

# Report

	TARA_ION_RAW
# contigs (>= 0 bp)	1608737
# contigs (>= 1000 bp)	1608737
# contigs (>= 5000 bp)	67292
# contigs (>= 10000 bp)	15920
# contigs (>= 25000 bp)	2271
# contigs (>= 50000 bp)	493
Total length (>= 0 bp)	3246736749
Total length (>= 1000 bp)	3246736749
Total length (>= 5000 bp)	636672775
Total length (>= 10000 bp)	295072419
Total length (>= 25000 bp)	101713095
Total length (>= 50000 bp)	42680448
# contigs	1608737
Largest contig	1188021
Total length	3246736749
Reference length	4234461
N50	2043
N75	1355
L50	406812
L75	904273
# 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	1608696 + 40 part
Unaligned length	3246732034
Genome fraction (%)	0.019
Duplication ratio	5.945
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13647.64
# indels per 100 kbp	0.00
Largest alignment	129
Total aligned length	3762

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

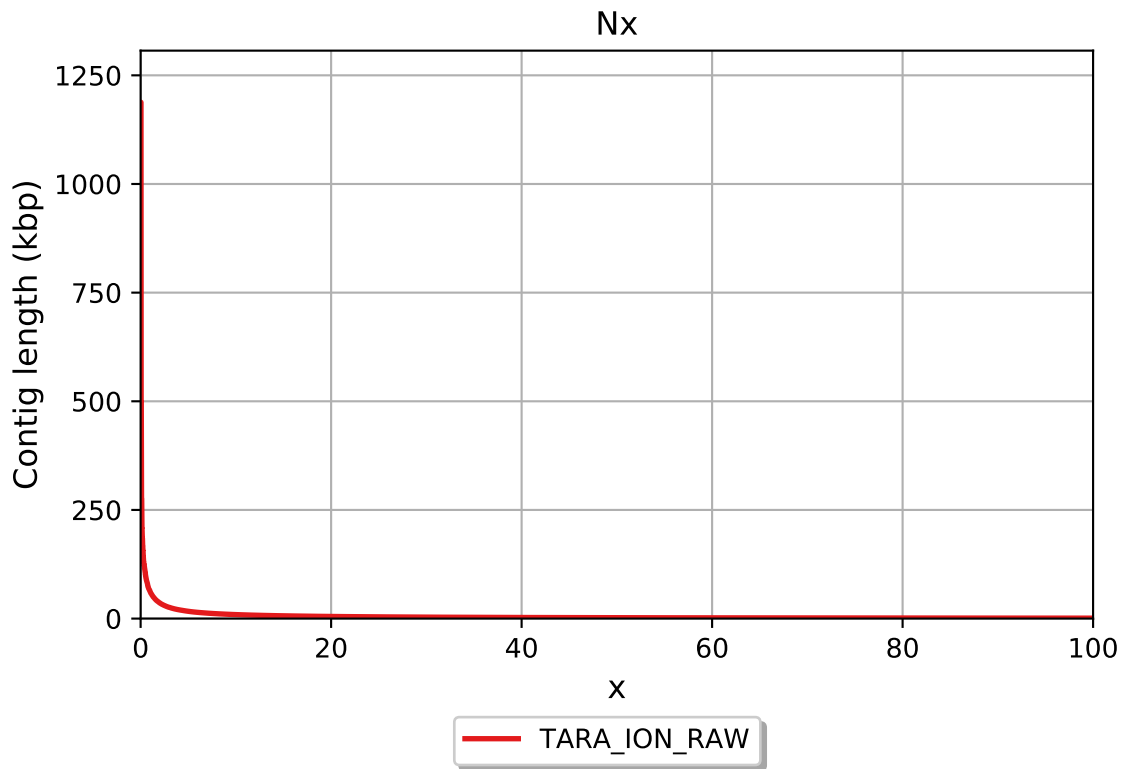
	TARA_ION_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	39
# possible misassemblies	42
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	110
# 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).

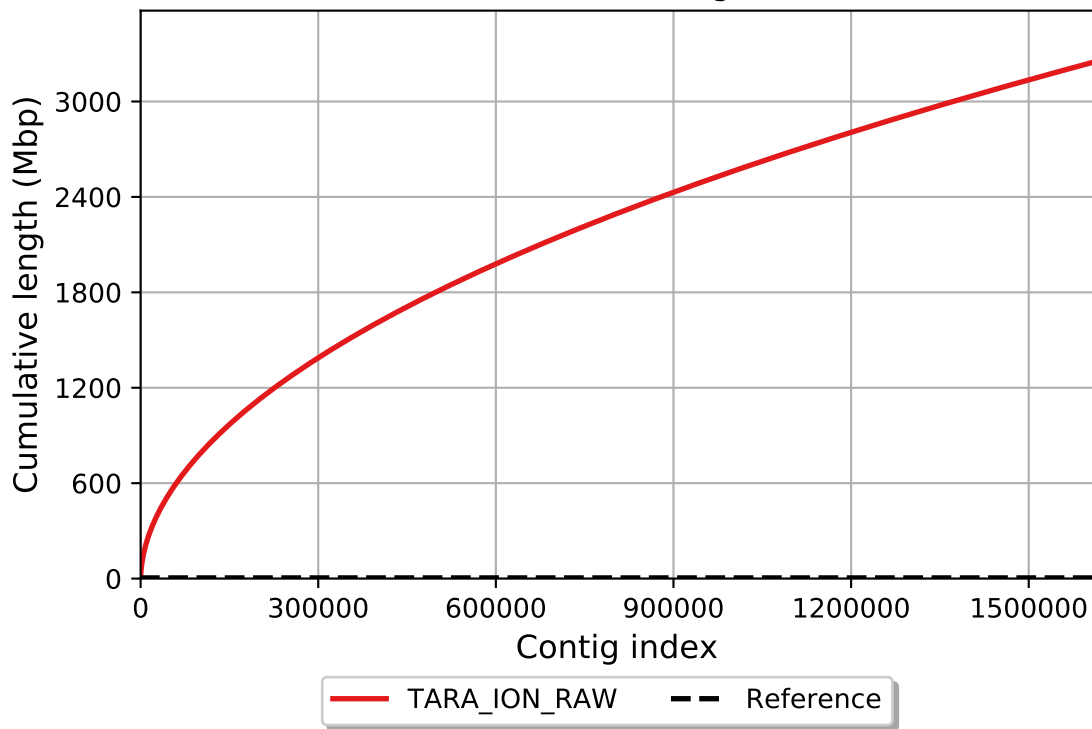
## Unaligned report

	TARA_ION_RAW
# fully unaligned contigs	1608696
Fully unaligned length	3246594711
# partially unaligned contigs	40
Partially unaligned length	137323
# N's	0

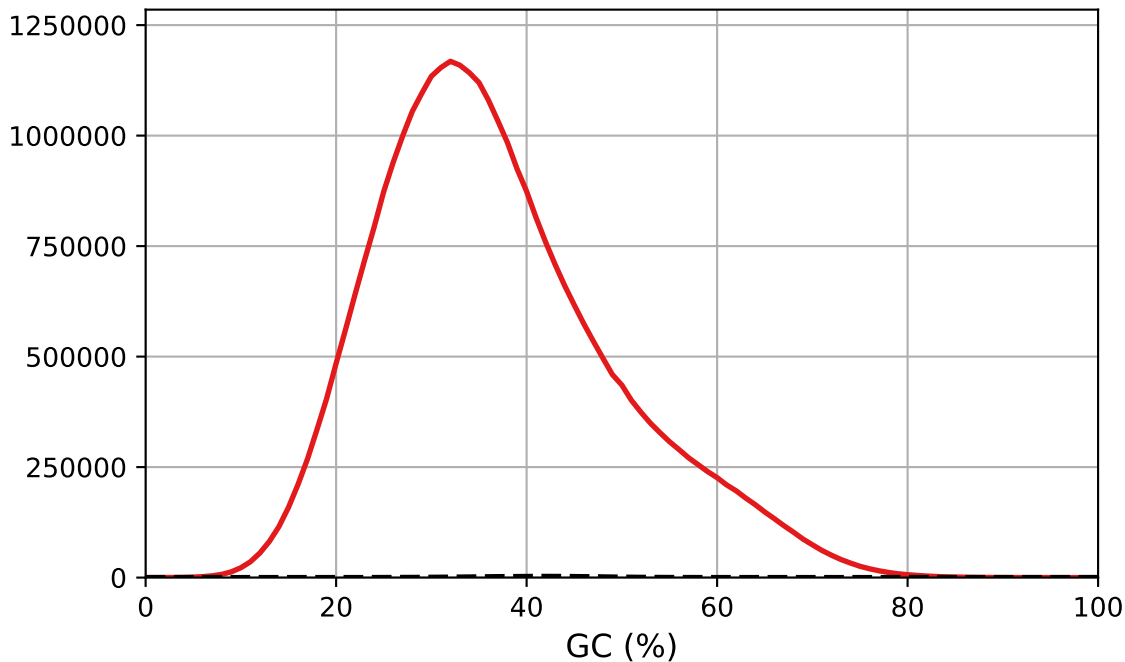
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



Cumulative length

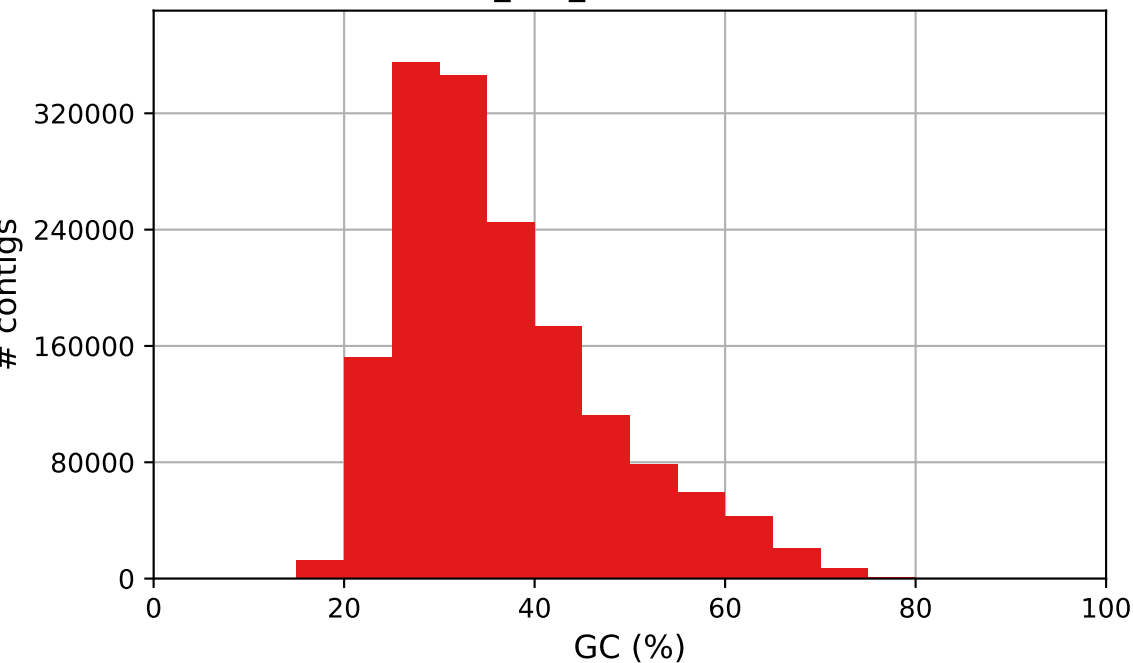


## GC content



— TARA\_ION\_RAW    - - Reference

TARA\_ION\_RAW GC content



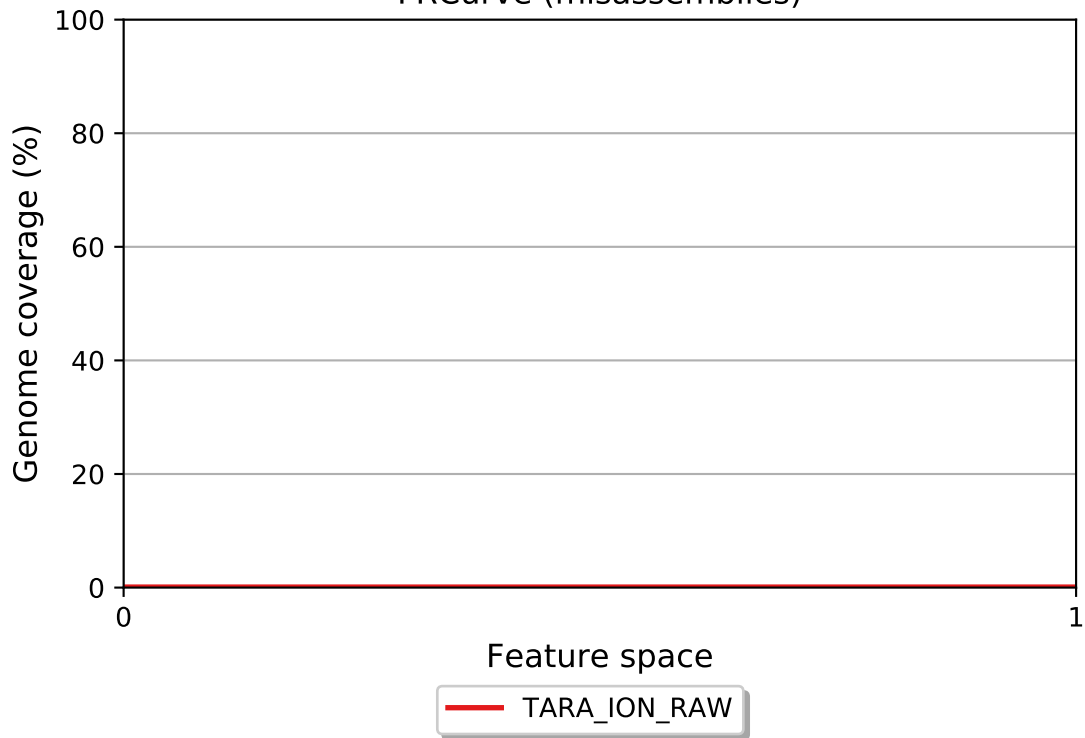
TARA\_ION\_RAW

## Misassemblies

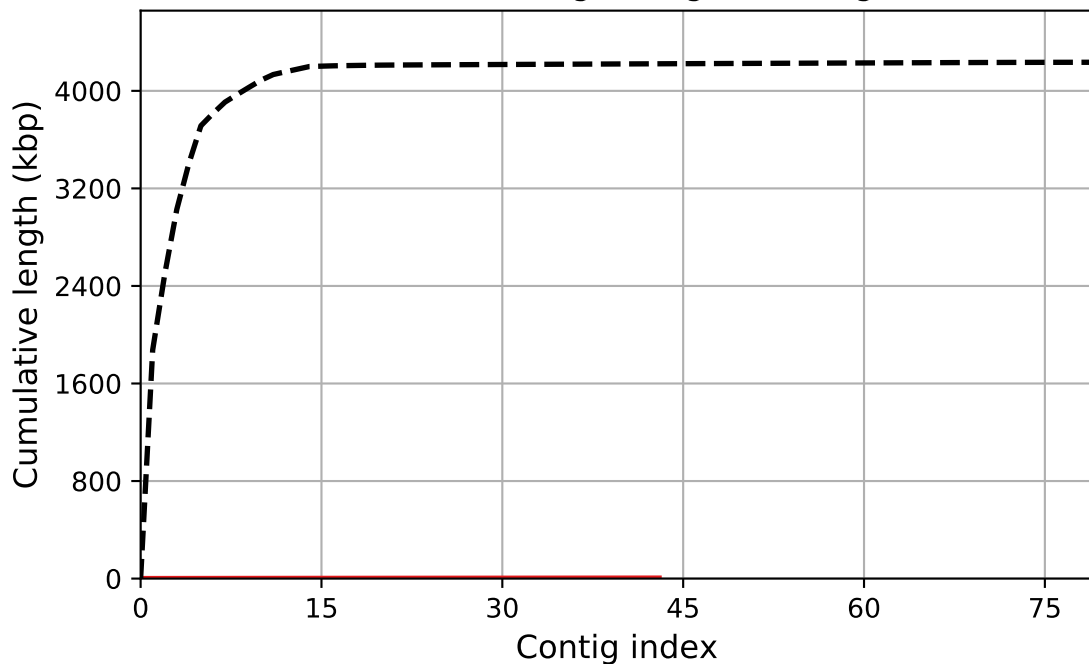




FRCurve (misassemblies)

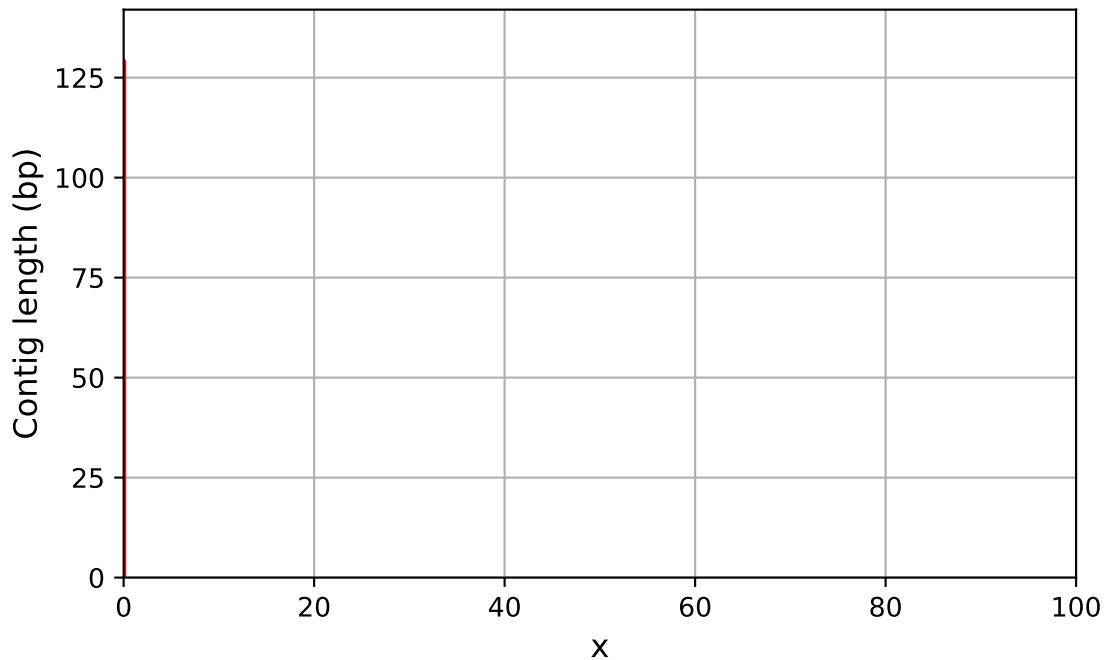


Cumulative length (aligned contigs)



TARA\_ION\_RAW      Reference

NAx



TARA\_ION\_RAW