

# Report

	4222_RB2_racon3
# contigs (>= 0 bp)	31
# contigs (>= 1000 bp)	31
# contigs (>= 5000 bp)	31
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	26
# contigs (>= 50000 bp)	25
Total length (>= 0 bp)	22539845
Total length (>= 1000 bp)	22539845
Total length (>= 5000 bp)	22539845
Total length (>= 10000 bp)	22524025
Total length (>= 25000 bp)	22487231
Total length (>= 50000 bp)	22452698
# contigs	31
Largest contig	4574793
Total length	22539845
Reference length	15074320
GC (%)	45.81
Reference GC (%)	48.02
N50	1016908
NG50	1358536
N75	795634
NG75	1016908
L50	6
LG50	3
L75	12
LG75	6
# misassemblies	25
# misassembled contigs	12
Misassembled contigs length	7891195
# local misassemblies	64
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	2 + 21 part
Unaligned length	7503986
Genome fraction (%)	99.579
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	75.54
# indels per 100 kbp	148.13
Largest alignment	1121328
Total aligned length	15026814
NA50	409349
NGA50	853626
NGA75	409349
LA50	14
LGA50	8
LGA75	14

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

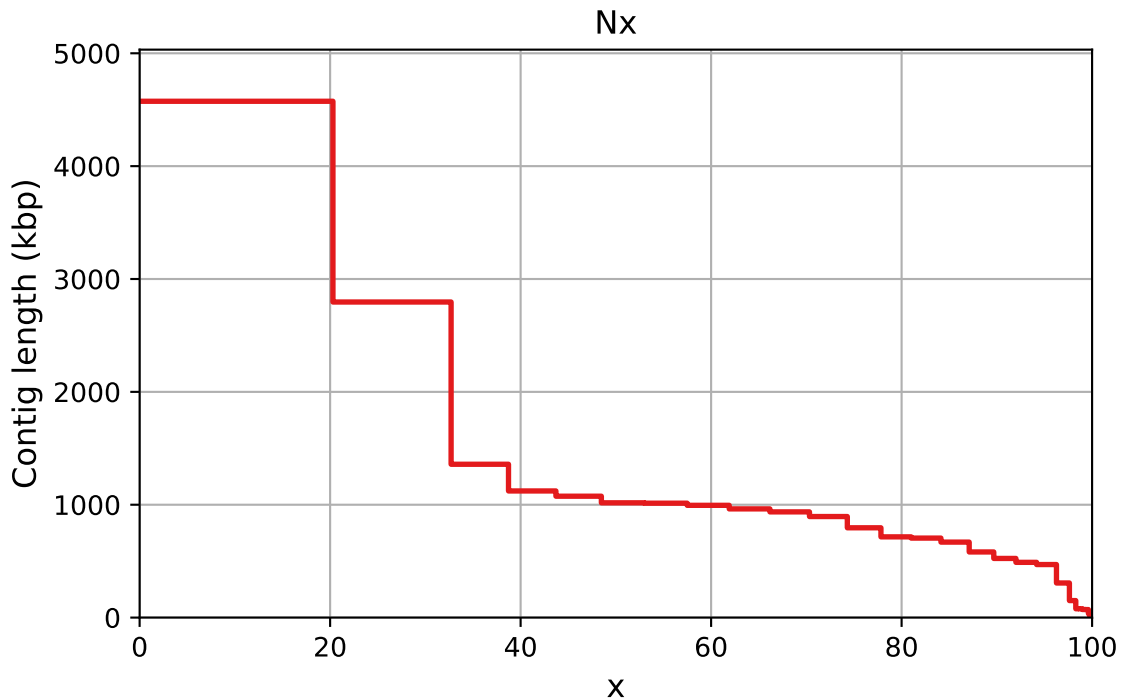
	4222_RB2_racon3
# misassemblies	25
# contig misassemblies	25
# c. relocations	23
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	7891195
# local misassemblies	64
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	11312
# indels	22182
# indels (<= 5 bp)	22052
# indels (> 5 bp)	130
Indels length	30948

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

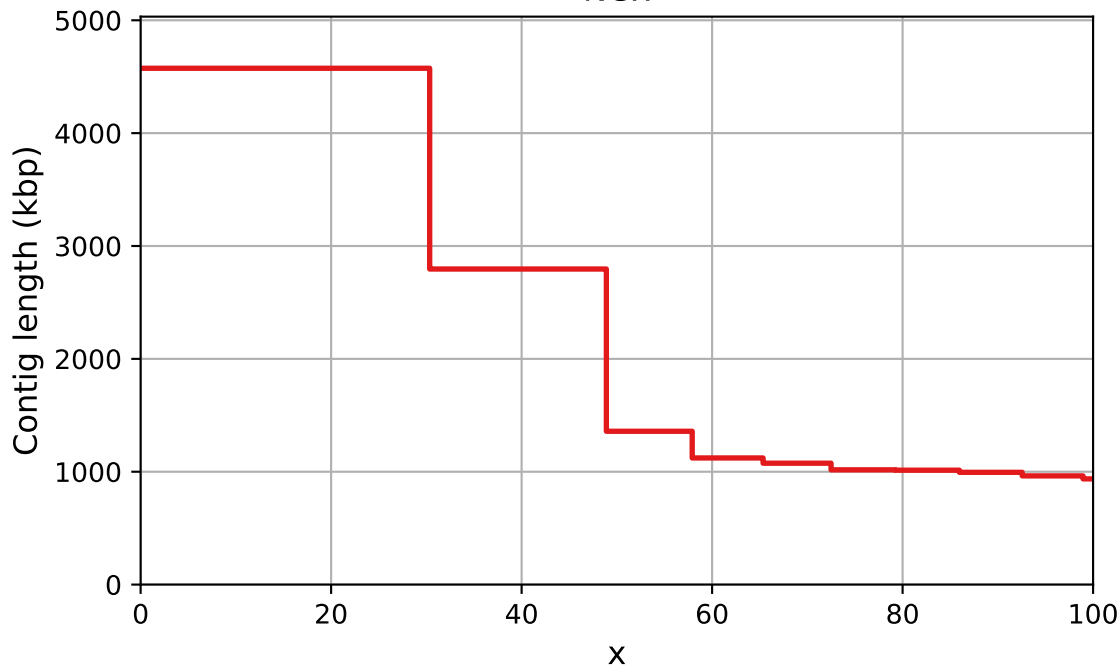
	4222_RB2_racon3
# fully unaligned contigs	2
Fully unaligned length	7370939
# partially unaligned contigs	21
Partially unaligned length	133047
# N's	0

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).



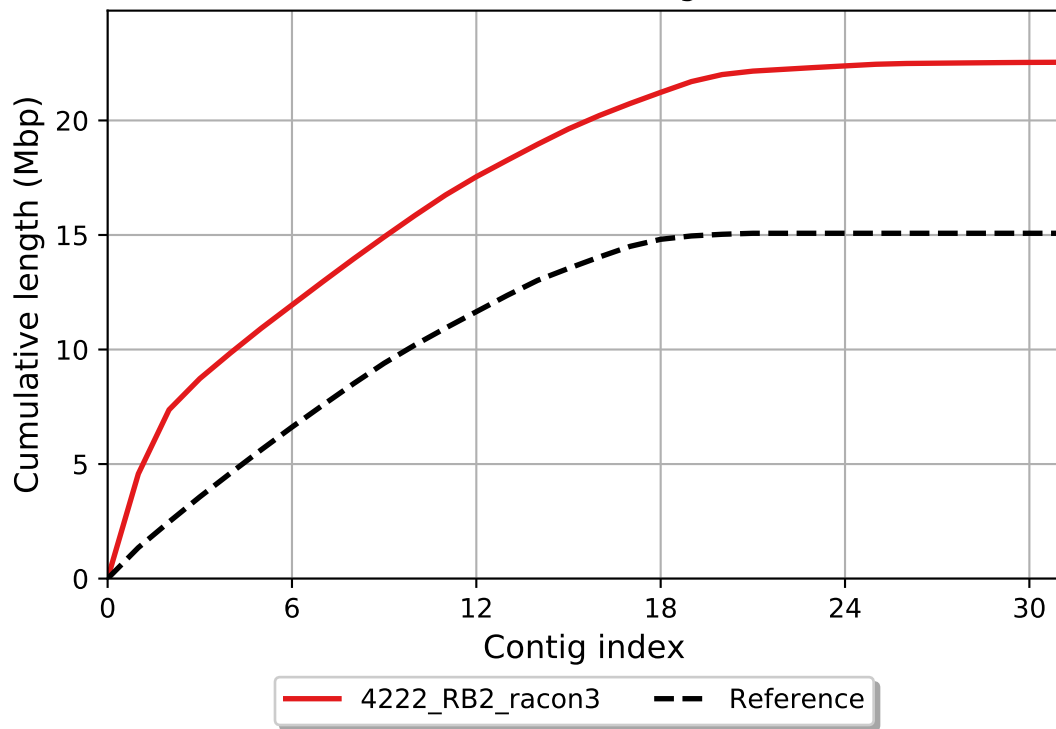
— 4222\_RB2\_racon3

NGx

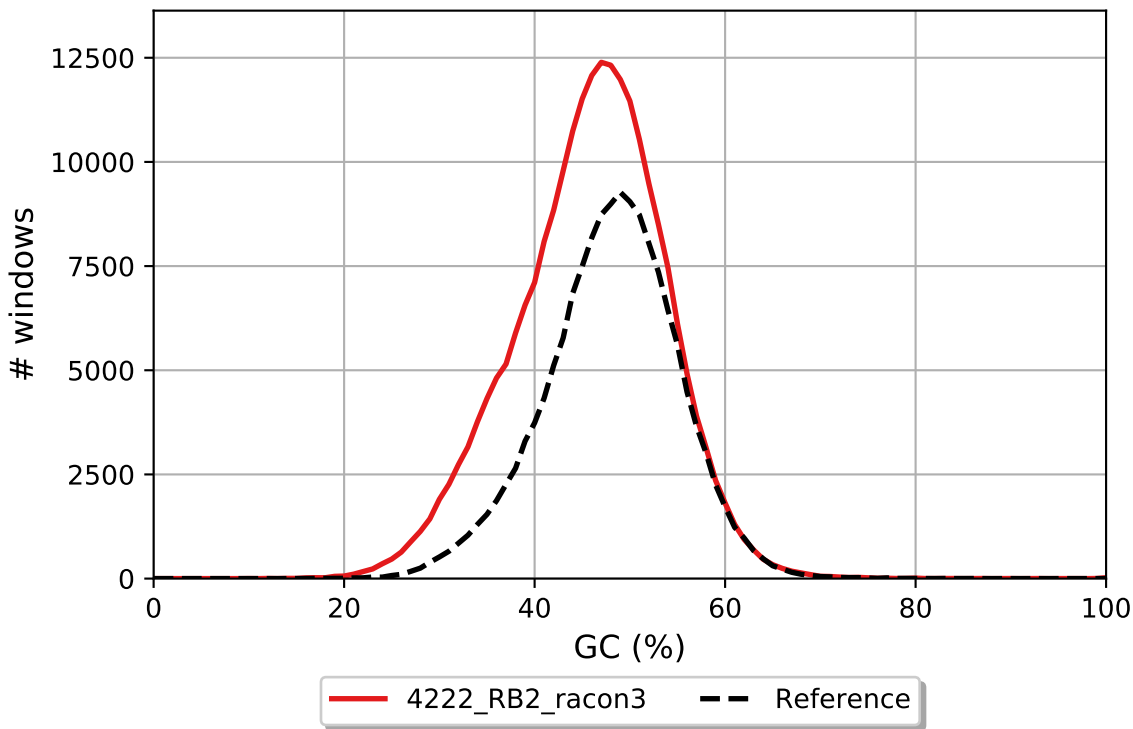


— 4222\_RB2\_racon3

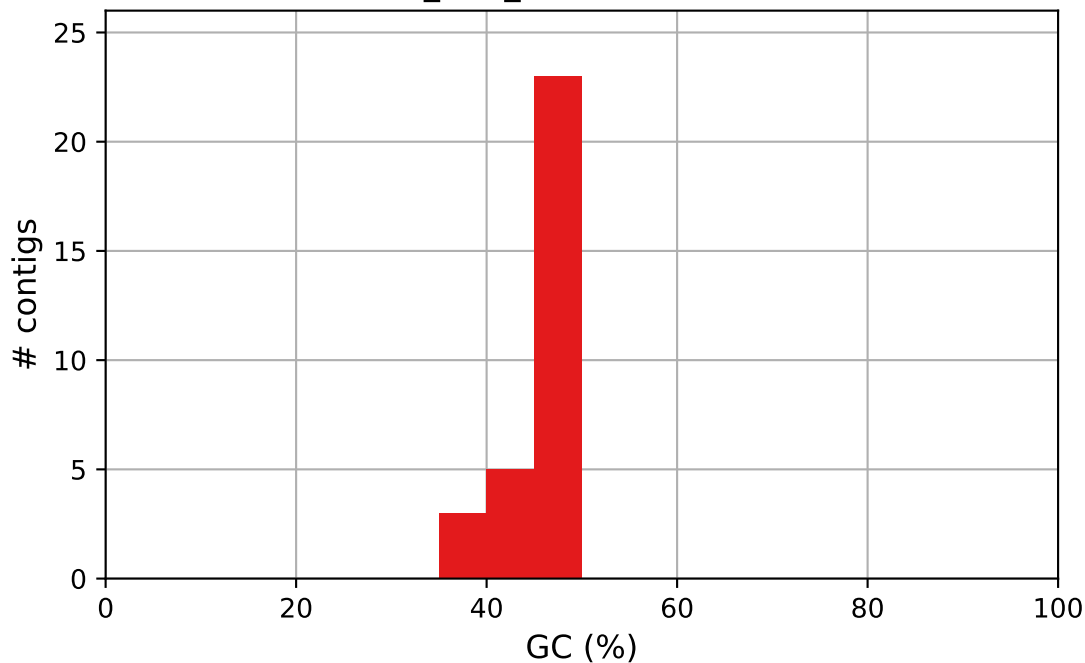
Cumulative length



# GC content



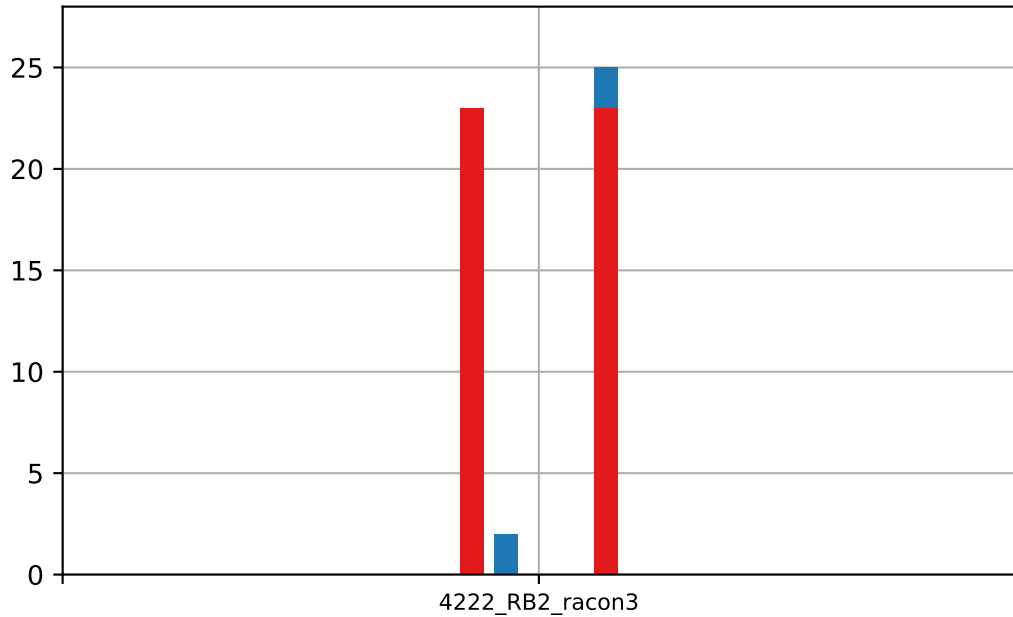
4222\_RB2\_racon3 GC content



4222\_RB2\_racon3



## Misassemblies

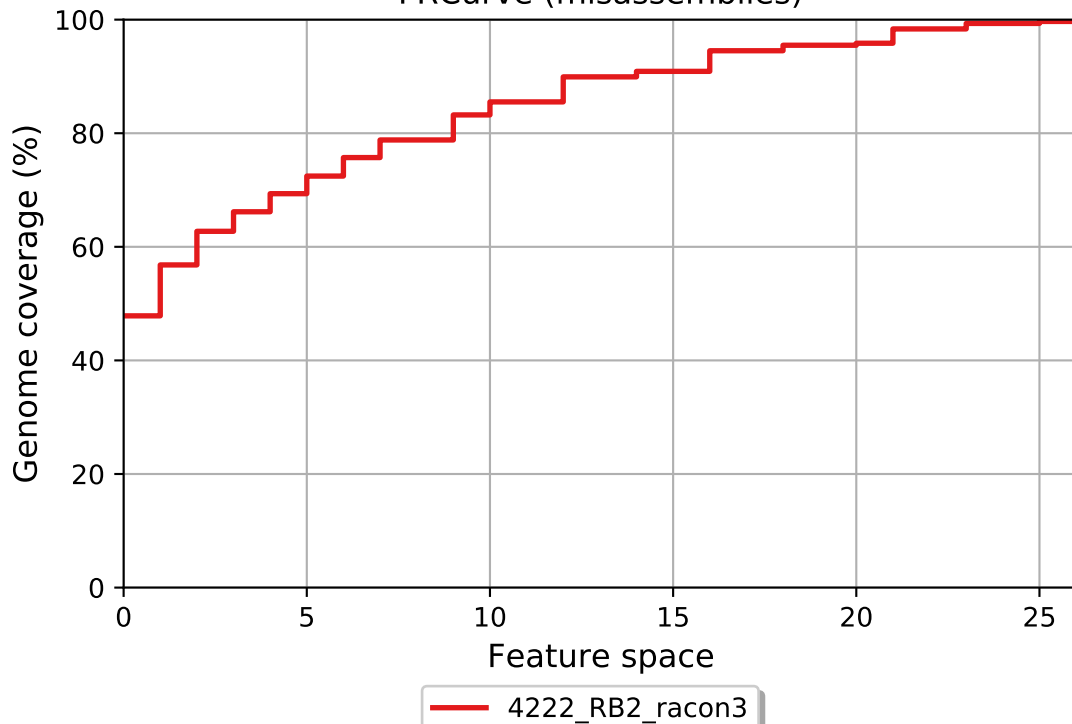


# relocations

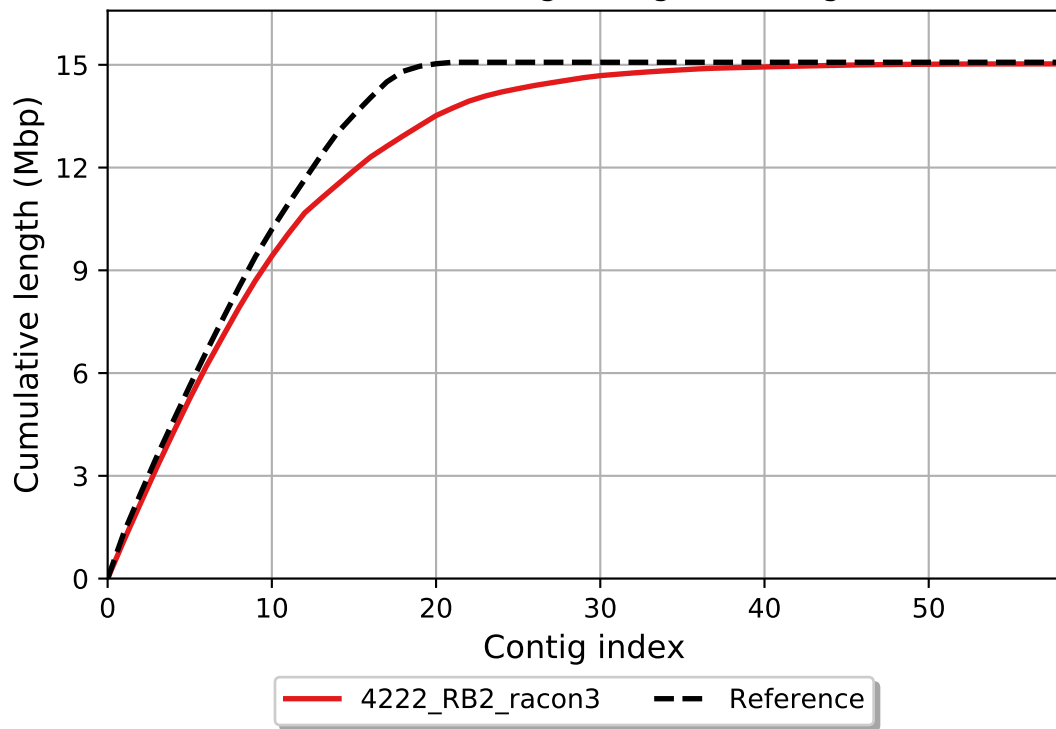


# translocations

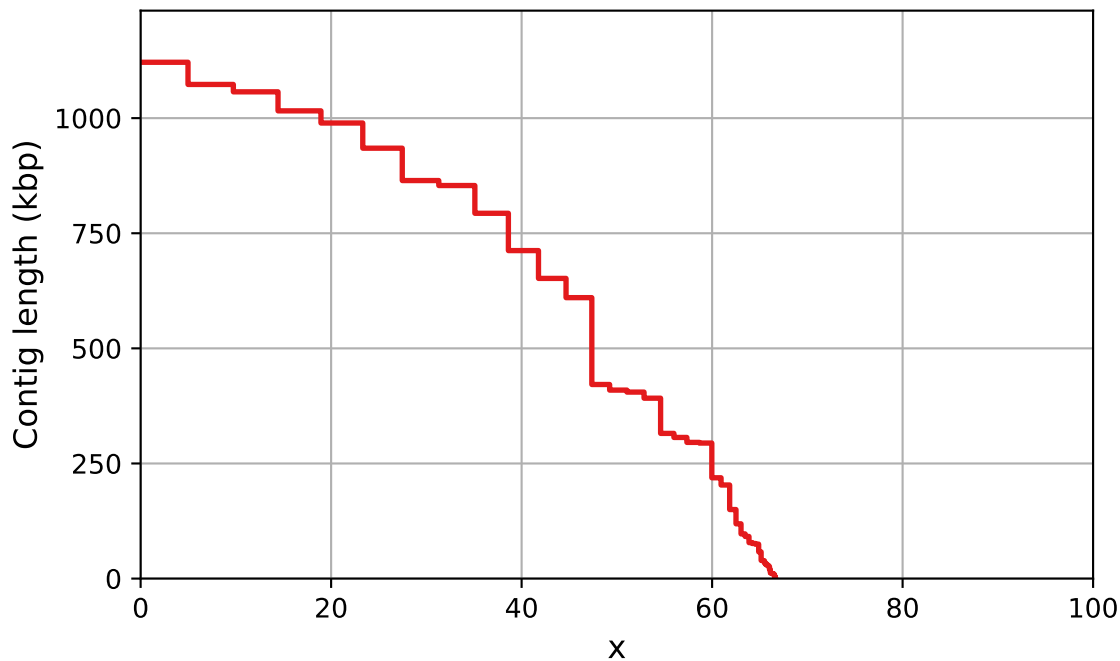
FRCurve (misassemblies)



Cumulative length (aligned contigs)

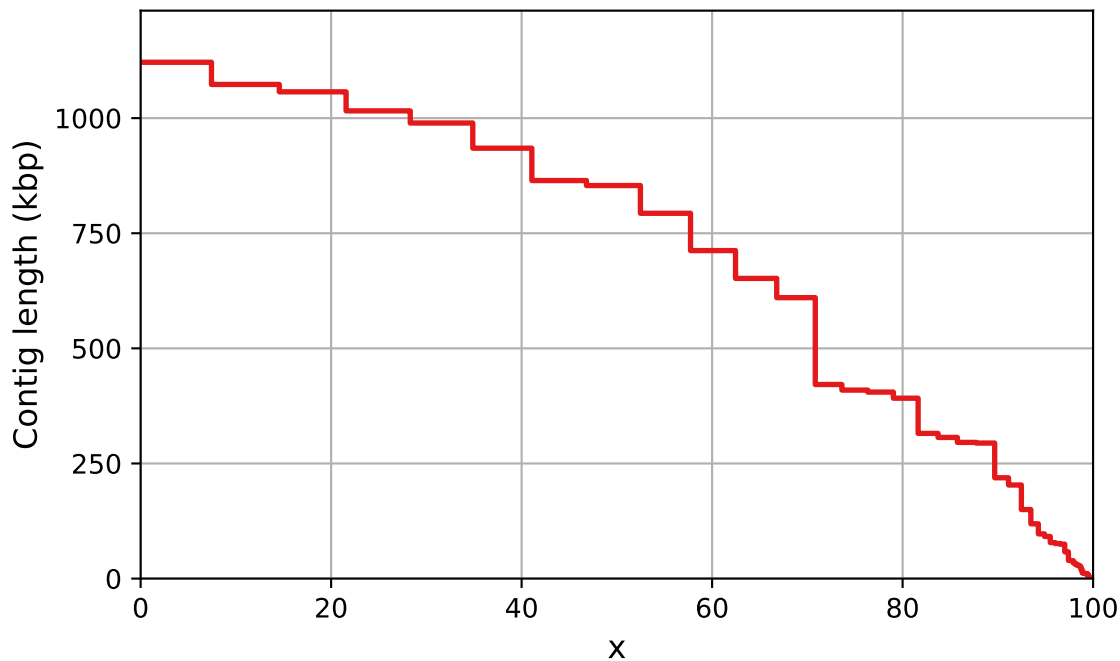


NAx



4222\_RB2\_racon3

# NGAx



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