

Report

GCA_030439665.1_ASM3043966v1_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)	1000122
Total length (>= 1000 bp)	1000122
Total length (>= 5000 bp)	1000122
Total length (>= 10000 bp)	1000122
Total length (>= 25000 bp)	984026
Total length (>= 50000 bp)	957520
# contigs	4
Largest contig	902811
Total length	1000122
Reference length	1521208
GC (%)	28.45
Reference GC (%)	28.18
N50	902811
NG50	902811
N90	902811
NG90	-
auN	818922.5
auNG	538402.7
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	16096
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2277
Genome fraction (%)	65.614
Duplication ratio	0.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	551.26
# indels per 100 kbp	21.27
# genomic features	1035 + 8 part
Largest alignment	902628
Total aligned length	996816
NA50	902628
NGA50	902628
NA90	902628
NGA90	-
auNA	818390.7
auNGA	538053.0
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

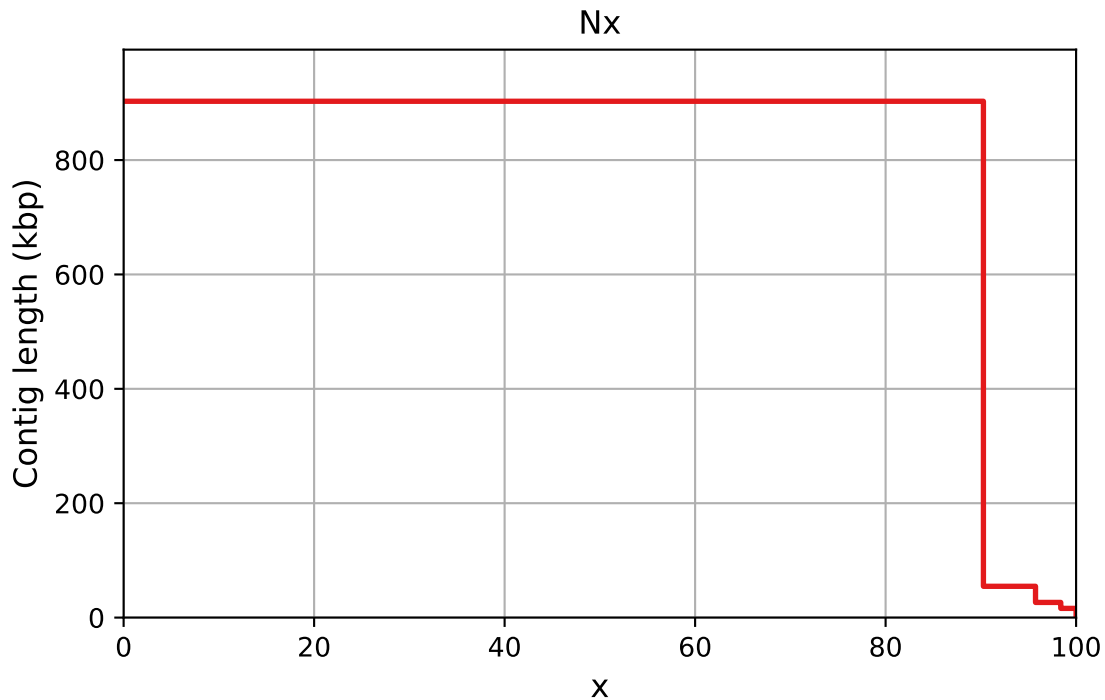
	GCA_030439665.1_ASM3043966v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	16096
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	5495
# indels	212
# indels (<= 5 bp)	185
# indels (> 5 bp)	27
Indels length	1463

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

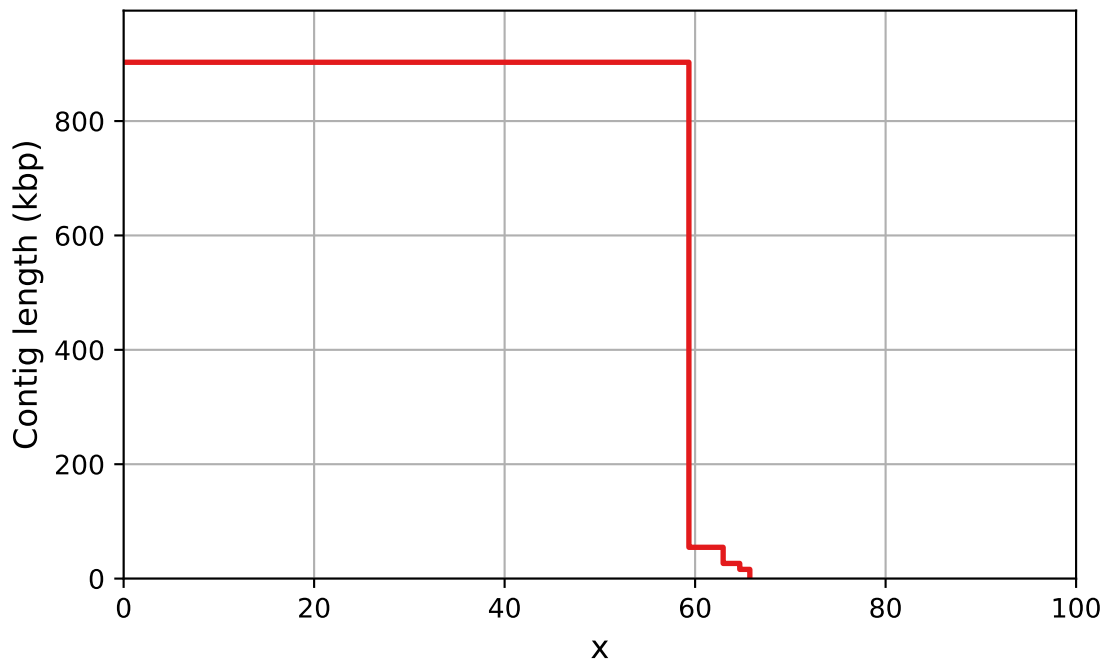
	GCA_030439665.1_ASM3043966v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2277
# N's	0

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).

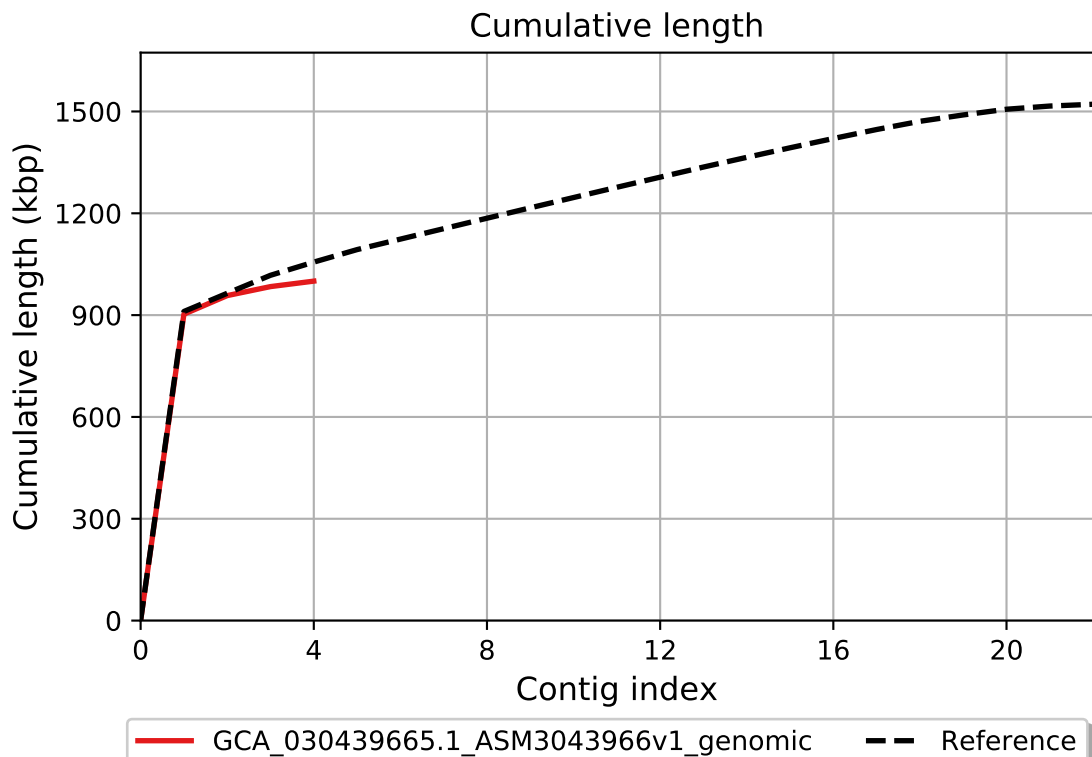


— GCA_030439665.1_ASM3043966v1_genomic

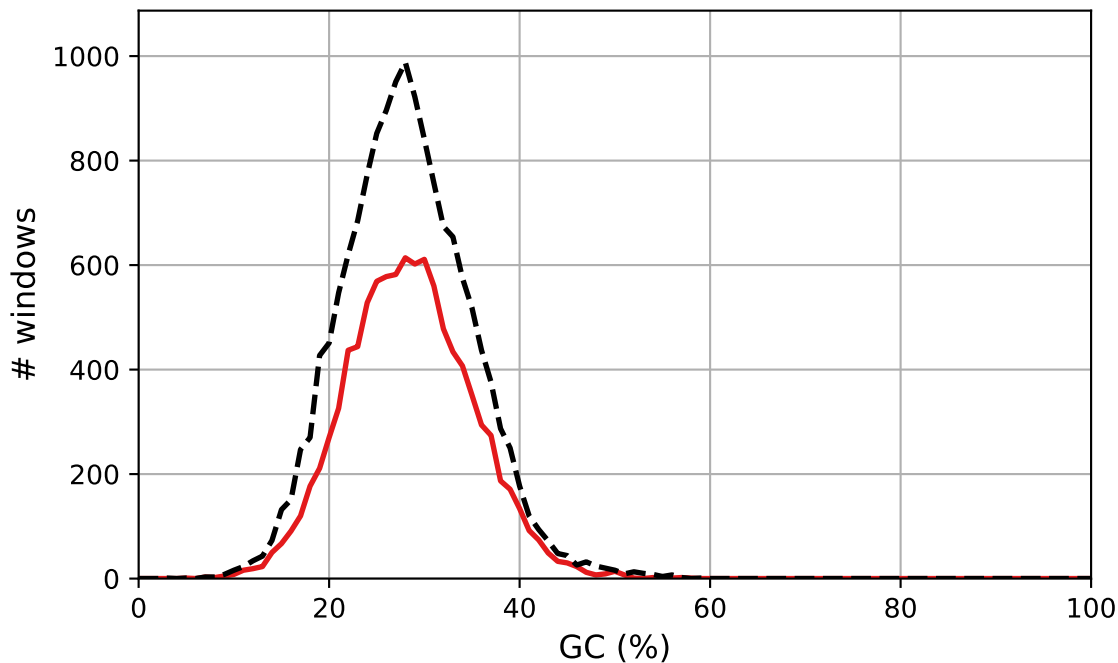
NGx



— GCA_030439665.1_ASM3043966v1_genomic



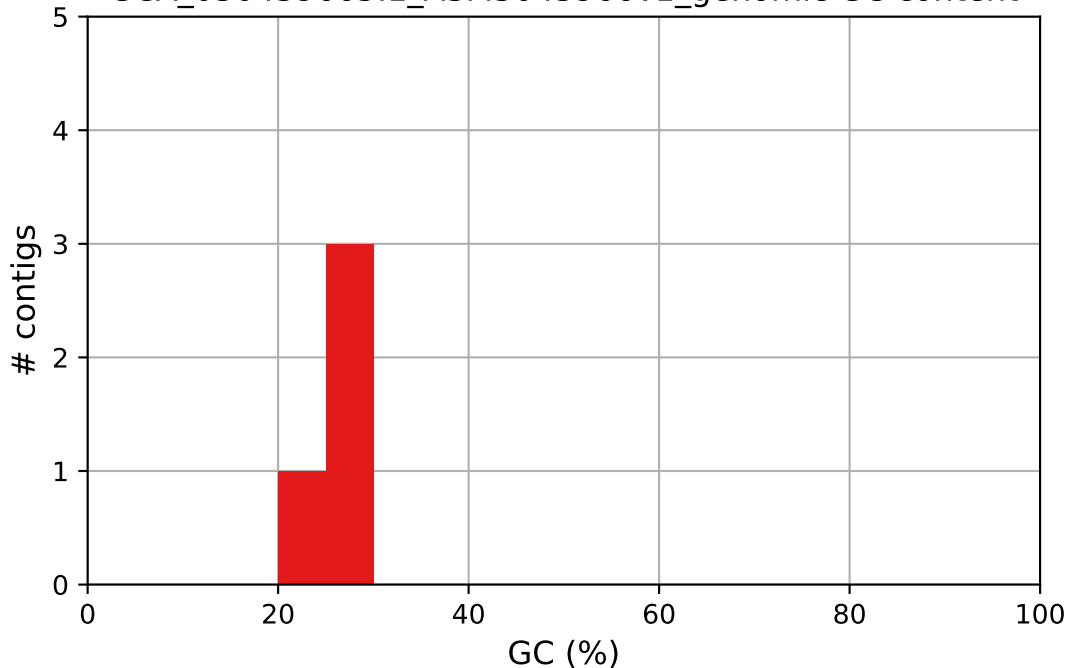
GC content



GCA_030439665.1_ASM3043966v1_genomic

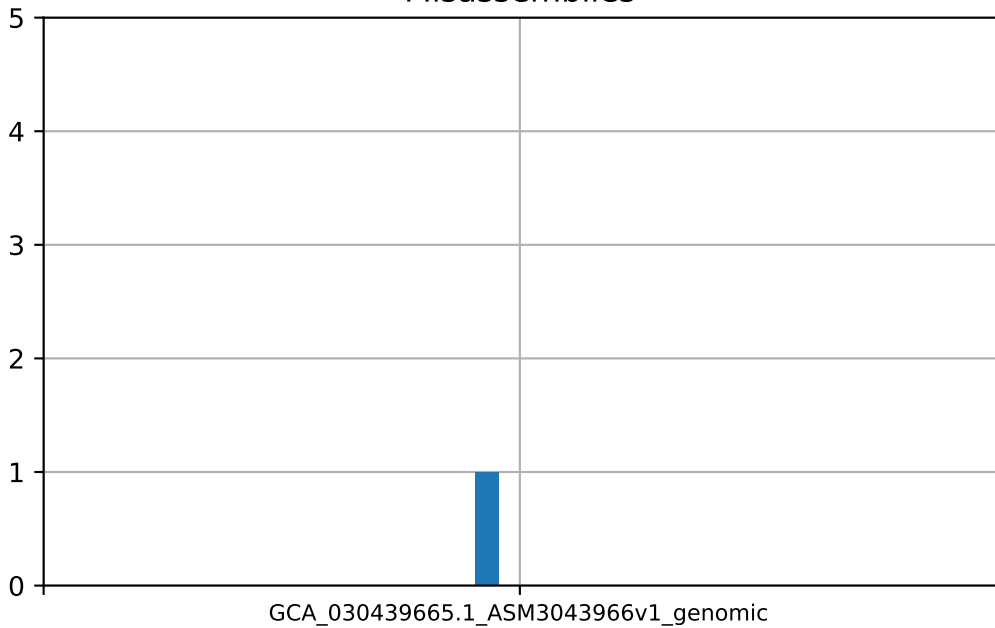
-- Reference

GCA_030439665.1_ASM3043966v1_genomic GC content



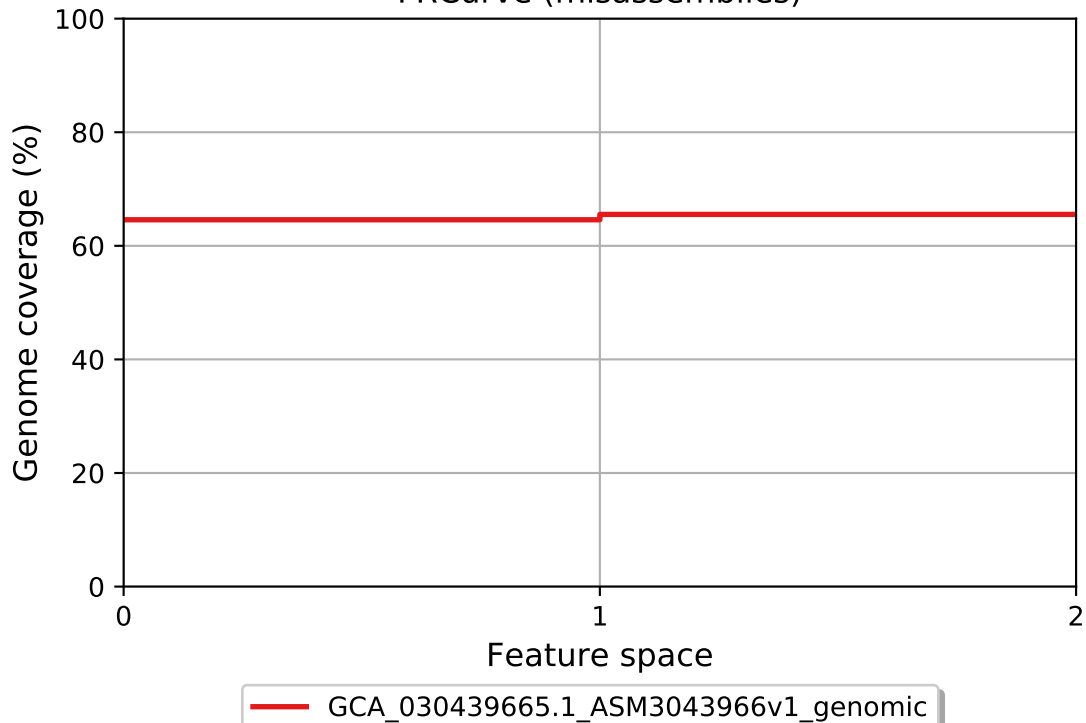
GCA_030439665.1_ASM3043966v1_genomic

Misassemblies

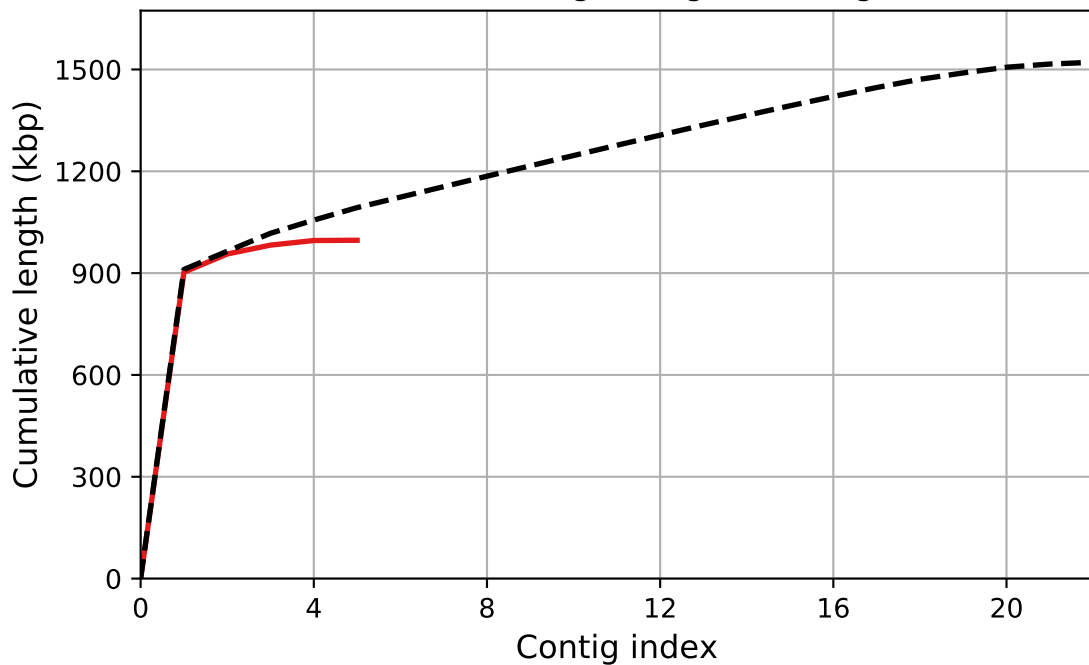


translocations

FRCurve (misassemblies)



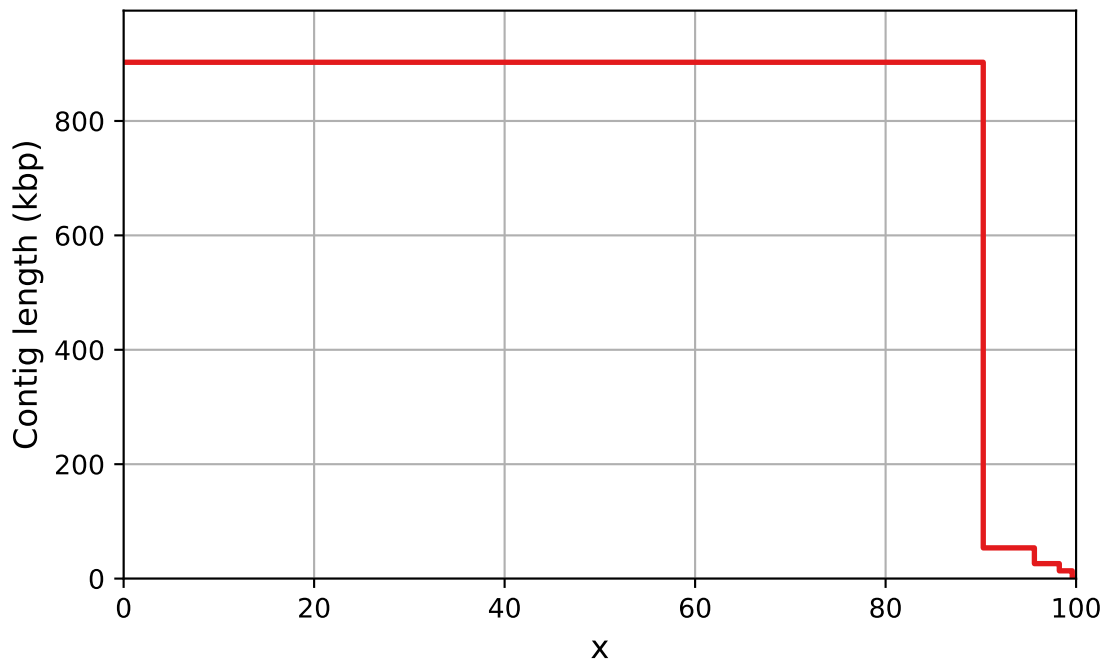
Cumulative length (aligned contigs)



GCA_030439665.1_ASM3043966v1_genomic

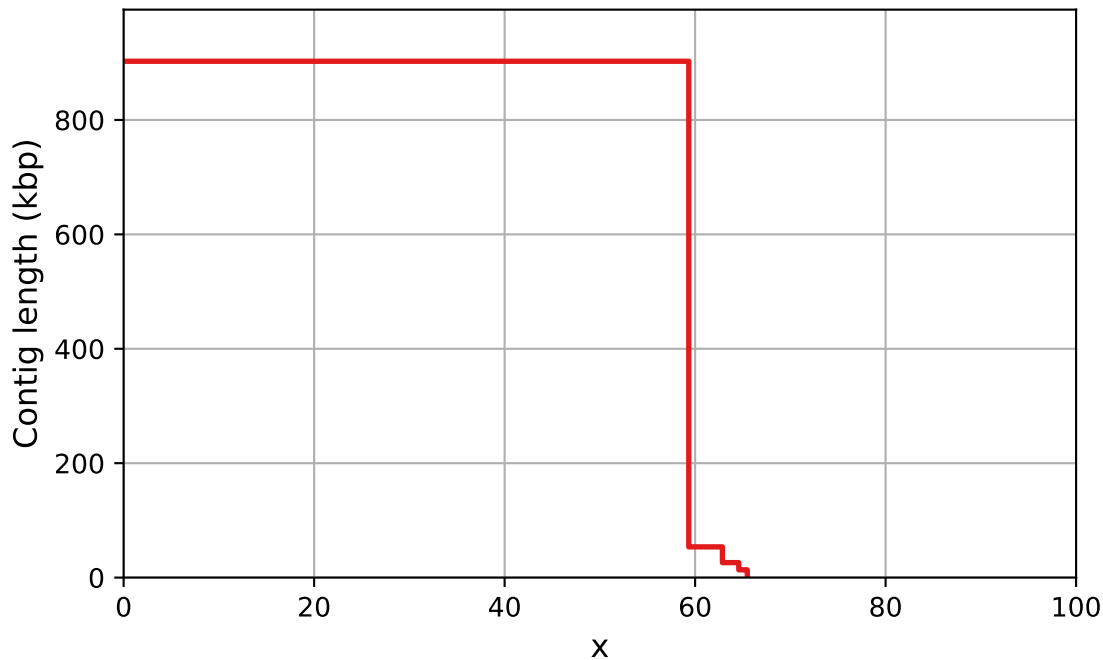
Reference

NAx

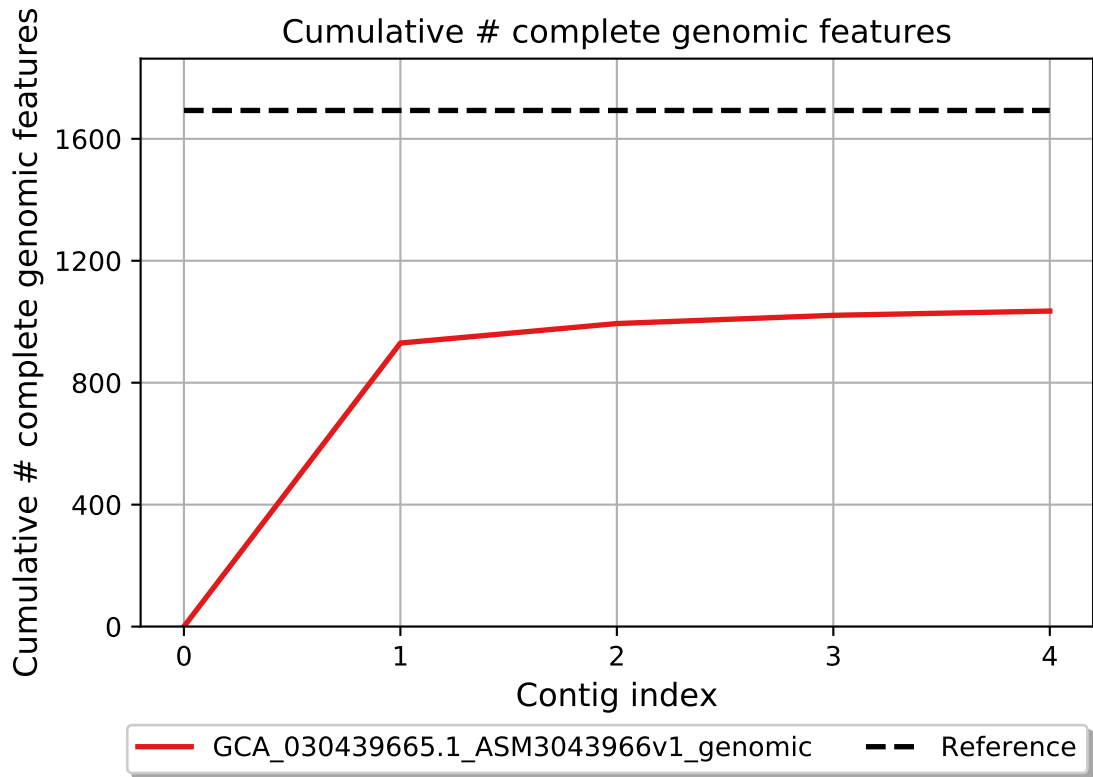


— GCA_030439665.1_ASM3043966v1_genomic

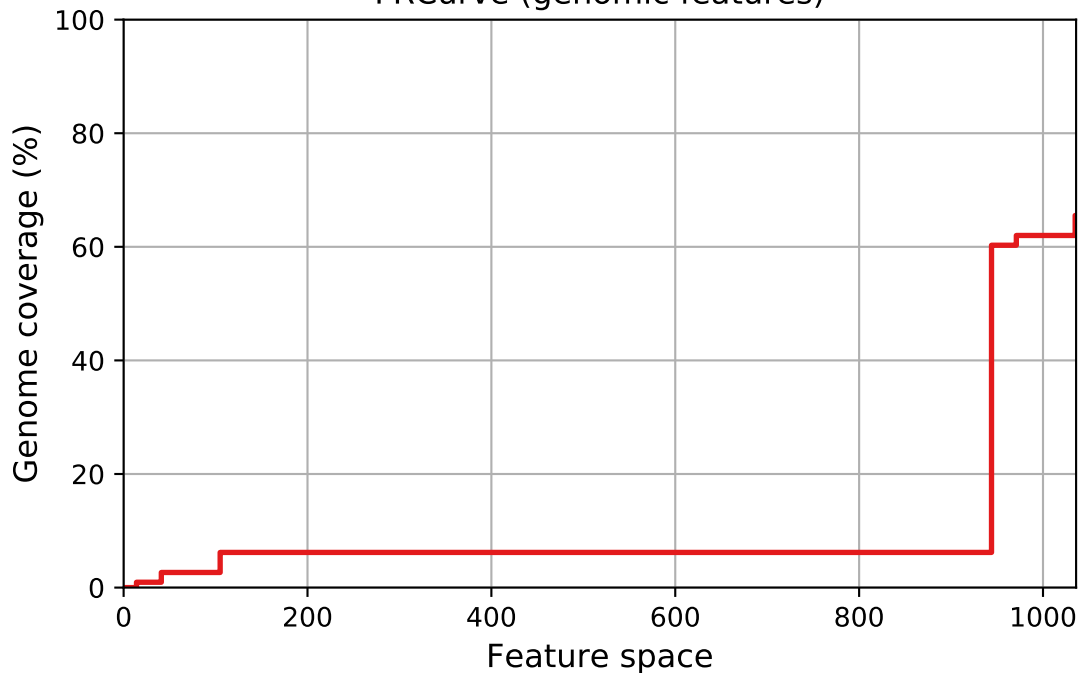
NGAx



— GCA_030439665.1_ASM3043966v1_genomic



FRCurve (genomic features)



— GCA_030439665.1_ASM3043966v1_genomic