Report

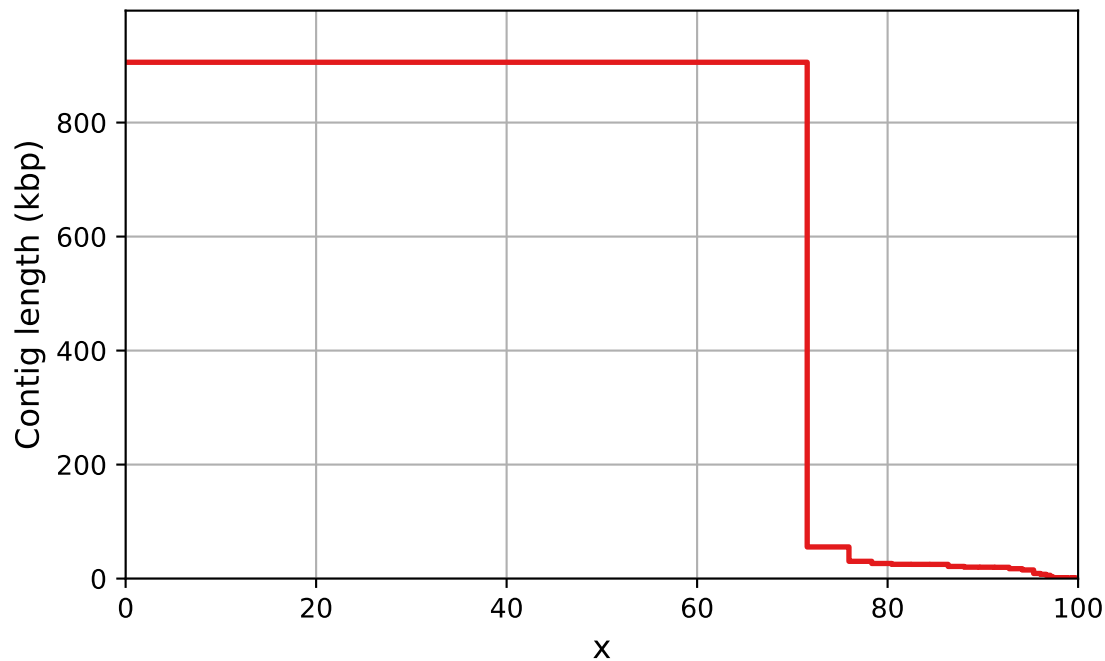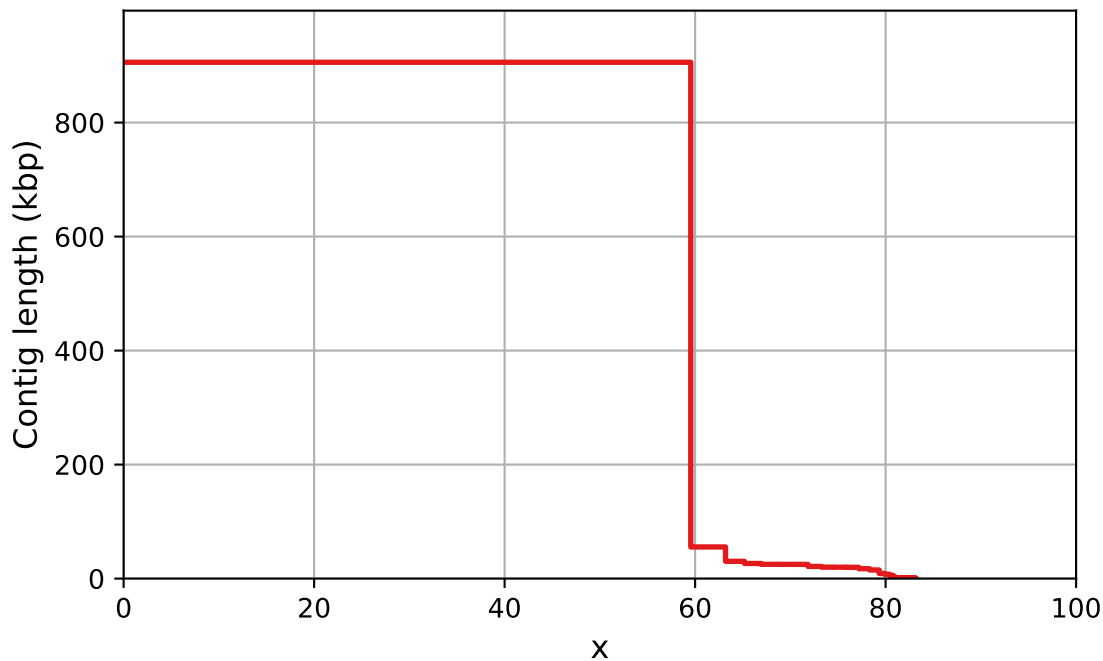|	UCT113H
# contigs (>= 0 bp)	253
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1304891
Total length (>= 1000 bp)	1241570
Total length (>= 5000 bp)	1228925
Total length (>= 10000 bp)	1206704
Total length (>= 25000 bp)	1043164
Total length (>= 50000 bp)	961288
# contigs	60
Largest contig	905788
Total length	1265811
Reference length	1521208
GC (%)	28.12
Reference GC (%)	28.18
N50	905788
NG50	905788
N90	19970
NG90	-
auN	655243.8
auNG	545234.4
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	19
# misassembled contigs	9
Misassembled contigs length	186222
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	16 + 12 part
Unaligned length	108208
Genome fraction (%)	75.122
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	683.13
# indels per 100 kbp	35.66
# genomic features	1178 + 63 part
Largest alignment	904982
Total aligned length	1155410
NA50	904982
NGA50	904982
NA90	912
NGA90	-
auNA	650666.7
auNGA	541425.7
LA50	1
LGA50	1
LA90	36
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

	UCT113H
# misassemblies	19
# contig misassemblies	19
# c. relocations	8
# c. translocations	9
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	186222
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	7893
# indels	412
# indels (<= 5 bp)	370
# indels (> 5 bp)	42
Indels length	1608

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).
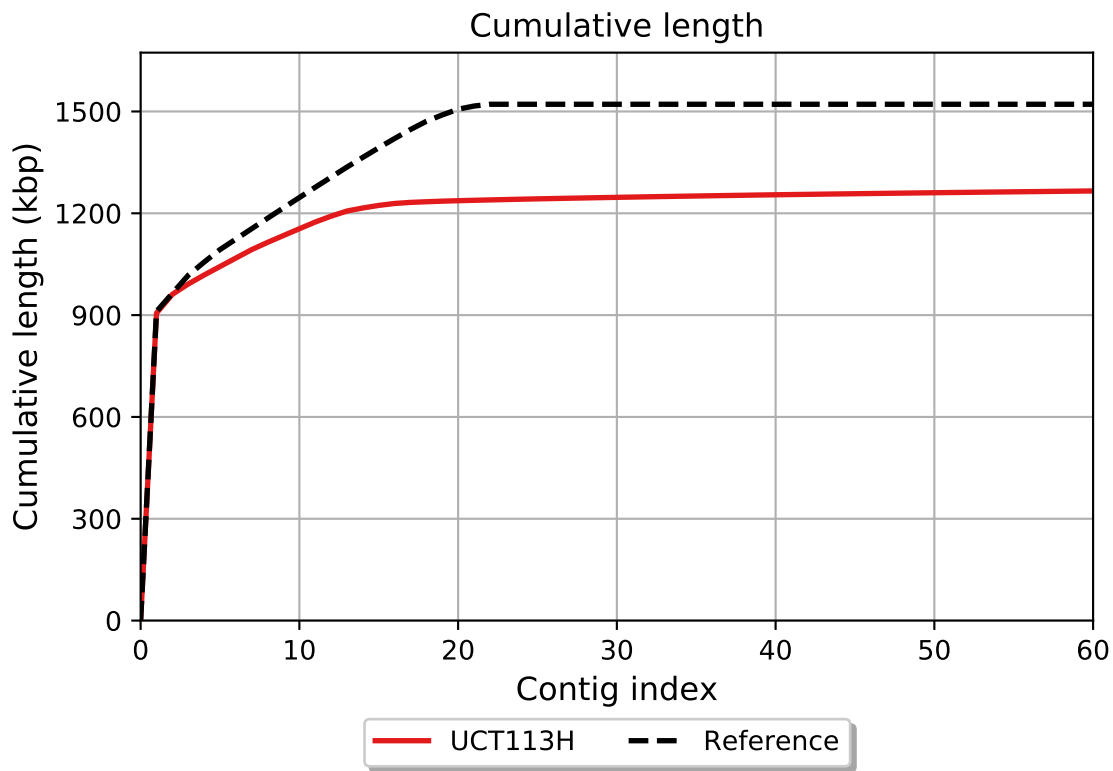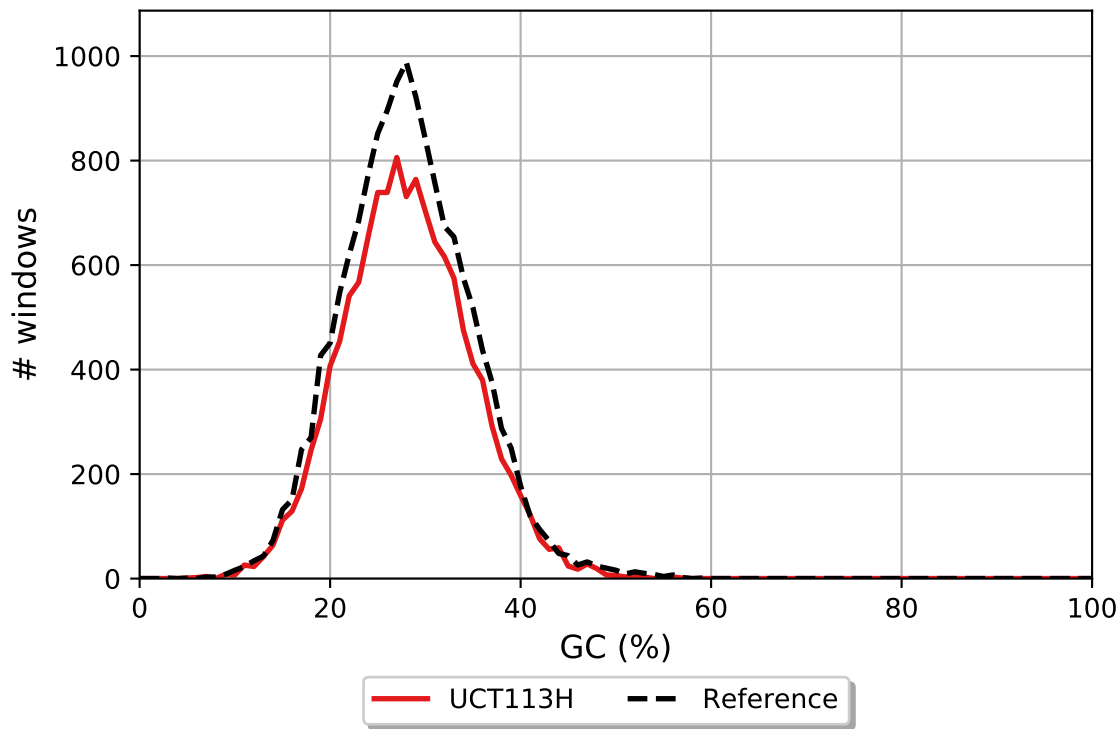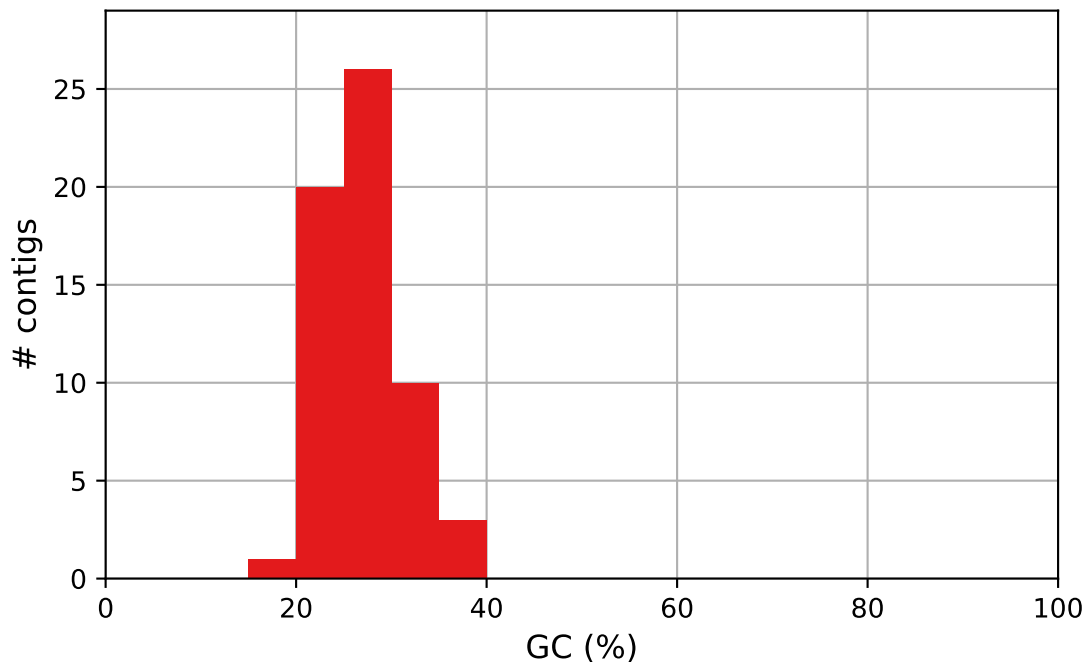
Unaligned report

	UCT113H
# fully unaligned contigs	16
Fully unaligned length	12936
# partially unaligned contigs	12
Partially unaligned length	95272
# 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)

x

UCT113H

NGx

Cumulative length

GC content

windows vs. GC (%)

Legend: UCT113H (red solid line), Reference (black dashed line)

UCT113H GC content

Misassemblies
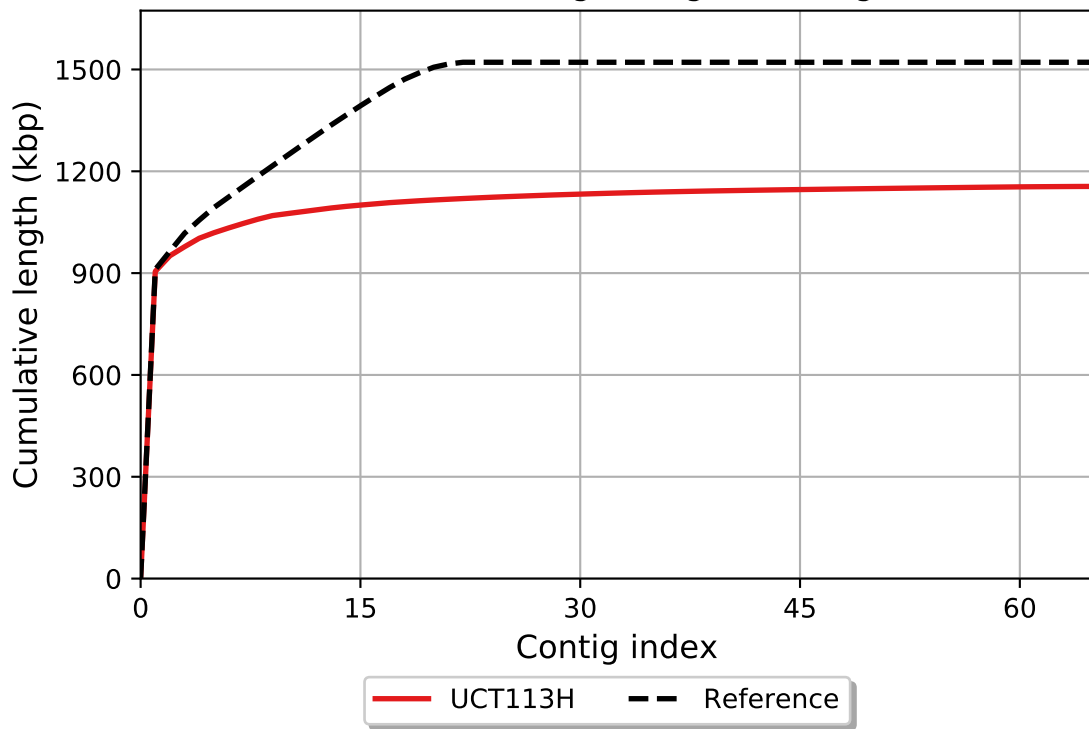
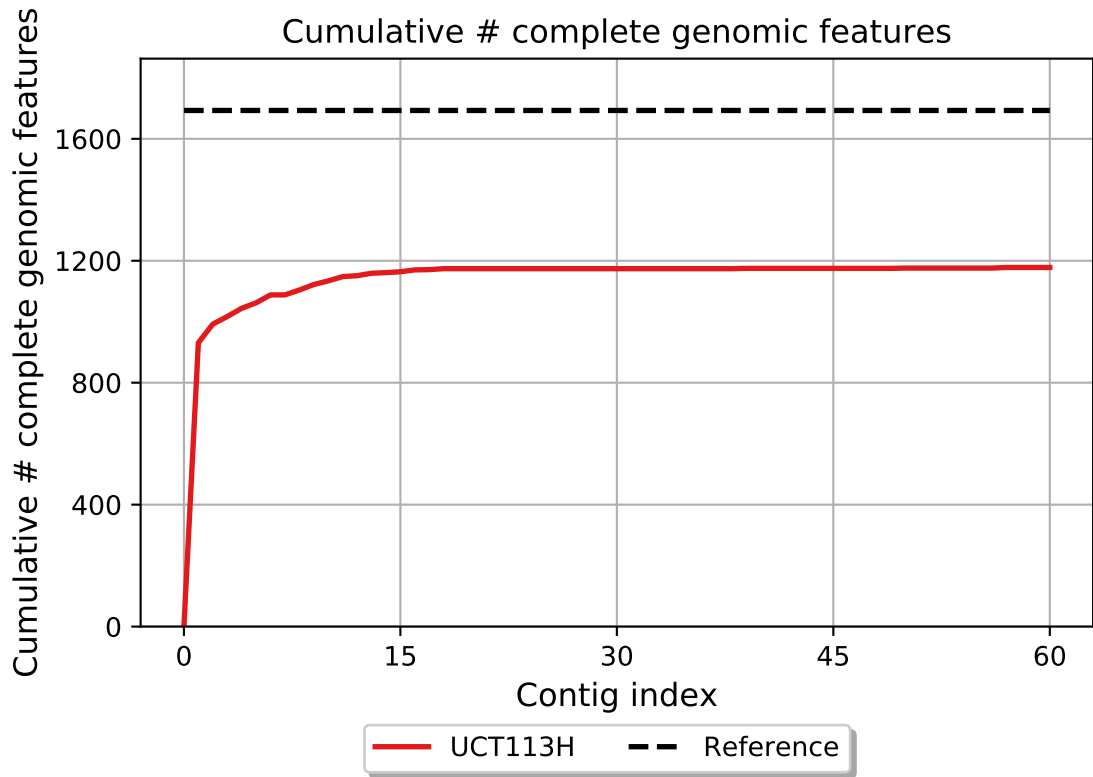FRCurve (misassemblies)
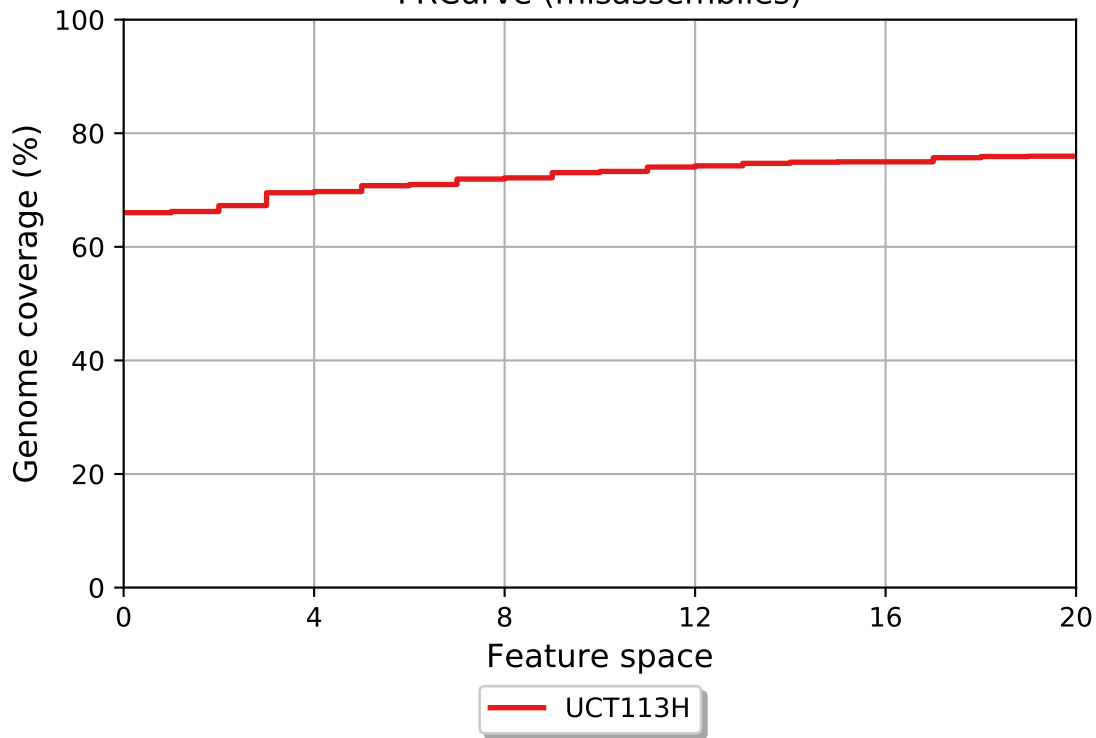
Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

UCT113H

NGAx

UCT113H

Cumulative # complete genomic features
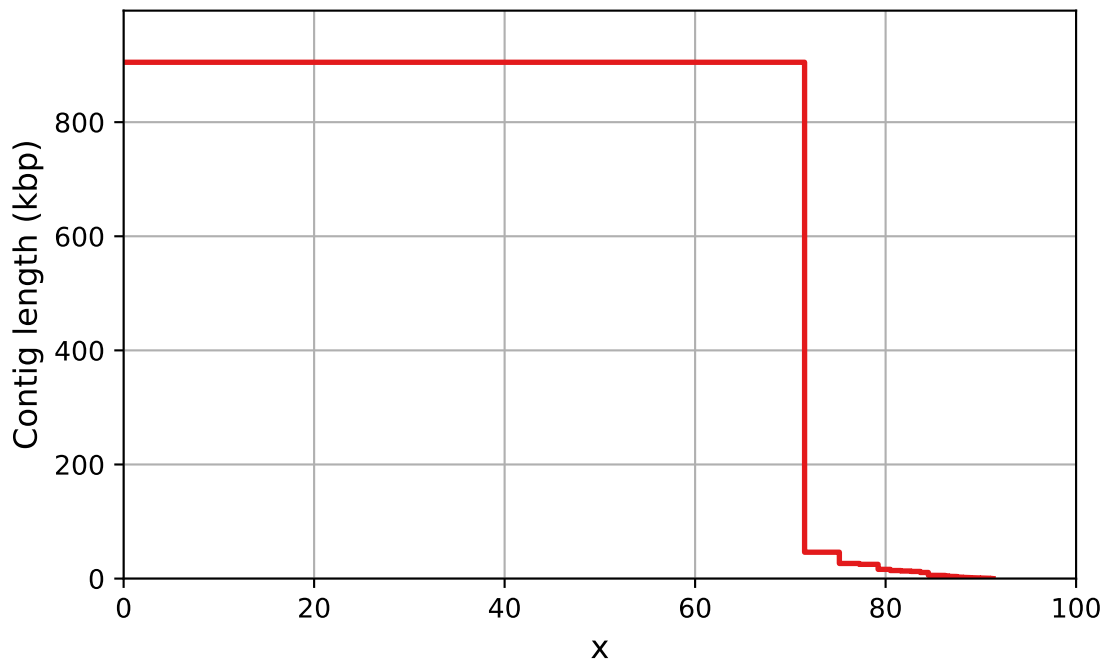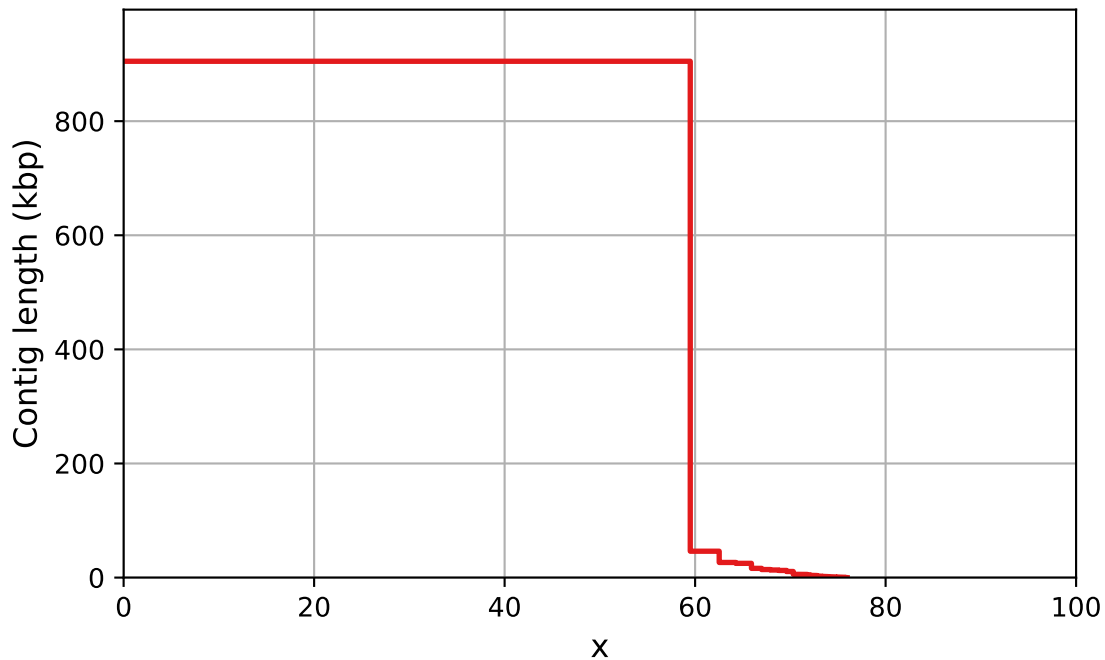
FRCurve (genomic features)