

Report

GCA_030445065.1_ASM3044506v1_genomic	
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1006503
Total length (>= 1000 bp)	1006503
Total length (>= 5000 bp)	1006503
Total length (>= 10000 bp)	1006503
Total length (>= 25000 bp)	989986
Total length (>= 50000 bp)	963461
# contigs	4
Largest contig	910229
Total length	1006503
Reference length	1521208
GC (%)	28.43
Reference GC (%)	28.18
N50	910229
NG50	910229
N90	910229
NG90	-
auN	826949.2
auNG	547148.6
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	16517
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.140
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	286.20
# indels per 100 kbp	12.82
# genomic features	1044 + 5 part
Largest alignment	910229
Total aligned length	1005955
NA50	910229
NGA50	910229
NA90	910229
NGA90	-
auNA	826887.8
auNGA	547108.0
LA50	1
LGA50	1
LA90	1
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

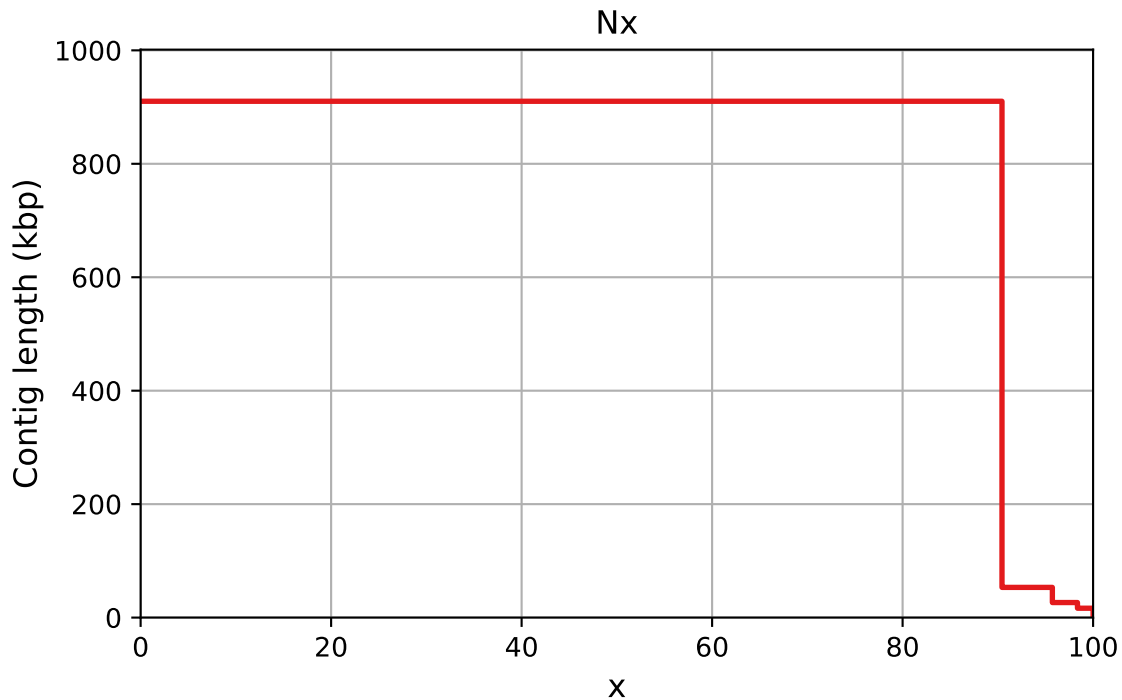
	GCA_030445065.1_ASM3044506v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	16517
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	2879
# indels	129
# indels (<= 5 bp)	115
# indels (> 5 bp)	14
Indels length	631

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

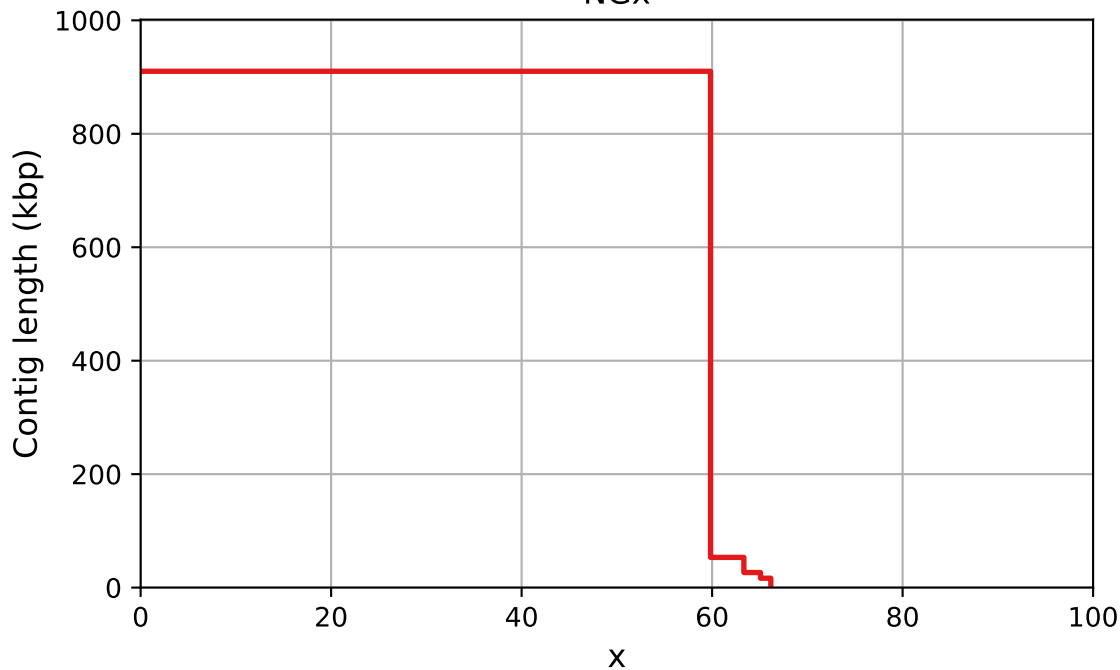
	GCA_030445065.1_ASM3044506v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

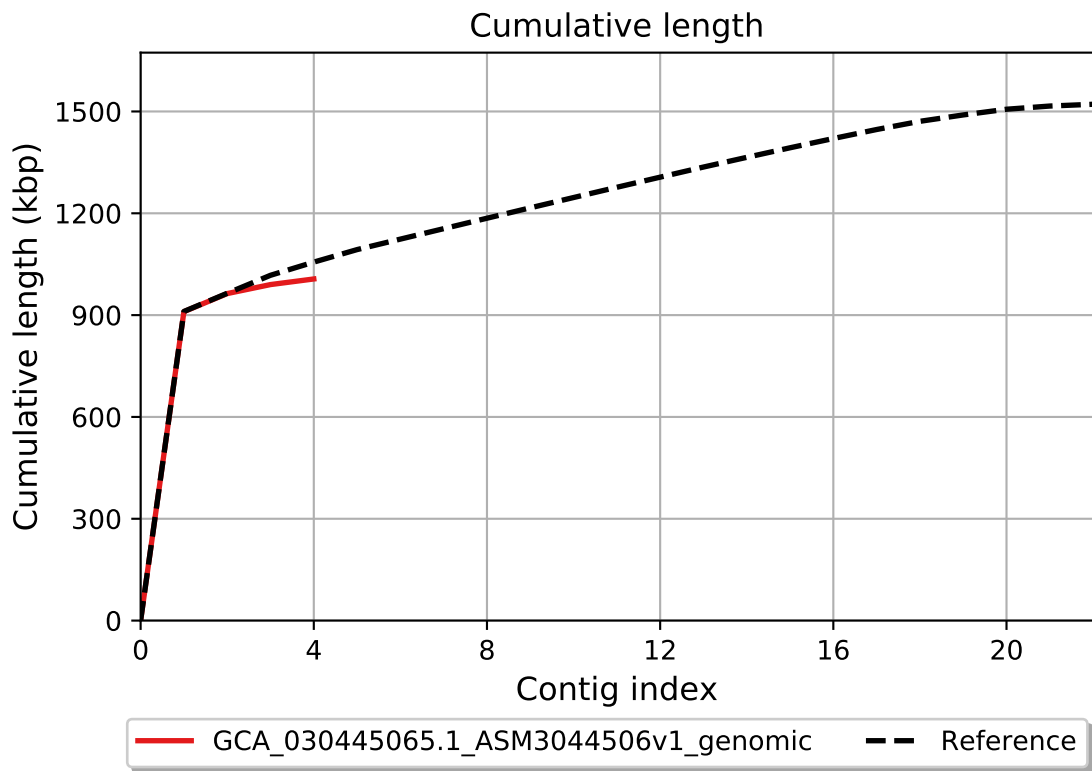


— GCA_030445065.1_ASM3044506v1_genomic

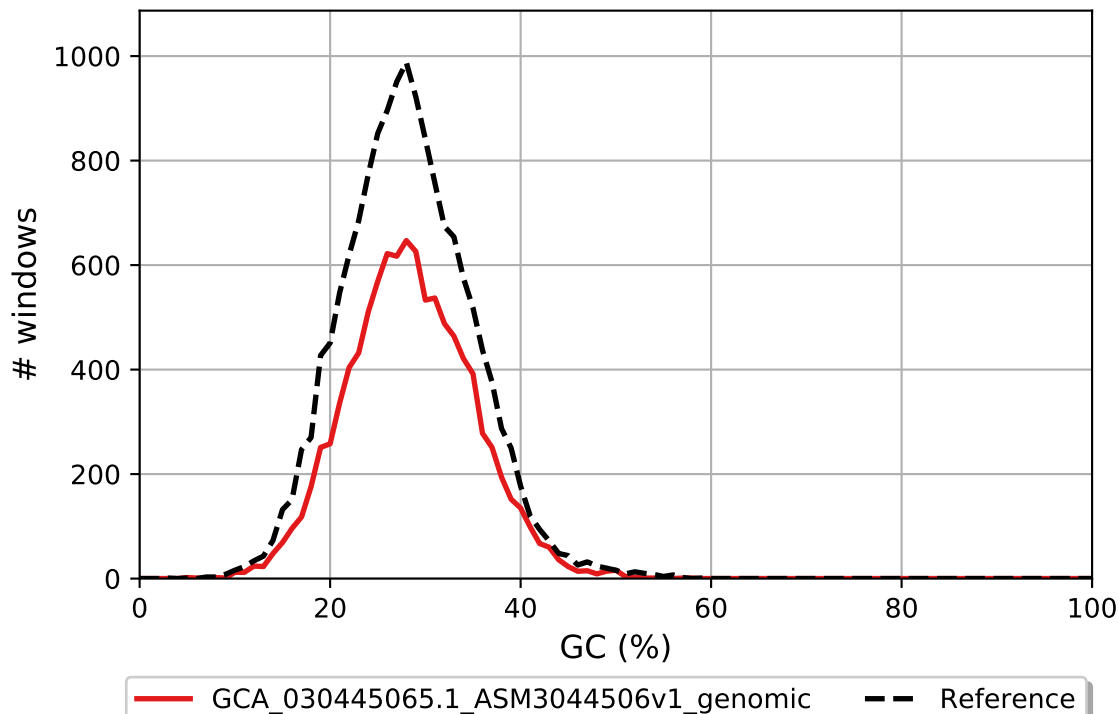
NGx



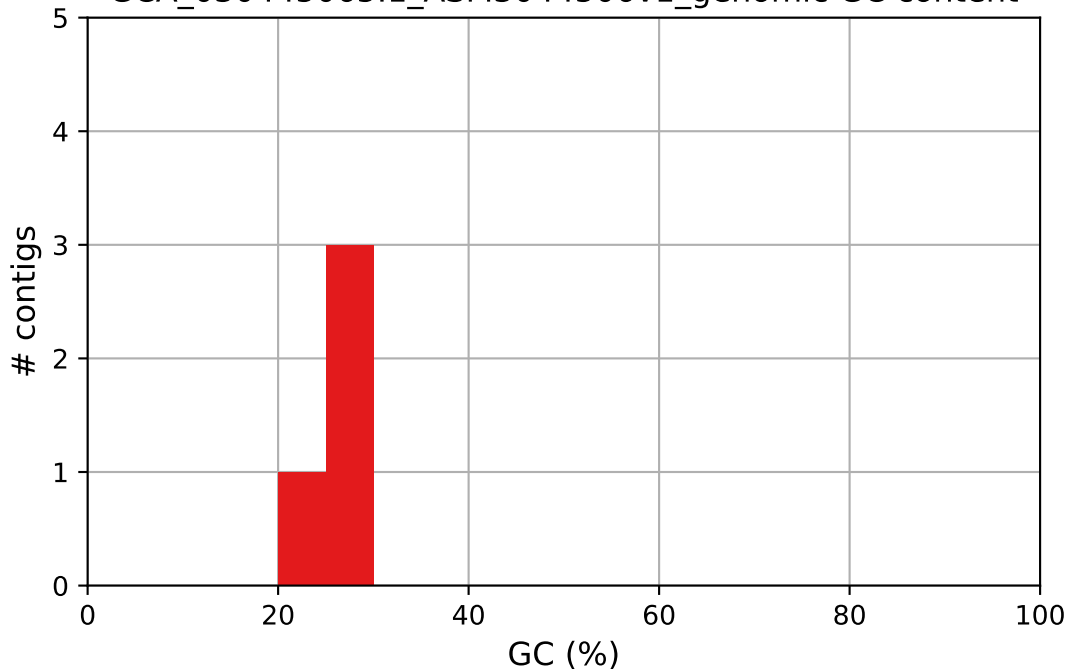
— GCA_030445065.1_ASM3044506v1_genomic



GC content

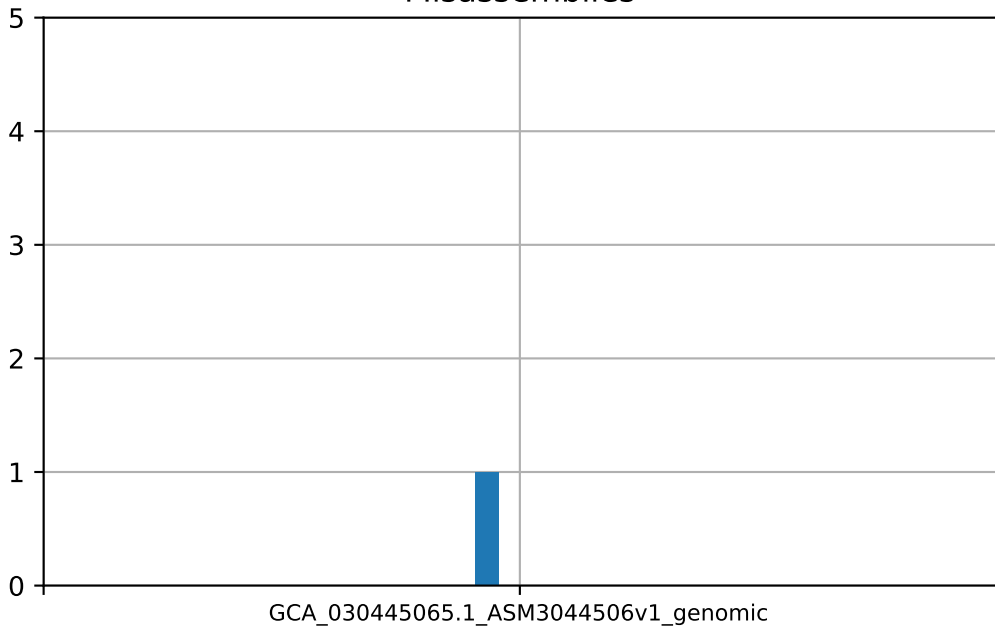


GCA_030445065.1_ASM3044506v1_genomic GC content



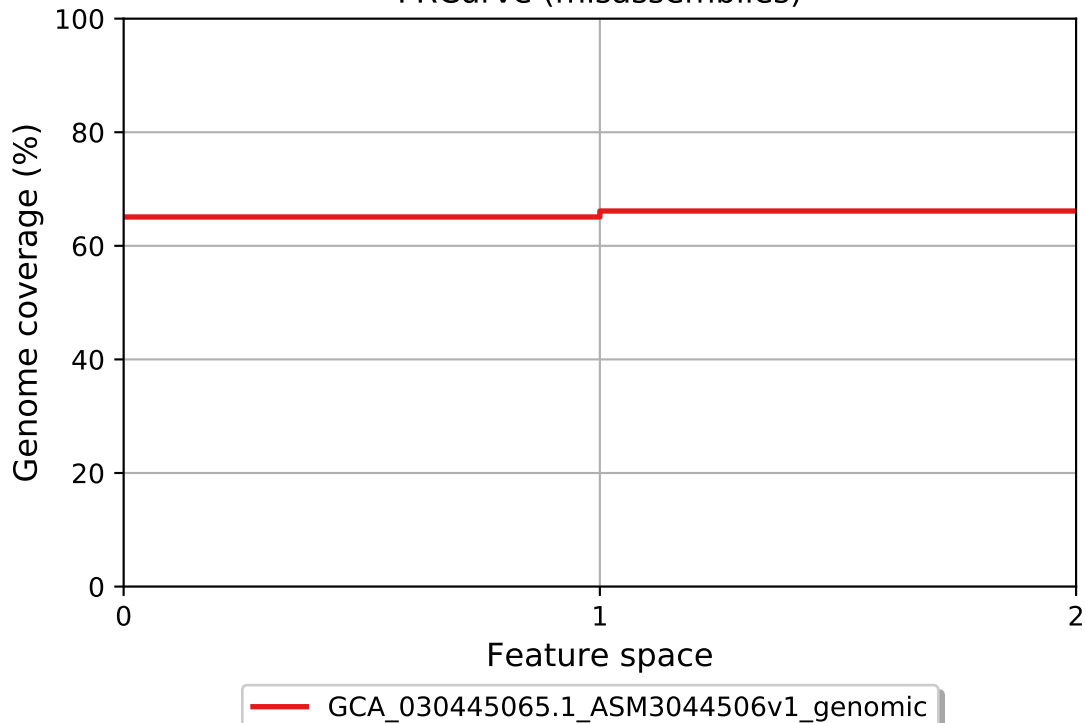
 GCA_030445065.1_ASM3044506v1_genomic

Misassemblies

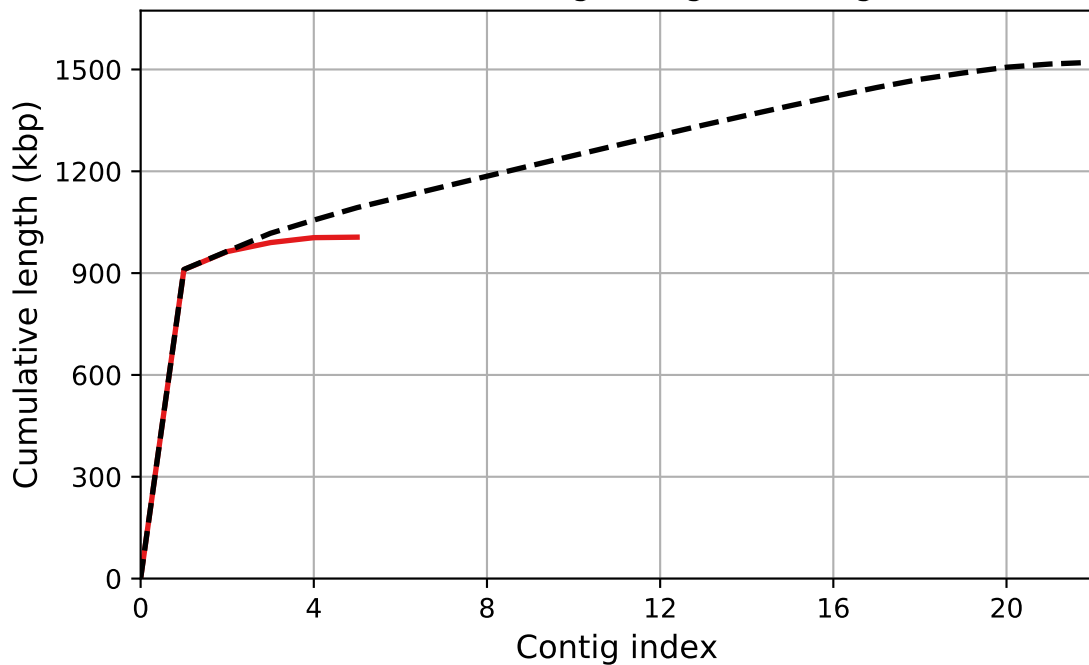


translocations

FRCurve (misassemblies)



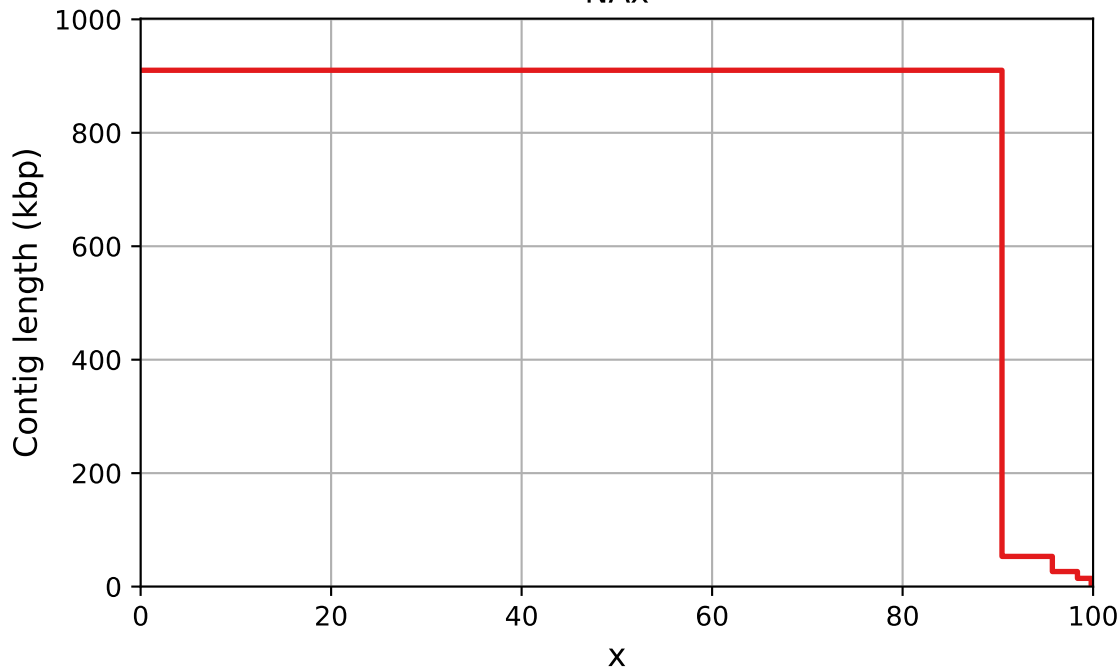
Cumulative length (aligned contigs)



GCA_030445065.1_ASM3044506v1_genomic

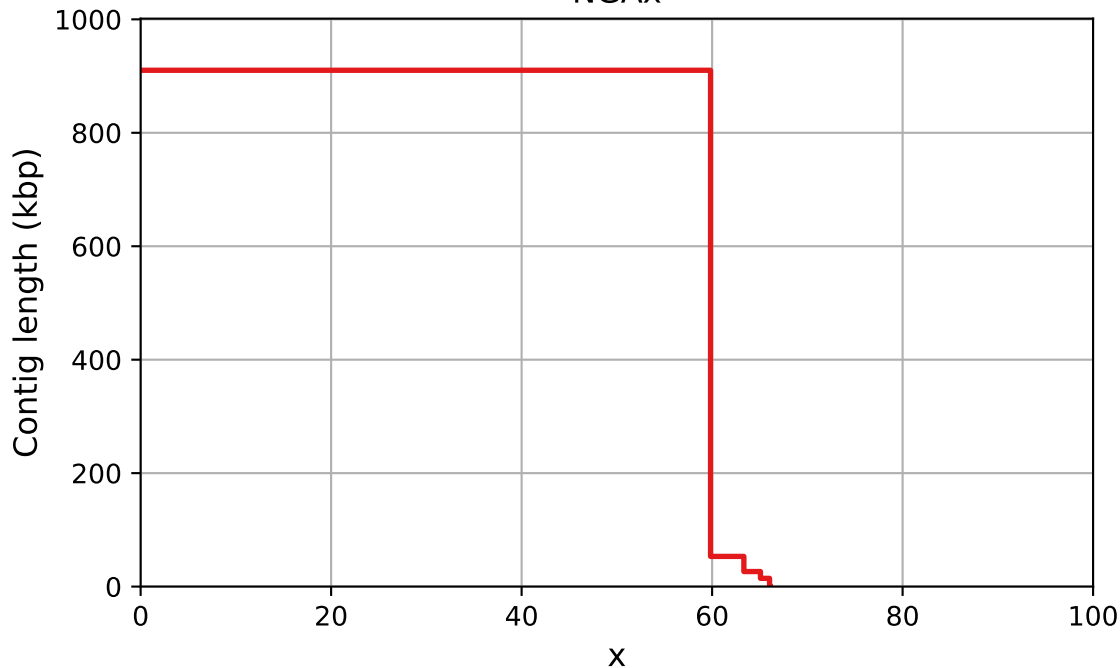
Reference

NAx

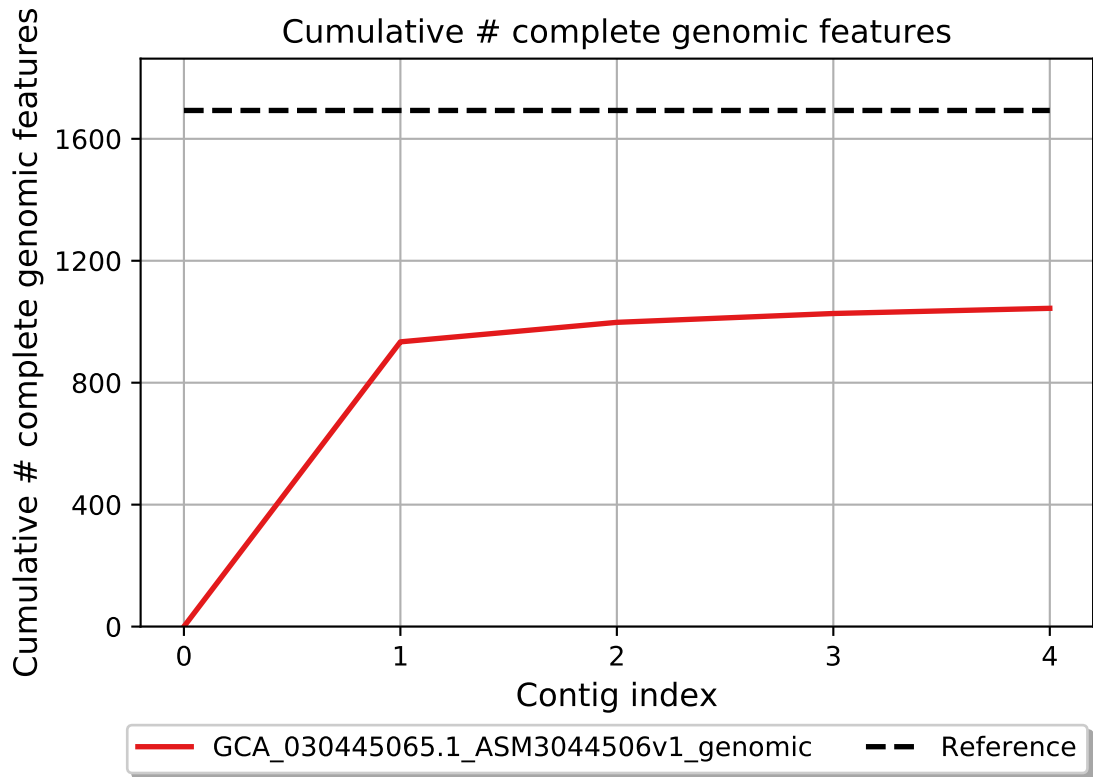


— GCA_030445065.1_ASM3044506v1_genomic

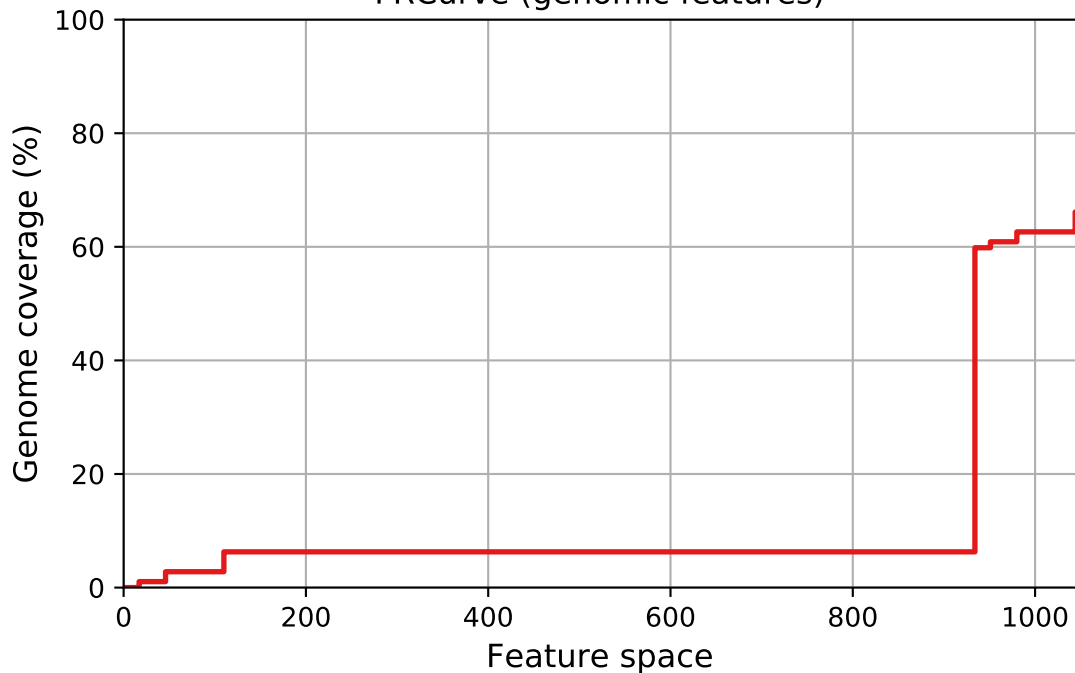
NGAx



— GCA_030445065.1_ASM3044506v1_genomic



FRCurve (genomic features)



— GCA_030445065.1_ASM3044506v1_genomic