

Report

	TARA_PSE_RAW
# contigs (>= 1000 bp)	52
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	214615
Total length (>= 5000 bp)	120515
Total length (>= 10000 bp)	114251
Total length (>= 25000 bp)	104193
Total length (>= 50000 bp)	104193
# contigs	52
Largest contig	104193
Total length	214615
Reference length	3561038
GC (%)	48.66
Reference GC (%)	41.87
N50	10058
N75	2373
L50	2
L75	17
# 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 + 48 part
Unaligned length	209993
Genome fraction (%)	0.028
Duplication ratio	4.650
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13179.07
# indels per 100 kbp	0.00
Largest alignment	200
Total aligned length	4622
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

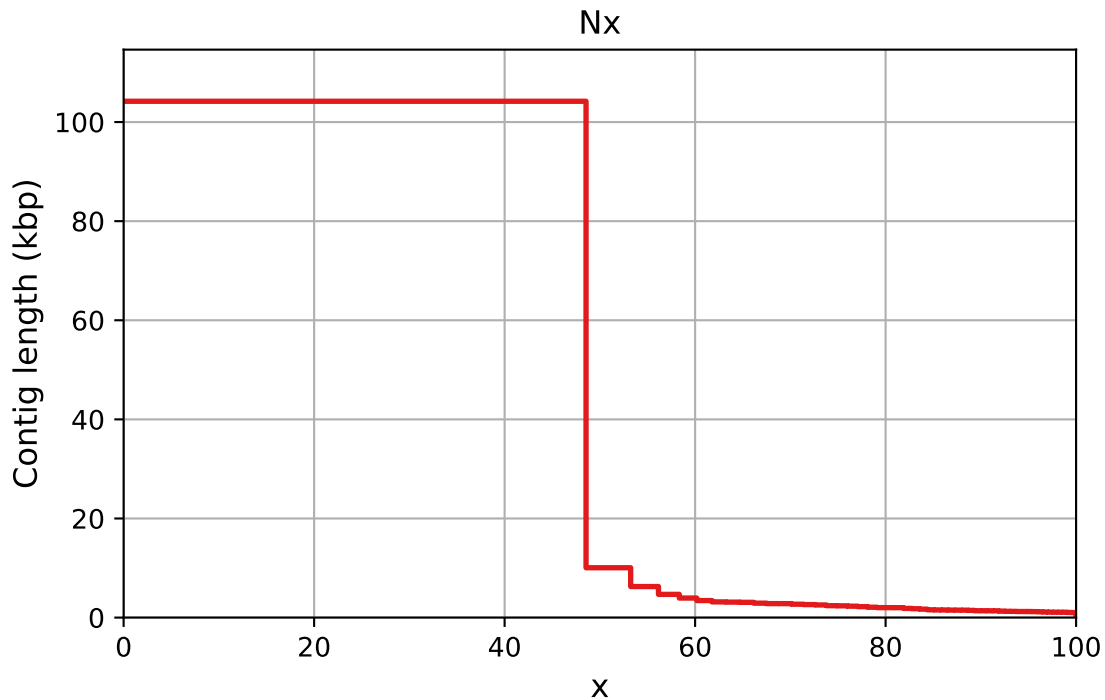
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	50
# possible misassemblies	59
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	131
# 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

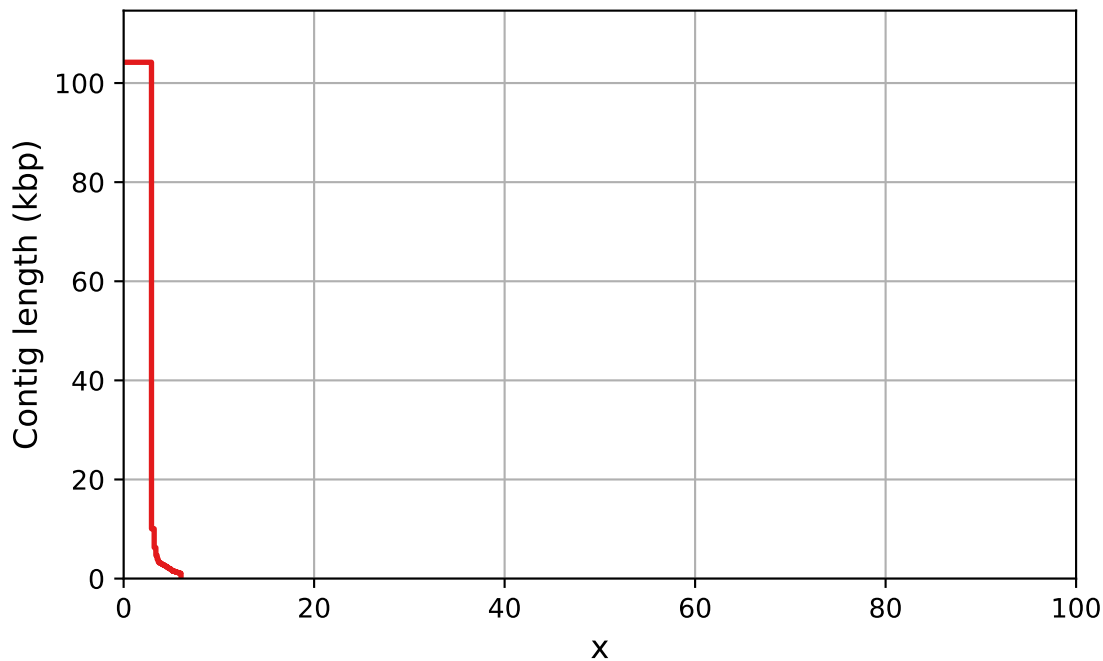
	TARA_PSE_RAW
# fully unaligned contigs	4
Fully unaligned length	6134
# partially unaligned contigs	48
Partially unaligned length	203859
# N's	0

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).

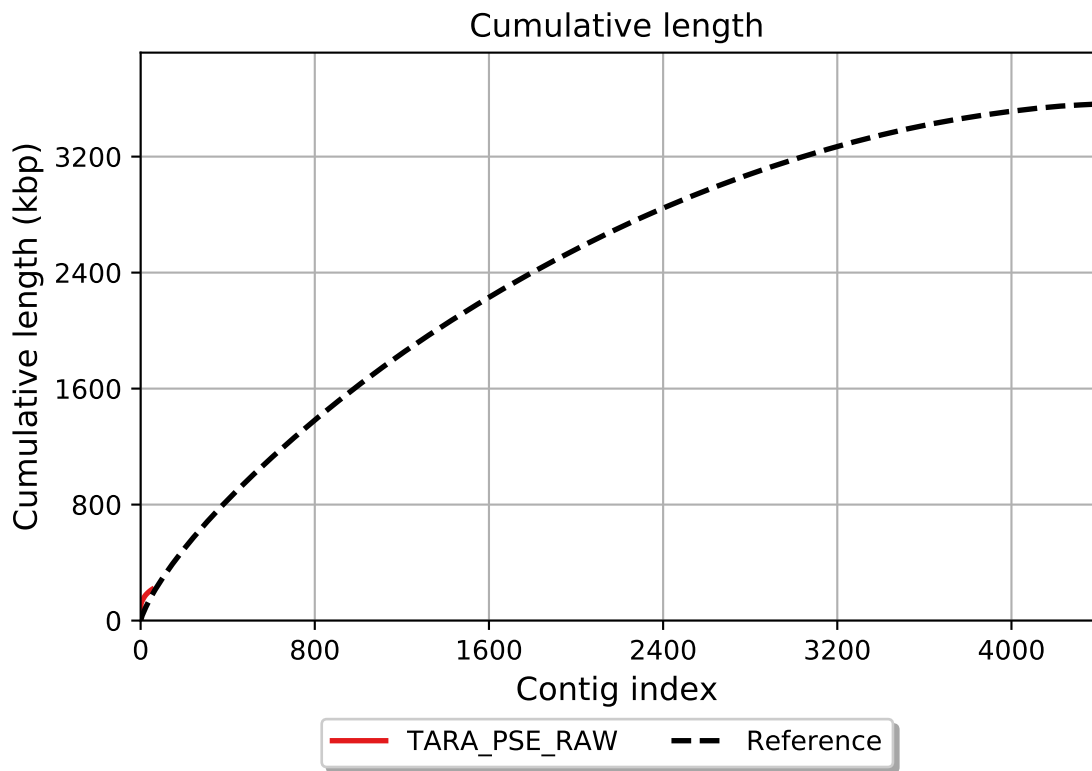


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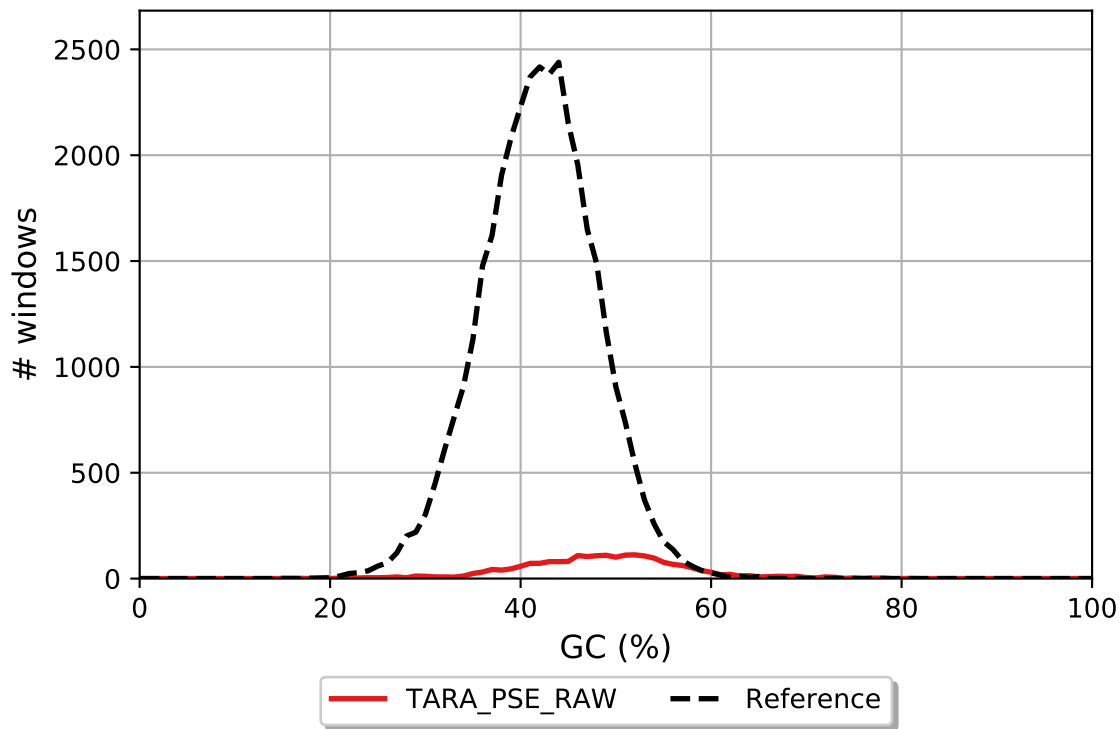
NGx



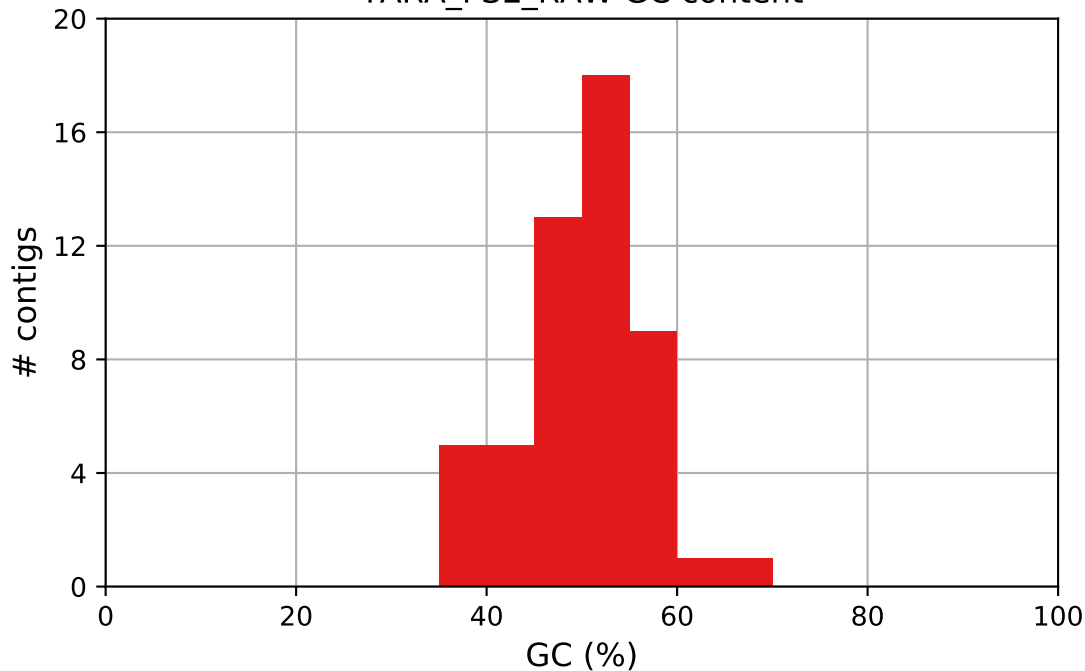
TARA_PSE_RAW



GC content

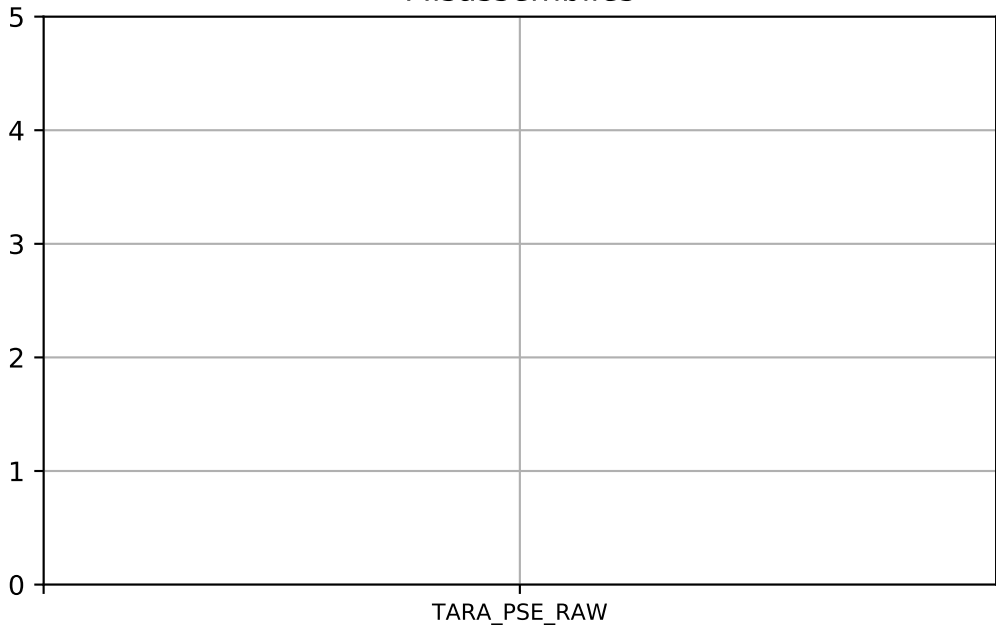


TARA_PSE_RAW GC content

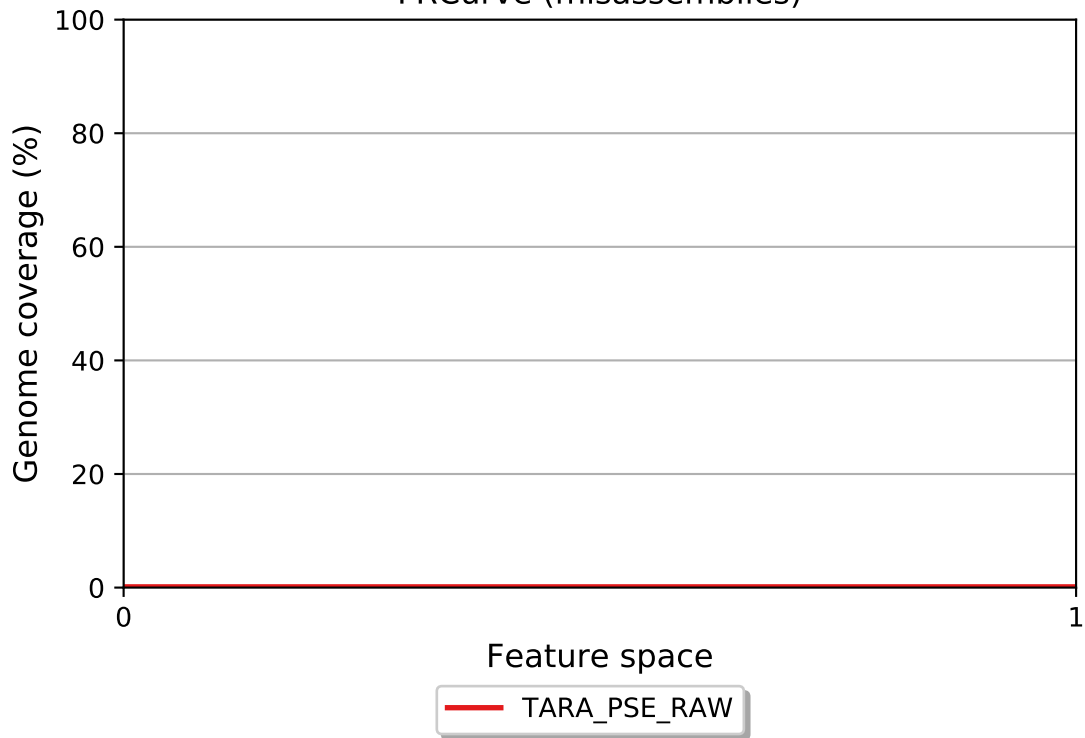


TARA_PSE_RAW

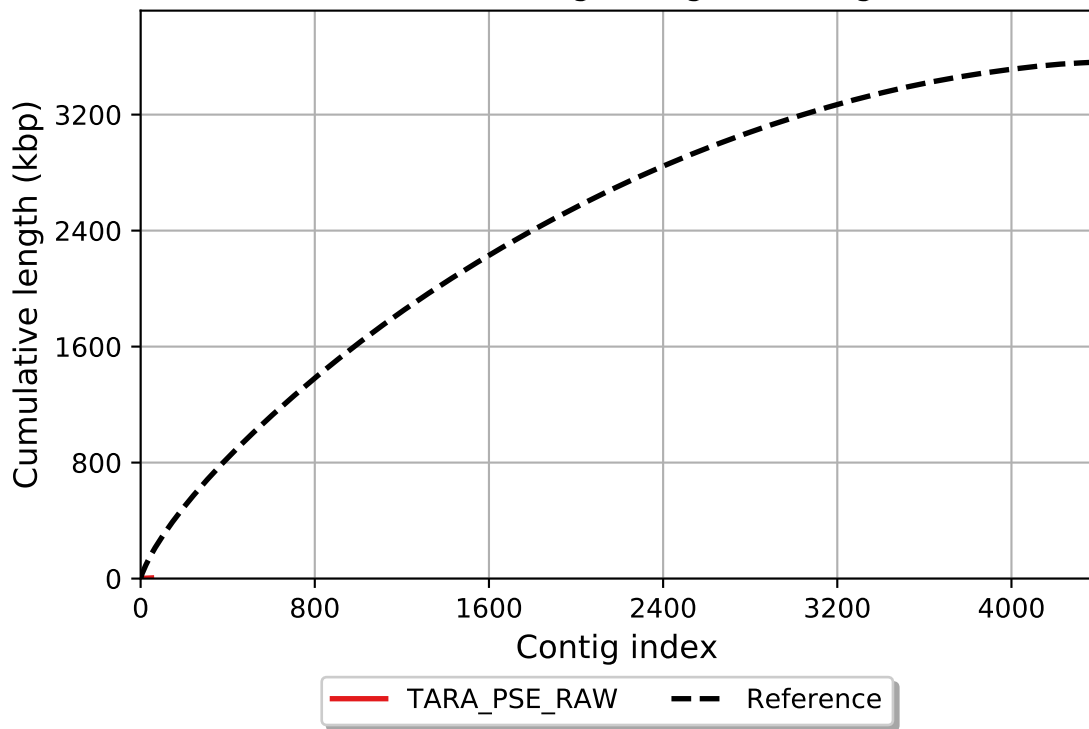
Misassemblies



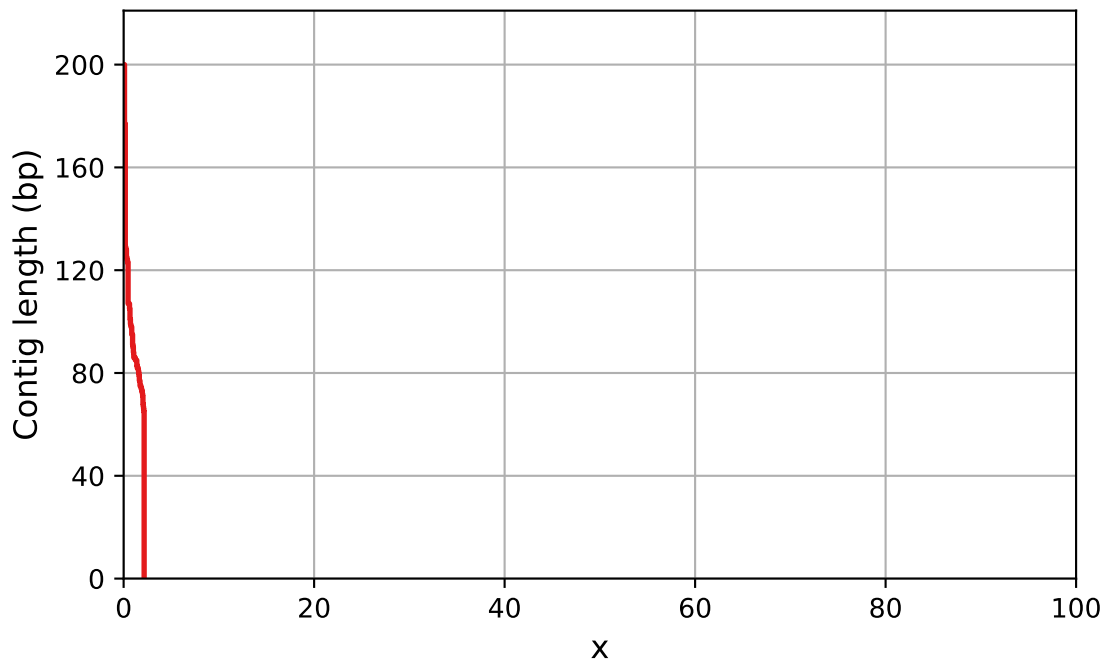
FRCurve (misassemblies)



Cumulative length (aligned contigs)

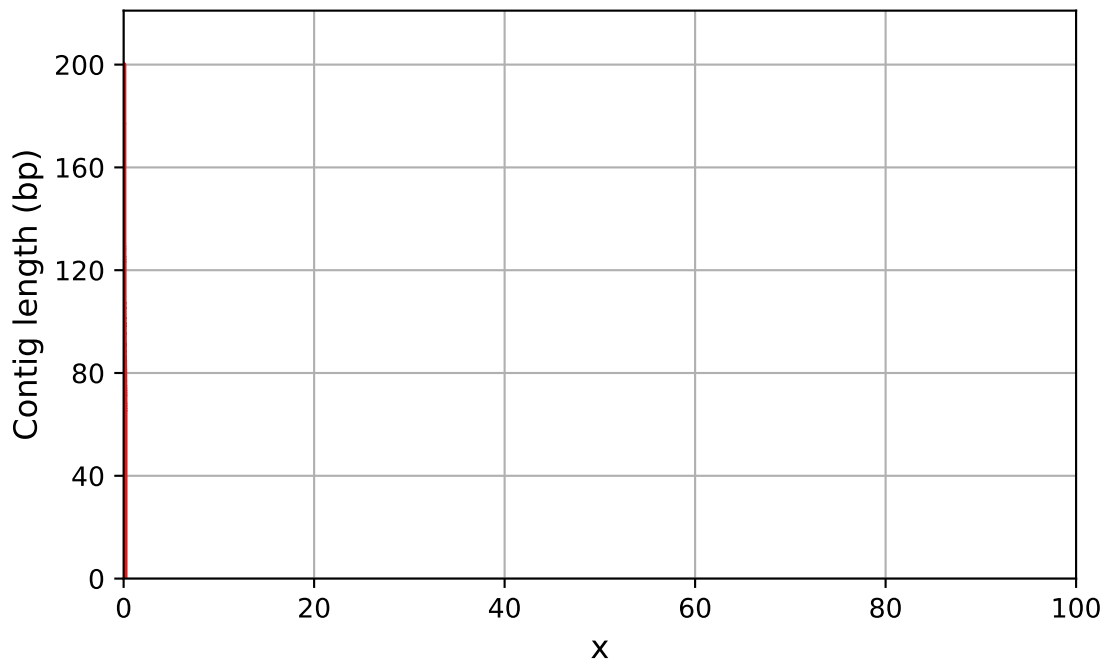


NAx



TARA_PSE_RAW

NGAx



TARA_PSE_RAW