

Report

	res_erreurs_tipping_bubbles_medium
# 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)	31
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	10
Largest contig	8848
Total length	30268
Reference length	29814
GC (%)	38.05
Reference GC (%)	38.01
N50	4493
NG50	4493
N75	3254
NG75	3254
L50	3
LG50	3
L75	5
LG75	5
# 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	3 + 0 part
Unaligned length	128
Genome fraction (%)	99.524
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.11
# indels per 100 kbp	6.74
Largest alignment	8716
Total aligned length	29688
NA50	4373
NGA50	4373
NA75	3226
NGA75	3226
LA50	3
LGA50	3
LA75	5
LGA75	5

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_medium
# 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

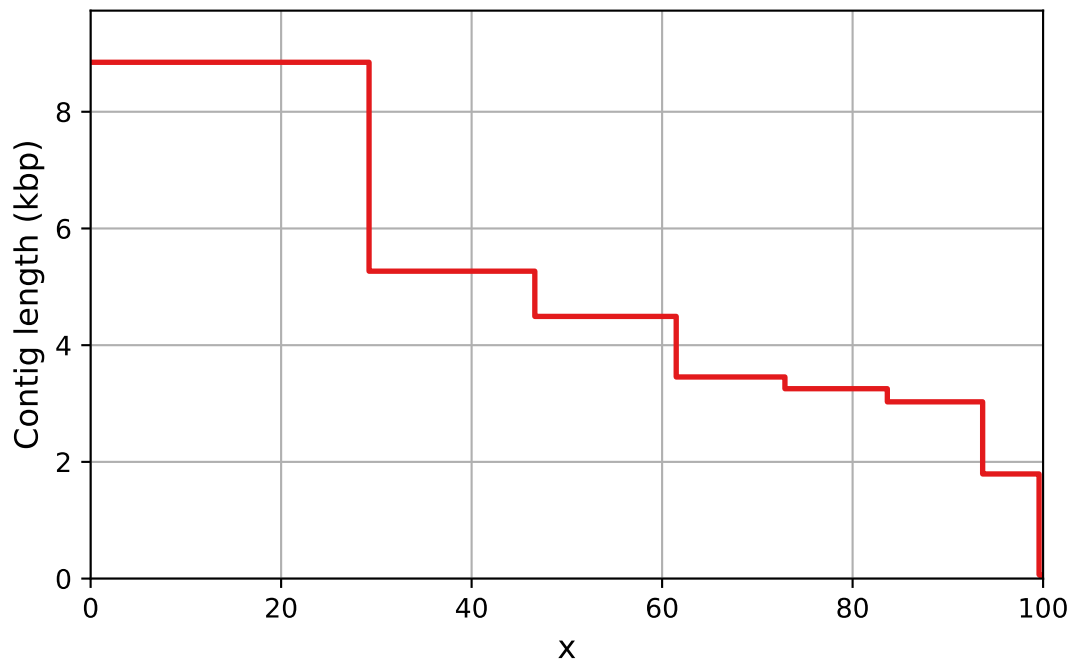
All statistics are based on contigs of size ≥ 31 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	res_erreurs_tipping_bubbles_medium
# fully unaligned contigs	3
Fully unaligned length	128
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

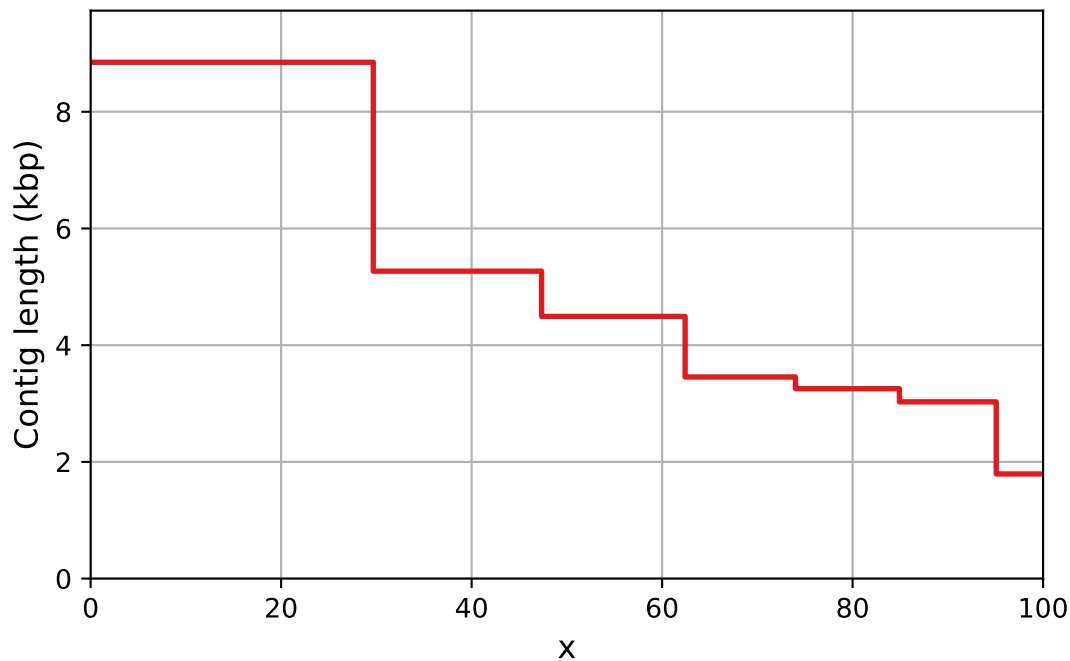
All statistics are based on contigs of size ≥ 31 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



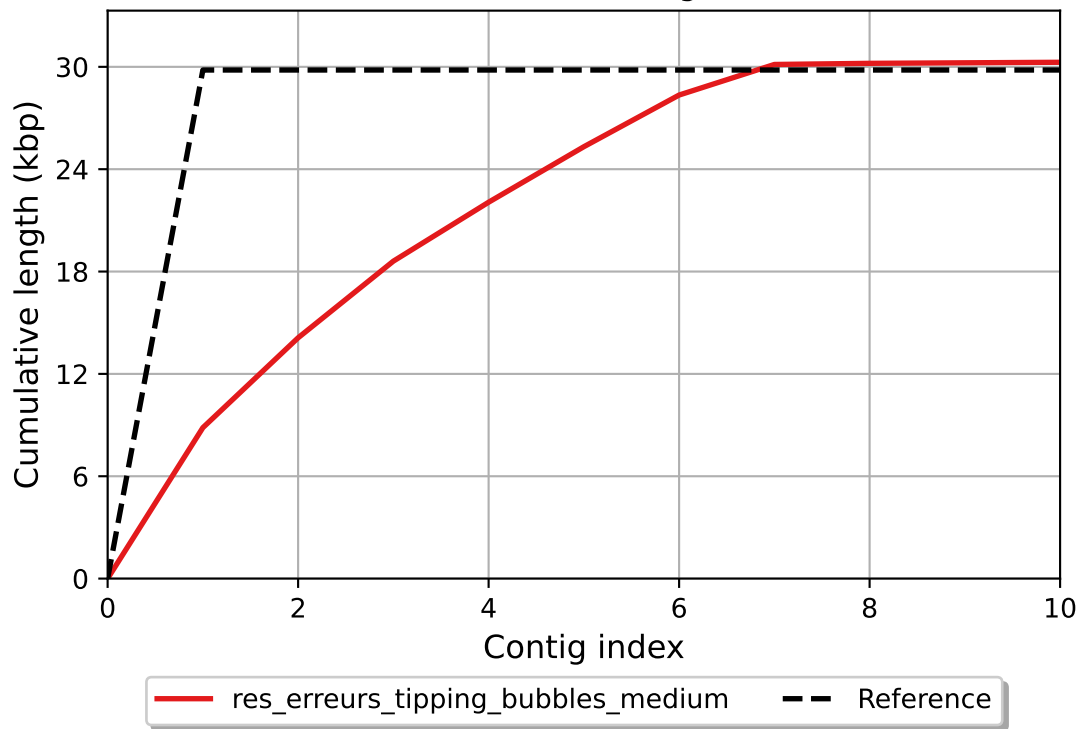
res_erreurs_tipping_bubbles_medium

NGx

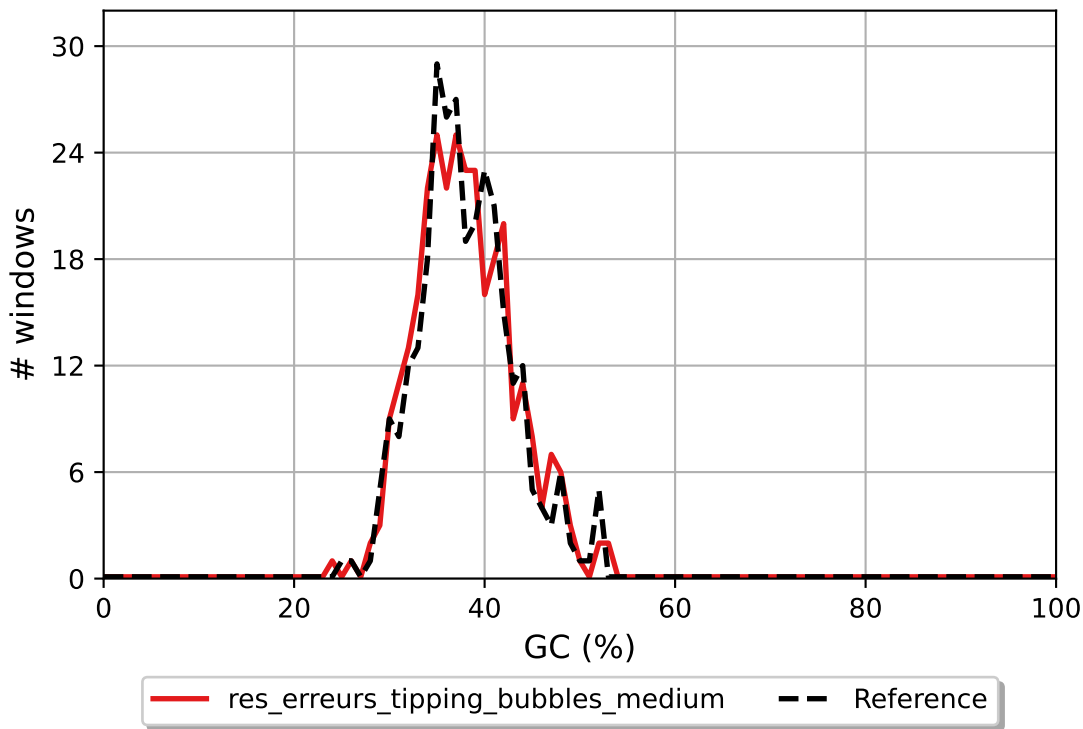


res_erreurs_tipping_bubbles_medium

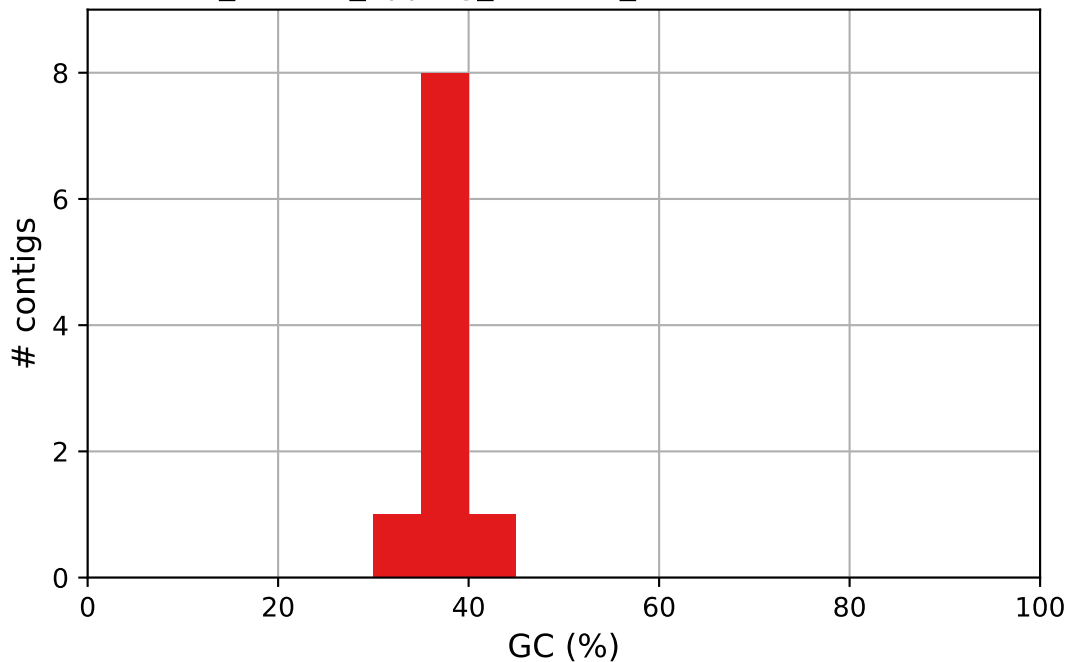
Cumulative length



GC content

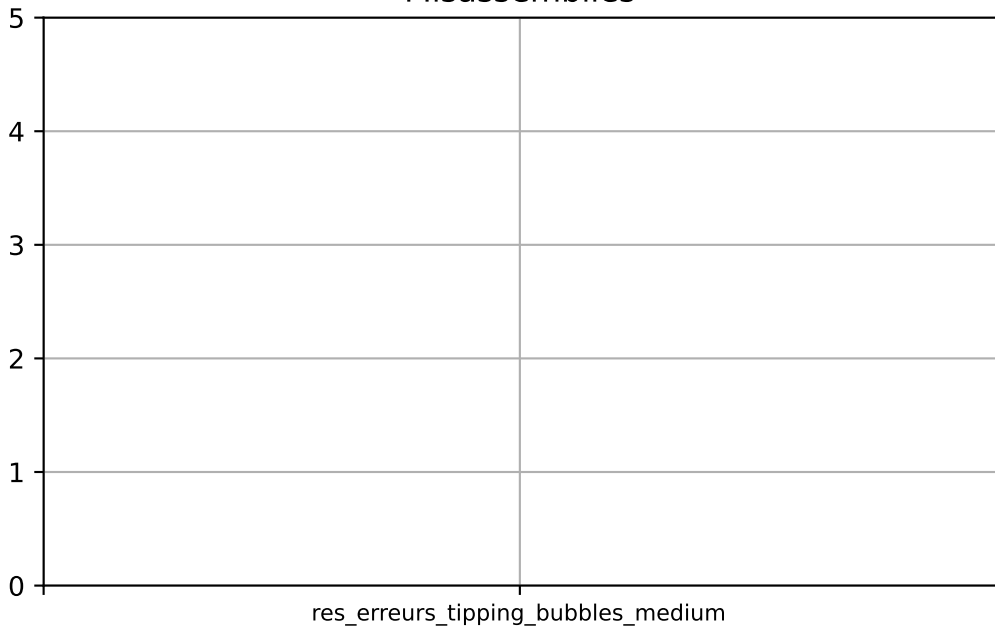


res_erreurs_tipping_bubbles_medium GC content



res_erreurs_tipping_bubbles_medium

Misassemblies

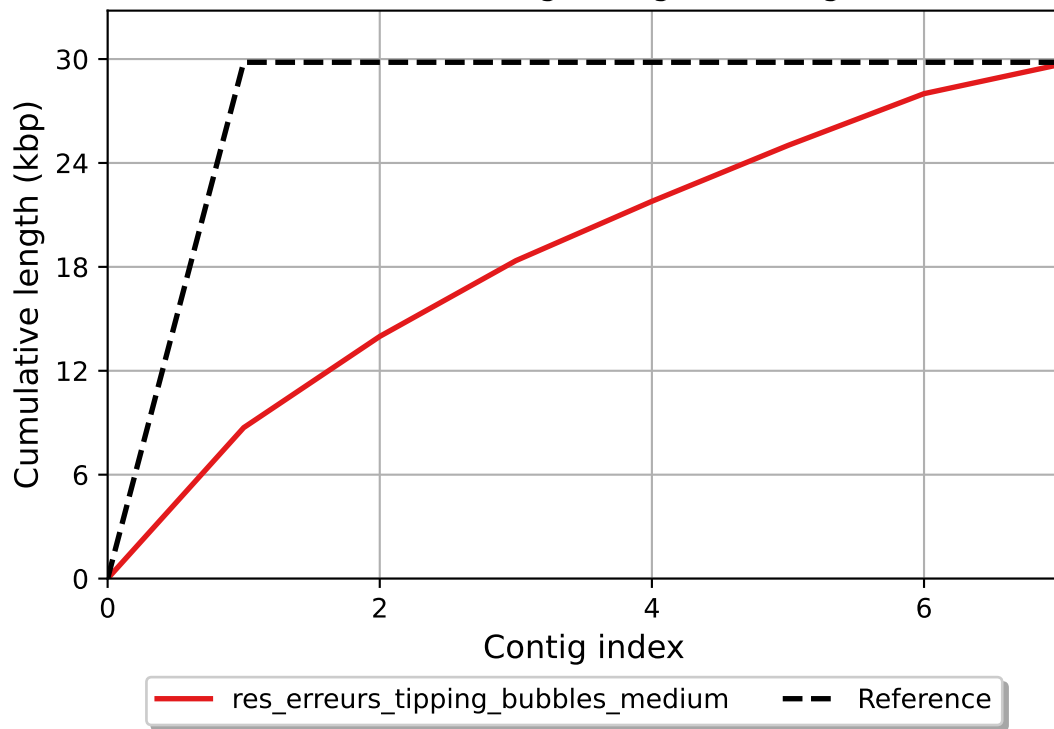


FRCurve (misassemblies)

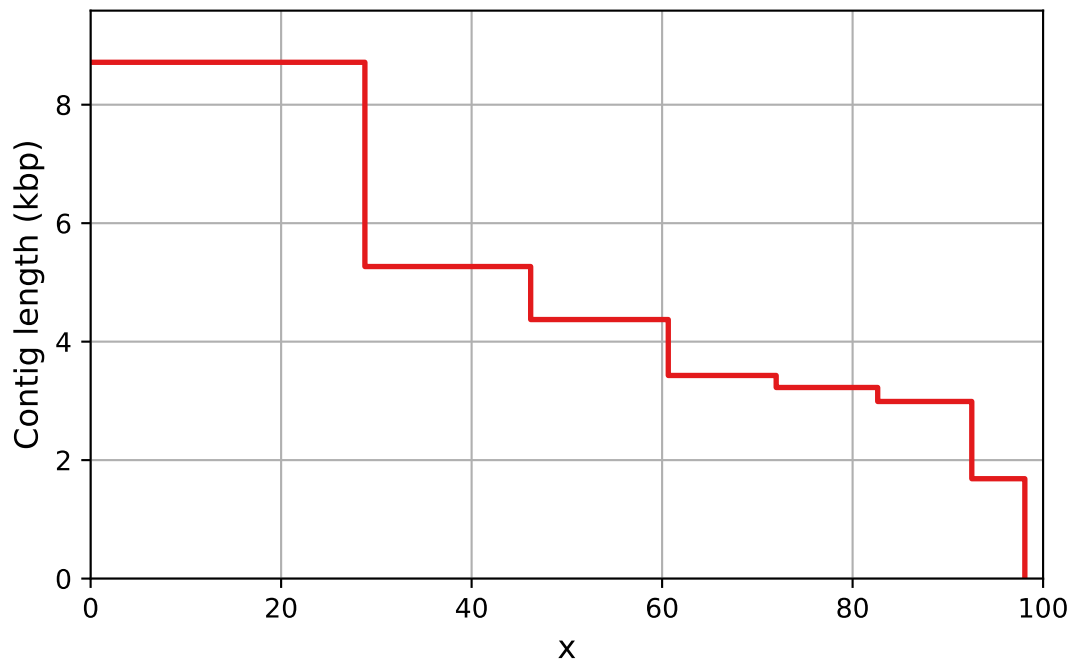


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Cumulative length (aligned contigs)

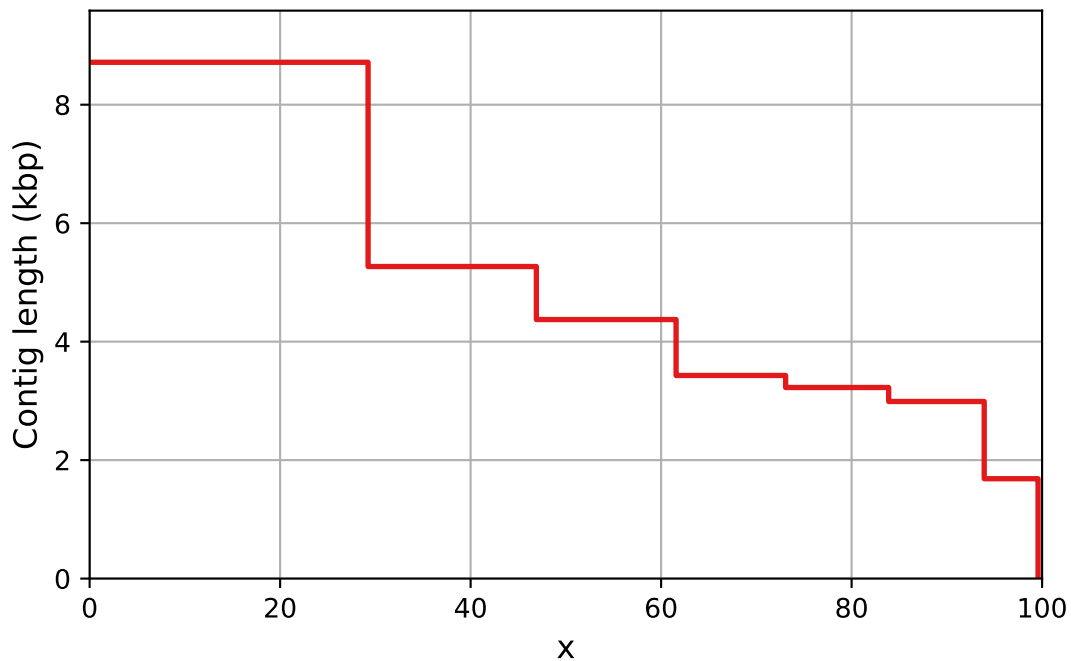


NAx



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NGAx



reserreurs_tipping_bubbles_medium