

Report

	GCF_000166635.1_ASM16663v1_genomic
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1339539
Total length (>= 1000 bp)	1339539
Total length (>= 5000 bp)	1339539
Total length (>= 10000 bp)	1330817
Total length (>= 25000 bp)	1253353
Total length (>= 50000 bp)	955977
# contigs	17
Largest contig	902191
Total length	1339539
Reference length	1521208
GC (%)	28.27
Reference GC (%)	28.18
N50	902191
NG50	902191
N90	26642
NG90	-
auN	617665.1
auNG	543901.0
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	15
# misassembled contigs	8
Misassembled contigs length	249274
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 13 part
Unaligned length	131991
Genome fraction (%)	79.113
Duplication ratio	1.003
# N's per 100 kbp	0.15
# mismatches per 100 kbp	825.88
# indels per 100 kbp	48.73
# genomic features	1255 + 51 part
Largest alignment	902026
Total aligned length	1206591
NA50	902026
NGA50	902026
NA90	550
NGA90	-
auNA	612325.5
auNGA	539199.0
LA50	1
LGA50	1
LA90	39
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

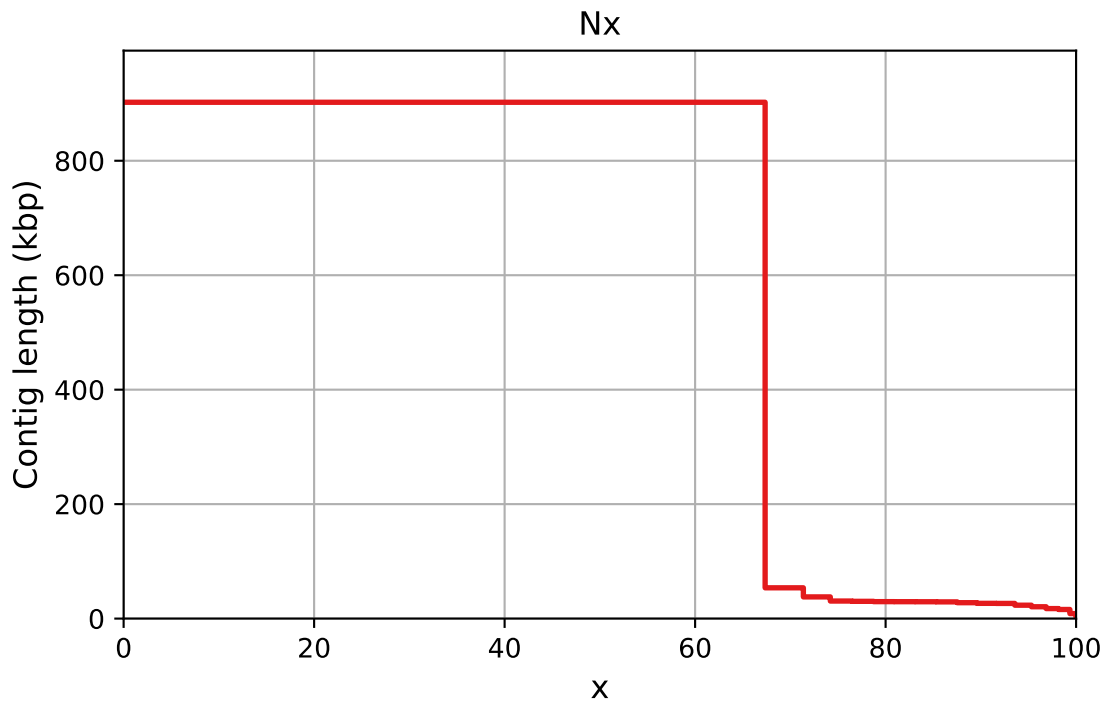
	GCF_000166635.1_ASM16663v1_genomic
# misassemblies	15
# contig misassemblies	15
# c. relocations	4
# c. translocations	11
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	249274
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9965
# indels	588
# indels (<= 5 bp)	524
# indels (> 5 bp)	64
Indels length	3233

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

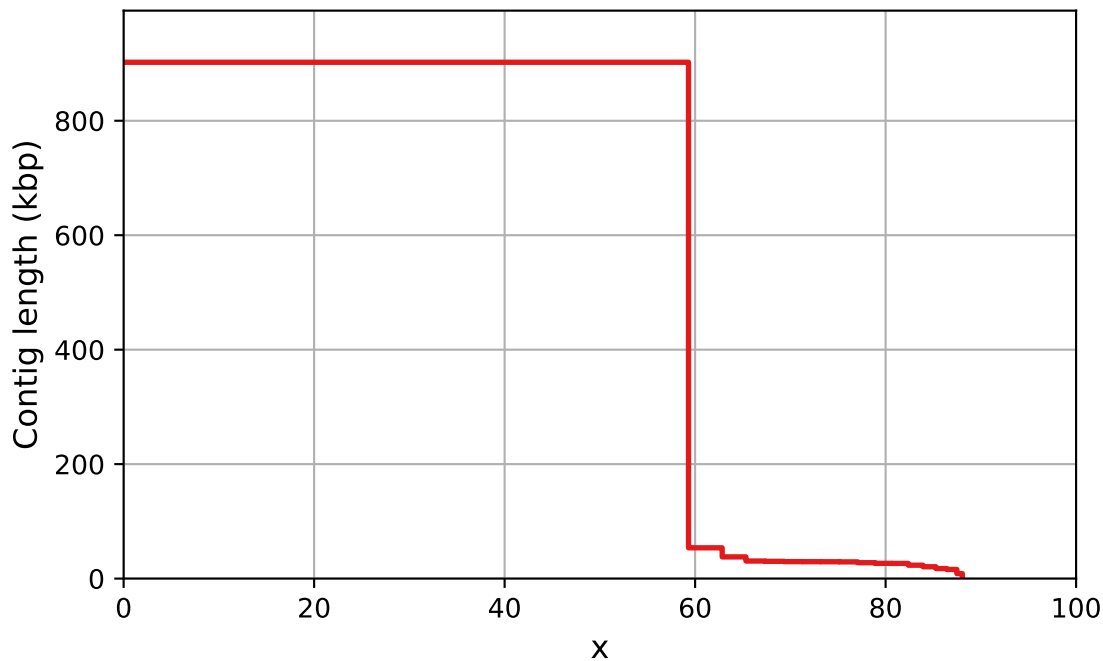
	GCF_000166635.1_ASM16663v1_genomic
# fully unaligned contigs	1
Fully unaligned length	27767
# partially unaligned contigs	13
Partially unaligned length	104224
# N's	2

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).

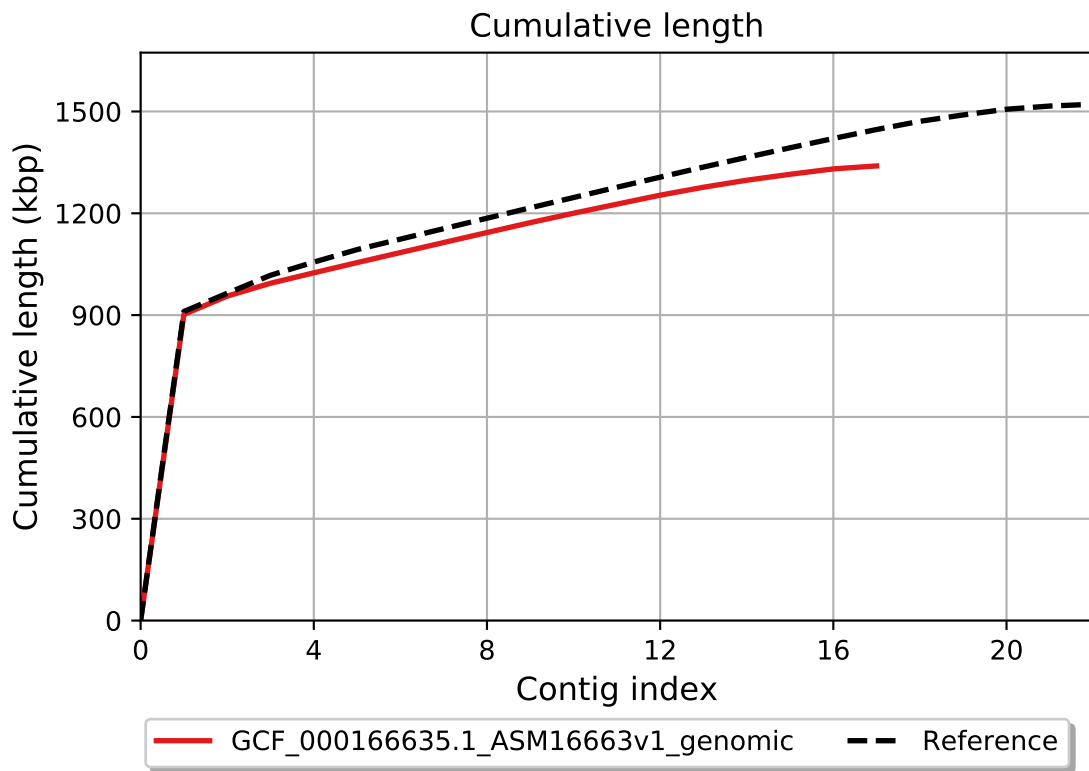


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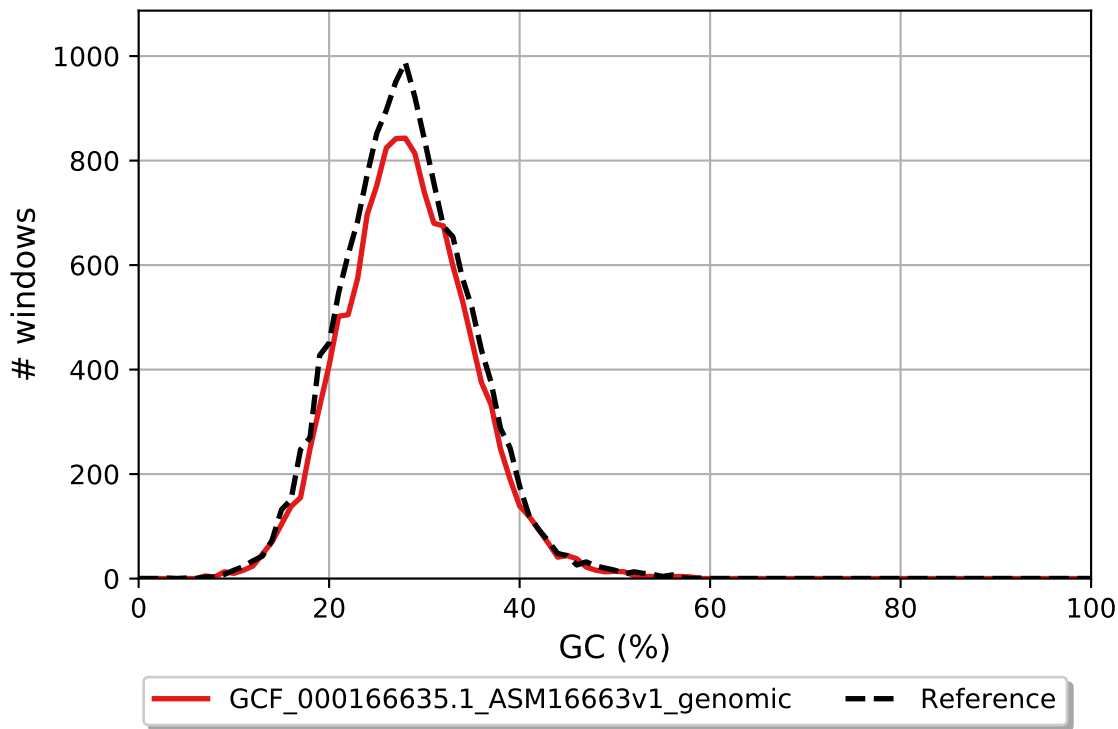
NGx



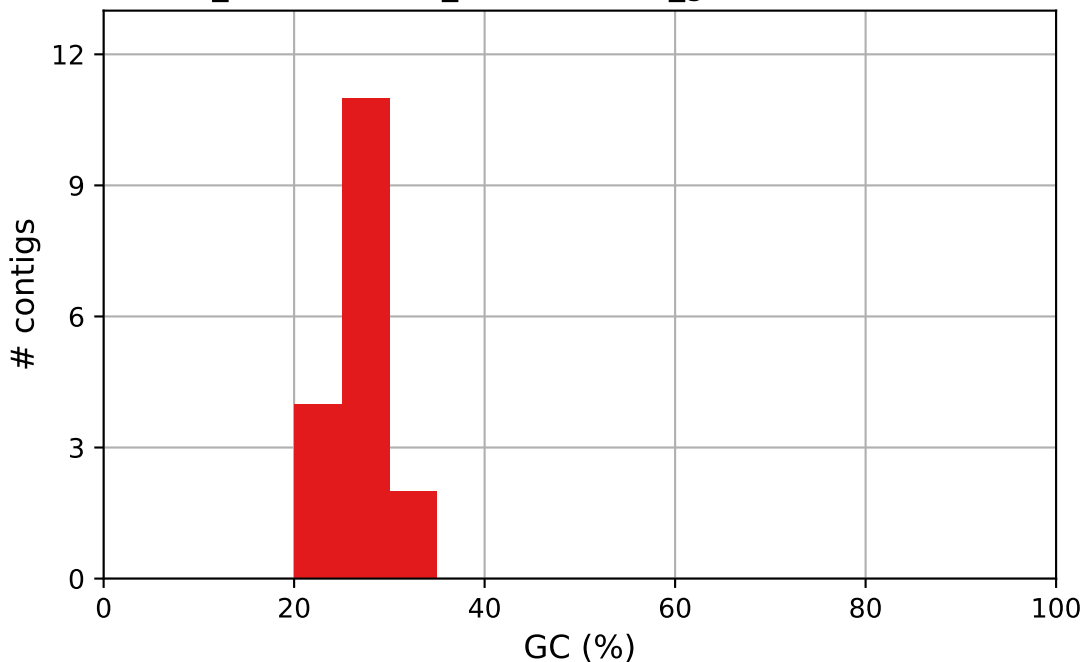
— GCF_000166635.1_ASM16663v1_genomic



GC content

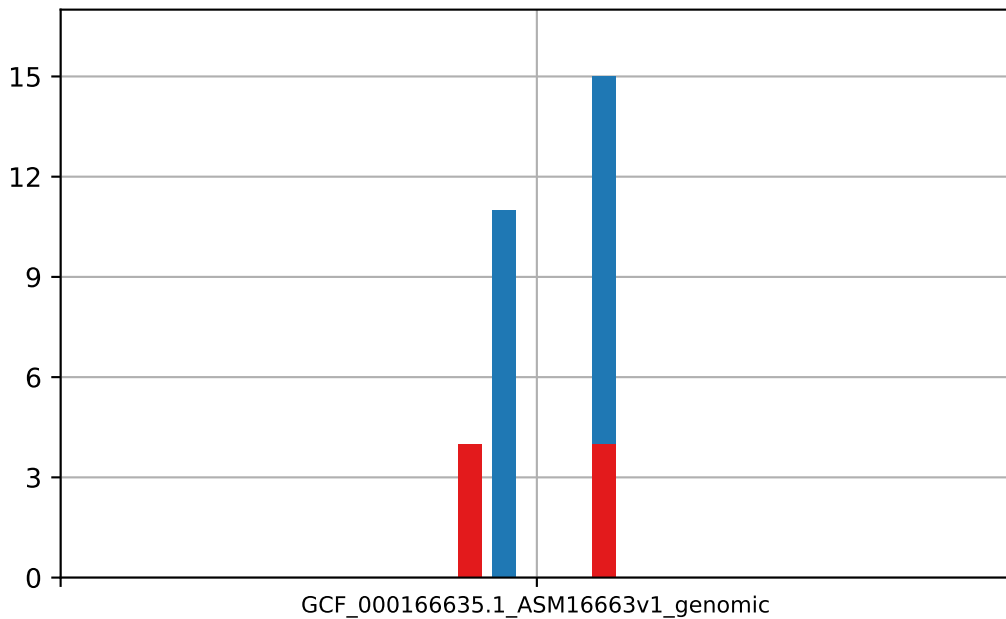


GCF_000166635.1_ASM16663v1_genomic GC content



GCF_000166635.1_ASM16663v1_genomic

Misassemblies

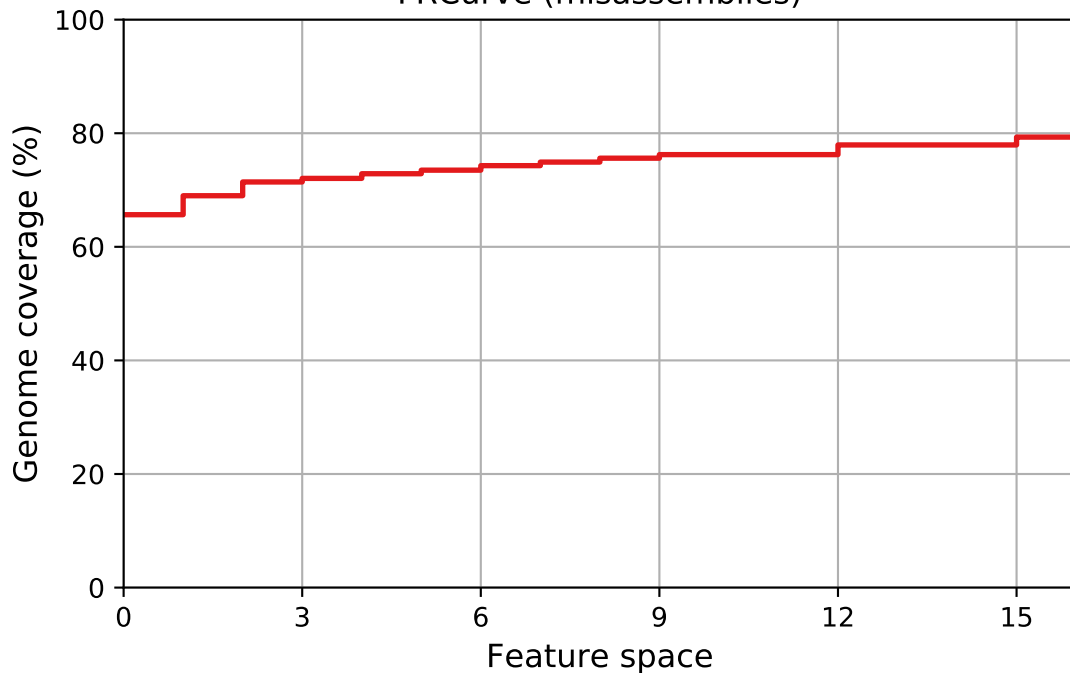


relocations



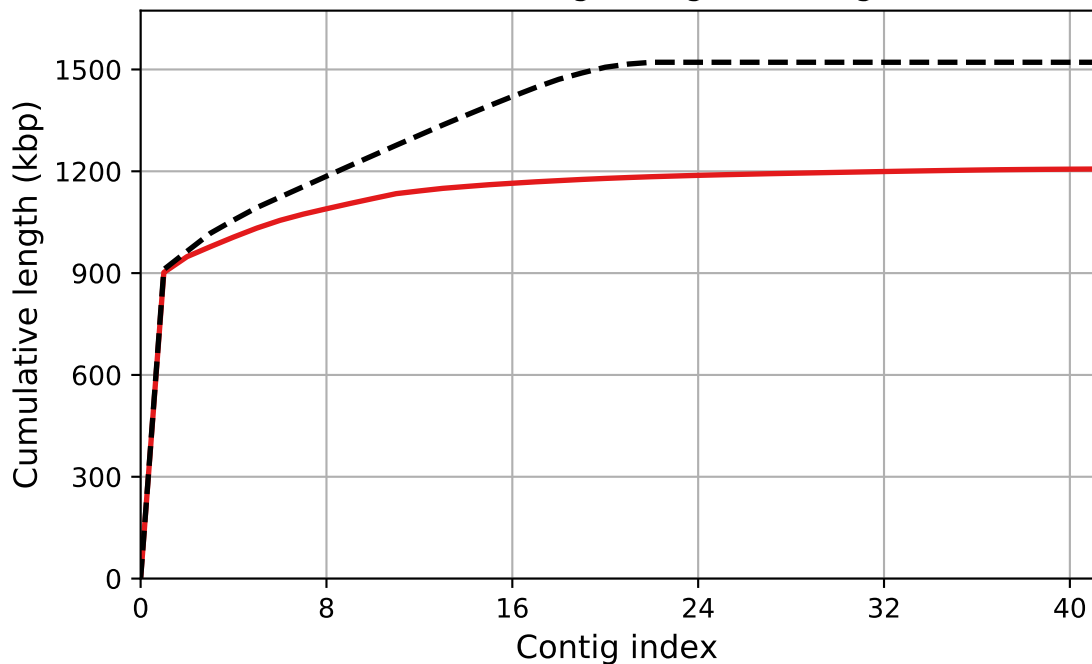
translocations

FRCurve (misassemblies)



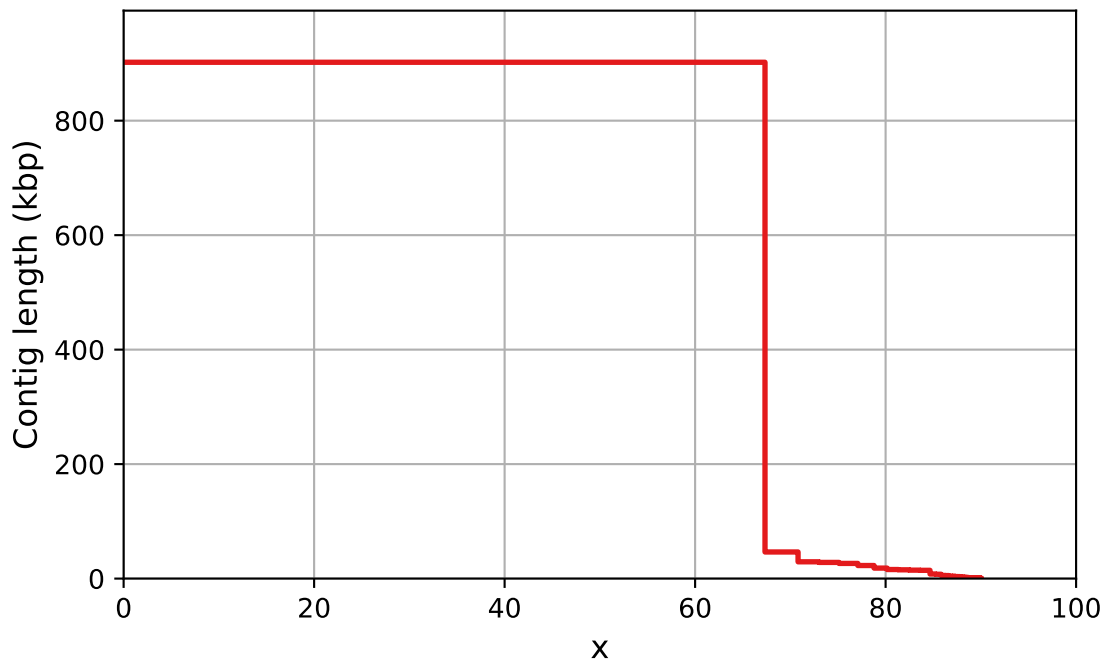
— GCF_000166635.1_ASM16663v1_genomic

Cumulative length (aligned contigs)



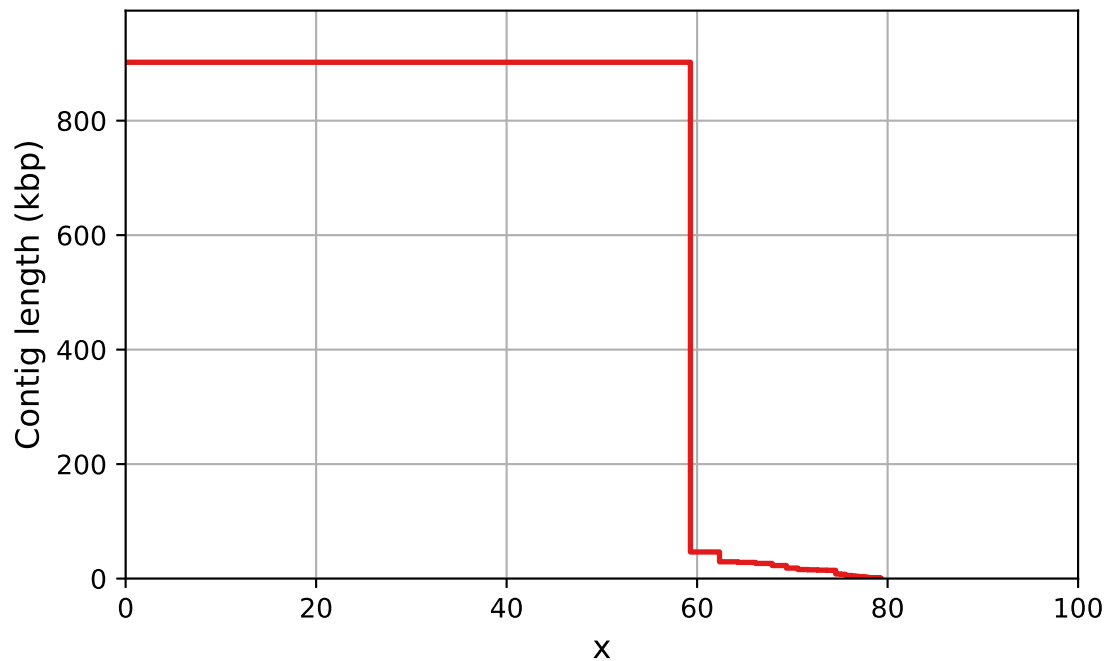
— GCF_000166635.1_ASM16663v1_genomic - - Reference

NAx



— GCF_000166635.1_ASM16663v1_genomic

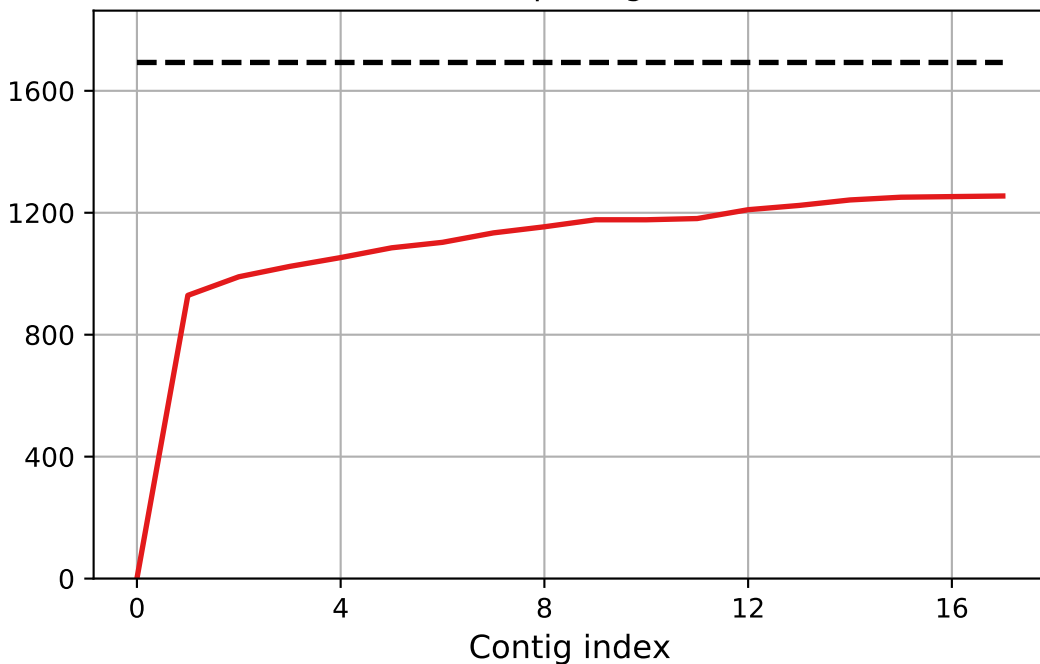
NGAx



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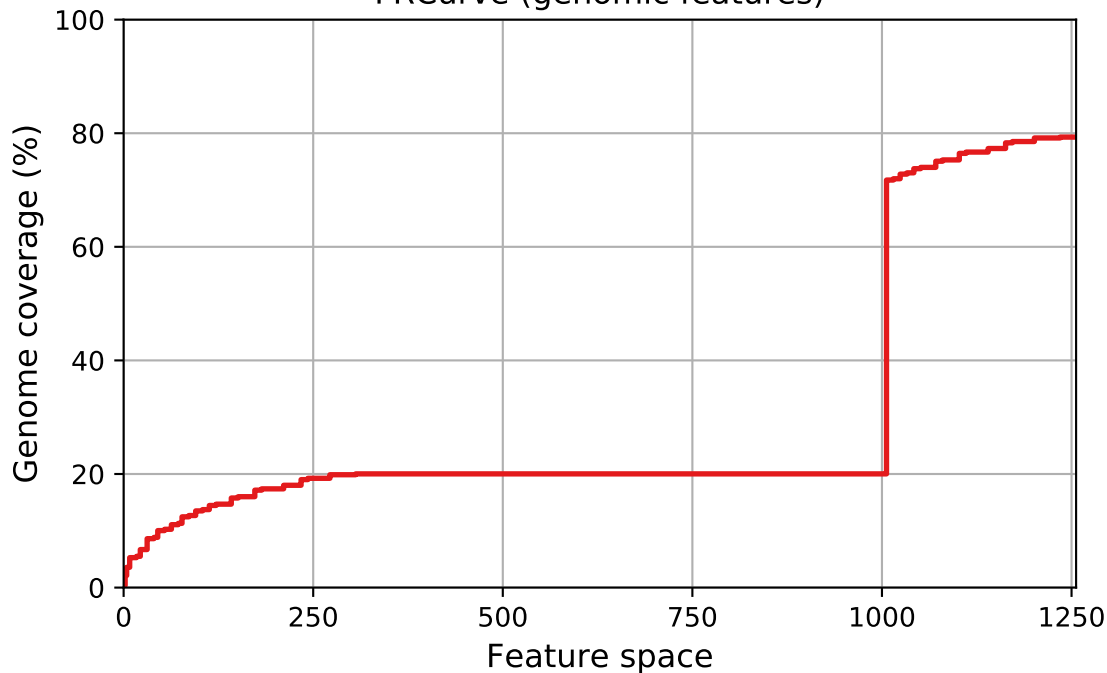
Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)



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