

Report

GCA_030439625.1_ASM3043962v1_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)	1007827
Total length (>= 1000 bp)	1007827
Total length (>= 5000 bp)	1007827
Total length (>= 10000 bp)	1007827
Total length (>= 25000 bp)	990606
Total length (>= 50000 bp)	964152
# contigs	4
Largest contig	910422
Total length	1007827
Reference length	1521208
GC (%)	28.41
Reference GC (%)	28.18
N50	910422
NG50	910422
N90	910422
NG90	-
auN	826284.2
auNG	547427.8
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	17221
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.236
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	331.98
# indels per 100 kbp	17.27
# genomic features	1047 + 3 part
Largest alignment	910422
Total aligned length	1007303
NA50	910422
NGA50	910422
NA90	910422
NGA90	-
auNA	826220.5
auNGA	547385.6
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

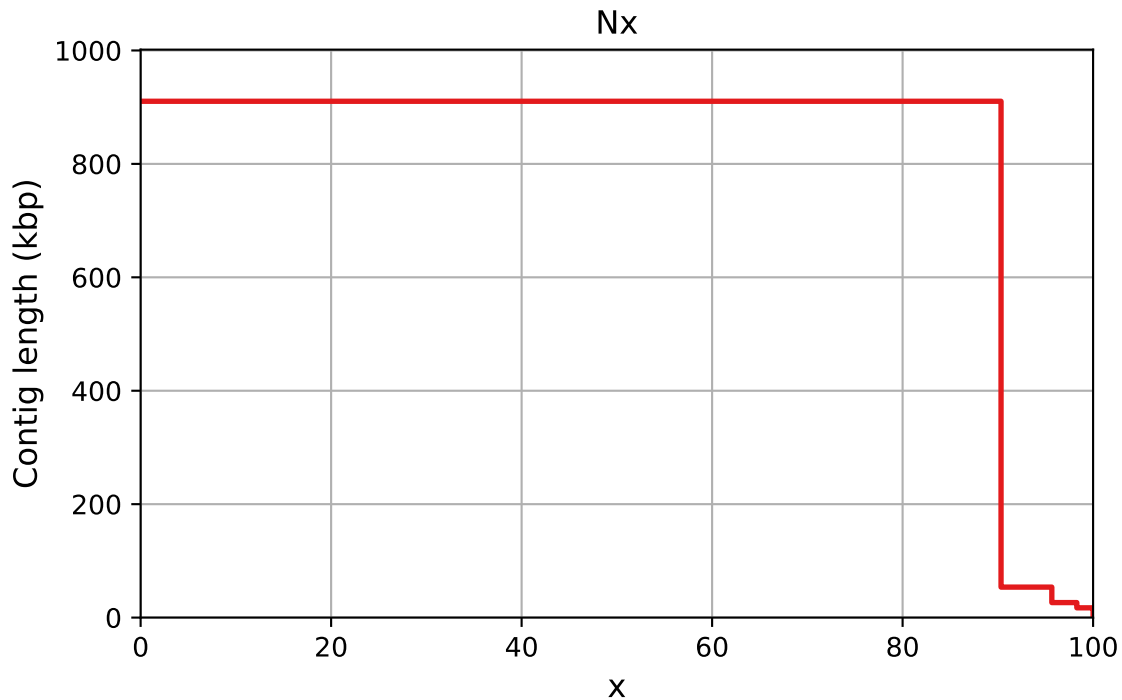
	GCA_030439625.1_ASM3043962v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	17221
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3344
# indels	174
# indels (<= 5 bp)	145
# indels (> 5 bp)	29
Indels length	1028

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

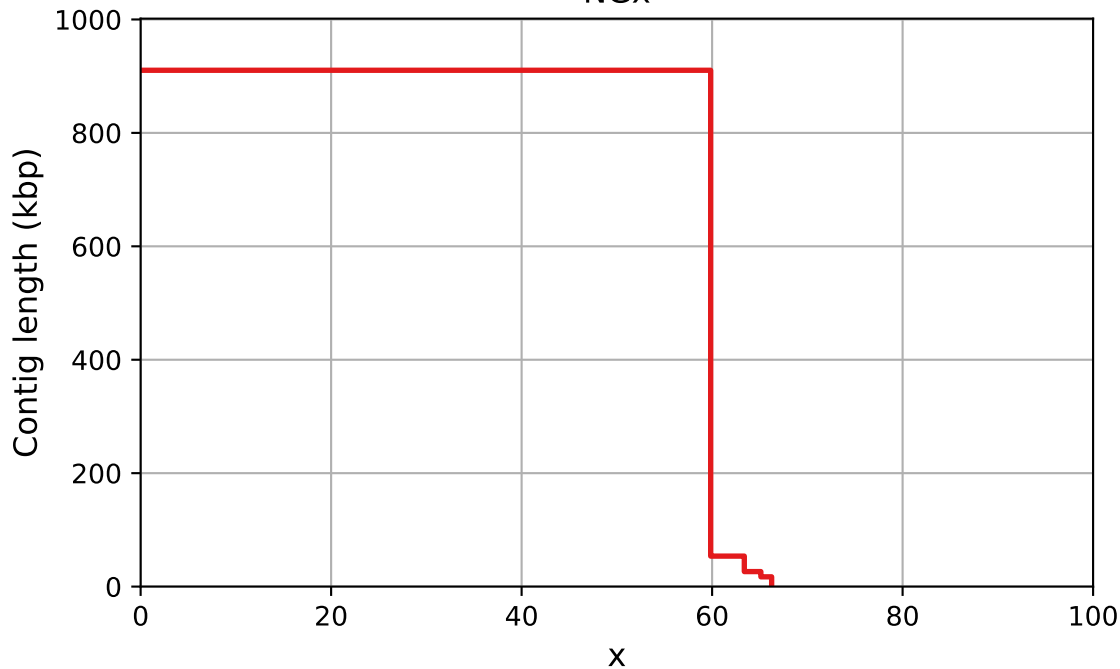
	GCA_030439625.1_ASM3043962v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

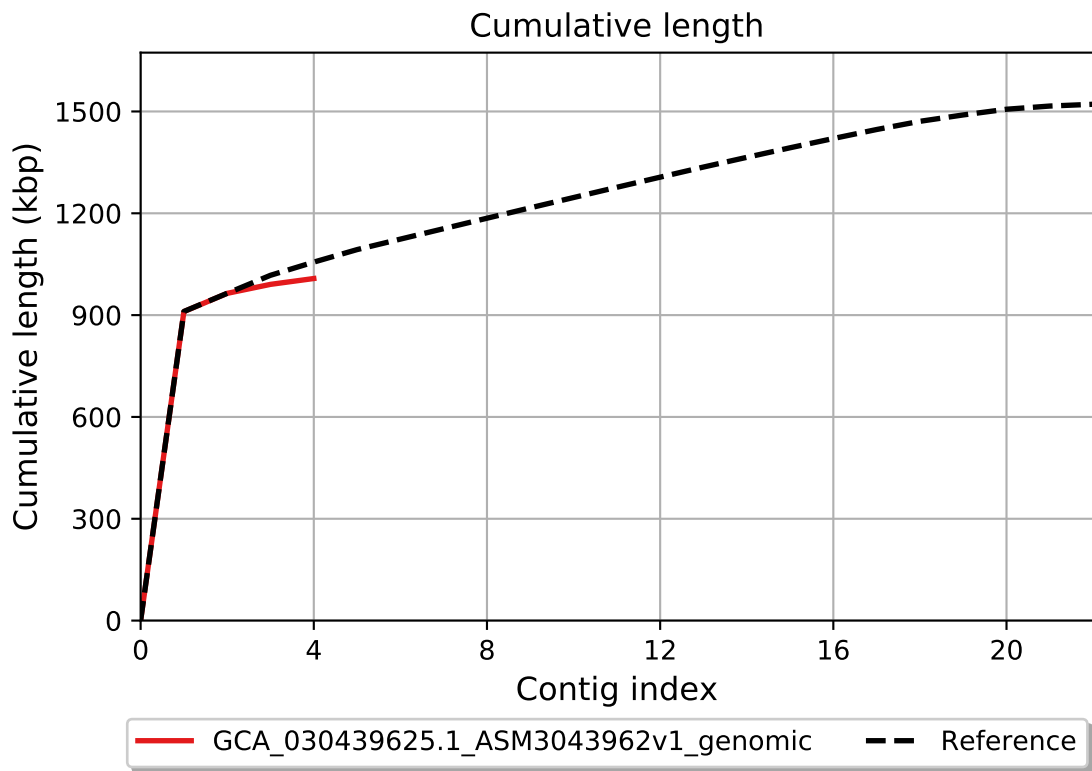


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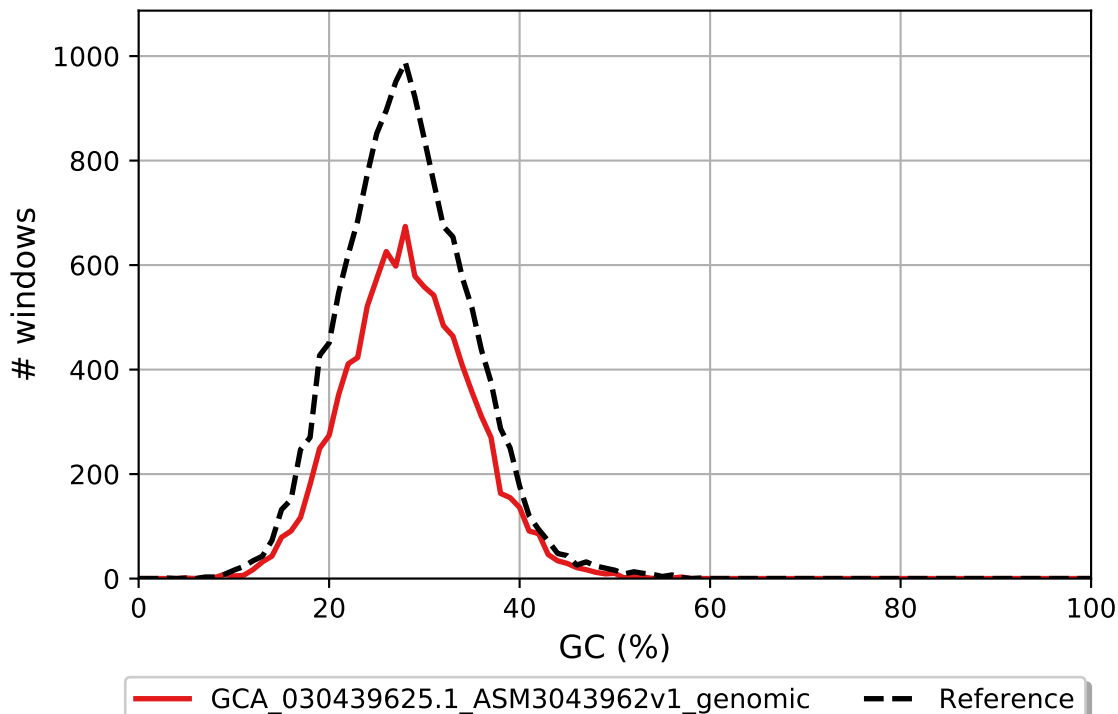
NGx



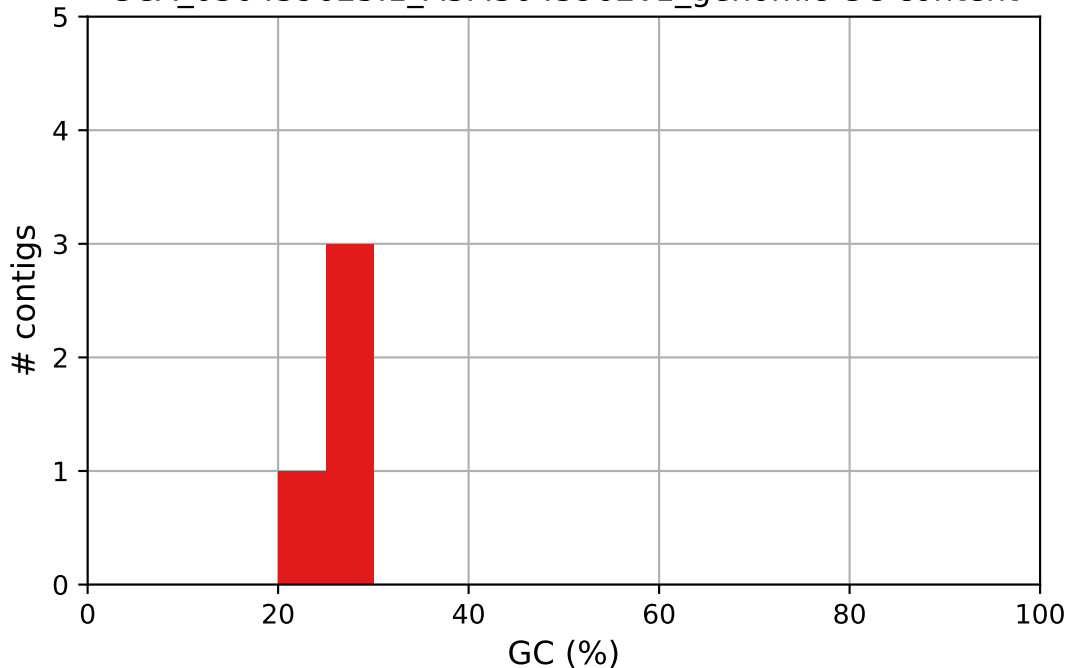
— GCA_030439625.1_ASM3043962v1_genomic



GC content

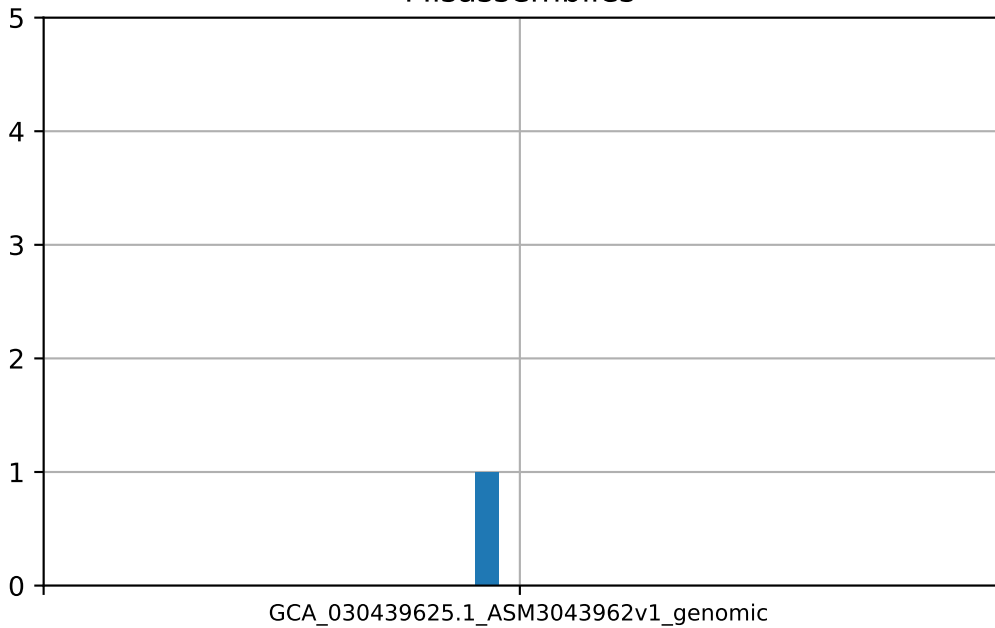


GCA_030439625.1_ASM3043962v1_genomic GC content



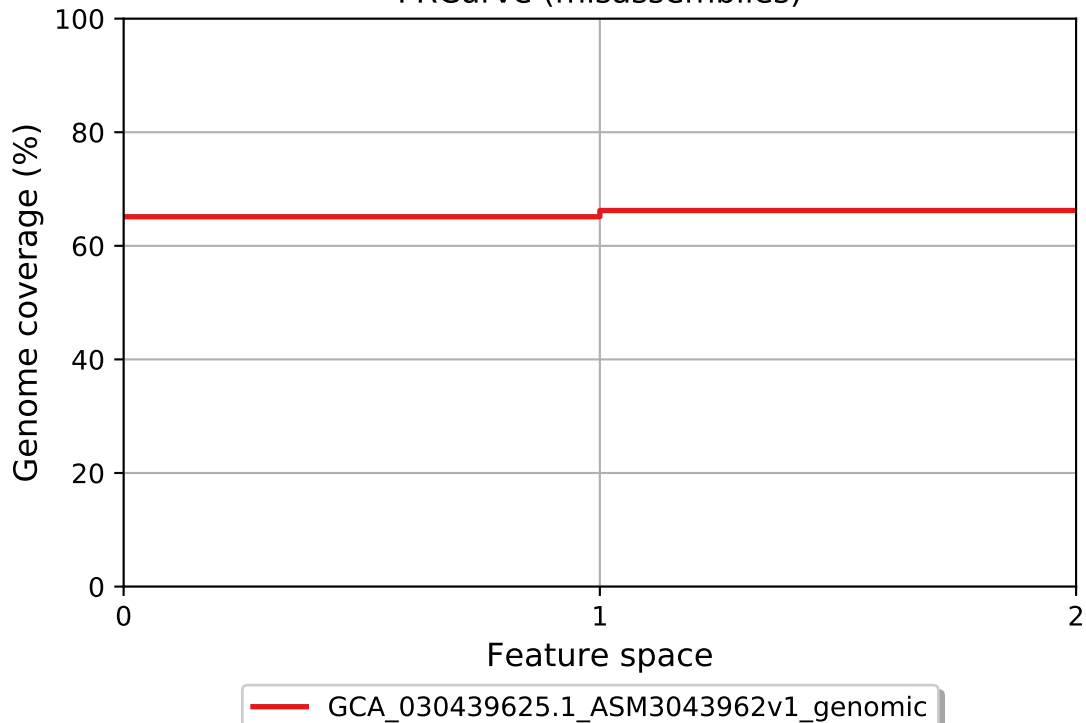
 GCA_030439625.1_ASM3043962v1_genomic

Misassemblies

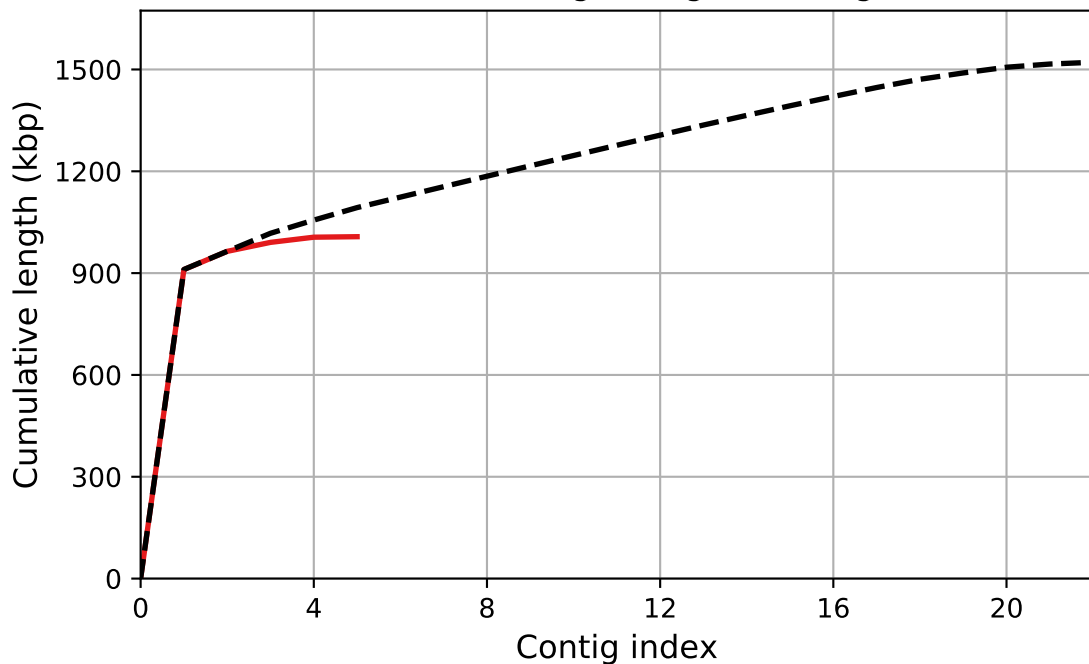


translocations

FRCurve (misassemblies)

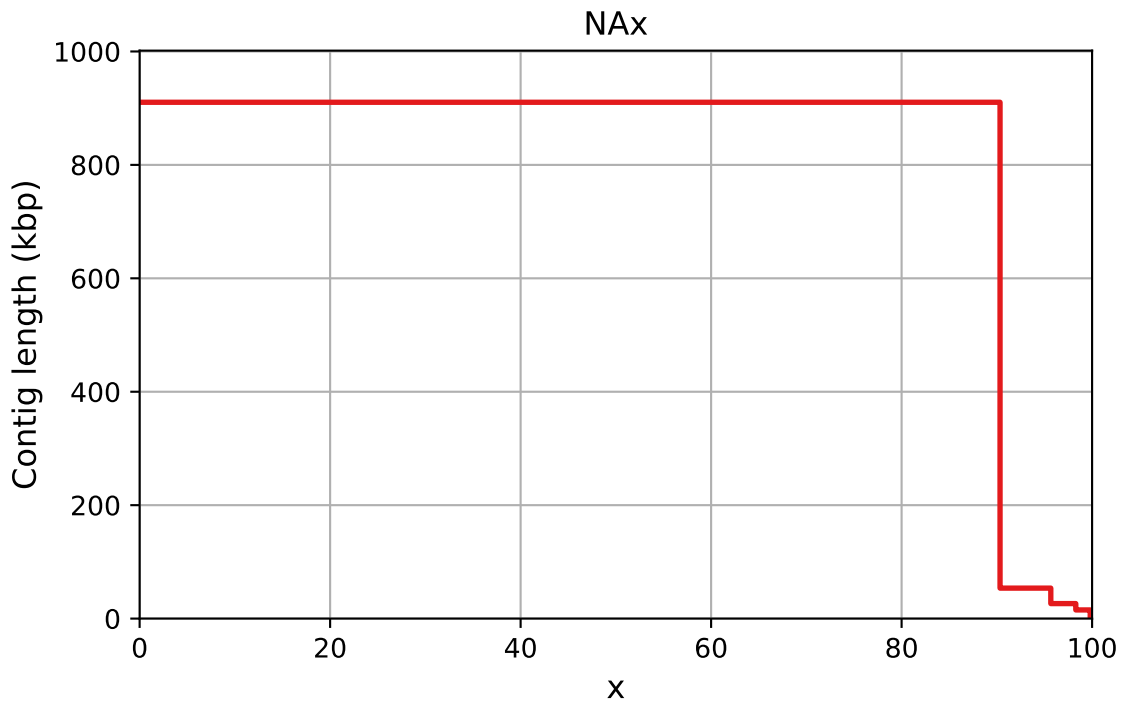


Cumulative length (aligned contigs)



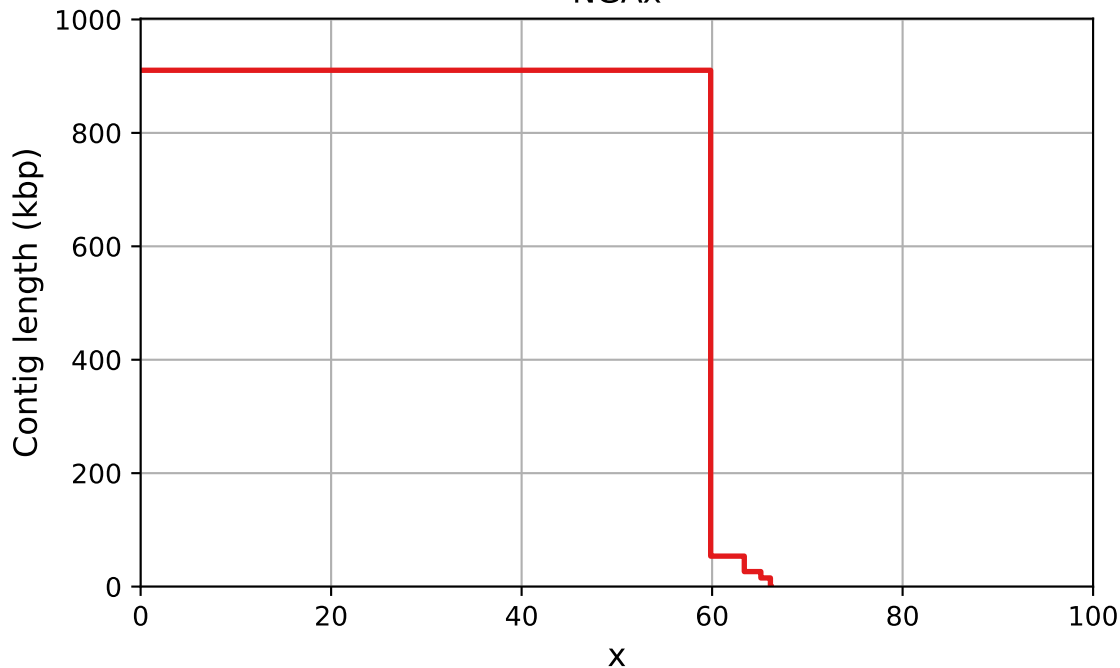
GCA_030439625.1_ASM3043962v1_genomic

Reference

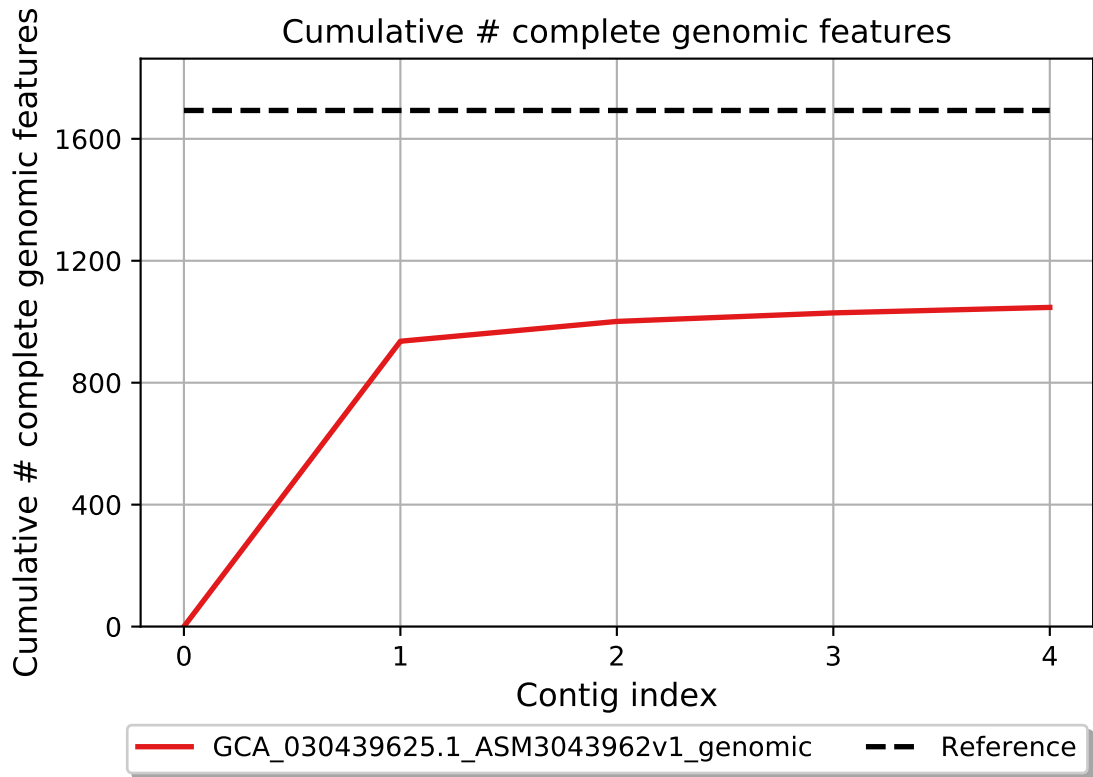


— GCA_030439625.1_ASM3043962v1_genomic

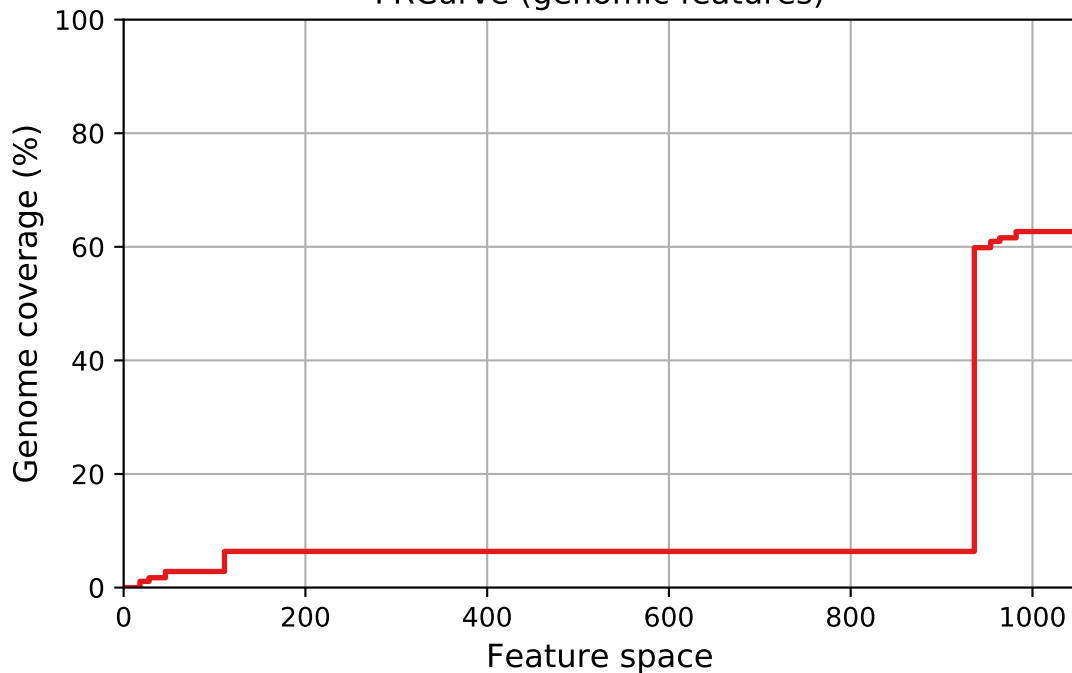
NGAx



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FRCurve (genomic features)



— GCA_030439625.1_ASM3043962v1_genomic