

# Report

	TARA_RED_RAW
# contigs ( $\geq 1000$ bp)	246
# contigs ( $\geq 5000$ bp)	50
# contigs ( $\geq 10000$ bp)	32
# contigs ( $\geq 25000$ bp)	15
# contigs ( $\geq 50000$ bp)	10
Total length ( $\geq 1000$ bp)	3493812
Total length ( $\geq 5000$ bp)	3090358
Total length ( $\geq 10000$ bp)	2963938
Total length ( $\geq 25000$ bp)	2702556
Total length ( $\geq 50000$ bp)	2529428
# contigs	246
Largest contig	811431
Total length	3493812
Reference length	5854900
GC (%)	49.32
Reference GC (%)	63.53
N50	527714
NG50	11420
N75	34206
L50	3
LG50	29
L75	13
# 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	5 + 241 part
Unaligned length	3474402
Genome fraction (%)	0.048
Duplication ratio	6.942
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13626.61
# indels per 100 kbp	35.77
Largest alignment	125
Total aligned length	19410
NGA50	-

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).

## Misassemblies report

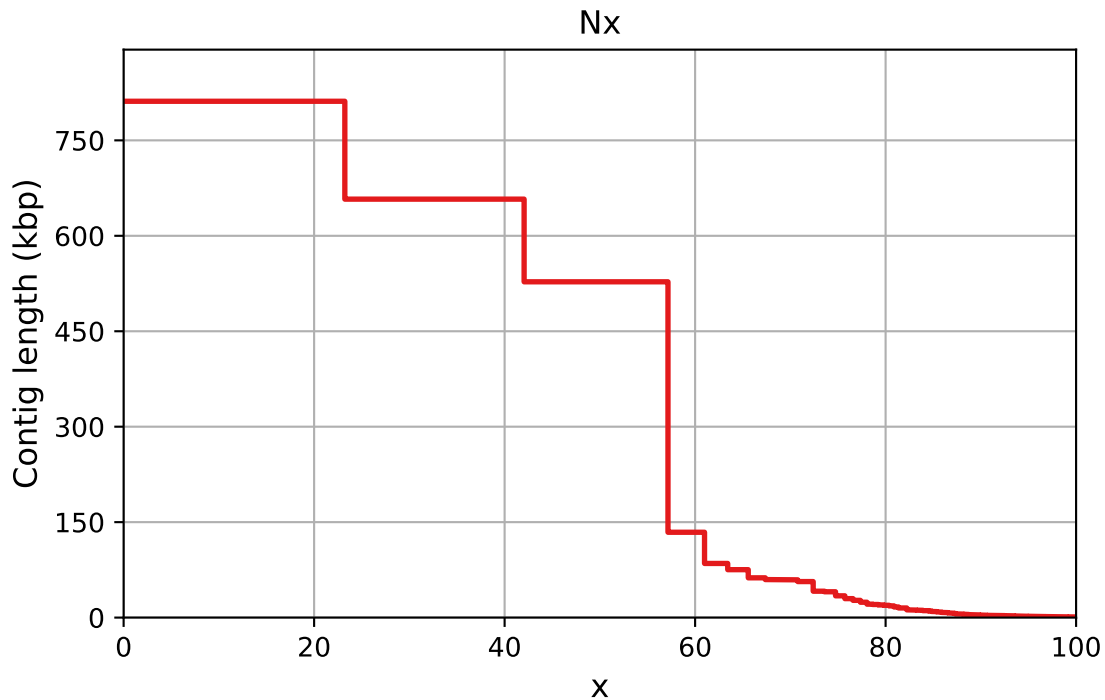
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	245
# possible misassemblies	307
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	381
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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## Unaligned report

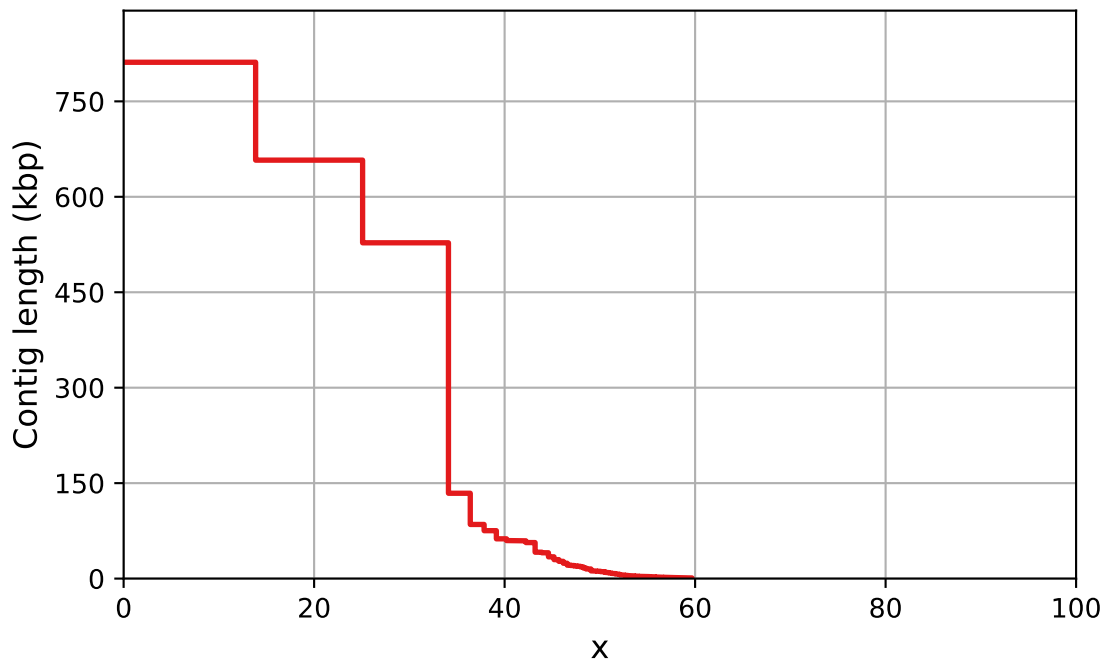
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# fully unaligned contigs	5
Fully unaligned length	18349
# partially unaligned contigs	241
Partially unaligned length	3456053
# N's	0

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).



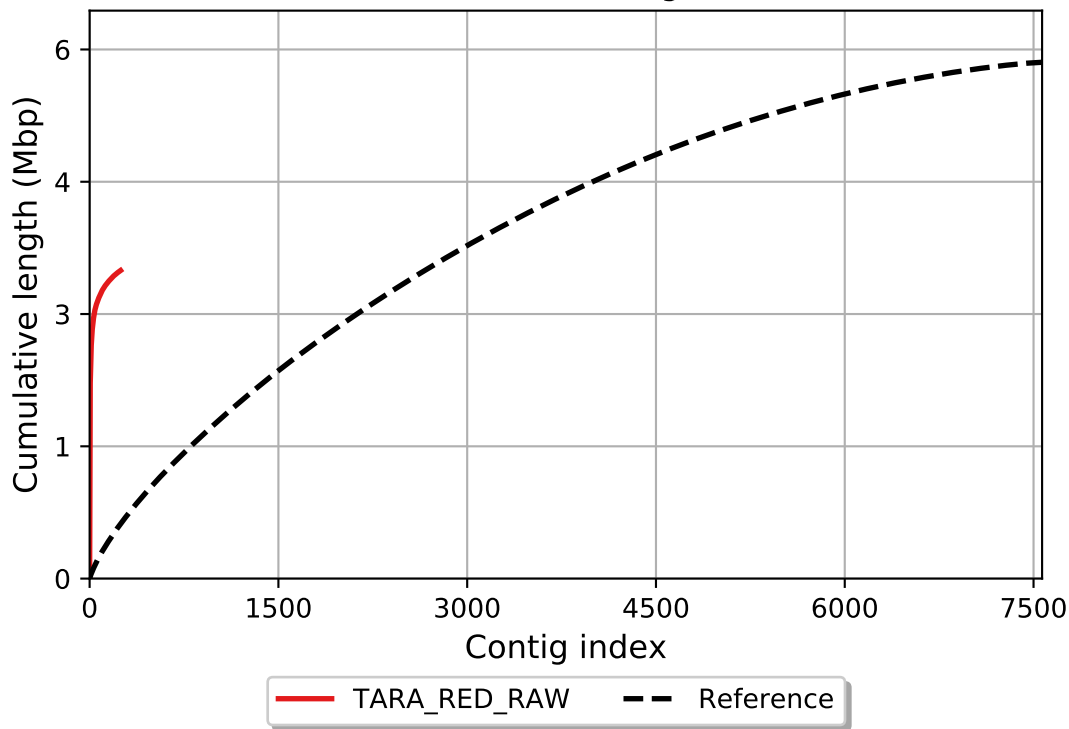
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NGx

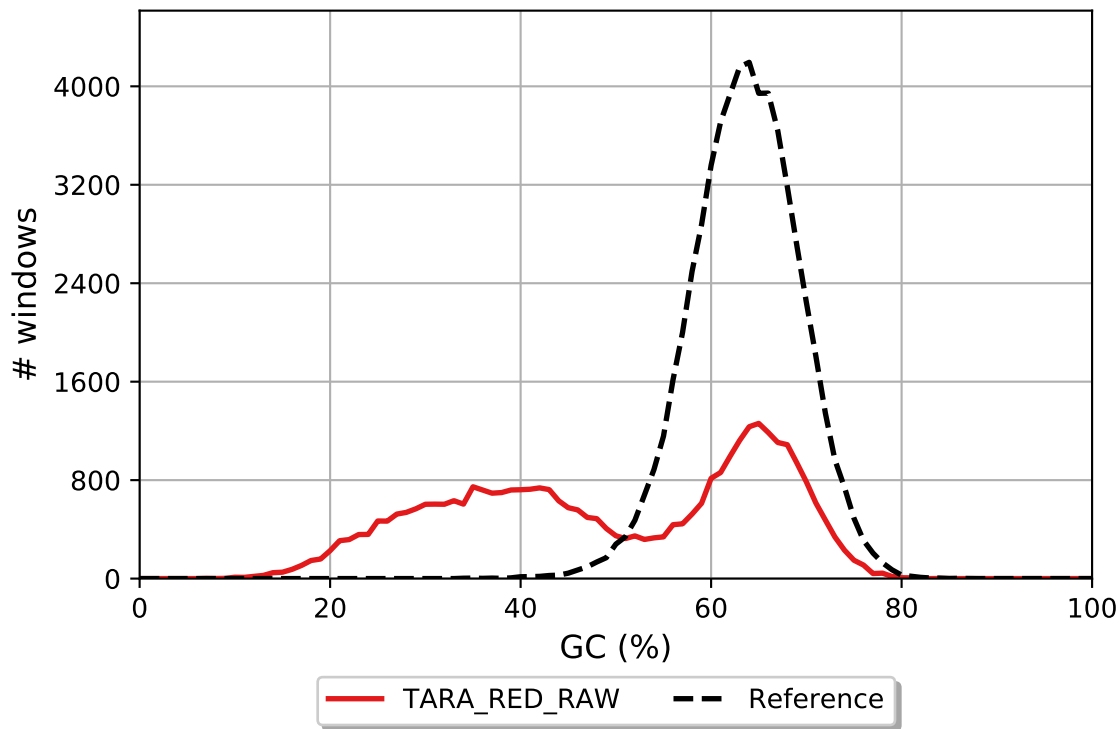


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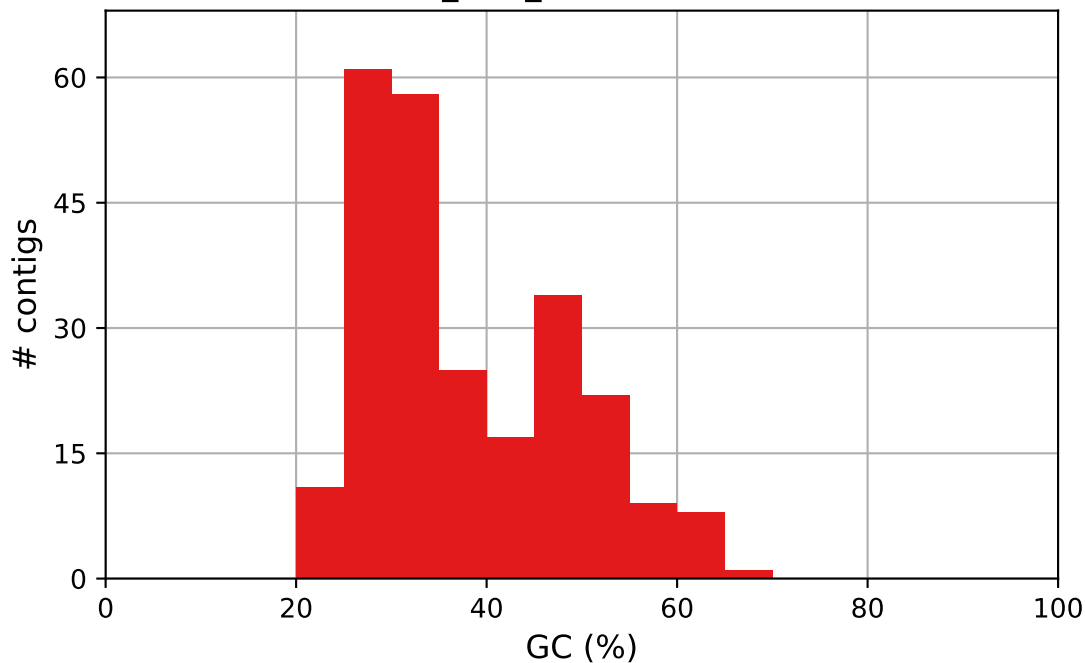
Cumulative length



GC content



TARA\_RED\_RAW GC content



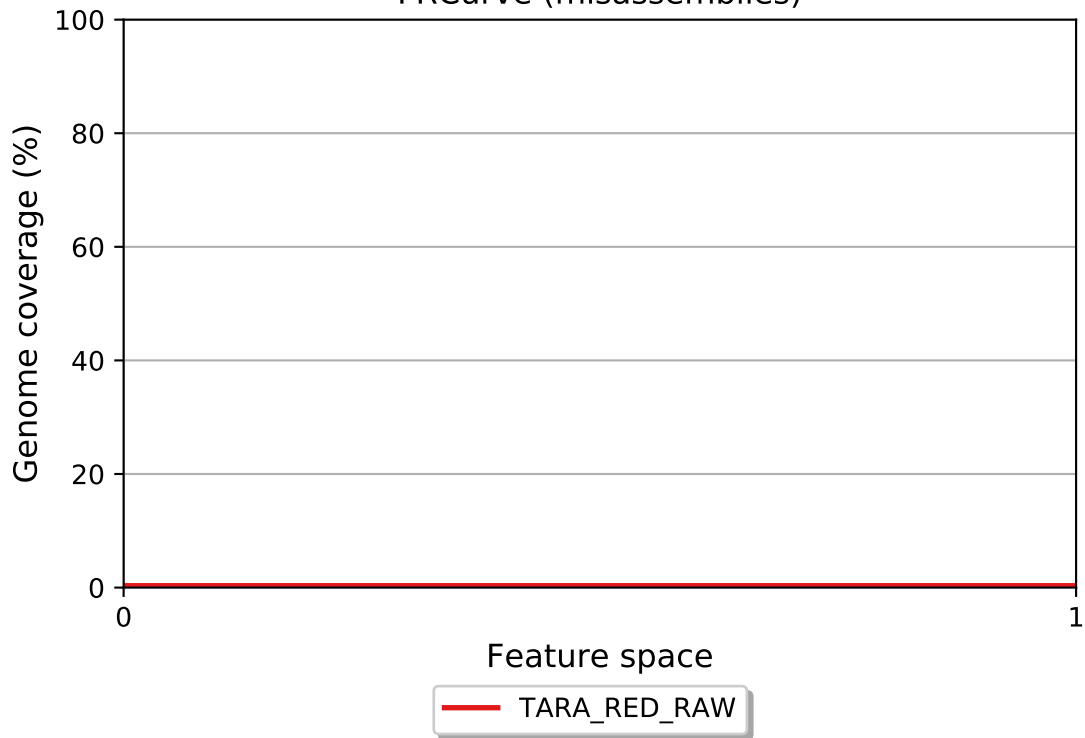
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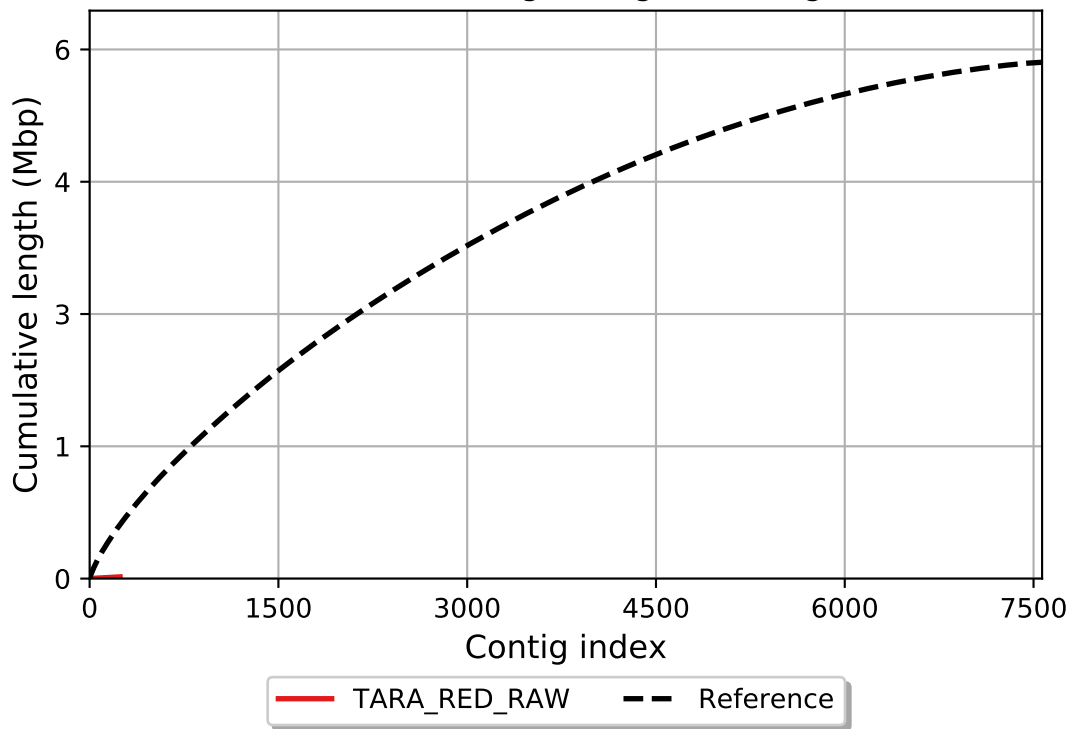
## Misassemblies



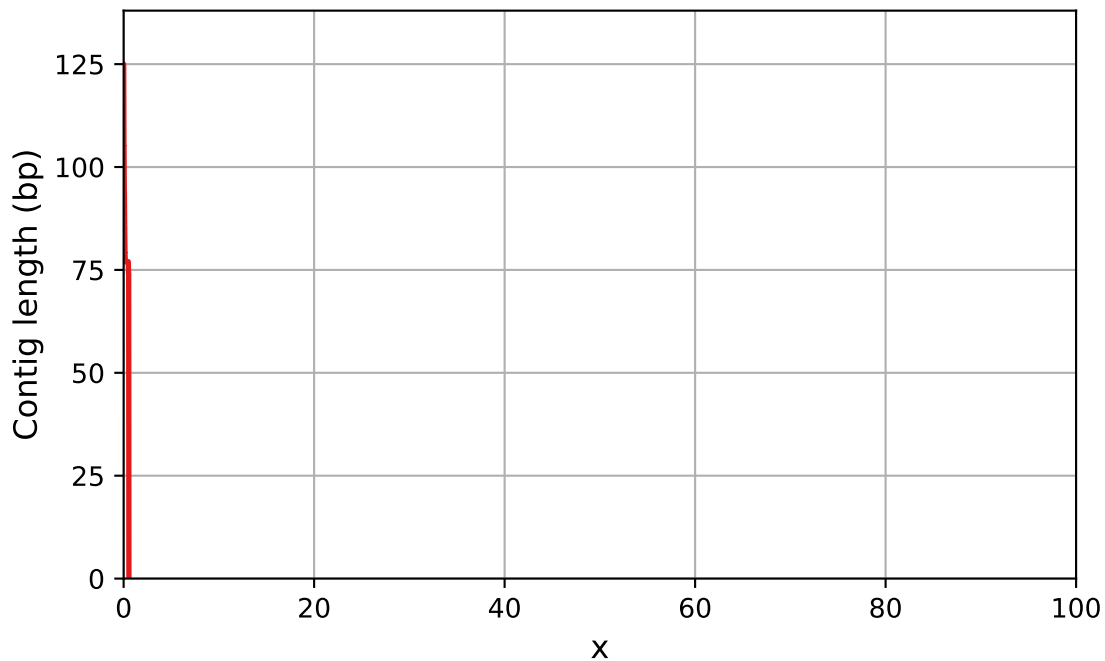
FRCurve (misassemblies)



Cumulative length (aligned contigs)

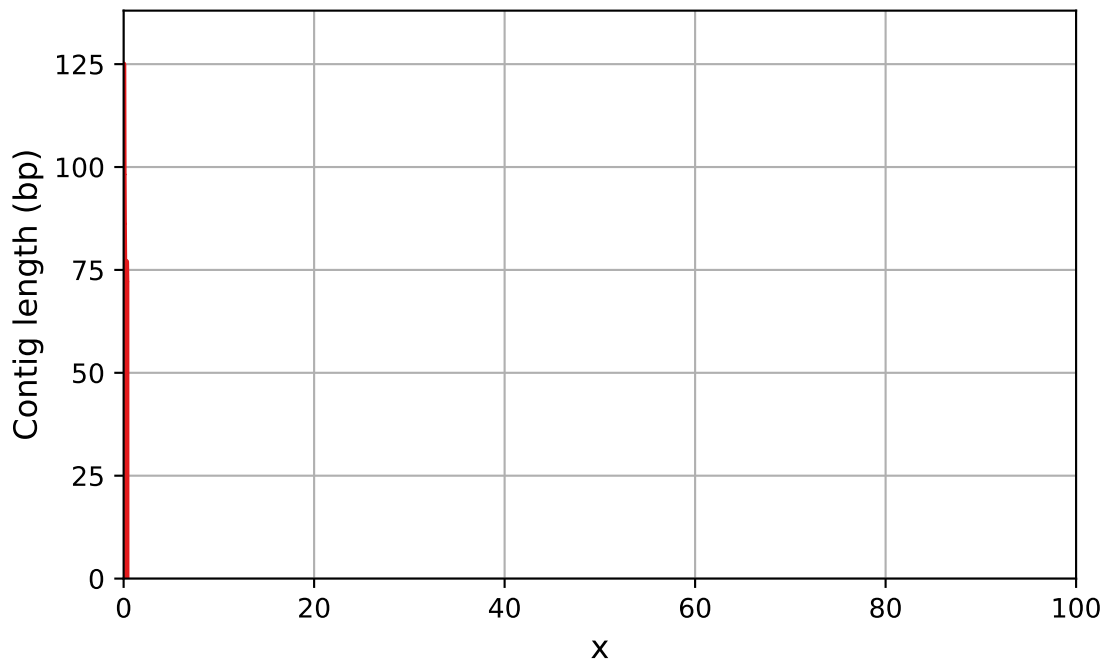


NAx



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# NGAx



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