

Report

	TARA_MED_RAW
# contigs (>= 1000 bp)	41
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	102976
Total length (>= 5000 bp)	16947
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	41
Largest contig	5751
Total length	102976
Reference length	4234461
GC (%)	48.05
Reference GC (%)	41.03
N50	3025
N75	2005
L50	13
L75	23
# 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	3
# unaligned contigs	3 + 38 part
Unaligned length	99331
Genome fraction (%)	0.028
Duplication ratio	3.129
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8583.69
# indels per 100 kbp	0.00
Largest alignment	174
Total aligned length	3645
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_MED_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	38
# possible misassemblies	45
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	100
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

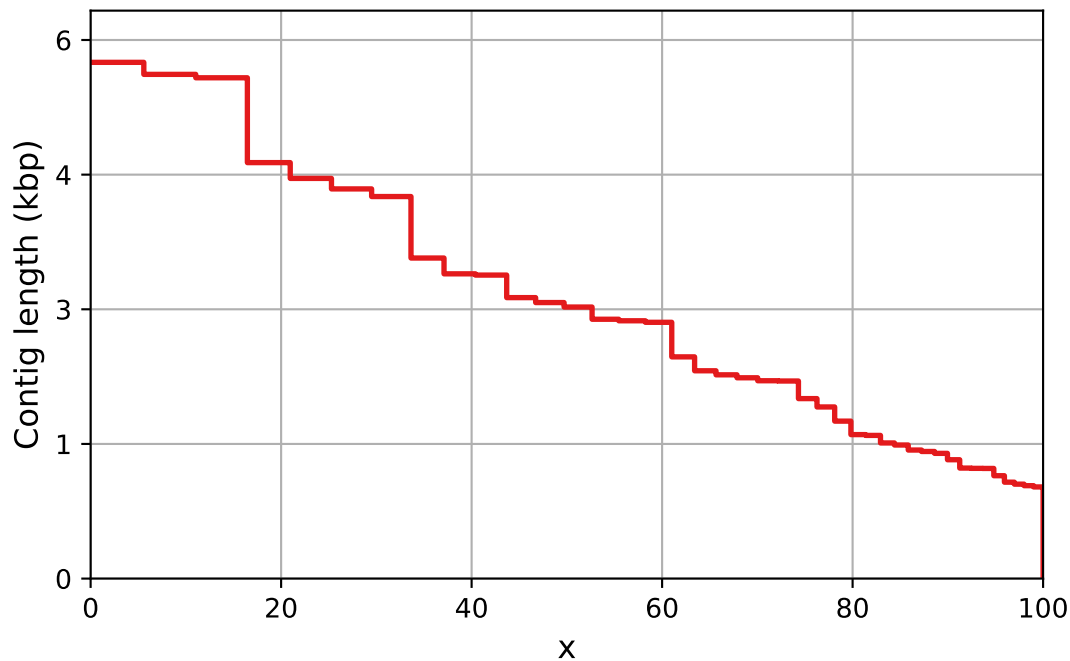
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_MED_RAW
# fully unaligned contigs	3
Fully unaligned length	5096
# partially unaligned contigs	38
Partially unaligned length	94235
# N's	0

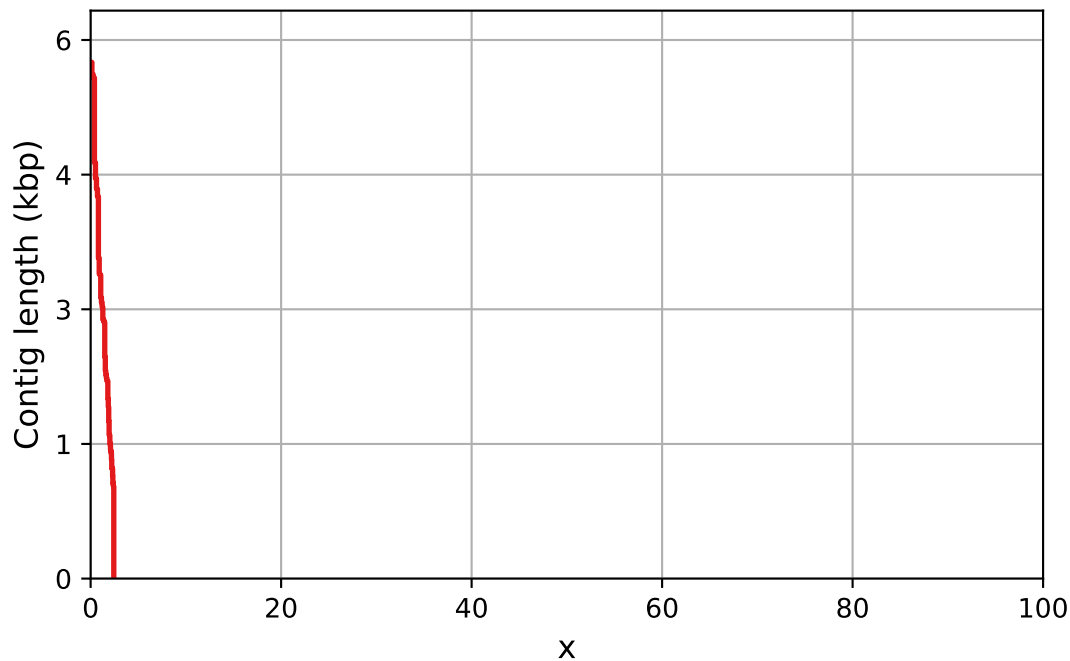
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

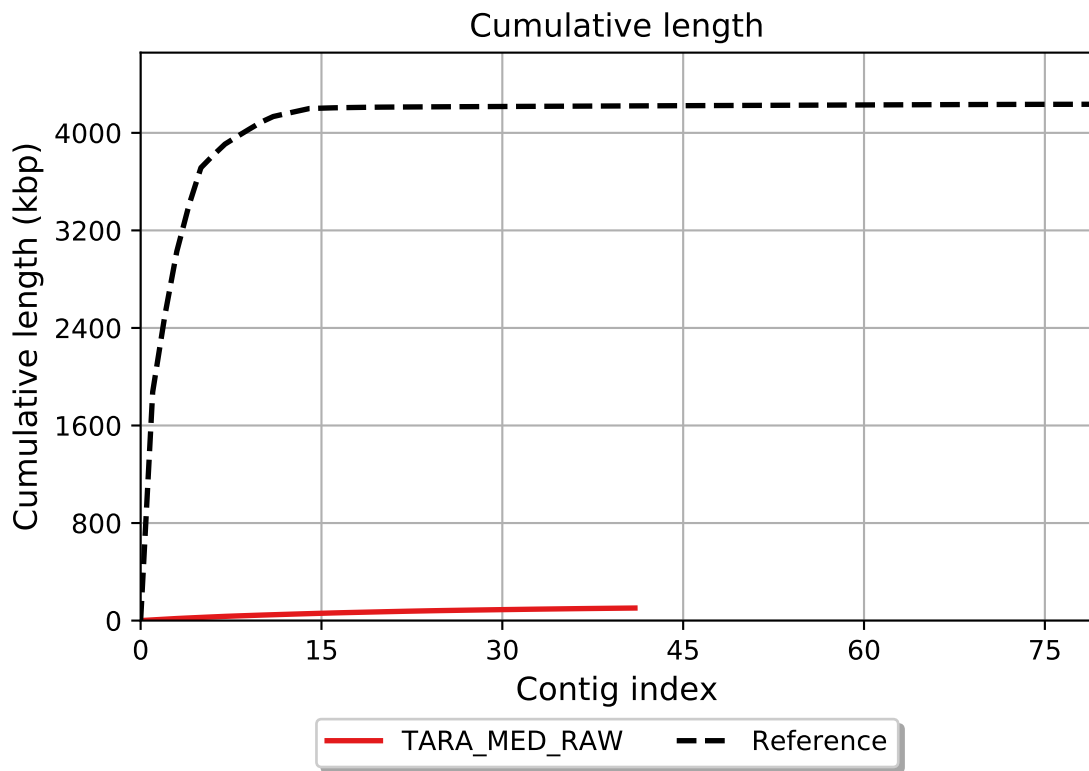


TARA_MED_RAW

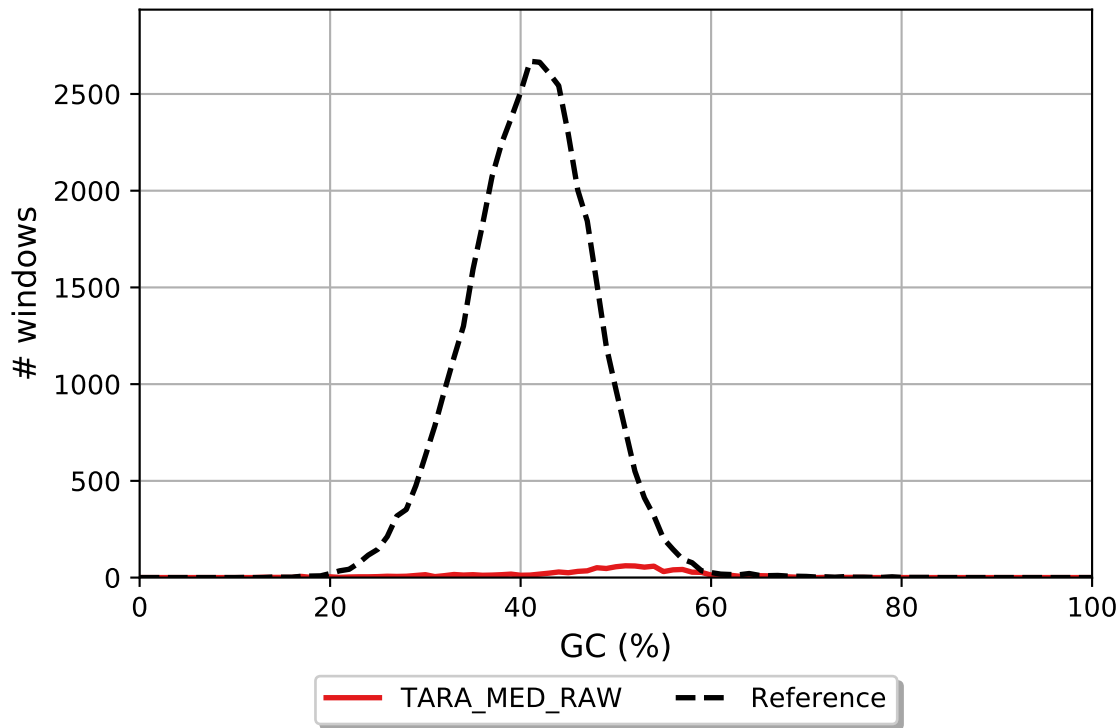
NGx



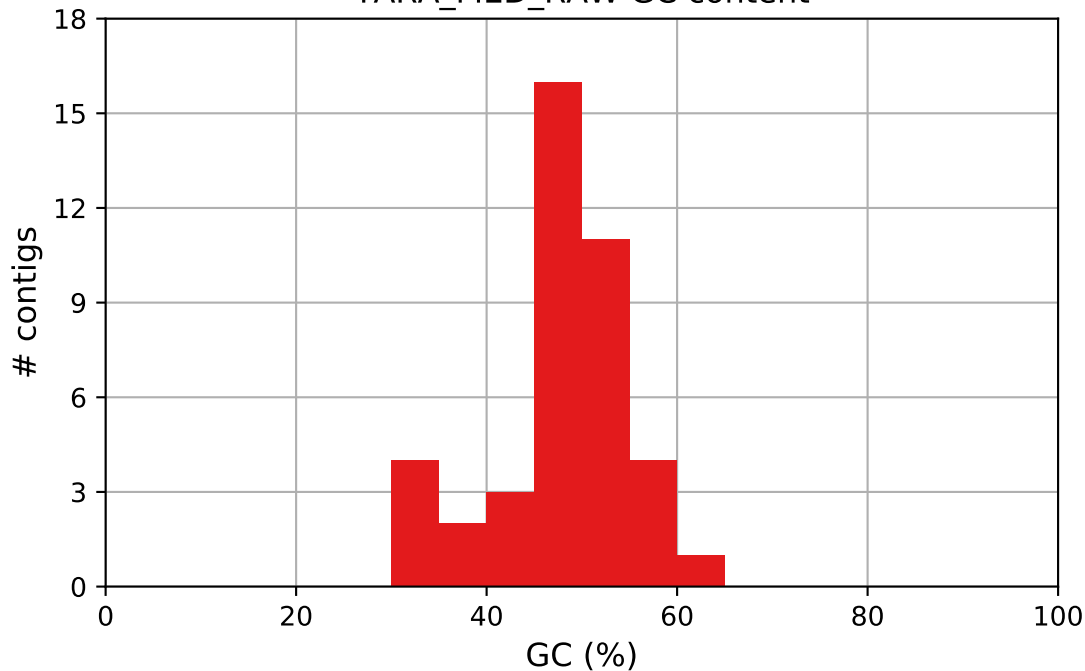
TARA_MED_RAW



GC content



TARA_MED_RAW GC content



TARA_MED_RAW

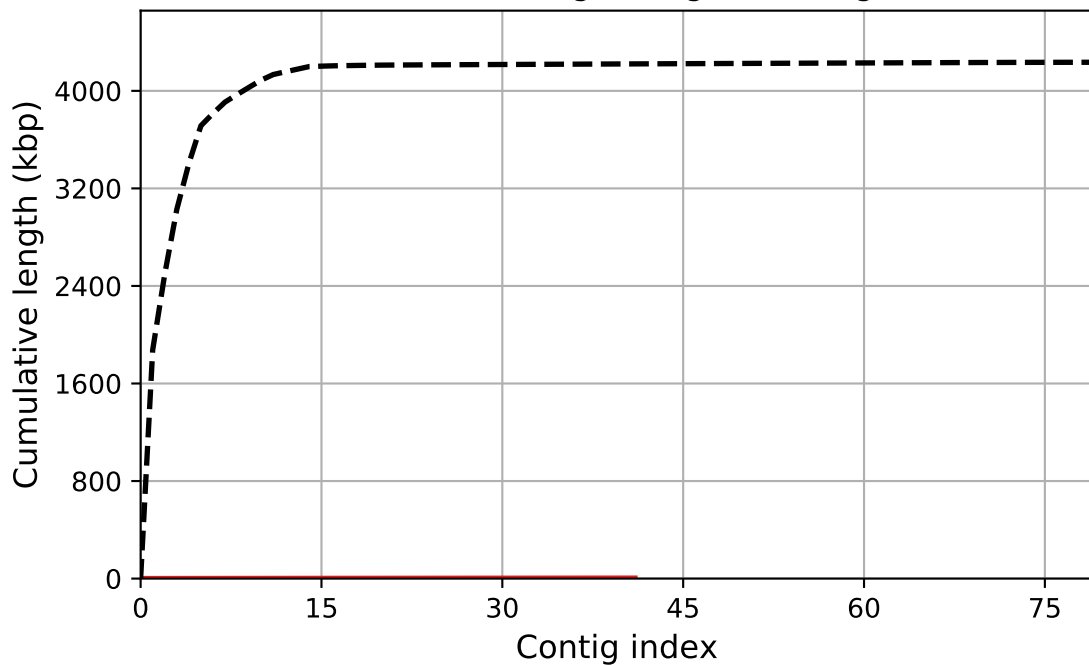
Misassemblies



FRCurve (misassemblies)

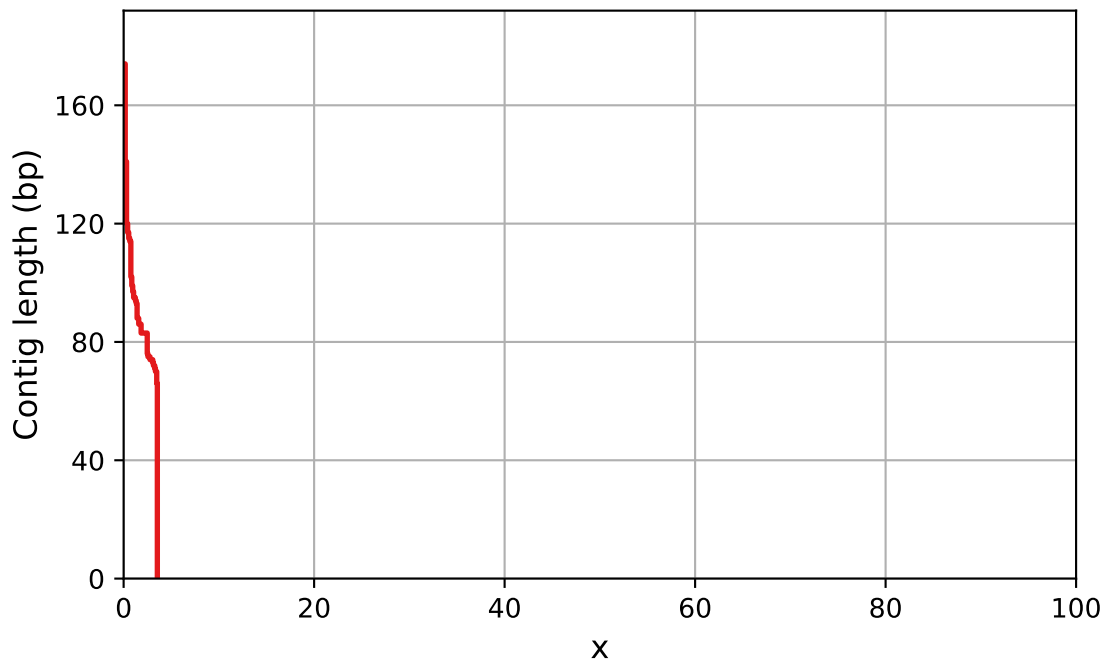


Cumulative length (aligned contigs)



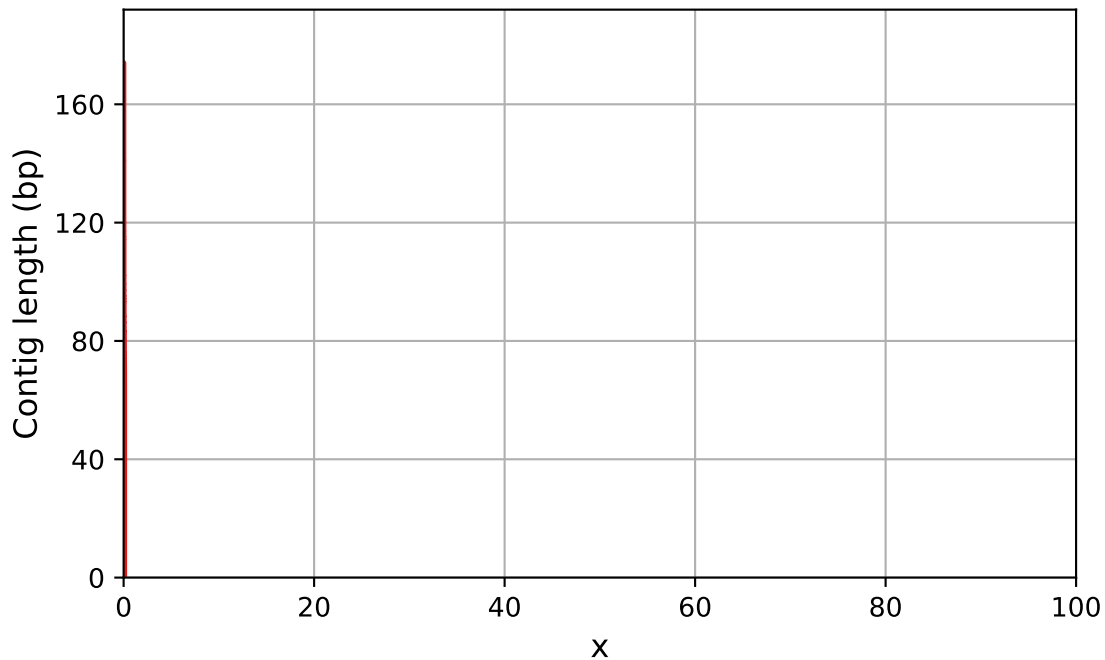
— TARA_MED_RAW - - Reference

NAx



TARA_MED_RAW

NGAx



TARA_MED_RAW