

Report

	URI56H
# contigs (>= 0 bp)	230
# contigs (>= 1000 bp)	48
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1297641
Total length (>= 1000 bp)	1233022
Total length (>= 5000 bp)	1170376
Total length (>= 10000 bp)	1099567
Total length (>= 25000 bp)	983573
Total length (>= 50000 bp)	957067
# contigs	84
Largest contig	903272
Total length	1259512
Reference length	1521208
GC (%)	28.10
Reference GC (%)	28.18
N50	903272
NG50	903272
N90	7895
NG90	-
auN	652857.3
auNG	540545.2
L50	1
LG50	1
L90	14
LG90	-
# misassemblies	14
# misassembled contigs	9
Misassembled contigs length	113180
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	14 + 17 part
Unaligned length	57814
Genome fraction (%)	77.927
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	728.86
# indels per 100 kbp	48.69
# genomic features	1203 + 81 part
Largest alignment	903068
Total aligned length	1197483
NA50	903068
NGA50	903068
NA90	2959
NGA90	-
auNA	651881.5
auNGA	539737.2
LA50	1
LGA50	1
LA90	21
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

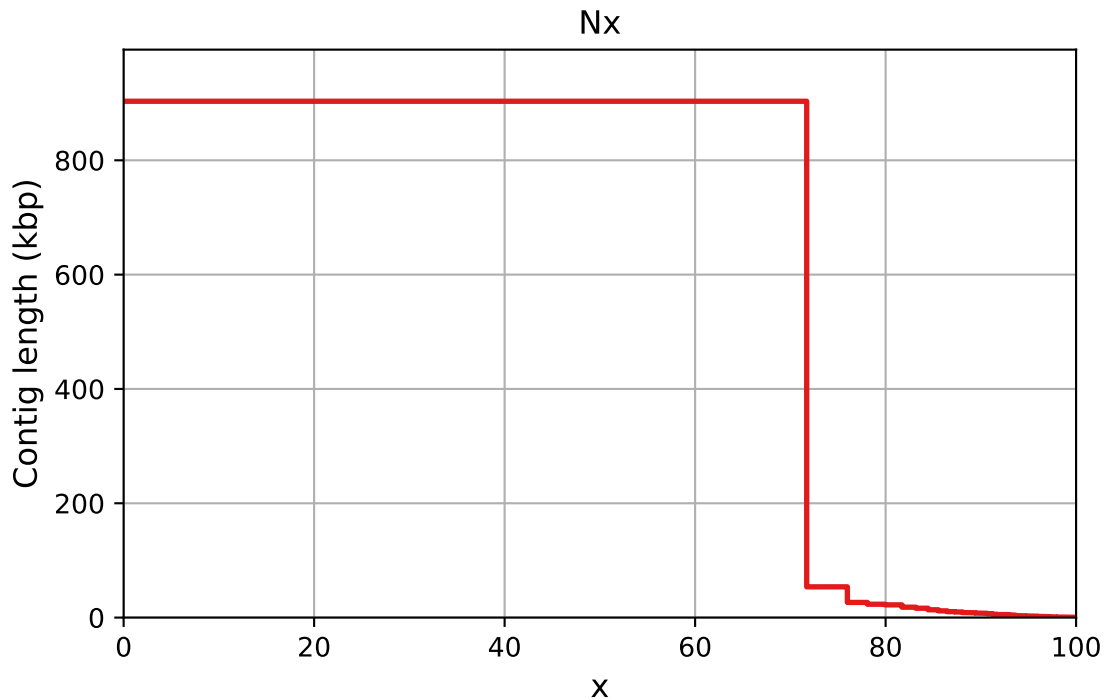
	URI56H
# misassemblies	14
# contig misassemblies	14
# c. relocations	3
# c. translocations	8
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	113180
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	8728
# indels	583
# indels (<= 5 bp)	510
# indels (> 5 bp)	73
Indels length	3192

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

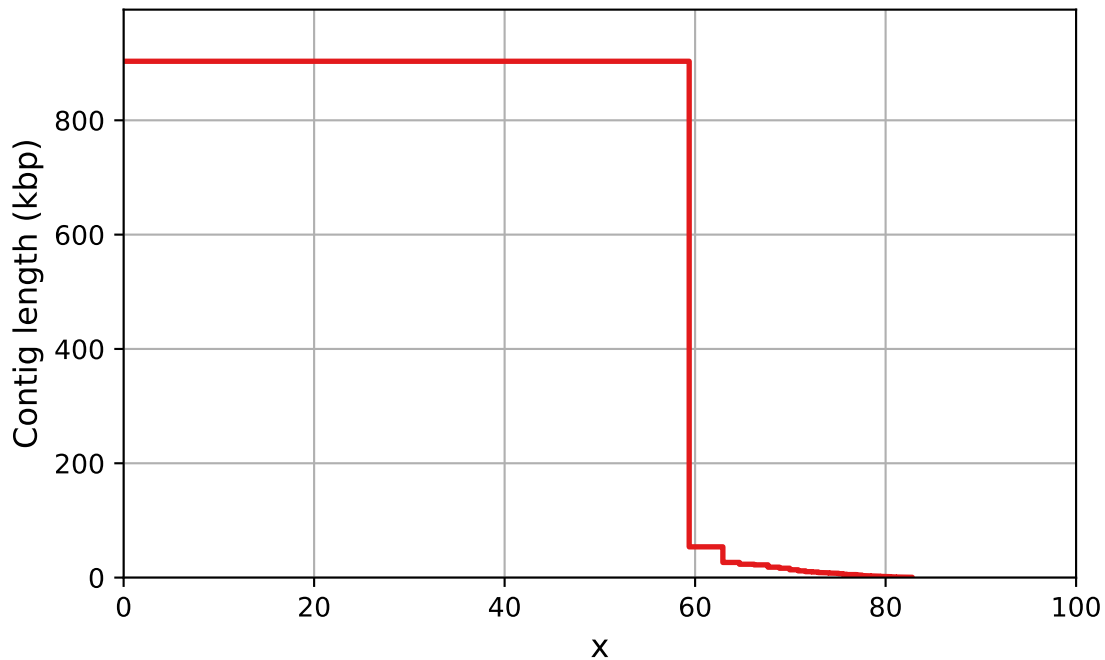
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# fully unaligned contigs	14
Fully unaligned length	18396
# partially unaligned contigs	17
Partially unaligned length	39418
# N's	0

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).

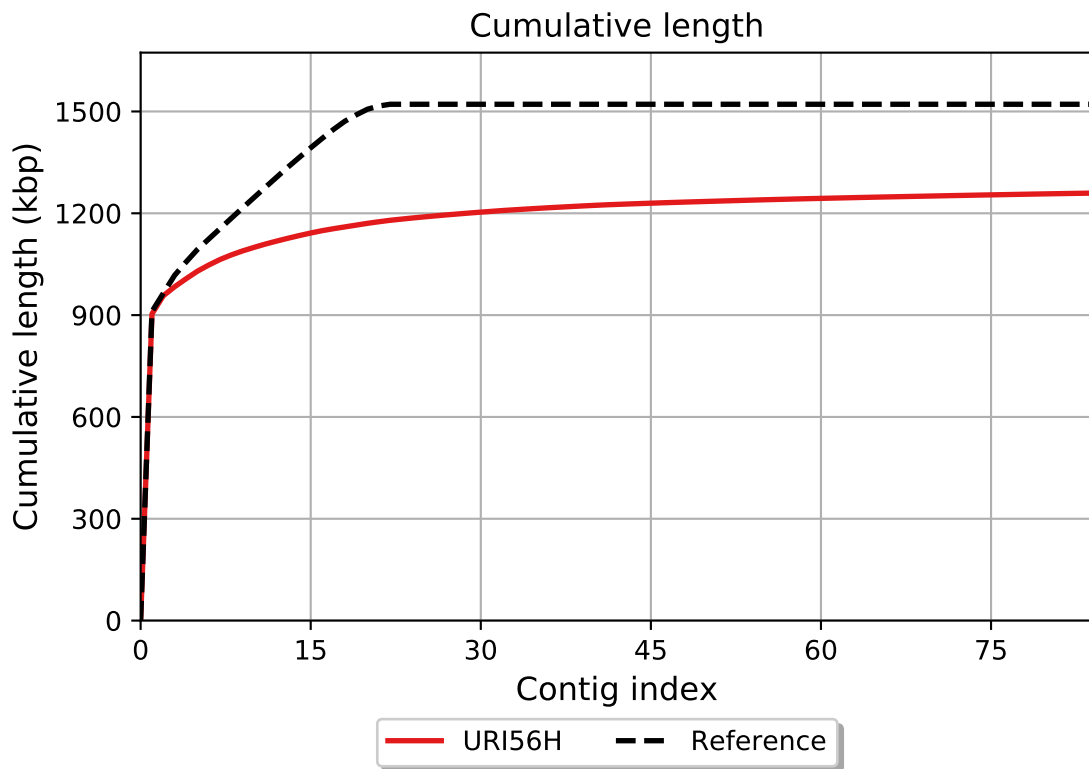


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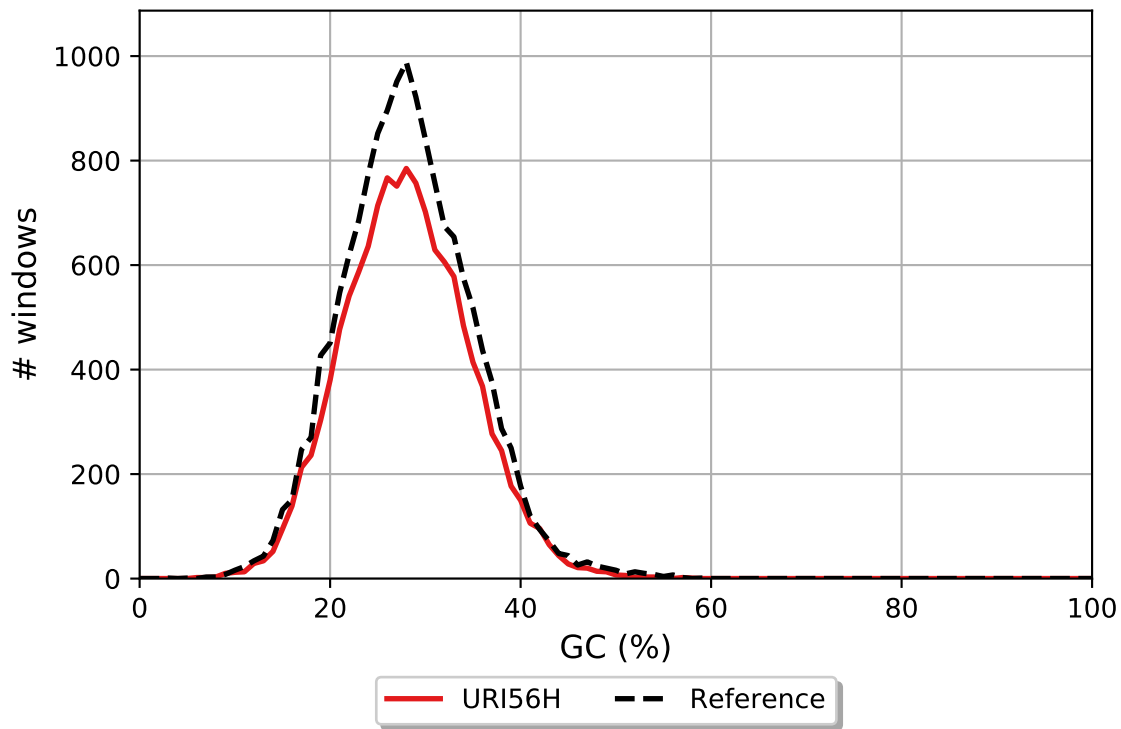
NGx



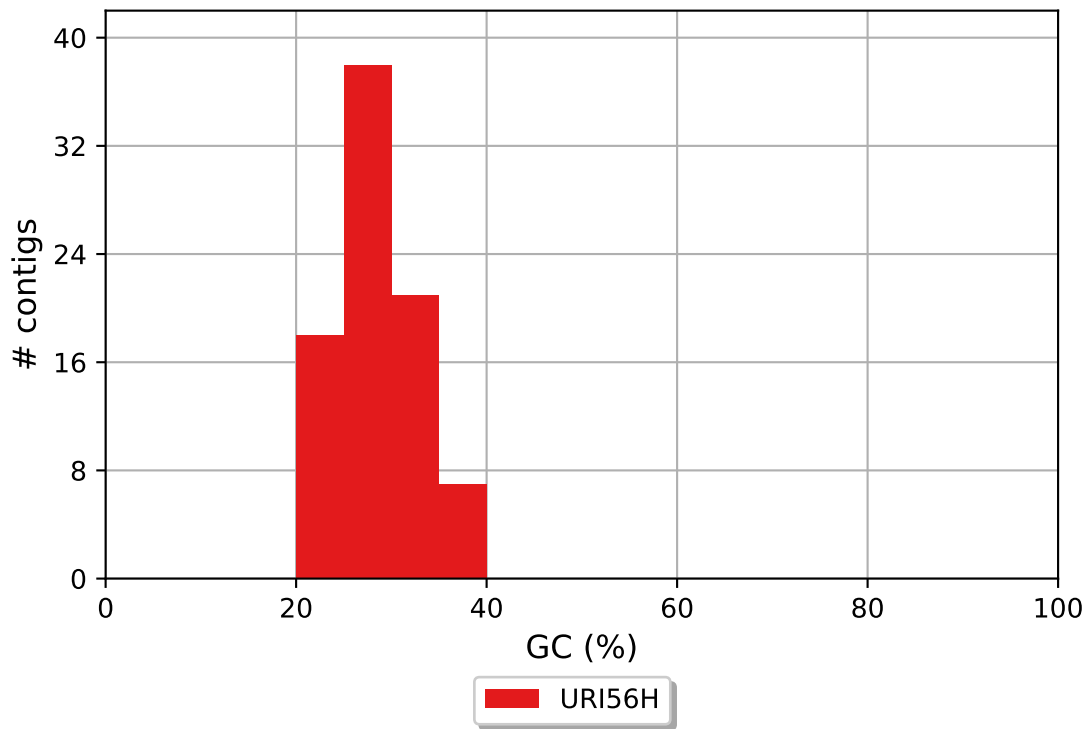
URI56H



GC content

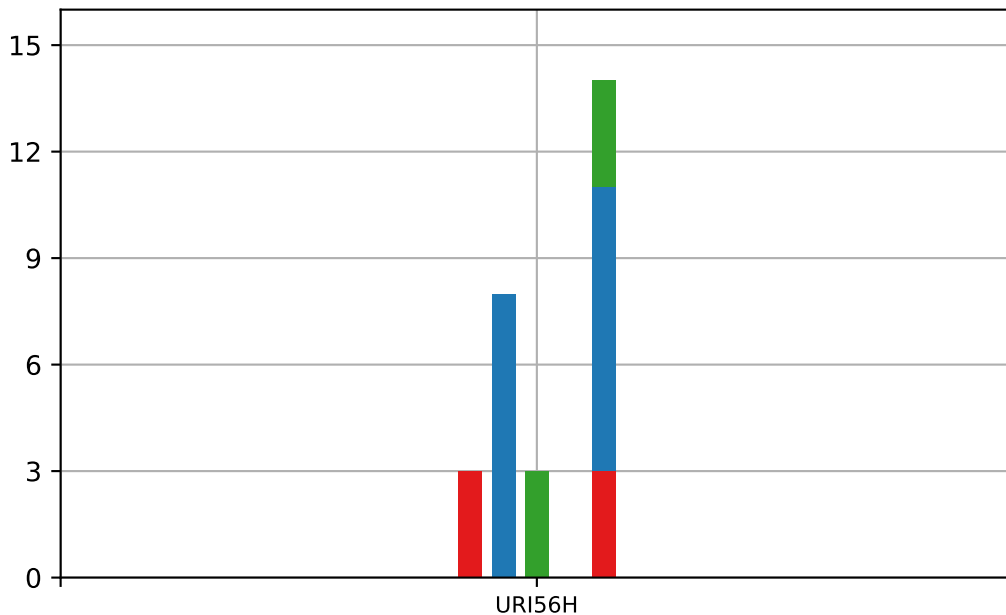


URI56H GC content





## Misassemblies



# relocations

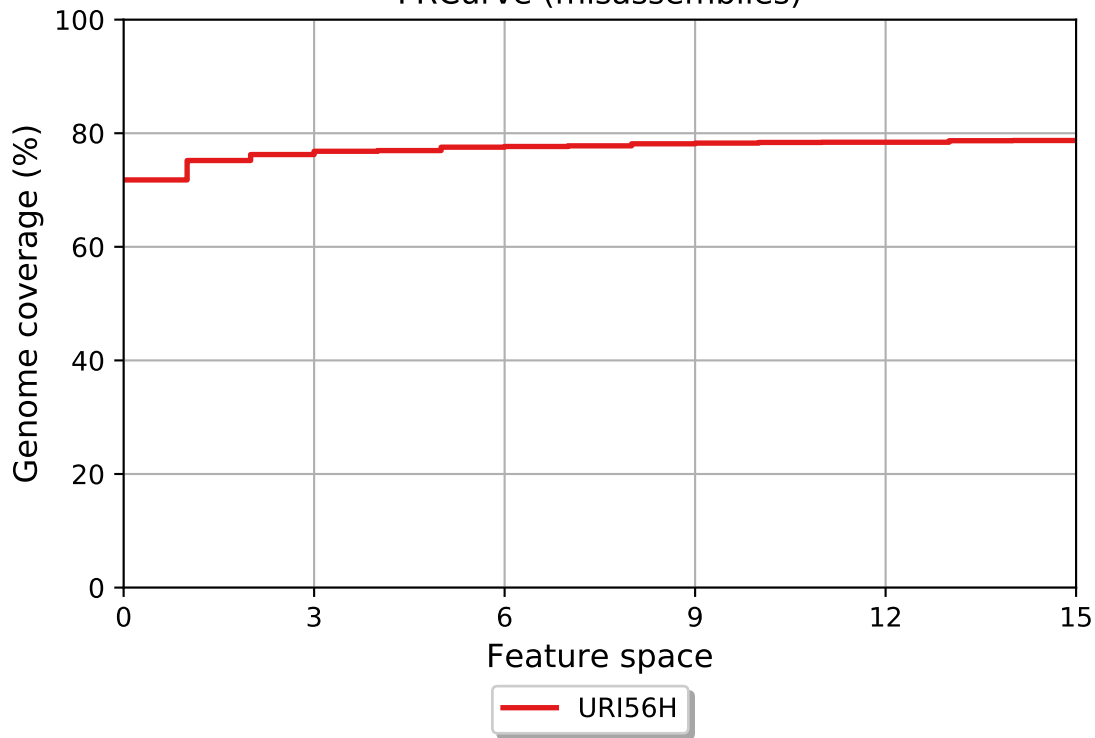


# translocations

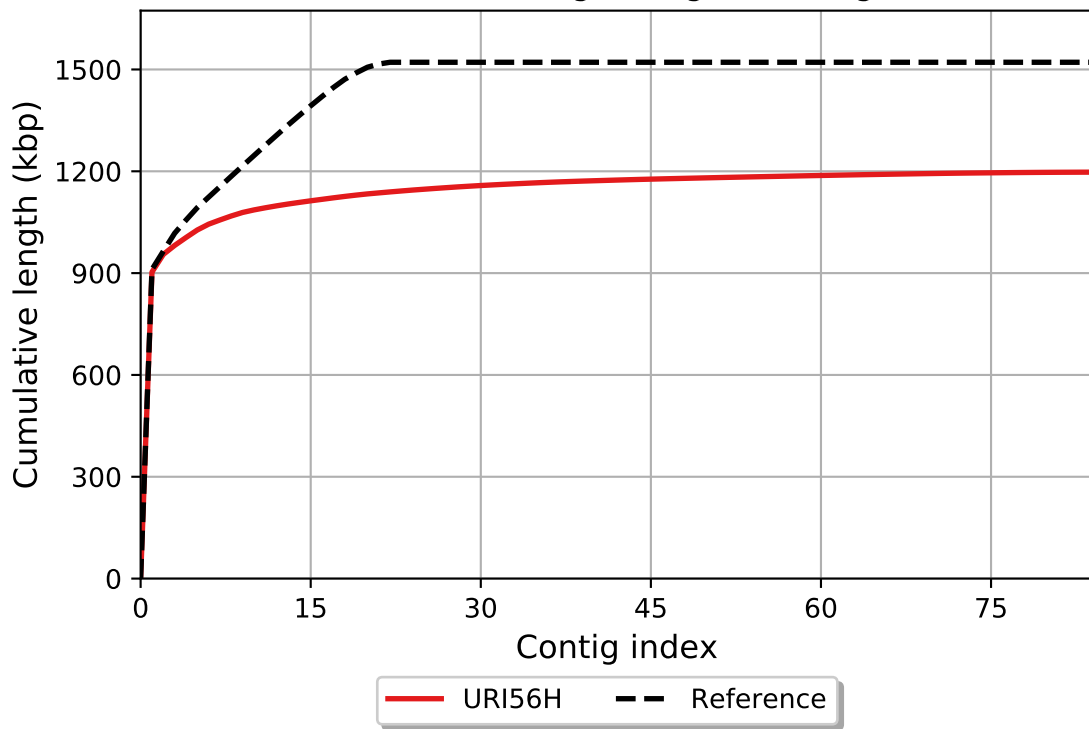


# inversions

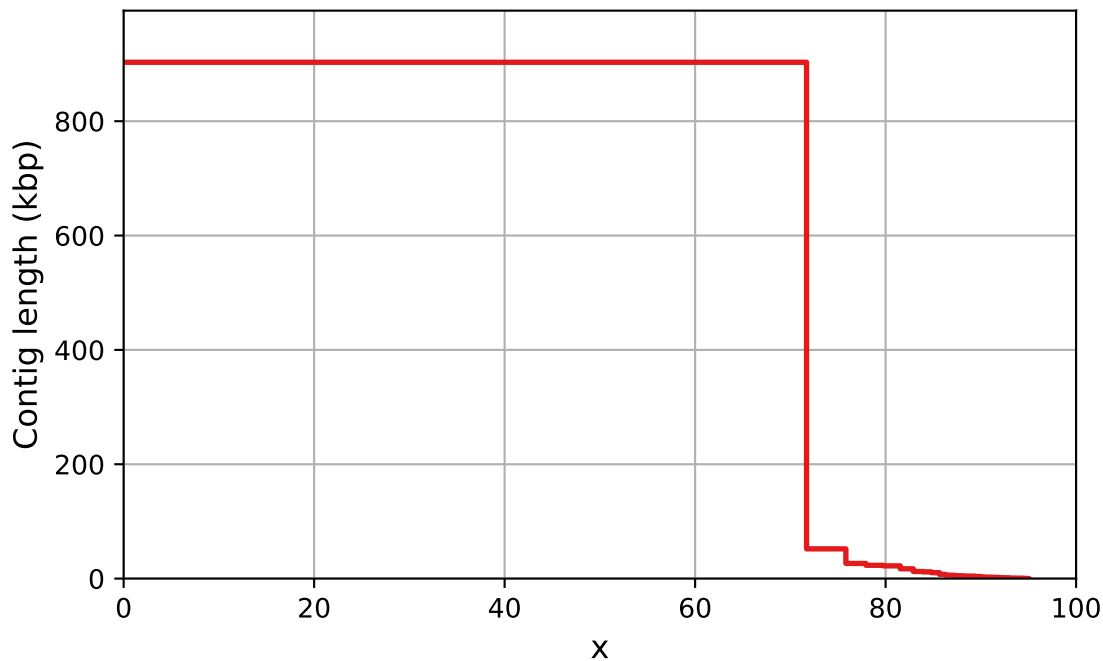
FRCurve (misassemblies)



Cumulative length (aligned contigs)

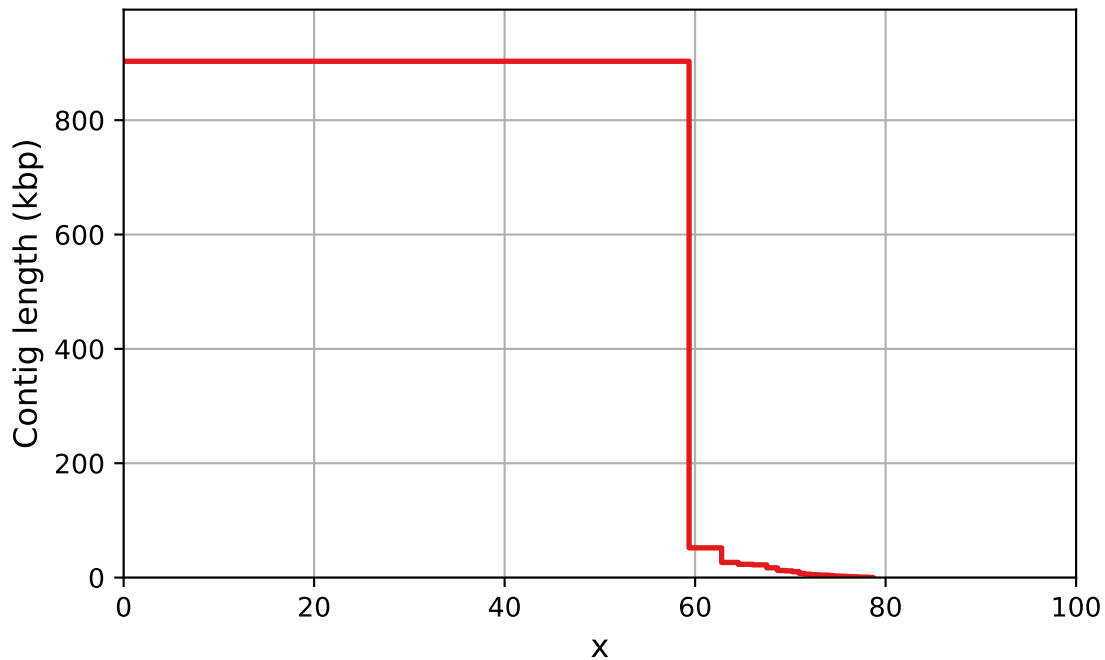


NAx

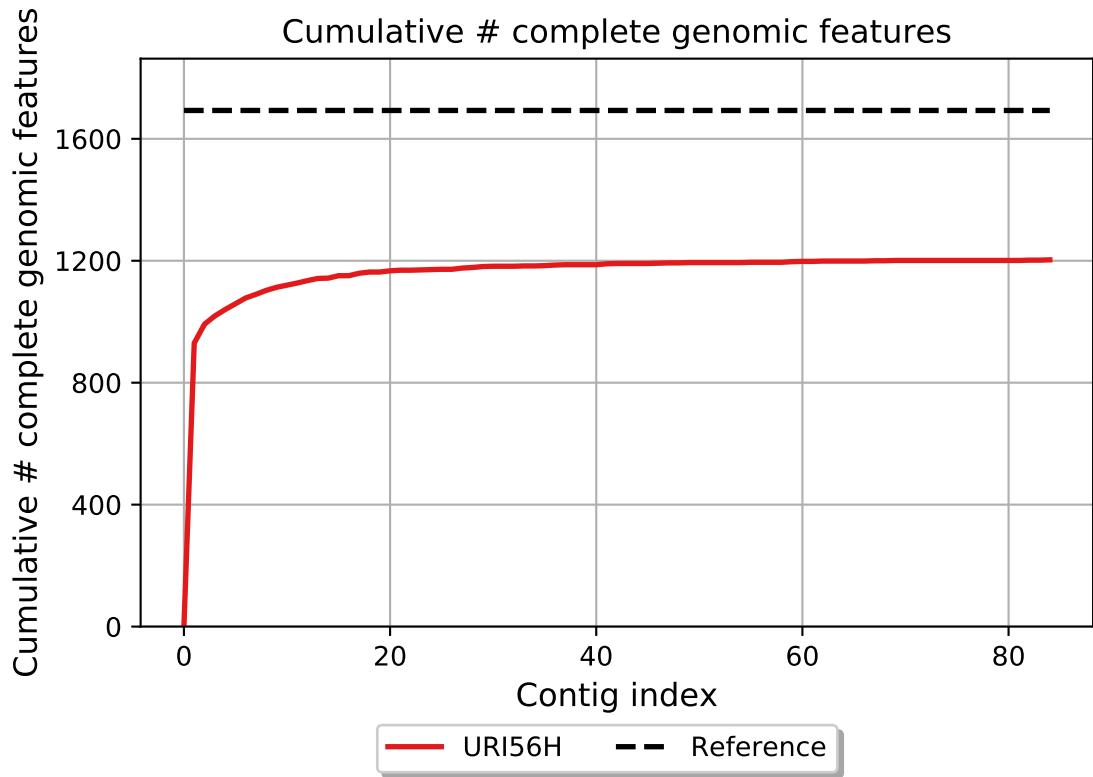


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# NGAx



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FRCurve (genomic features)

