Report

	res_erreurs_tipping_bubbles_hard
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2718
Total length (>= 1000 bp)	2718
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	26
Largest contig	5327
Total length	29928
Reference length	29814
GC (%)	37.90
Reference GC (%)	38.01
N50	2495
NG50	2495
N75	2124
NG75	2124
L50	5
LG50	5
L75	8
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	11 + 0 part
Unaligned length	376
Genome fraction (%)	96.713
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.40
# indels per 100 kbp	6.94
Largest alignment	5298
Total aligned length	29001
NA50	2466
NGA50	2466
NA75	2121
NGA75	2121
LA50	5
LGA50	5
LA75	8
LGA75	8

All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

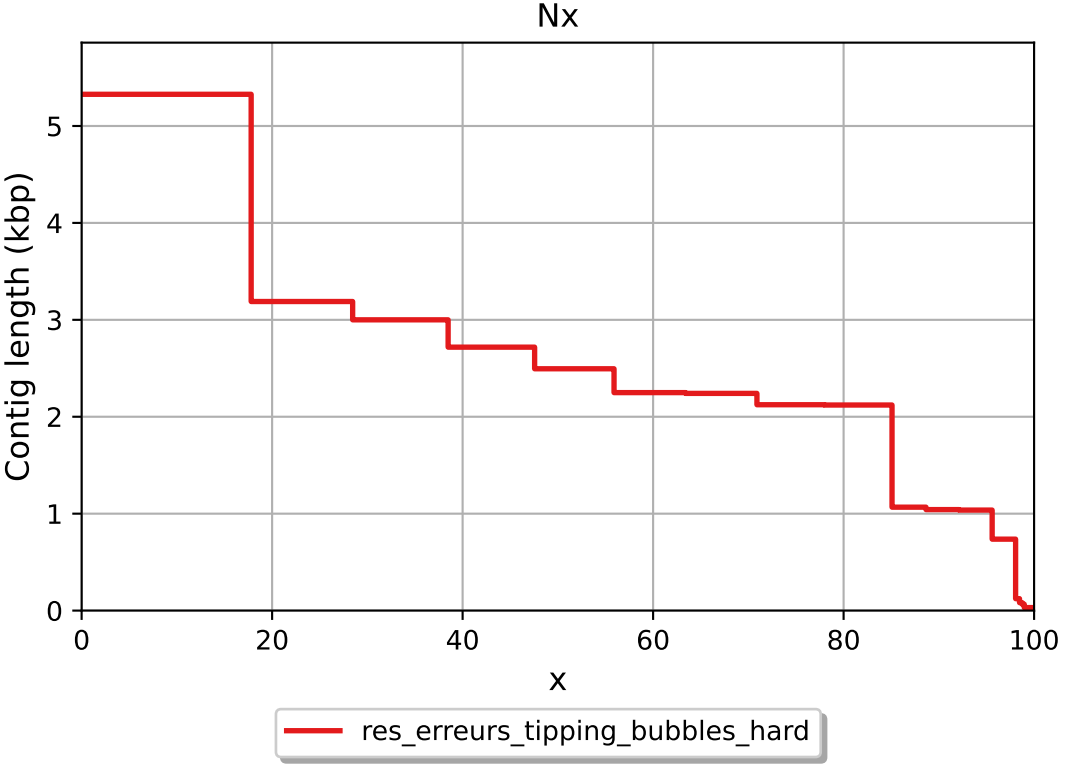
	res_erreurs_tipping_bubbles_hard
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3
# indels	2
# indels (<= 5 bp)	0
# indels (> 5 bp)	2
Indels length	15

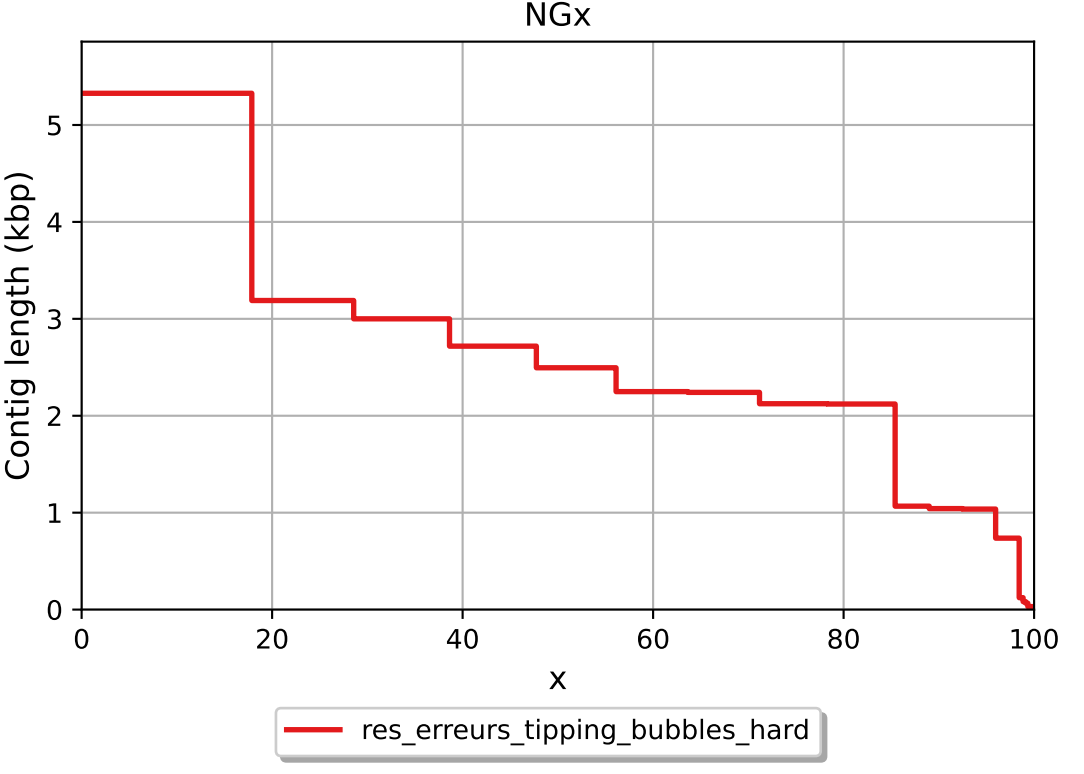
All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

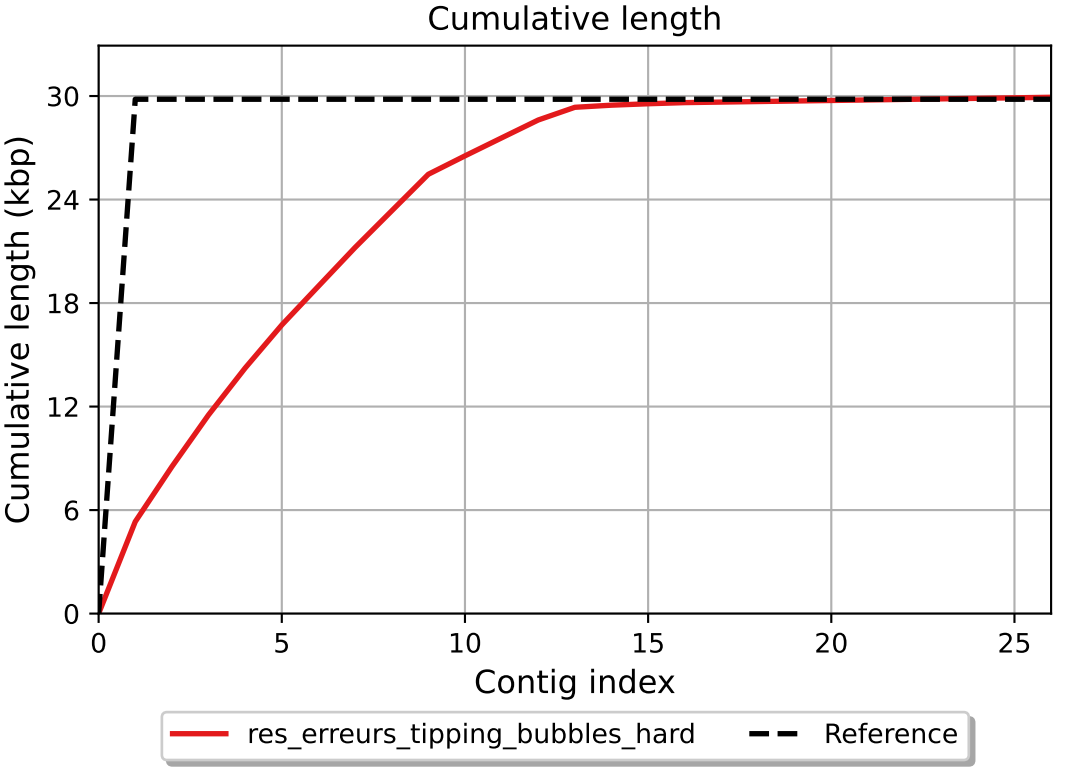
Unaligned report

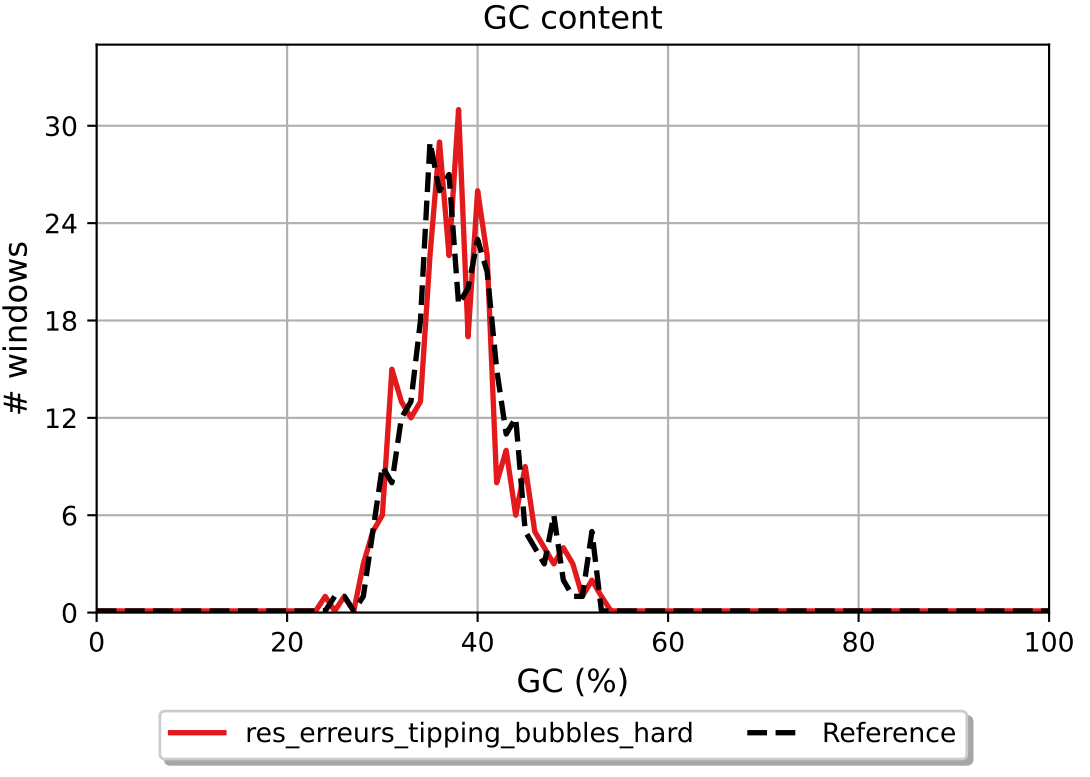
	res_erreurs_tipping_bubbles_hard
# fully unaligned contigs	11
Fully unaligned length	376
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

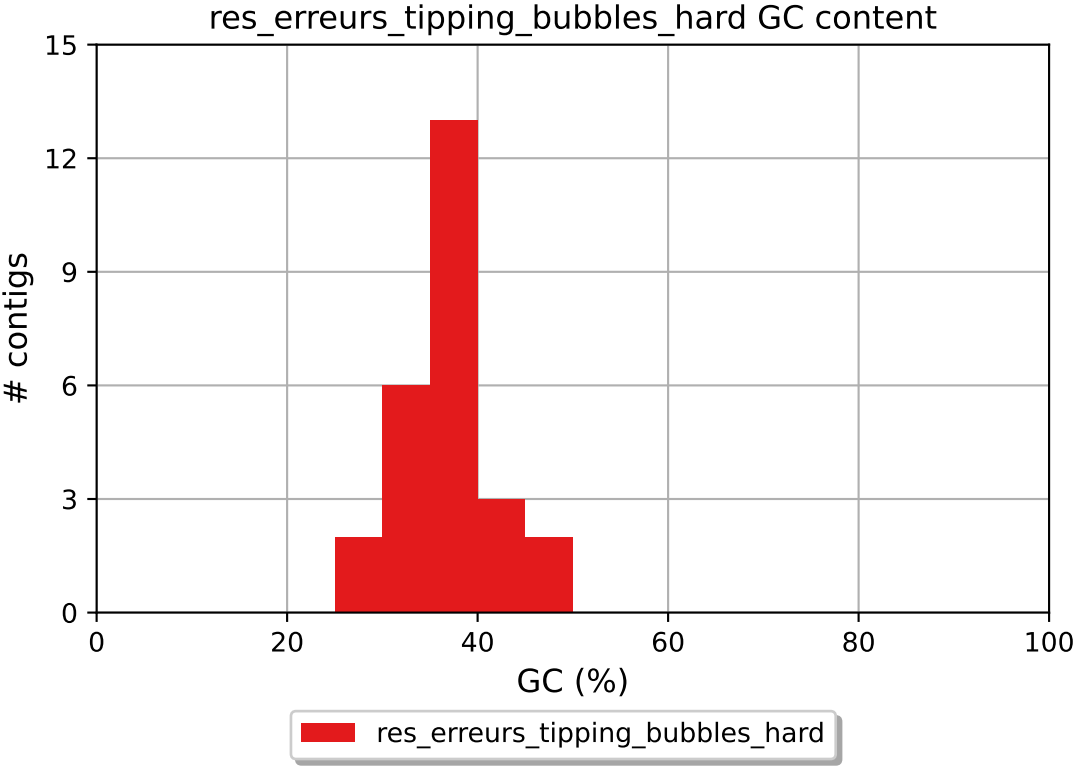
All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
res_erreurs_tipping_bubbles_hard

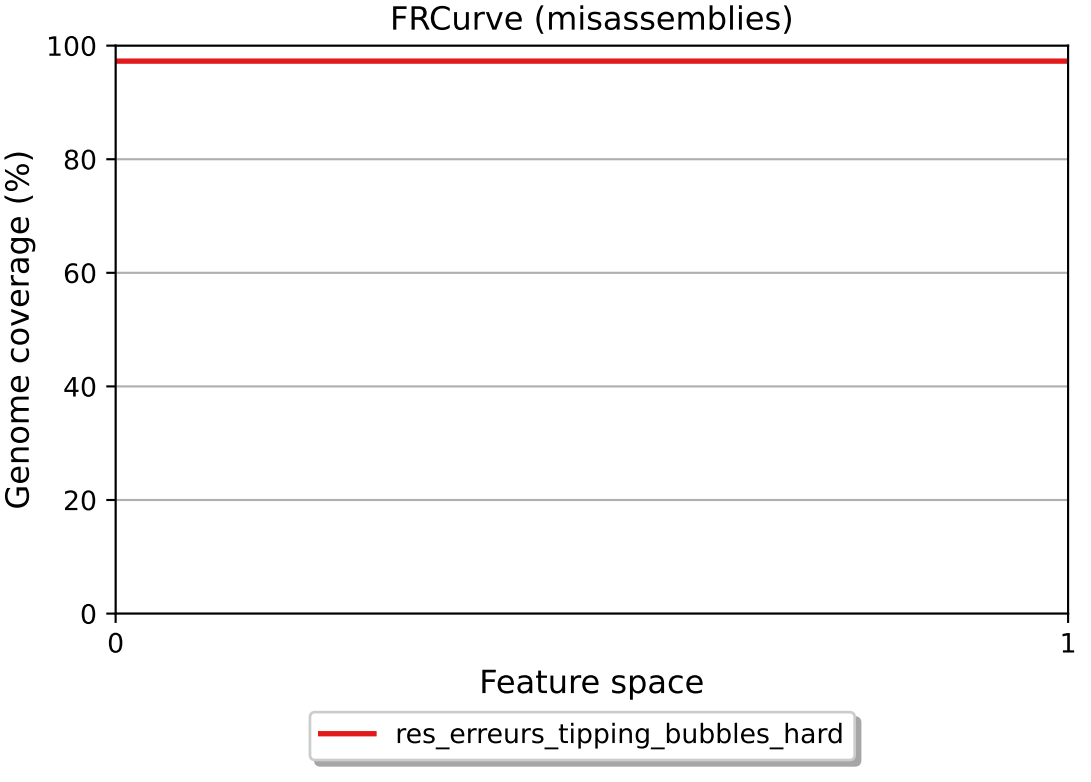

NGx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
res_erreurs_tipping_bubbles_hard

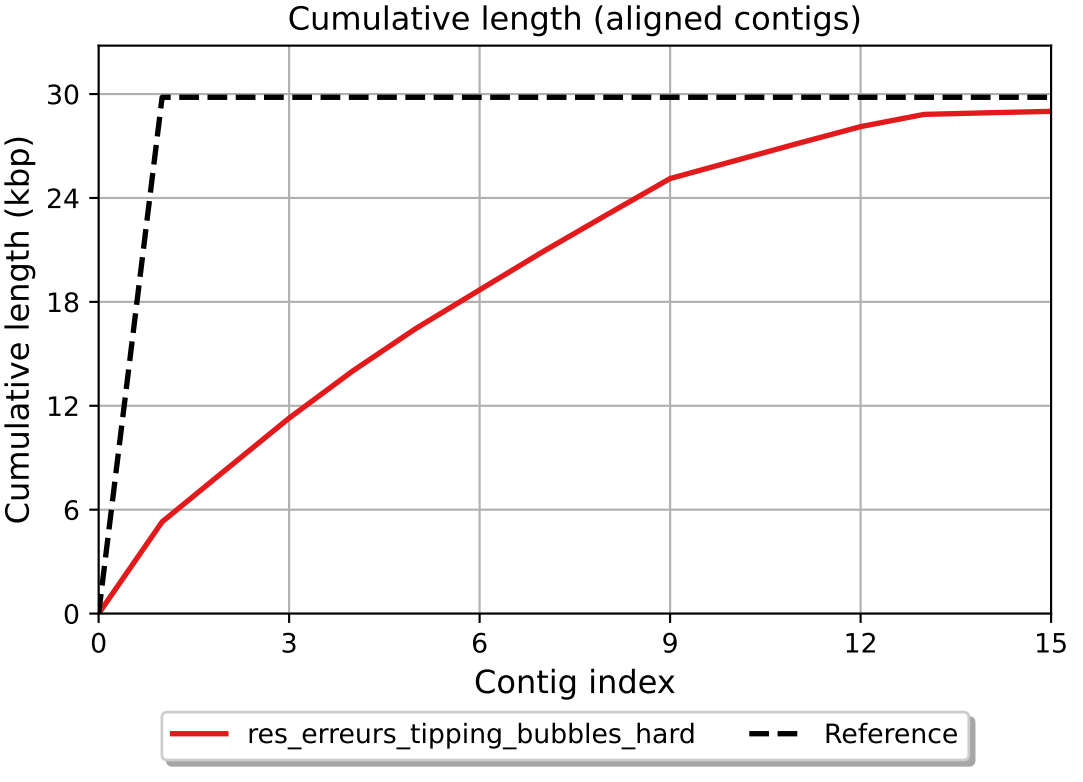

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
5
10
15
20
25
Contig index
res_erreurs_tipping_bubbles_hard
Reference

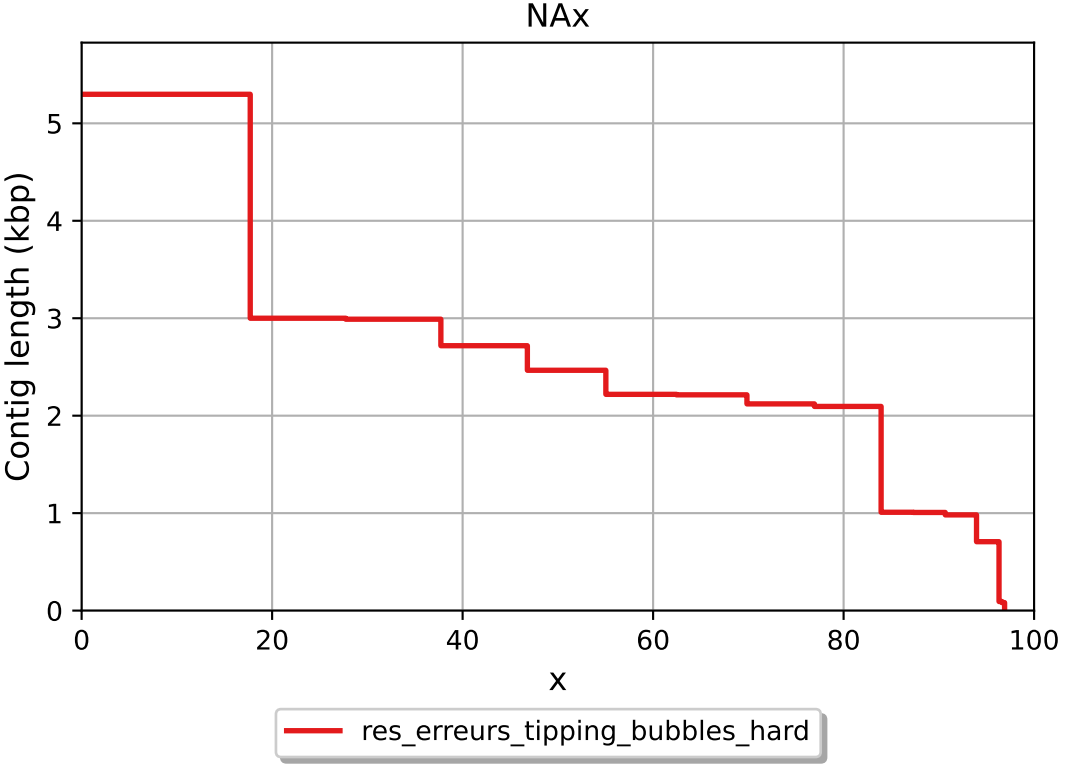

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
res_erreurs_tipping_bubbles_hard
Reference

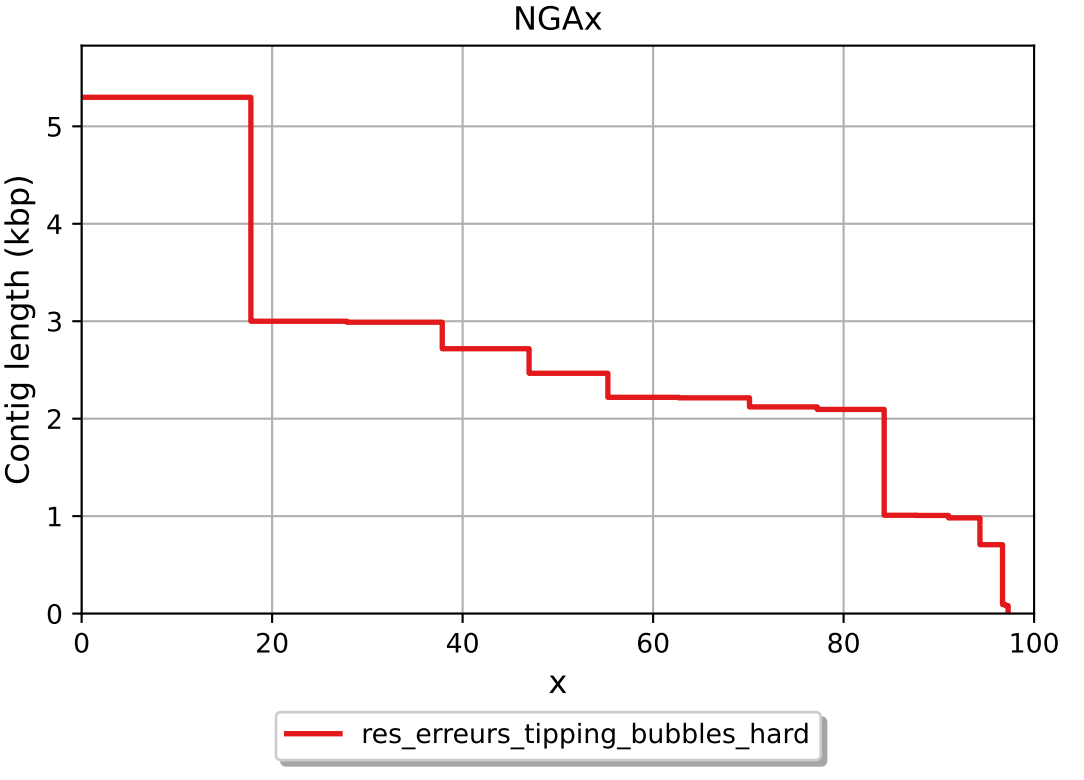

res_erreurs_tipping_bubbles_hard GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
res_erreurs_tipping_bubbles_hard

Misassemblies
5
4
3
2
1
0
res_erreurs_tipping_bubbles_hard


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
res_erreurs_tipping_bubbles_hard


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
3
6
9
12
15
Contig index
res_erreurs_tipping_bubbles_hard
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
res_erreurs_tipping_bubbles_hard


NGAx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
res_erreurs_tipping_bubbles_hard