

Report

GCF_019134655.1_ASM1913465v1_genomic	
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1217256
Total length (>= 1000 bp)	1217256
Total length (>= 5000 bp)	1217256
Total length (>= 10000 bp)	1217256
Total length (>= 25000 bp)	1199051
Total length (>= 50000 bp)	961768
# contigs	11
Largest contig	909995
Total length	1217256
Reference length	1521208
GC (%)	28.45
Reference GC (%)	28.18
N50	909995
NG50	909995
N90	29645
NG90	-
auN	688566.0
auNG	550983.9
L50	1
LG50	1
L90	7
LG90	-
# misassemblies	13
# misassembled contigs	6
Misassembled contigs length	179875
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	74069
Genome fraction (%)	73.334
Duplication ratio	1.018
# N's per 100 kbp	1.64
# mismatches per 100 kbp	837.36
# indels per 100 kbp	39.56
# genomic features	1160 + 32 part
Largest alignment	904588
Total aligned length	1135119
NA50	904588
NGA50	904588
NA90	7716
NGA90	-
auNA	676857.7
auNGA	541615.1
LA50	1
LGA50	1
LA90	11
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

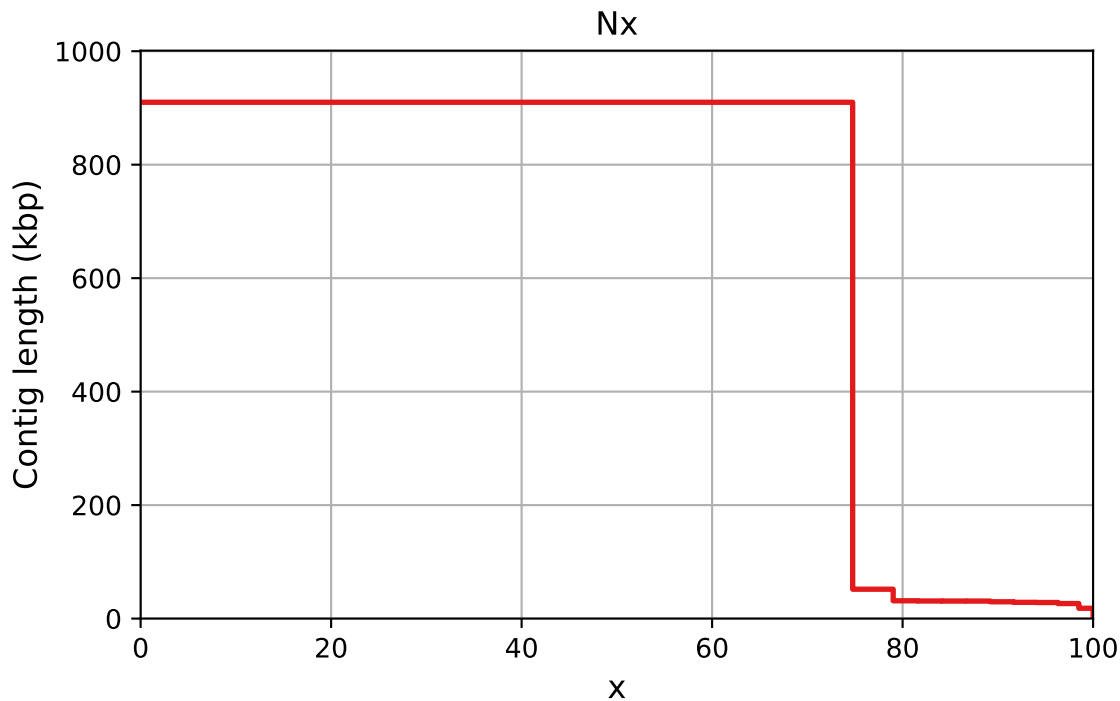
	GCF_019134655.1_ASM1913465v1_genomic
# misassemblies	13
# contig misassemblies	13
# c. relocations	1
# c. translocations	12
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	179875
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	9505
# indels	449
# indels (<= 5 bp)	402
# indels (> 5 bp)	47
Indels length	1949

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

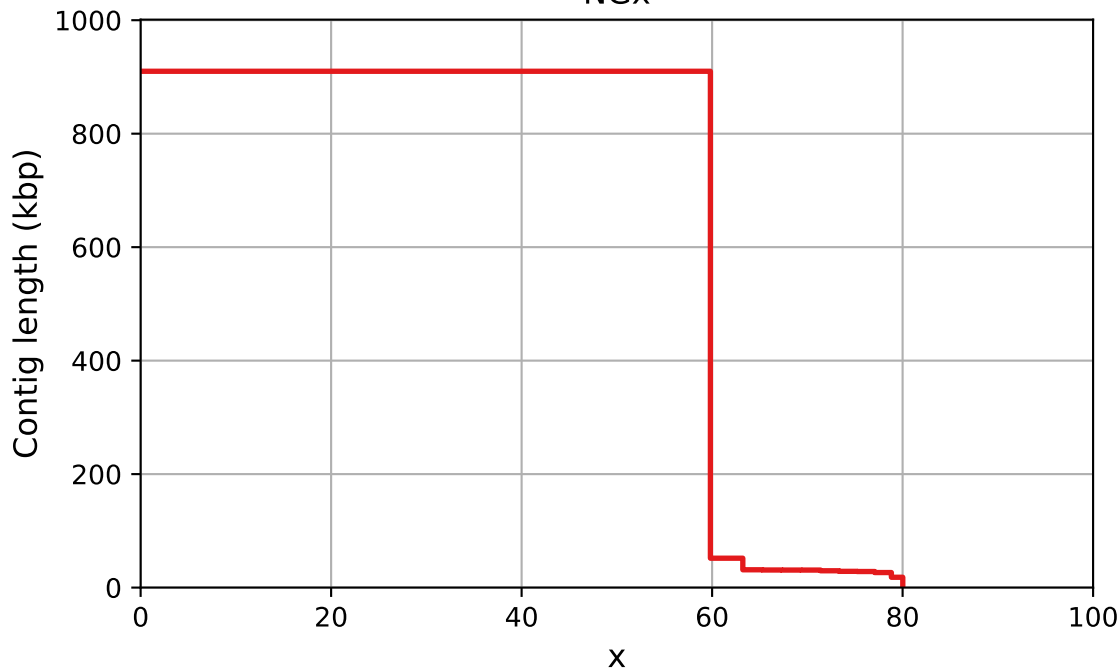
	GCF_019134655.1_ASM1913465v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	74069
# N's	20

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).

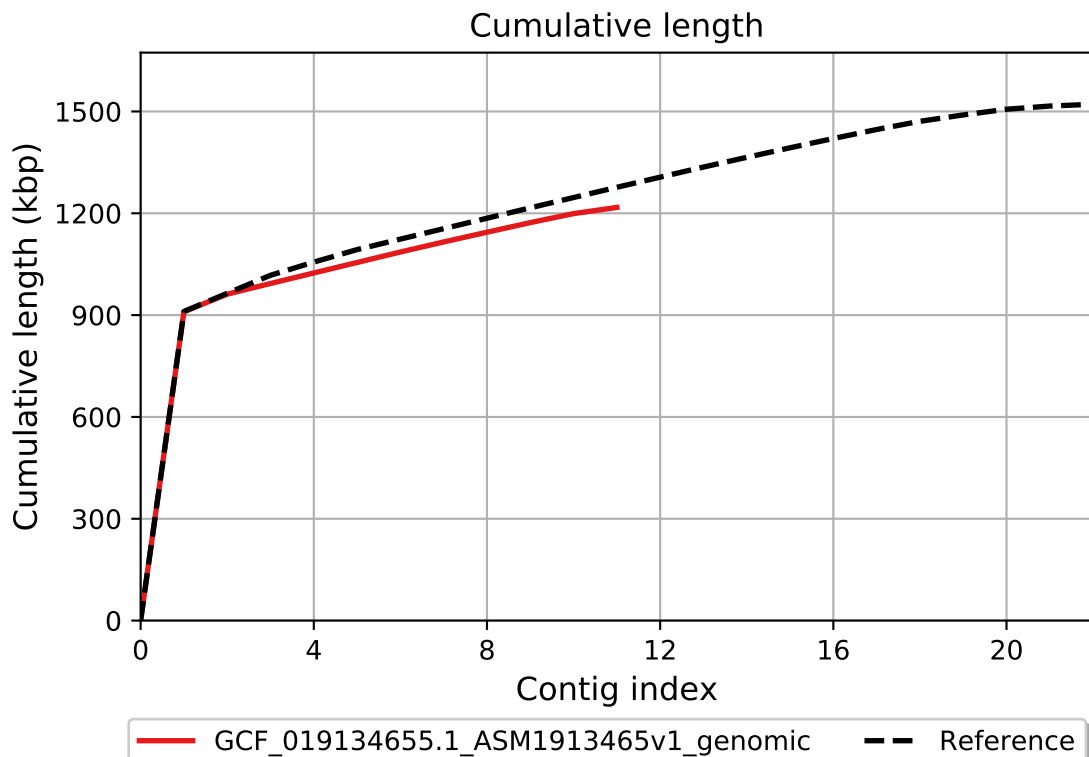


— GCF_019134655.1_ASM1913465v1_genomic

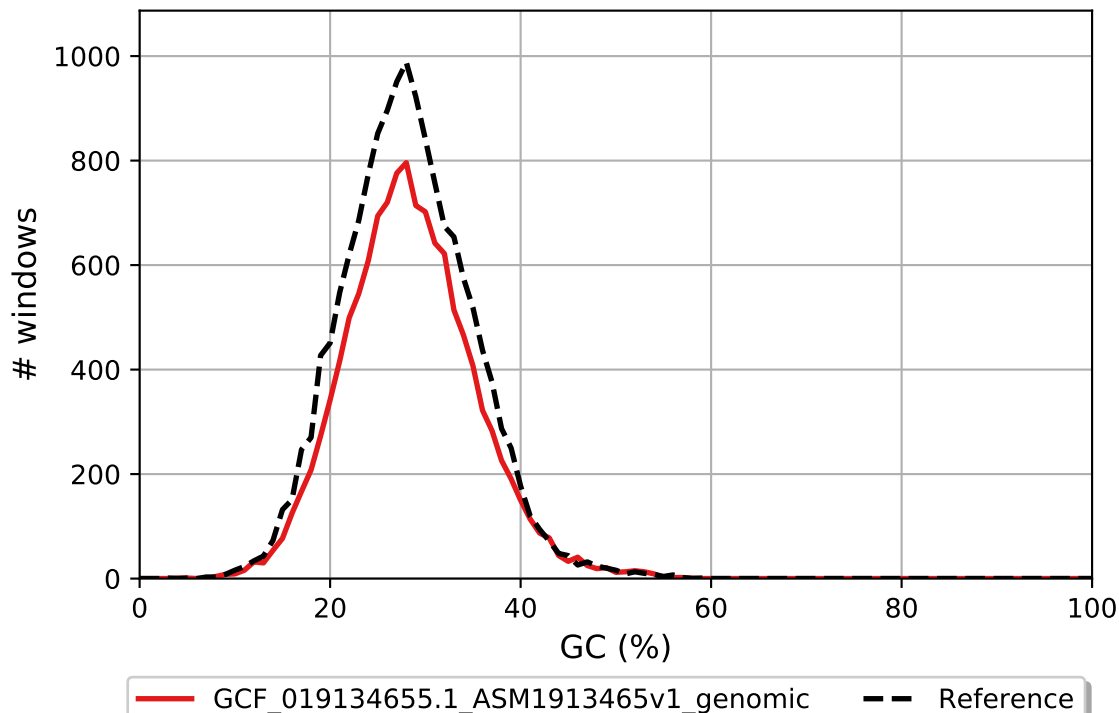
NGx



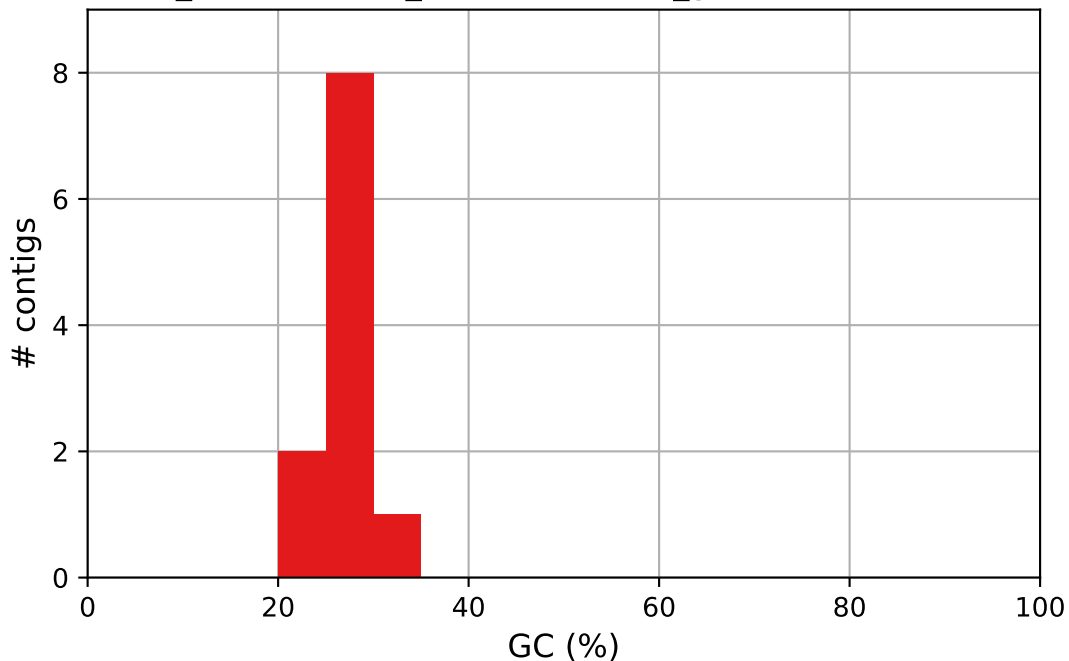
— GCF_019134655.1_ASM1913465v1_genomic



GC content

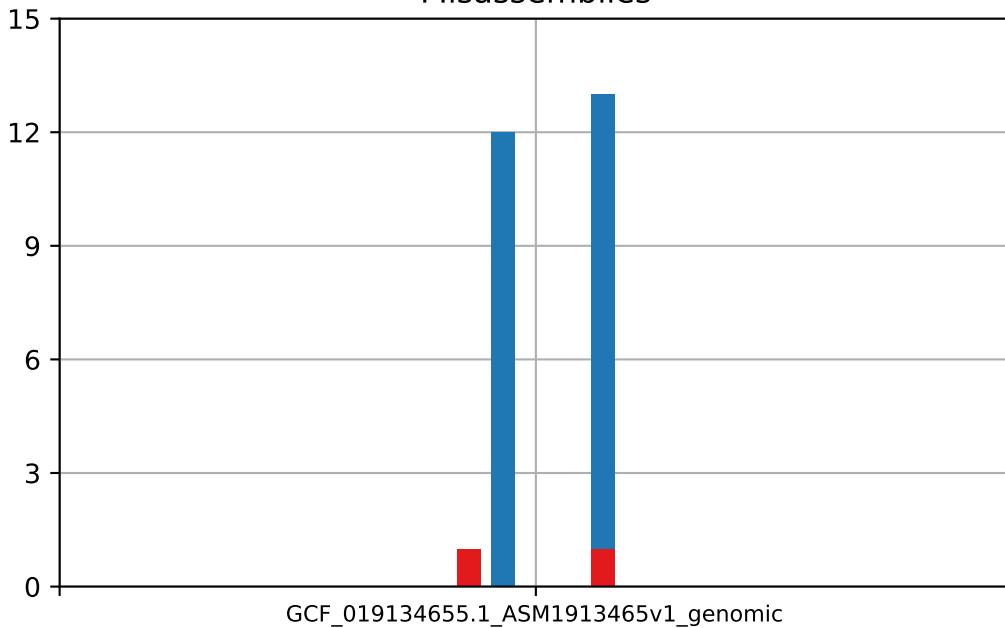


GCF_019134655.1_ASM1913465v1_genomic GC content



■ GCF_019134655.1_ASM1913465v1_genomic

Misassemblies

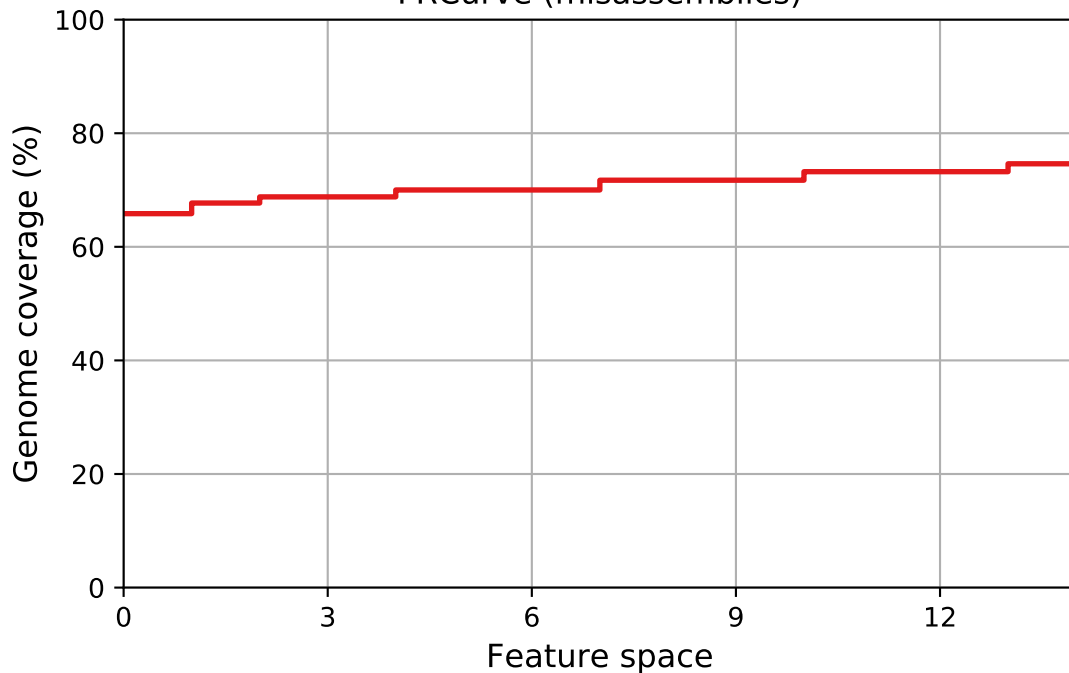


relocations



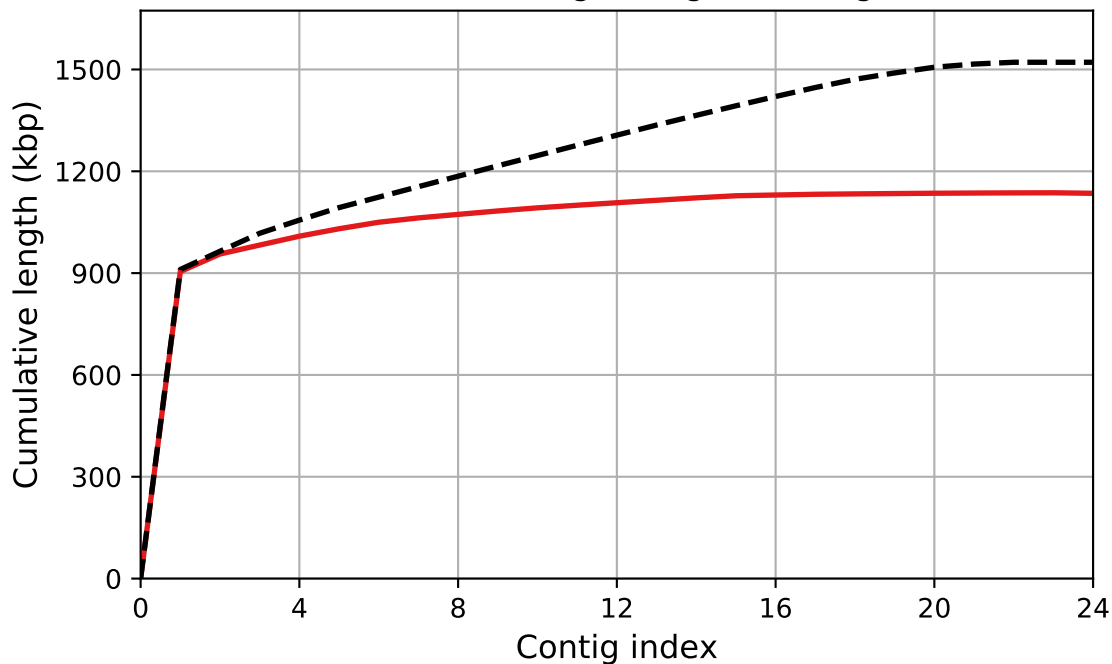
translocations

FRCurve (misassemblies)



— GCF_019134655.1_ASM1913465v1_genomic

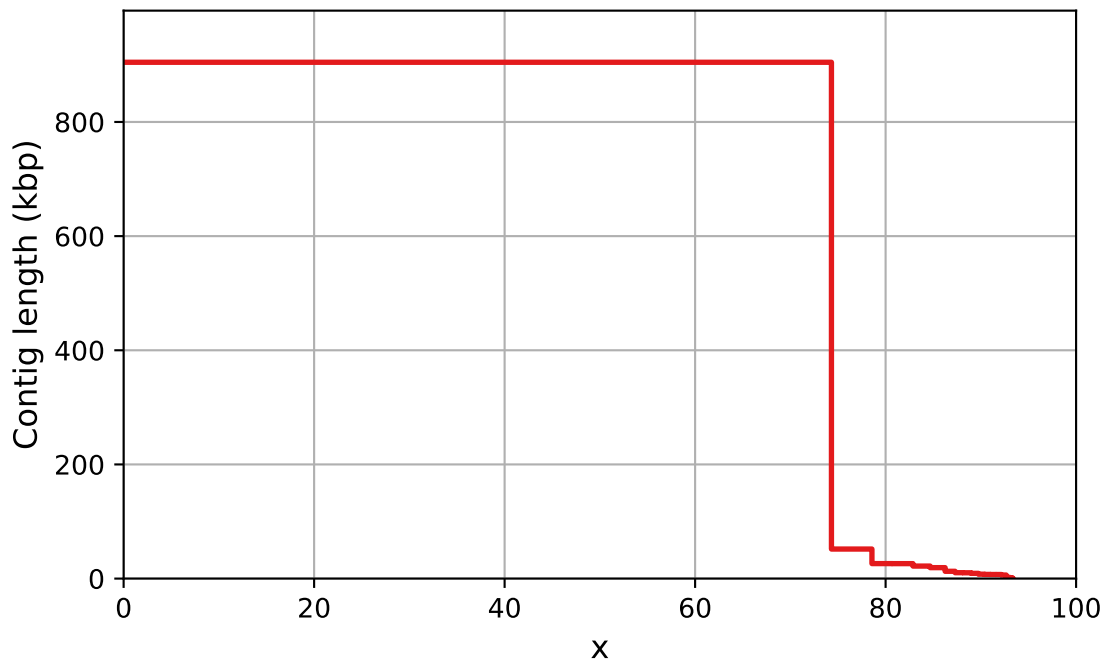
Cumulative length (aligned contigs)



GCF_019134655.1_ASM1913465v1_genomic

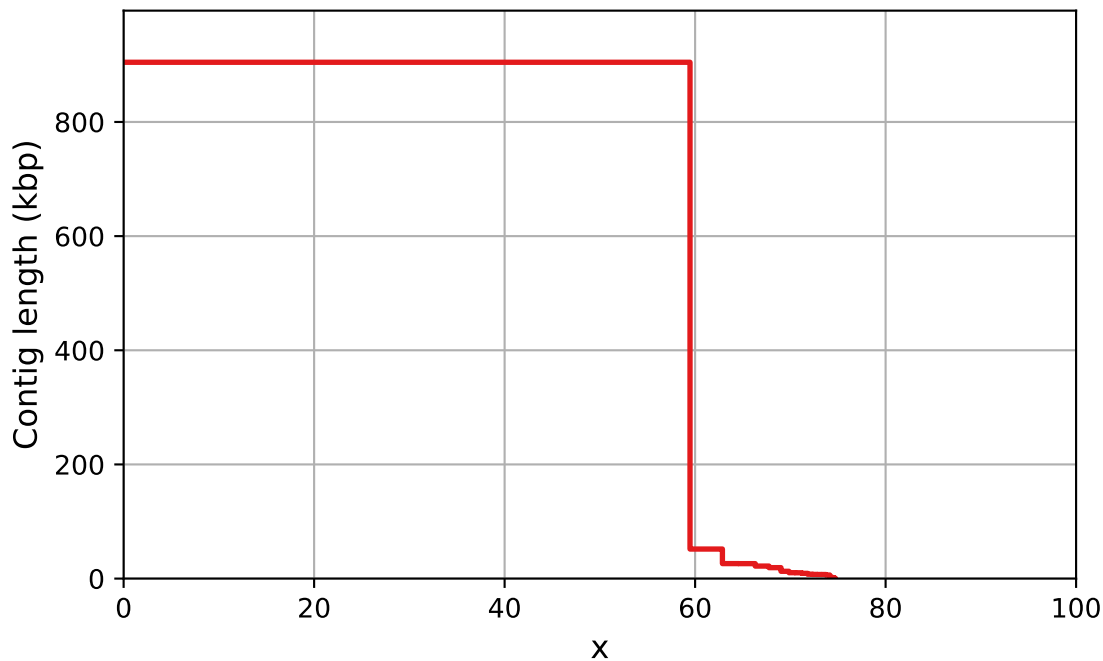
Reference

NAx

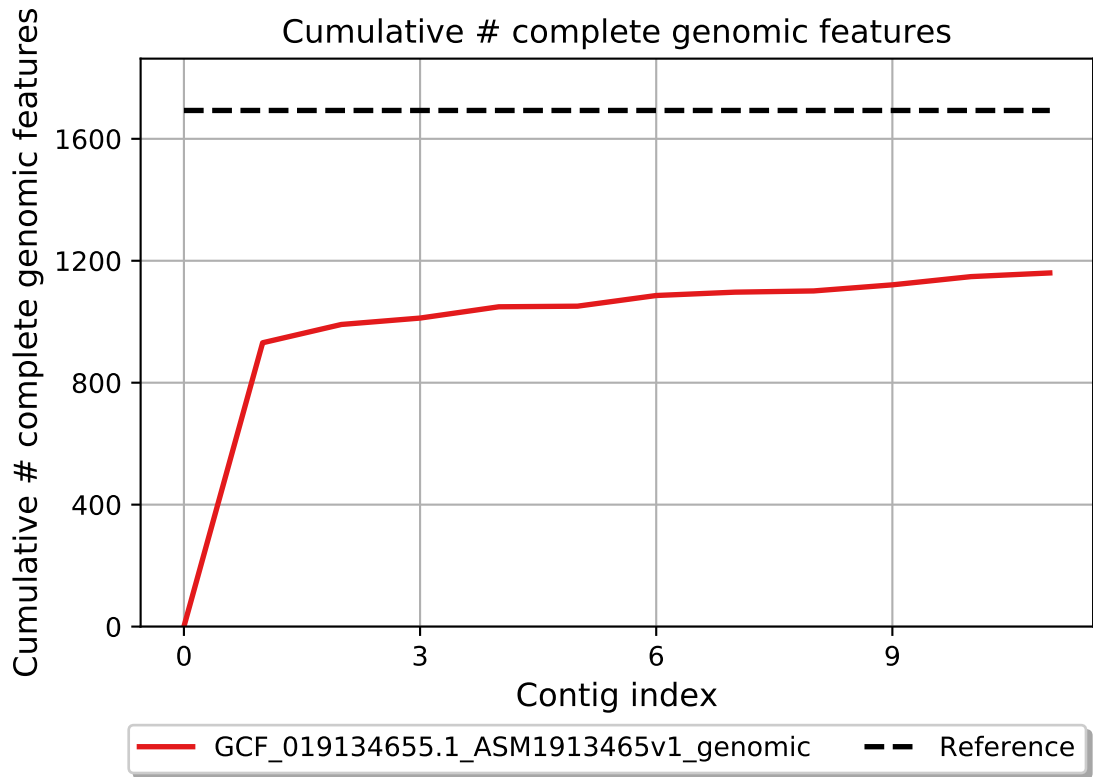


— GCF_019134655.1_ASM1913465v1_genomic

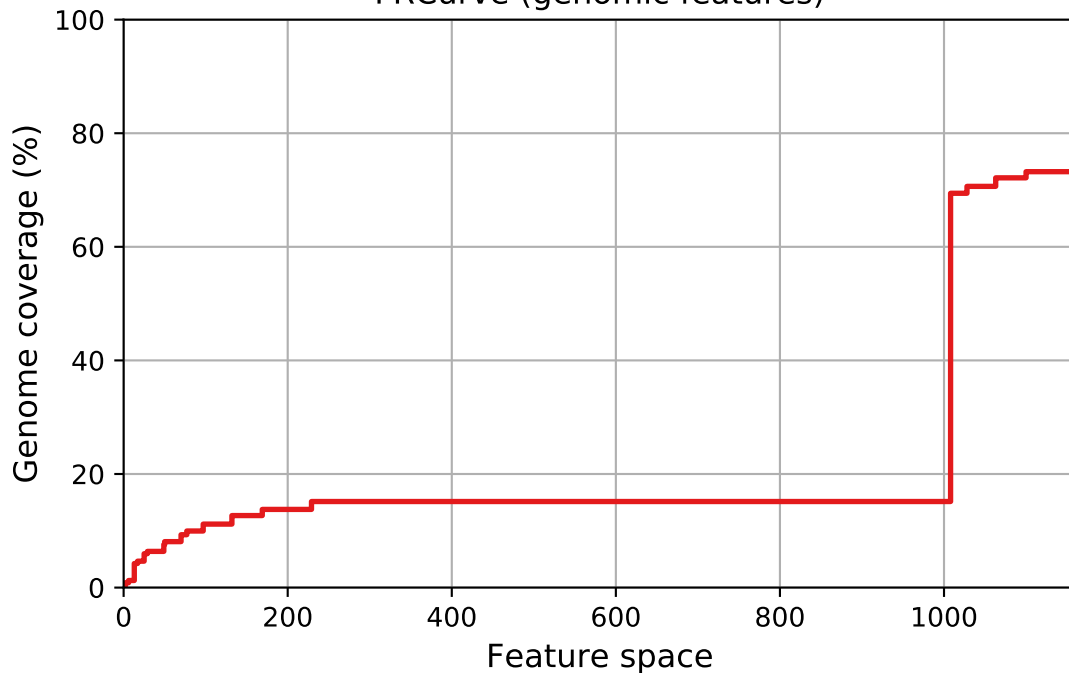
NGAx



— GCF_019134655.1_ASM1913465v1_genomic



FRCurve (genomic features)



— GCF_019134655.1_ASM1913465v1_genomic