

# Report

	33_3_80.30
# contigs (>= 1000 bp)	31
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	224694
Total length (>= 5000 bp)	178252
Total length (>= 10000 bp)	117526
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	35
Largest contig	19486
Total length	228097
Reference length	29903
GC (%)	37.99
Reference GC (%)	37.97
N50	10094
NG50	19486
N75	5559
NG75	19485
L50	8
LG50	1
L75	15
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.993
Duplication ratio	7.705
# N's per 100 kbp	0.00
# mismatches per 100 kbp	131.75
# indels per 100 kbp	64.18
Largest alignment	19486
Total aligned length	228064
NA50	10093
NGA50	19486
NA75	5558
NGA75	19484
LA50	8
LGA50	1
LA75	15
LGA75	2

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

	33_3_80.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	39
# indels	19
# indels (<= 5 bp)	19
# indels (> 5 bp)	0
Indels length	19

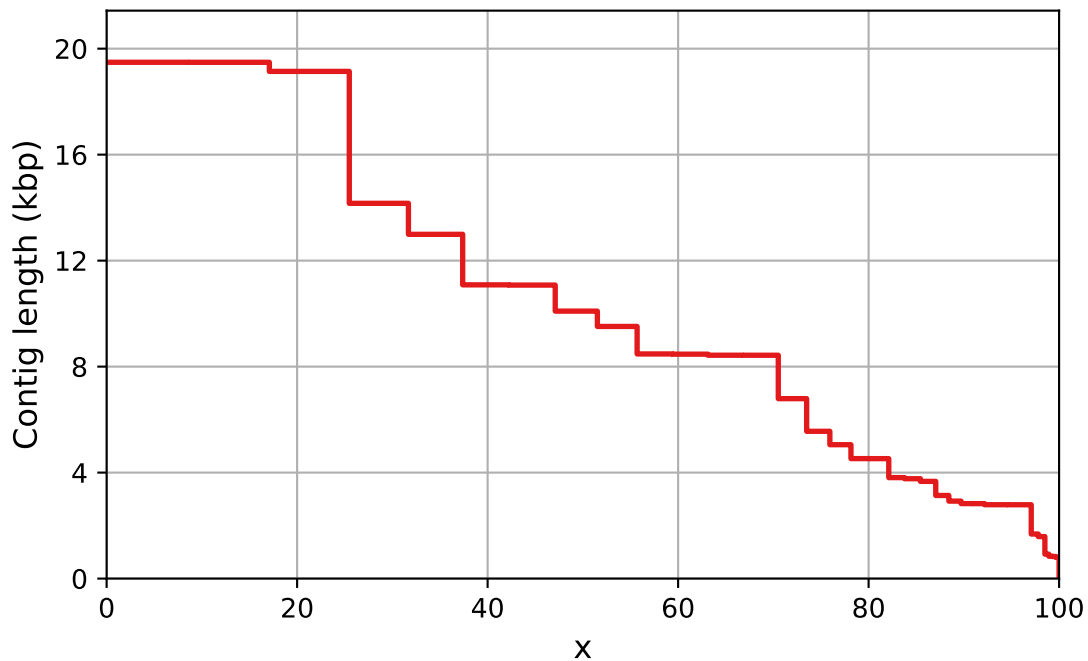
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	33_3_80.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

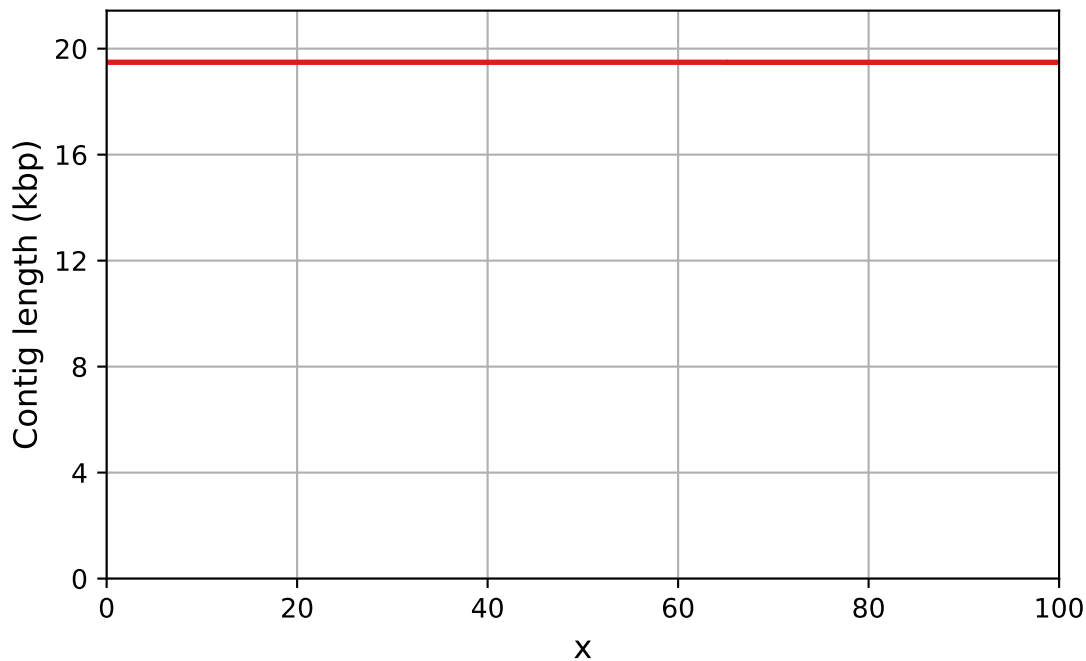
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

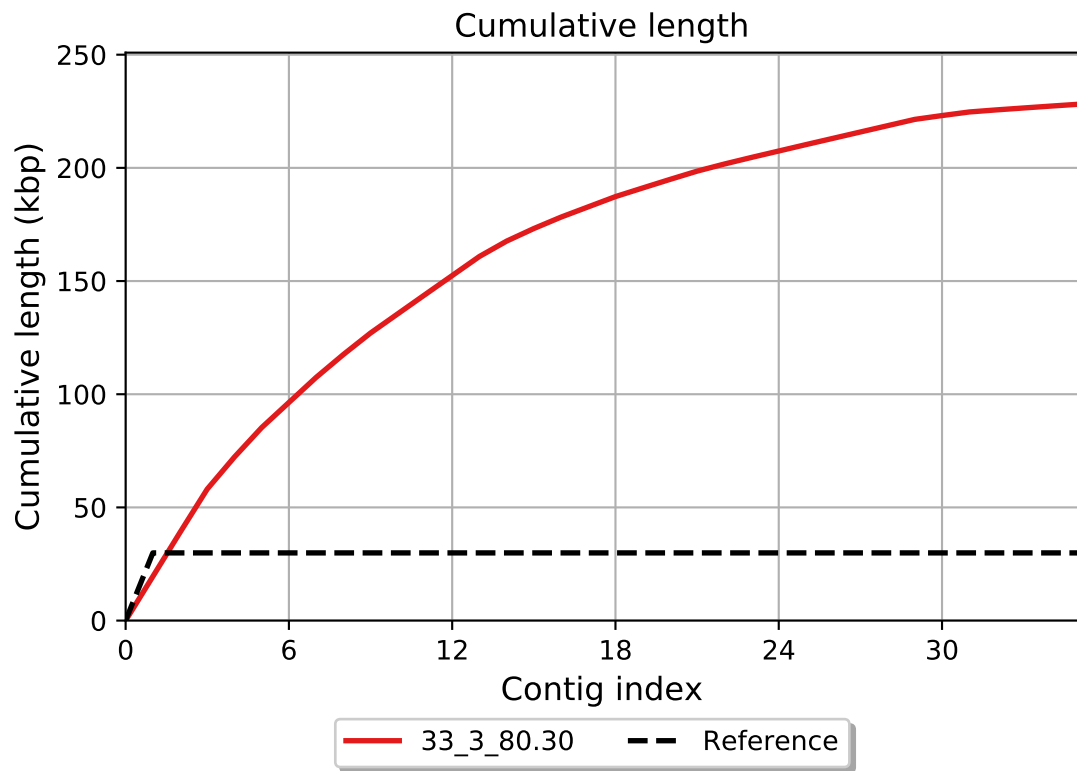


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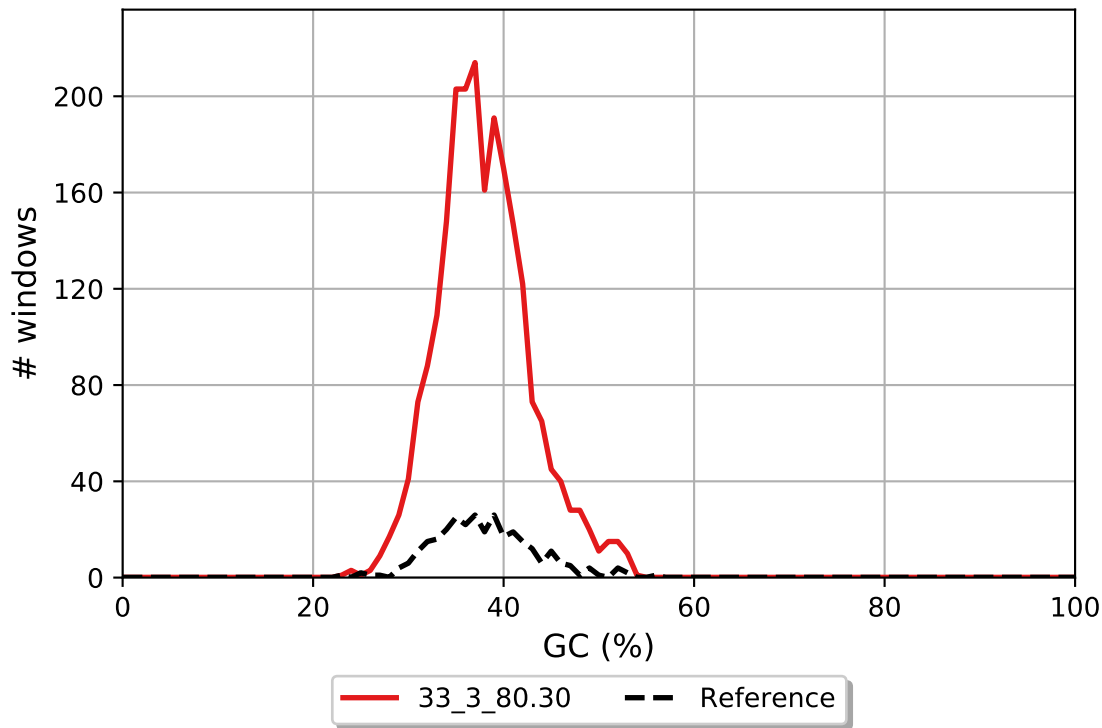
NGx



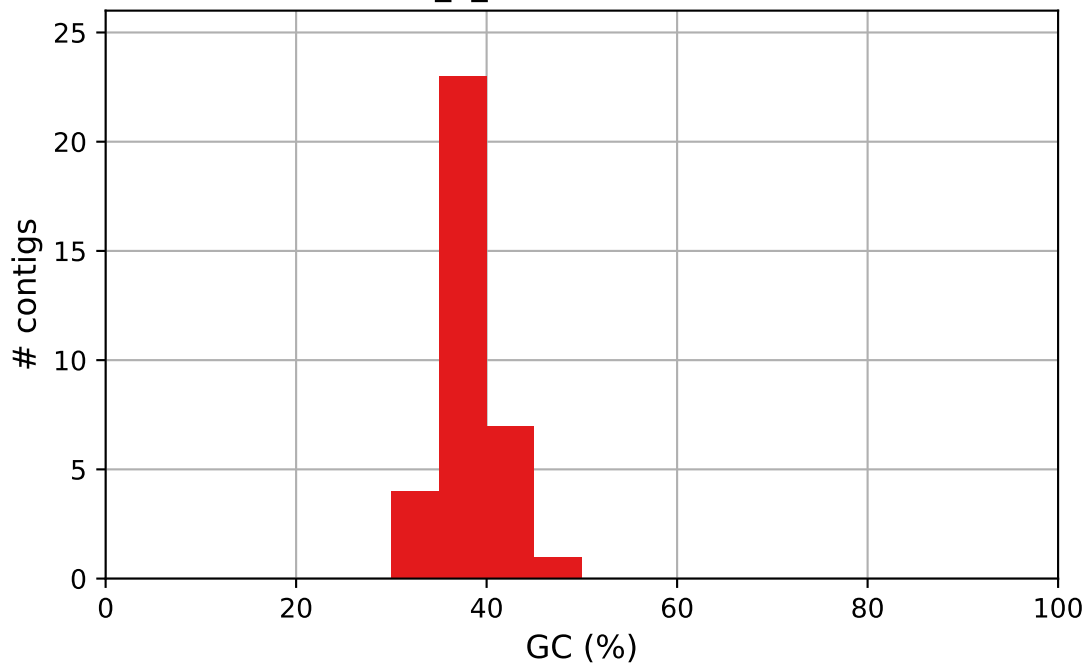
33\_3\_80.30



## GC content



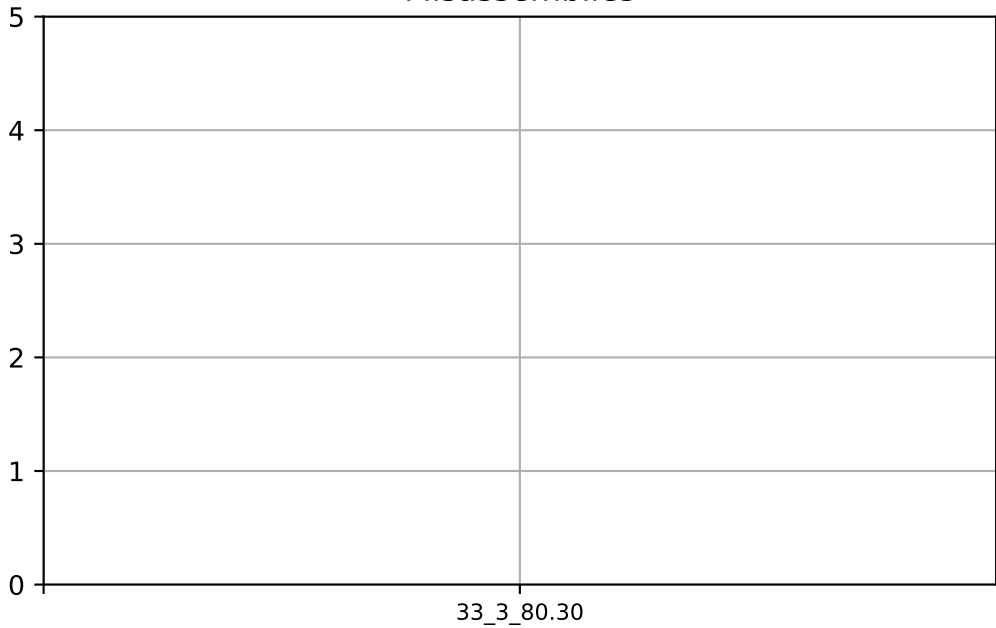
33\_3\_80.30 GC content



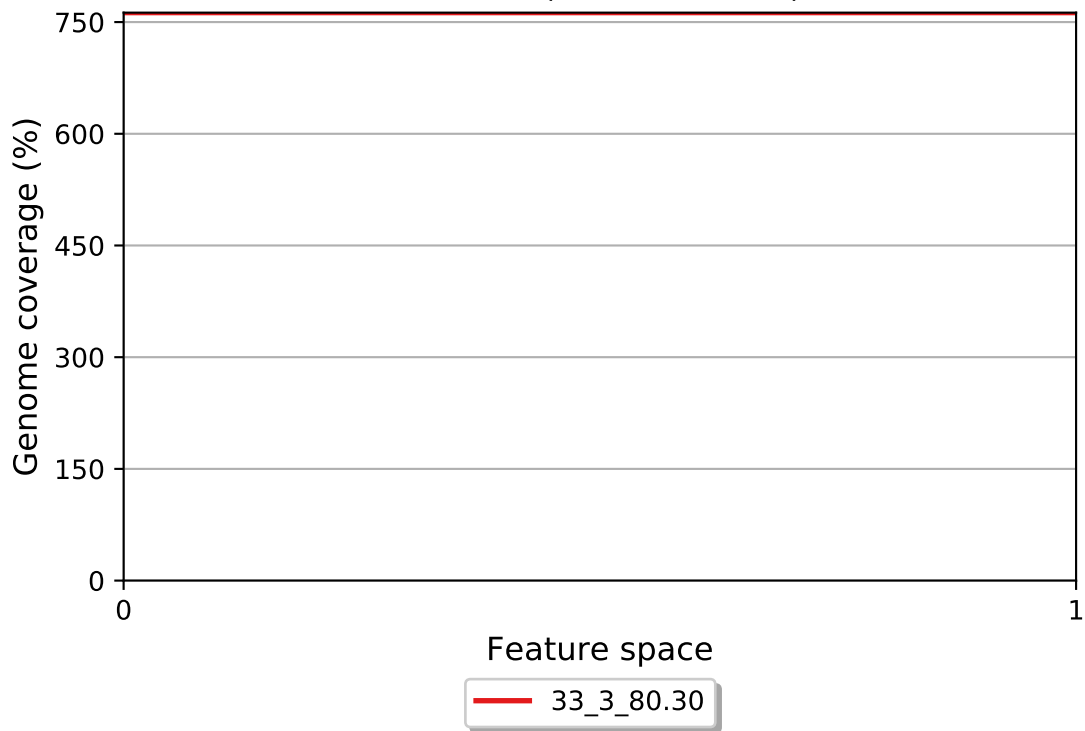
33\_3\_80.30



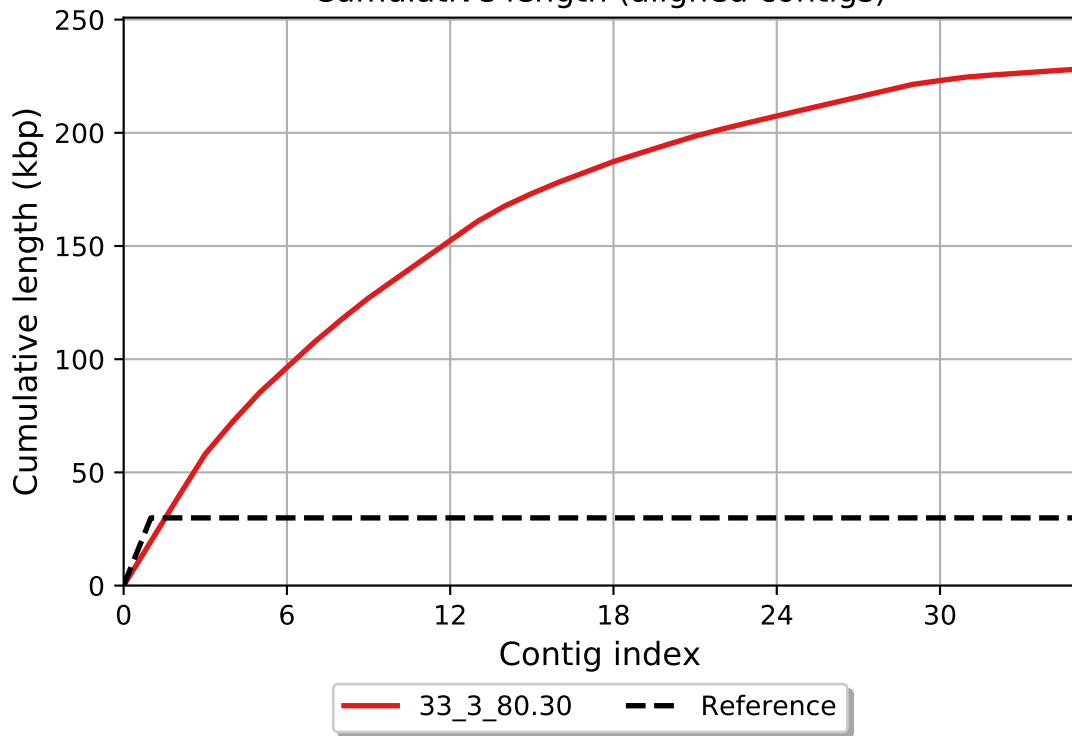
## Misassemblies



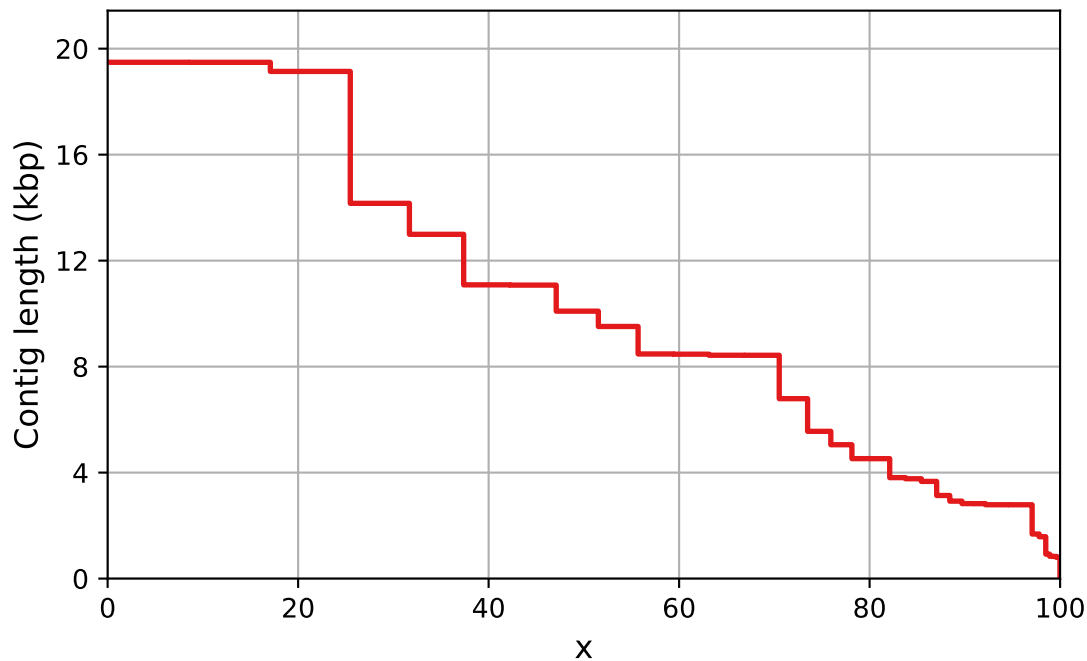
FRCurve (misassemblies)



Cumulative length (aligned contigs)

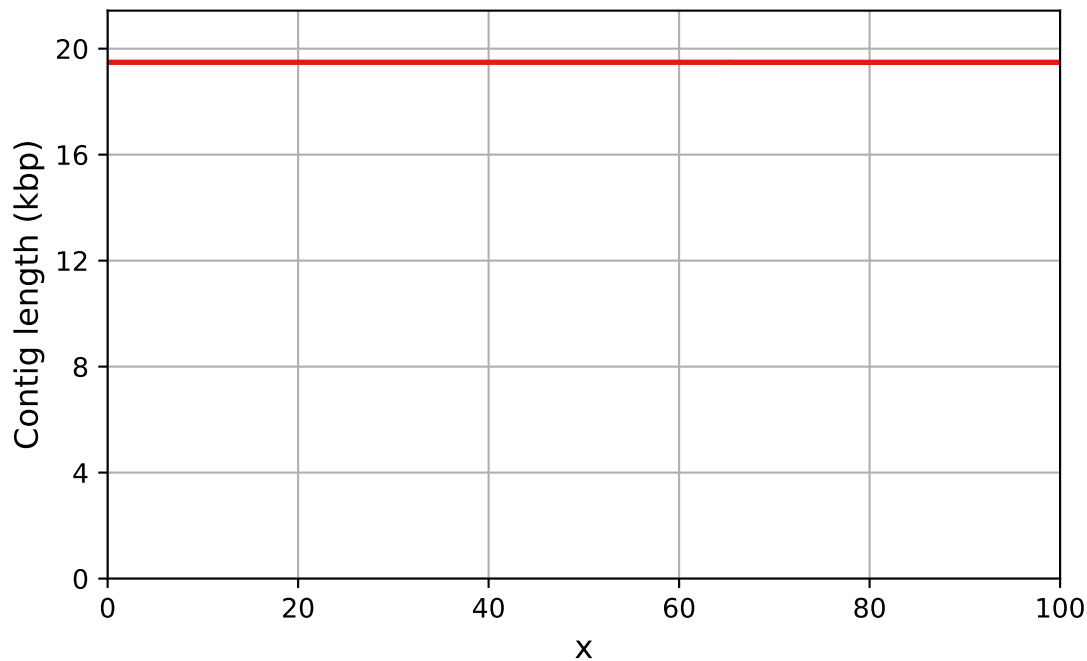


NAx



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NGAx



33\_3\_80.30