

Report

	UNY1032P
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1459435
Total length (>= 1000 bp)	1459435
Total length (>= 5000 bp)	1459435
Total length (>= 10000 bp)	1459435
Total length (>= 25000 bp)	1418114
Total length (>= 50000 bp)	1017137
# contigs	18
Largest contig	910572
Total length	1459435
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	910572
NG50	910572
N90	29838
NG90	27414
auN	581190.3
auNG	557589.4
L50	1
LG50	1
L90	13
LG90	15
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	91704
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	7014
Genome fraction (%)	93.671
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	88.25
# indels per 100 kbp	15.50
# genomic features	1555 + 22 part
Largest alignment	910572
Total aligned length	1451592
NA50	910572
NGA50	910572
NA90	26597
NGA90	24180
auNA	580255.8
auNGA	556692.9
LA50	1
LGA50	1
LA90	13
LGA90	15

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

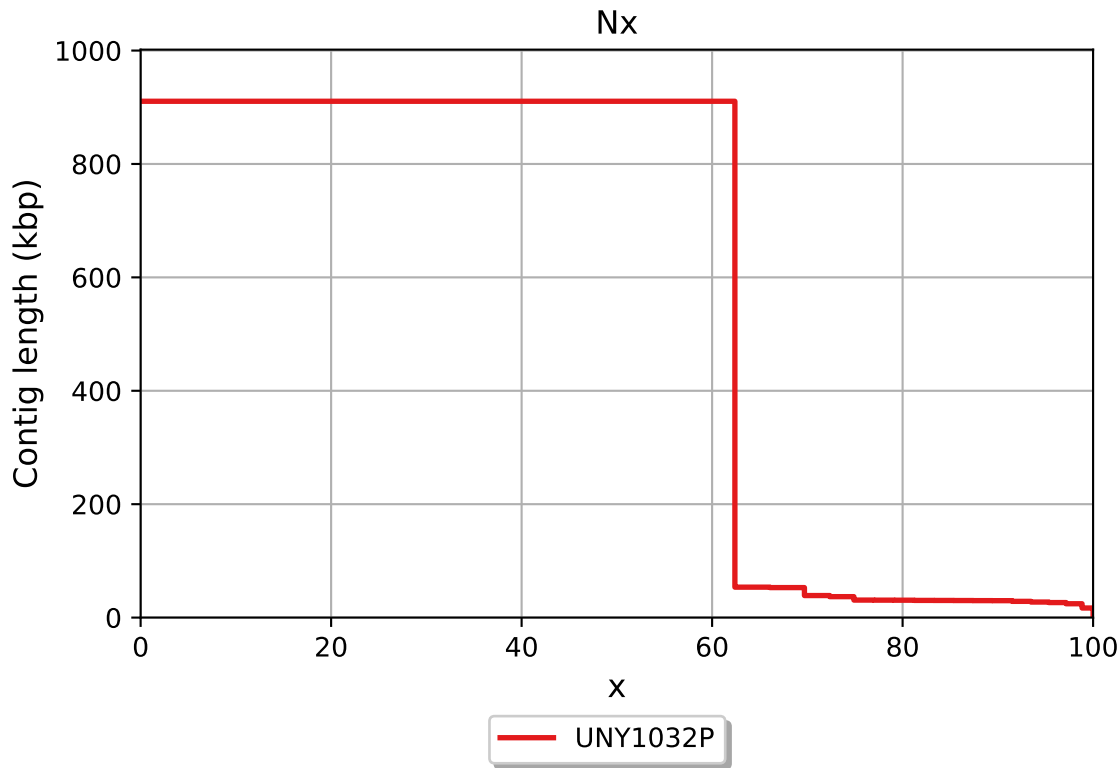
	UNY1032P
# misassemblies	3
# contig misassemblies	3
# c. relocations	1
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	91704
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1281
# indels	225
# indels (<= 5 bp)	183
# indels (> 5 bp)	42
Indels length	1804

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).

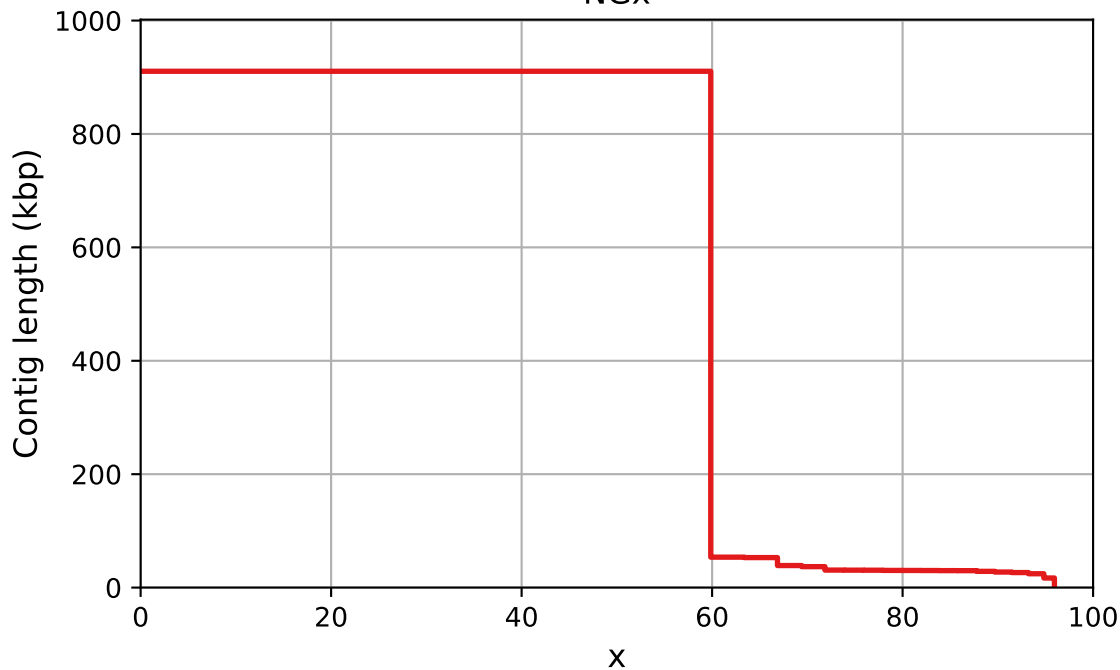
Unaligned report

	UNY1032P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	7014
# N's	0

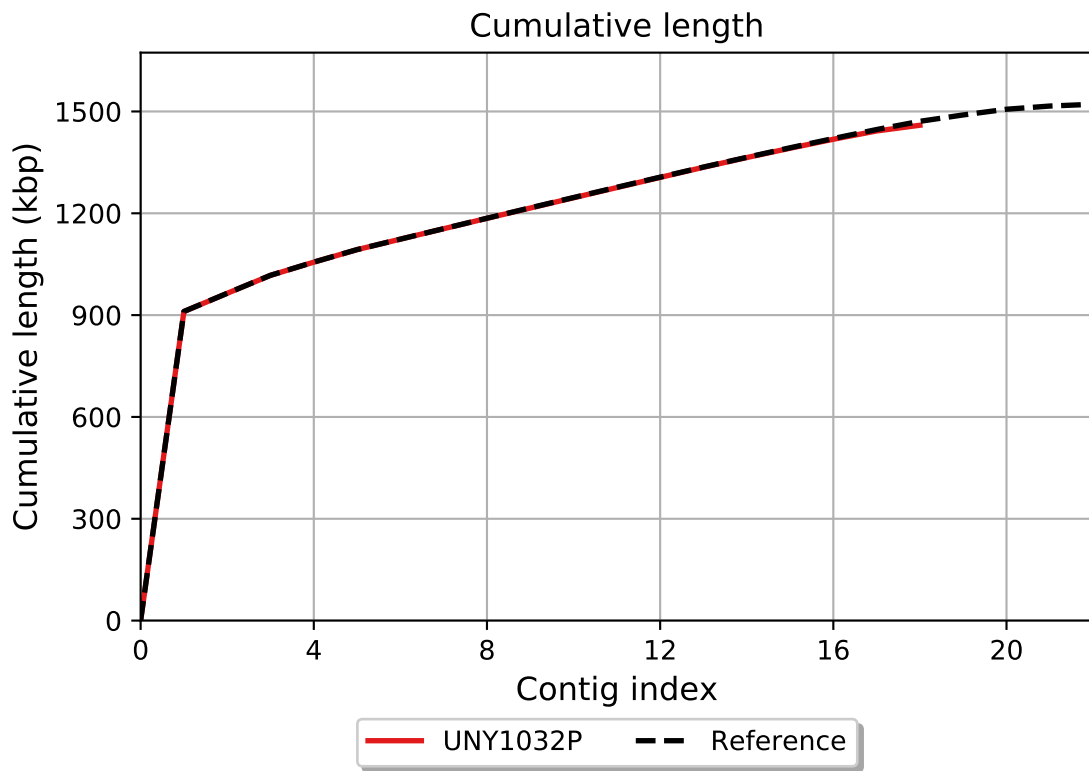
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



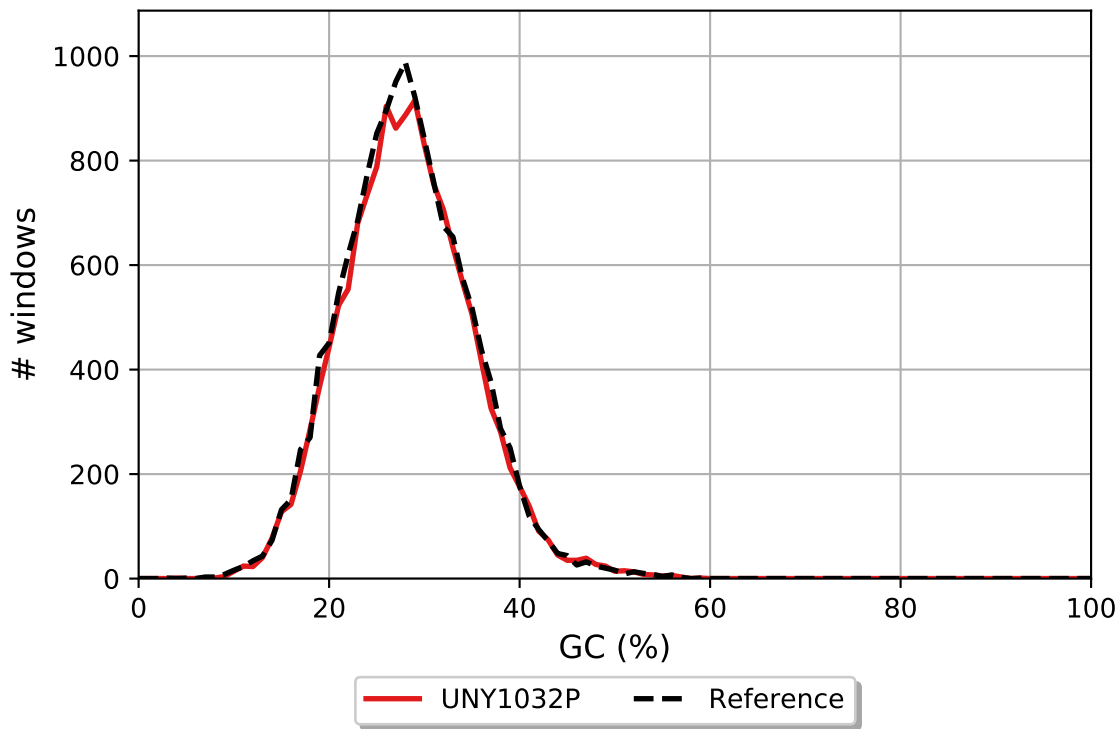
NGx



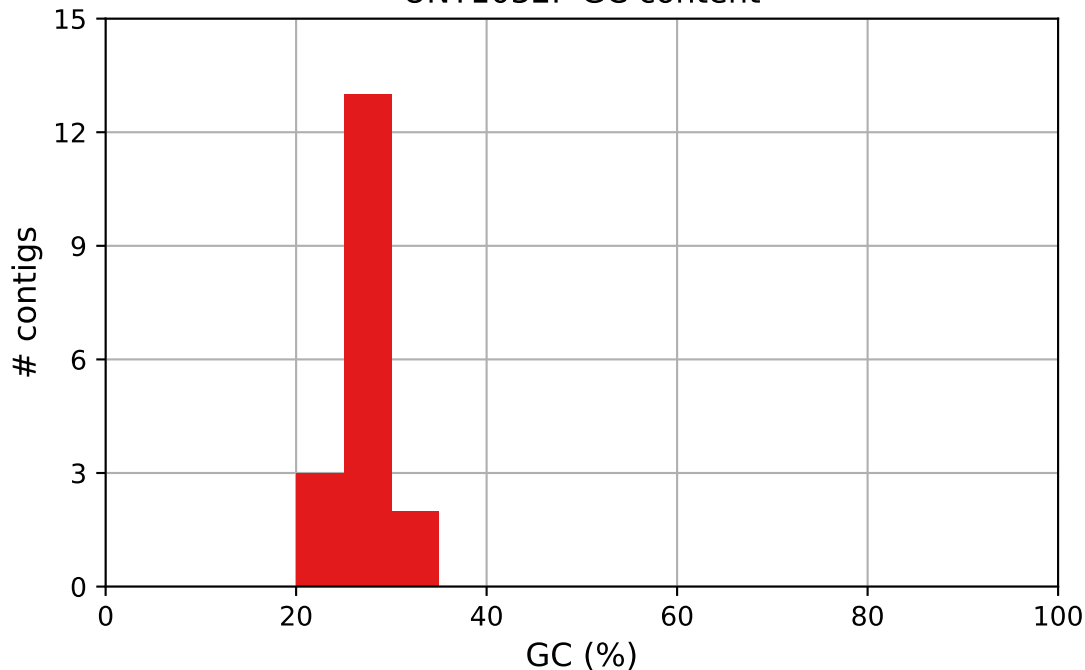
UNY1032P



GC content

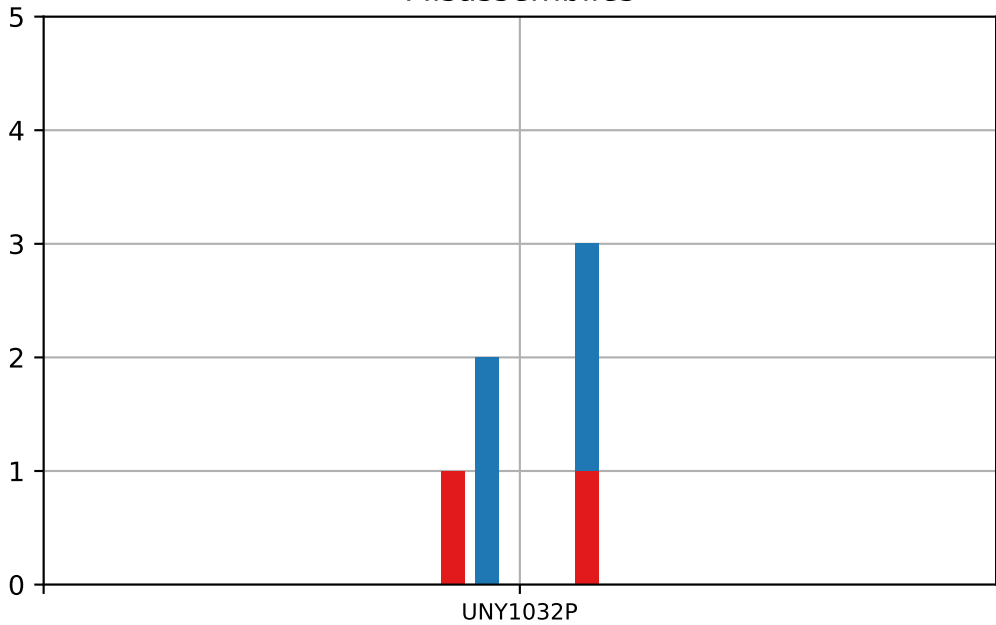


UNY1032P GC content



UNY1032P

Misassemblies

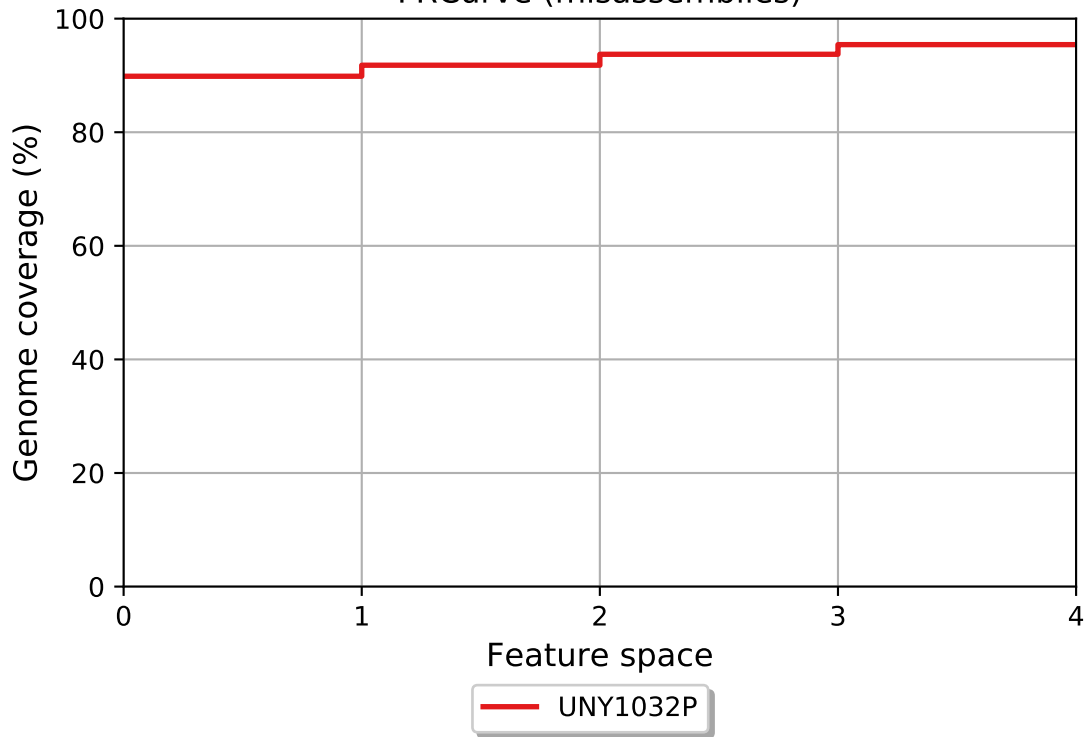


relocations

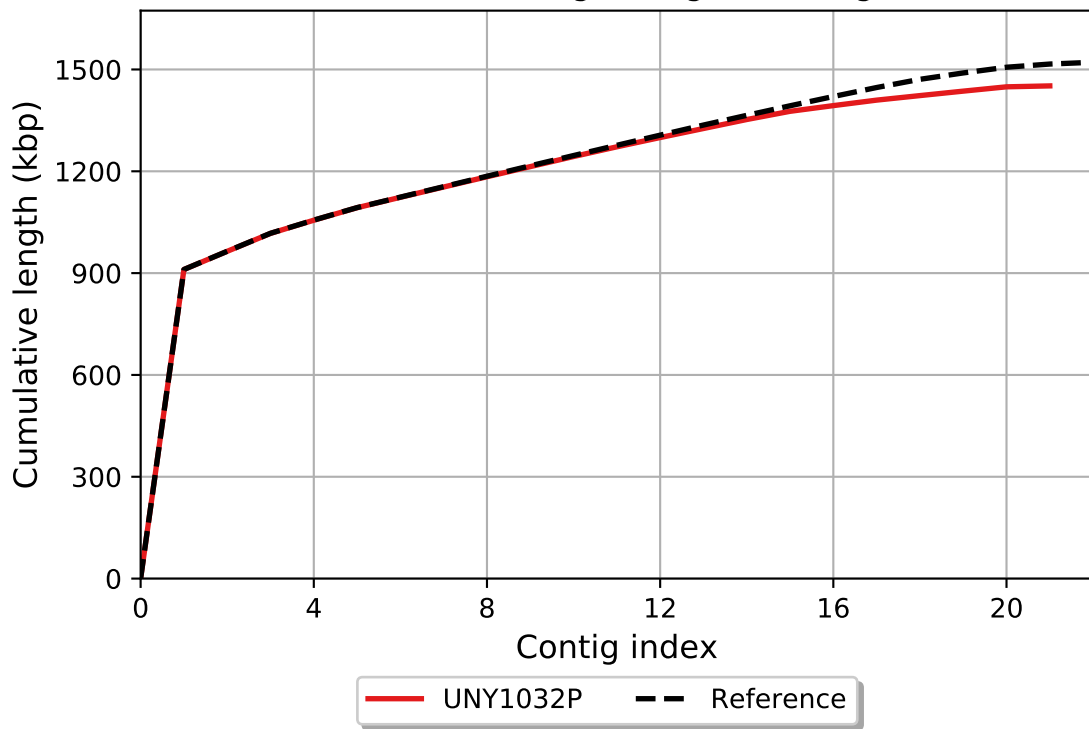


translocations

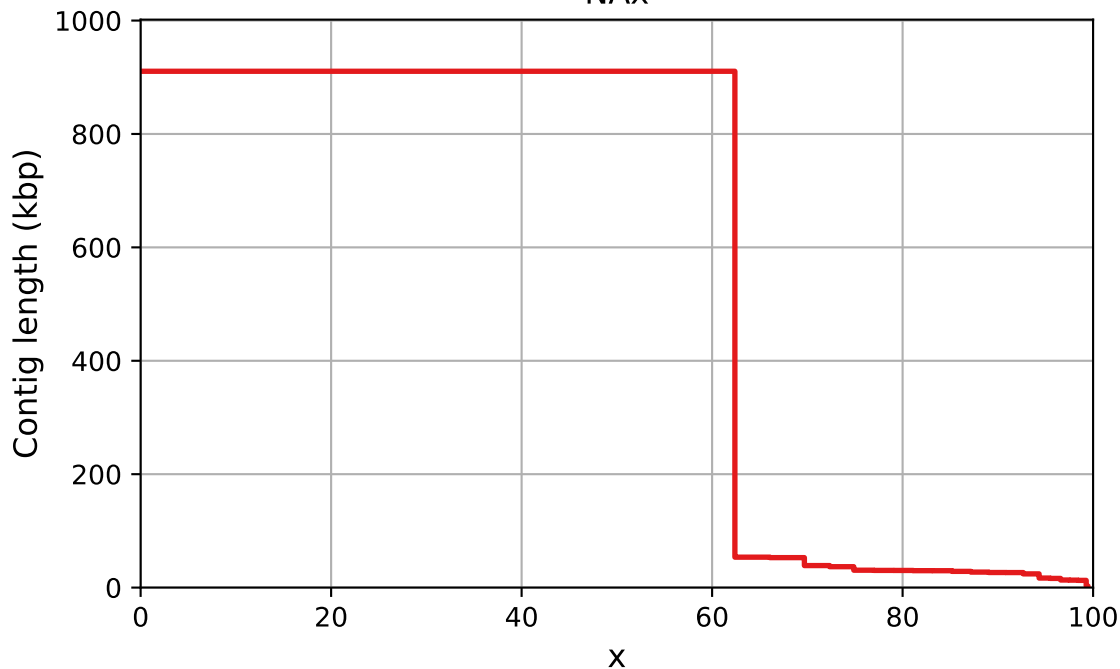
FRCurve (misassemblies)



Cumulative length (aligned contigs)

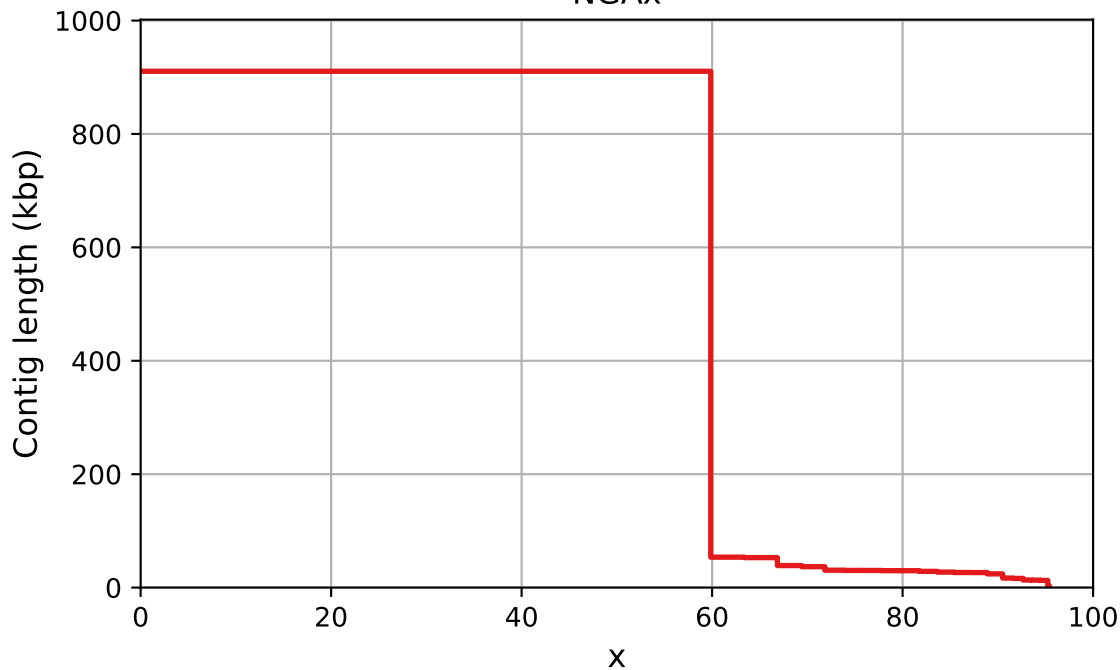


NAx

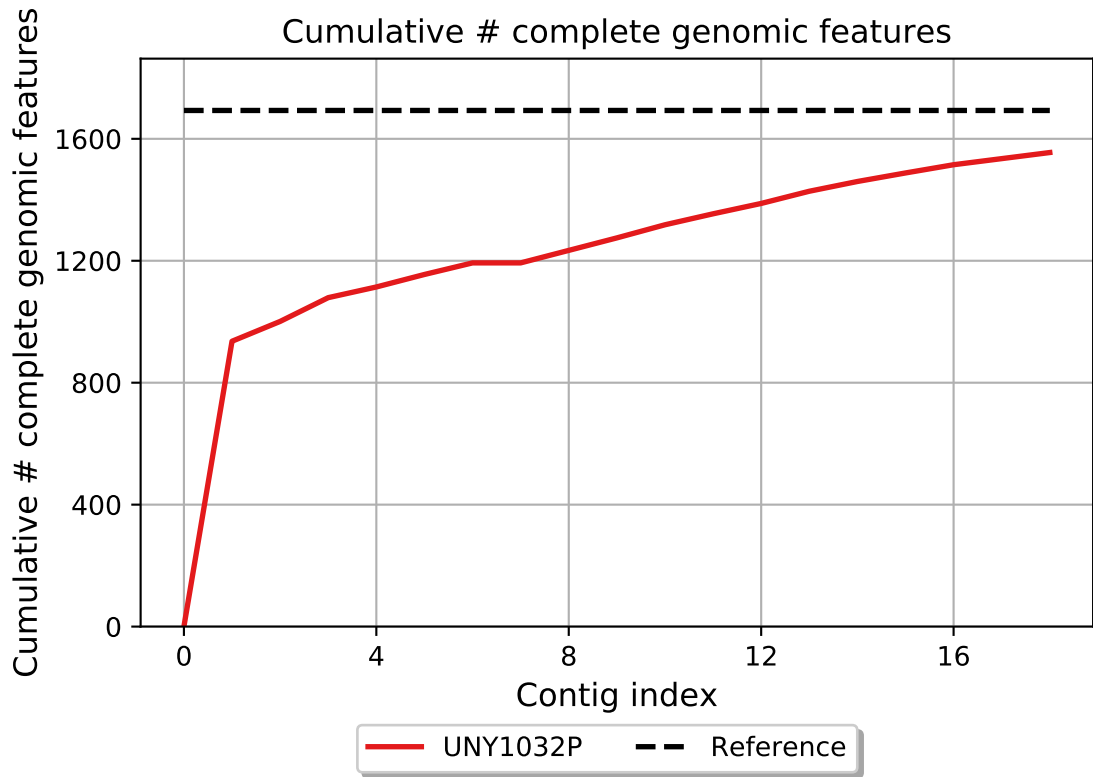


— UNY1032P

NGAx



UNY1032P



FRCurve (genomic features)

