

Report

	URI41H
# contigs (>= 0 bp)	84
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1468867
Total length (>= 1000 bp)	1447925
Total length (>= 5000 bp)	1441808
Total length (>= 10000 bp)	1441808
Total length (>= 25000 bp)	1404162
Total length (>= 50000 bp)	1028130
# contigs	34
Largest contig	914354
Total length	1457112
Reference length	1521208
GC (%)	28.25
Reference GC (%)	28.18
N50	914354
NG50	914354
N90	29838
NG90	26498
auN	587000.6
auNG	562267.3
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	13
# misassembled contigs	5
Misassembled contigs length	198557
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 4 part
Unaligned length	22425
Genome fraction (%)	91.732
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	166.82
# indels per 100 kbp	22.52
# genomic features	1509 + 42 part
Largest alignment	910732
Total aligned length	1429648
NA50	910732
NGA50	910732
NA90	19399
NGA90	13215
auNA	578990.2
auNGA	554594.5
LA50	1
LGA50	1
LA90	15
LGA90	18

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

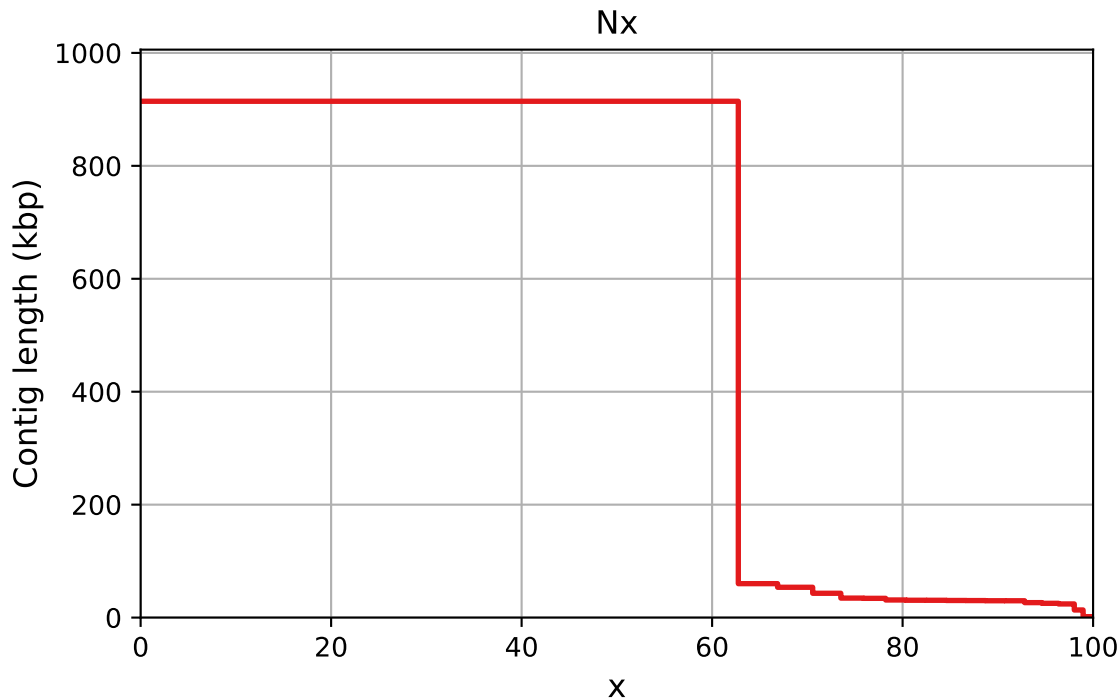
	URI41H
# misassemblies	13
# contig misassemblies	13
# c. relocations	4
# c. translocations	7
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	198557
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	2385
# indels	322
# indels (<= 5 bp)	269
# indels (> 5 bp)	53
Indels length	3488

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

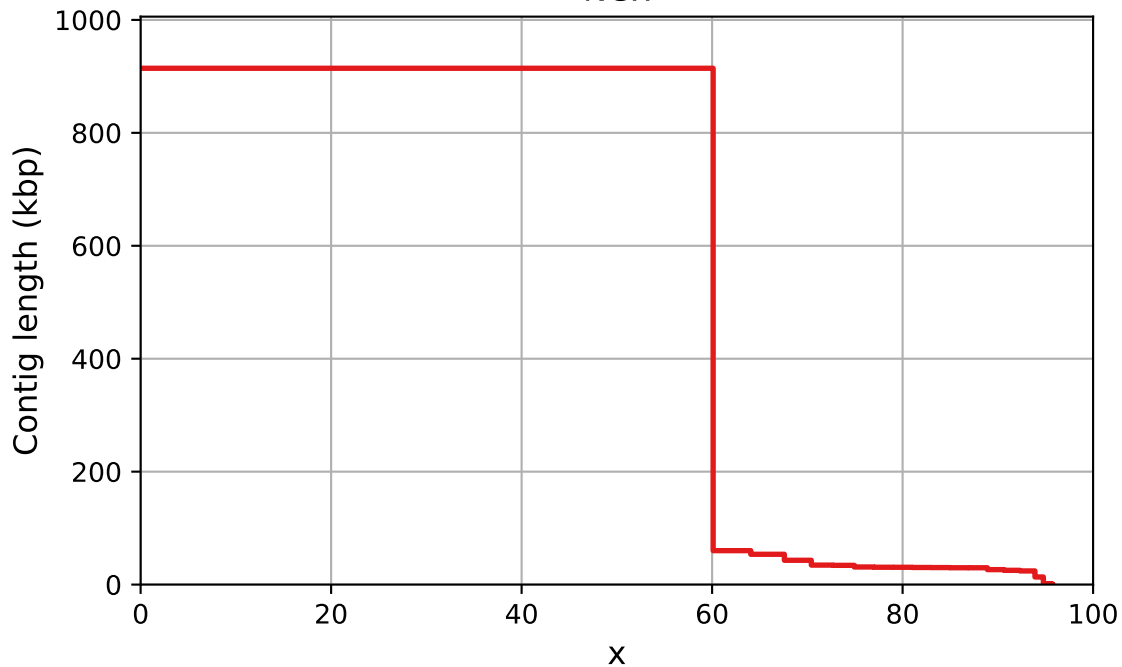
	URI41H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	22425
# N's	0

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).

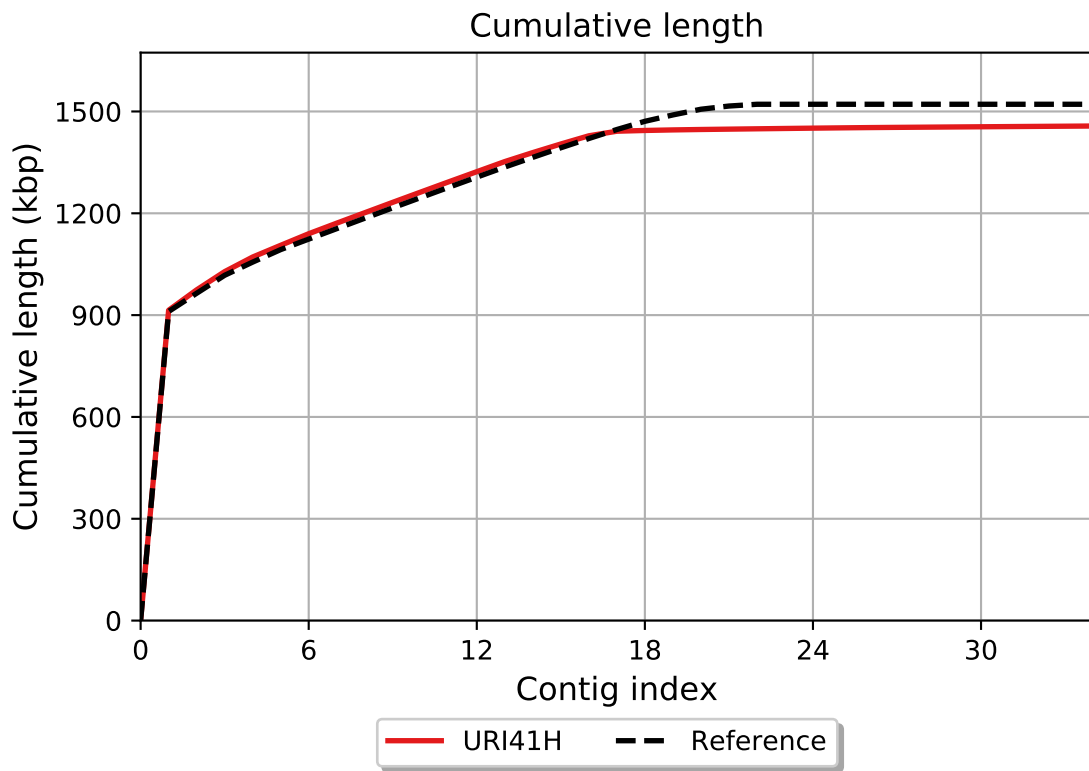


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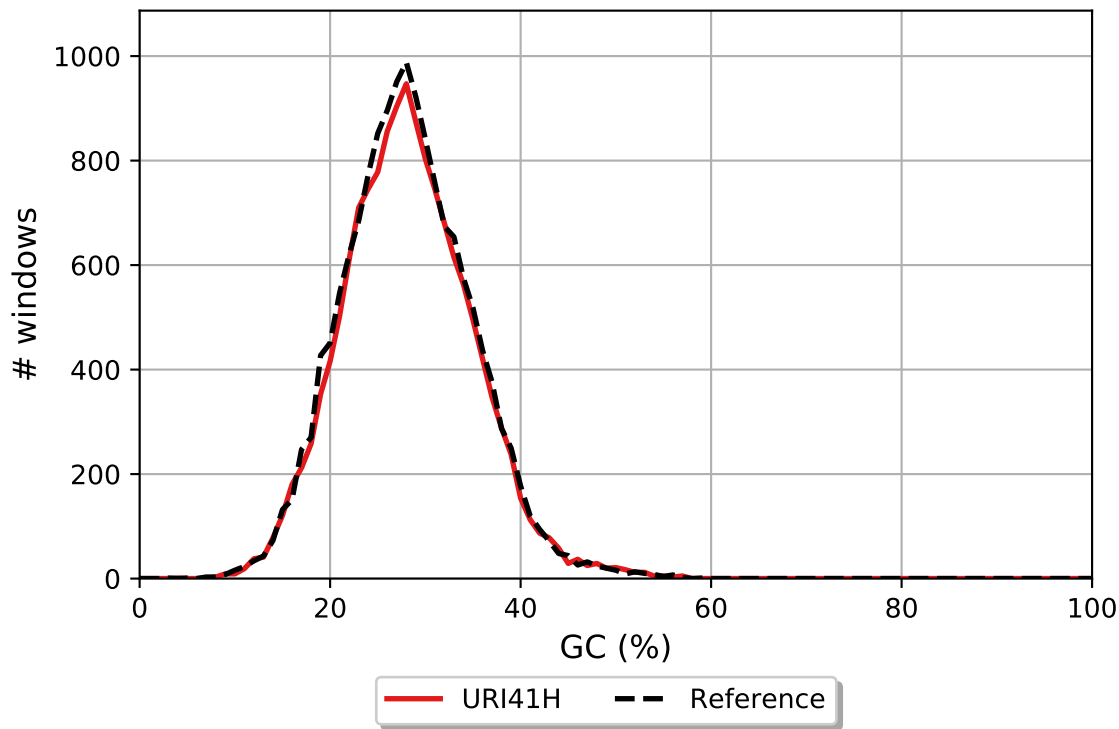
NGx



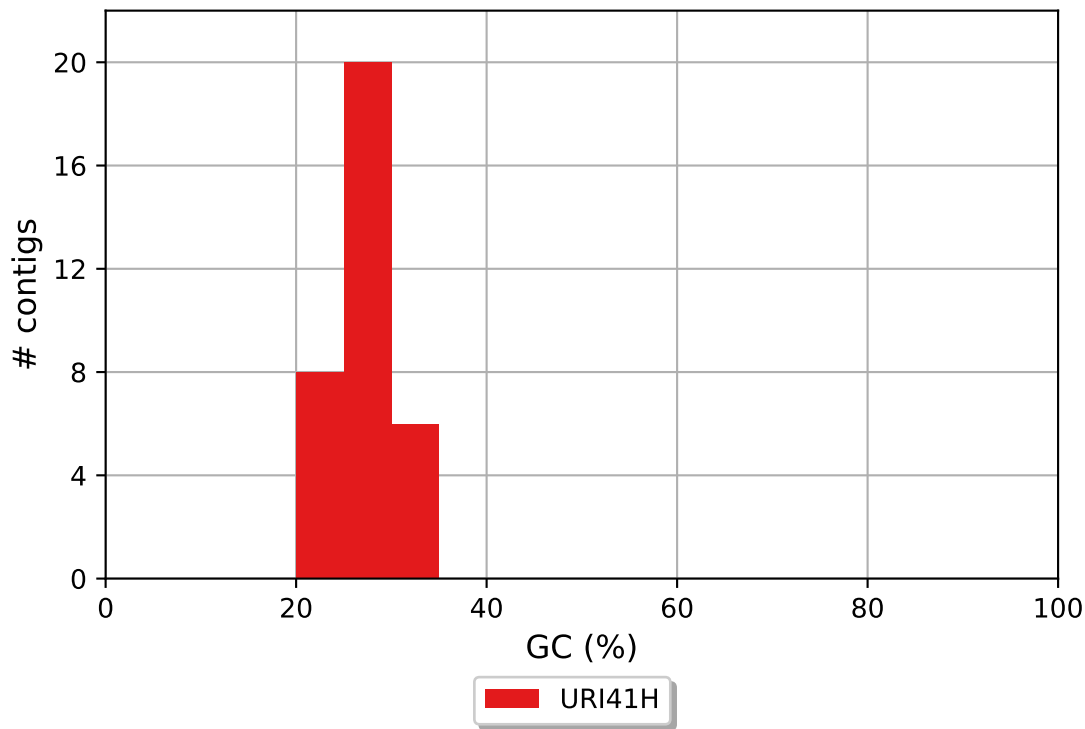
URI41H



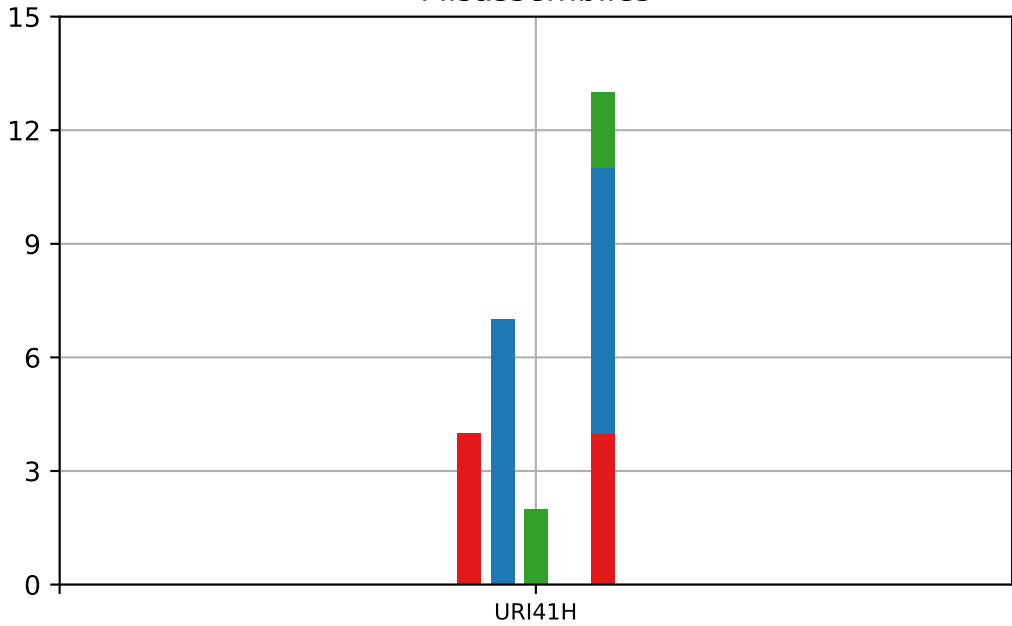
GC content



URI41H GC content



Misassemblies



relocations

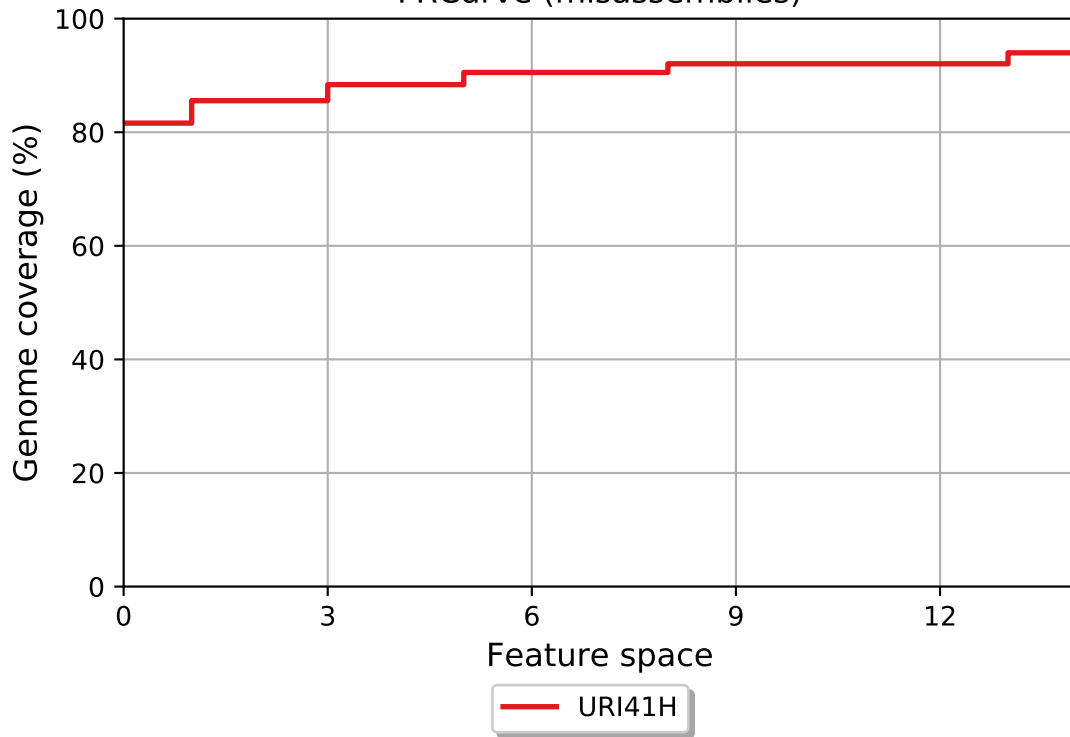


translocations

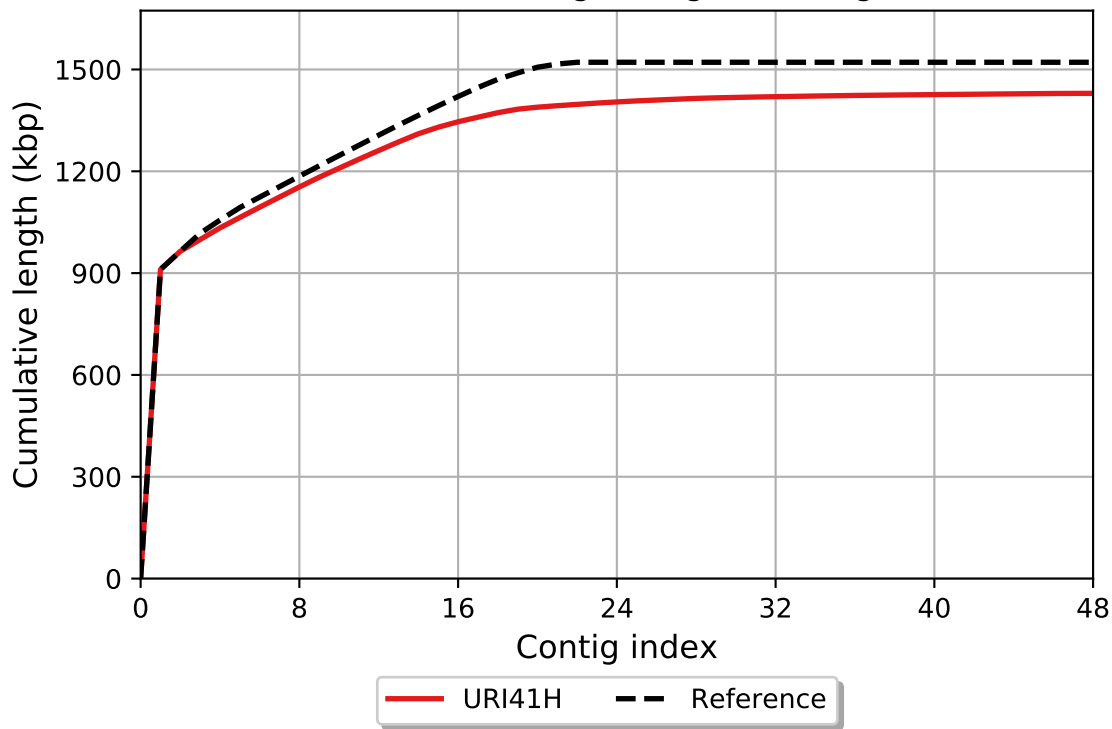


inversions

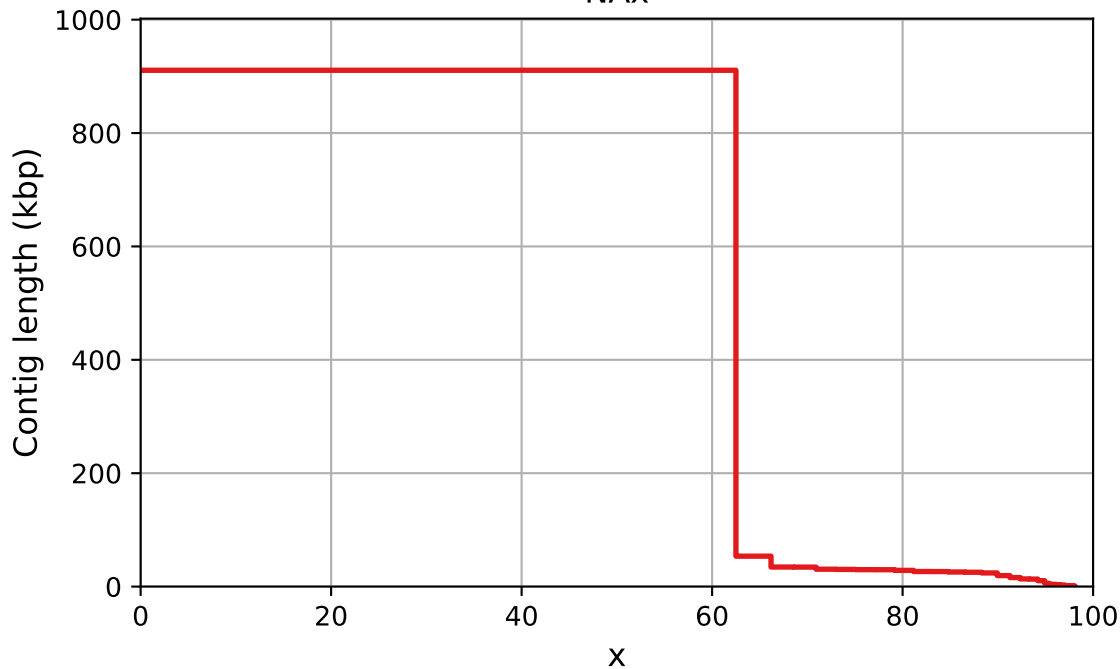
FRCurve (misassemblies)



Cumulative length (aligned contigs)

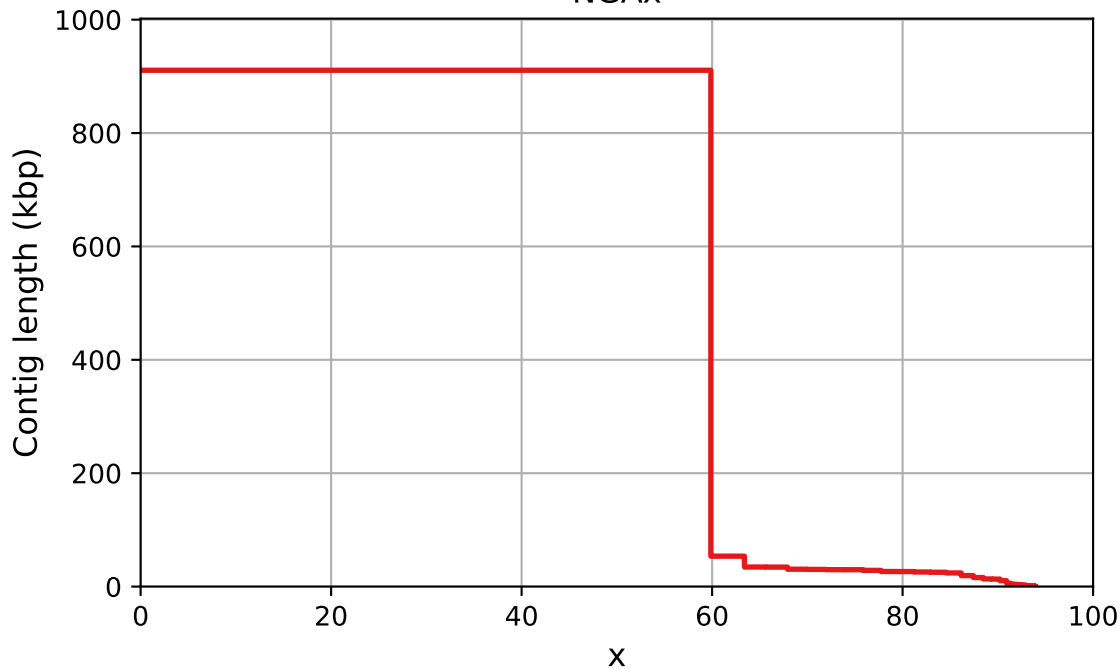


NAx

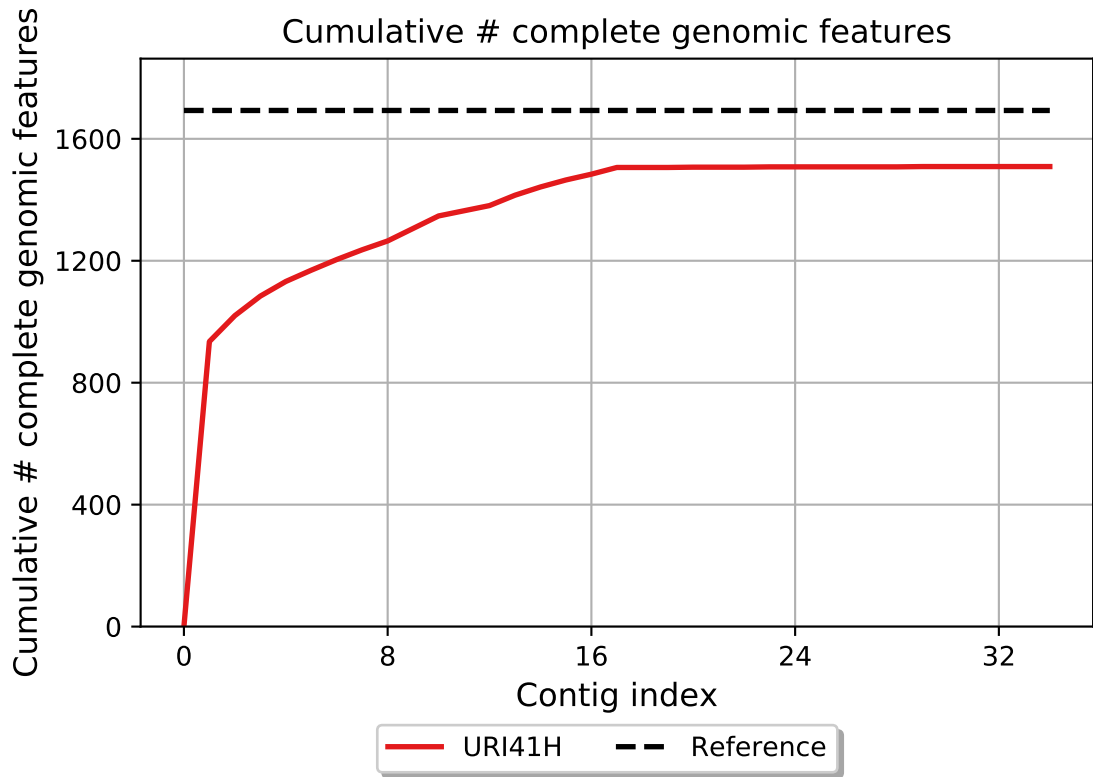


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NGAx



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FRCurve (genomic features)

