

Report

	UWI263P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1409038
Total length (>= 1000 bp)	1409038
Total length (>= 5000 bp)	1409038
Total length (>= 10000 bp)	1399612
Total length (>= 25000 bp)	1312125
Total length (>= 50000 bp)	961828
# contigs	19
Largest contig	907926
Total length	1409038
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	907926
NG50	907926
N90	26519
NG90	20998
auN	595812.4
auNG	551878.7
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	25
# misassembled contigs	9
Misassembled contigs length	286890
# local misassemblies	13
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 15 part
Unaligned length	162477
Genome fraction (%)	78.613
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	829.11
# indels per 100 kbp	51.82
# genomic features	1246 + 54 part
Largest alignment	904819
Total aligned length	1236994
NA50	904819
NGA50	904819
NA90	-
NGA90	-
auNA	585398.8
auNGA	542233.0
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

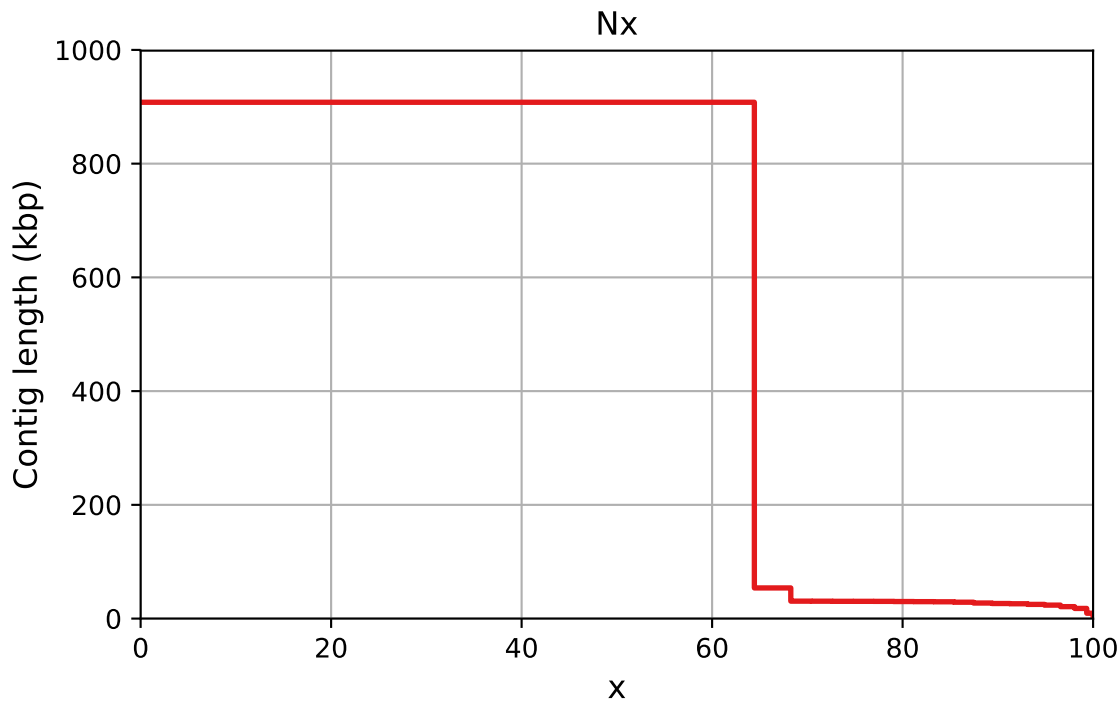
	UWI263P
# misassemblies	25
# contig misassemblies	25
# c. relocations	3
# c. translocations	22
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	286890
# local misassemblies	13
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	10256
# indels	641
# indels (<= 5 bp)	579
# indels (> 5 bp)	62
Indels length	2238

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

## Unaligned report

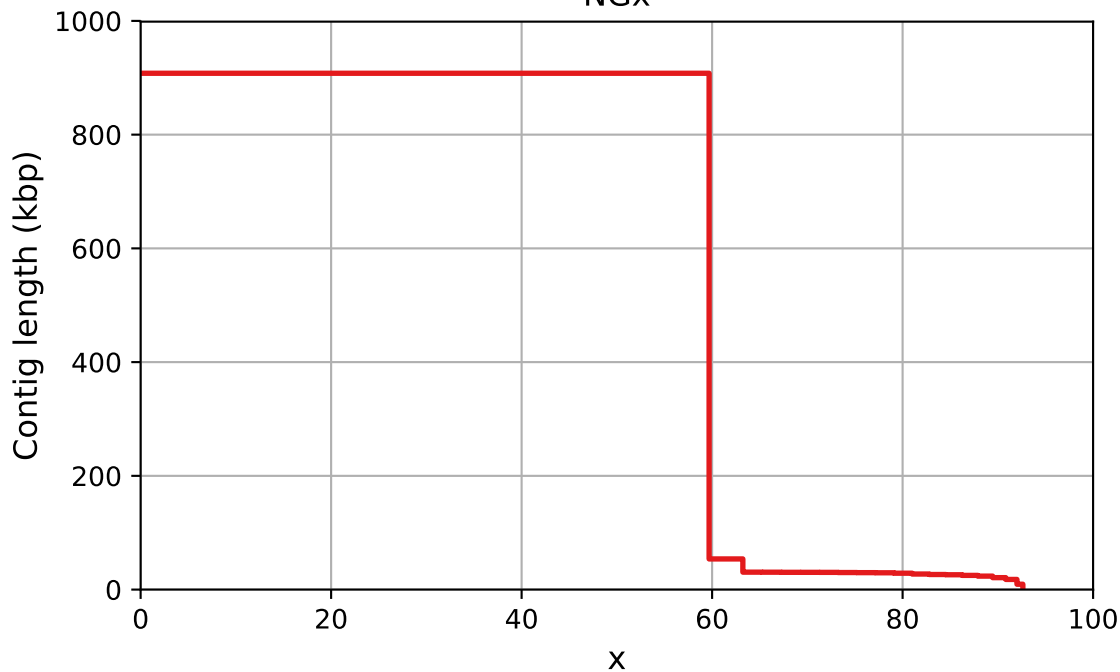
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# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	162477
# N's	0

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

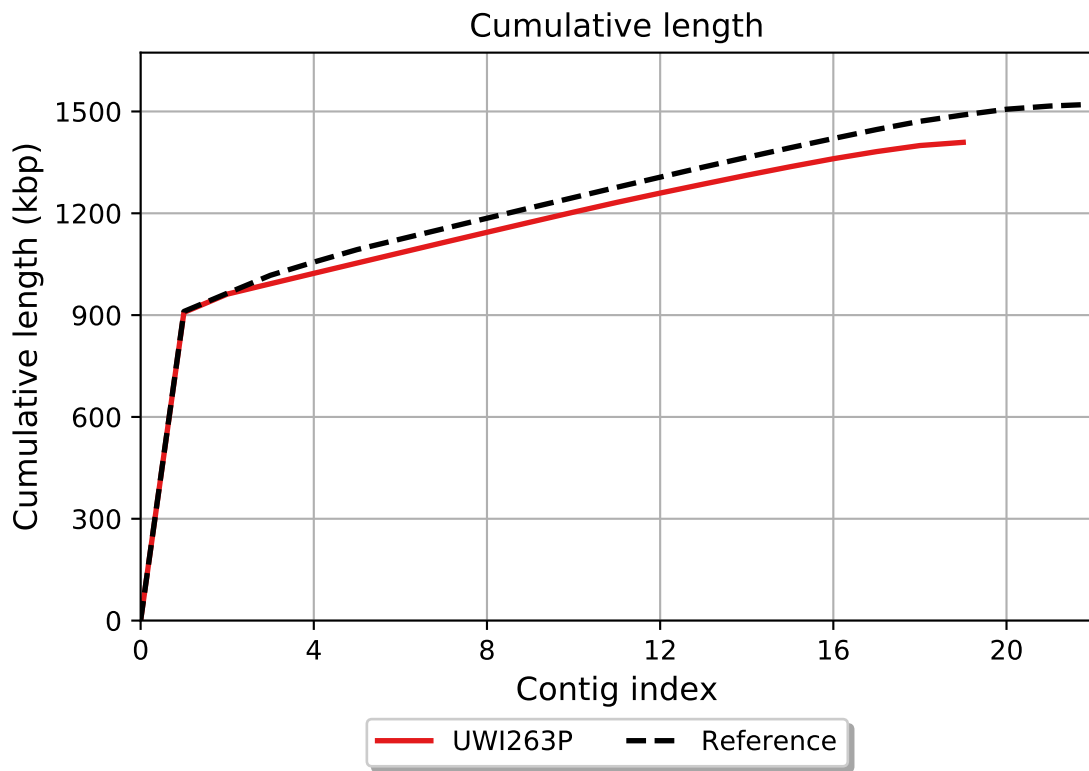


— UWI263P

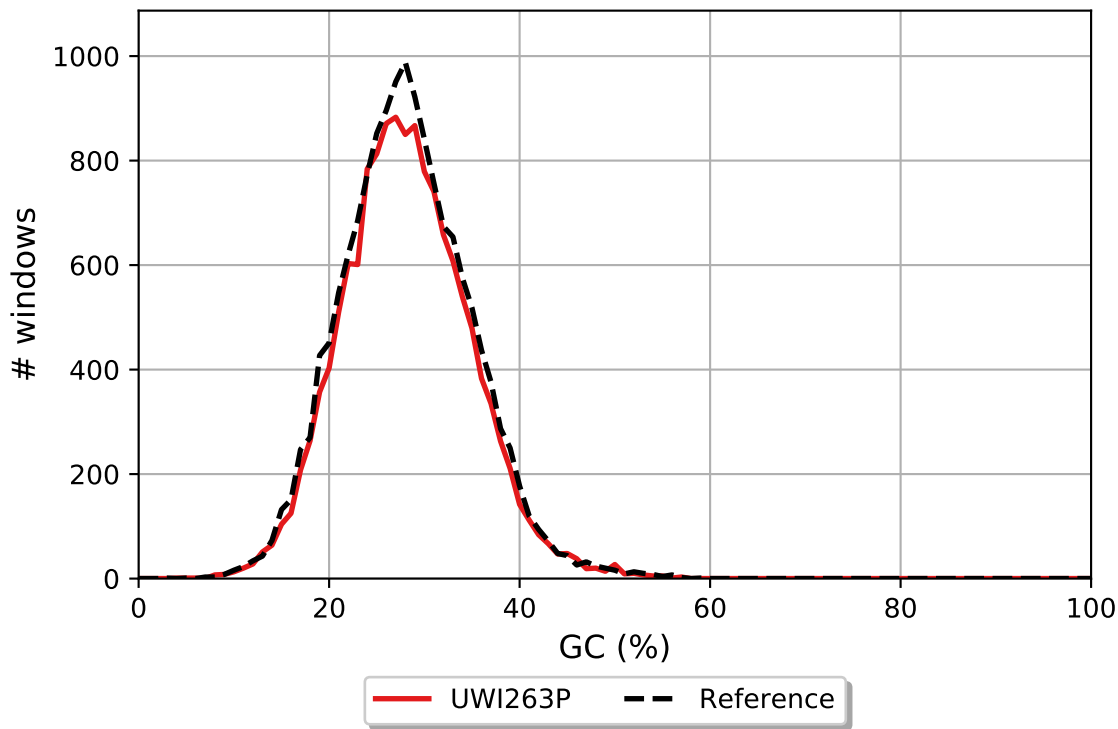
NGx



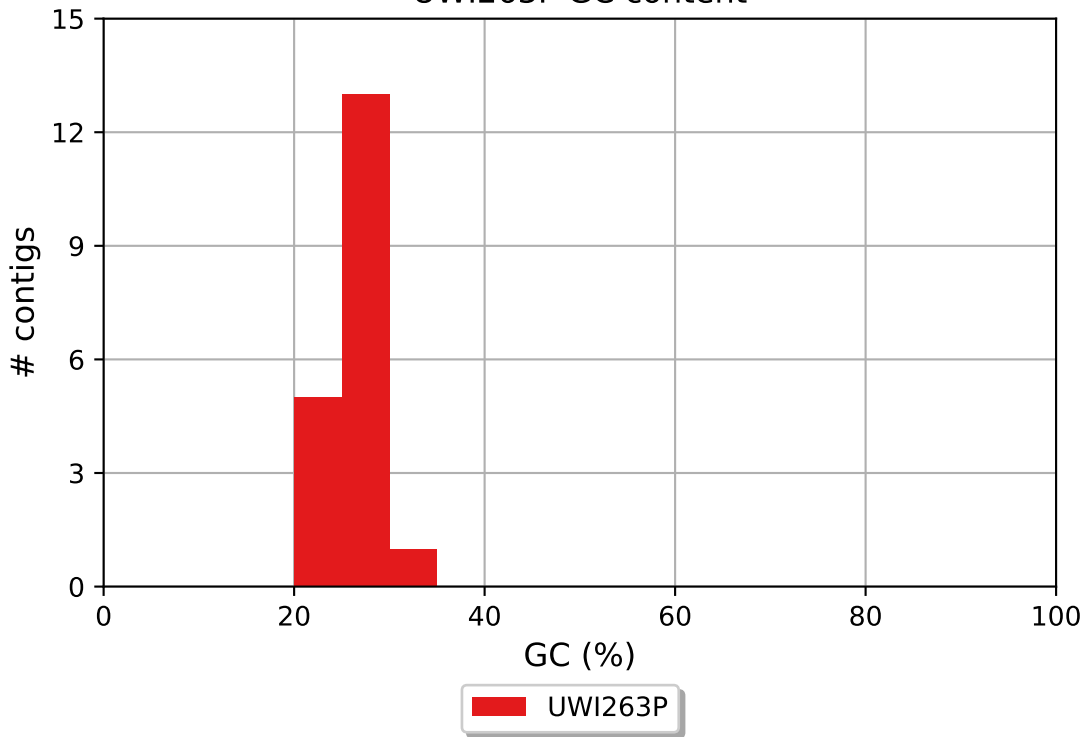
UWI263P



## GC content

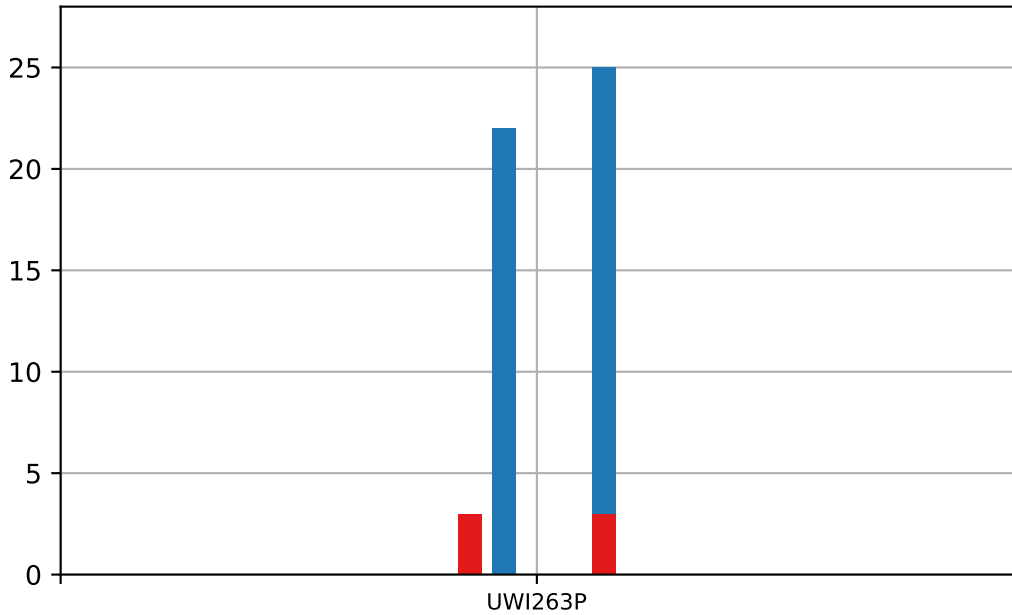


UWI263P GC content





## Misassemblies

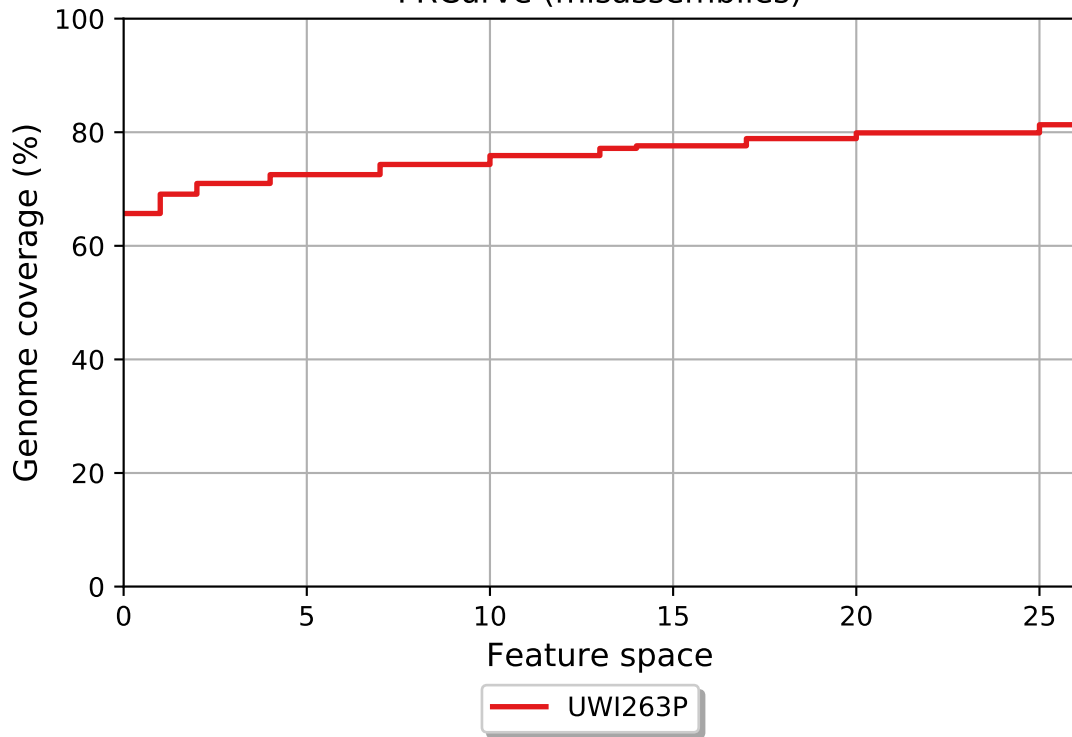


# relocations

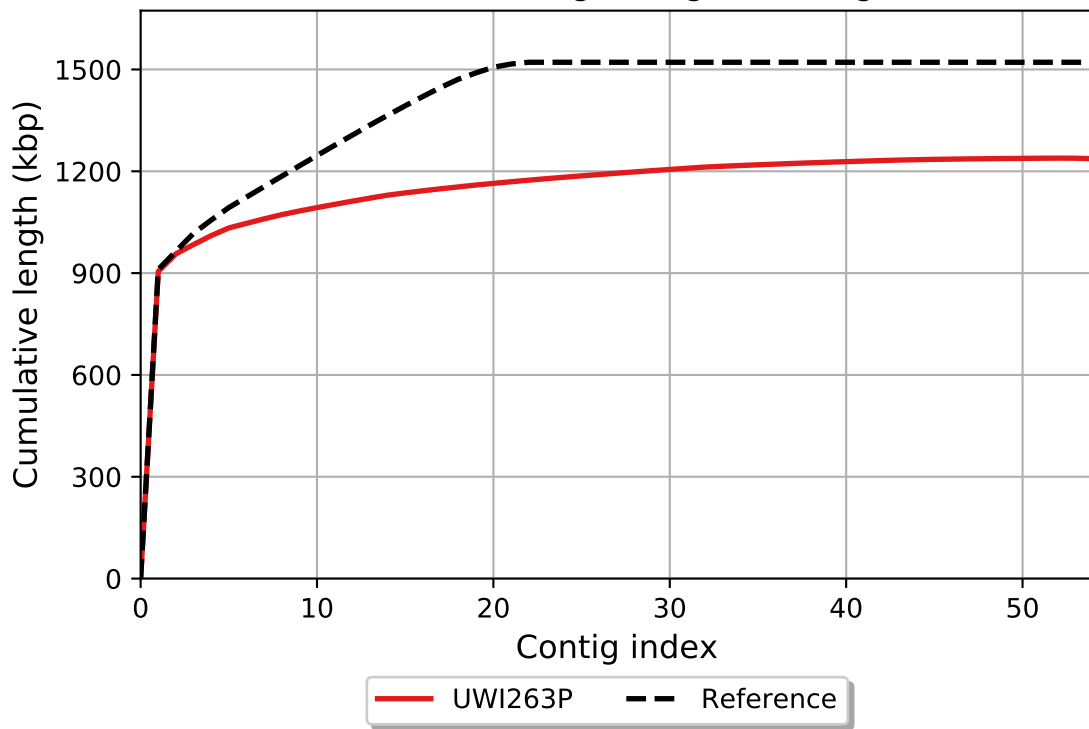


# translocations

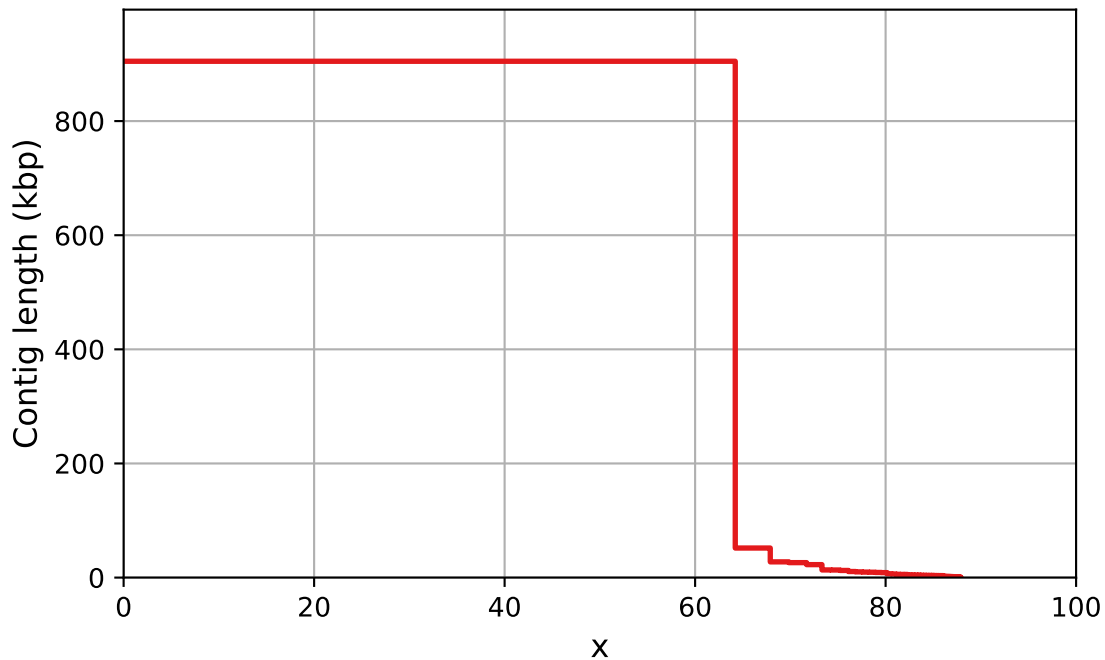
FRCurve (misassemblies)



Cumulative length (aligned contigs)

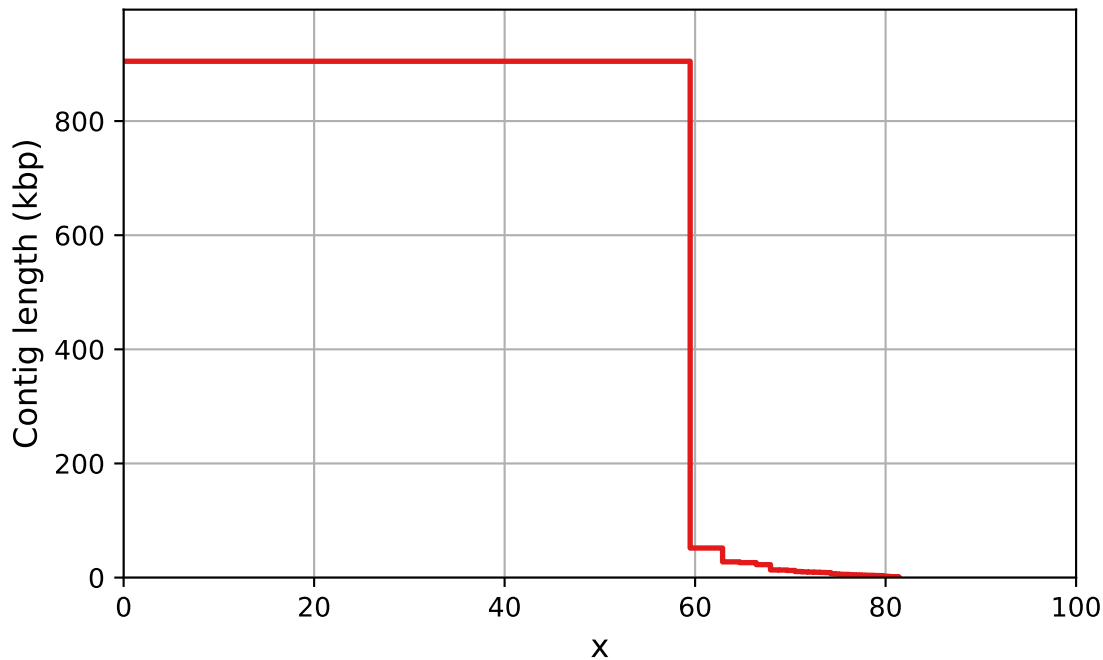


NAx



— UWI263P

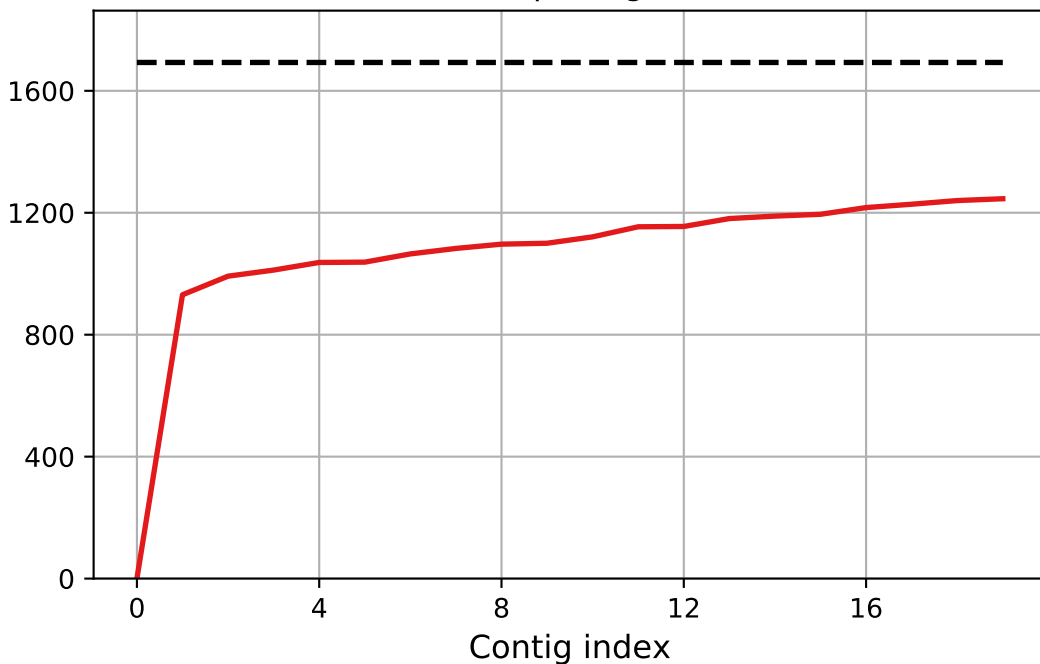
NGAx



UWI263P

Cumulative # complete genomic features

Cumulative # complete genomic features



— UWI263P    - - Reference

FRCurve (genomic features)

