

Report

	GCF_000021405.1_ASM2140v1_genomic
# contigs (>= 0 bp)	15
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1345494
Total length (>= 1000 bp)	1345494
Total length (>= 5000 bp)	1345494
Total length (>= 10000 bp)	1345494
Total length (>= 25000 bp)	1280480
Total length (>= 50000 bp)	960322
# contigs	15
Largest contig	906707
Total length	1345494
Reference length	1521208
GC (%)	28.27
Reference GC (%)	28.18
N50	906707
NG50	906707
N90	28885
NG90	-
auN	622101.9
auNG	550243.2
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	1012994
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 6 part
Unaligned length	71256
Genome fraction (%)	83.267
Duplication ratio	1.003
# N's per 100 kbp	0.37
# mismatches per 100 kbp	511.34
# indels per 100 kbp	38.10
# genomic features	1349 + 27 part
Largest alignment	903539
Total aligned length	1270379
NA50	903539
NGA50	903539
NA90	17211
NGA90	-
auNA	614395.0
auNGA	543426.5
LA50	1
LGA50	1
LA90	12
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

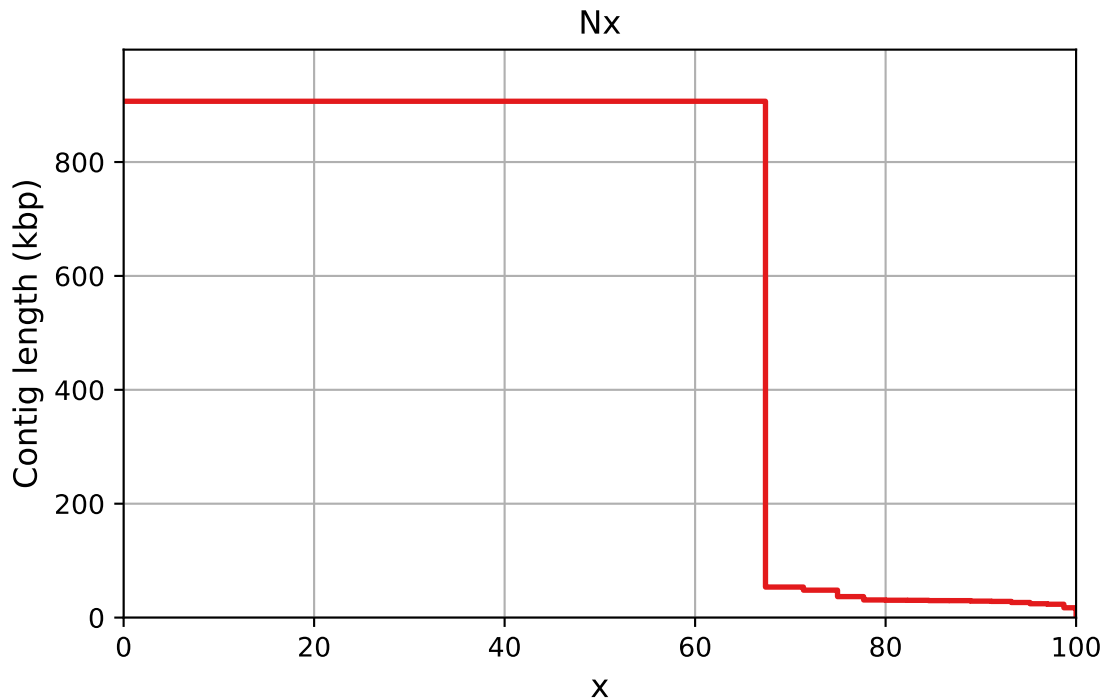
	GCF_000021405.1_ASM2140v1_genomic
# misassemblies	7
# contig misassemblies	7
# c. relocations	2
# c. translocations	5
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	1012994
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	6496
# indels	484
# indels (<= 5 bp)	424
# indels (> 5 bp)	60
Indels length	3091

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

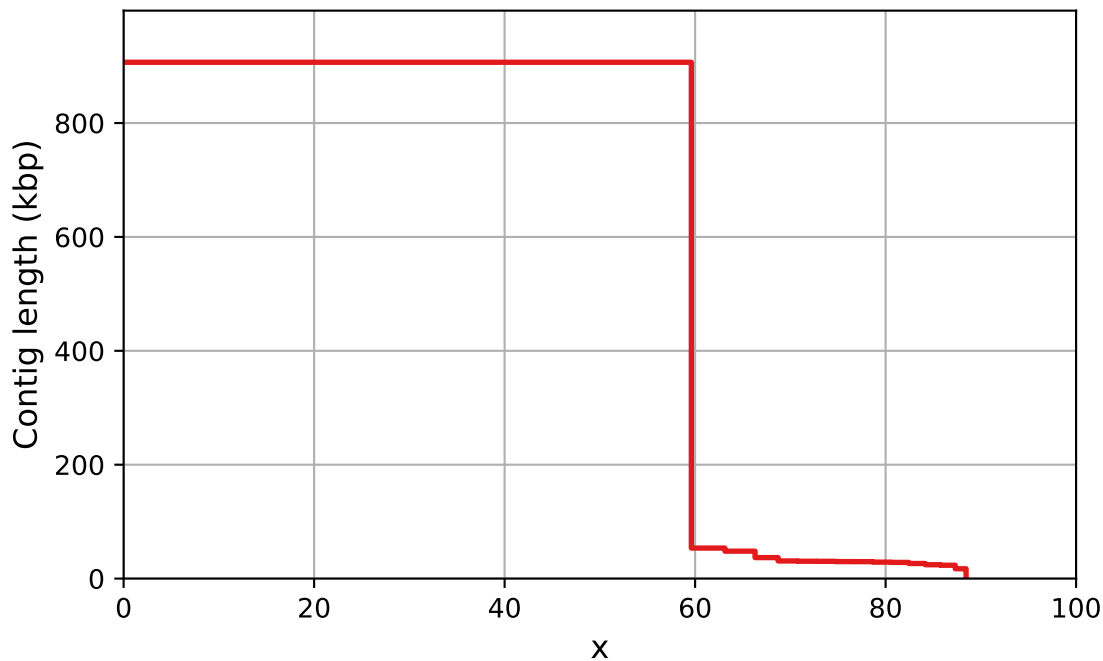
	GCF_000021405.1_ASM2140v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	71256
# N's	5

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).

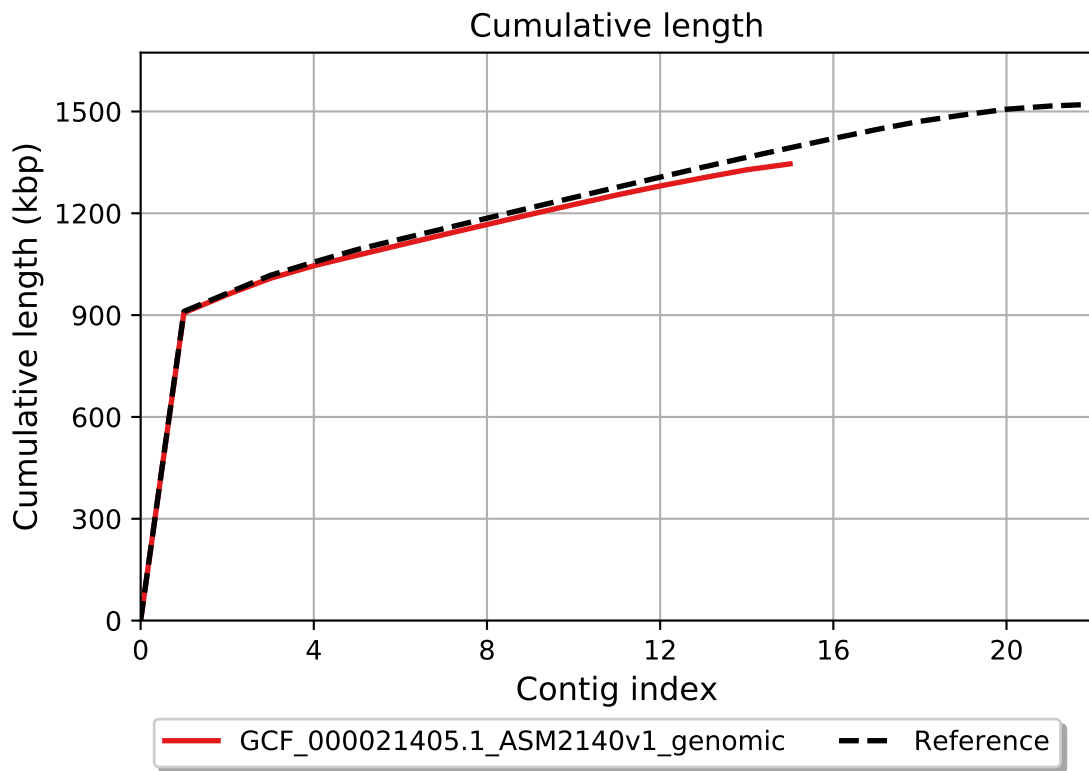


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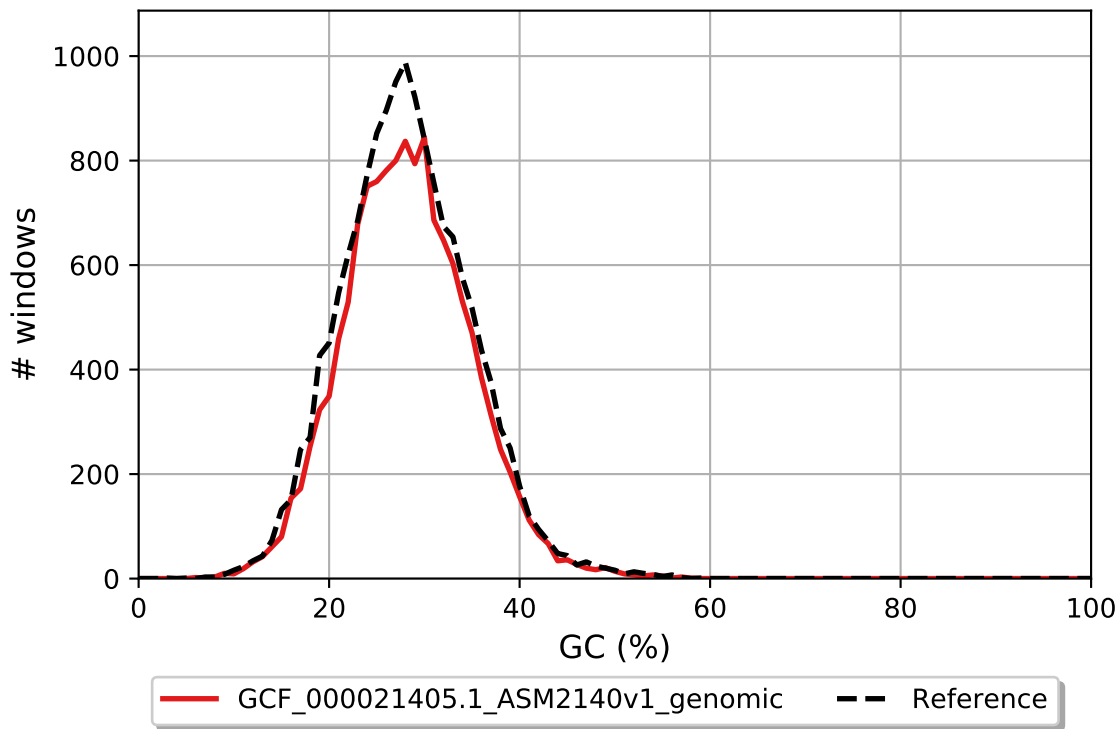
NGx



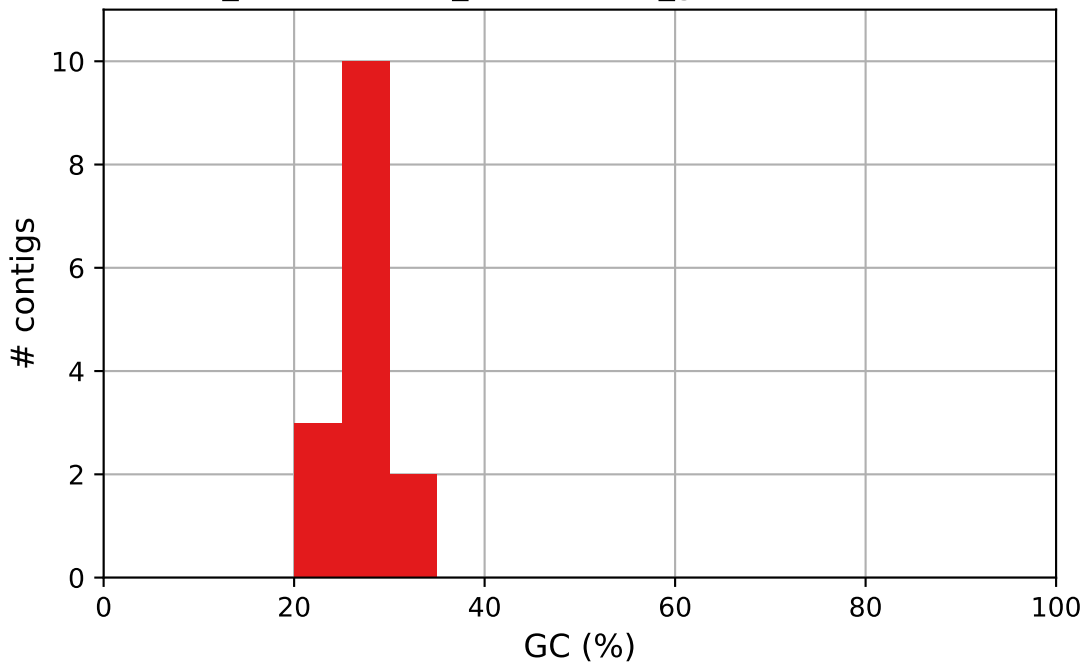
— GCF\_000021405.1\_ASM2140v1\_genomic



## GC content



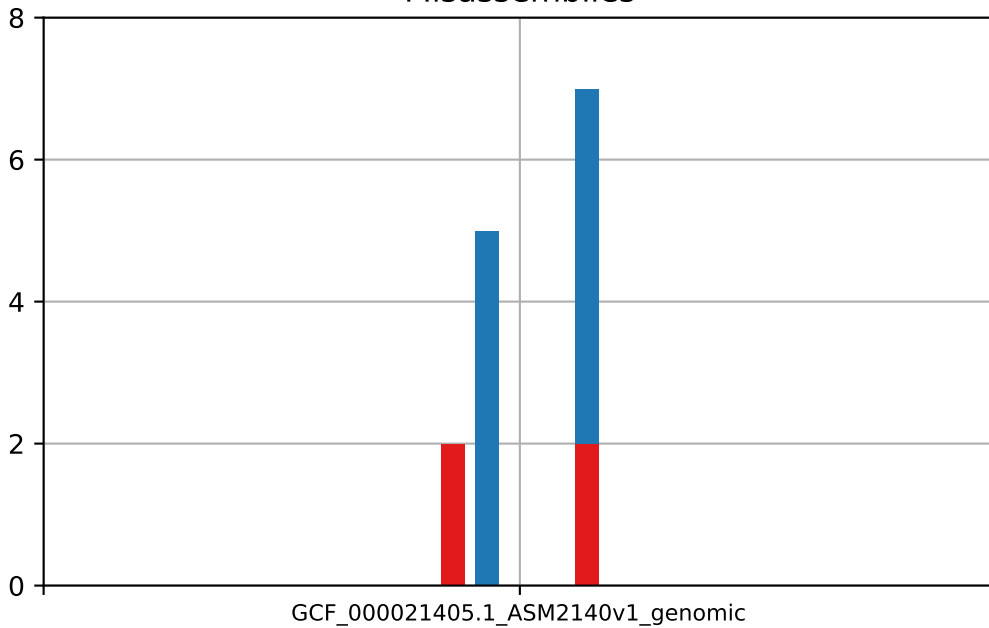
GCF\_000021405.1\_ASM2140v1\_genomic GC content



GCF\_000021405.1\_ASM2140v1\_genomic



## Misassemblies

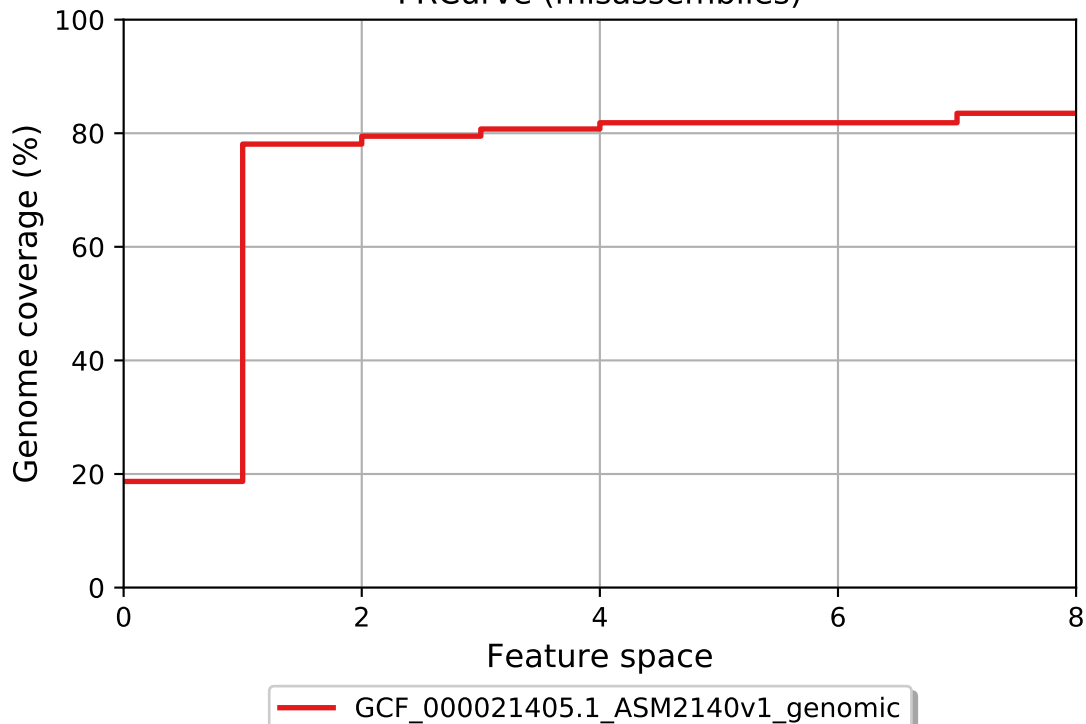


# relocations

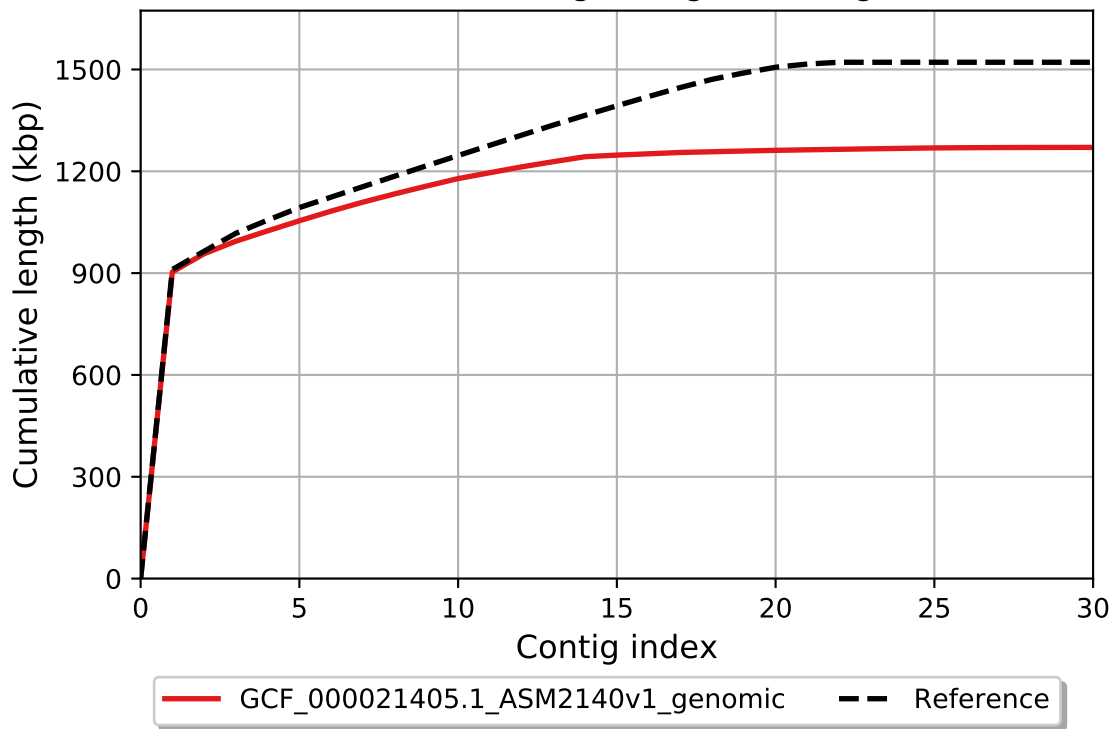


# translocations

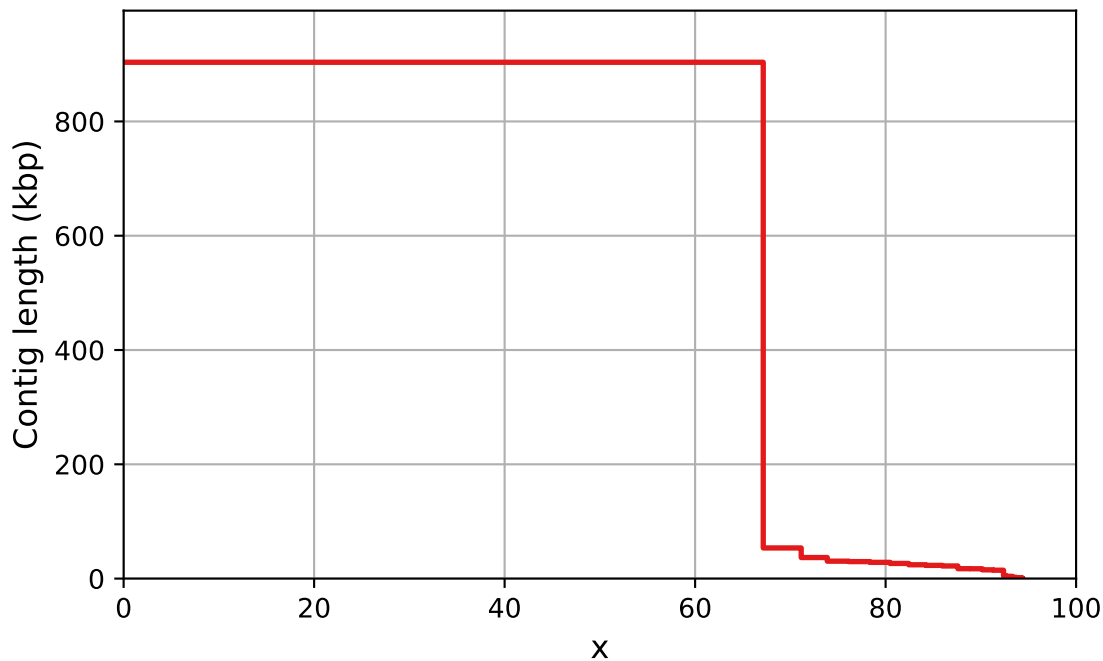
FRCurve (misassemblies)



Cumulative length (aligned contigs)

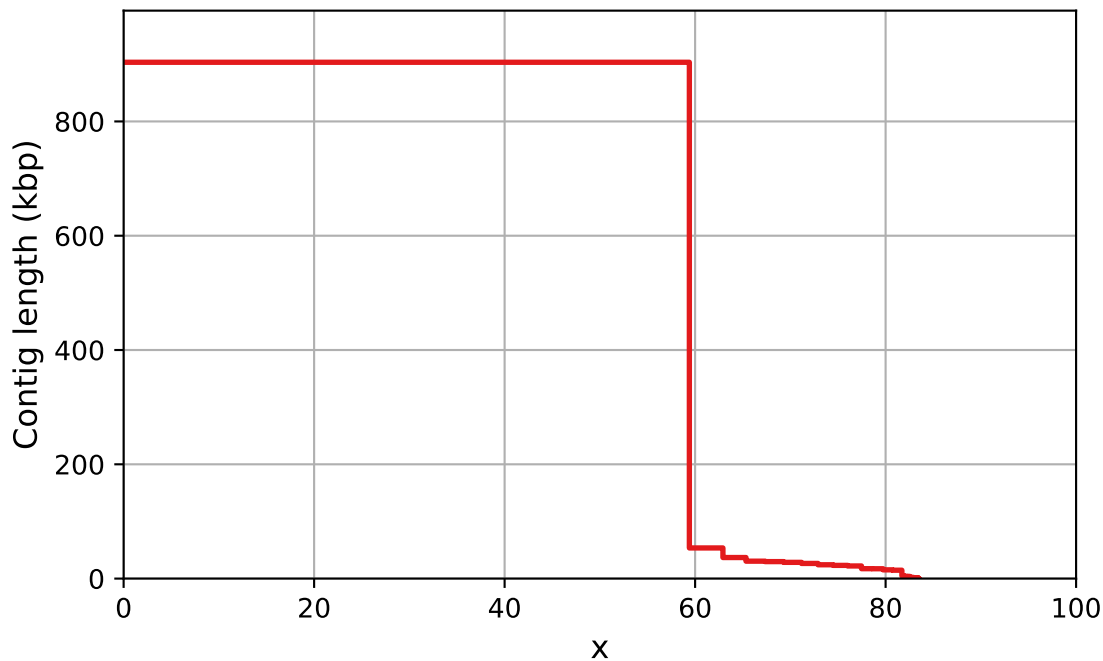


NAx



— GCF\_000021405.1\_ASM2140v1\_genomic

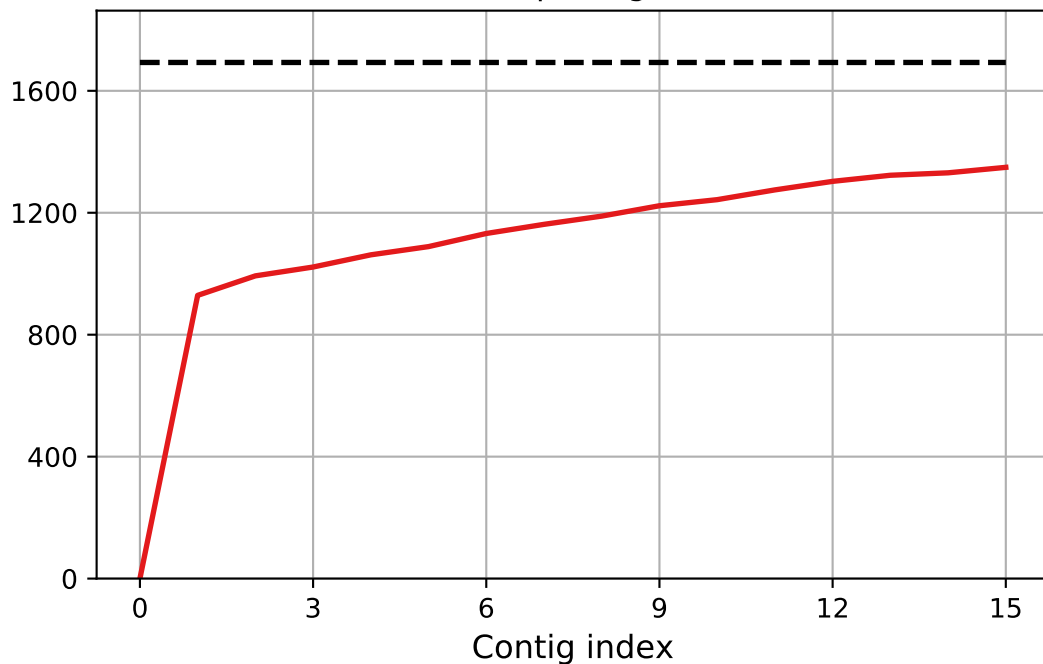
# NGAx



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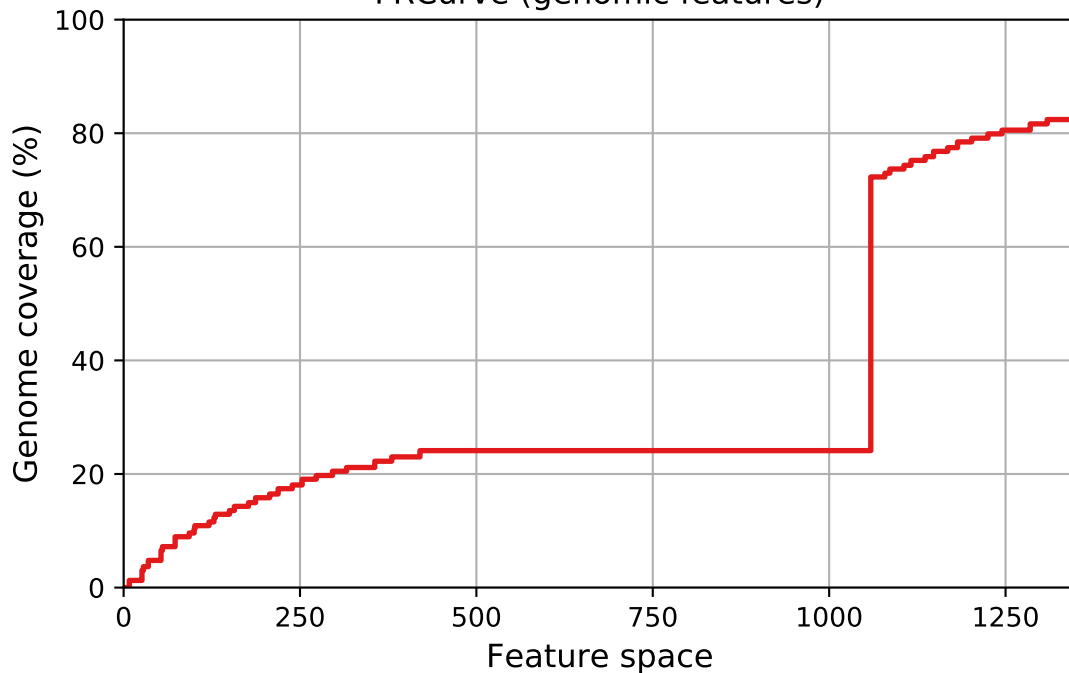
Cumulative # complete genomic features

Cumulative # complete genomic features



— GCF\_000021405.1\_ASM2140v1\_genomic      - - Reference

FRCurve (genomic features)



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