

# Report

	TARA_RED_RAW
# contigs (>= 1000 bp)	42
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	784988
Total length (>= 5000 bp)	714950
Total length (>= 10000 bp)	709256
Total length (>= 25000 bp)	632141
Total length (>= 50000 bp)	603011
# contigs	42
Largest contig	527714
Total length	784988
Reference length	3561038
GC (%)	41.90
Reference GC (%)	41.87
N50	527714
N75	75297
L50	1
L75	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	2
# unaligned contigs	4 + 38 part
Unaligned length	781530
Genome fraction (%)	0.025
Duplication ratio	3.947
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10502.28
# indels per 100 kbp	0.00
Largest alignment	129
Total aligned length	3458
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

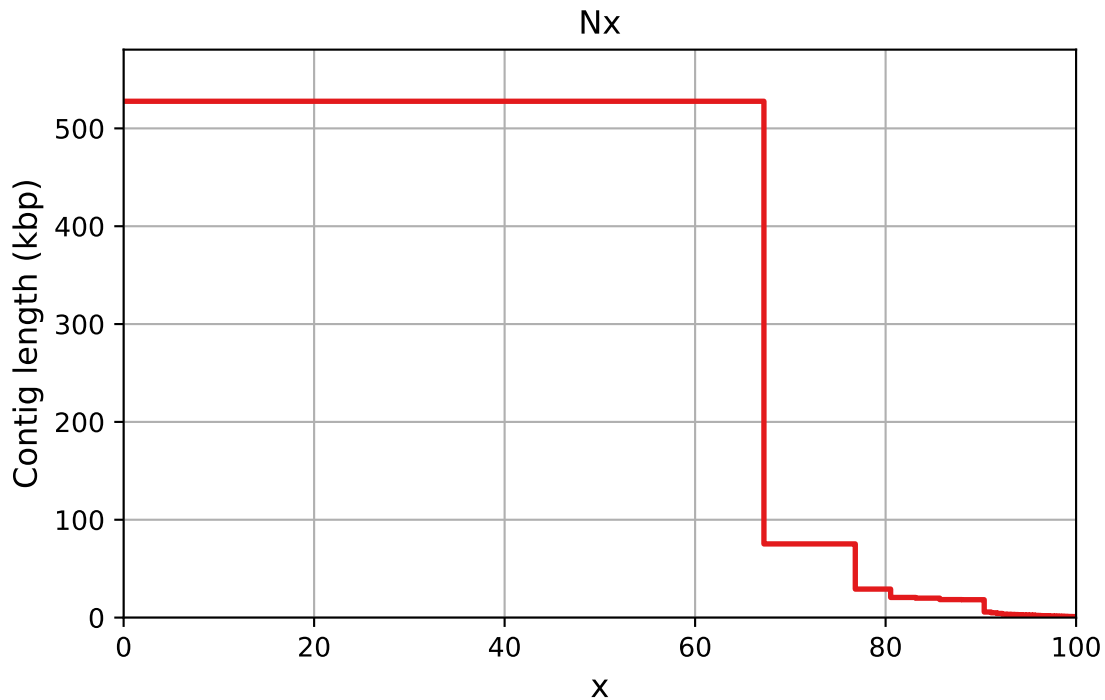
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	40
# possible misassemblies	44
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	92
# 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

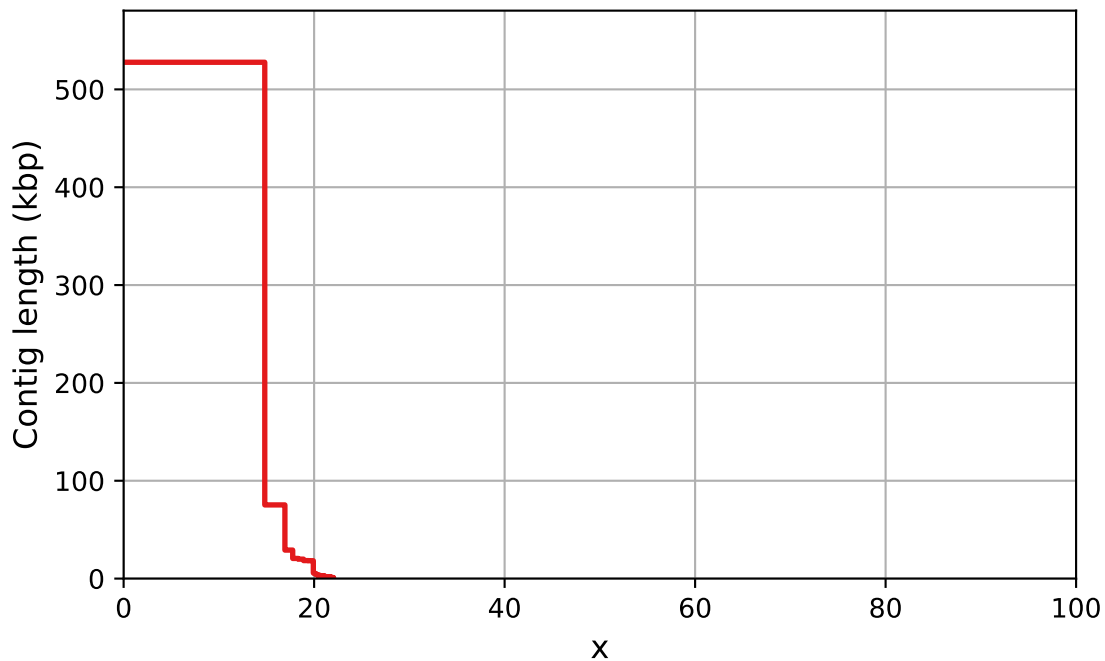
	TARA_RED_RAW
# fully unaligned contigs	4
Fully unaligned length	9263
# partially unaligned contigs	38
Partially unaligned length	772267
# N's	0

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).

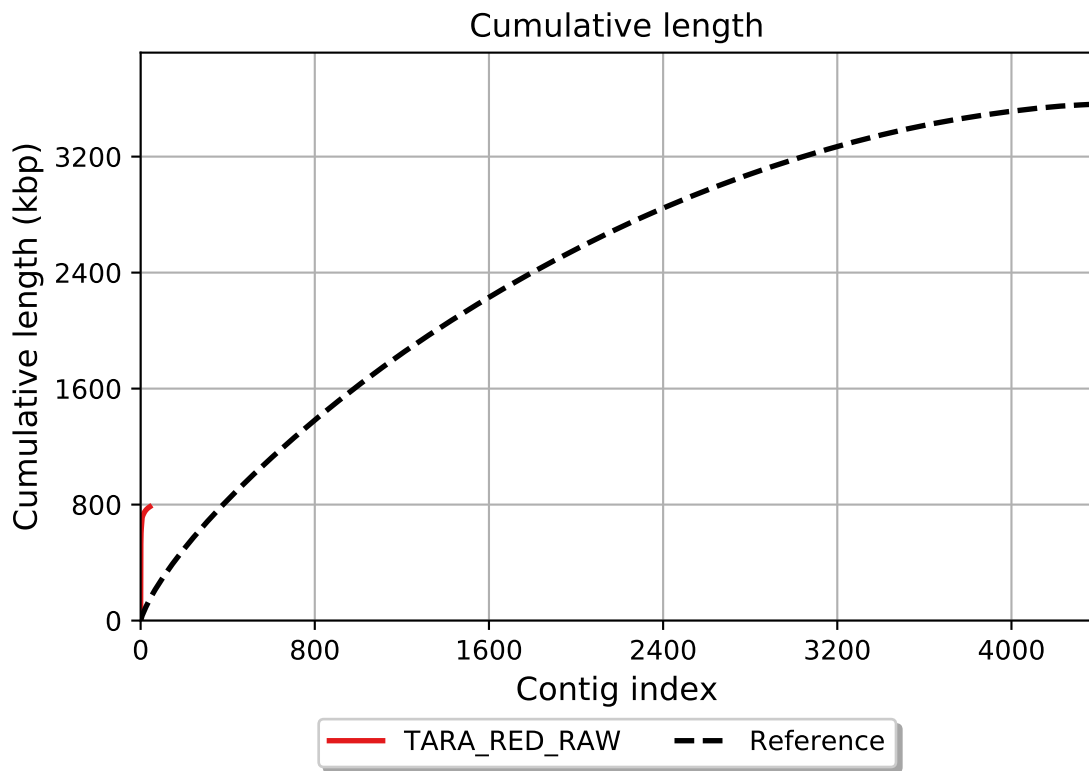


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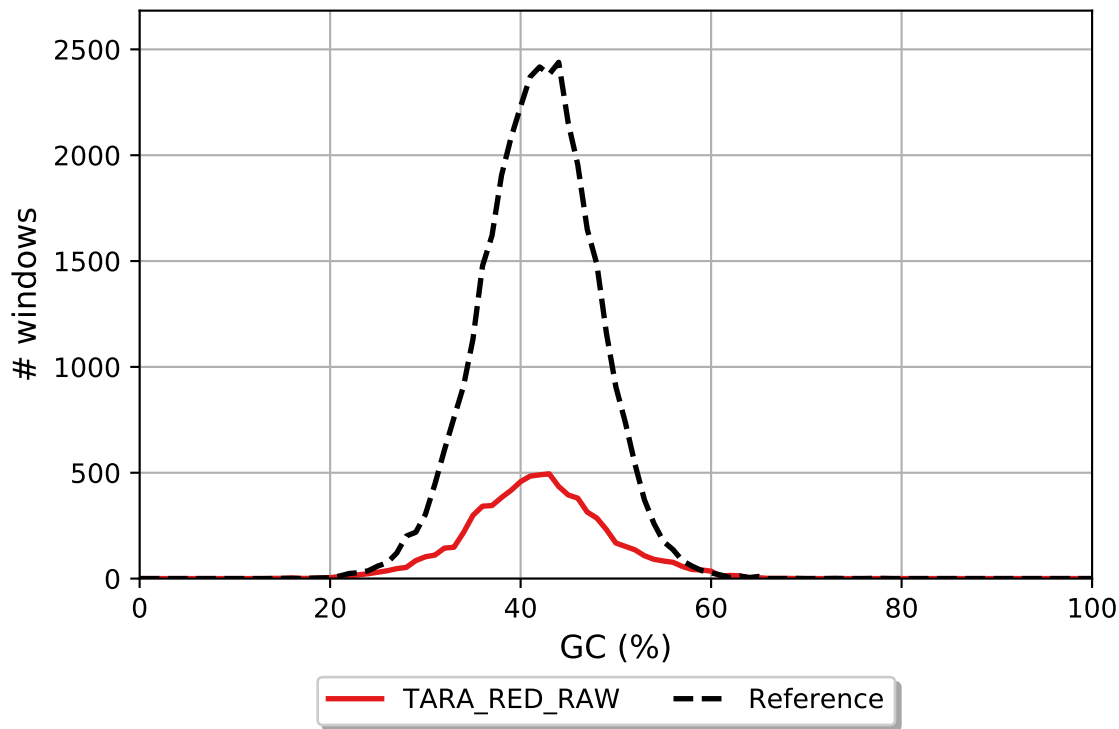
NGx



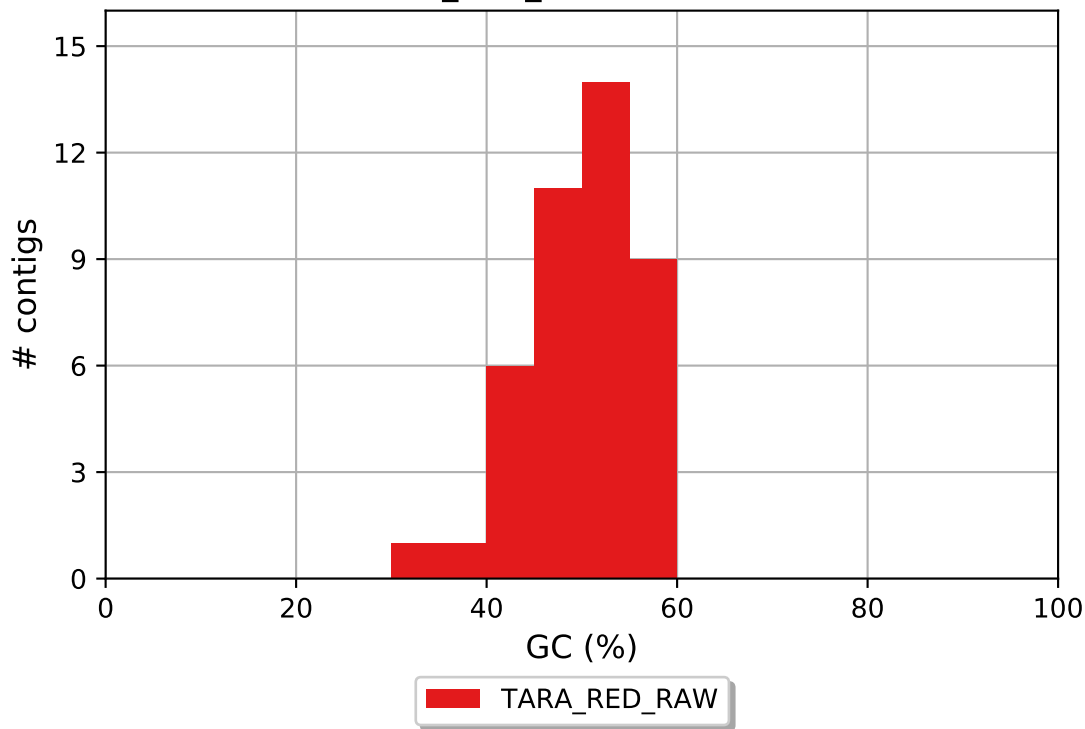
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## GC content



TARA\_RED\_RAW GC content

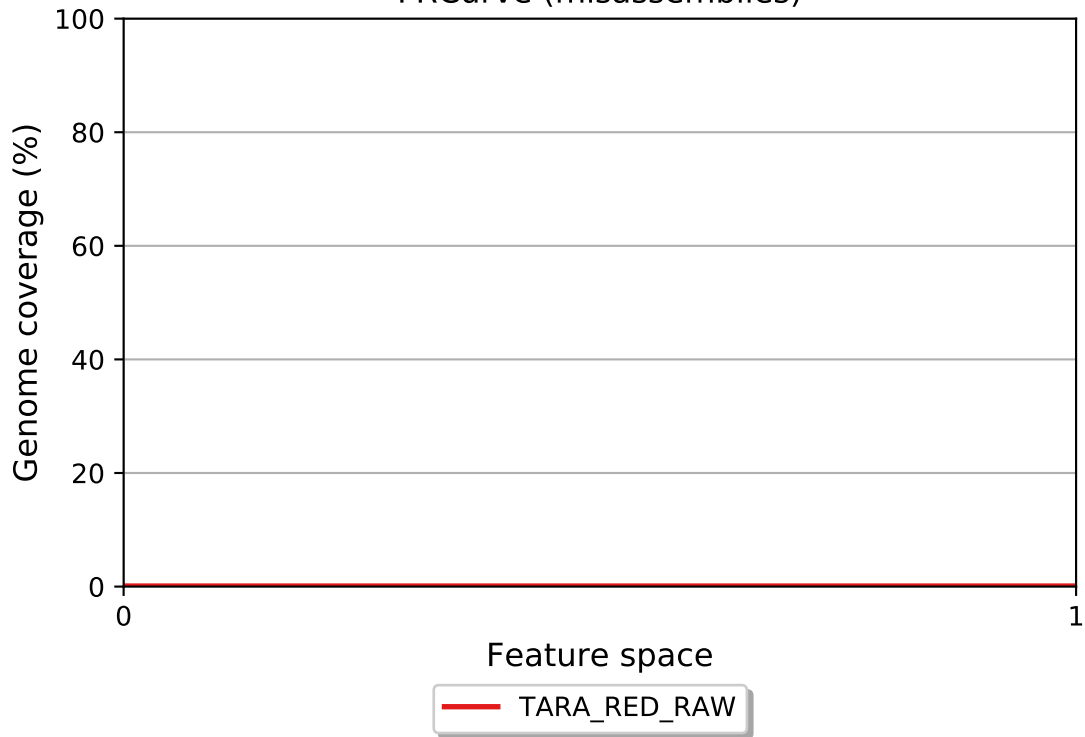




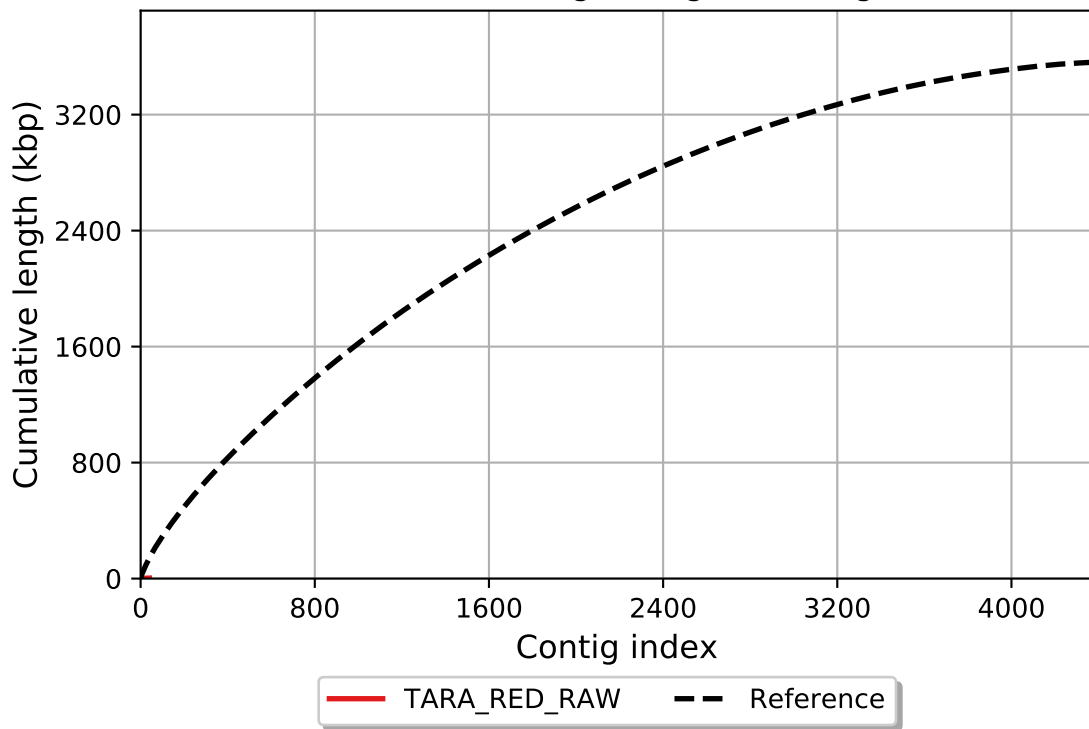
## Misassemblies



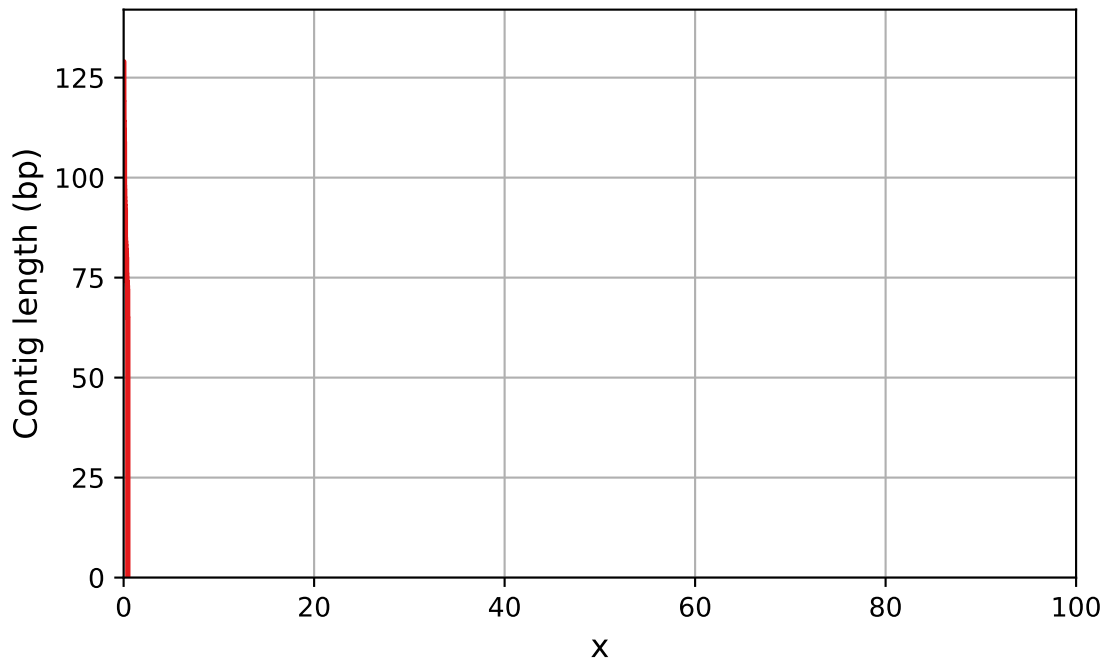
FRCurve (misassemblies)



Cumulative length (aligned contigs)

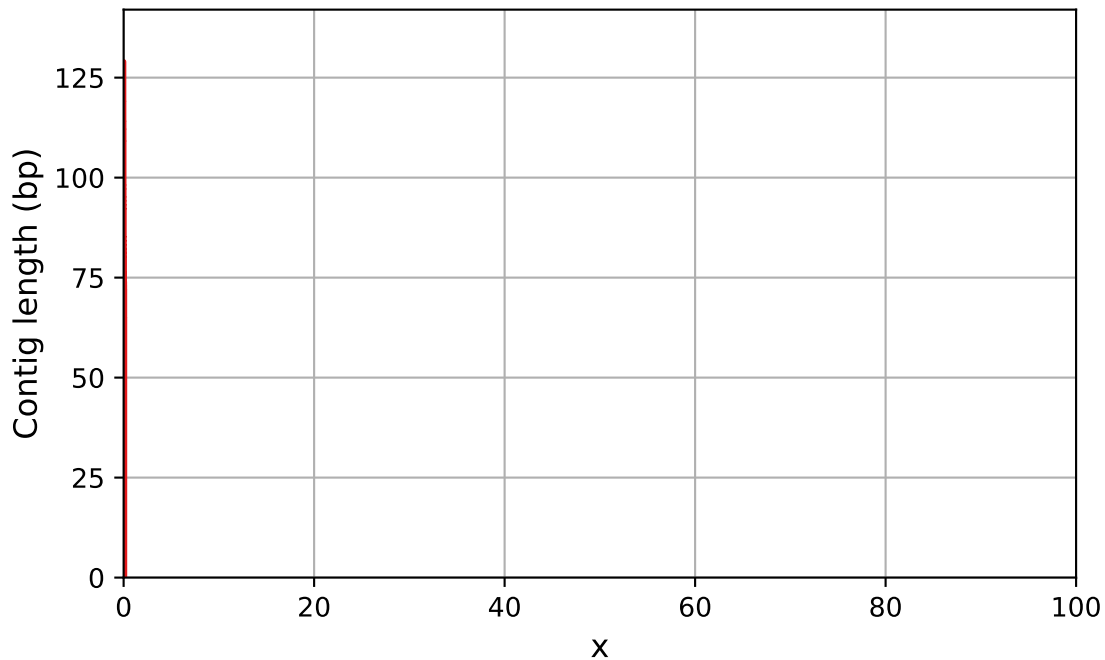


NAx



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# NGAx



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