

Report

	UNY1083P
# contigs (>= 0 bp)	226
# contigs (>= 1000 bp)	33
# contigs (>= 5000 bp)	23
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1494188
Total length (>= 1000 bp)	1433590
Total length (>= 5000 bp)	1410159
Total length (>= 10000 bp)	1376368
Total length (>= 25000 bp)	1221987
Total length (>= 50000 bp)	1032502
# contigs	59
Largest contig	923130
Total length	1449517
Reference length	1521208
GC (%)	28.28
Reference GC (%)	28.18
N50	923130
NG50	923130
N90	16711
NG90	13481
auN	598346.9
auNG	570148.2
L50	1
LG50	1
L90	14
LG90	18
# misassemblies	28
# misassembled contigs	12
Misassembled contigs length	1177439
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	21 + 19 part
Unaligned length	192215
Genome fraction (%)	80.312
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	795.09
# indels per 100 kbp	55.07
# genomic features	1279 + 56 part
Largest alignment	909598
Total aligned length	1251049
NA50	909598
NGA50	909598
NA90	-
NGA90	-
auNA	575253.7
auNGA	548143.3
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

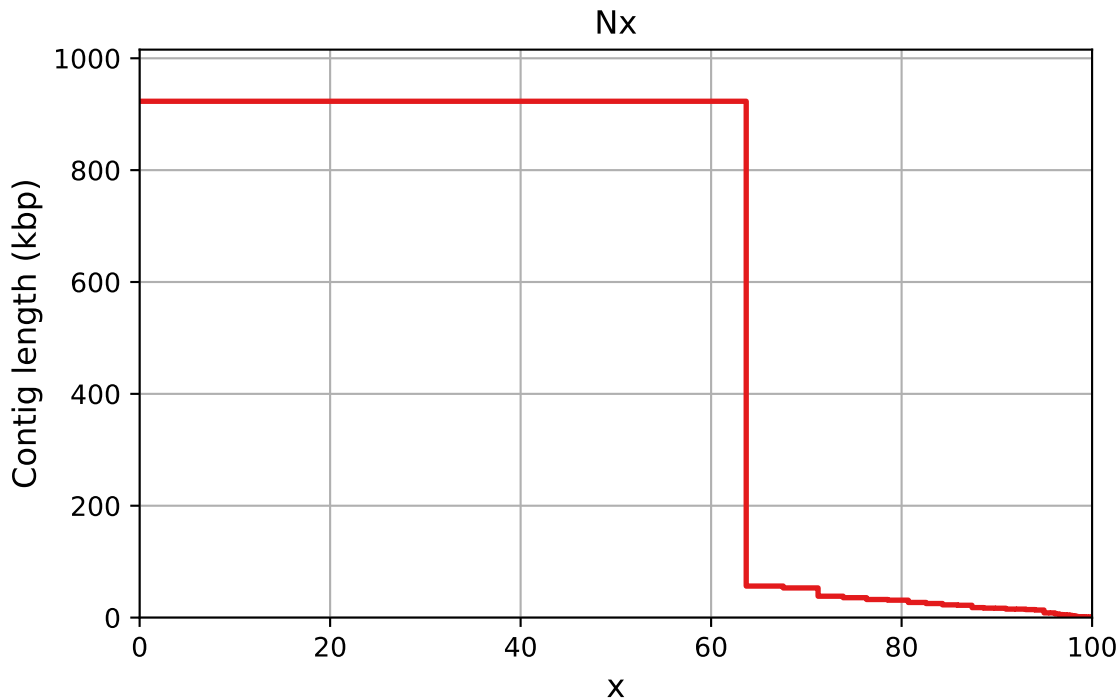
	UNY1083P
# misassemblies	28
# contig misassemblies	28
# c. relocations	4
# c. translocations	24
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	1177439
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	9947
# indels	689
# indels (<= 5 bp)	612
# indels (> 5 bp)	77
Indels length	3667

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

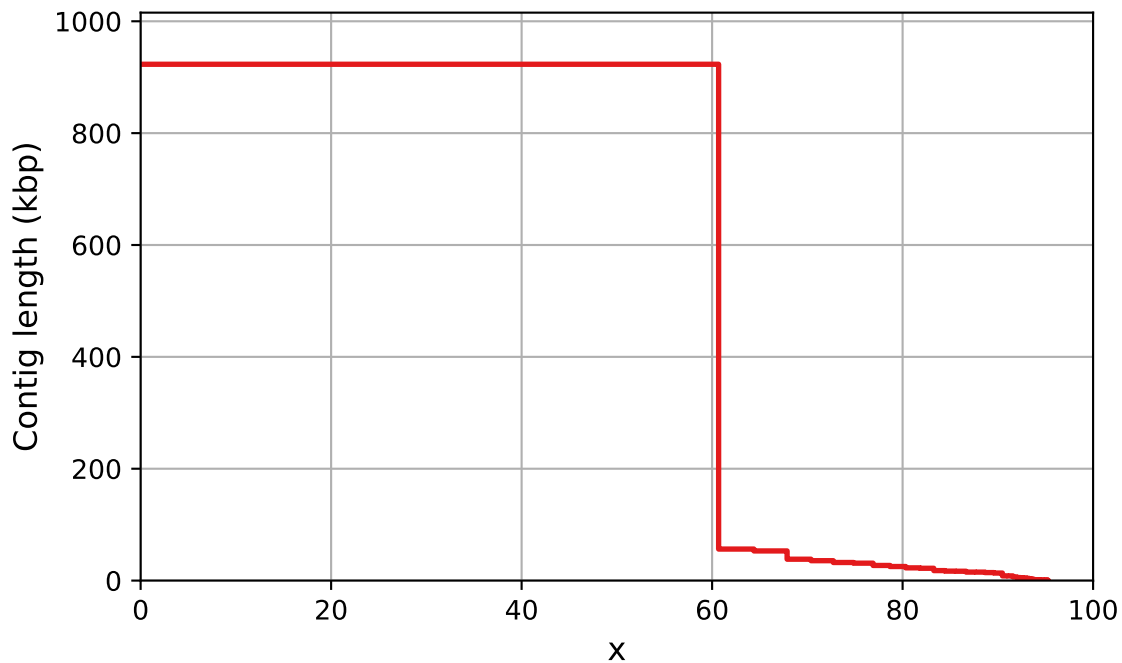
	UNY1083P
# fully unaligned contigs	21
Fully unaligned length	21724
# partially unaligned contigs	19
Partially unaligned length	170491
# N's	0

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).

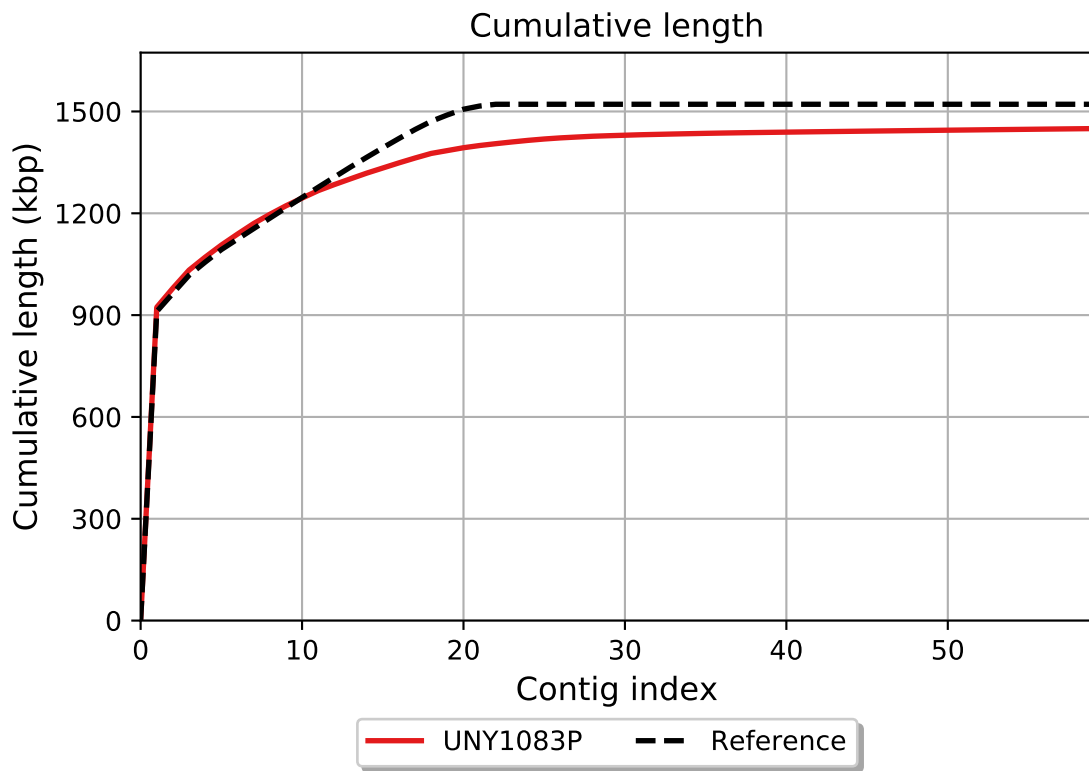


— UNY1083P

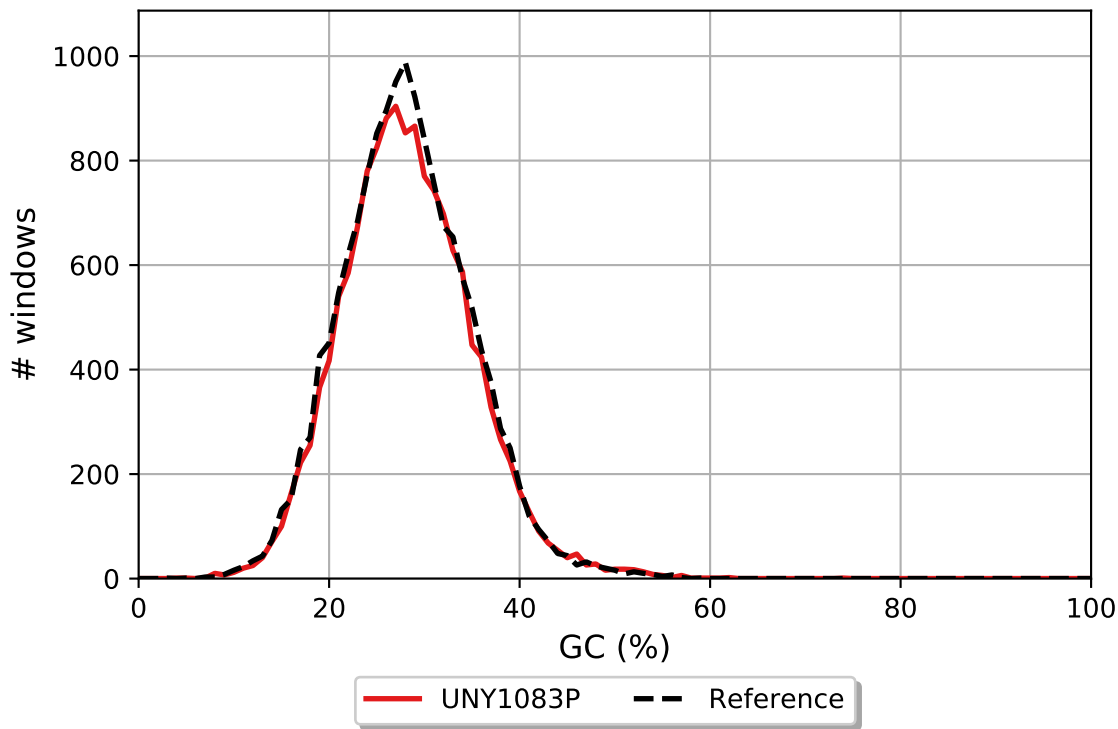
NGx



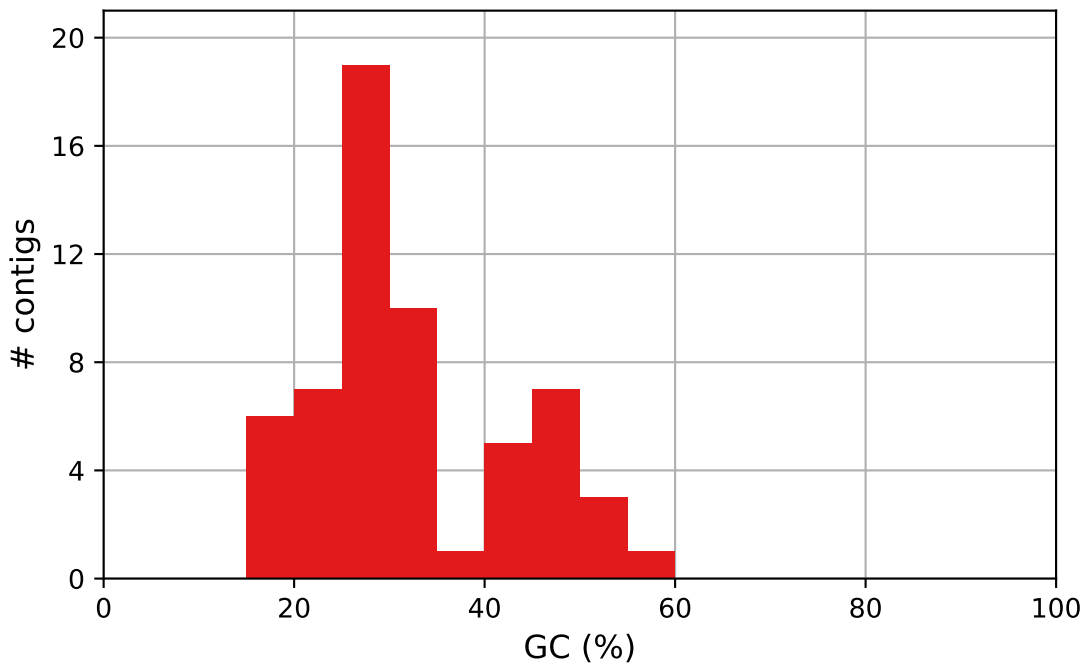
— UNY1083P



GC content

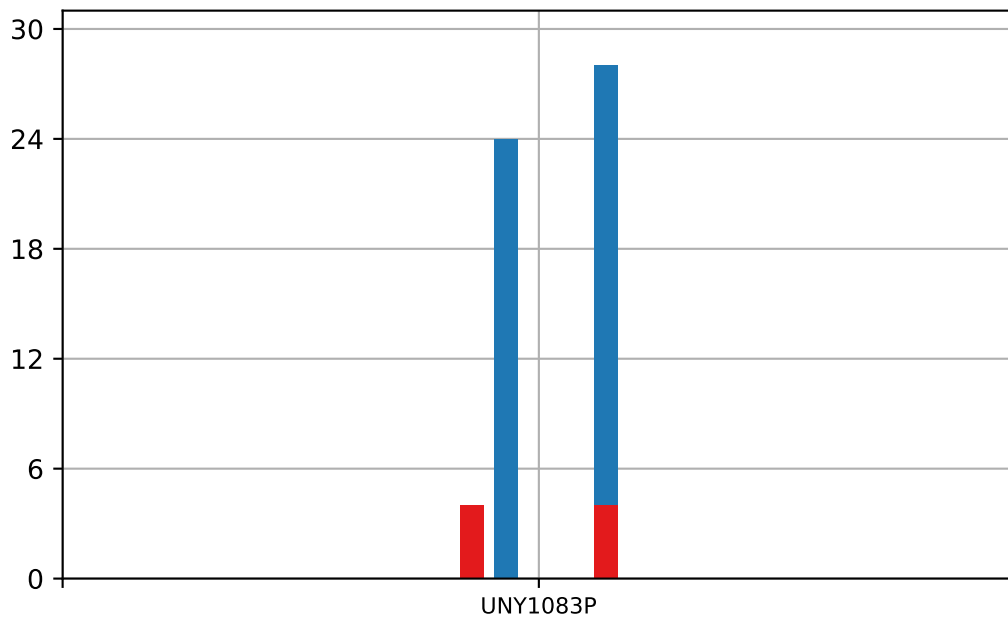


UNY1083P GC content



UNY1083P

Misassemblies

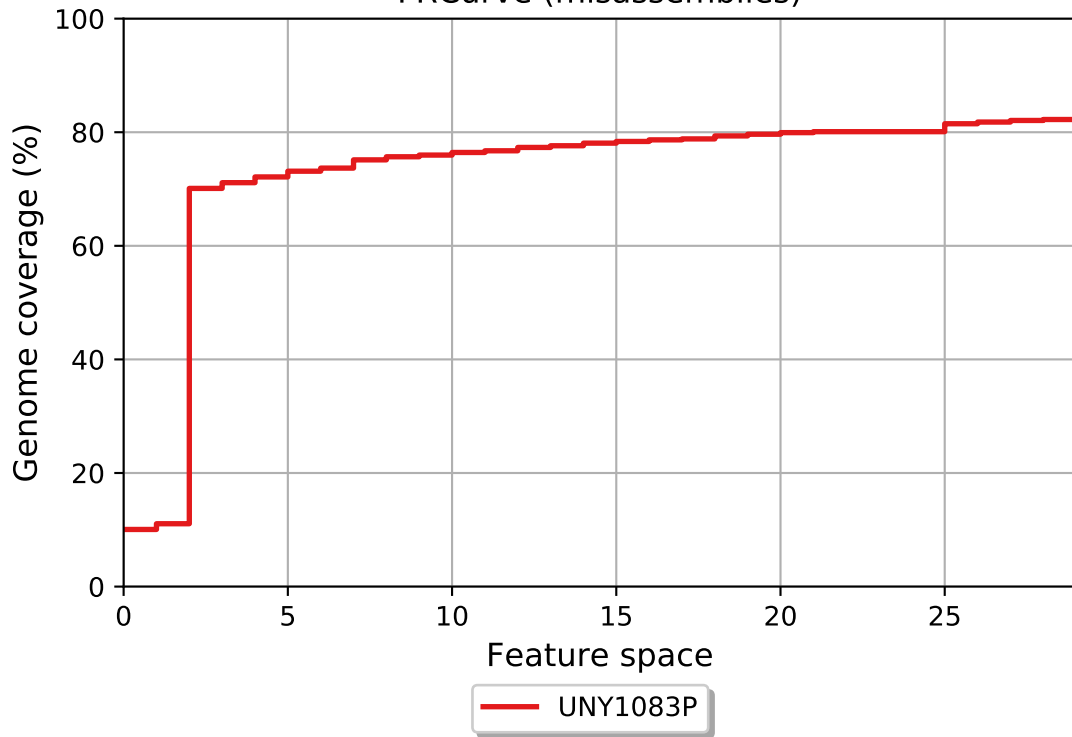


relocations

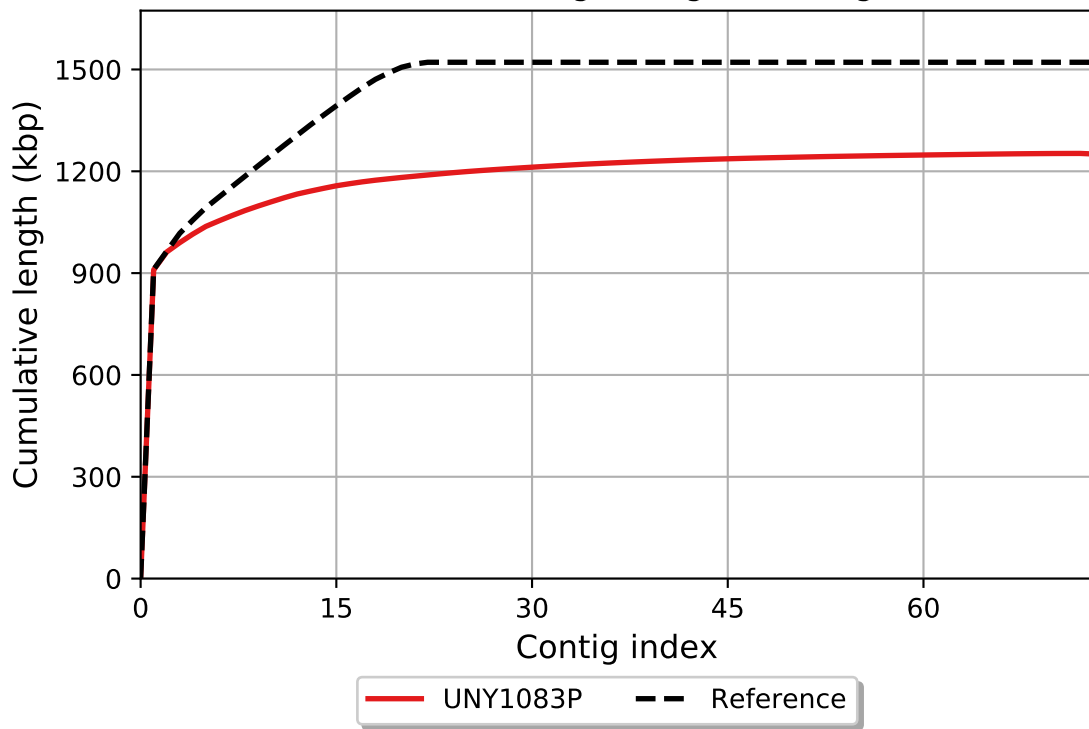


translocations

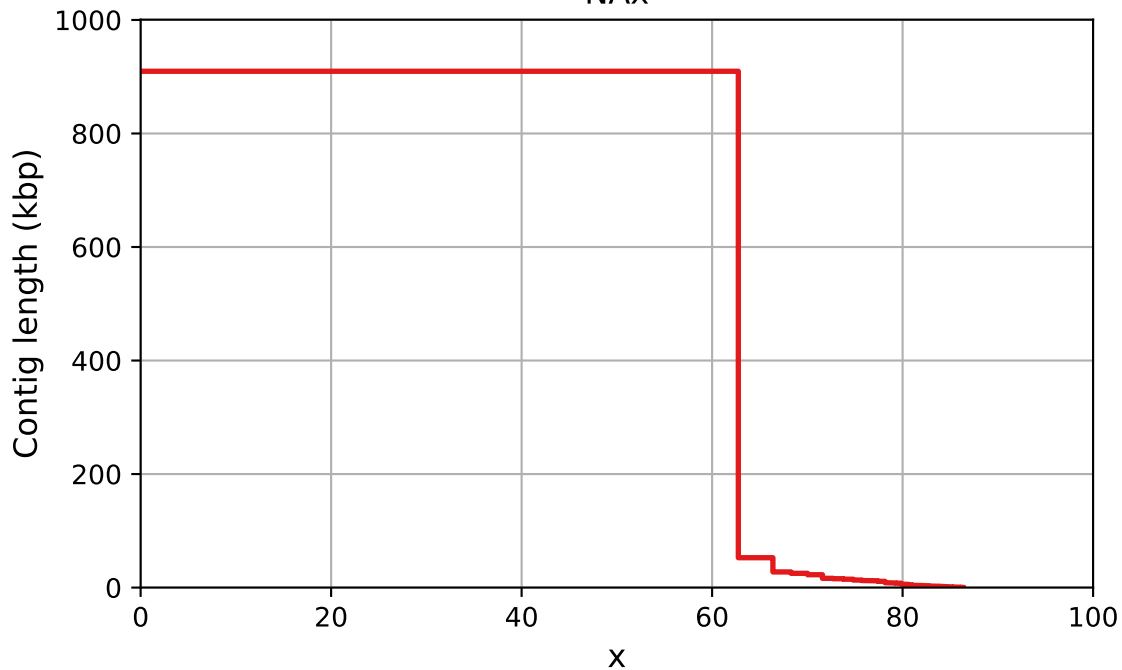
FRCurve (misassemblies)



Cumulative length (aligned contigs)

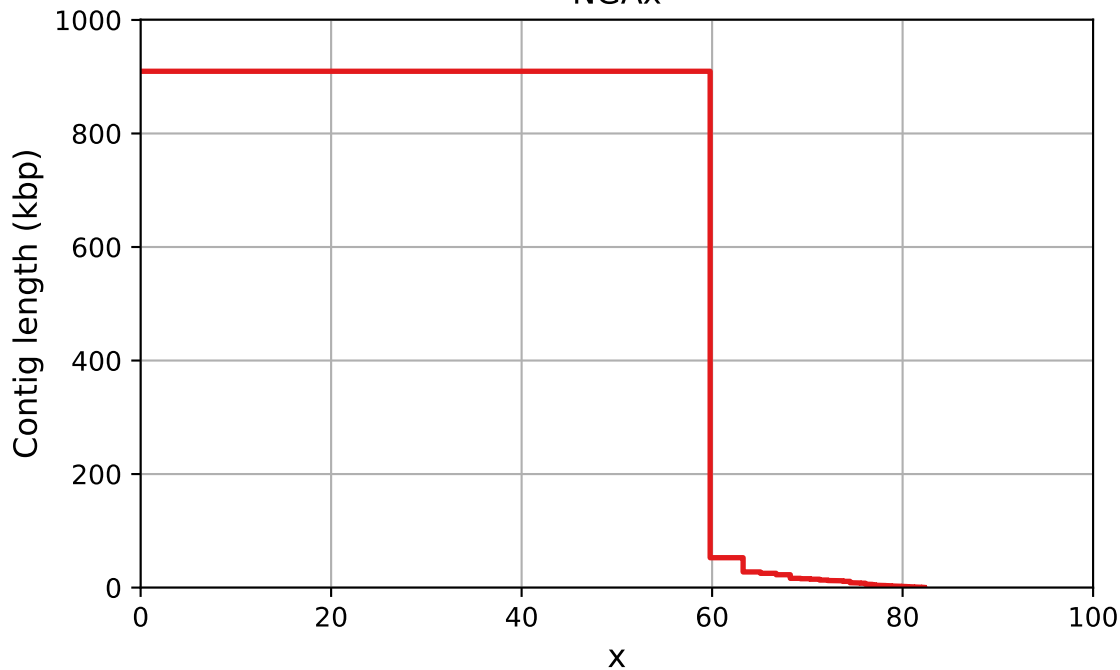


NAx

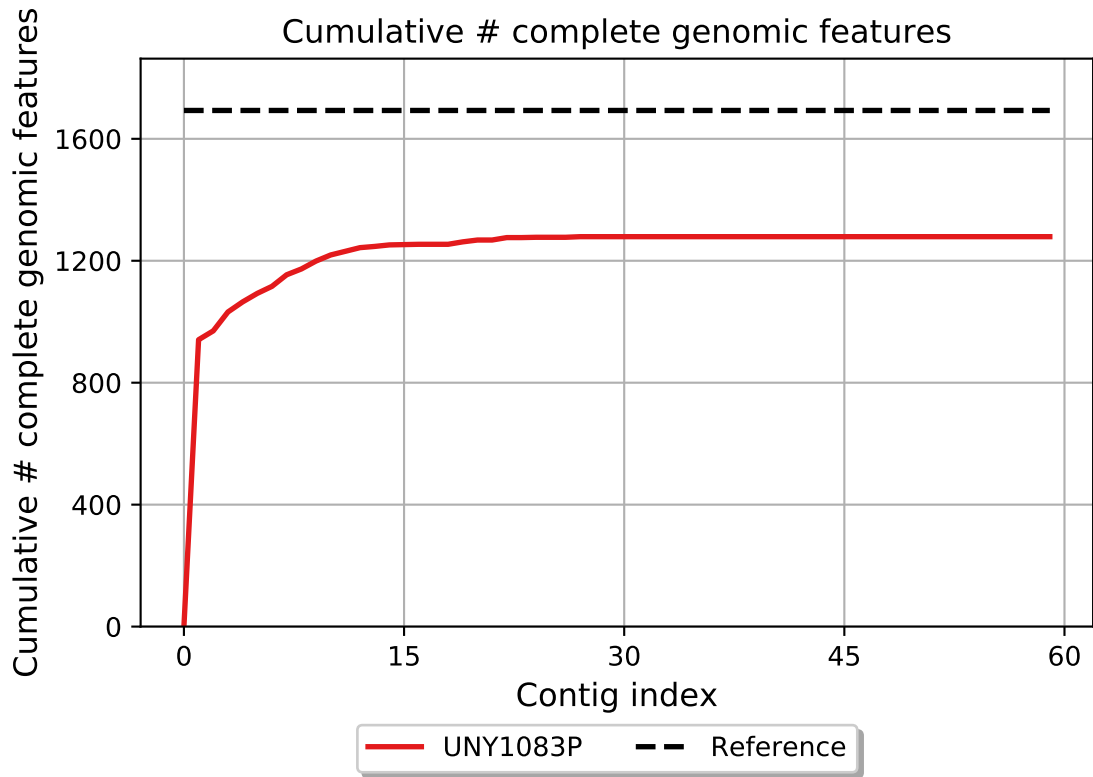


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NGAx



— UNY1083P



FRCurve (genomic features)

