

Report

	UNY1038P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1403595
Total length (>= 1000 bp)	1403595
Total length (>= 5000 bp)	1403595
Total length (>= 10000 bp)	1394201
Total length (>= 25000 bp)	1288571
Total length (>= 50000 bp)	969567
# contigs	19
Largest contig	915733
Total length	1403595
Reference length	1521208
GC (%)	28.19
Reference GC (%)	28.18
N50	915733
NG50	915733
N90	26514
NG90	20343
auN	607789.6
auNG	560798.0
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	18
# misassembled contigs	10
Misassembled contigs length	1178740
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 15 part
Unaligned length	198293
Genome fraction (%)	78.419
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	743.29
# indels per 100 kbp	45.05
# genomic features	1243 + 49 part
Largest alignment	905458
Total aligned length	1207607
NA50	905458
NGA50	905458
NA90	-
NGA90	-
auNA	588024.0
auNGA	542560.6
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

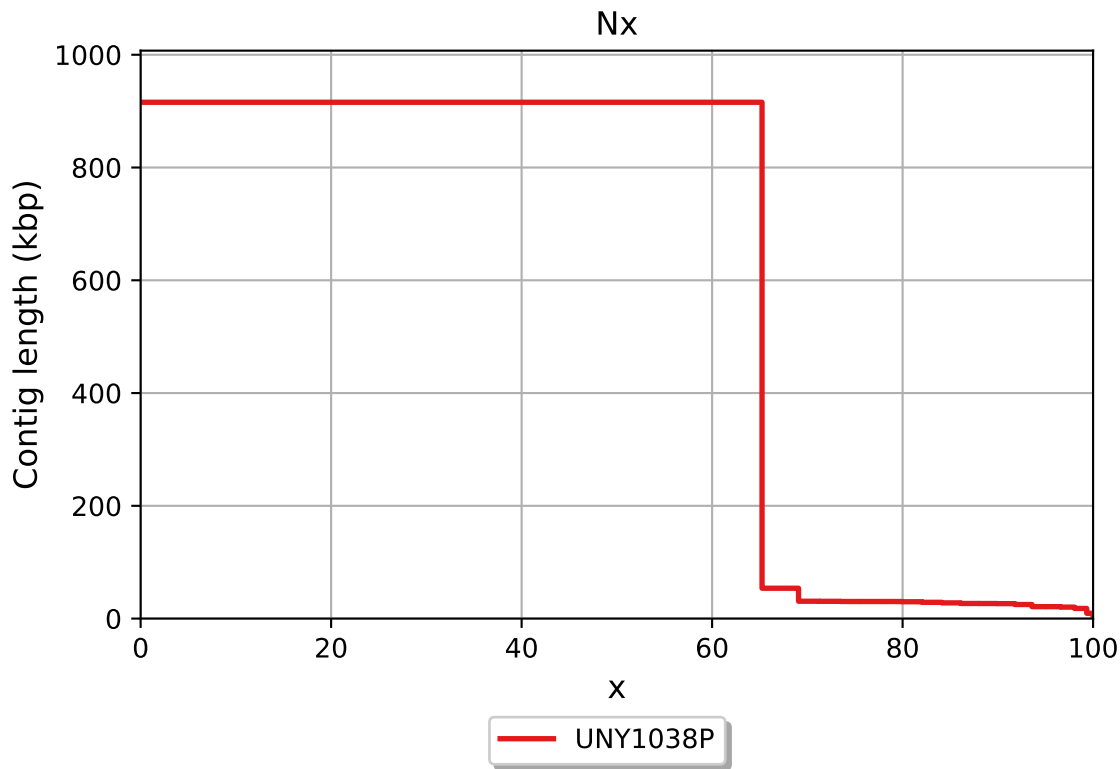
	UNY1038P
# misassemblies	18
# contig misassemblies	18
# c. relocations	5
# c. translocations	13
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	1178740
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	8976
# indels	544
# indels (<= 5 bp)	489
# indels (> 5 bp)	55
Indels length	3591

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).

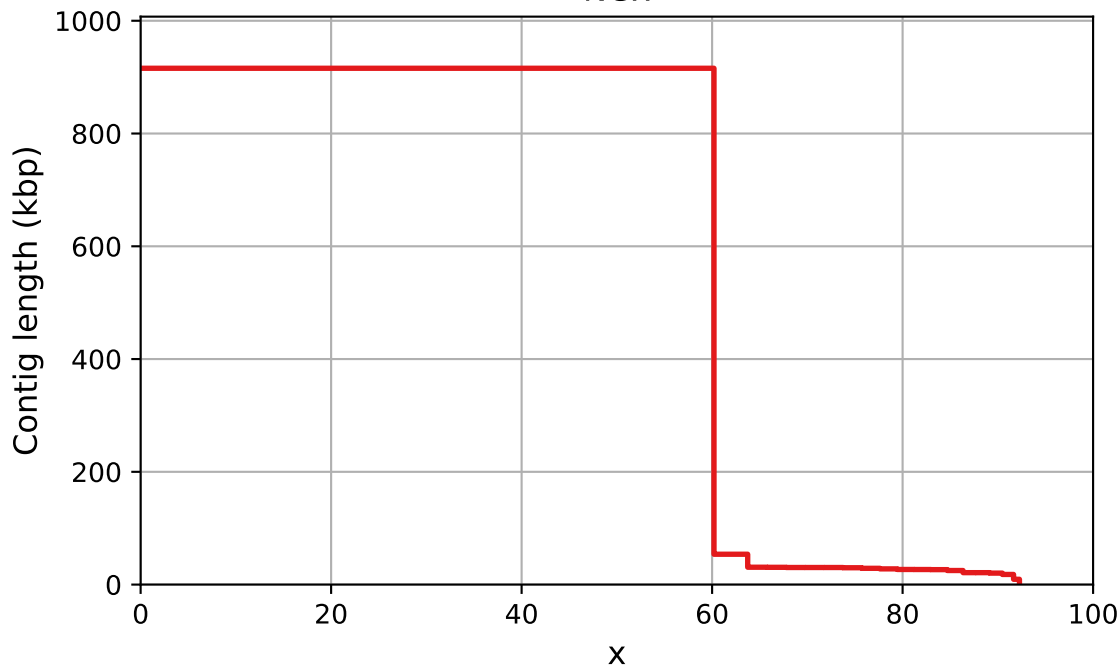
Unaligned report

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# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	198293
# N's	0

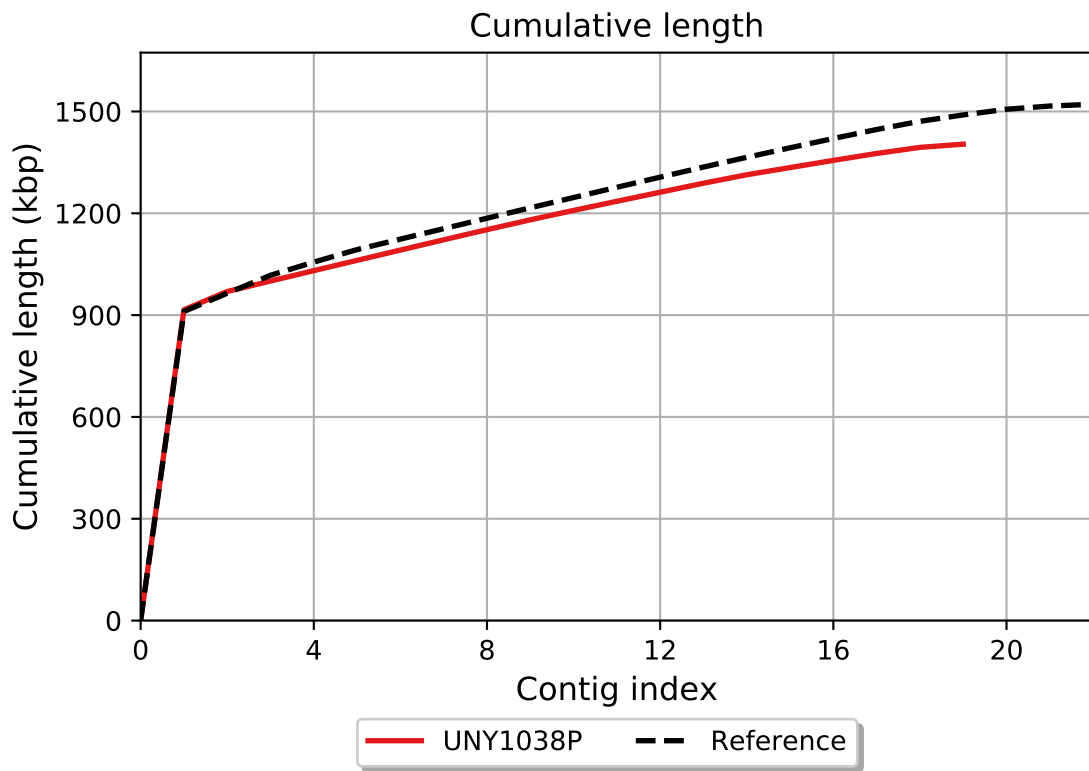
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



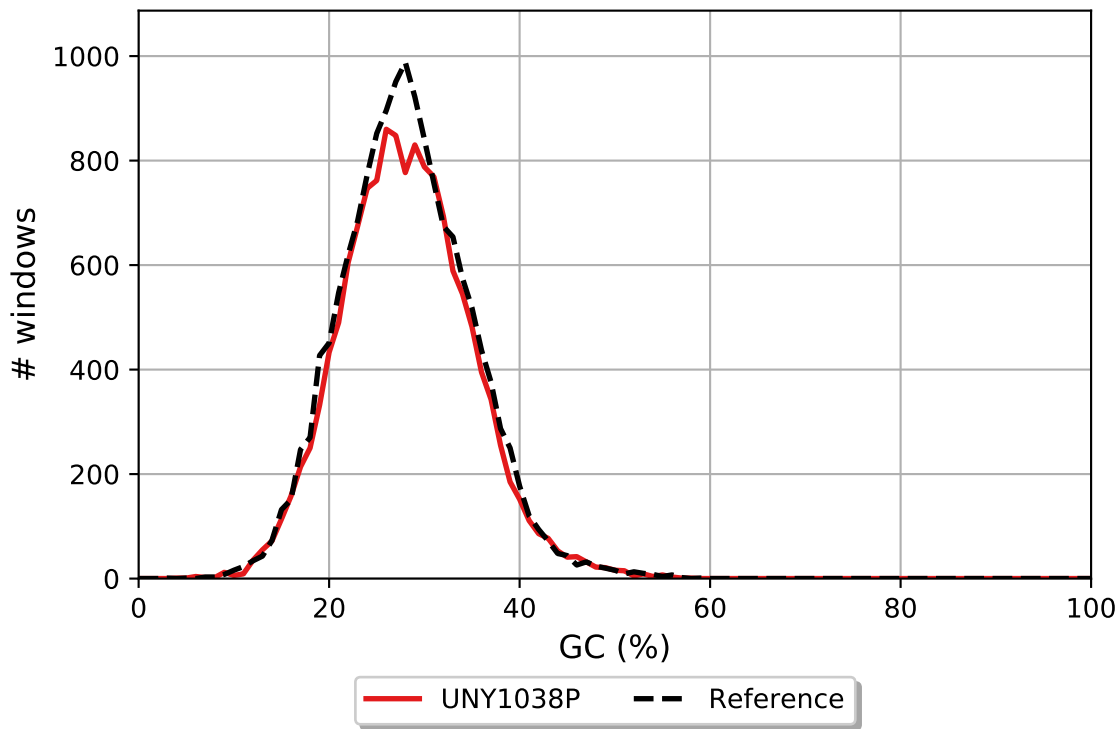
NGx



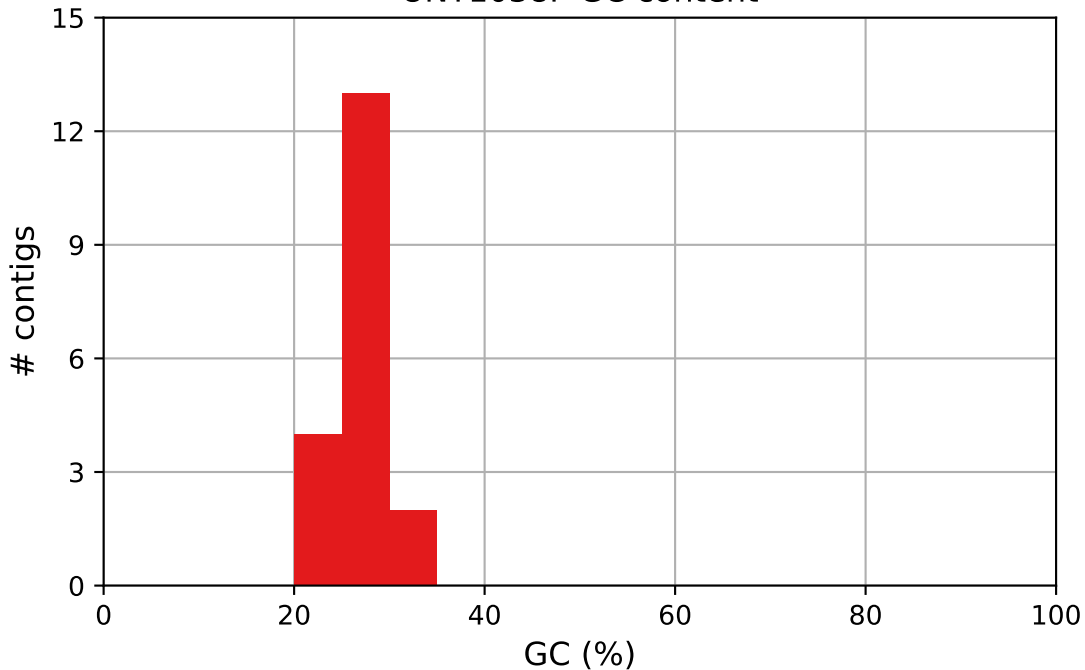
UNY1038P



GC content

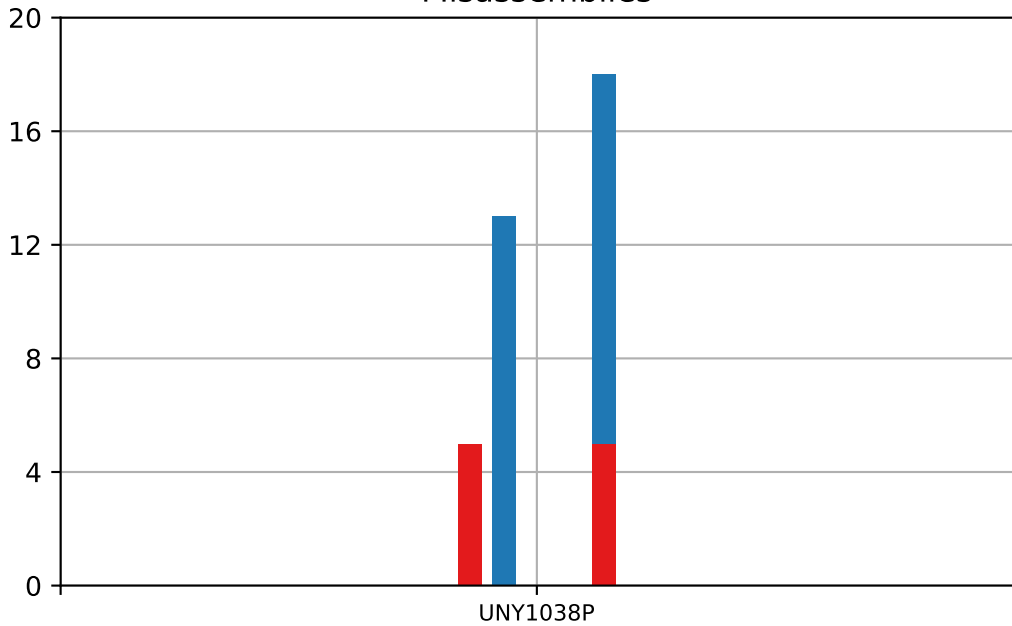


UNY1038P GC content



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Misassemblies

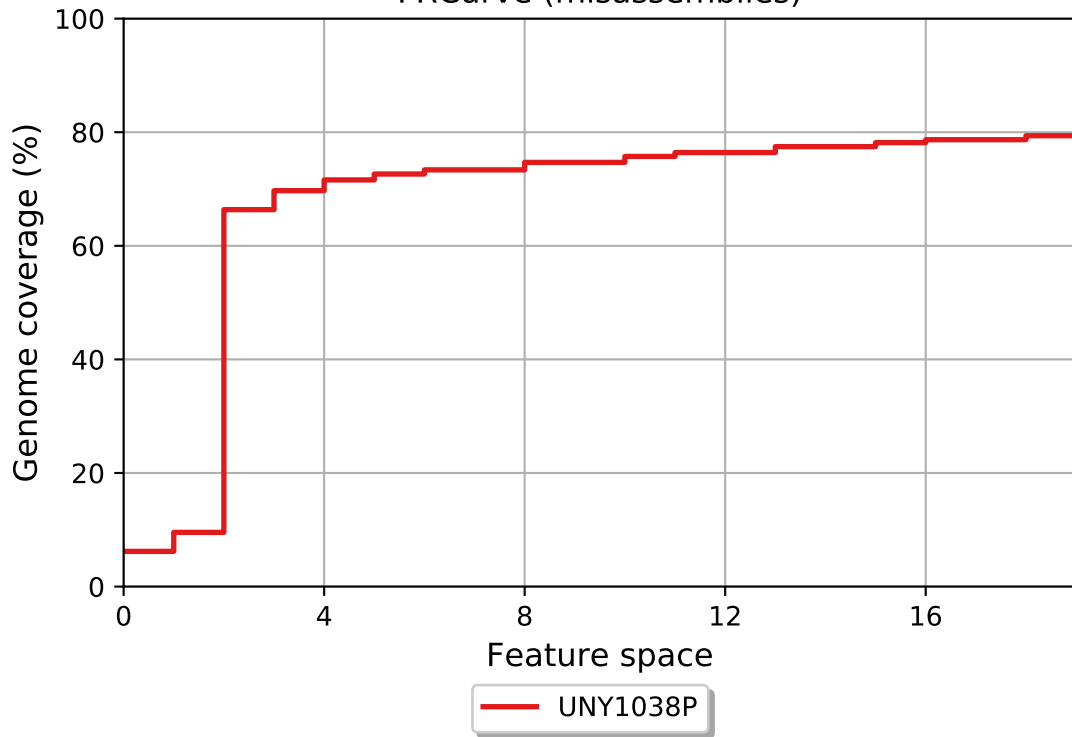


relocations

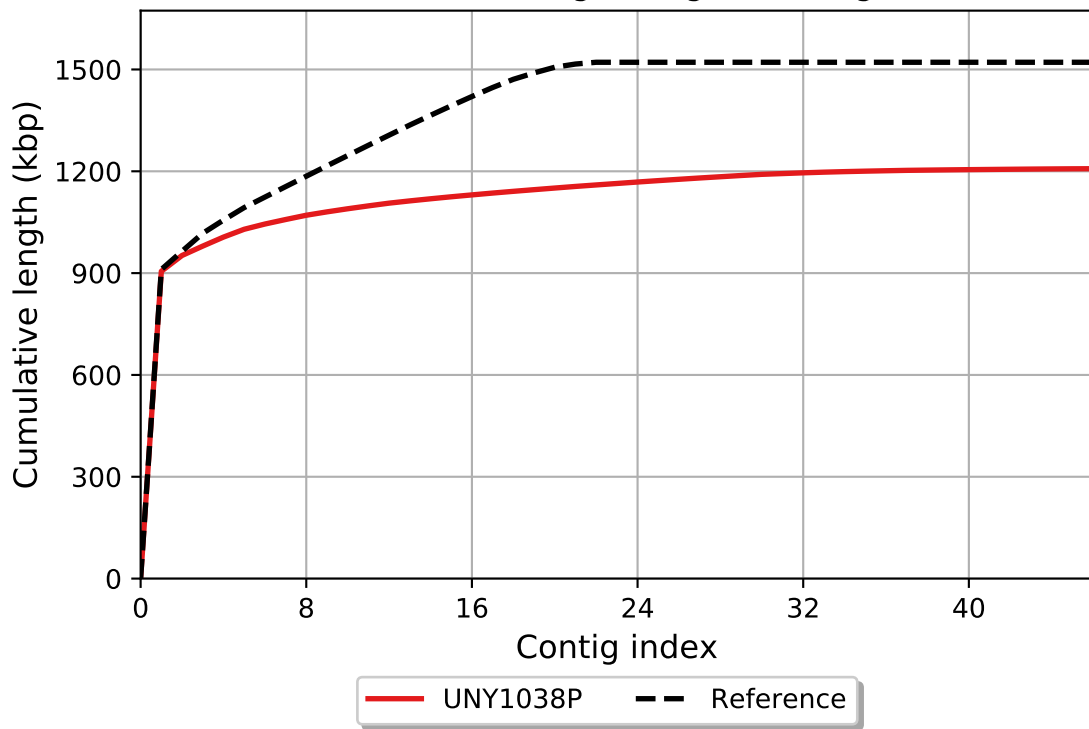


translocations

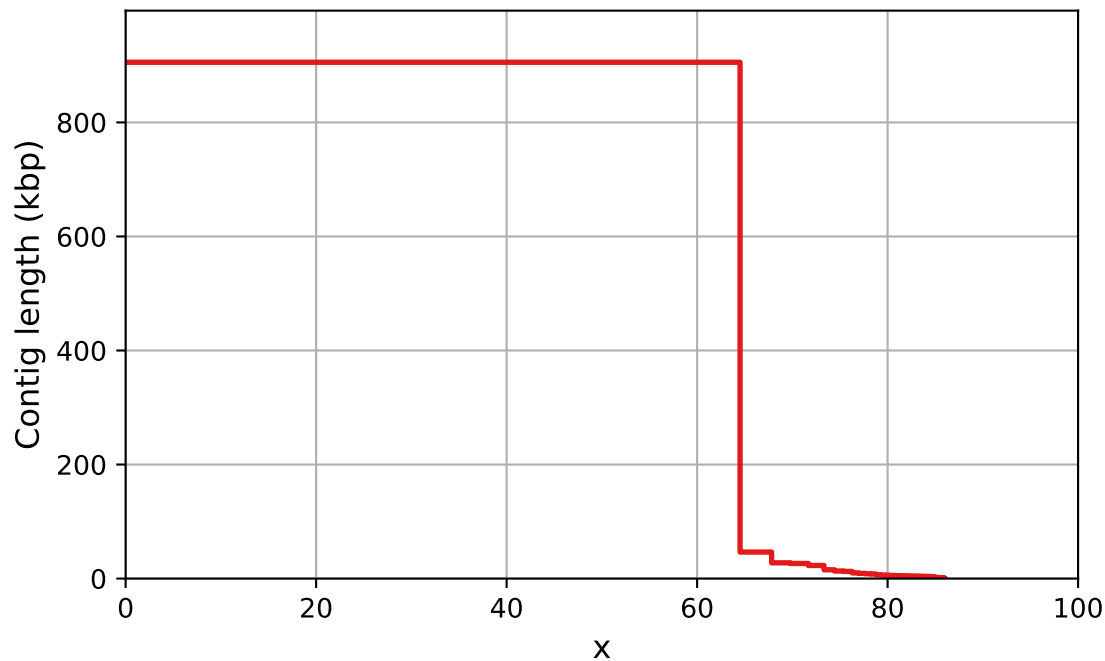
FRCurve (misassemblies)



Cumulative length (aligned contigs)

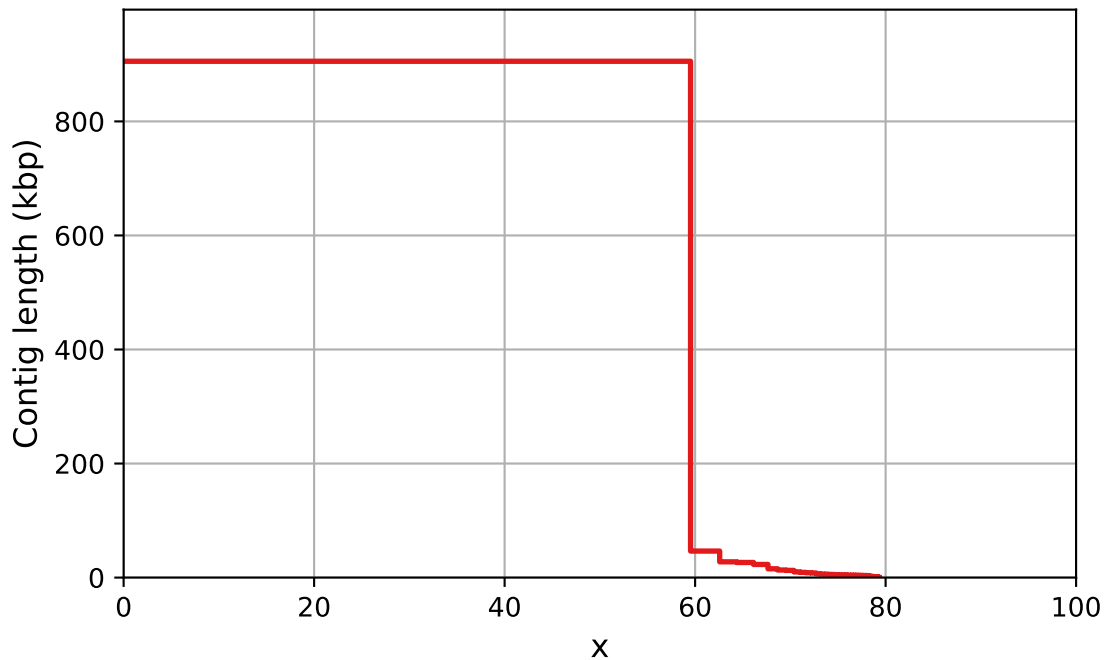


NAx



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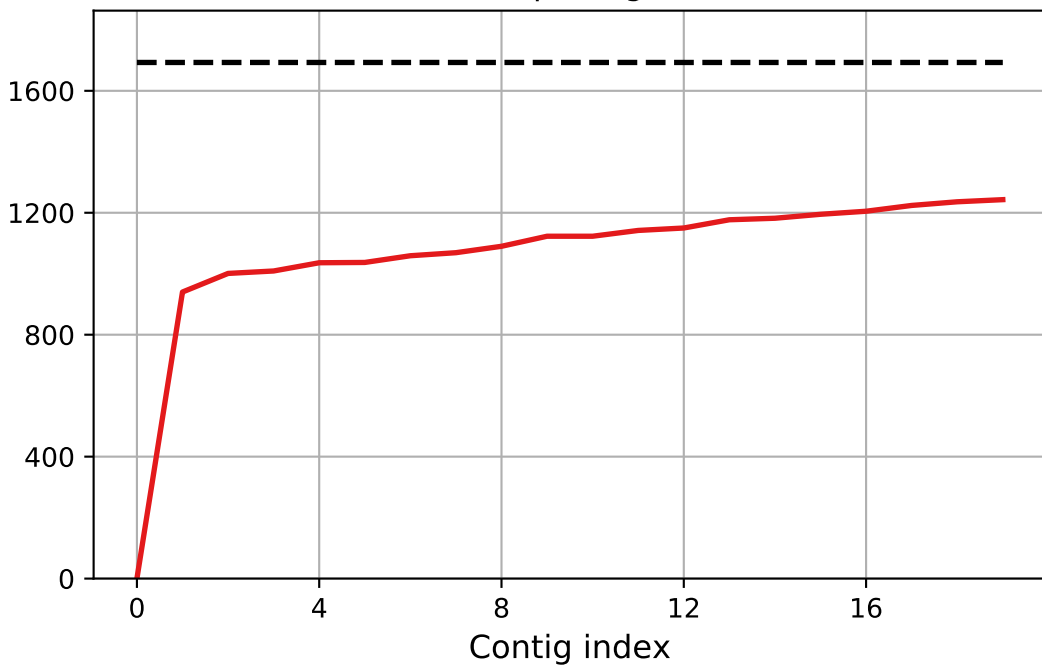
NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

