

Report

	UNY203P
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1326072
Total length (>= 1000 bp)	1326072
Total length (>= 5000 bp)	1326072
Total length (>= 10000 bp)	1312122
Total length (>= 25000 bp)	1253245
Total length (>= 50000 bp)	963850
# contigs	17
Largest contig	910084
Total length	1326072
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	910084
NG50	910084
N90	27810
NG90	-
auN	634069.6
auNG	552733.1
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	15
# misassembled contigs	6
Misassembled contigs length	156154
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 12 part
Unaligned length	163060
Genome fraction (%)	74.574
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	731.32
# indels per 100 kbp	33.69
# genomic features	1184 + 50 part
Largest alignment	904630
Total aligned length	1157499
NA50	904630
NGA50	904630
NA90	-
NGA90	-
auNA	620935.1
auNGA	541283.4
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

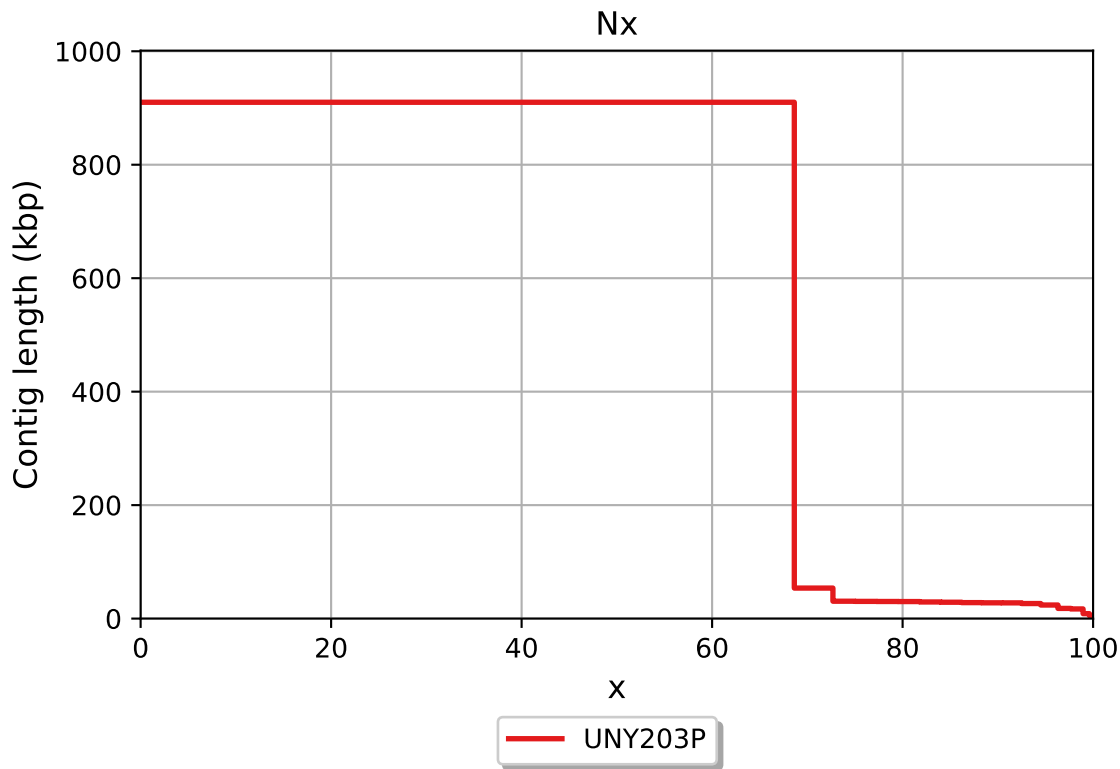
	UNY203P
# misassemblies	15
# contig misassemblies	15
# c. relocations	1
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	156154
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	8465
# indels	390
# indels (<= 5 bp)	353
# indels (> 5 bp)	37
Indels length	1466

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).

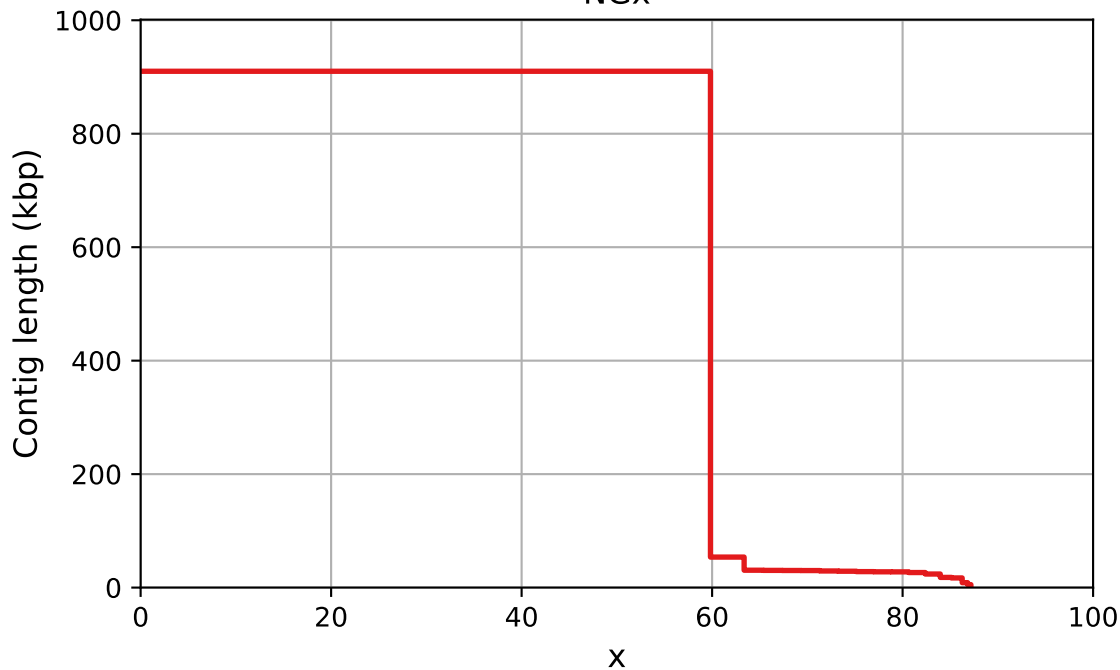
Unaligned report

	UNY203P
# fully unaligned contigs	1
Fully unaligned length	27704
# partially unaligned contigs	12
Partially unaligned length	135356
# N's	0

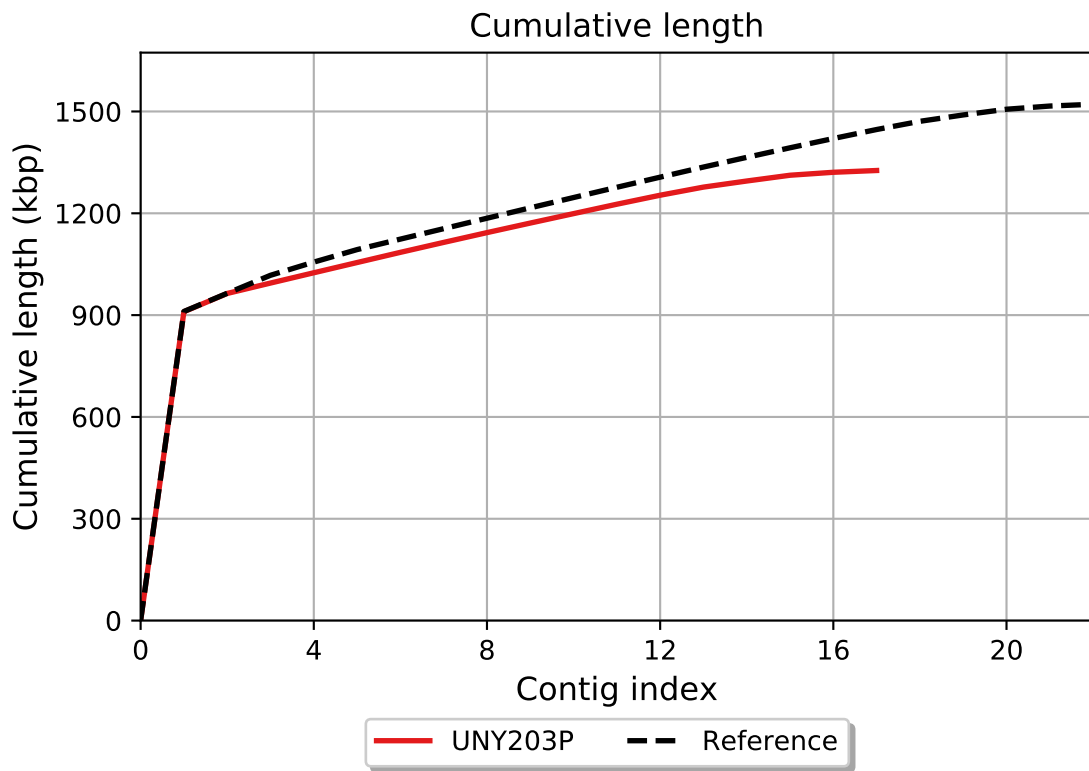
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



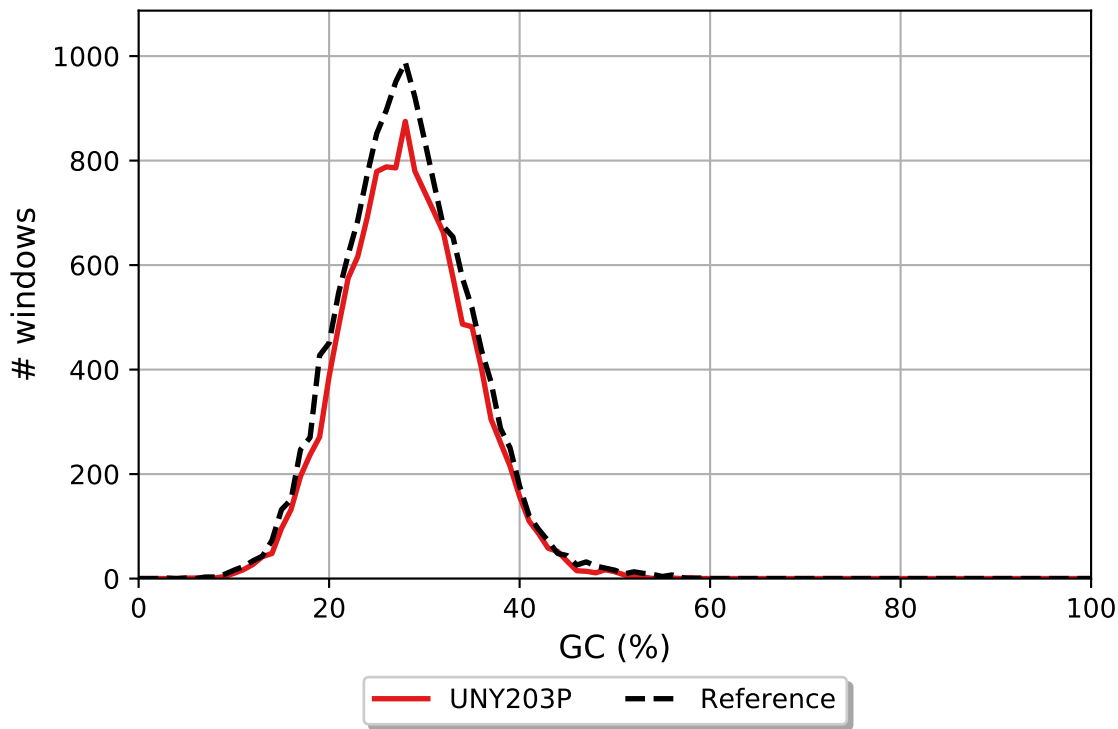
NGx



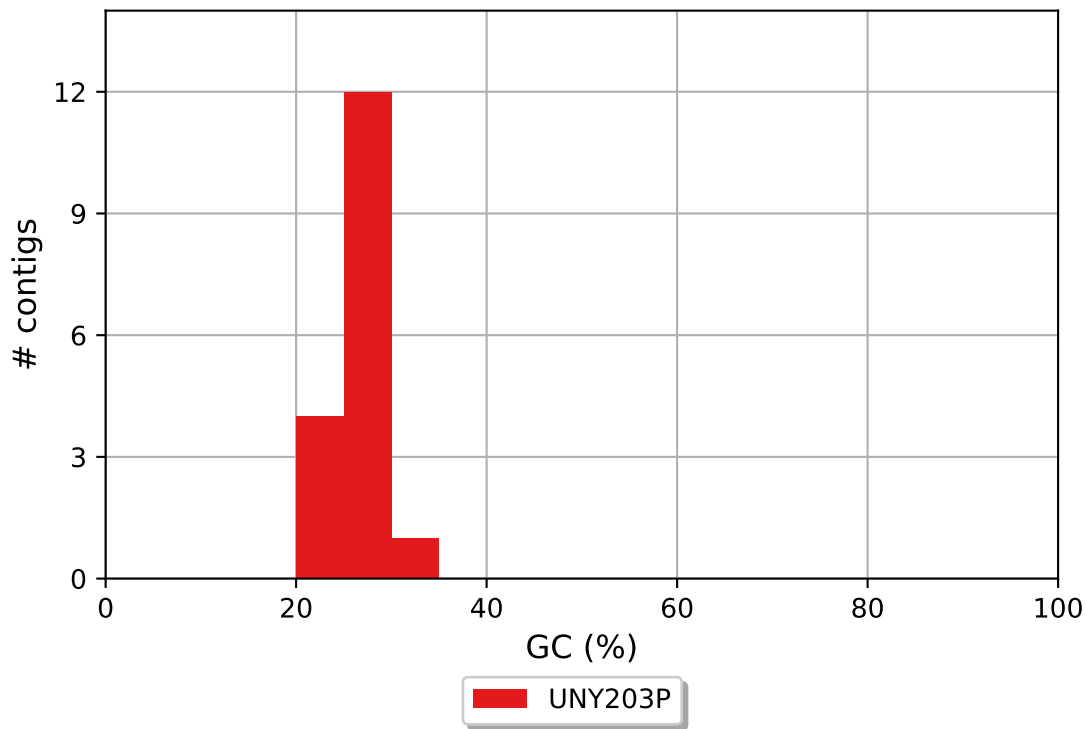
— UNY203P



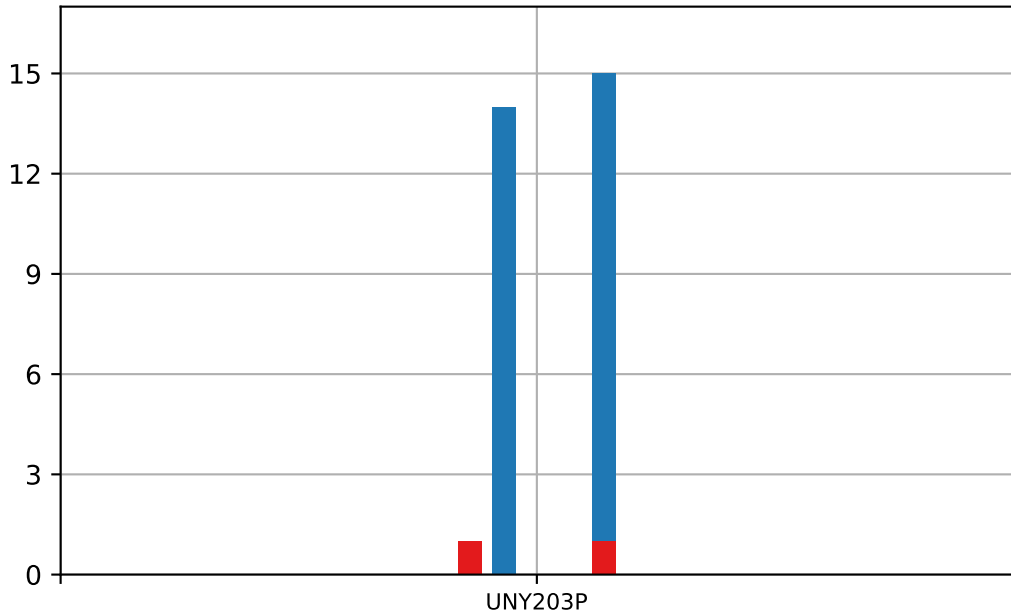
GC content



UNY203P GC content



Misassemblies

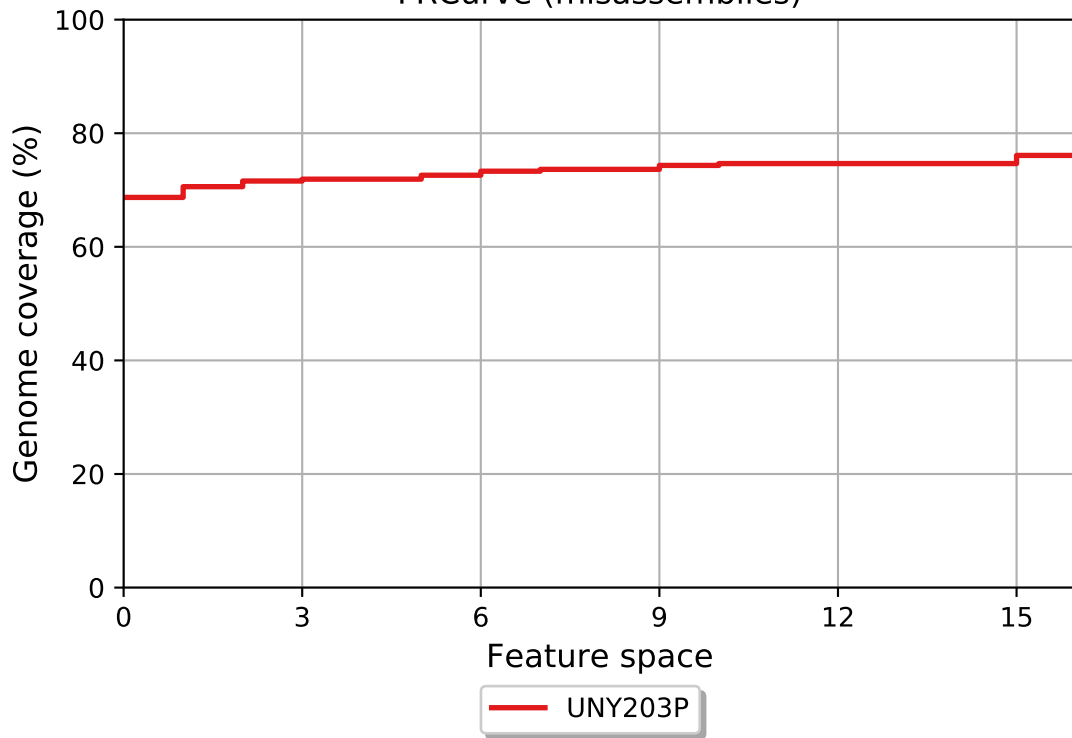


relocations

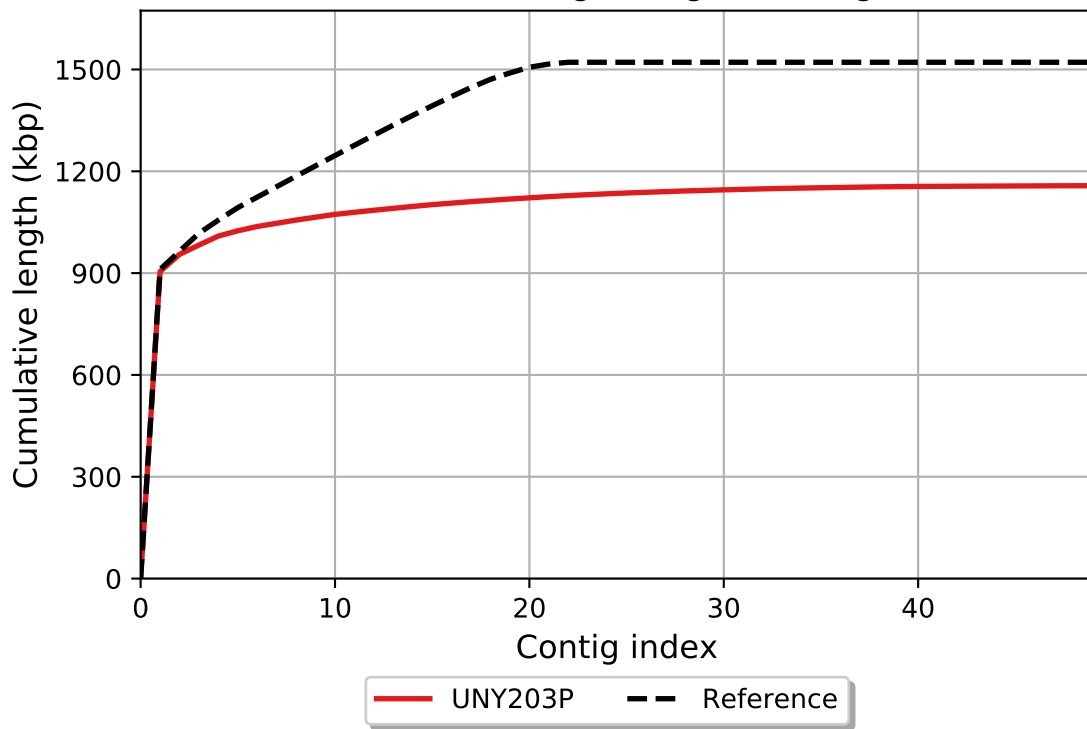


translocations

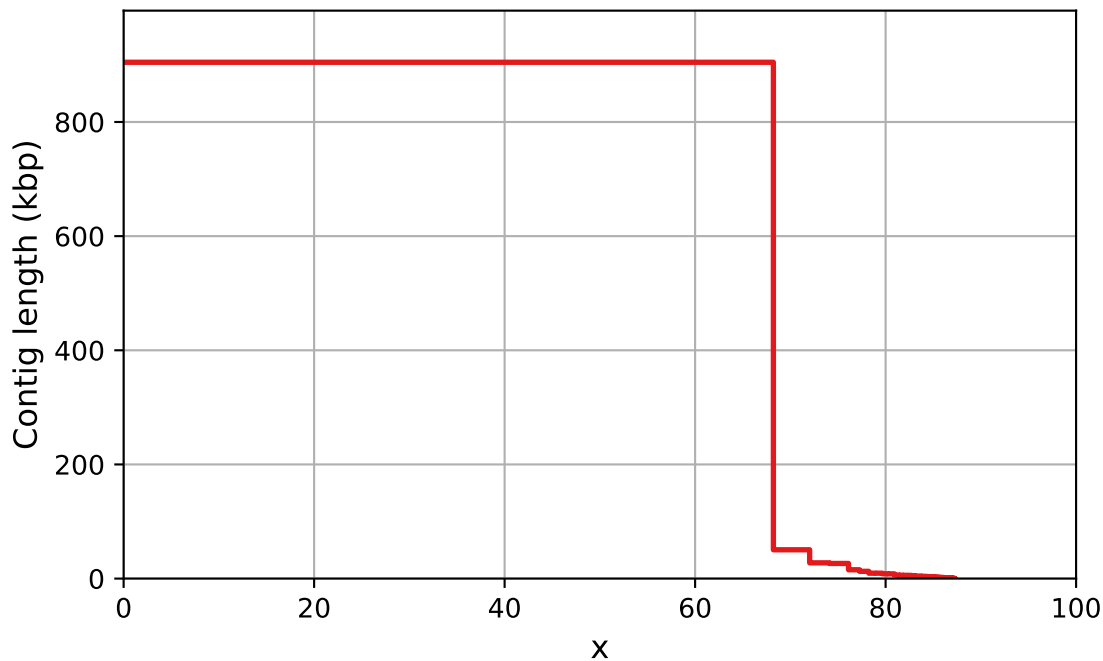
FRCurve (misassemblies)



Cumulative length (aligned contigs)

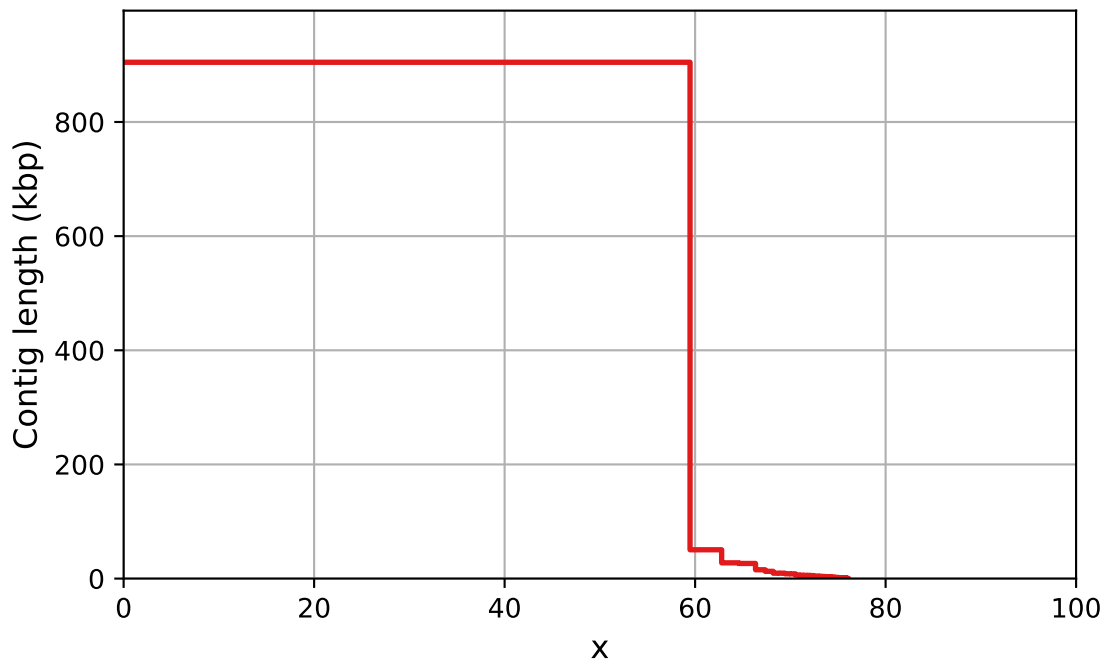


NAx

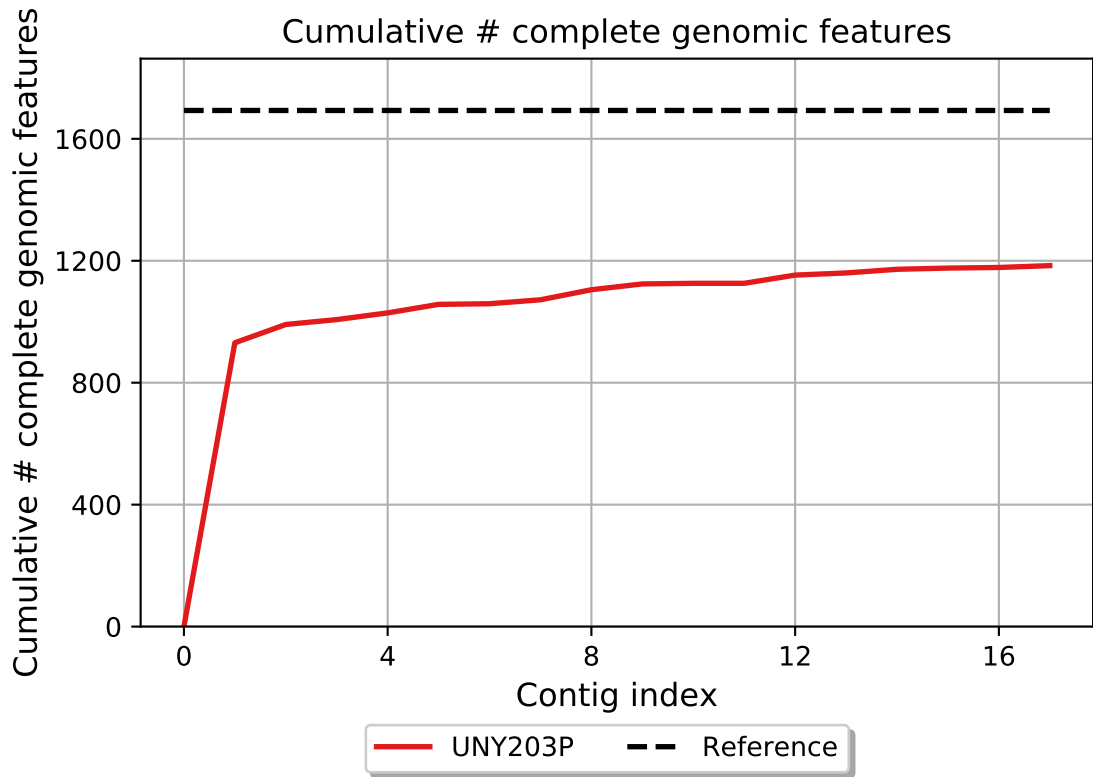


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NGAx



— UNY203P



FRCurve (genomic features)

