

## Report

	TARA_MED_RAW
# contigs (>= 0 bp)	1146485
# contigs (>= 1000 bp)	1146485
# contigs (>= 5000 bp)	75053
# contigs (>= 10000 bp)	21465
# contigs (>= 25000 bp)	3865
# contigs (>= 50000 bp)	899
Total length (>= 0 bp)	2674153874
Total length (>= 1000 bp)	2674153874
Total length (>= 5000 bp)	788856372
Total length (>= 10000 bp)	427670459
Total length (>= 25000 bp)	173275639
Total length (>= 50000 bp)	73958586
# contigs	1146485
Largest contig	743739
Total length	2674153874
Reference length	5854900
N50	2548
N75	1484
L50	235584
L75	589432
# 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	1146043 + 442 part
Unaligned length	2674118594
Genome fraction (%)	0.066
Duplication ratio	9.756
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19190.87
# indels per 100 kbp	25.93
Largest alignment	339
Total aligned length	35280

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

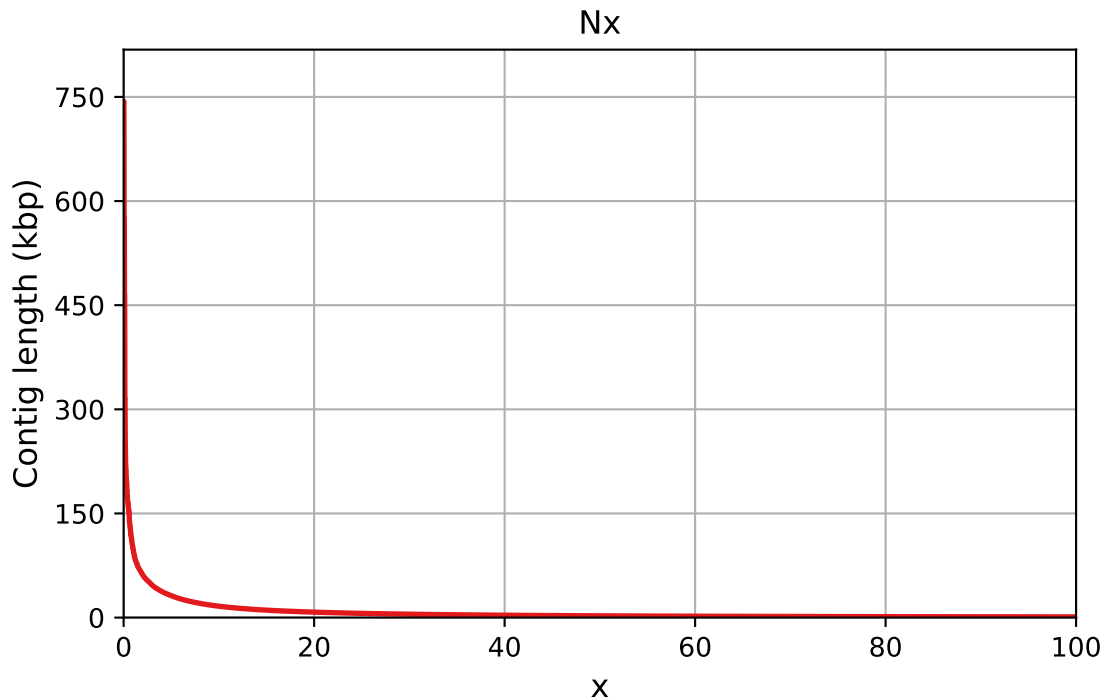
	TARA_MED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	440
# possible misassemblies	554
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	740
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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

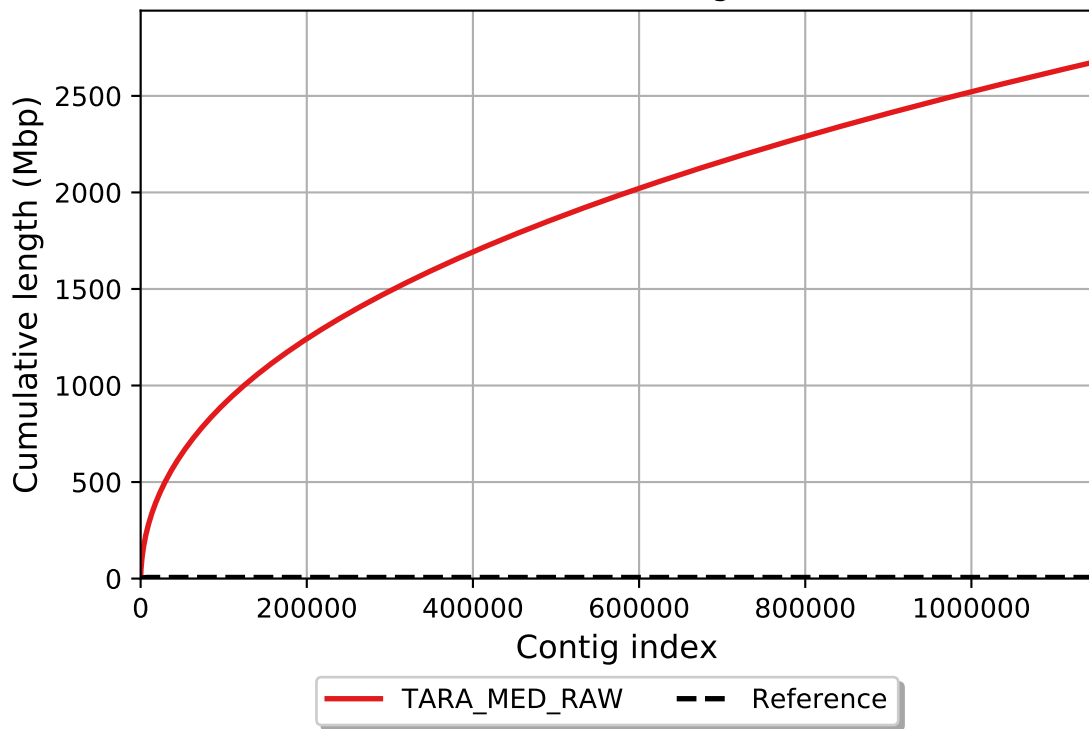
	TARA_MED_RAW
# fully unaligned contigs	1146043
Fully unaligned length	2670734762
# partially unaligned contigs	442
Partially unaligned length	3383832
# N's	0

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).

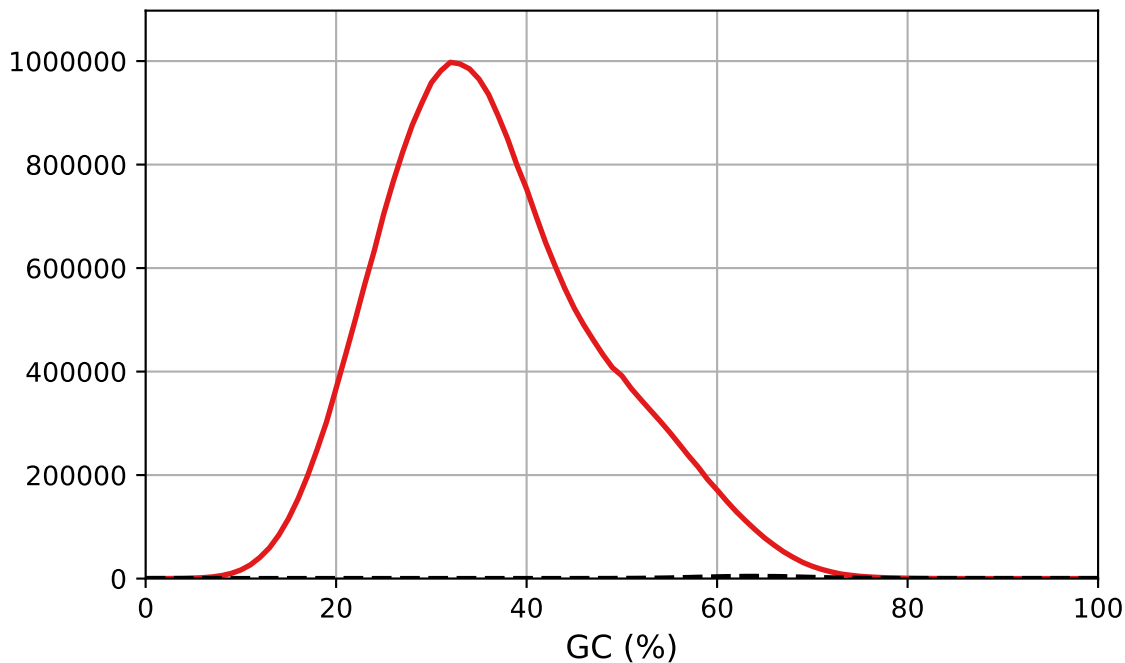


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Cumulative length

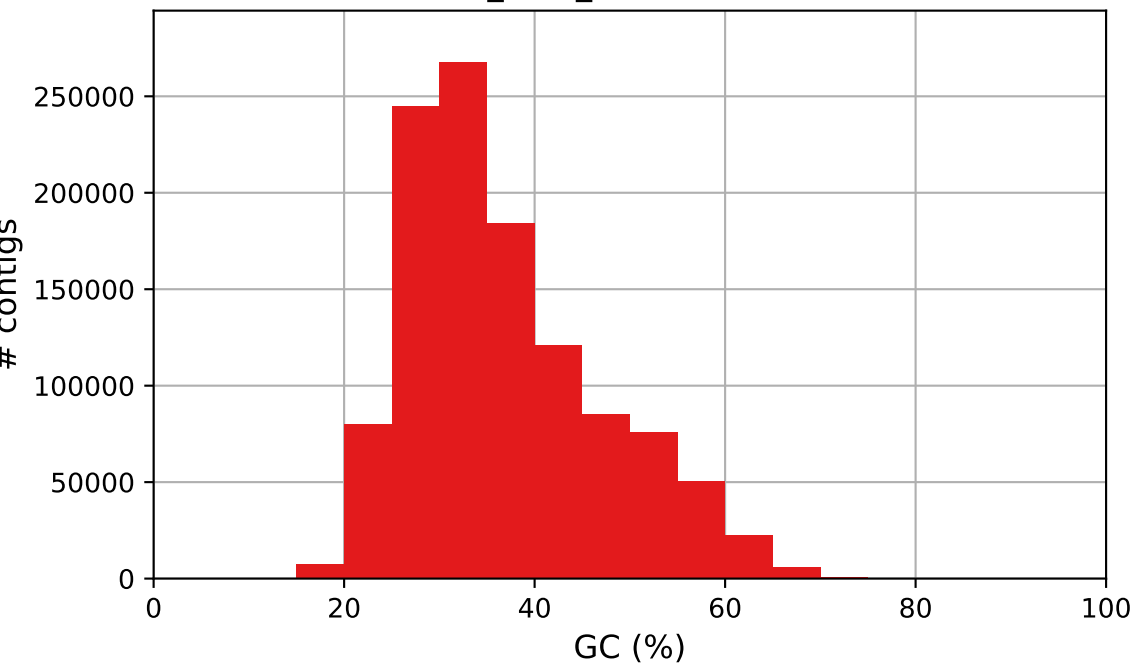


GC content



— TARA\_MED\_RAW    - - Reference

TARA\_MED\_RAW GC content



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## Misassemblies

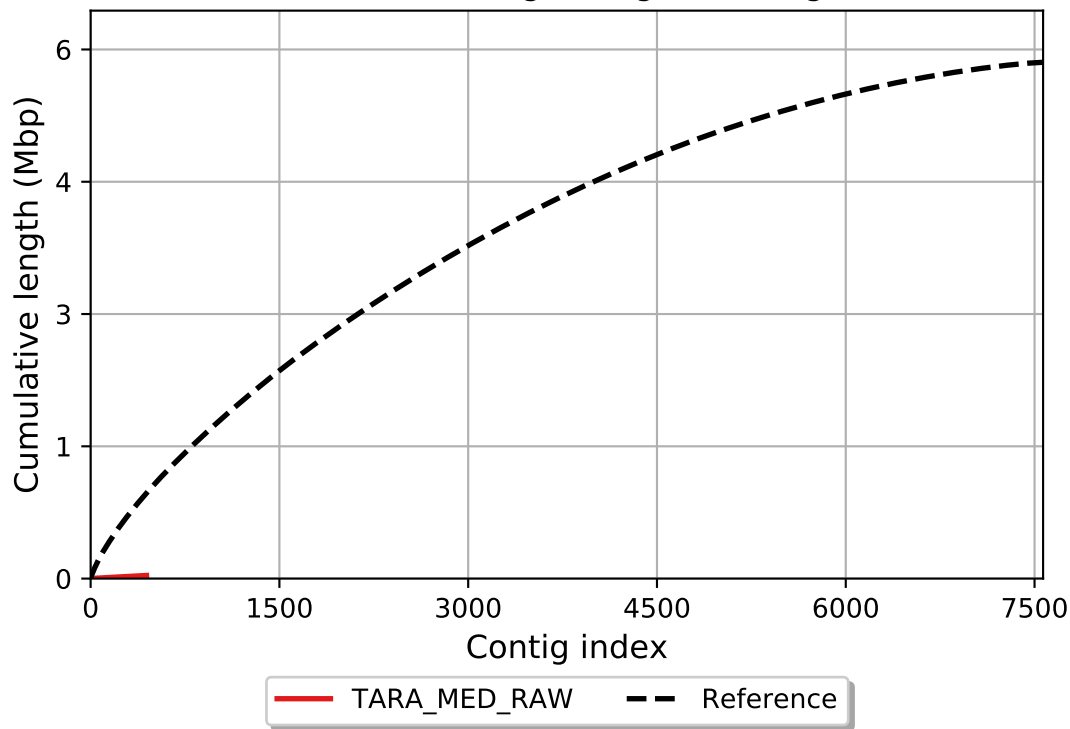




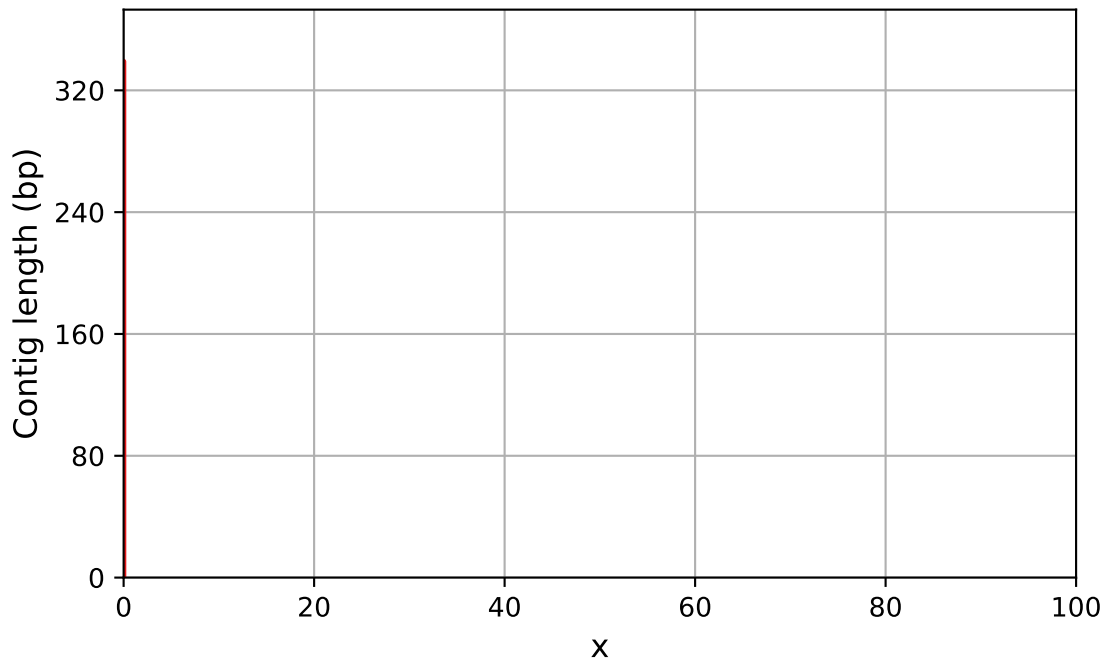
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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