

Report

	TARA_IOS_RAW
# contigs (>= 0 bp)	1475271
# contigs (>= 1000 bp)	1475271
# contigs (>= 5000 bp)	53523
# contigs (>= 10000 bp)	11784
# contigs (>= 25000 bp)	1601
# contigs (>= 50000 bp)	355
Total length (>= 0 bp)	2864496476
Total length (>= 1000 bp)	2864496476
Total length (>= 5000 bp)	494394129
Total length (>= 10000 bp)	217798872
Total length (>= 25000 bp)	74213818
Total length (>= 50000 bp)	32929696
# contigs	1475271
Largest contig	584819
Total length	2864496476
Reference length	5854900
N50	1934
N75	1323
L50	391314
L75	846793
# 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	6
# unaligned contigs	1474913 + 358 part
Unaligned length	2864467194
Genome fraction (%)	0.075
Duplication ratio	7.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14282.48
# indels per 100 kbp	0.00
Largest alignment	335
Total aligned length	29282

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

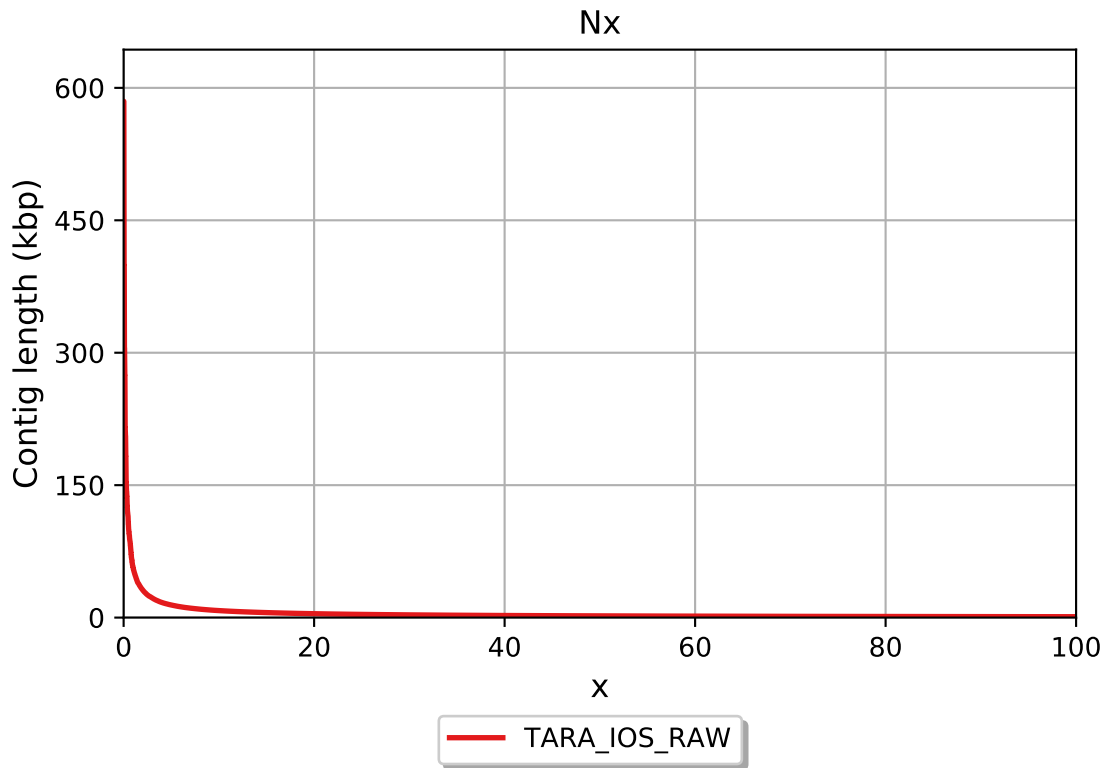
	TARA_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	352
# possible misassemblies	427
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	630
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

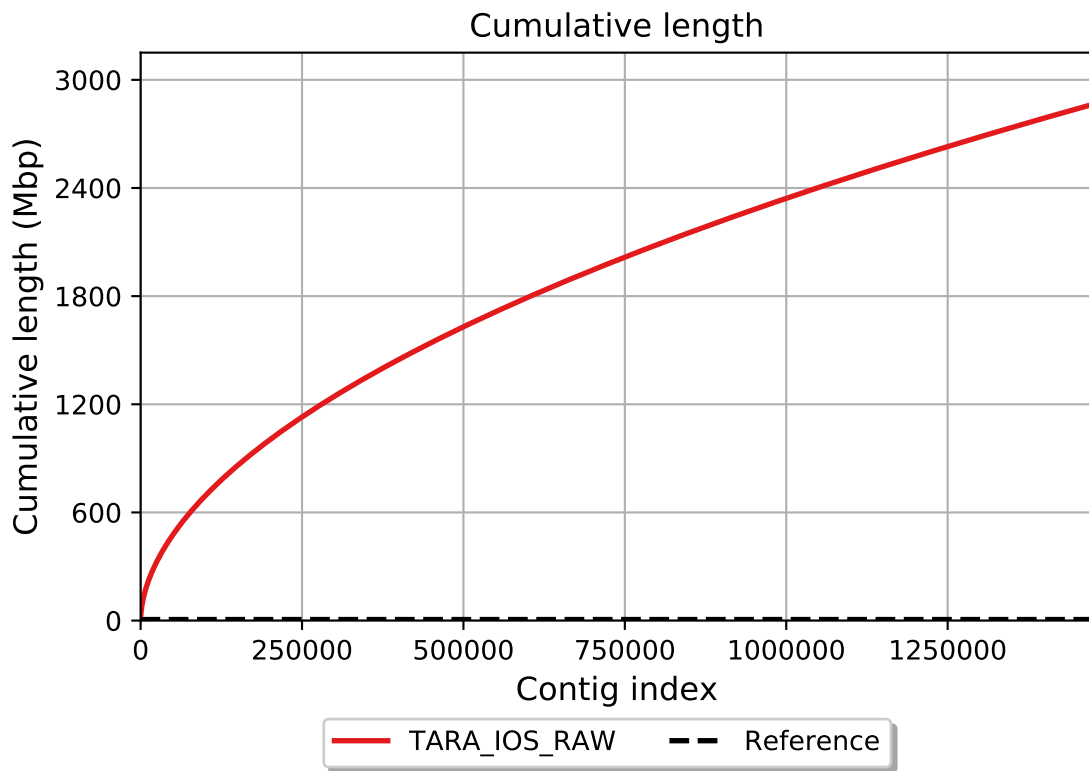
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

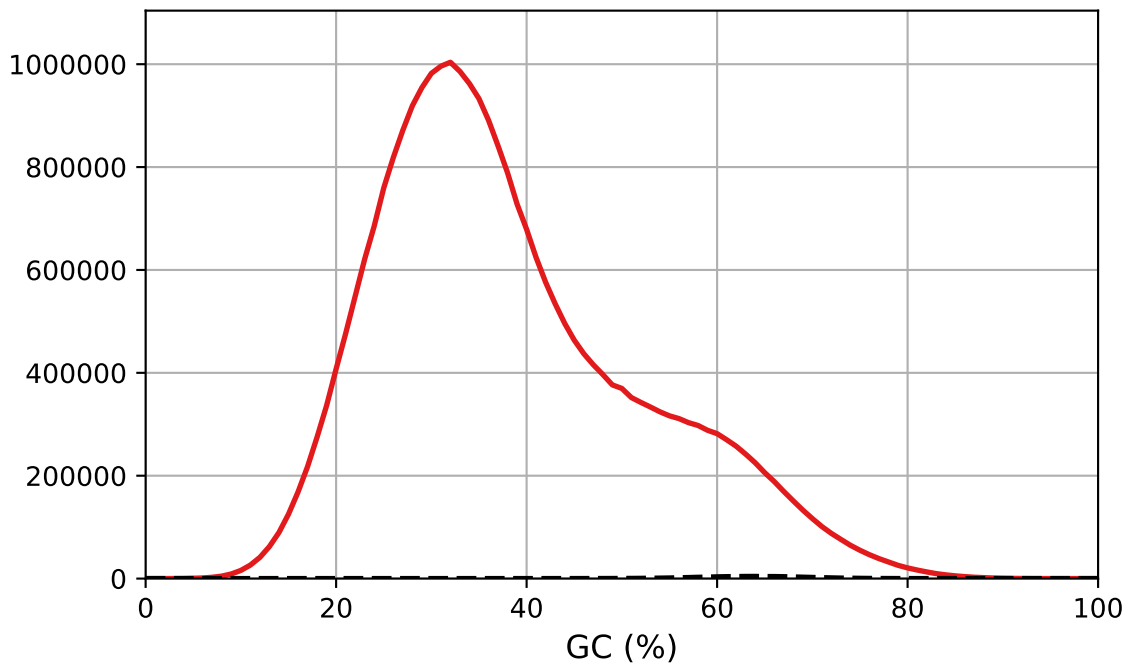
	TARA_IOS_RAW
# fully unaligned contigs	1474913
Fully unaligned length	2862862331
# partially unaligned contigs	358
Partially unaligned length	1604863
# N's	0

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).



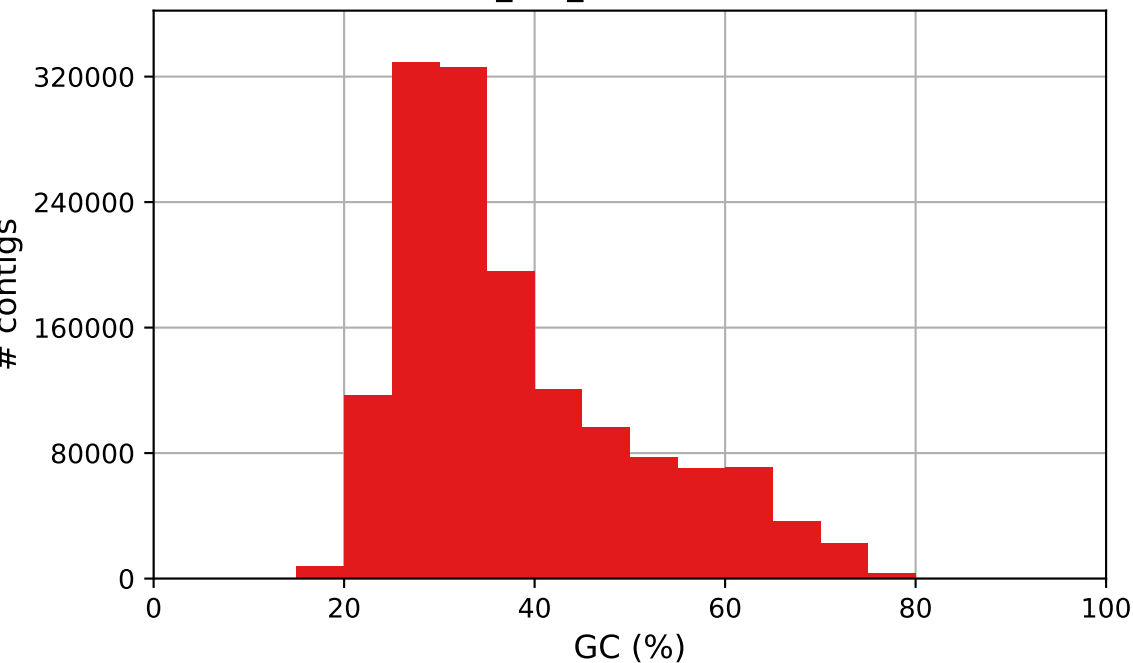


GC content



— TARA_IOS_RAW - - Reference

TARA_IOS_RAW GC content

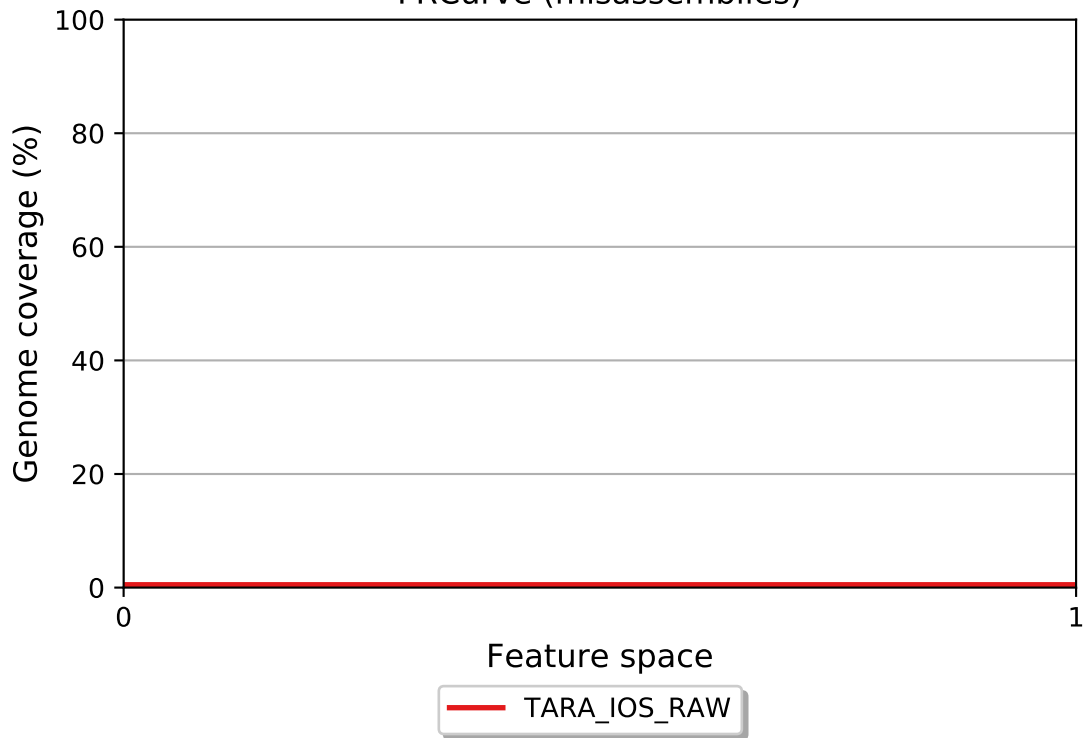


TARA_IOS_RAW

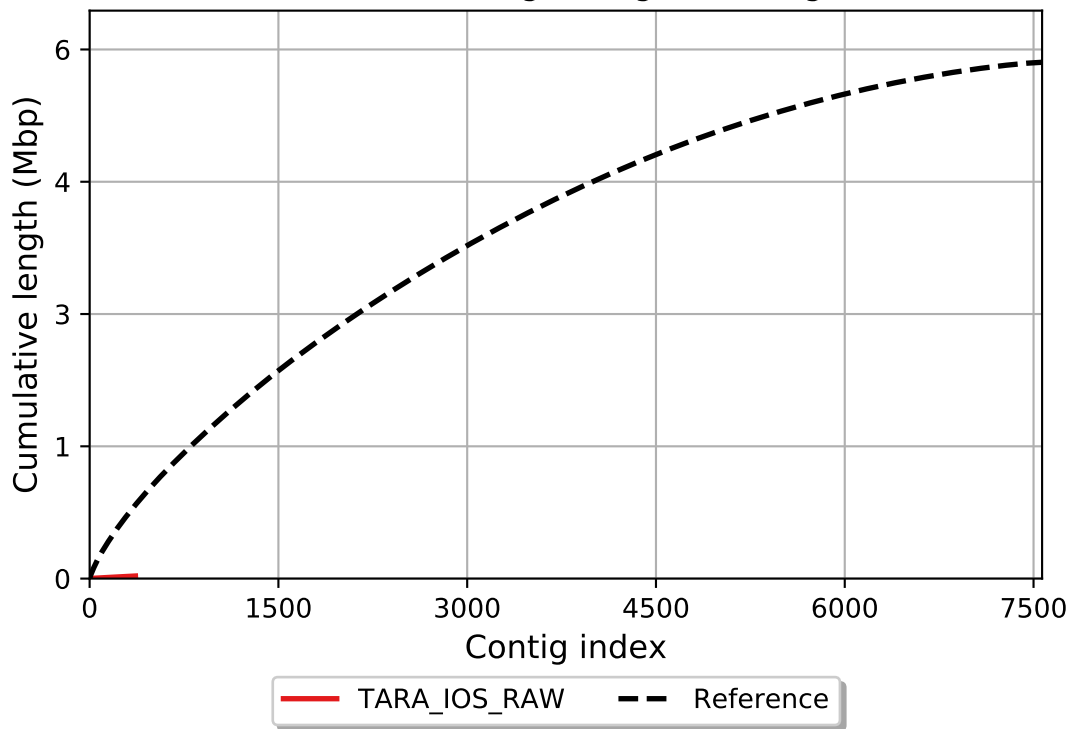
Misassemblies



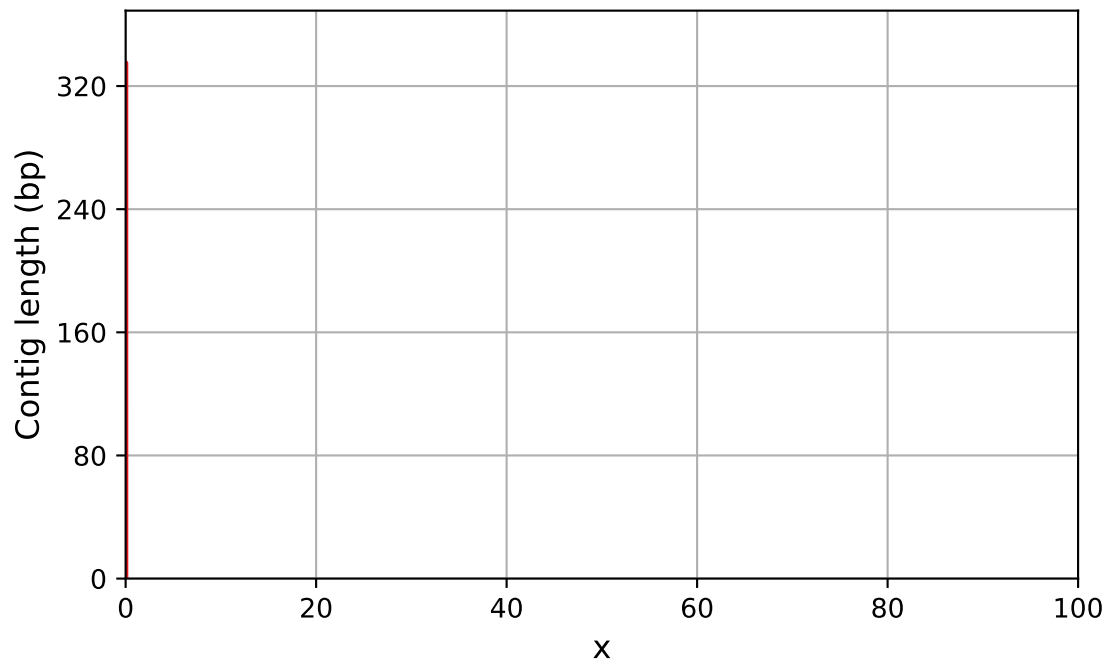
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



TARA_IOS_RAW