

Report

	GCA_024662195.1_ASM2466219v1_genomic
# contigs (≥ 0 bp)	21
# contigs (≥ 1000 bp)	21
# contigs (≥ 5000 bp)	21
# contigs (≥ 10000 bp)	20
# contigs (≥ 25000 bp)	17
# contigs (≥ 50000 bp)	3
Total length (≥ 0 bp)	1513701
Total length (≥ 1000 bp)	1513701
Total length (≥ 5000 bp)	1513701
Total length (≥ 10000 bp)	1504314
Total length (≥ 25000 bp)	1444849
Total length (≥ 50000 bp)	1015796
# contigs	21
Largest contig	909655
Total length	1513701
Reference length	1521208
GC (%)	28.20
Reference GC (%)	28.18
N50	909655
NG50	909655
N90	28447
NG90	28332
auN	560014.8
auNG	557251.1
L50	1
LG50	1
L90	14
LG90	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.439
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.98
# indels per 100 kbp	4.36
# genomic features	1669 + 16 part
Largest alignment	909651
Total aligned length	1512668
NA50	909651
NGA50	909651
NA90	28332
NGA90	27991
auNA	559971.8
auNGA	557208.4
LA50	1
LGA50	1
LA90	14
LGA90	15

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

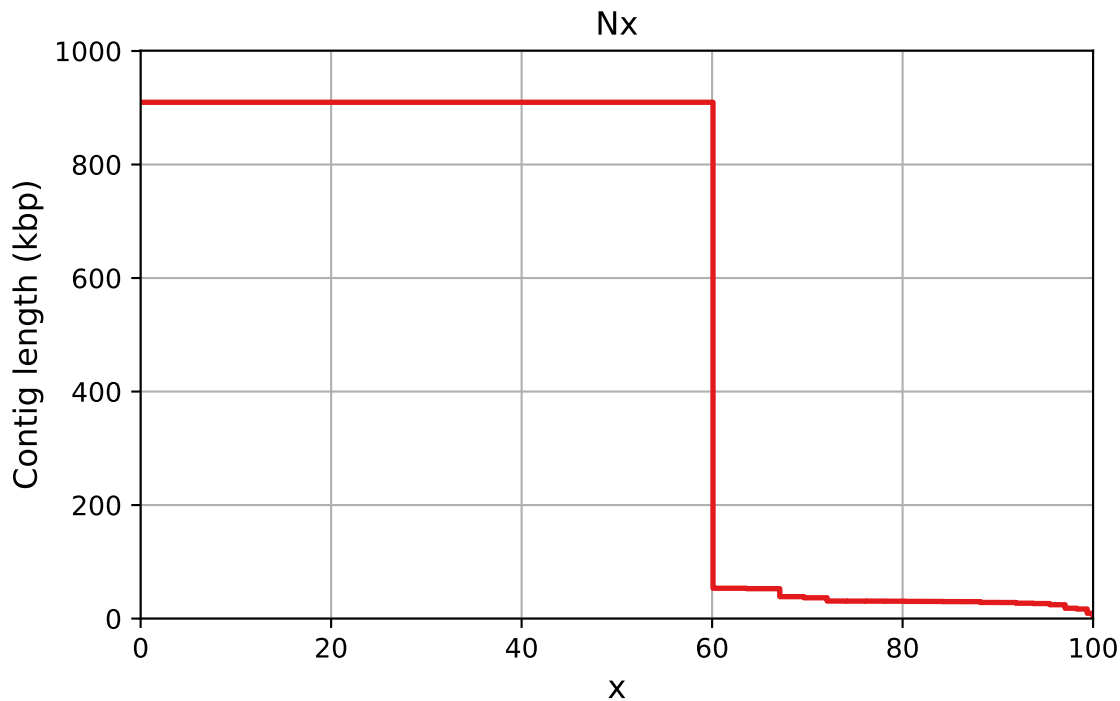
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# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	30
# indels	66
# indels (<= 5 bp)	66
# indels (> 5 bp)	0
Indels length	69

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

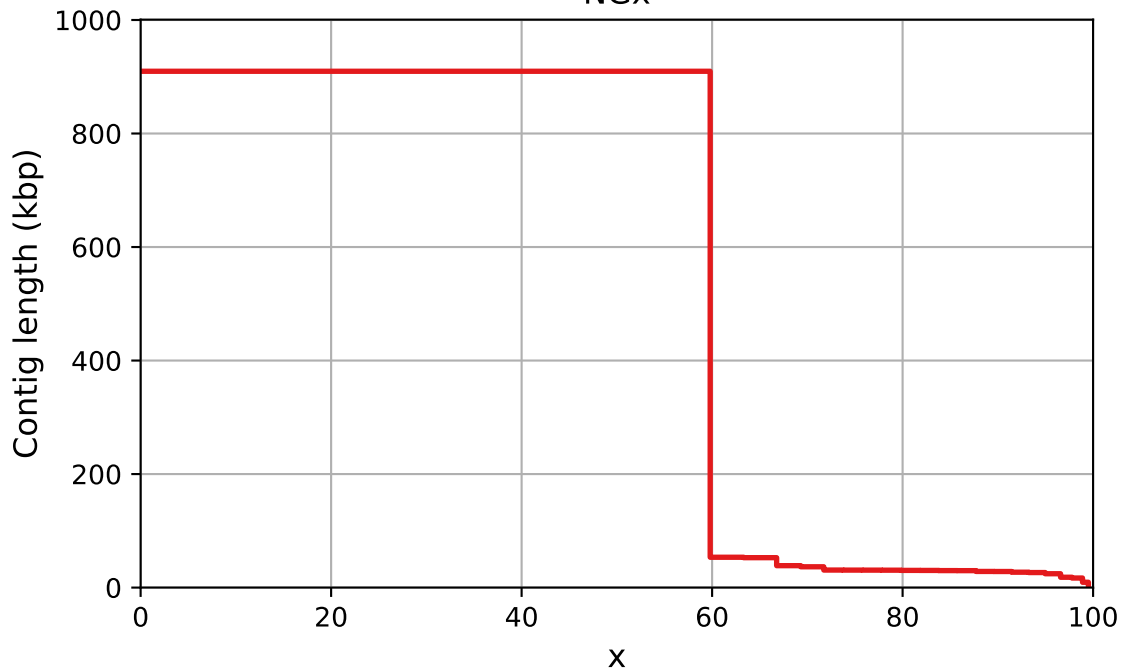
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# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

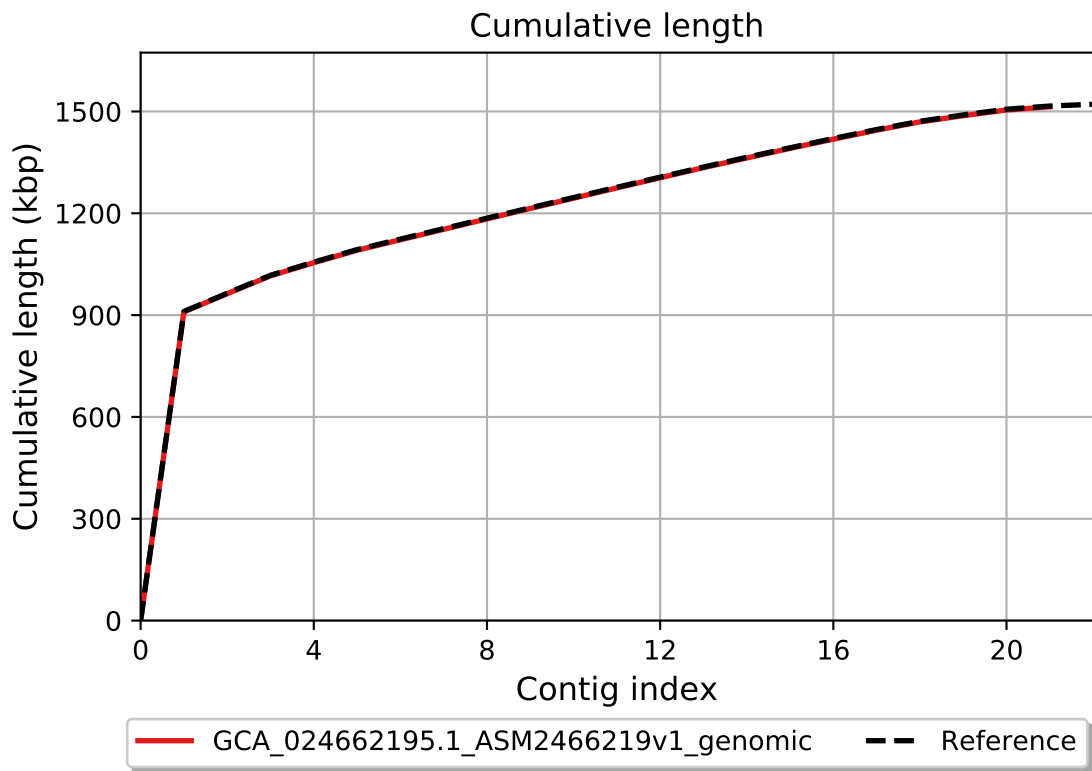


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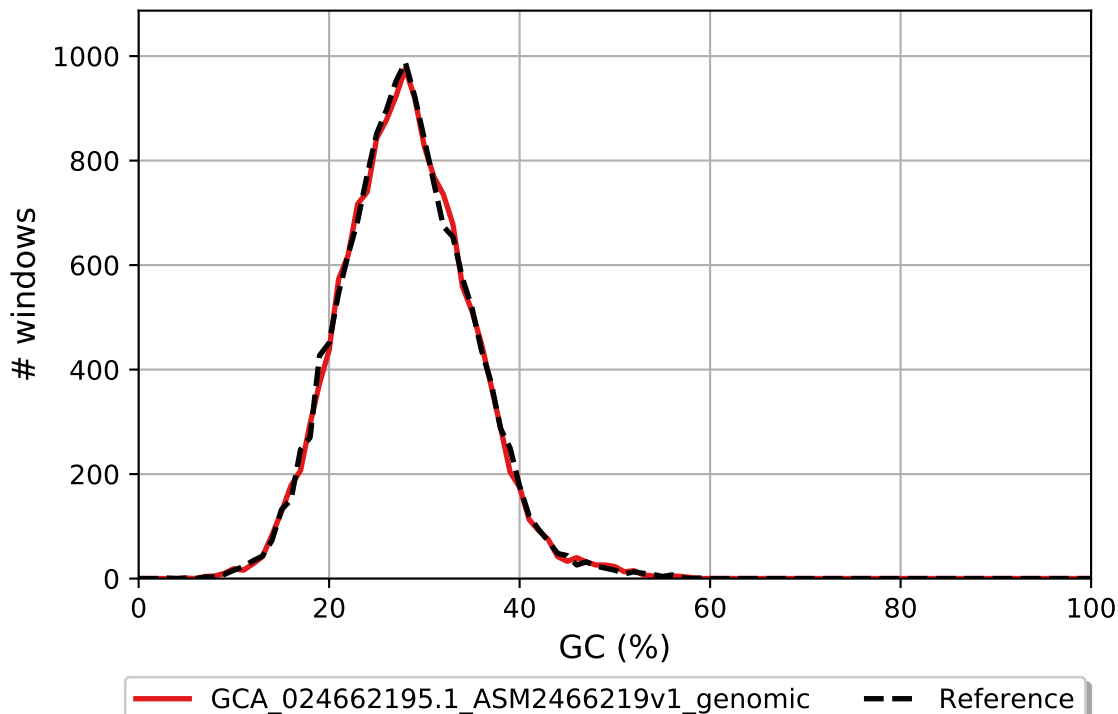
NGx



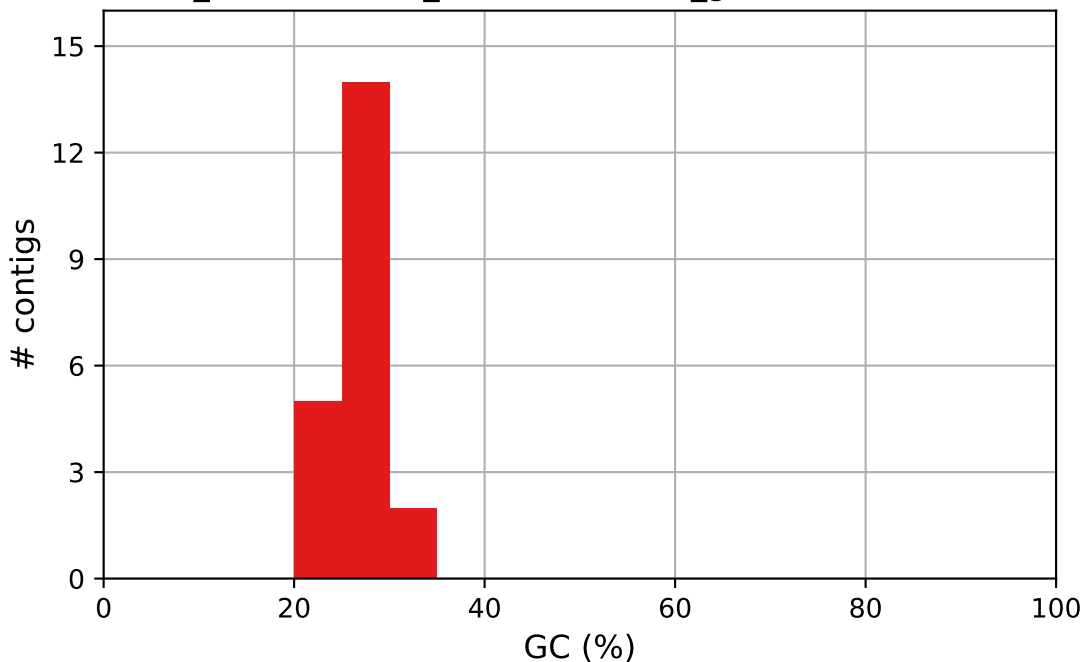
— GCA_024662195.1_ASM2466219v1_genomic



GC content

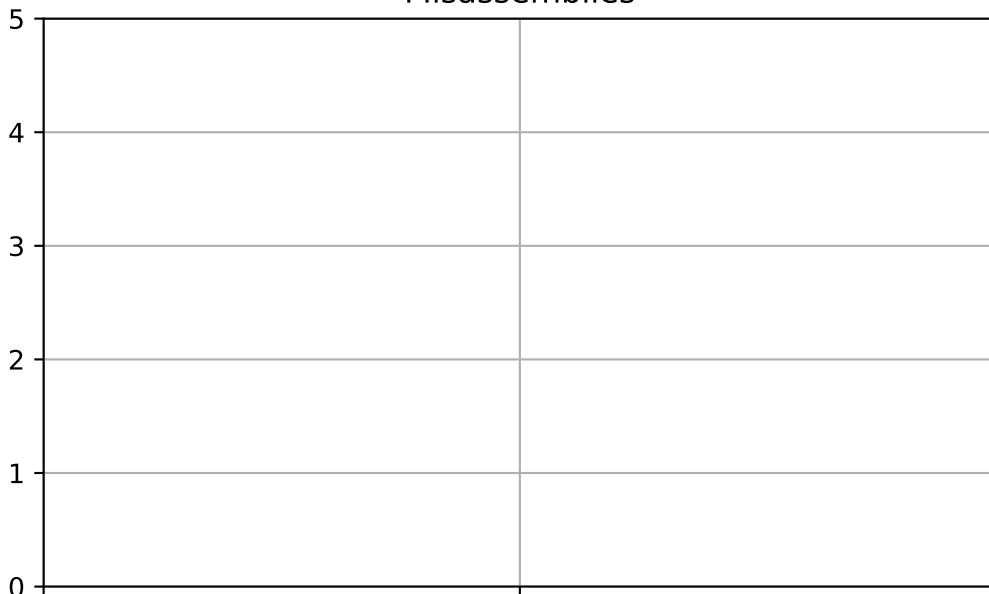


GCA_024662195.1_ASM2466219v1_genomic GC content



GCA_024662195.1_ASM2466219v1_genomic

Misassemblies



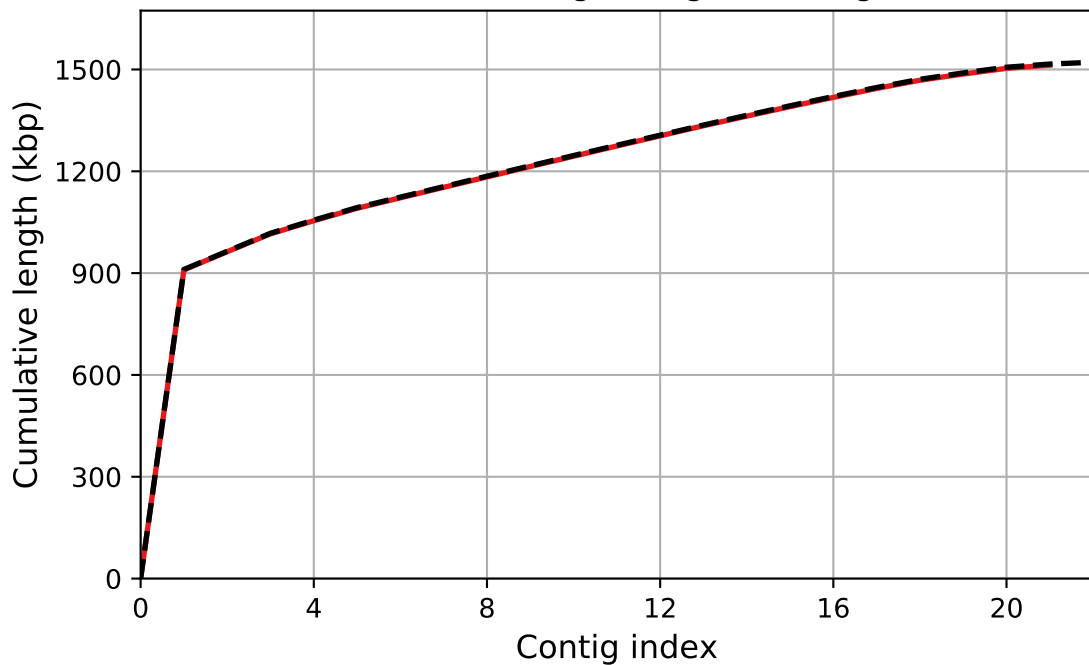
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FRCurve (misassemblies)



— GCA_024662195.1_ASM2466219v1_genomic

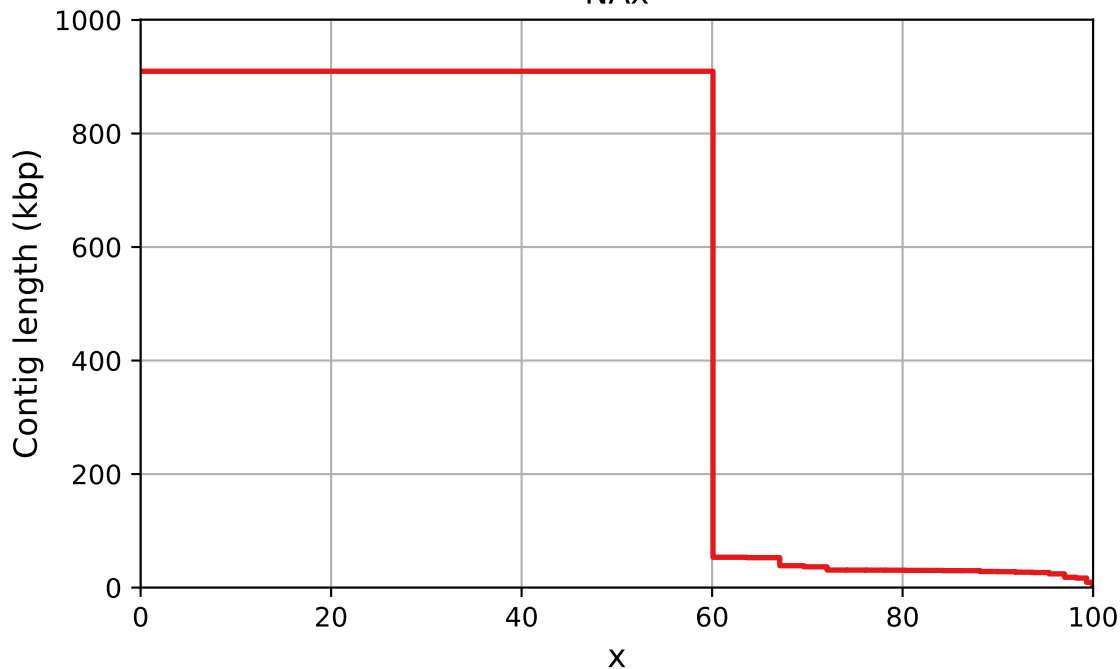
Cumulative length (aligned contigs)



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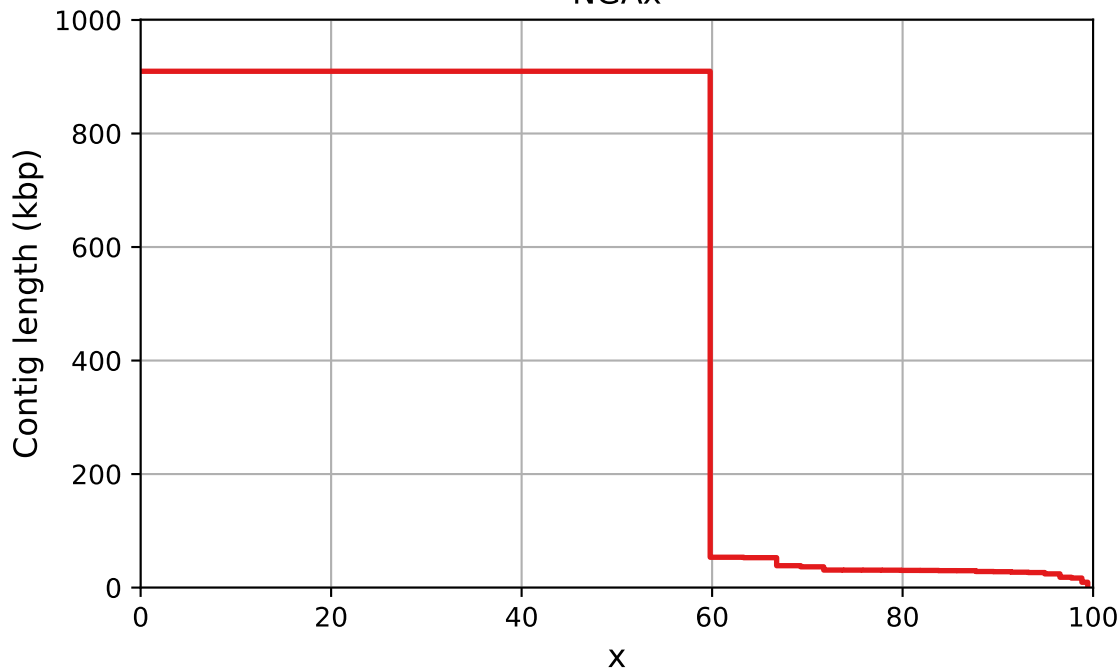
Reference

NAx

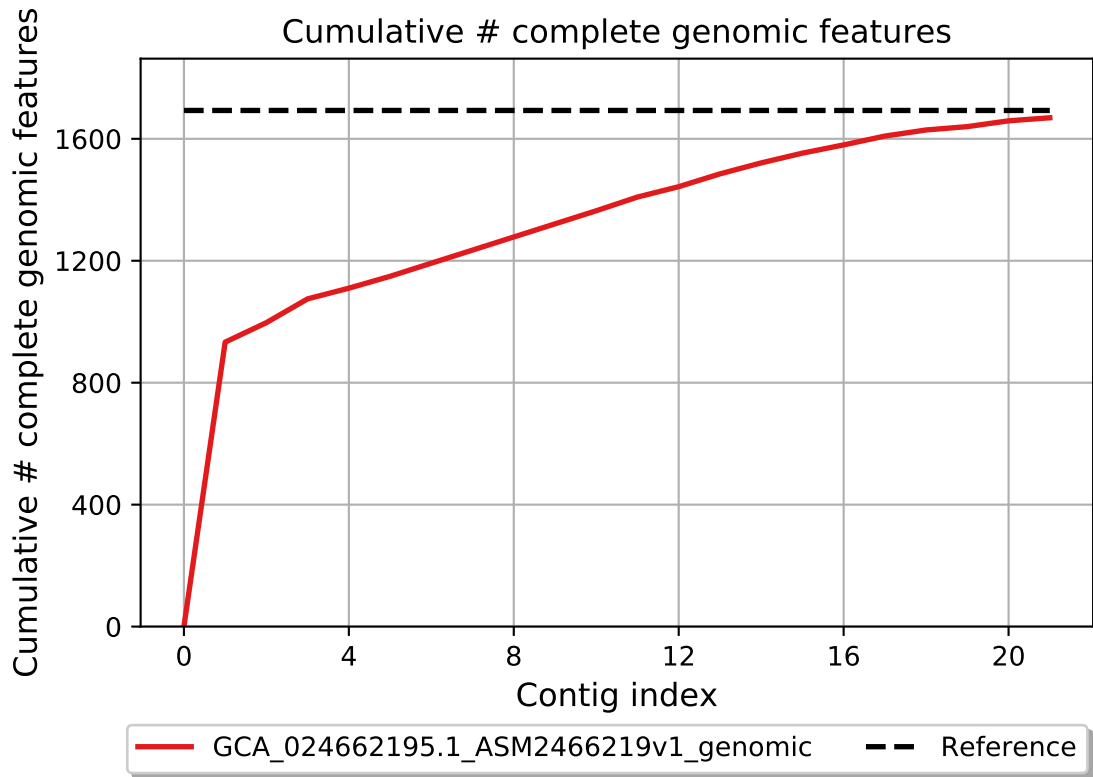


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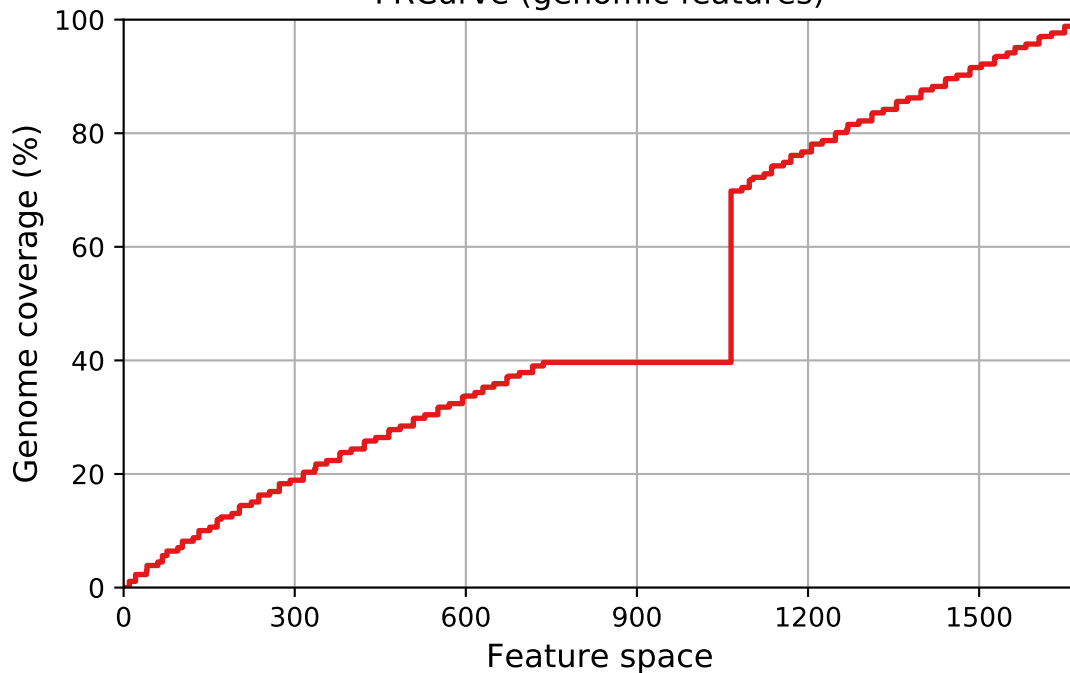
NGAx



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FRCurve (genomic features)



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