

Report

	contigs_k35
# 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)	1020
Total length (>= 1000 bp)	1020
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	1020
Total length	1020
Reference length	1040
GC (%)	51.37
Reference GC (%)	51.25
N50	1020
NG50	1020
N90	1020
NG90	1020
auN	1020.0
auNG	1000.4
L50	1
LG50	1
L90	1
LG90	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 (%)	100.000
Duplication ratio	0.981
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	98.04
Largest alignment	1020
Total aligned length	1020
NA50	1020
NGA50	1020
NA90	1020
NGA90	1020
auNA	1020.0
auNGA	1000.4
LA50	1
LGA50	1
LA90	1
LGA90	1

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

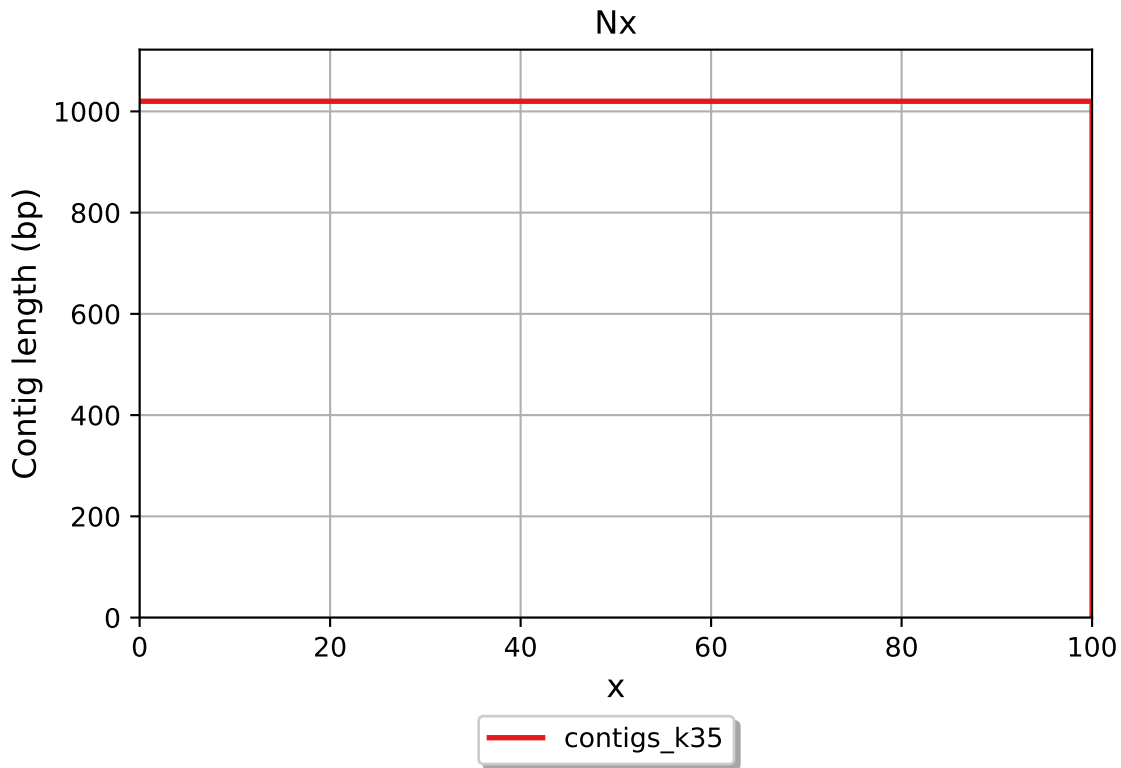
	contigs_k35
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

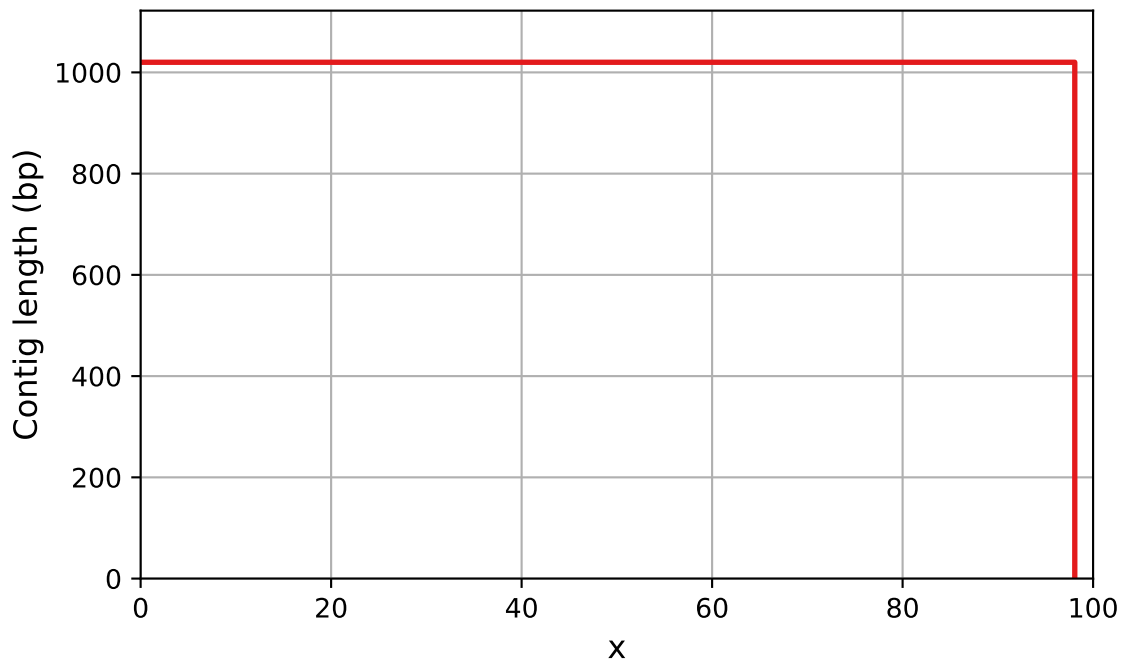
## Unaligned report

	contigs_k35
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

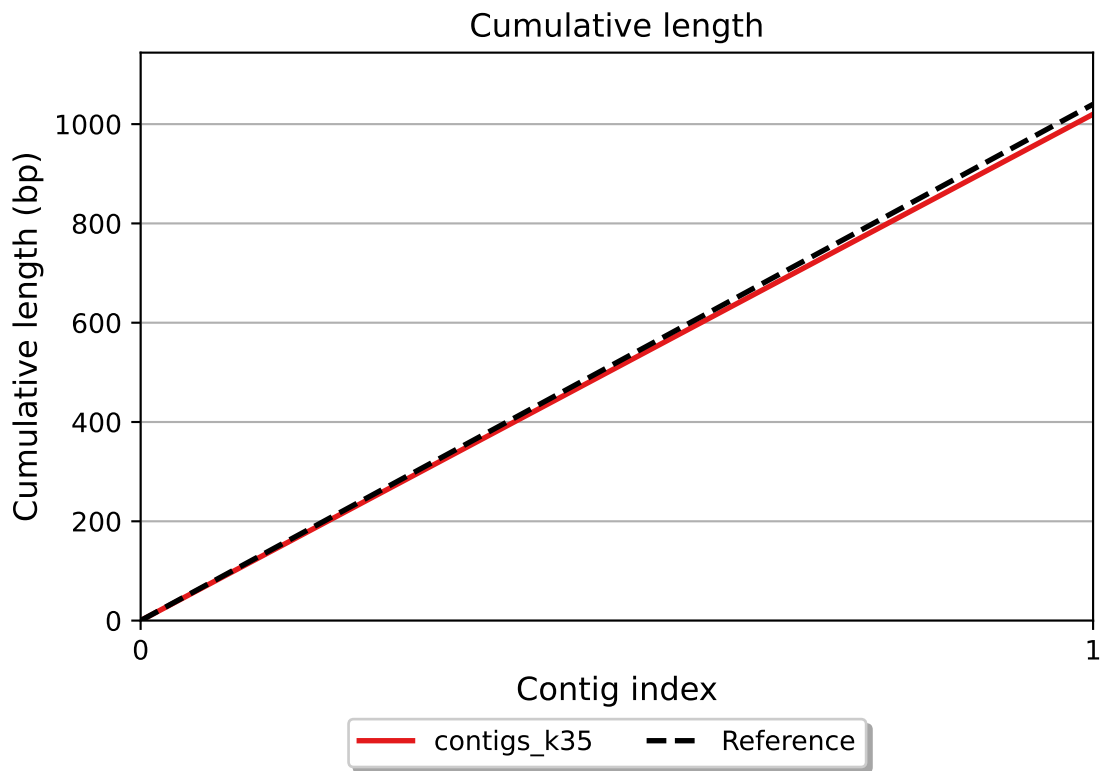
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



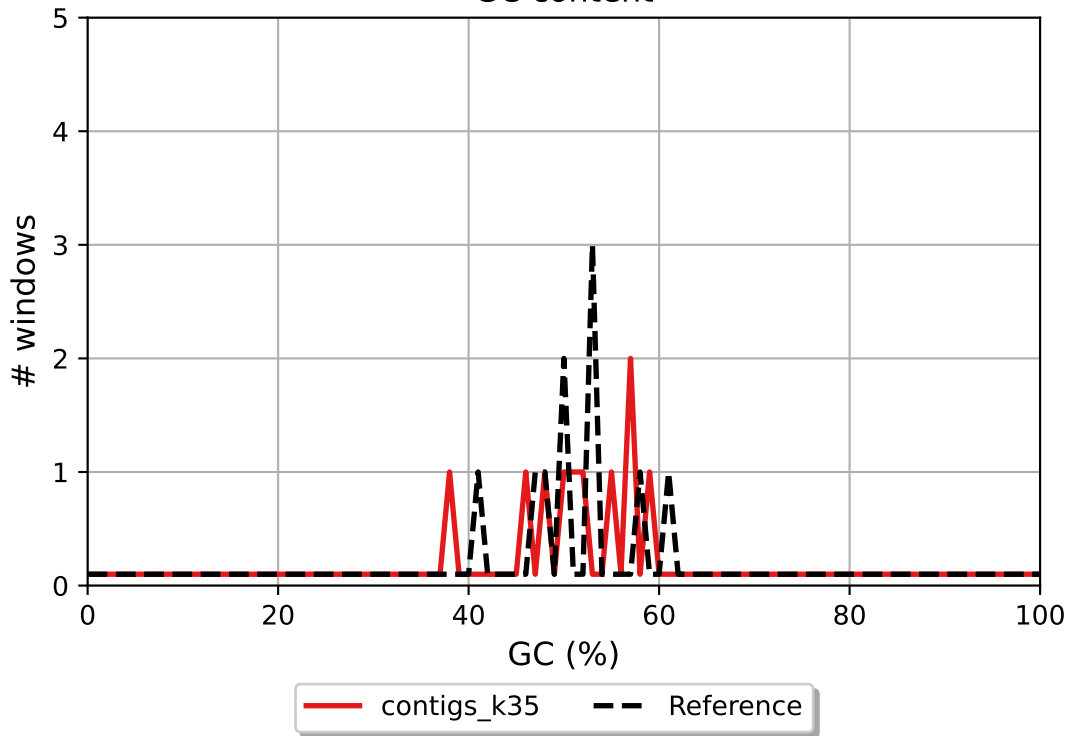
NGx



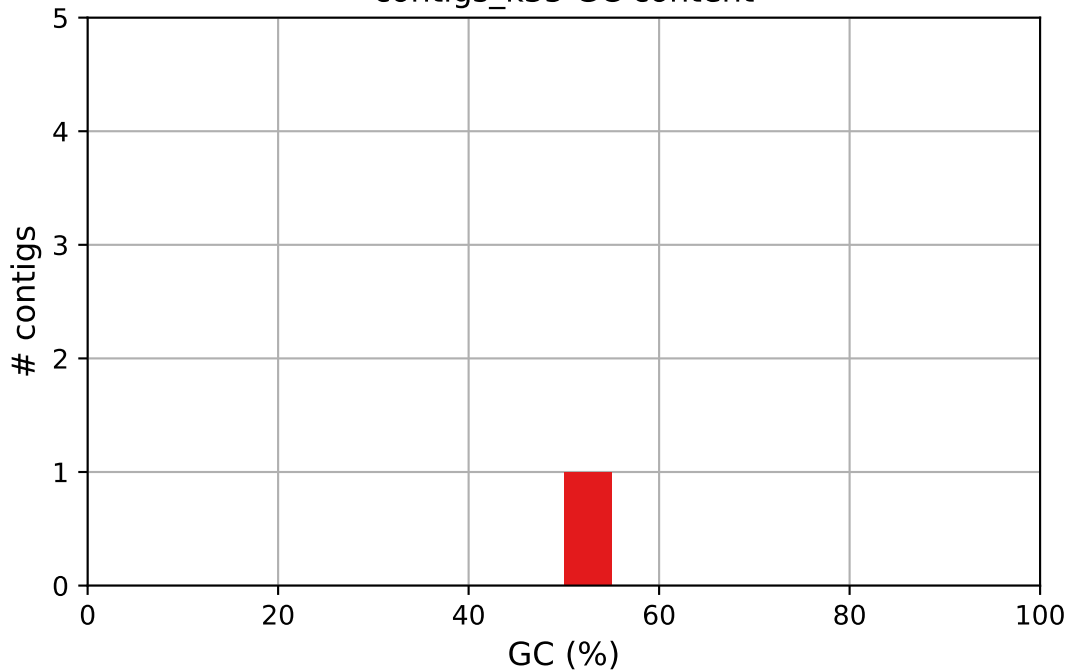
contigs\_k35



# GC content



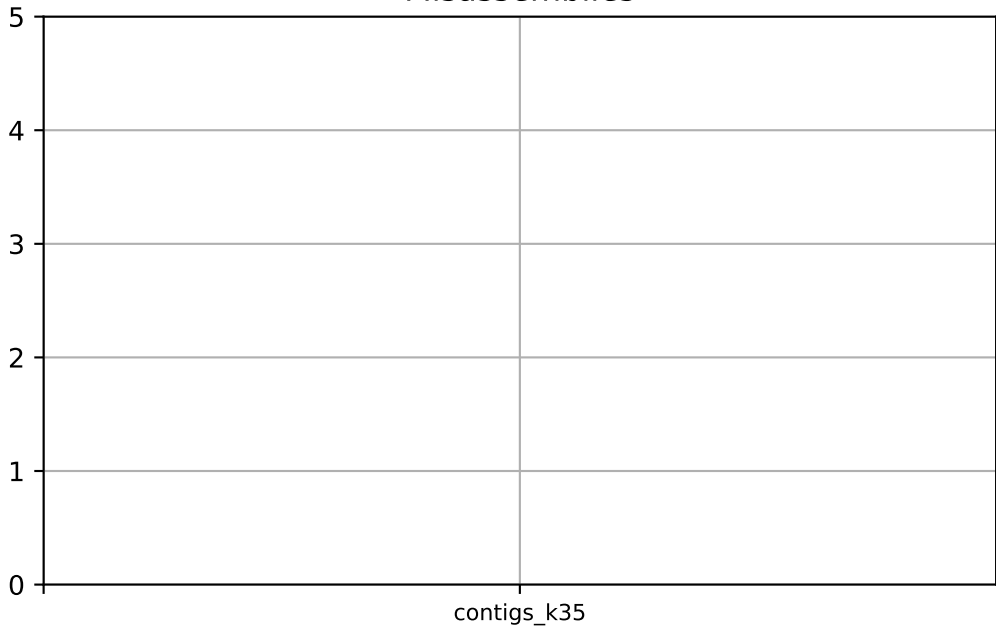
contigs\_k35 GC content



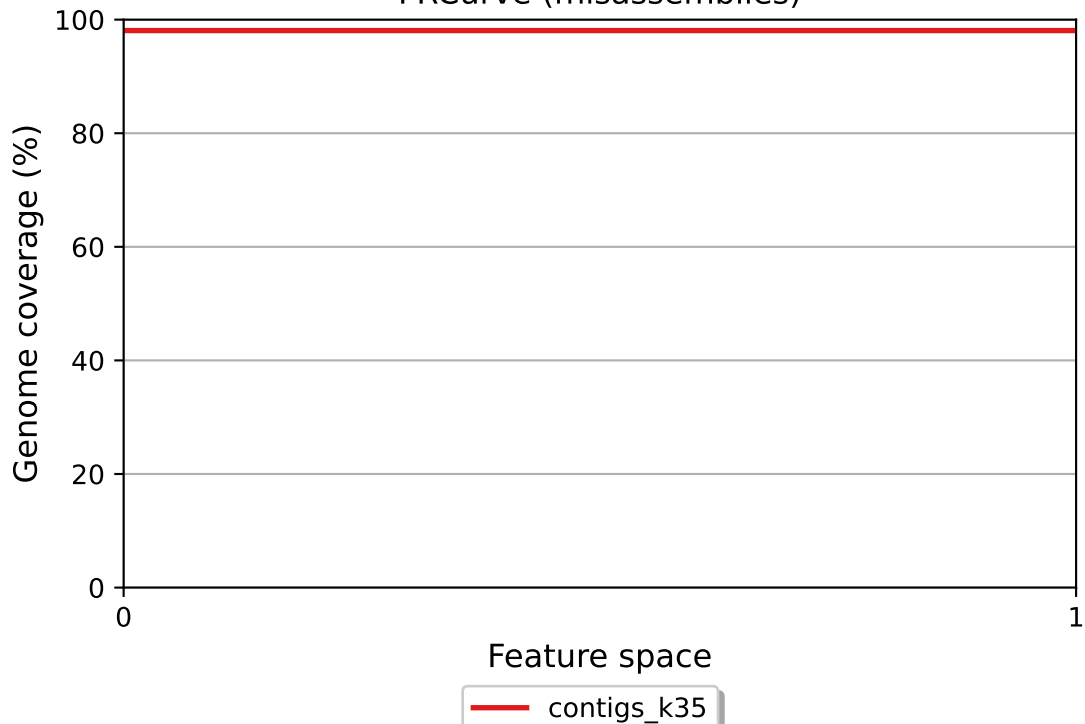
contigs\_k35



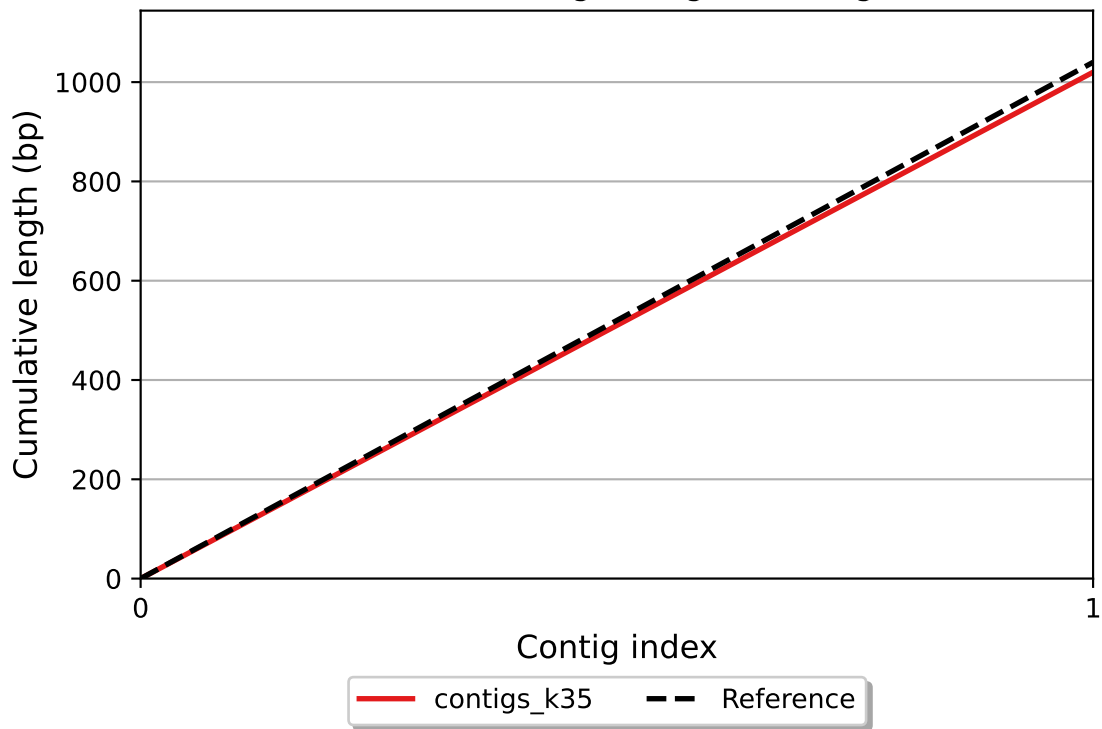
# Misassemblies



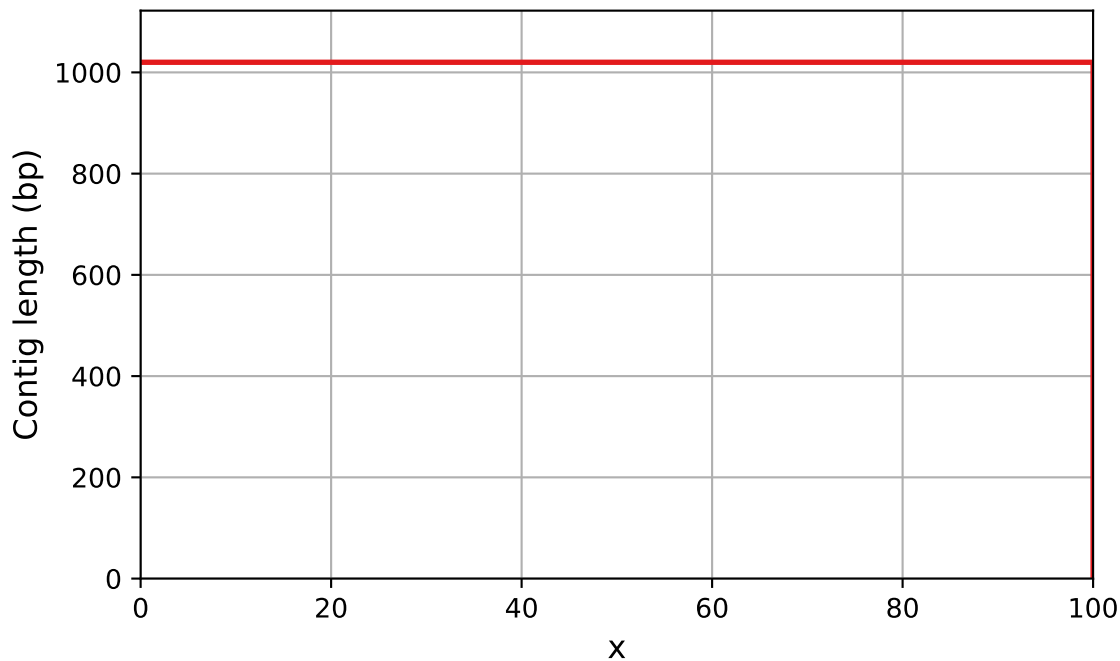
FRCurve (misassemblies)



Cumulative length (aligned contigs)

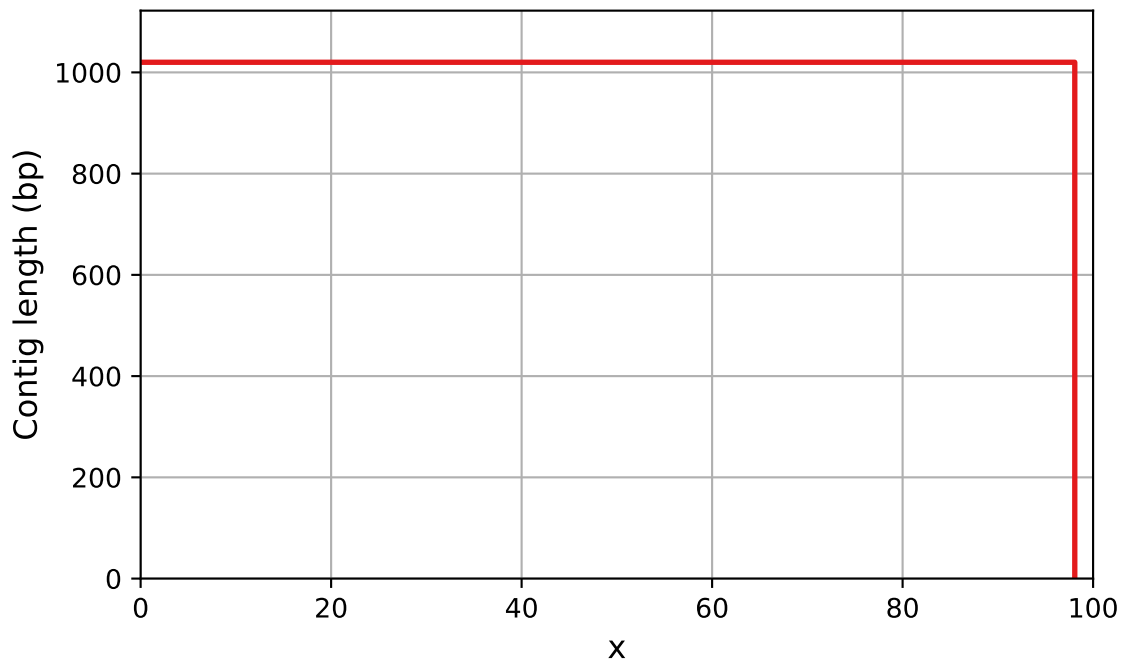


NAx



— contigs\_k35

# NGAx



contigs\_k35