

Report

	GCF_000181575.2_ASM18157v2_genomic
# contigs (>= 0 bp)	20
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1321434
Total length (>= 1000 bp)	1321434
Total length (>= 5000 bp)	1318733
Total length (>= 10000 bp)	1318733
Total length (>= 25000 bp)	1234899
Total length (>= 50000 bp)	962871
# contigs	20
Largest contig	471200
Total length	1321434
Reference length	1521208
GC (%)	28.59
Reference GC (%)	28.18
N50	170966
NG50	170966
N90	28200
NG90	-
auN	229884.1
auNG	199694.3
L50	3
LG50	3
L90	13
LG90	-
# misassemblies	10
# misassembled contigs	6
Misassembled contigs length	156416
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	2 + 7 part
Unaligned length	112501
Genome fraction (%)	77.384
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	571.41
# indels per 100 kbp	34.76
# genomic features	1242 + 33 part
Largest alignment	471194
Total aligned length	1208236
NA50	170966
NGA50	170966
NA90	3362
NGA90	-
auNA	226335.3
auNGA	196611.6
LA50	3
LGA50	3
LA90	19
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

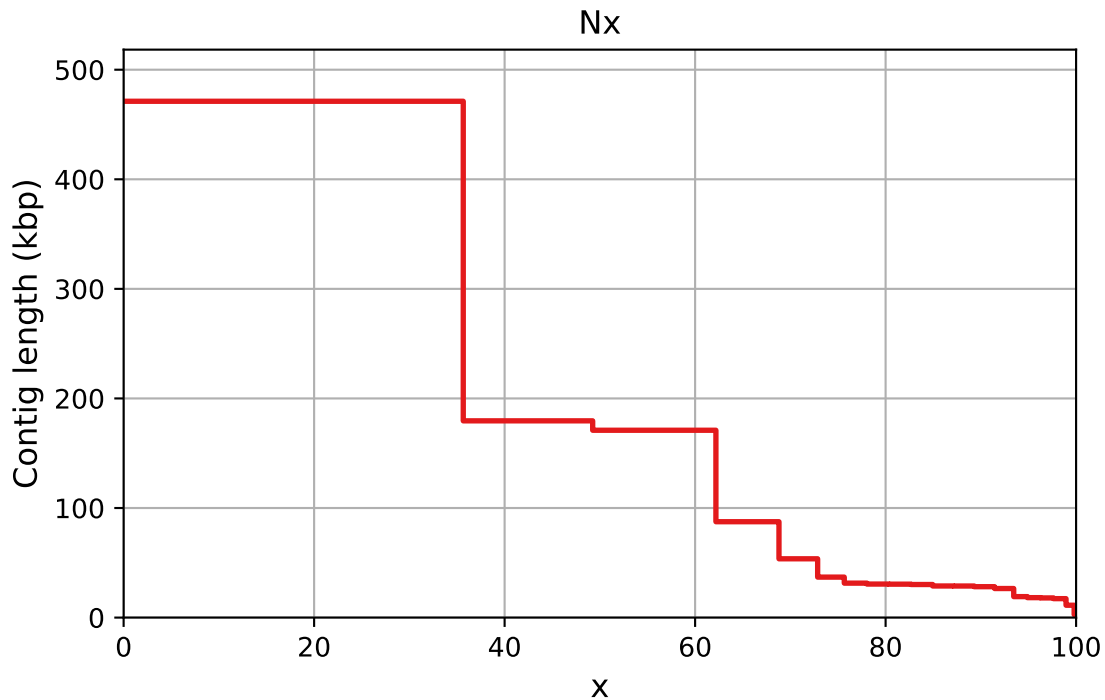
	GCF_000181575.2_ASM18157v2_genomic
# misassemblies	10
# contig misassemblies	10
# c. relocations	1
# c. translocations	9
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	156416
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	6904
# indels	420
# indels (<= 5 bp)	365
# indels (> 5 bp)	55
Indels length	1810

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

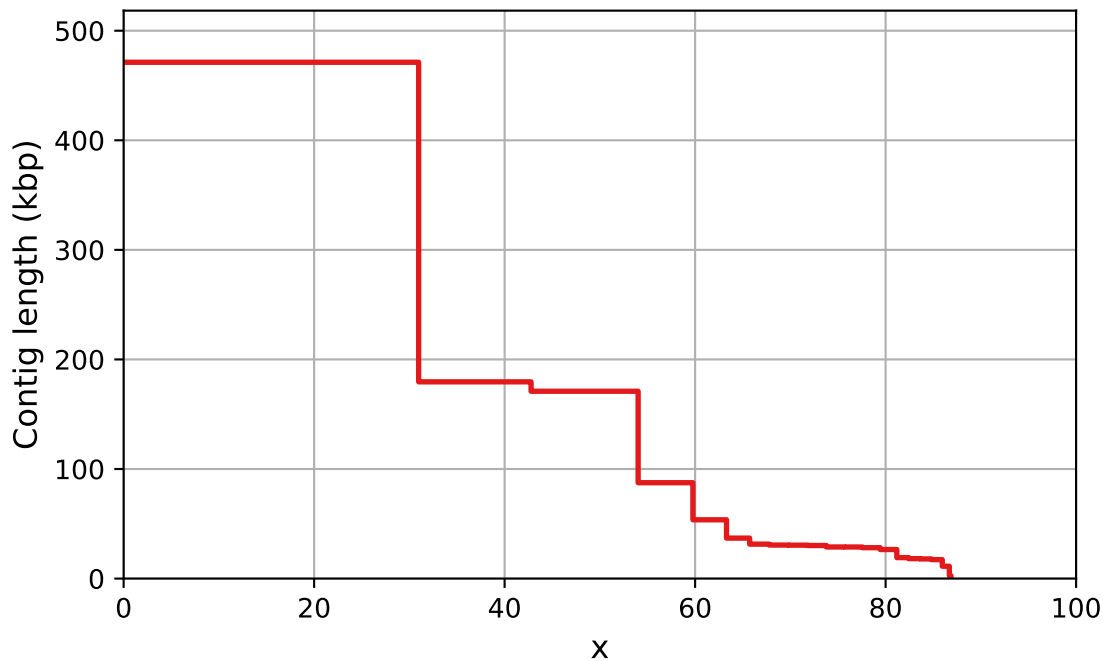
	GCF_000181575.2_ASM18157v2_genomic
# fully unaligned contigs	2
Fully unaligned length	46141
# partially unaligned contigs	7
Partially unaligned length	66360
# N's	0

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).

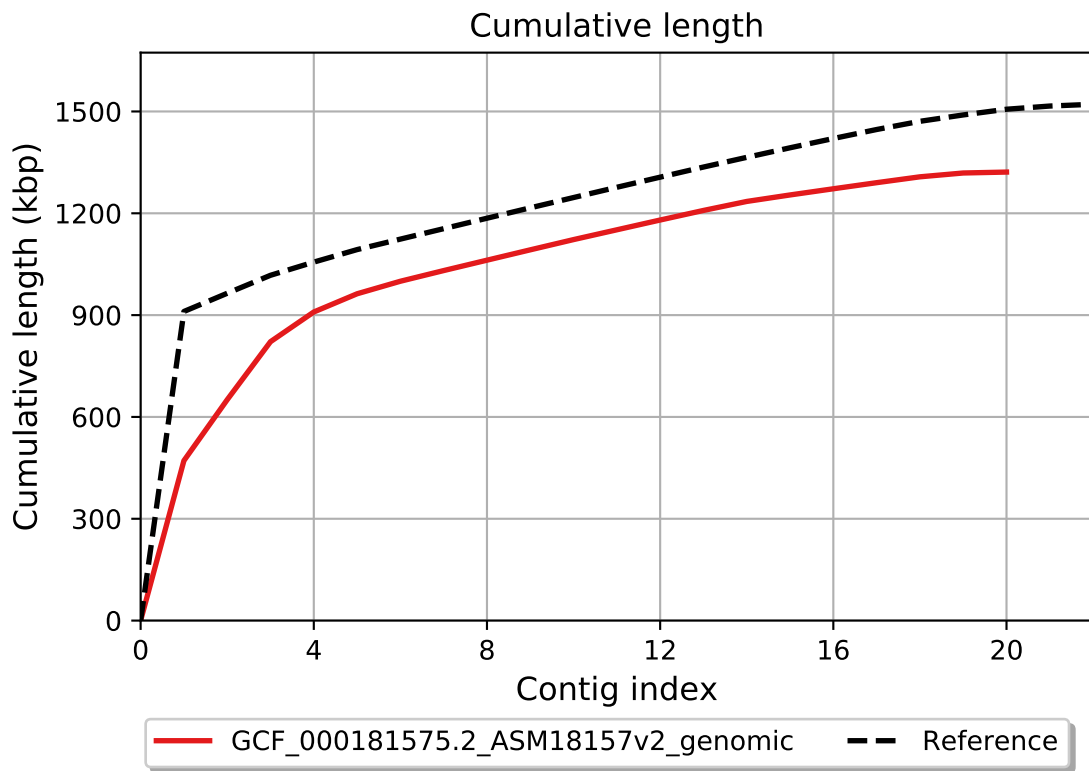


— GCF_000181575.2_ASM18157v2_genomic

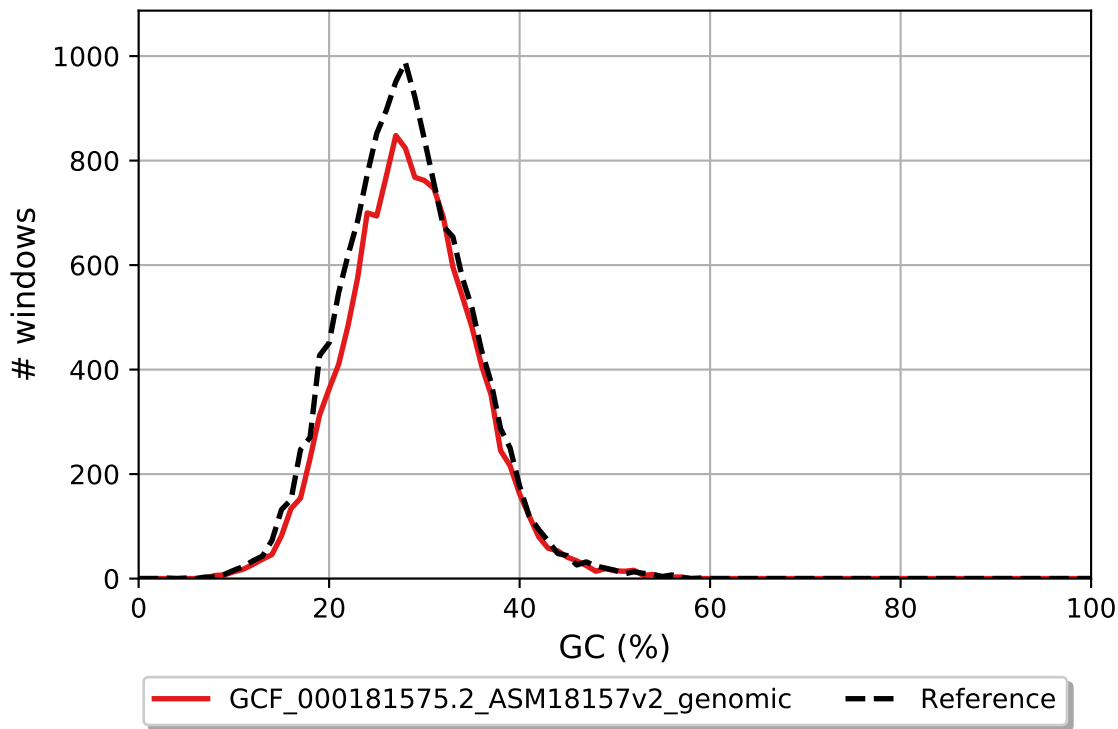
NGx



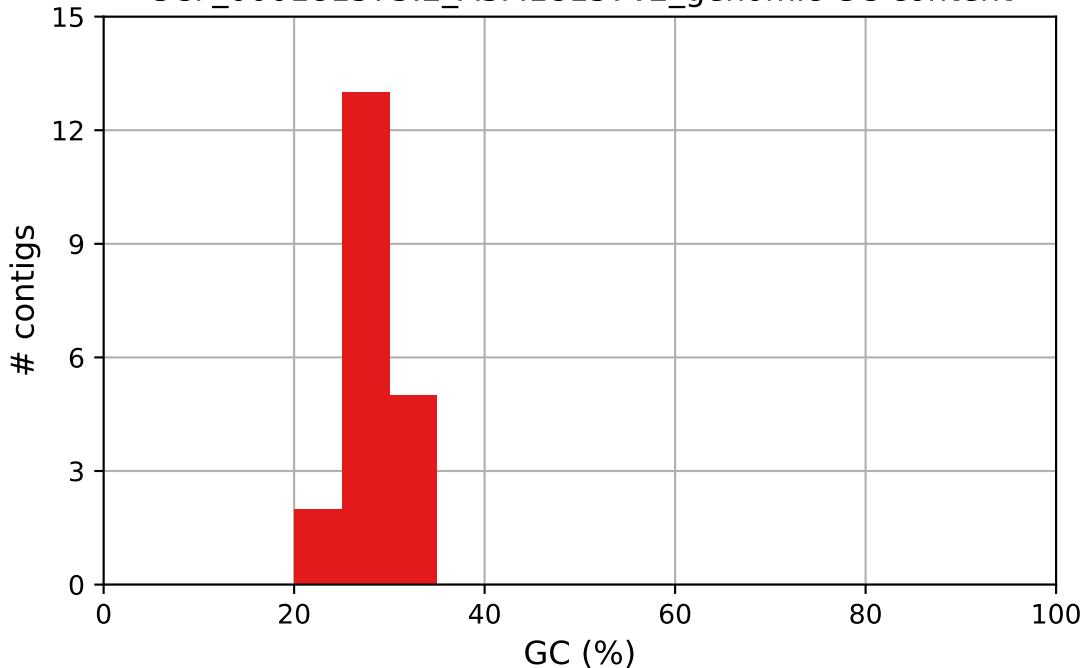
— GCF_000181575.2_ASM18157v2_genomic



GC content

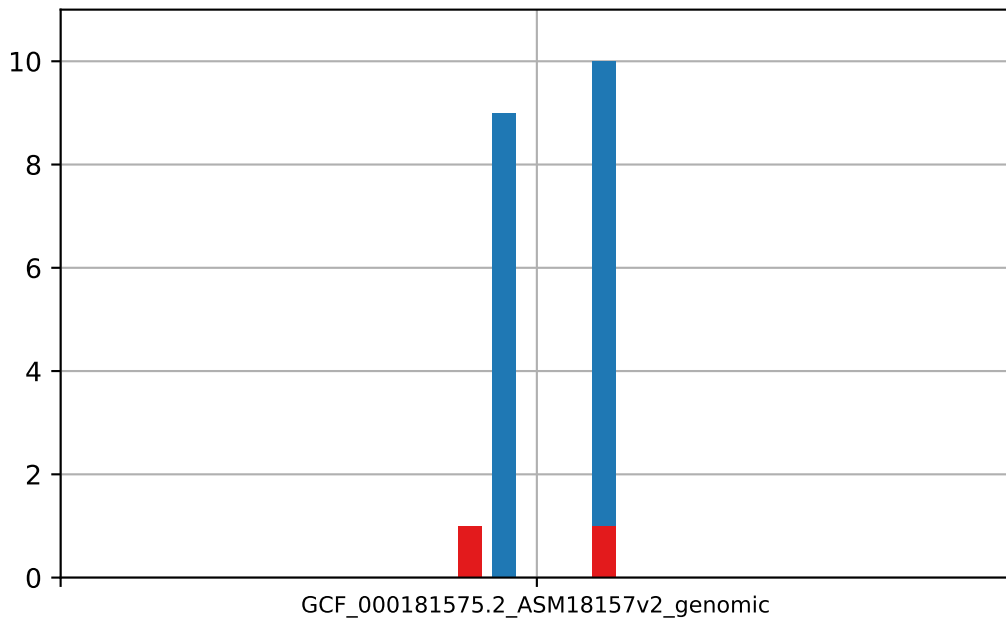


GCF_000181575.2_ASM18157v2_genomic GC content



GCF_000181575.2_ASM18157v2_genomic

Misassemblies

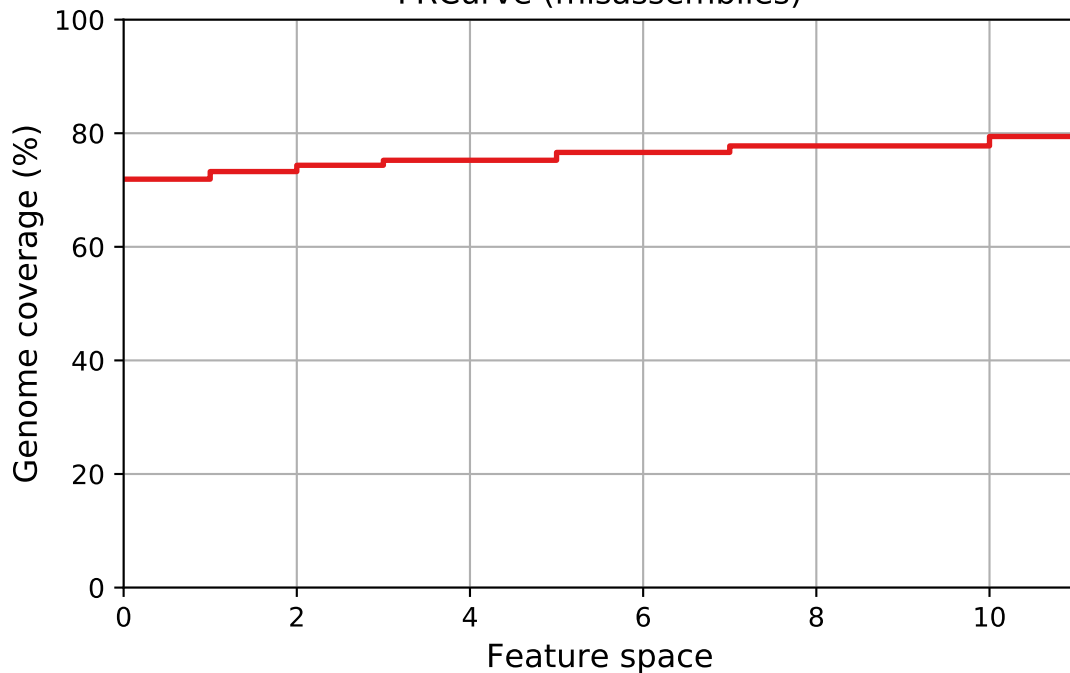


relocations



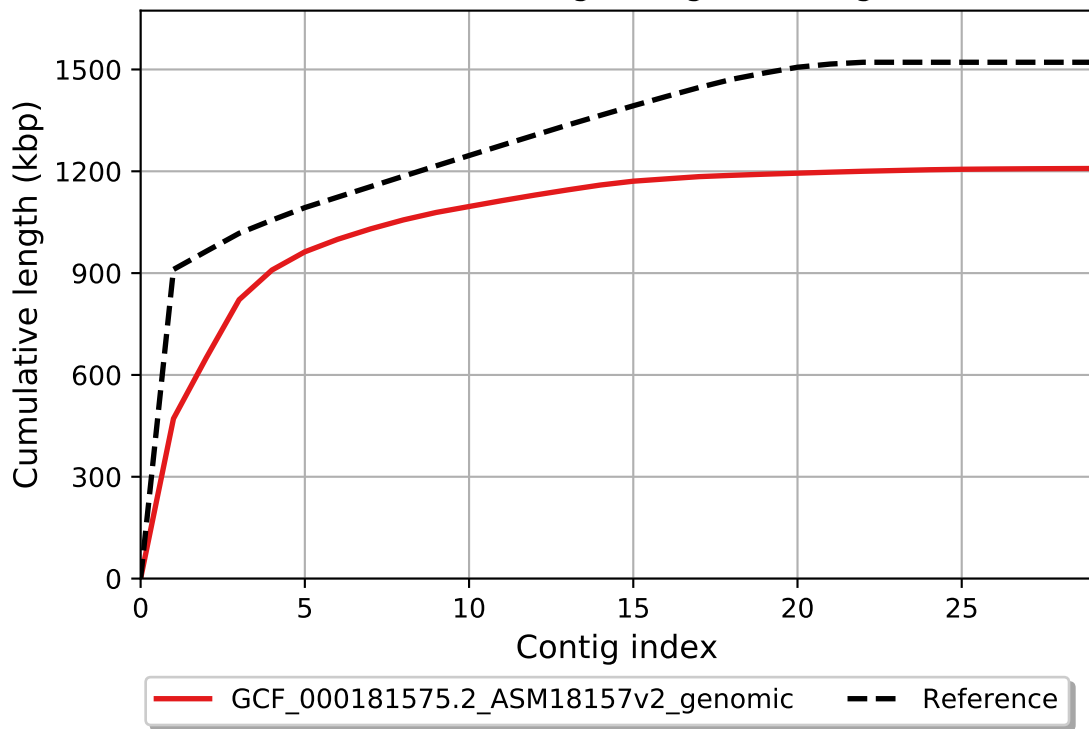
translocations

FRCurve (misassemblies)

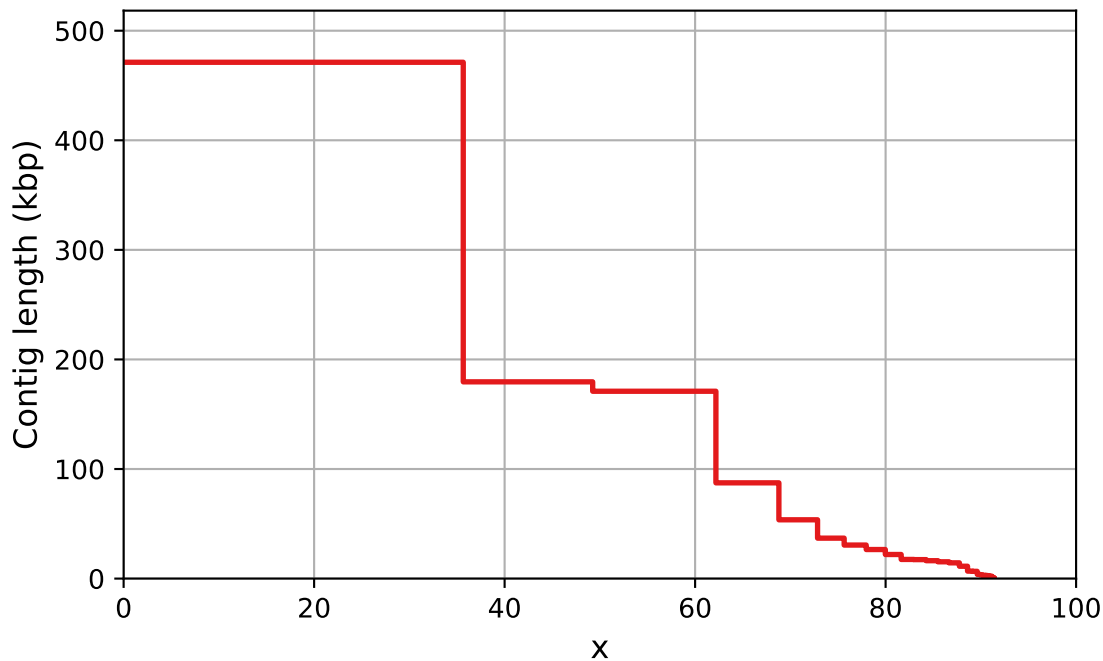


— GCF_000181575.2_ASM18157v2_genomic

Cumulative length (aligned contigs)

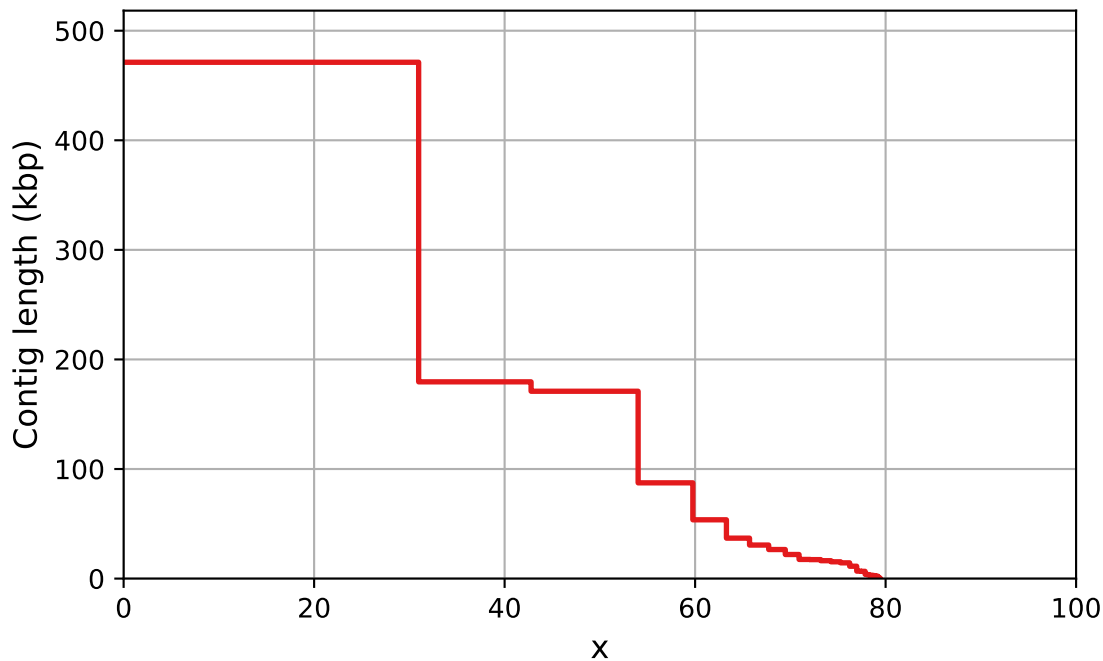


NAx



— GCF_000181575.2_ASM18157v2_genomic

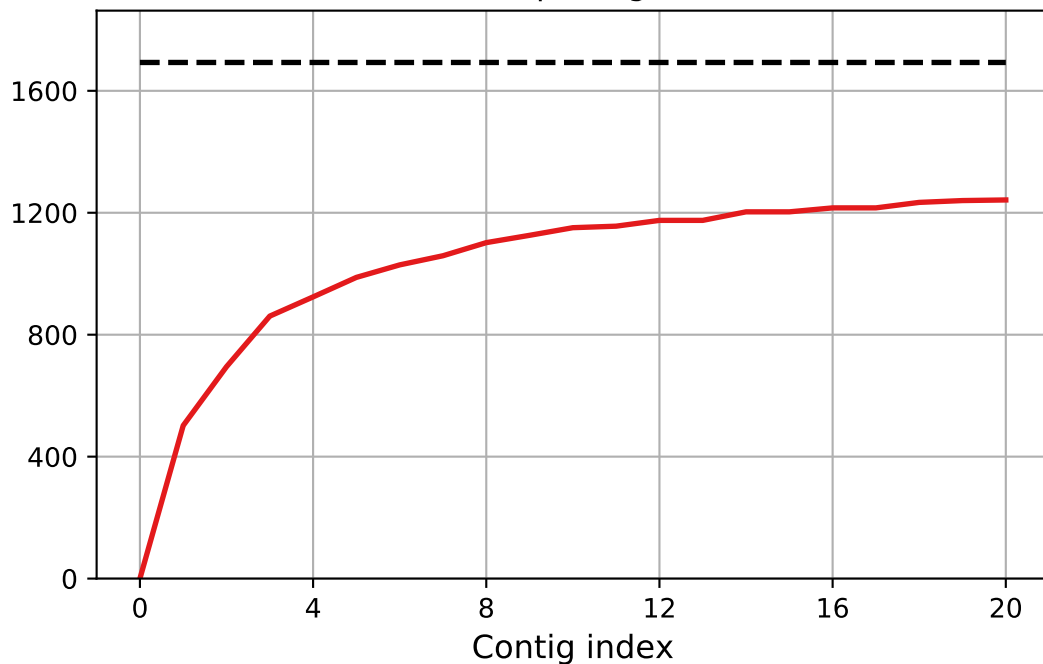
NGAx



— GCF_000181575.2_ASM18157v2_genomic

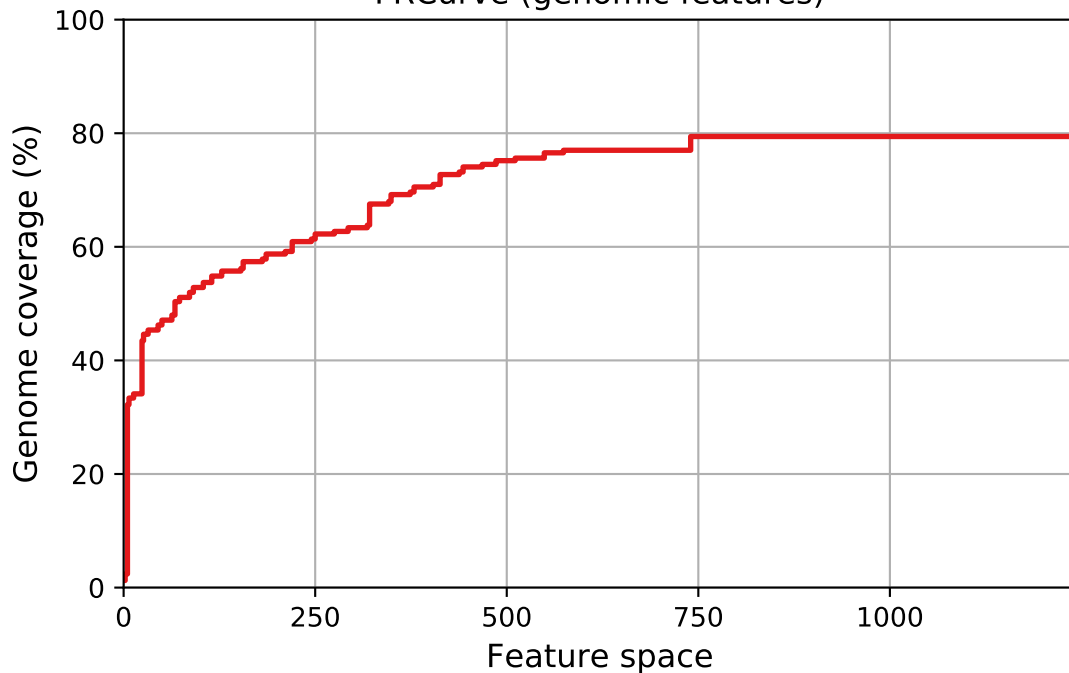
Cumulative # complete genomic features

Cumulative # complete genomic features



— GCF_000181575.2_ASM18157v2_genomic - - Reference

FRCurve (genomic features)



— GCF_000181575.2_ASM18157v2_genomic