

Report

	G11_RB6_2022_racon3
# contigs (>= 0 bp)	28
# contigs (>= 1000 bp)	28
# contigs (>= 5000 bp)	26
# contigs (>= 10000 bp)	26
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	22
Total length (>= 0 bp)	15364424
Total length (>= 1000 bp)	15364424
Total length (>= 5000 bp)	15359065
Total length (>= 10000 bp)	15359065
Total length (>= 25000 bp)	15333701
Total length (>= 50000 bp)	15252298
# contigs	28
Largest contig	1367294
Total length	15364424
Reference length	15074320
GC (%)	47.96
Reference GC (%)	48.02
N50	925304
NG50	925304
N75	746866
NG75	746866
L50	8
LG50	8
L75	12
LG75	12
# misassemblies	159
# misassembled contigs	19
Misassembled contigs length	13363424
# local misassemblies	177
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	2 + 24 part
Unaligned length	1023832
Genome fraction (%)	94.879
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	486.91
# indels per 100 kbp	190.31
Largest alignment	951854
Total aligned length	14337244
NA50	195720
NGA50	195720
NA75	95484
NGA75	103928
LA50	18
LGA50	18
LA75	46
LGA75	43

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

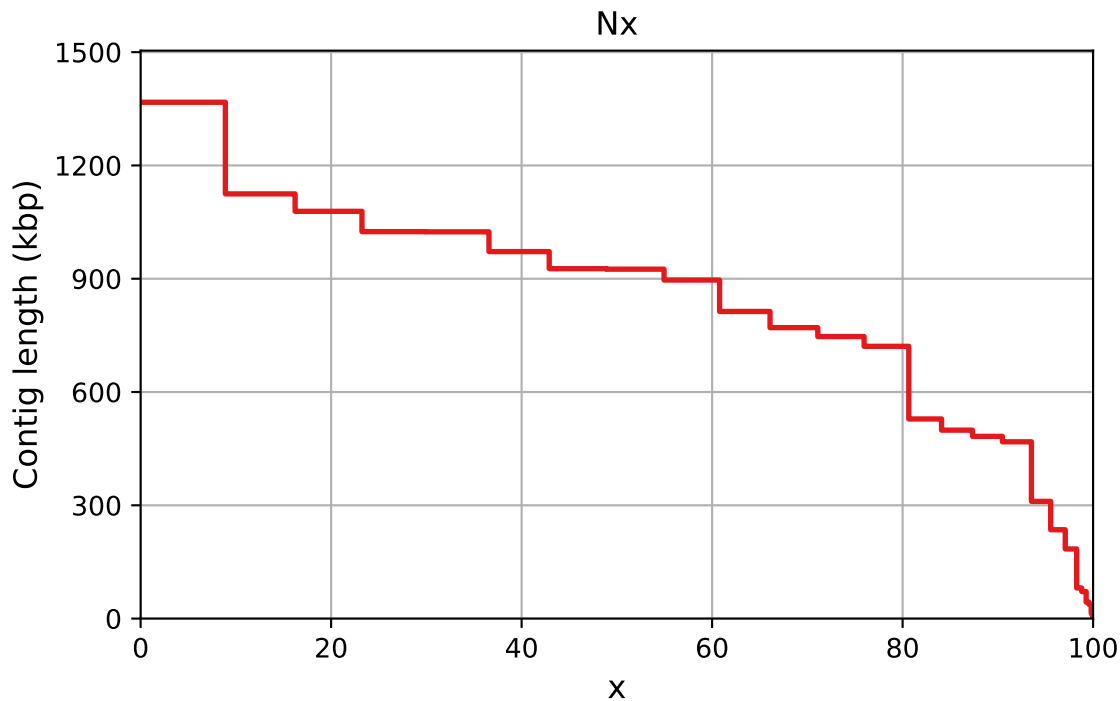
	G11_RB6_2022_racon3
# misassemblies	159
# contig misassemblies	159
# c. relocations	92
# c. translocations	56
# c. inversions	11
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	19
Misassembled contigs length	13363424
# local misassemblies	177
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	69472
# indels	27153
# indels (<= 5 bp)	24187
# indels (> 5 bp)	2966
Indels length	83814

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).

Unaligned report

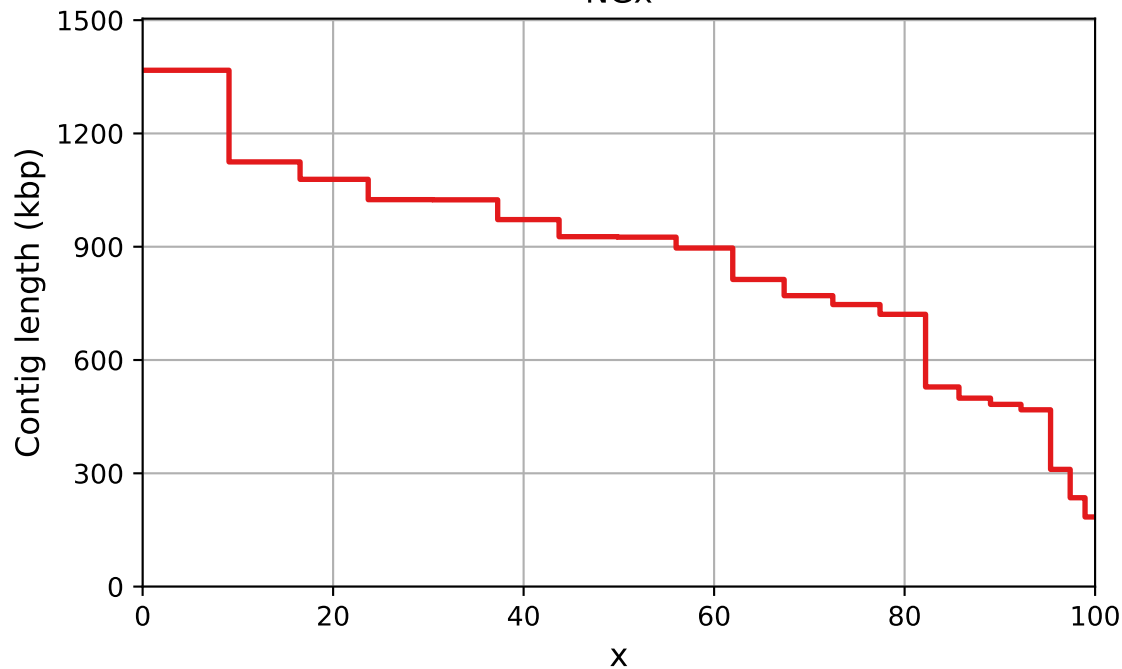
	G11_RB6_2022_racon3
# fully unaligned contigs	2
Fully unaligned length	14616
# partially unaligned contigs	24
Partially unaligned length	1009216
# N's	0

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).



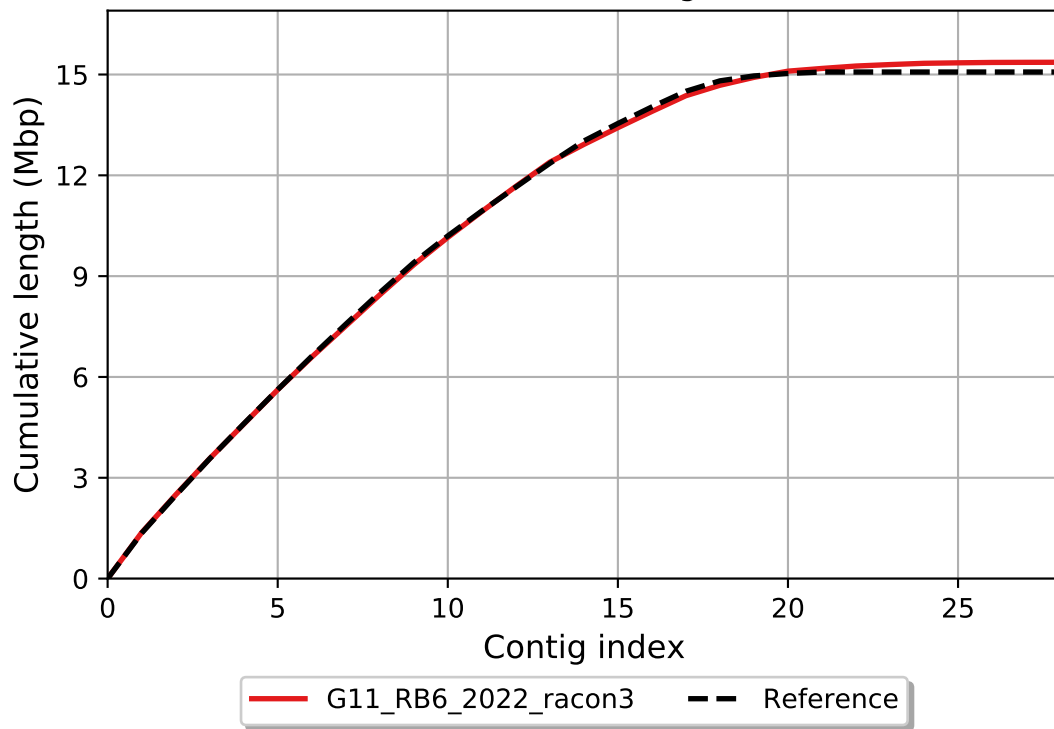
G11_RB6_2022_racon3

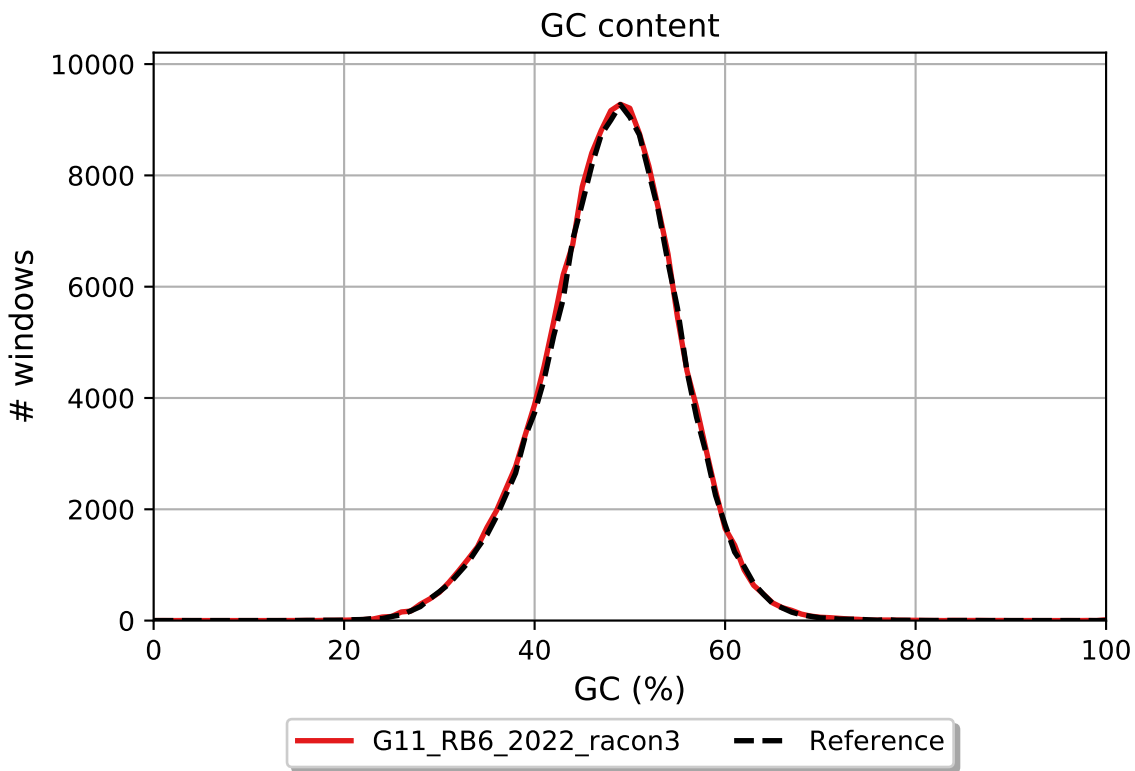
NGx



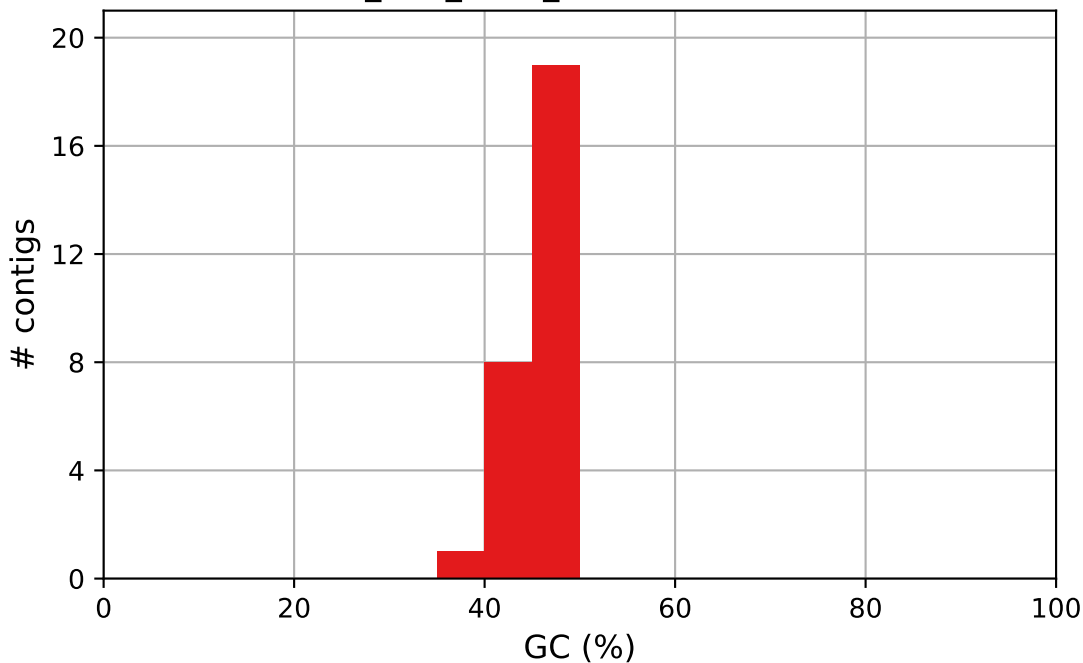
G11_RB6_2022_racon3

Cumulative length



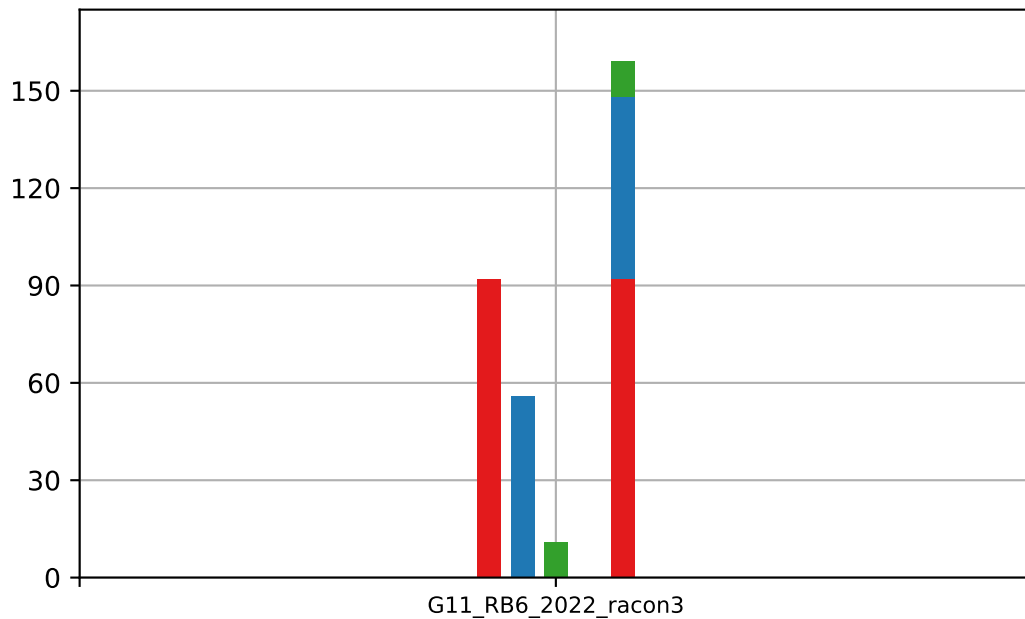


G11_RB6_2022_racon3 GC content



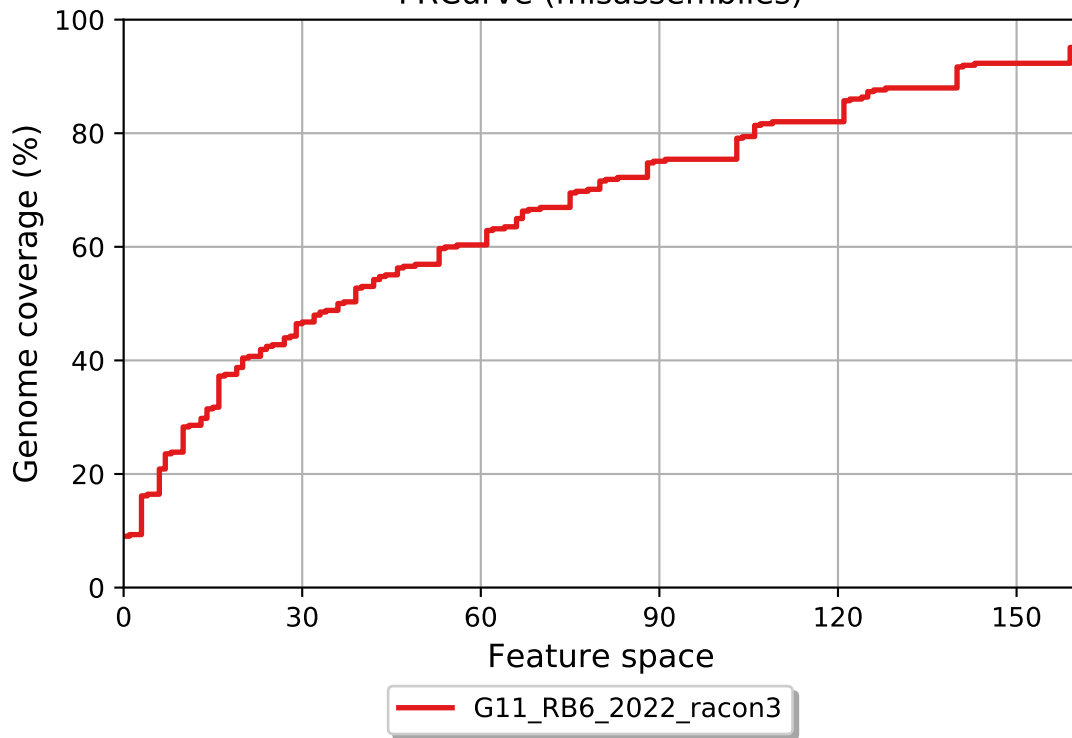
G11_RB6_2022_racon3

Misassemblies

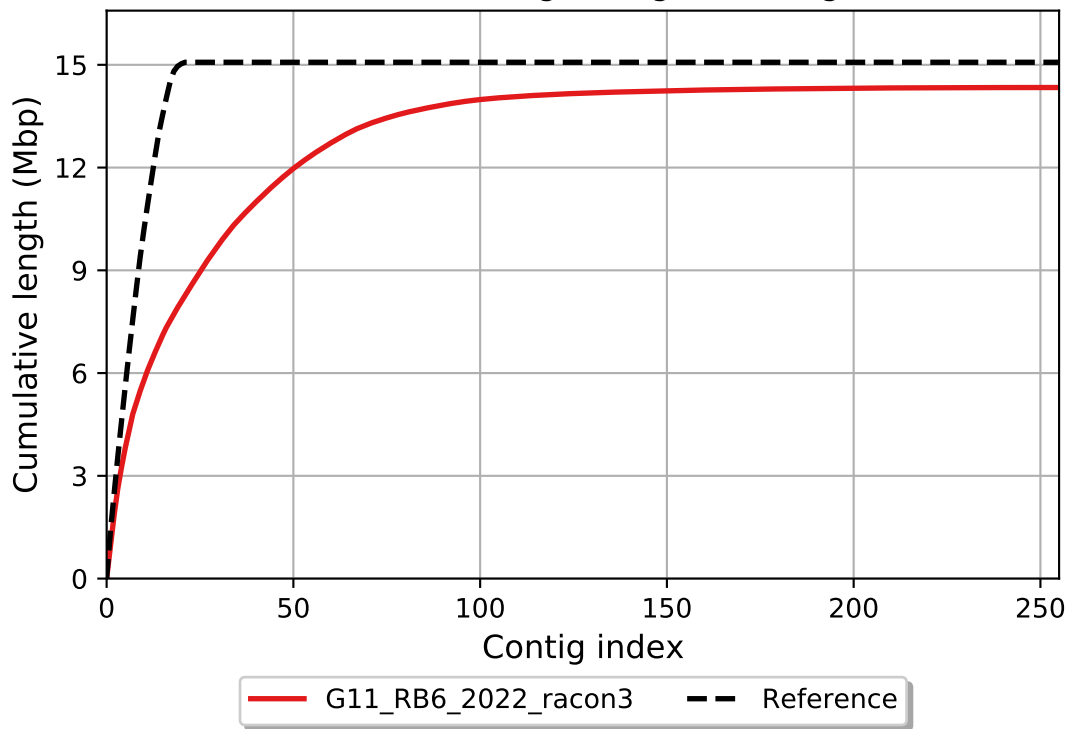


■ # relocations ■ # translocations ■ # inversions

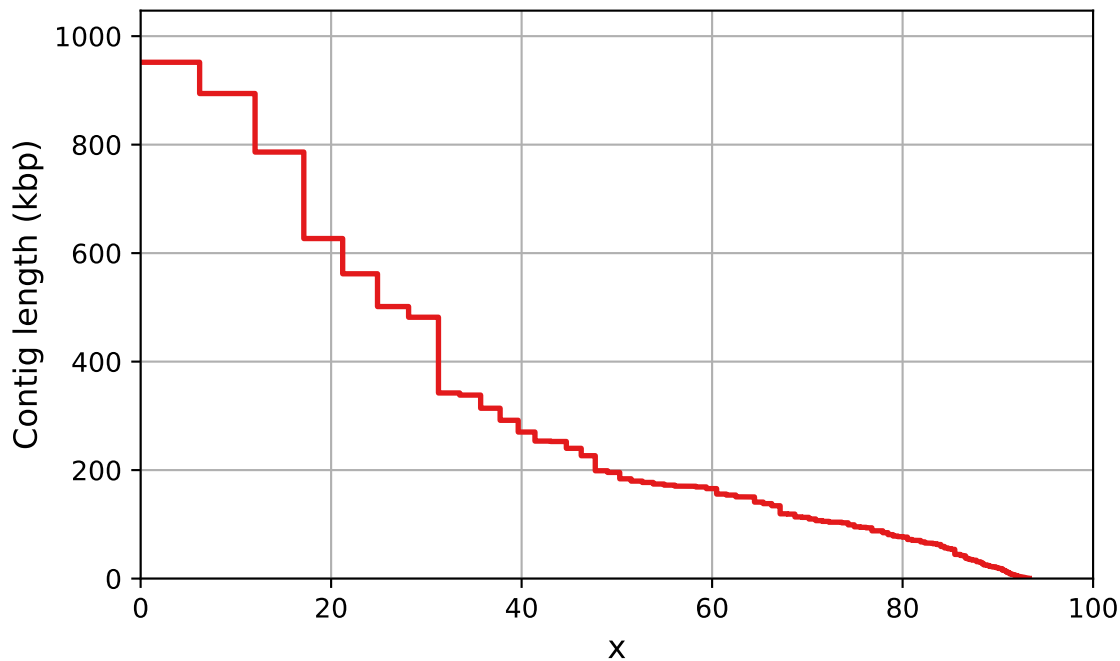
FRCurve (misassemblies)



Cumulative length (aligned contigs)

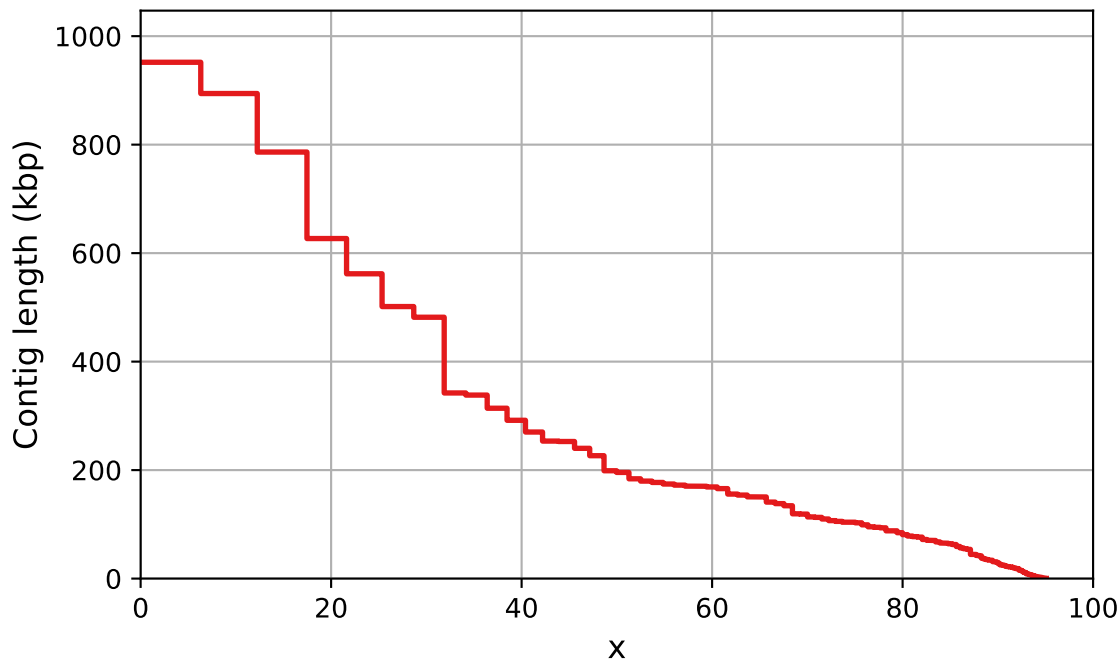


NAx



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NGAx



G11_RB6_2022_racon3