Report

	URI118H
# contigs (>= 0 bp)	109
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1380118
Total length (>= 1000 bp)	1351956
Total length (>= 5000 bp)	1343032
Total length (>= 10000 bp)	1329643
Total length (>= 25000 bp)	1231478
Total length (>= 50000 bp)	974805
# contigs	40
Largest contig	920957
Total length	1363534
Reference length	1521208
GC (%)	28.20
Reference GC (%)	28.18
N50	920957
NG50	920957
N90	26073
NG90	-
auN	631071.1
auNG	565660.3
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	21
# misassembled contigs	11
Misassembled contigs length	1180331
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	7 + 15 part
Unaligned length	144888
Genome fraction (%)	78.827
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	777.62
# indels per 100 kbp	48.77
# genomic features	1253 + 54 part
Largest alignment	905370
Total aligned length	1213829
NA50	905370
NGA50	905370
NA90	-
NGA90	-
auNA	605306.7
auNGA	542566.3
LA50	1
LGA50	1
LA90	-
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).
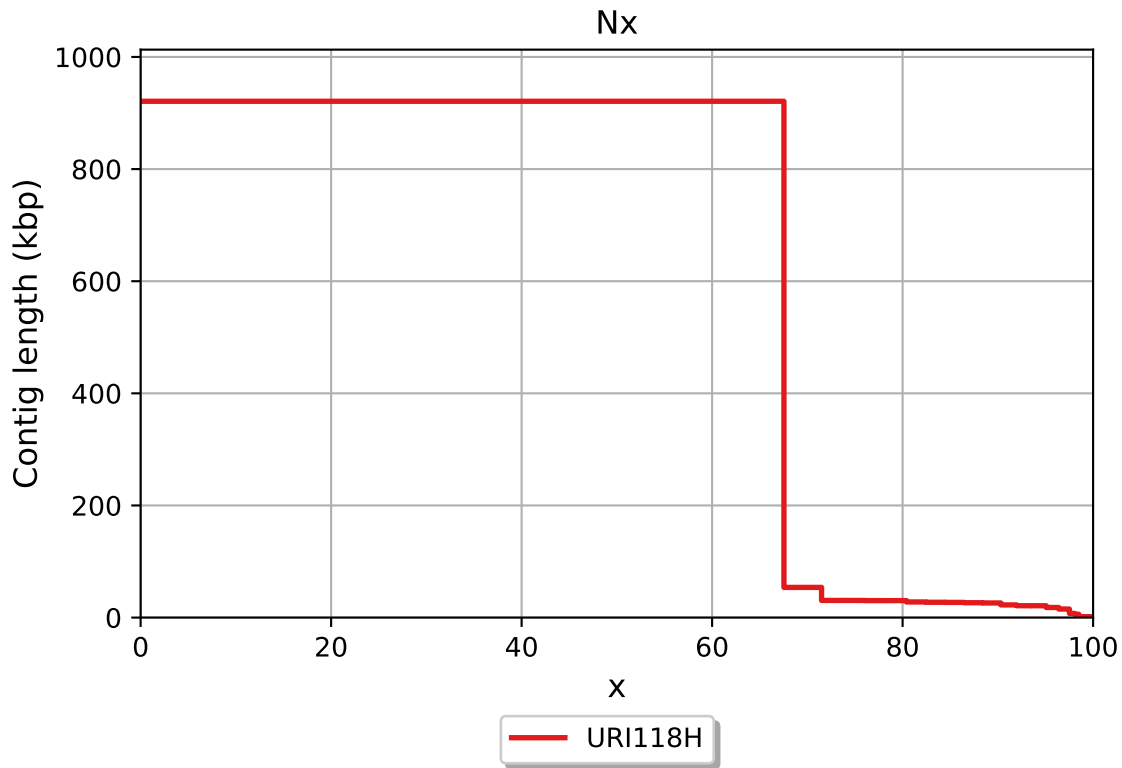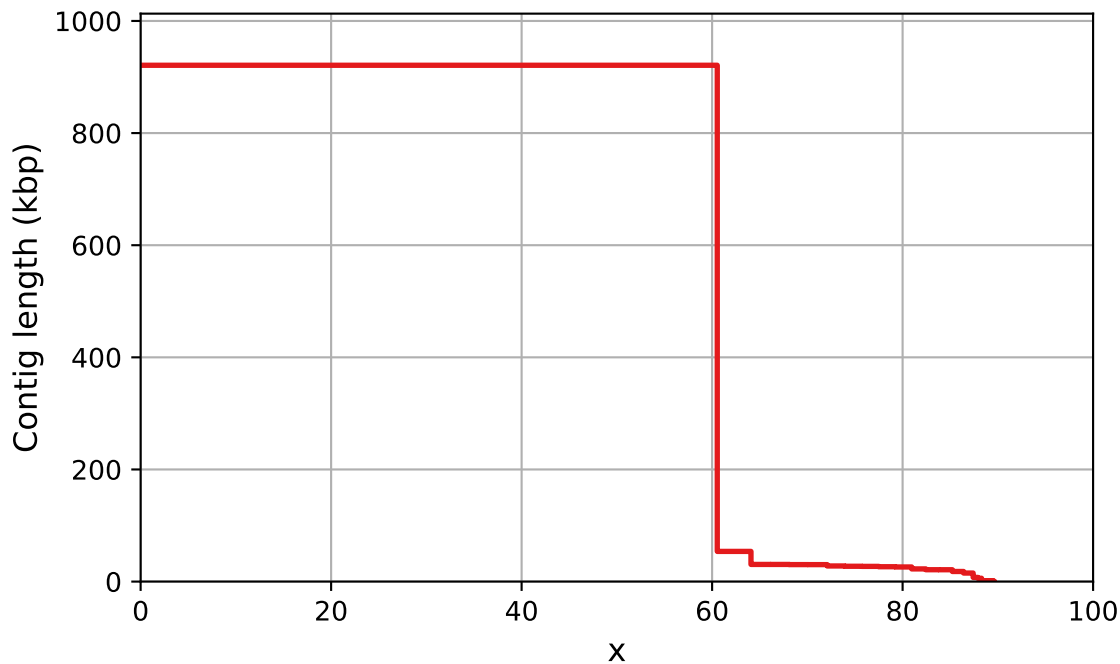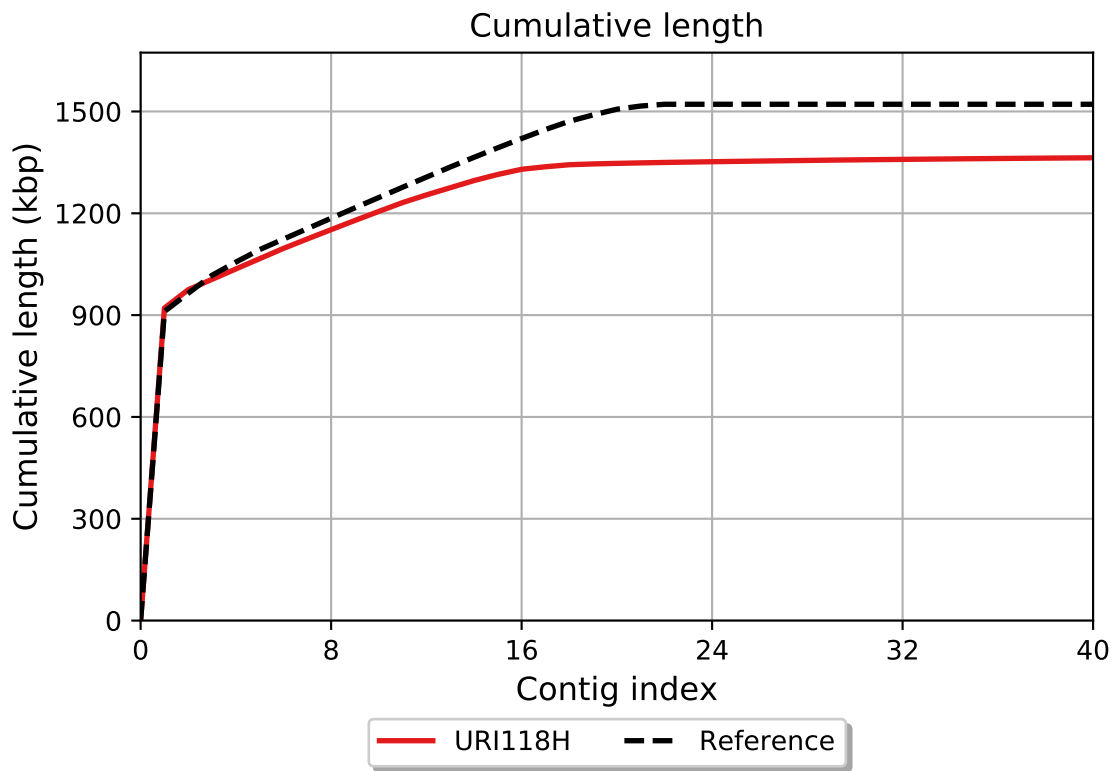
Misassemblies report

	URI118H
# misassemblies	21
# contig misassemblies	21
# c. relocations	6
# c. translocations	13
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1180331
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9439
# indels	592
# indels (<= 5 bp)	529
# indels (> 5 bp)	63
Indels length	3975

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
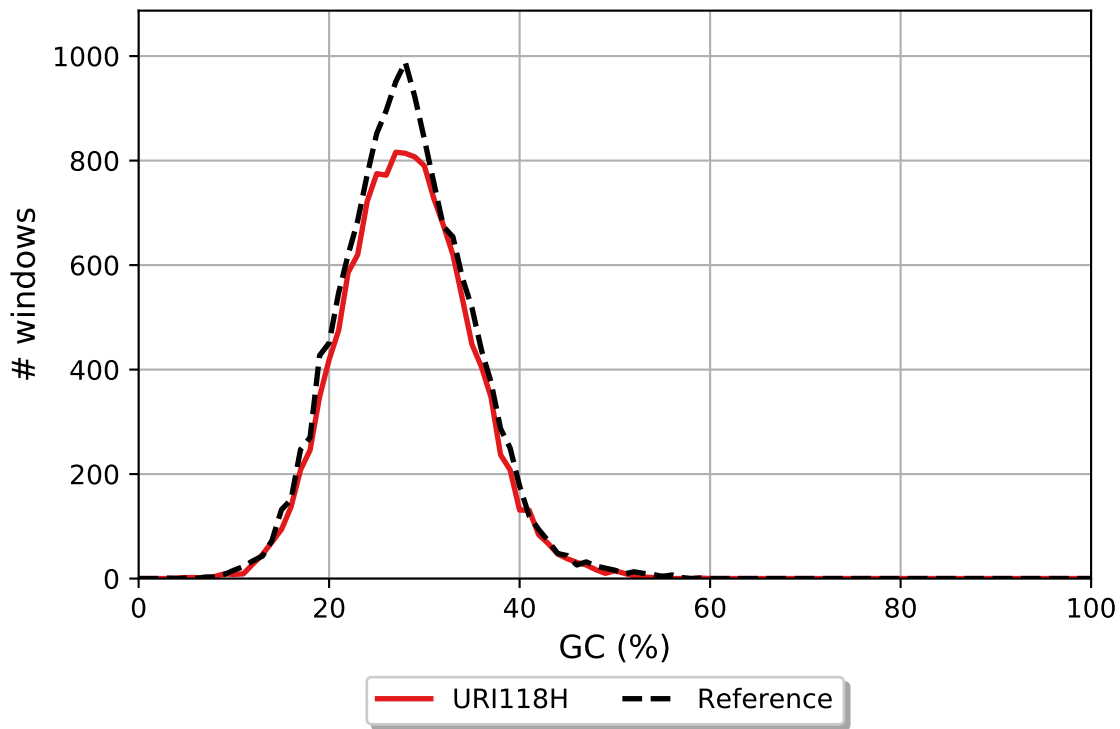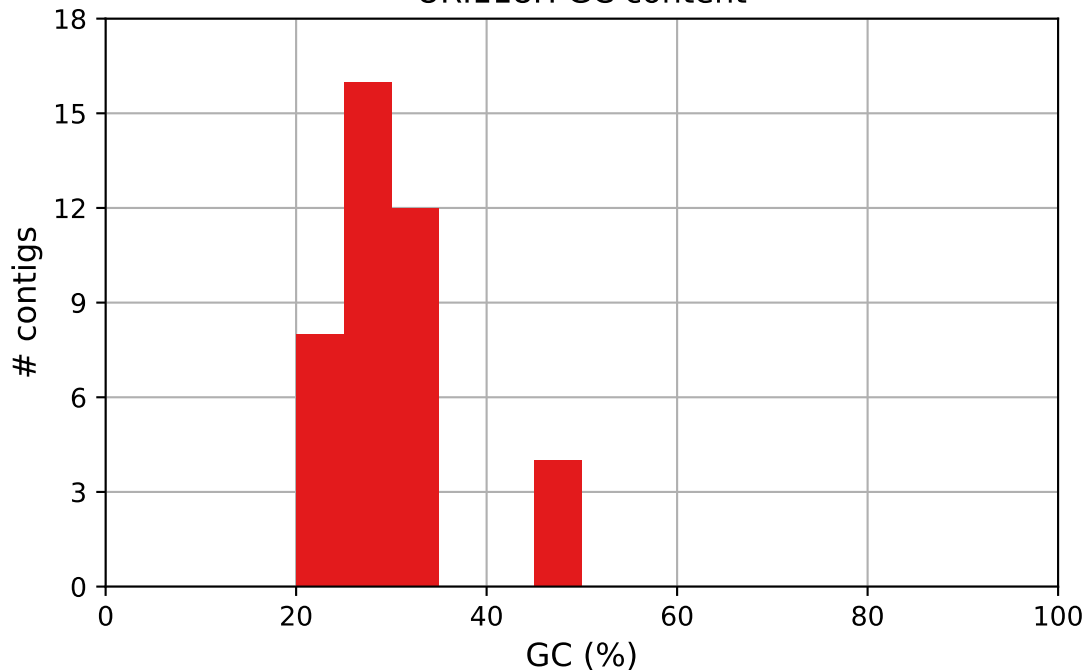
	URI118H
# fully unaligned contigs	7
Fully unaligned length	10984
# partially unaligned contigs	15
Partially unaligned length	133904
# N's	0

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).

Nx

Contig length (kbp) vs x

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NGx

URI118H

Cumulative length

GC content

URI118H GC content

Misassemblies

FRCurve (misassemblies)
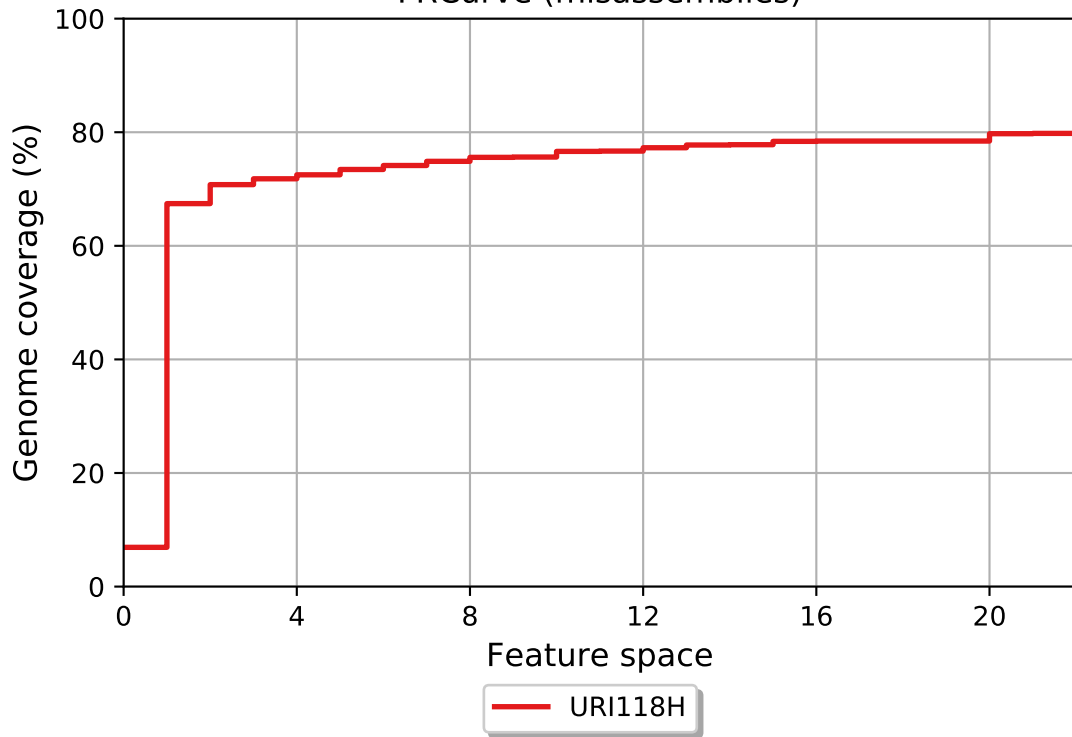
Cumulative length (aligned contigs)

NAx

NGAx

Cumulative # complete genomic features
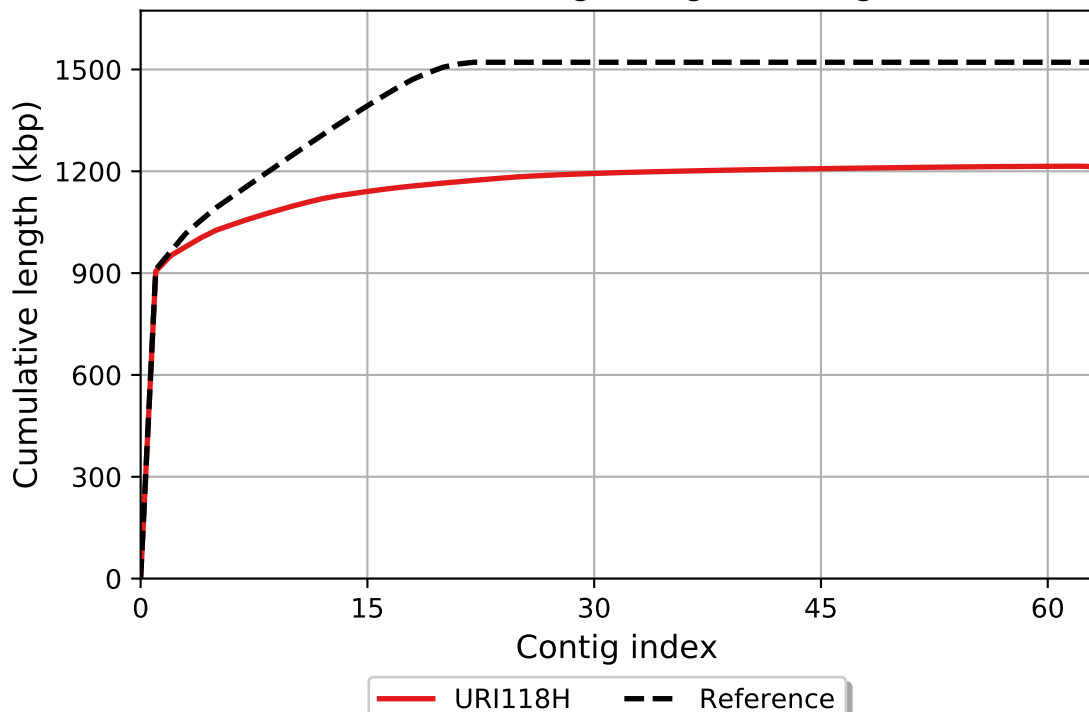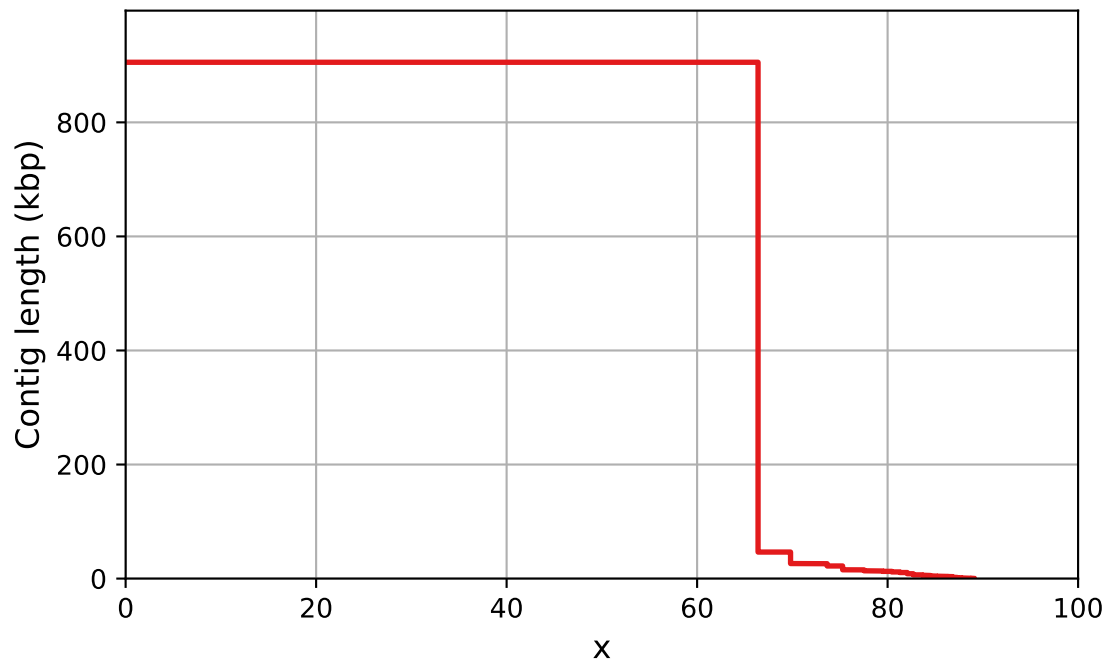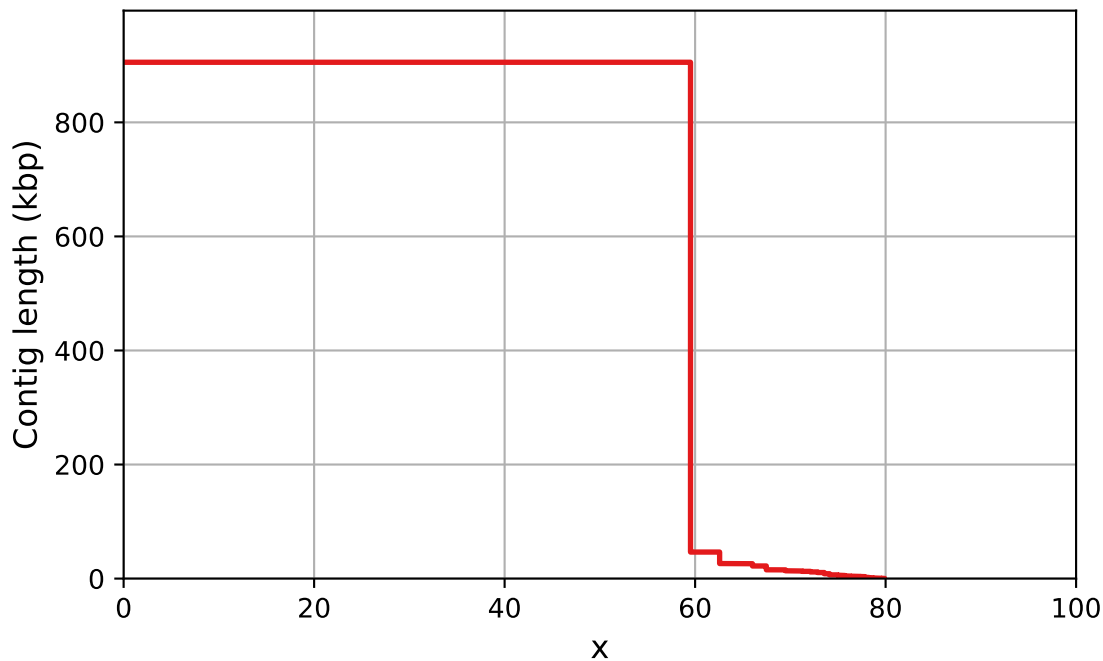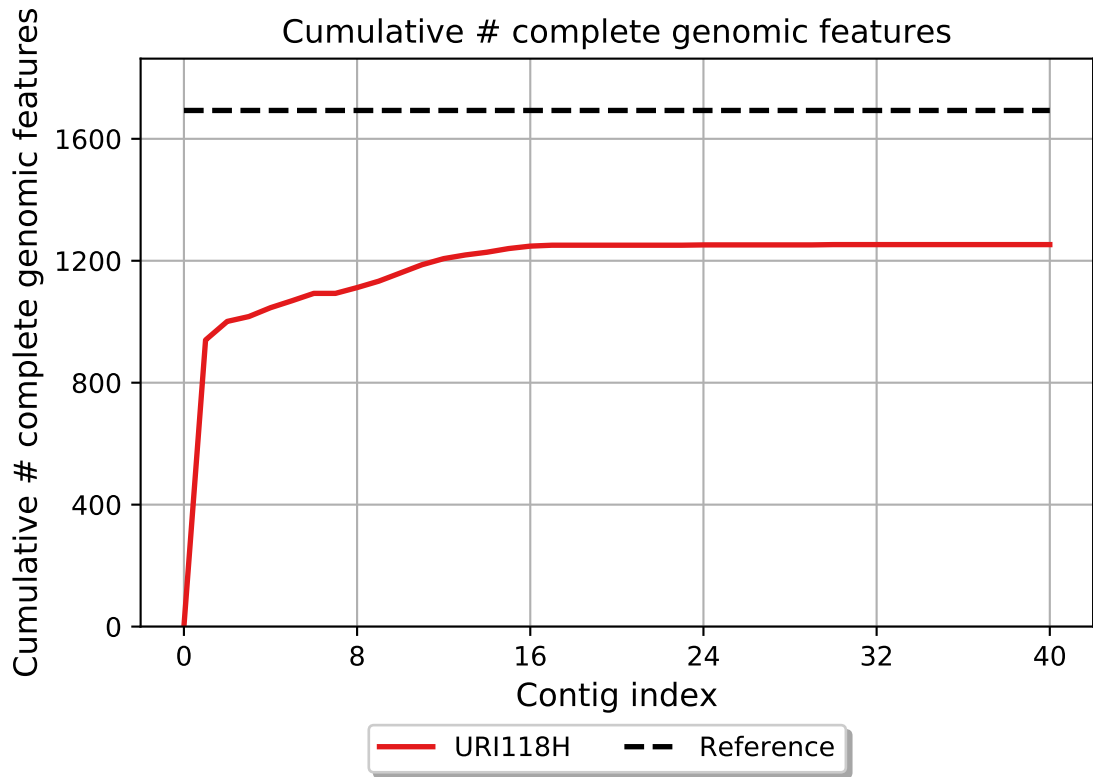
FRCurve (genomic features)

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