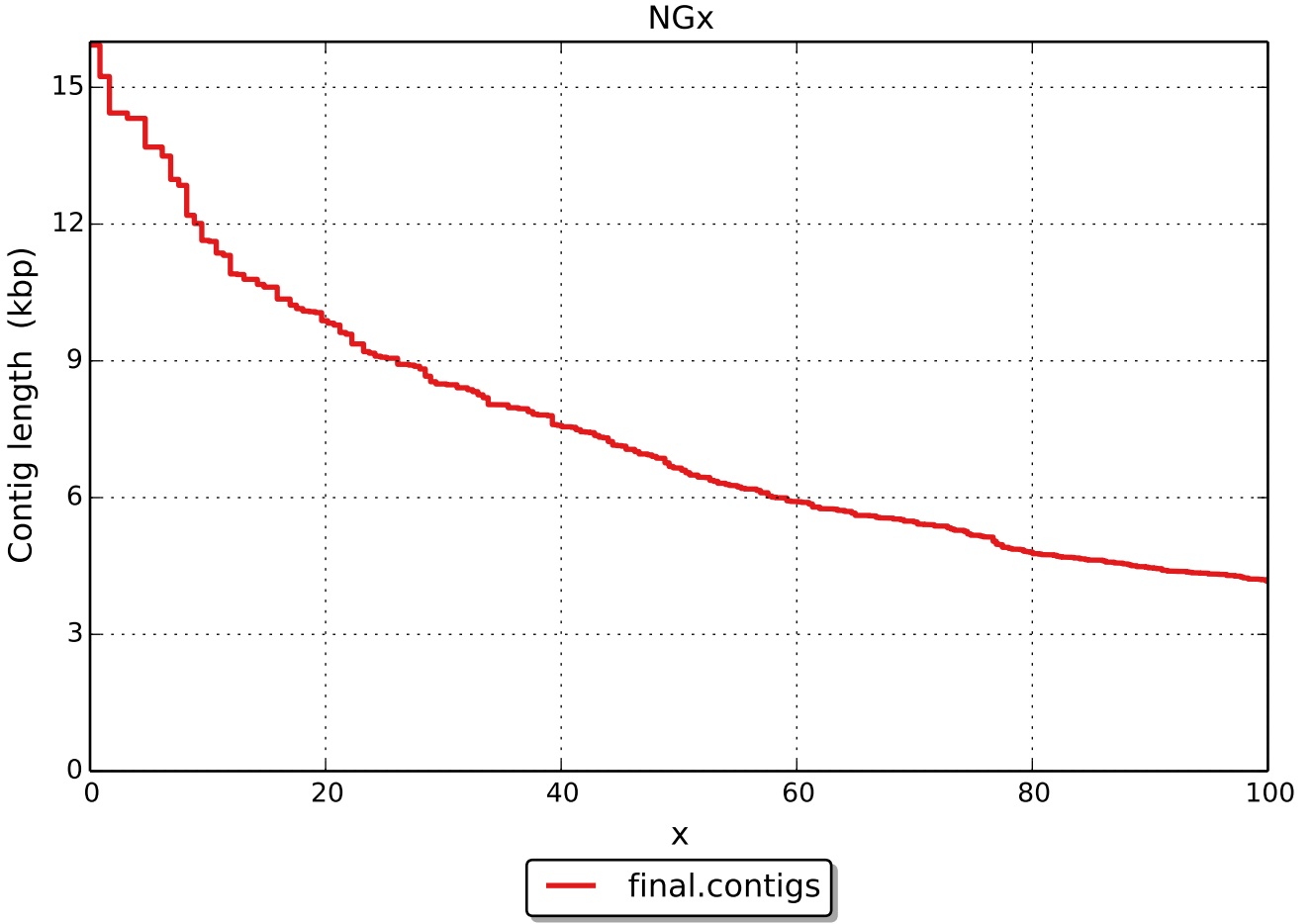
	final.contigs
# fully unaligned contigs	99
Fully unaligned length	311955
# partially unaligned contigs	72
# with misassembly	9
# both parts are significant	38
Partially unaligned length	201053
# N's	0

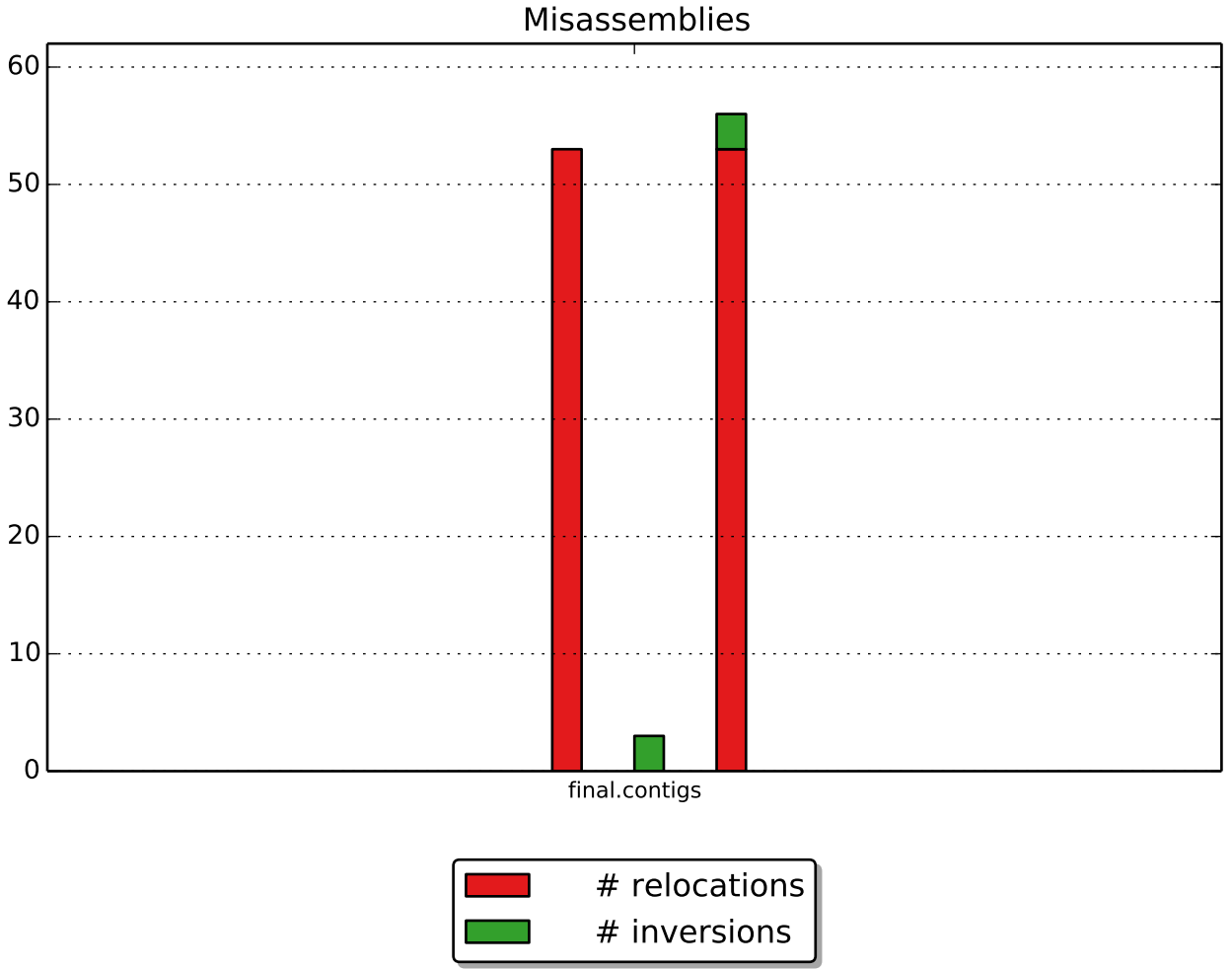
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

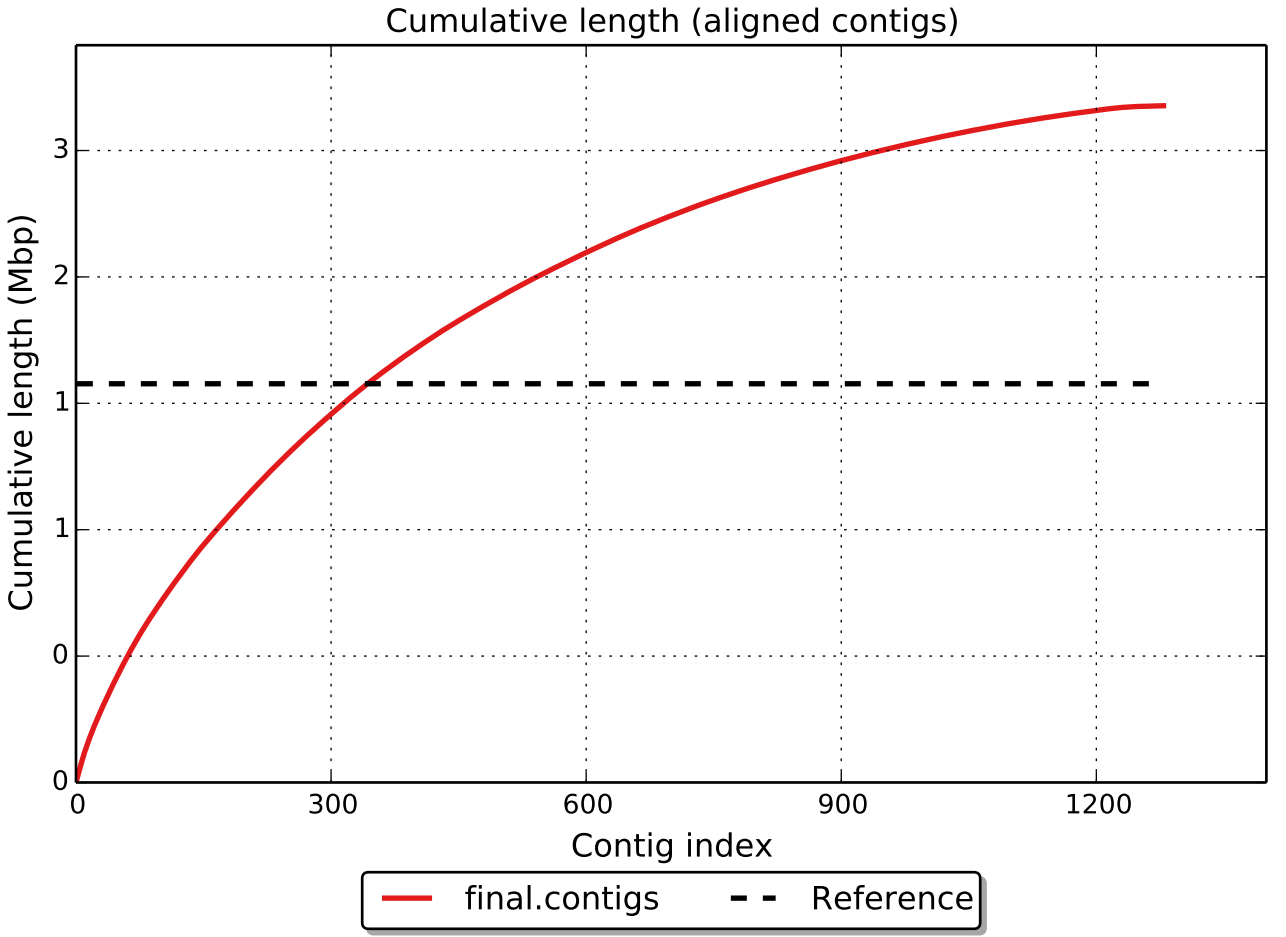

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
300
600
900
1200
Contig index
final.contigs
Reference

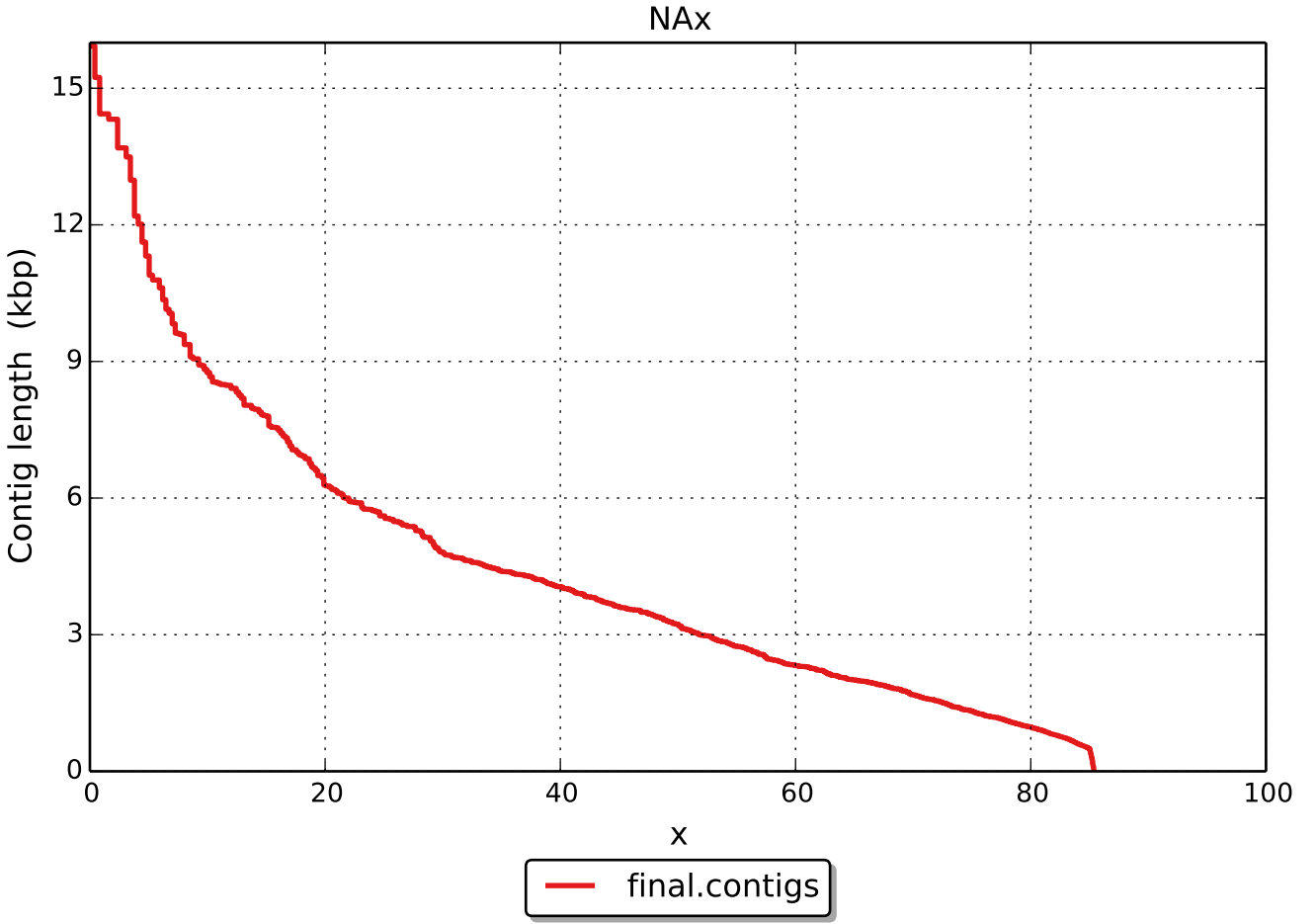

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

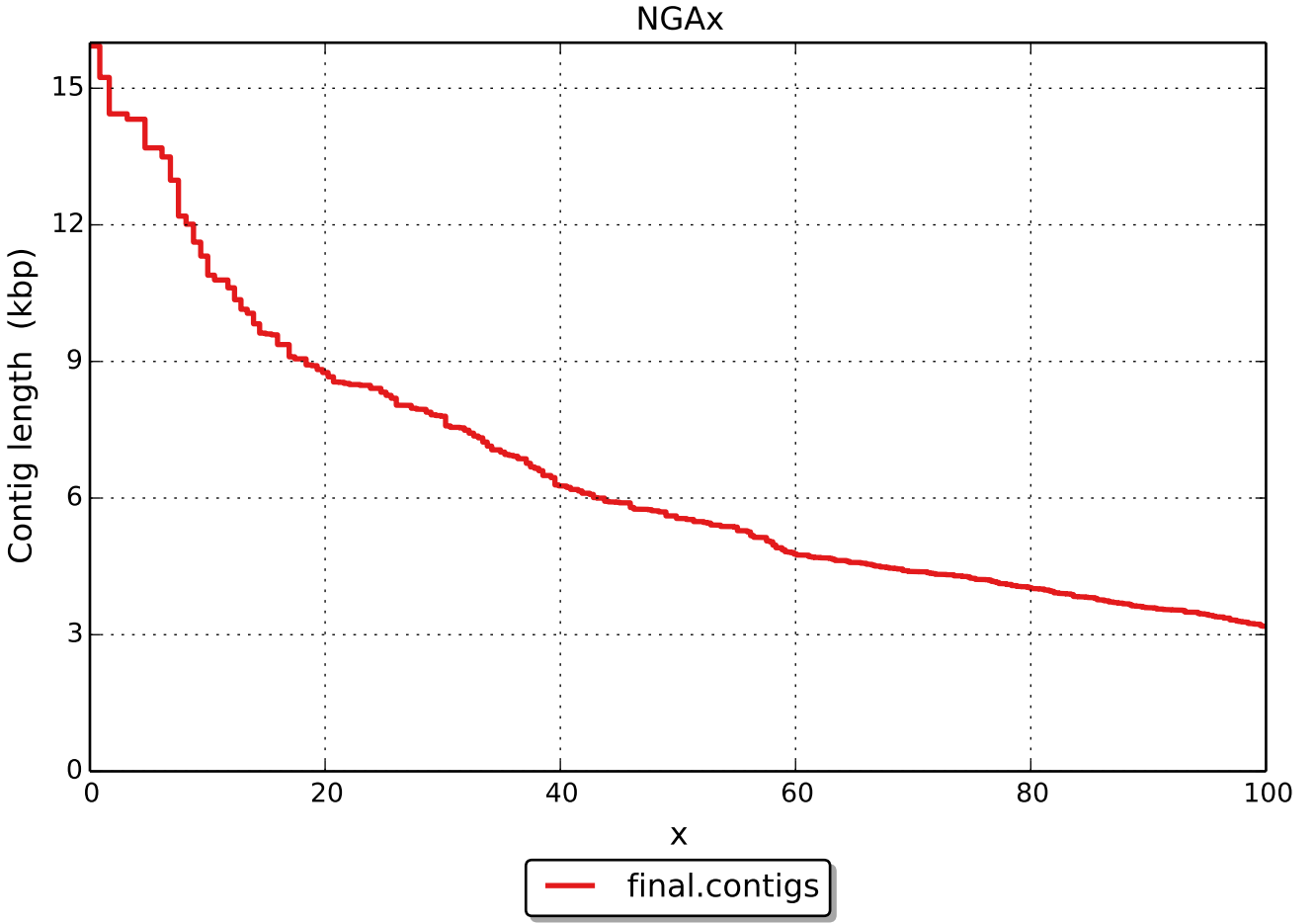

Nx
Contig length (kbp)
0
3
6
9
12
15
0
20
40
60
80
100
x
final.contigs


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


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
3
2
1
1
0
0
0
300
600
900
1200
Contig index
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