

Report

	mini-ava-pb_10
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	4234782
Total length (>= 1000 bp)	4234782
Total length (>= 5000 bp)	4234782
Total length (>= 10000 bp)	4234782
Total length (>= 25000 bp)	4234782
Total length (>= 50000 bp)	4234782
# contigs	17
Largest contig	897414
Total length	4234782
Reference length	4686137
GC (%)	50.78
Reference GC (%)	50.78
N50	309908
NG50	303237
N90	98806
NG90	58230
auN	448603.3
auNG	405395.1
L50	4
LG50	5
L90	12
LG90	17
# 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 (%)	89.032
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.19
Largest alignment	897414
Total aligned length	4234782
NA50	309908
NGA50	303237
NA90	98806
NGA90	58230
auNA	448603.3
auNGA	405395.1
LA50	4
LGA50	5
LA90	12
LGA90	17

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

	mini-ava-pb_10
# 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	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	11

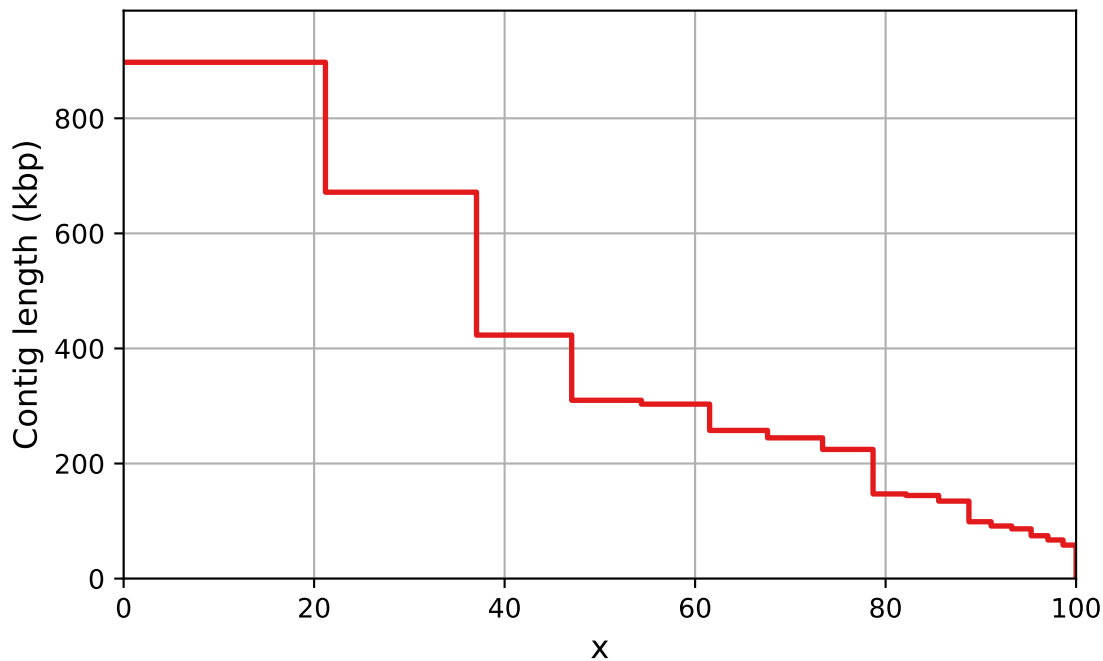
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	mini-ava-pb_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

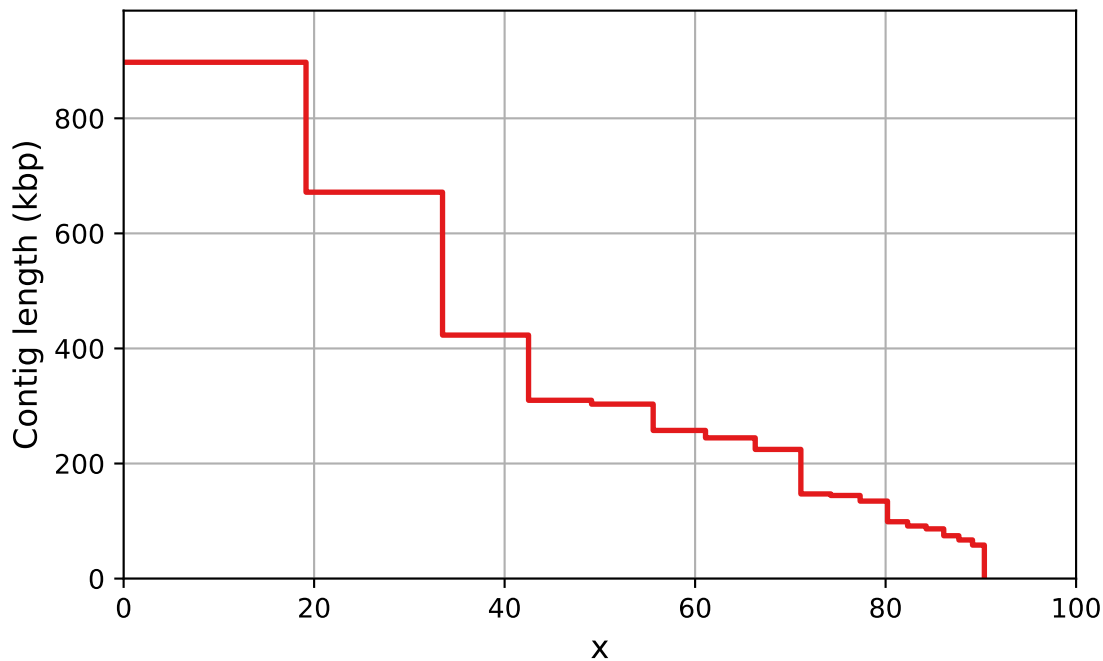
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

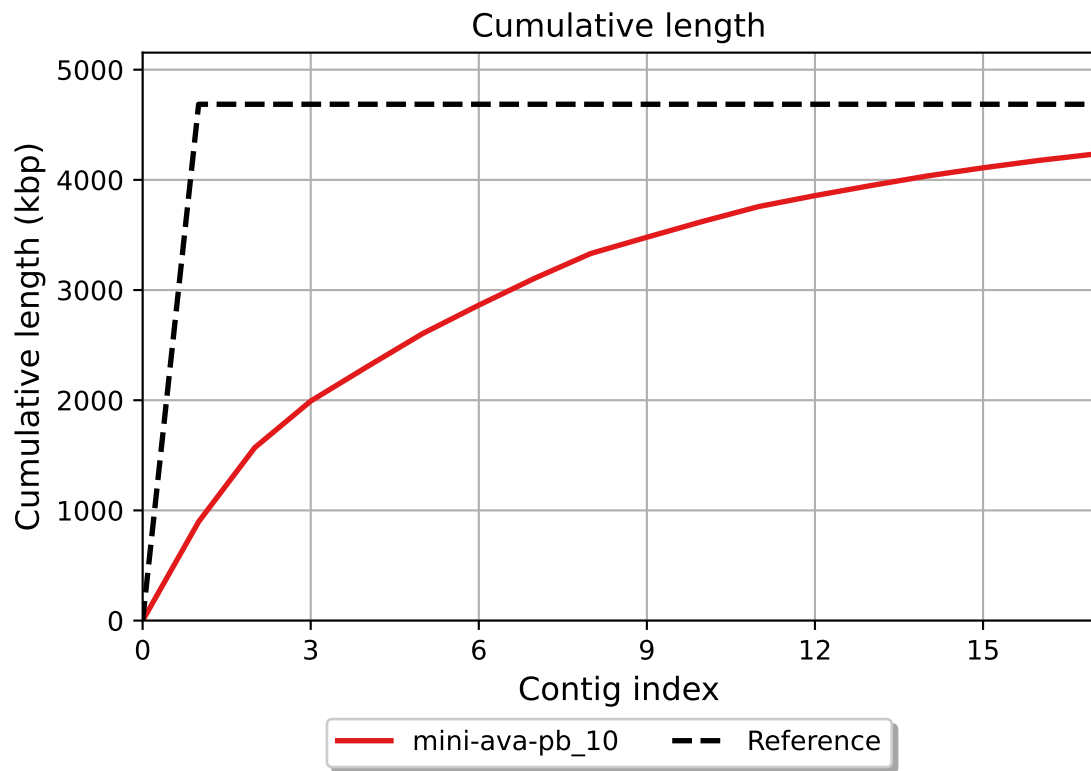


mini-ava-pb\_10

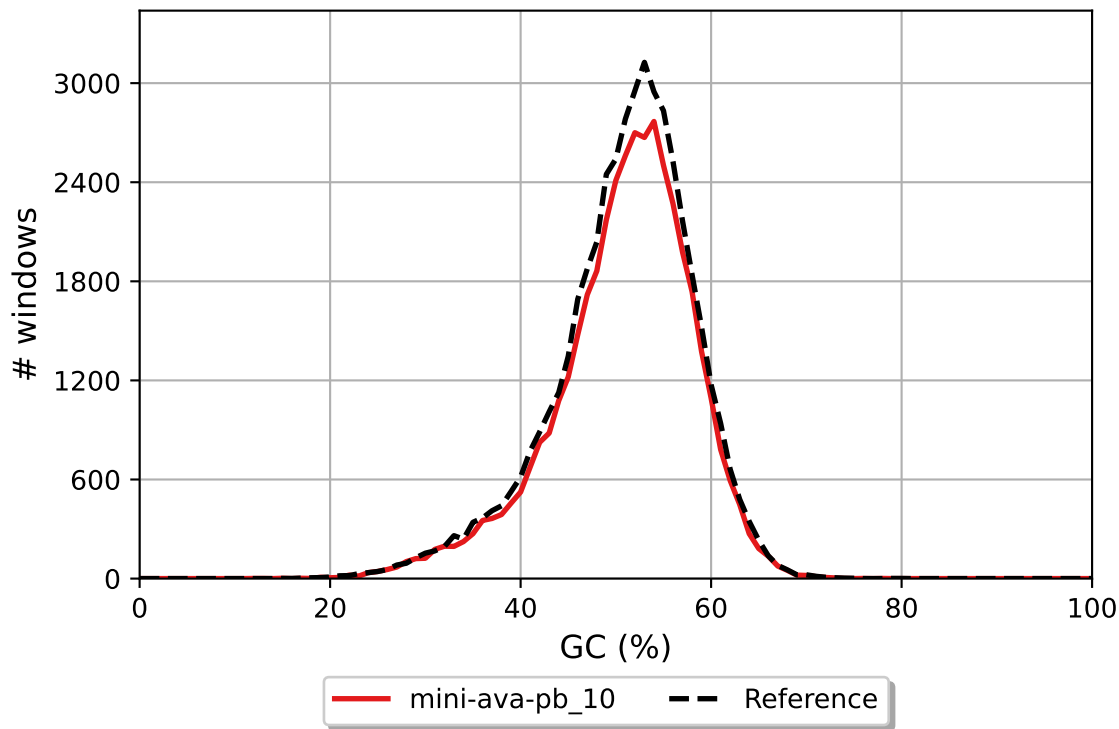
# NGx



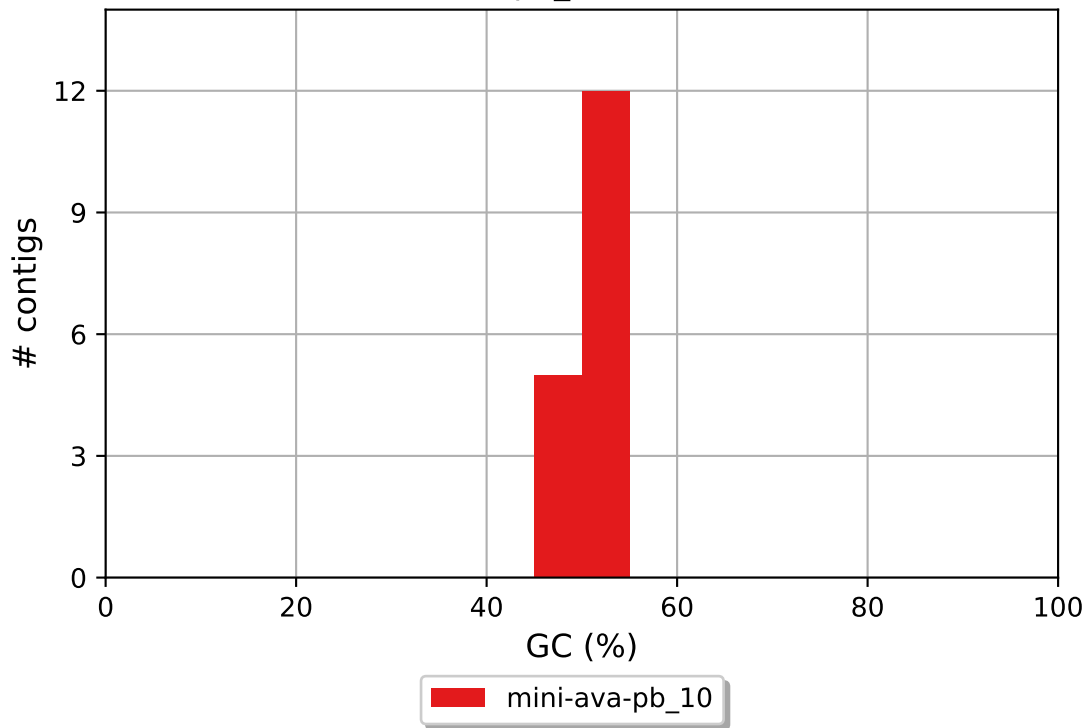
mini-ava-pb\_10



GC content

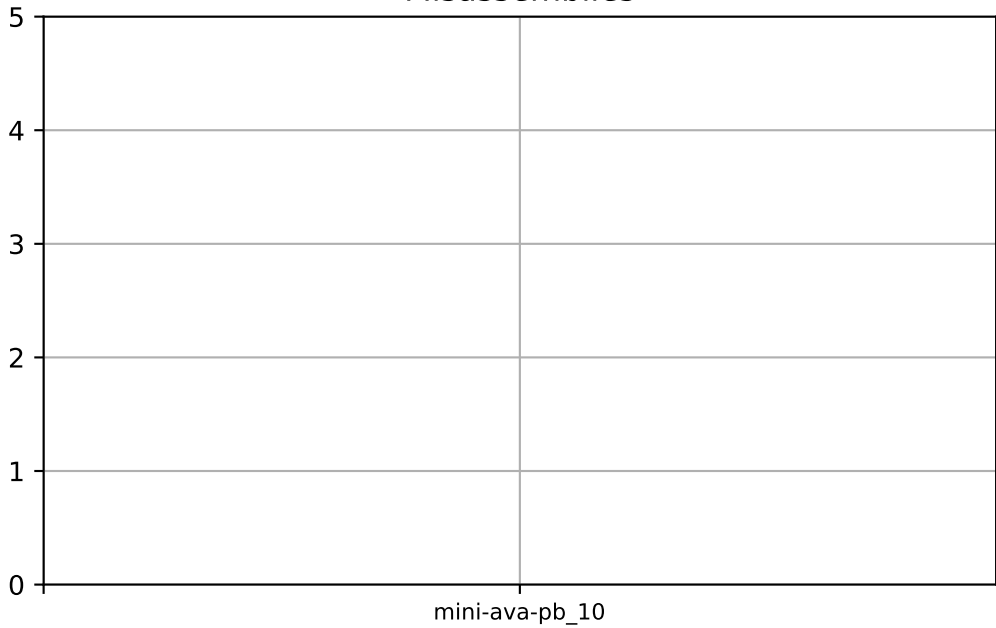


mini-ava-pb\_10 GC content

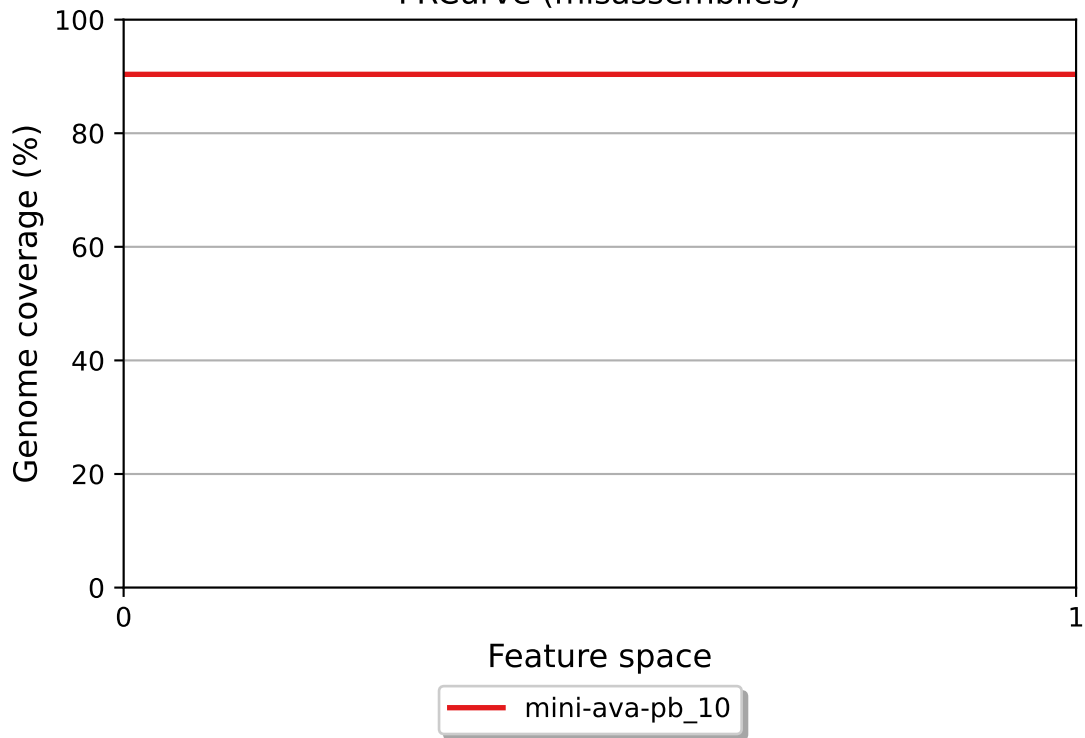




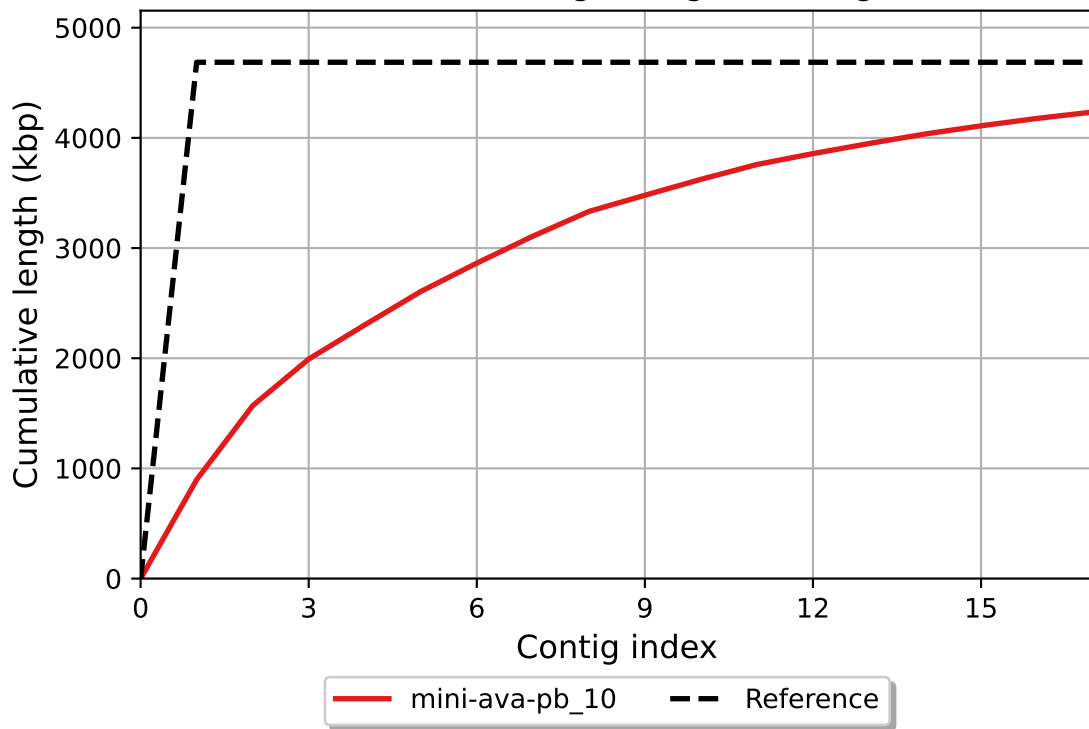
## Misassemblies



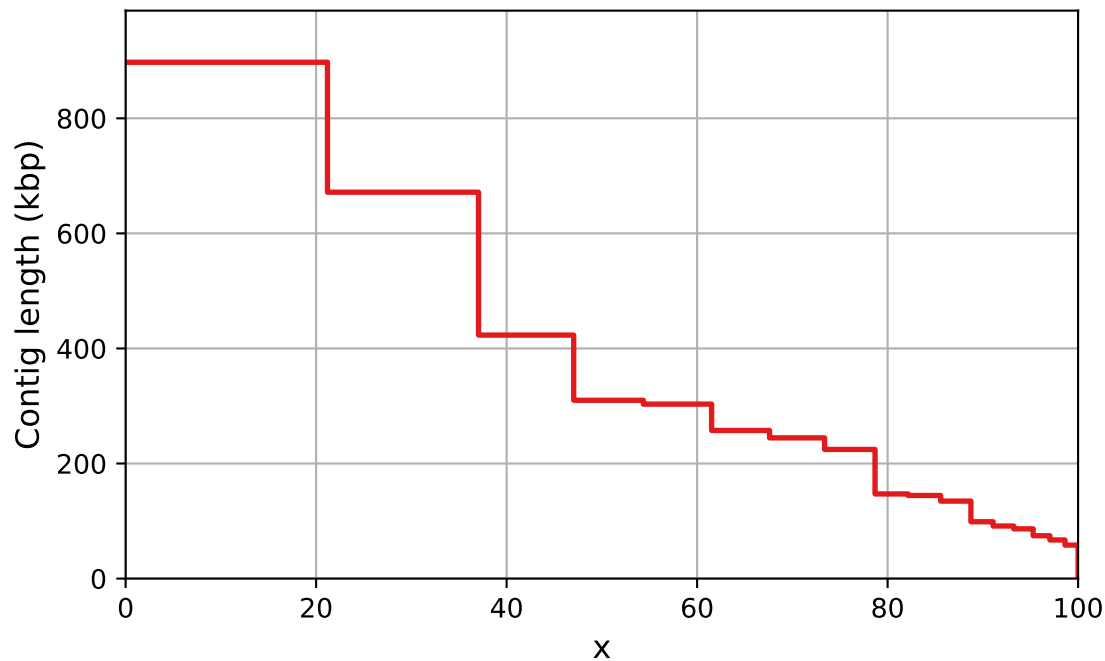
FRCurve (misassemblies)



Cumulative length (aligned contigs)

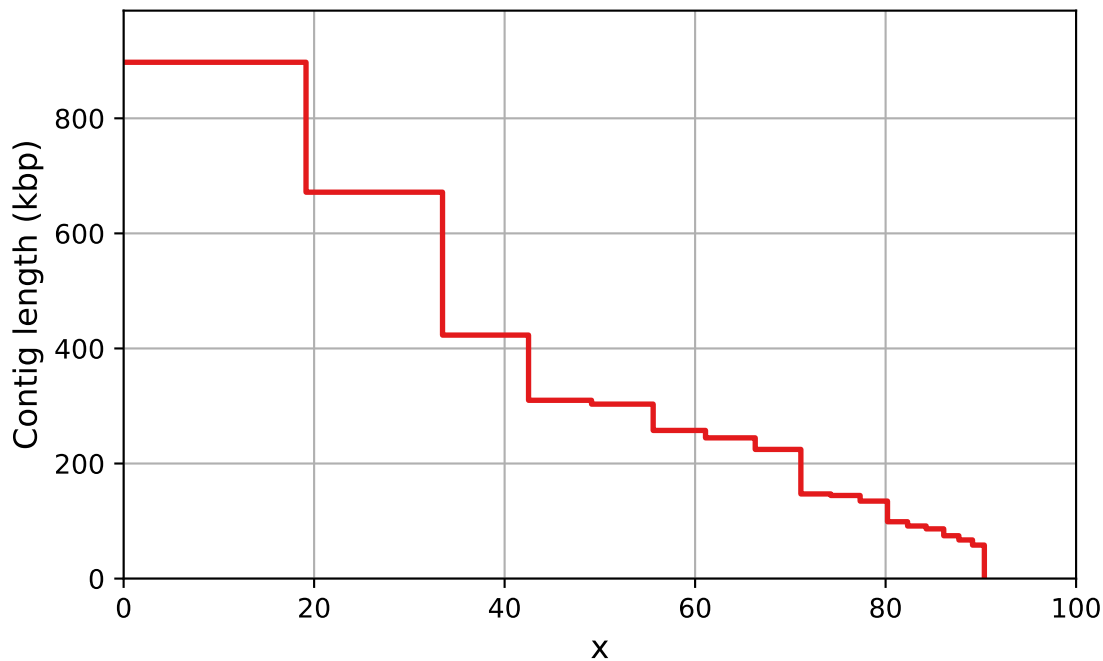


NAx



— mini-ava-pb\_10

# NGAx



— mini-ava-pb\_10