

Report

GCF_000171735.2_ASM17173v2_genomic	
# contigs (≥ 0 bp)	27
# contigs (≥ 1000 bp)	26
# contigs (≥ 5000 bp)	26
# contigs (≥ 10000 bp)	25
# contigs (≥ 25000 bp)	21
# contigs (≥ 50000 bp)	8
Total length (≥ 0 bp)	1453013
Total length (≥ 1000 bp)	1452092
Total length (≥ 5000 bp)	1452092
Total length (≥ 10000 bp)	1443400
Total length (≥ 25000 bp)	1366151
Total length (≥ 50000 bp)	969313
# contigs	27
Largest contig	231415
Total length	1453013
Reference length	1521208
GC (%)	28.19
Reference GC (%)	28.18
N50	85309
NG50	85309
N90	27336
NG90	24765
auN	112945.7
auNG	107882.4
L50	5
LG50	5
L90	19
LG90	22
# misassemblies	16
# misassembled contigs	9
Misassembled contigs length	502351
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# unaligned contigs	1 + 17 part
Unaligned length	232255
Genome fraction (%)	78.160
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	811.09
# indels per 100 kbp	42.01
# genomic features	1229 + 56 part
Largest alignment	204462
Total aligned length	1223536
NA50	79026
NGA50	66837
NA90	-
NGA90	-
auNA	96273.3
auNGA	91957.4
LA50	5
LGA50	6
LA90	-
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

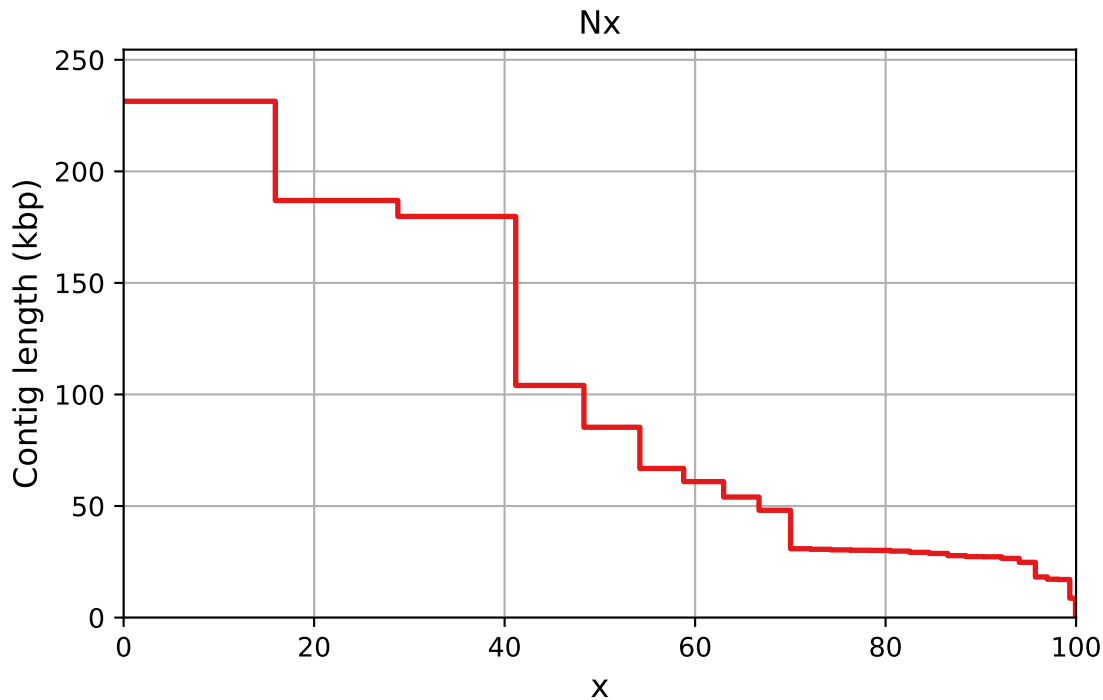
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# misassemblies	16
# contig misassemblies	16
# c. relocations	3
# c. translocations	12
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	502351
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	9924
# indels	514
# indels (<= 5 bp)	471
# indels (> 5 bp)	43
Indels length	2183

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

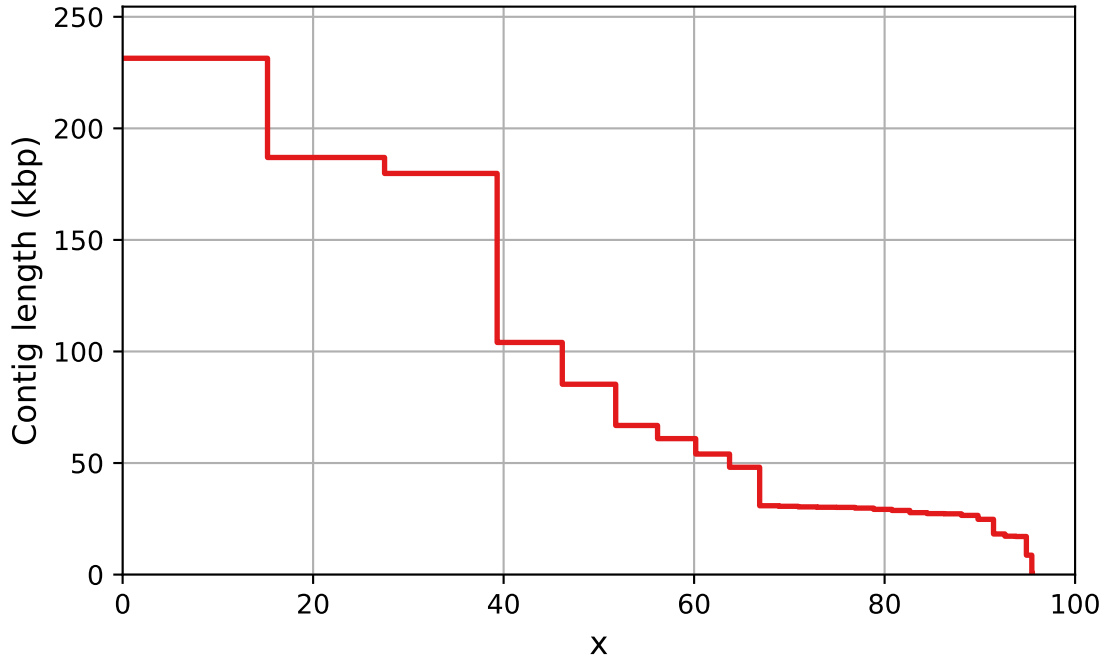
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# fully unaligned contigs	1
Fully unaligned length	17205
# partially unaligned contigs	17
Partially unaligned length	215050
# N's	0

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).

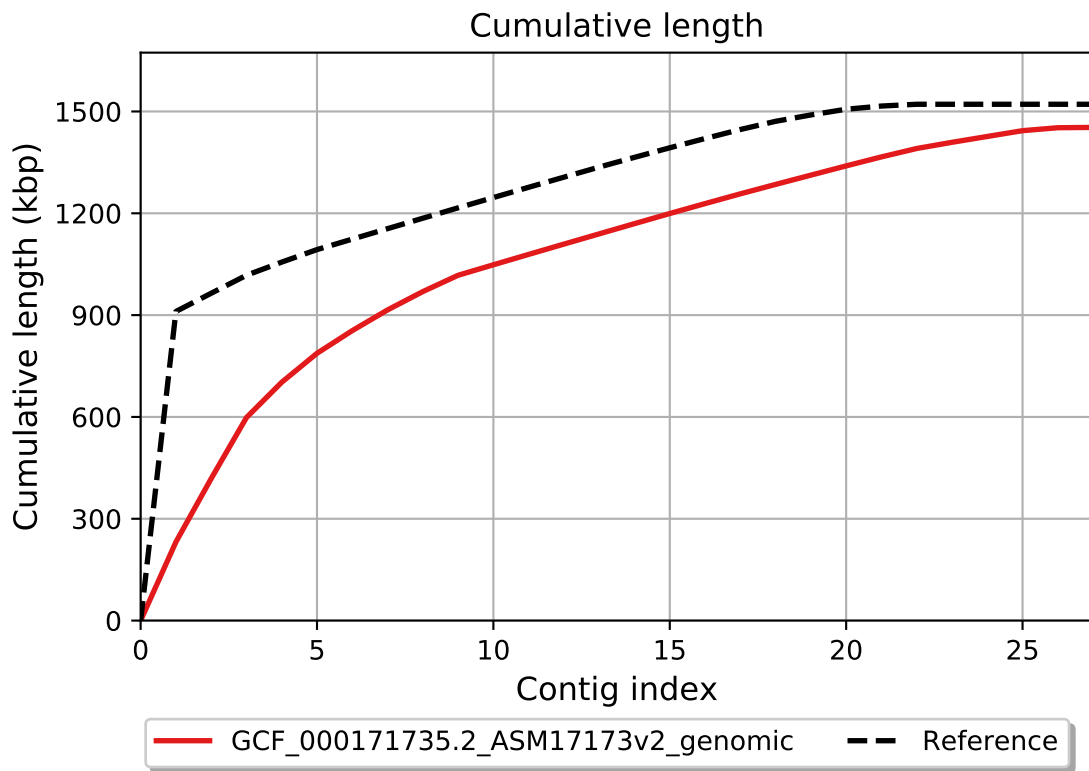


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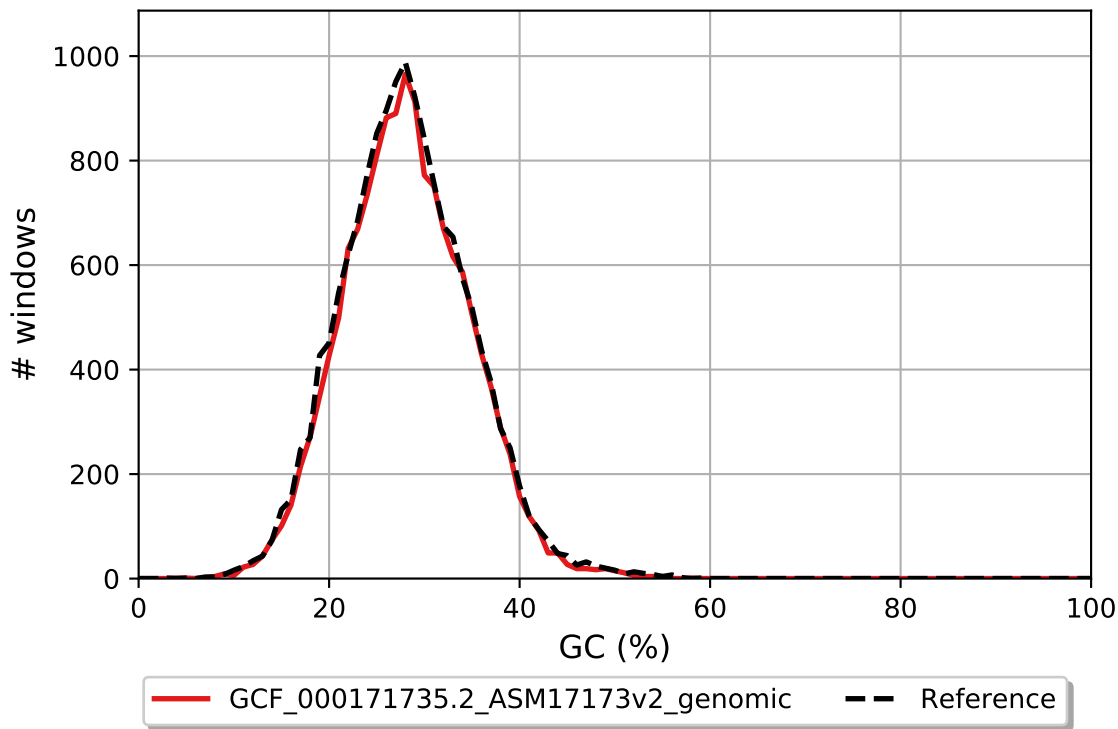
NGx



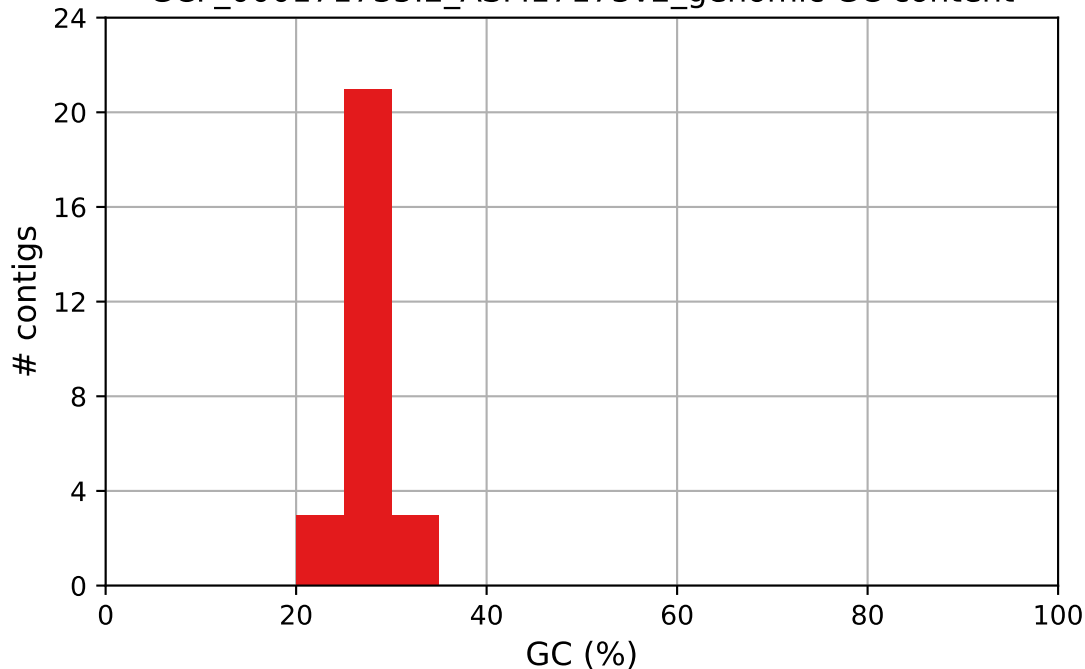
— GCF_000171735.2_ASM17173v2_genomic



GC content

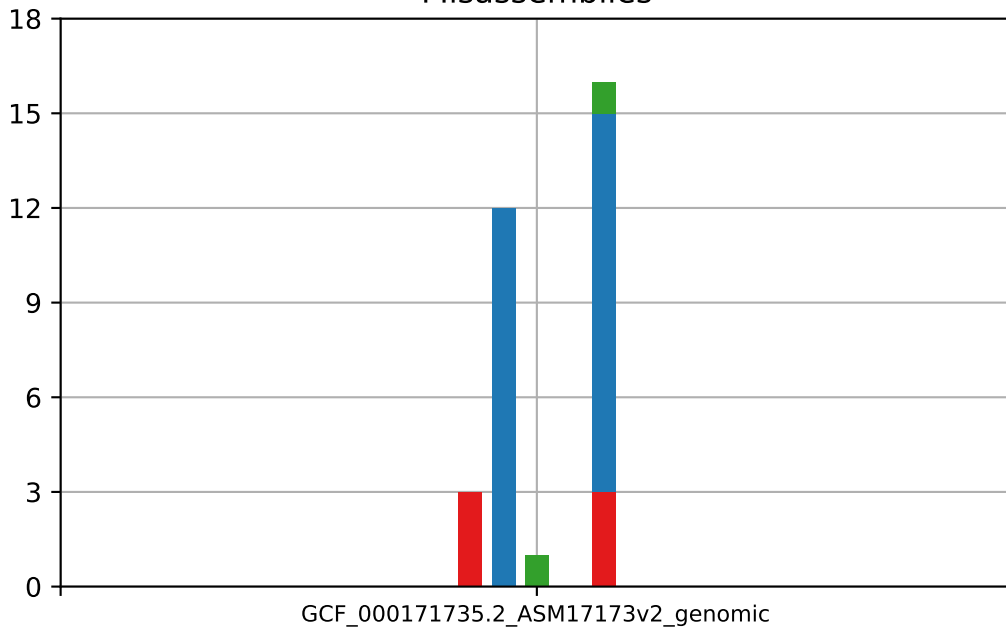


GCF_000171735.2_ASM17173v2_genomic GC content



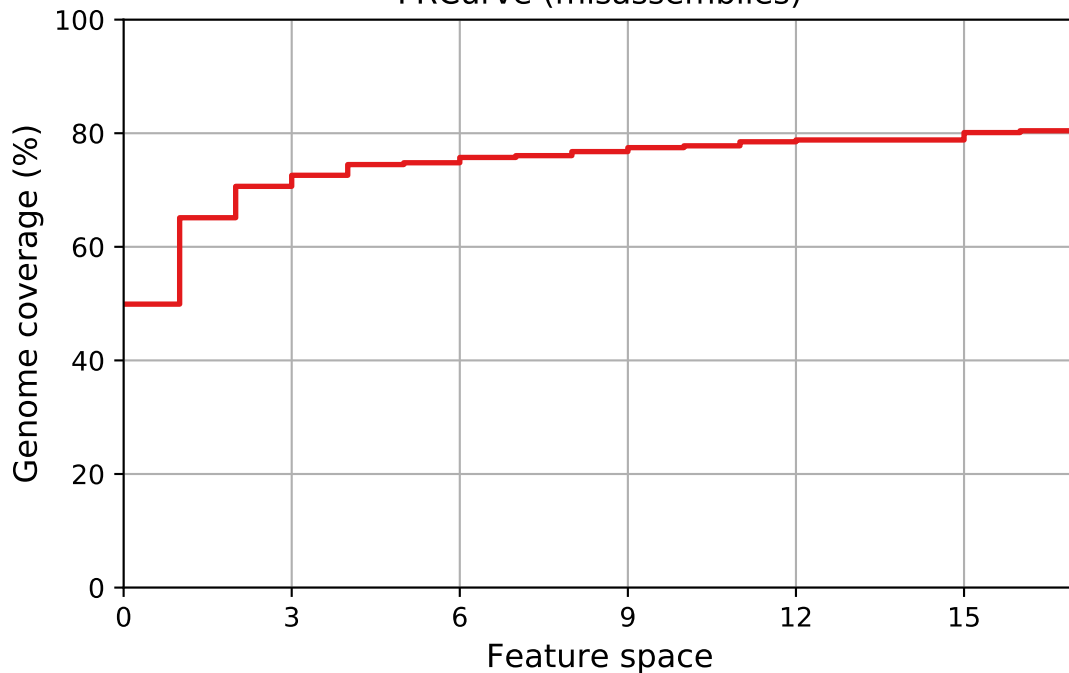
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Misassemblies



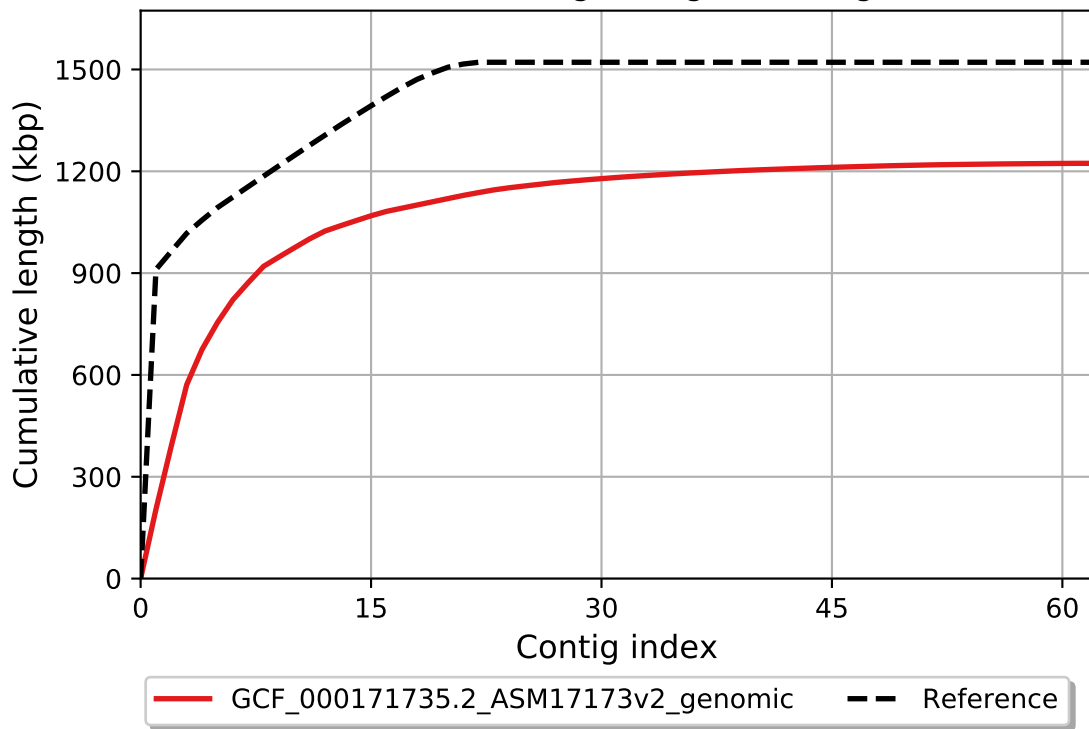
■ # relocations ■ # translocations ■ # inversions

FRCurve (misassemblies)

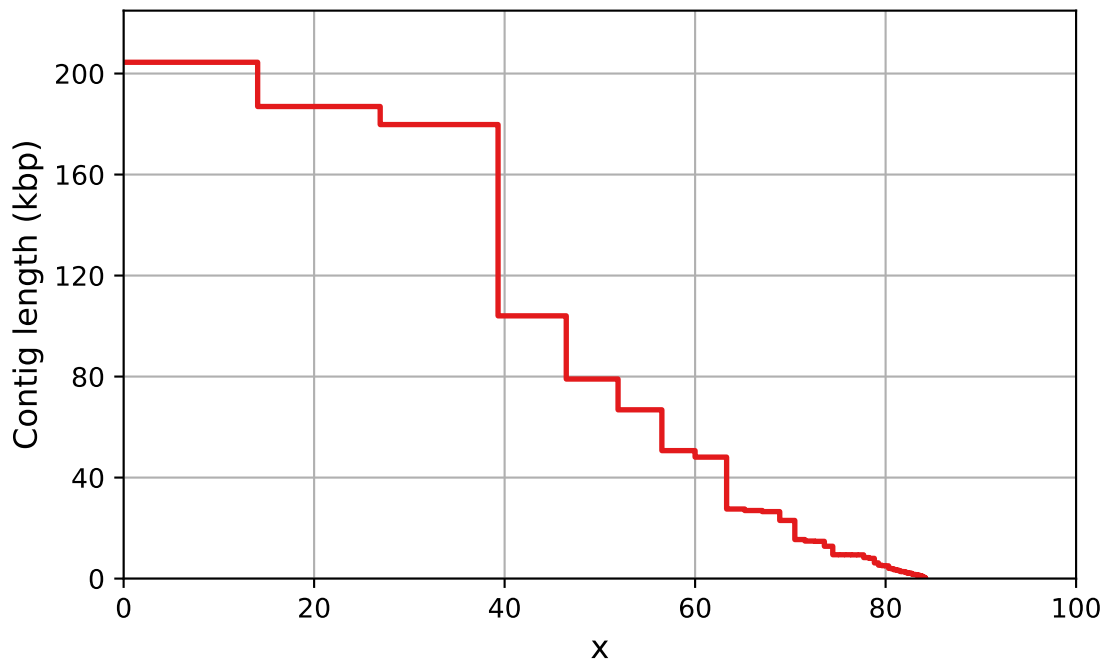


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Cumulative length (aligned contigs)

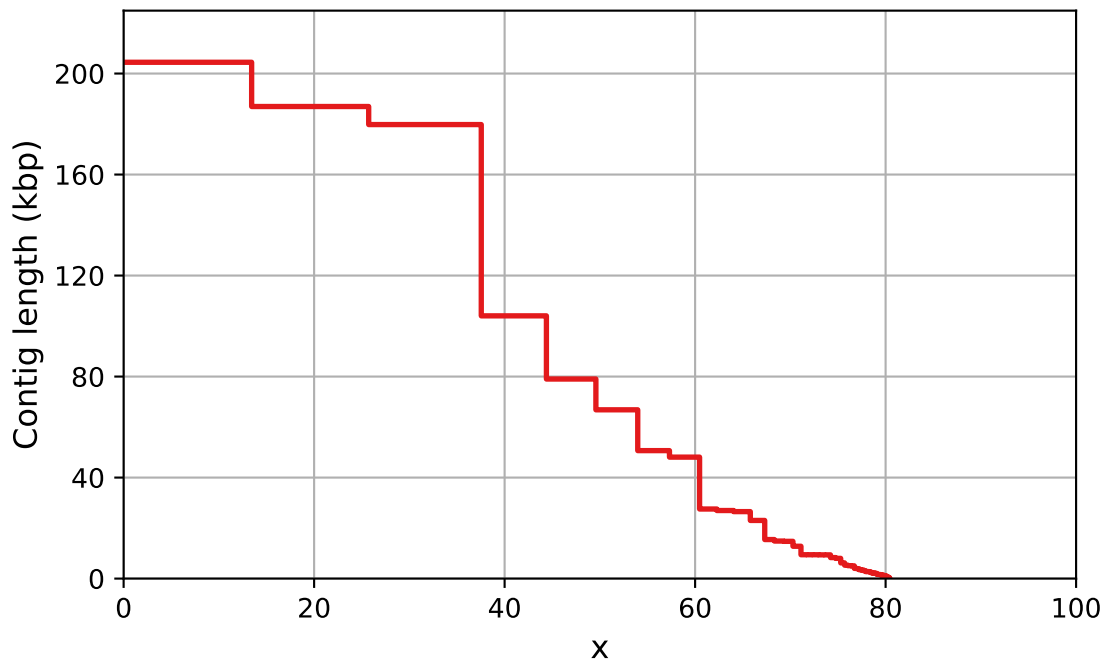


NAx



— GCF_000171735.2_ASM17173v2_genomic

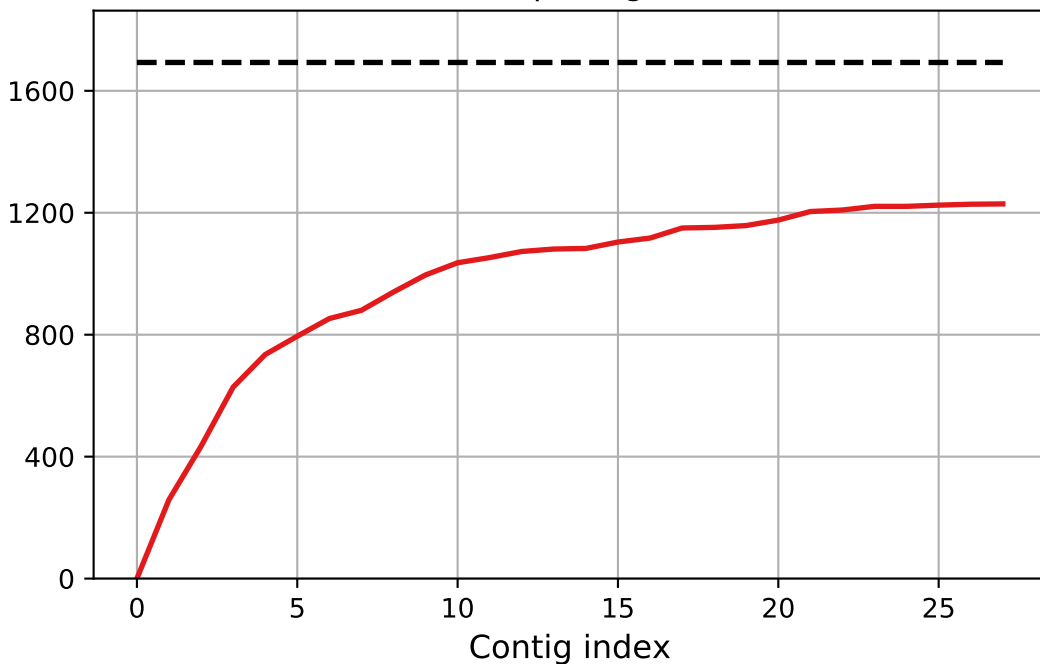
NGAx



— GCF_000171735.2_ASM17173v2_genomic

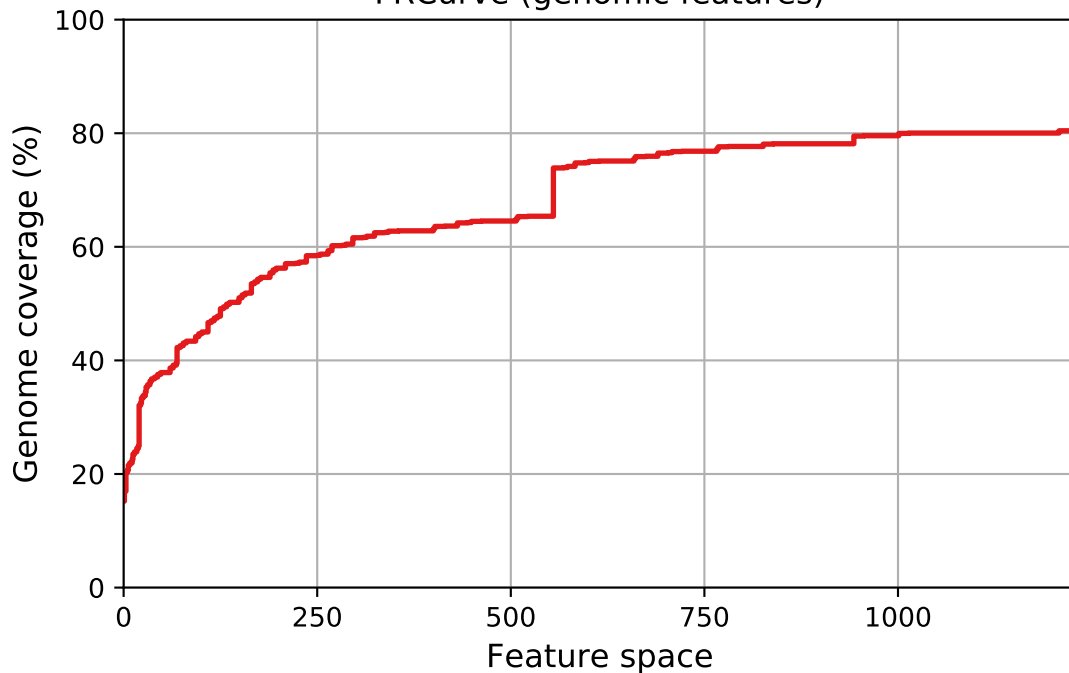
Cumulative # complete genomic features

Cumulative # complete genomic features



— GCF_000171735.2_ASM17173v2_genomic - - Reference

FRCurve (genomic features)



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