

Report

	B418PP
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1376853
Total length (>= 1000 bp)	1376853
Total length (>= 5000 bp)	1376853
Total length (>= 10000 bp)	1368131
Total length (>= 25000 bp)	1289988
Total length (>= 50000 bp)	956578
# contigs	18
Largest contig	902773
Total length	1376853
Reference length	1521208
GC (%)	28.32
Reference GC (%)	28.18
N50	902773
NG50	902773
N90	27767
NG90	8722
auN	602623.9
auNG	545437.9
L50	1
LG50	1
L90	12
LG90	18
# misassemblies	16
# misassembled contigs	8
Misassembled contigs length	251361
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 14 part
Unaligned length	137251
Genome fraction (%)	80.193
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	851.29
# indels per 100 kbp	51.15
# genomic features	1270 + 48 part
Largest alignment	902593
Total aligned length	1235661
NA50	902593
NGA50	902593
NA90	-
NGA90	-
auNA	597197.3
auNGA	540526.2
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

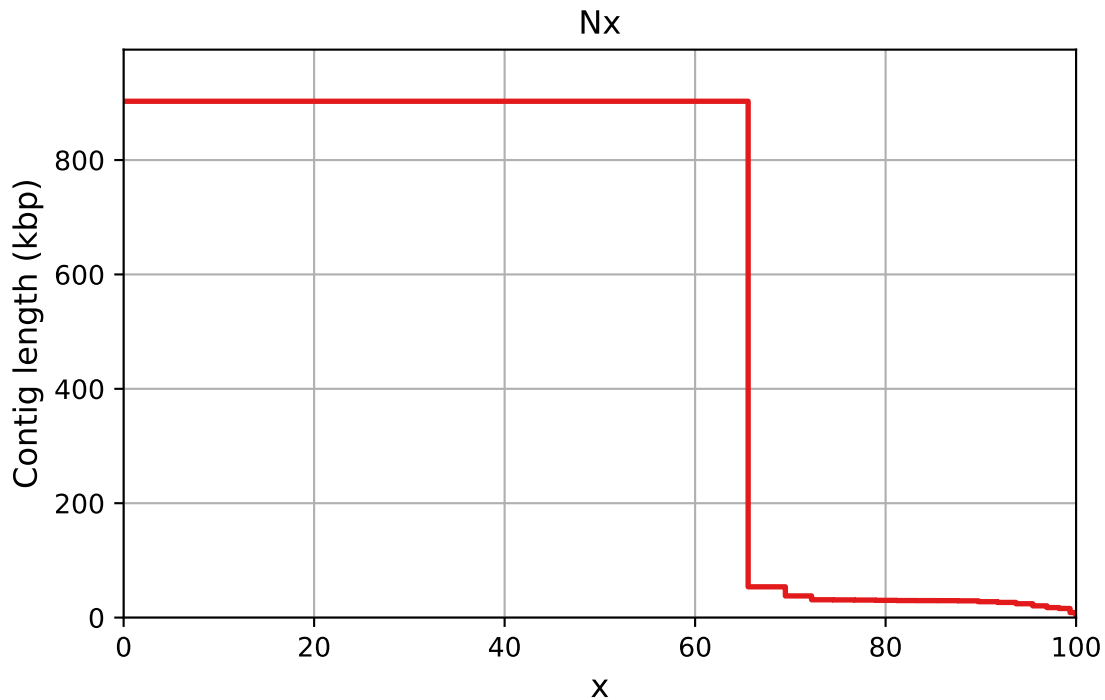
	B418PP
# misassemblies	16
# contig misassemblies	16
# c. relocations	4
# c. translocations	12
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	251361
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	10519
# indels	632
# indels (<= 5 bp)	559
# indels (> 5 bp)	73
Indels length	3259

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

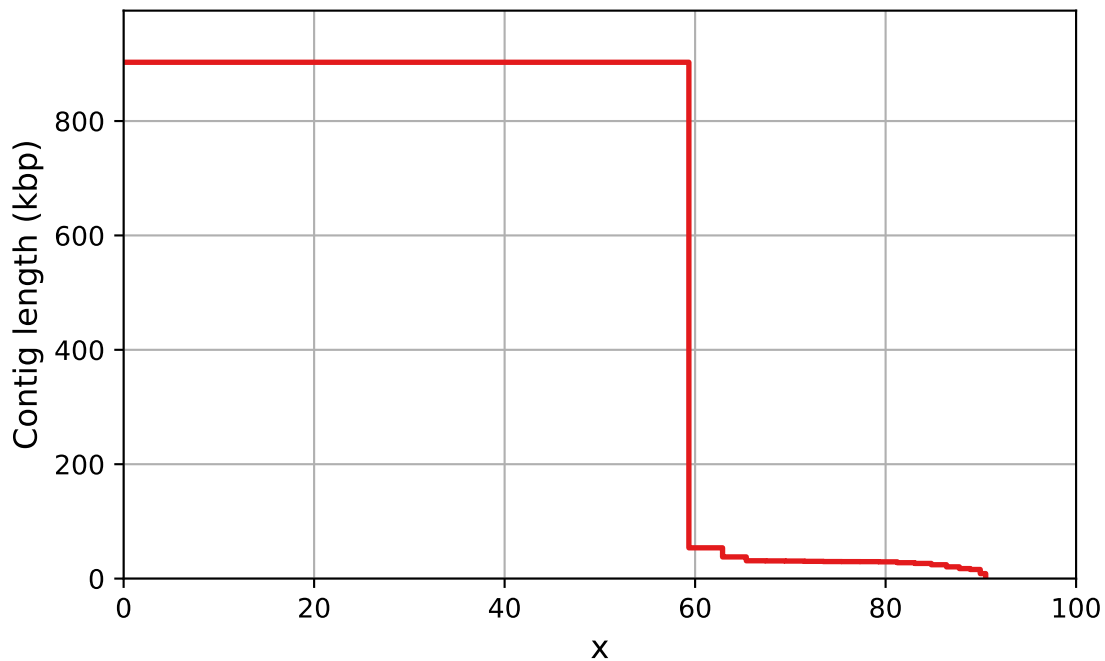
	B418PP
# fully unaligned contigs	1
Fully unaligned length	27767
# partially unaligned contigs	14
Partially unaligned length	109484
# N's	0

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).

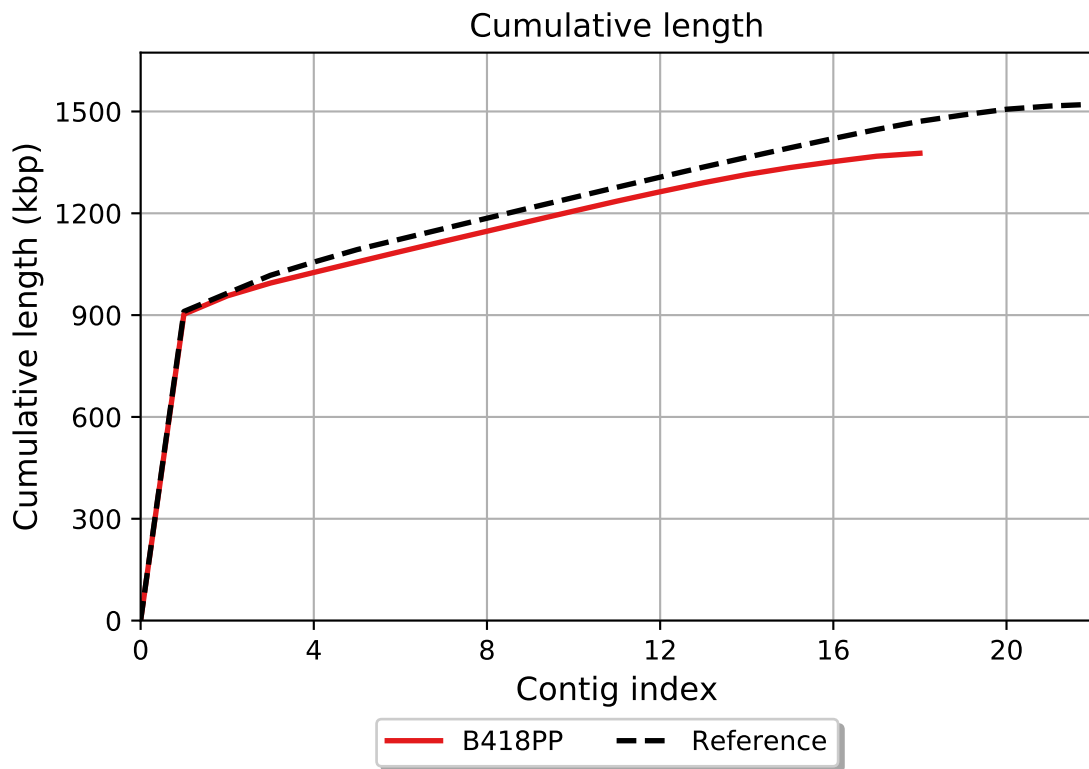


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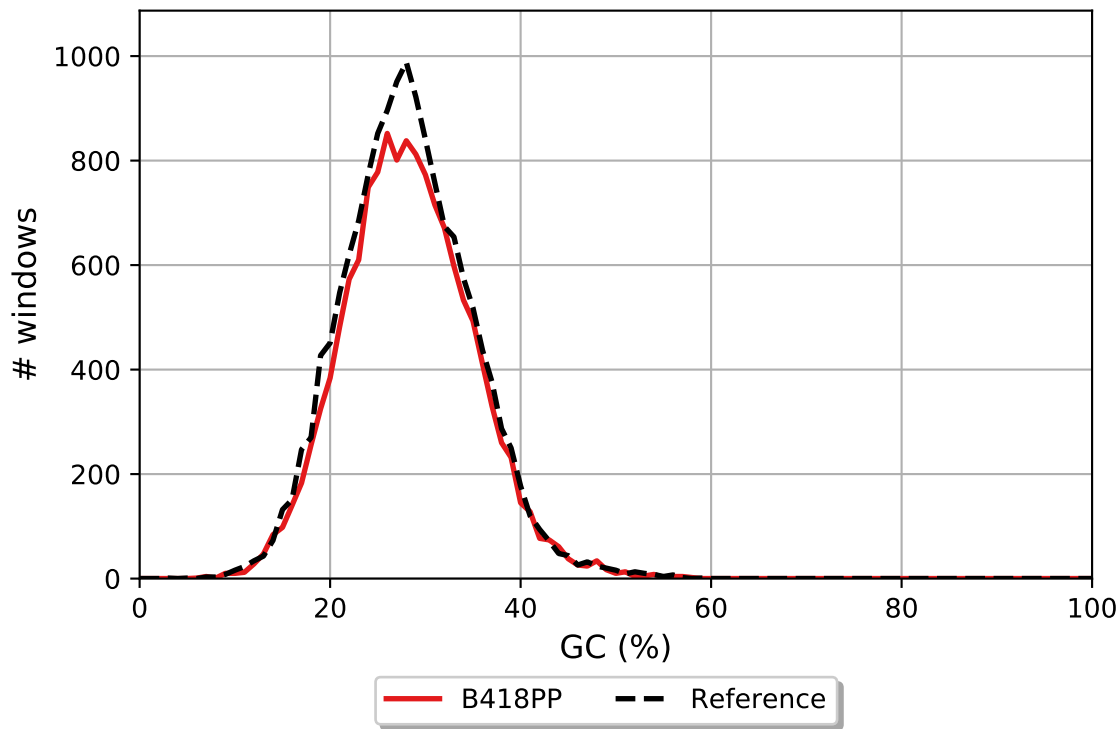
NGx



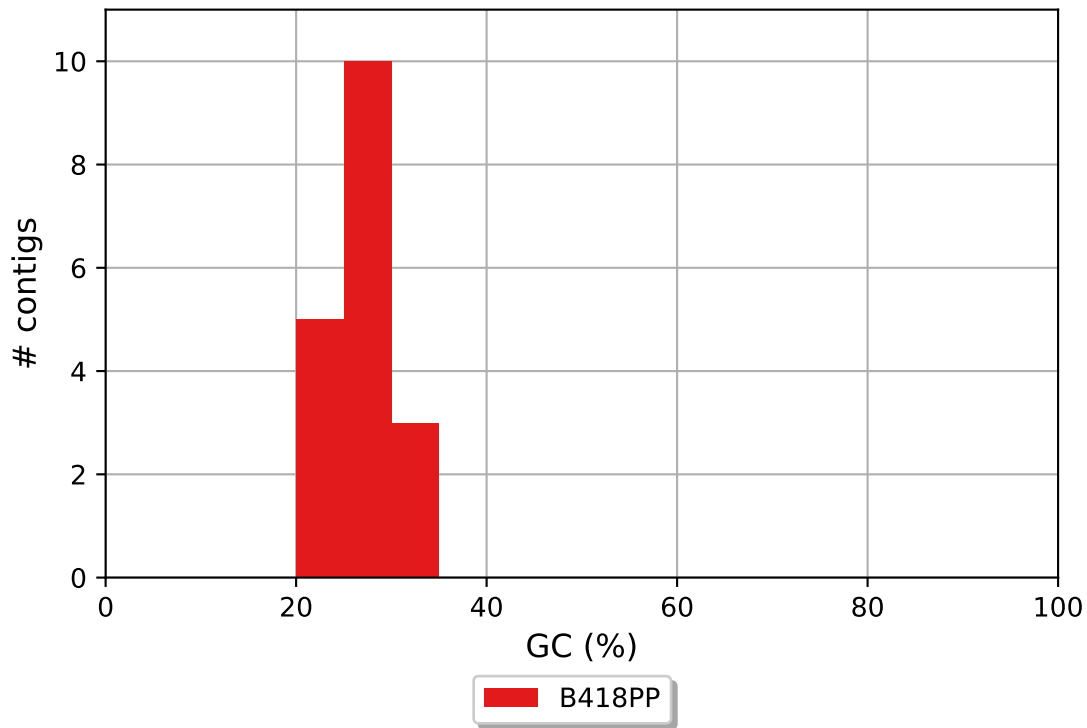
B418PP



## GC content

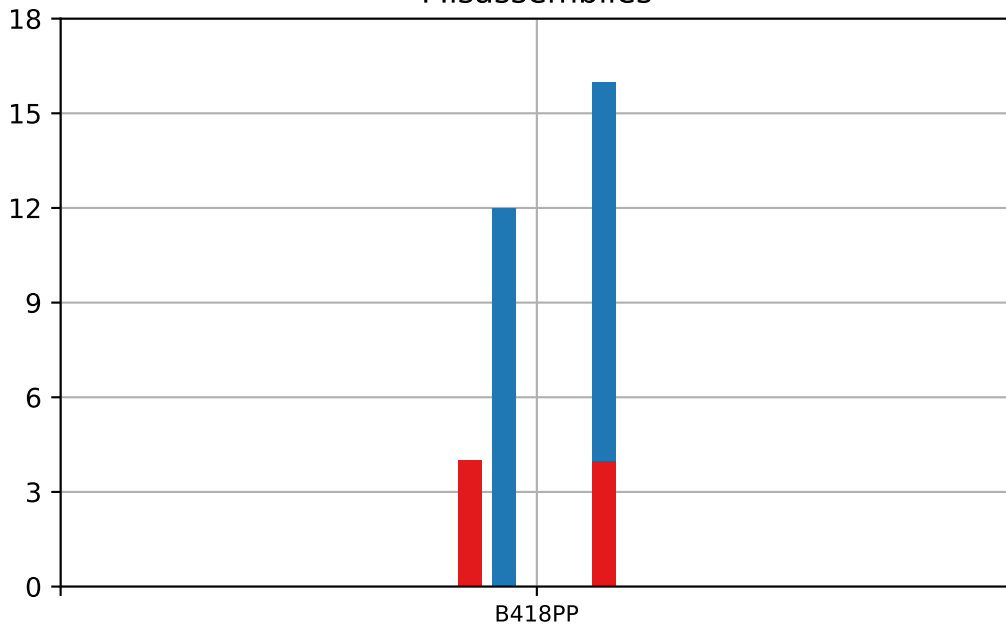


B418PP GC content





## Misassemblies

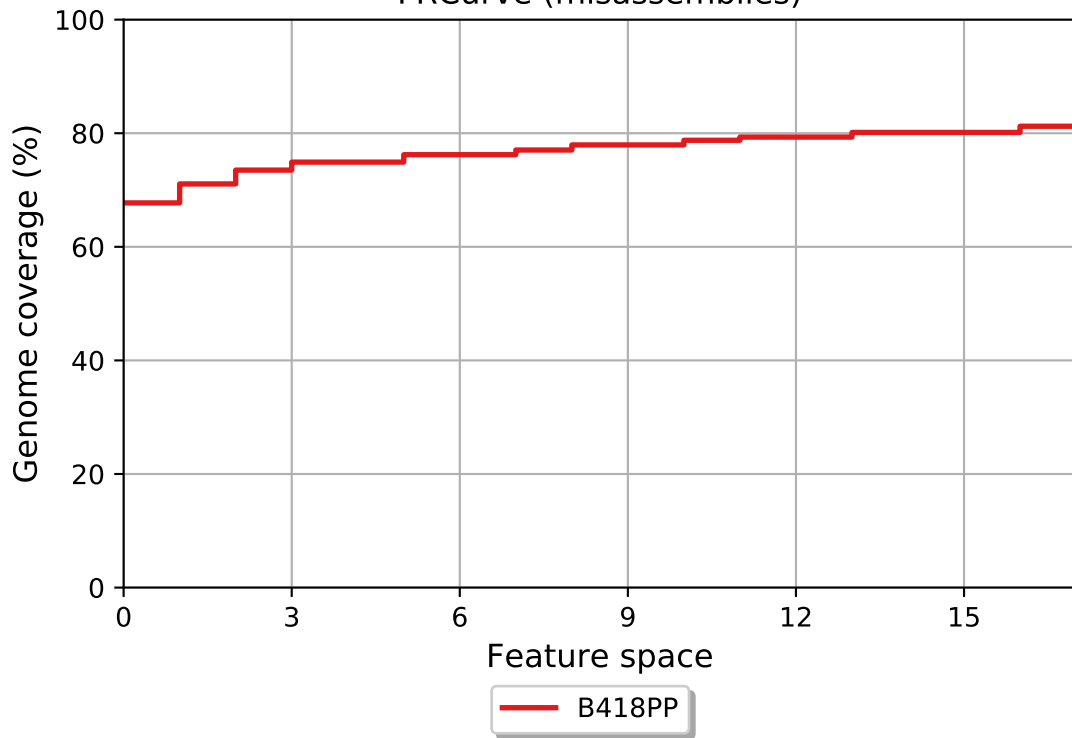


# relocations

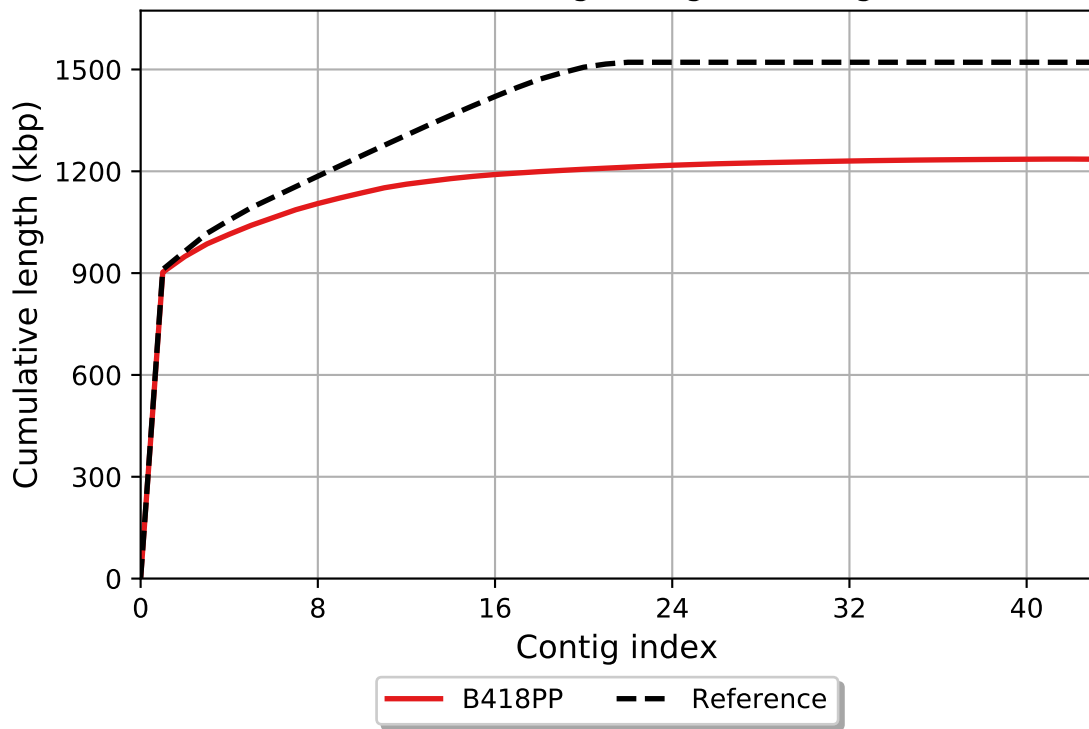


# translocations

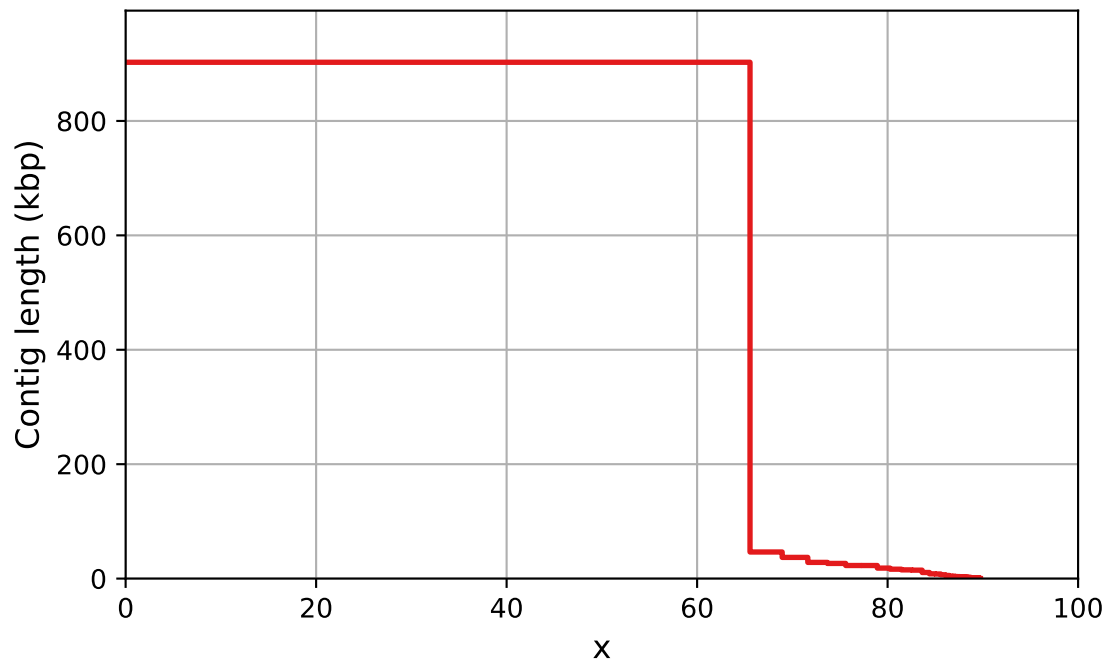
FRCurve (misassemblies)



Cumulative length (aligned contigs)

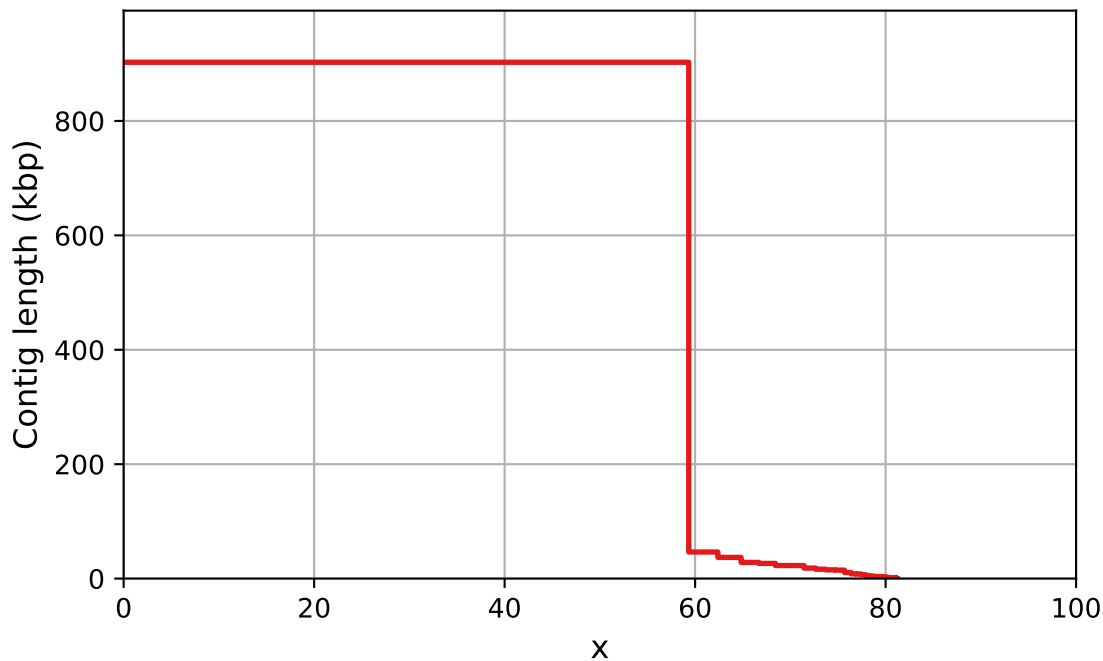


NAx

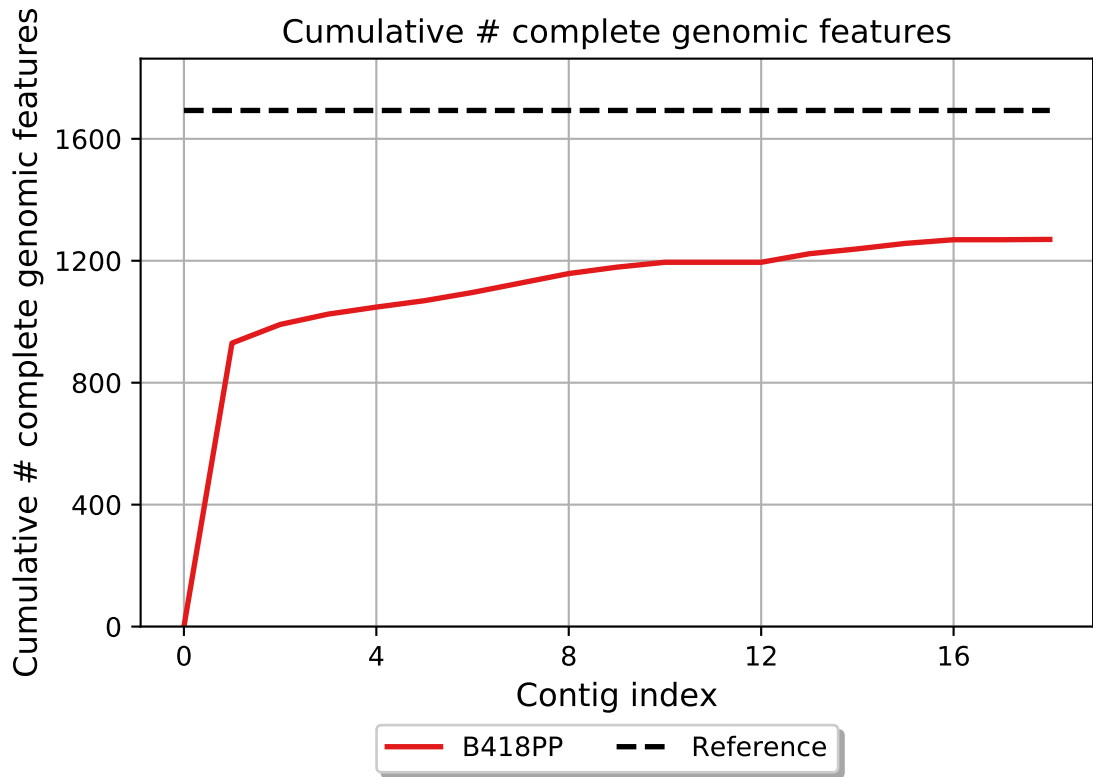


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NGAx



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FRCurve (genomic features)

