

# 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	3561038
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	0
# unaligned contigs	1475233 + 38 part
Unaligned length	2864492956
Genome fraction (%)	0.027
Duplication ratio	3.824
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11975.44
# indels per 100 kbp	0.00
Largest alignment	166
Total aligned length	3520

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

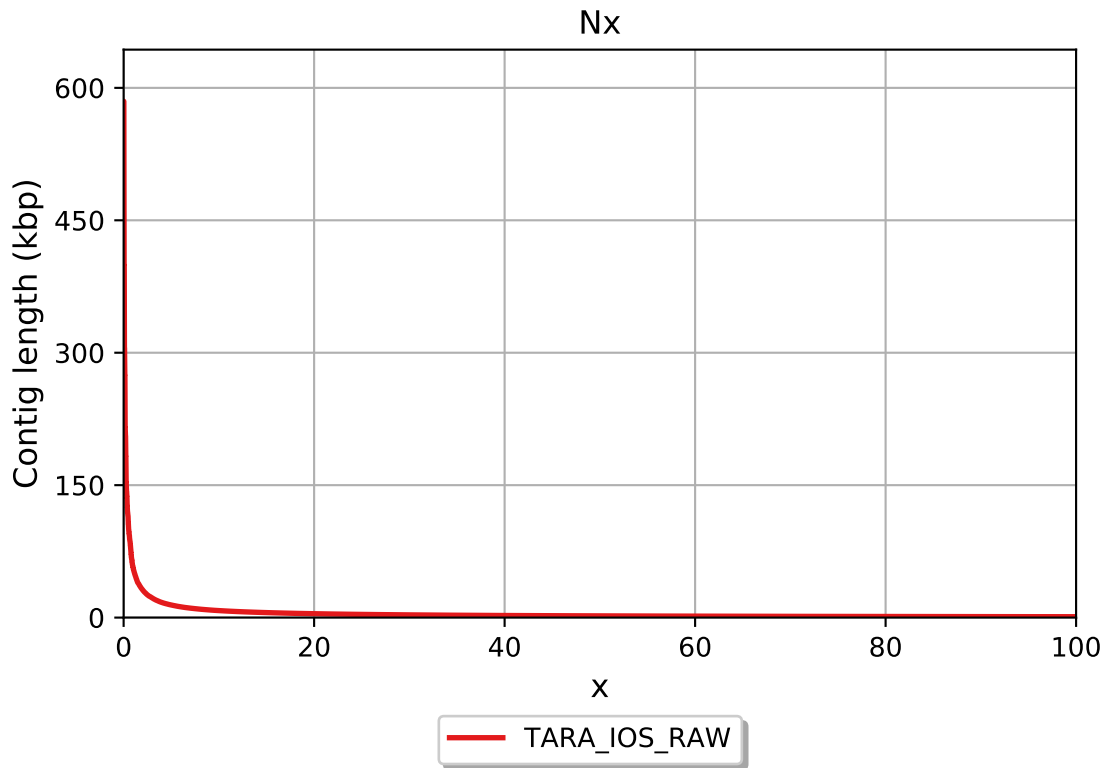
	TARA_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	38
# possible misassemblies	42
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	117
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

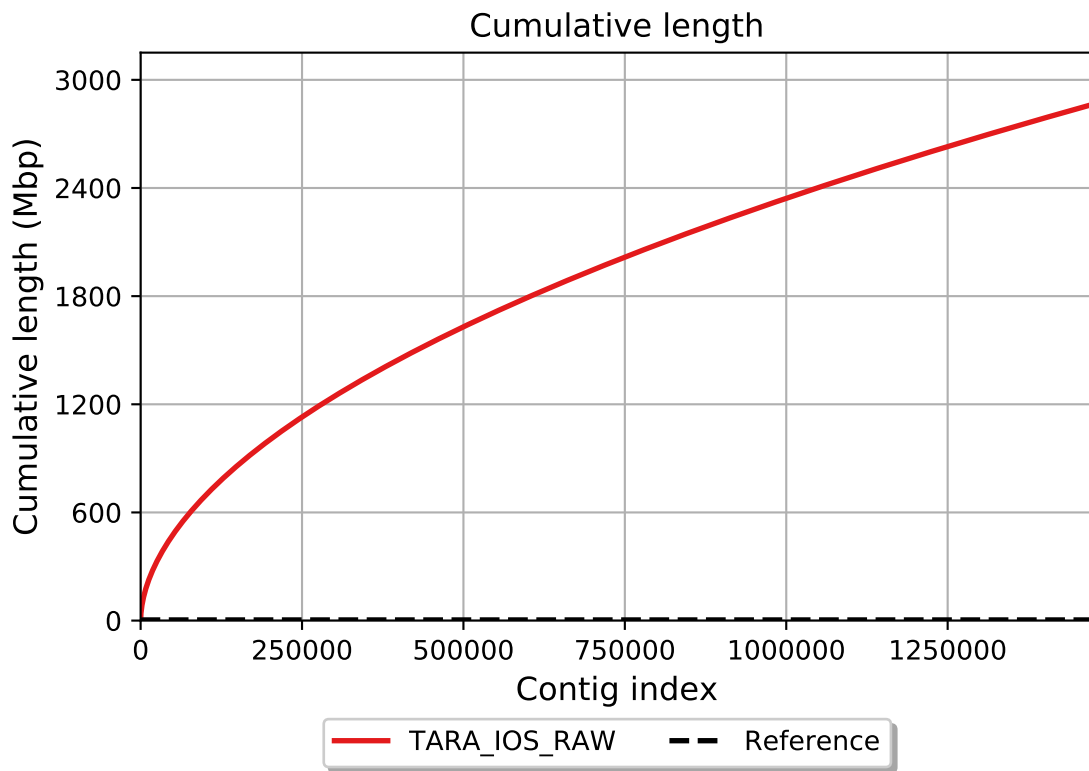
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

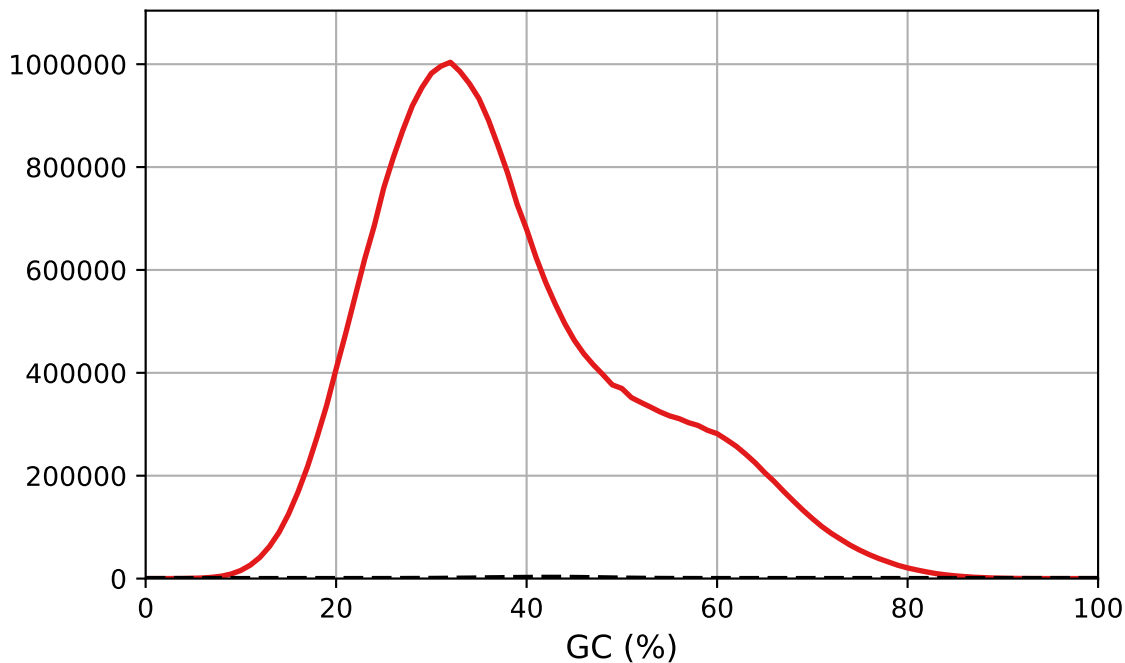
	TARA_IOS_RAW
# fully unaligned contigs	1475233
Fully unaligned length	2864349880
# partially unaligned contigs	38
Partially unaligned length	143076
# N's	0

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



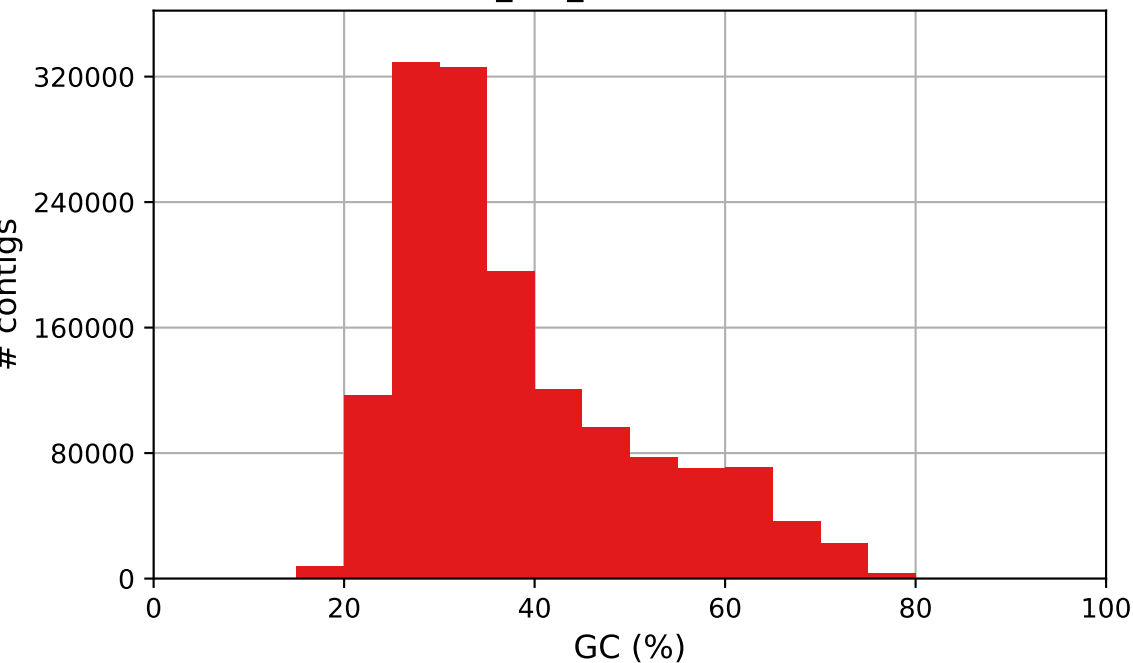


## GC content



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TARA\_IOS\_RAW GC content



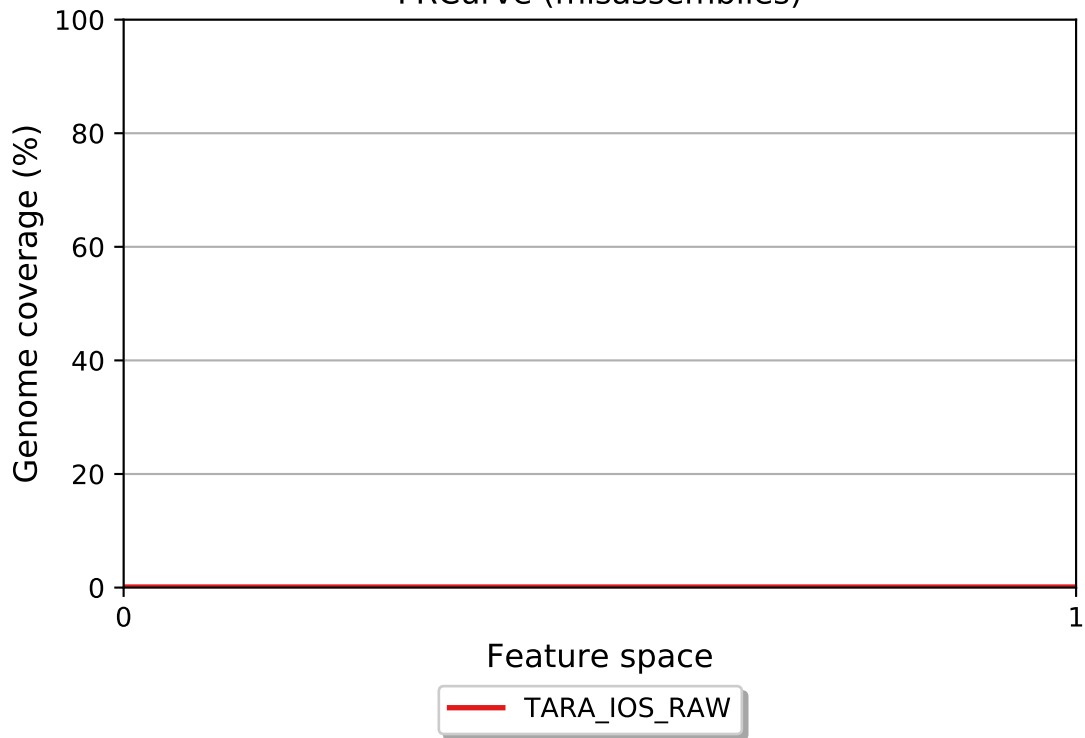
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## Misassemblies

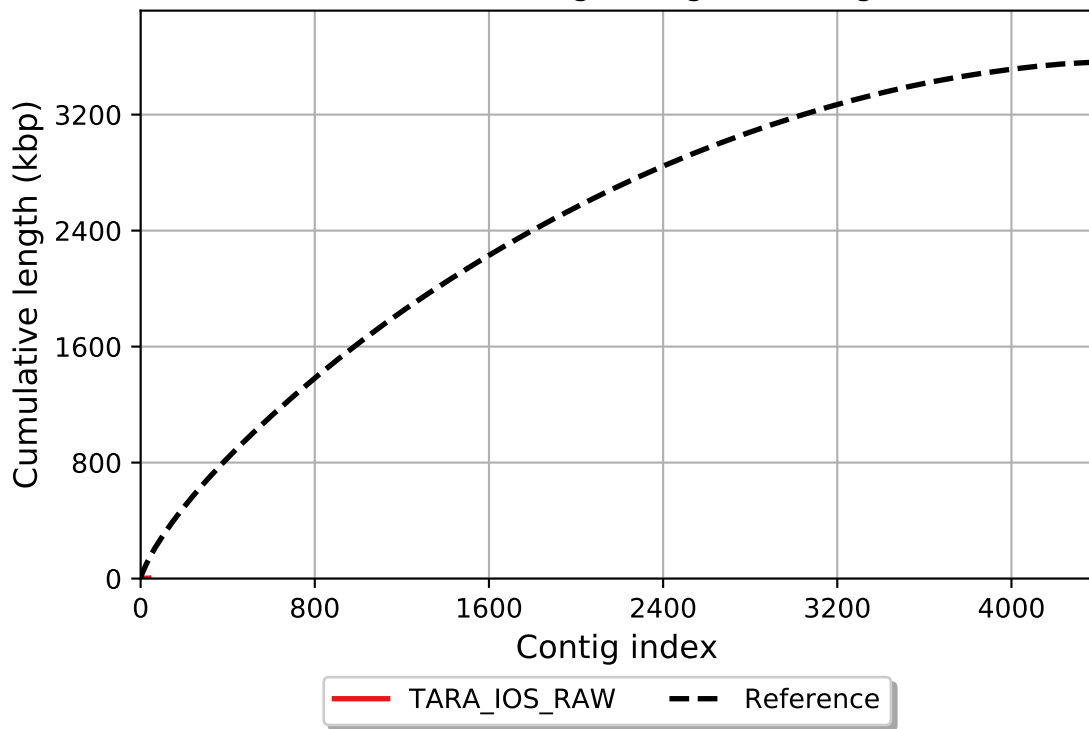




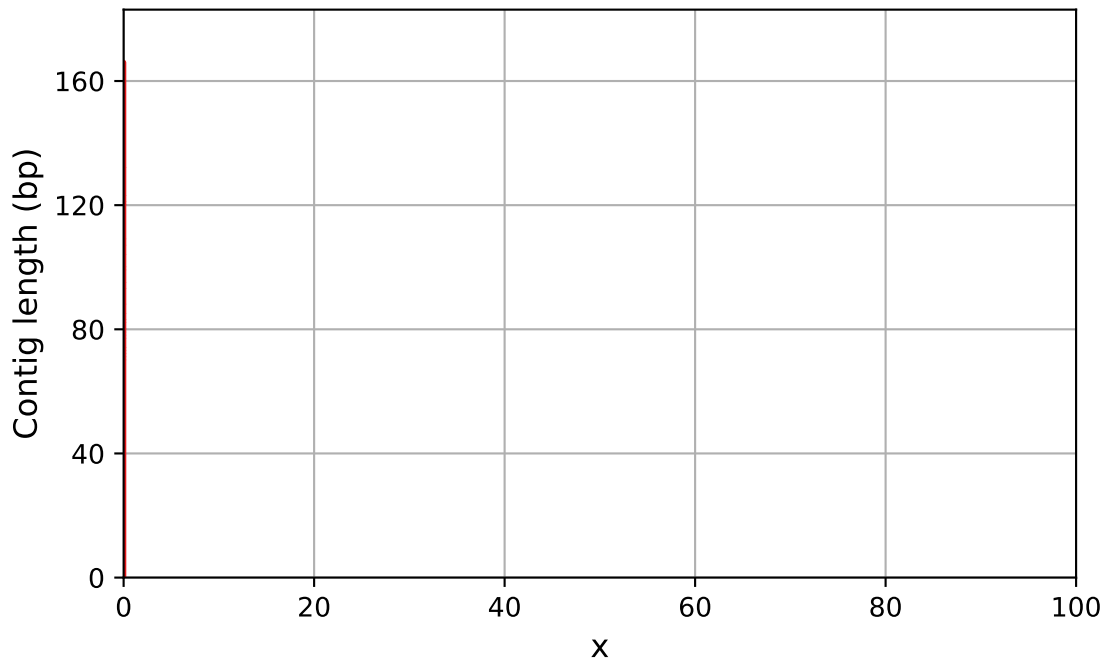
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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