

# Report

GCA_032595535.1_ASM3259553v1_genomic	
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1005759
Total length (>= 1000 bp)	1005759
Total length (>= 5000 bp)	1005759
Total length (>= 10000 bp)	1005759
Total length (>= 25000 bp)	985923
Total length (>= 50000 bp)	960224
# contigs	4
Largest contig	909722
Total length	1005759
Reference length	1521208
GC (%)	28.44
Reference GC (%)	28.18
N50	909722
NG50	909722
N90	909722
NG90	-
auN	826439.0
auNG	546406.9
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	929558
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	10
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	8440
Genome fraction (%)	64.803
Duplication ratio	1.000
# N's per 100 kbp	1129.50
# mismatches per 100 kbp	569.01
# indels per 100 kbp	19.27
# genomic features	1013 + 23 part
Largest alignment	896938
Total aligned length	985924
NA50	896938
NGA50	896938
NA90	50457
NGA90	-
auNA	803201.3
auNGA	531043.0
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

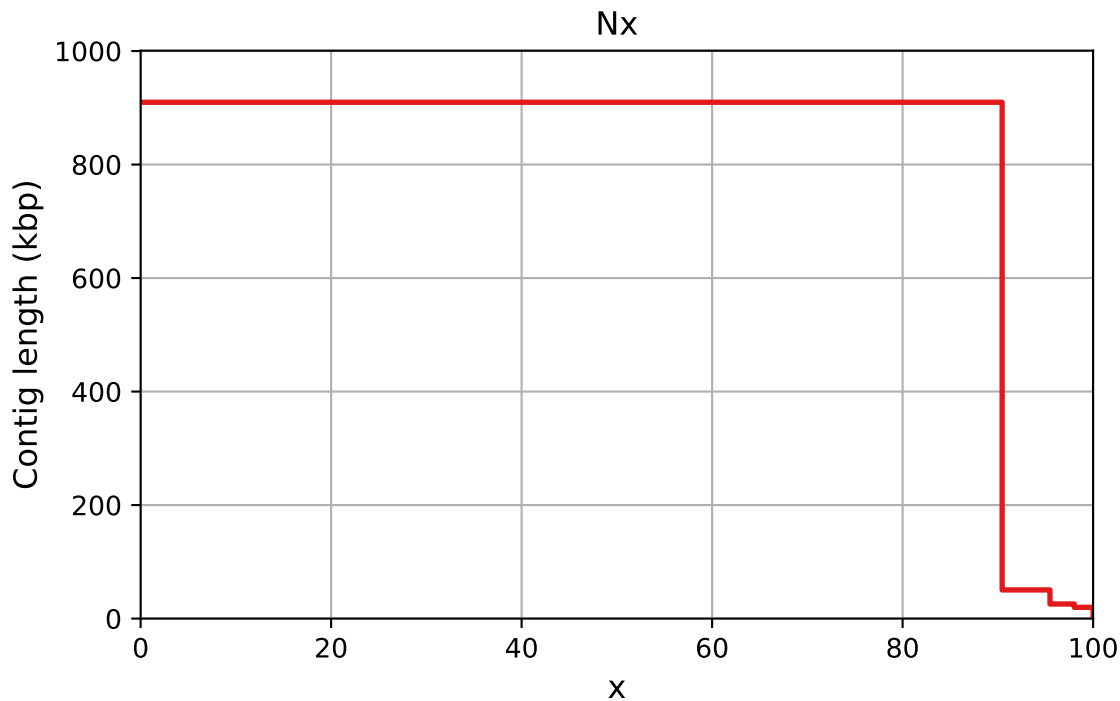
	GCA_032595535.1_ASM3259553v1_genomic
# misassemblies	2
# contig misassemblies	2
# c. relocations	0
# c. translocations	1
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	929558
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	10
# unaligned mis. contigs	0
# mismatches	5610
# indels	190
# indels (<= 5 bp)	166
# indels (> 5 bp)	24
Indels length	954

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

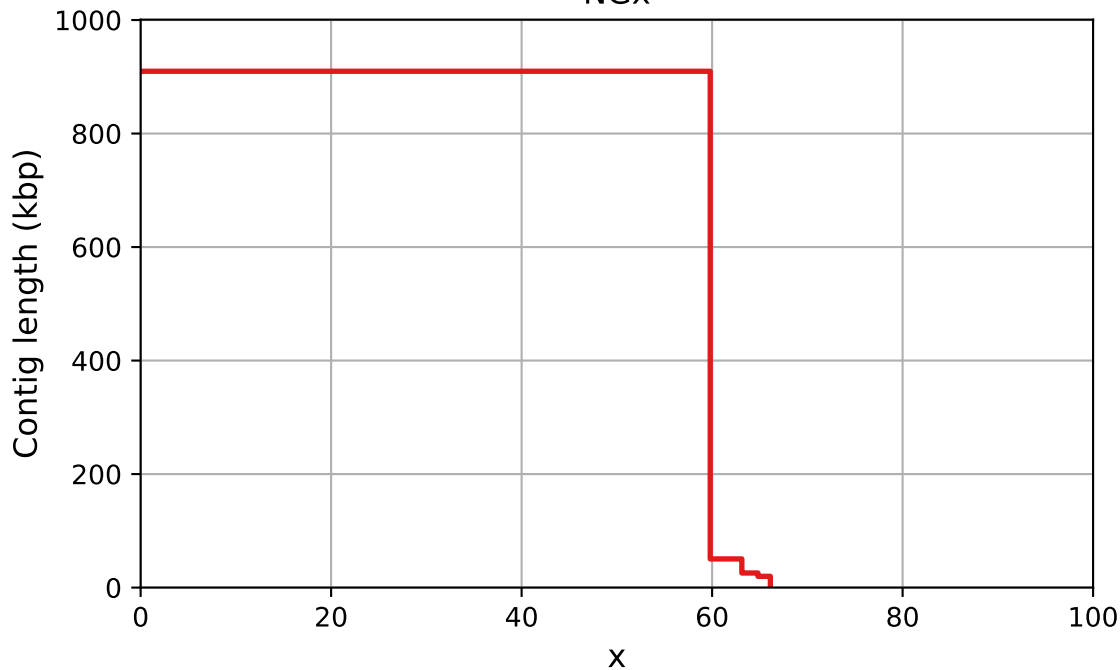
	GCA_032595535.1_ASM3259553v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	8440
# N's	11360

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).

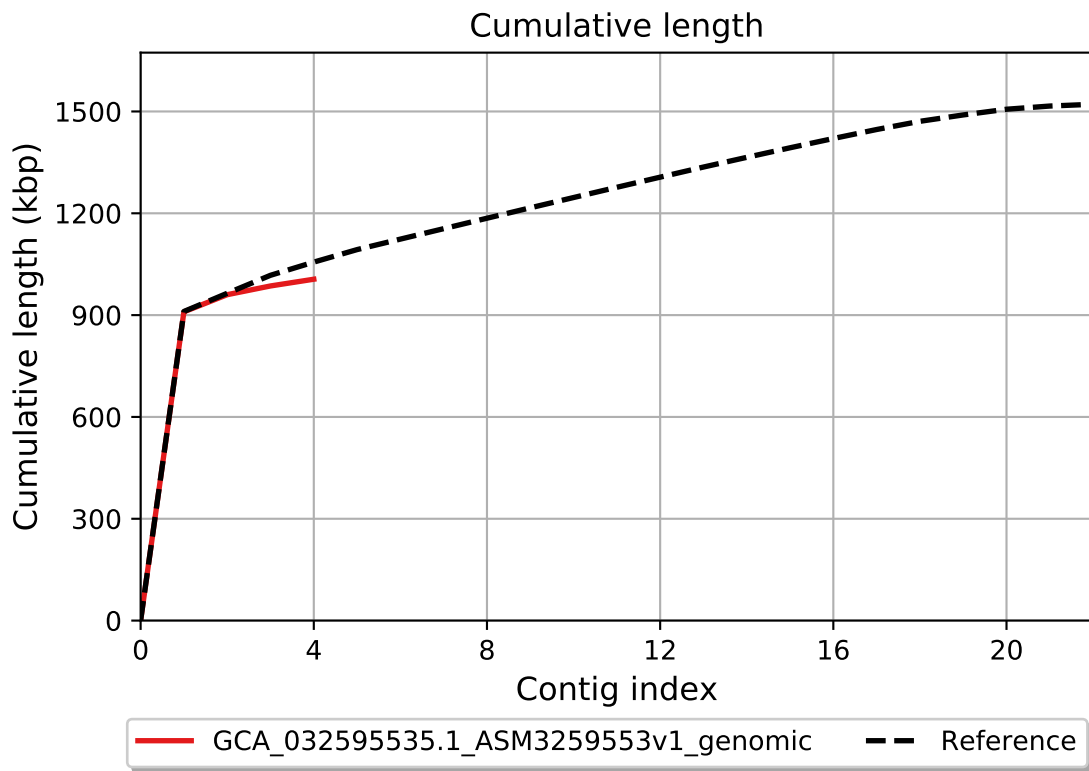


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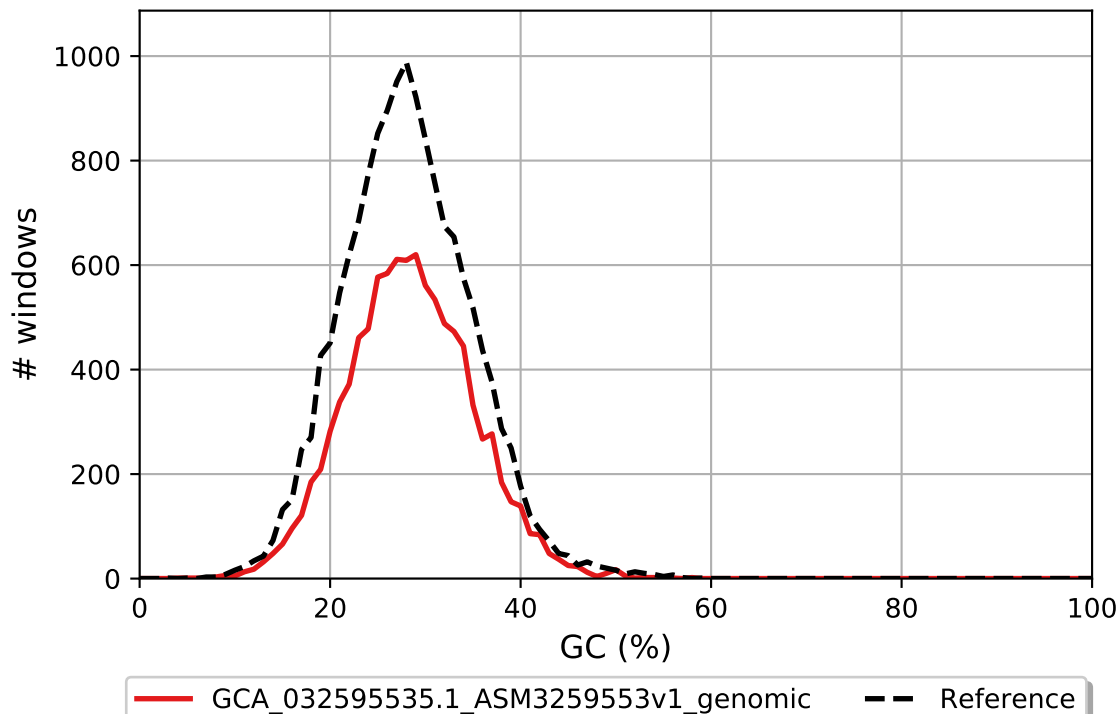
NGx



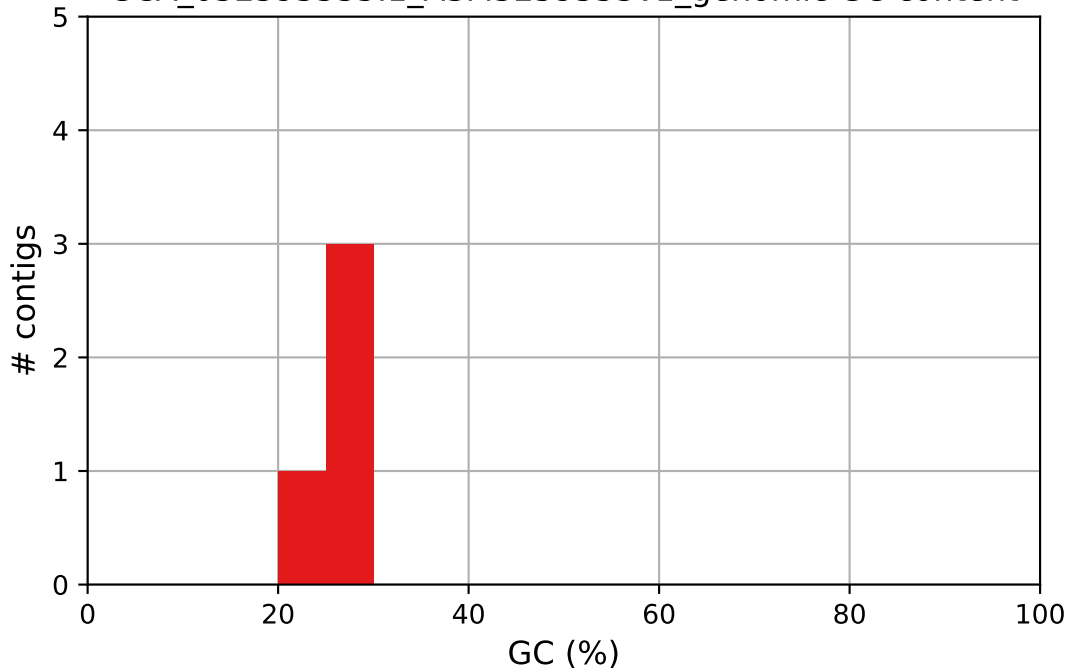
— GCA\_032595535.1\_ASM3259553v1\_genomic



## GC content



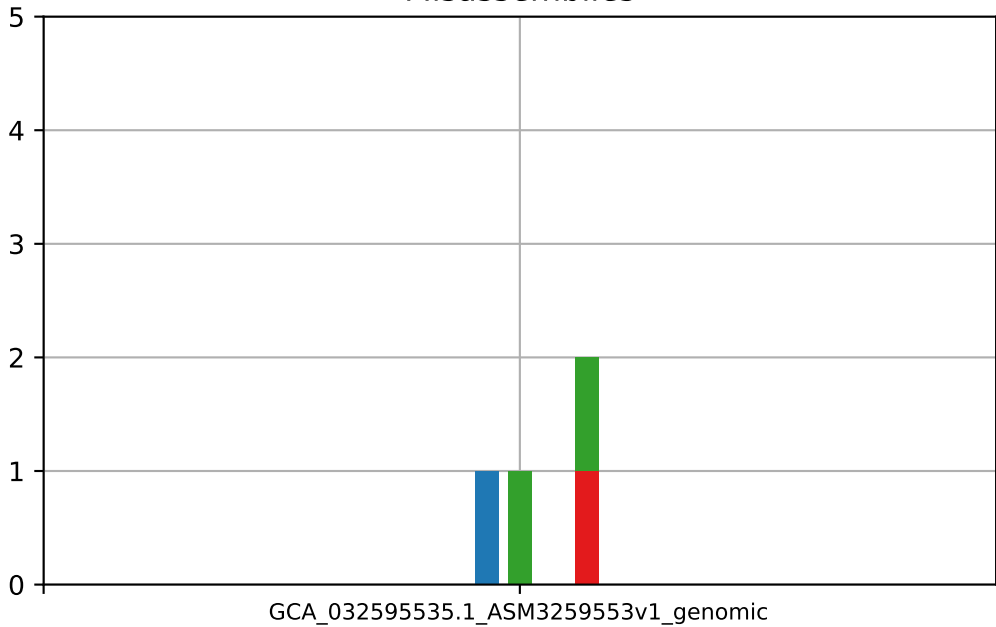
GCA\_032595535.1\_ASM3259553v1\_genomic GC content



GCA\_032595535.1\_ASM3259553v1\_genomic



## Misassemblies

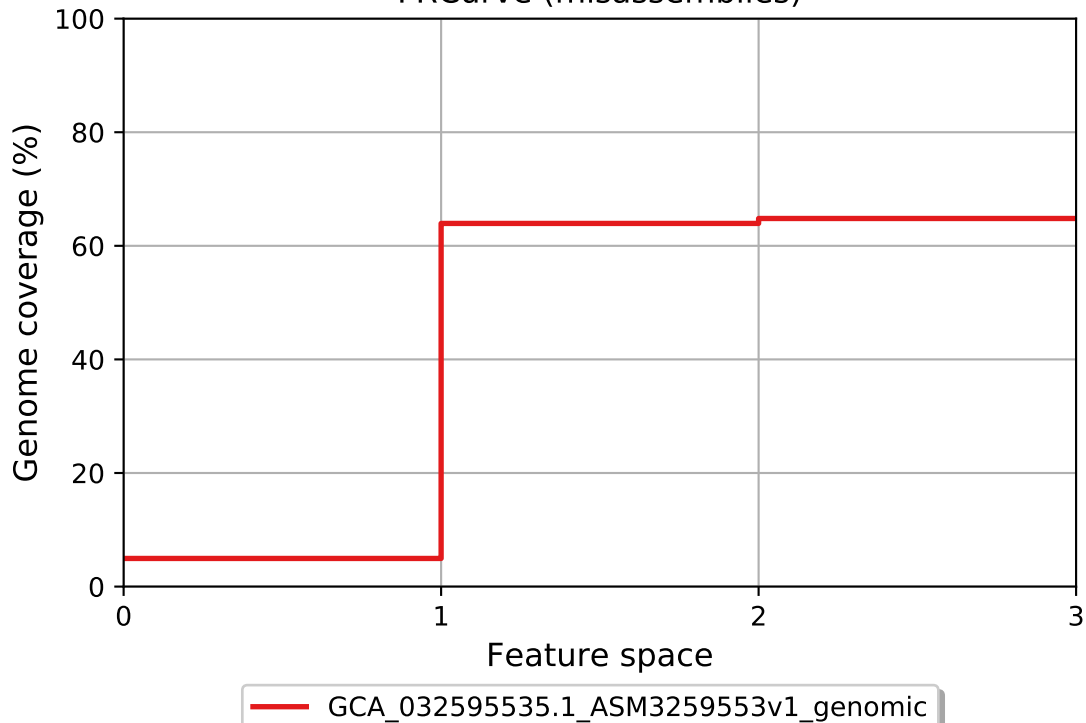


# translocations

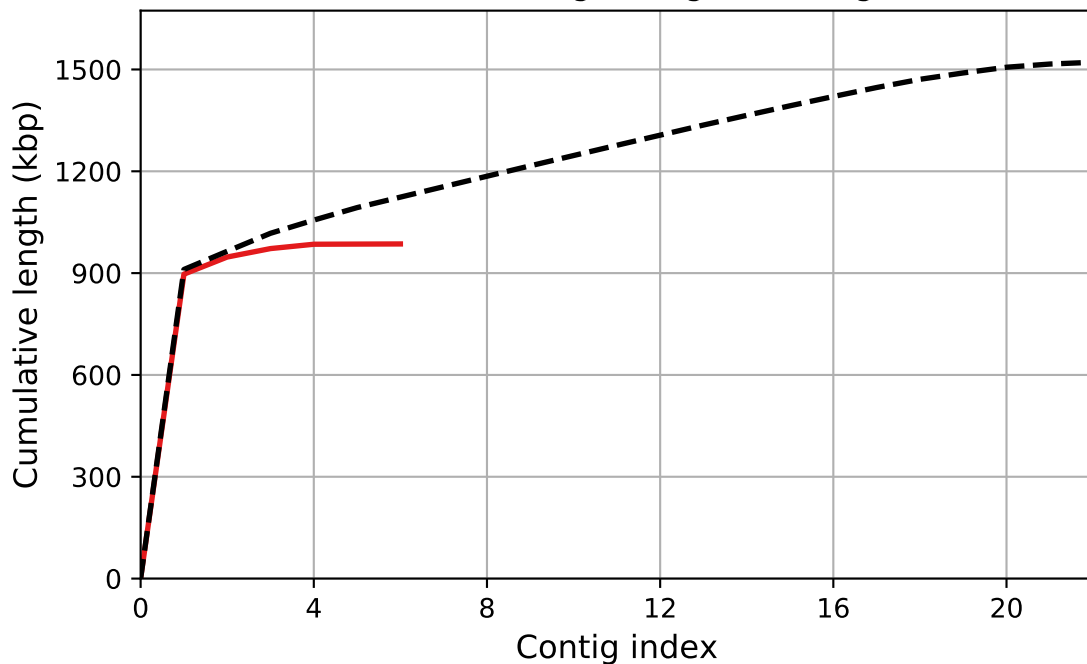


# inversions

FRCurve (misassemblies)



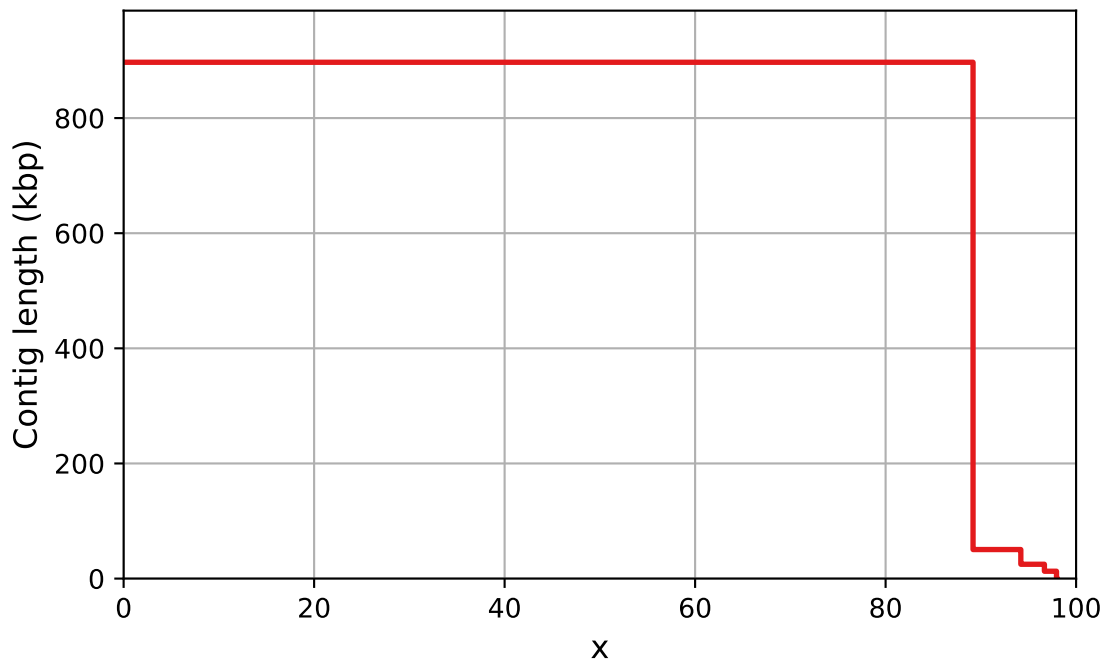
Cumulative length (aligned contigs)



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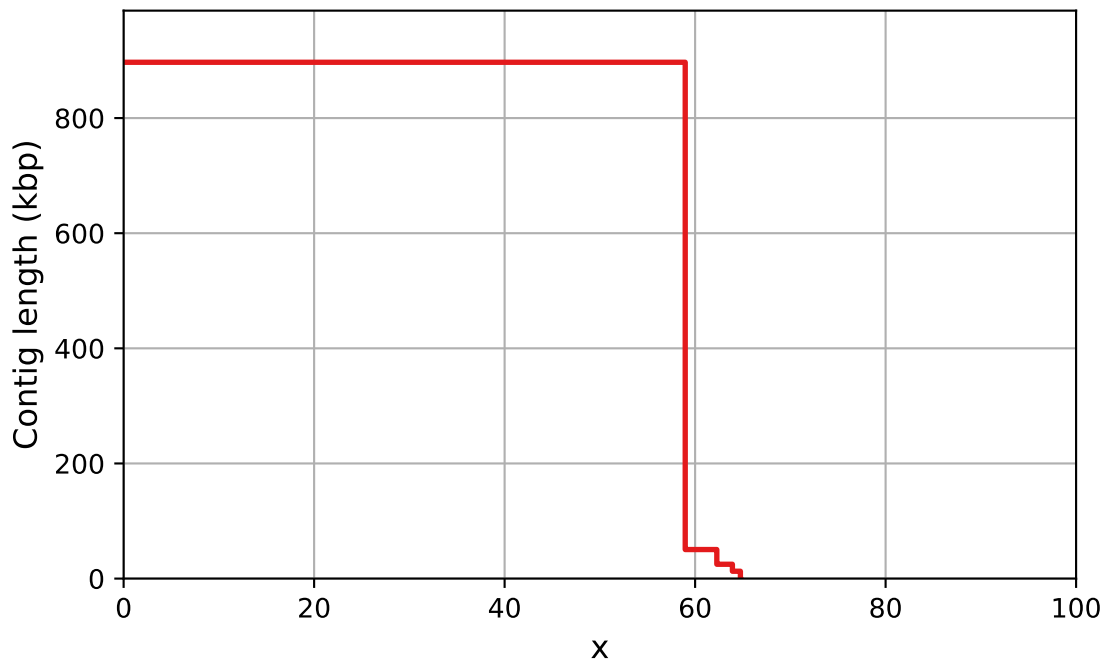
Reference

NAx

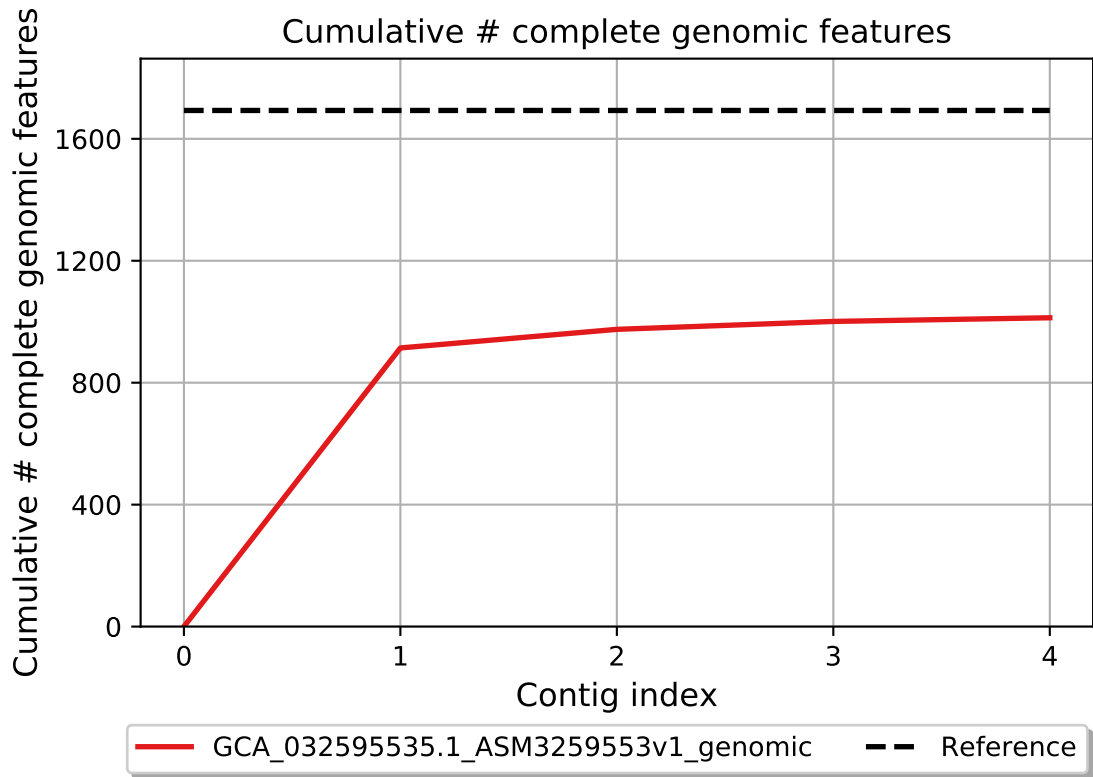


— GCA\_032595535.1\_ASM3259553v1\_genomic

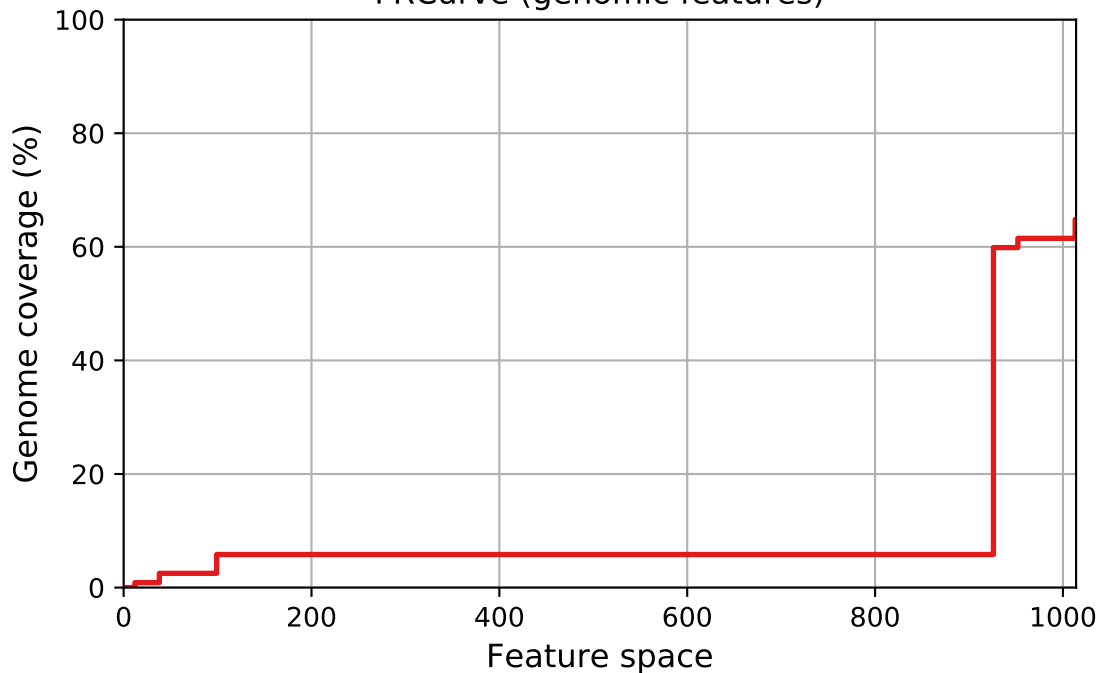
NGAx



— GCA\_032595535.1\_ASM3259553v1\_genomic



FRCurve (genomic features)



— GCA\_032595535.1\_ASM3259553v1\_genomic