

Report

	UNY149P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1427032
Total length (>= 1000 bp)	1427032
Total length (>= 5000 bp)	1427032
Total length (>= 10000 bp)	1427032
Total length (>= 25000 bp)	1318132
Total length (>= 50000 bp)	969575
# contigs	19
Largest contig	915733
Total length	1427032
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	915733
NG50	915733
N90	26726
NG90	21172
auN	598460.0
auNG	561410.1
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	21
# misassembled contigs	11
Misassembled contigs length	1211948
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 16 part
Unaligned length	190341
Genome fraction (%)	79.957
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	841.47
# indels per 100 kbp	49.76
# genomic features	1284 + 51 part
Largest alignment	905458
Total aligned length	1236049
NA50	905458
NGA50	905458
NA90	-
NGA90	-
auNA	578834.4
auNGA	542999.5
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

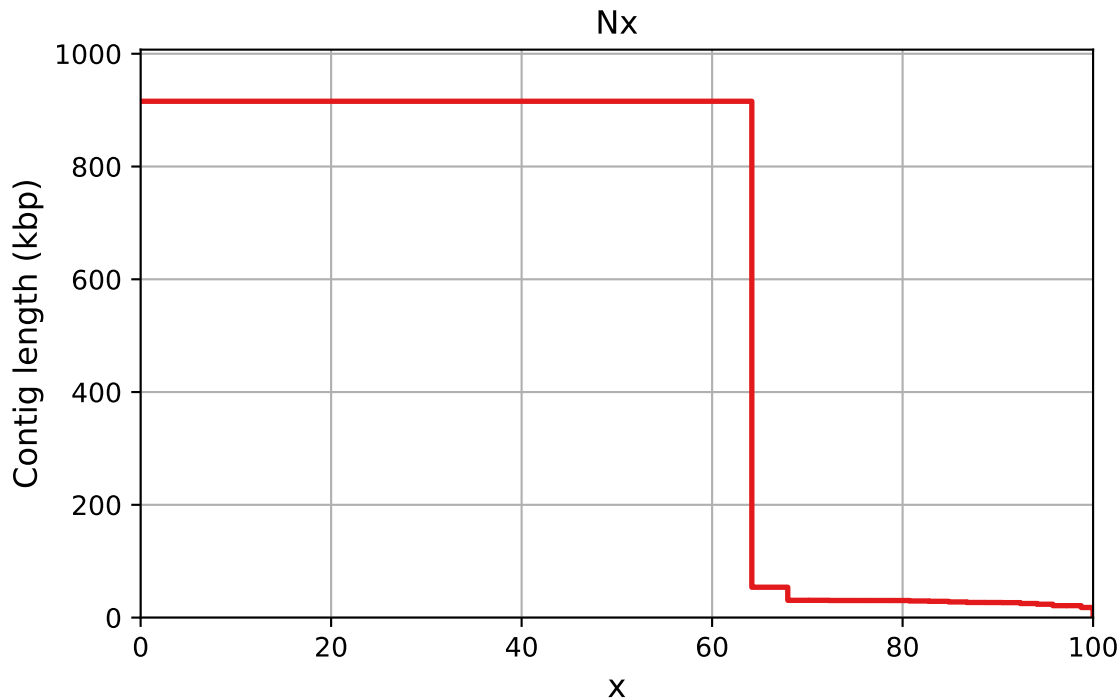
	UNY149P
# misassemblies	21
# contig misassemblies	21
# c. relocations	5
# c. translocations	16
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1211948
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	10401
# indels	615
# indels (<= 5 bp)	552
# indels (> 5 bp)	63
Indels length	3393

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

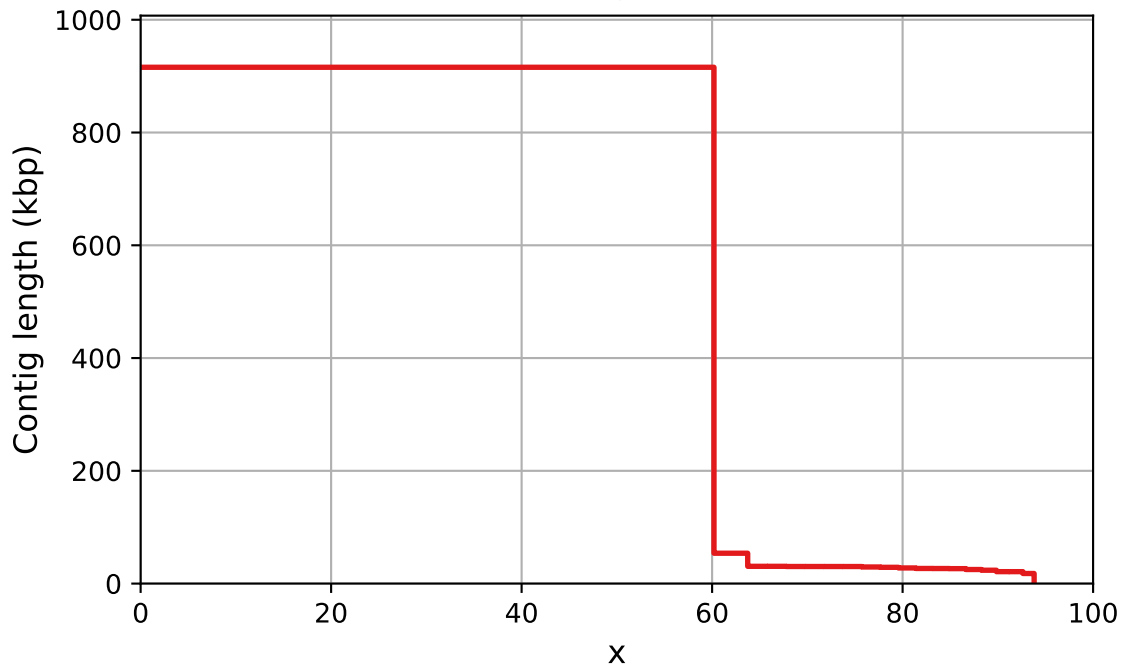
	UNY149P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
Partially unaligned length	190341
# N's	0

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).

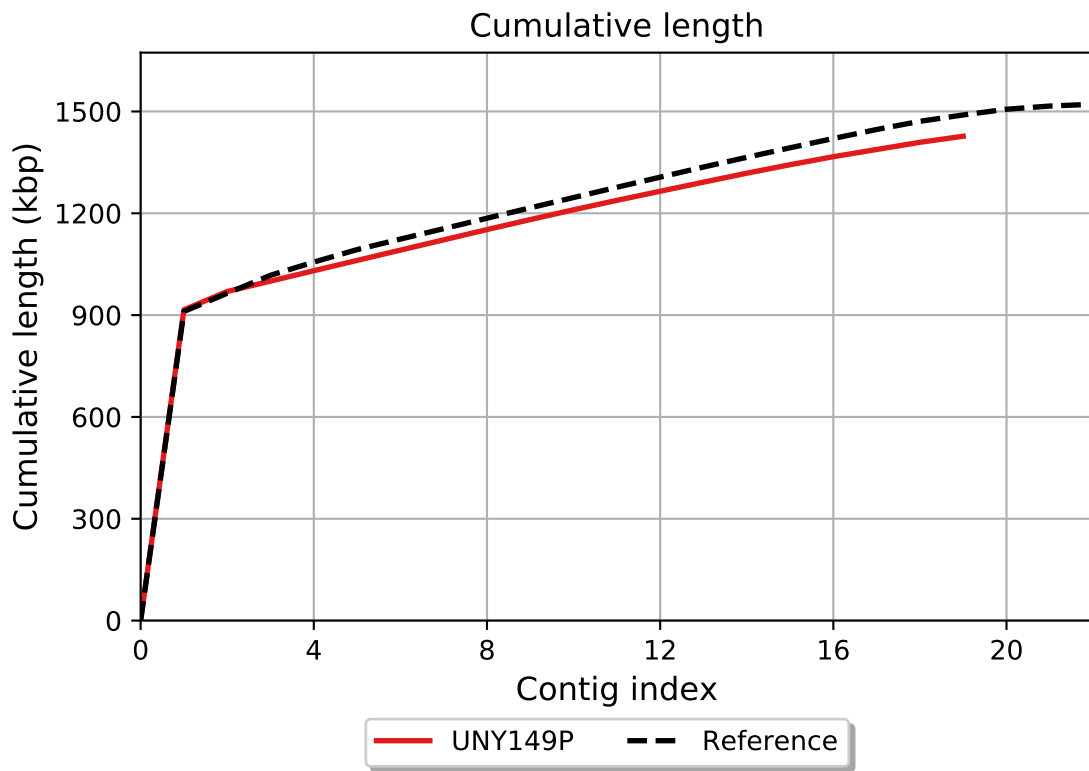


— UNY149P

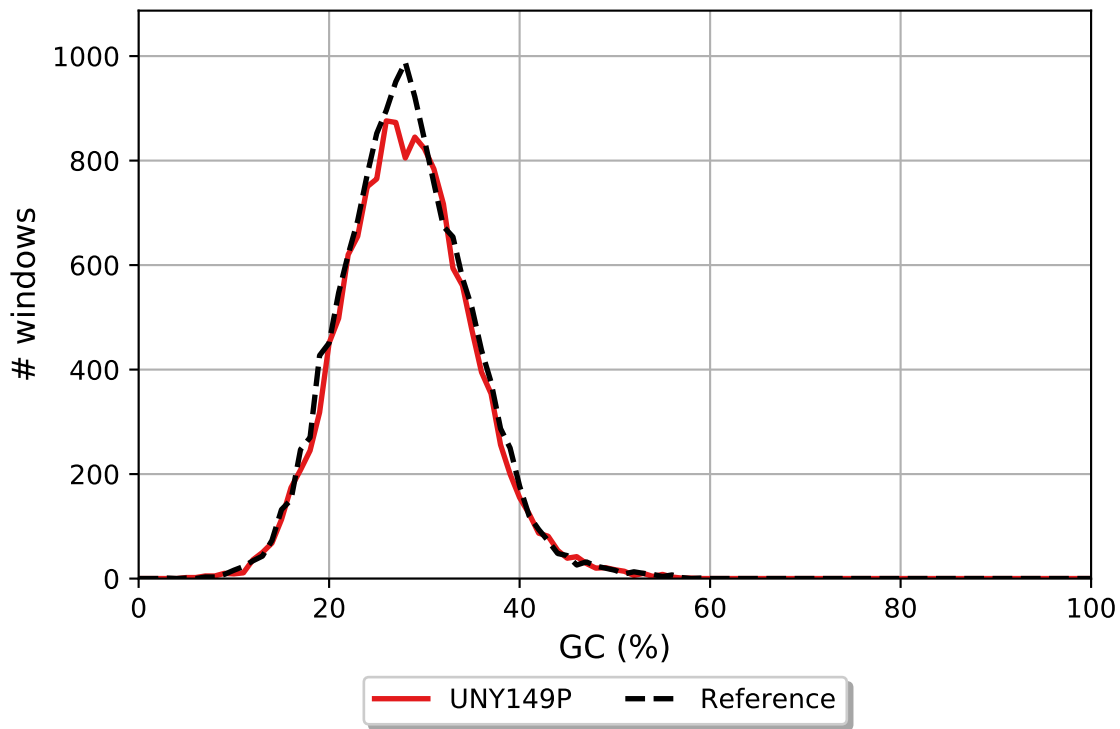
NGx



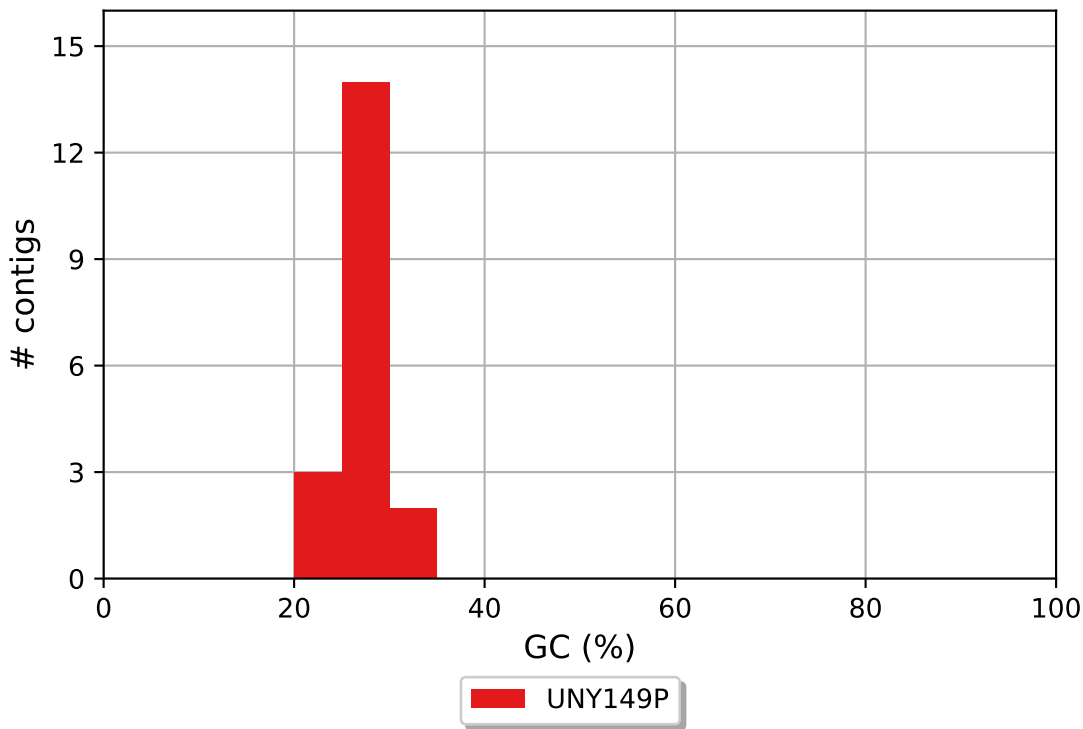
— UNY149P



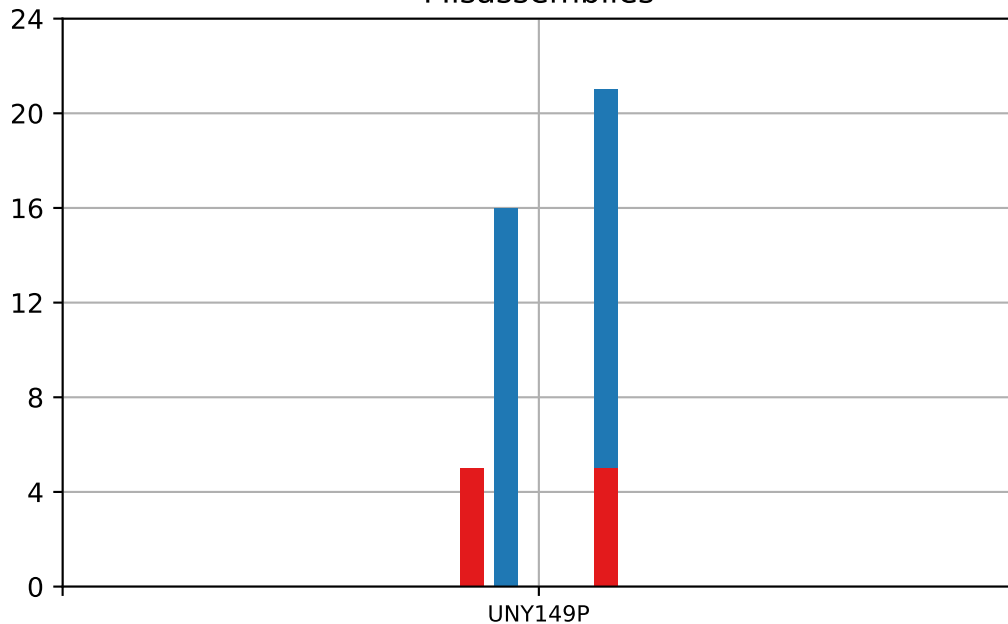
GC content



UNY149P GC content



Misassemblies

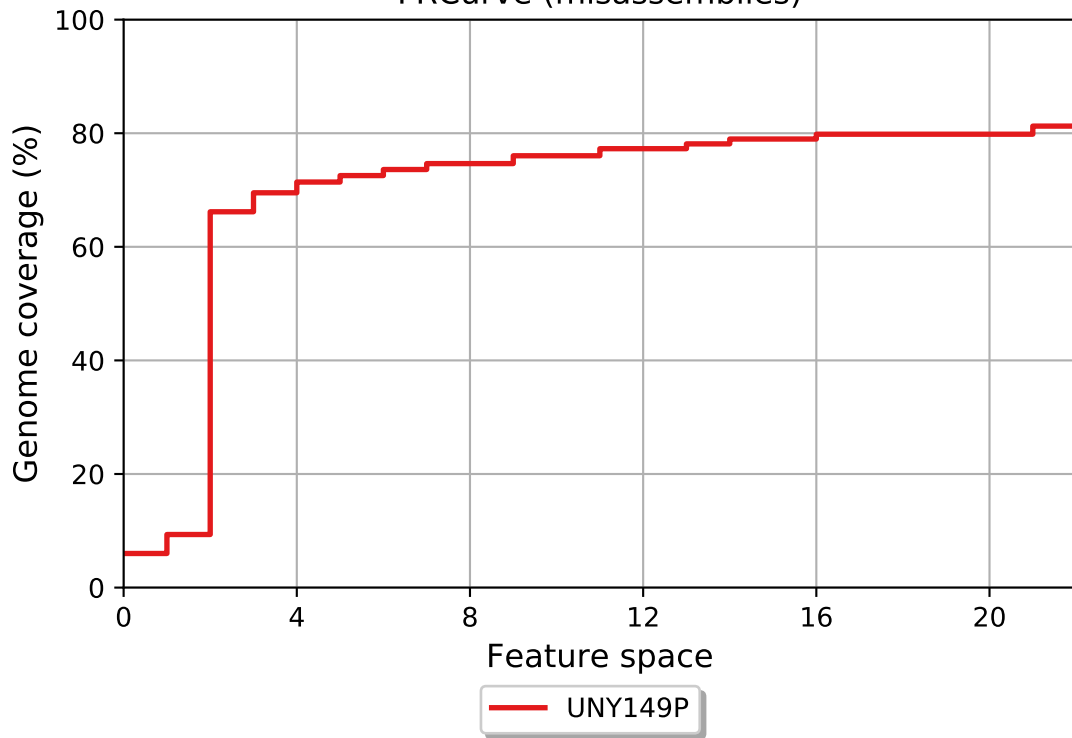


relocations

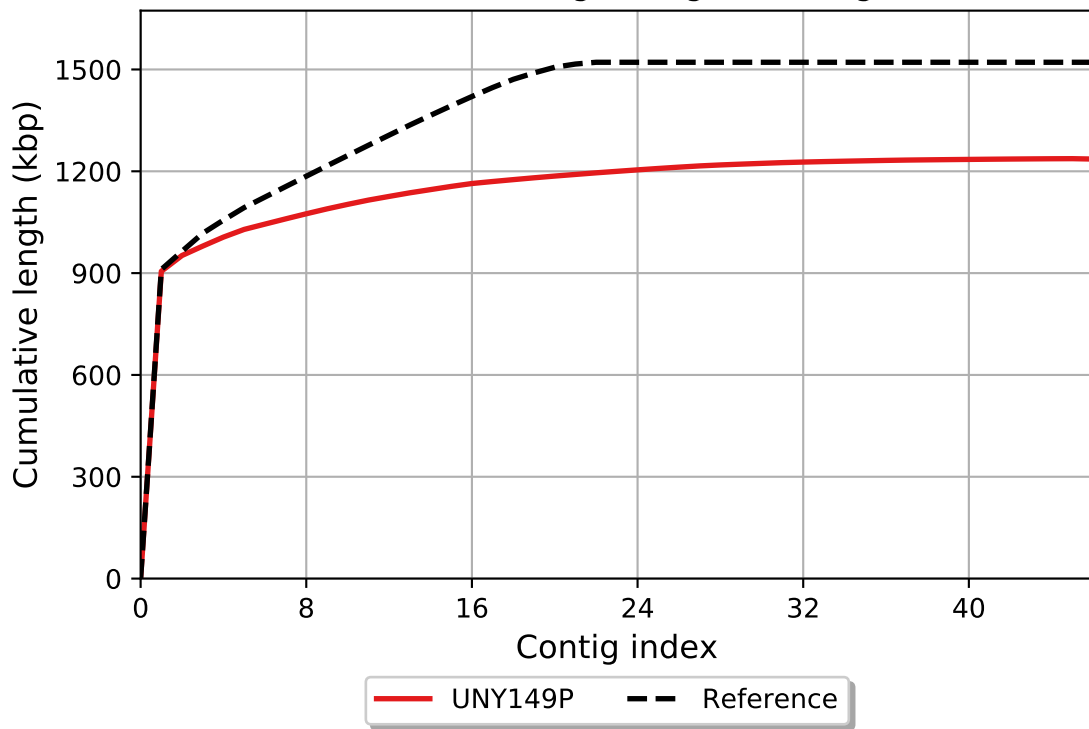


translocations

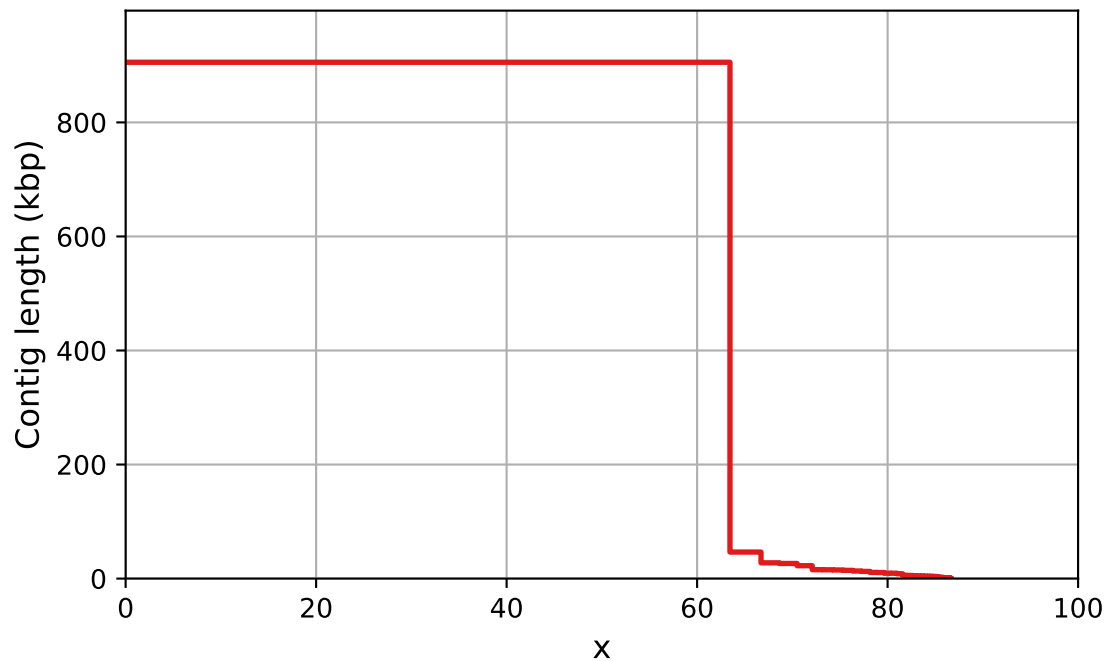
FRCurve (misassemblies)



Cumulative length (aligned contigs)

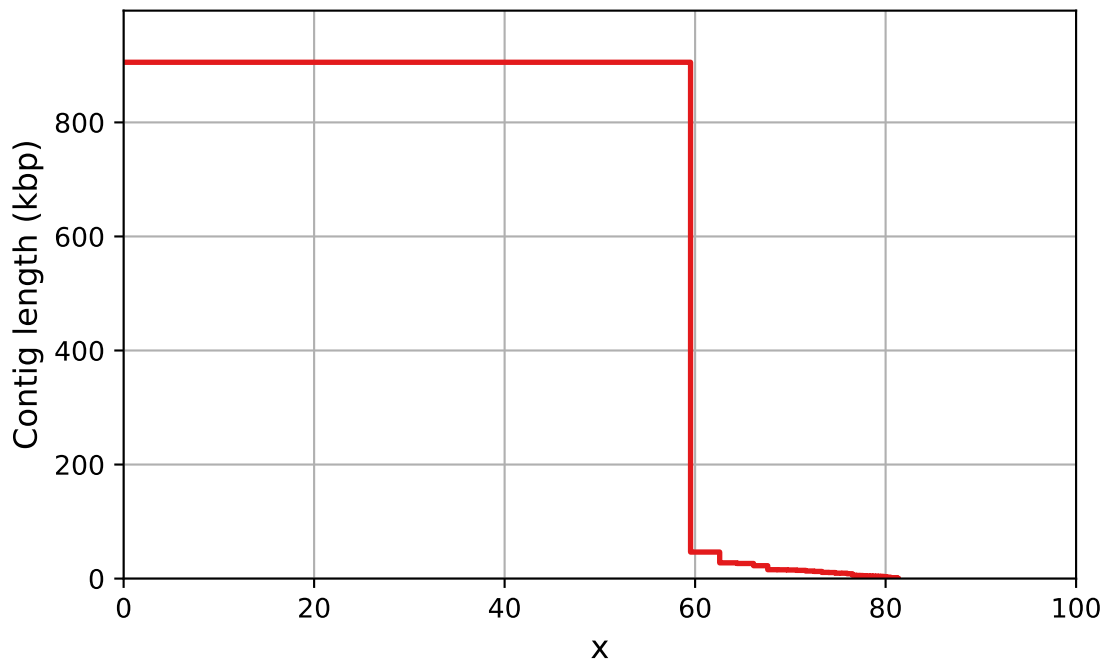


NAx



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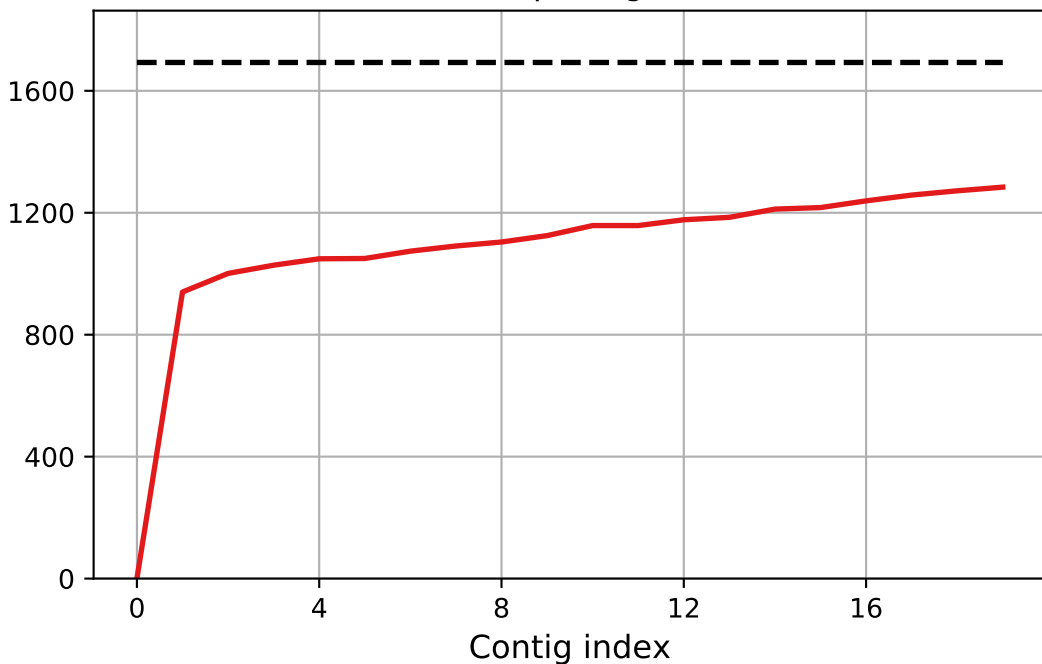
NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



UNY149P Reference

FRCurve (genomic features)

