

Report

	UNY1085P
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1409080
Total length (>= 1000 bp)	1409080
Total length (>= 5000 bp)	1409080
Total length (>= 10000 bp)	1409080
Total length (>= 25000 bp)	1323667
Total length (>= 50000 bp)	957251
# contigs	18
Largest contig	903386
Total length	1409080
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	903386
NG50	903386
N90	27704
NG90	22534
auN	590587.9
auNG	547055.8
L50	1
LG50	1
L90	12
LG90	16
# misassemblies	19
# misassembled contigs	7
Misassembled contigs length	218340
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	2 + 11 part
Unaligned length	163200
Genome fraction (%)	79.803
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	878.26
# indels per 100 kbp	57.40
# genomic features	1261 + 45 part
Largest alignment	903207
Total aligned length	1242119
NA50	903207
NGA50	903207
NA90	-
NGA90	-
auNA	584534.5
auNGA	541448.5
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

	UNY1085P
# misassemblies	19
# contig misassemblies	19
# c. relocations	3
# c. translocations	16
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	218340
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	10909
# indels	713
# indels (<= 5 bp)	615
# indels (> 5 bp)	98
Indels length	3266

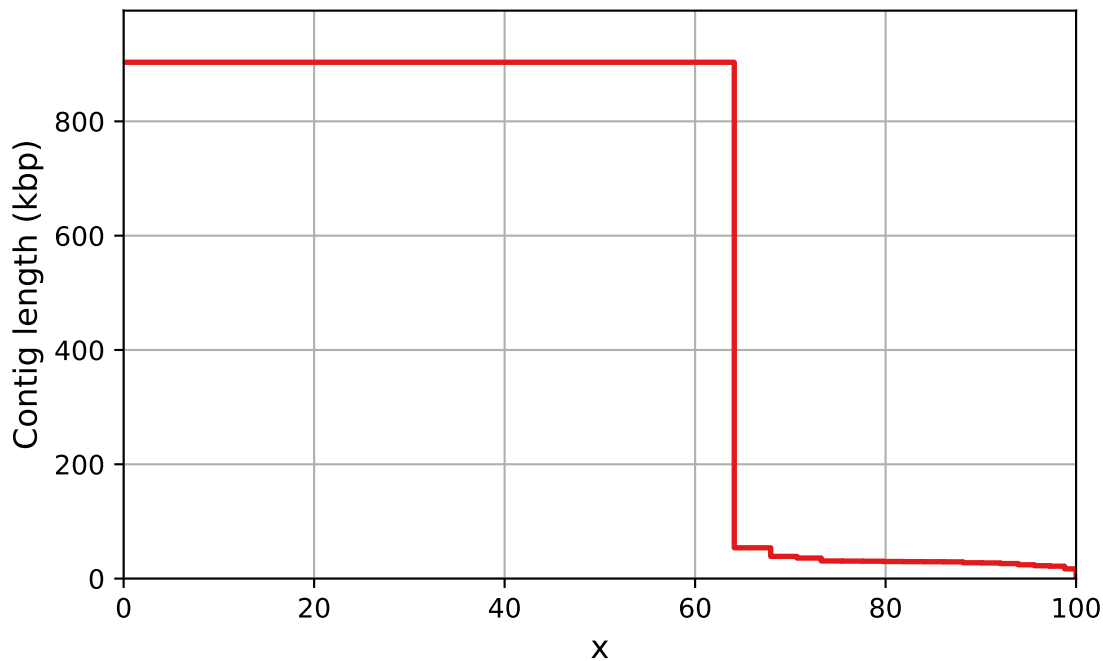
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	UNY1085P
# fully unaligned contigs	2
Fully unaligned length	63650
# partially unaligned contigs	11
Partially unaligned length	99550
# N's	0

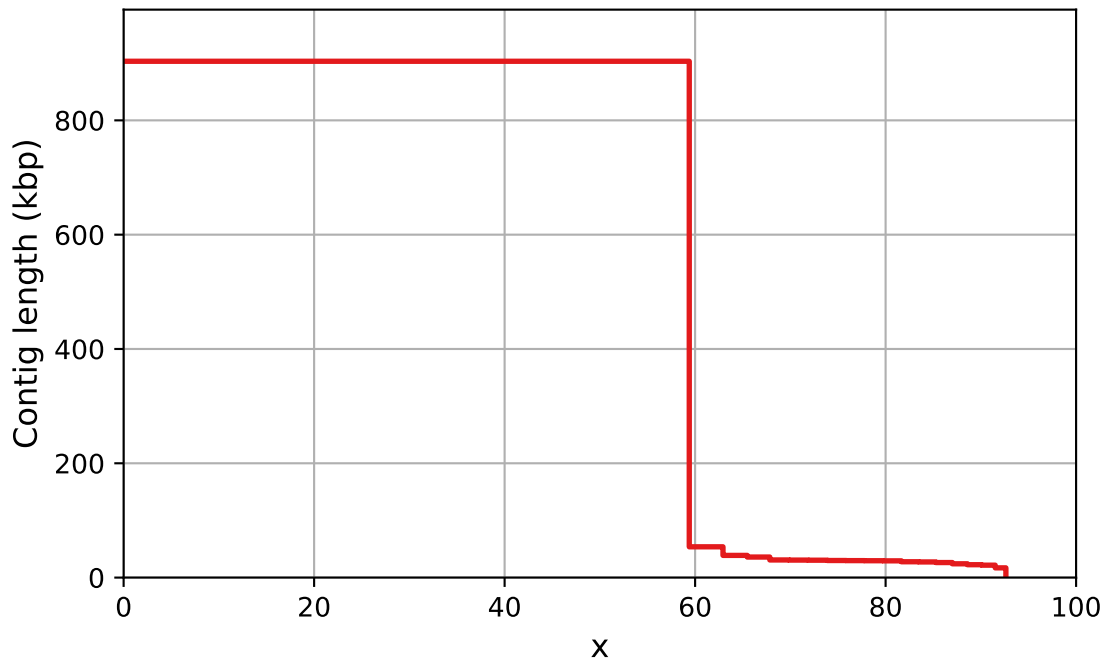
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

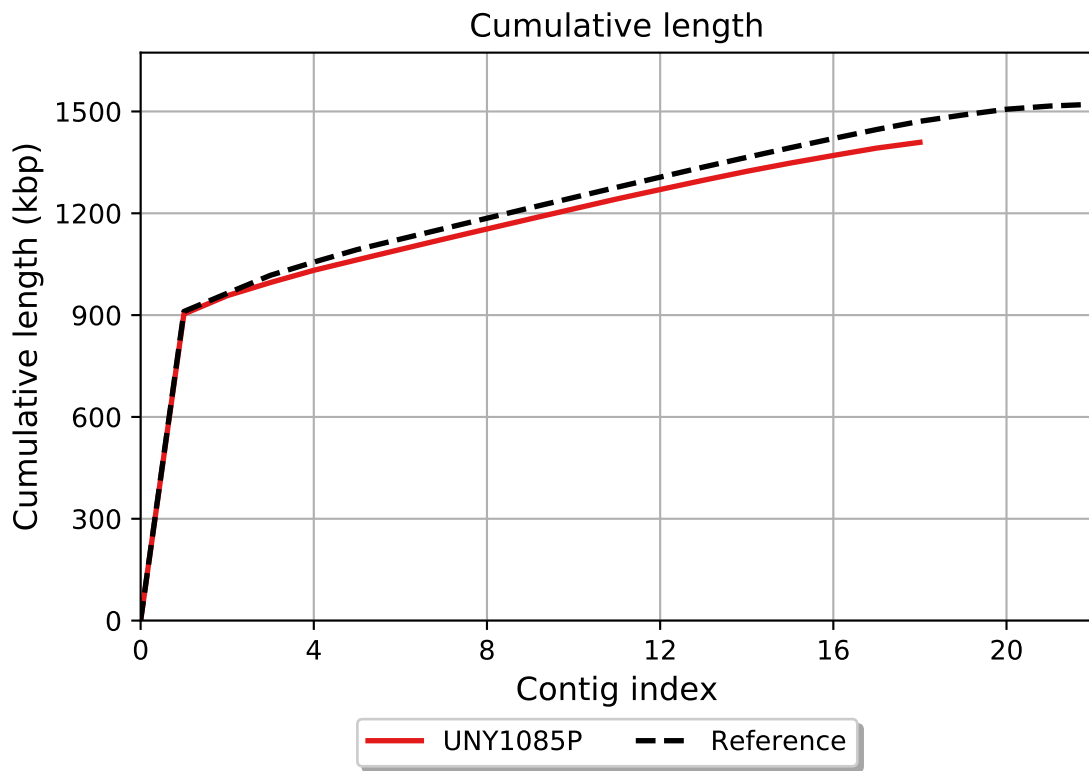


UNY1085P

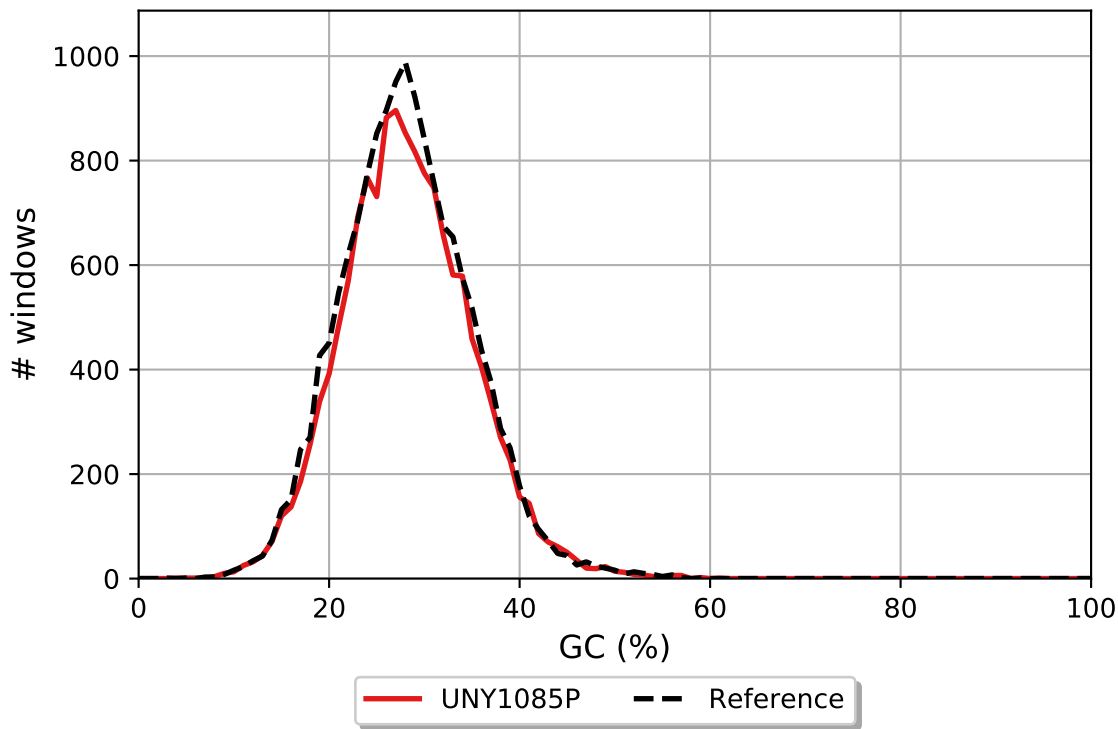
NGx



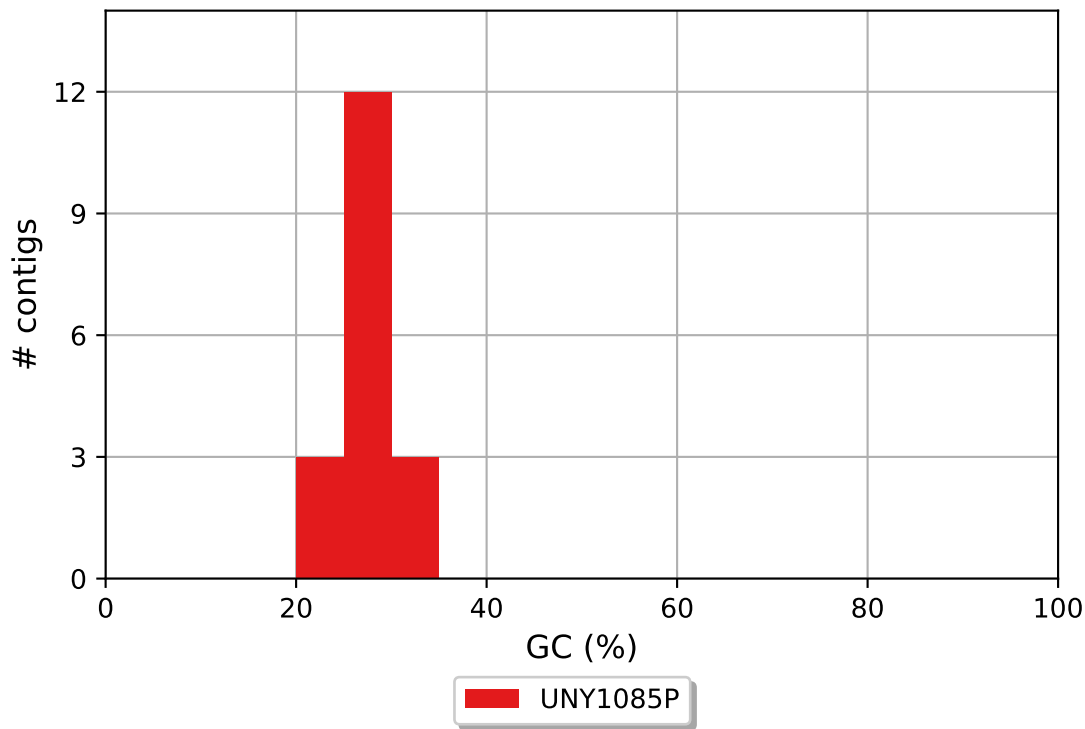
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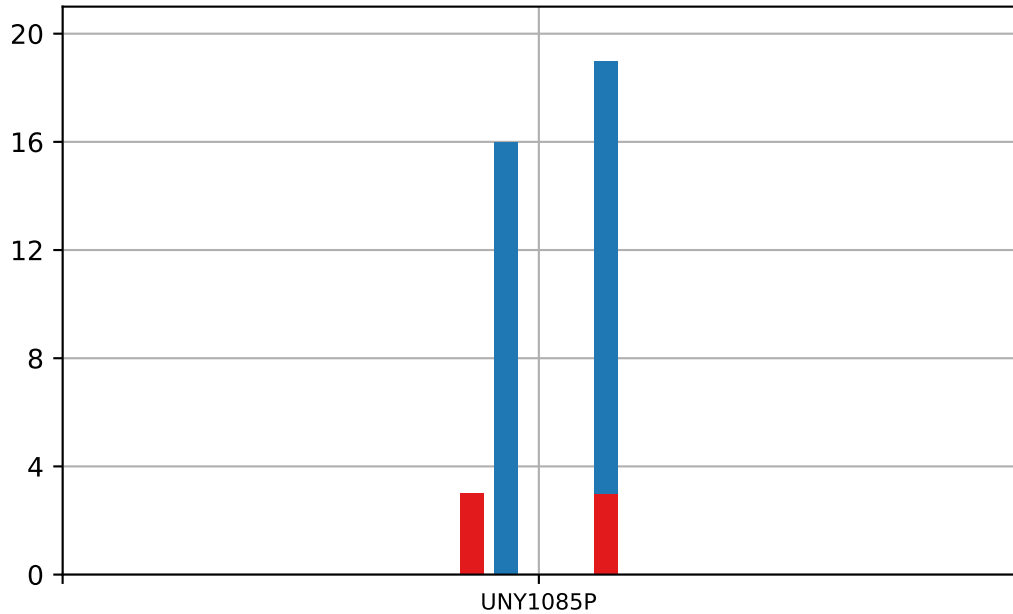
GC content



UNY1085P GC content



Misassemblies

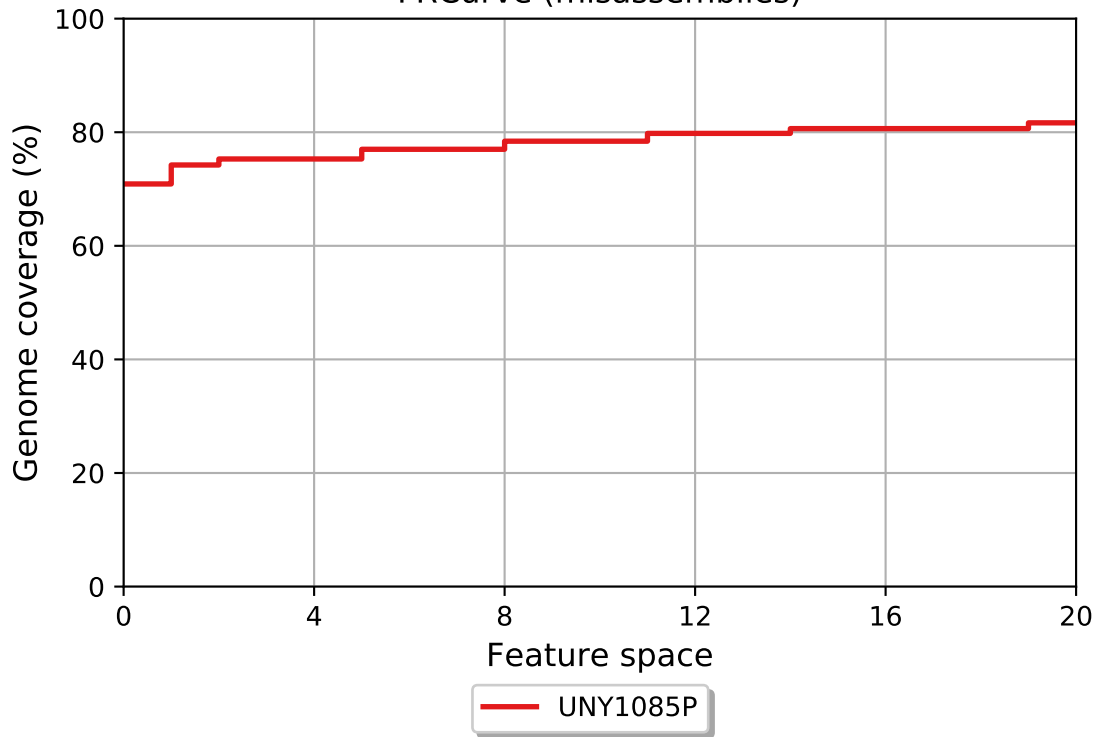


relocations

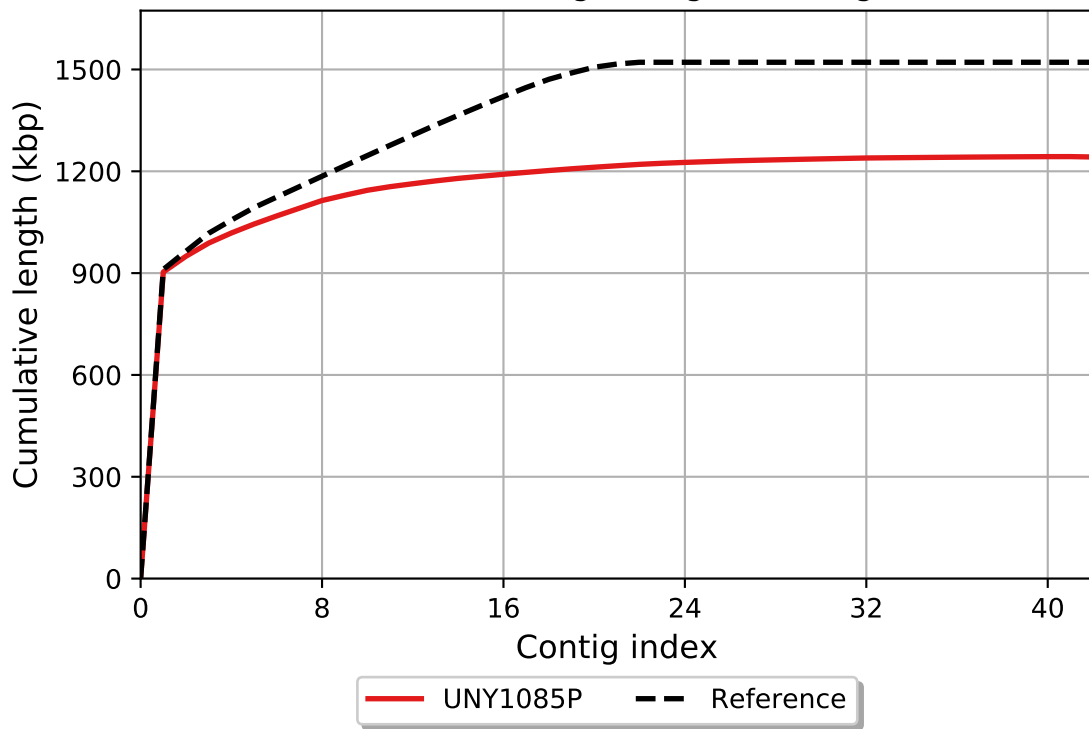


translocations

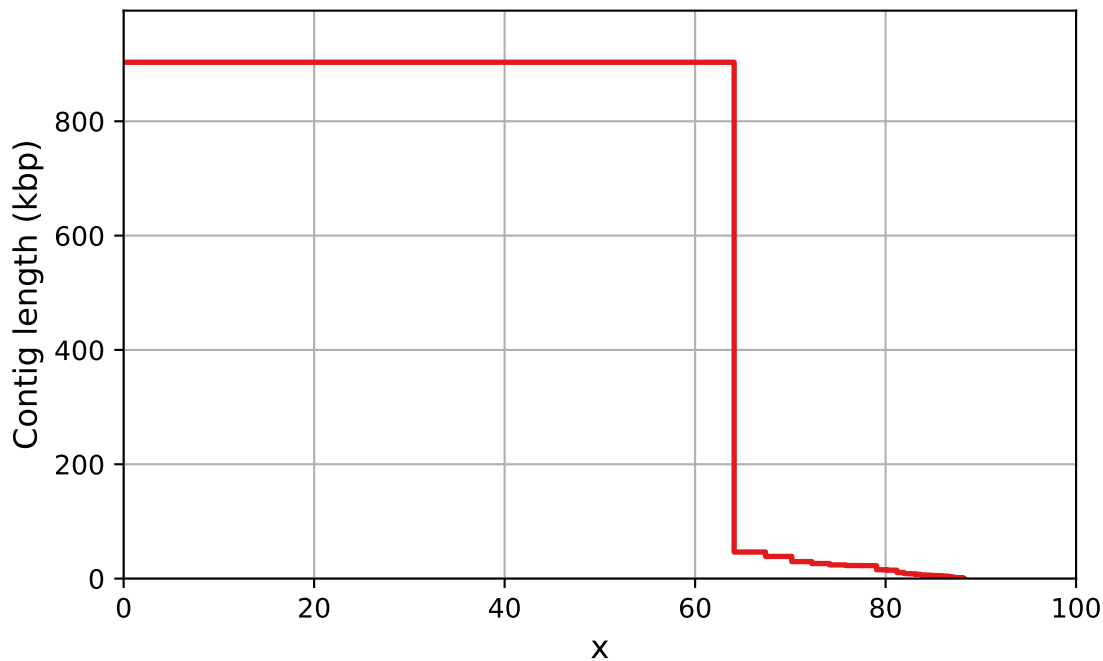
FRCurve (misassemblies)



Cumulative length (aligned contigs)

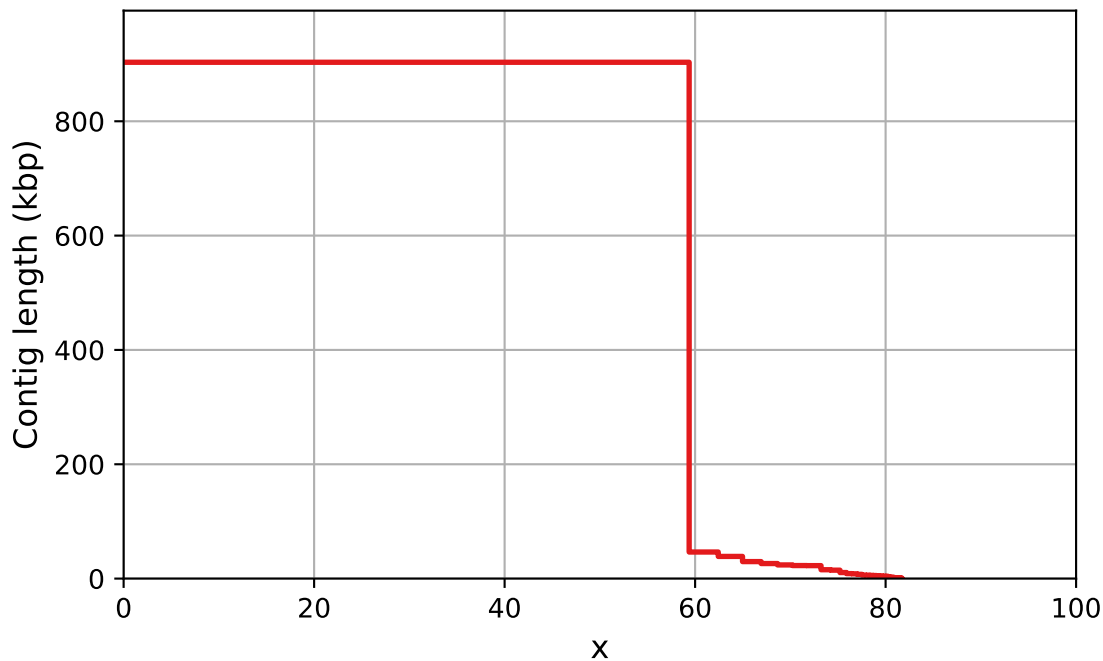


NAx

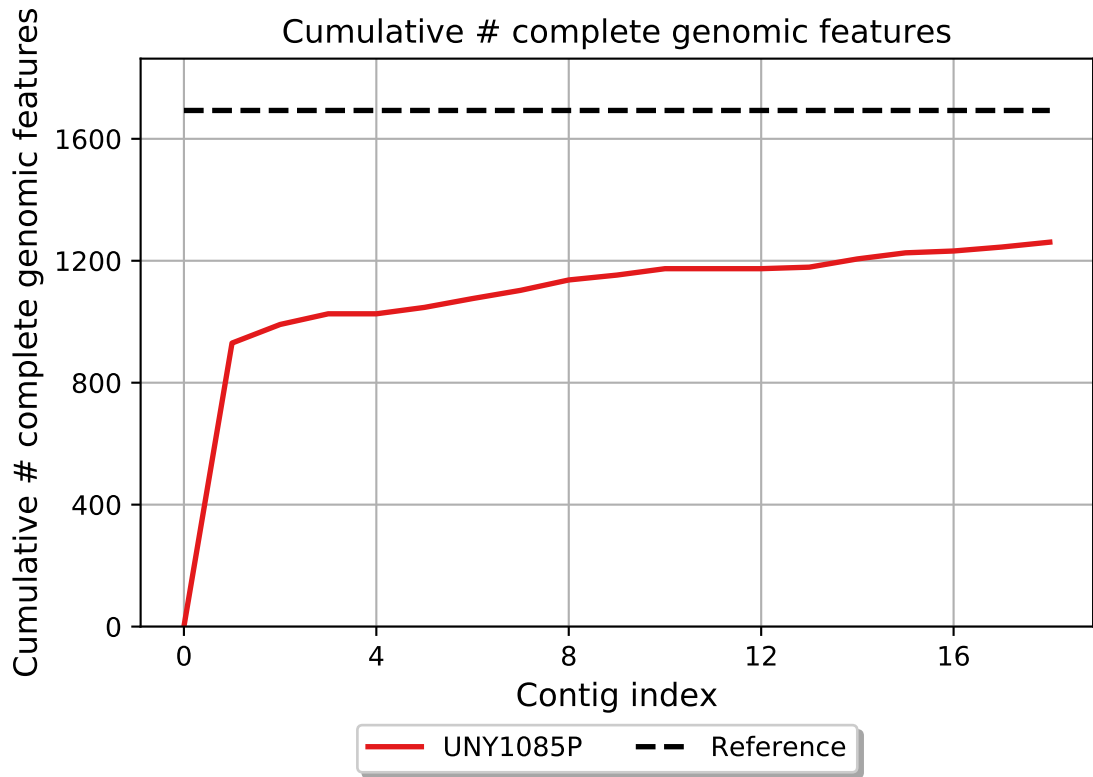


UNY1085P

NGAx



UNY1085P



FRCurve (genomic features)

