Report

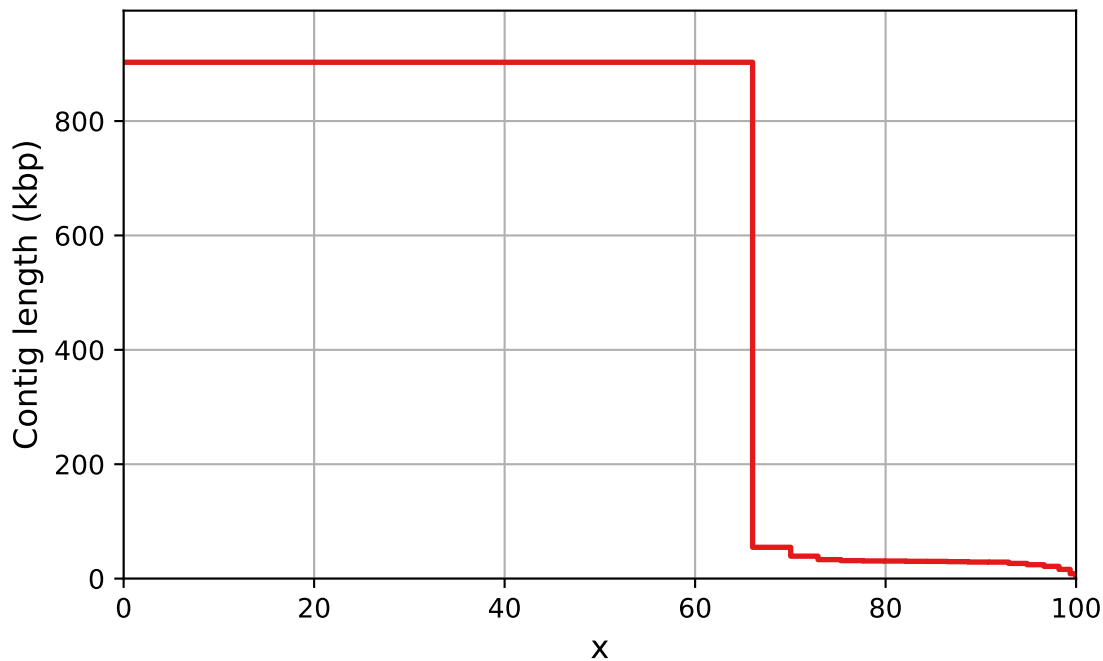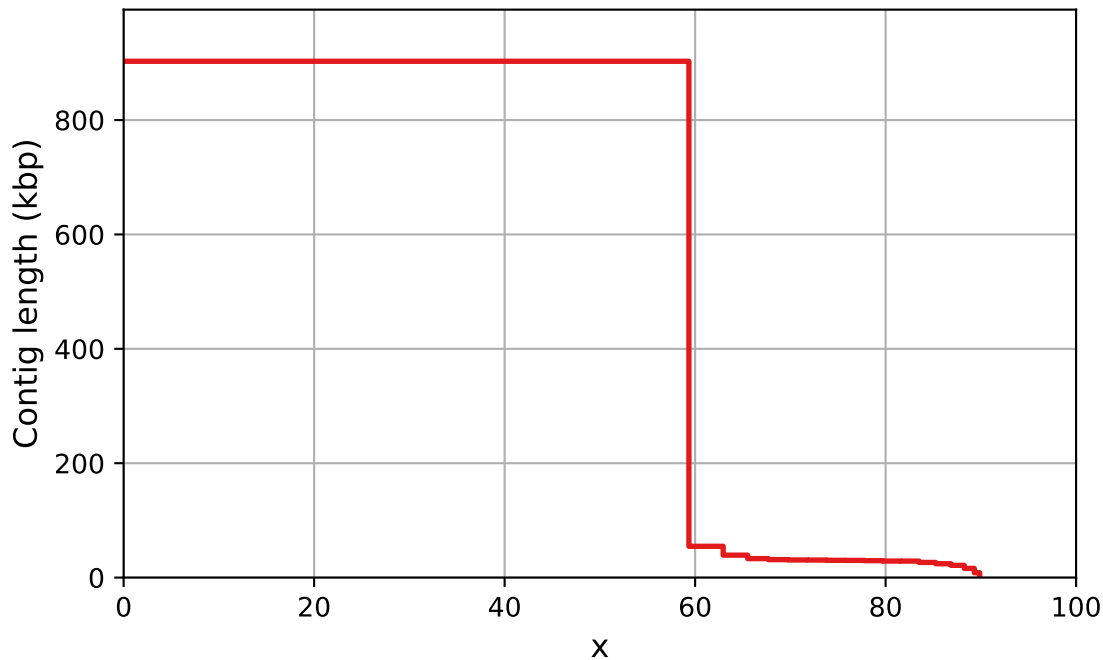|	UNY990P
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1367194
Total length (>= 1000 bp)	1367194
Total length (>= 5000 bp)	1367194
Total length (>= 10000 bp)	1358674
Total length (>= 25000 bp)	1296898
Total length (>= 50000 bp)	957523
# contigs	17
Largest contig	902813
Total length	1367194
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	902813
NG50	902813
N90	28907
NG90	-
auN	607096.7
auNG	545631.5
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	14
# misassembled contigs	6
Misassembled contigs length	164428
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 14 part
Unaligned length	140300
Genome fraction (%)	78.845
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	807.88
# indels per 100 kbp	53.28
# genomic features	1252 + 40 part
Largest alignment	902629
Total aligned length	1223702
NA50	902629
NGA50	902629
NA90	-
NGA90	-
auNA	601931.5
auNGA	540989.2
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
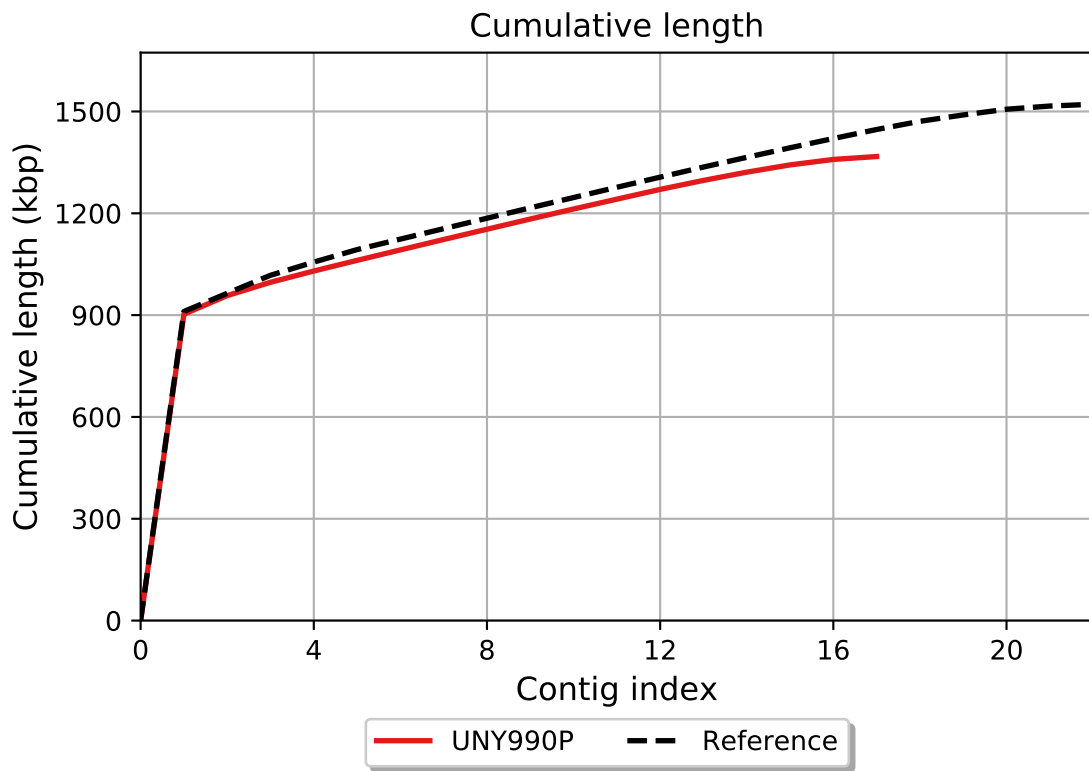
	UNY990P
# misassemblies	14
# contig misassemblies	14
# c. relocations	1
# c. translocations	12
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	164428
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9886
# indels	652
# indels (<= 5 bp)	580
# indels (> 5 bp)	72
Indels length	3594

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

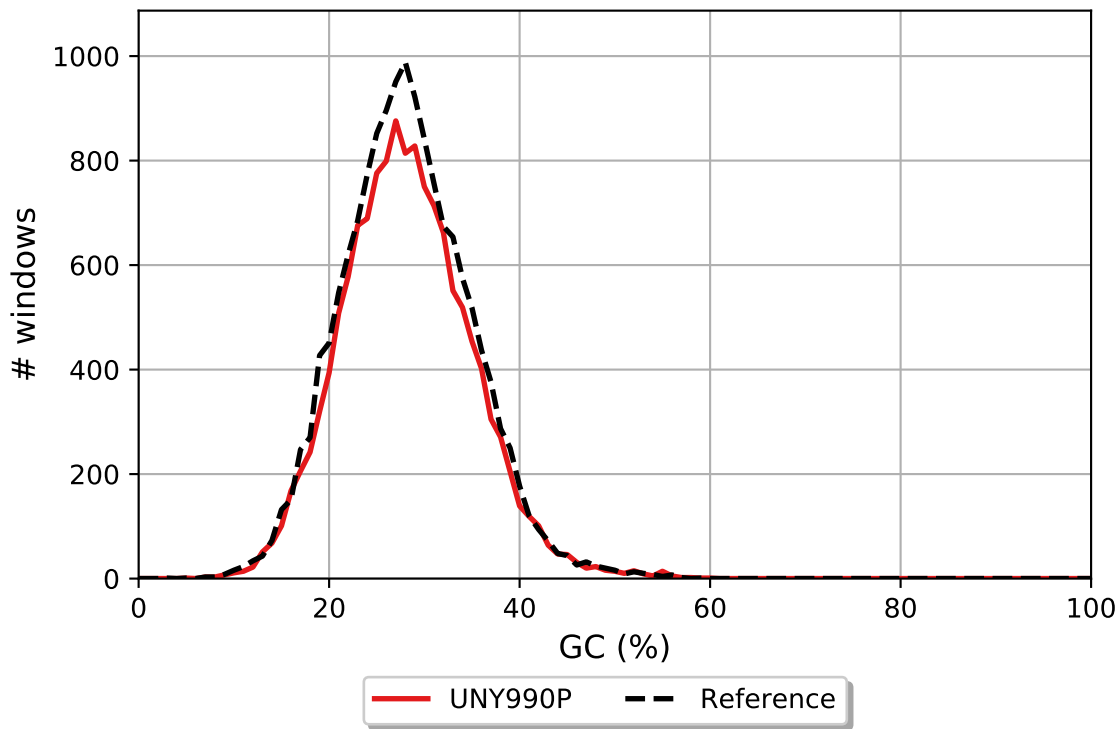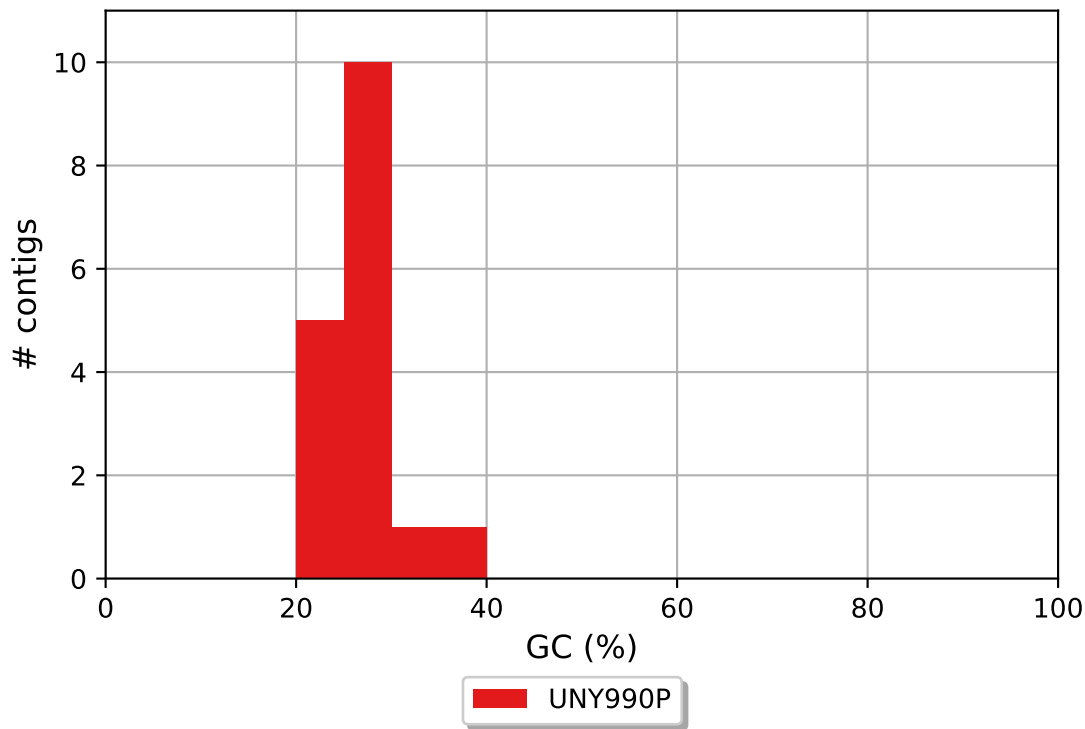|	UNY990P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	140300
# N's	0

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
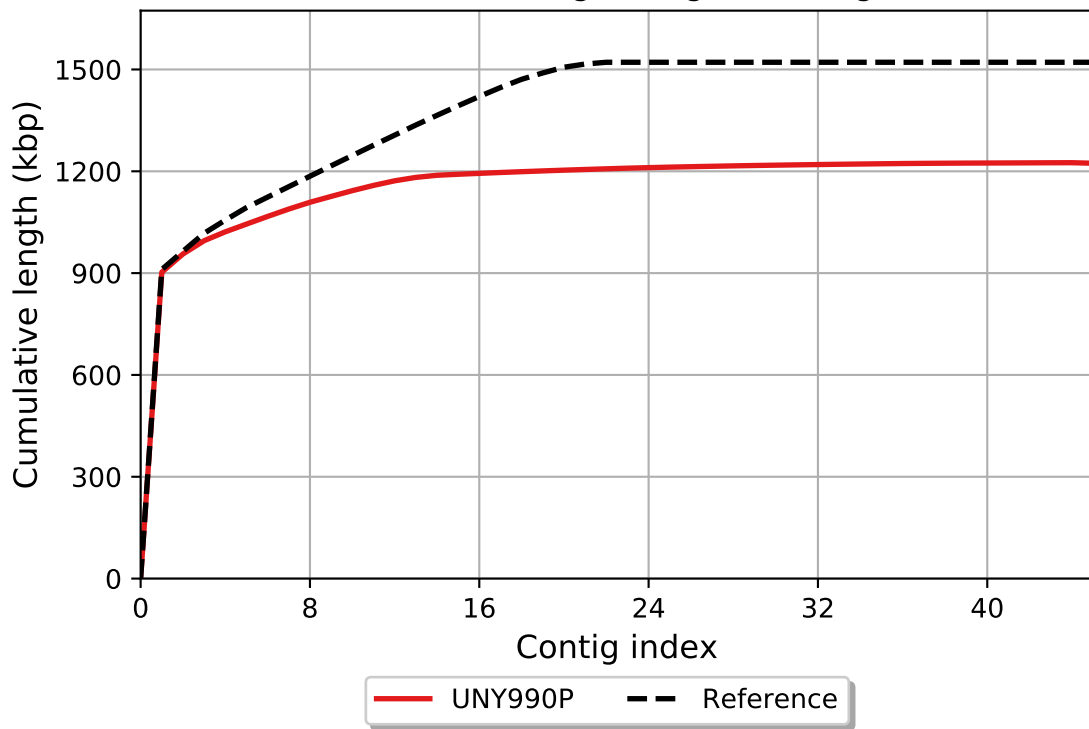
GC content

UNY990P GC content
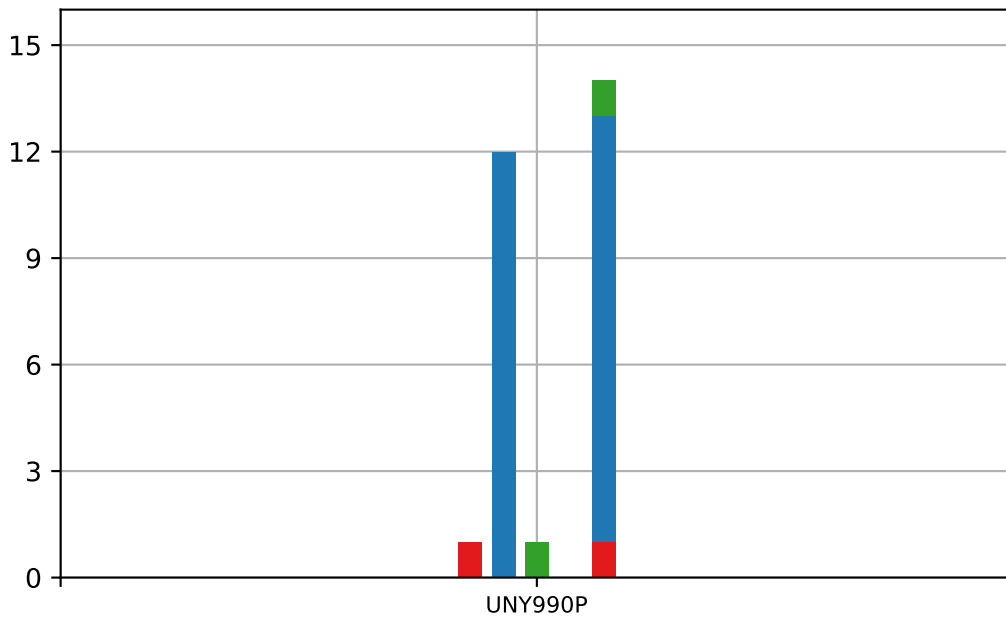
Misassemblies

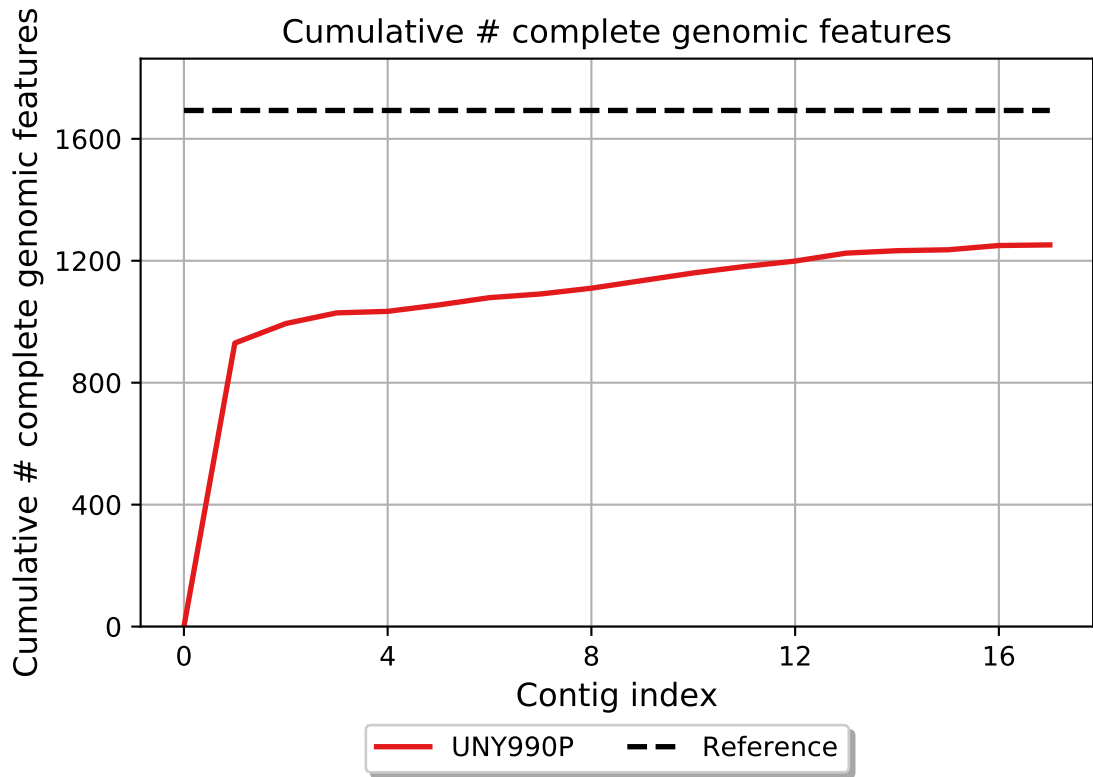FRCurve (misassemblies)
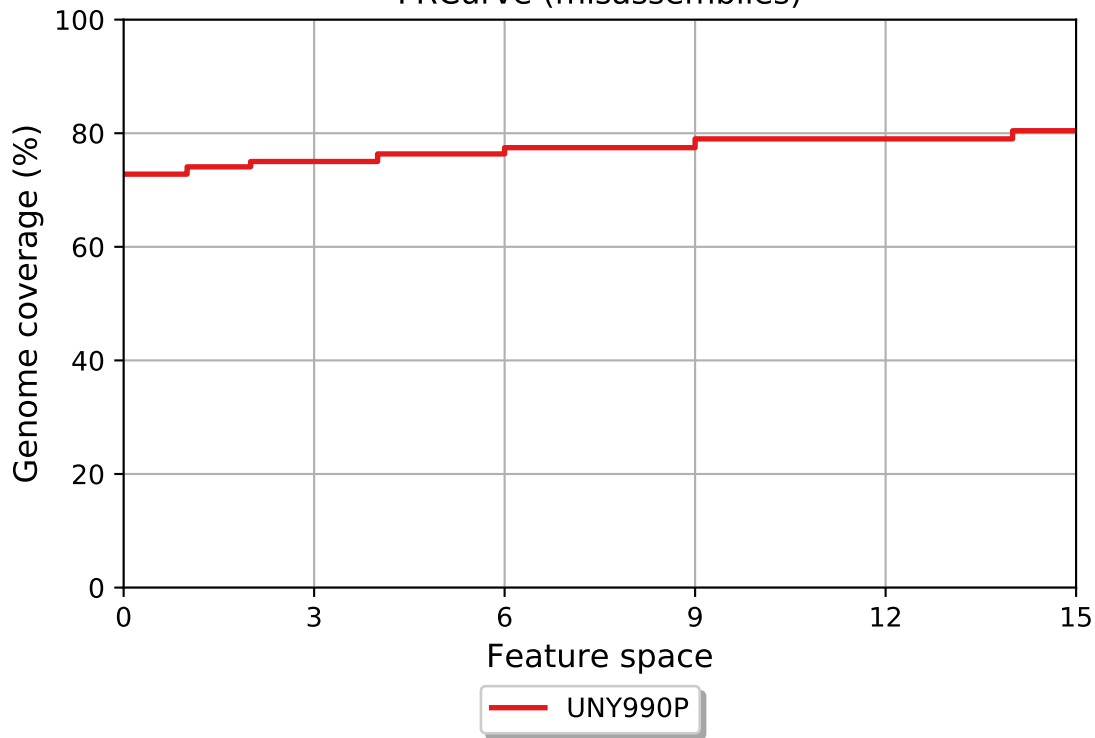
Cumulative length (aligned contigs)

NAx

x

Contig length (kbp)

UNY990P

NGAx

Cumulative # complete genomic features
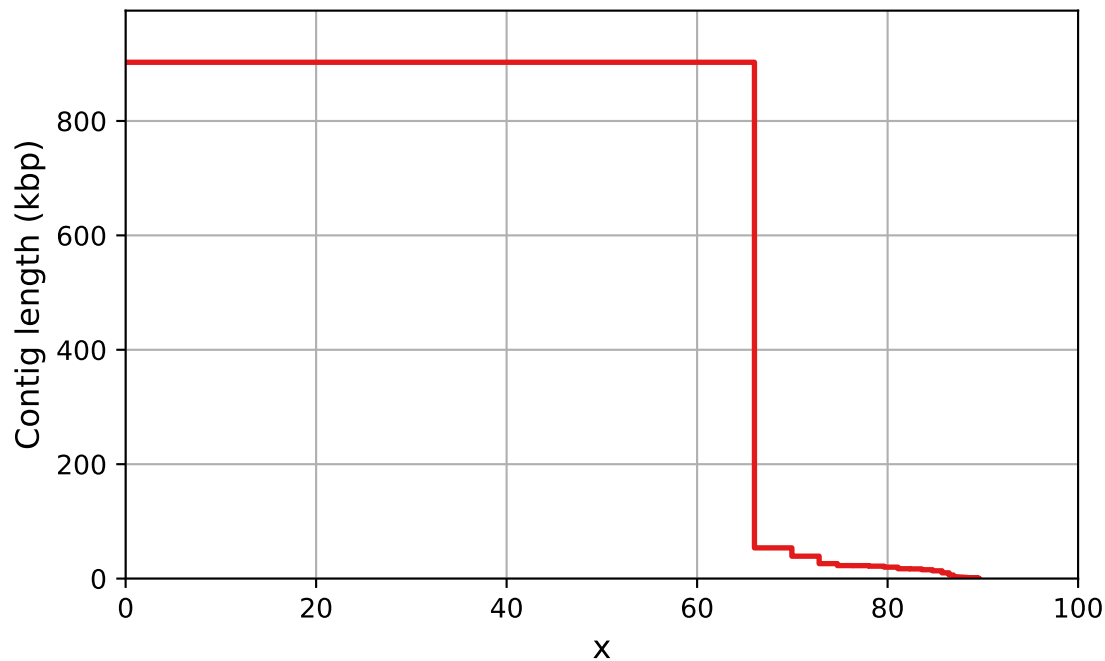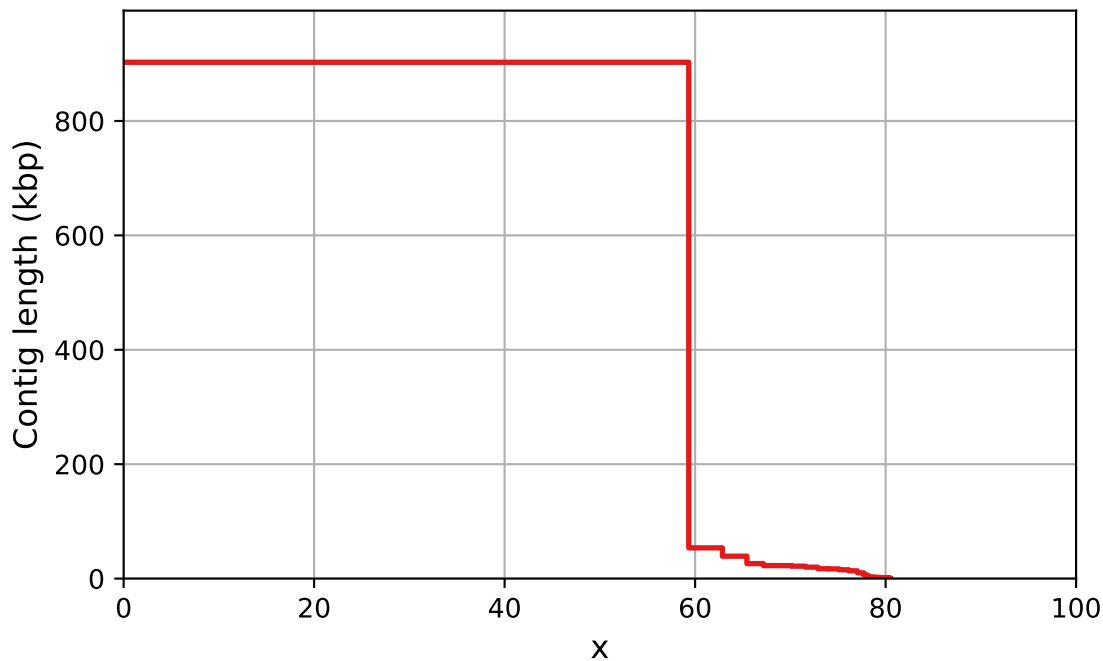
FRCurve (genomic features)