

Report

	UNY1090P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1413250
Total length (>= 1000 bp)	1413250
Total length (>= 5000 bp)	1413250
Total length (>= 10000 bp)	1413250
Total length (>= 25000 bp)	1287170
Total length (>= 50000 bp)	966596
# contigs	19
Largest contig	912713
Total length	1413250
Reference length	1521208
GC (%)	28.35
Reference GC (%)	28.18
N50	912713
NG50	912713
N90	25500
NG90	21337
auN	600073.1
auNG	557486.8
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	17
# misassembled contigs	9
Misassembled contigs length	263584
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	0 + 16 part
Unaligned length	168851
Genome fraction (%)	78.991
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	827.41
# indels per 100 kbp	42.21
# genomic features	1273 + 35 part
Largest alignment	904987
Total aligned length	1236632
NA50	904987
NGA50	904987
NA90	-
NGA90	-
auNA	584325.4
auNGA	542856.7
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

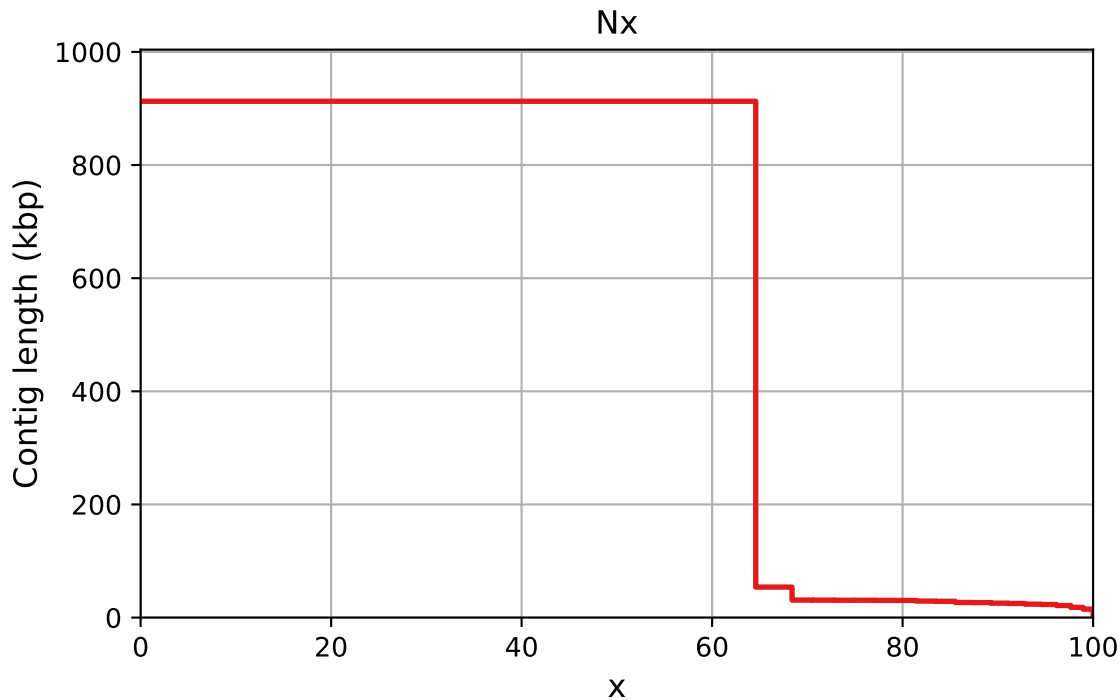
	UNY1090P
# misassemblies	17
# contig misassemblies	17
# c. relocations	3
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	263584
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	10232
# indels	522
# indels (<= 5 bp)	469
# indels (> 5 bp)	53
Indels length	2307

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

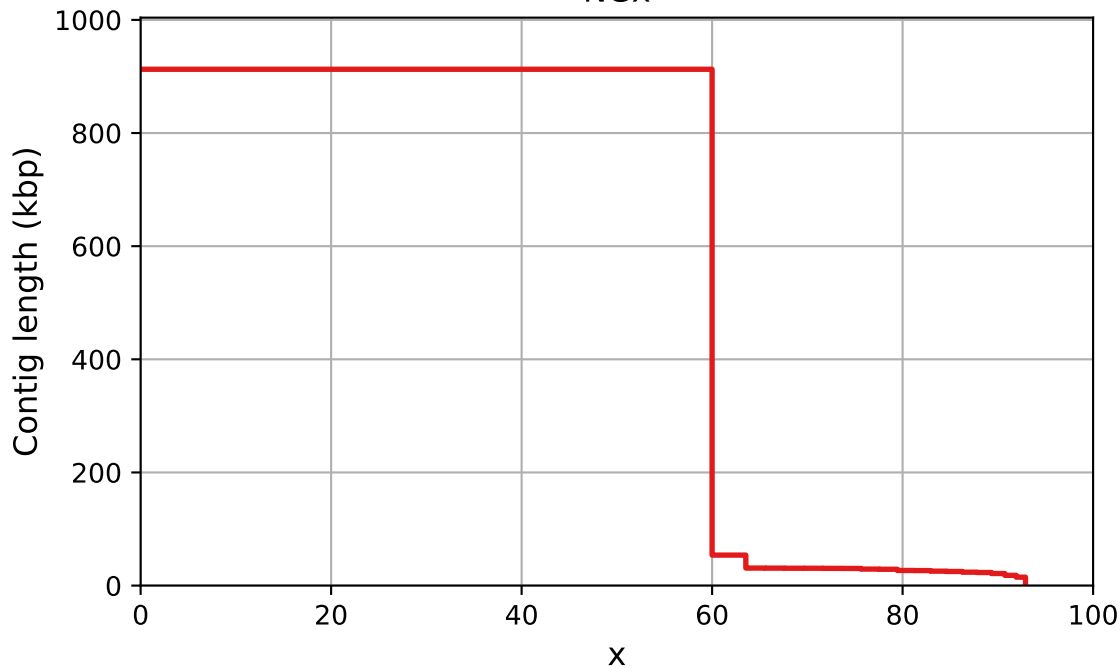
	UNY1090P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
Partially unaligned length	168851
# N's	0

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).

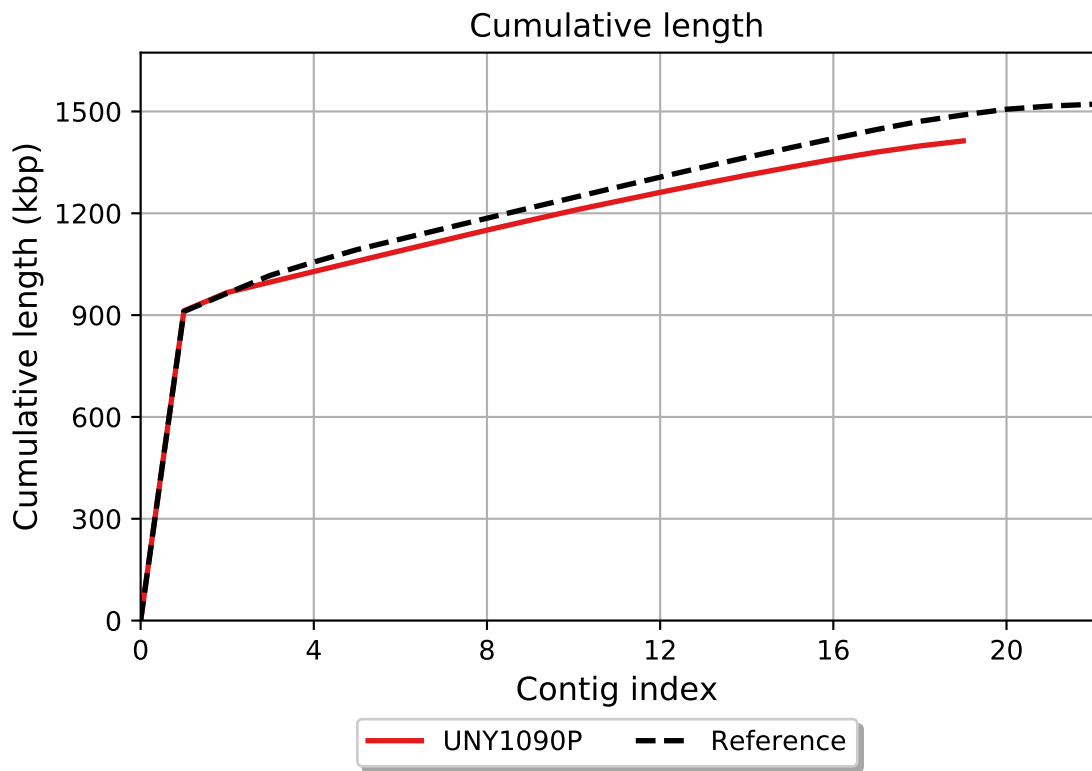


— UNY1090P

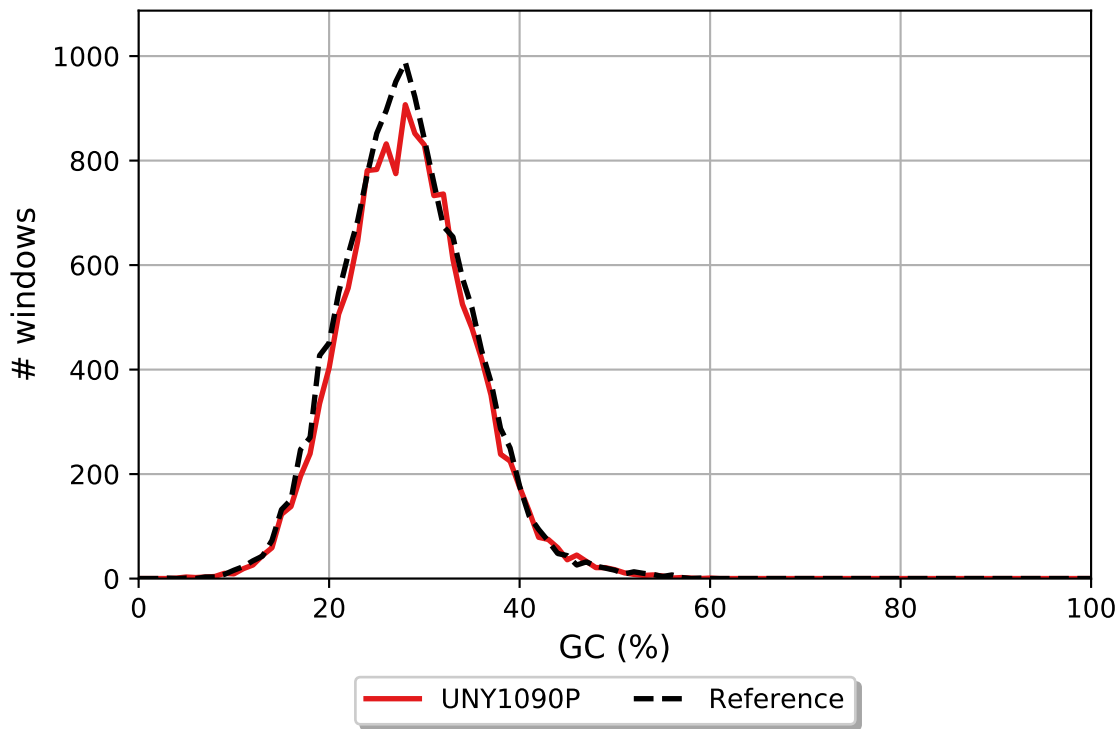
NGx



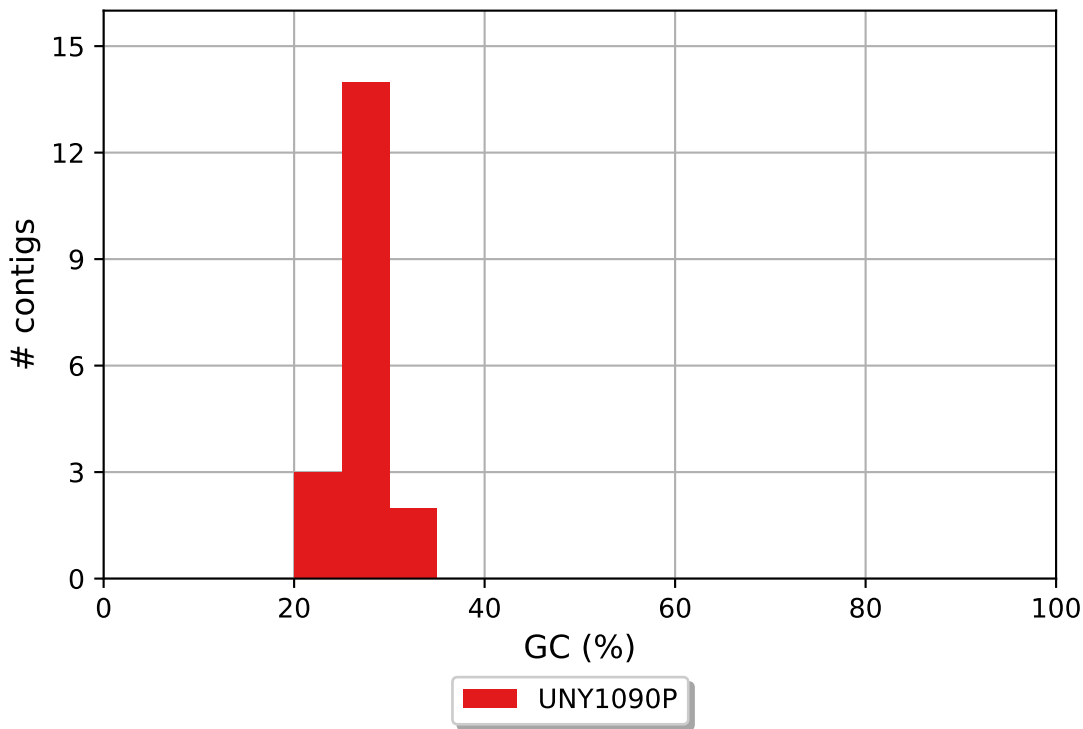
— UNY1090P



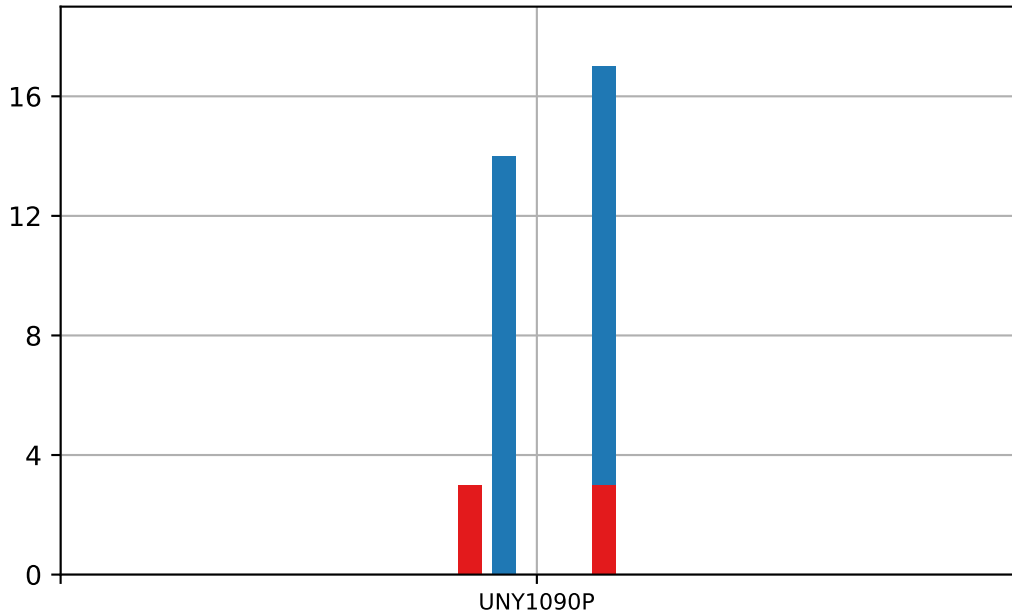
GC content



UNY1090P GC content



Misassemblies

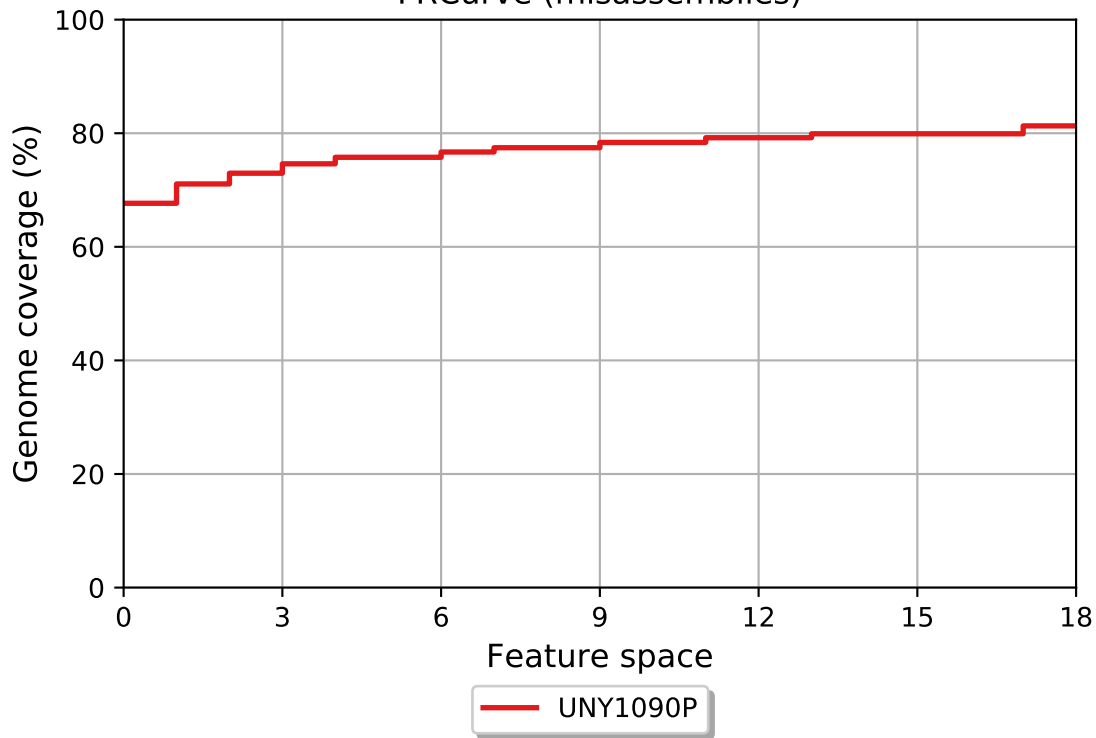


relocations

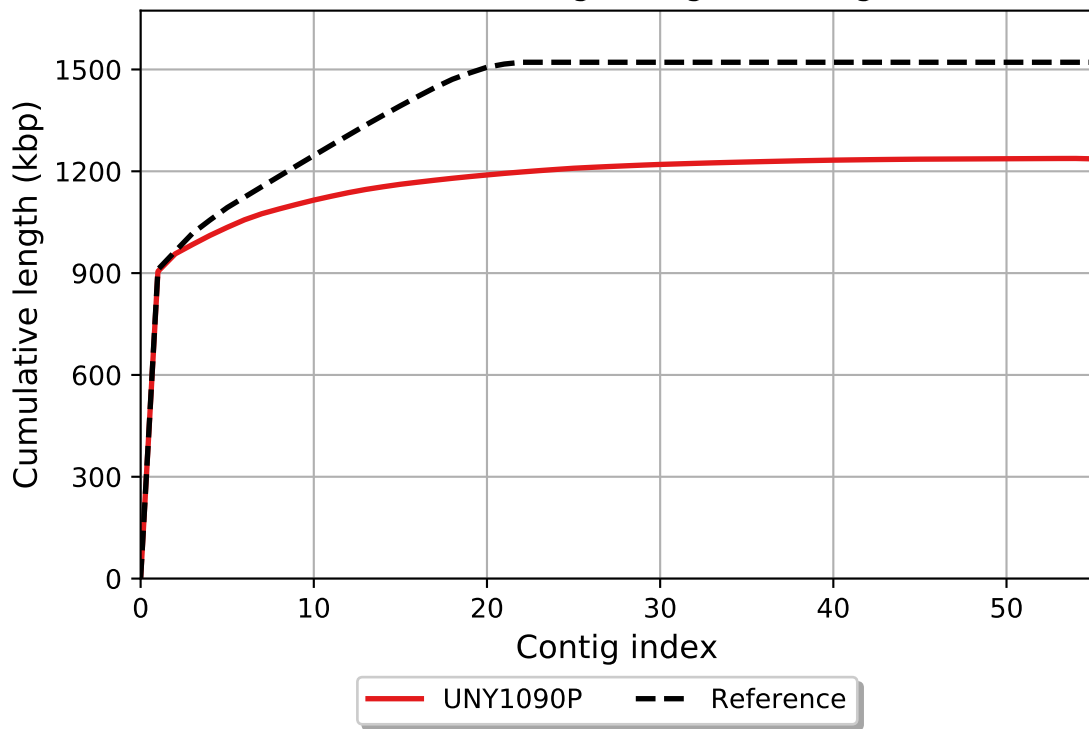


translocations

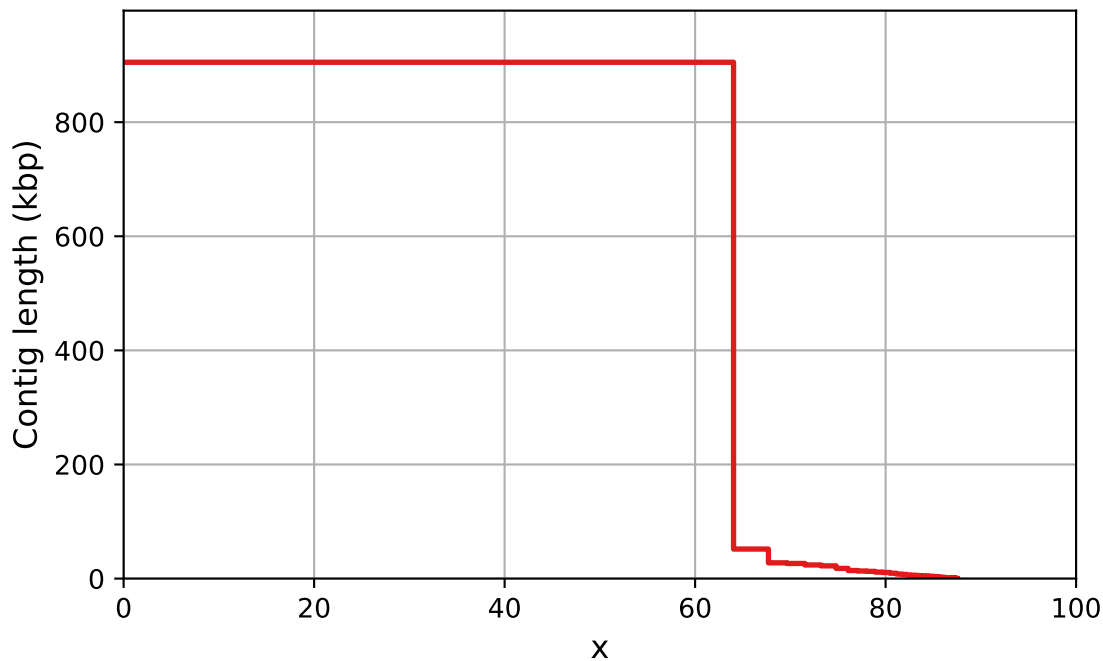
FRCurve (misassemblies)



Cumulative length (aligned contigs)

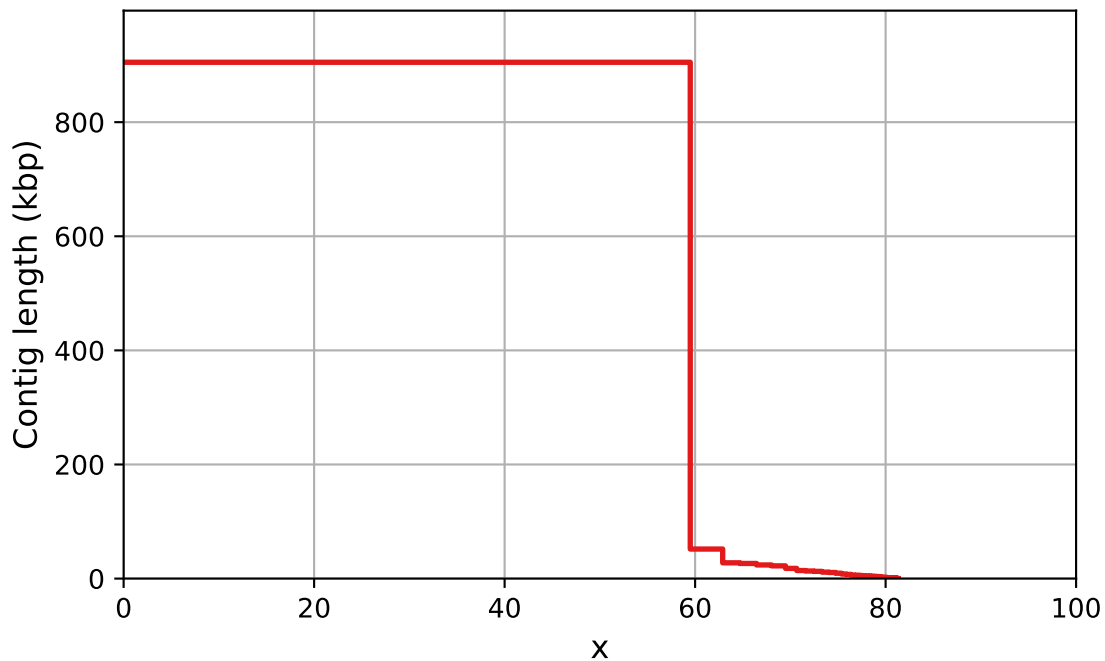


NAx

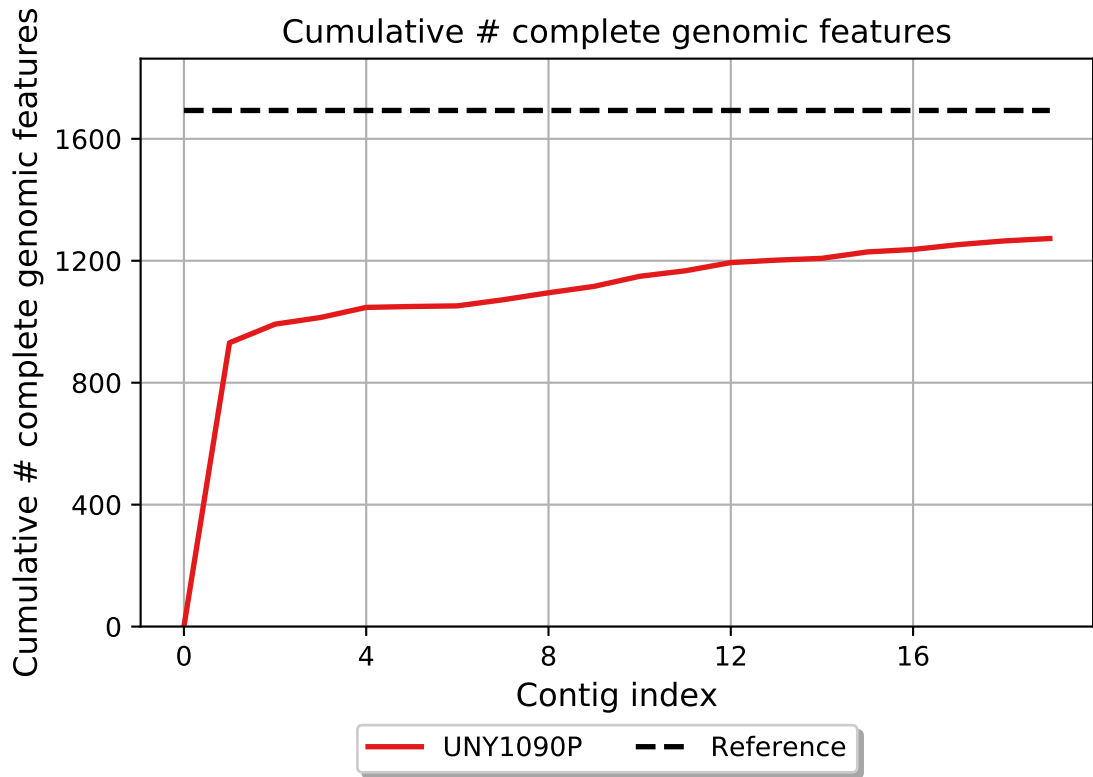


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NGAx



— UNY1090P



FRCurve (genomic features)

