

Report

	Racon_on_data_37_data_39_and_data_30
# contigs (>= 0 bp)	88
# contigs (>= 1000 bp)	85
Total length (>= 0 bp)	1977764
Total length (>= 1000 bp)	1975490
# contigs	88
Largest contig	412867
Total length	1977764
Reference length	875732047
GC (%)	35.84
Reference GC (%)	33.51
N50	36368
N75	18983
L50	10
L75	27
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	39657
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	36
# unaligned contigs	27 + 56 part
Unaligned length	1665394
Genome fraction (%)	0.041
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1438.88
# indels per 100 kbp	1131.16
# genomic features	0 + 0 part
Largest alignment	12629
Total aligned length	310915
NGA50	-

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

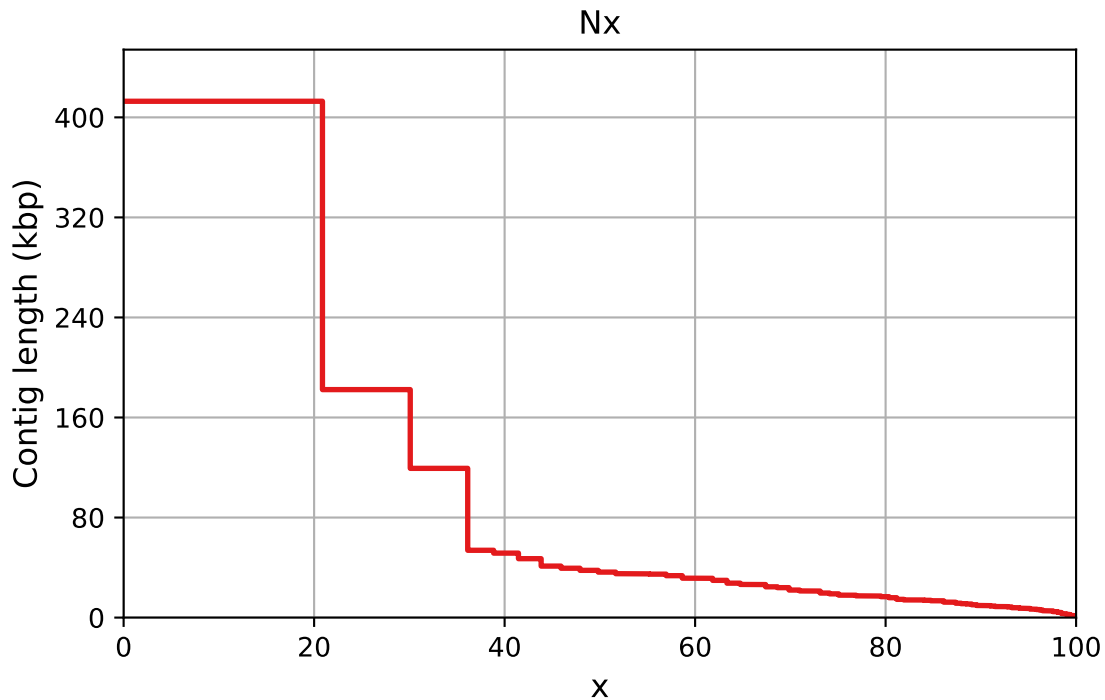
	Racon_on_data_37__data_39__and_data_30
# misassemblies	3
# contig misassemblies	3
# c. relocations	2
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	39657
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	36
# mismatches	4372
# indels	3437
# indels (<= 5 bp)	3368
# indels (> 5 bp)	69
Indels length	5488

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

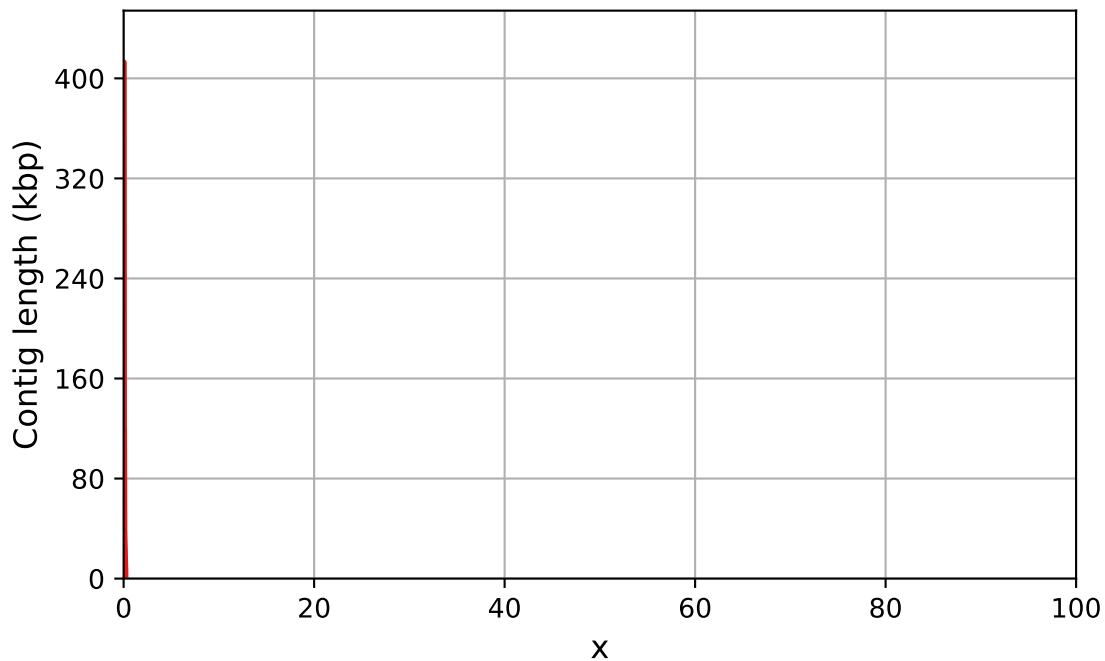
	Racon_on_data_37__data_39__and_data_30
# fully unaligned contigs	27
Fully unaligned length	244897
# partially unaligned contigs	56
Partially unaligned length	1420497
# N's	0

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).

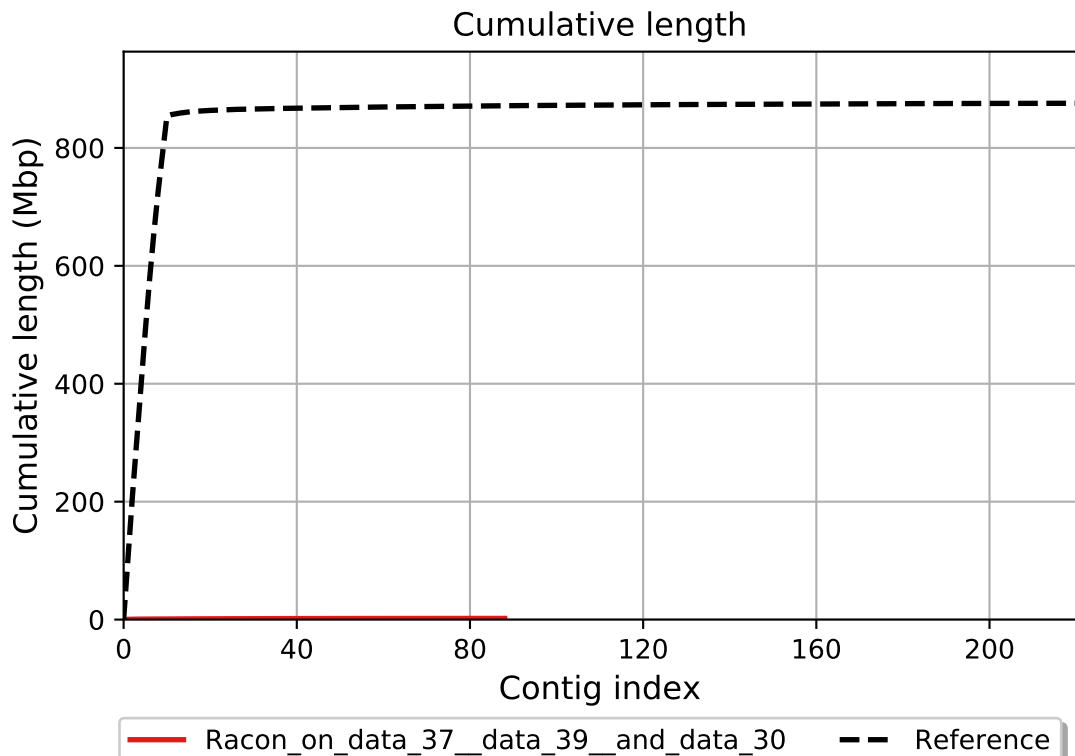


— Racon_on_data_37__data_39__and_data_30

NGx

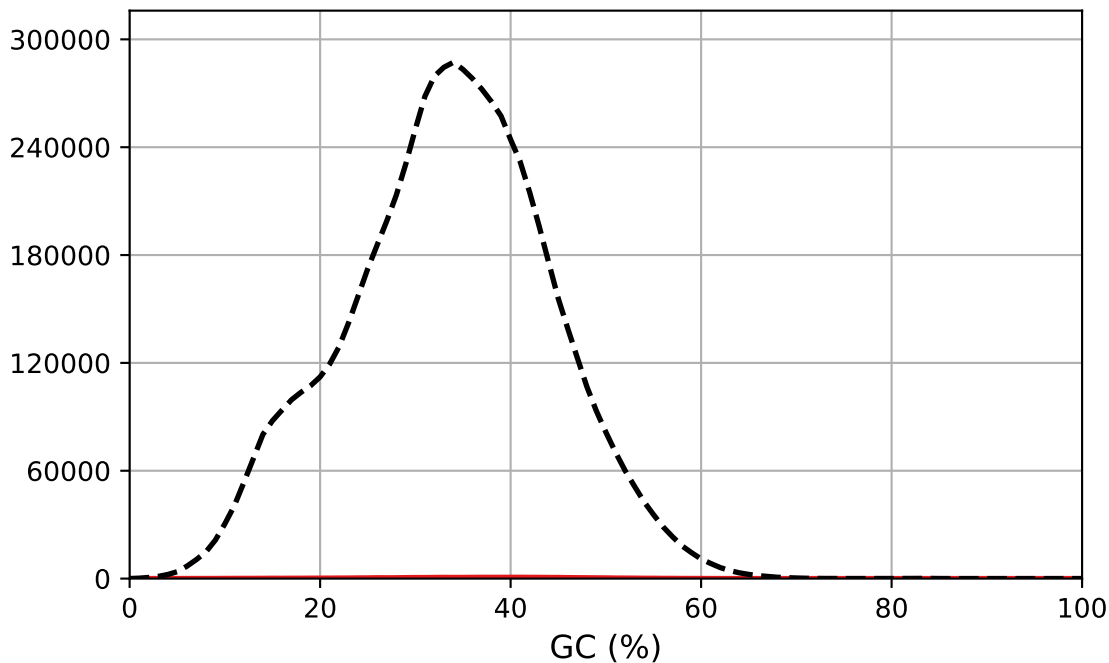


Racon_on_data_37_data_39_and_data_30



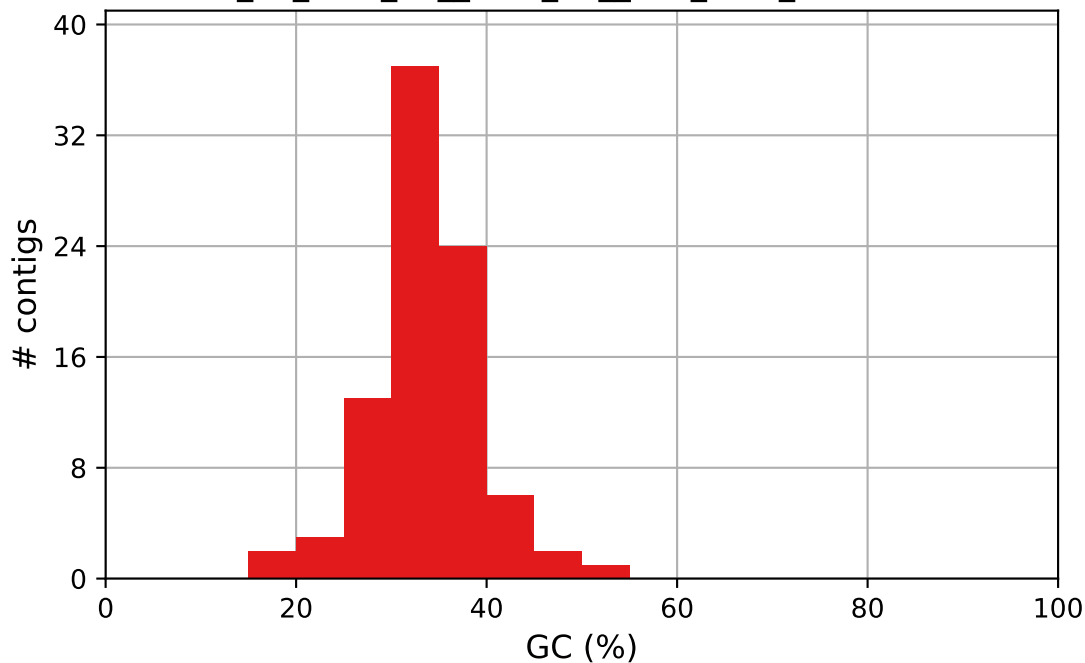
windows

GC content



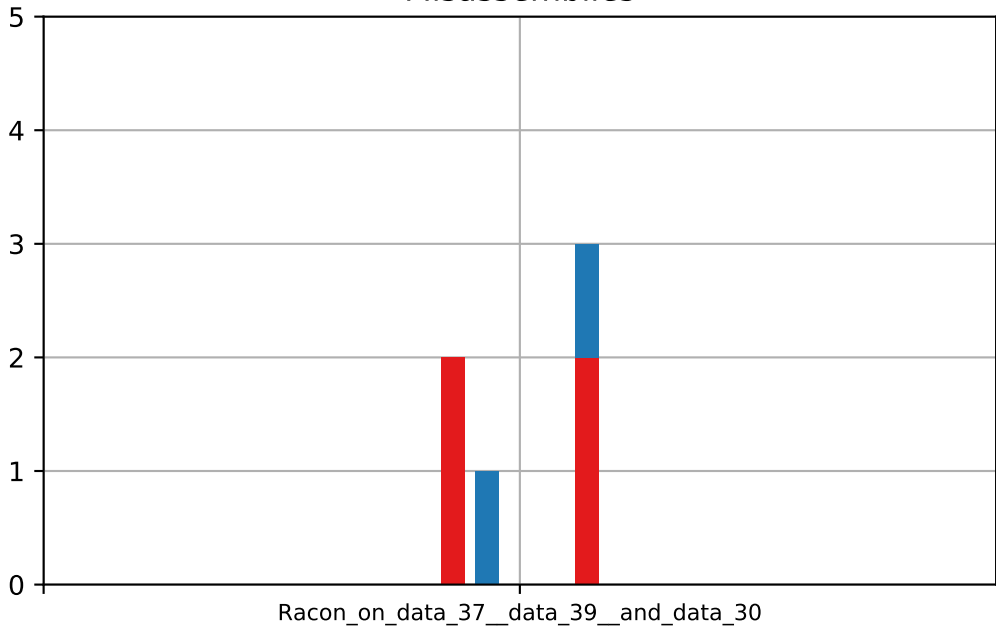
— Racon_on_data_37_data_39_and_data_30 - - Reference

Racon_on_data_37__data_39__and_data_30 GC content



Racon_on_data_37__data_39__and_data_30

Misassemblies

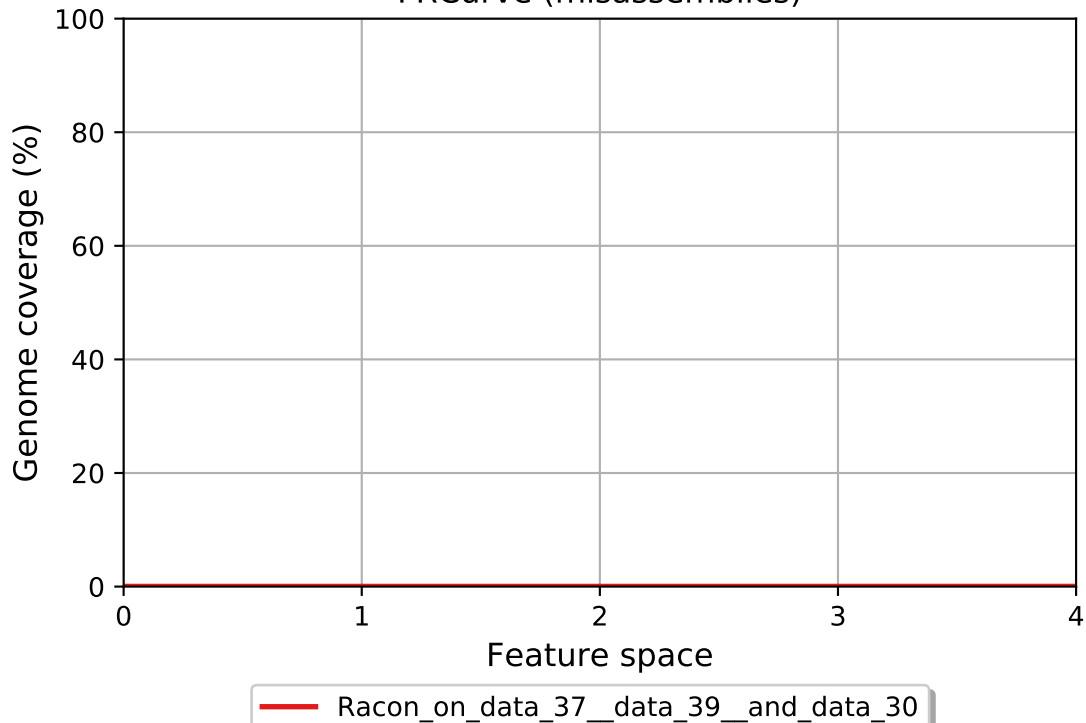


relocations

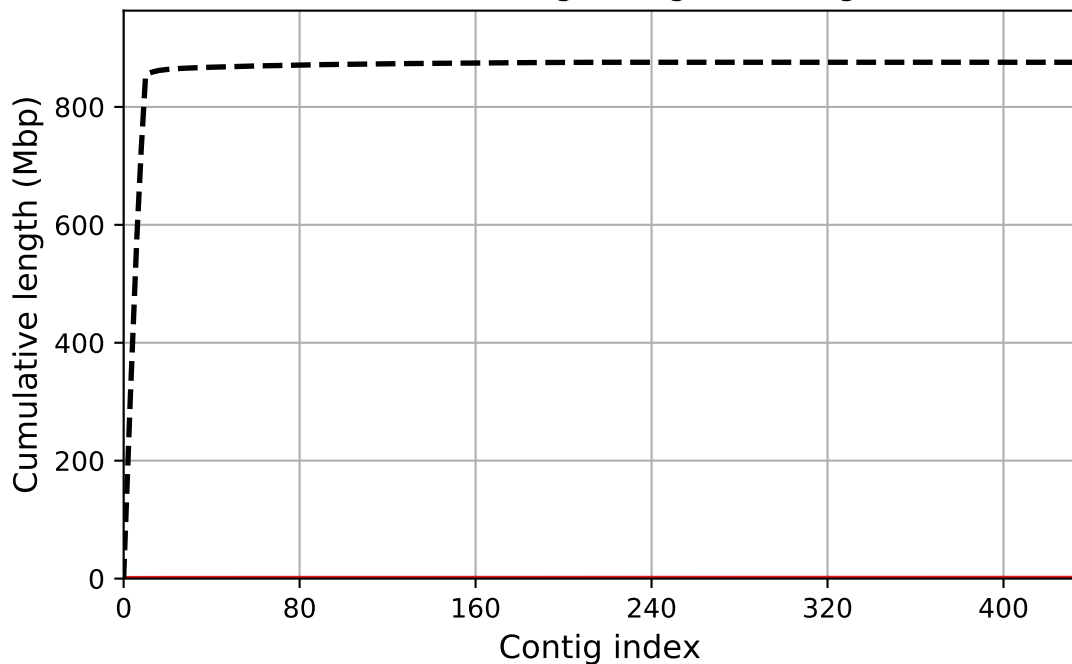


translocations

FRCurve (misassemblies)

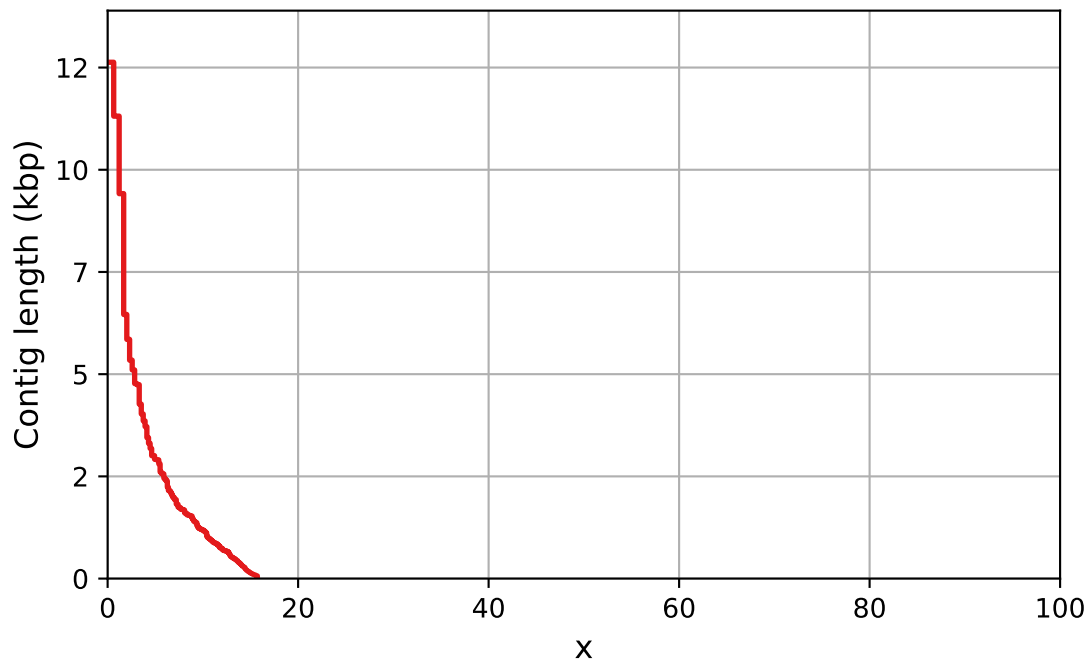


Cumulative length (aligned contigs)



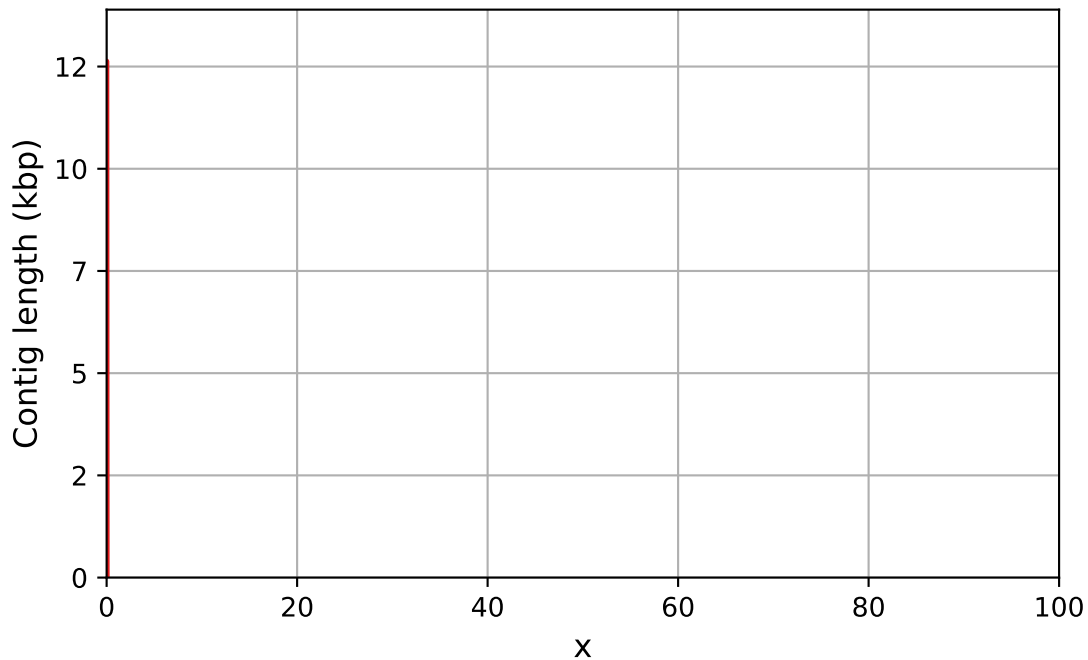
— Racon_on_data_37_data_39_and_data_30 - - Reference

NAx



— Racon_on_data_37__data_39__and_data_30

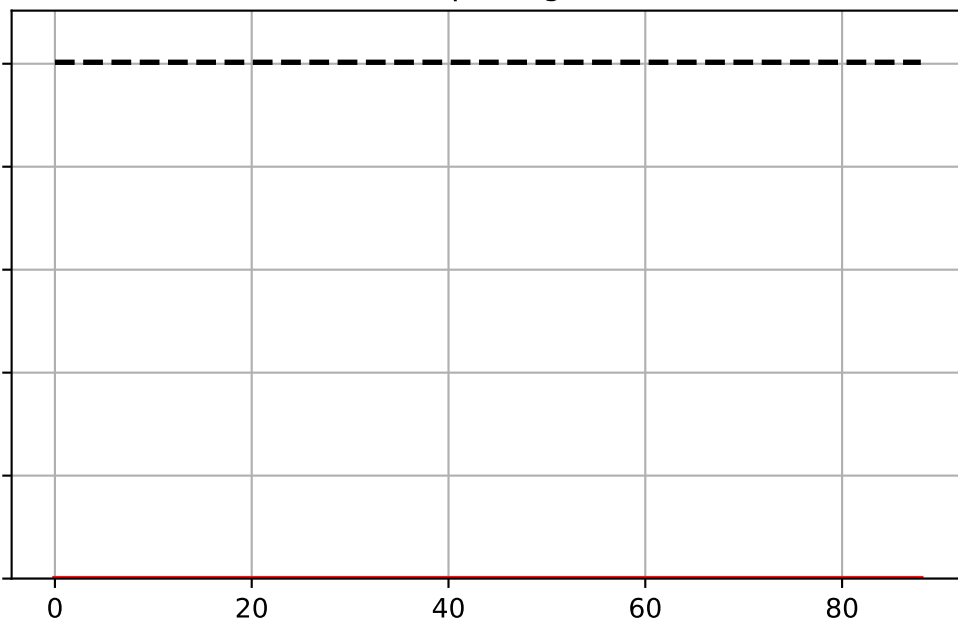
NGAx



Racon_on_data_37__data_39__and_data_30

Cumulative # complete genomic features

Cumulative # complete genomic features



— Racon_on_data_37_data_39_and_data_30 - - Reference

FRCurve (genomic features)

