Report

	URI112H
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1431440
Total length (>= 1000 bp)	1407410
Total length (>= 5000 bp)	1397089
Total length (>= 10000 bp)	1382483
Total length (>= 25000 bp)	1245305
Total length (>= 50000 bp)	1028355
# contigs	41
Largest contig	903099
Total length	1420550
Reference length	1521208
GC (%)	28.13
Reference GC (%)	28.18
N50	903099
NG50	903099
N90	24214
NG90	12616
auN	586784.8
auNG	547957.4
L50	1
LG50	1
L90	12
LG90	16
# misassemblies	26
# misassembled contigs	10
Misassembled contigs length	290299
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	4 + 18 part
Unaligned length	177877
Genome fraction (%)	79.202
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	827.54
# indels per 100 kbp	54.85
# genomic features	1250 + 64 part
Largest alignment	903082
Total aligned length	1239704
NA50	903082
NGA50	903082
NA90	-
NGA90	-
auNA	578157.0
auNGA	539900.5
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).
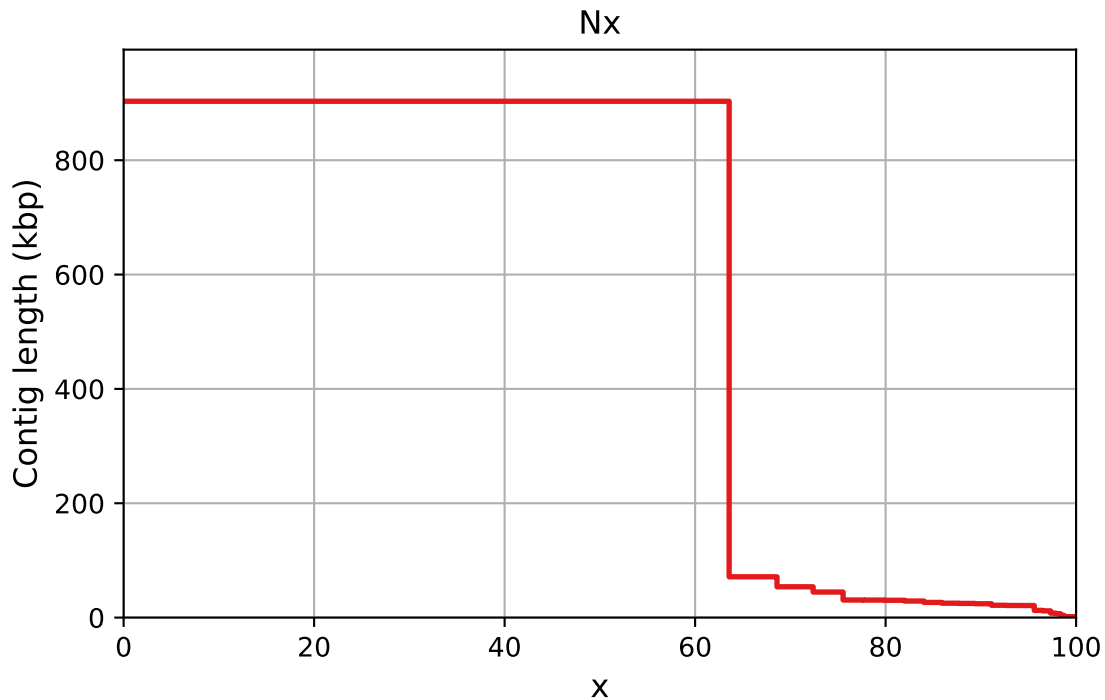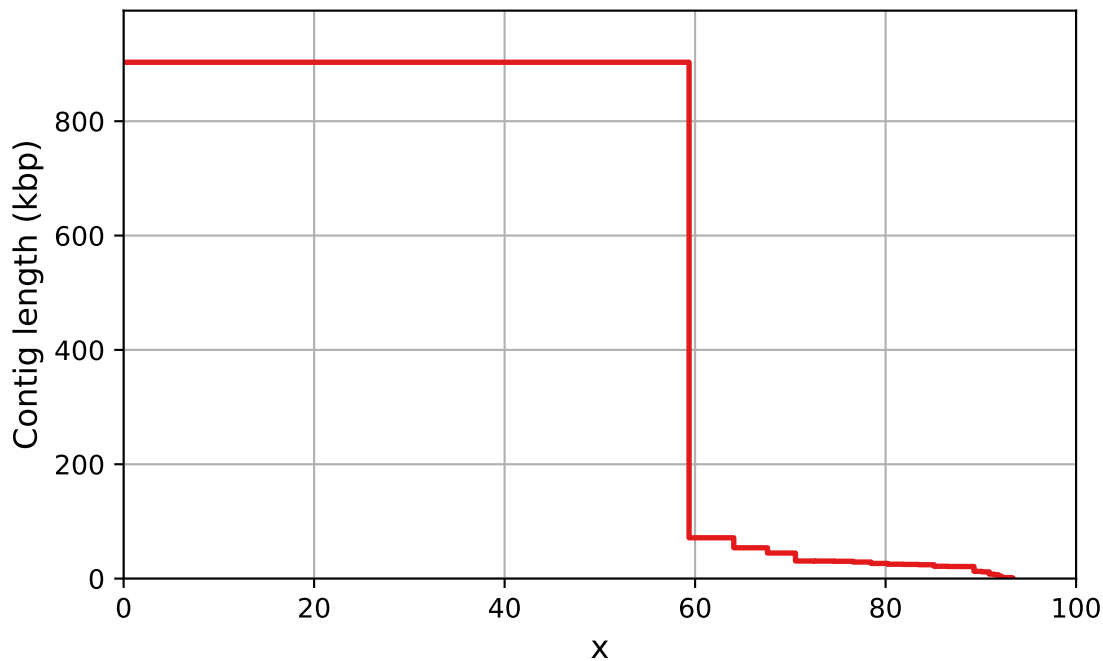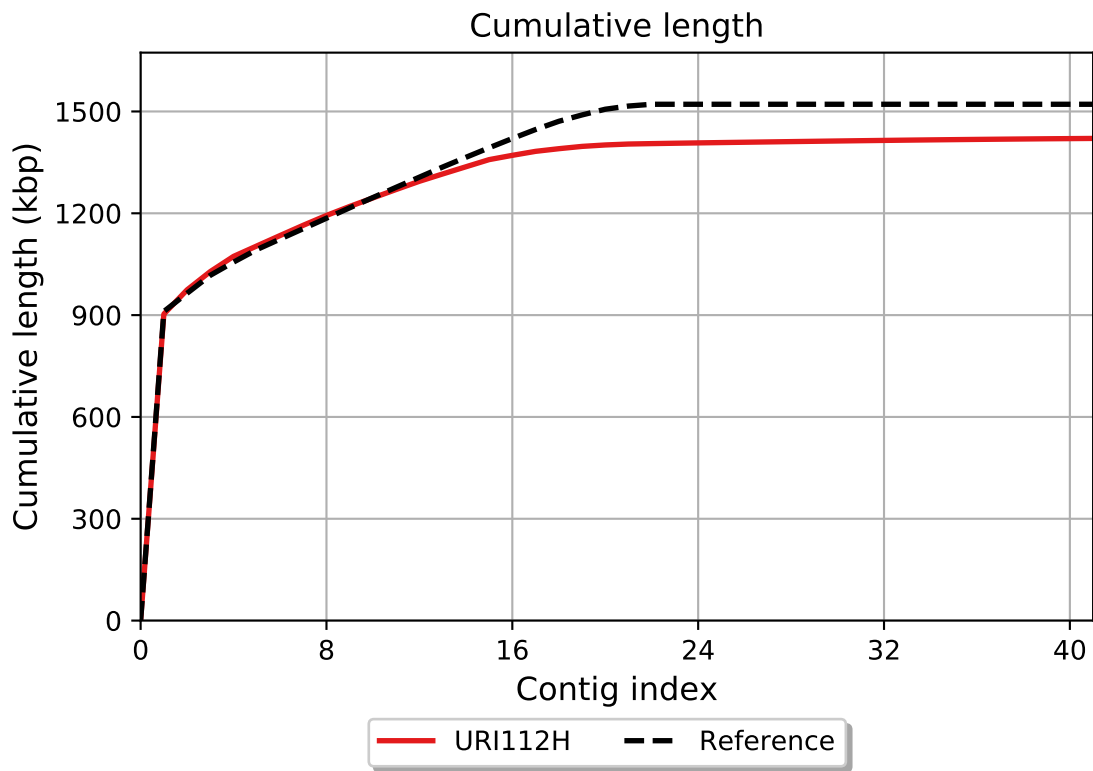
Misassemblies report
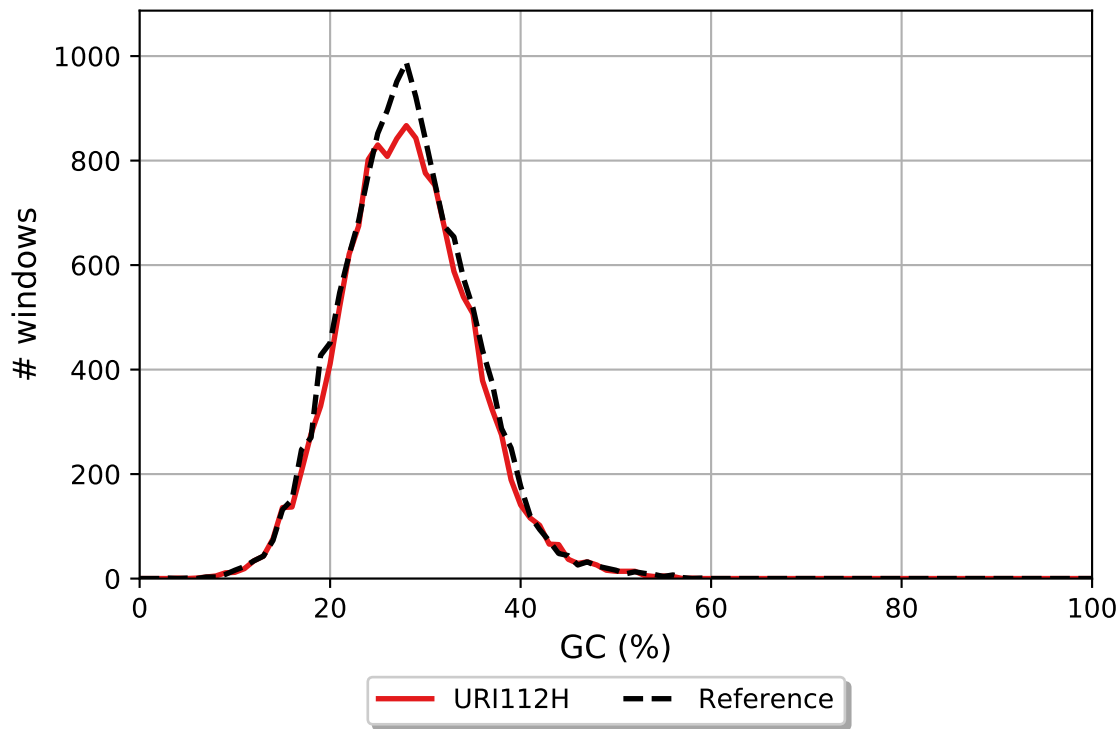
	URI112H
# misassemblies	26
# contig misassemblies	26
# c. relocations	5
# c. translocations	17
# c. inversions	4
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	290299
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	10259
# indels	680
# indels (<= 5 bp)	609
# indels (> 5 bp)	71
Indels length	4432

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

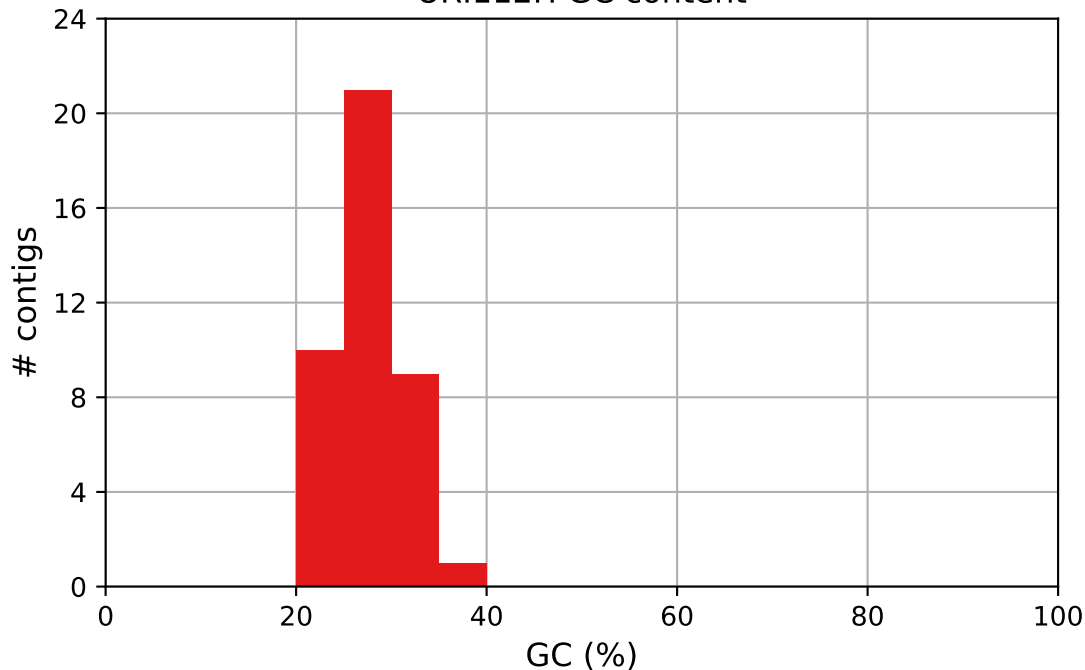|	URI112H
# fully unaligned contigs	4
Fully unaligned length	3569
# partially unaligned contigs	18
Partially unaligned length	174308
# N's	0

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

NGx

Cumulative length

GC content

URI112H GC content

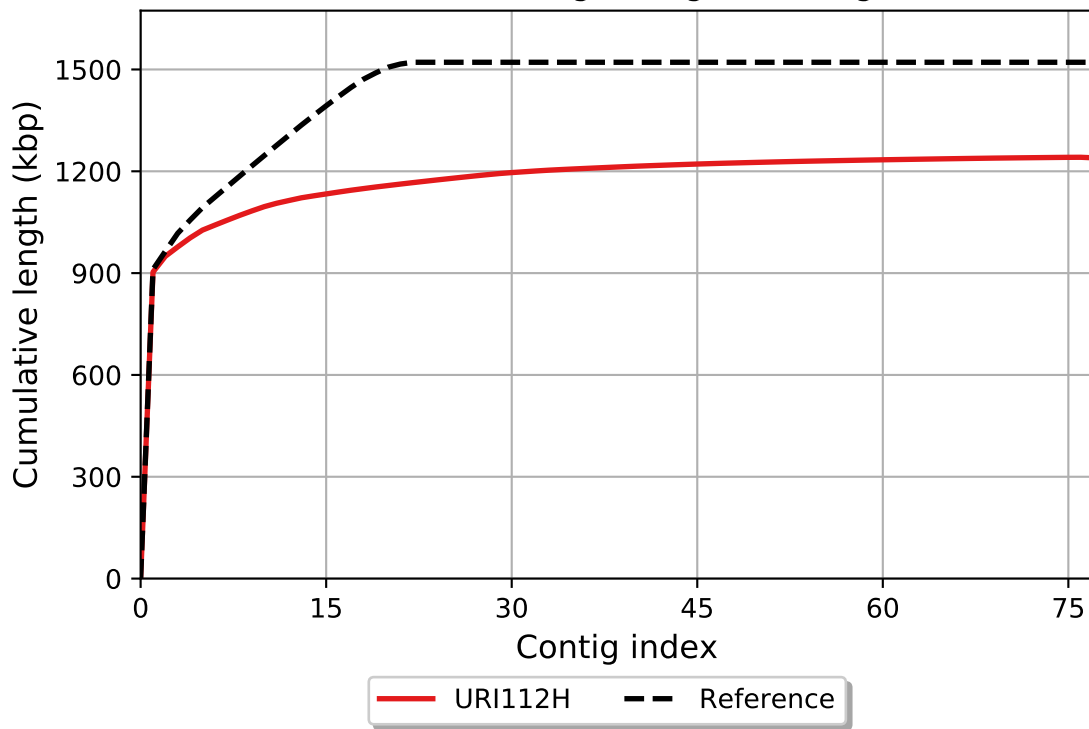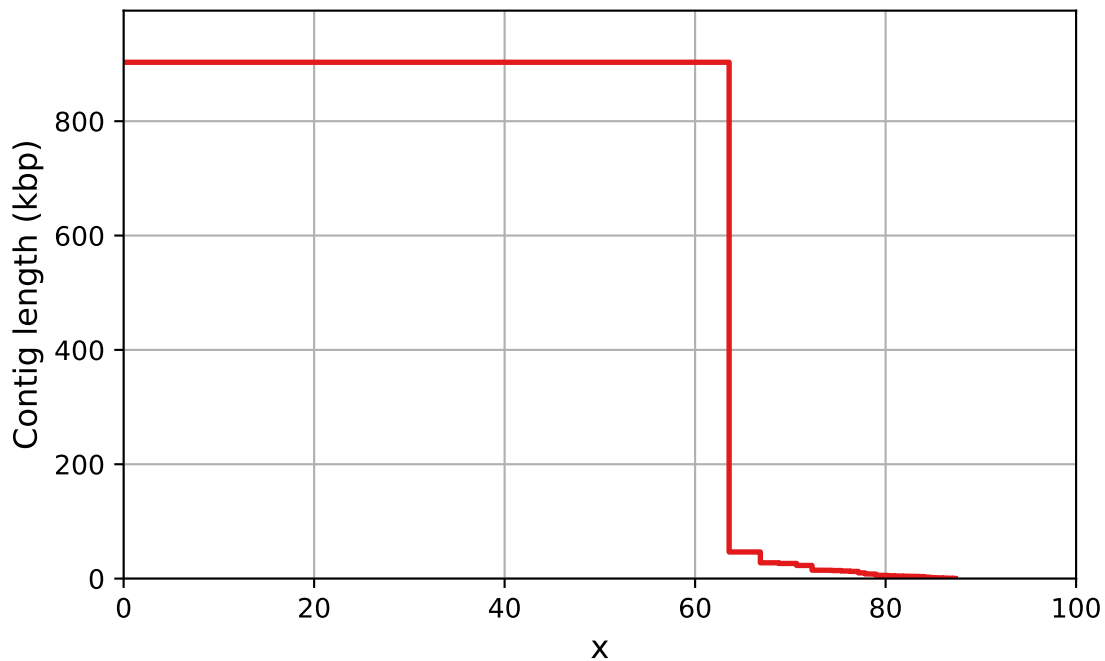Misassemblies

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relocations   # translocations   # inversions

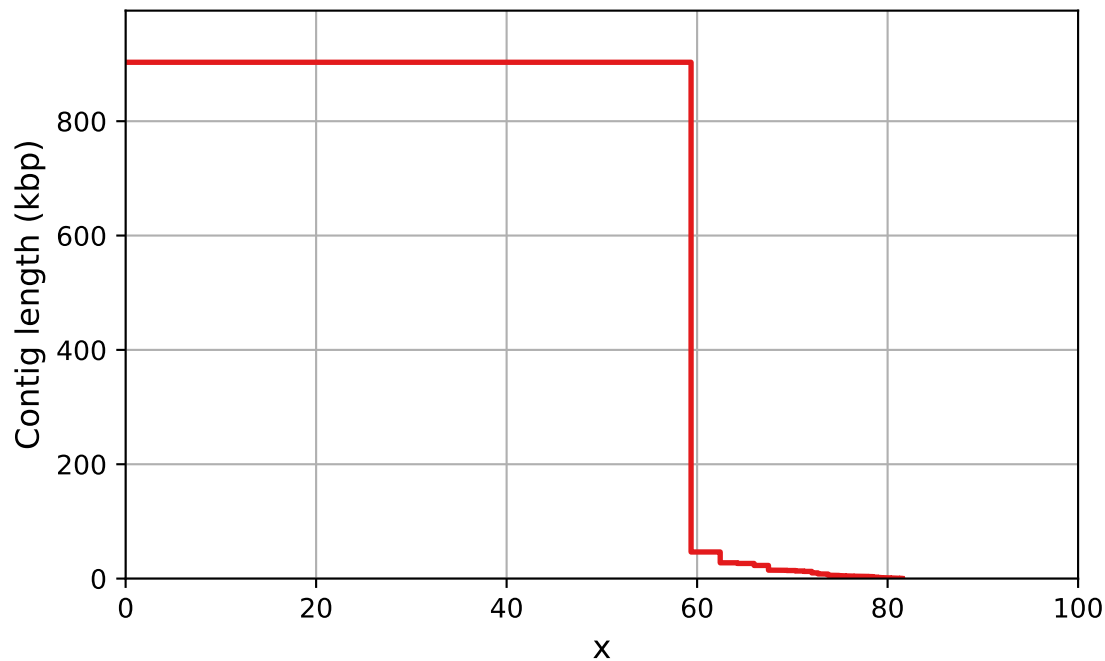FRCurve (misassemblies)
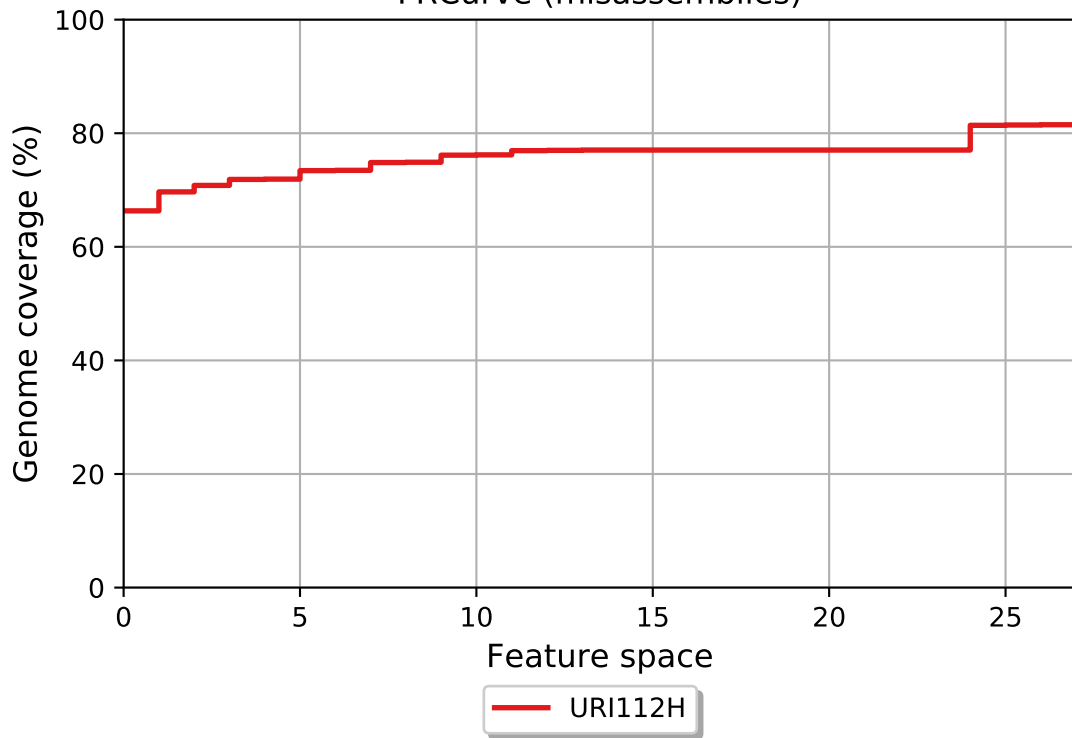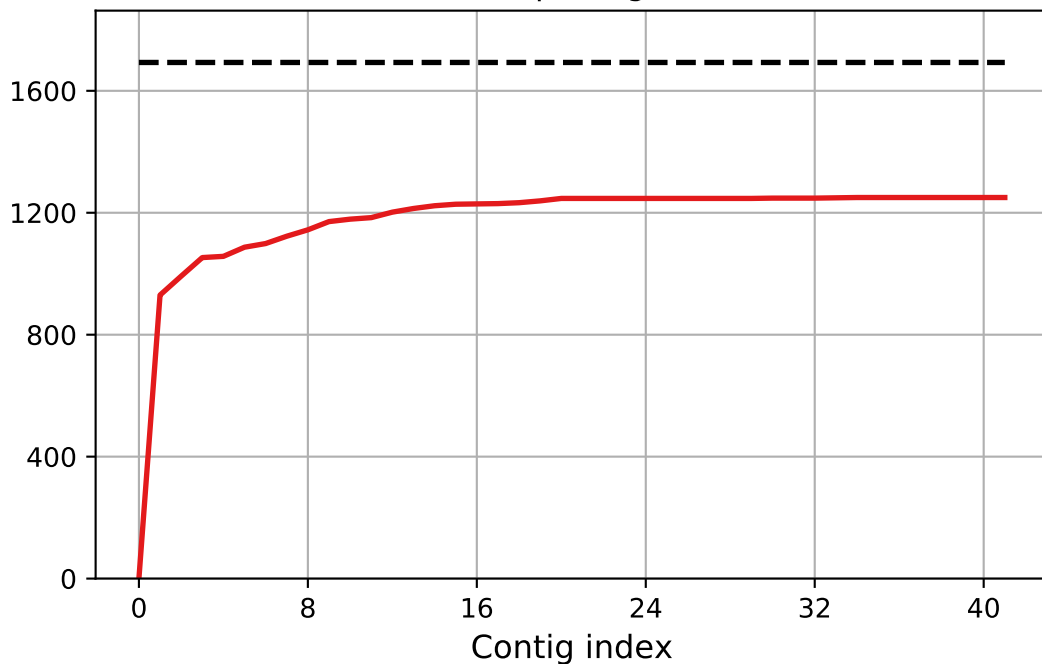
Cumulative length (aligned contigs)

NAx

URI112H

NGAx

Cumulative # complete genomic features

FRCurve (genomic features)