

Report

	TARA_ANW_RAW
# contigs (≥ 1000 bp)	382
# contigs (≥ 5000 bp)	96
# contigs (≥ 10000 bp)	64
# contigs (≥ 25000 bp)	32
# contigs (≥ 50000 bp)	14
Total length (≥ 1000 bp)	3313539
Total length (≥ 5000 bp)	2725225
Total length (≥ 10000 bp)	2514318
Total length (≥ 25000 bp)	1983831
Total length (≥ 50000 bp)	1340183
# contigs	382
Largest contig	206415
Total length	3313539
Reference length	5854900
GC (%)	51.92
Reference GC (%)	63.53
N50	37051
NG50	2801
N75	11132
L50	22
LG50	150
L75	62
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	1200
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	21 + 360 part
Unaligned length	3280522
Genome fraction (%)	0.171
Duplication ratio	3.290
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6008.97
# indels per 100 kbp	19.93
Largest alignment	556
Total aligned length	32464
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

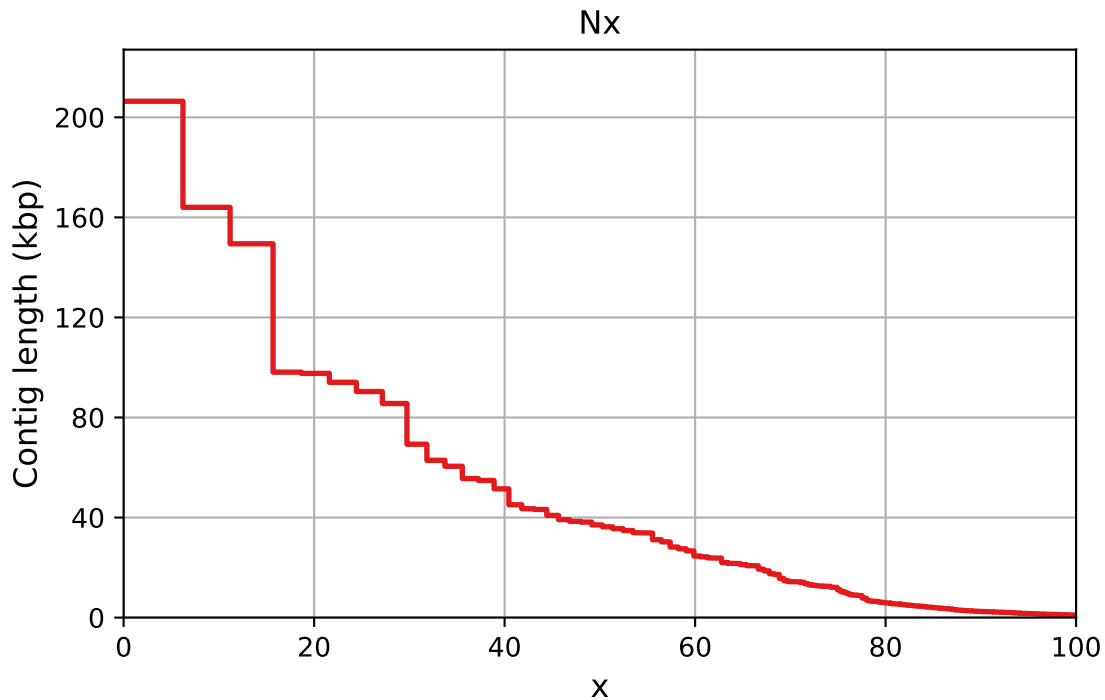
	TARA_ANW_RAW
# misassemblies	2
# contig misassemblies	2
# c. relocations	0
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	1200
# possibly misassembled contigs	375
# possible misassemblies	496
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	603
# indels	2
# indels (<= 5 bp)	1
# indels (> 5 bp)	1
Indels length	25

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).

Unaligned report

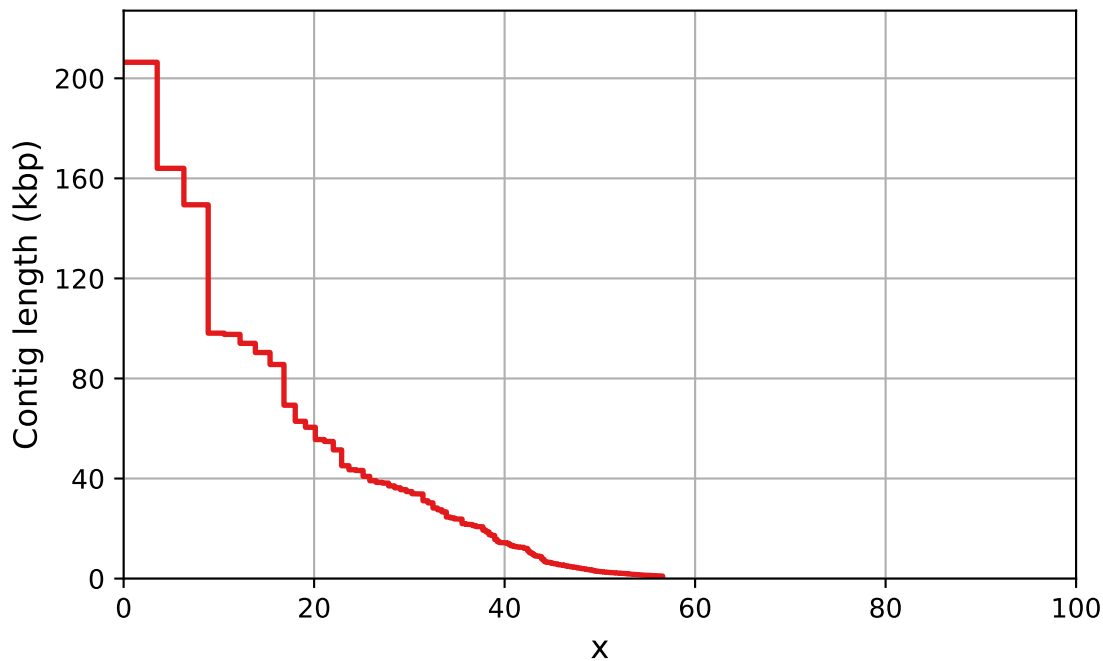
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# fully unaligned contigs	21
Fully unaligned length	348391
# partially unaligned contigs	360
Partially unaligned length	2932131
# N's	0

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).



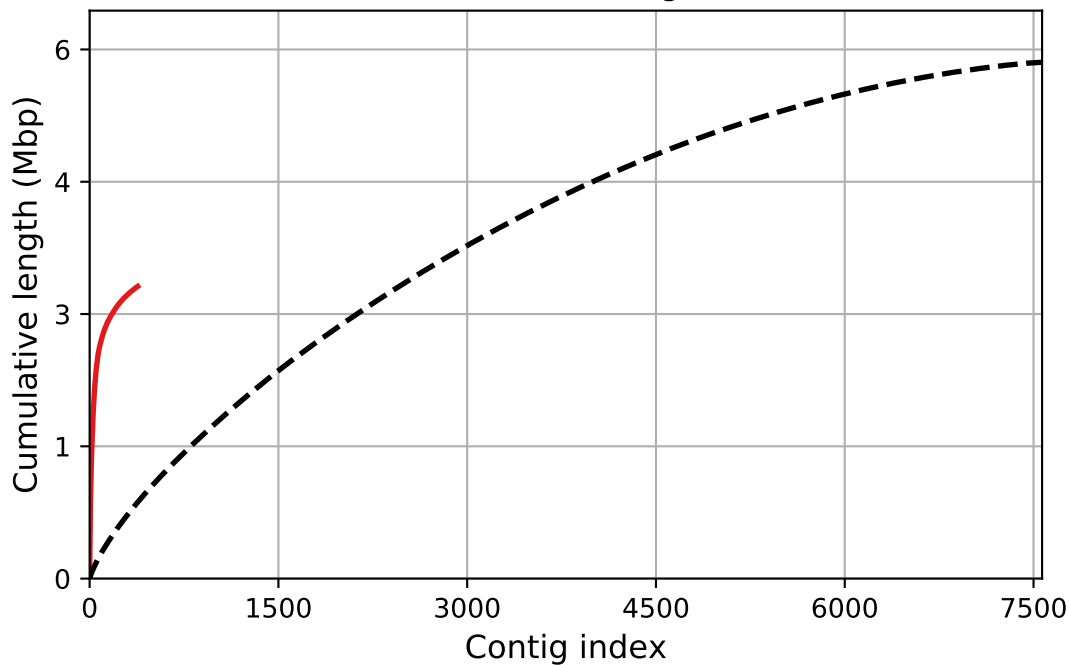
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NGx



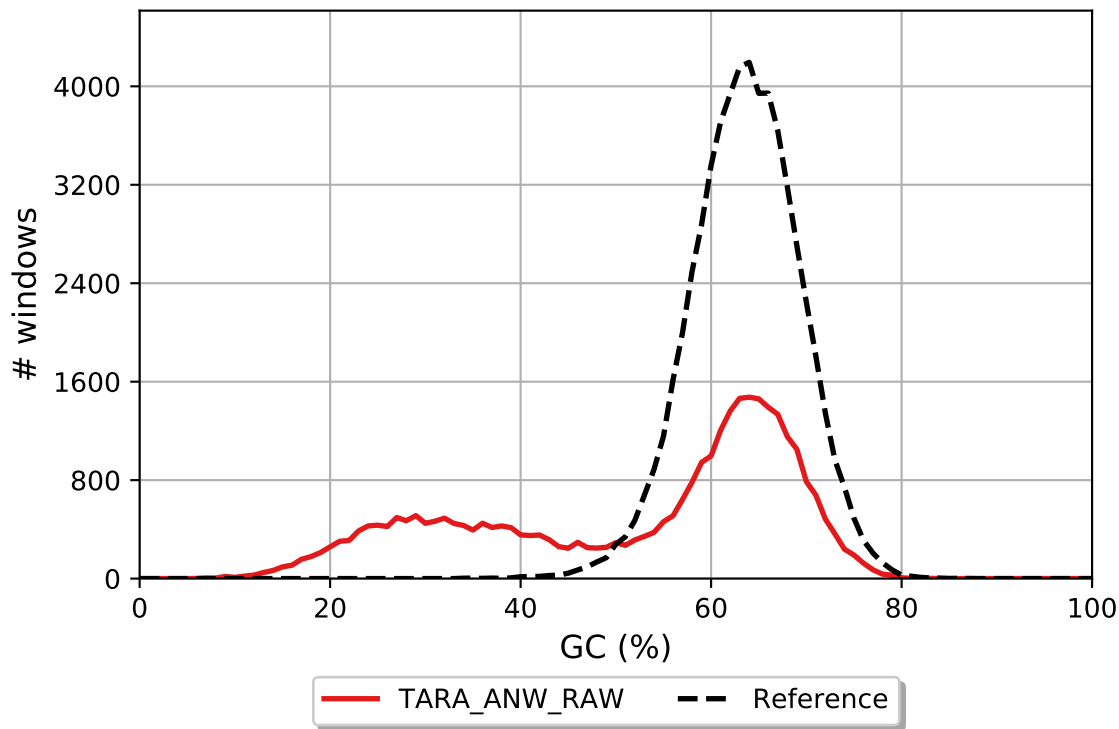
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Cumulative length

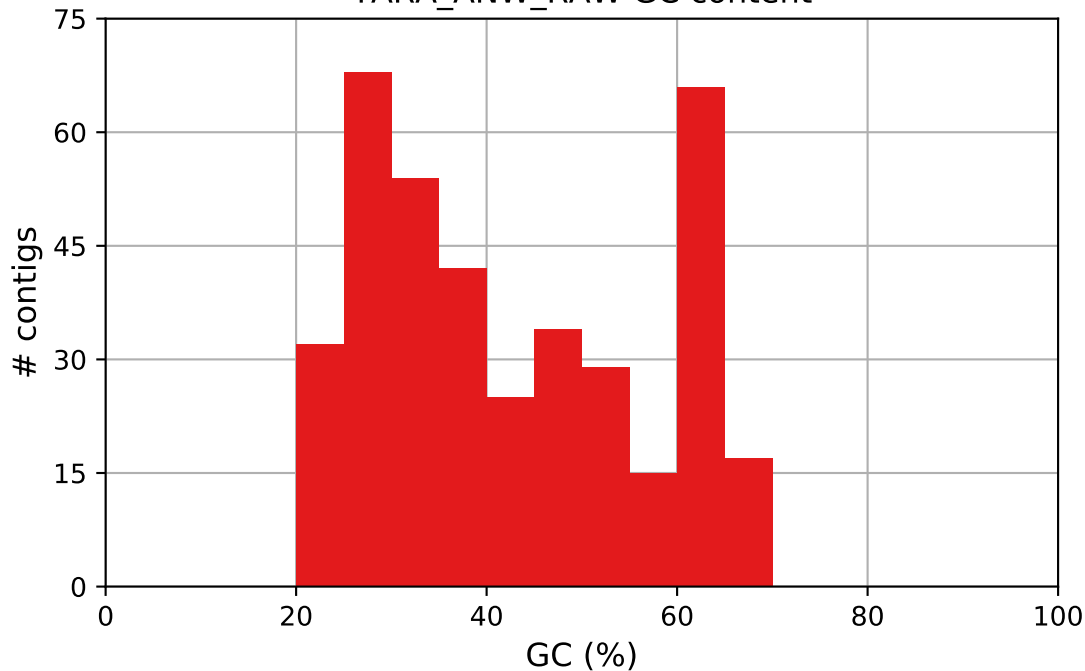


— TARA_ANW_RAW - - Reference

GC content

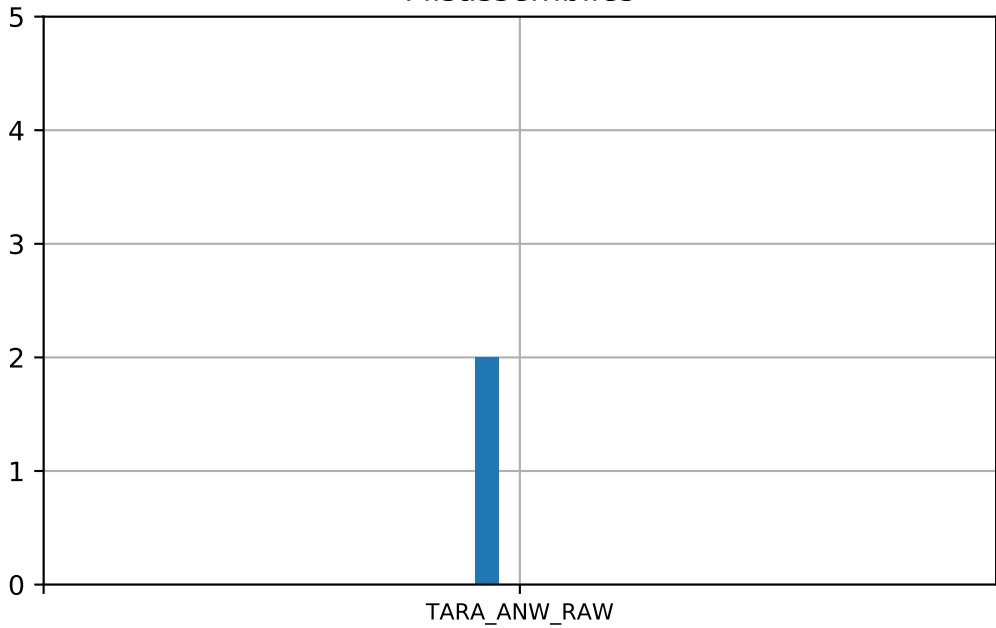


TARA_ANW_RAW GC content



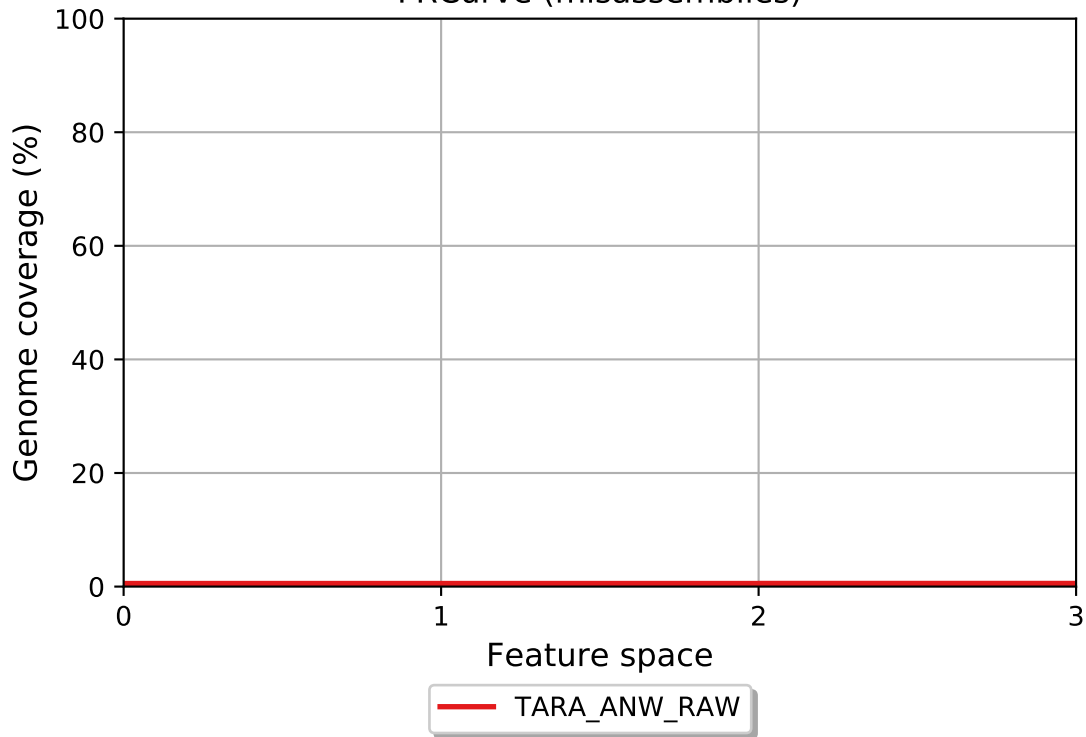
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Misassemblies

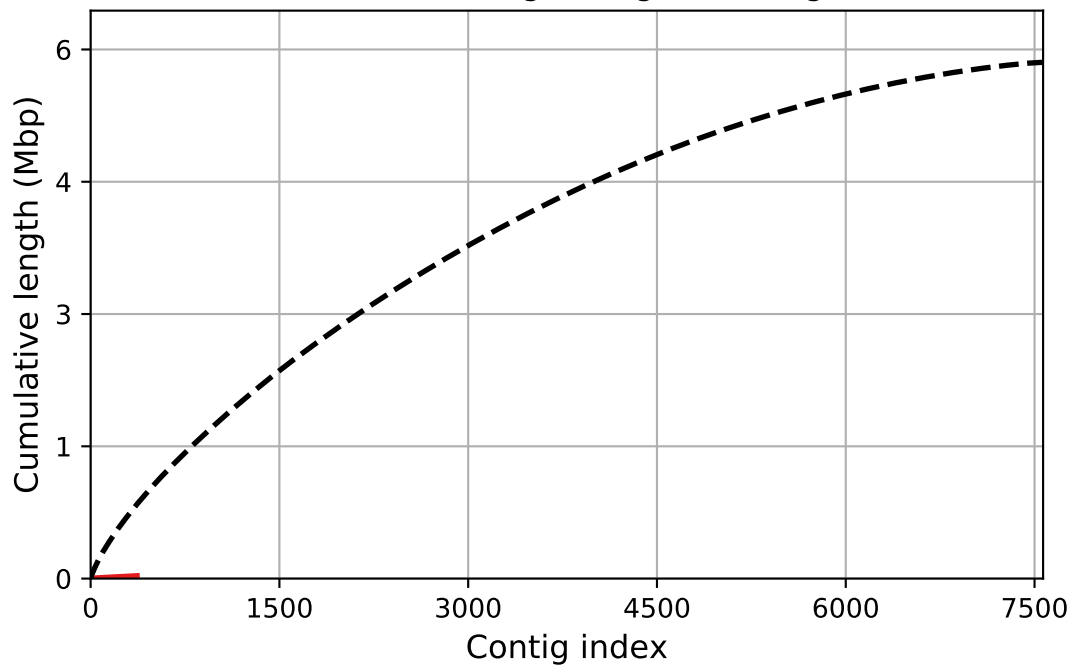


 # translocations

FRCurve (misassemblies)

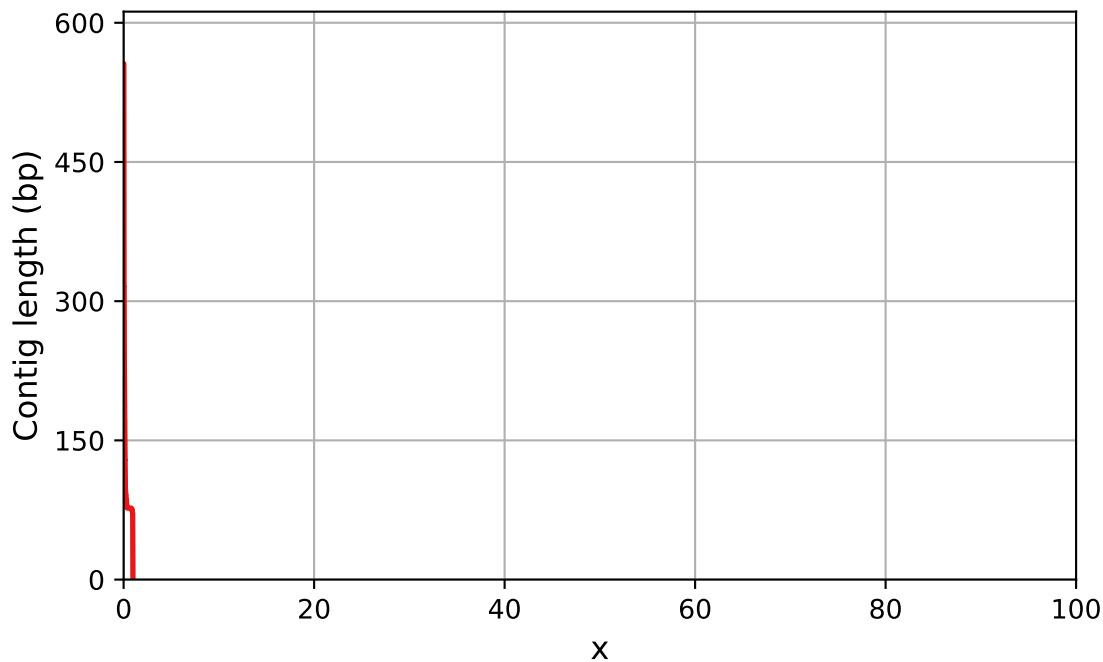


Cumulative length (aligned contigs)



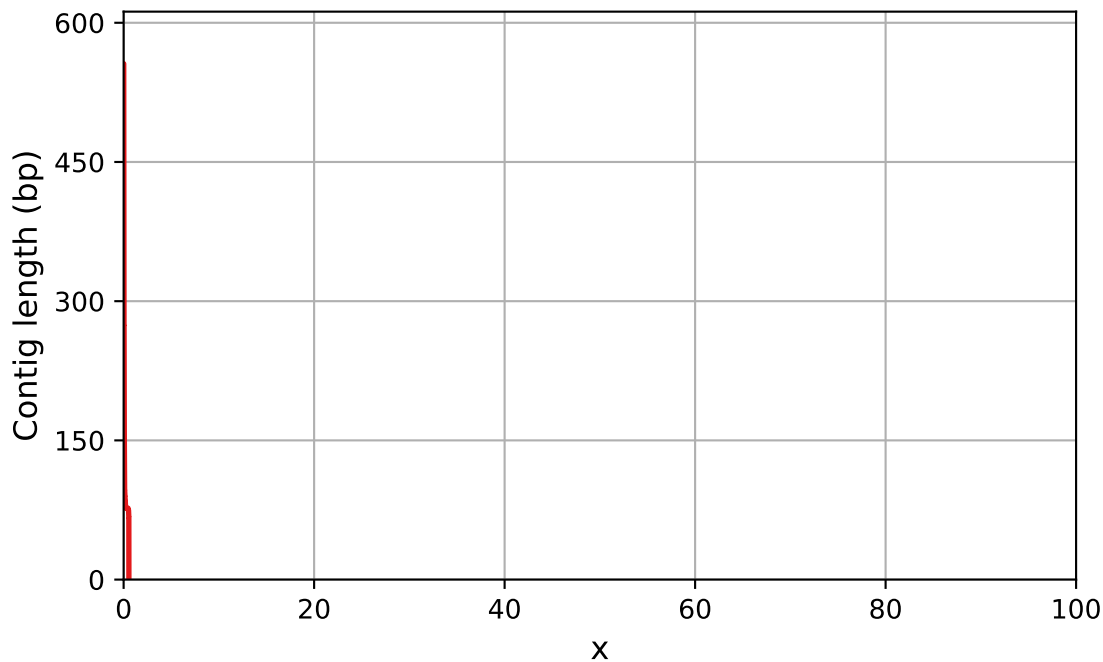
— TARA_ANW_RAW - - Reference

NAx



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NGAx



TARA_ANW_RAW