

Report

	TARA_ASE_RAW
# contigs (>= 1000 bp)	146
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	326665
Total length (>= 5000 bp)	85069
Total length (>= 10000 bp)	40117
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	146
Largest contig	14515
Total length	326665
Reference length	7658814
GC (%)	42.97
Reference GC (%)	63.29
N50	2404
N75	1504
L50	36
L75	79
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	5552
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	5 + 141 part
Unaligned length	311981
Genome fraction (%)	0.083
Duplication ratio	2.303
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4831.37
# indels per 100 kbp	62.75
Largest alignment	1795
Total aligned length	14684
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_ASE_RAW
# misassemblies	2
# contig misassemblies	2
# c. relocations	0
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	5552
# possibly misassembled contigs	141
# possible misassemblies	158
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	308
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	6

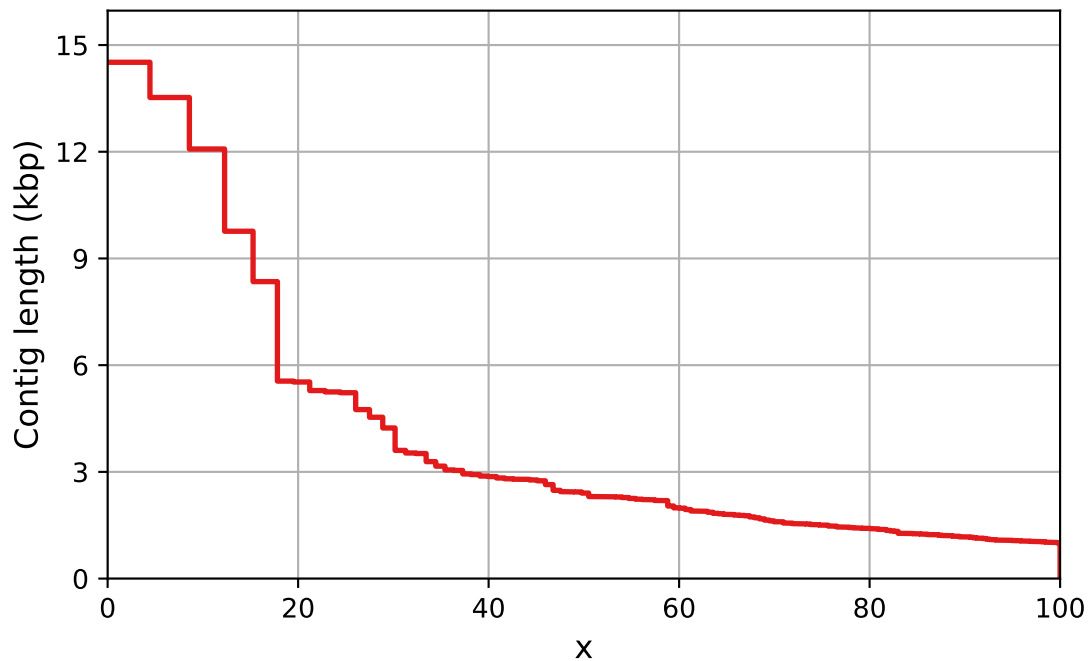
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	5
Fully unaligned length	9073
# partially unaligned contigs	141
Partially unaligned length	302908
# N's	0

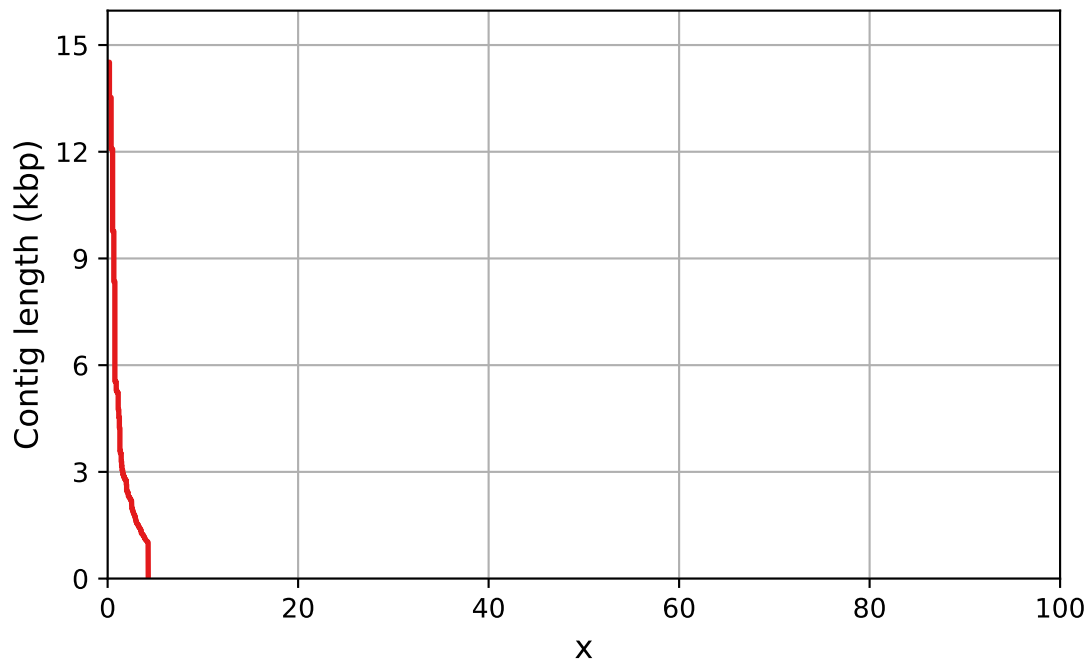
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



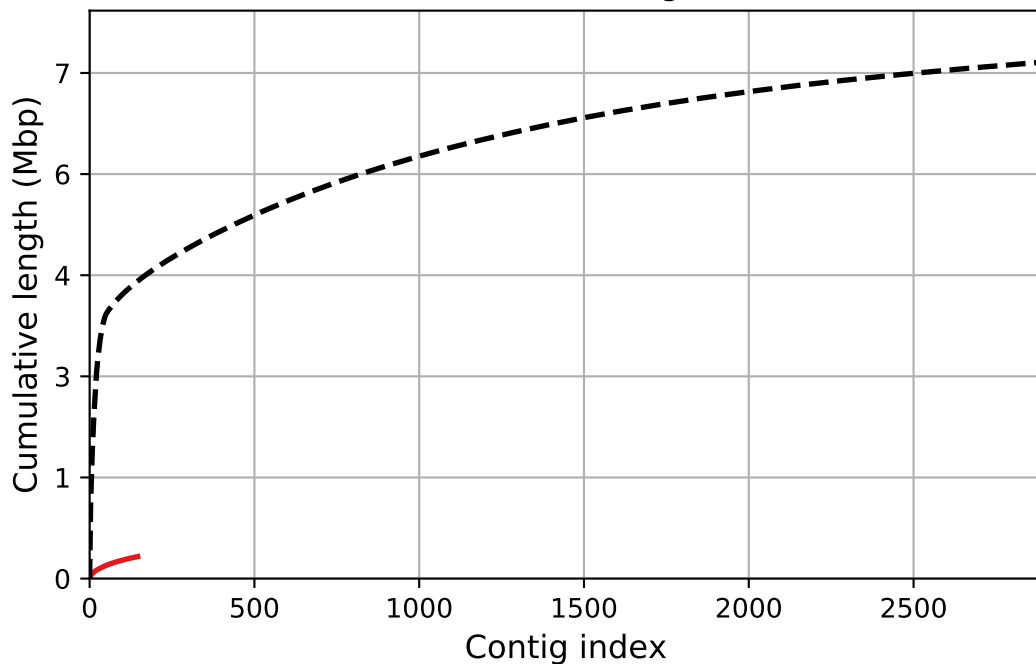
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NGx



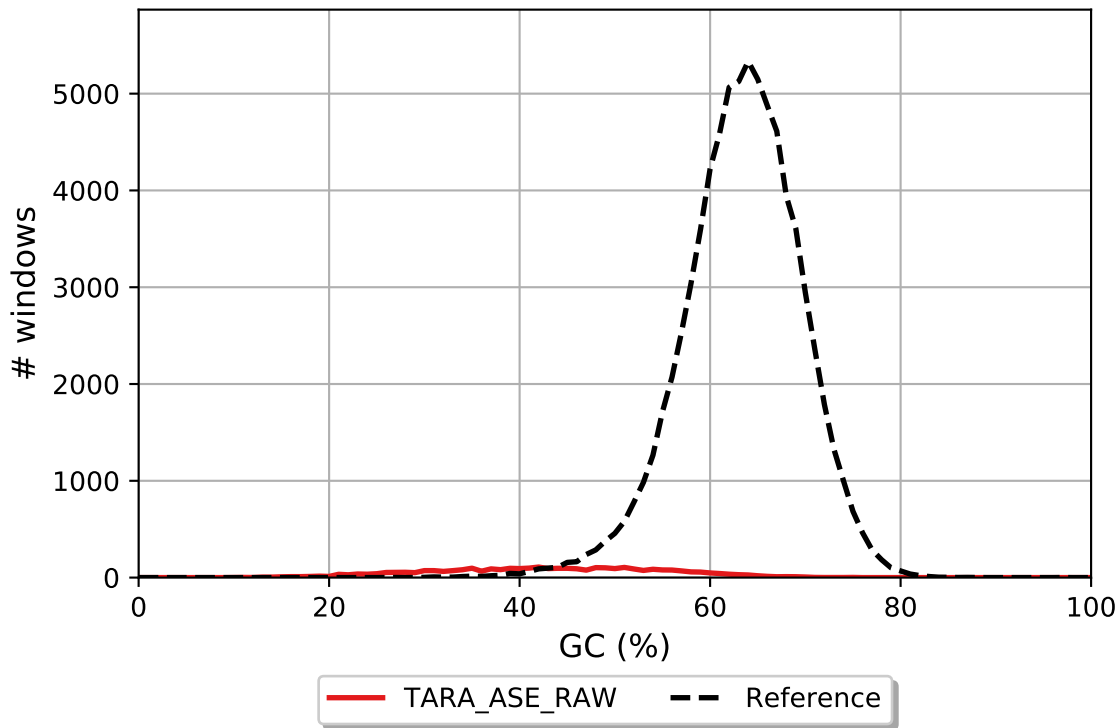
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Cumulative length

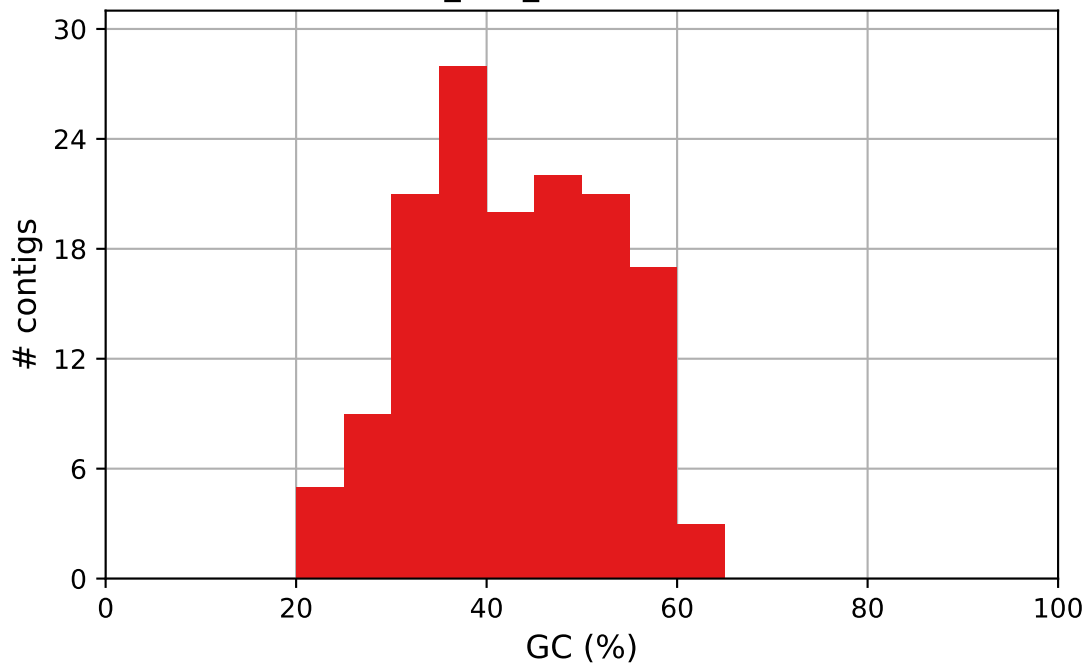


TARA_ASE_RAW Reference

GC content

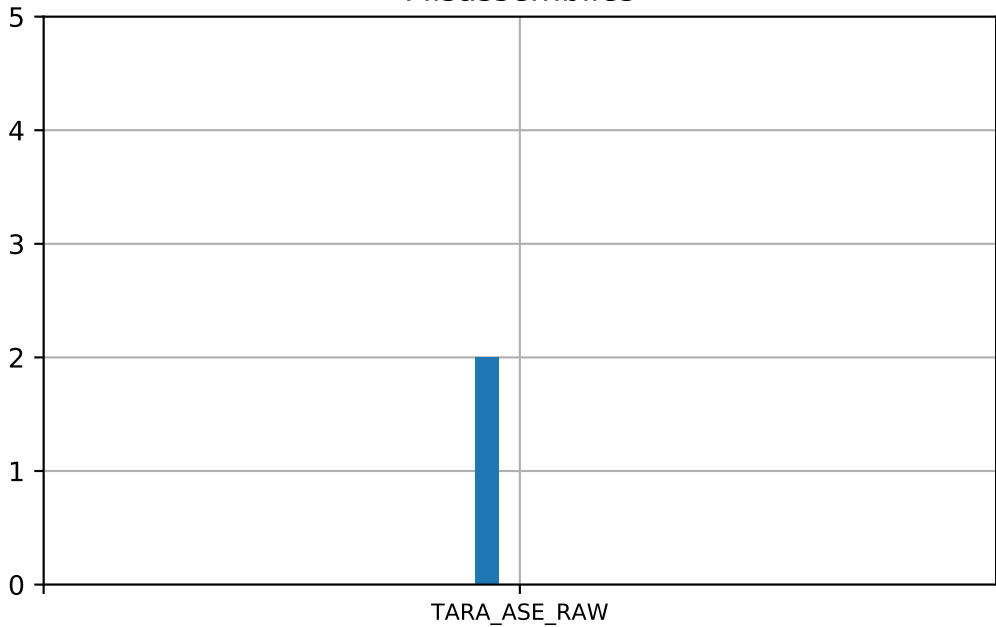


TARA_ASE_RAW GC content



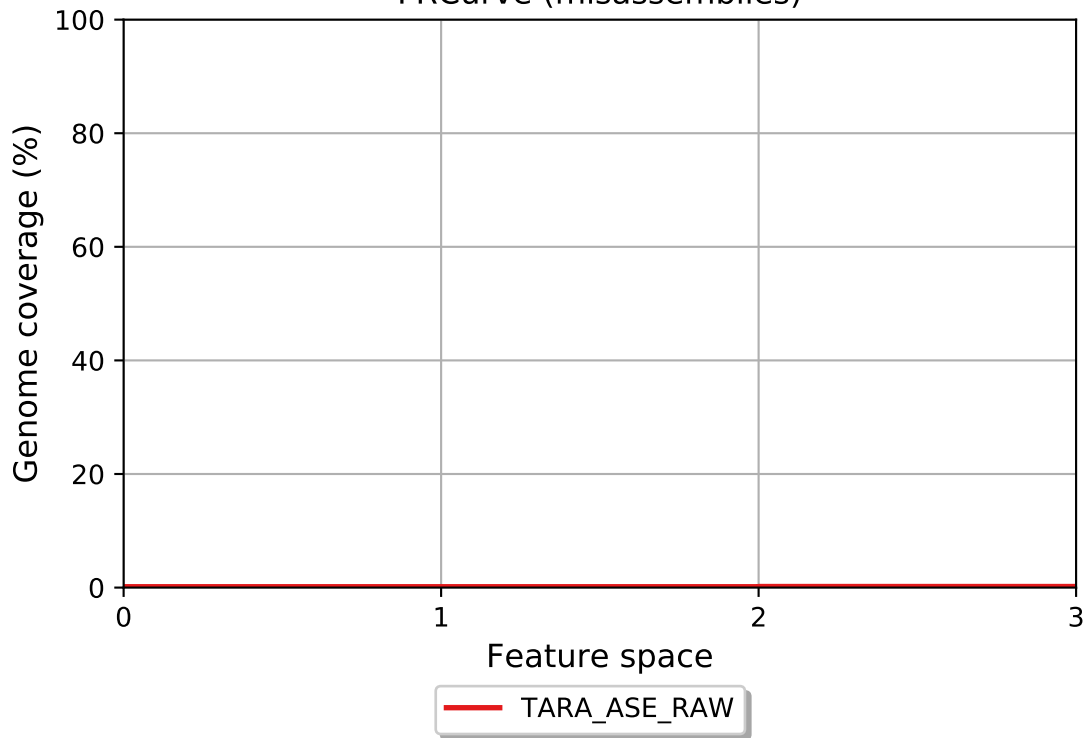
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Misassemblies

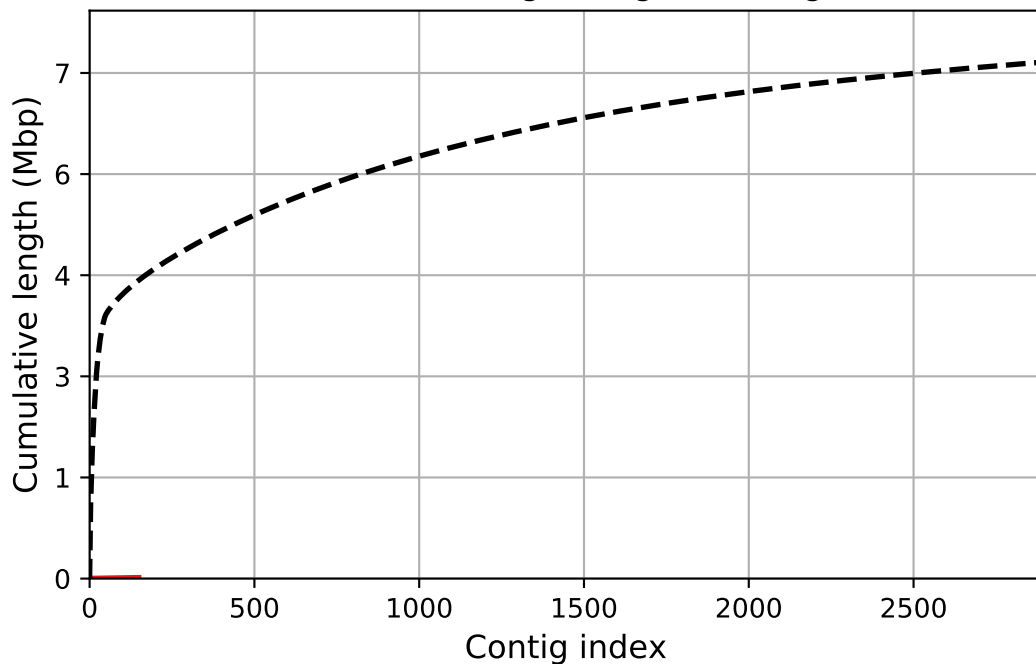


 # translocations

FRCurve (misassemblies)

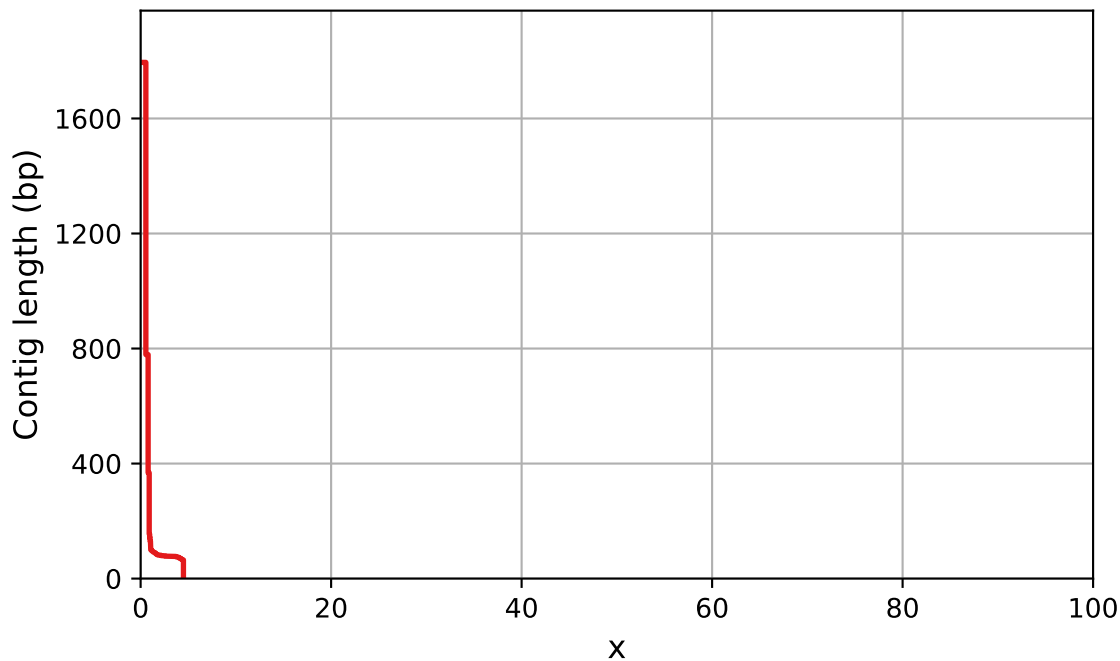


Cumulative length (aligned contigs)



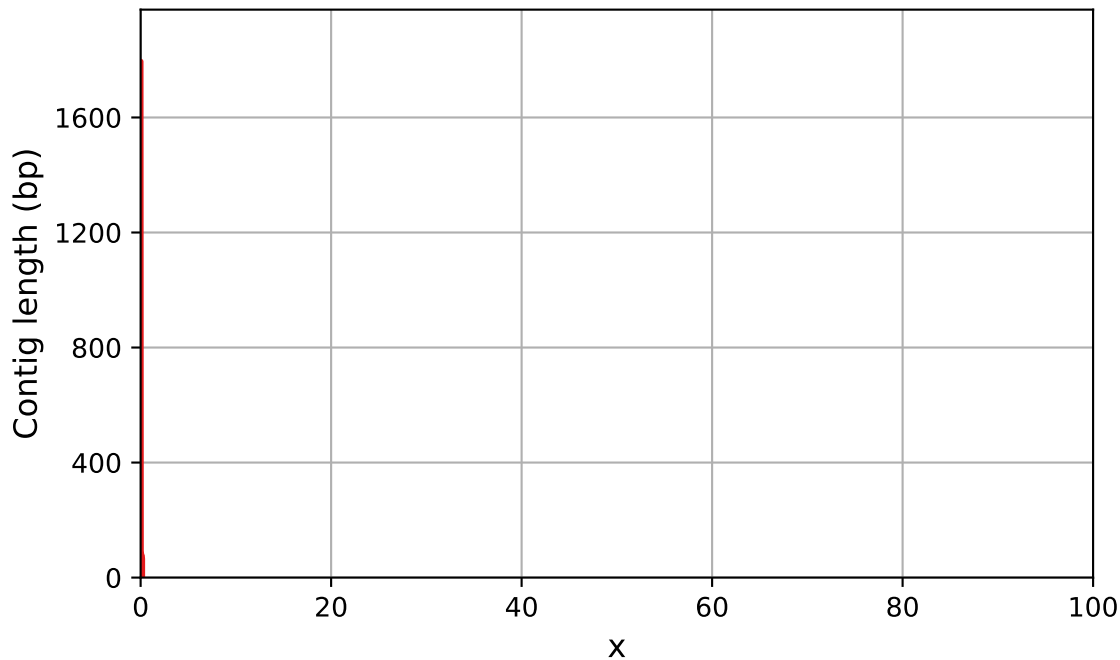
— TARA_ASE_RAW - - Reference

NAx



TARA_ASE_RAW

NGAx



TARA_ASE_RAW