

Report

	B331PP
# 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)	1409078
Total length (>= 1000 bp)	1409078
Total length (>= 5000 bp)	1409078
Total length (>= 10000 bp)	1400364
Total length (>= 25000 bp)	1318606
Total length (>= 50000 bp)	957412
# contigs	19
Largest contig	903654
Total length	1409078
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	903654
NG50	903654
N90	27641
NG90	18340
auN	590638.9
auNG	547102.2
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	24
# misassembled contigs	12
Misassembled contigs length	374752
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 13 part
Unaligned length	113060
Genome fraction (%)	78.783
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	932.37
# indels per 100 kbp	60.88
# genomic features	1250 + 39 part
Largest alignment	903464
Total aligned length	1294341
NA50	903464
NGA50	903464
NA90	2247
NGA90	-
auNA	585147.2
auNGA	542015.4
LA50	1
LGA50	1
LA90	30
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

	B331PP
# misassemblies	24
# contig misassemblies	24
# c. relocations	2
# c. translocations	20
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	374752
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	12068
# indels	788
# indels (<= 5 bp)	706
# indels (> 5 bp)	82
Indels length	3797

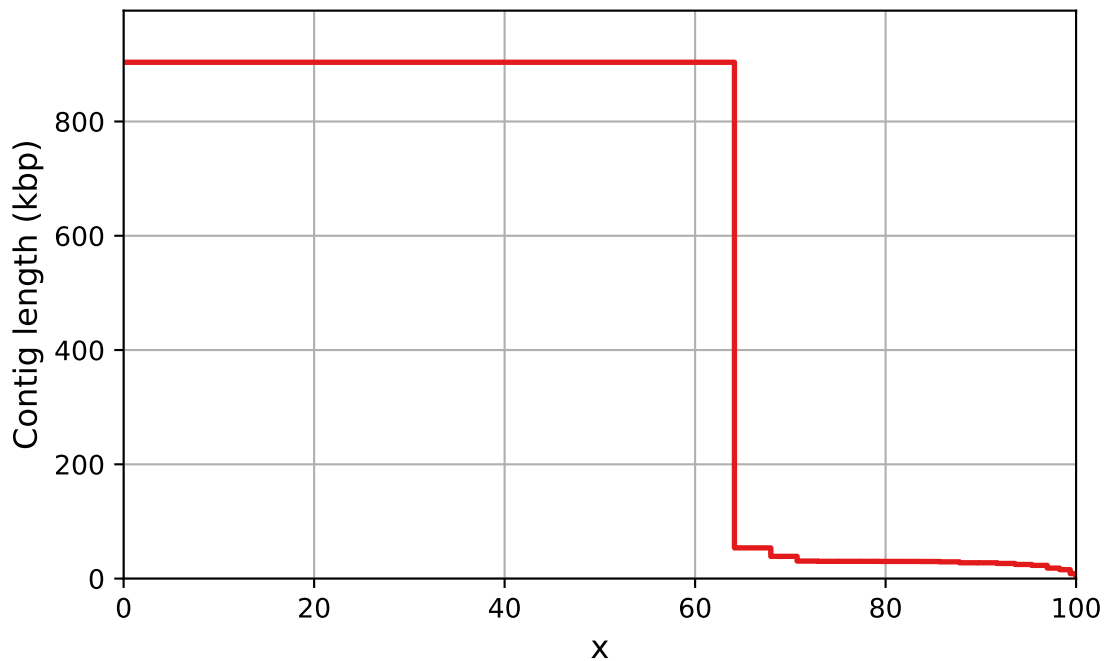
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	B331PP
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	113060
# N's	0

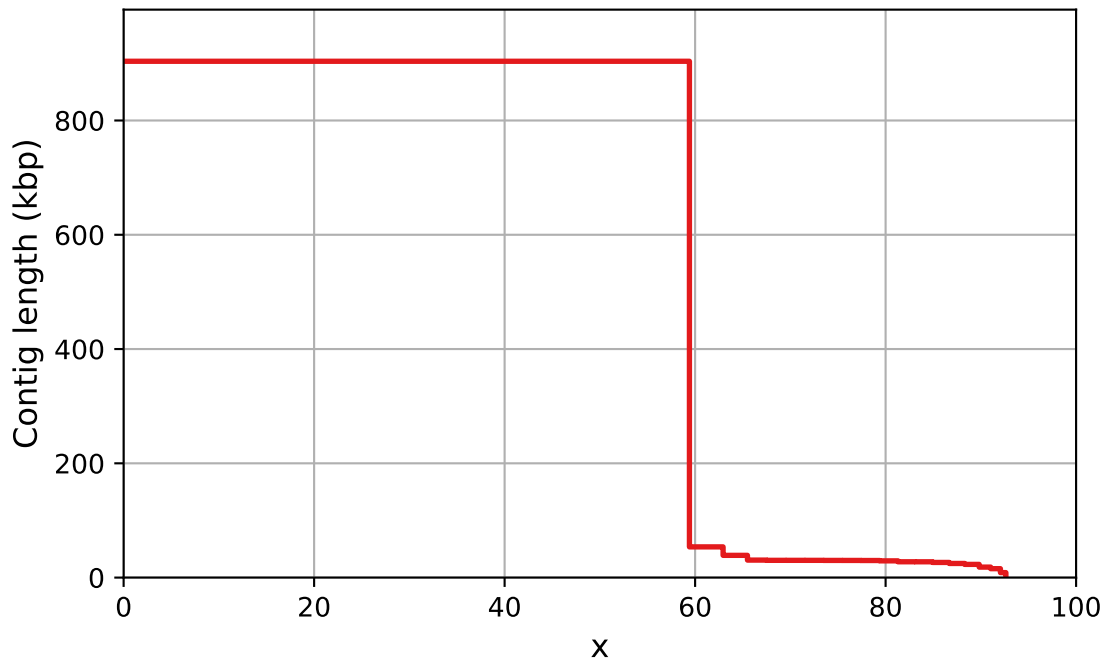
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

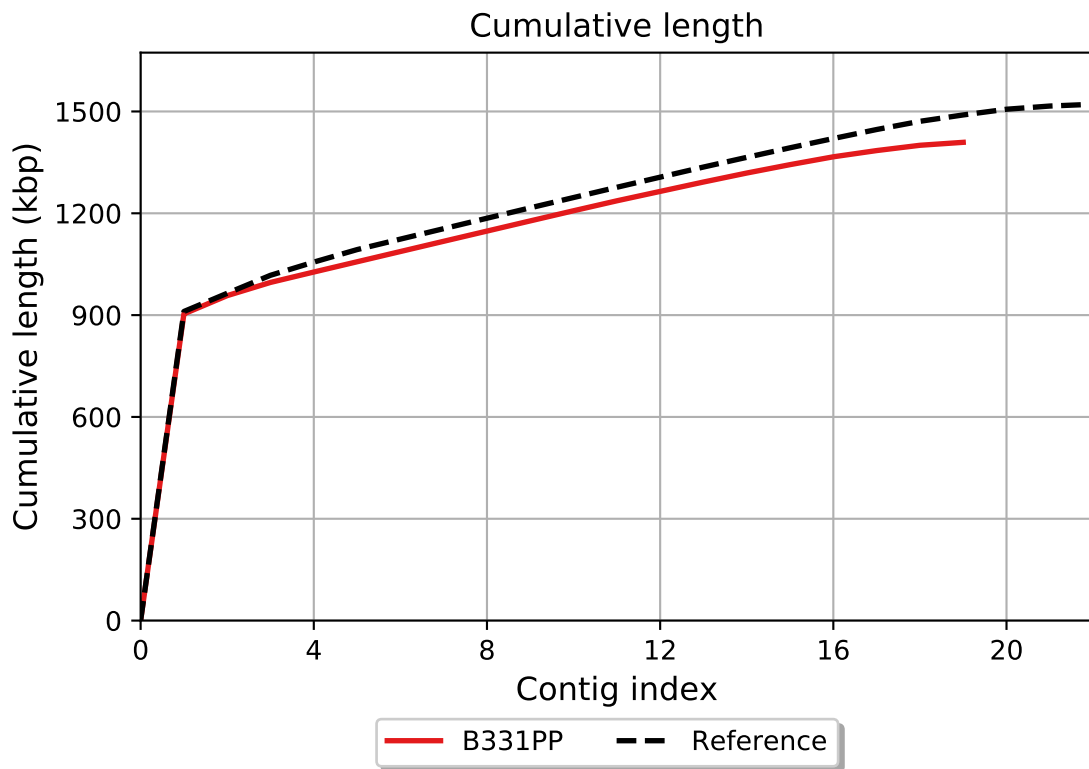


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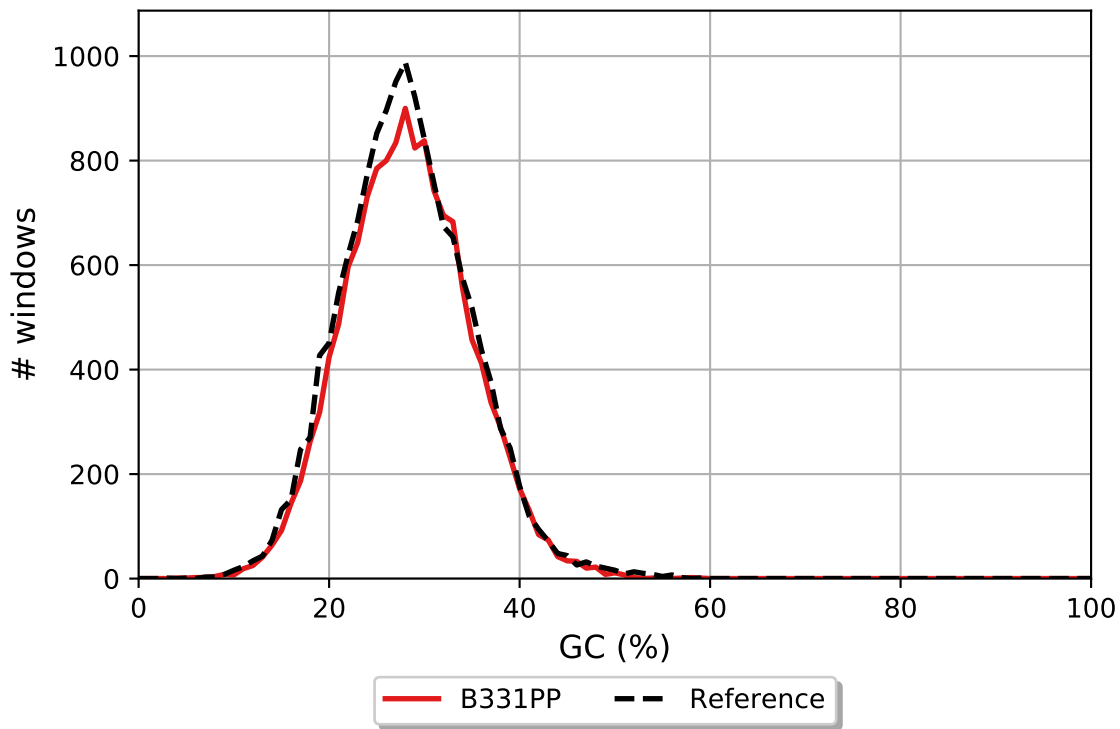
NGx



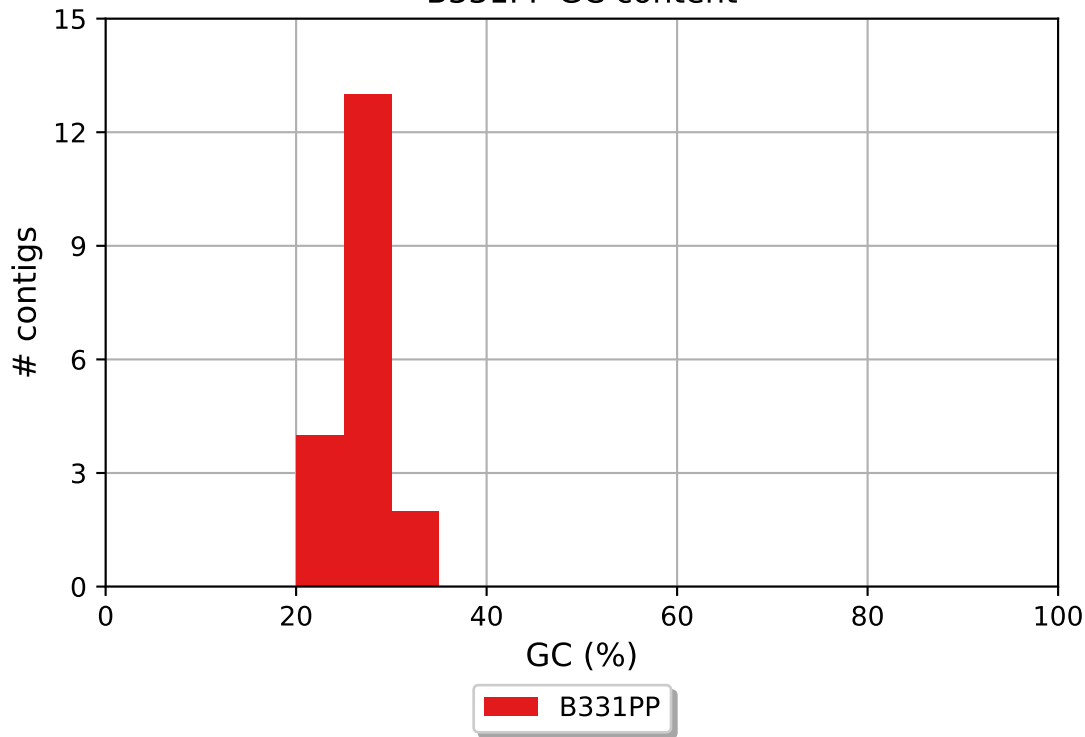
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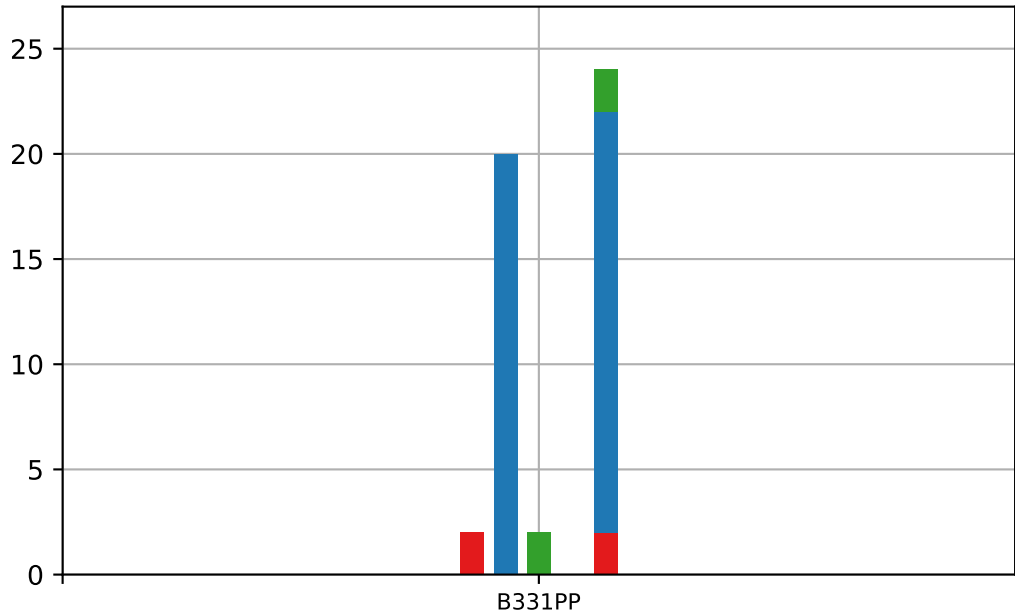
GC content



B331PP GC content



Misassemblies



relocations

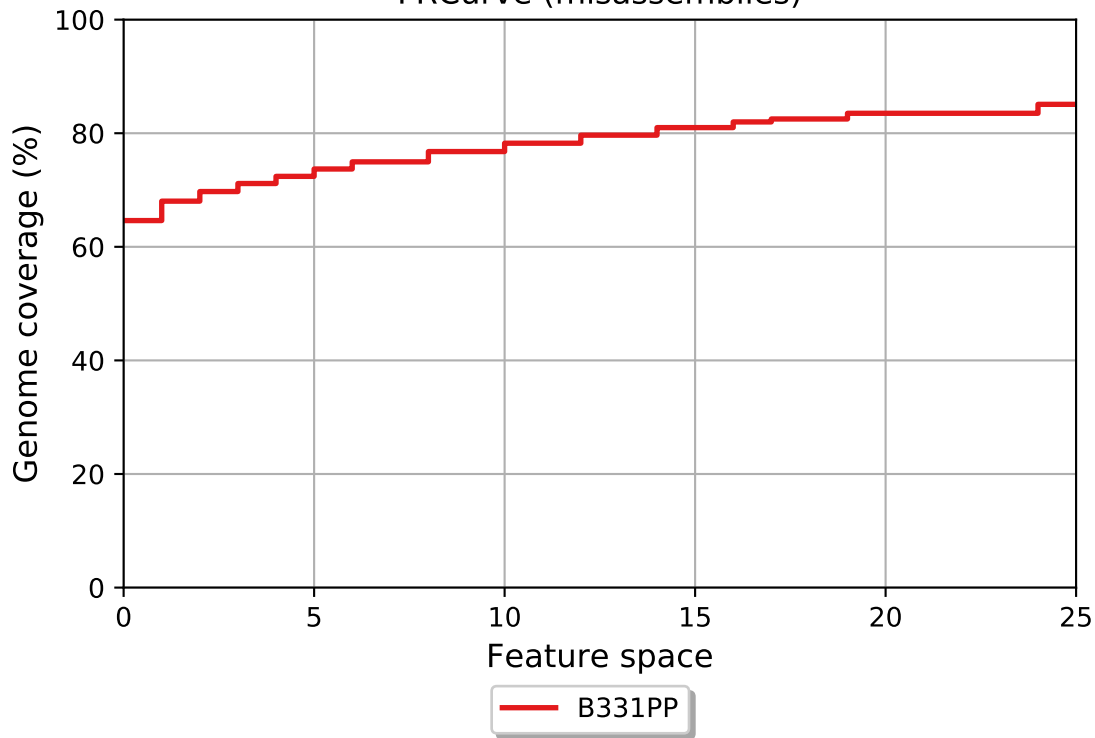


translocations

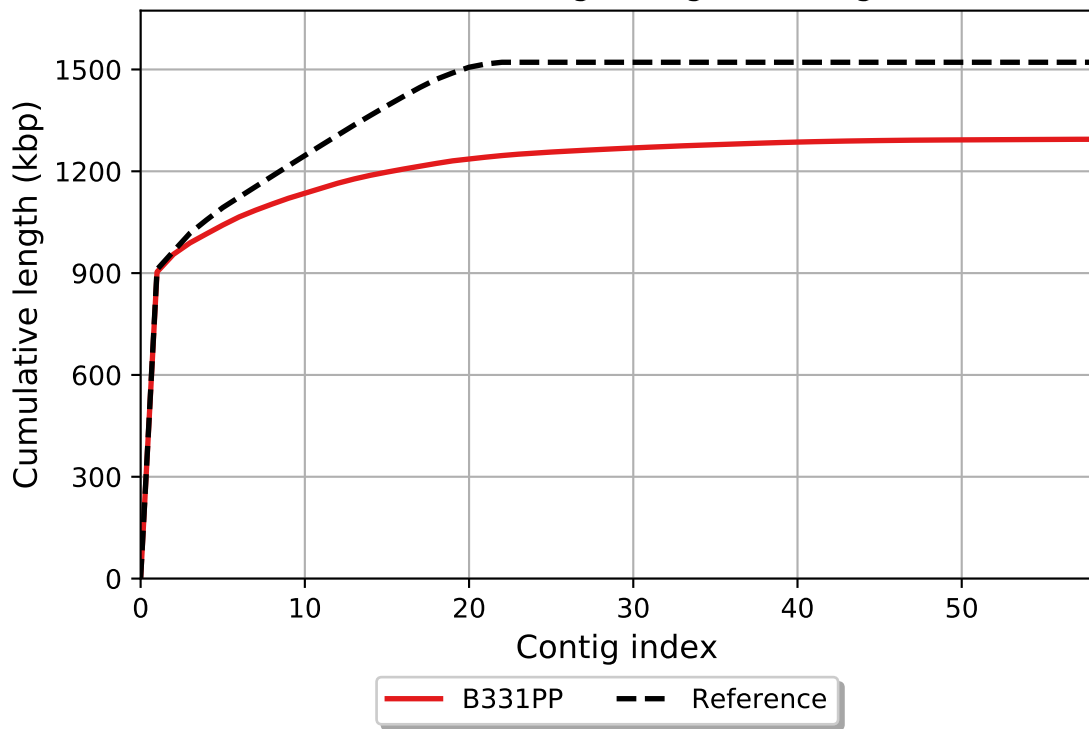


inversions

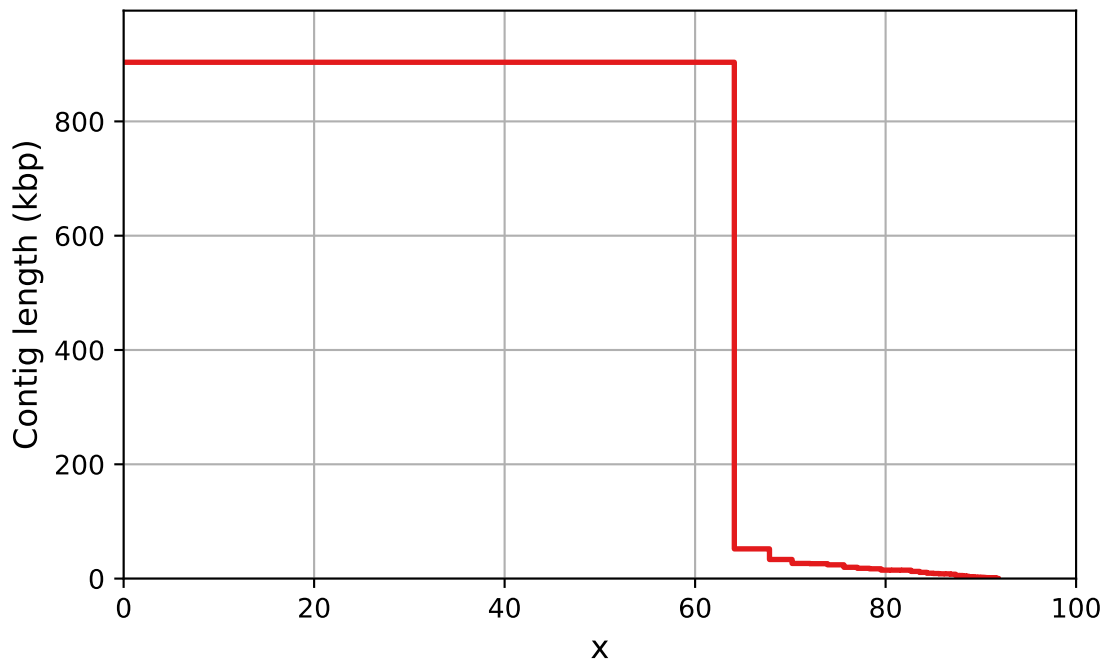
FRCurve (misassemblies)



Cumulative length (aligned contigs)

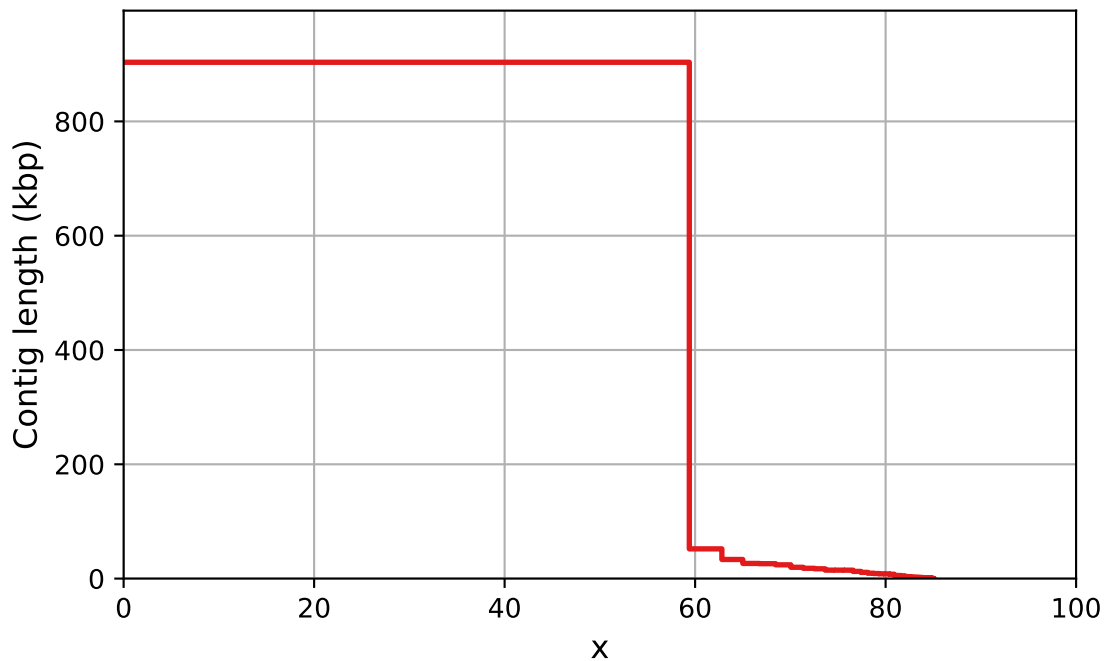


NAx



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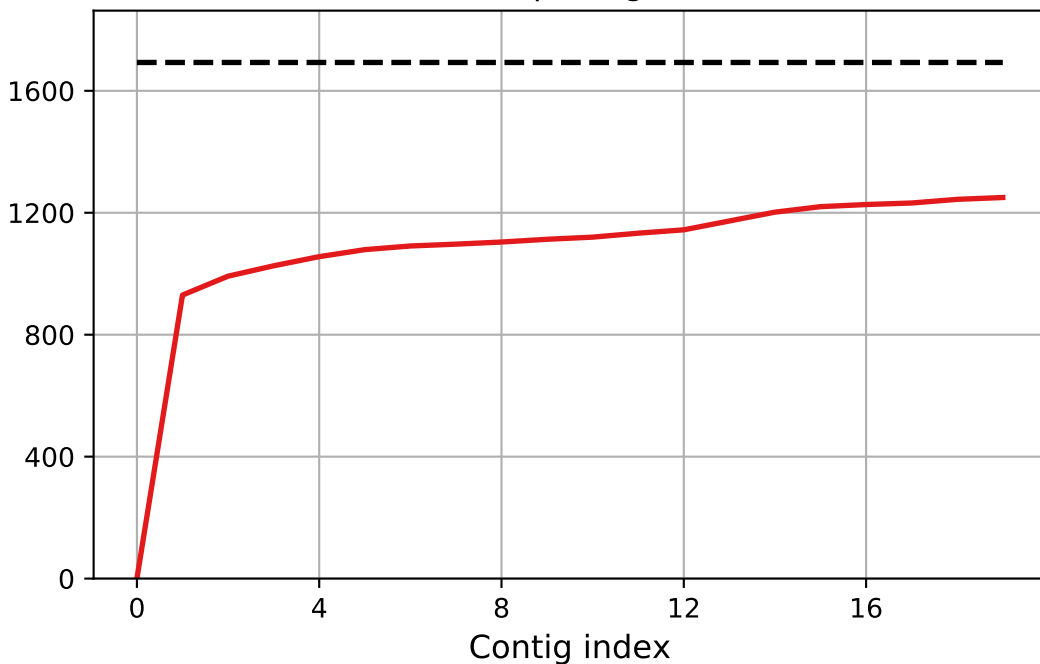
NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

