

Report

	TARA_PSW_RAW
# contigs (>= 1000 bp)	54
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	439264
Total length (>= 5000 bp)	356217
Total length (>= 10000 bp)	322655
Total length (>= 25000 bp)	289201
Total length (>= 50000 bp)	222419
# contigs	54
Largest contig	222419
Total length	439264
Reference length	3561038
GC (%)	50.36
Reference GC (%)	41.87
N50	222419
N75	8043
L50	1
L75	6
# 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	1
# unaligned contigs	11 + 43 part
Unaligned length	435239
Genome fraction (%)	0.024
Duplication ratio	4.763
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13964.50
# indels per 100 kbp	0.00
Largest alignment	200
Total aligned length	4025
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

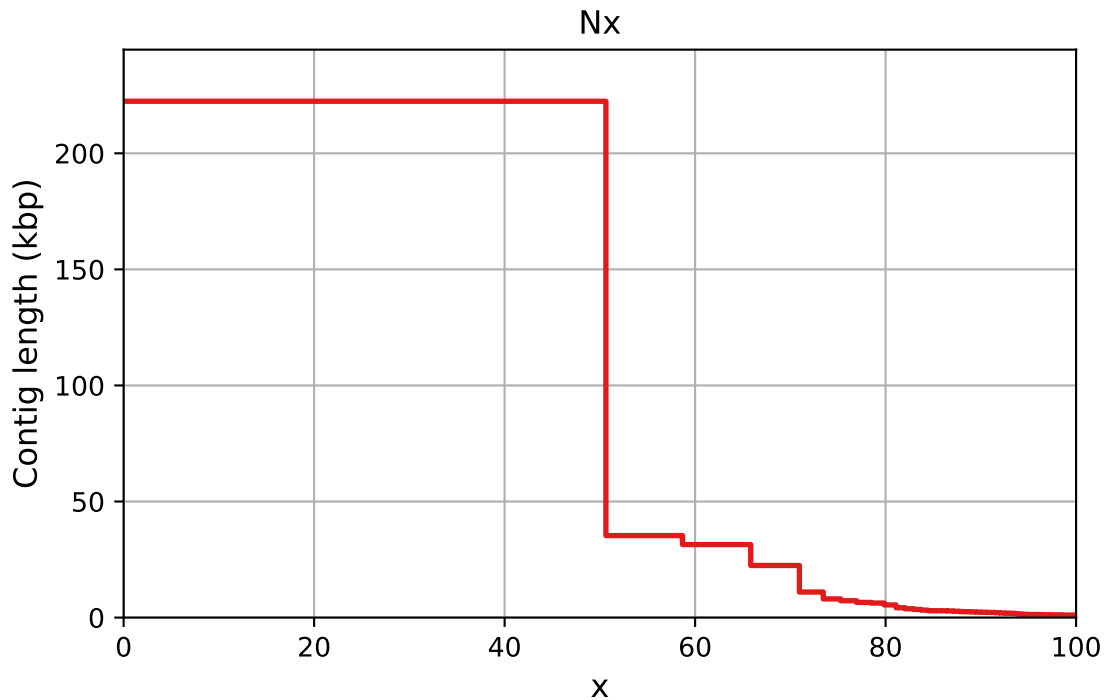
	TARA_PSW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	53
# possible misassemblies	64
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	118
# 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

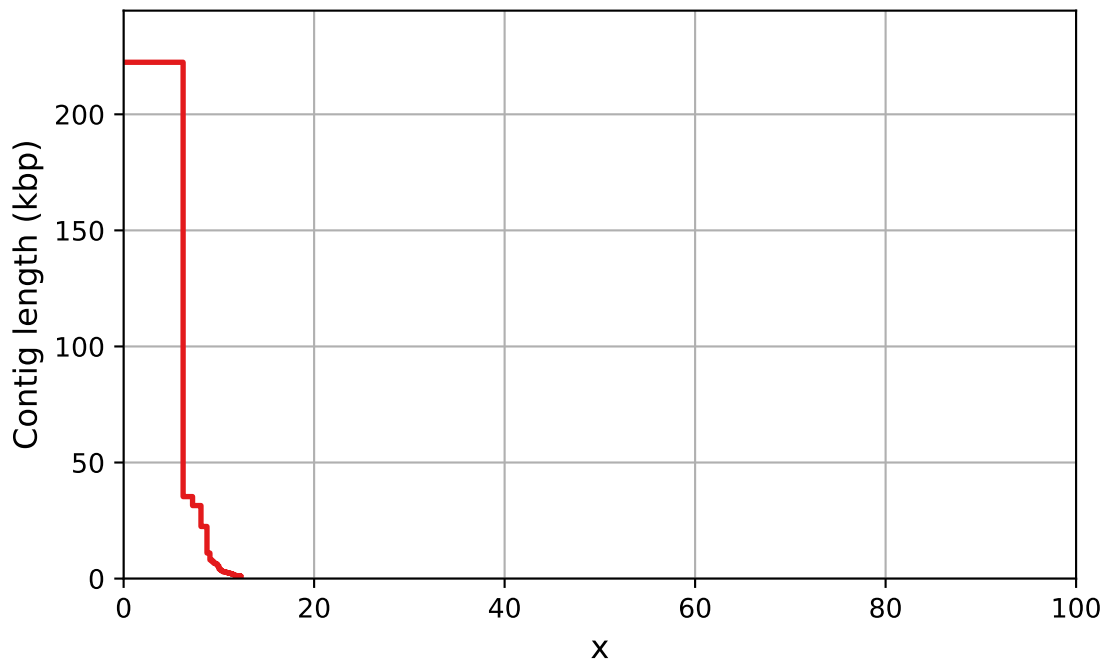
	TARA_PSW_RAW
# fully unaligned contigs	11
Fully unaligned length	249031
# partially unaligned contigs	43
Partially unaligned length	186208
# N's	0

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).

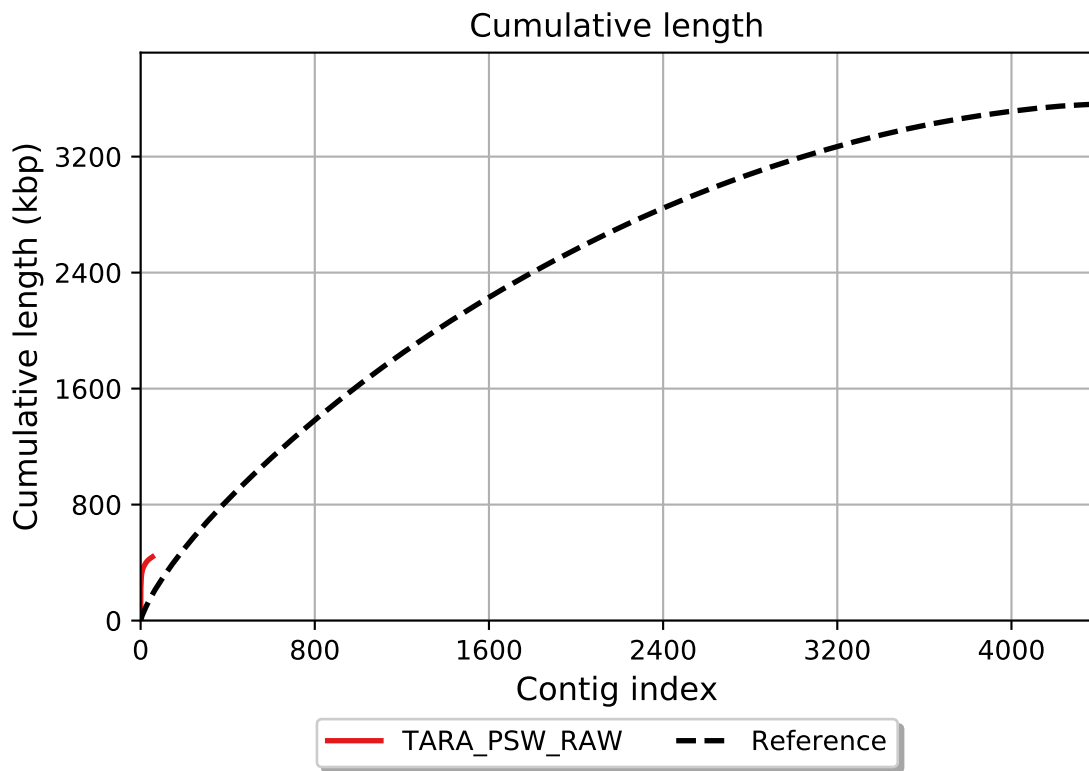


TARA_PSW_RAW

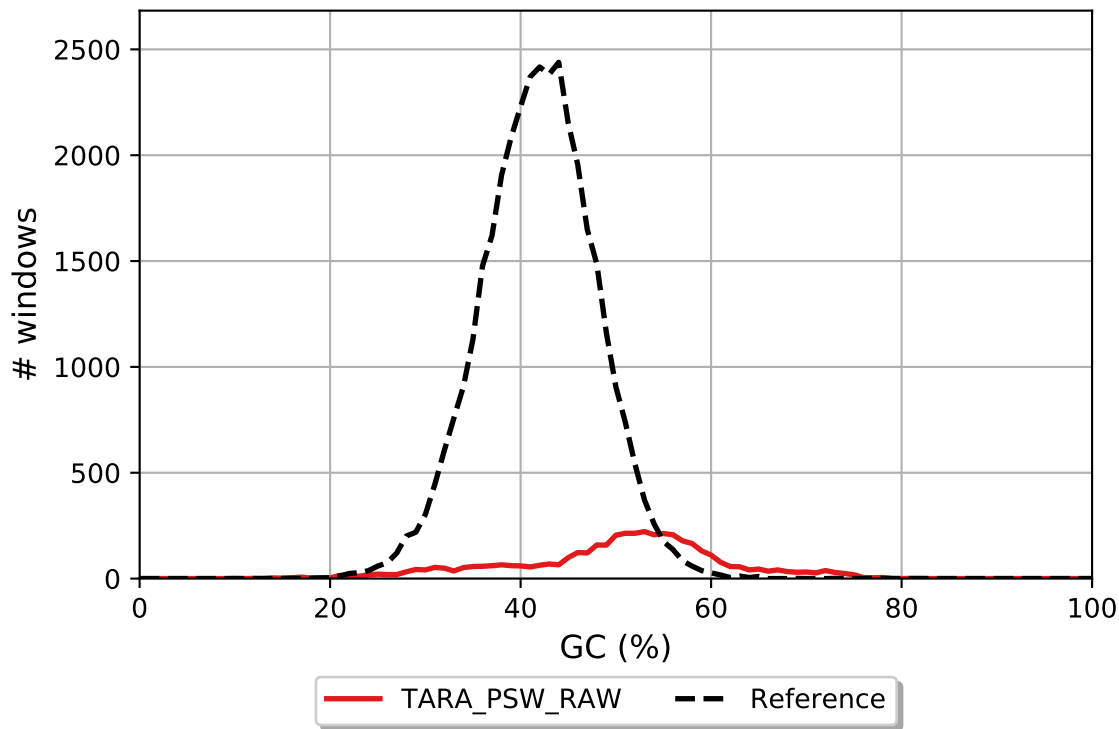
NGx



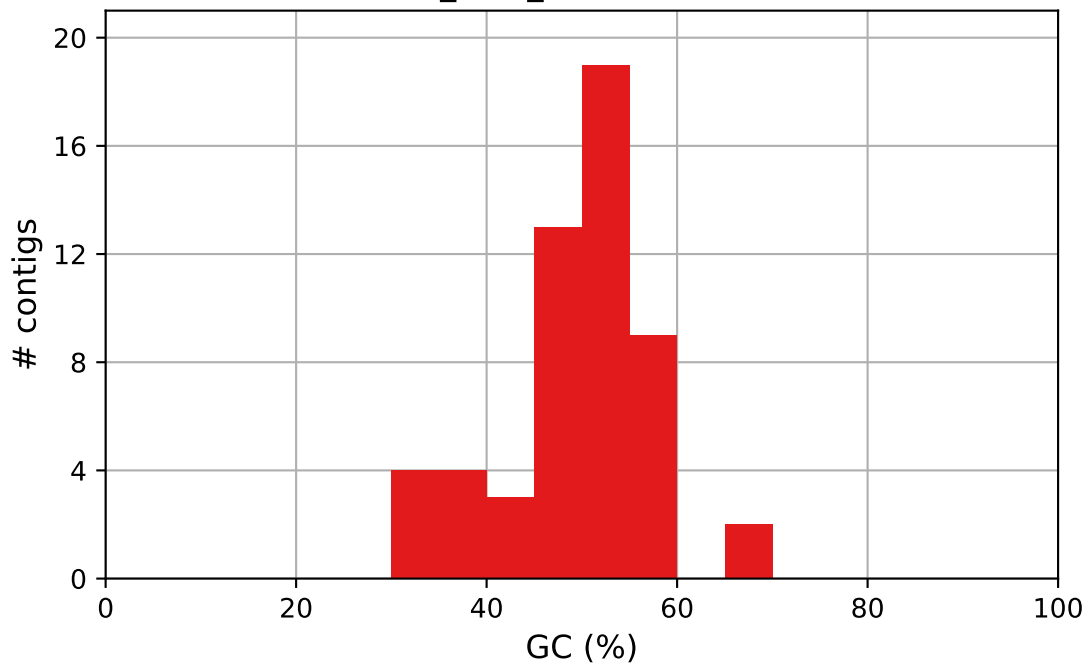
TARA_PSW_RAW



GC content



TARA_PSW_RAW GC content

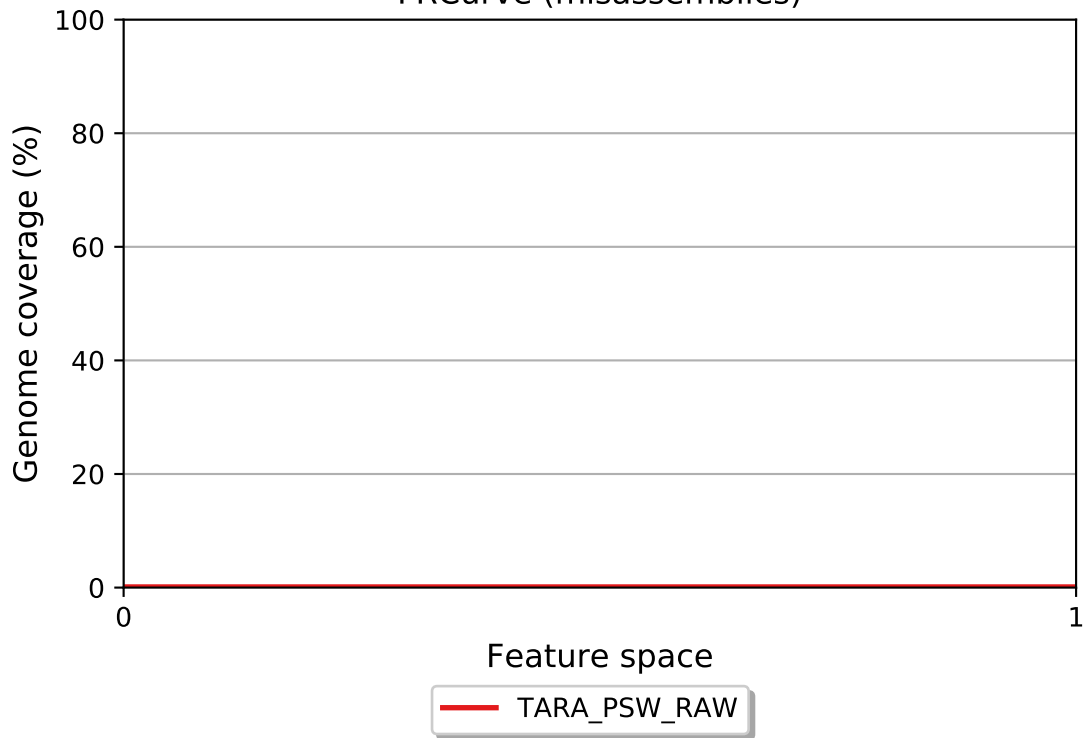


TARA_PSW_RAW

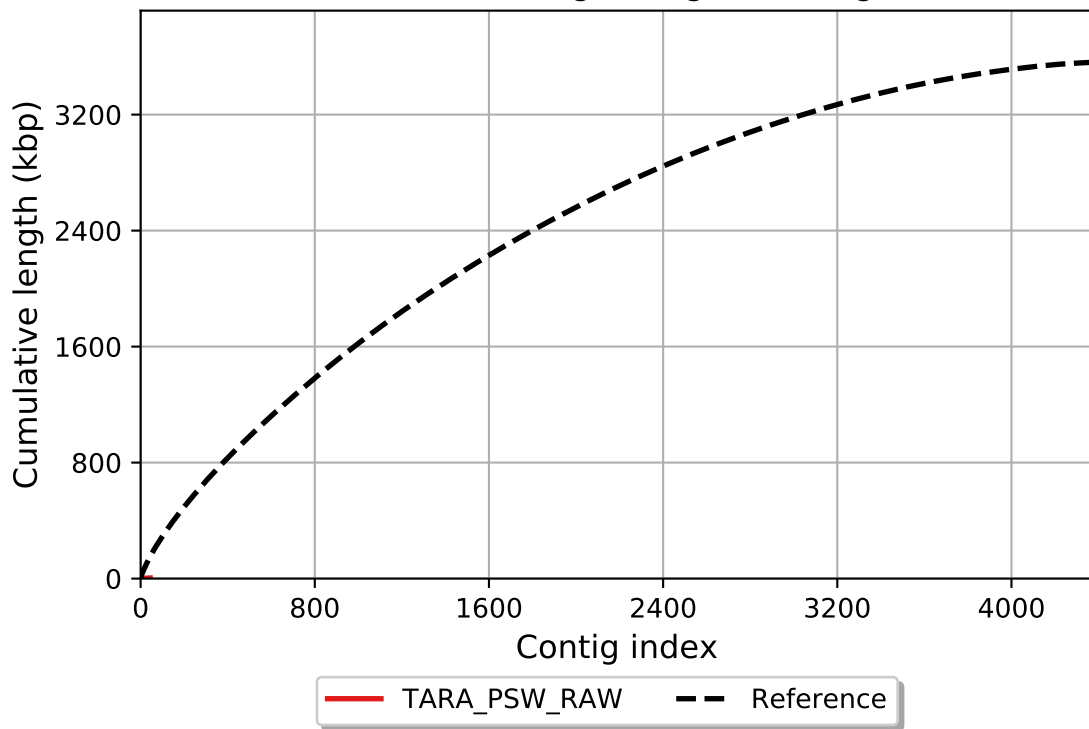
Misassemblies



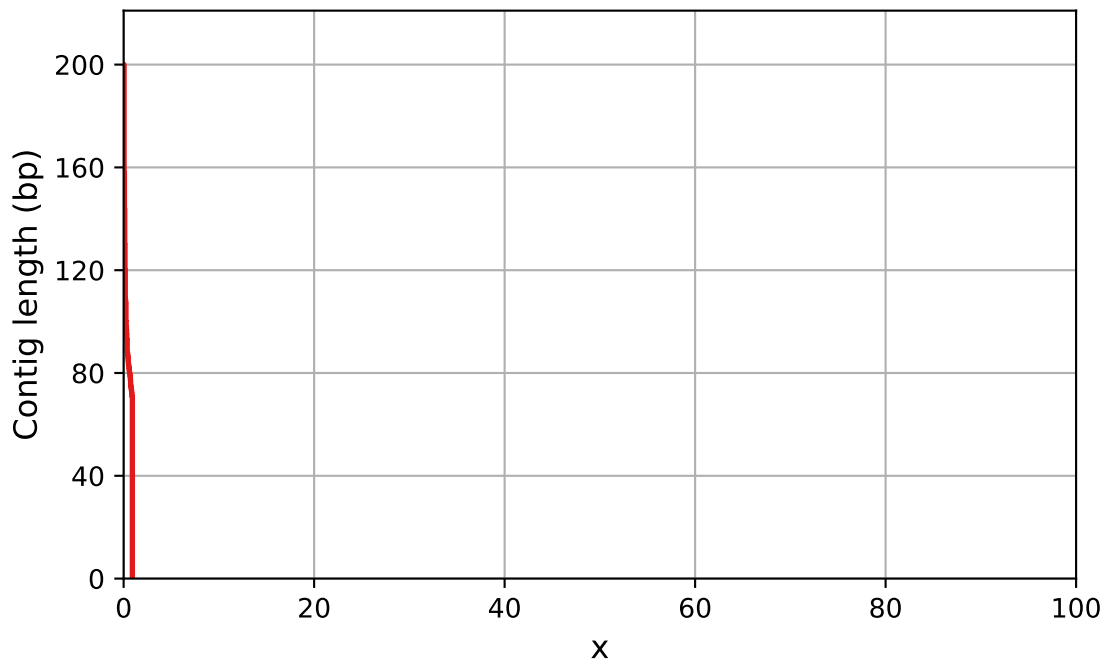
FRCurve (misassemblies)



Cumulative length (aligned contigs)

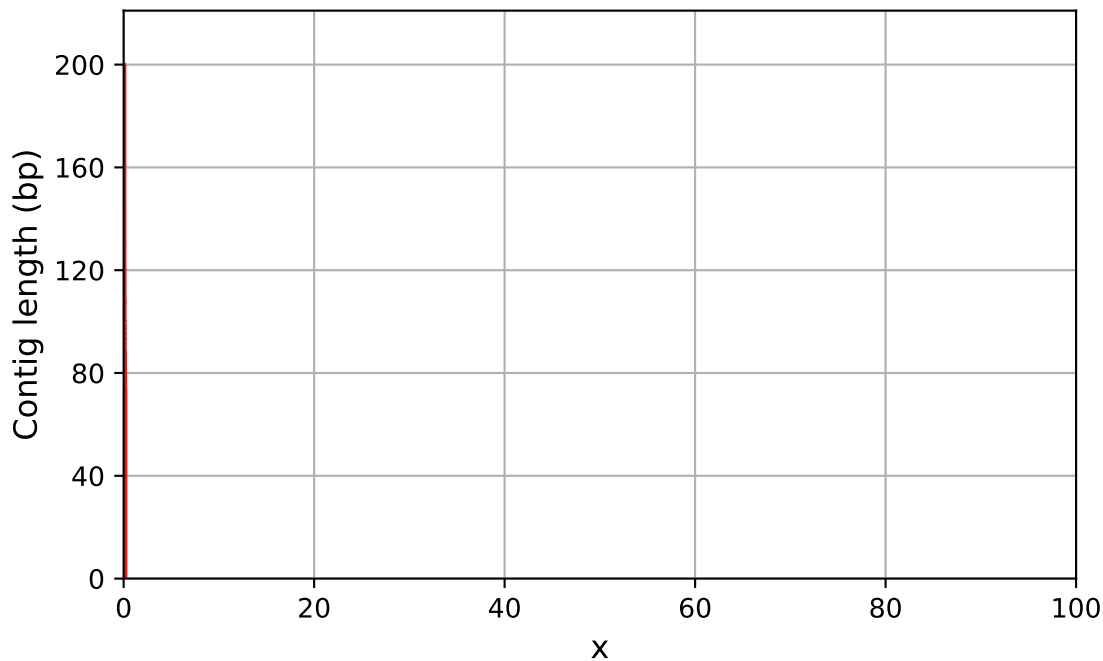


NAx



TARA_PSW_RAW

NGAx



TARA_PSW_RAW