

Report

GCF_000181855.2_ASM18185v2_genomic	
# contigs (>= 0 bp)	54
# contigs (>= 1000 bp)	52
# contigs (>= 5000 bp)	44
# contigs (>= 10000 bp)	38
# contigs (>= 25000 bp)	25
# contigs (>= 50000 bp)	6
Total length (>= 0 bp)	1427907
Total length (>= 1000 bp)	1426086
Total length (>= 5000 bp)	1404416
Total length (>= 10000 bp)	1364903
Total length (>= 25000 bp)	1137135
Total length (>= 50000 bp)	510948
# contigs	54
Largest contig	147840
Total length	1427907
Reference length	1521208
GC (%)	28.31
Reference GC (%)	28.18
N50	36967
NG50	33777
N90	16824
NG90	8706
auN	53385.5
auNG	50111.2
L50	11
LG50	12
L90	33
LG90	39
# misassemblies	24
# misassembled contigs	14
Misassembled contigs length	394426
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 15 part
Unaligned length	114883
Genome fraction (%)	80.442
Duplication ratio	1.072
# N's per 100 kbp	0.00
# mismatches per 100 kbp	939.06
# indels per 100 kbp	76.21
# genomic features	1236 + 60 part
Largest alignment	147832
Total aligned length	1312160
NA50	33777
NGA50	28321
NA90	2330
NGA90	-
auNA	48433.7
auNGA	45463.1
LA50	11
LGA50	13
LA90	59
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

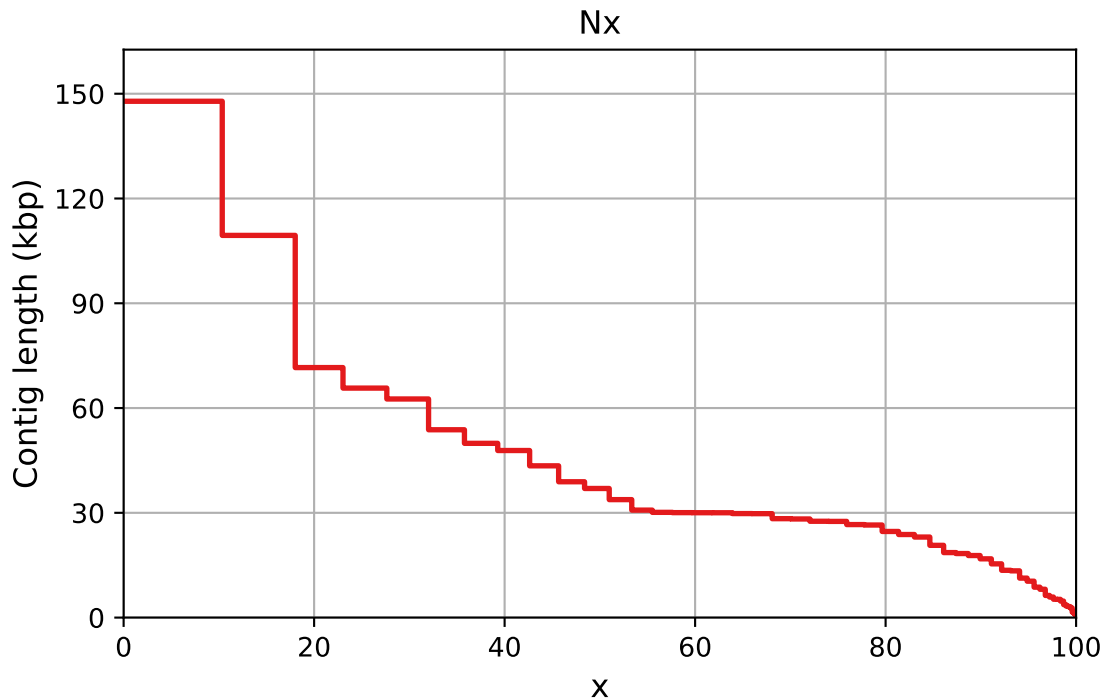
	GCF_000181855.2_ASM18185v2_genomic
# misassemblies	24
# contig misassemblies	24
# c. relocations	4
# c. translocations	17
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	14
Misassembled contigs length	394426
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	12322
# indels	1000
# indels (<= 5 bp)	912
# indels (> 5 bp)	88
Indels length	4044

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

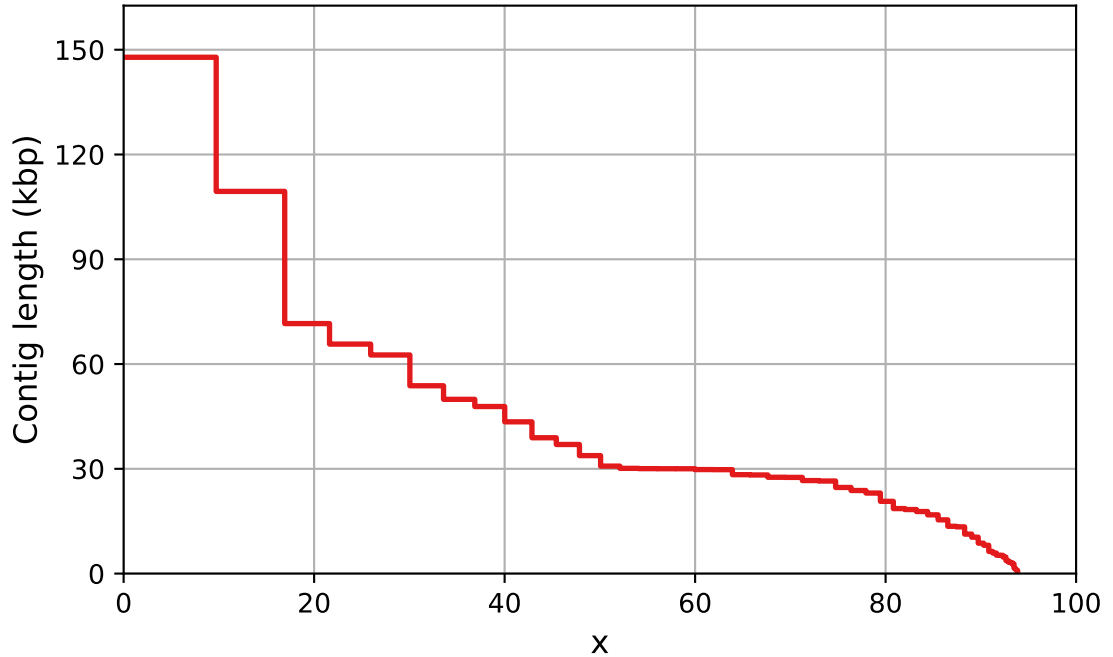
	GCF_000181855.2_ASM18185v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	114883
# N's	0

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).

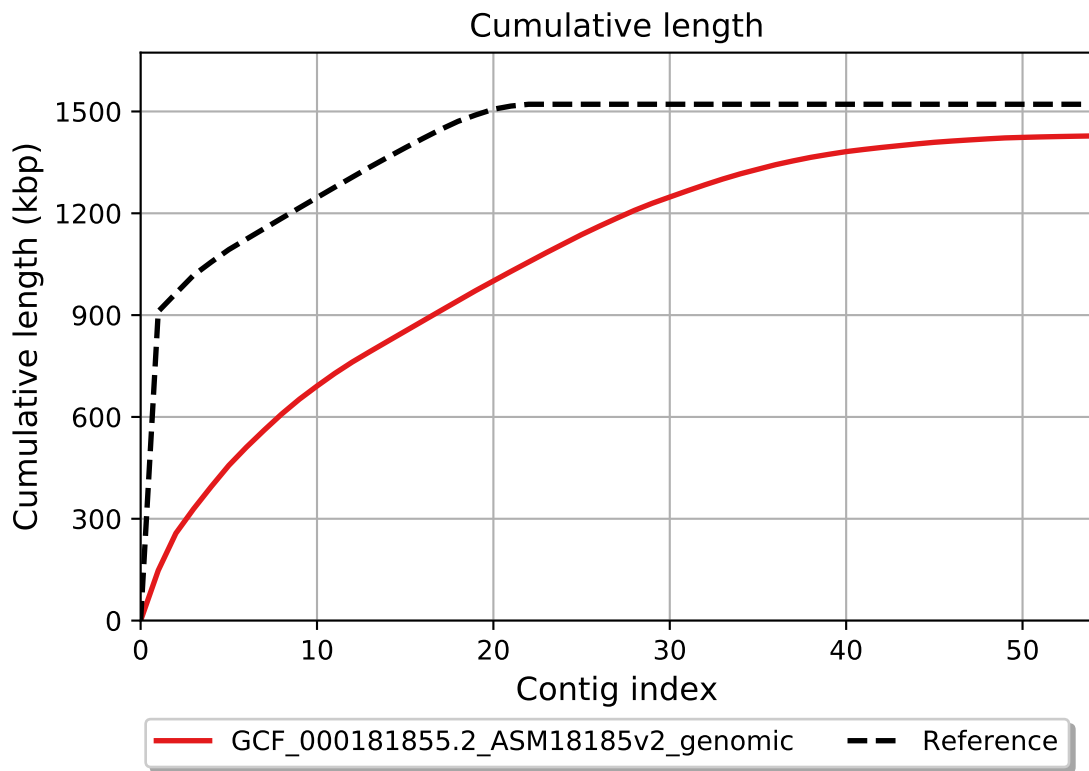


— GCF_000181855.2_ASM18185v2_genomic

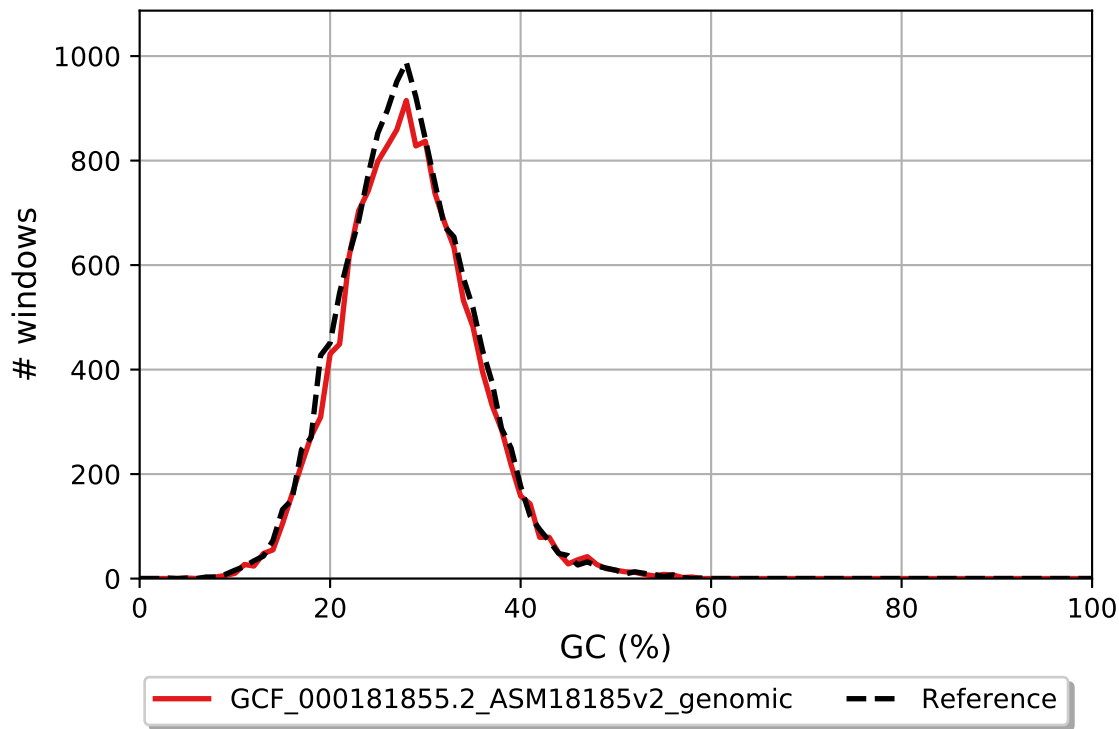
NGx



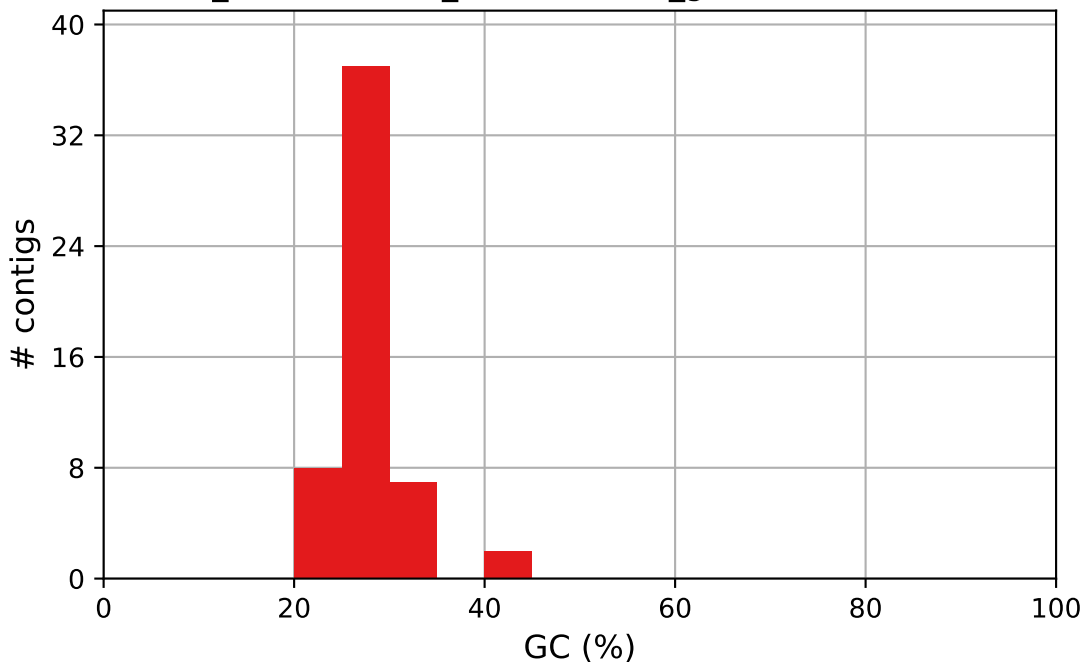
GCF_000181855.2_ASM18185v2_genomic



GC content

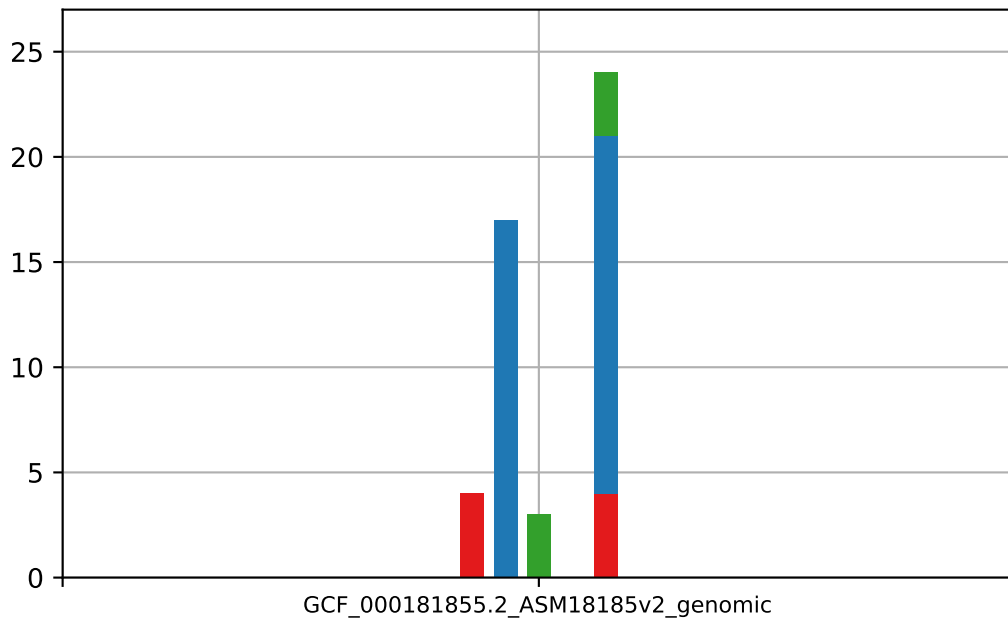


GCF_000181855.2_ASM18185v2_genomic GC content



GCF_000181855.2_ASM18185v2_genomic

Misassemblies



relocations

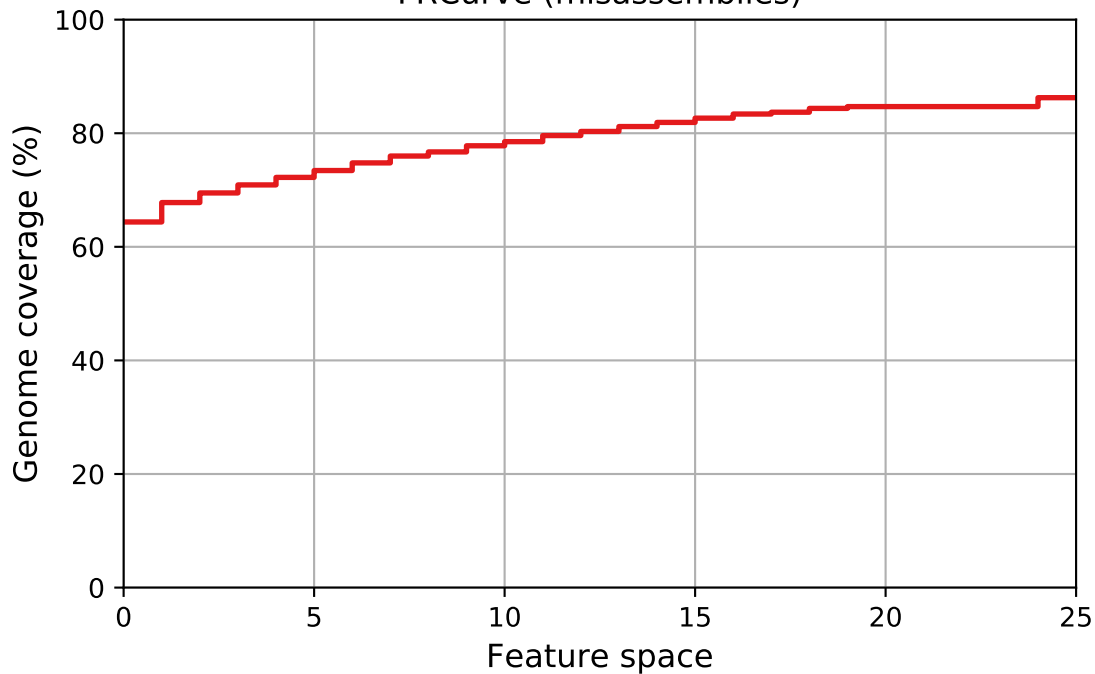


translocations



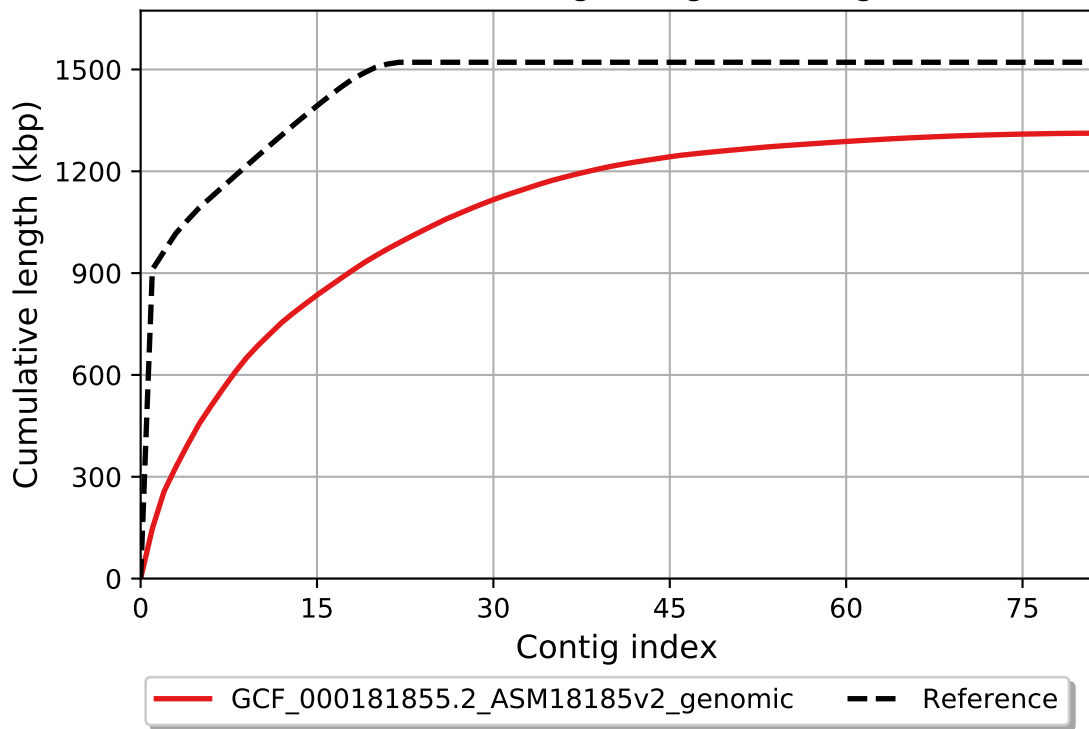
inversions

FRCurve (misassemblies)

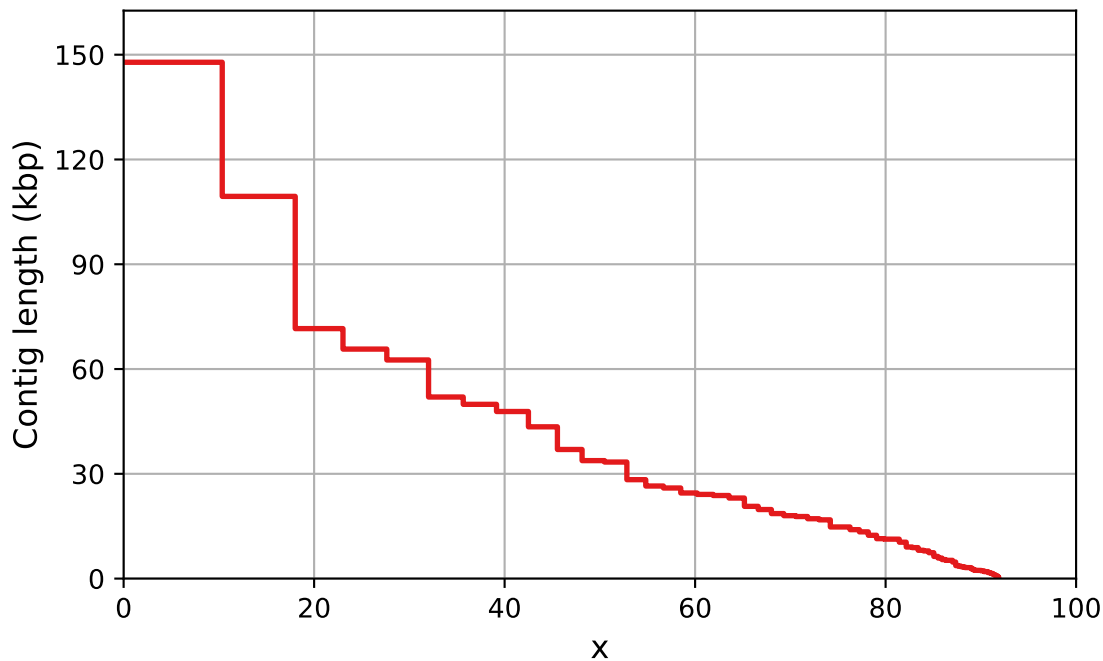


— GCF_000181855.2_ASM18185v2_genomic

Cumulative length (aligned contigs)

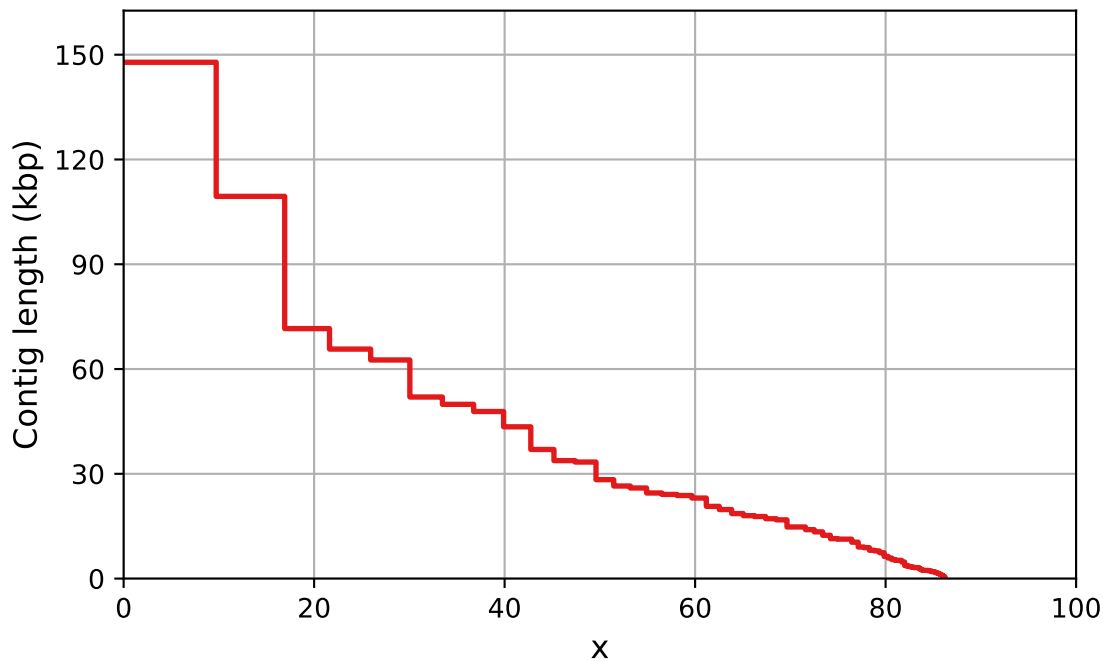


NAx



— GCF_000181855.2_ASM18185v2_genomic

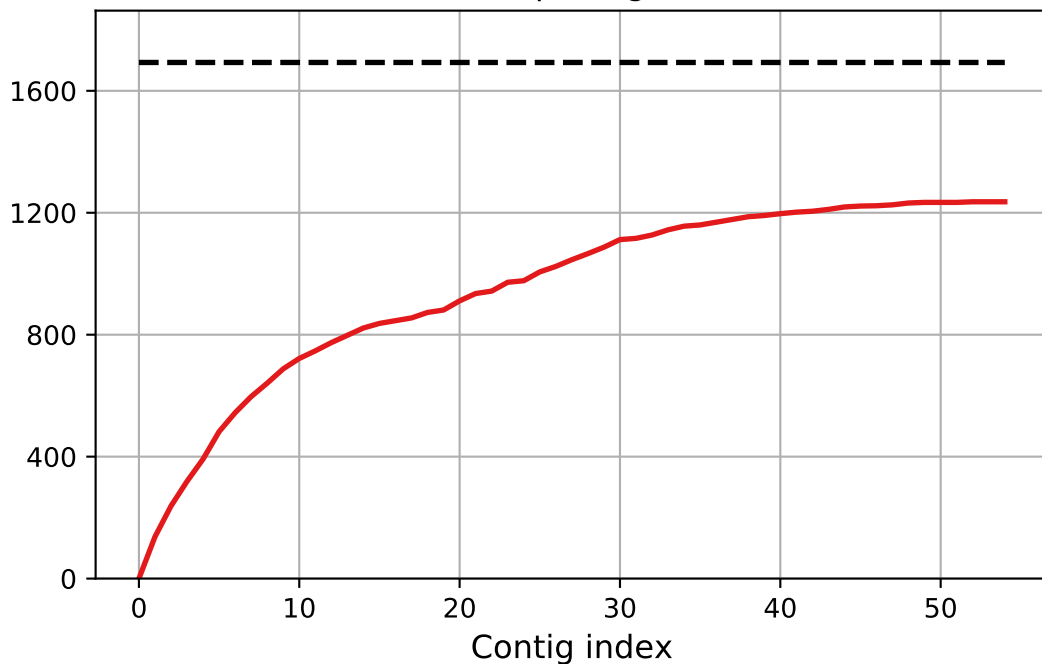
NGAx



— GCF_000181855.2_ASM18185v2_genomic

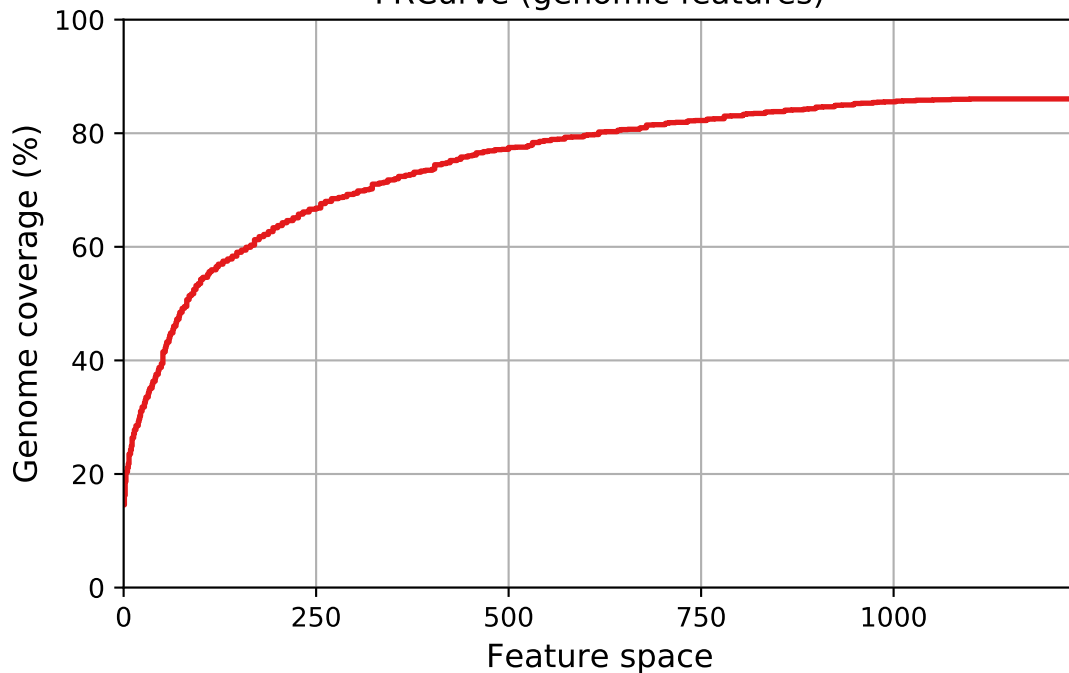
Cumulative # complete genomic features

Cumulative # complete genomic features



GCF_000181855.2_ASM18185v2_genomic -- Reference

FRCurve (genomic features)



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