

Report

	GCF_000172335.2_ASM17233v2_genomic
# contigs (>= 0 bp)	24
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	24
# contigs (>= 10000 bp)	24
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	1485884
Total length (>= 1000 bp)	1485884
Total length (>= 5000 bp)	1485884
Total length (>= 10000 bp)	1485884
Total length (>= 25000 bp)	1435683
Total length (>= 50000 bp)	1008991
# contigs	24
Largest contig	408550
Total length	1485884
Reference length	1521208
GC (%)	28.43
Reference GC (%)	28.18
N50	169176
NG50	87194
N90	28645
NG90	26992
auN	174006.7
auNG	169966.1
L50	3
LG50	4
L90	18
LG90	19
# misassemblies	12
# misassembled contigs	9
Misassembled contigs length	665506
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 7 part
Unaligned length	87676
Genome fraction (%)	88.174
Duplication ratio	1.042
# N's per 100 kbp	0.13
# mismatches per 100 kbp	444.76
# indels per 100 kbp	34.50
# genomic features	1425 + 40 part
Largest alignment	218302
Total aligned length	1396946
NA50	169176
NGA50	87194
NA90	9720
NGA90	7195
auNA	113374.9
auNGA	110742.3
LA50	4
LGA50	5
LA90	24
LGA90	28

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

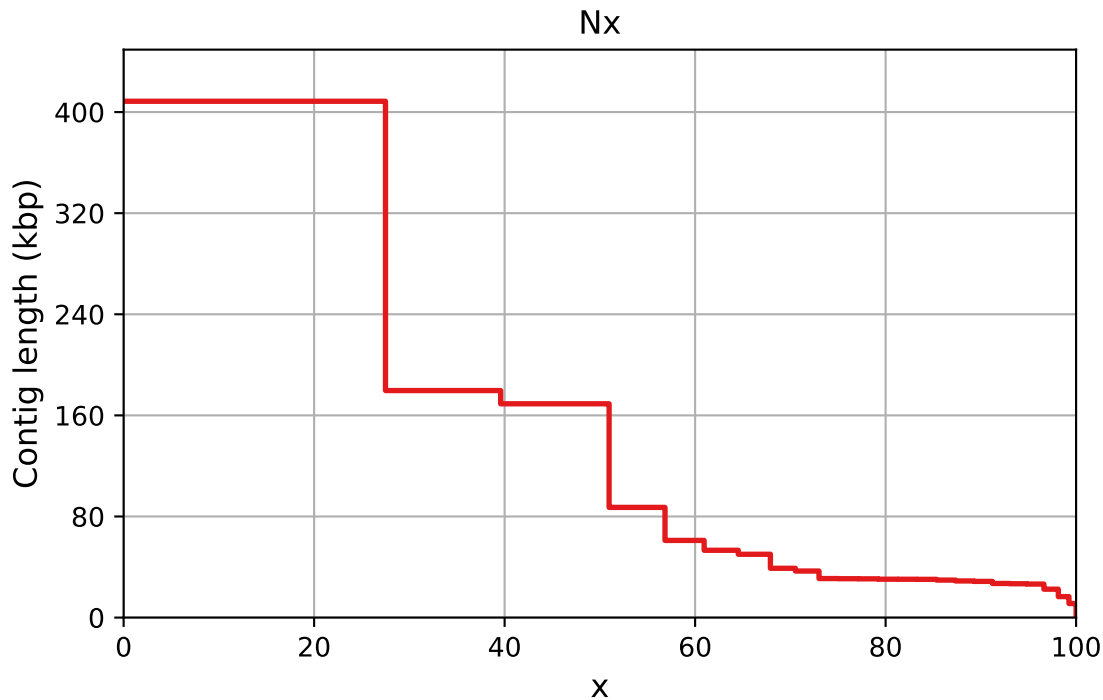
	GCF_000172335.2_ASM17233v2_genomic
# misassemblies	12
# contig misassemblies	12
# c. relocations	3
# c. translocations	9
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	665506
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	6213
# indels	482
# indels (<= 5 bp)	436
# indels (> 5 bp)	46
Indels length	2421

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

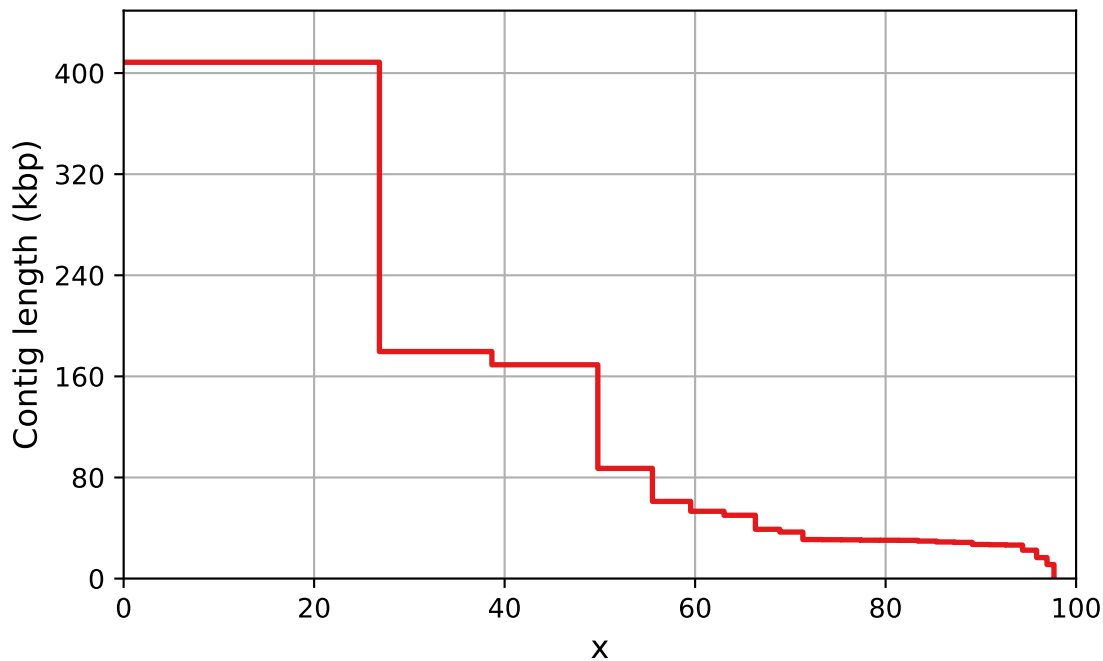
	GCF_000172335.2_ASM17233v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	87676
# N's	2

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).

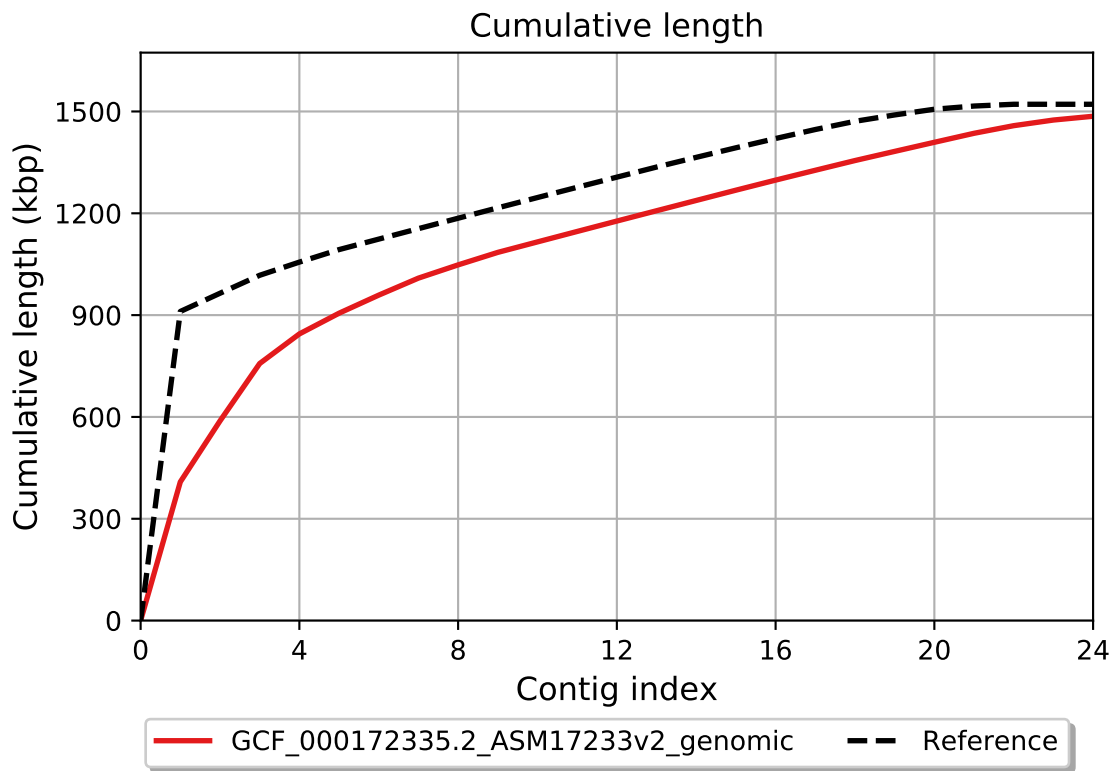


— GCF_000172335.2_ASM17233v2_genomic

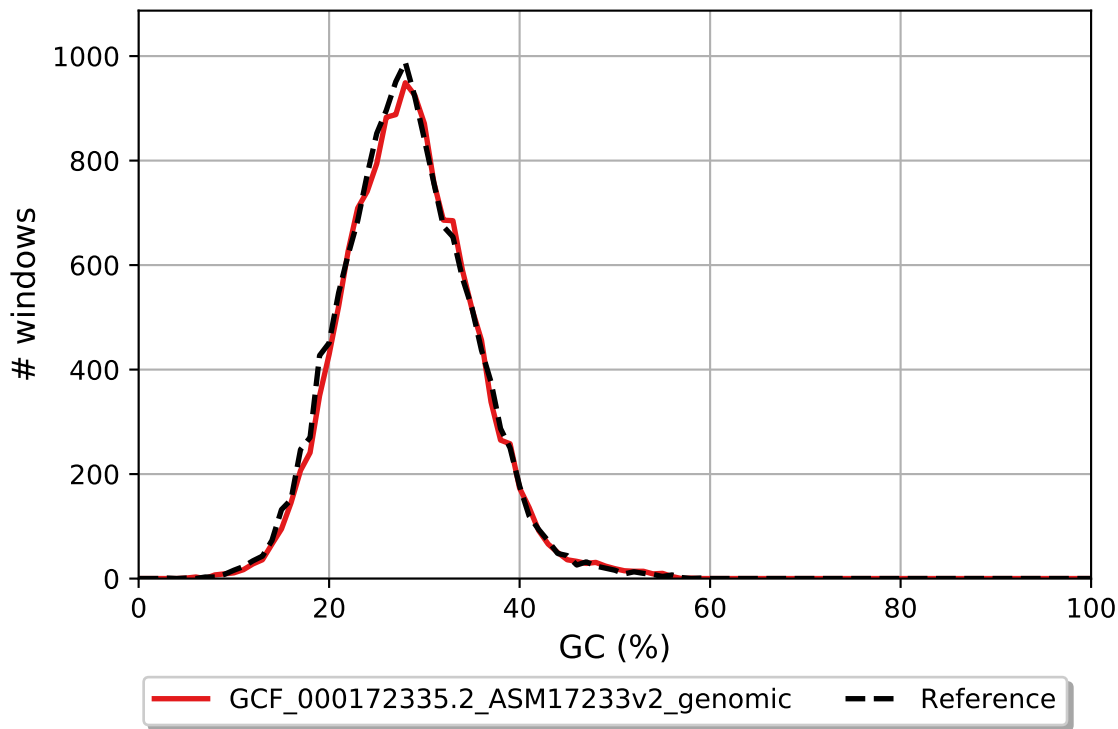
NGx



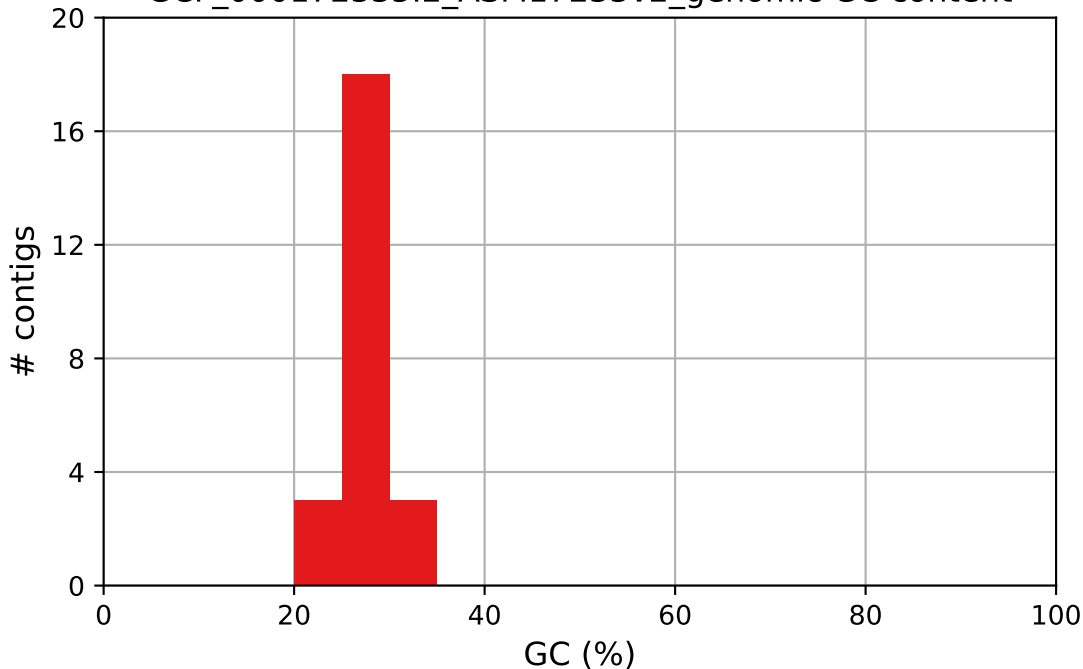
— GCF_000172335.2_ASM17233v2_genomic



GC content

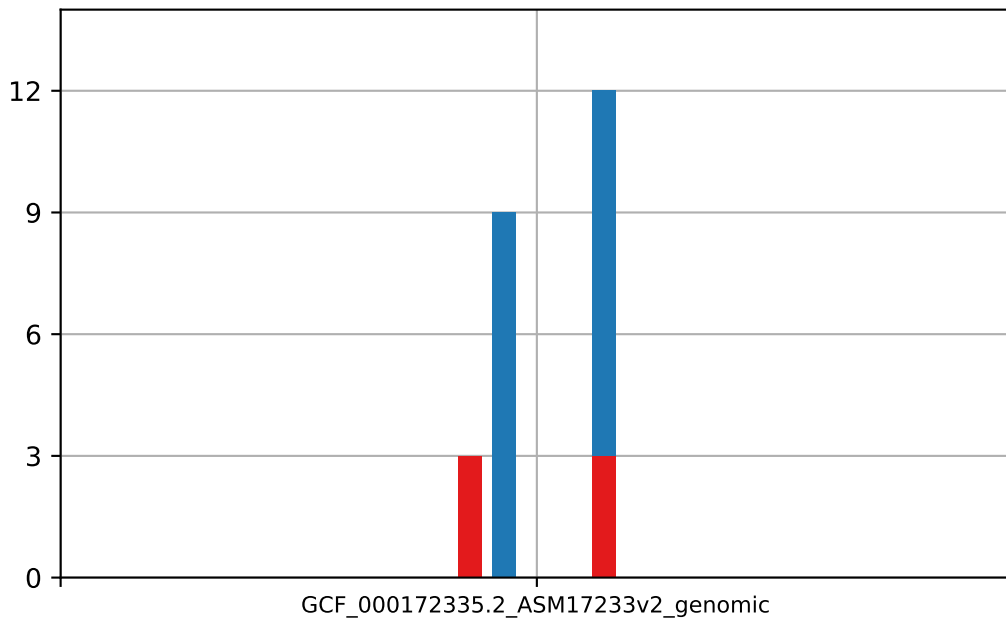


GCF_000172335.2_ASM17233v2_genomic GC content



GCF_000172335.2_ASM17233v2_genomic

Misassemblies

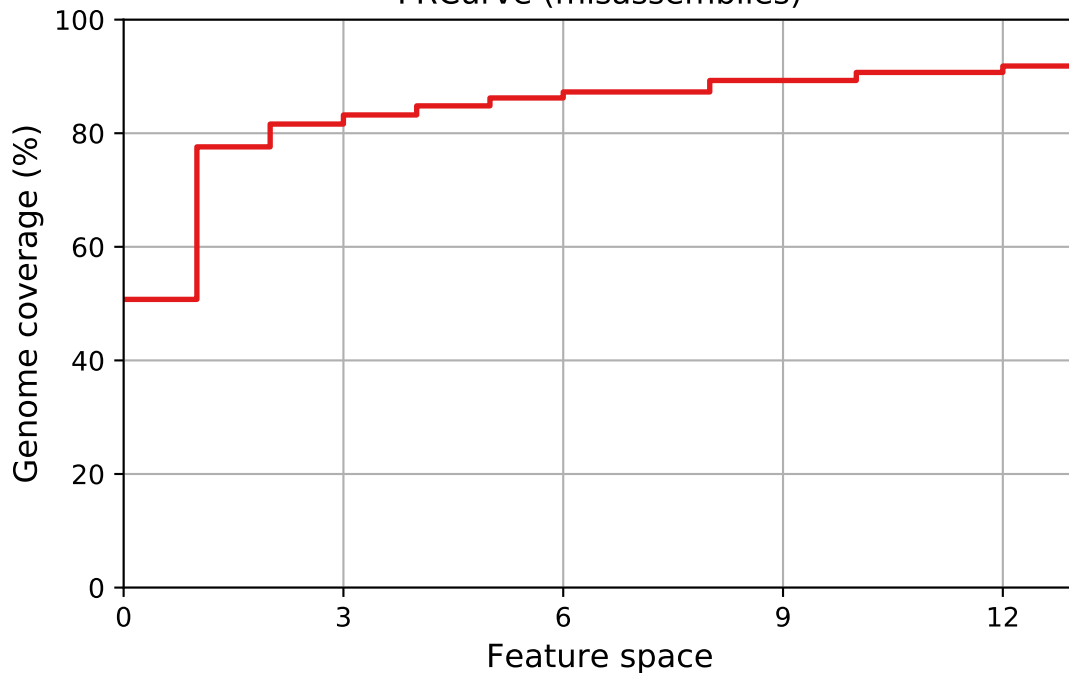


relocations



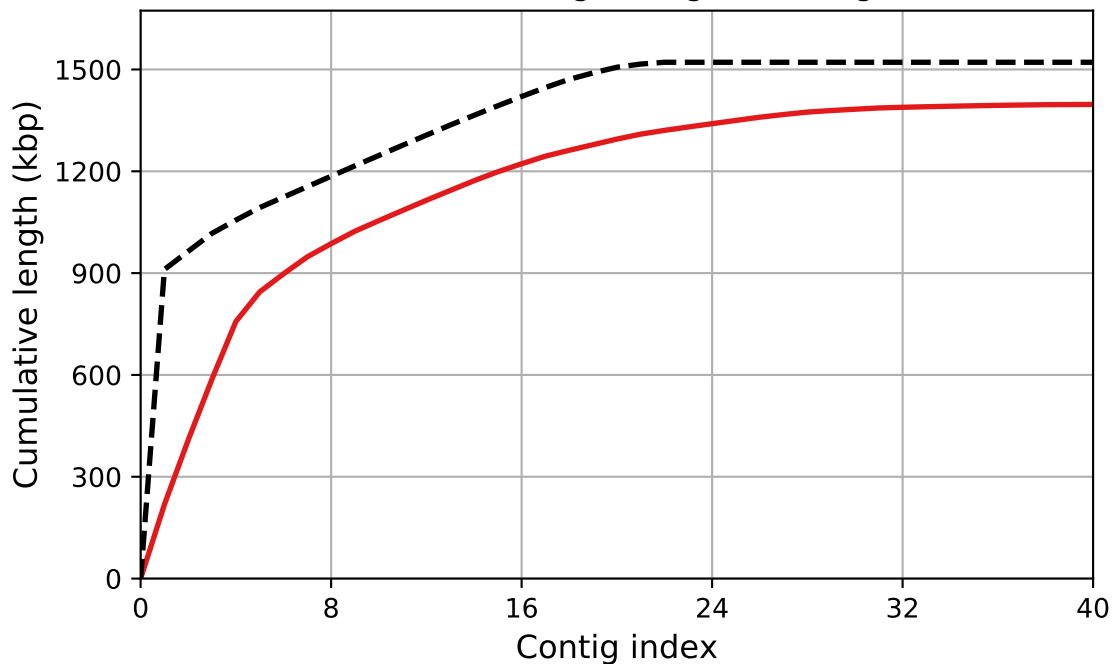
translocations

FRCurve (misassemblies)



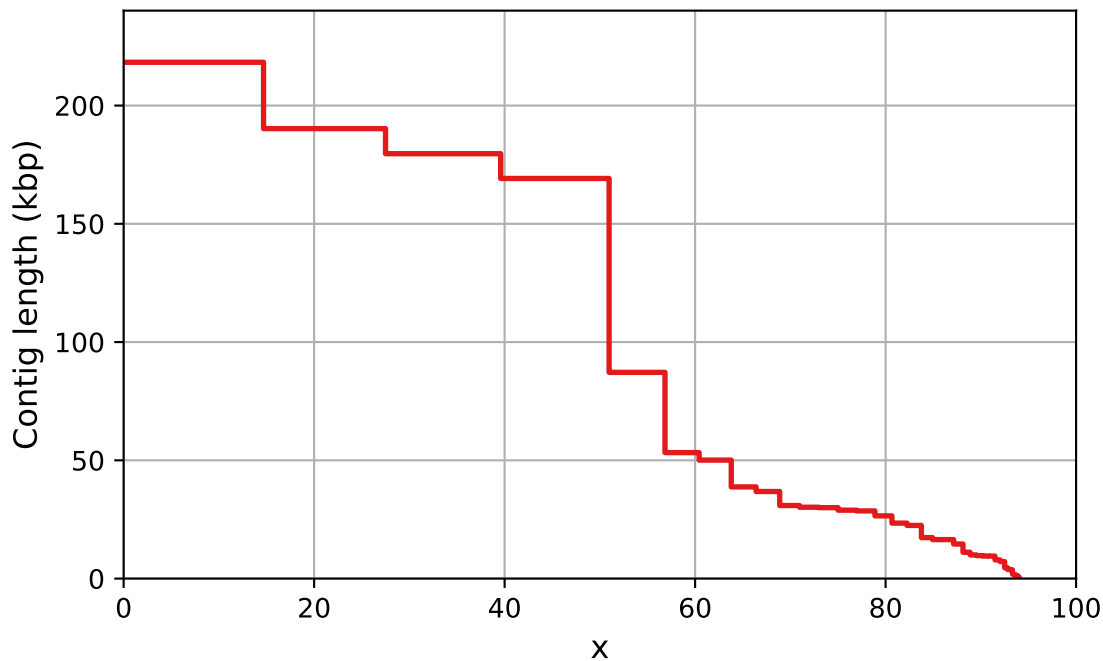
— GCF_000172335.2_ASM17233v2_genomic

Cumulative length (aligned contigs)



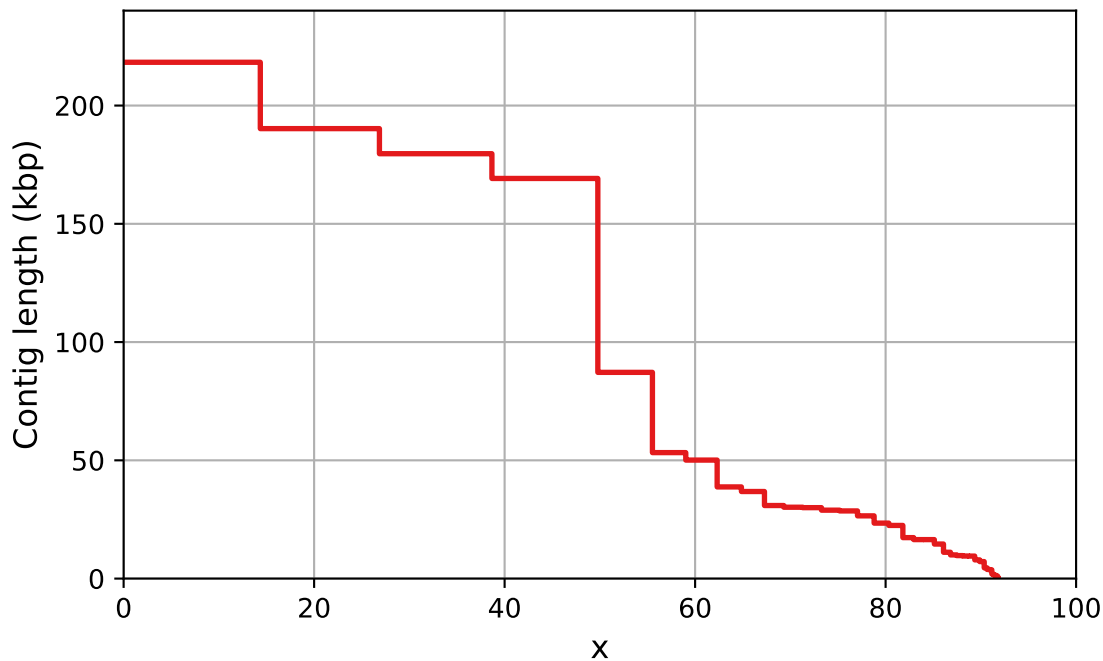
— GCF_000172335.2_ASM17233v2_genomic - - Reference

NAx

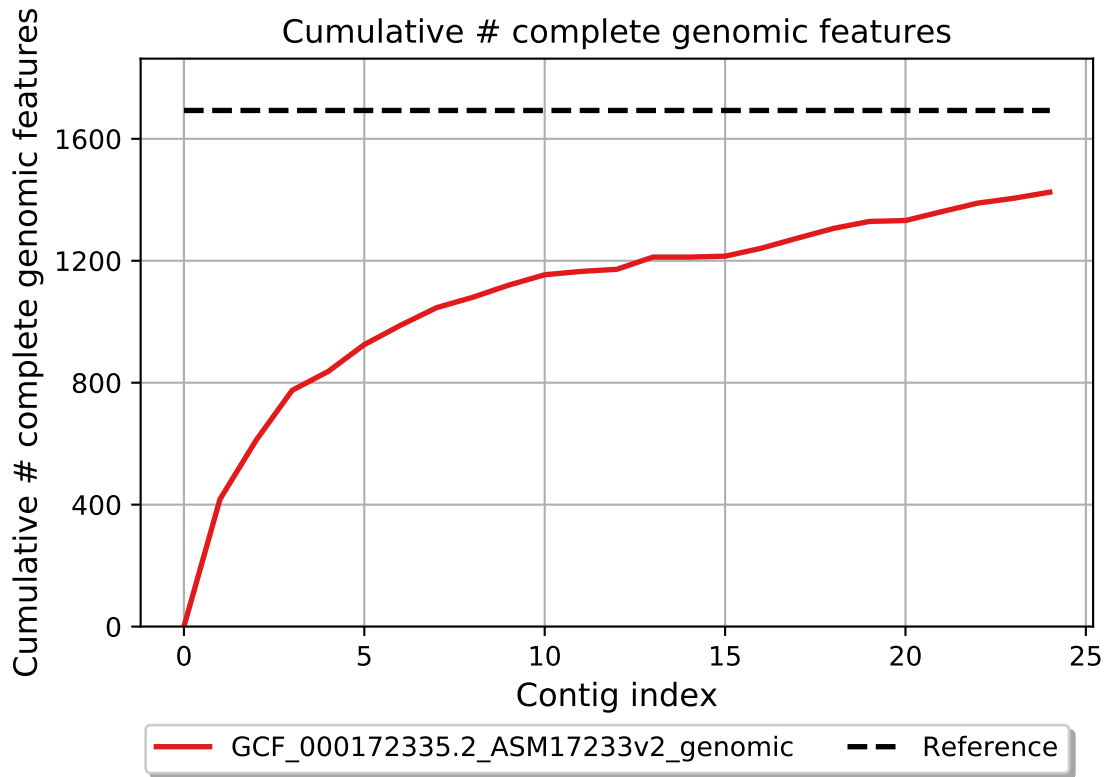


— GCF_000172335.2_ASM17233v2_genomic

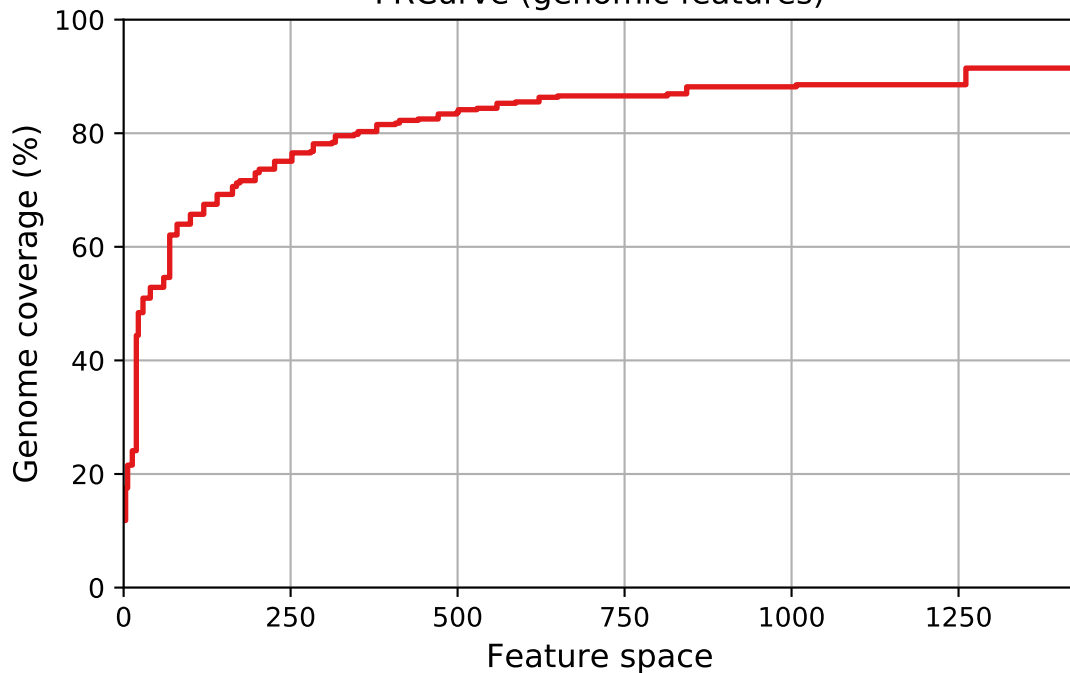
NGAx



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FRCurve (genomic features)



— GCF_000172335.2_ASM17233v2_genomic