Report

	final.contigs
# contigs (>= 0 bp)	2417
# contigs (>= 1000 bp)	1401
Total length (>= 0 bp)	3576845
Total length (>= 1000 bp)	2837658
# contigs	2417
Largest contig	7824
Total length	3576845
Reference length	1892775
GC (%)	32.30
Reference GC (%)	32.26
N50	1844
NG50	2834
N75	1098
NG75	2231
L50	629
LG50	258
L75	1253
LG75	447
# misassemblies	77
# misassembled contigs	77
Misassembled contigs length	141726
# local misassemblies	0
# unaligned contigs	5 + 5 part
Unaligned length	8552
Genome fraction (%)	95.844
Duplication ratio	1.967
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1772.23
# indels per 100 kbp	1.38
Largest alignment	7824
NA50	1811
NGA50	2793
NA75	1068
NGA75	2187
LA50	640
LGA50	261
LA75	1281
LGA75	454

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

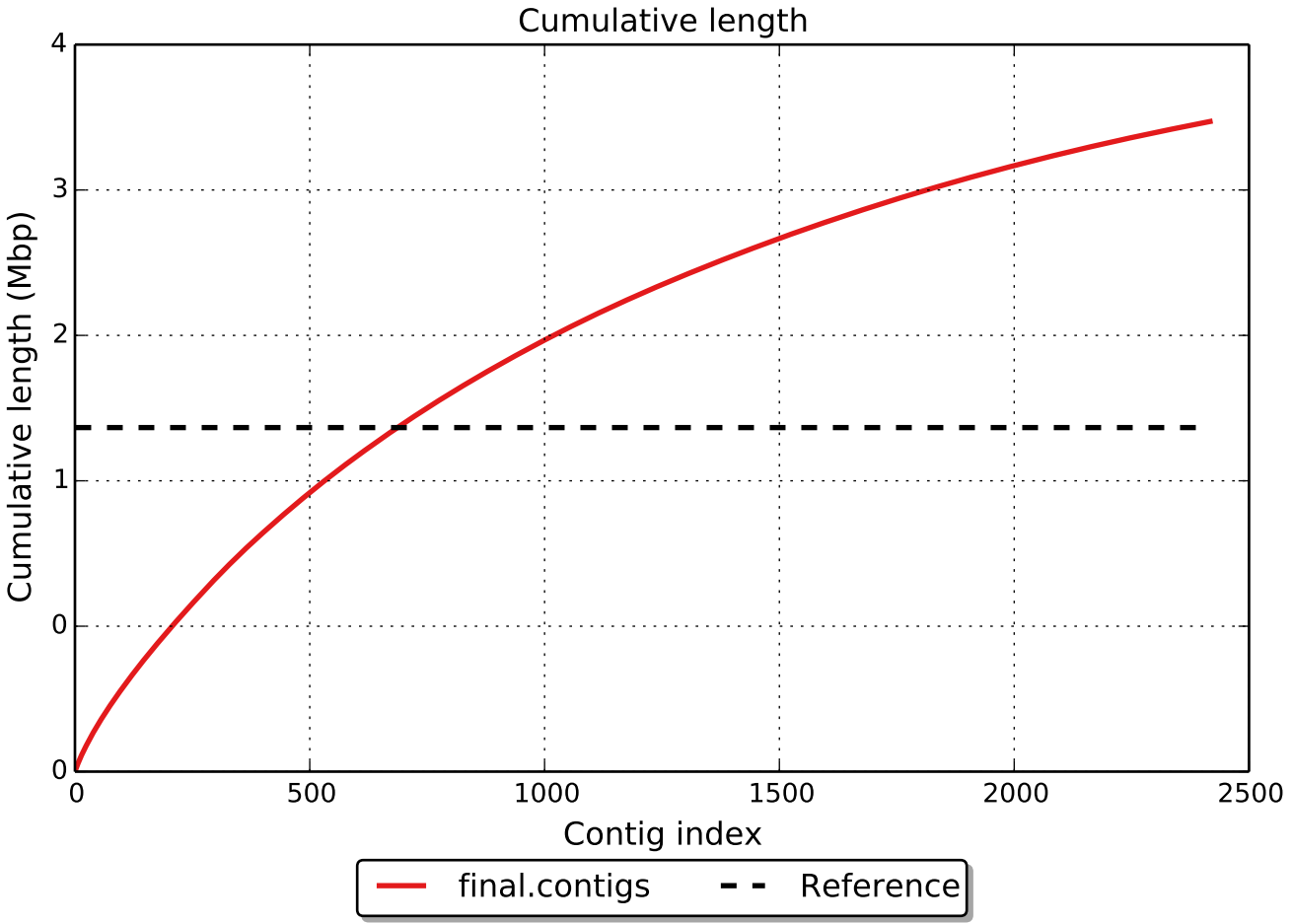
	final.contigs
# misassemblies	77
# relocations	76
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	77
Misassembled contigs length	141726
# local misassemblies	0
# mismatches	32150
# indels	25
# short indels	25
# long indels	0
Indels length	25

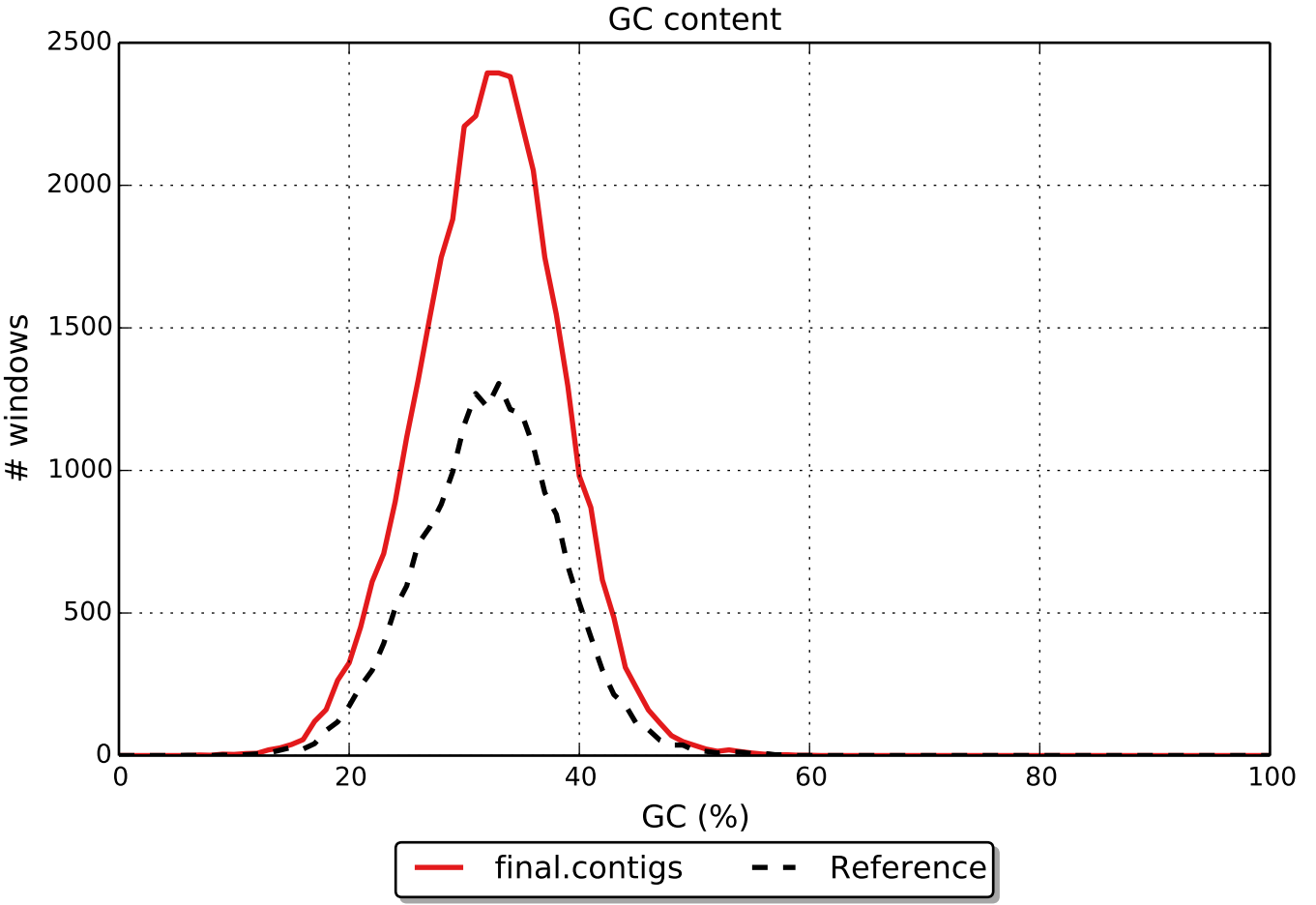
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

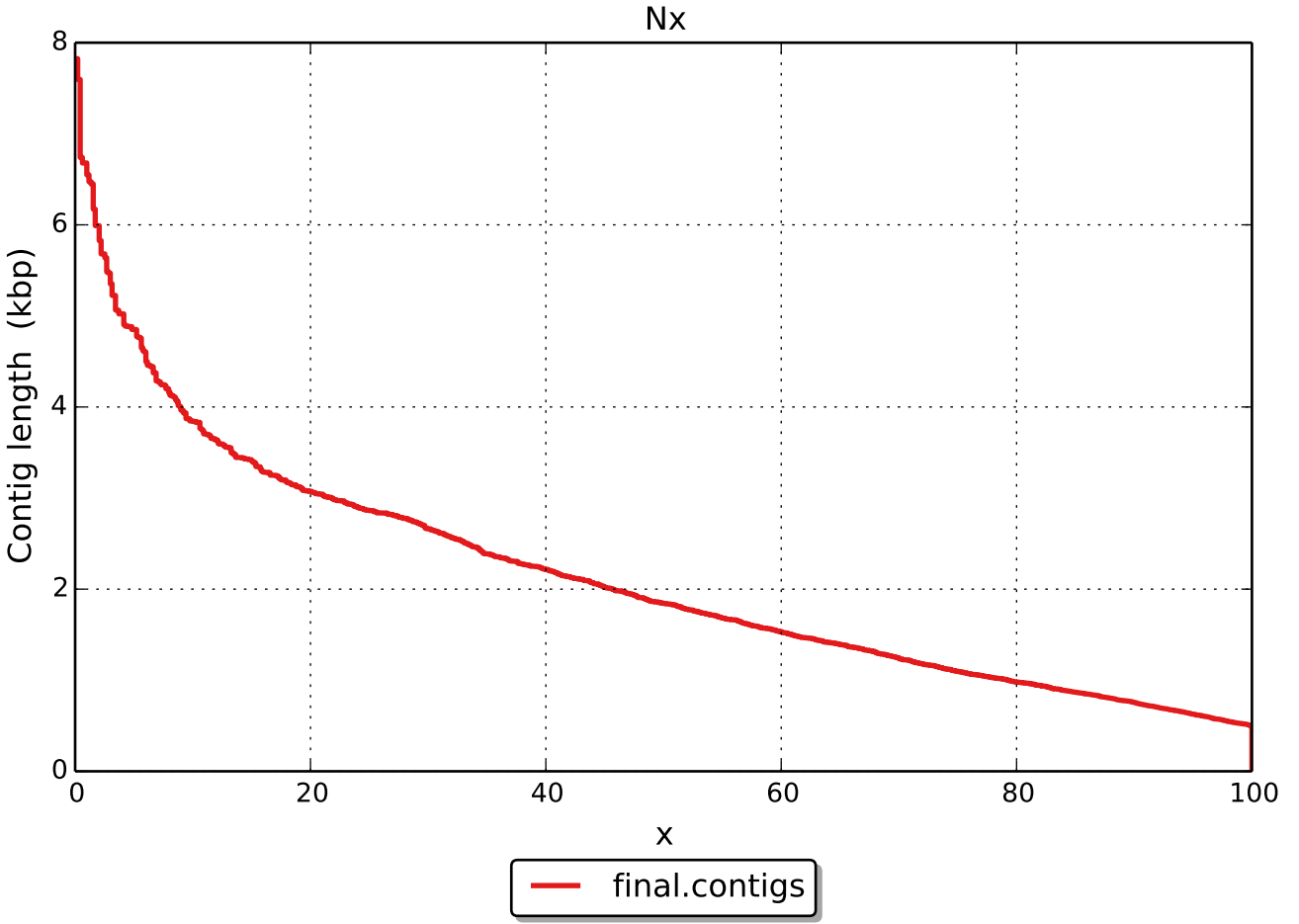
Unaligned report

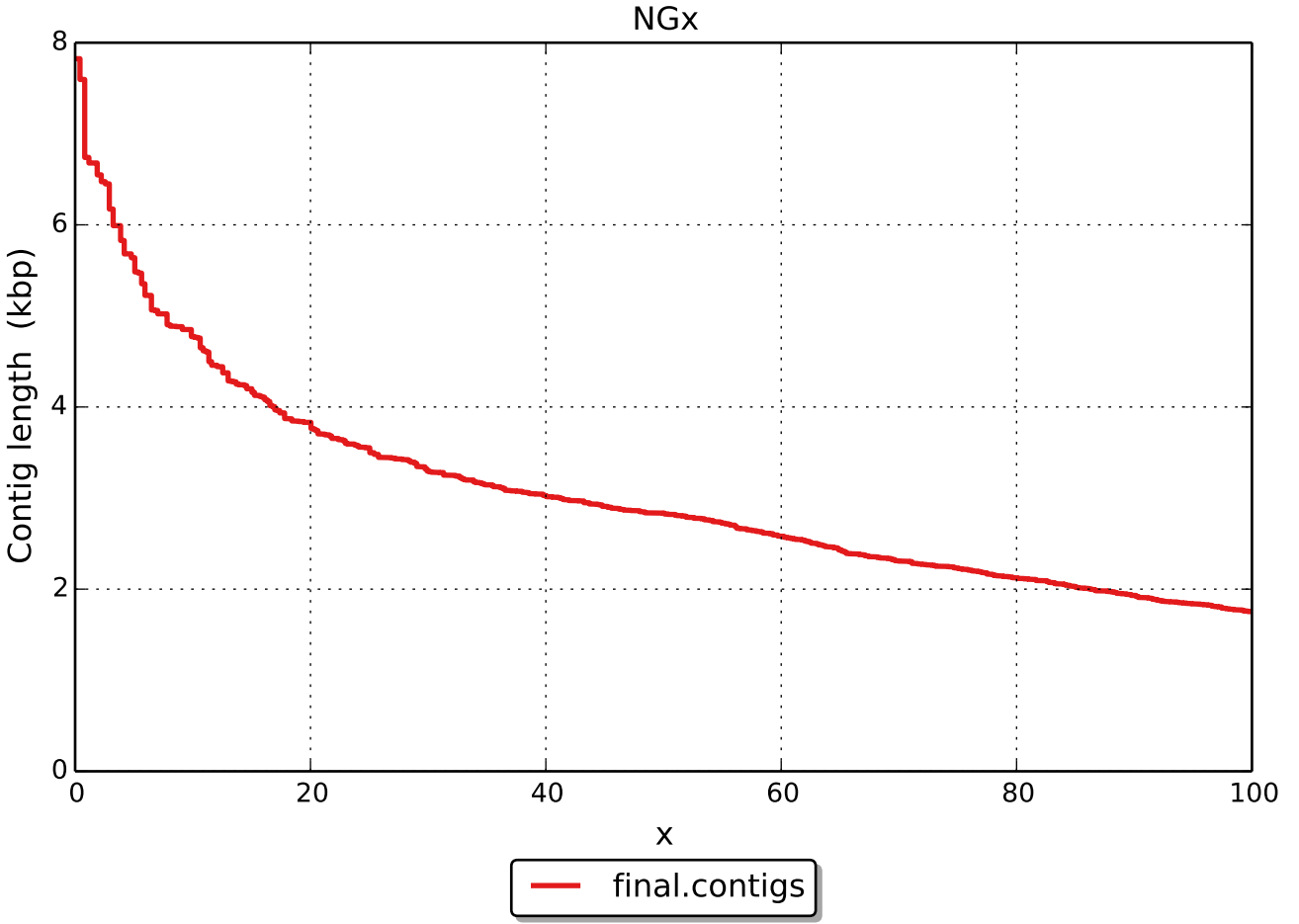
	final.contigs
# fully unaligned contigs	5
Fully unaligned length	6425
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2127
# N's	0

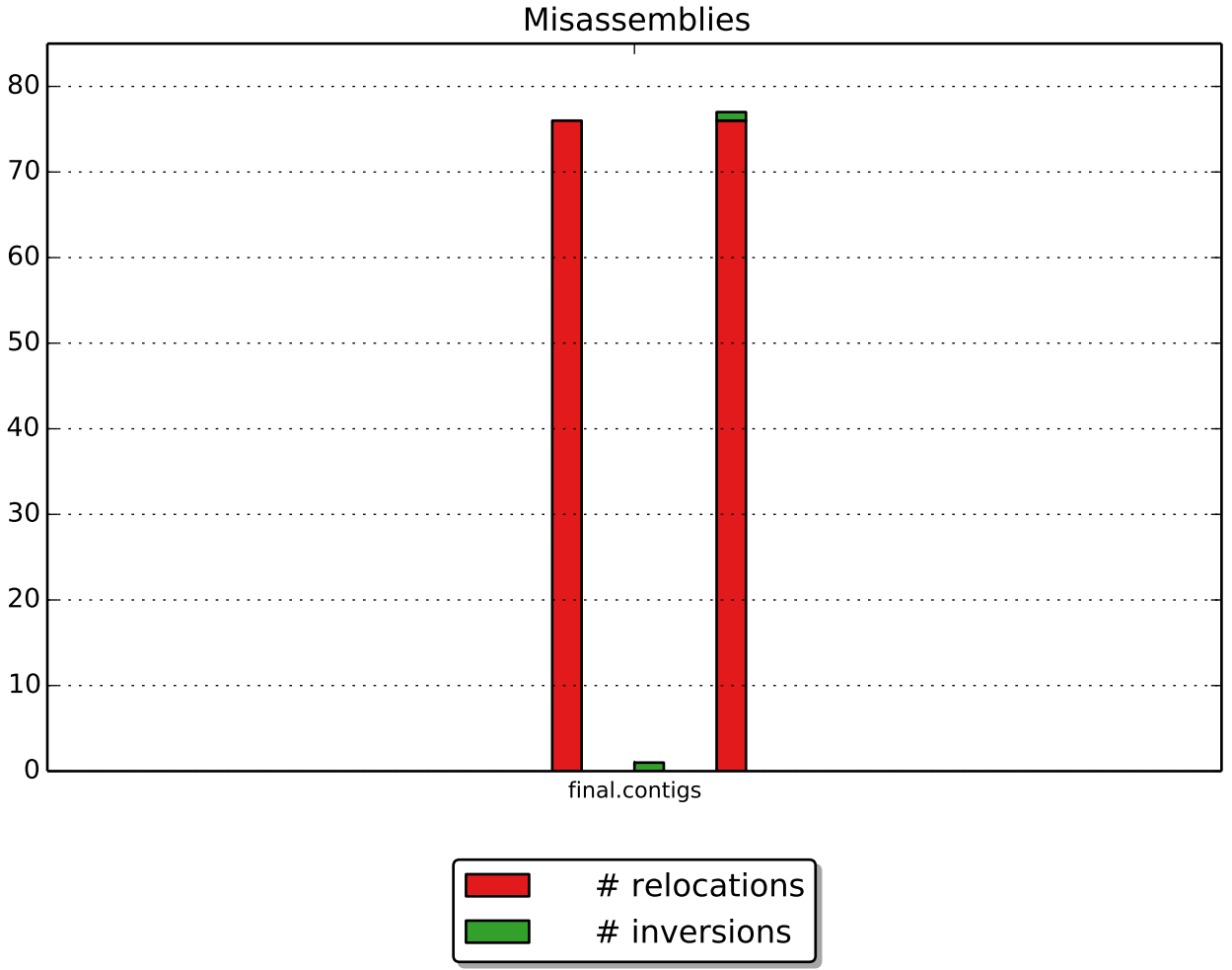
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

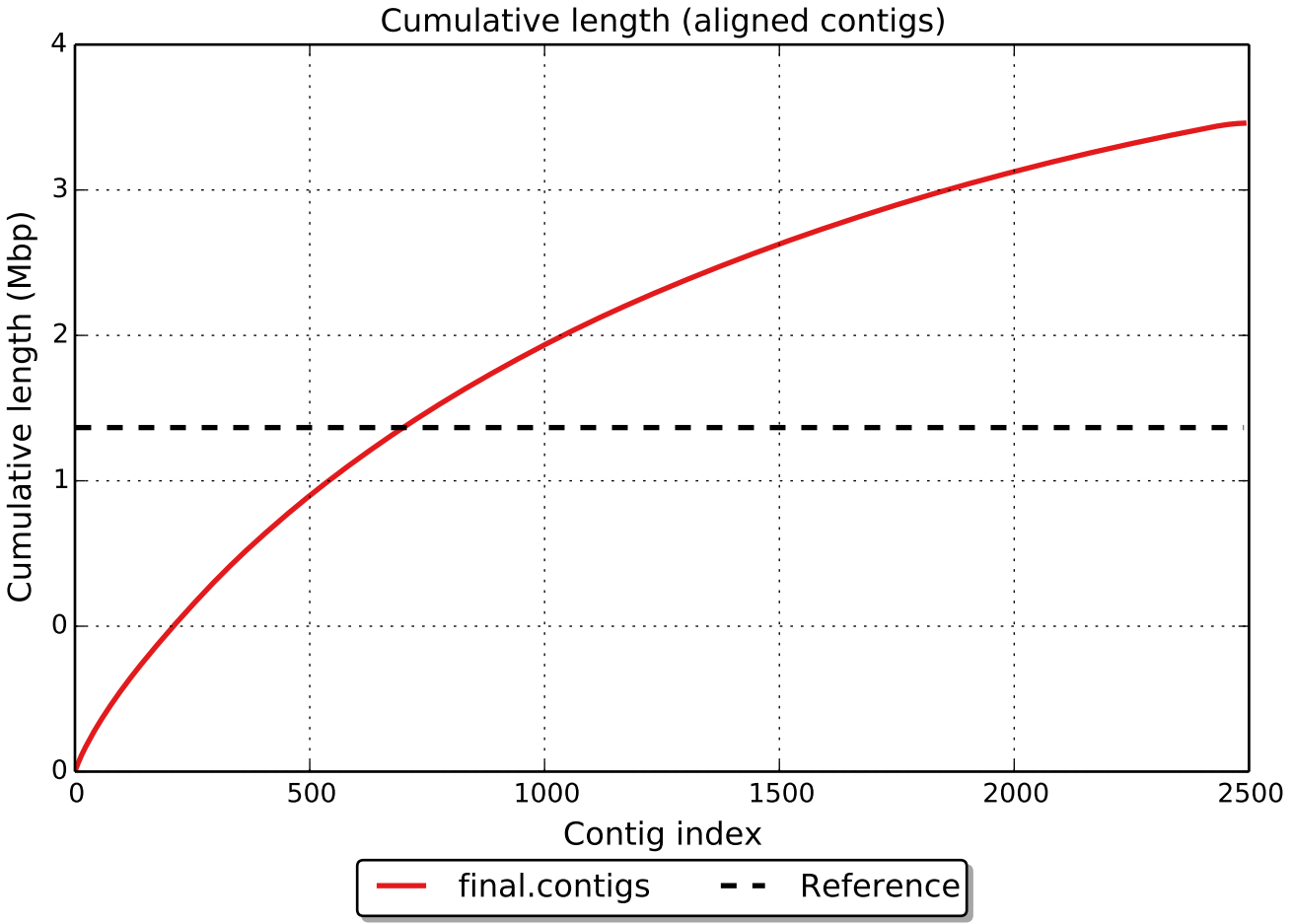

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

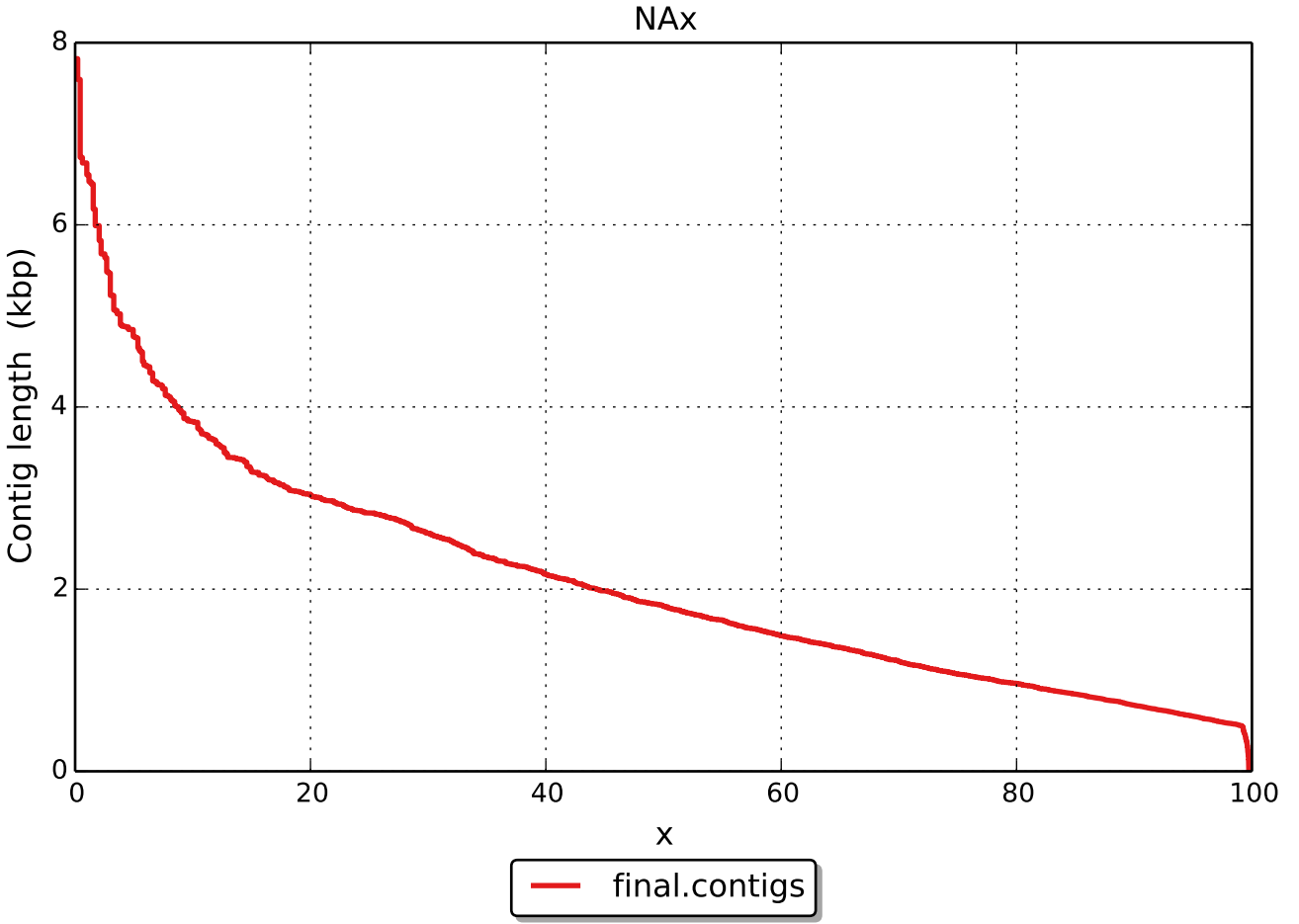

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

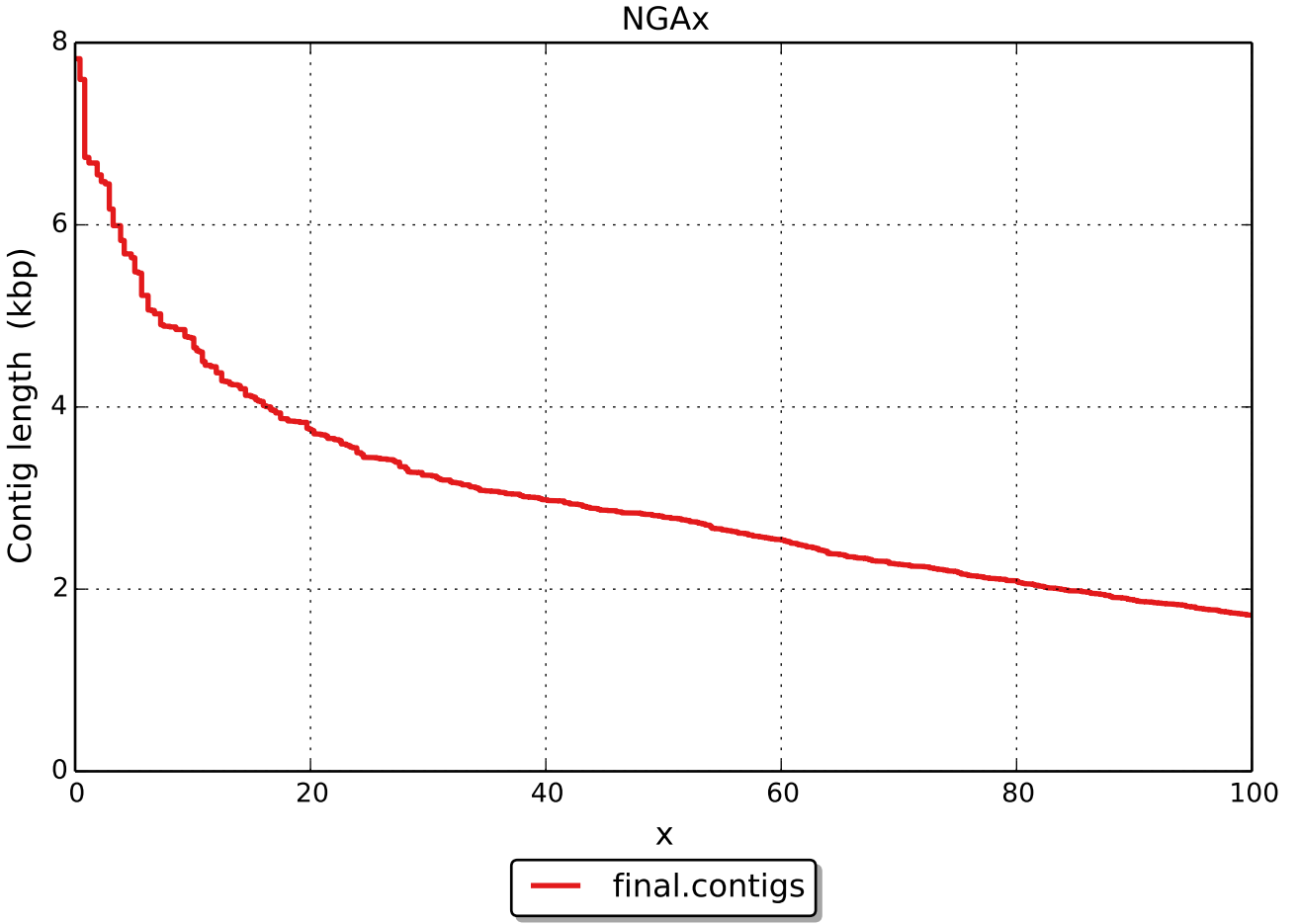

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
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
500
1000
1500
2000
2500
final.contigs
Reference


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


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