

Report

	sortie_sequencagesserreur
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	45123
Total length (>= 1000 bp)	45123
Total length (>= 5000 bp)	45123
Total length (>= 10000 bp)	45123
Total length (>= 25000 bp)	45123
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	45123
Total length	45123
Reference length	48576
GC (%)	49.54
Reference GC (%)	49.87
N50	45123
NG50	45123
N75	45123
NG75	45123
L50	1
LG50	1
L75	1
LG75	1
# 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	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.850
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	2.22
Largest alignment	45123
Total aligned length	45123
NA50	45123
NGA50	45123
NA75	45123
NGA75	45123
LA50	1
LGA50	1
LA75	1
LGA75	1

All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	sortie_sequencageserreur
# 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	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	20

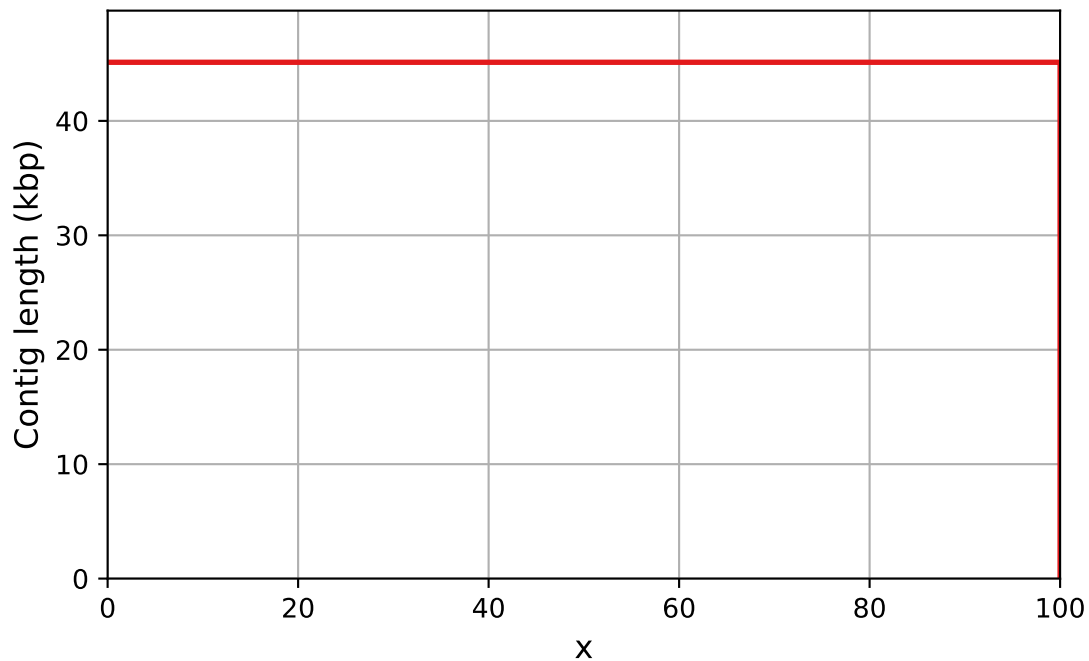
All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sortie_sequencagesserreur
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

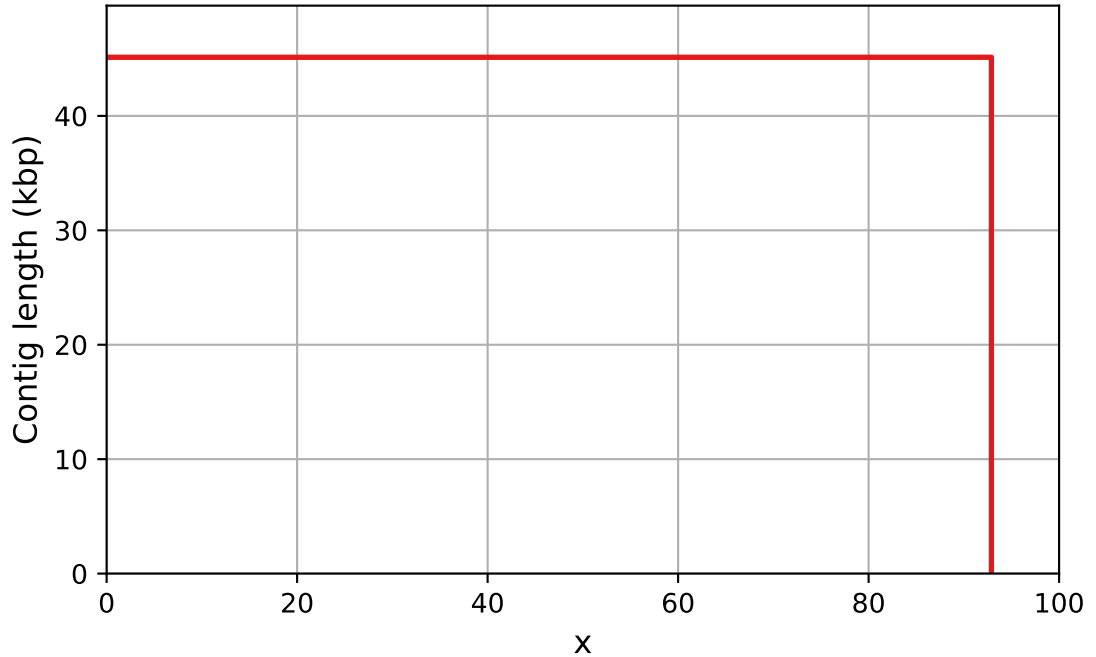
All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



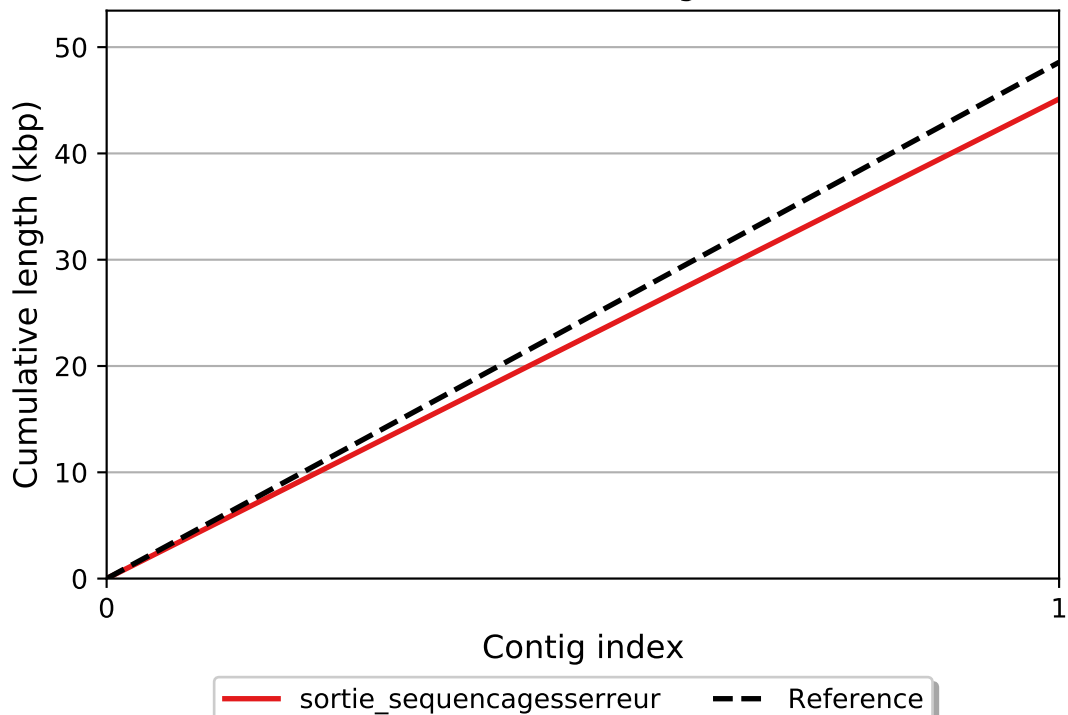
— sortie_sequencagesserreur

NGx

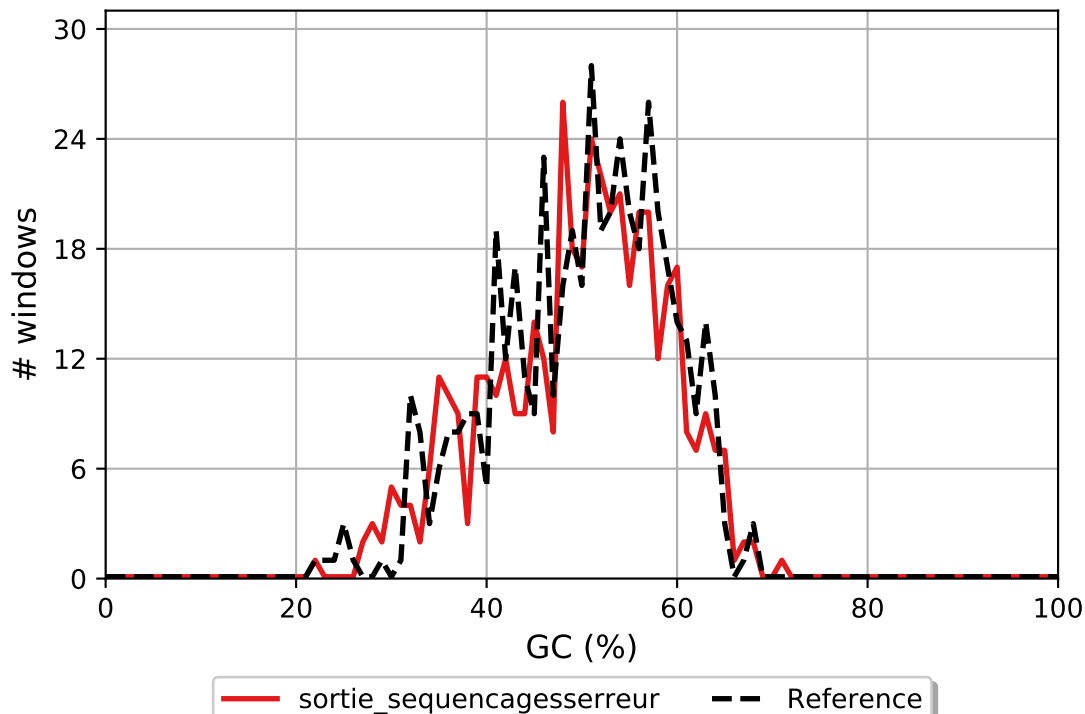


— sortie_sequencagesserreur

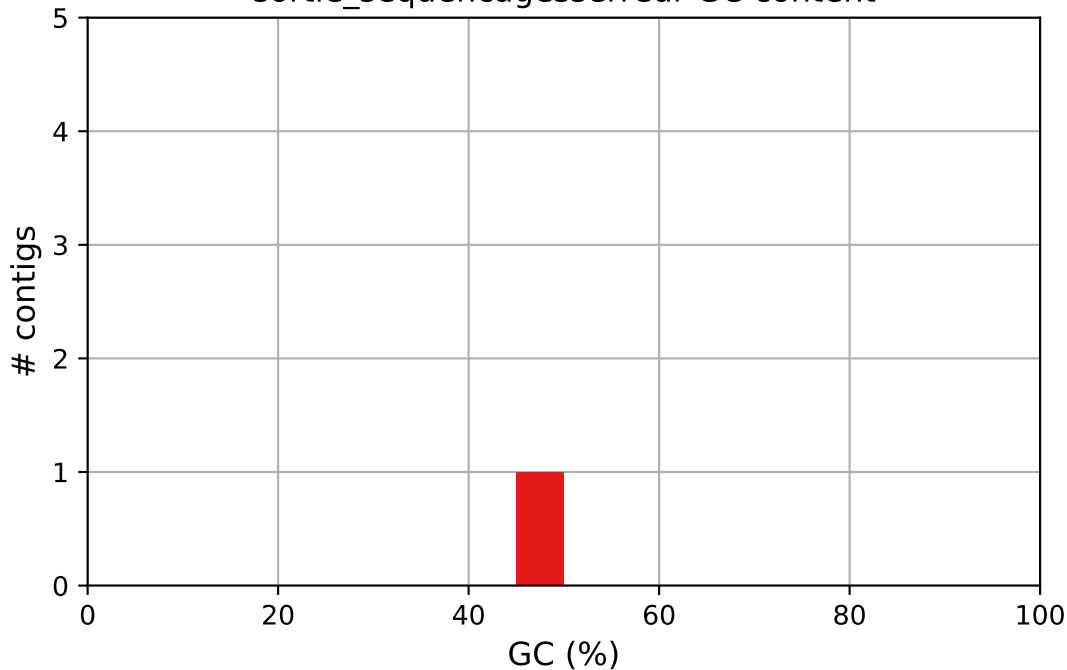
Cumulative length



GC content



sortie_sequencagesserreur GC content

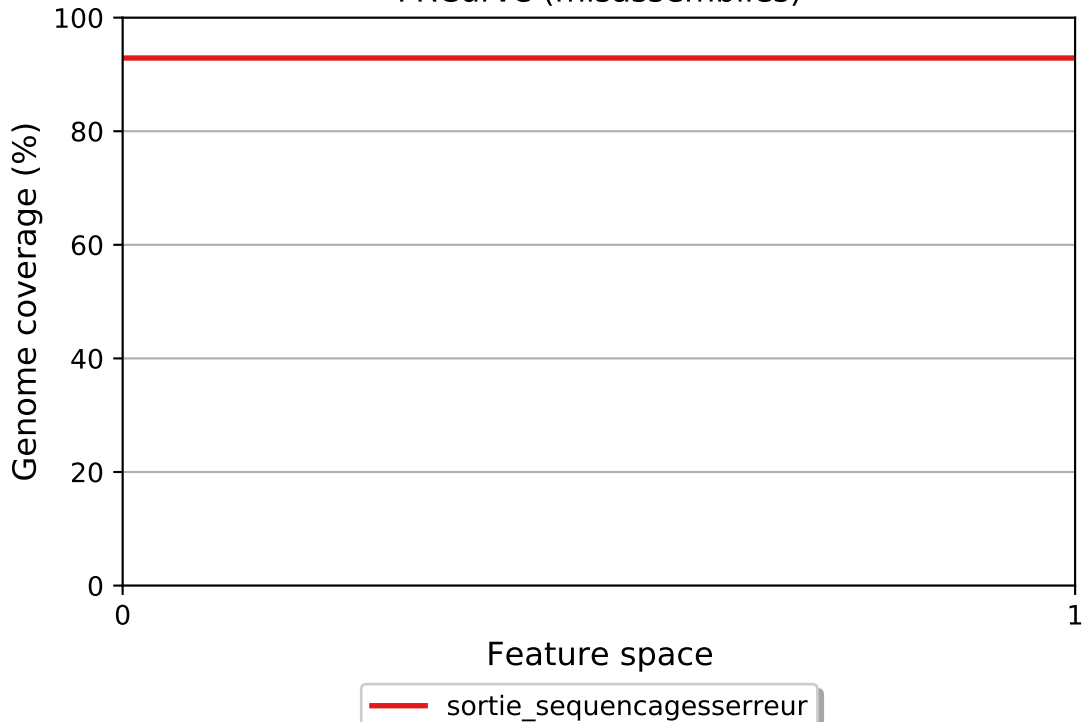


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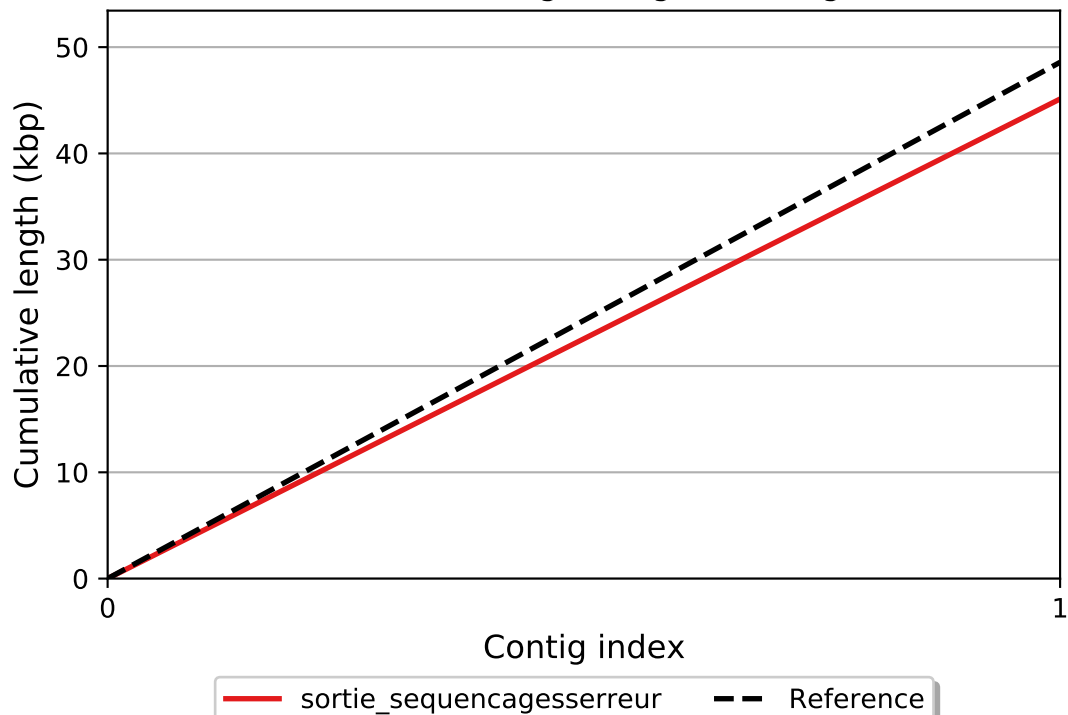
Misassemblies



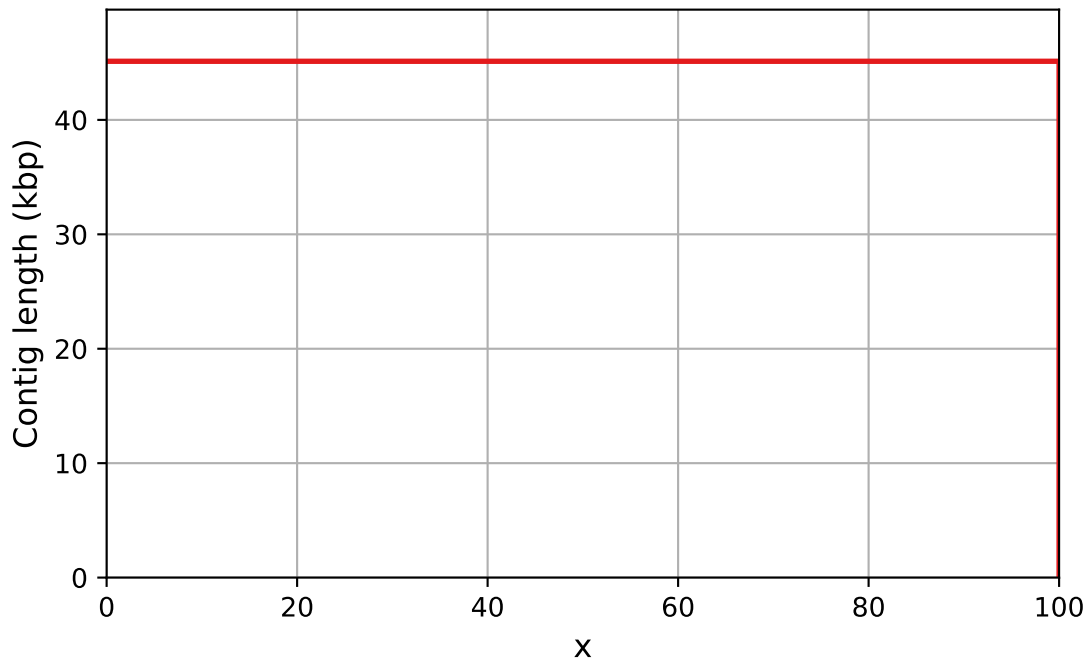
FRCurve (misassemblies)



Cumulative length (aligned contigs)

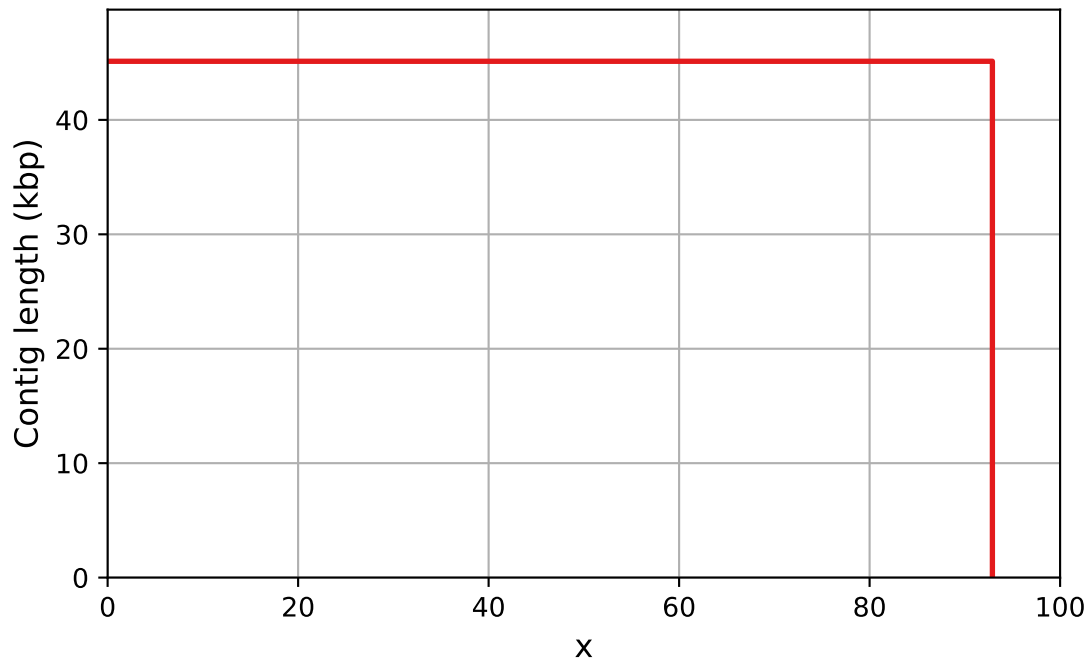


NAx



— sortie_sequencagesserreur

NGAx



— sortie_sequencagesserreur