

# Report

	TARA_ANW_RAW
# contigs (>= 1000 bp)	51
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	200221
Total length (>= 5000 bp)	121401
Total length (>= 10000 bp)	105935
Total length (>= 25000 bp)	105935
Total length (>= 50000 bp)	105935
# contigs	51
Largest contig	105935
Total length	200221
Reference length	3561038
GC (%)	41.62
Reference GC (%)	41.87
N50	105935
N75	2041
L50	1
L75	14
# 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	1
# unaligned contigs	10 + 41 part
Unaligned length	196465
Genome fraction (%)	0.022
Duplication ratio	4.719
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14698.49
# indels per 100 kbp	0.00
Largest alignment	145
Total aligned length	3756
NGA50	-

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

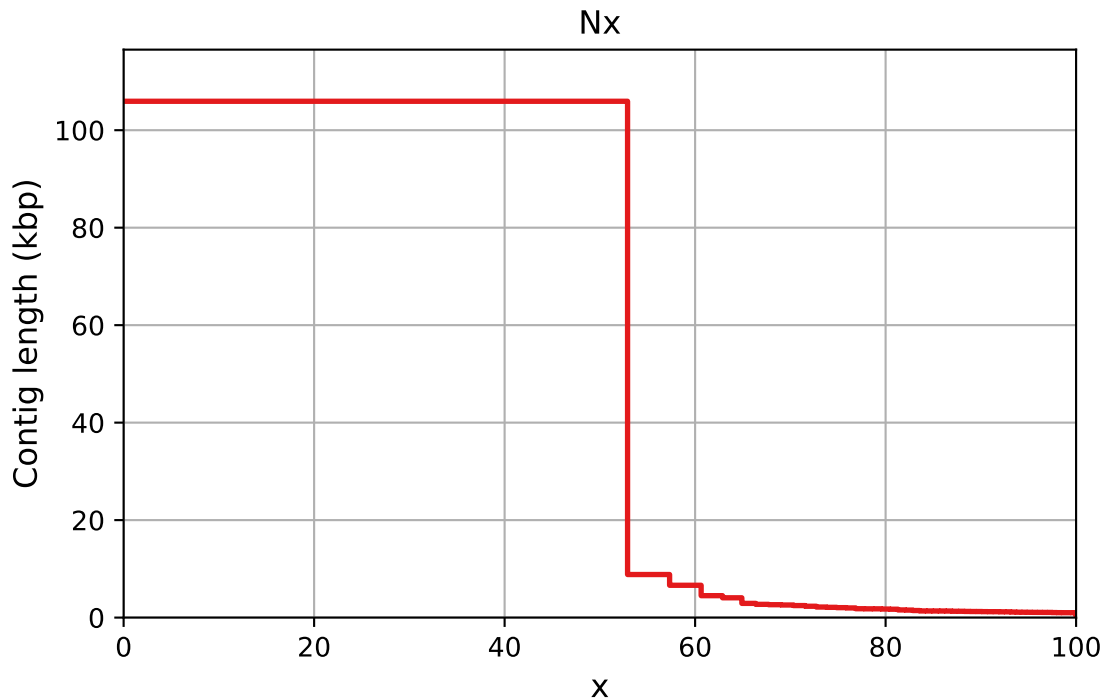
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	49
# possible misassemblies	56
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	117
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

## Unaligned report

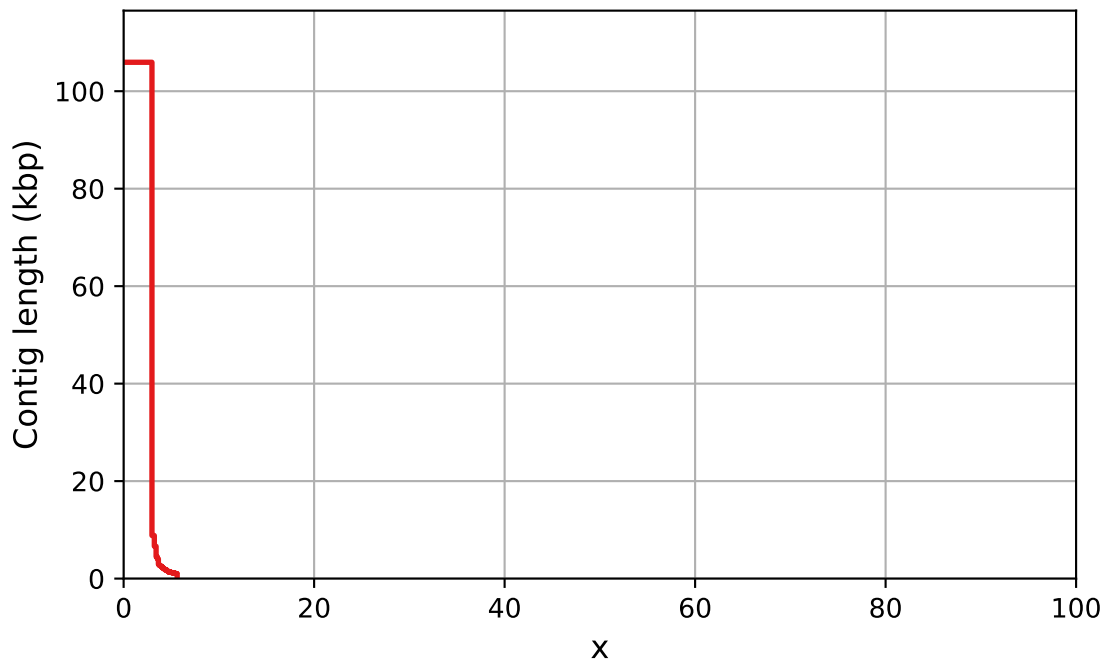
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# fully unaligned contigs	10
Fully unaligned length	21714
# partially unaligned contigs	41
Partially unaligned length	174751
# N's	0

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).

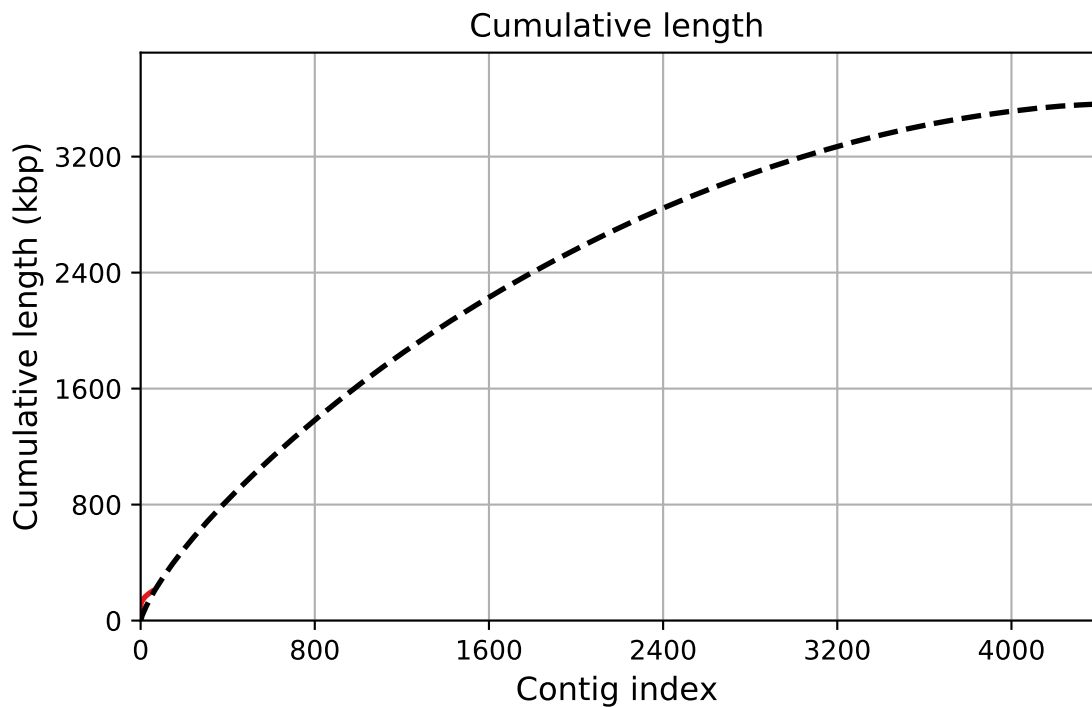


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NGx

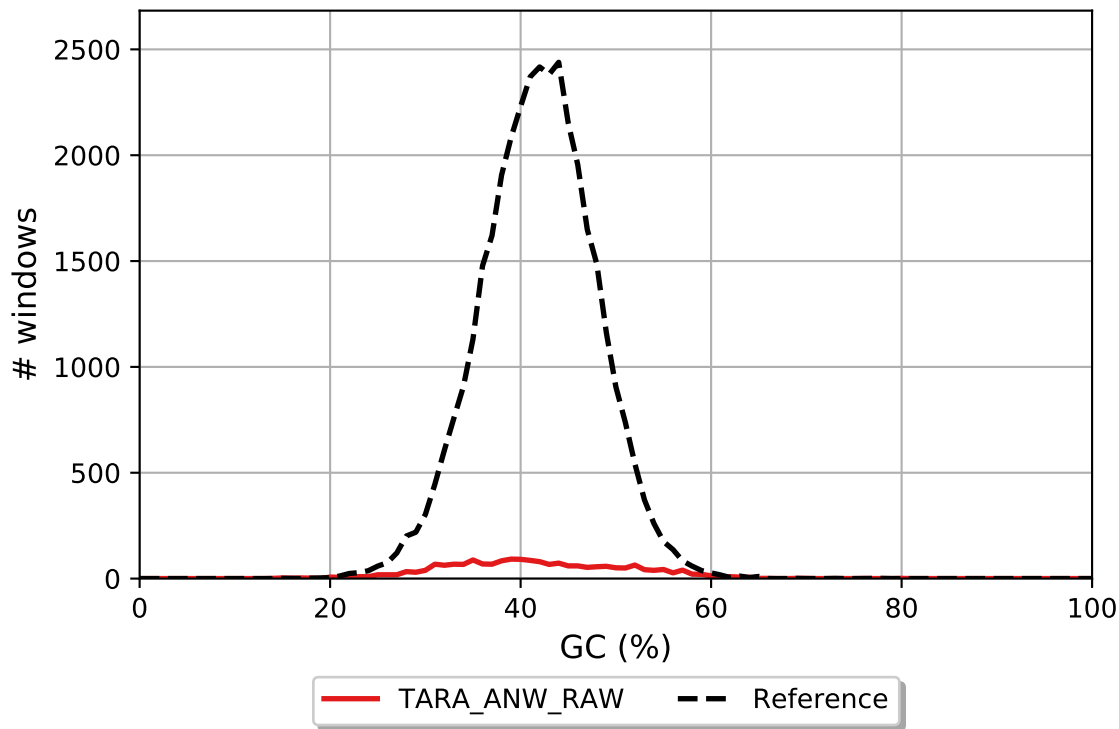


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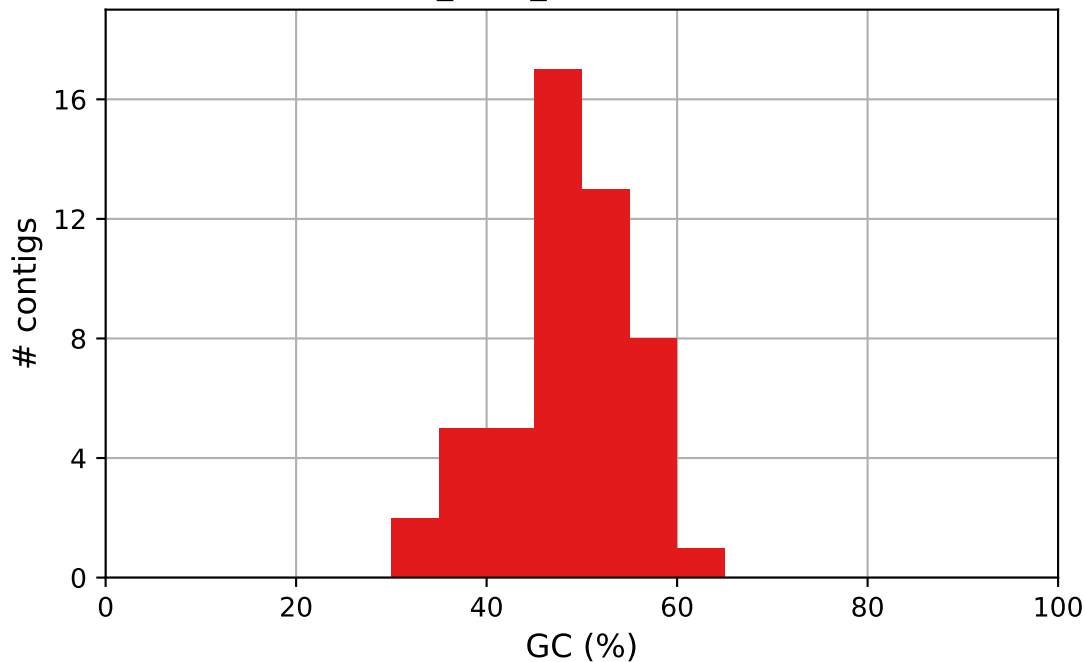


— TARA\_ANW\_RAW      - - Reference

## GC content



TARA\_ANW\_RAW GC content



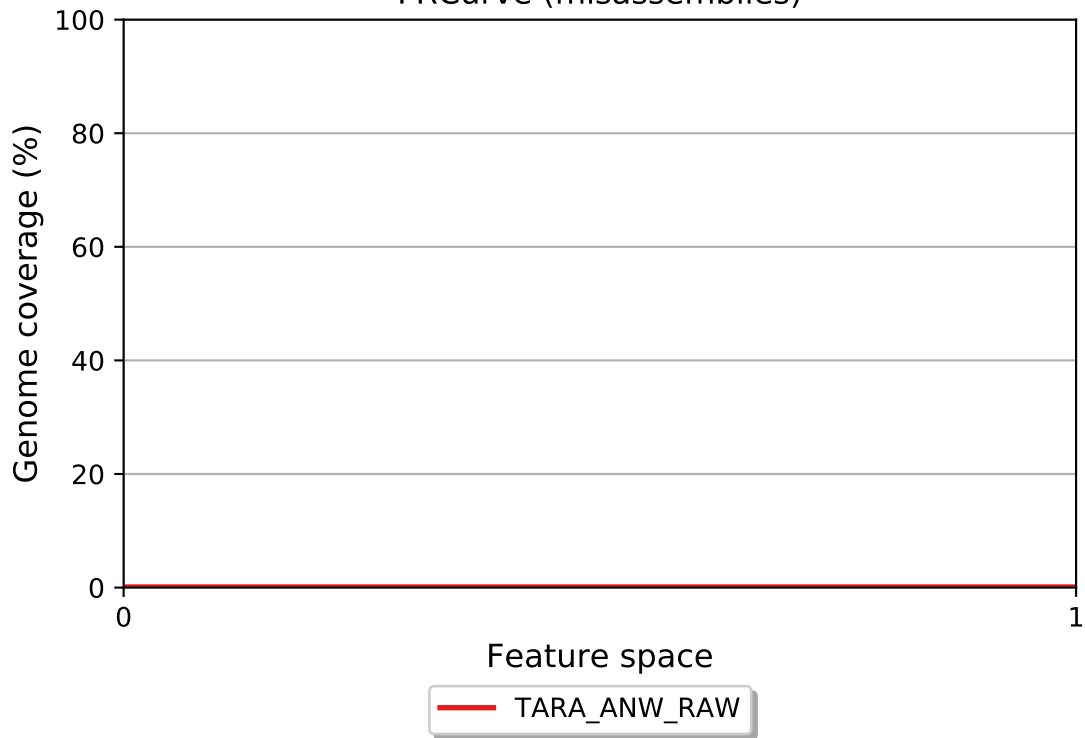
TARA\_ANW\_RAW



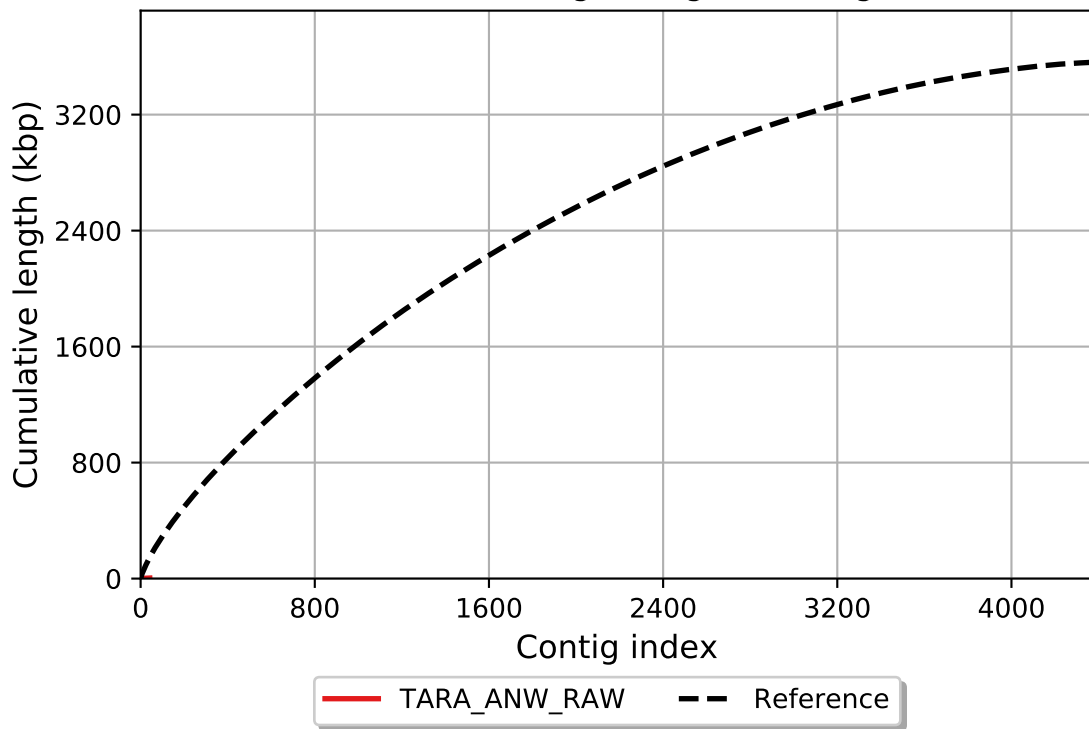
## Misassemblies



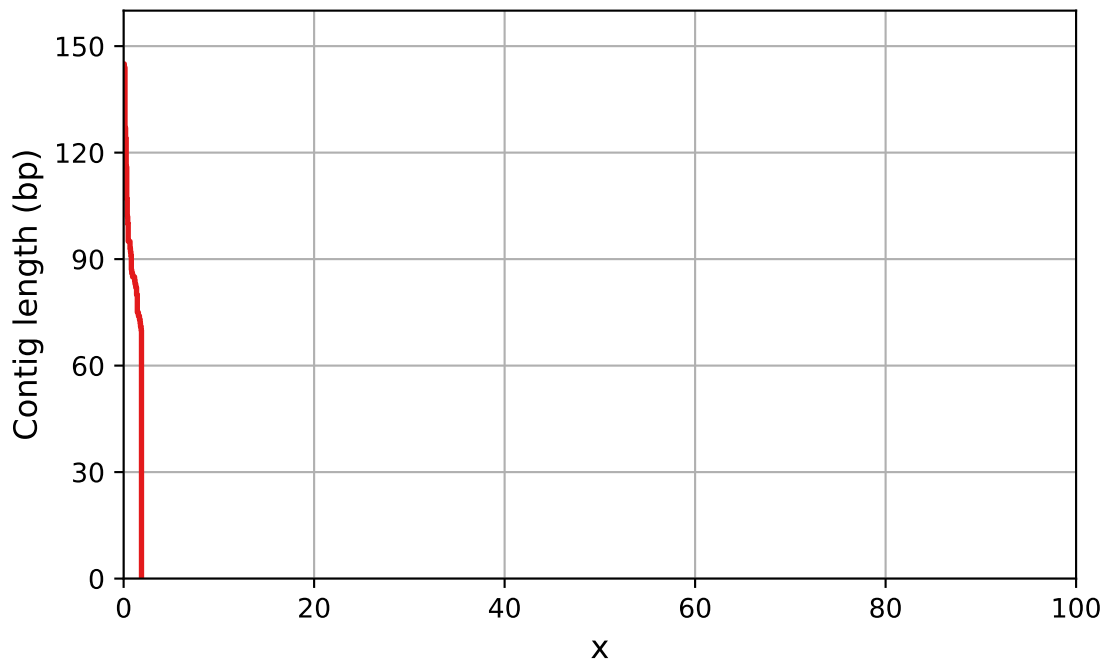
FRCurve (misassemblies)



Cumulative length (aligned contigs)

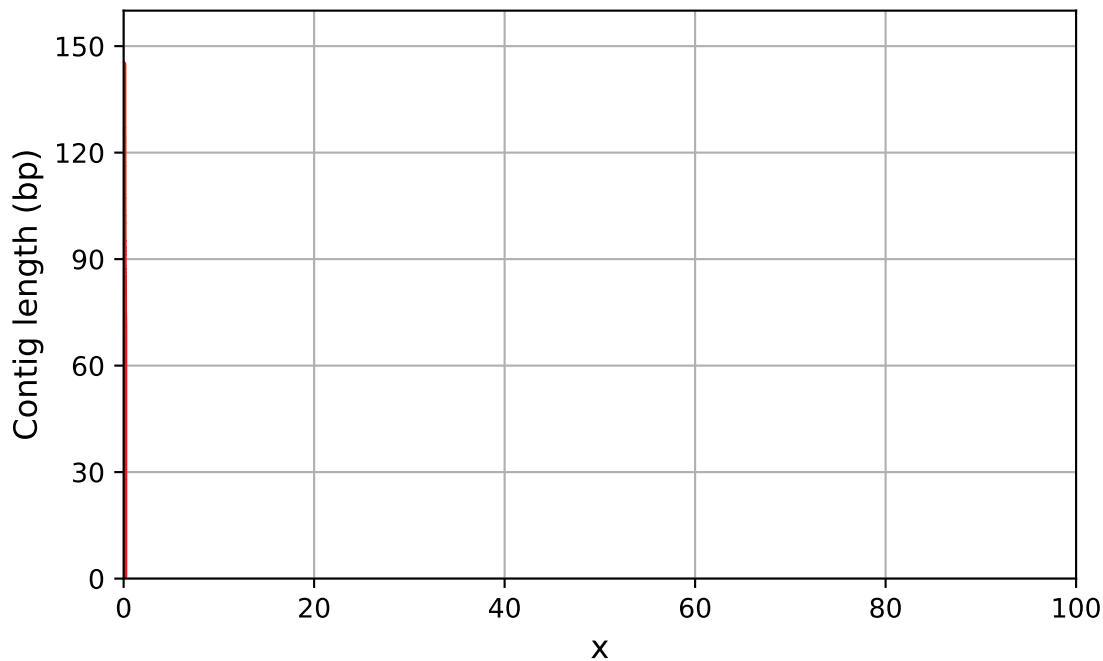


NAx



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# NGAx



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