

Report

	TARA_IOS_RAW
# contigs (>= 1000 bp)	358
# contigs (>= 5000 bp)	56
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	1634145
Total length (>= 5000 bp)	1030952
Total length (>= 10000 bp)	790682
Total length (>= 25000 bp)	601574
Total length (>= 50000 bp)	418129
# contigs	358
Largest contig	152236
Total length	1634145
Reference length	5854900
GC (%)	39.05
Reference GC (%)	63.53
N50	9561
N75	2813
L50	25
L75	112
# 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	5
# unaligned contigs	6 + 352 part
Unaligned length	1605462
Genome fraction (%)	0.061
Duplication ratio	8.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15941.62
# indels per 100 kbp	0.00
Largest alignment	335
Total aligned length	28683
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

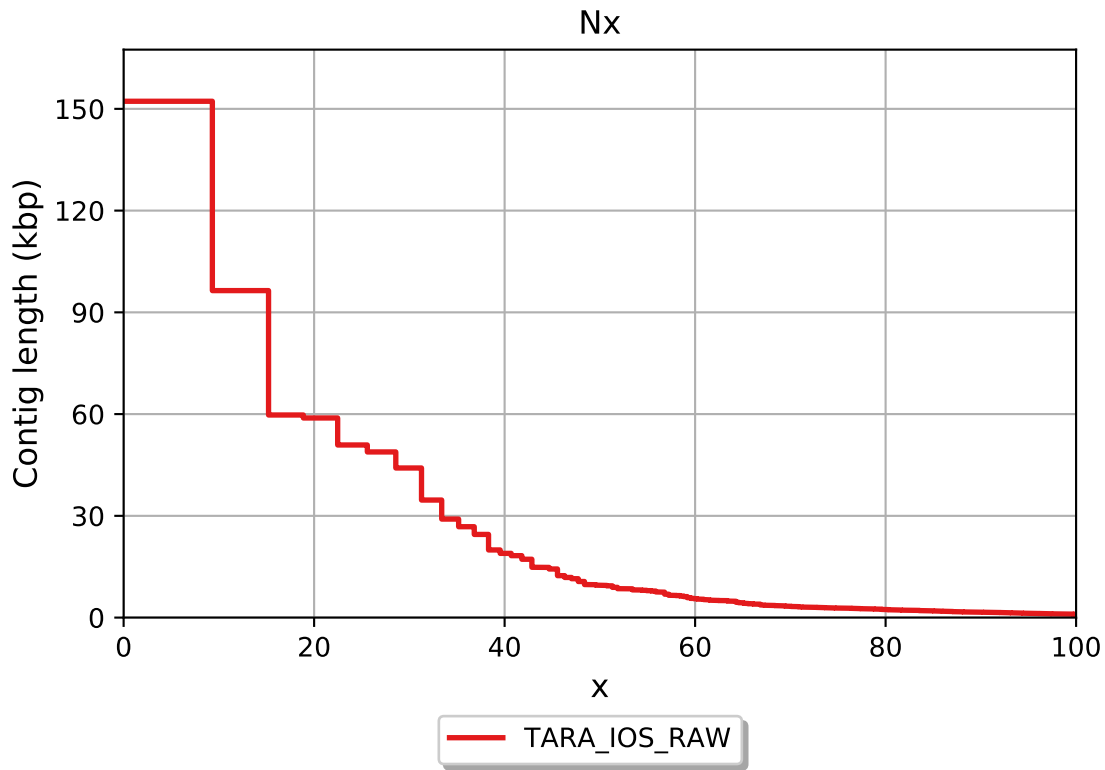
	TARA_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	352
# possible misassemblies	427
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	568
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

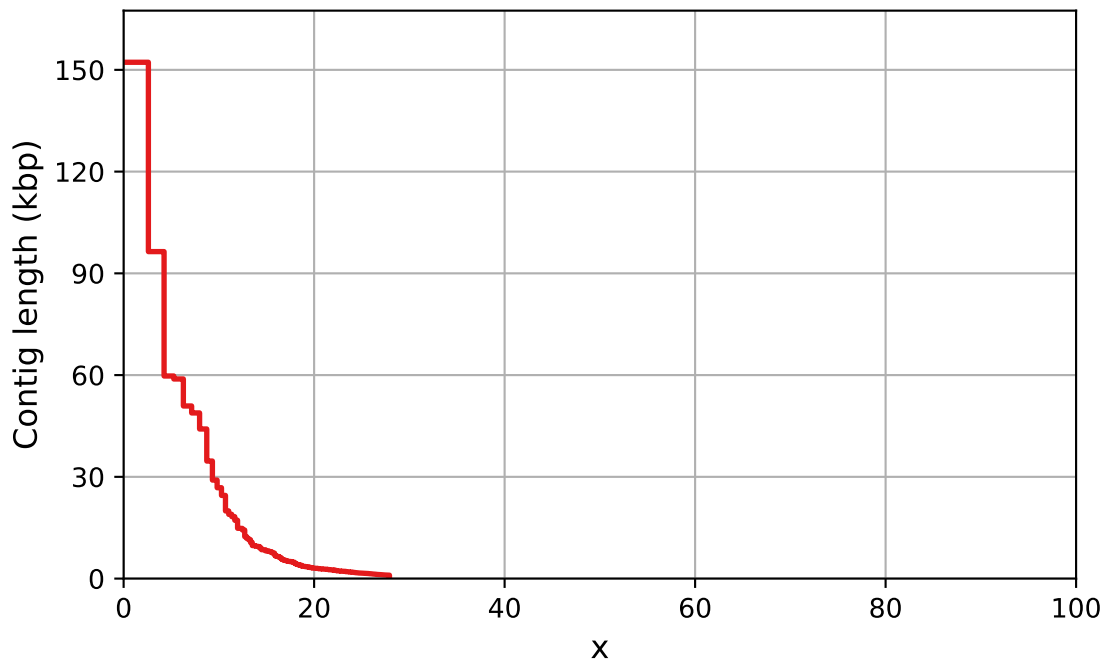
Unaligned report

	TARA_IOS_RAW
# fully unaligned contigs	6
Fully unaligned length	106630
# partially unaligned contigs	352
Partially unaligned length	1498832
# N's	0

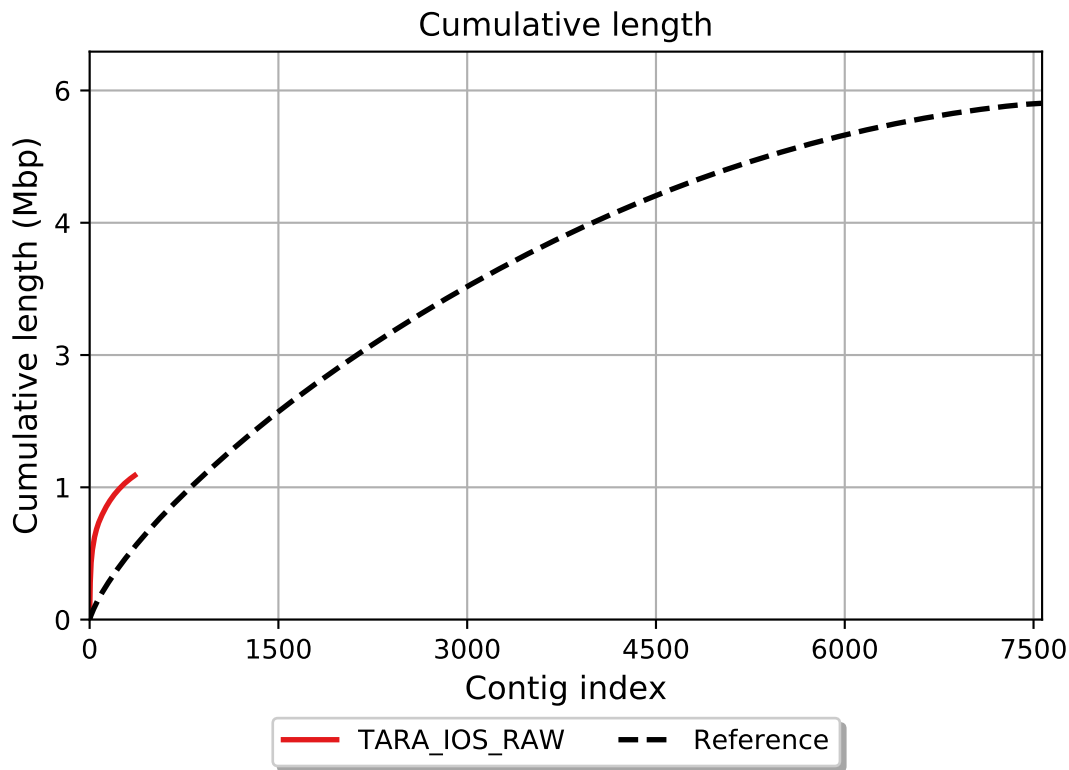
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



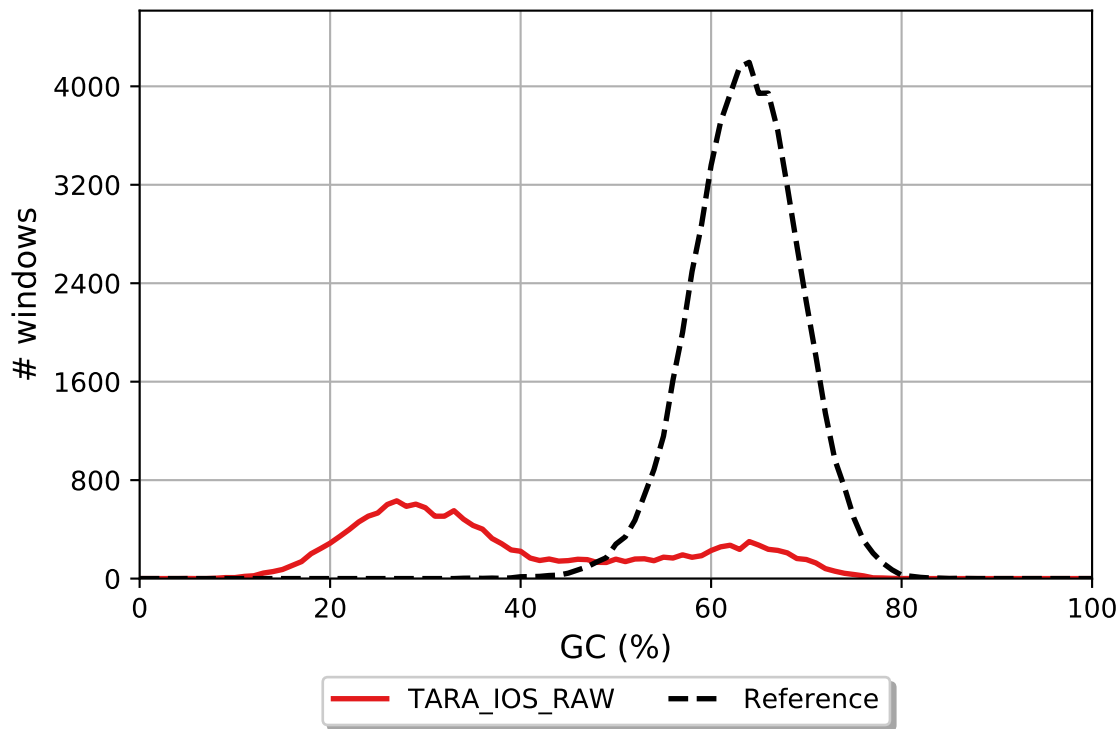
NGx



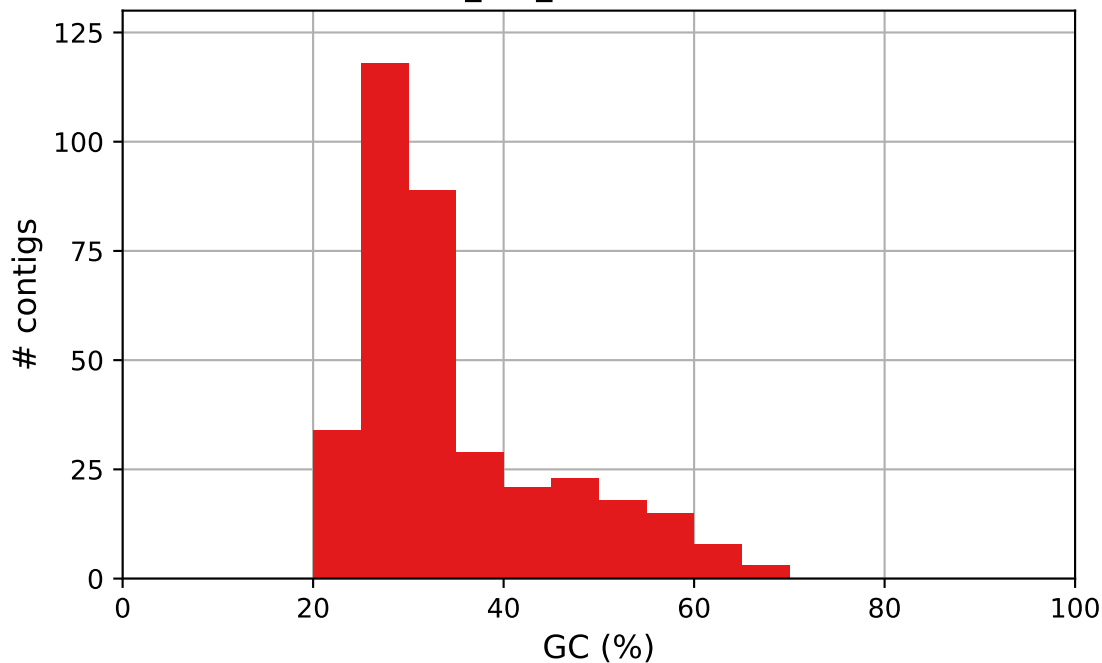
TARA_IOS_RAW



GC content



TARA_IOS_RAW GC content

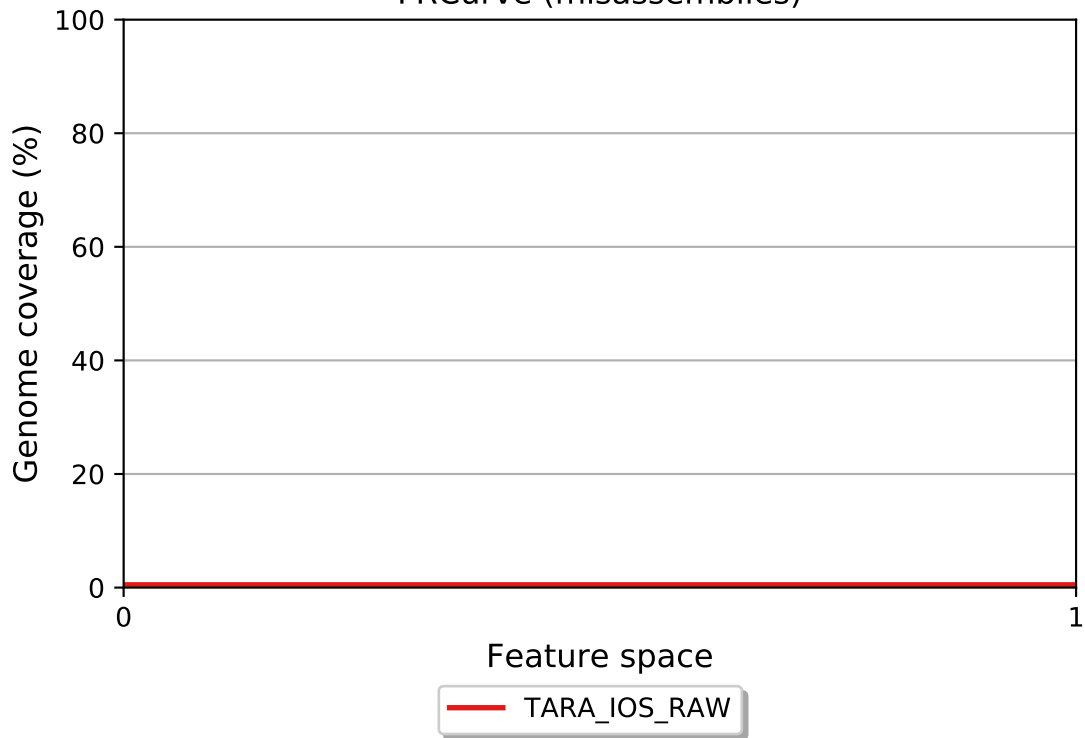


TARA_IOS_RAW

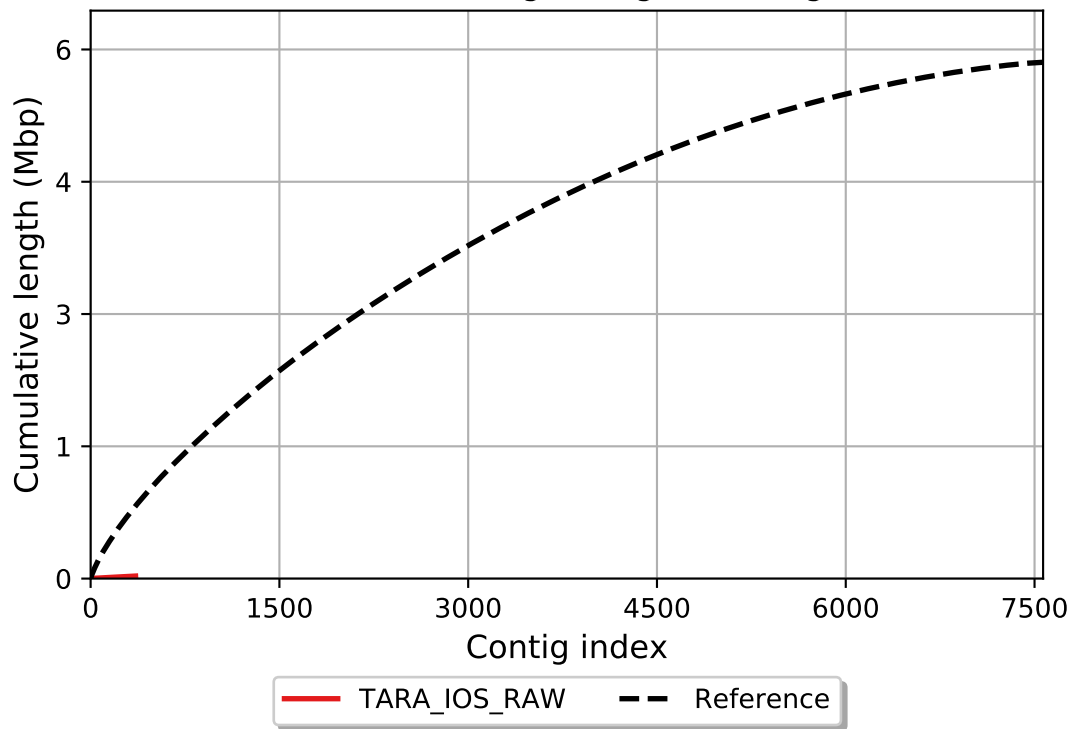
Misassemblies



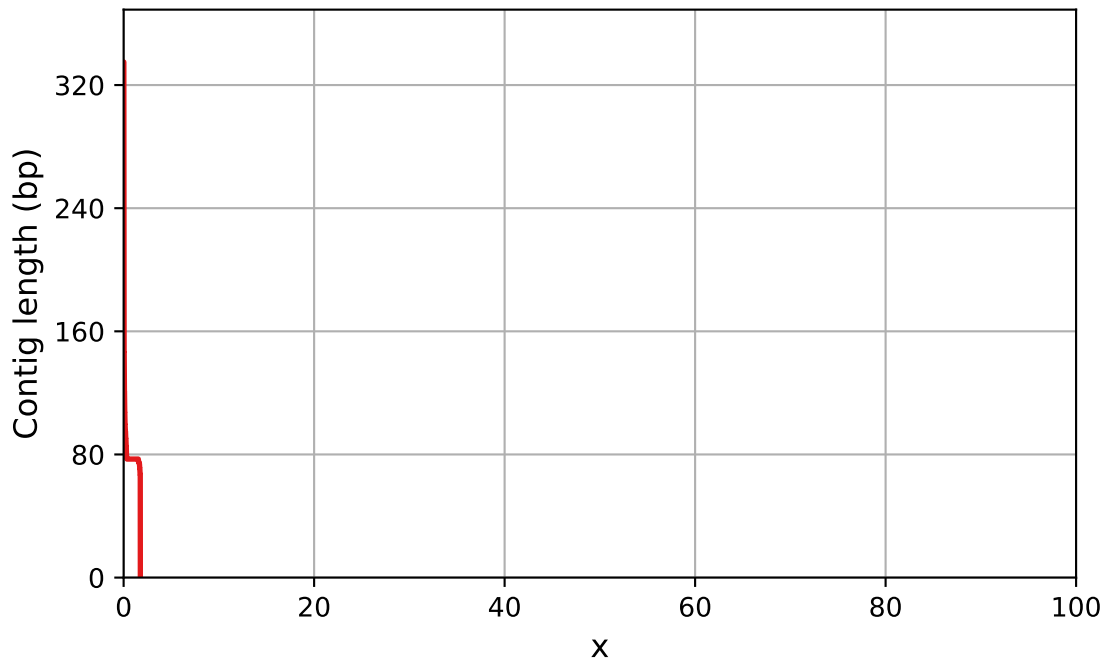
FRCurve (misassemblies)



Cumulative length (aligned contigs)

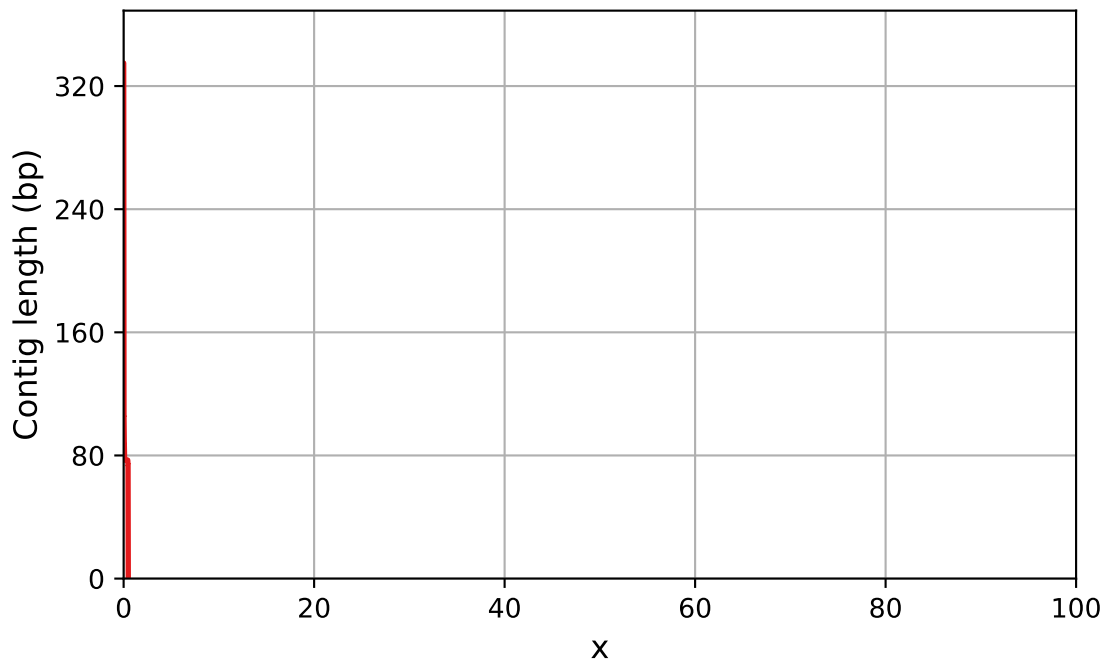


NAx



TARA_IOS_RAW

NGAx



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