

# Report

	TARA_ION_RAW
# contigs (>= 1000 bp)	39
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	127668
Total length (>= 5000 bp)	54650
Total length (>= 10000 bp)	49455
Total length (>= 25000 bp)	36852
Total length (>= 50000 bp)	0
# contigs	39
Largest contig	36852
Total length	127668
Reference length	3561038
GC (%)	46.81
Reference GC (%)	41.87
N50	3082
N75	2138
L50	6
L75	18
# 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	4 + 35 part
Unaligned length	124617
Genome fraction (%)	0.018
Duplication ratio	4.828
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13291.14
# indels per 100 kbp	0.00
Largest alignment	129
Total aligned length	3051
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_ION_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	37
# possible misassemblies	40
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	84
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

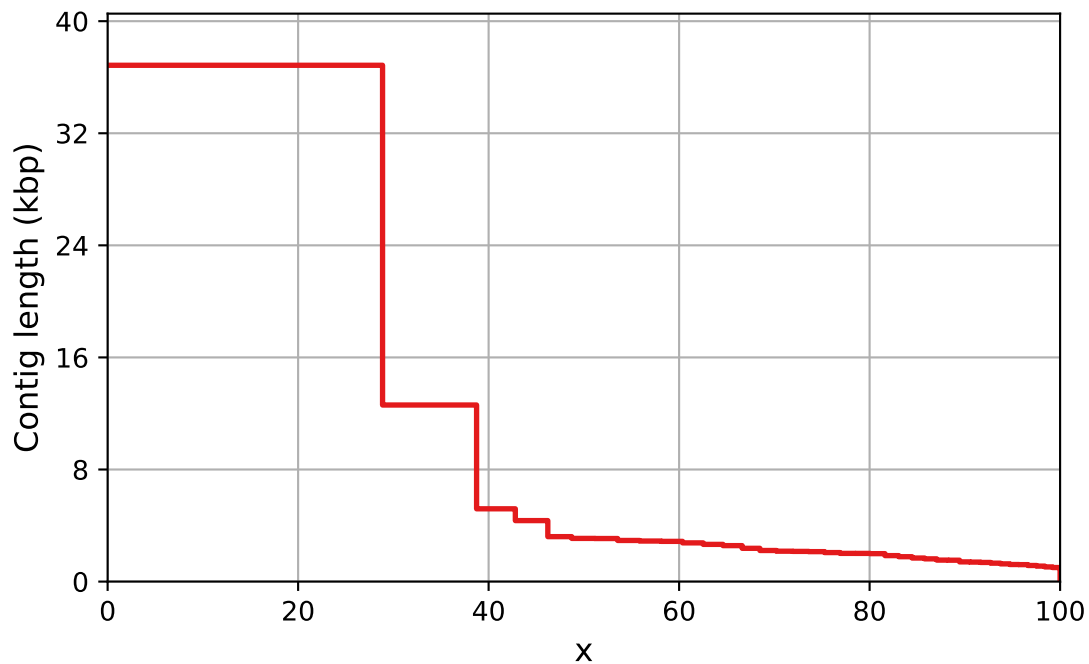
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_ION_RAW
# fully unaligned contigs	4
Fully unaligned length	12280
# partially unaligned contigs	35
Partially unaligned length	112337
# N's	0

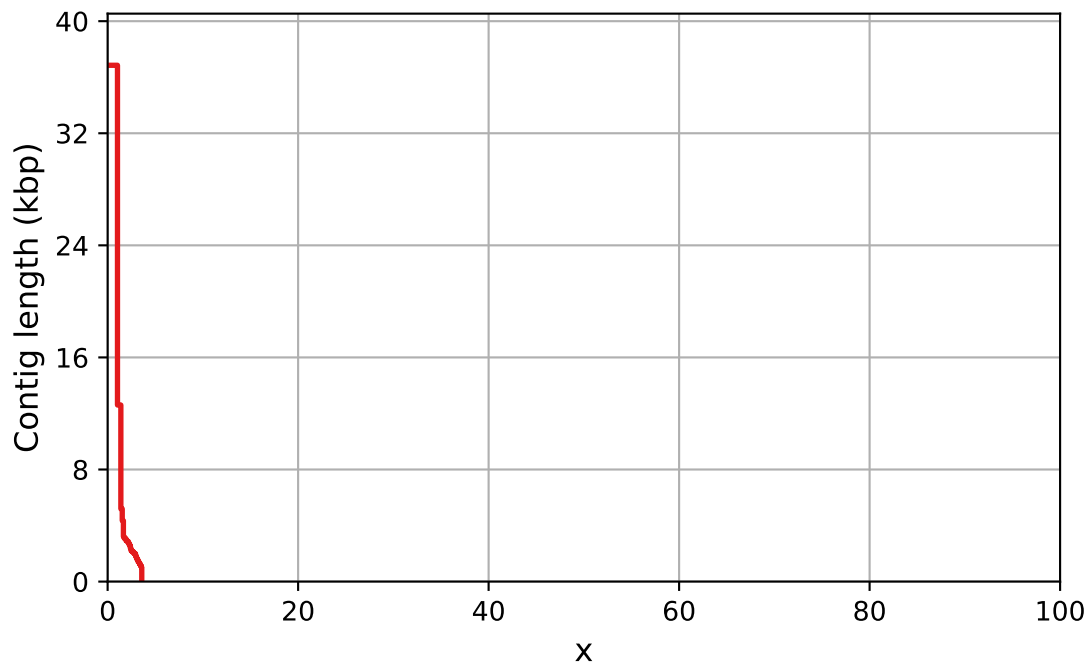
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

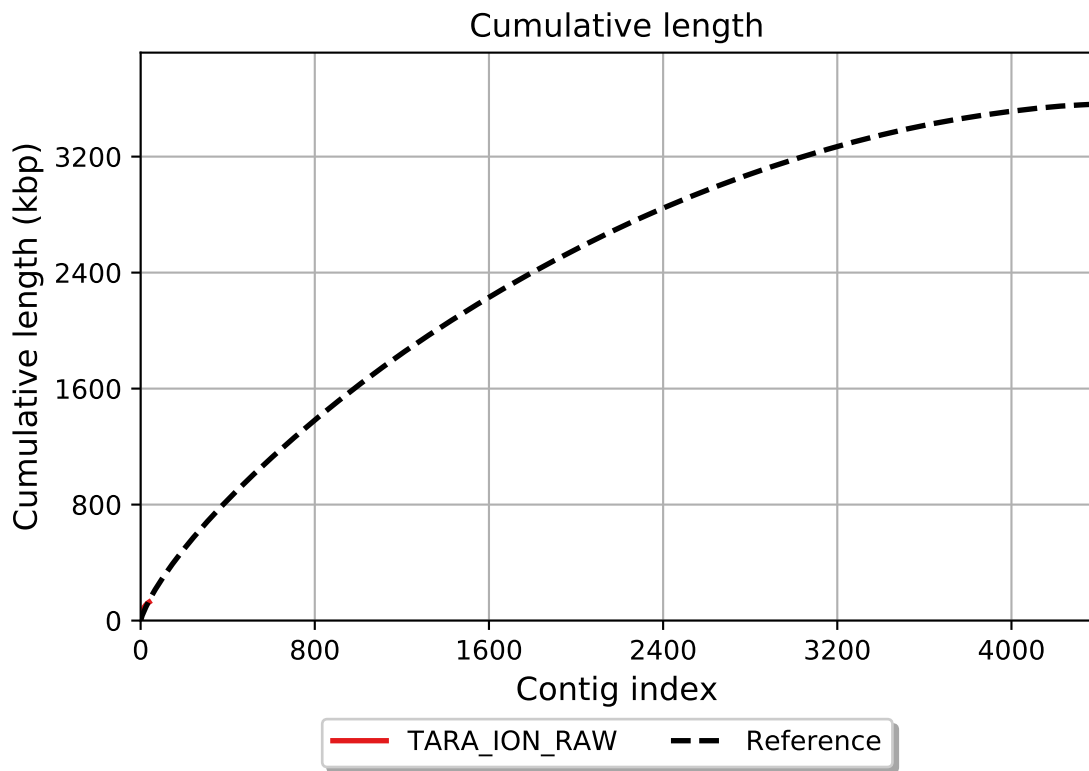


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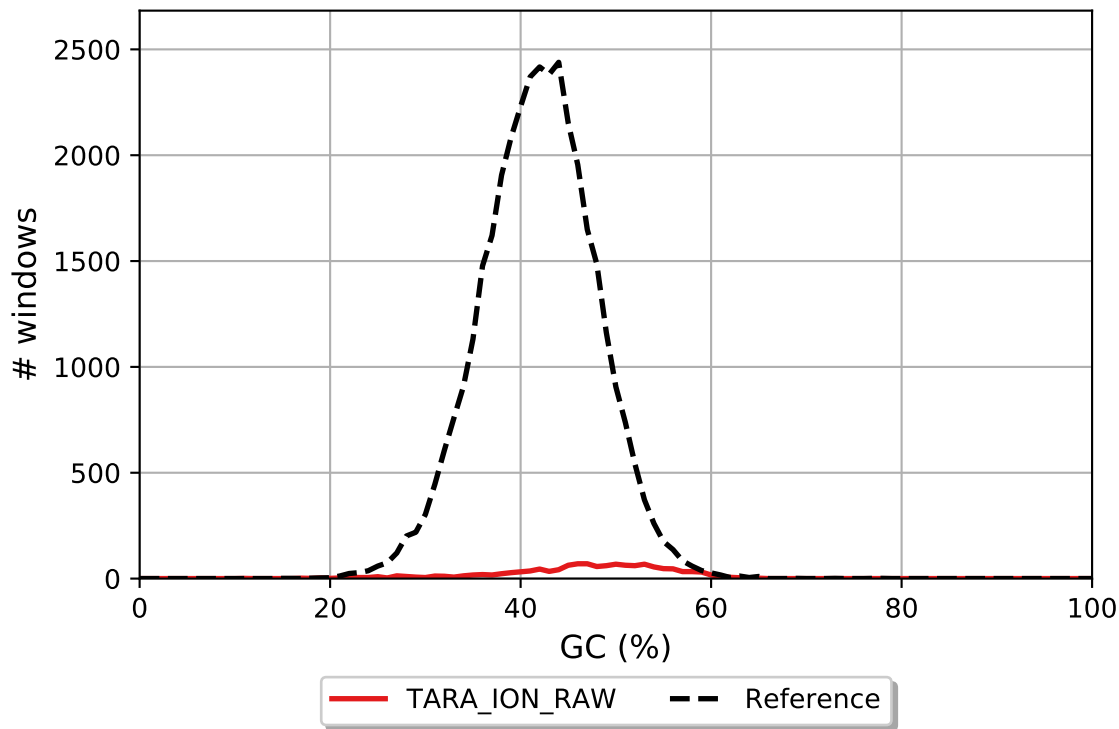
NGx



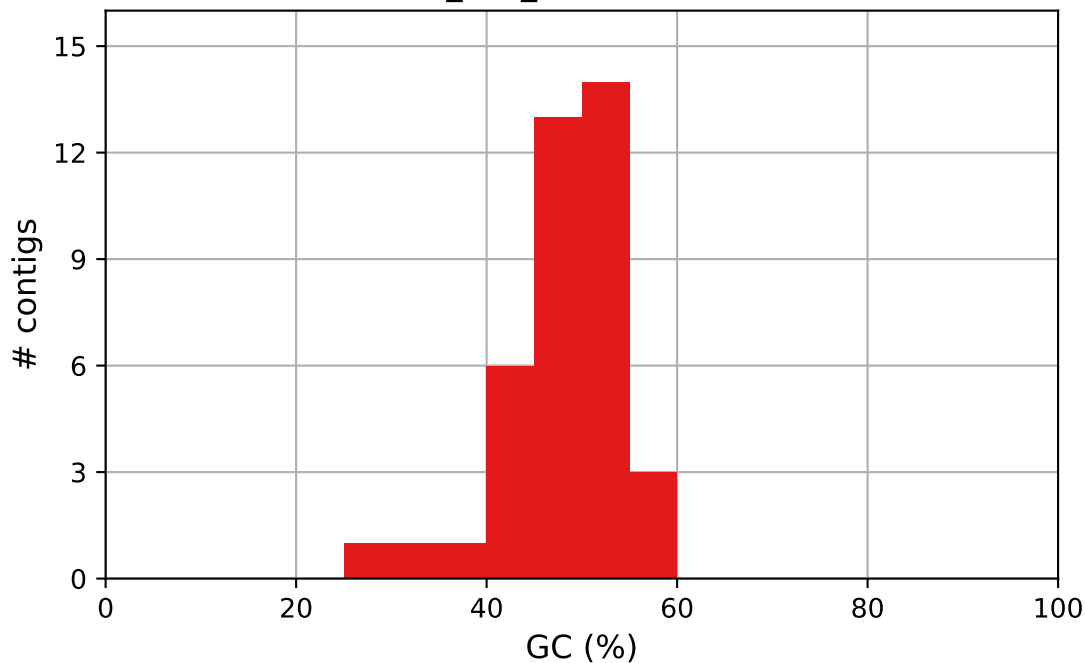
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## GC content



TARA\_ION\_RAW GC content



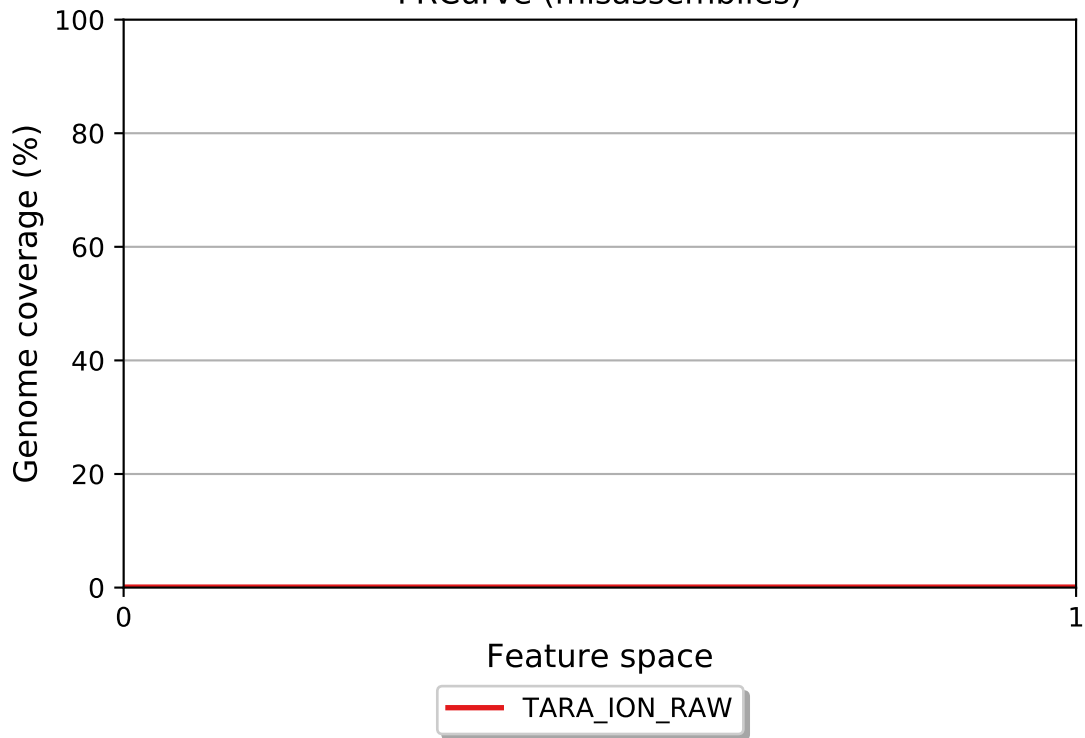
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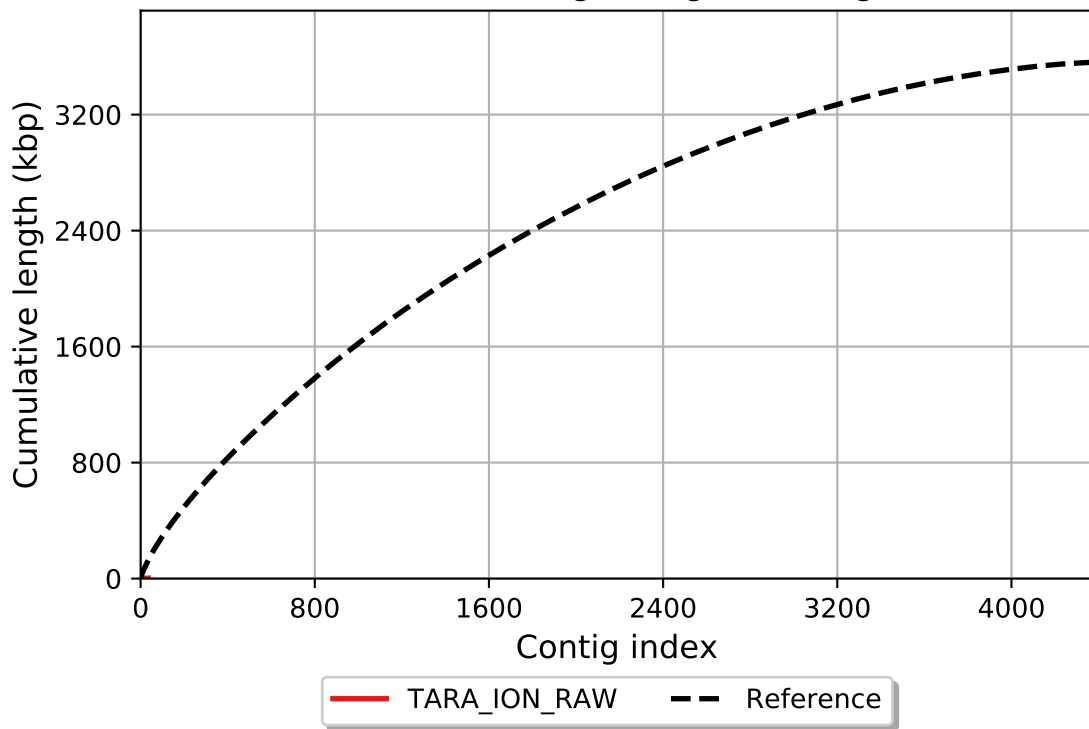
## Misassemblies



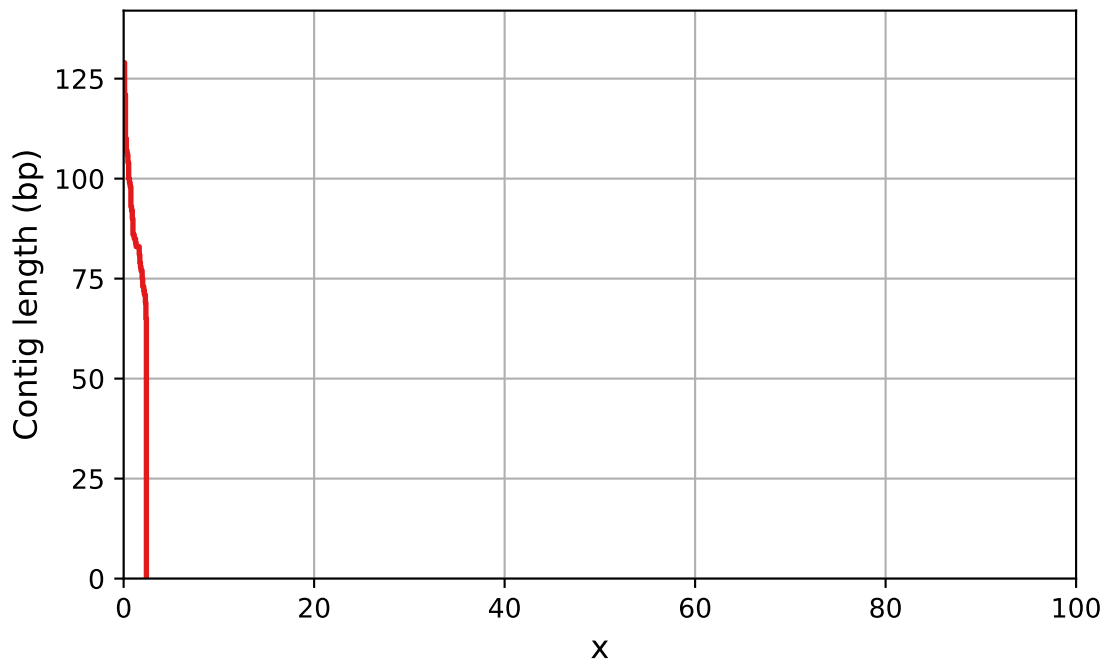
FRCurve (misassemblies)



Cumulative length (aligned contigs)

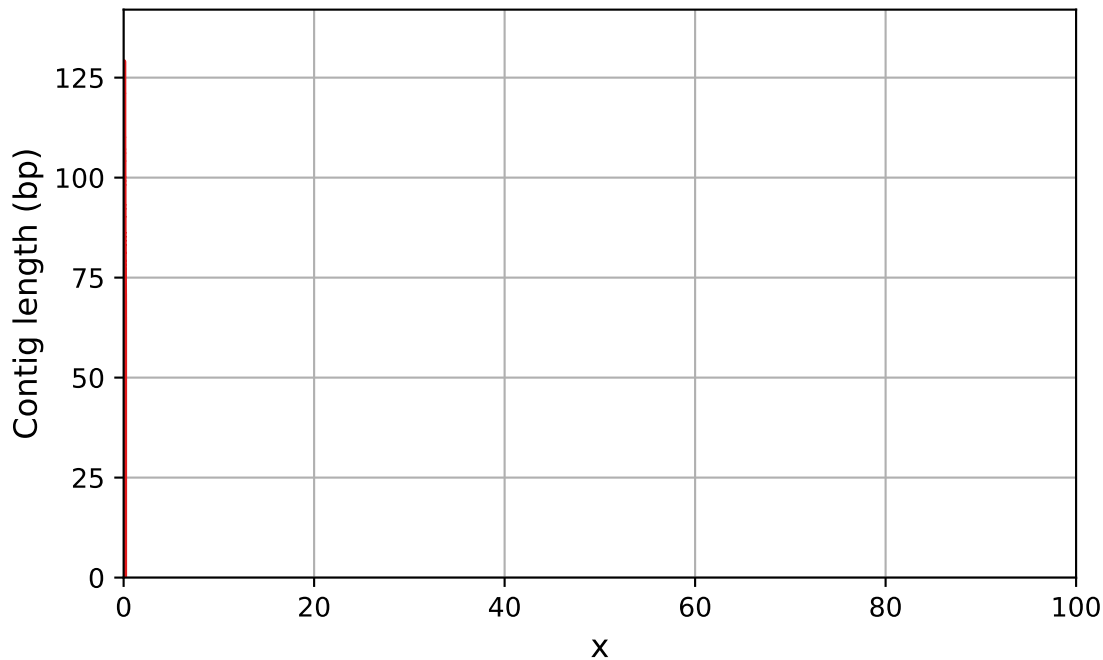


NAx



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# NGAx



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