

Report

	TARA_SOC_RAW
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	610754
Total length (>= 5000 bp)	407931
Total length (>= 10000 bp)	356788
Total length (>= 25000 bp)	278308
Total length (>= 50000 bp)	122423
# contigs	107
Largest contig	63887
Total length	610754
Reference length	5854900
GC (%)	33.34
Reference GC (%)	63.53
N50	15901
N75	3933
L50	8
L75	31
# 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	5 + 102 part
Unaligned length	602230
Genome fraction (%)	0.045
Duplication ratio	3.256
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6569.90
# indels per 100 kbp	0.00
Largest alignment	266
Total aligned length	8524
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_SOC_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	104
# possible misassemblies	130
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	172
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

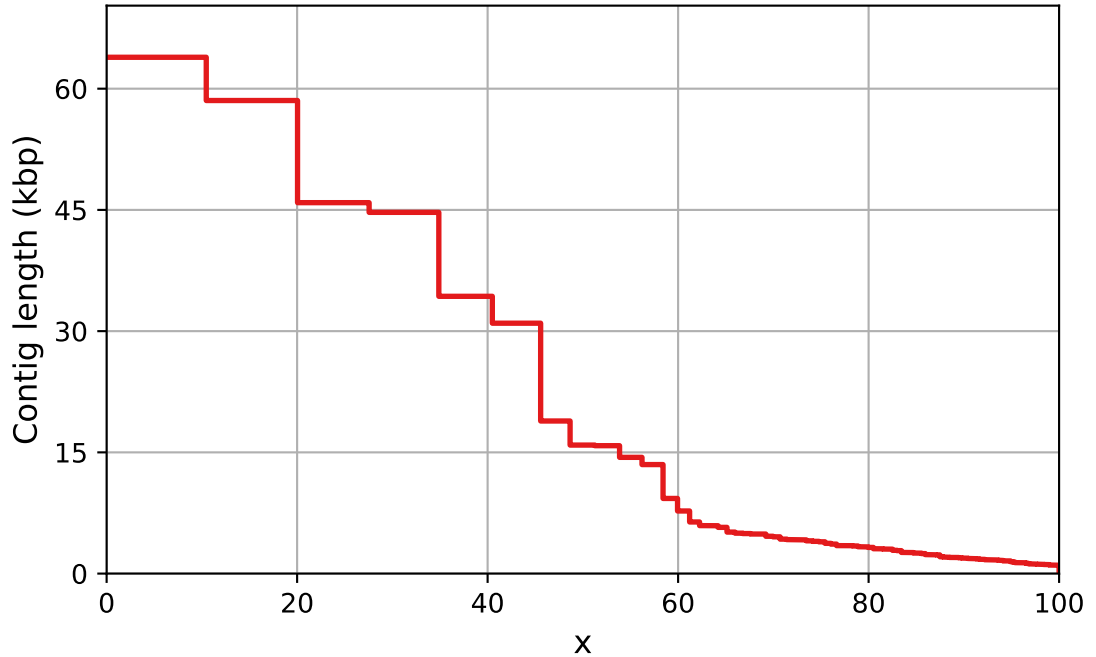
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_SOC_RAW
# fully unaligned contigs	5
Fully unaligned length	16057
# partially unaligned contigs	102
Partially unaligned length	586173
# N's	0

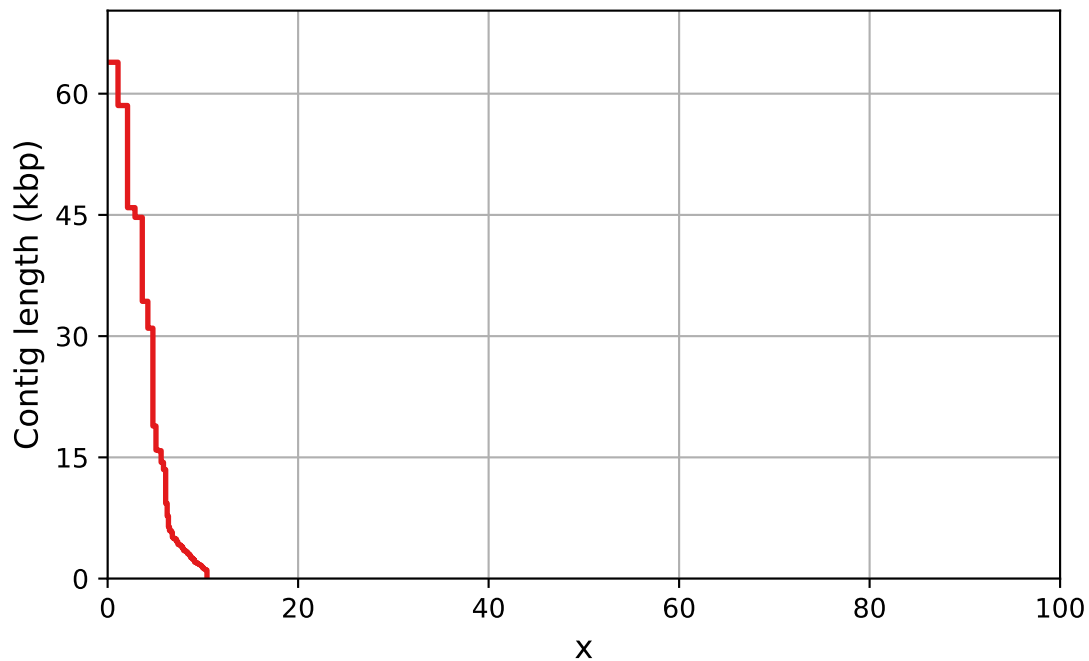
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



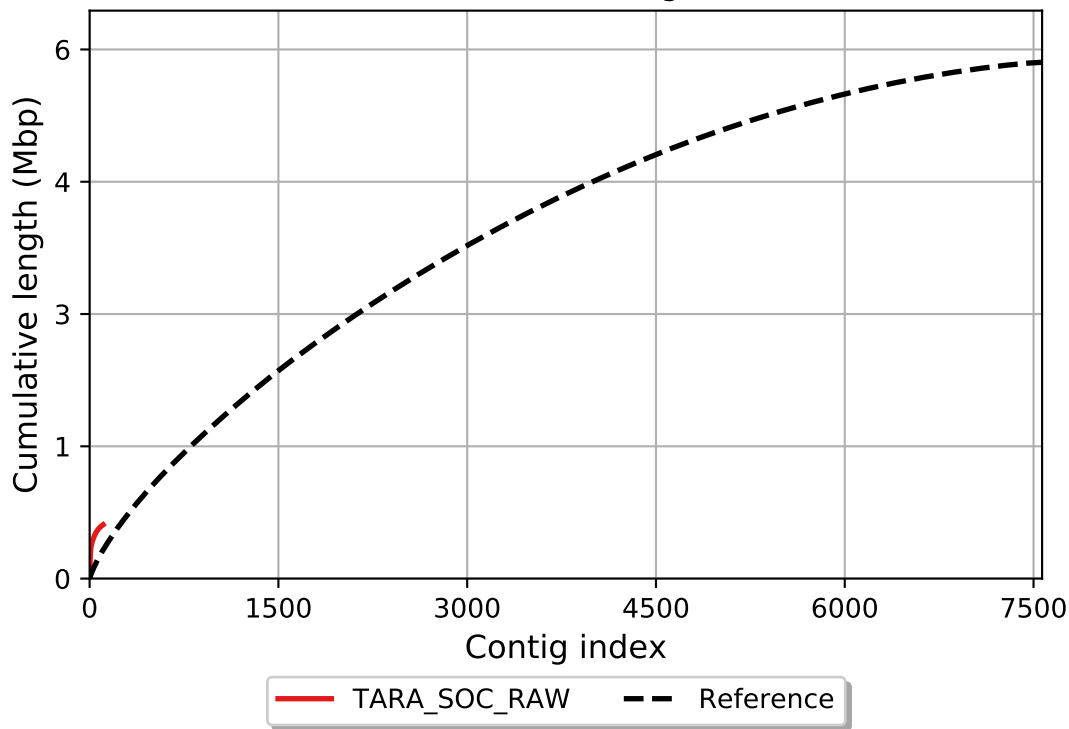
TARA_SOC_RAW

NGx

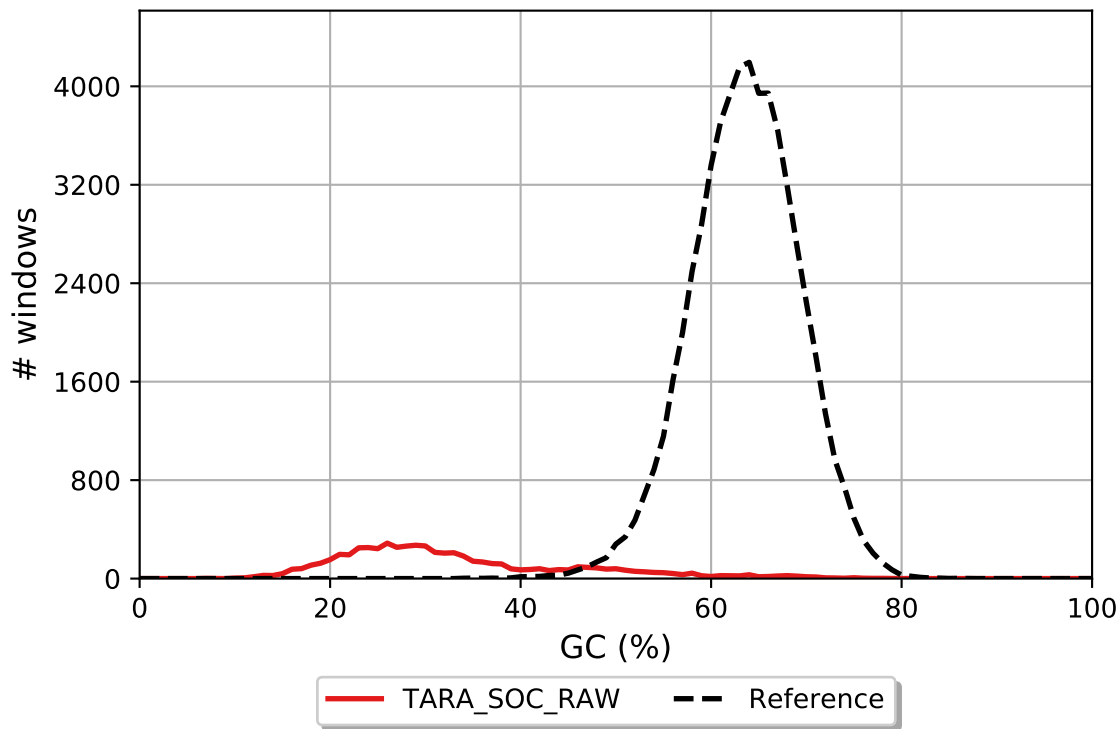


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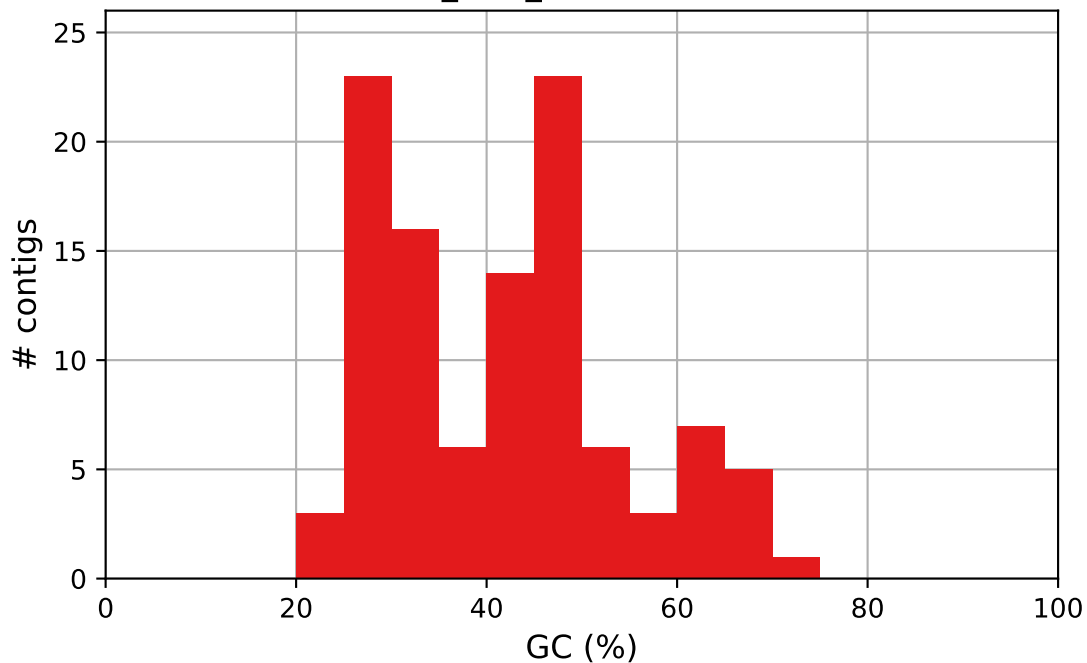
Cumulative length



GC content

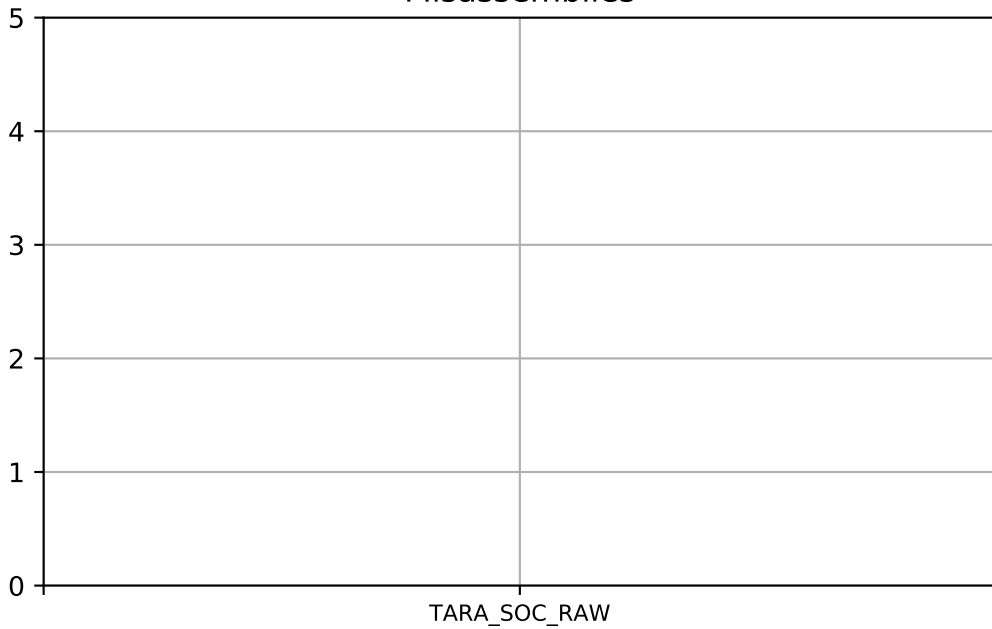


TARA_SOC_RAW GC content

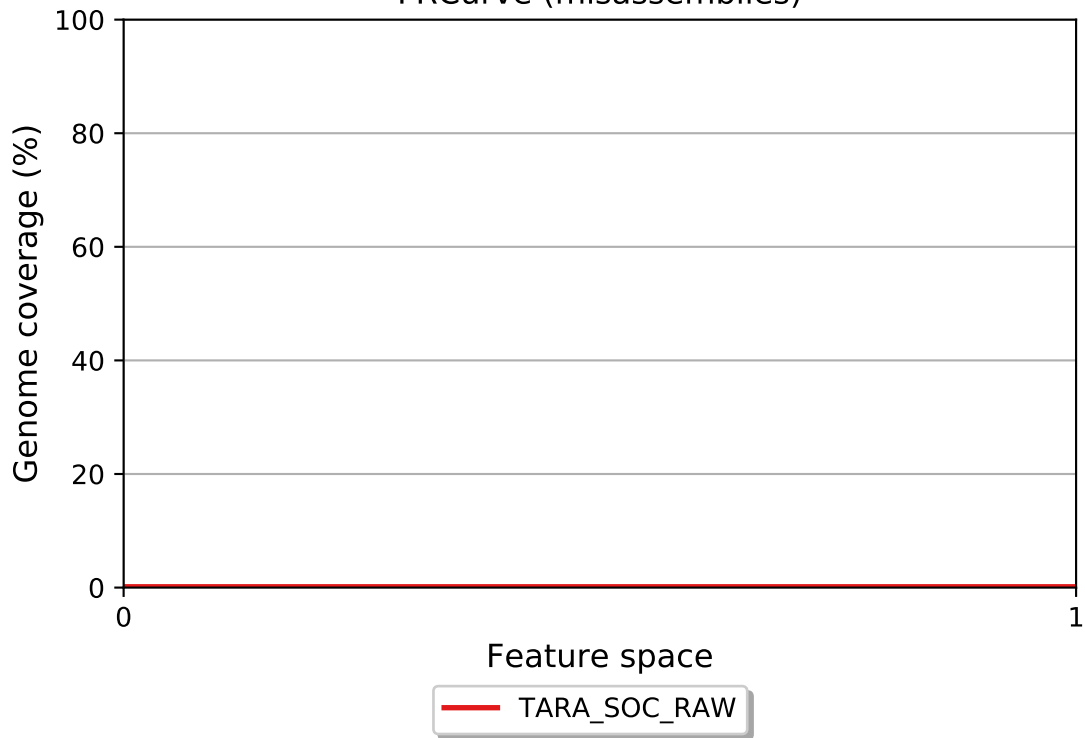


TARA_SOC_RAW

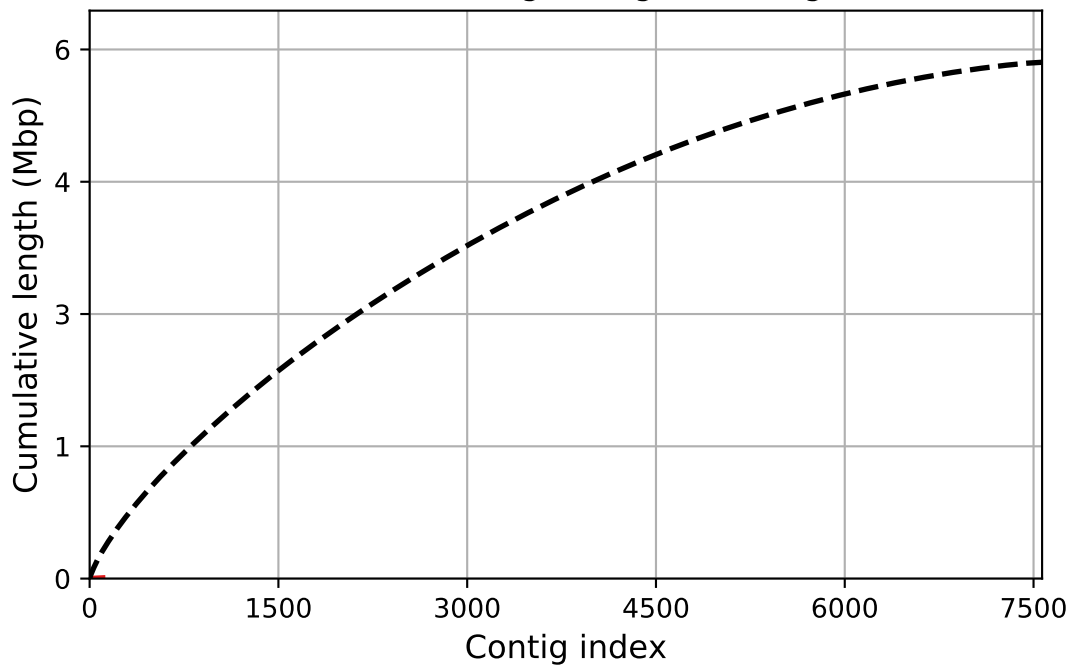
Misassemblies



FRCurve (misassemblies)

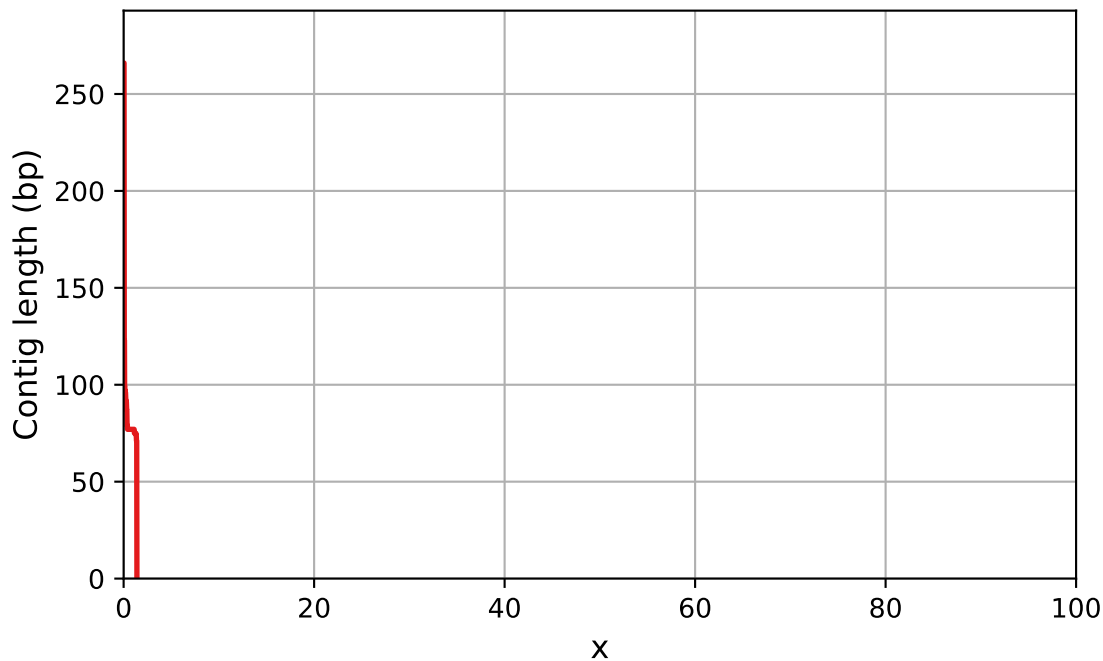


Cumulative length (aligned contigs)



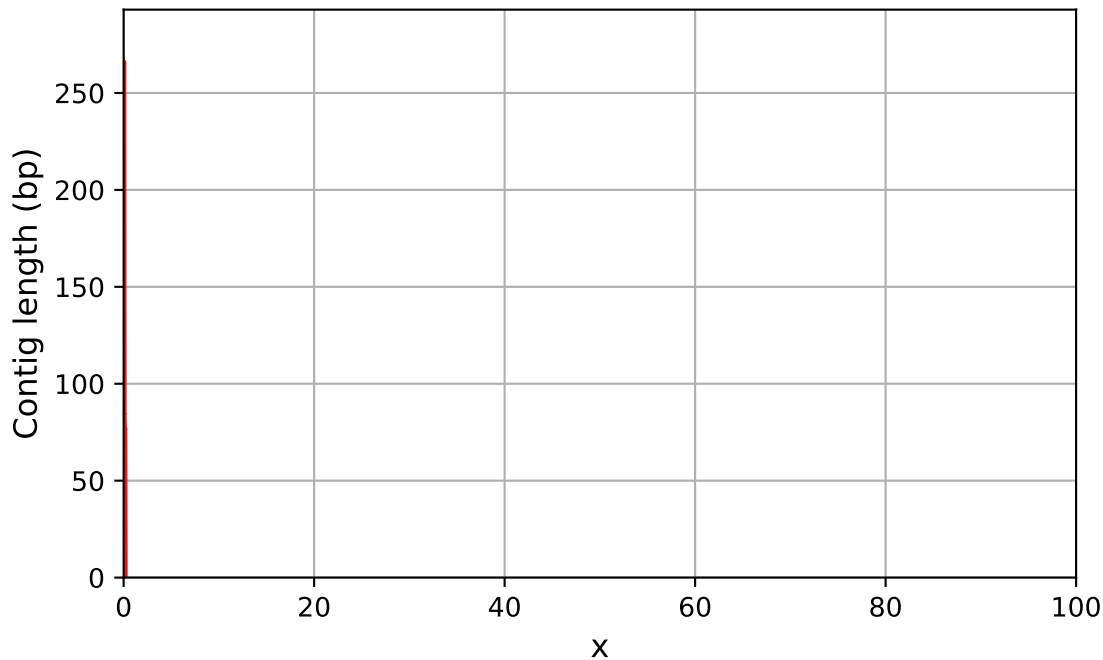
— TARA_SOC_RAW - - Reference

NAx



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NGAx



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