

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	7658814
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	4
# unaligned contigs	1608354 + 382 part
Unaligned length	3246704486
Genome fraction (%)	0.063
Duplication ratio	6.884
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12214.37
# indels per 100 kbp	166.18
Largest alignment	159
Total aligned length	31324

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

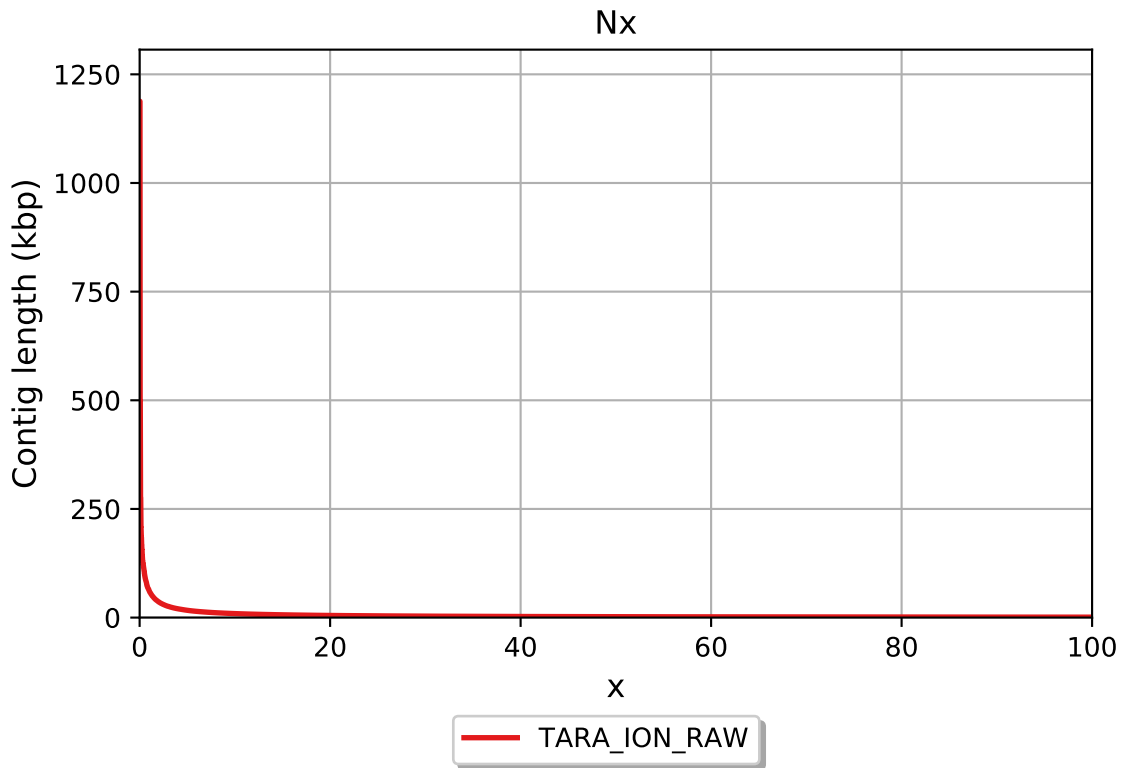
	TARA_ION_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	378
# possible misassemblies	457
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	588
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	11

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).

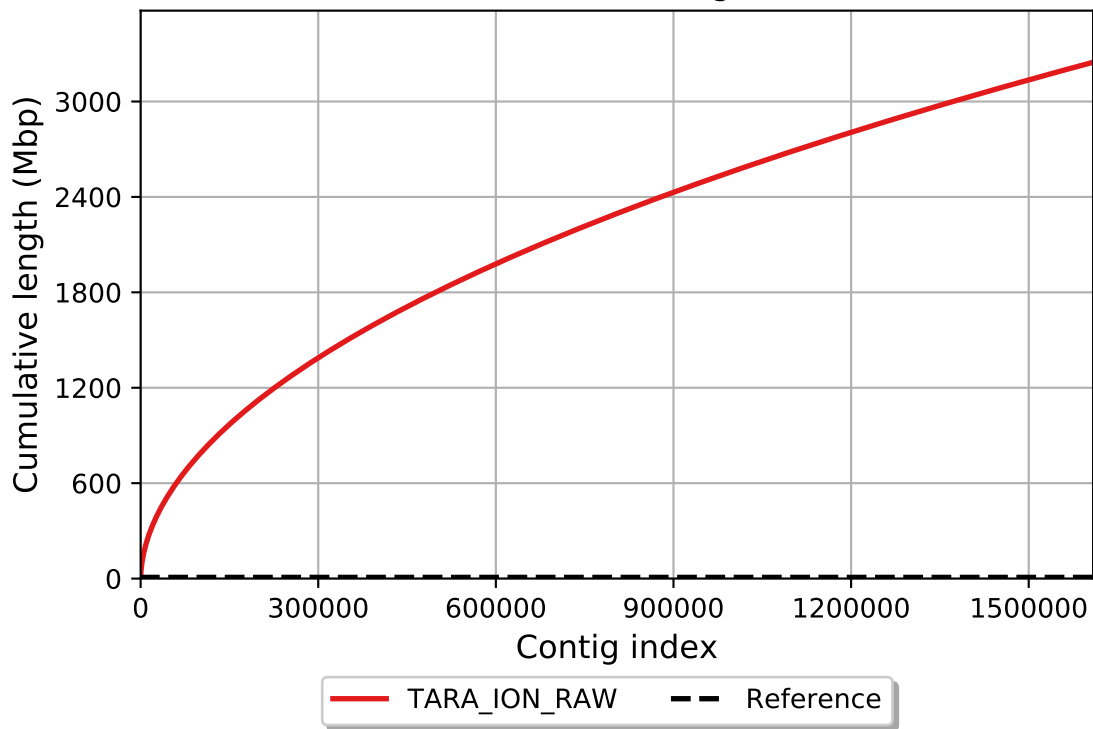
Unaligned report

	TARA_ION_RAW
# fully unaligned contigs	1608354
Fully unaligned length	3244794546
# partially unaligned contigs	382
Partially unaligned length	1909940
# N's	0

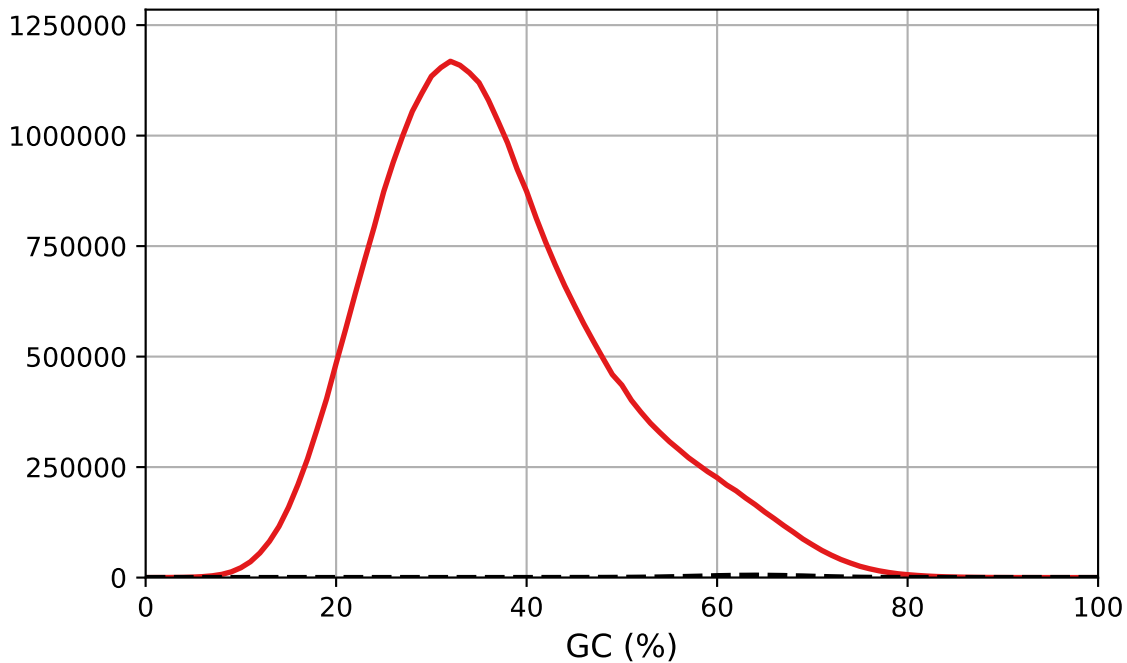
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



Cumulative length

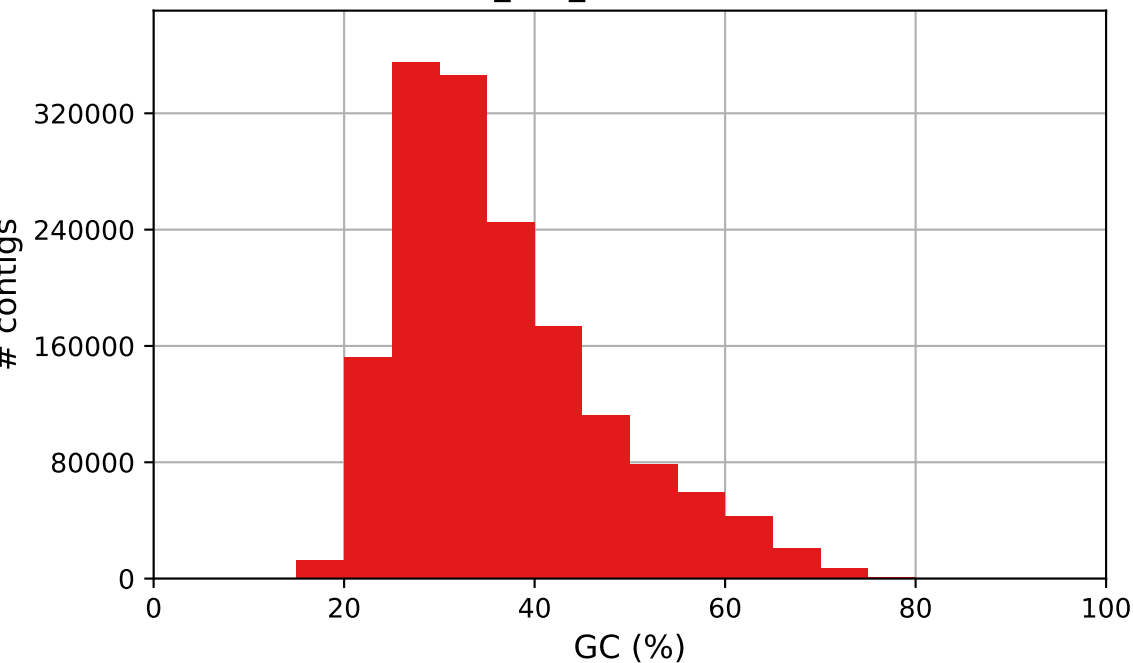


GC content



— TARA_ION_RAW - - Reference

TARA_ION_RAW GC content

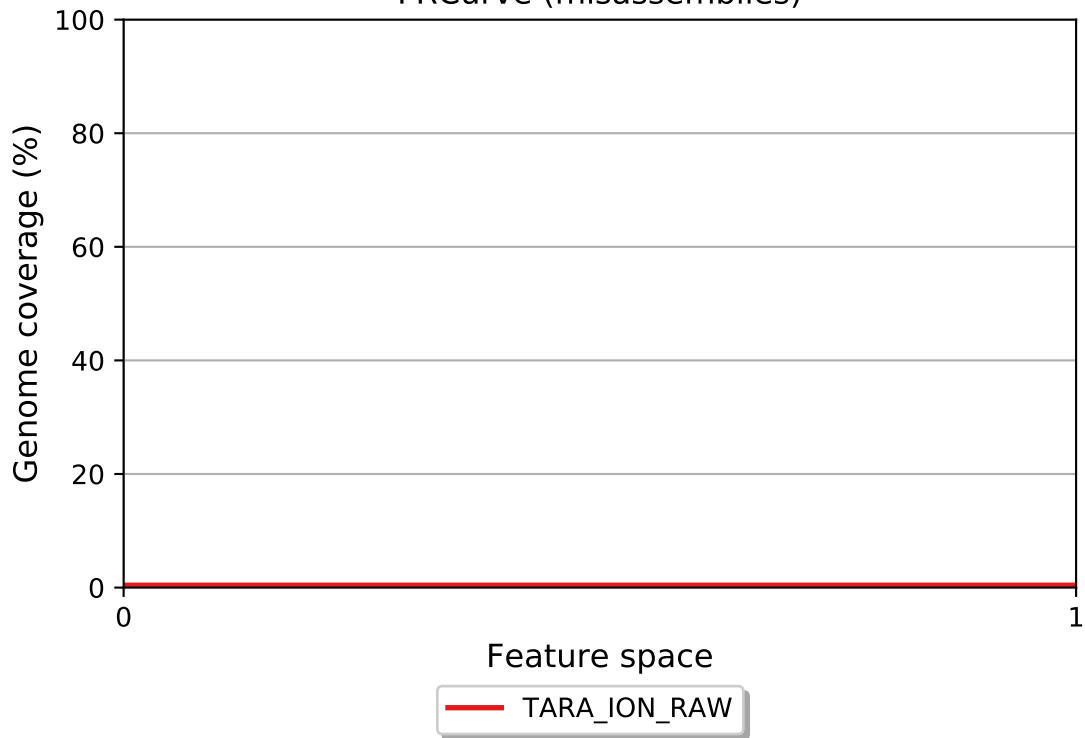


TARA_ION_RAW

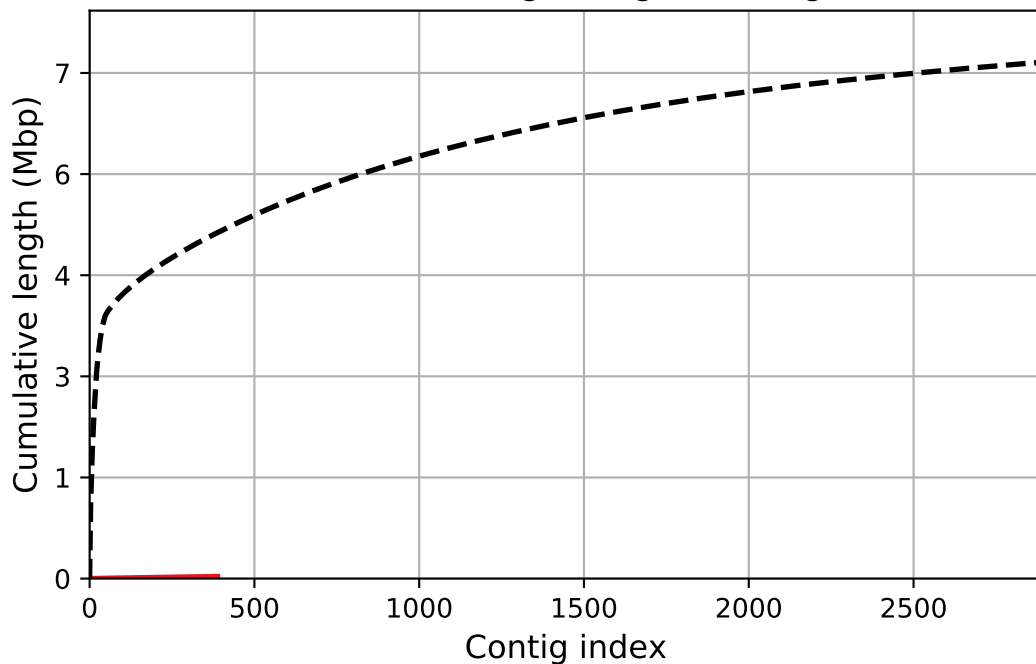
Misassemblies



FRCurve (misassemblies)

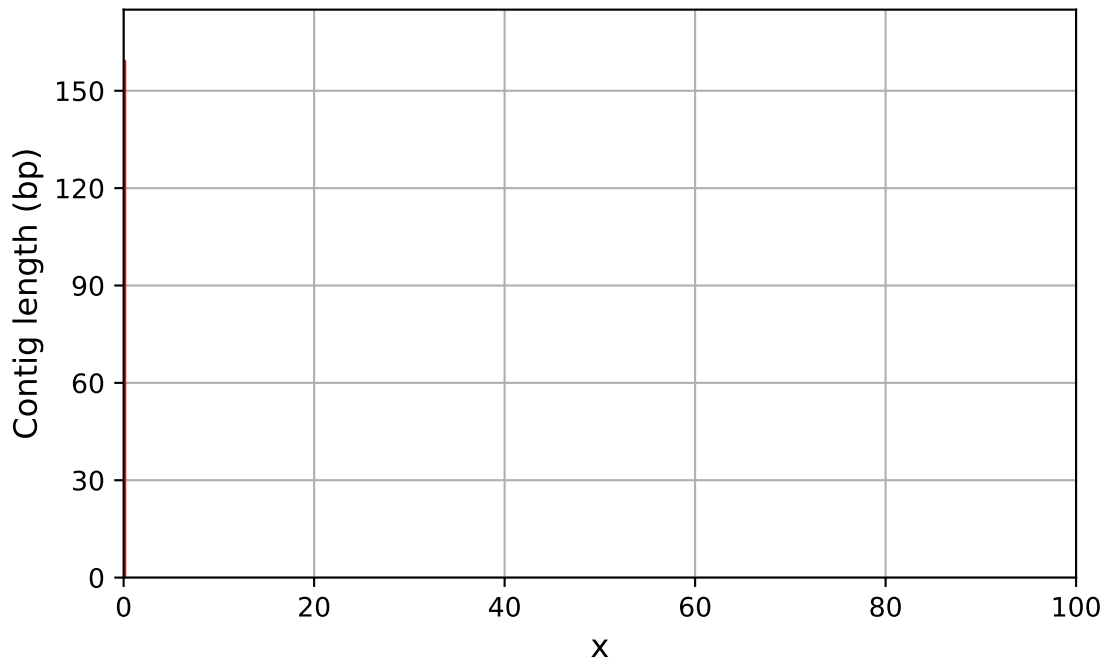


Cumulative length (aligned contigs)



— TARA_ION_RAW - - Reference

NAx



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