

Report

GCF_019464575.1_ASM1946457v1_genomic	
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1429304
Total length (>= 1000 bp)	1429304
Total length (>= 5000 bp)	1429304
Total length (>= 10000 bp)	1429304
Total length (>= 25000 bp)	1346823
Total length (>= 50000 bp)	957418
# contigs	19
Largest contig	903660
Total length	1429304
Reference length	1521208
GC (%)	28.21
Reference GC (%)	28.18
N50	903660
NG50	903660
N90	27715
NG90	24387
auN	582816.1
auNG	547605.2
L50	1
LG50	1
L90	13
LG90	16
# misassemblies	30
# misassembled contigs	14
Misassembled contigs length	427297
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 13 part
Unaligned length	100342
Genome fraction (%)	81.123
Duplication ratio	1.076
# N's per 100 kbp	0.00
# mismatches per 100 kbp	948.06
# indels per 100 kbp	69.76
# genomic features	1278 + 40 part
Largest alignment	903470
Total aligned length	1327445
NA50	903470
NGA50	903470
NA90	3158
NGA90	-
auNA	577381.0
auNGA	542498.4
LA50	1
LGA50	1
LA90	26
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

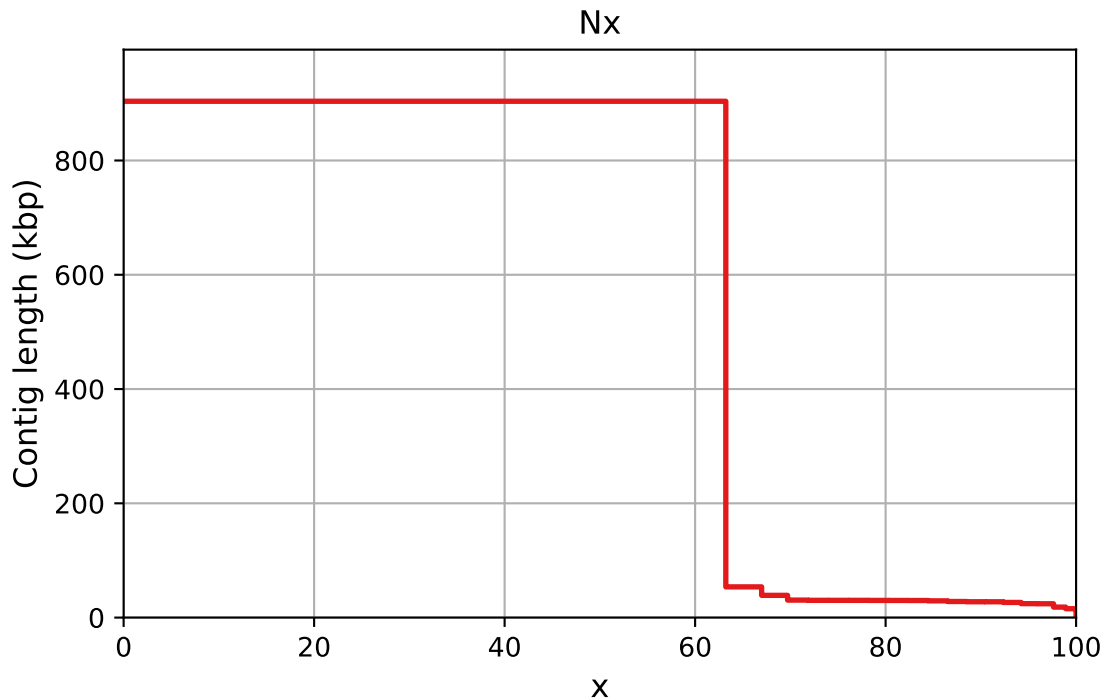
	GCF_019464575.1_ASM1946457v1_genomic
# misassemblies	30
# contig misassemblies	30
# c. relocations	3
# c. translocations	23
# c. inversions	4
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	14
Misassembled contigs length	427297
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	12585
# indels	926
# indels (<= 5 bp)	815
# indels (> 5 bp)	111
Indels length	6588

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

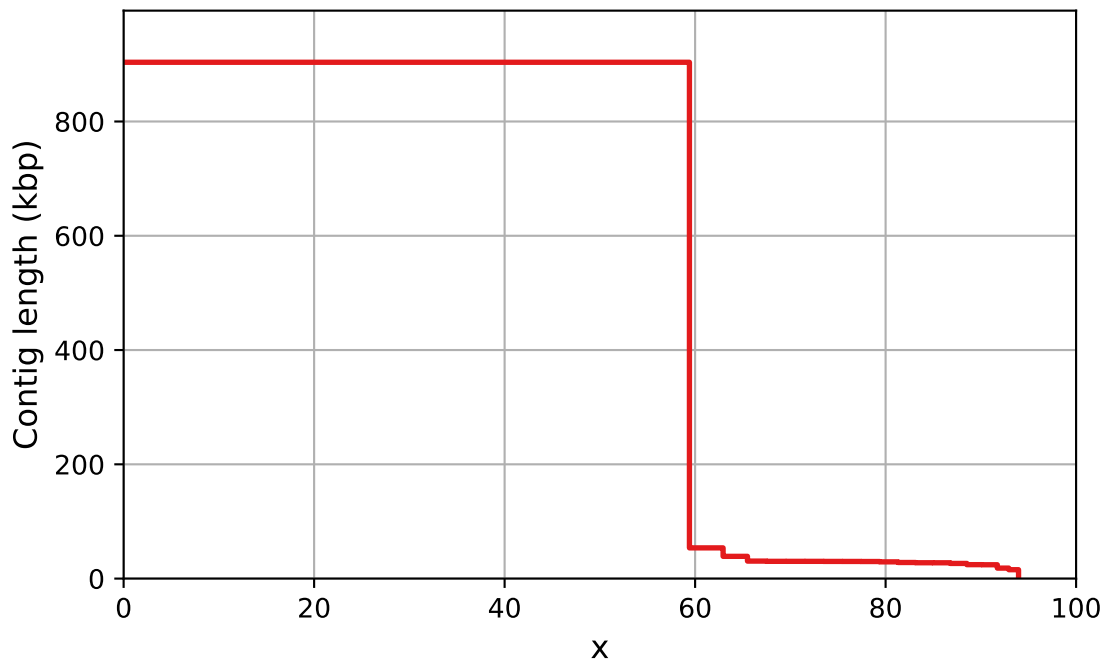
	GCF_019464575.1_ASM1946457v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	100342
# N's	0

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).

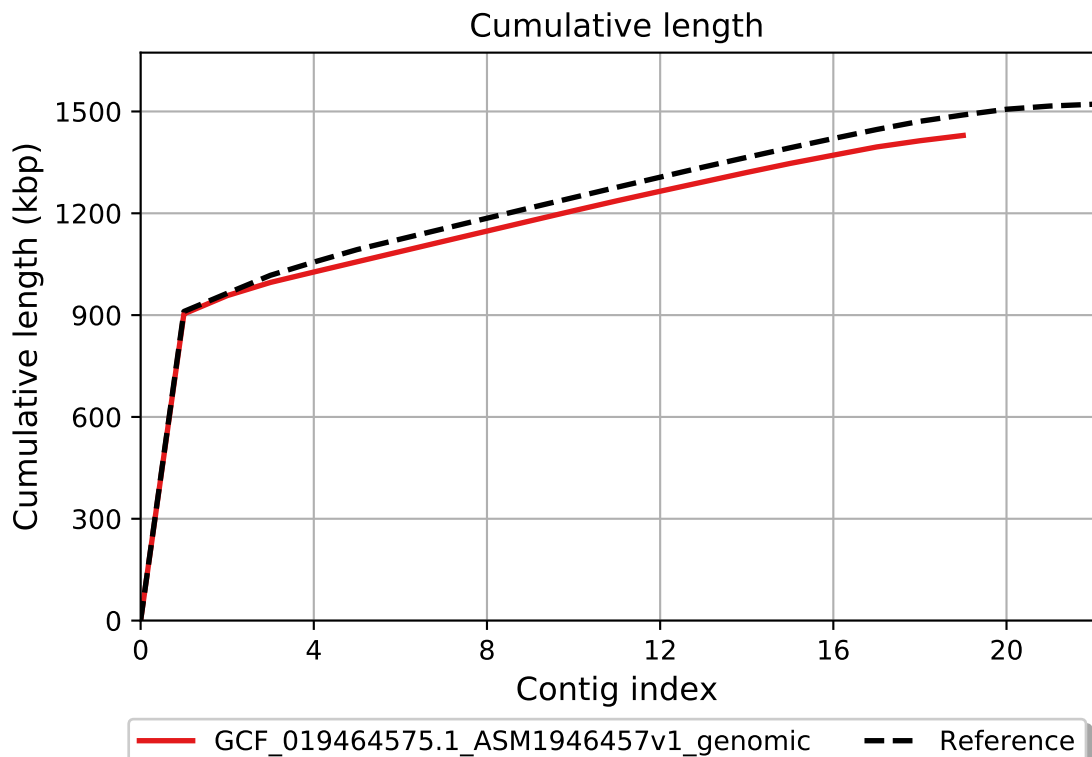


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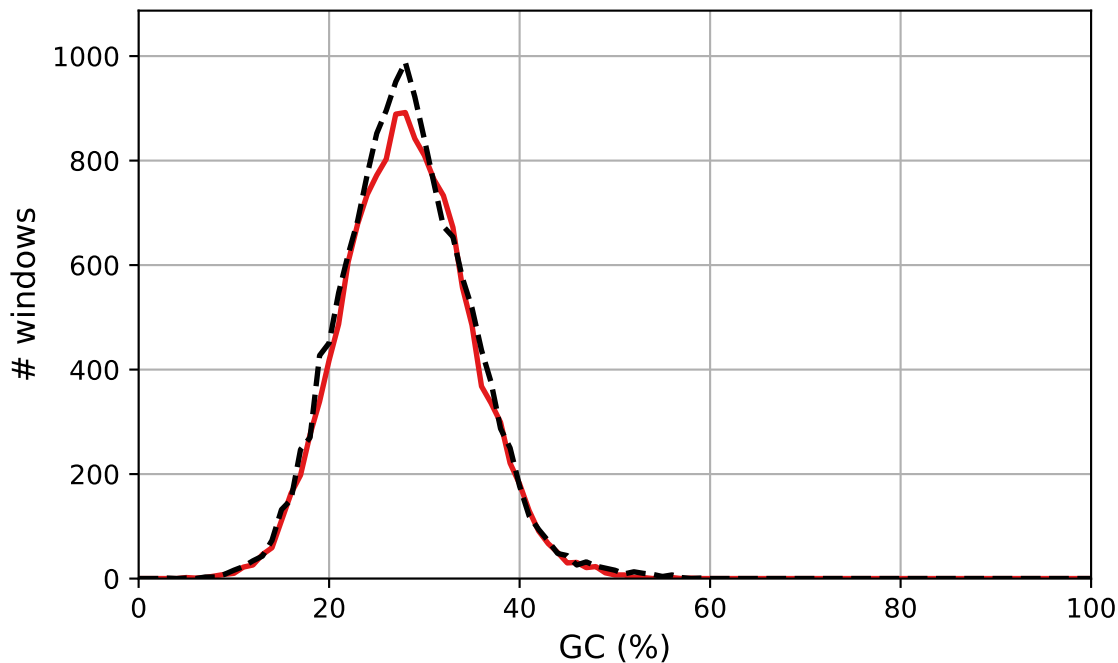
NGx



— GCF_019464575.1_ASM1946457v1_genomic

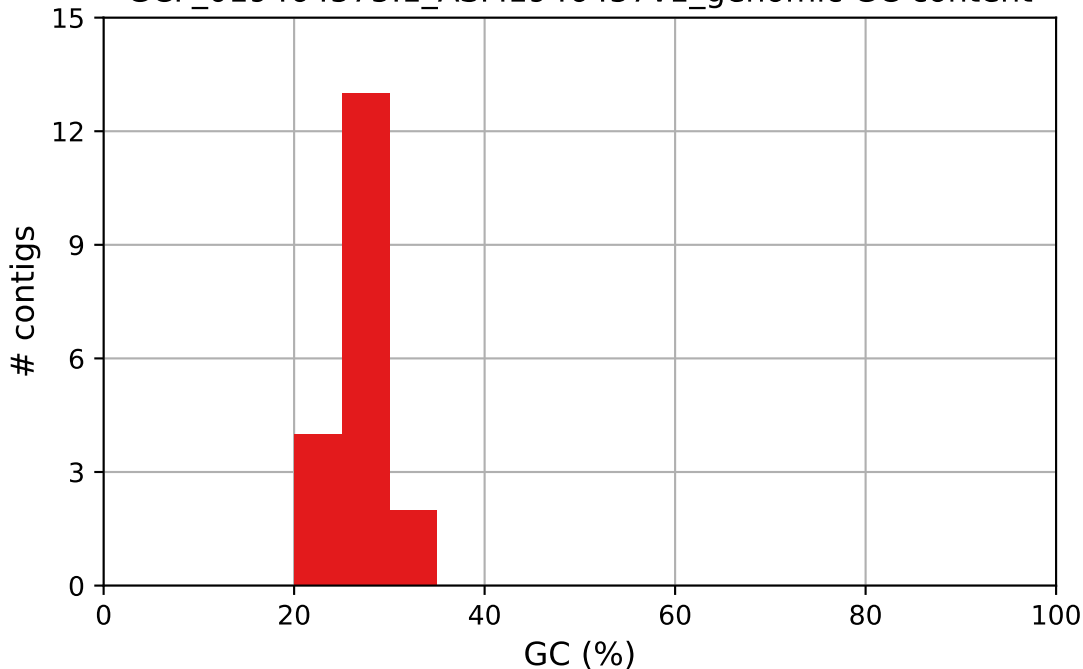


GC content



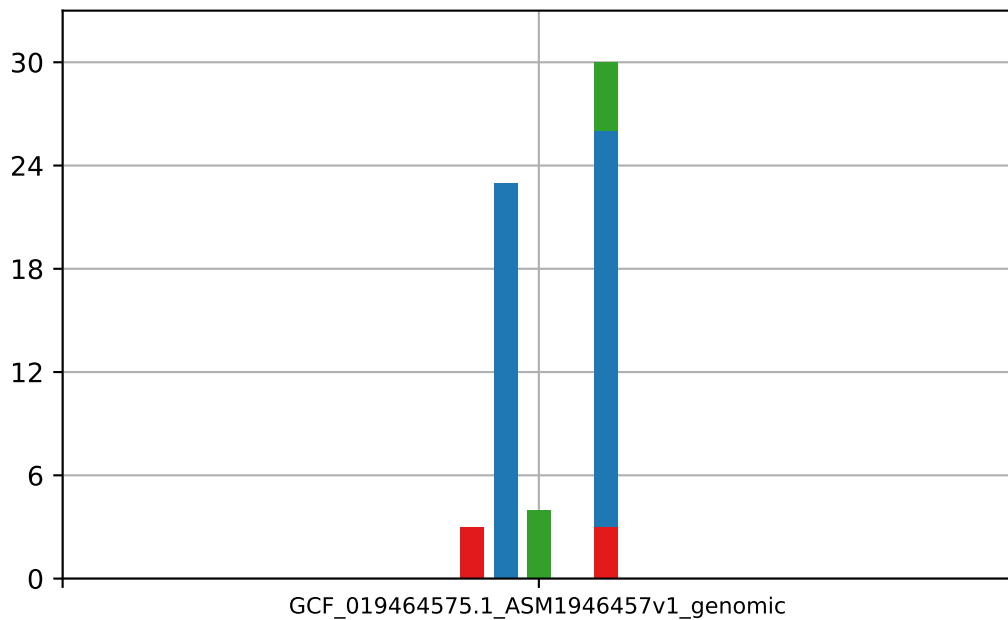
— GCF_019464575.1_ASM1946457v1_genomic - - Reference

GCF_019464575.1_ASM1946457v1_genomic GC content



 GCF_019464575.1_ASM1946457v1_genomic

Misassemblies



relocations

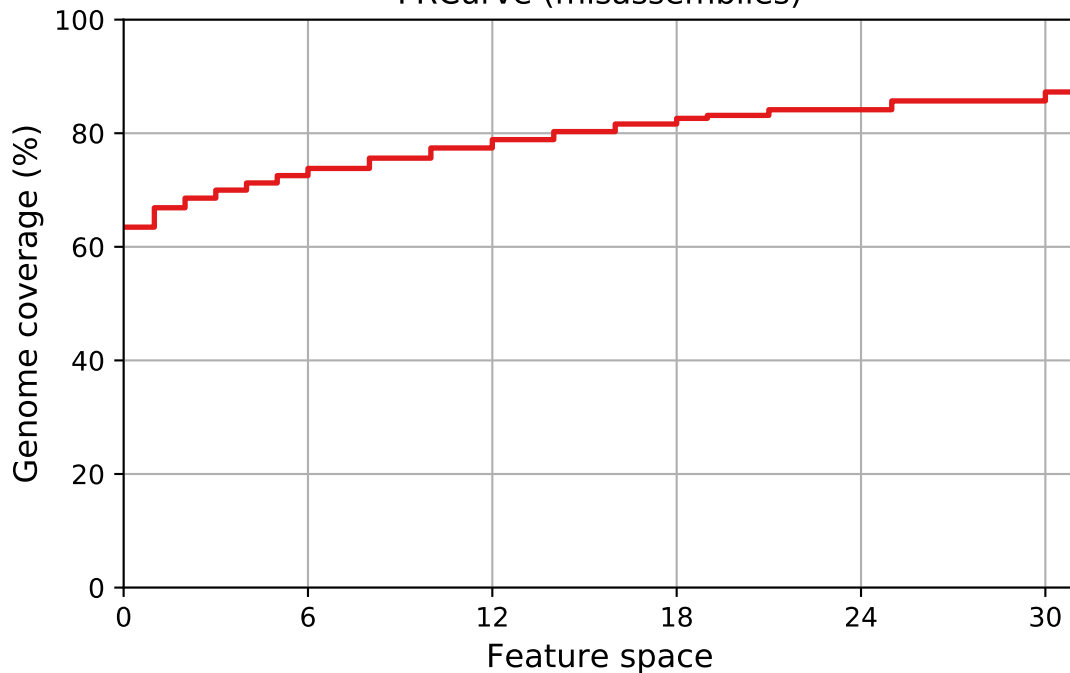


translocations



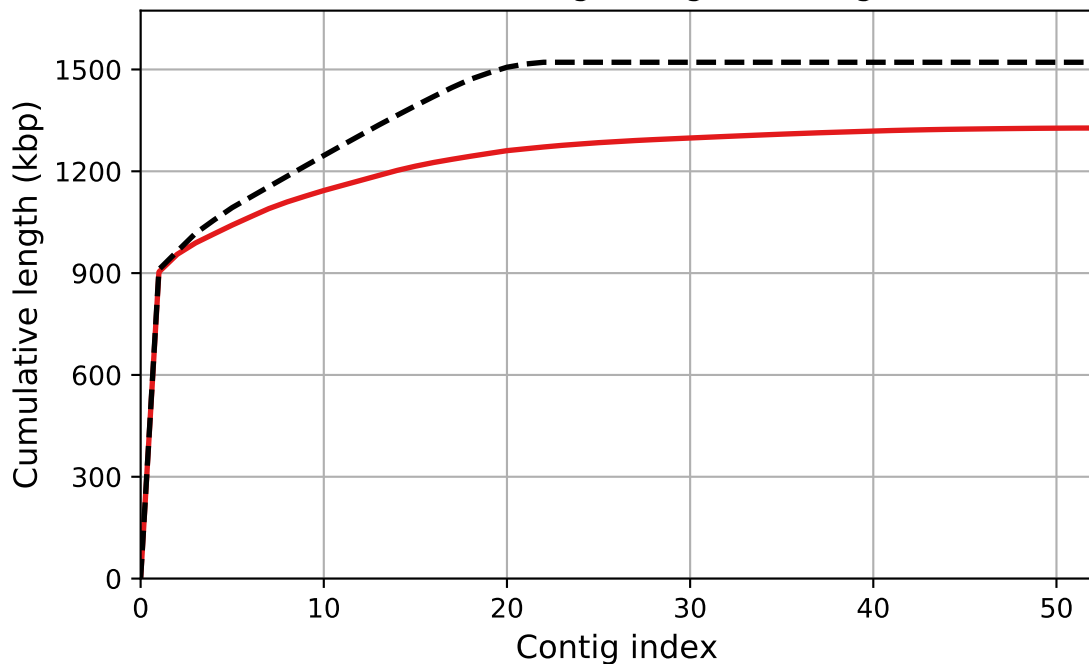
inversions

FRCurve (misassemblies)



— GCF_019464575.1_ASM1946457v1_genomic

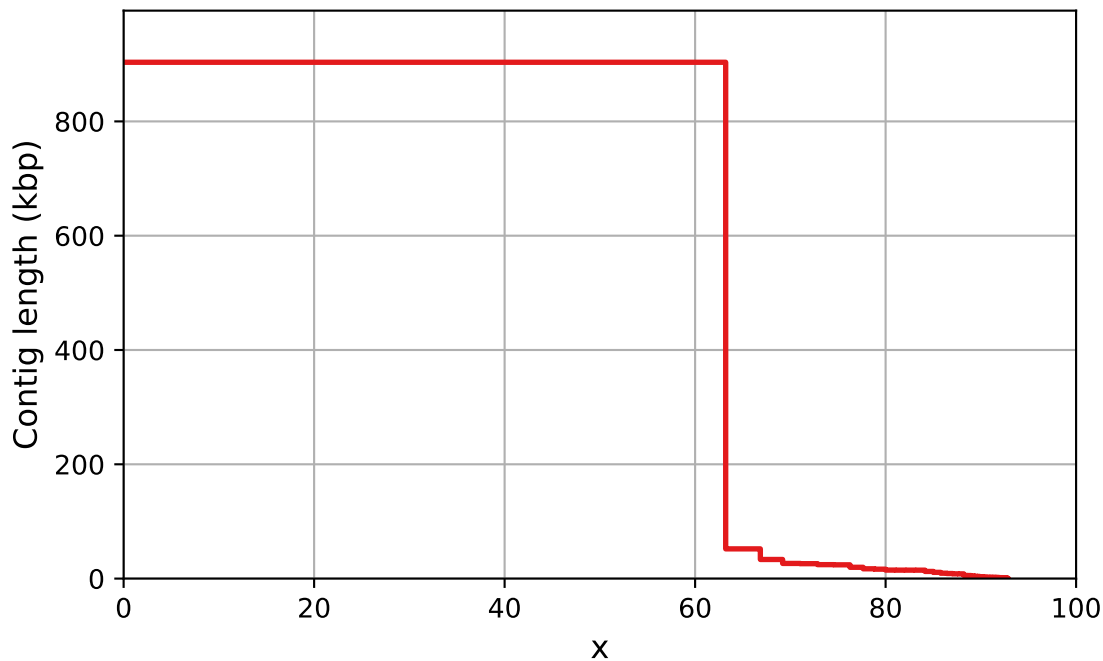
Cumulative length (aligned contigs)



GCF_019464575.1_ASM1946457v1_genomic

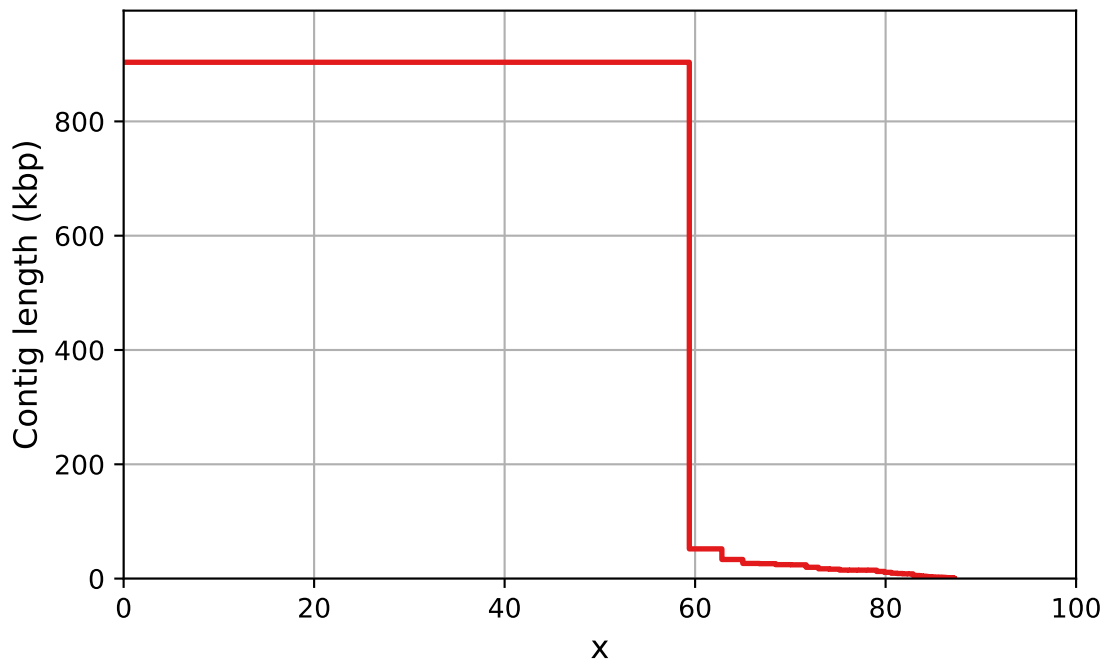
Reference

NAx



— GCF_019464575.1_ASM1946457v1_genomic

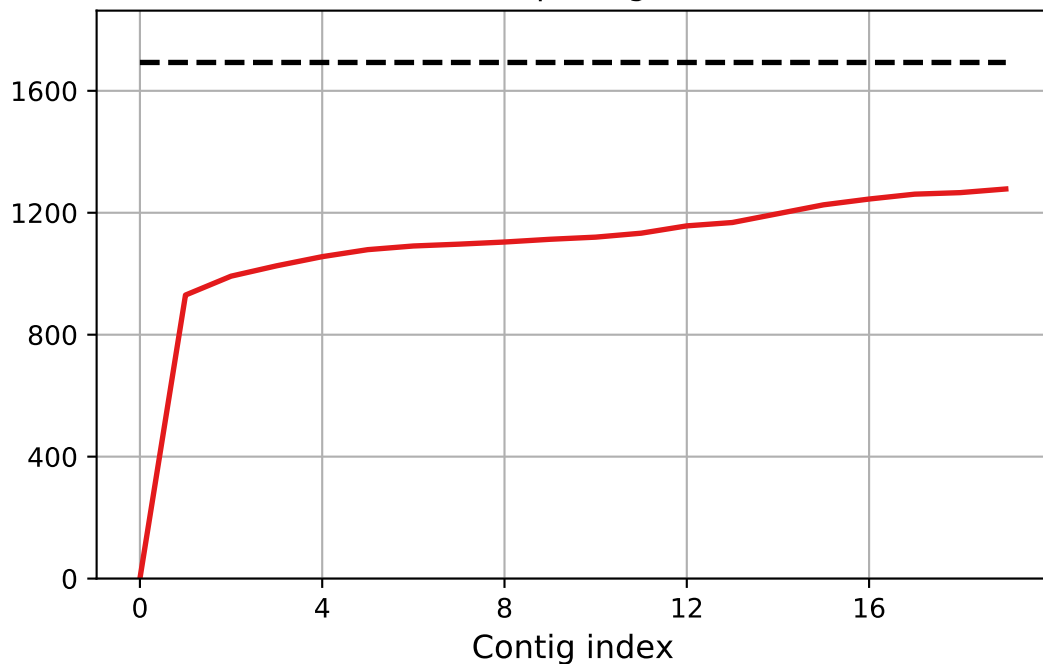
NGAx



— GCF_019464575.1_ASM1946457v1_genomic

Cumulative # complete genomic features

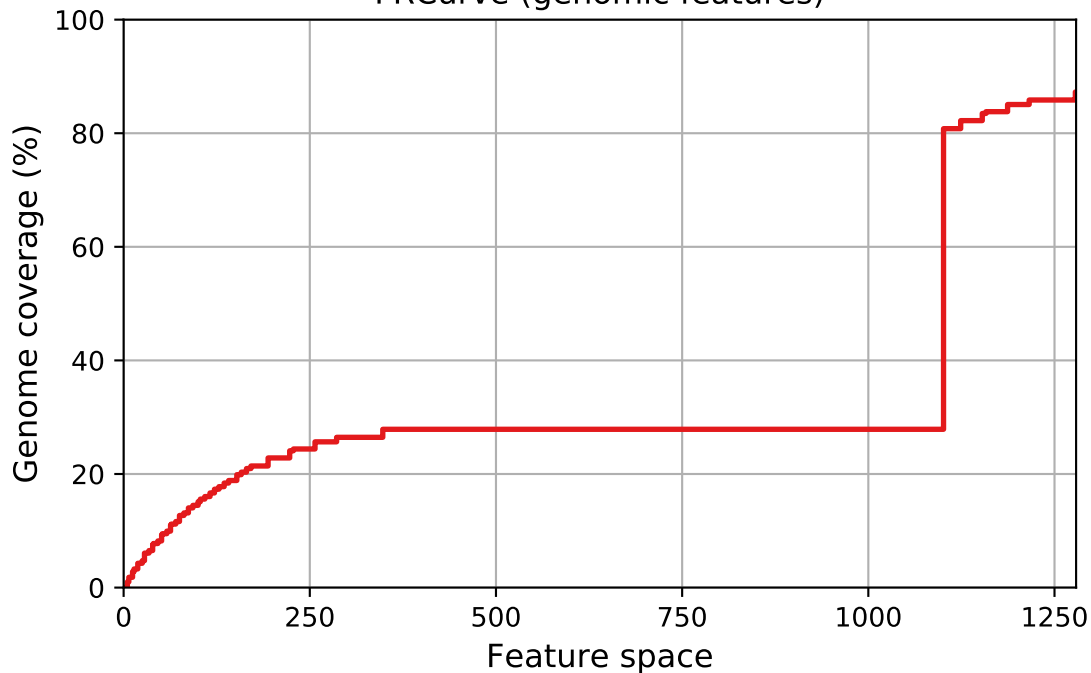
Cumulative # complete genomic features



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Reference

FRCurve (genomic features)



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