

# Report

	TARA_PSE_RAW
# contigs (>= 1000 bp)	955
# contigs (>= 5000 bp)	212
# contigs (>= 10000 bp)	105
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	6714178
Total length (>= 5000 bp)	5178741
Total length (>= 10000 bp)	4406378
Total length (>= 25000 bp)	3713963
Total length (>= 50000 bp)	2604987
# contigs	955
Largest contig	320051
Total length	6714178
Reference length	7658814
GC (%)	47.70
Reference GC (%)	63.29
N50	30545
NG50	21333
N75	6006
NG75	2935
L50	48
LG50	66
L75	187
LG75	360
# 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	13
# unaligned contigs	21 + 933 part
Unaligned length	6635638
Genome fraction (%)	0.164
Duplication ratio	6.262
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10747.89
# indels per 100 kbp	47.84
Largest alignment	523
Total aligned length	77644
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

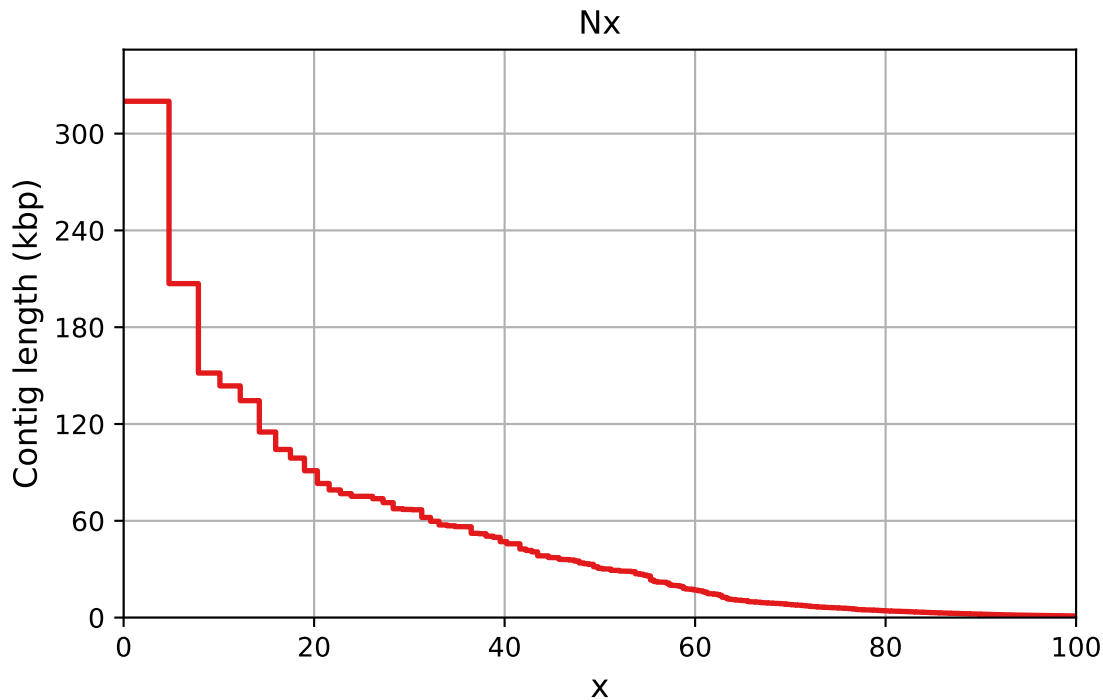
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	941
# possible misassemblies	1169
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	13
# mismatches	1348
# indels	6
# indels (<= 5 bp)	6
# indels (> 5 bp)	0
Indels length	8

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

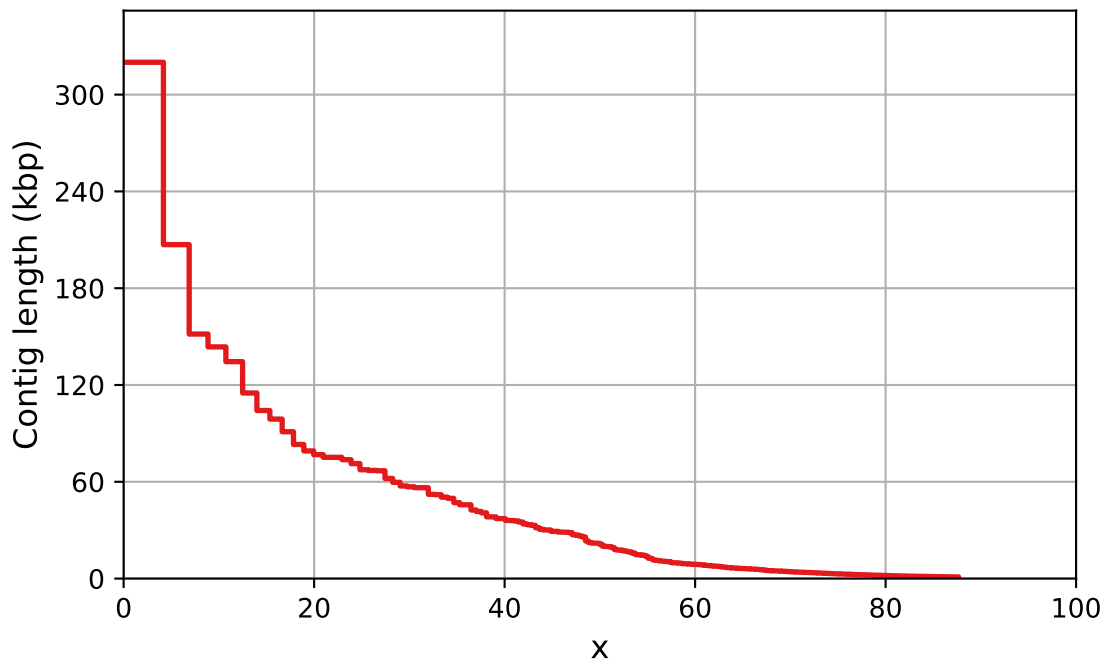
	TARA_PSE_RAW
# fully unaligned contigs	21
Fully unaligned length	284393
# partially unaligned contigs	933
Partially unaligned length	6351245
# N's	0

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).



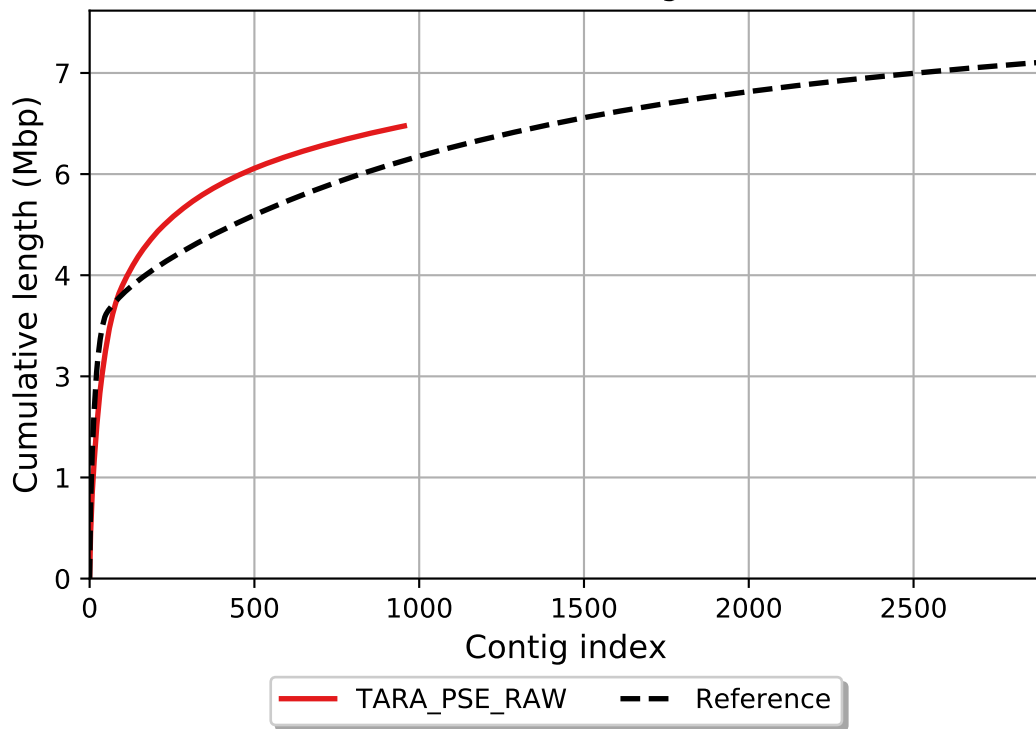
TARA\_PSE\_RAW

# NGx

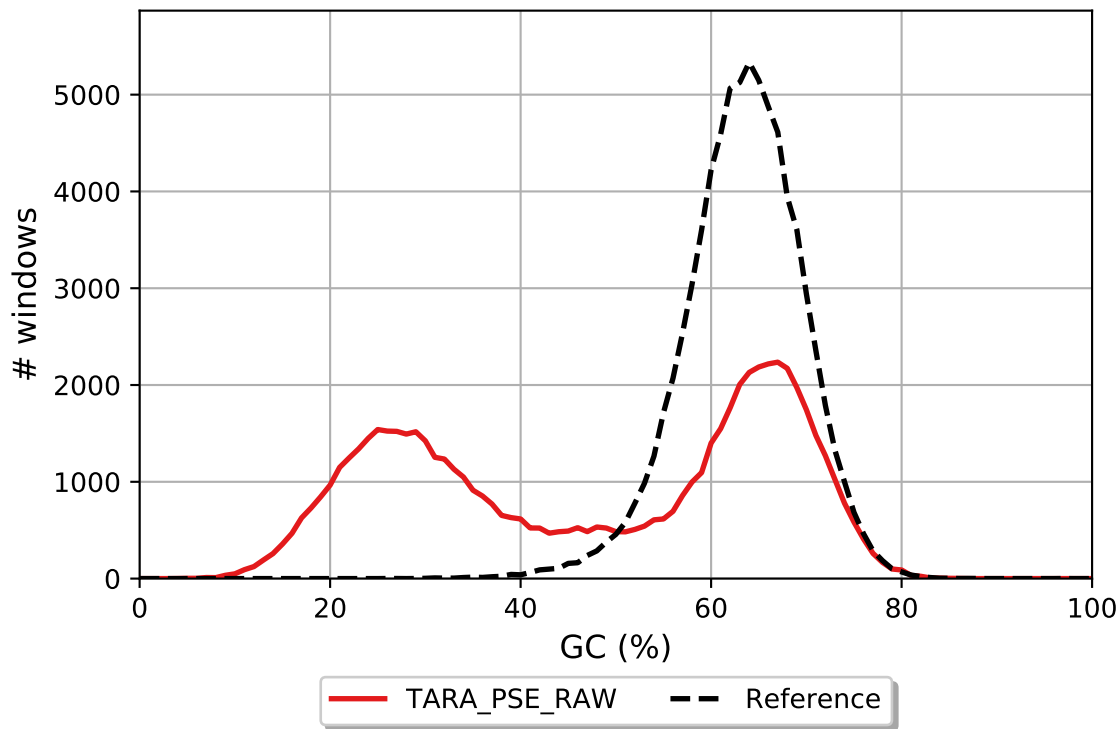


TARA\_PSE\_RAW

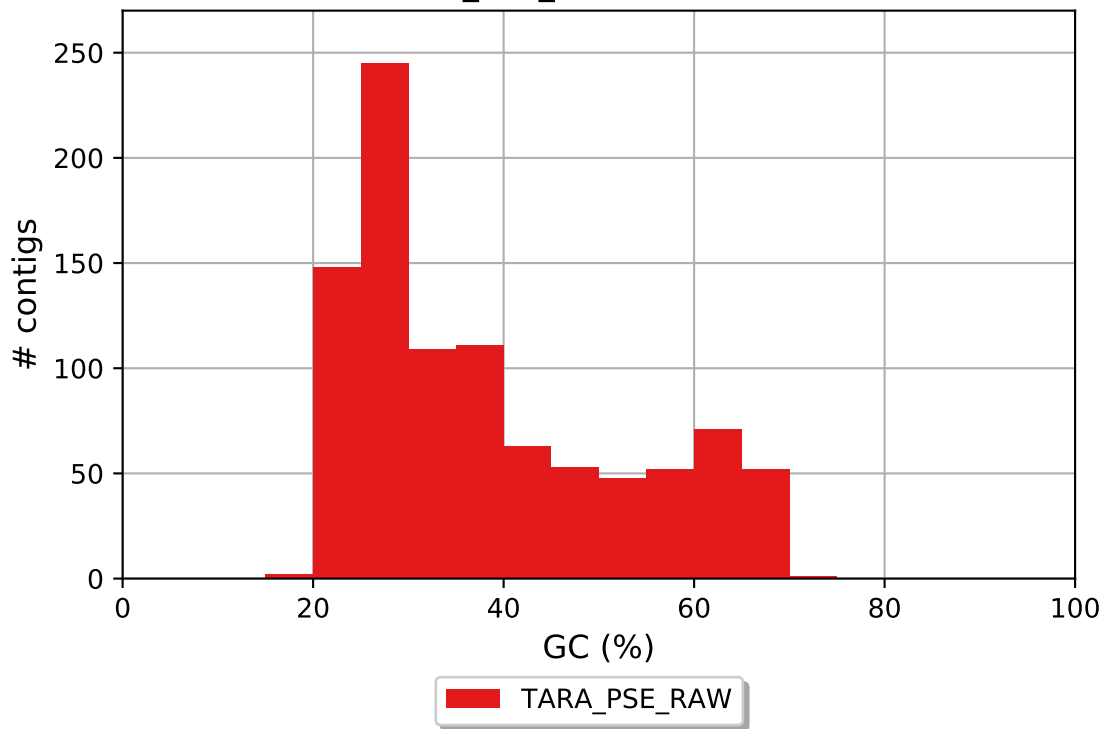
Cumulative length



GC content

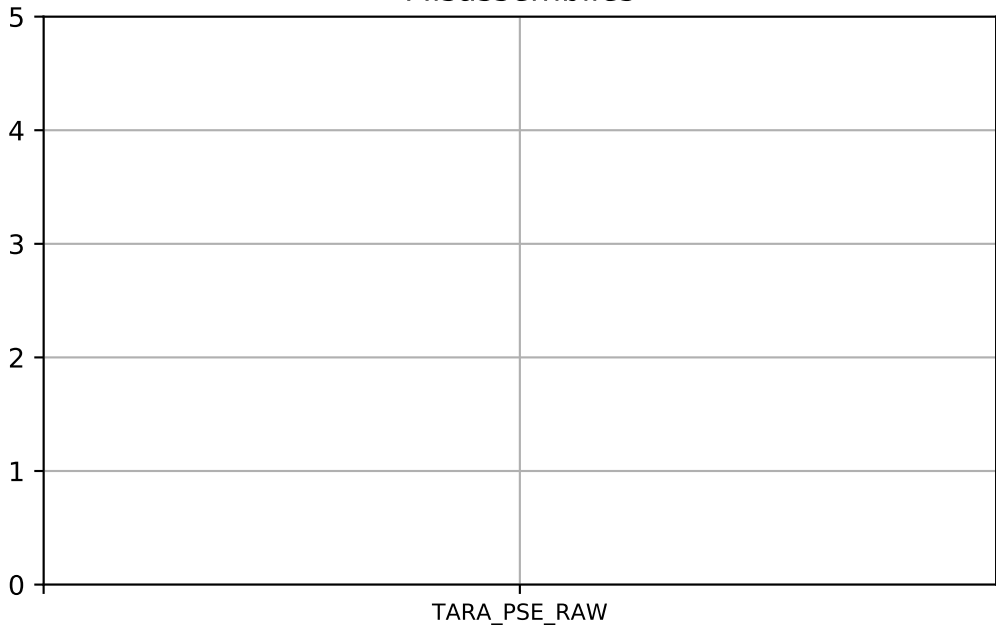


TARA\_PSE\_RAW GC content

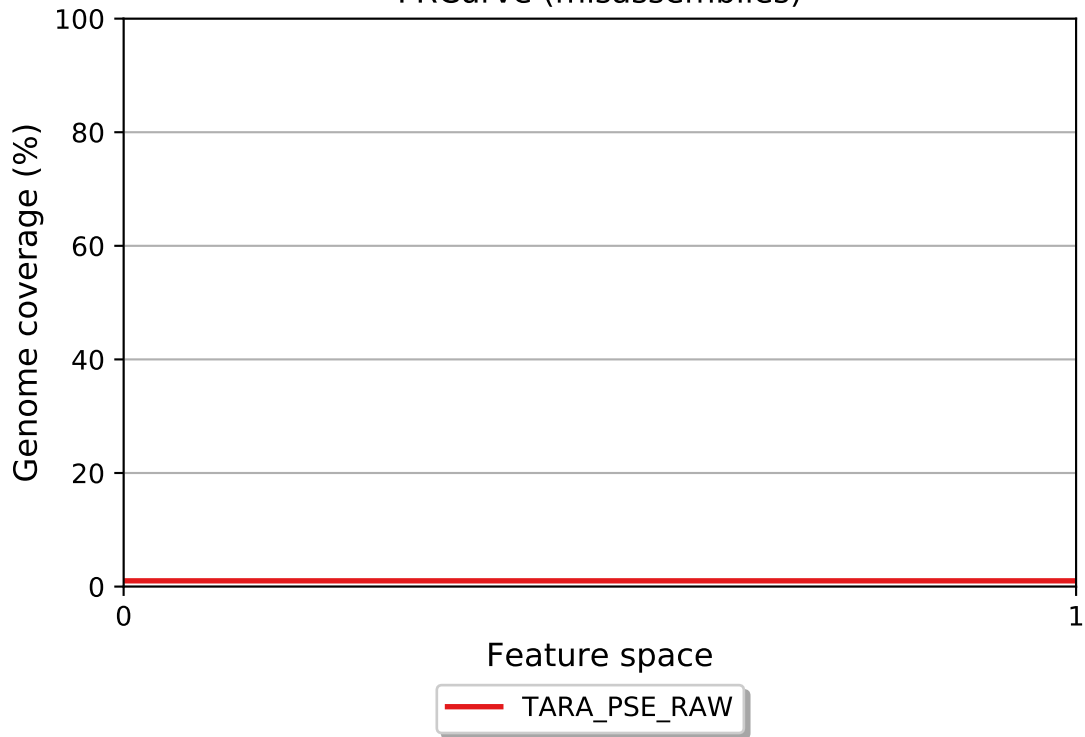




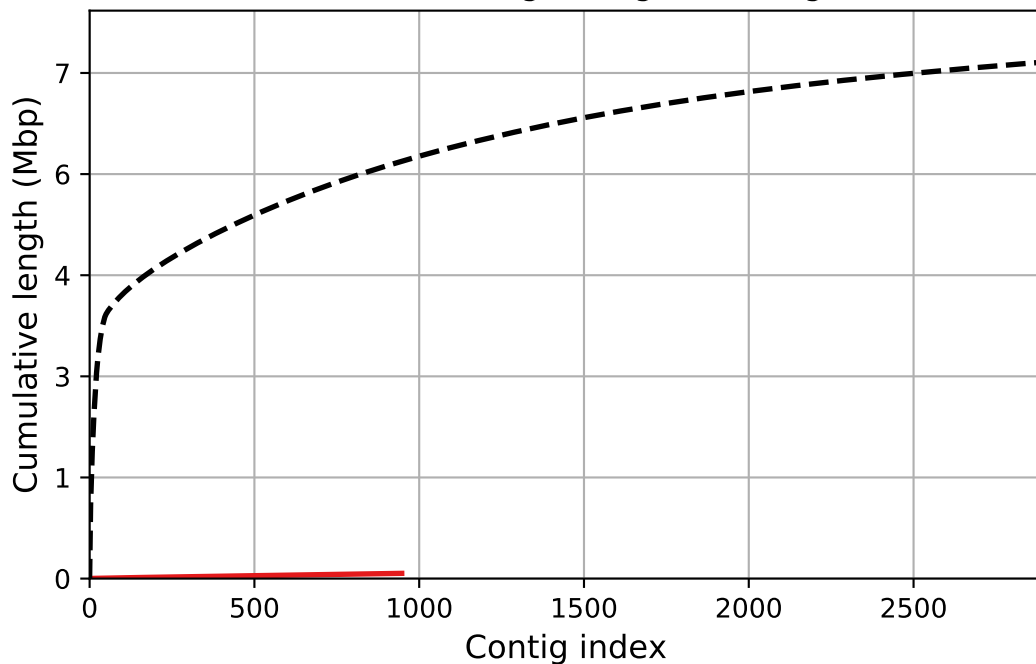
## Misassemblies



FRCurve (misassemblies)

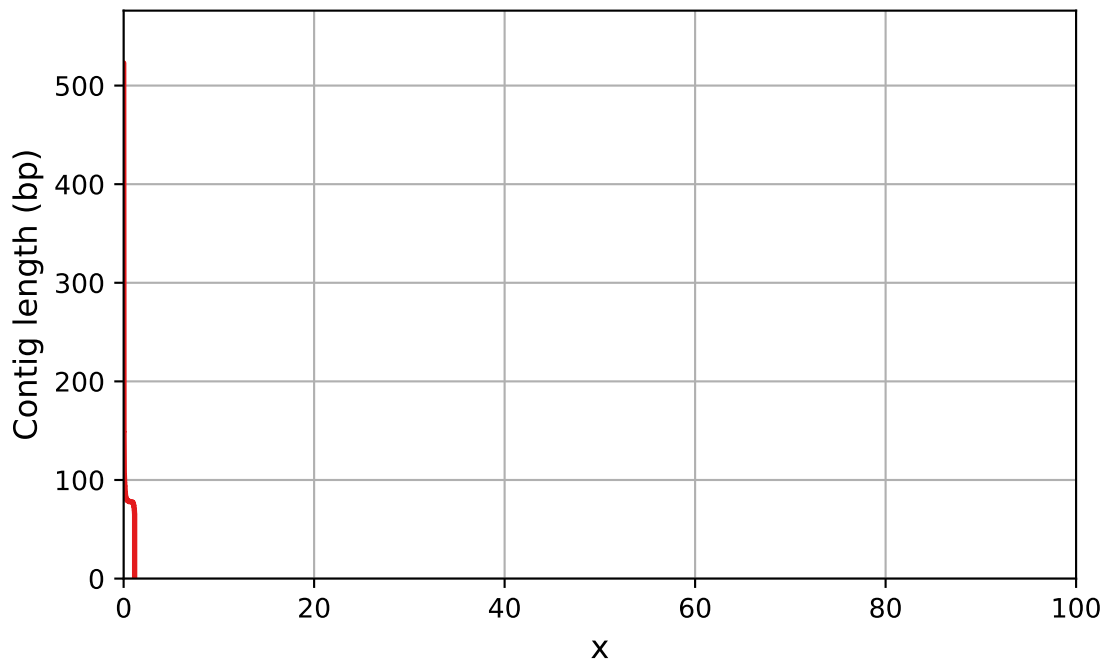


Cumulative length (aligned contigs)



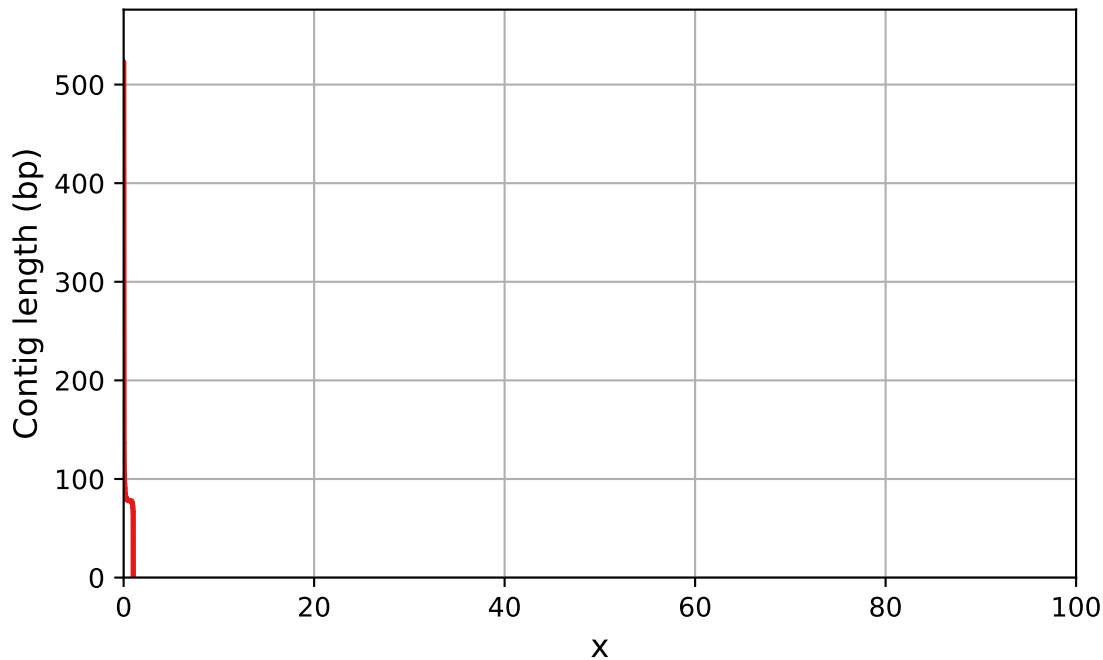
TARA\_PSE\_RAW      Reference

NAx



TARA\_PSE\_RAW

# NGAx



TARA\_PSE\_RAW