

# 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	5854900
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	1
# unaligned contigs	1608391 + 345 part
Unaligned length	3246708421
Genome fraction (%)	0.059
Duplication ratio	8.544
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14482.76
# indels per 100 kbp	28.74
Largest alignment	159
Total aligned length	27389

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

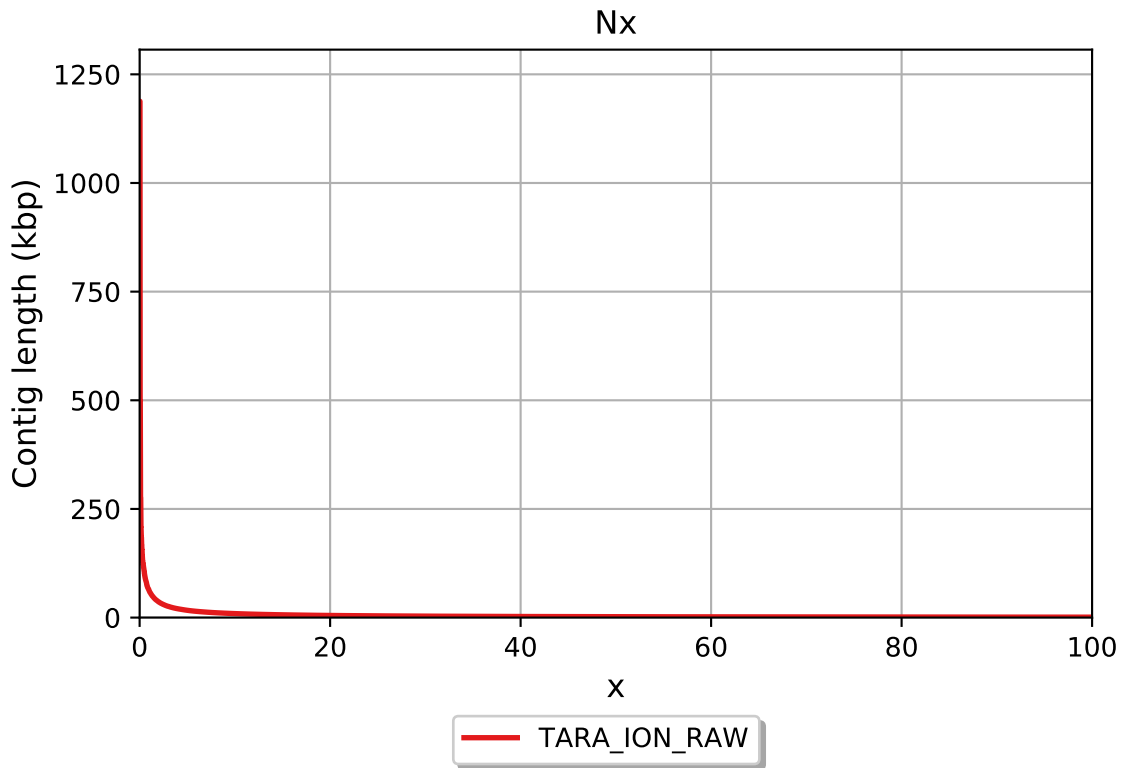
	TARA_ION_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	344
# possible misassemblies	414
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	504
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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).

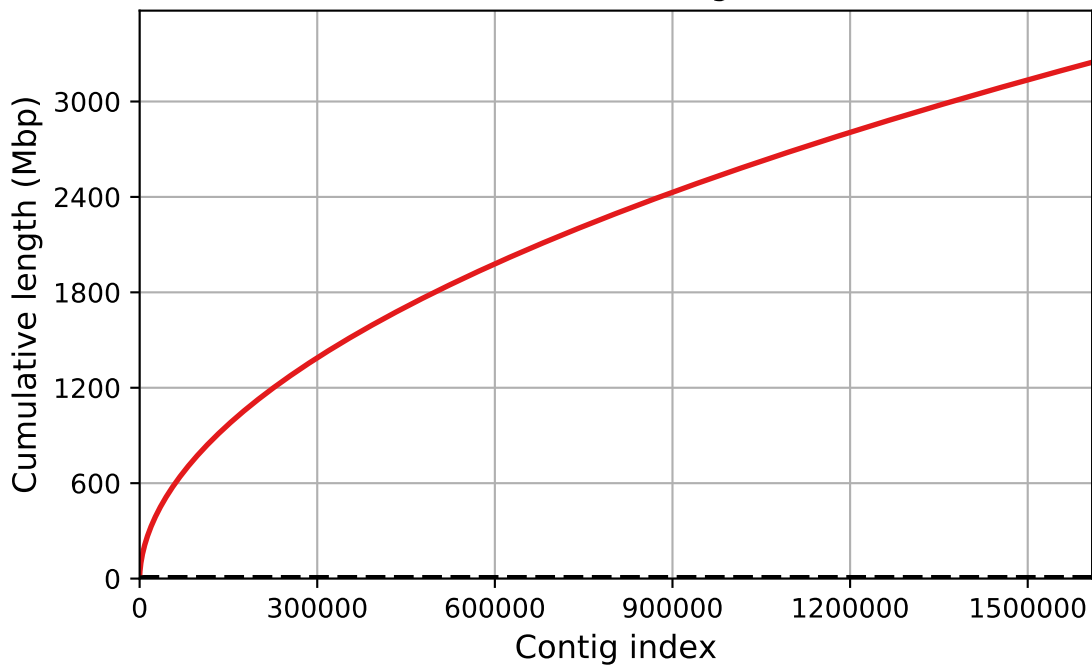
## Unaligned report

	TARA_ION_RAW
# fully unaligned contigs	1608391
Fully unaligned length	3245218917
# partially unaligned contigs	345
Partially unaligned length	1489504
# 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).

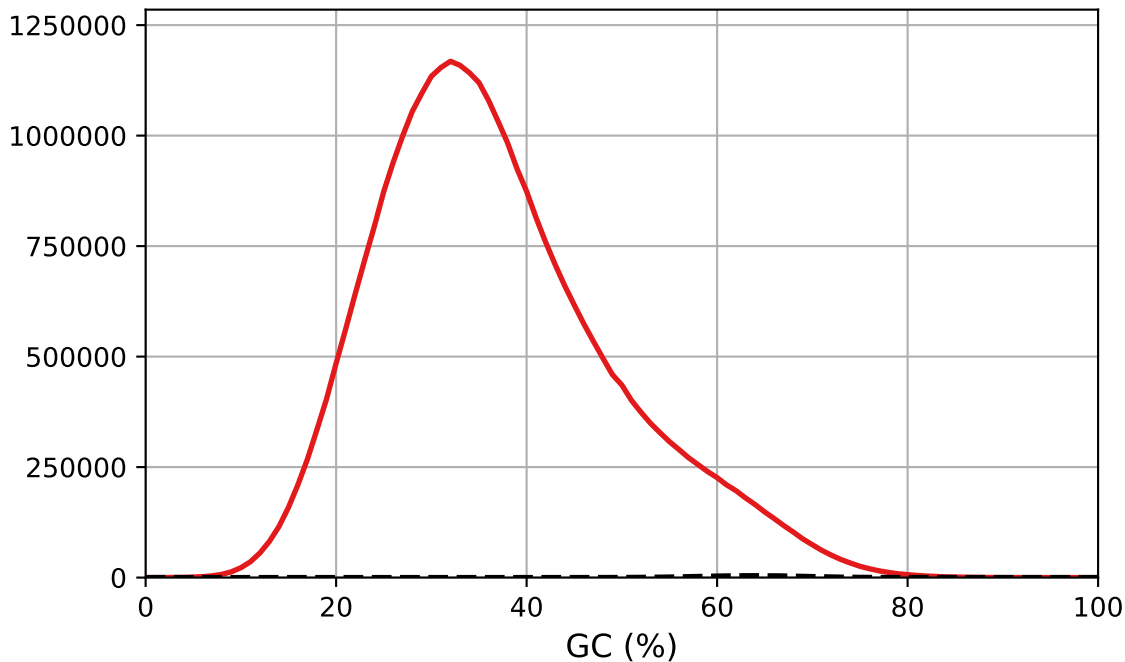


Cumulative length



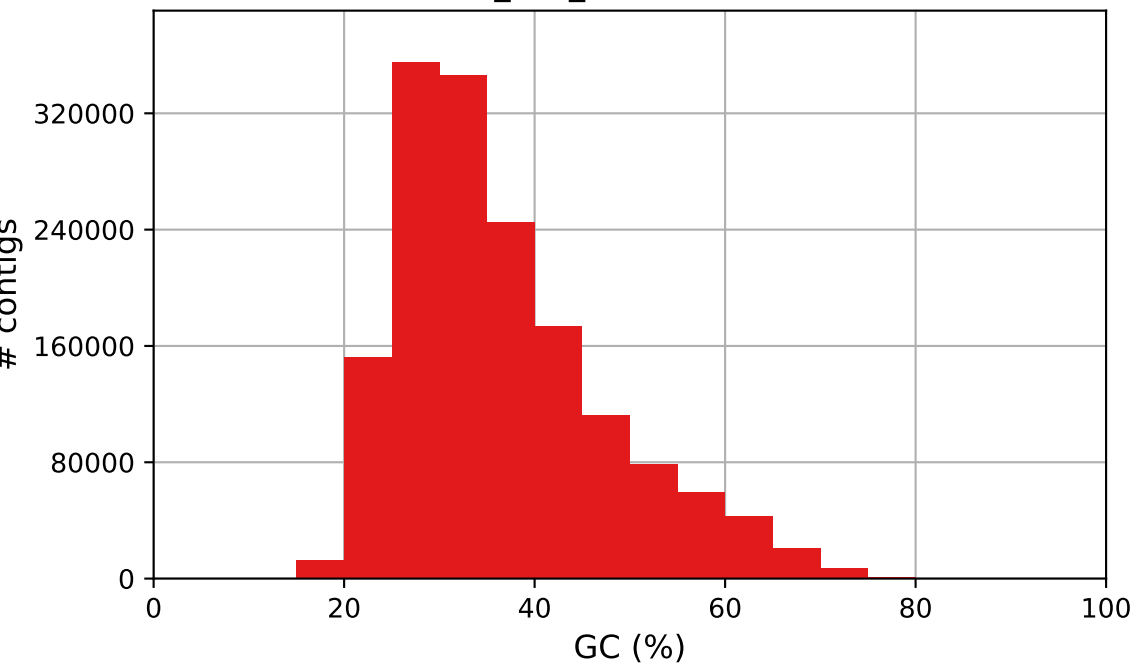
— TARA\_ION\_RAW    - - Reference

## GC content



— TARA\_ION\_RAW    - - Reference

TARA\_ION\_RAW GC content



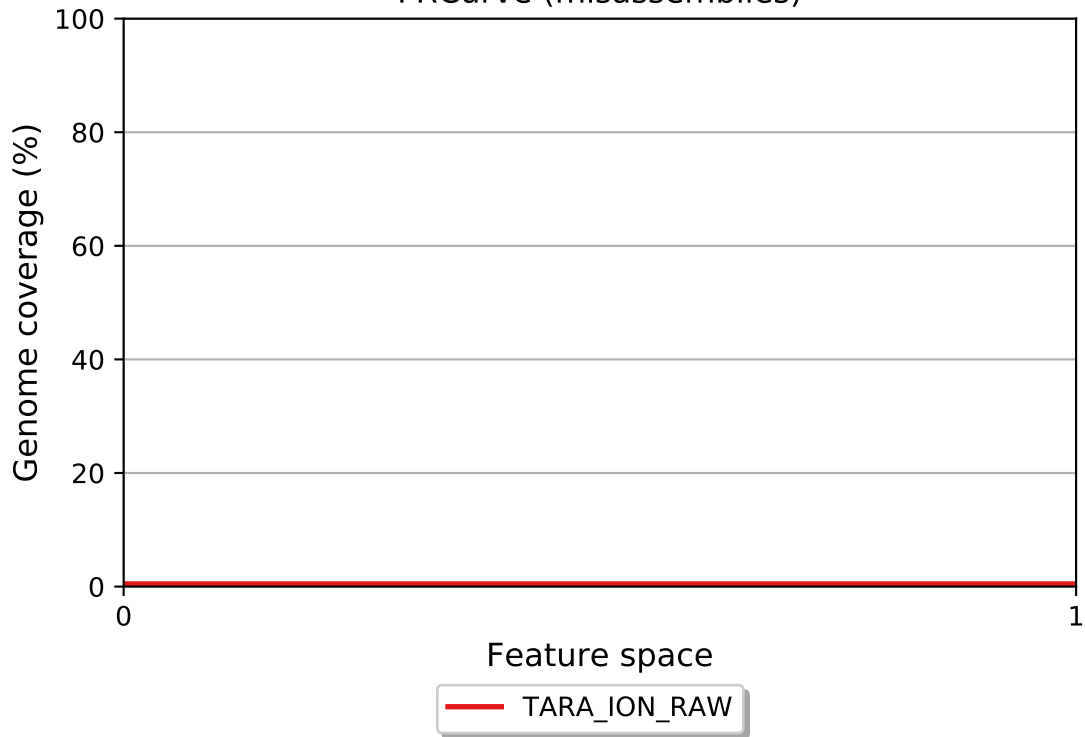
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## Misassemblies

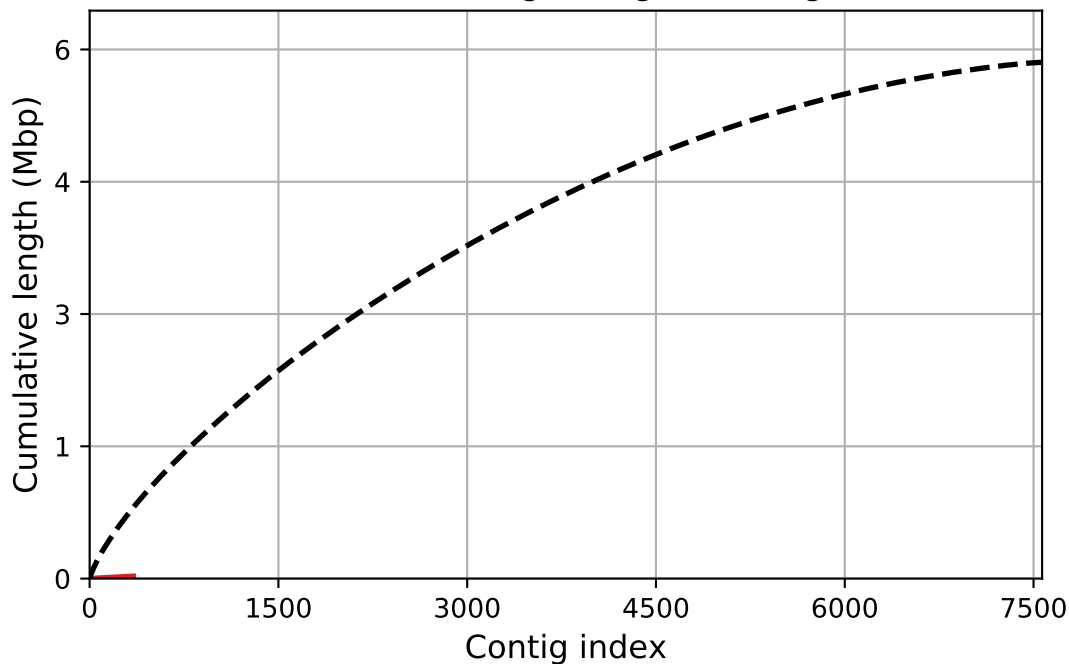




FRCurve (misassemblies)

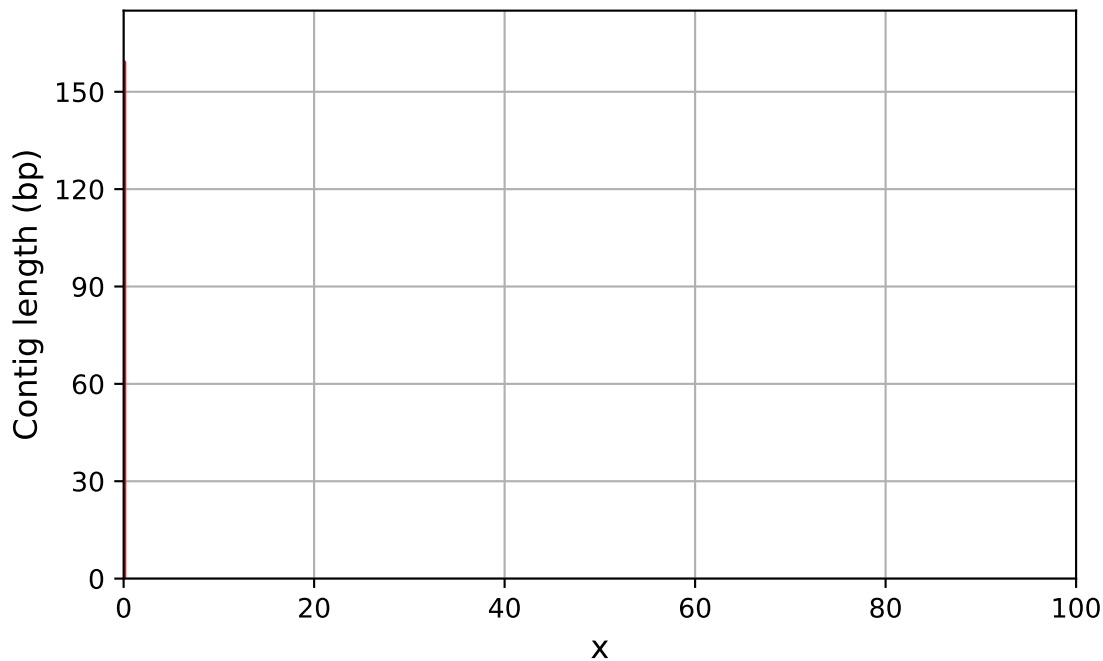


Cumulative length (aligned contigs)



TARA\_ION\_RAW    Reference

NAx



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