

Report

	GCA_032595515.1_ASM3259551v1_genomic
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	1004596
Total length (>= 1000 bp)	1004596
Total length (>= 5000 bp)	1004596
Total length (>= 10000 bp)	1004596
Total length (>= 25000 bp)	987311
Total length (>= 50000 bp)	911399
# contigs	4
Largest contig	911399
Total length	1004596
Reference length	1521208
GC (%)	28.40
Reference GC (%)	28.18
N50	911399
NG50	911399
N90	911399
NG90	-
auN	830273.7
auNG	548307.4
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	928684
# local misassemblies	2
# scaffold gap ext. mis.	2
# scaffold gap loc. mis.	7
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	65.163
Duplication ratio	1.003
# N's per 100 kbp	982.88
# mismatches per 100 kbp	338.46
# indels per 100 kbp	17.20
# genomic features	1016 + 17 part
Largest alignment	901525
Total aligned length	994219
NA50	901525
NGA50	901525
NA90	49389
NGA90	-
auNA	812393.0
auNGA	536499.1
LA50	1
LGA50	1
LA90	2
LGA90	-

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

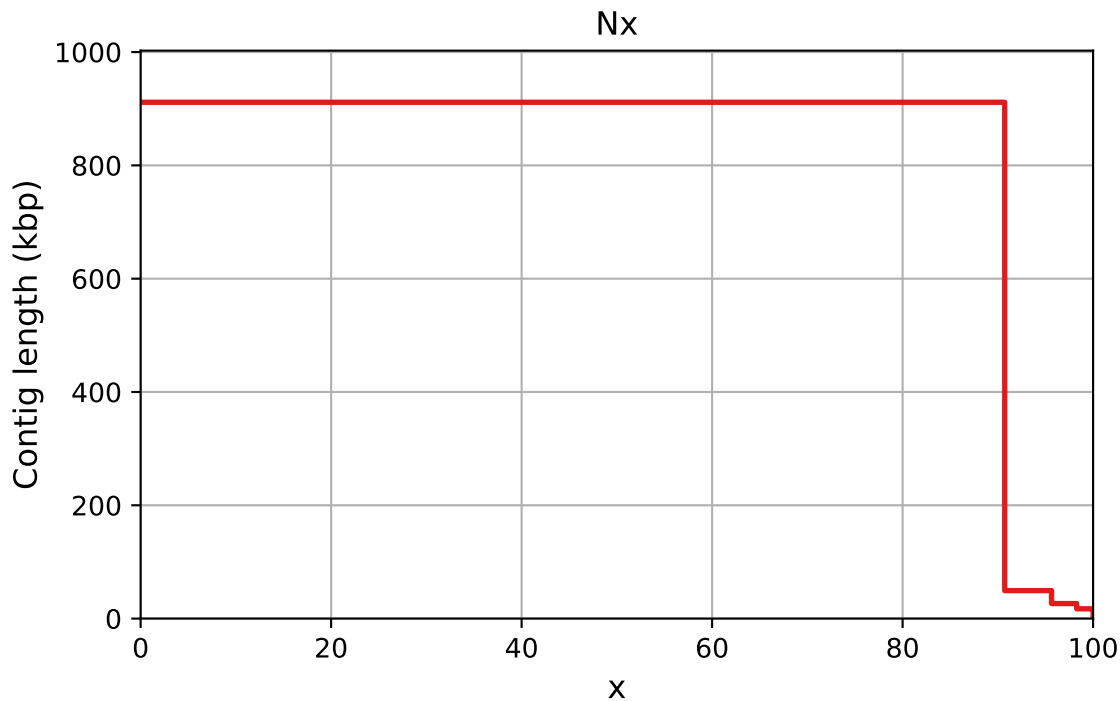
	GCA_032595515.1_ASM3259551v1_genomic
# misassemblies	2
# contig misassemblies	2
# c. relocations	1
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	928684
# local misassemblies	2
# scaffold gap ext. mis.	2
# scaffold gap loc. mis.	7
# unaligned mis. contigs	0
# mismatches	3365
# indels	171
# indels (<= 5 bp)	147
# indels (> 5 bp)	24
Indels length	683

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

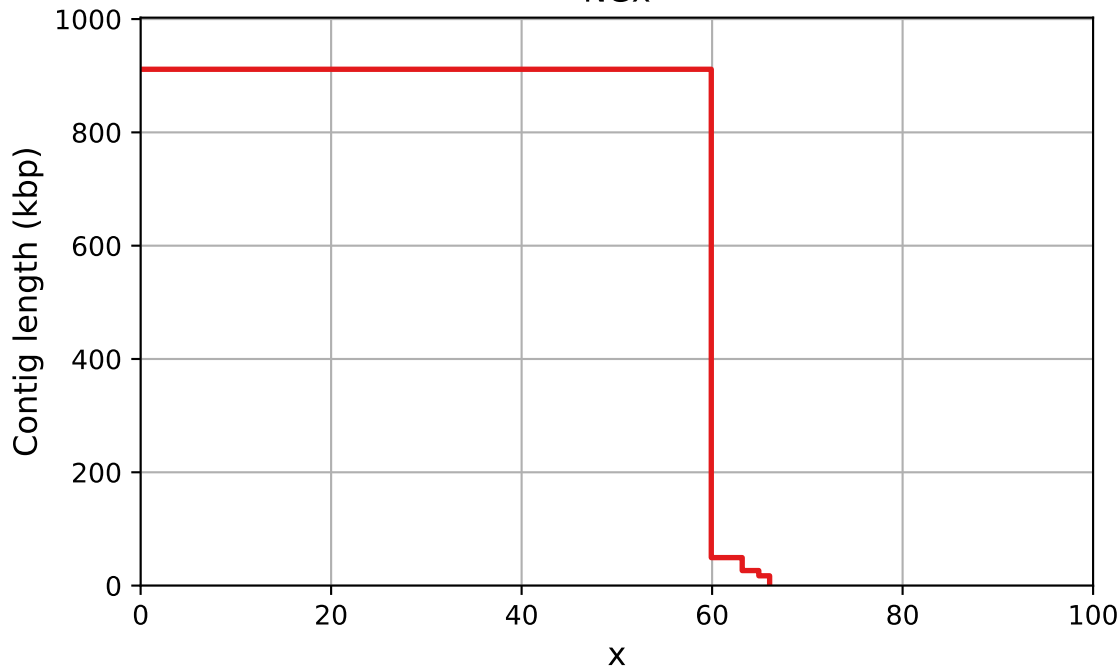
	GCA_032595515.1_ASM3259551v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	9874

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).

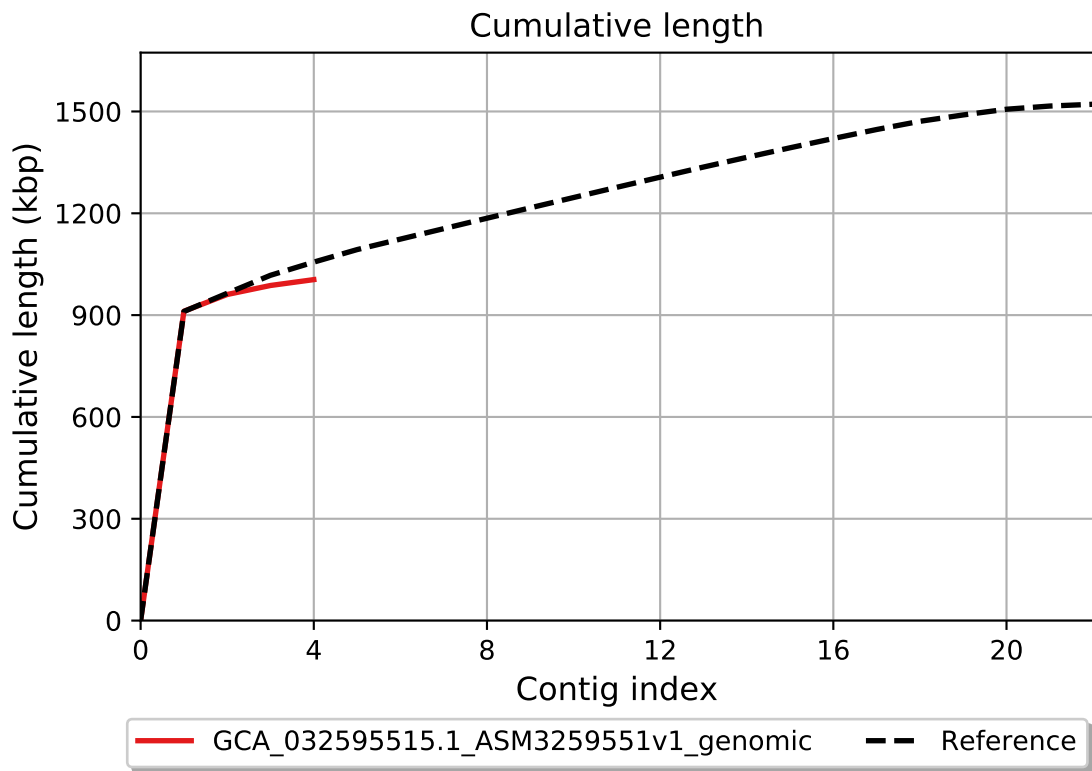


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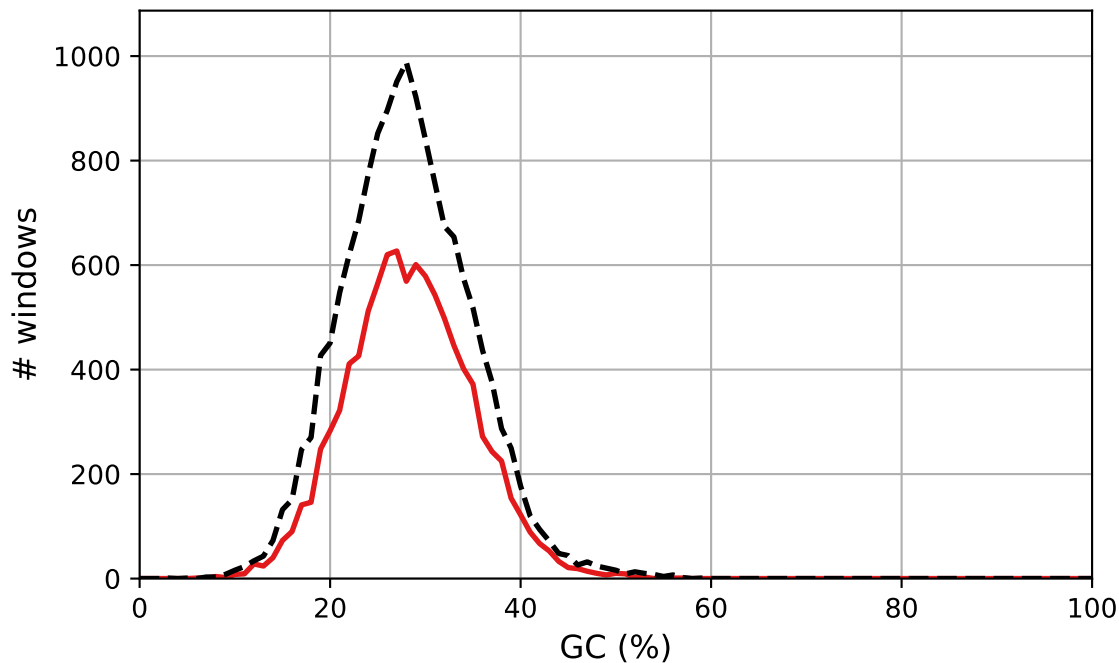
NGx



— GCA_032595515.1_ASM3259551v1_genomic



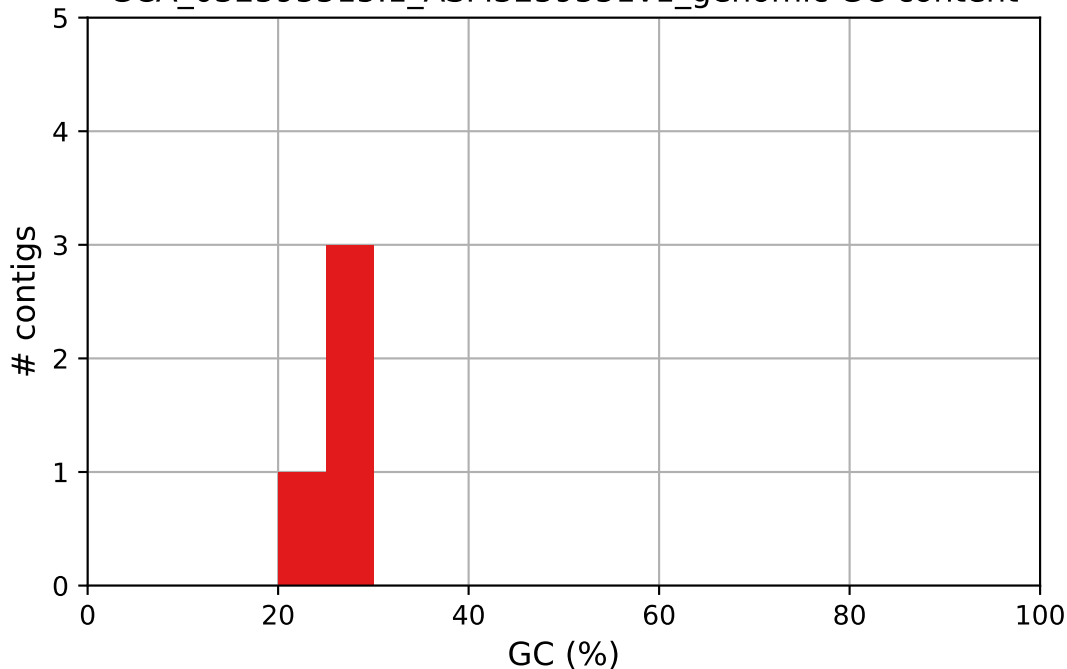
GC content



GCA_032595515.1_ASM3259551v1_genomic

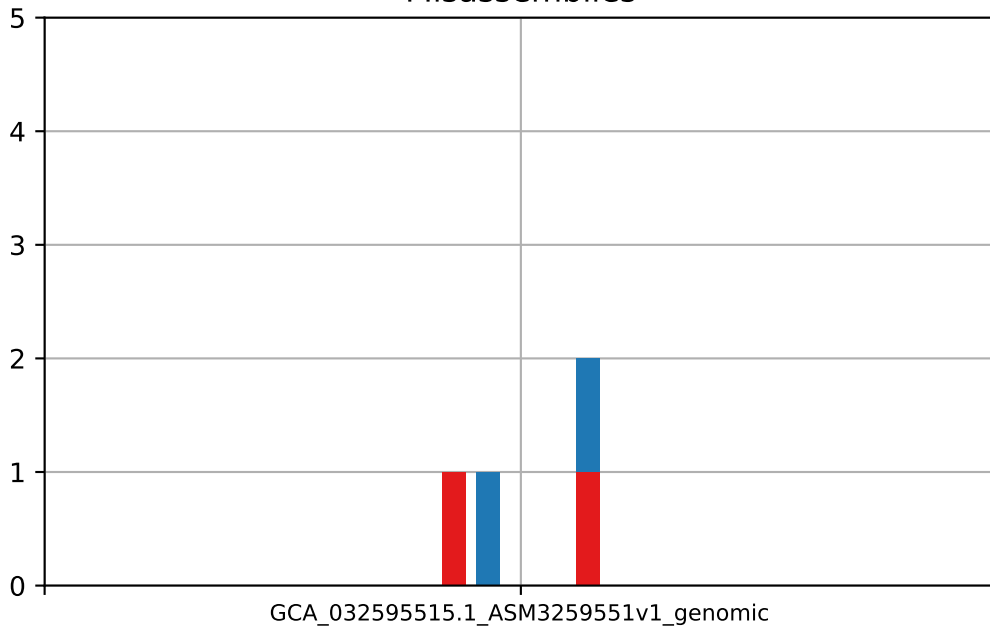
Reference

GCA_032595515.1_ASM3259551v1_genomic GC content



 GCA_032595515.1_ASM3259551v1_genomic

Misassemblies

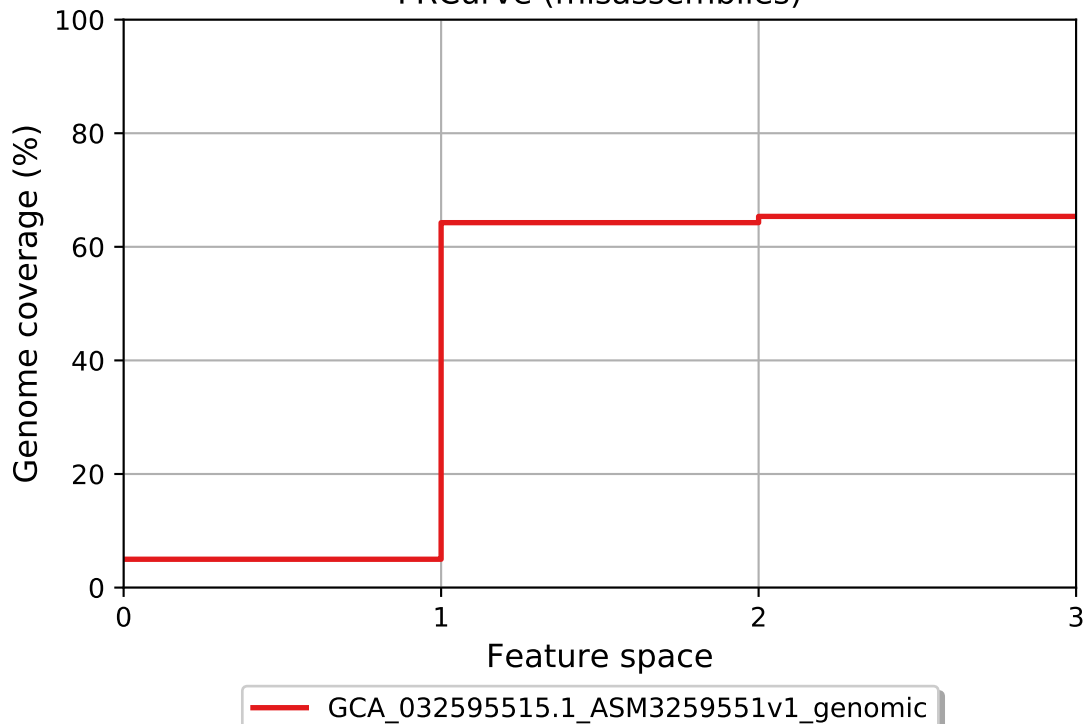


relocations

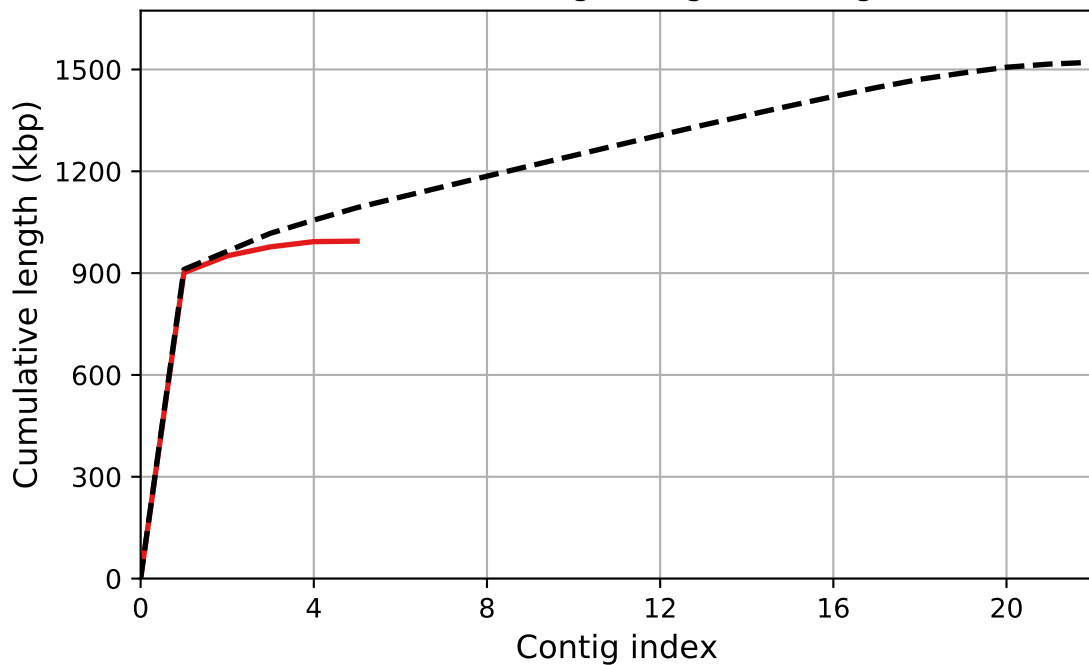


translocations

FRCurve (misassemblies)



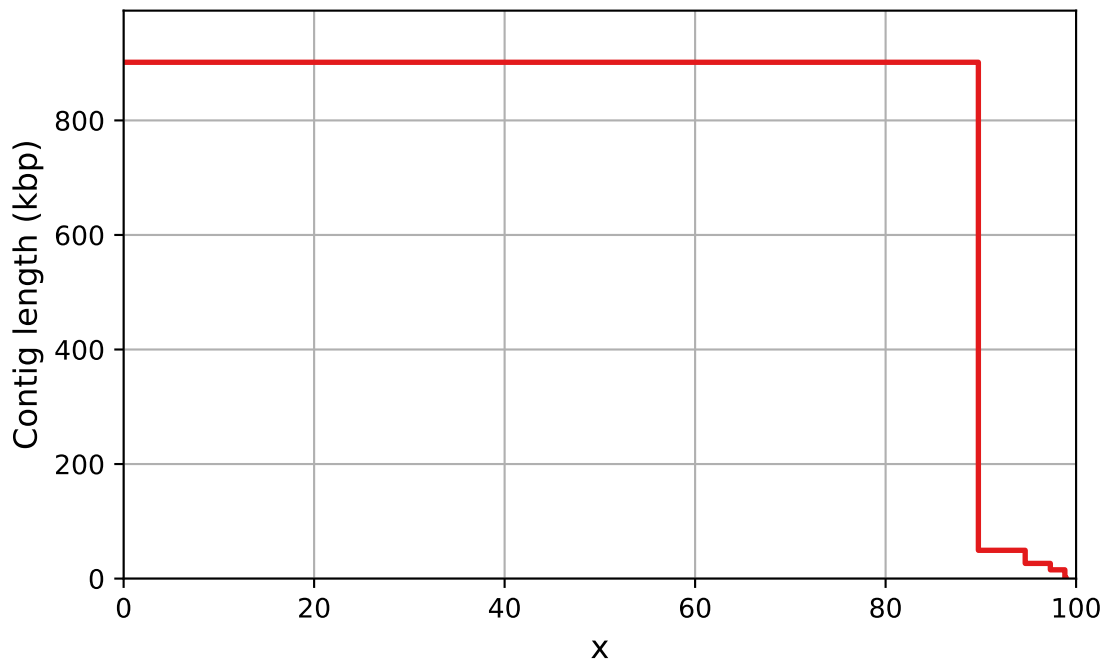
Cumulative length (aligned contigs)



GCA_032595515.1_ASM3259551v1_genomic

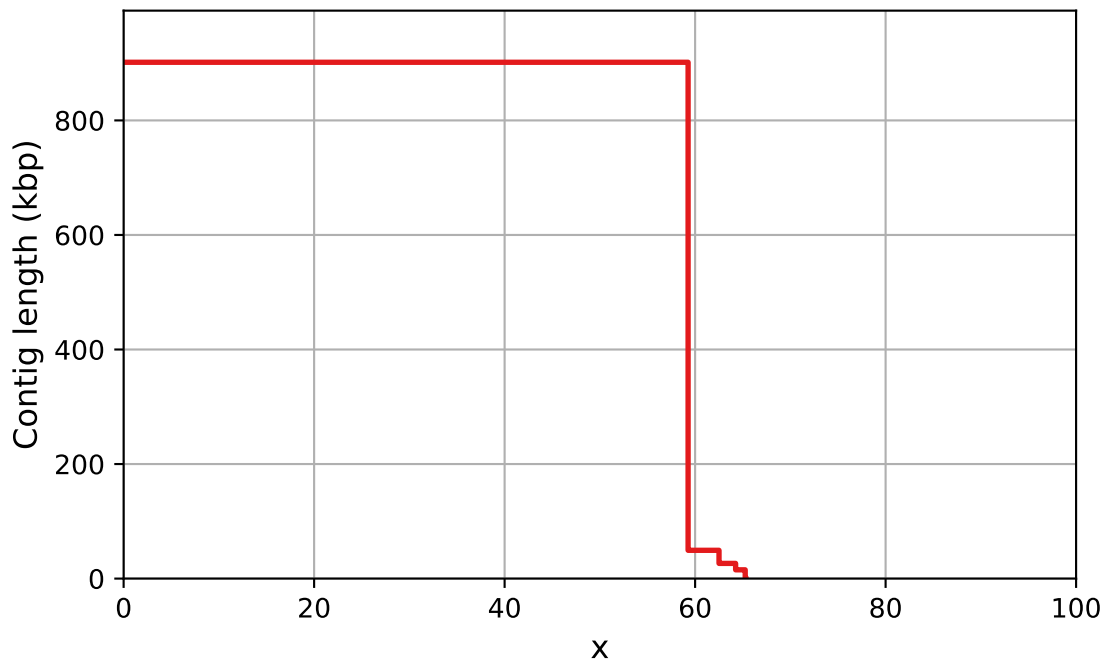
Reference

NAx

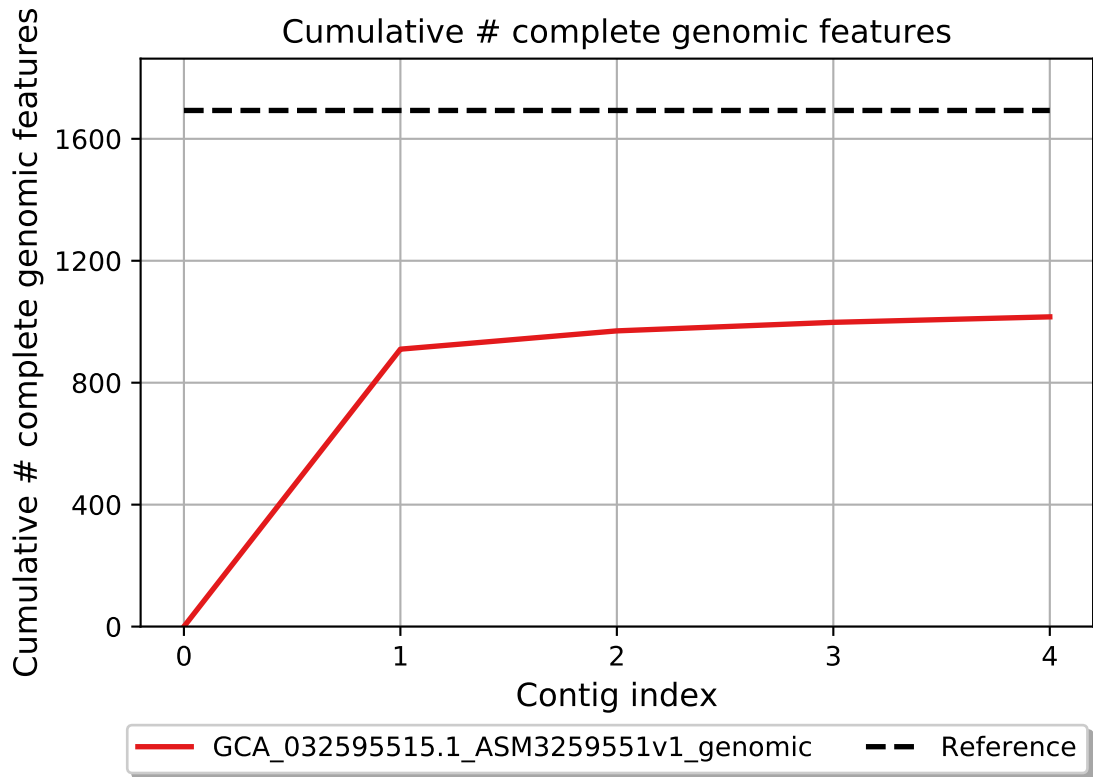


— GCA_032595515.1_ASM3259551v1_genomic

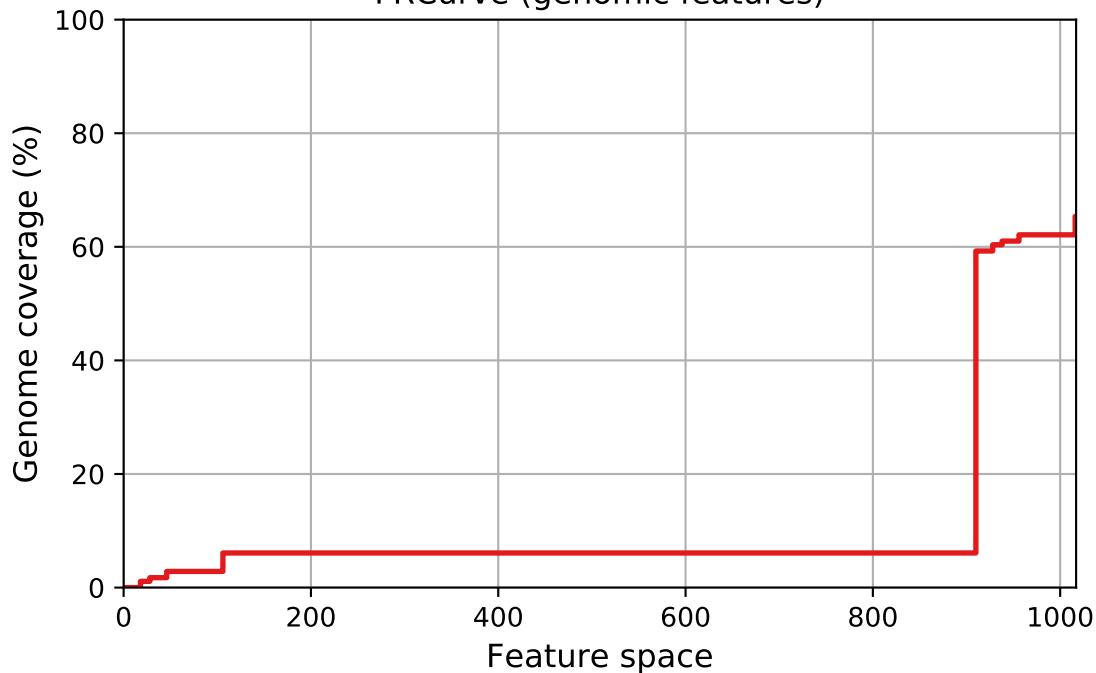
NGAx



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FRCurve (genomic features)



— GCA_032595515.1_ASM3259551v1_genomic