

Report

	res_erreurs_tipping_bubbles
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	43
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8
Largest contig	18475
Total length	48682
Reference length	48576
GC (%)	49.87
Reference GC (%)	49.87
N50	15785
NG50	15785
N75	10899
NG75	10899
L50	2
LG50	2
L75	3
LG75	3
# 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	4 + 0 part
Unaligned length	137
Genome fraction (%)	99.813
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	18475
Total aligned length	48545
NA50	15785
NGA50	15785
NA75	10899
NGA75	10899
LA50	2
LGA50	2
LA75	3
LGA75	3

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
# 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	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

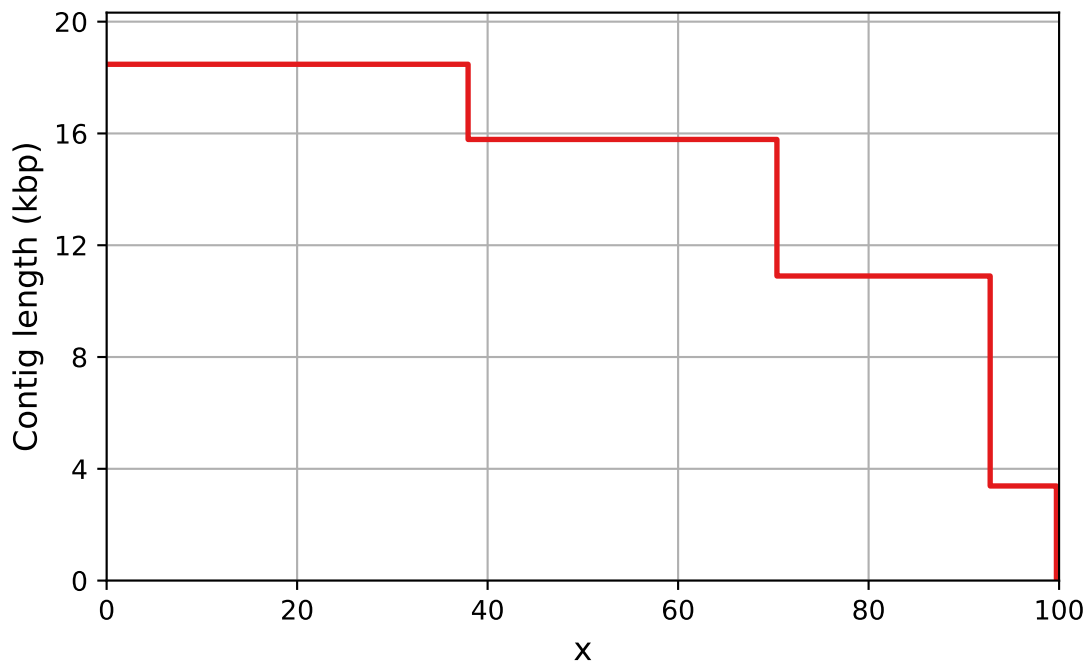
All statistics are based on contigs of size ≥ 31 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	res_erreurs_tipping_bubbles
# fully unaligned contigs	4
Fully unaligned length	137
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

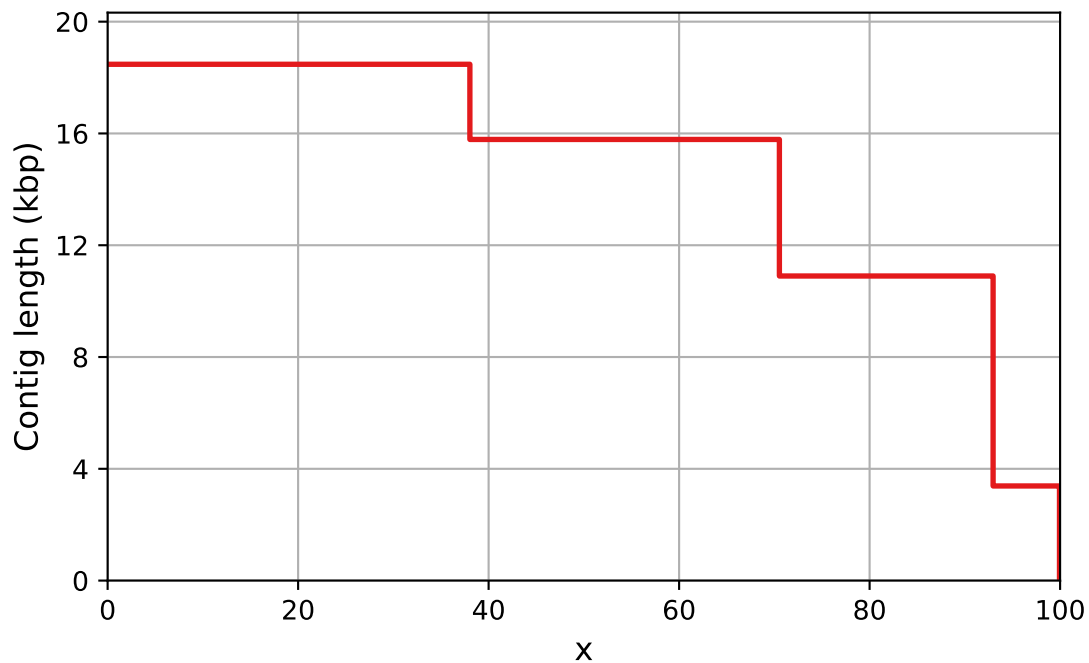
All statistics are based on contigs of size ≥ 31 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



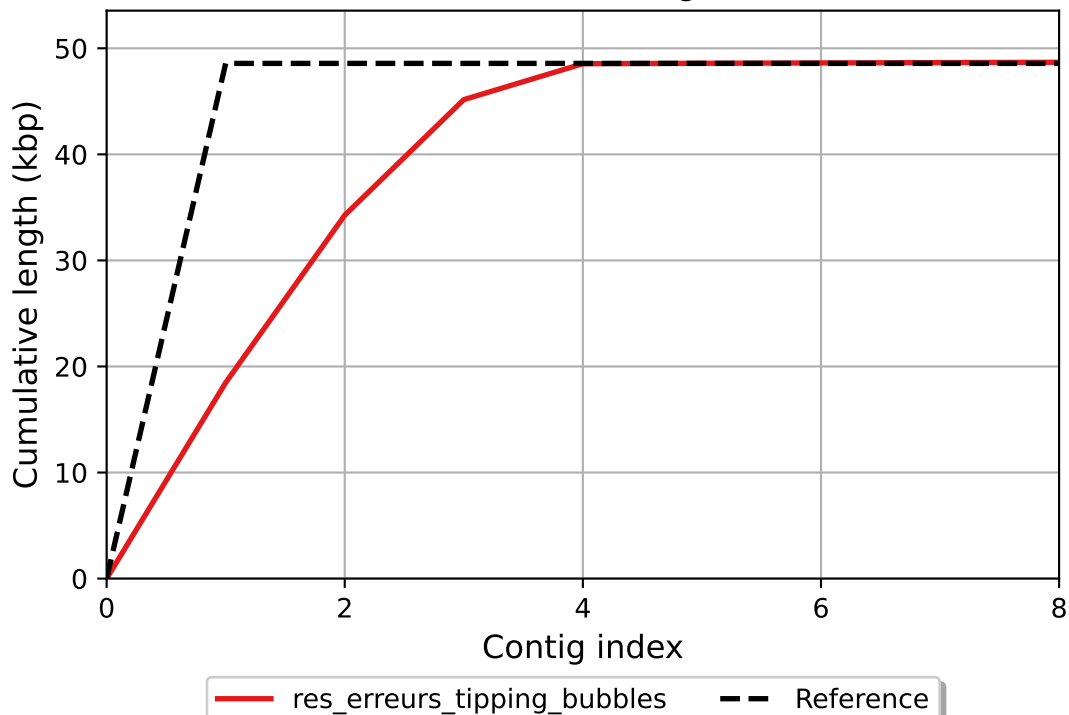
— reserreurs_tipping_bubbles

NGx

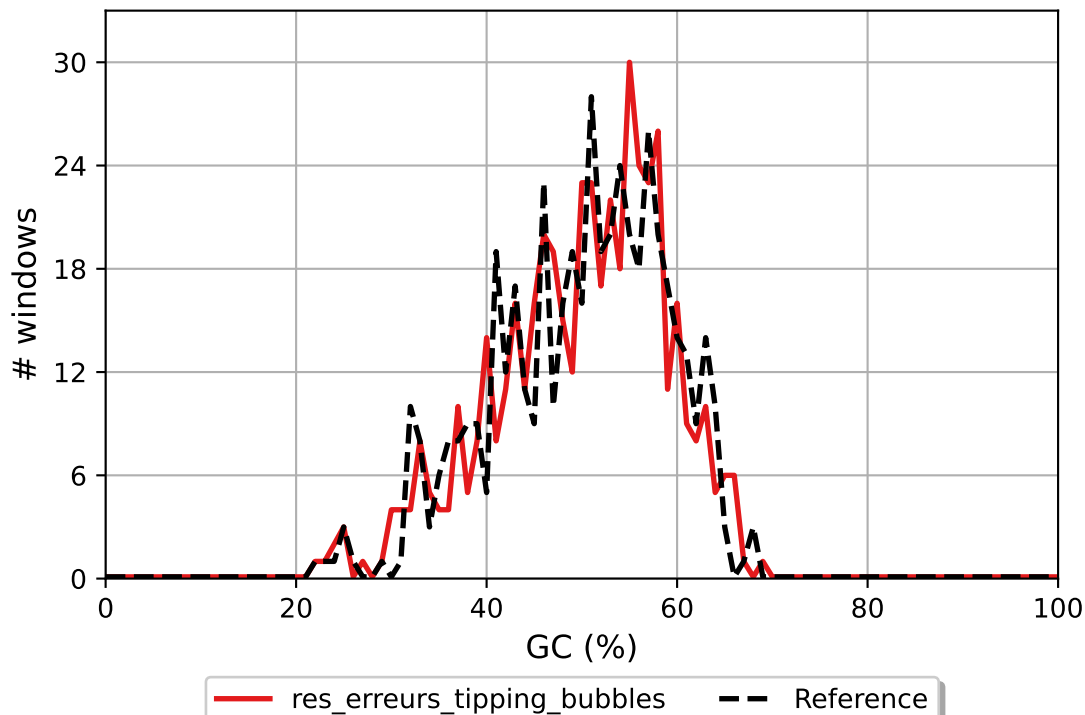


— reserreurs_tipping_bubbles

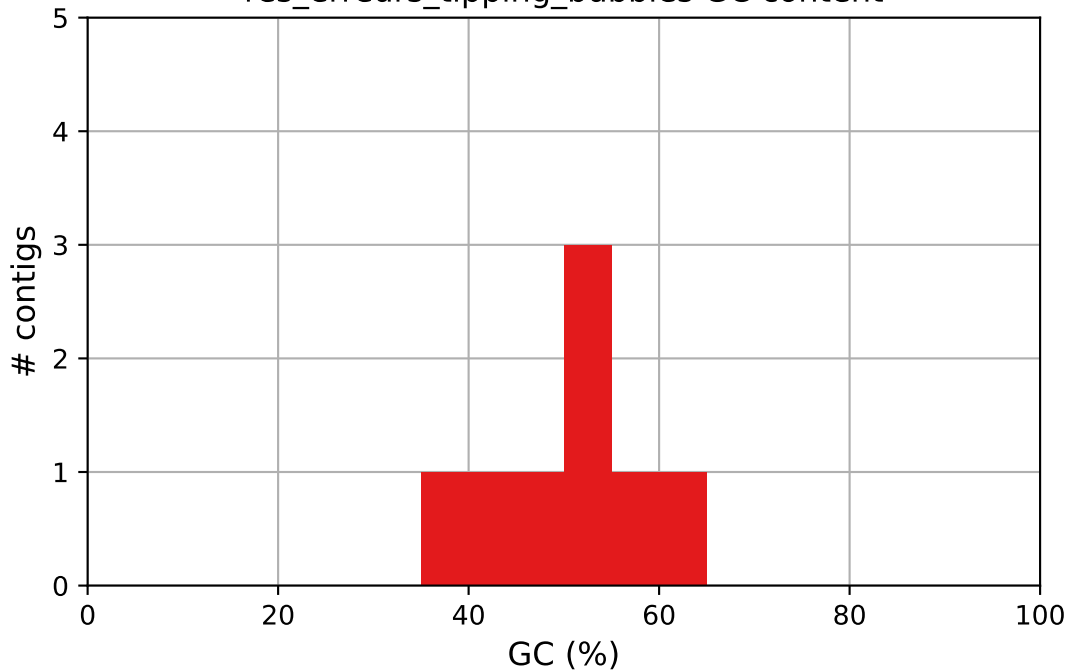
Cumulative length



GC content

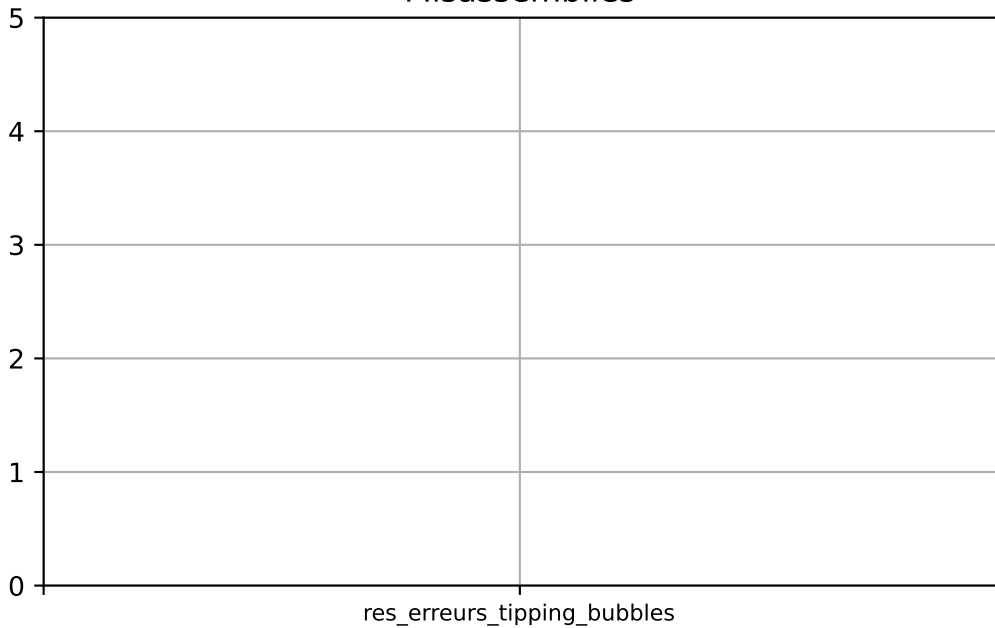


res_erreurs_tipping_bubbles GC content

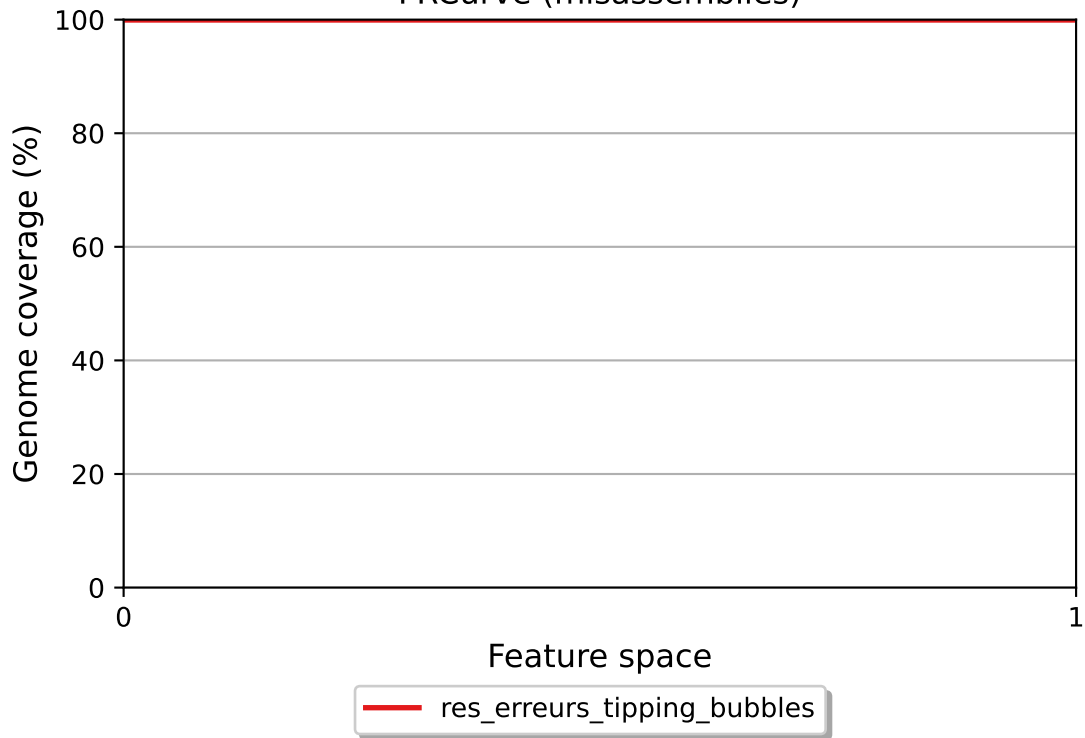


res_erreurs_tipping_bubbles

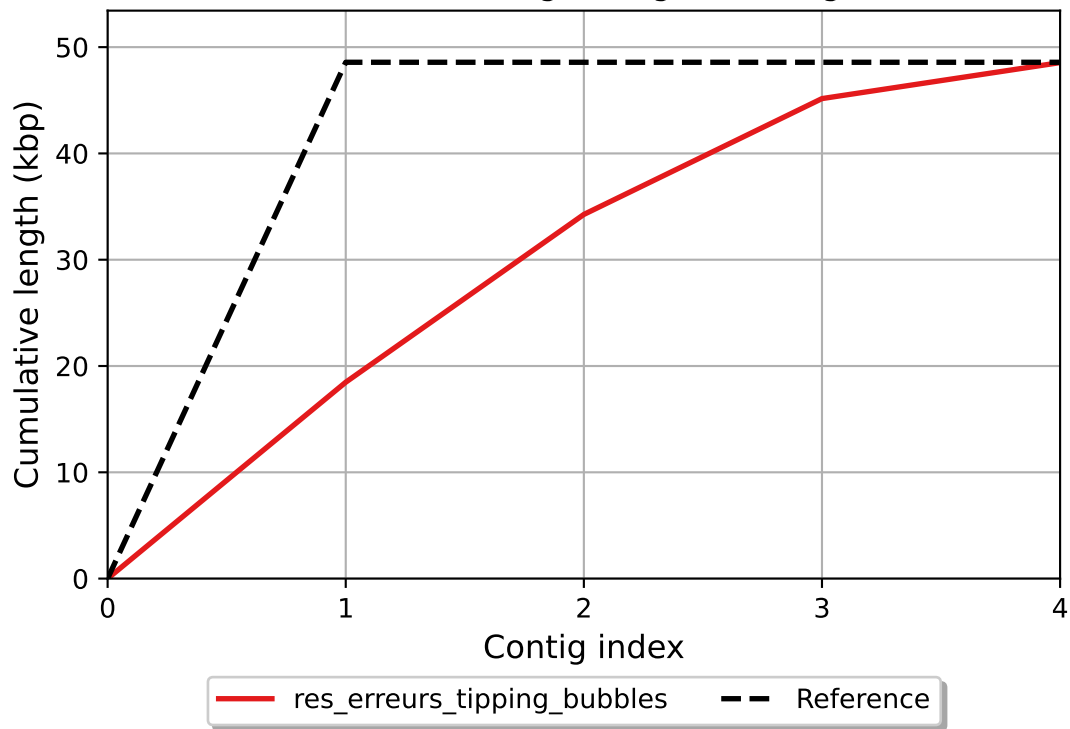
Misassemblies



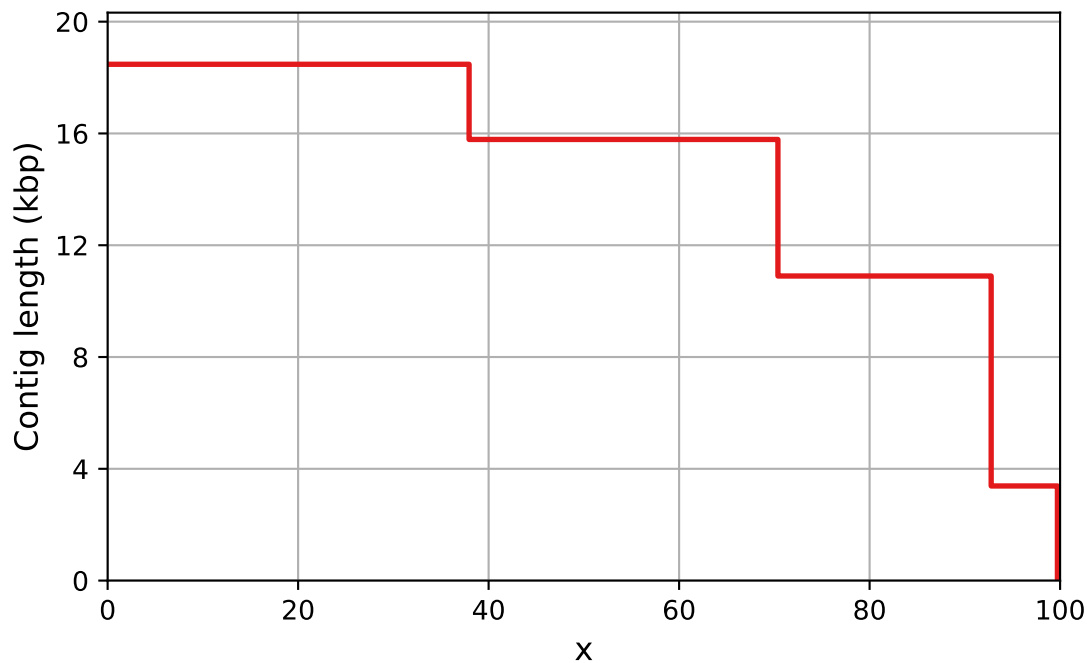
FRCurve (misassemblies)



Cumulative length (aligned contigs)

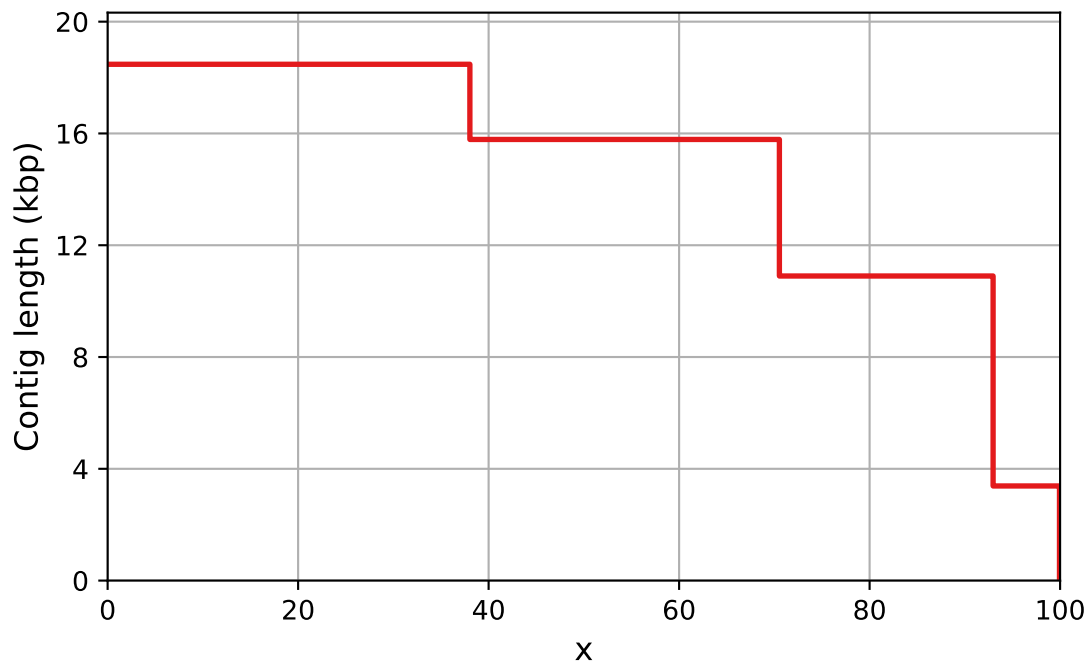


NAx



— reserreurs_tipping_bubbles

NGAx



— reserreurs_tipping_bubbles