

Report

	TARA_IOS_RAW
# contigs (>= 1000 bp)	390
# contigs (>= 5000 bp)	63
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	7
Total length (>= 1000 bp)	2109625
Total length (>= 5000 bp)	1461348
Total length (>= 10000 bp)	1209972
Total length (>= 25000 bp)	964754
Total length (>= 50000 bp)	781309
# contigs	390
Largest contig	205375
Total length	2109625
Reference length	7658814
GC (%)	43.11
Reference GC (%)	63.29
N50	18934
N75	3330
L50	17
L75	94
# 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	5
# unaligned contigs	10 + 380 part
Unaligned length	2077865
Genome fraction (%)	0.059
Duplication ratio	7.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13774.83
# indels per 100 kbp	88.30
Largest alignment	585
Total aligned length	31760
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

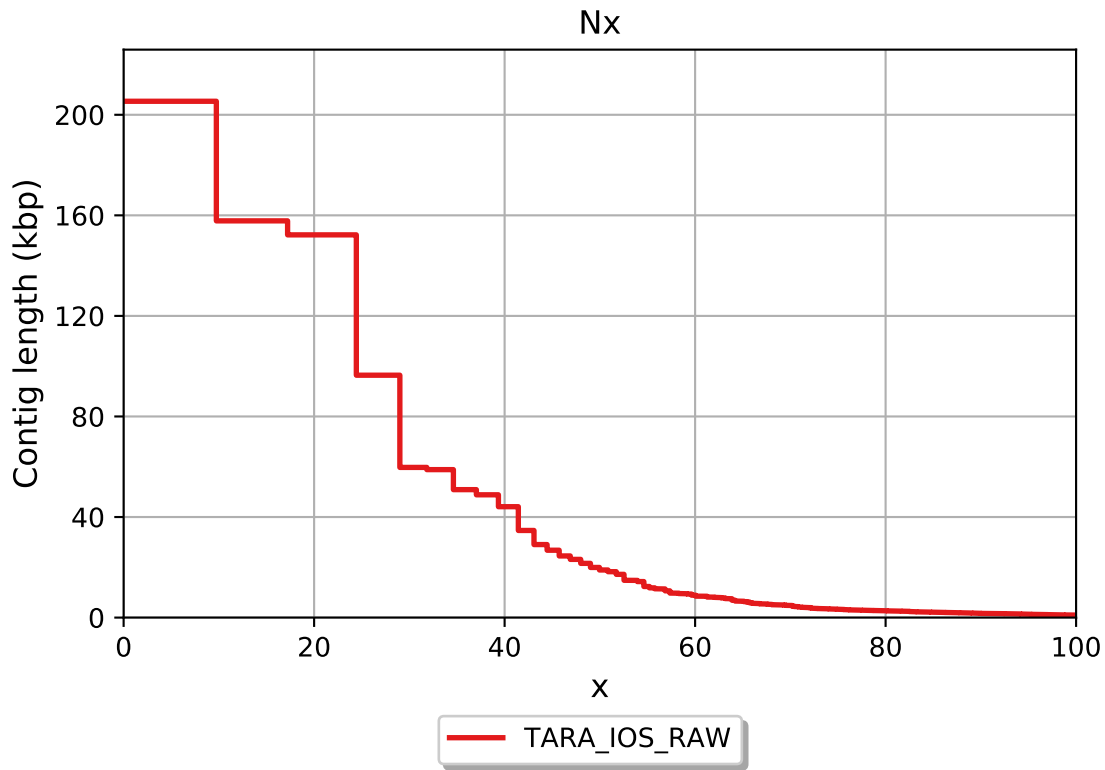
	TARA_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	383
# possible misassemblies	463
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	624
# 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).

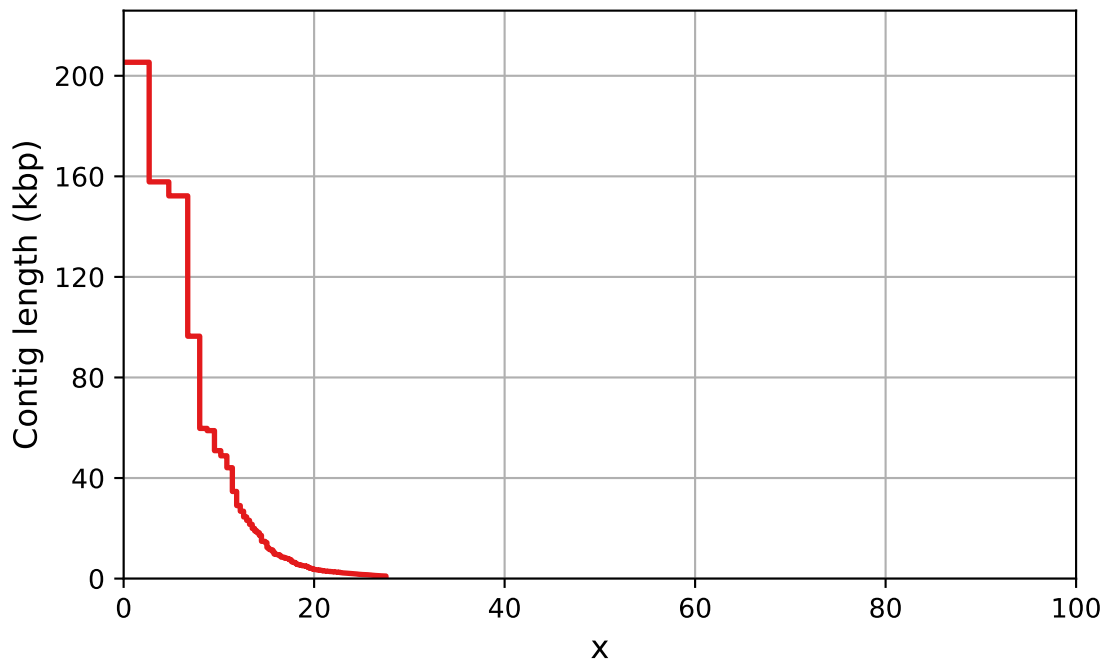
Unaligned report

	TARA_IOS_RAW
# fully unaligned contigs	10
Fully unaligned length	270843
# partially unaligned contigs	380
Partially unaligned length	1807022
# 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).

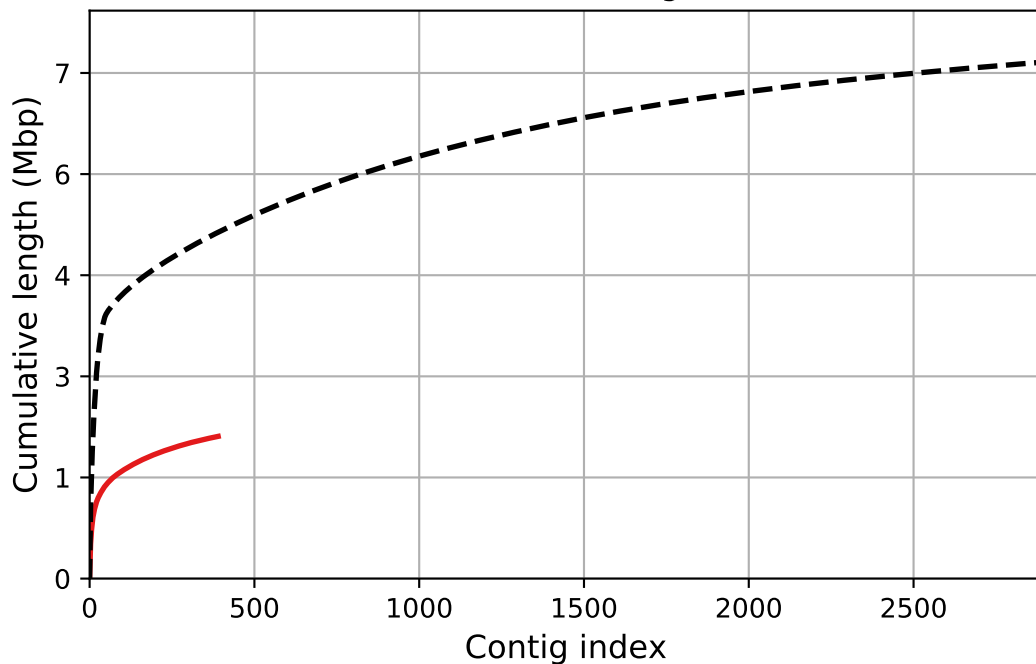


NGx



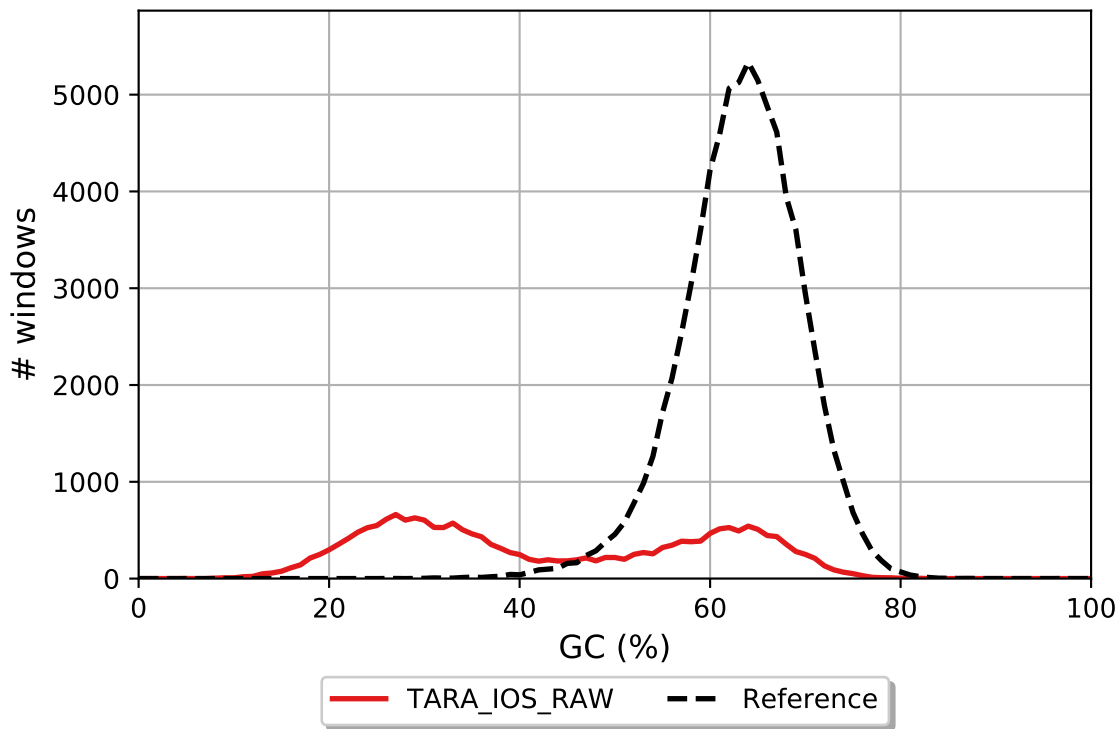
TARA_IOS_RAW

Cumulative length

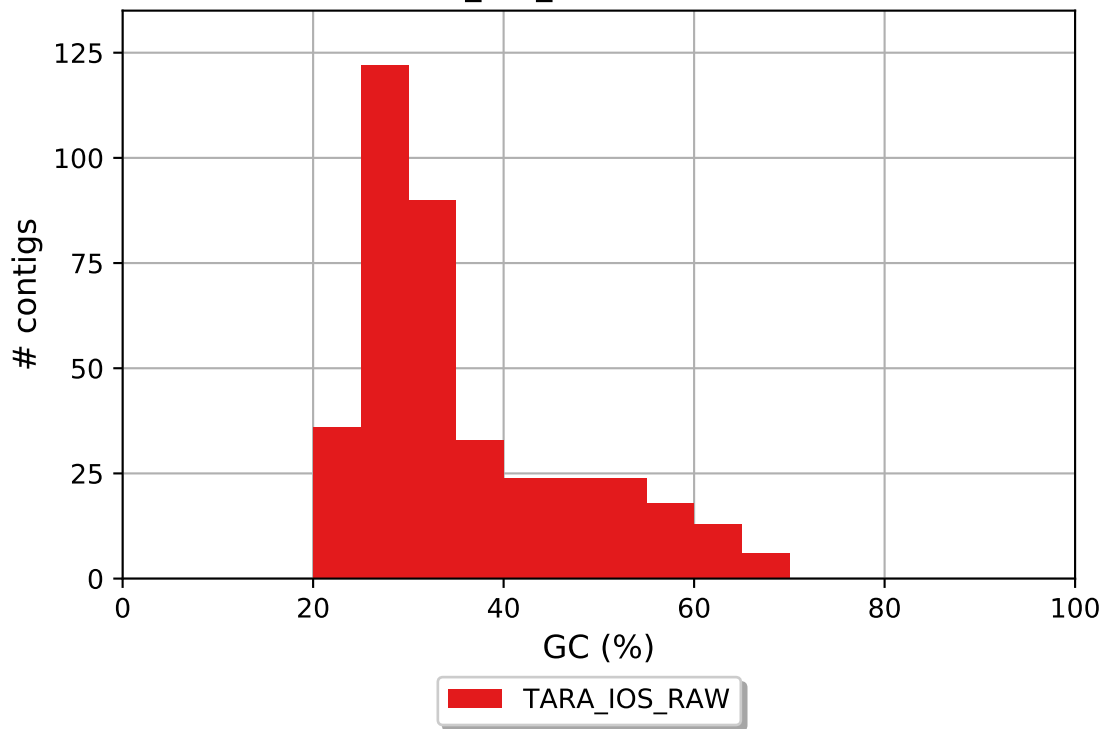


— TARA_IOS_RAW - - Reference

GC content



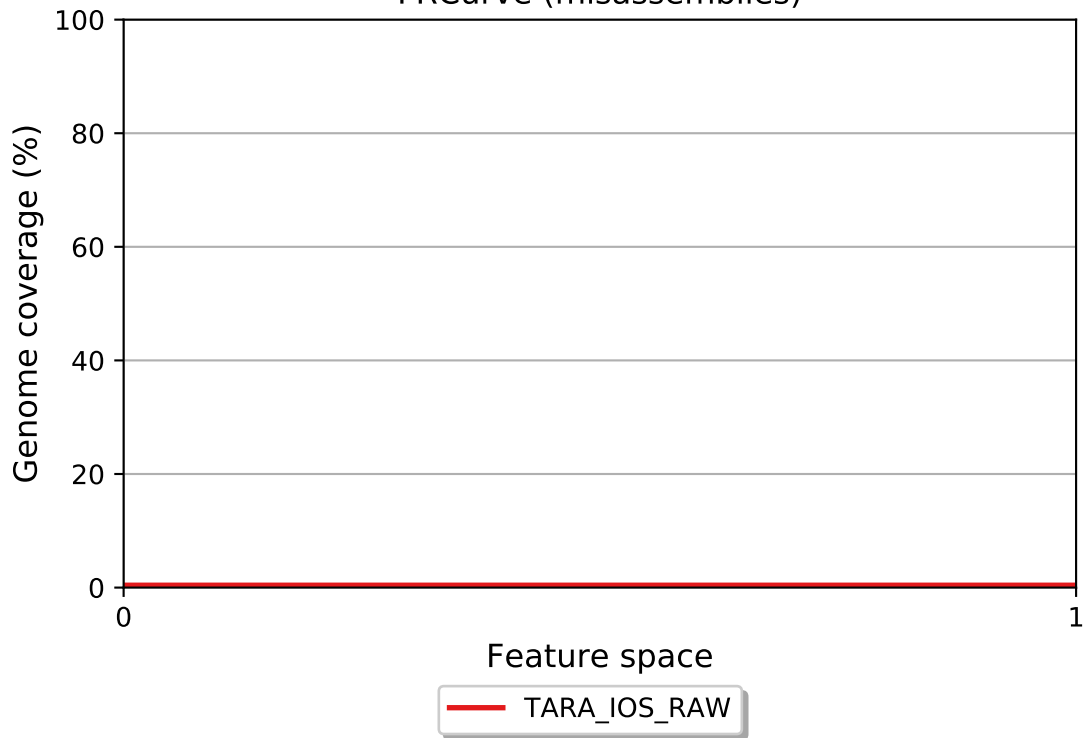
TARA_IOS_RAW GC content



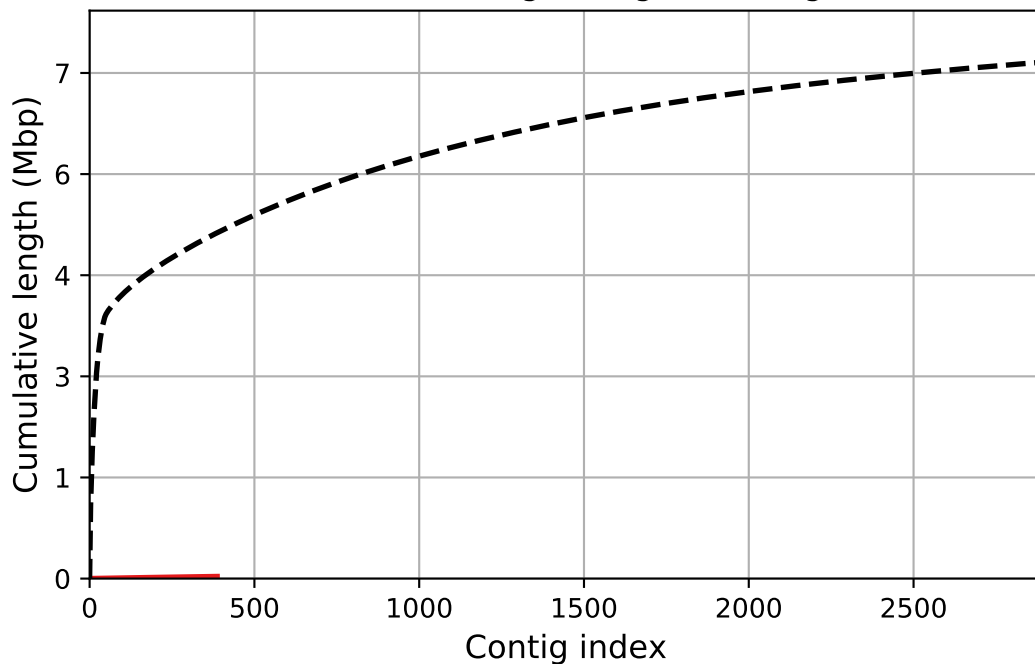
Misassemblies



FRCurve (misassemblies)

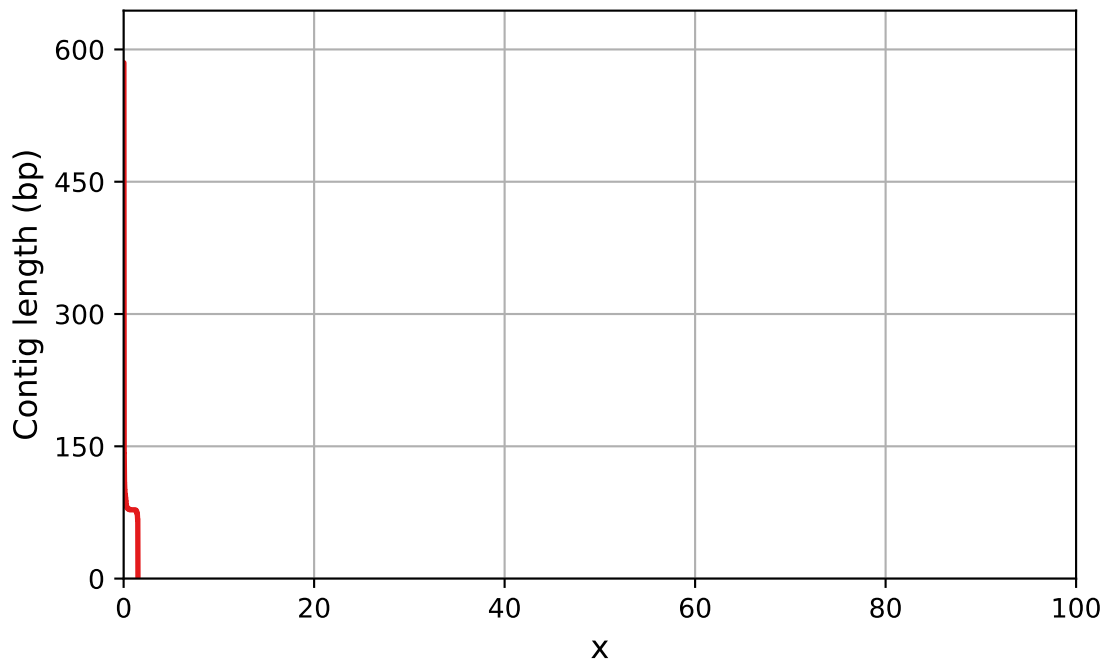


Cumulative length (aligned contigs)



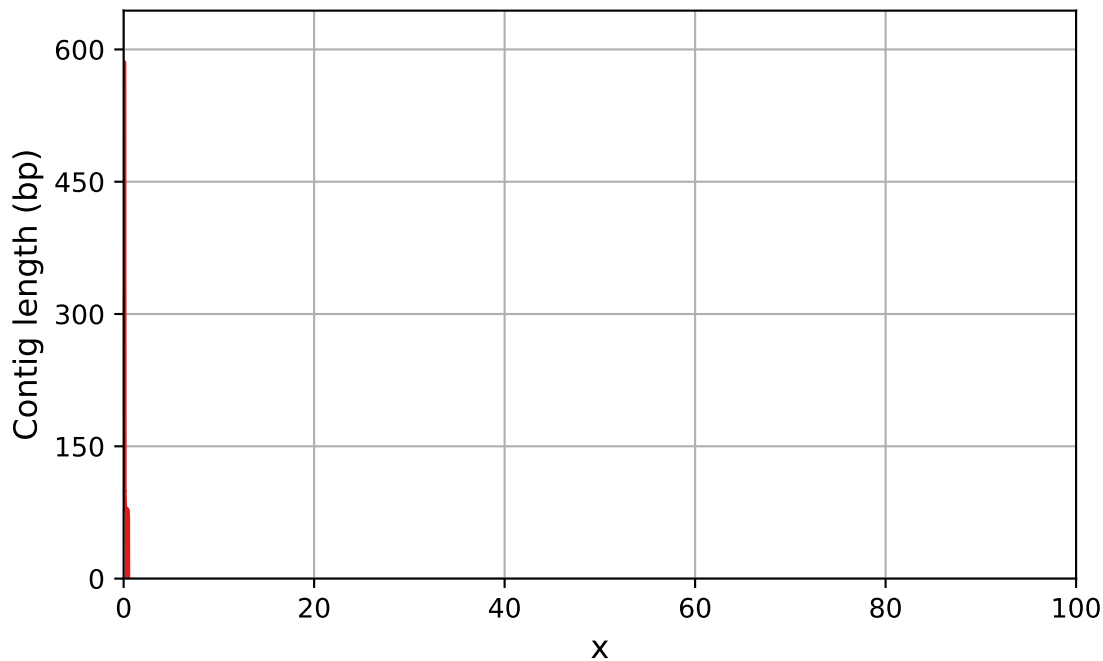
— TARA_IOS_RAW - - Reference

NAx



TARA_IOS_RAW

NGAx



— TARA_IOS_RAW