

Report

	URI111H
# contigs (>= 0 bp)	23
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1539609
Total length (>= 1000 bp)	1539157
Total length (>= 5000 bp)	1536822
Total length (>= 10000 bp)	1536822
Total length (>= 25000 bp)	1514726
Total length (>= 50000 bp)	1043298
# contigs	21
Largest contig	910611
Total length	1539157
Reference length	1521208
GC (%)	28.15
Reference GC (%)	28.18
N50	910611
NG50	910611
N90	30260
NG90	30299
auN	554805.9
auNG	561352.2
L50	1
LG50	1
L90	14
LG90	13
# misassemblies	21
# misassembled contigs	12
Misassembled contigs length	430100
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	30201
Genome fraction (%)	94.226
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	251.16
# indels per 100 kbp	28.36
# genomic features	1546 + 35 part
Largest alignment	910611
Total aligned length	1502246
NA50	910611
NGA50	910611
NA90	16822
NGA90	17432
auNA	548962.5
auNGA	555439.8
LA50	1
LGA50	1
LA90	18
LGA90	17

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

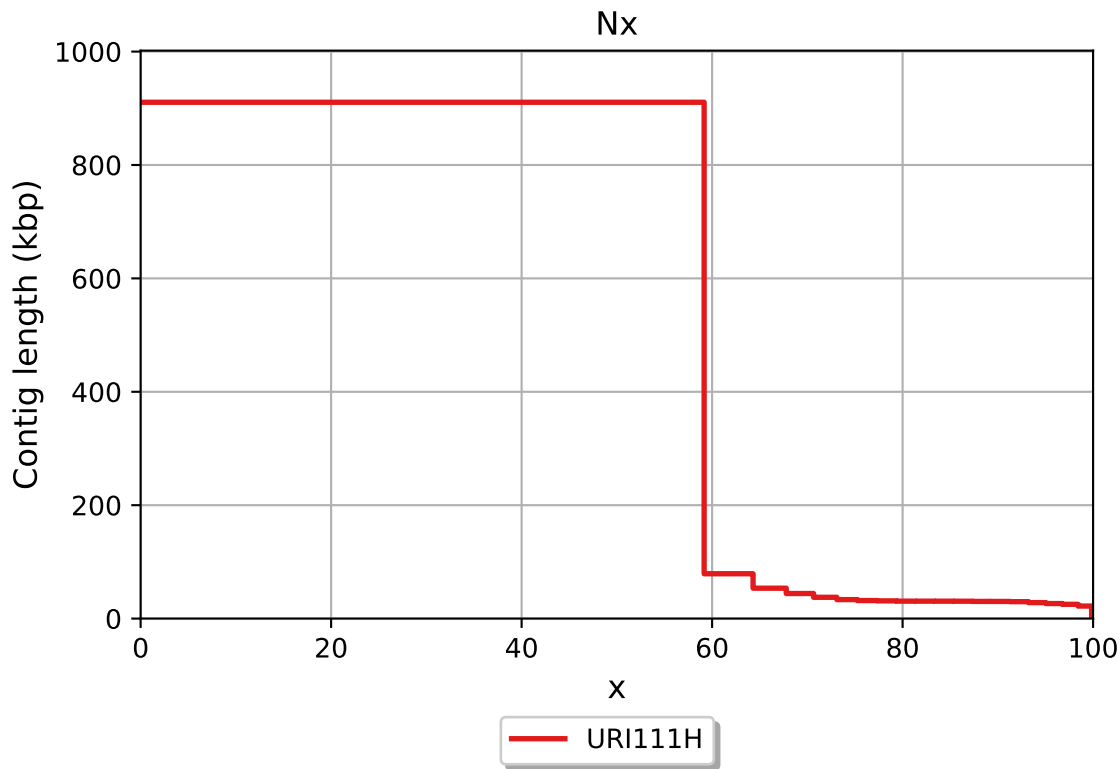
	URI111H
# misassemblies	21
# contig misassemblies	21
# c. relocations	8
# c. translocations	11
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	430100
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3773
# indels	426
# indels (<= 5 bp)	360
# indels (> 5 bp)	66
Indels length	3925

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

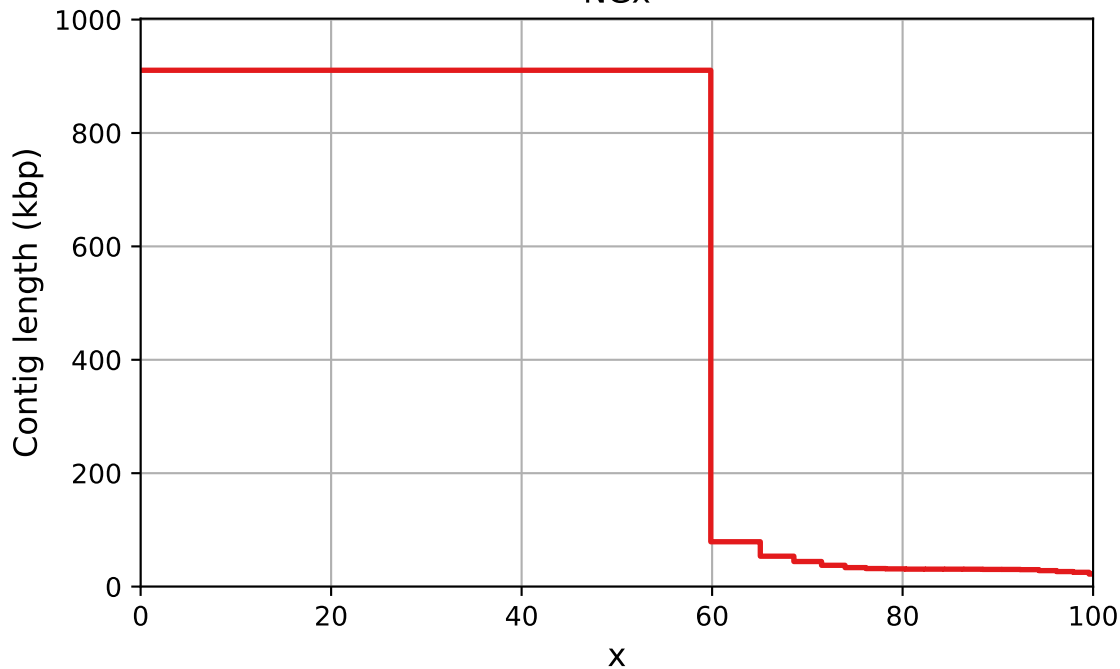
## Unaligned report

	URI111H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	30201
# N's	0

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

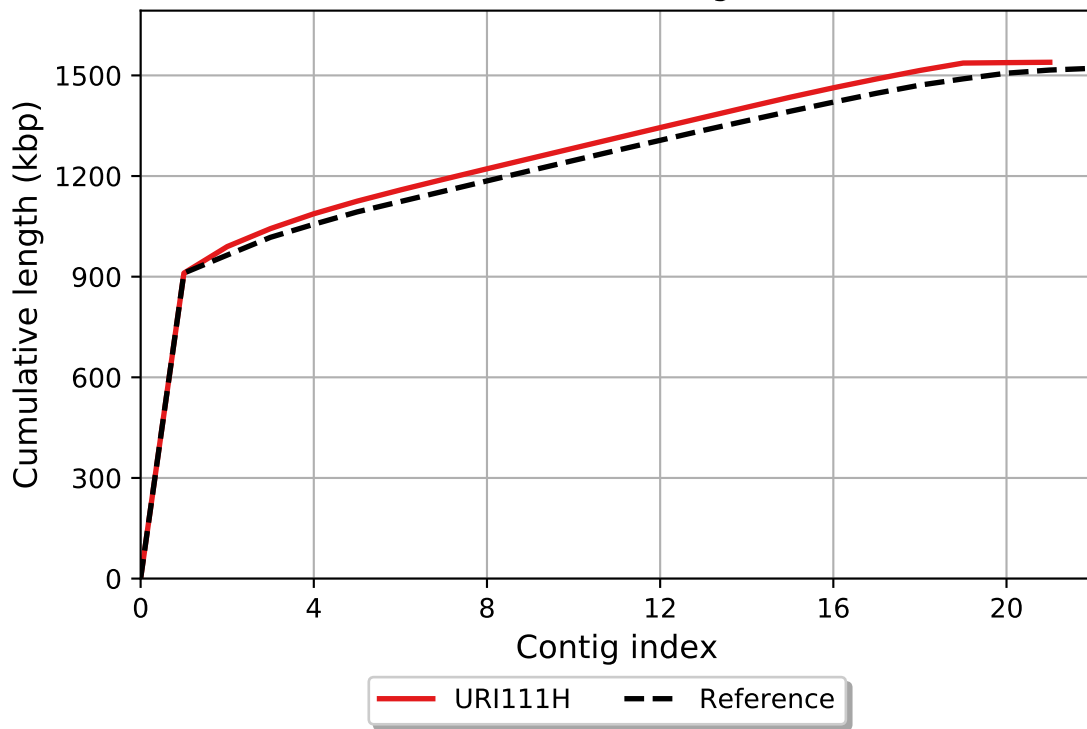


NGx

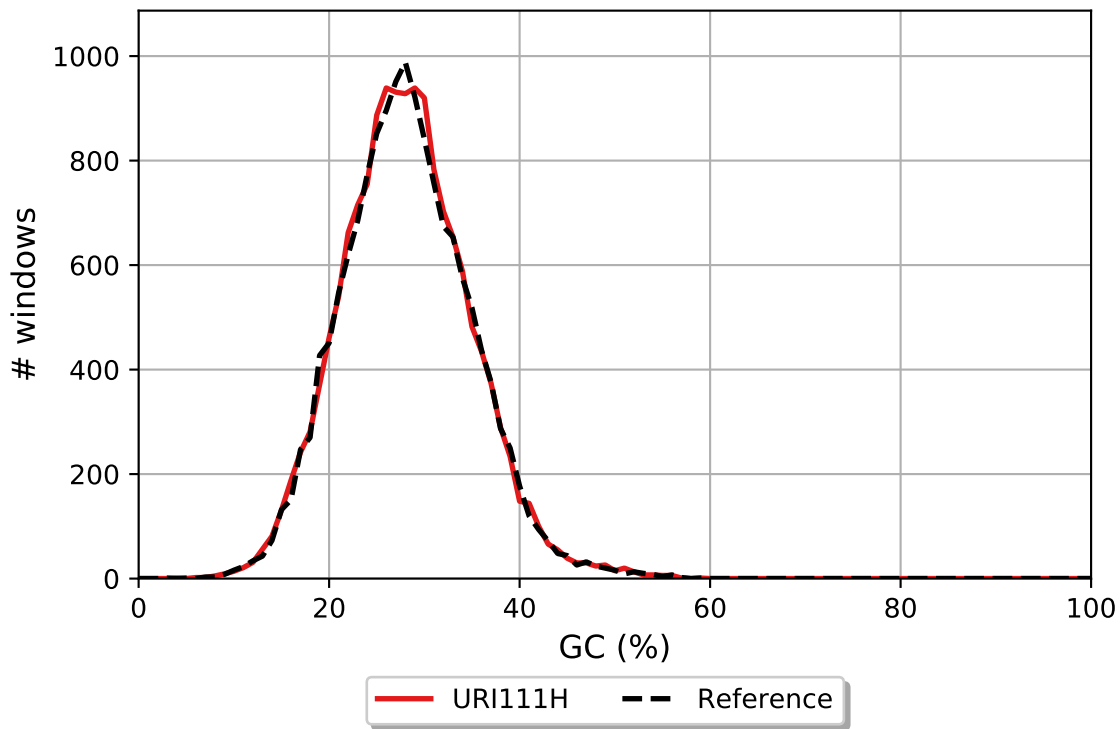


— URI111H

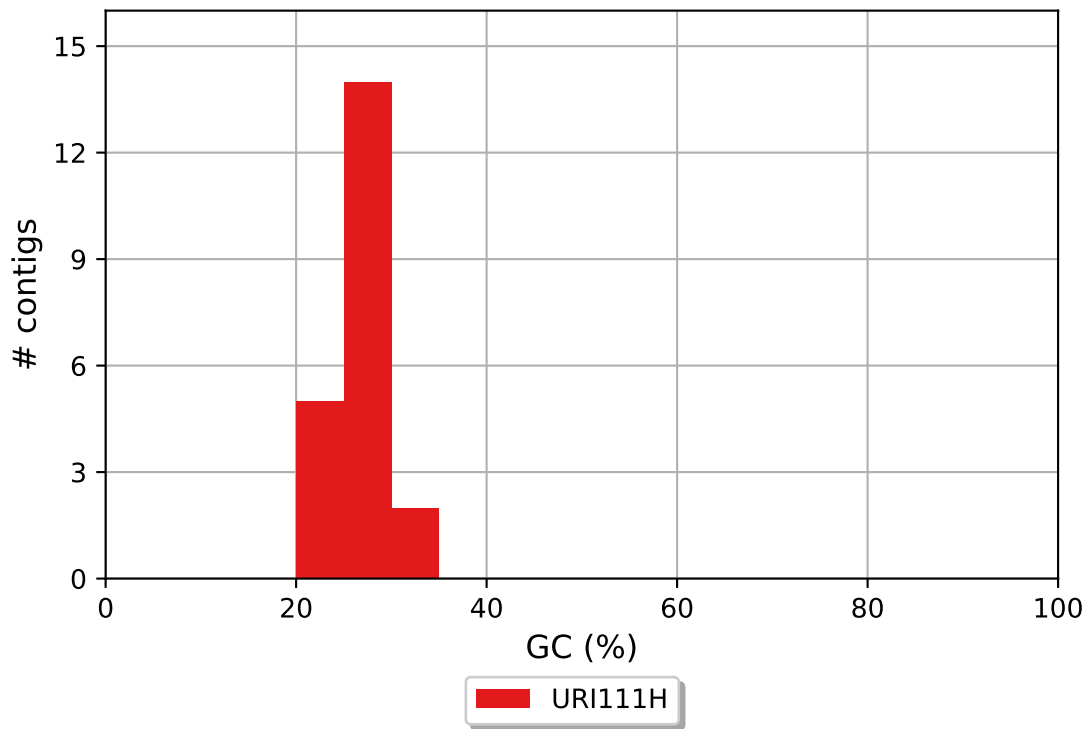
Cumulative length



GC content

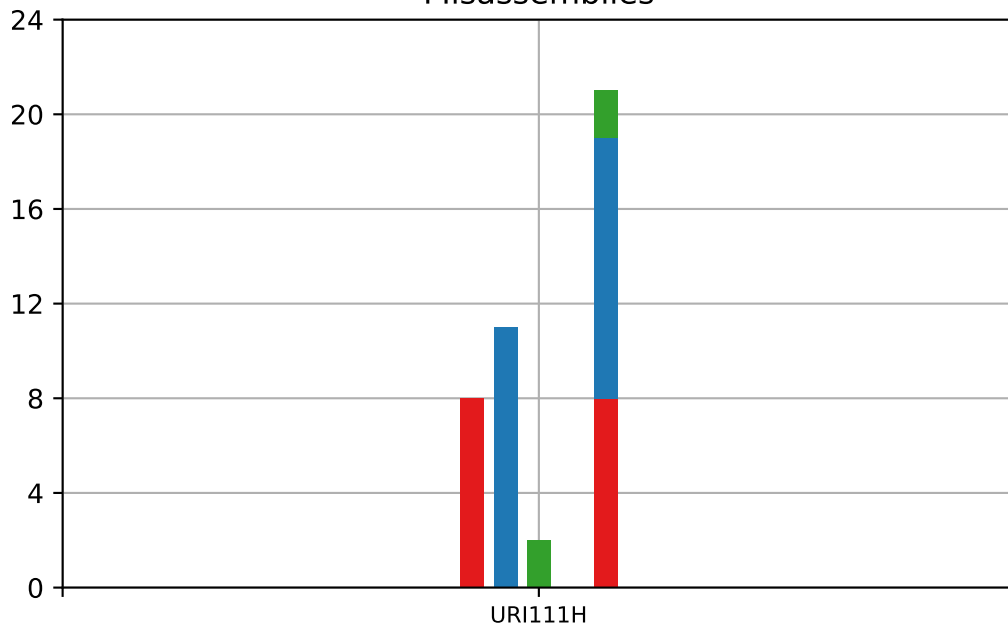


URI111H GC content



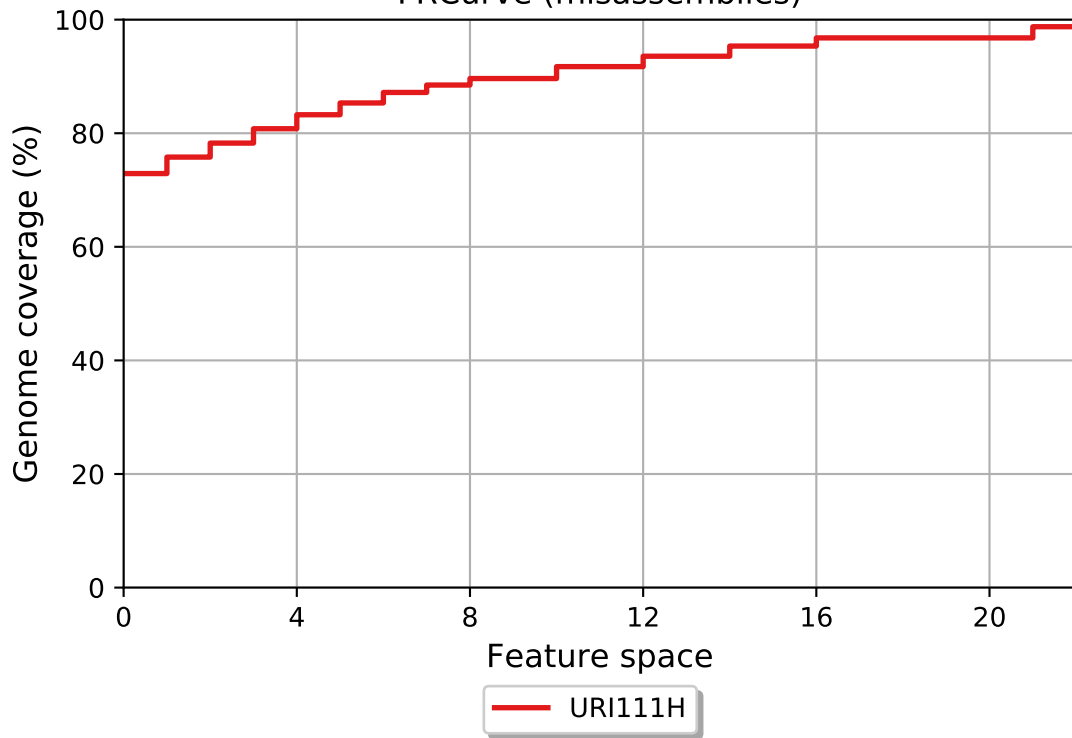


## Misassemblies

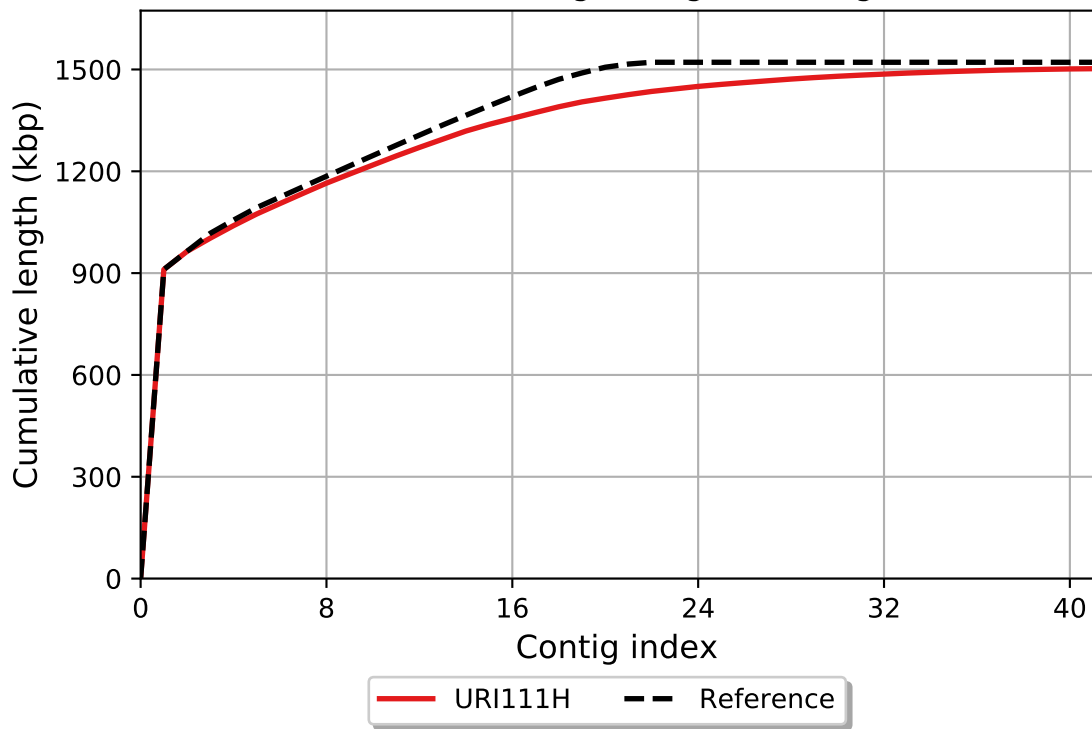


# relocations    # translocations    # inversions

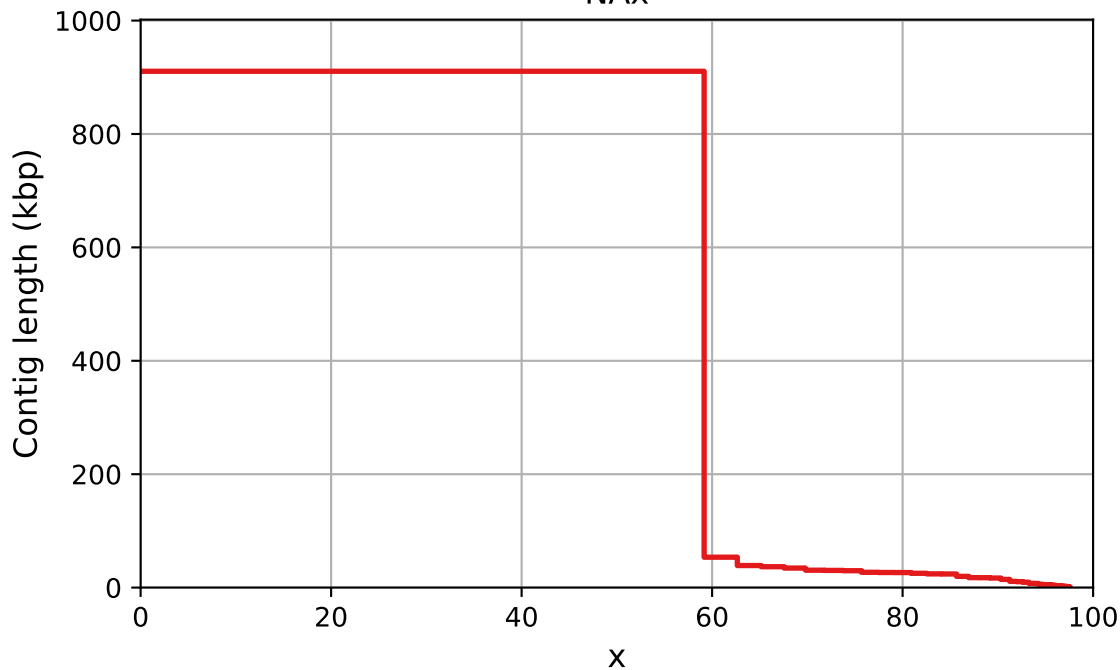
FRCurve (misassemblies)



Cumulative length (aligned contigs)

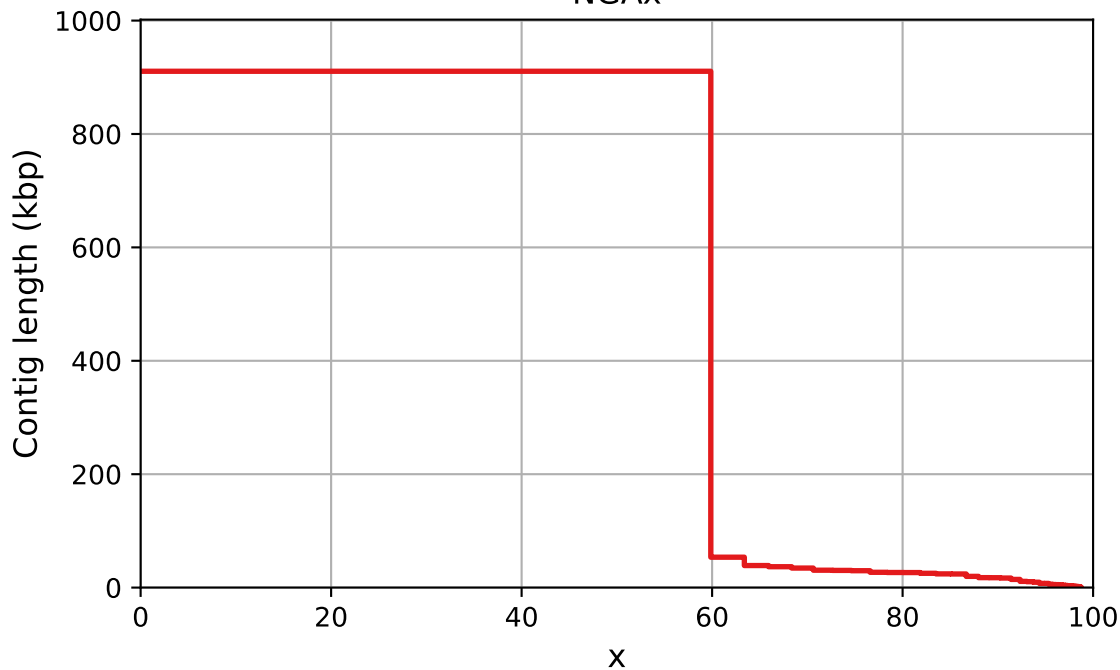


NAx



— URI111H

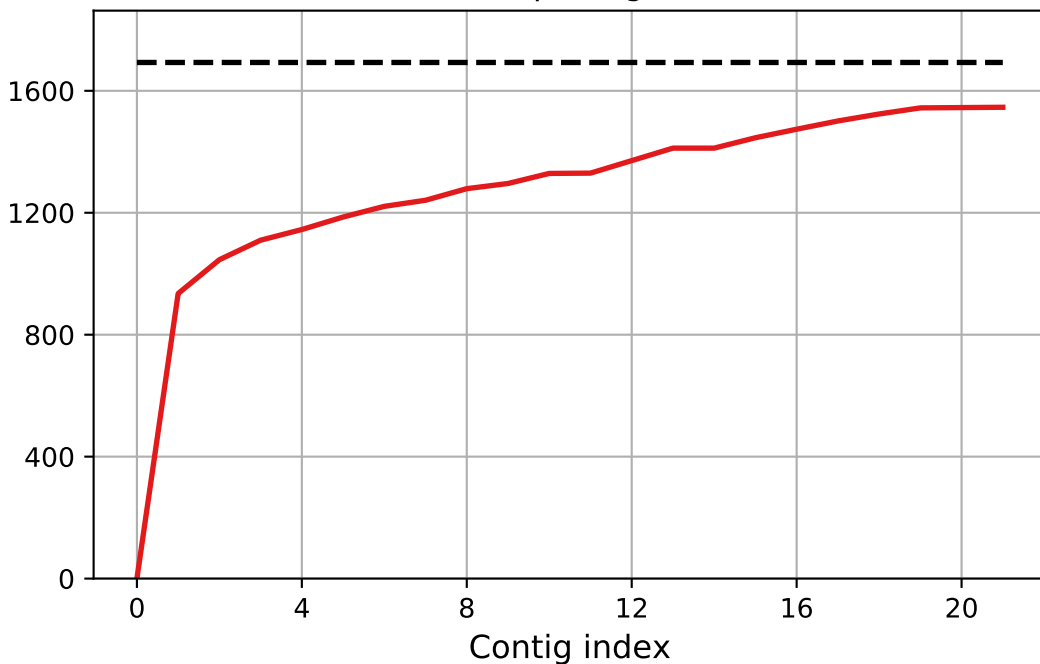
NGAx



URI111H

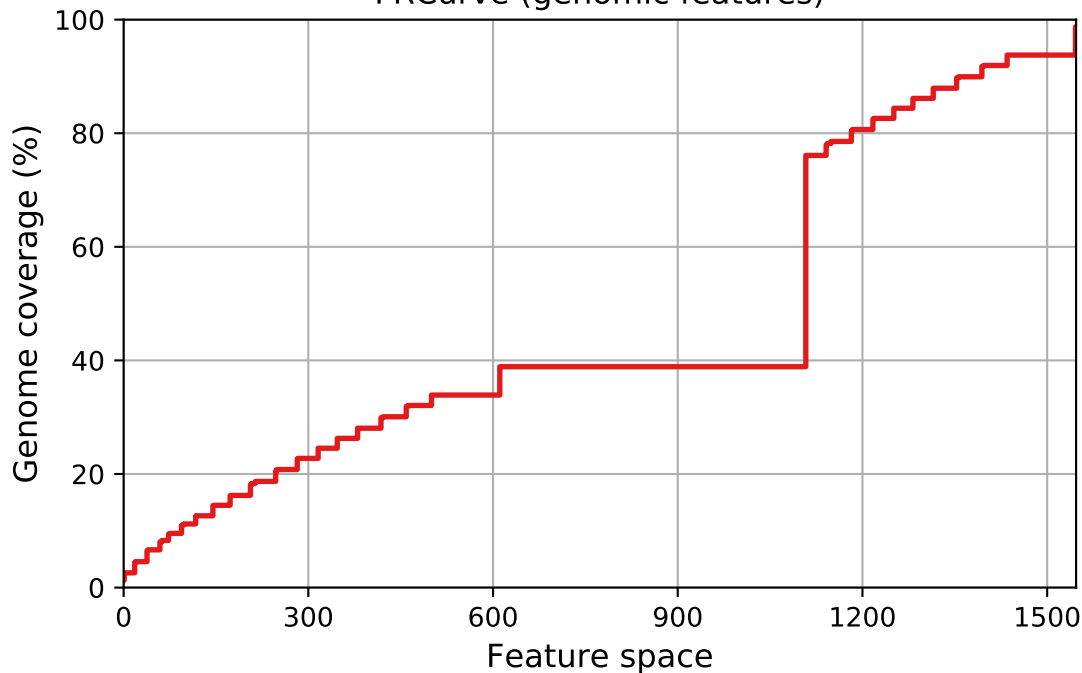
Cumulative # complete genomic features

Cumulative # complete genomic features



— URI111H    - - Reference

FRCurve (genomic features)



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