

Report

	UNY172P
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1352494
Total length (>= 1000 bp)	1352494
Total length (>= 5000 bp)	1352494
Total length (>= 10000 bp)	1352494
Total length (>= 25000 bp)	1267080
Total length (>= 50000 bp)	957249
# contigs	16
Largest contig	903384
Total length	1352494
Reference length	1521208
GC (%)	28.28
Reference GC (%)	28.18
N50	903384
NG50	903384
N90	27706
NG90	-
auN	614108.0
auNG	545998.6
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	17
# misassembled contigs	6
Misassembled contigs length	188537
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	2 + 9 part
Unaligned length	131995
Genome fraction (%)	78.963
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	841.18
# indels per 100 kbp	53.26
# genomic features	1245 + 38 part
Largest alignment	903205
Total aligned length	1216738
NA50	903205
NGA50	903205
NA90	575
NGA90	-
auNA	608841.9
auNGA	541316.5
LA50	1
LGA50	1
LA90	31
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

	UNY172P
# misassemblies	17
# contig misassemblies	17
# c. relocations	2
# c. translocations	15
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	188537
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	10235
# indels	648
# indels (<= 5 bp)	561
# indels (> 5 bp)	87
Indels length	2596

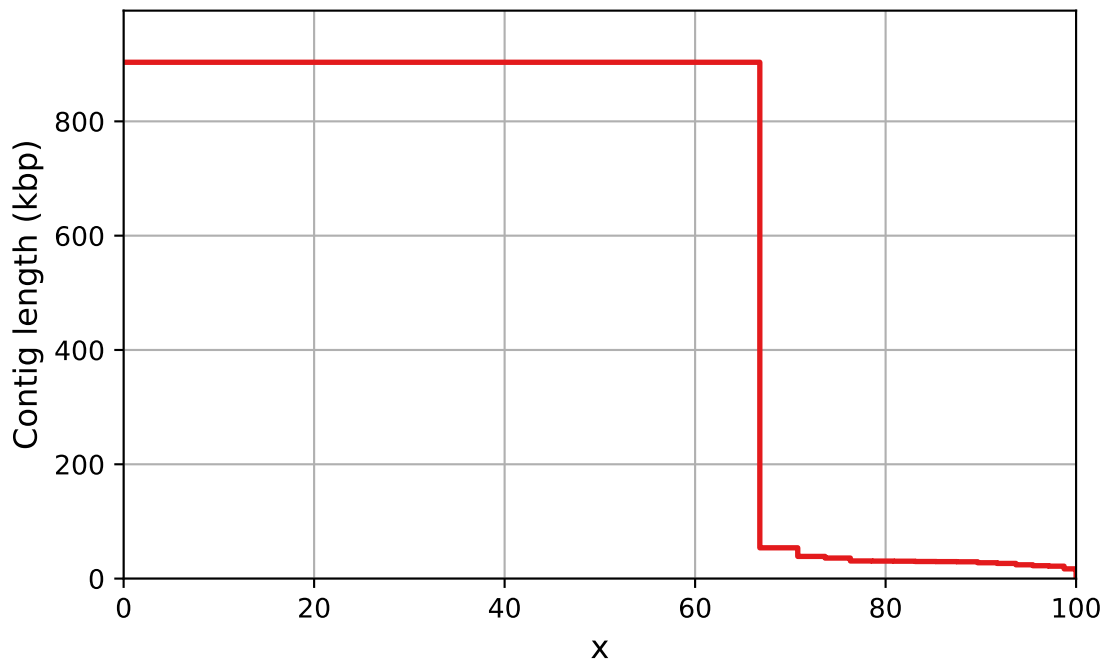
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	UNY172P
# fully unaligned contigs	2
Fully unaligned length	63631
# partially unaligned contigs	9
Partially unaligned length	68364
# N's	0

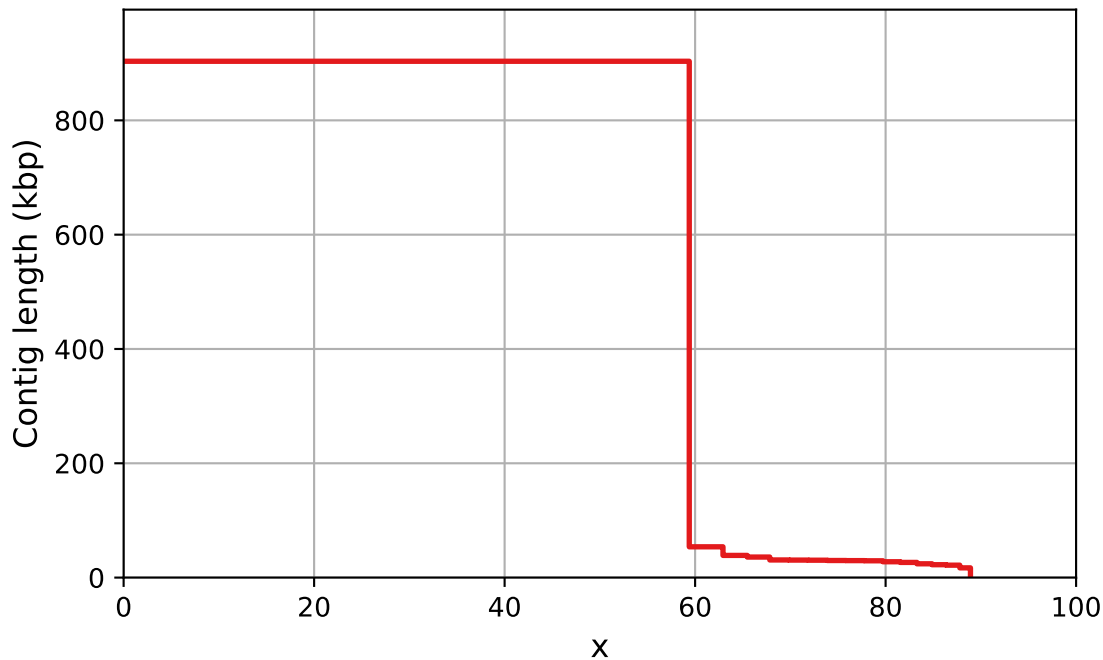
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

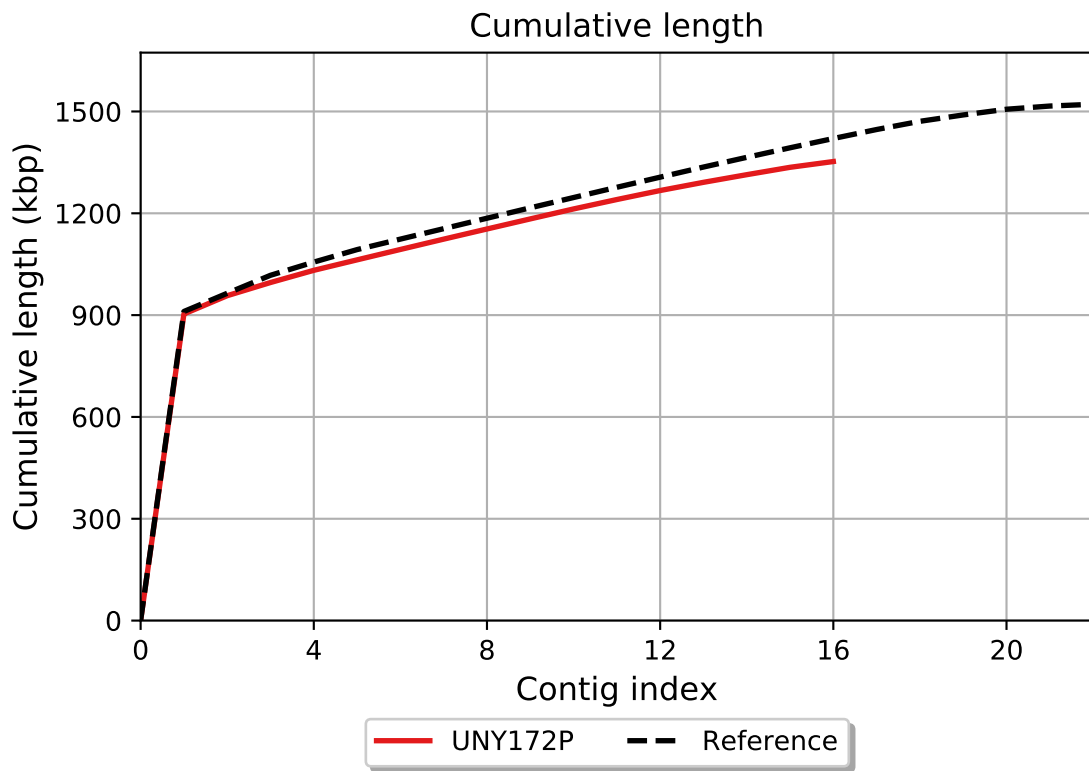


— UNY172P

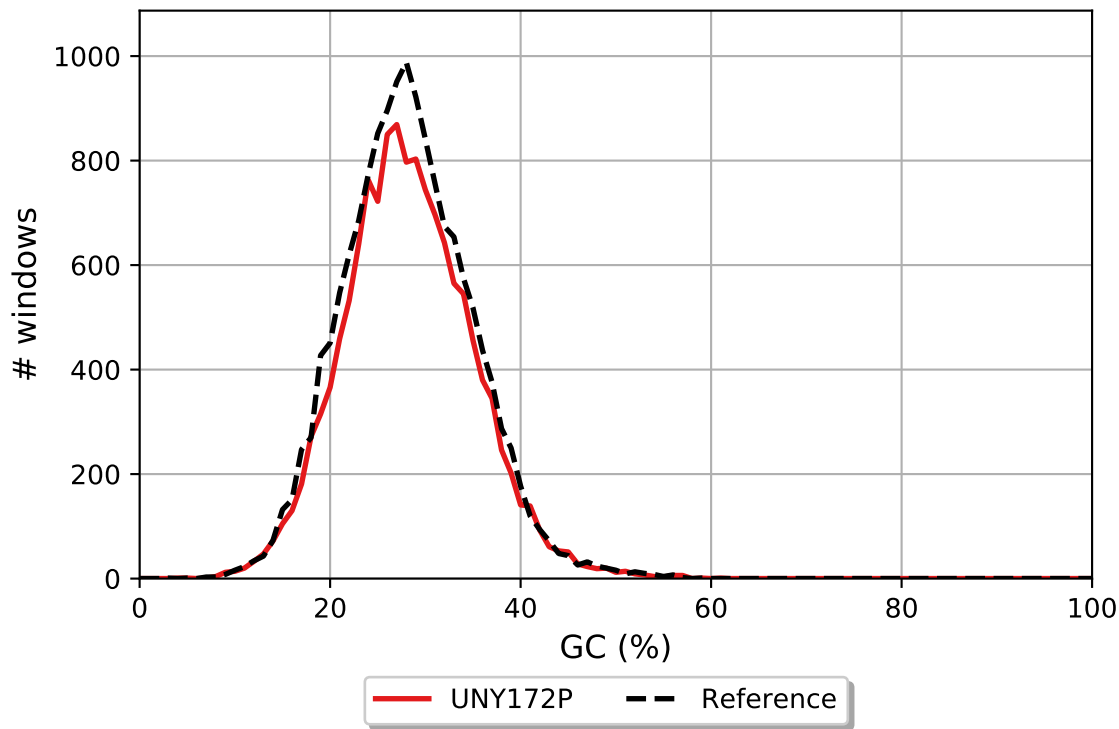
NGx



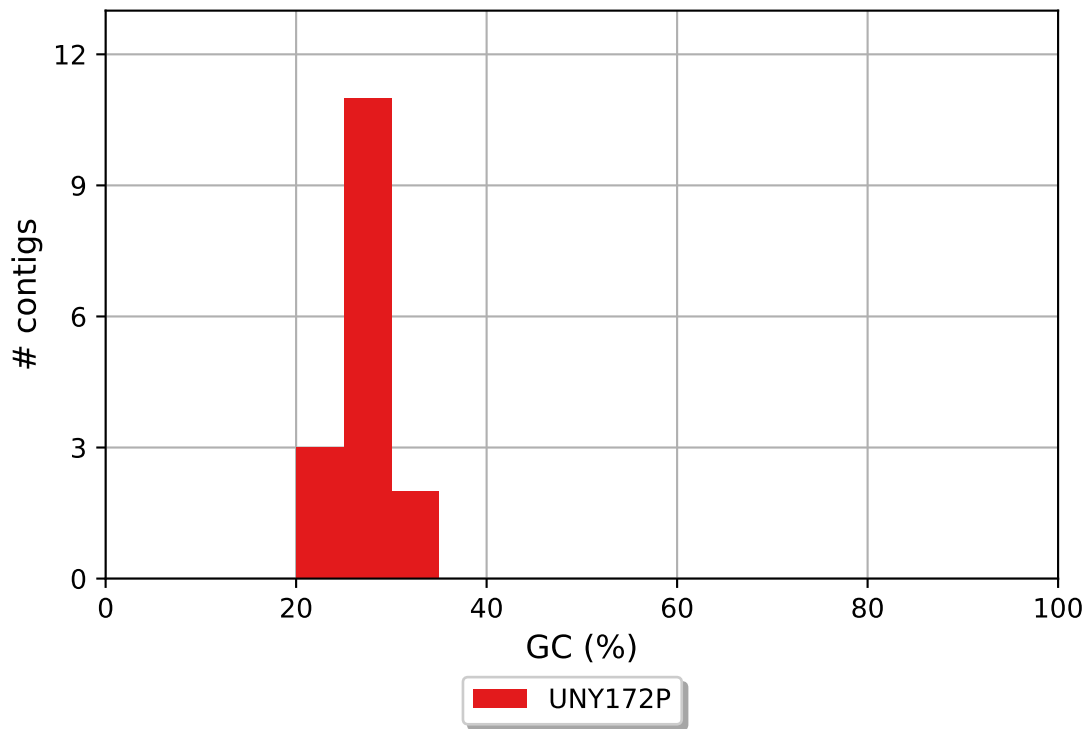
— UNY172P



## GC content

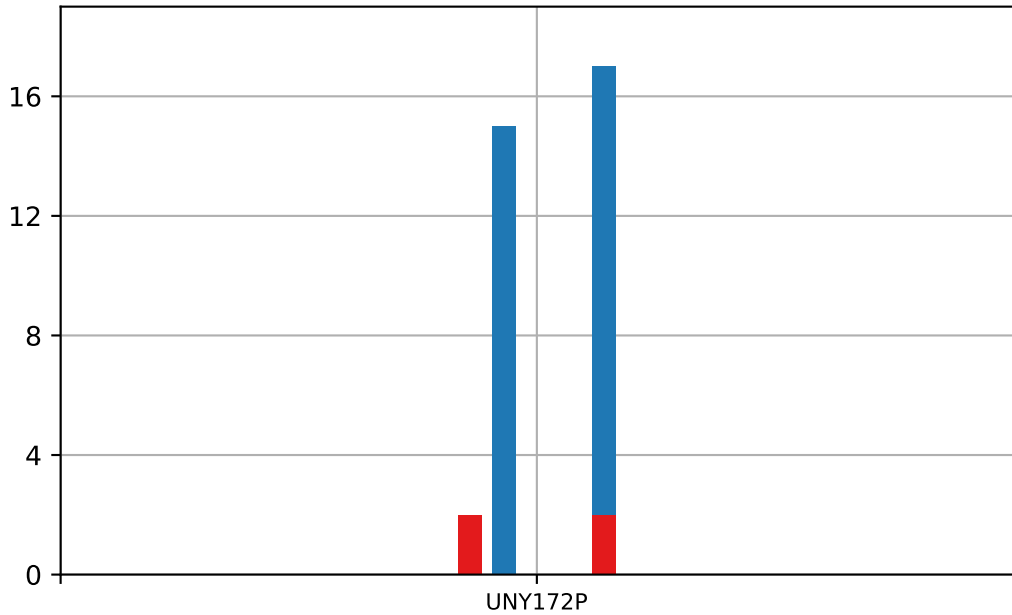


UNY172P GC content





## Misassemblies

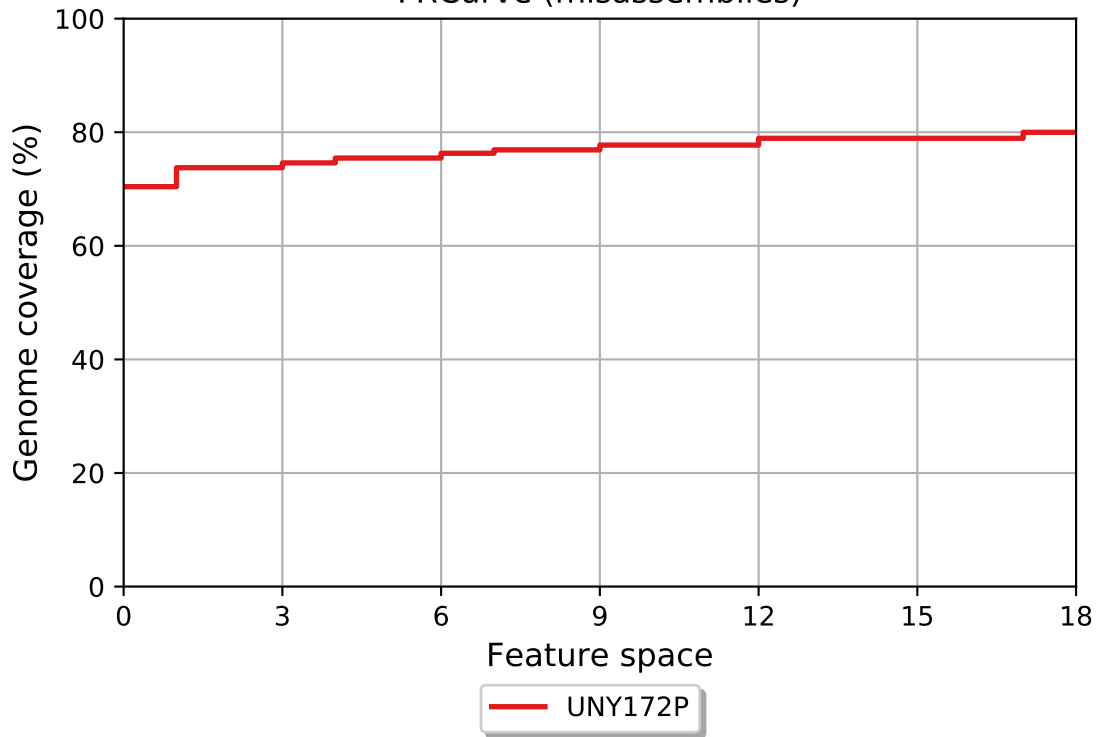


# relocations

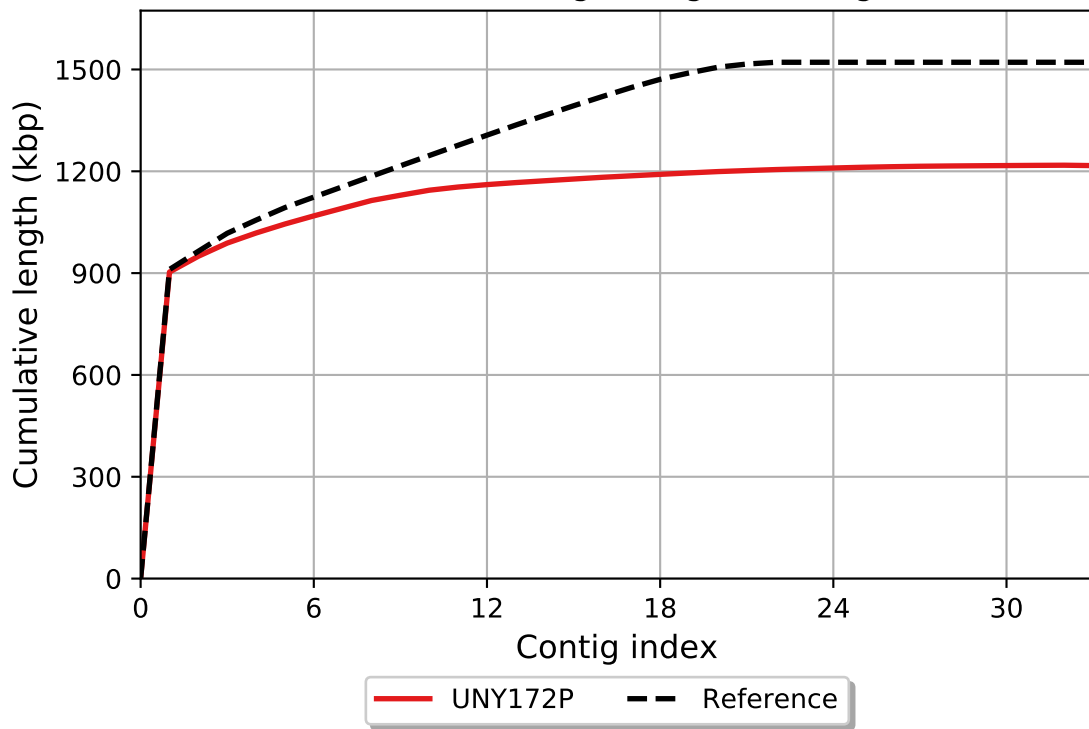


# translocations

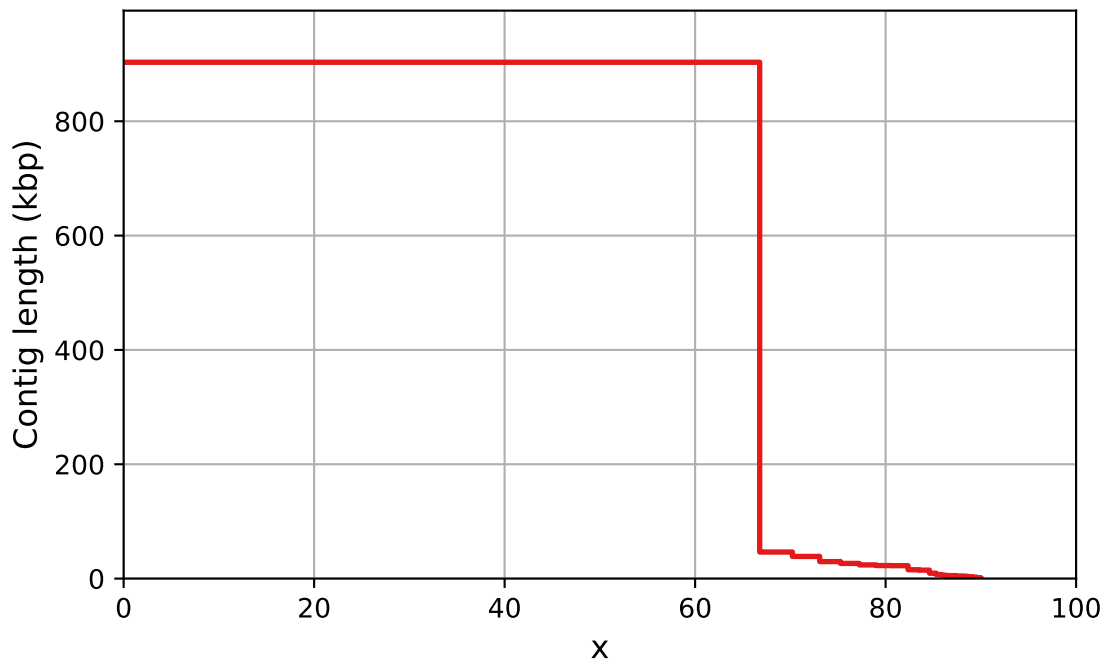
FRCurve (misassemblies)



Cumulative length (aligned contigs)

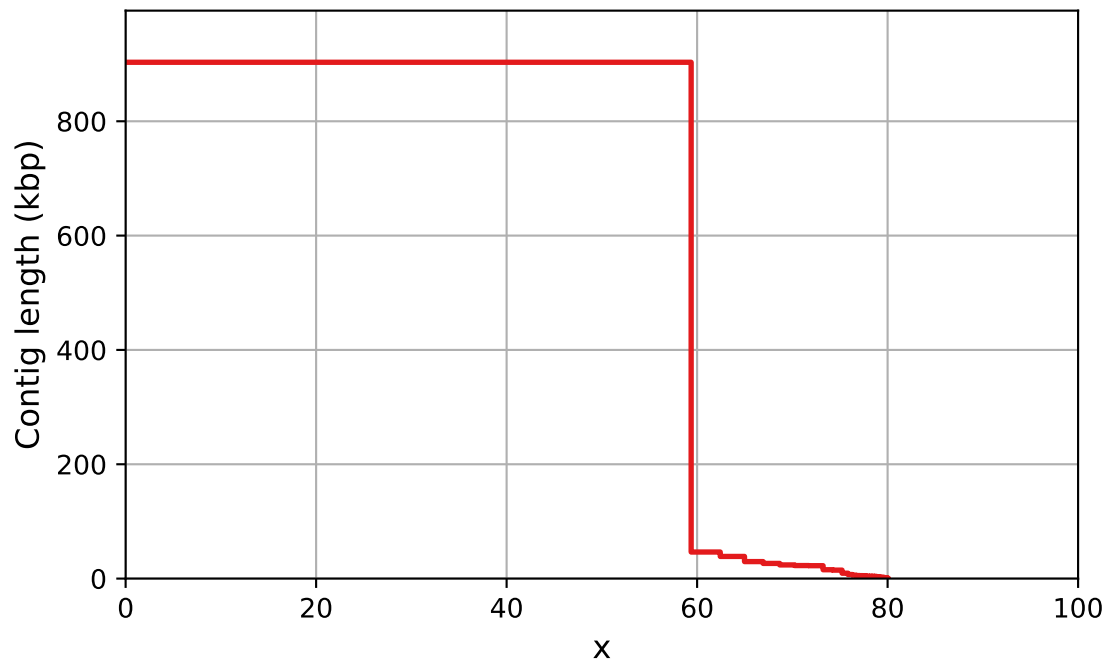


NAx

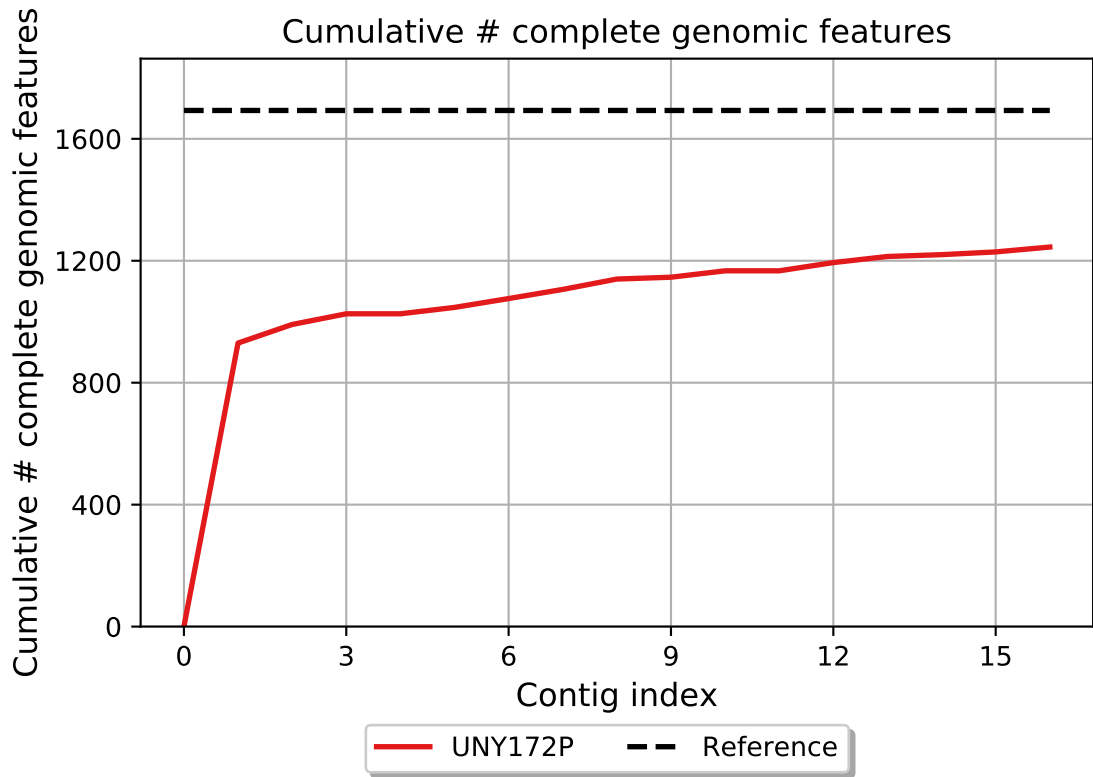


— UNY172P

NGAx



— UNY172P



FRCurve (genomic features)

