

Report

	URI36H
# contigs (>= 0 bp)	53
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1482383
Total length (>= 1000 bp)	1470916
Total length (>= 5000 bp)	1463555
Total length (>= 10000 bp)	1454827
Total length (>= 25000 bp)	1308923
Total length (>= 50000 bp)	981497
# contigs	34
Largest contig	927732
Total length	1476993
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	927732
NG50	927732
N90	24799
NG90	23172
auN	593546.1
auNG	576294.2
L50	1
LG50	1
L90	14
LG90	16
# misassemblies	39
# misassembled contigs	16
Misassembled contigs length	1339384
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	11 + 17 part
Unaligned length	124272
Genome fraction (%)	82.581
Duplication ratio	1.074
# N's per 100 kbp	0.00
# mismatches per 100 kbp	973.06
# indels per 100 kbp	63.98
# genomic features	1295 + 53 part
Largest alignment	903450
Total aligned length	1348941
NA50	903450
NGA50	903450
NA90	1976
NGA90	-
auNA	558503.2
auNGA	542269.9
LA50	1
LGA50	1
LA90	42
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

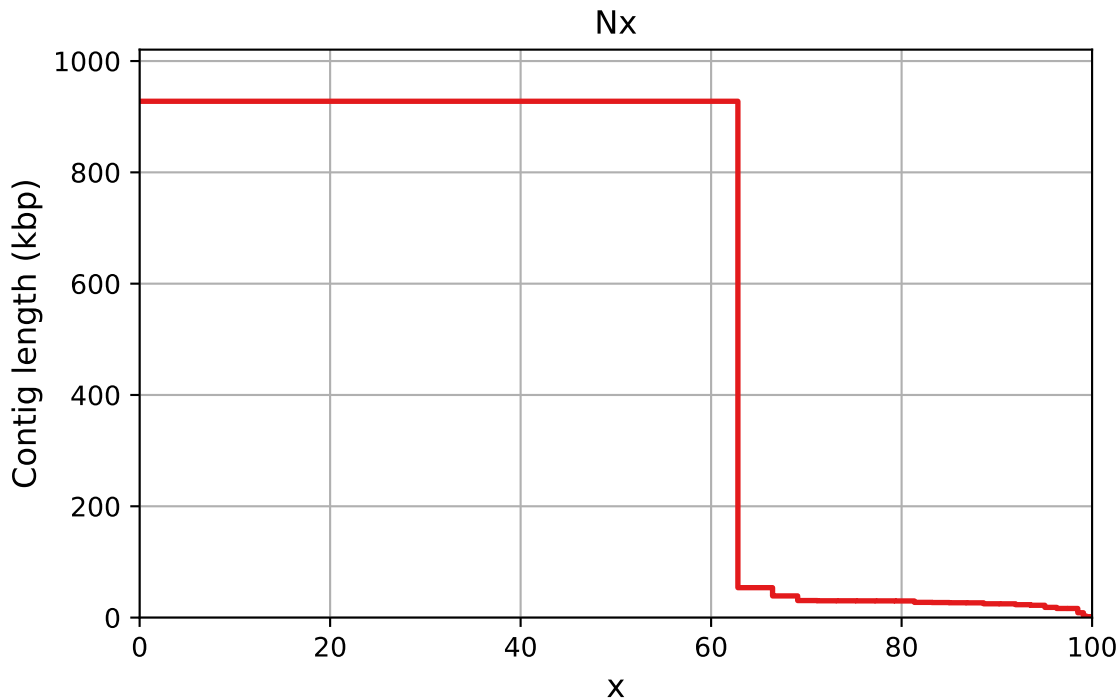
	URI36H
# misassemblies	39
# contig misassemblies	39
# c. relocations	6
# c. translocations	31
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	16
Misassembled contigs length	1339384
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	13126
# indels	863
# indels (<= 5 bp)	771
# indels (> 5 bp)	92
Indels length	3988

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

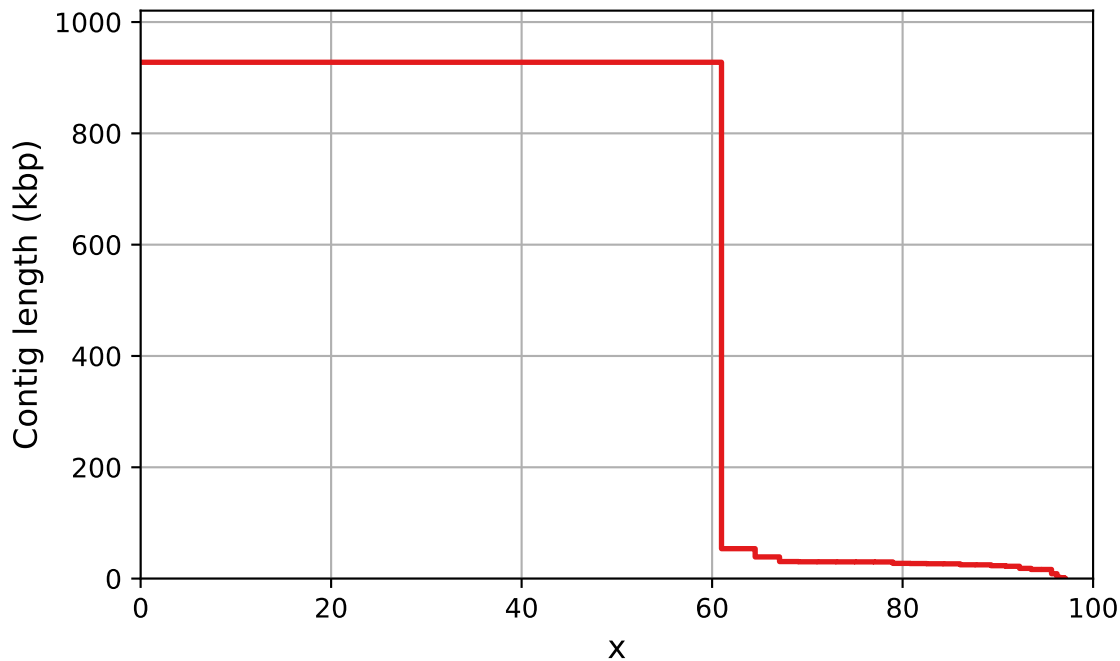
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# fully unaligned contigs	11
Fully unaligned length	8315
# partially unaligned contigs	17
Partially unaligned length	115957
# N's	0

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).

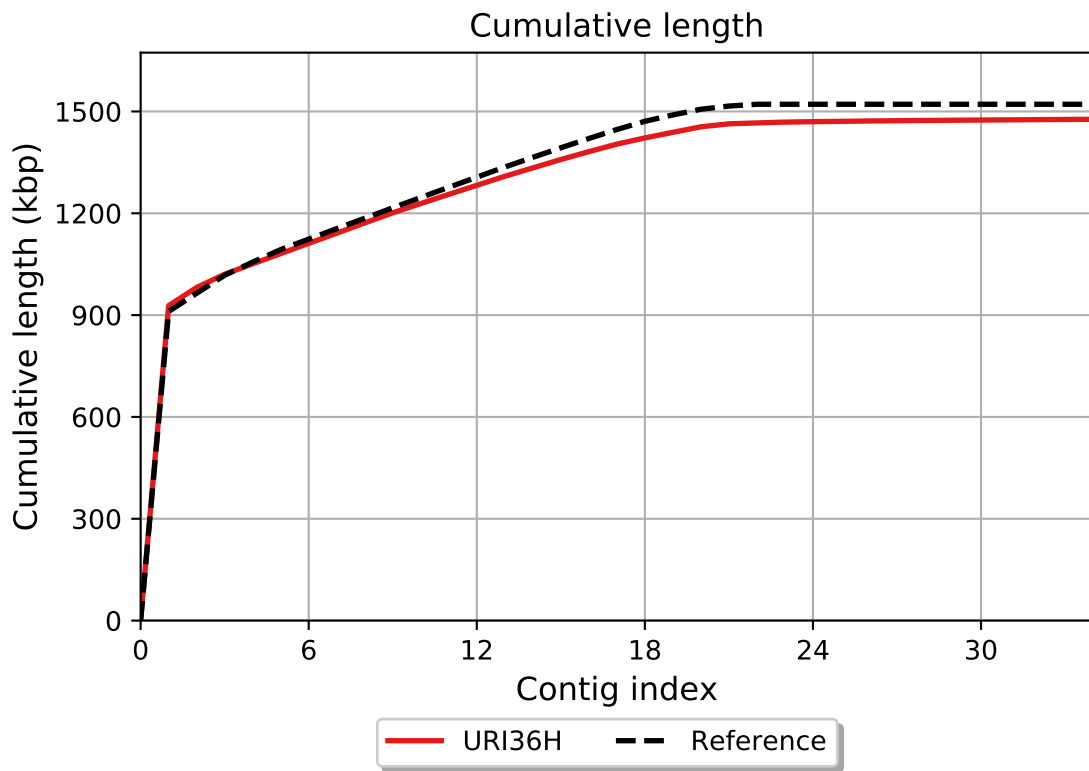


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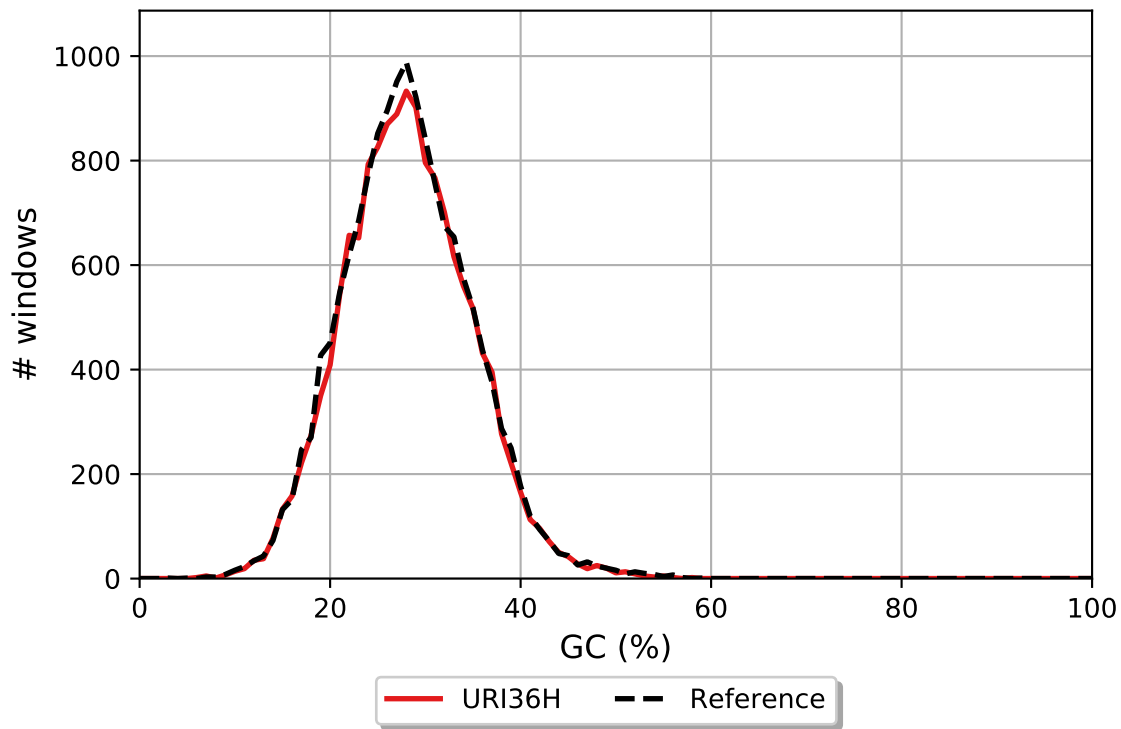
NGx



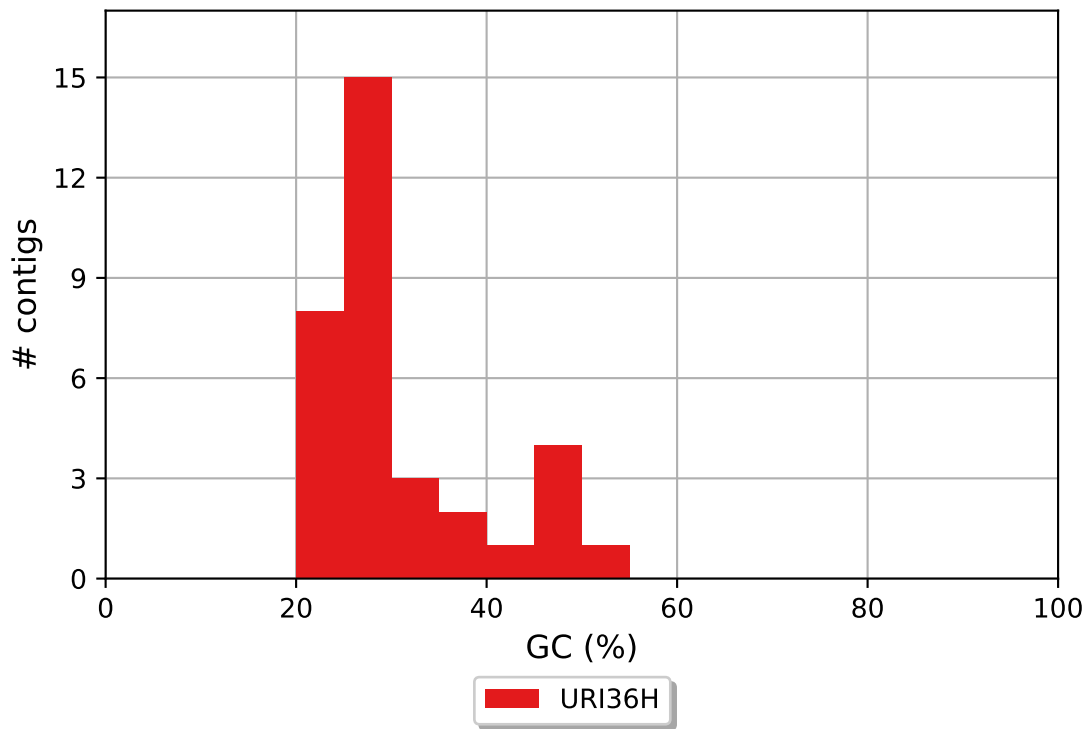
URI36H



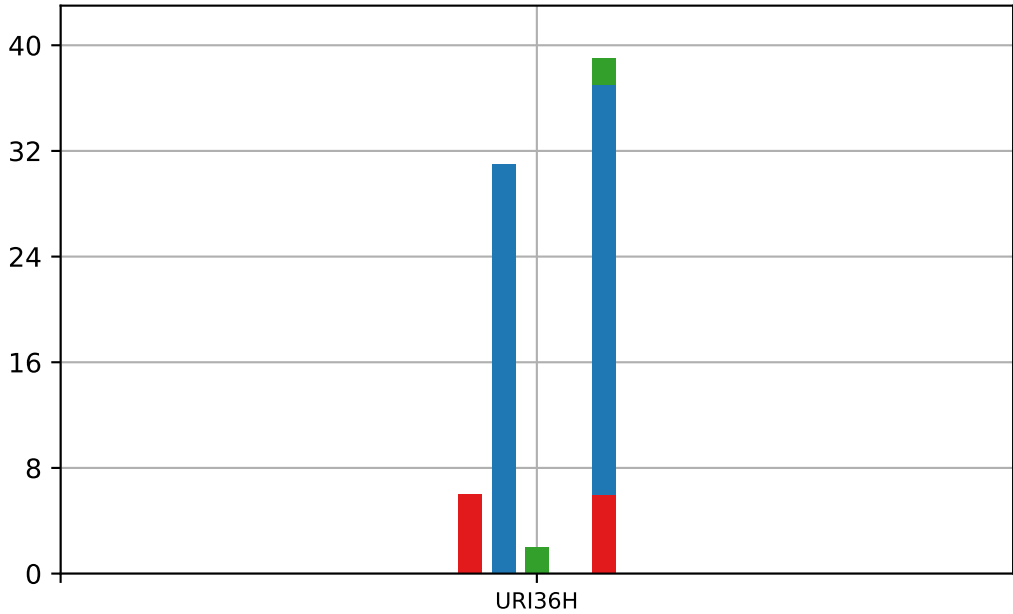
GC content



URI36H GC content



Misassemblies



relocations

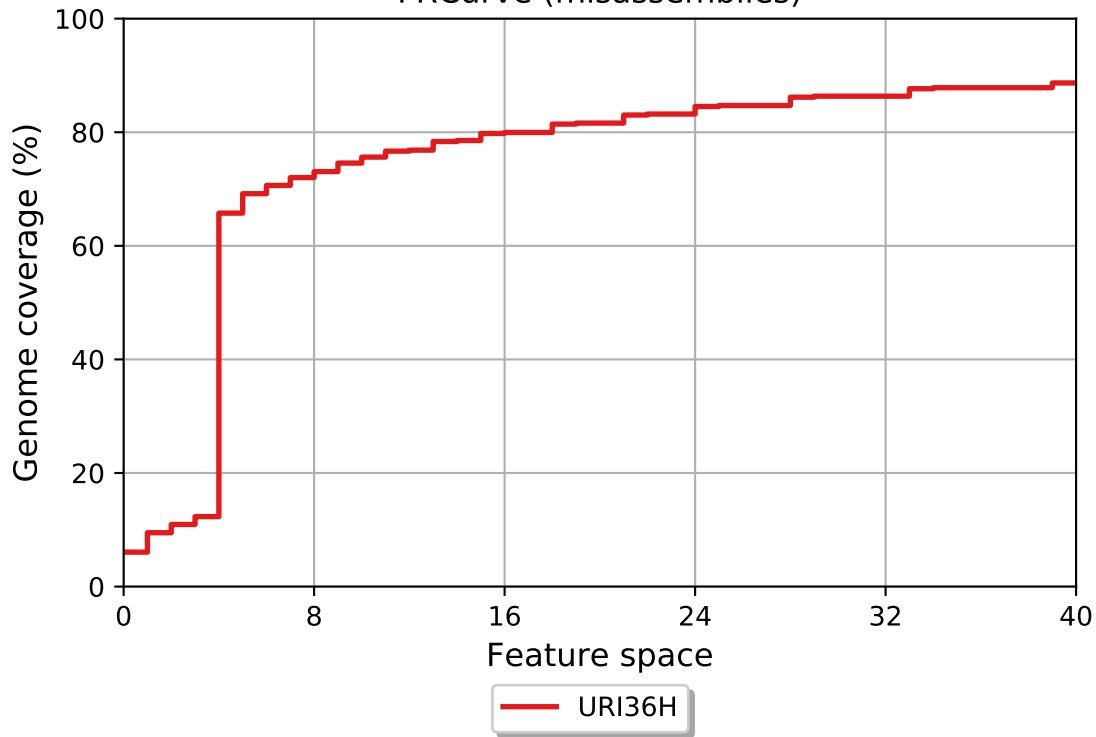


translocations

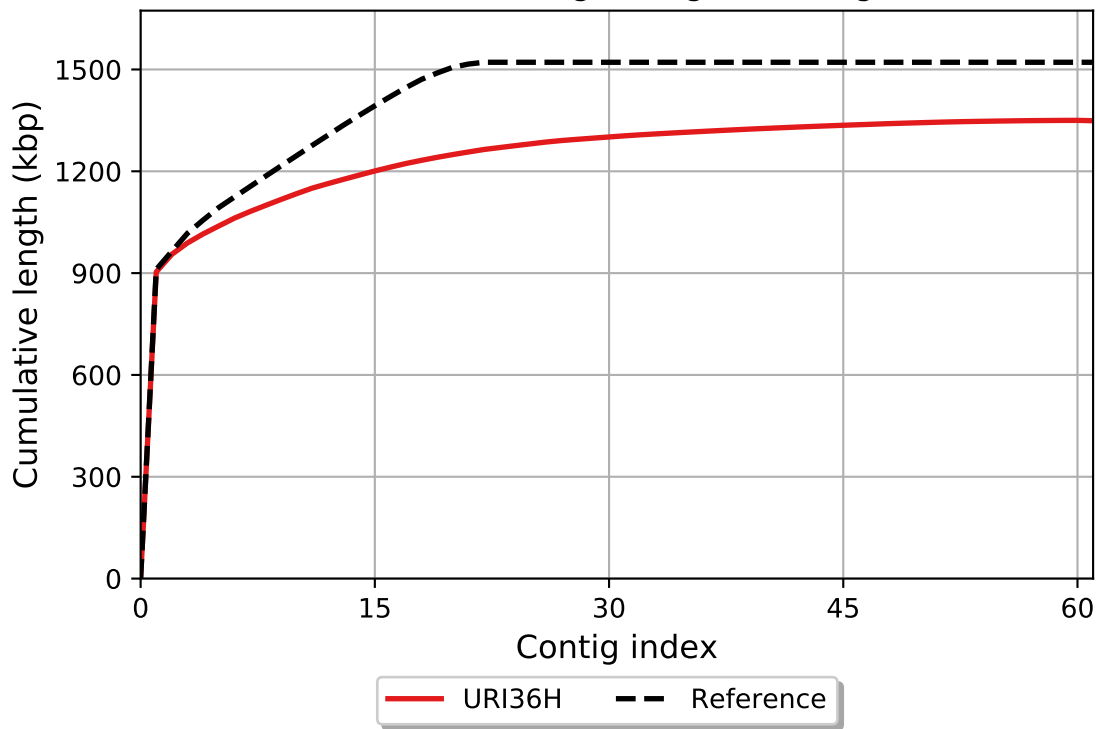


inversions

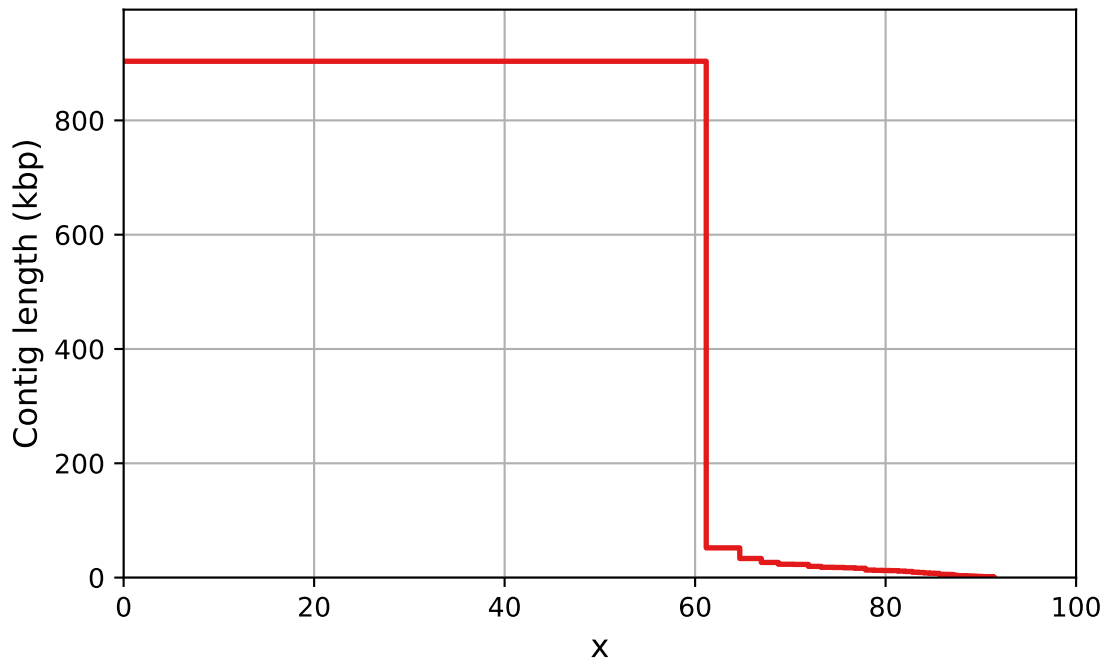
FRCurve (misassemblies)



Cumulative length (aligned contigs)

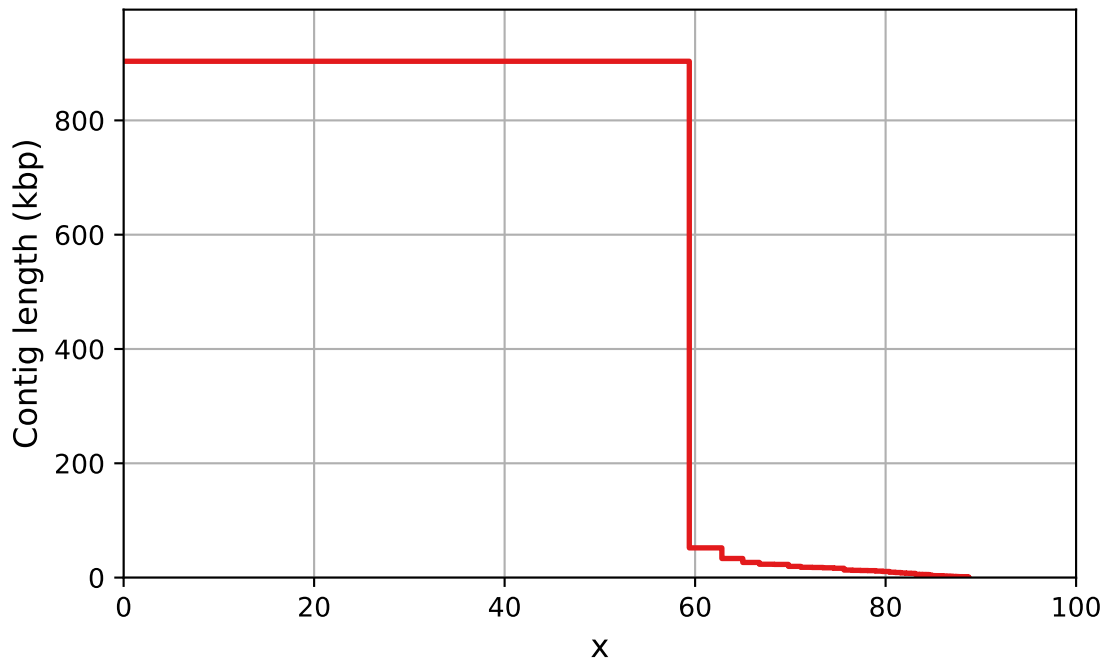


NAx

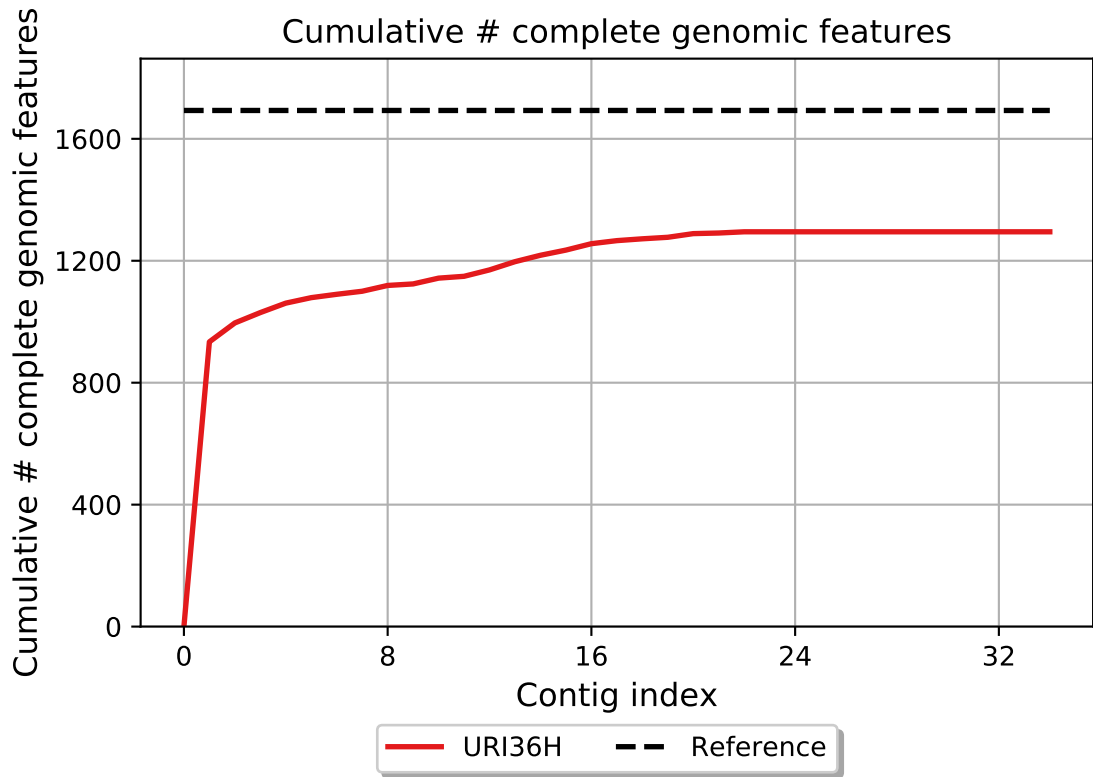


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NGAx



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FRCurve (genomic features)

