

# Report

GCA_030444985.1_ASM3044498v1_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)	1007632
Total length (>= 1000 bp)	1007632
Total length (>= 5000 bp)	1007632
Total length (>= 10000 bp)	1007632
Total length (>= 25000 bp)	990728
Total length (>= 50000 bp)	964230
# contigs	4
Largest contig	910563
Total length	1007632
Reference length	1521208
GC (%)	28.42
Reference GC (%)	28.18
N50	910563
NG50	910563
N90	910563
NG90	-
auN	826683.8
auNG	547586.5
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.243
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.73
# indels per 100 kbp	4.07
# genomic features	1050 + 0 part
Largest alignment	910563
Total aligned length	1007503
NA50	910563
NGA50	910563
NA90	910563
NGA90	-
auNA	826677.9
auNGA	547582.7
LA50	1
LGA50	1
LA90	1
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

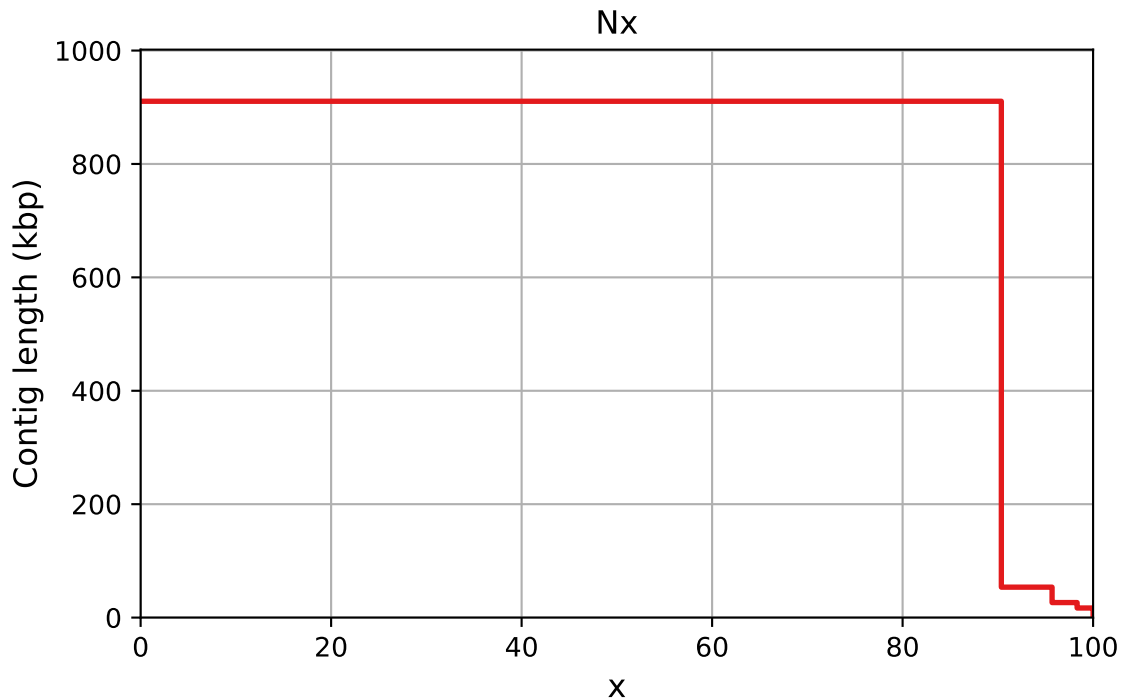
	GCA_030444985.1_ASM3044498v1_genomic
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	88
# indels	41
# indels (<= 5 bp)	37
# indels (> 5 bp)	4
Indels length	243

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

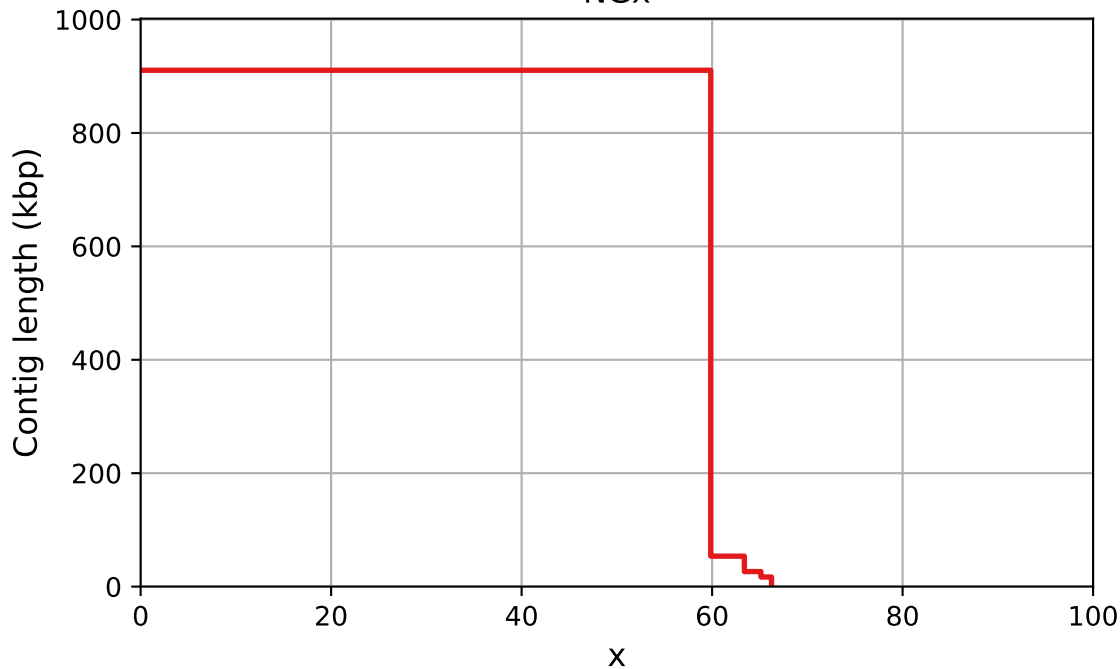
	GCA_030444985.1_ASM3044498v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

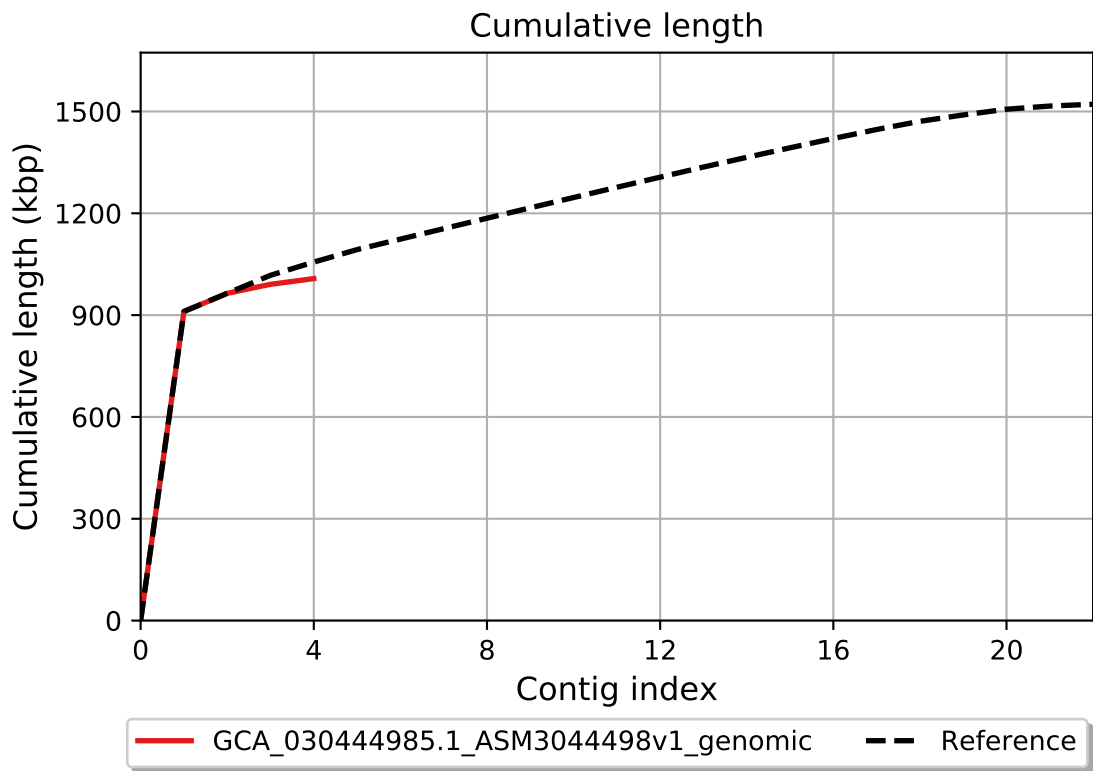


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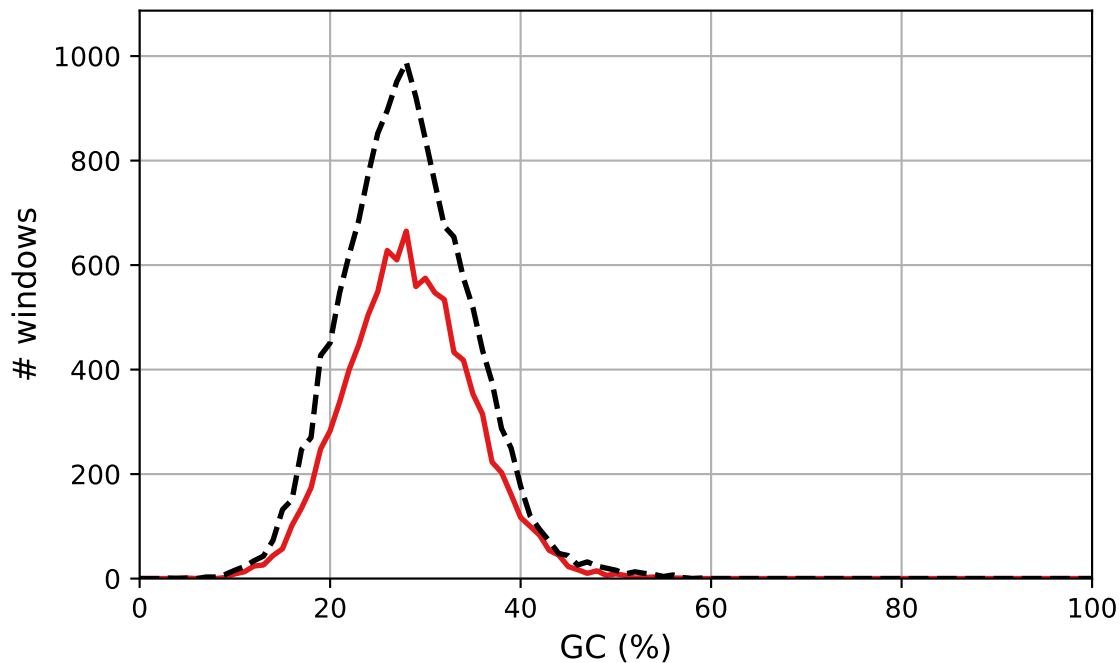
NGx



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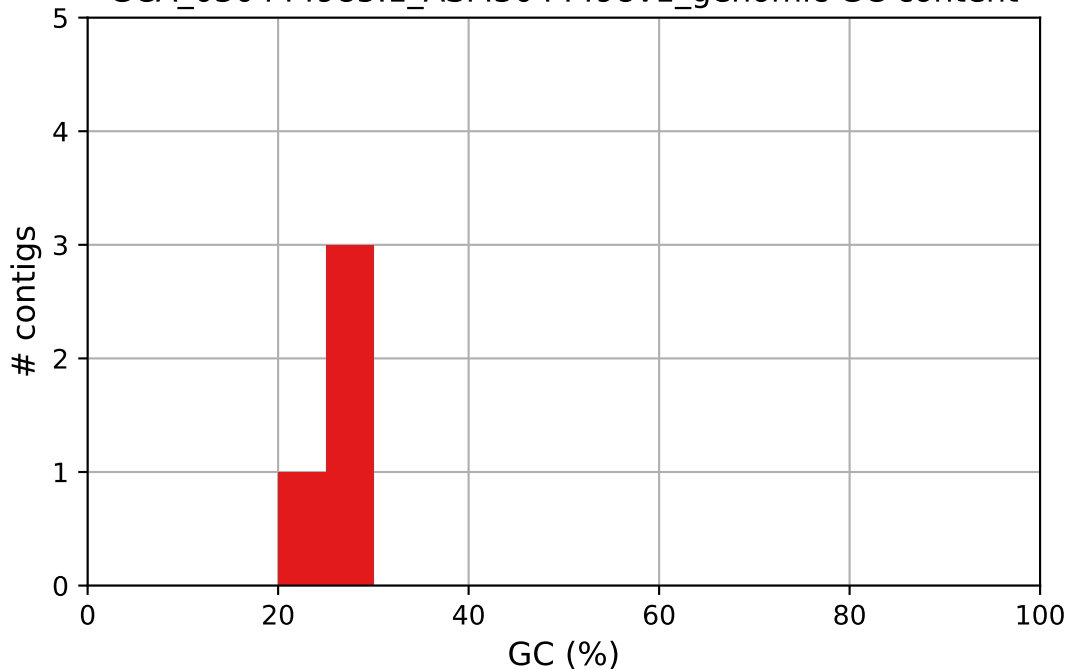
## GC content



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-- Reference

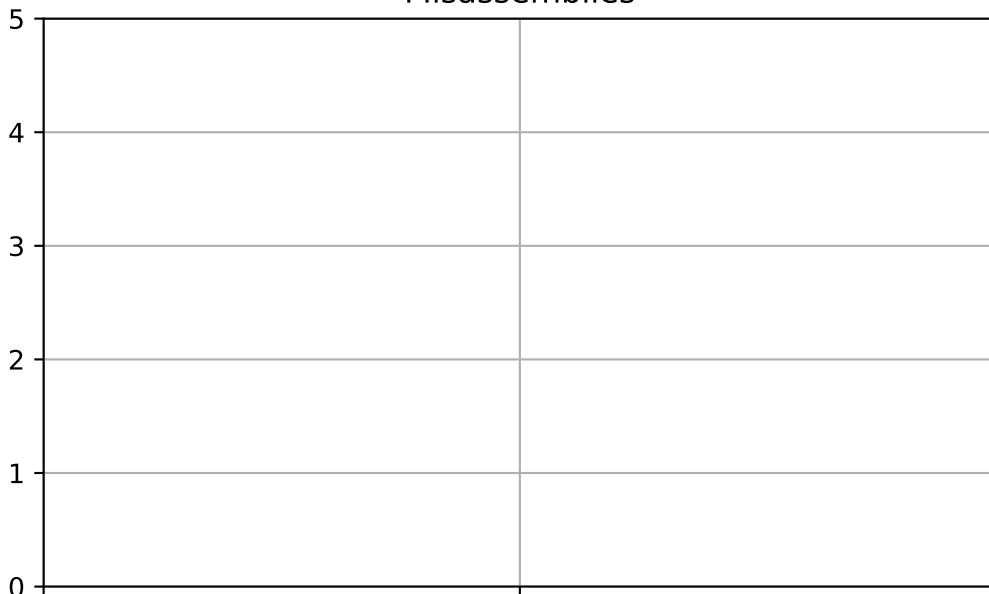
GCA\_030444985.1\_ASM3044498v1\_genomic GC content



GCA\_030444985.1\_ASM3044498v1\_genomic

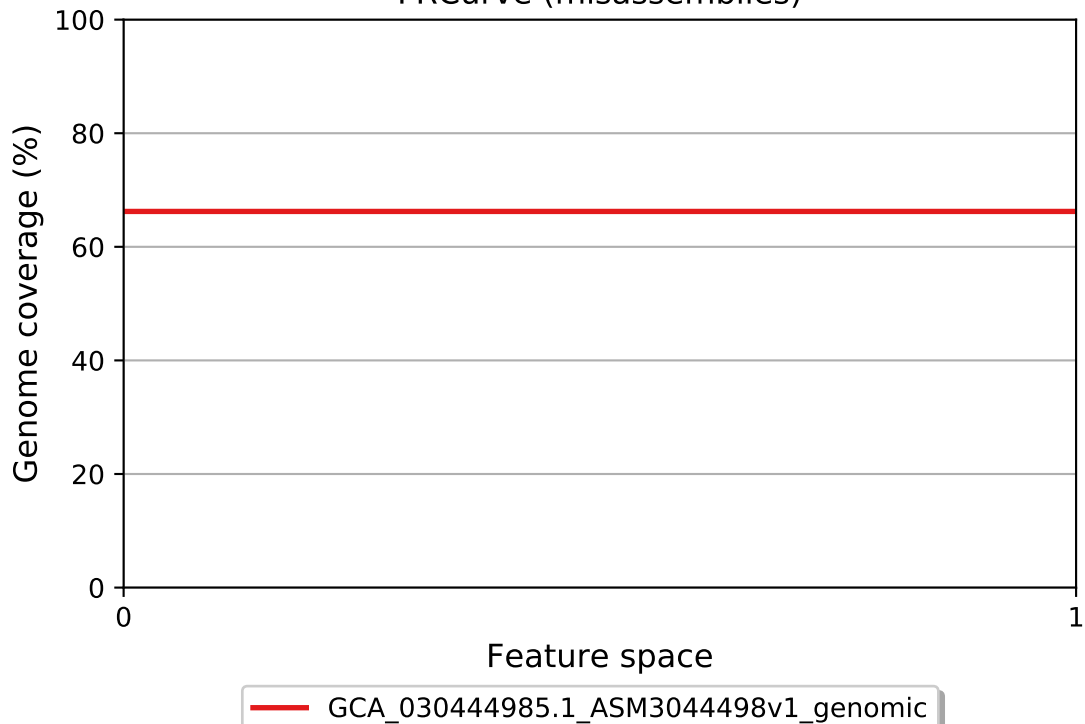


## Misassemblies

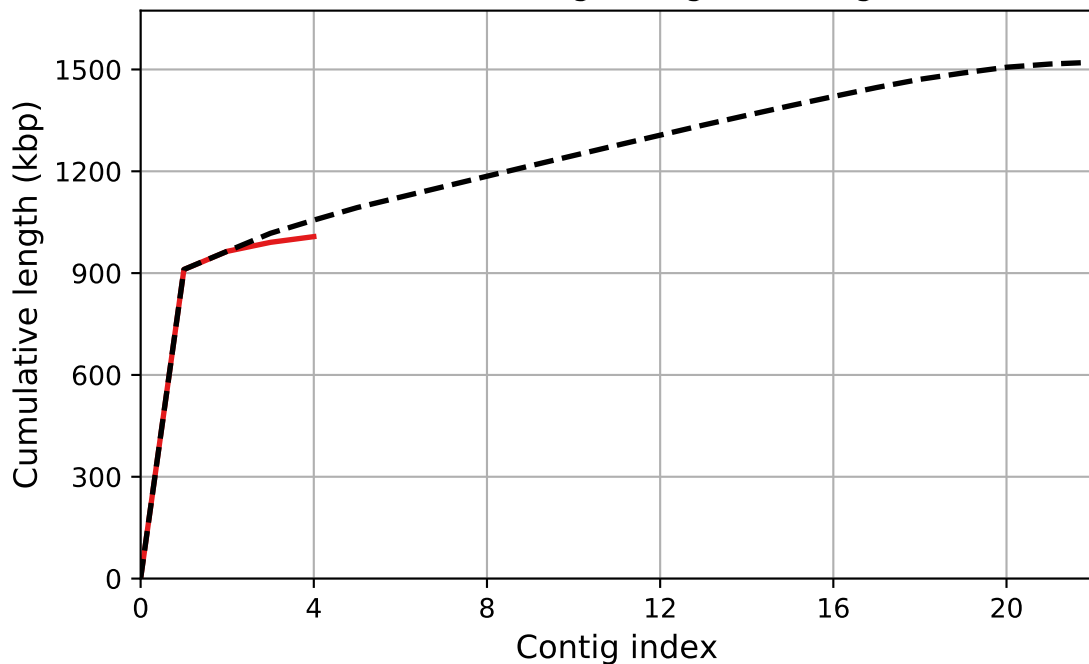


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FRCurve (misassemblies)



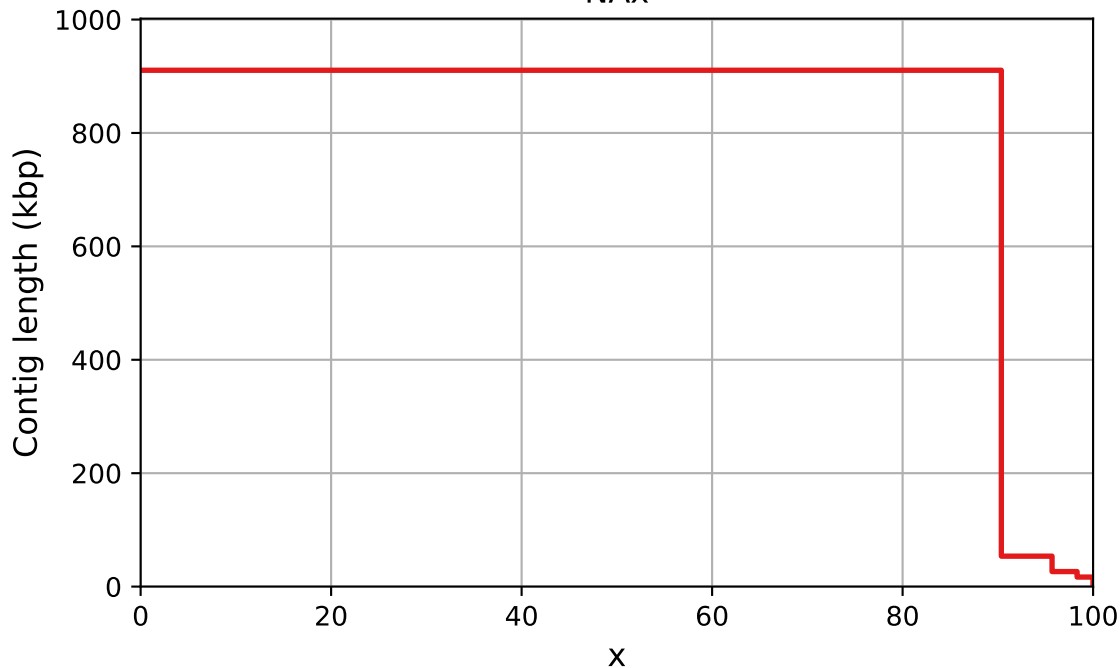
Cumulative length (aligned contigs)



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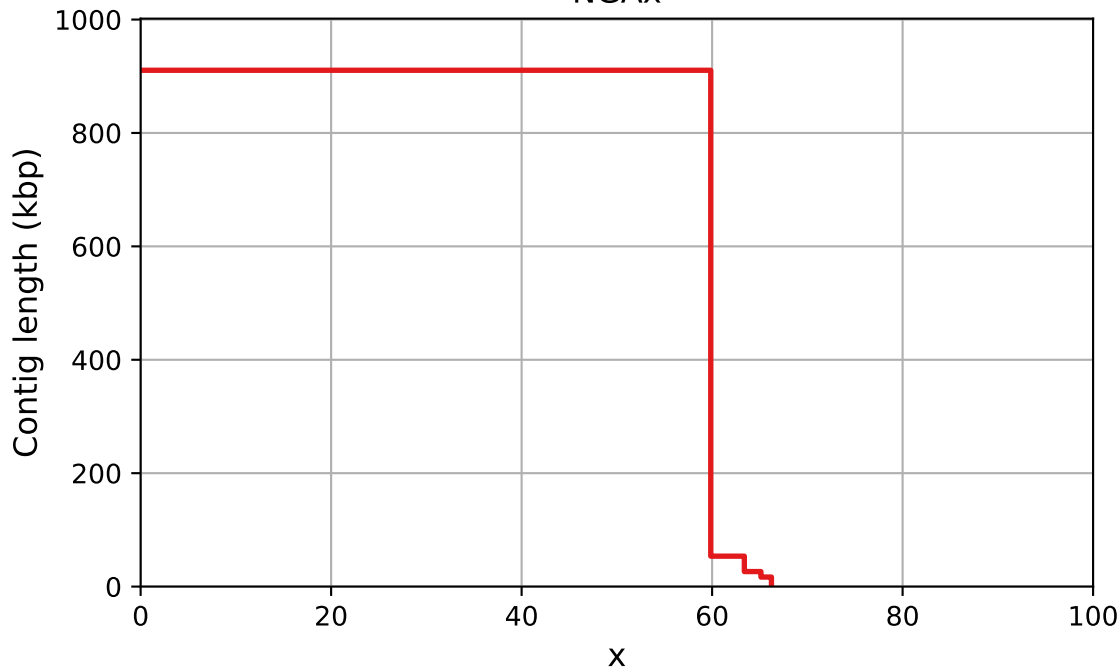
Reference

NAx

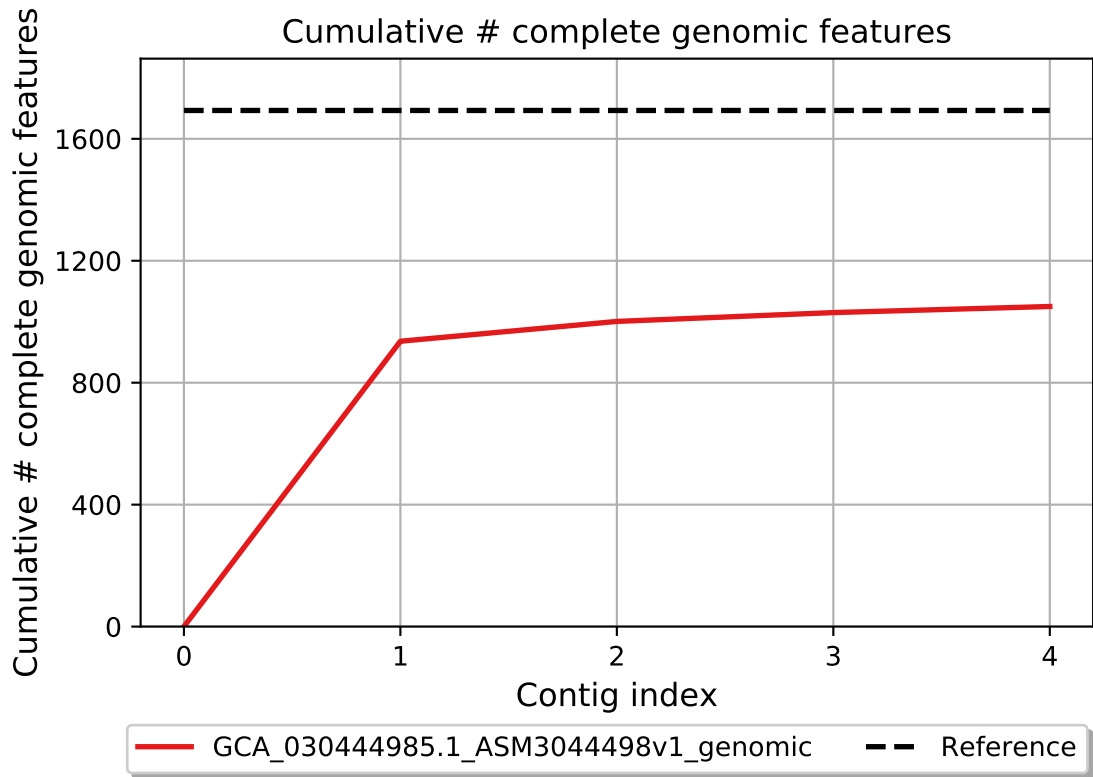


— GCA\_030444985.1\_ASM3044498v1\_genomic

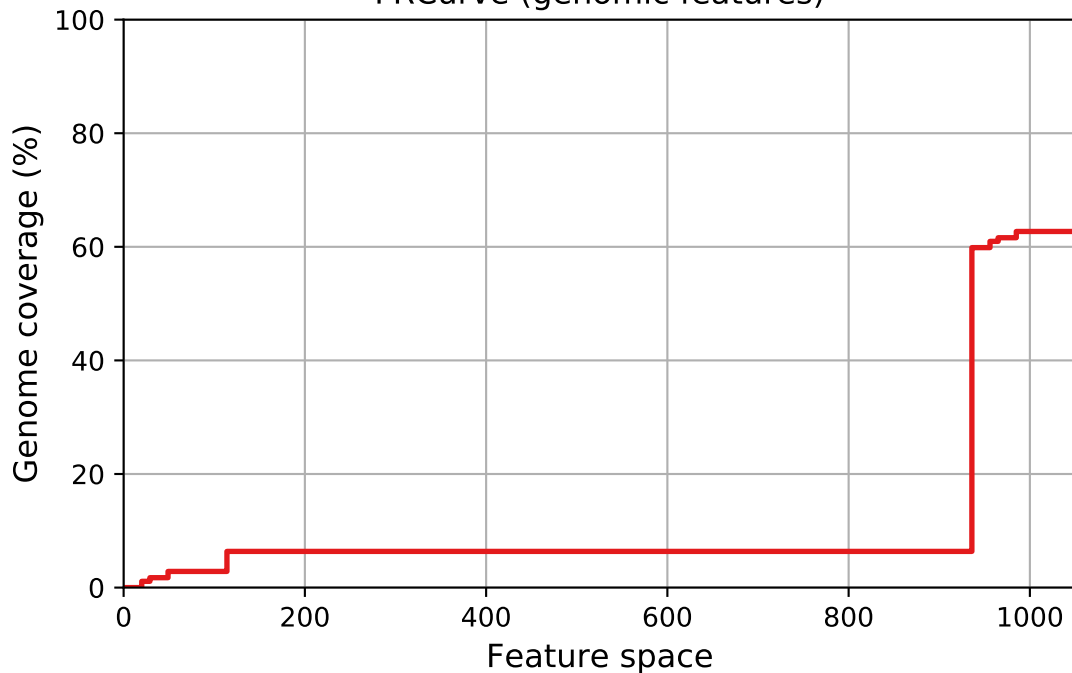
NGAx



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FRCurve (genomic features)



— GCA\_030444985.1\_ASM3044498v1\_genomic