

Report

	GCA_038801875.1_ASM3880187v1_genomic
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	946504
Total length (>= 1000 bp)	946504
Total length (>= 5000 bp)	946504
Total length (>= 10000 bp)	946504
Total length (>= 25000 bp)	946504
Total length (>= 50000 bp)	919990
# contigs	2
Largest contig	919990
Total length	946504
Reference length	1521208
GC (%)	28.44
Reference GC (%)	28.18
N50	919990
NG50	919990
N90	919990
NG90	-
auN	894961.5
auNG	556849.9
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	919990
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	3008
Genome fraction (%)	62.046
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	522.63
# indels per 100 kbp	18.34
# genomic features	968 + 4 part
Largest alignment	905455
Total aligned length	943489
NA50	905455
NGA50	905455
NA90	905455
NGA90	-
auNA	867069.0
auNGA	539495.1
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

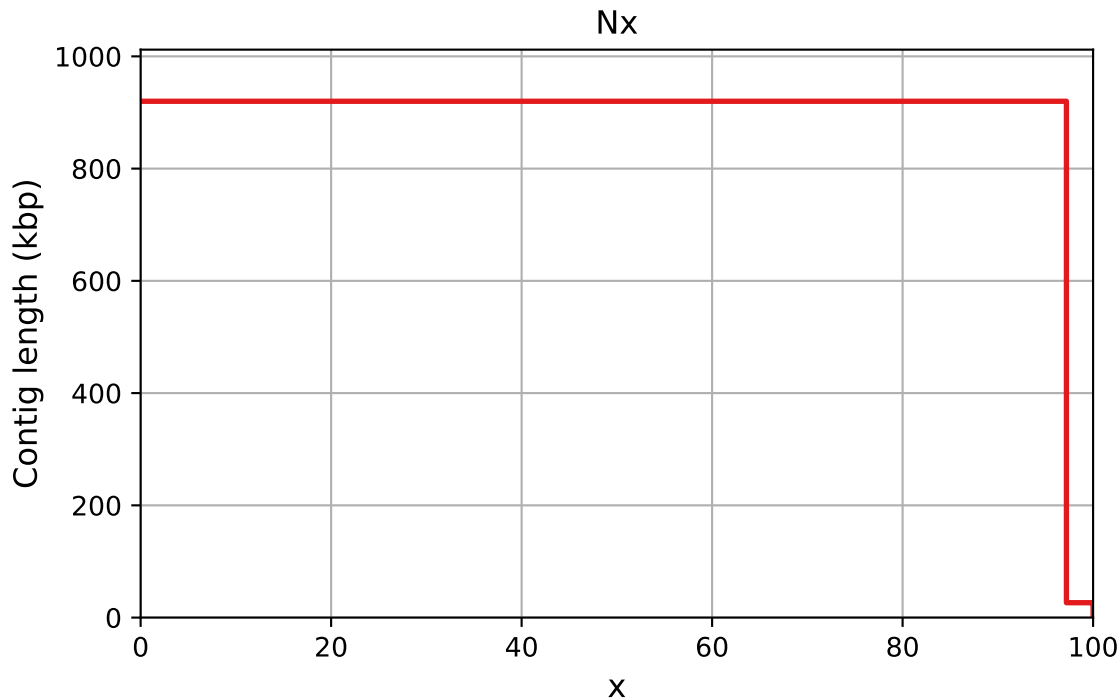
	GCA_038801875.1_ASM3880187v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	919990
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	4931
# indels	173
# indels (<= 5 bp)	148
# indels (> 5 bp)	25
Indels length	1500

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

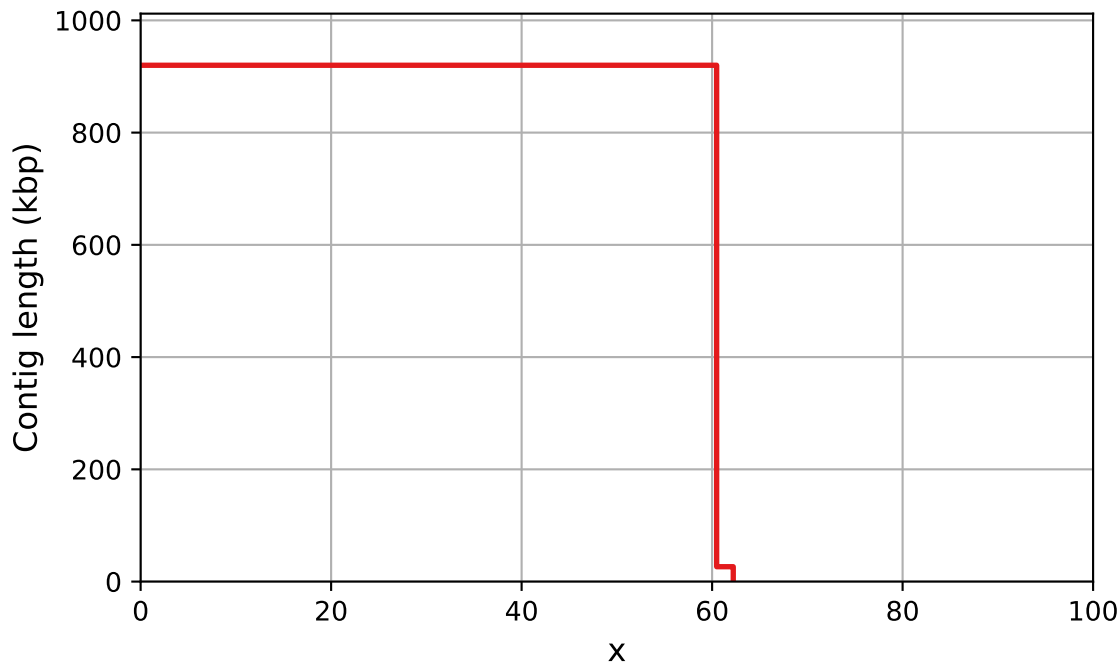
	GCA_038801875.1_ASM3880187v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	3008
# N's	0

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).

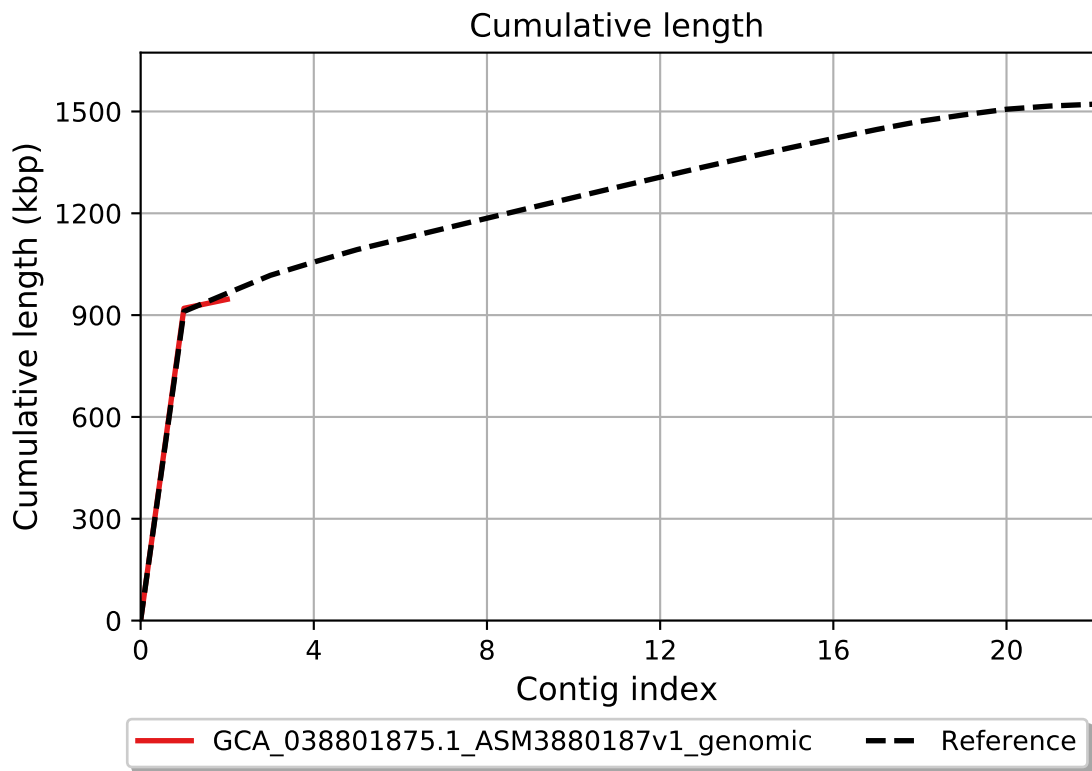


— GCA_038801875.1_ASM3880187v1_genomic

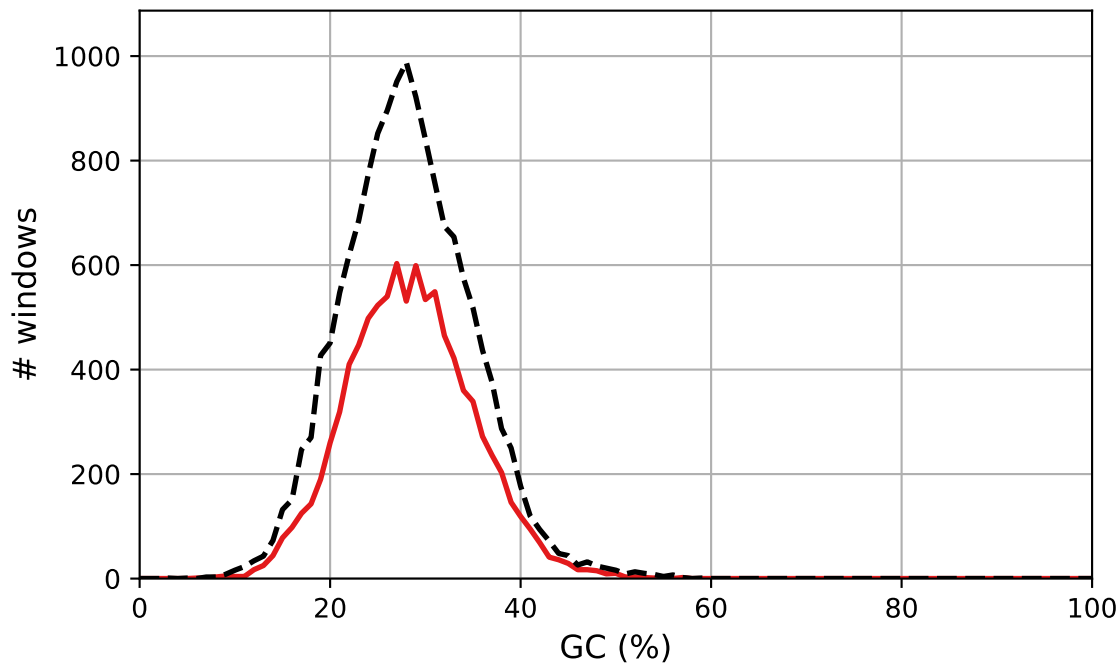
NGx



— GCA_038801875.1_ASM3880187v1_genomic



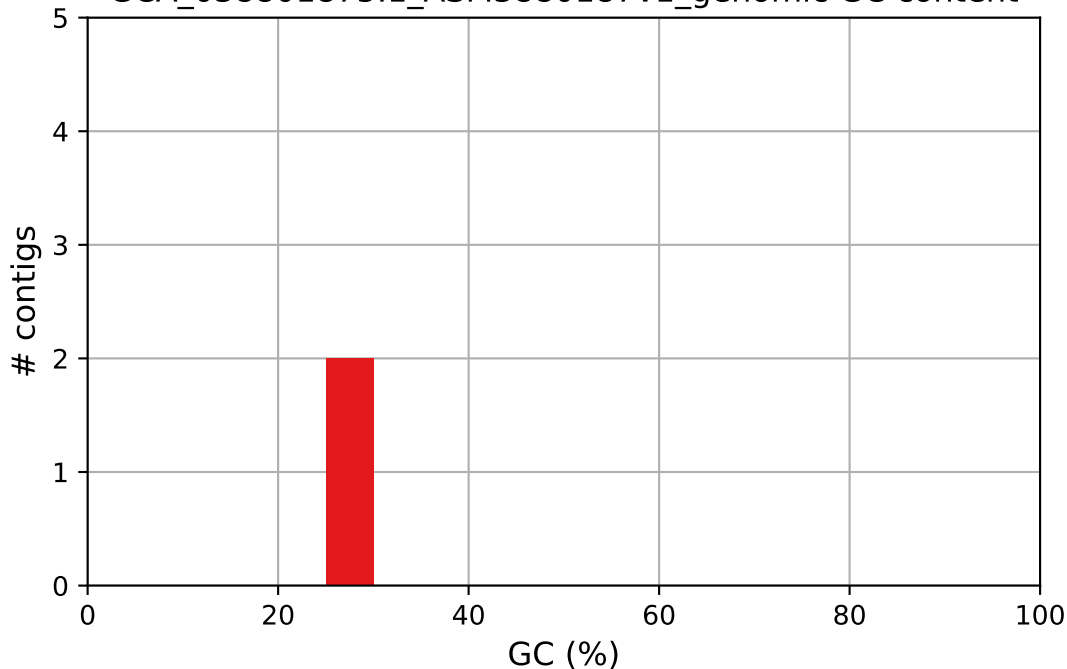
GC content




GCA_038801875.1_ASM3880187v1_genomic

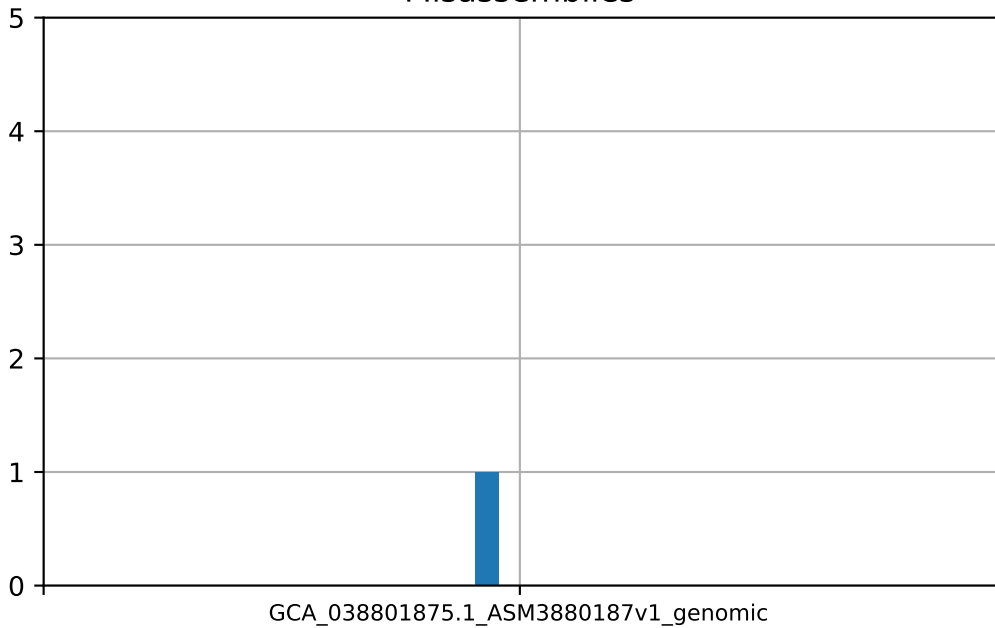
Reference

GCA_038801875.1_ASM3880187v1_genomic GC content



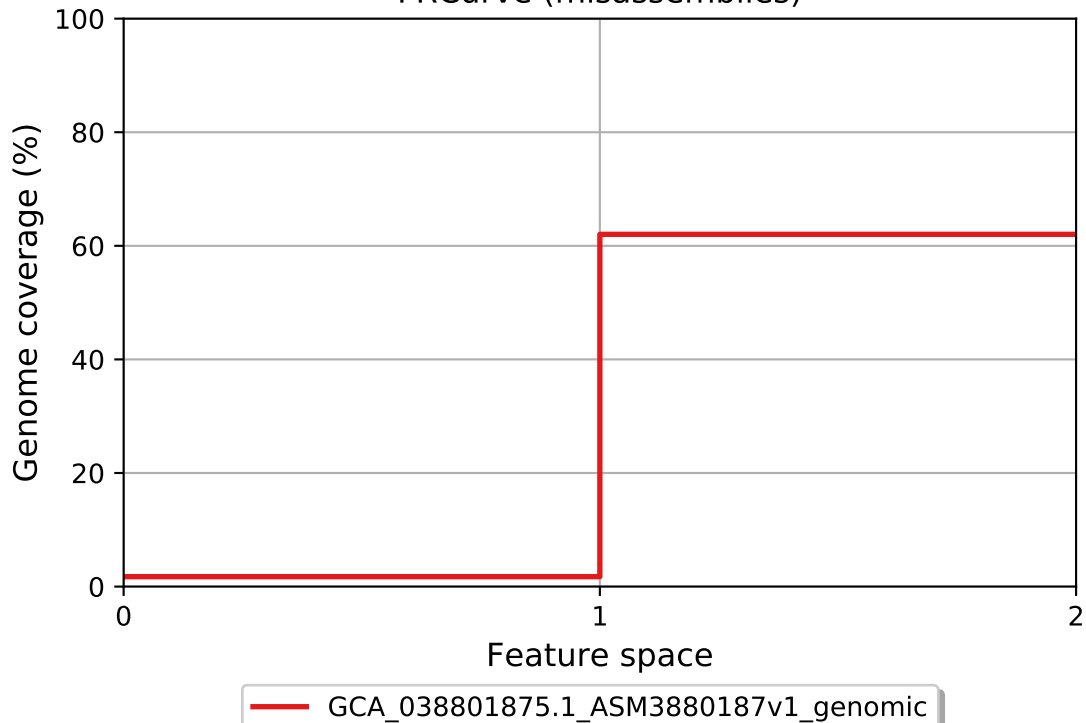
 GCA_038801875.1_ASM3880187v1_genomic

Misassemblies

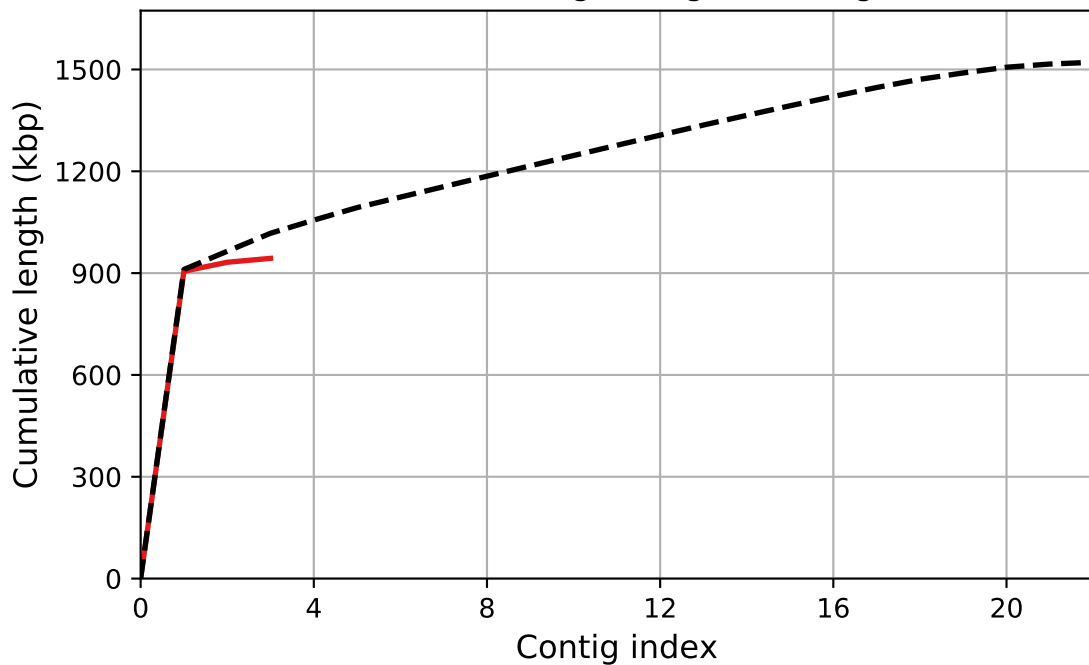


translocations

FRCurve (misassemblies)



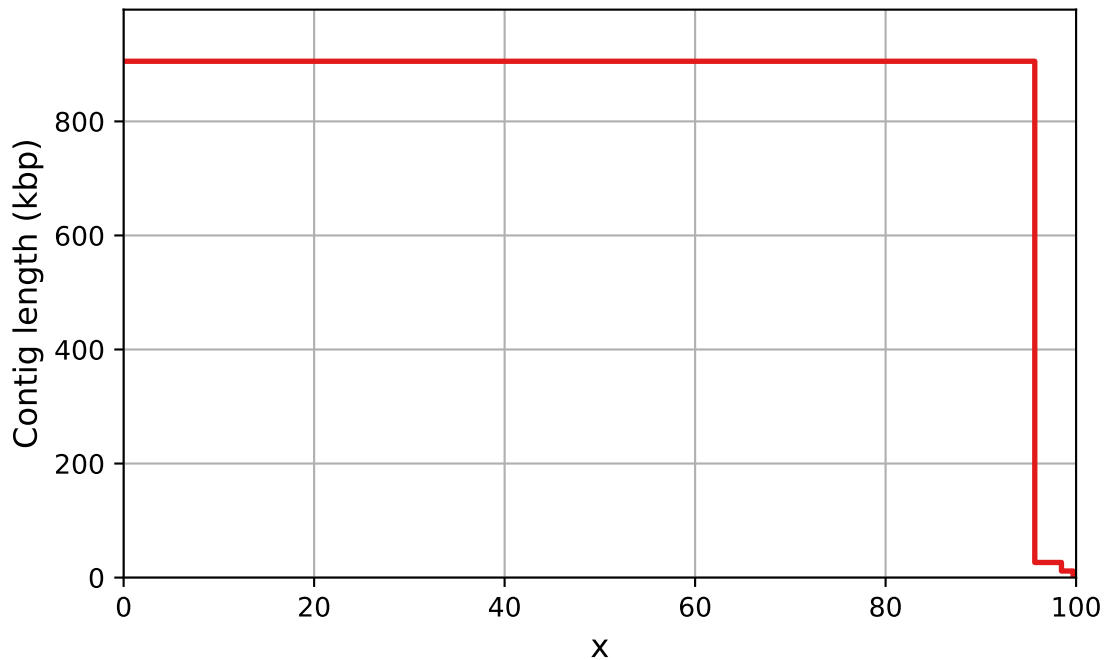
Cumulative length (aligned contigs)



GCA_038801875.1_ASM3880187v1_genomic

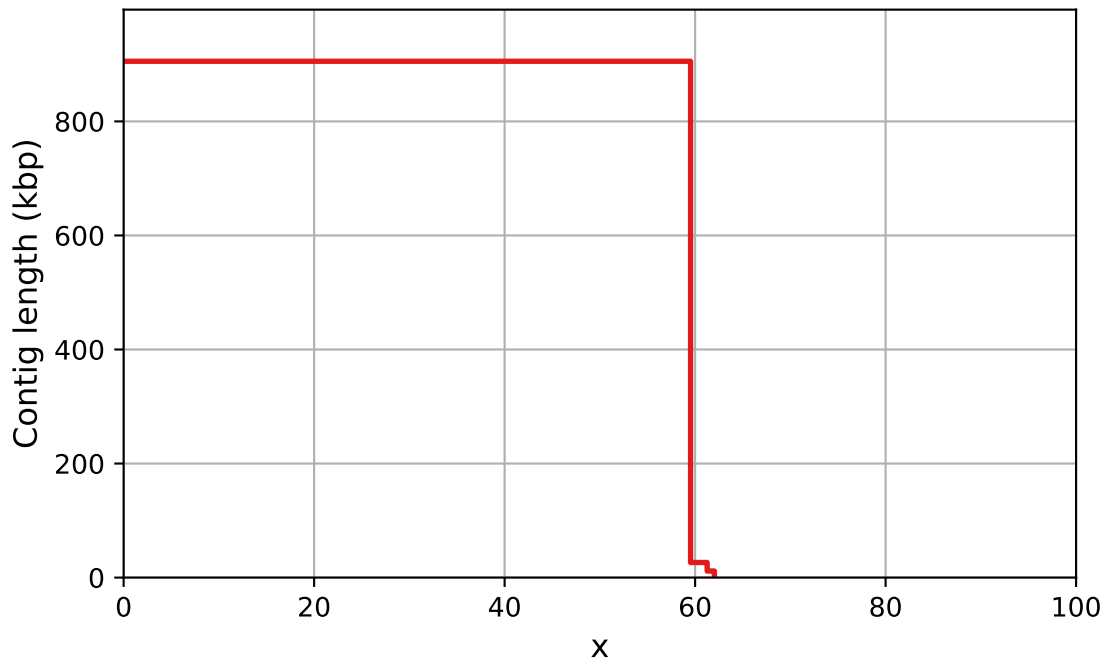
Reference

NAx

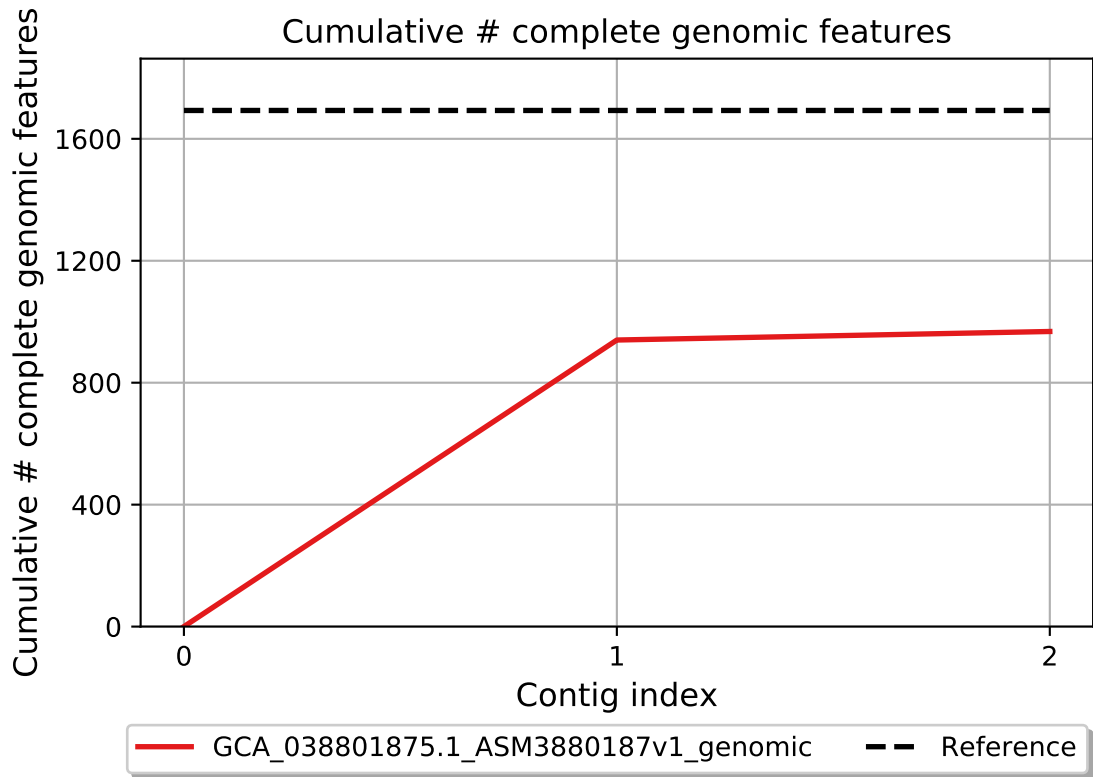


— GCA_038801875.1_ASM3880187v1_genomic

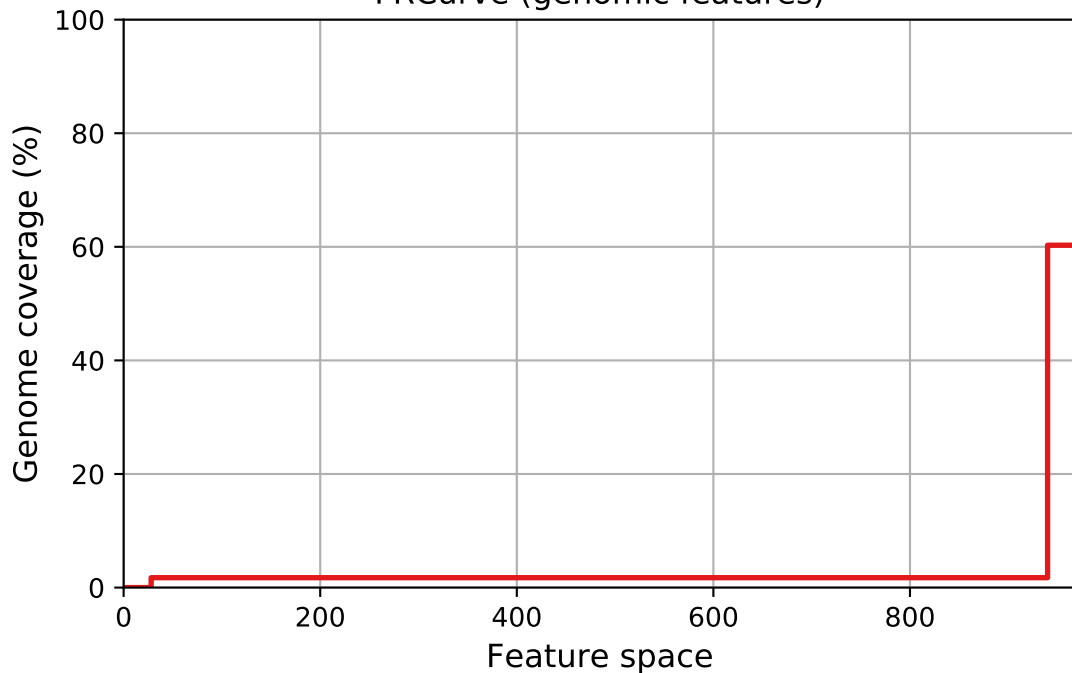
NGAx



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FRCurve (genomic features)



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