

Report

	TARA_RED_RAW
# contigs (>= 1000 bp)	272
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	34
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	11
Total length (>= 1000 bp)	3735593
Total length (>= 5000 bp)	3296265
Total length (>= 10000 bp)	3147012
Total length (>= 25000 bp)	2861032
Total length (>= 50000 bp)	2687904
# contigs	272
Largest contig	811431
Total length	3735593
Reference length	7658814
GC (%)	48.89
Reference GC (%)	63.29
N50	527714
N75	34206
L50	3
L75	14
# 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	8 + 264 part
Unaligned length	3714032
Genome fraction (%)	0.042
Duplication ratio	6.782
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13180.25
# indels per 100 kbp	0.00
Largest alignment	125
Total aligned length	21561
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

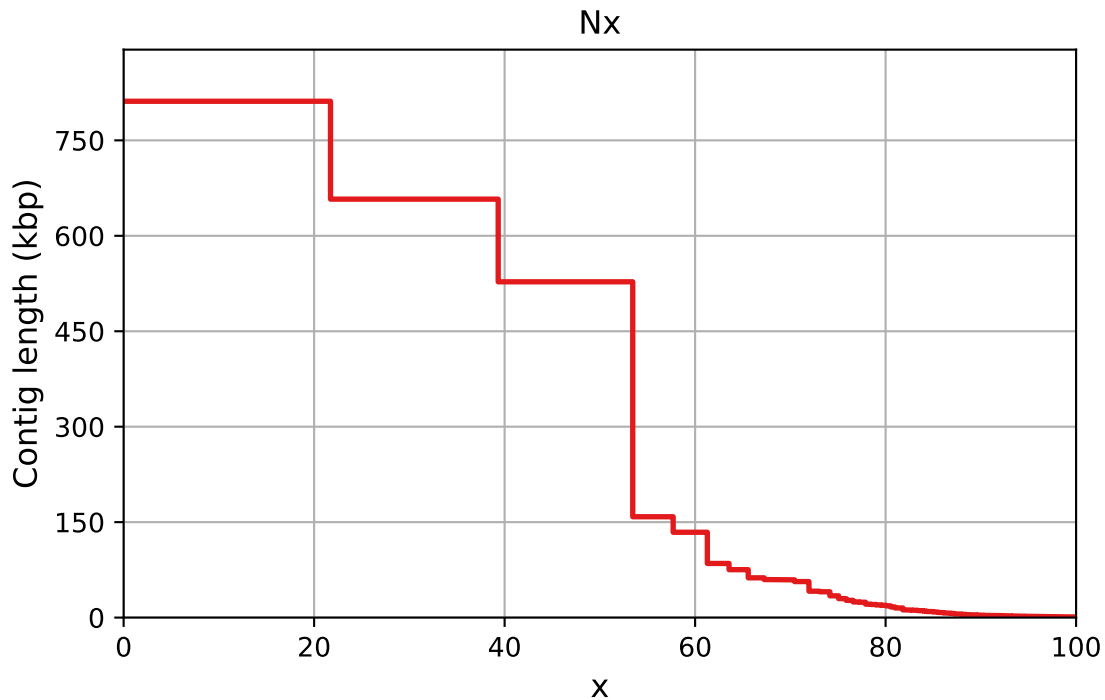
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	269
# possible misassemblies	333
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	419
# 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

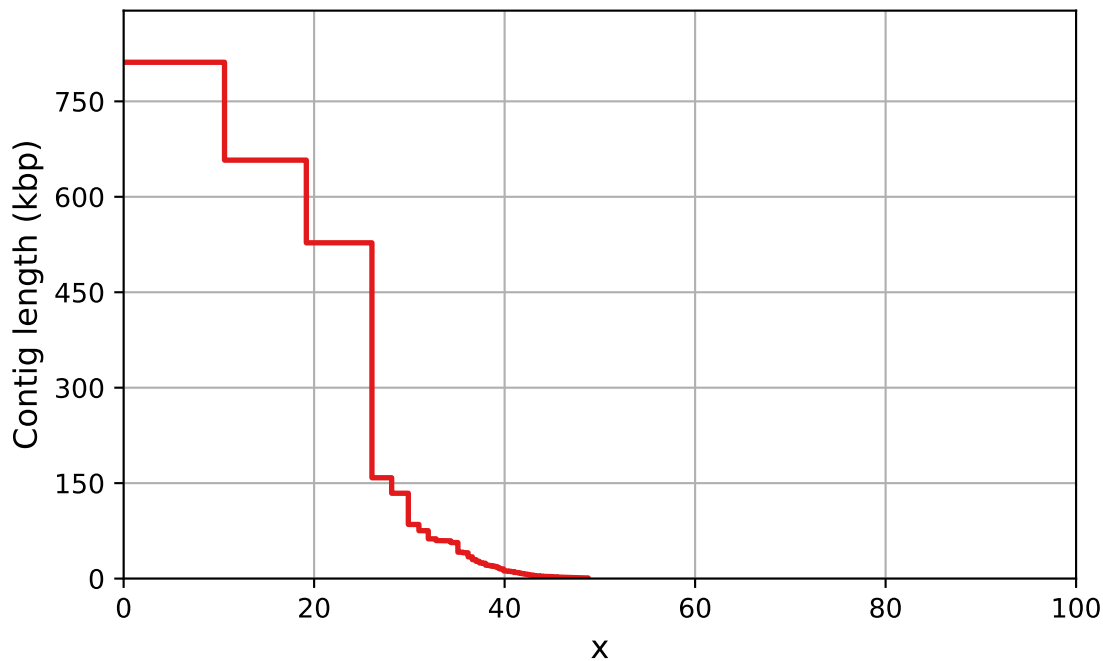
	TARA_RED_RAW
# fully unaligned contigs	8
Fully unaligned length	22109
# partially unaligned contigs	264
Partially unaligned length	3691923
# N's	0

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).



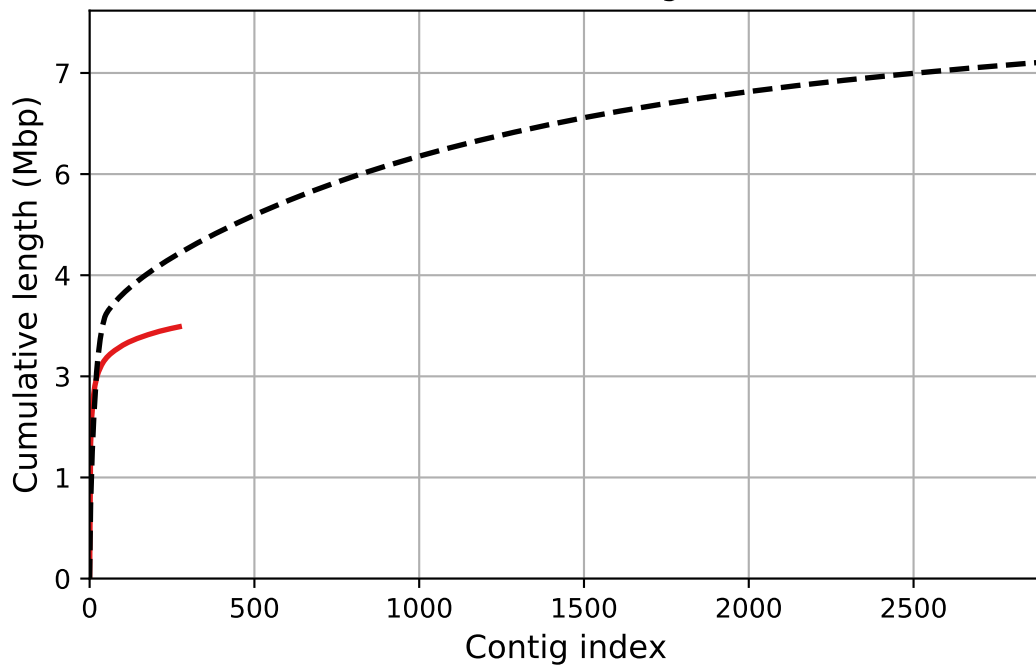
— TARA_RED_RAW

NGx



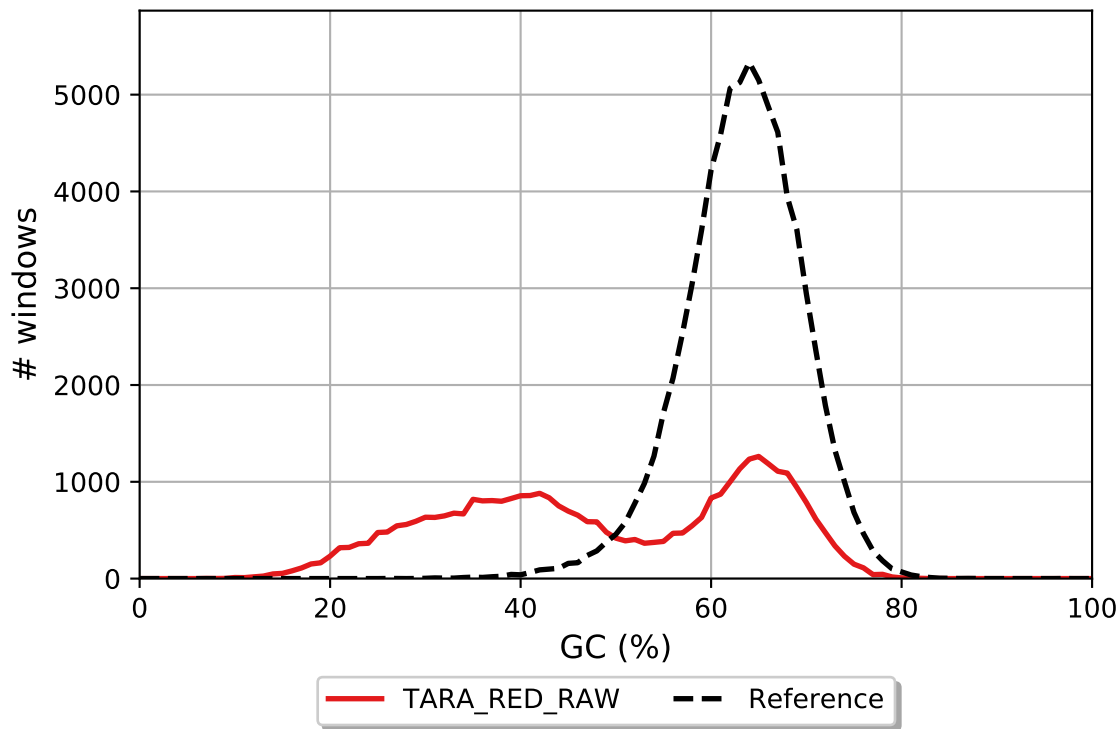
TARA_RED_RAW

Cumulative length

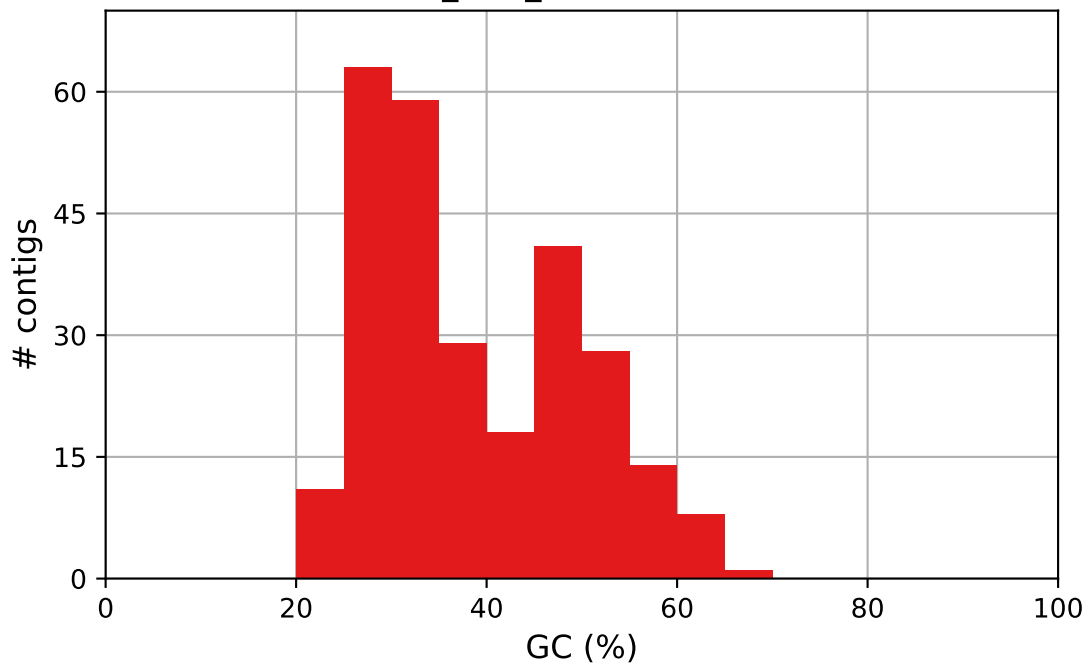


— TARA_RED_RAW - - Reference

GC content



TARA_RED_RAW GC content



TARA_RED_RAW

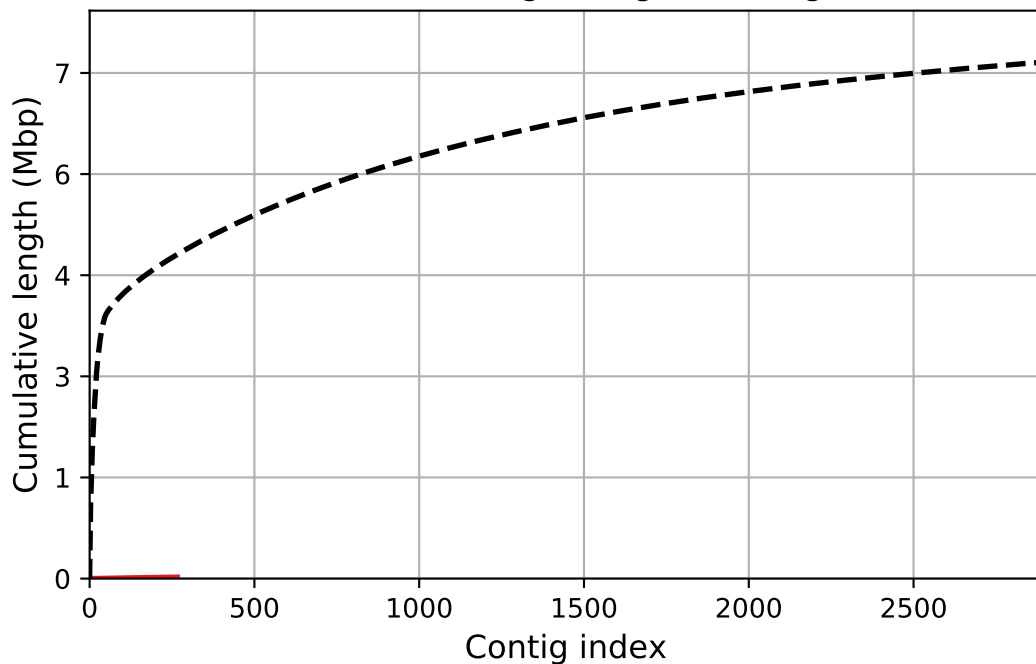
Misassemblies



FRCurve (misassemblies)

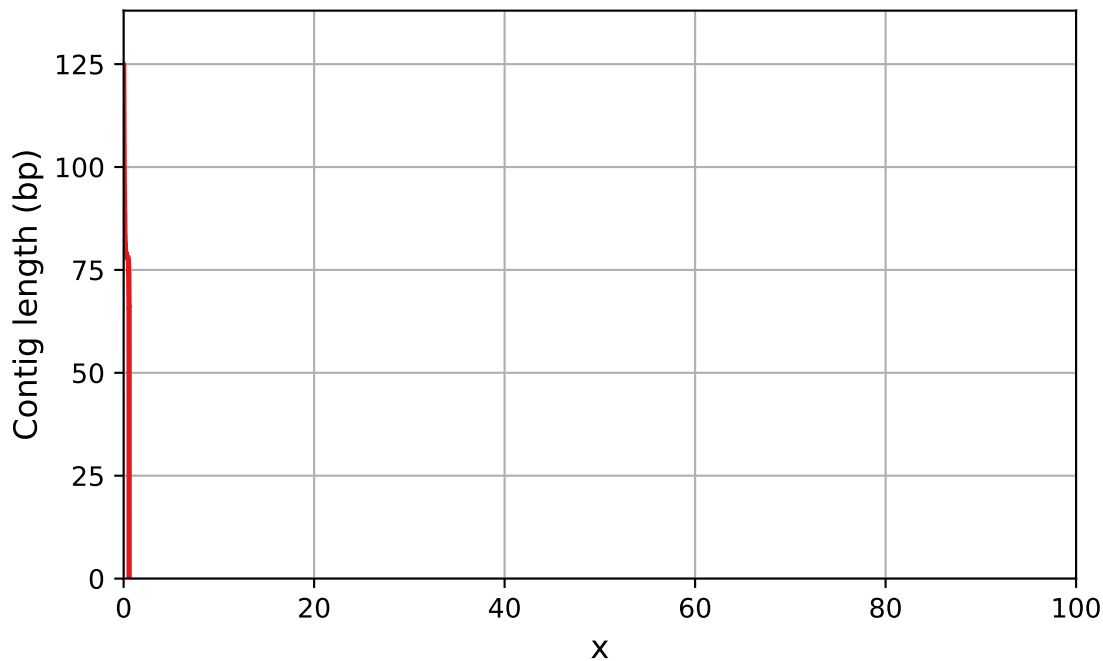


Cumulative length (aligned contigs)



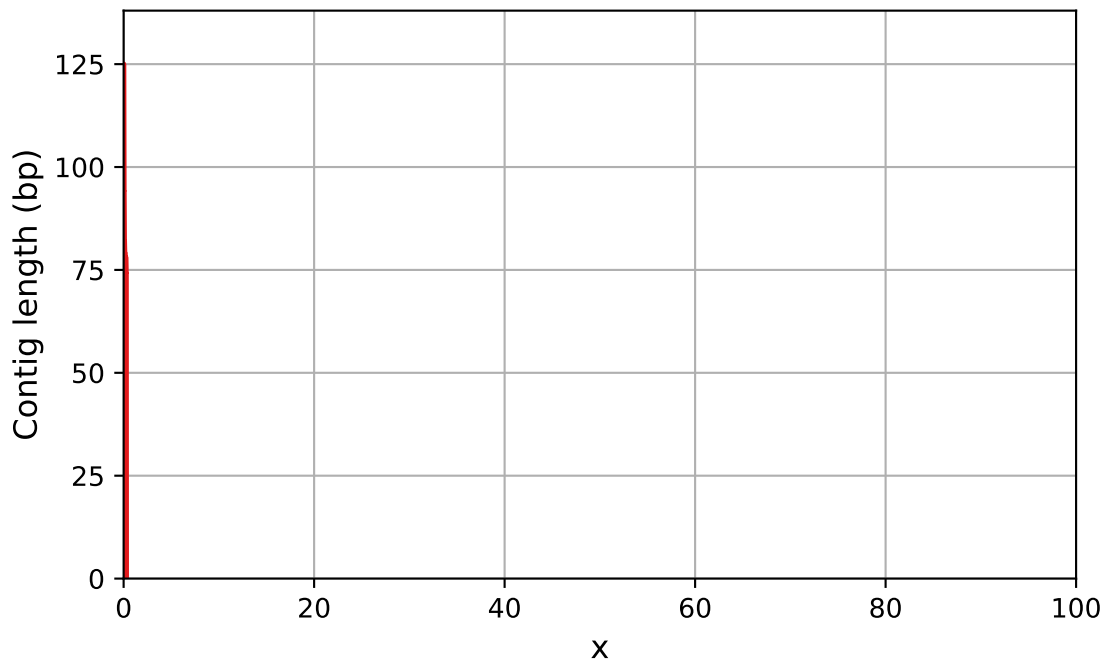
— TARA_RED_RAW - - Reference

NAx



TARA_RED_RAW

NGAx



TARA_RED_RAW