

Report

	TARA_PSE_RAW
# contigs (>= 1000 bp)	836
# contigs (>= 5000 bp)	190
# contigs (>= 10000 bp)	92
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	5933543
Total length (>= 5000 bp)	4599783
Total length (>= 10000 bp)	3891291
Total length (>= 25000 bp)	3263243
Total length (>= 50000 bp)	2359935
# contigs	836
Largest contig	320051
Total length	5933543
Reference length	5854900
GC (%)	46.35
Reference GC (%)	63.53
N50	31537
NG50	33015
N75	6019
NG75	6293
L50	41
LG50	40
L75	164
LG75	154
# 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	6
# unaligned contigs	9 + 825 part
Unaligned length	5865421
Genome fraction (%)	0.143
Duplication ratio	8.126
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12883.22
# indels per 100 kbp	23.86
Largest alignment	370
Total aligned length	66240
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

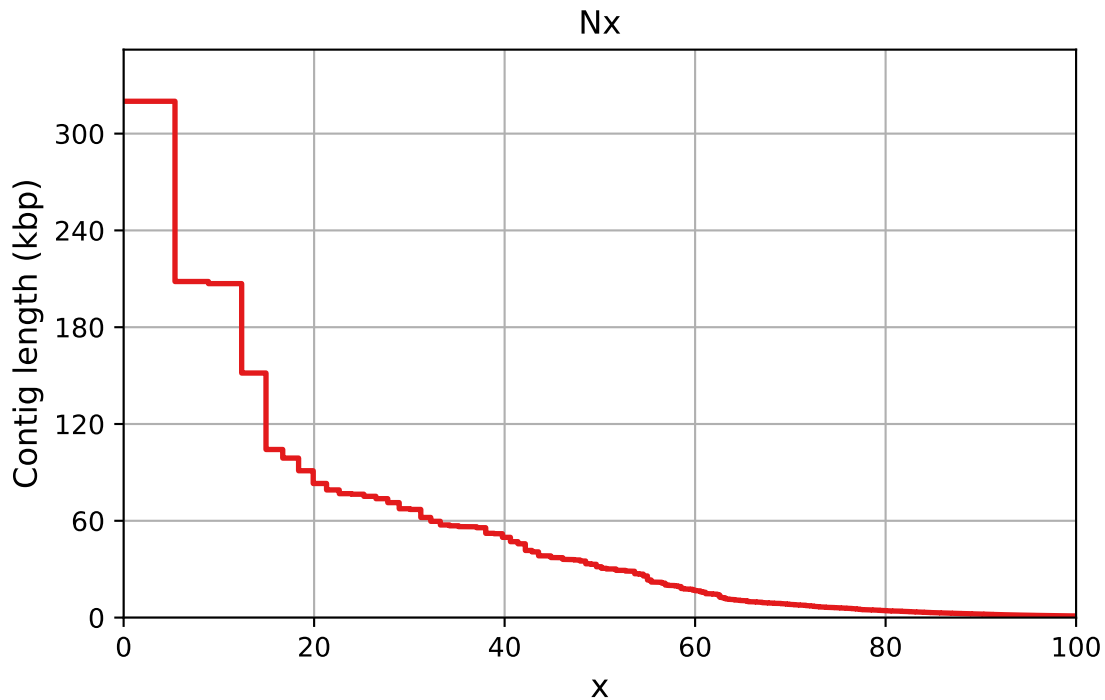
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	828
# possible misassemblies	1033
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	1080
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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

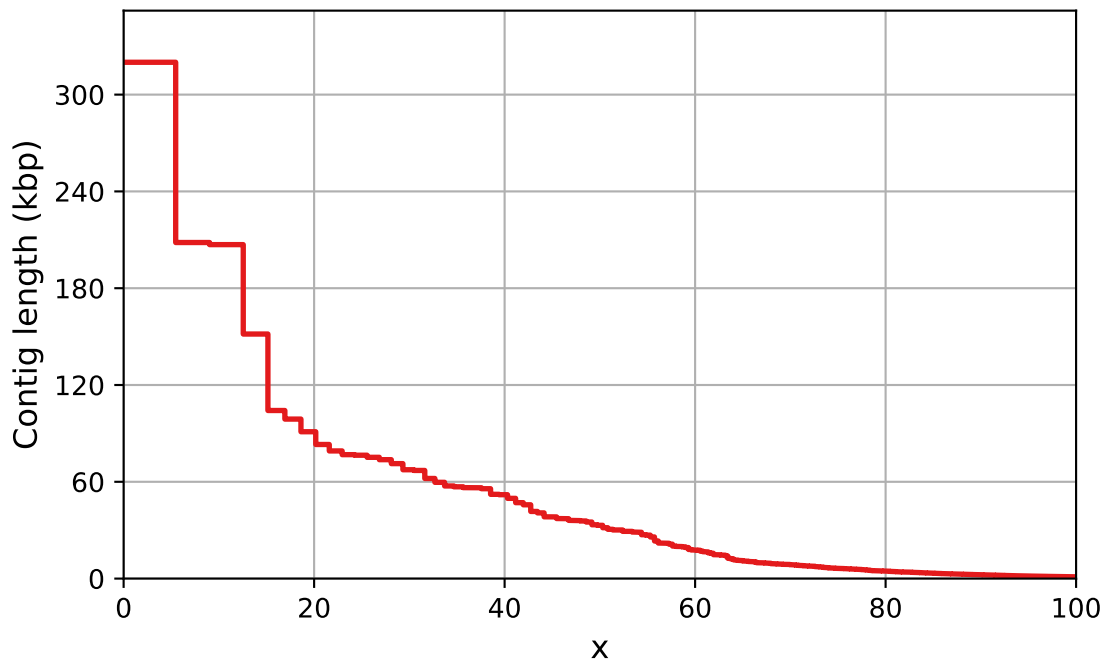
	TARA_PSE_RAW
# fully unaligned contigs	9
Fully unaligned length	162329
# partially unaligned contigs	825
Partially unaligned length	5703092
# N's	0

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).



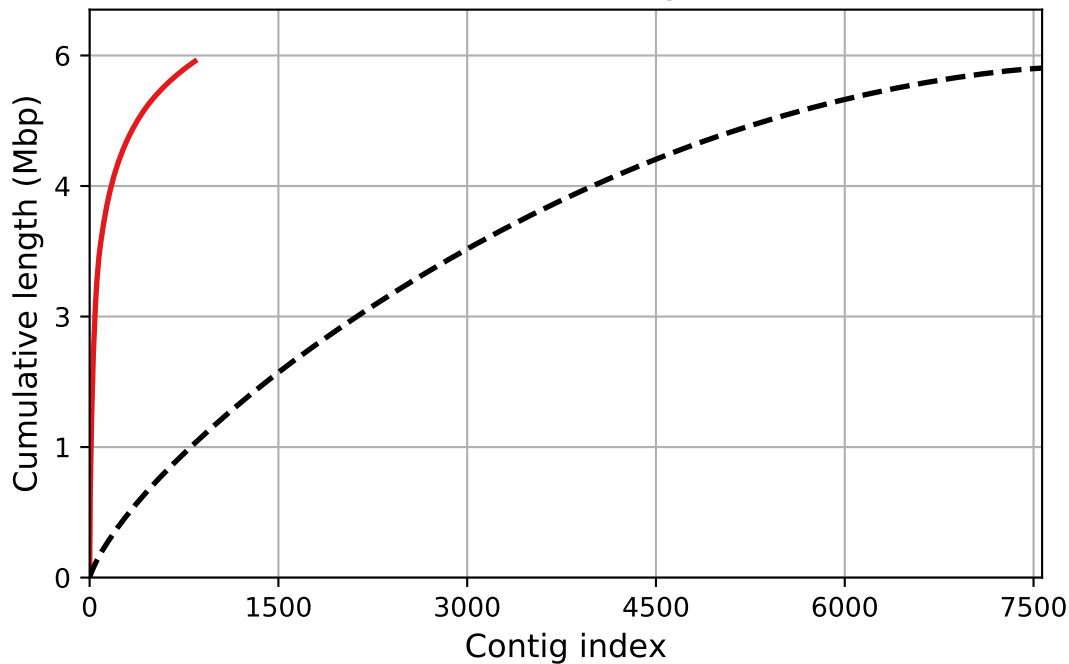
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NGx



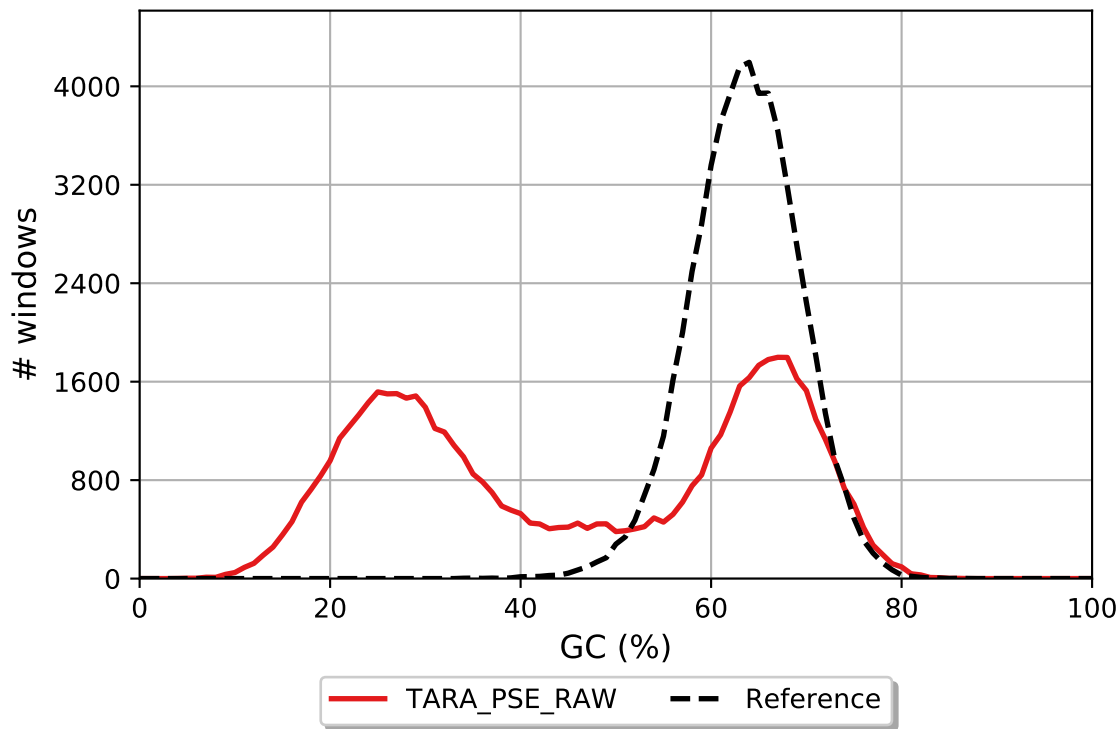
TARA_PSE_RAW

Cumulative length

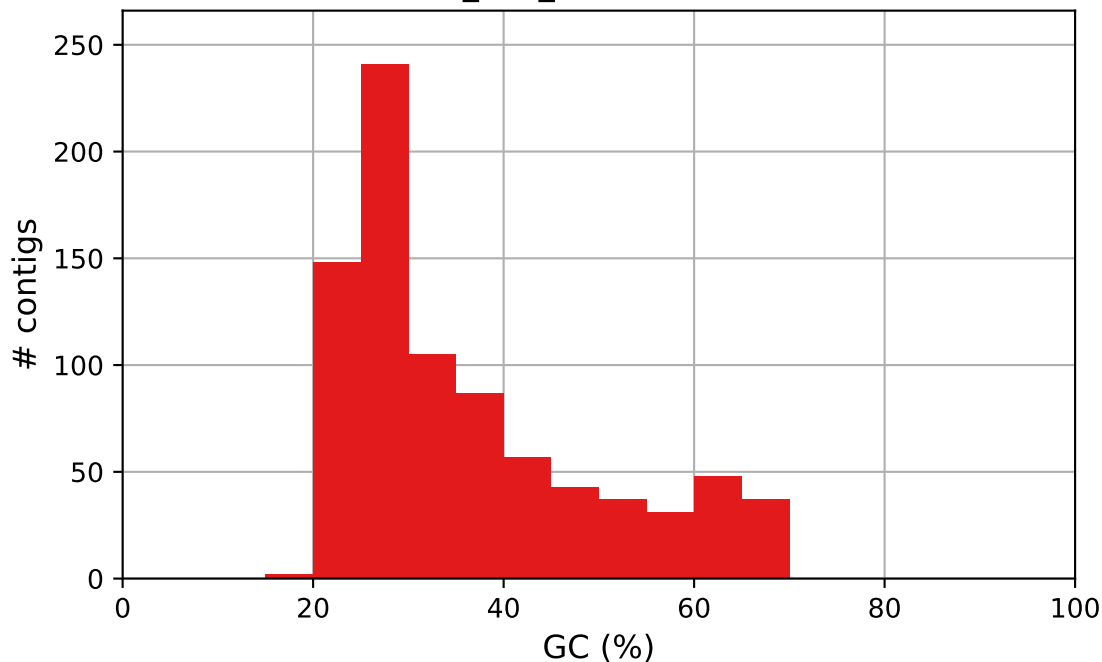


— TARA_PSE_RAW - - Reference

GC content

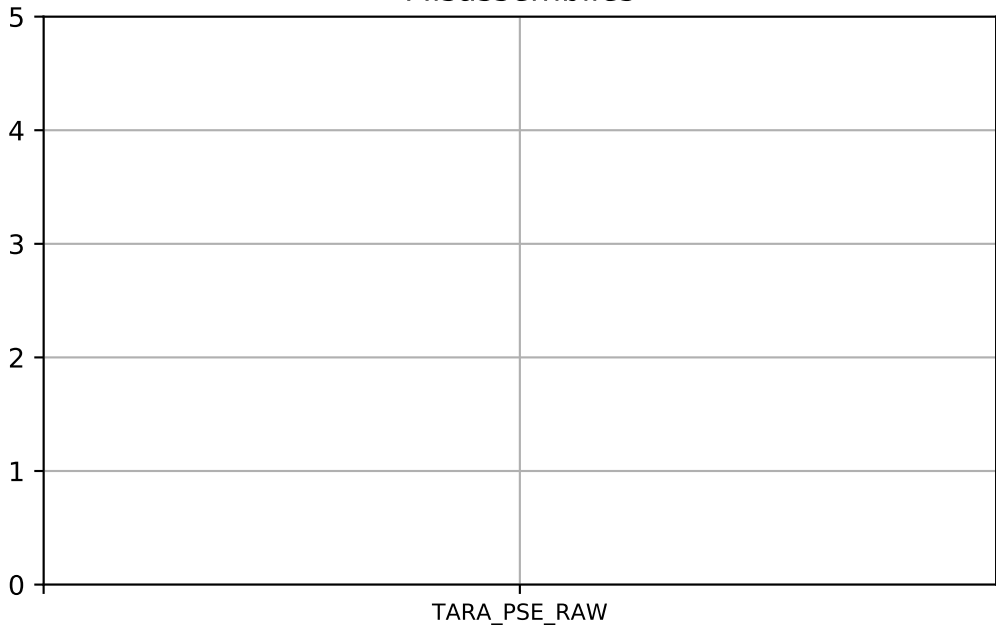


TARA_PSE_RAW GC content

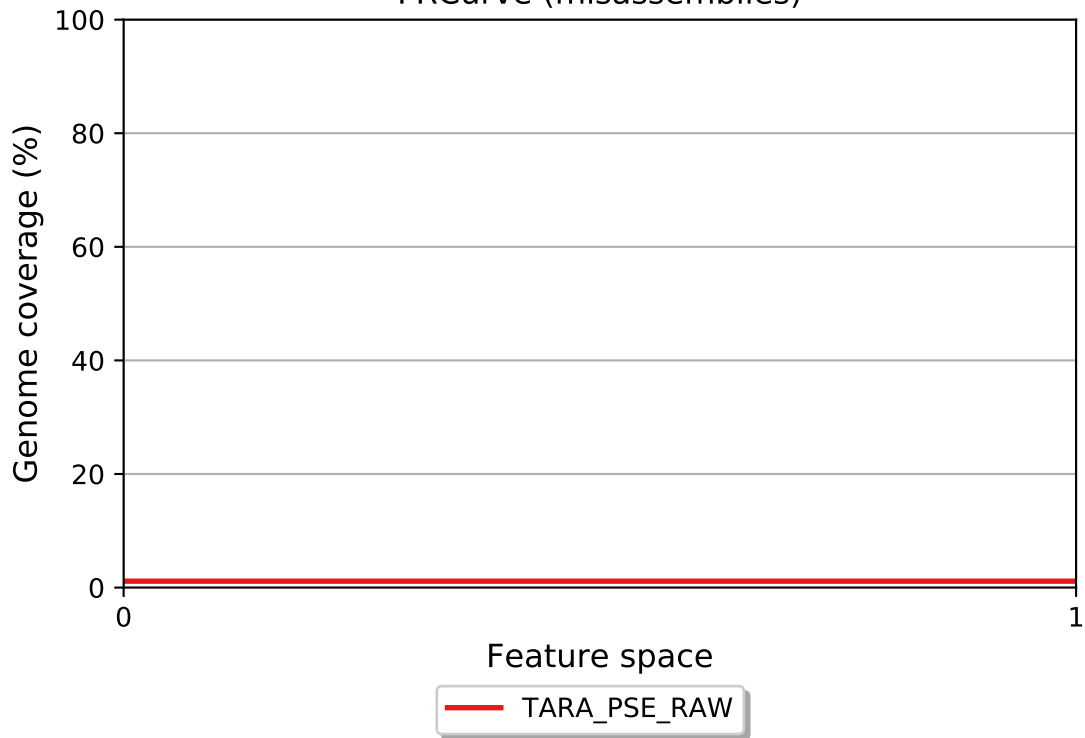


TARA_PSE_RAW

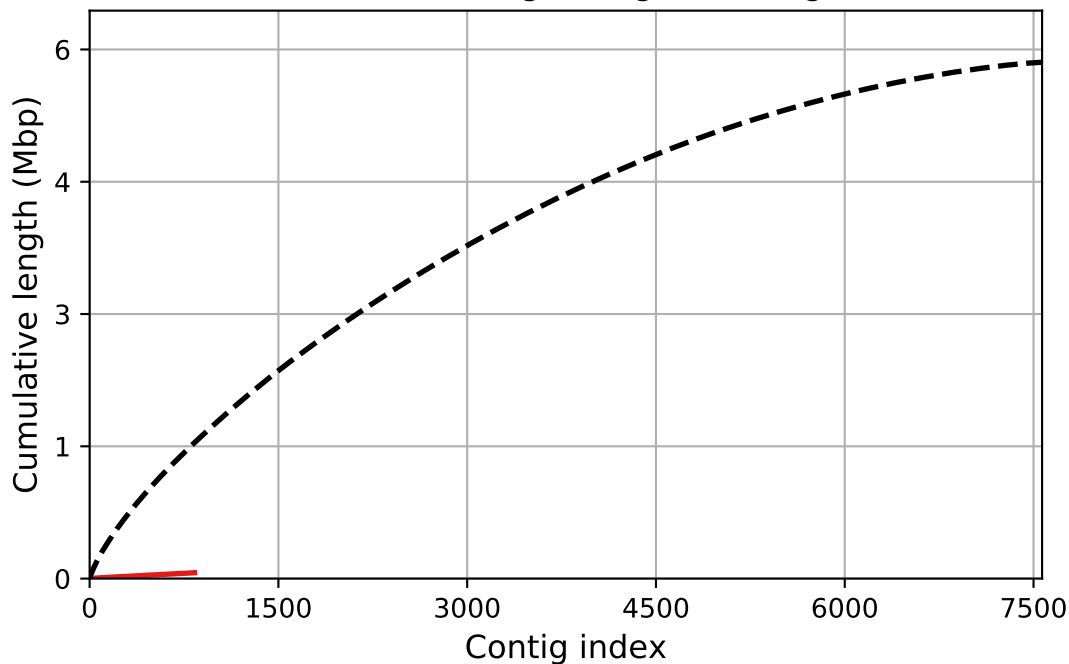
Misassemblies



FRCurve (misassemblies)

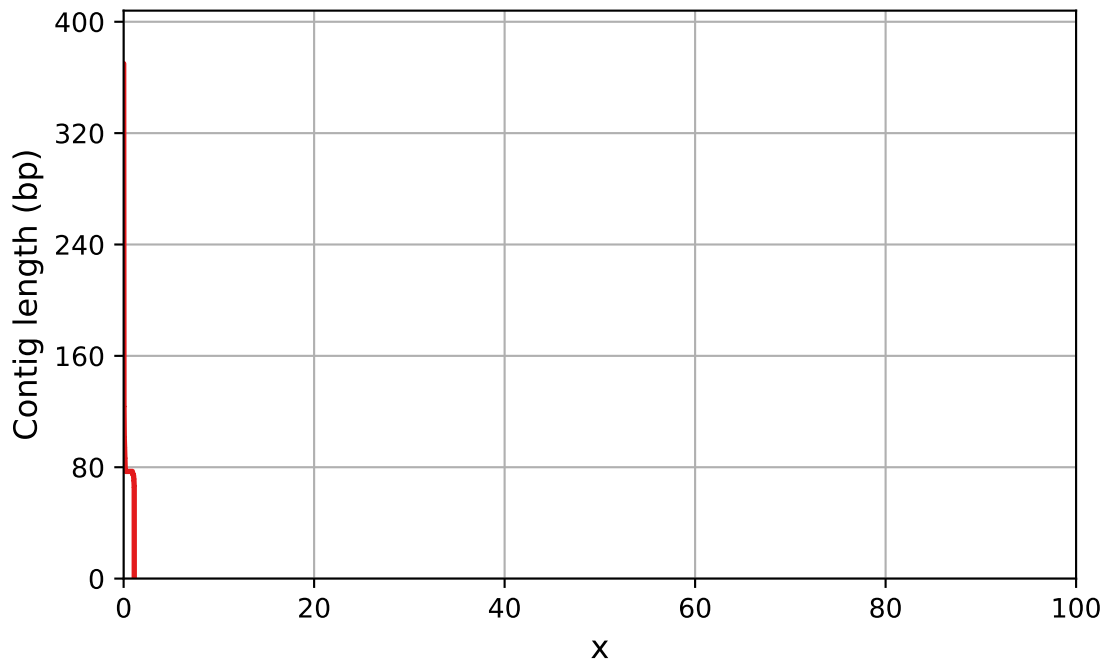


Cumulative length (aligned contigs)



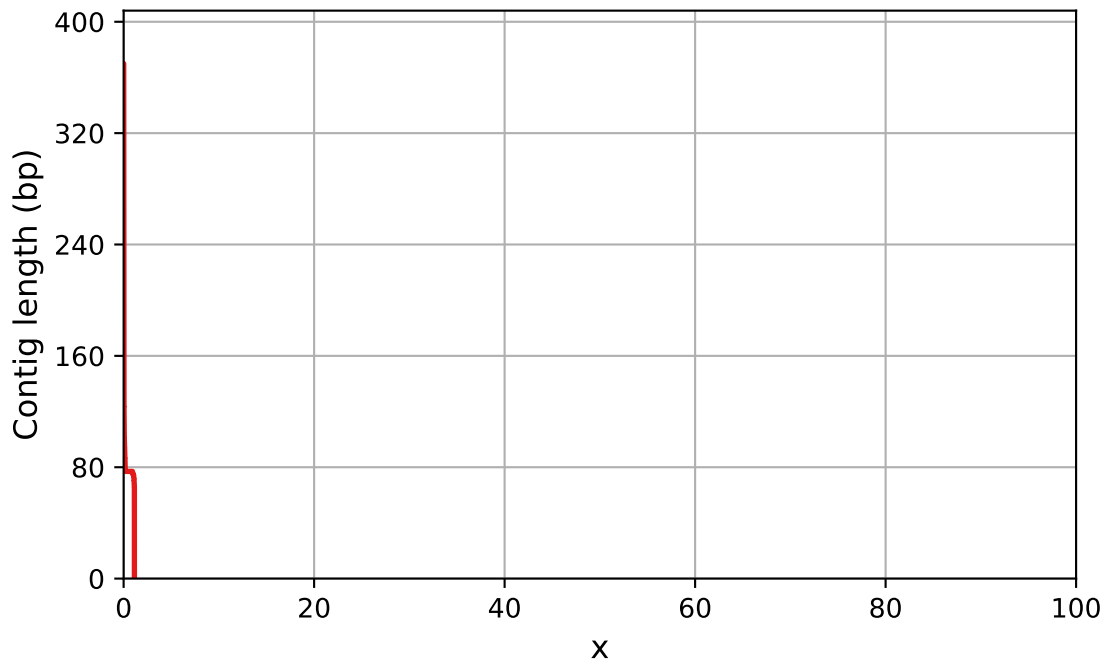
— TARA_PSE_RAW - - Reference

NAx



TARA_PSE_RAW

NGAx



TARA_PSE_RAW