

# 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	4234461
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	3
# unaligned contigs	1146444 + 41 part
Unaligned length	2674149701
Genome fraction (%)	0.039
Duplication ratio	2.646
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7826.61
# indels per 100 kbp	0.00
Largest alignment	174
Total aligned length	4173

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

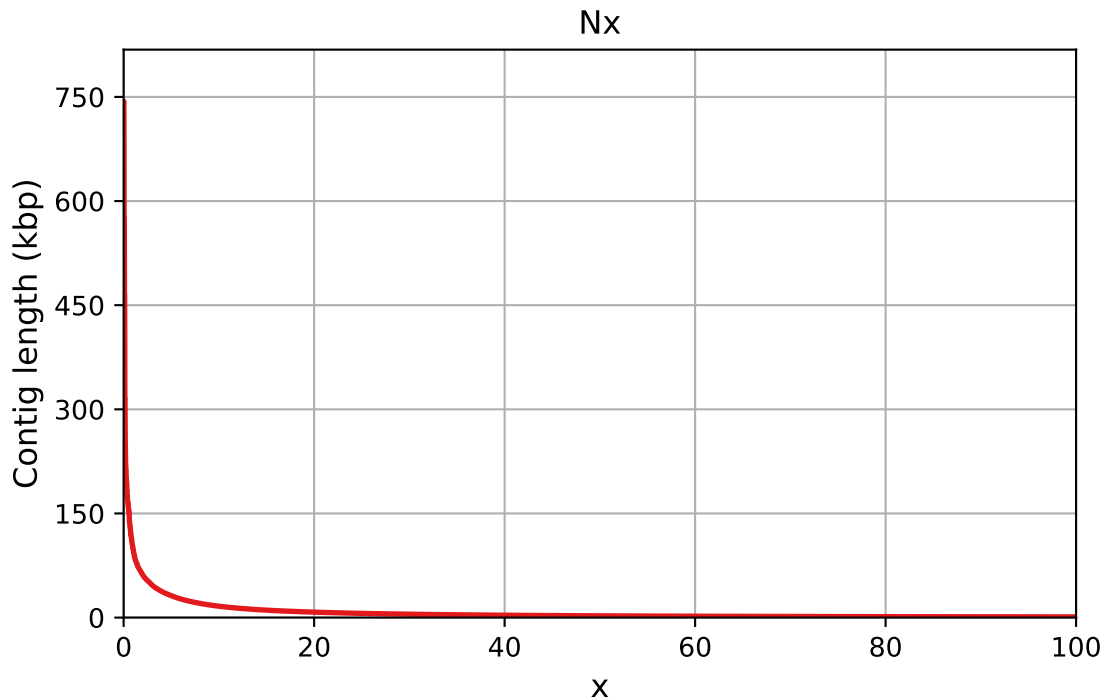
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# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	38
# possible misassemblies	45
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	130
# 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

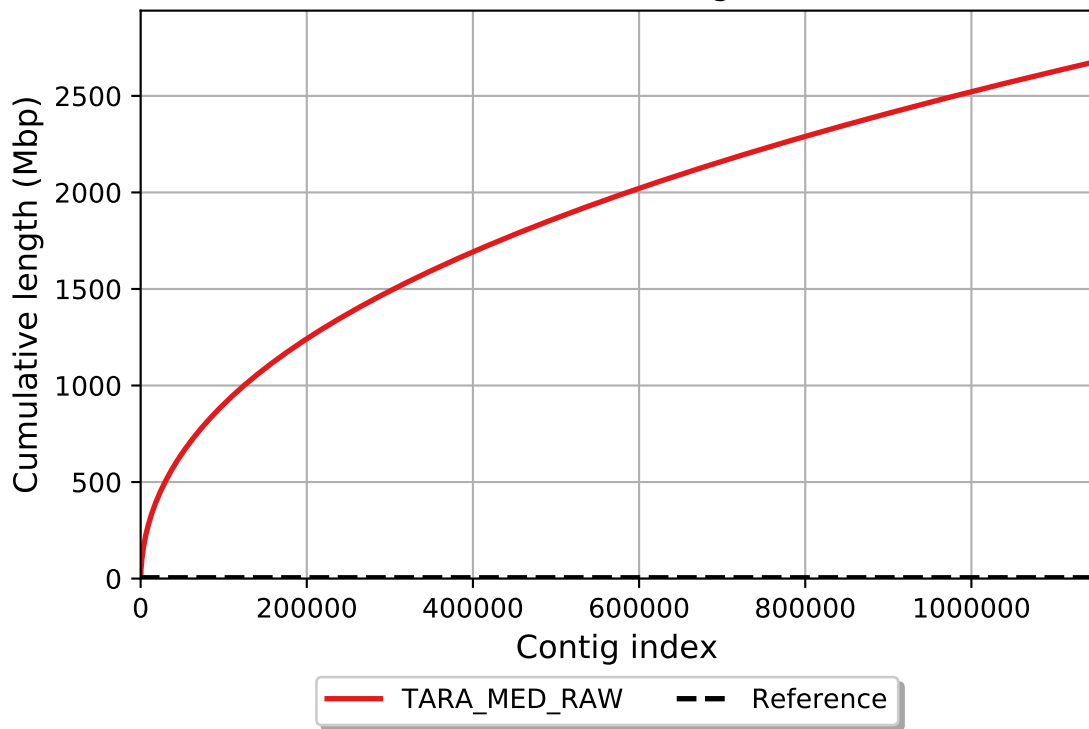
	TARA_MED_RAW
# fully unaligned contigs	1146444
Fully unaligned length	2674050898
# partially unaligned contigs	41
Partially unaligned length	98803
# N's	0

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).

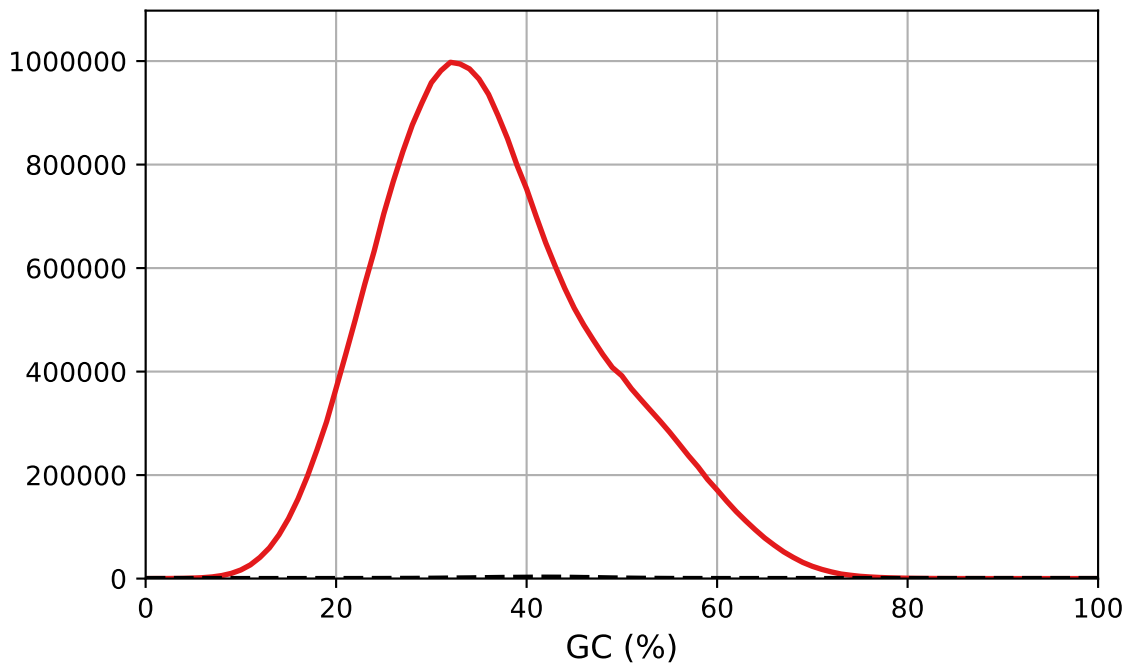


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Cumulative length

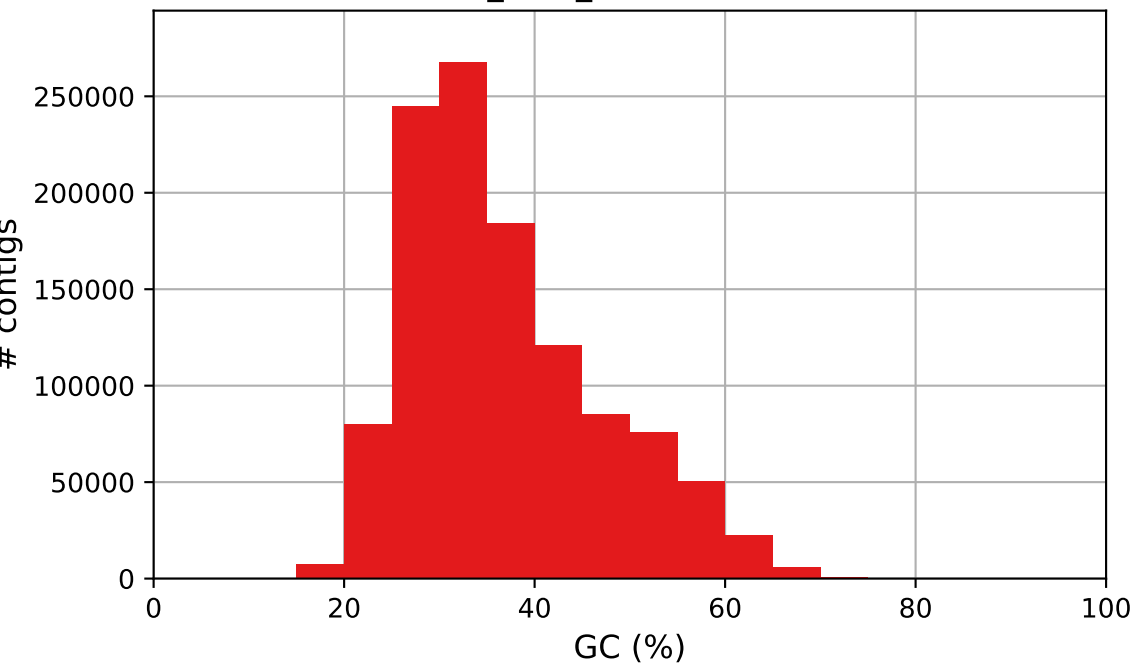


## GC content



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TARA\_MED\_RAW GC content



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## Misassemblies

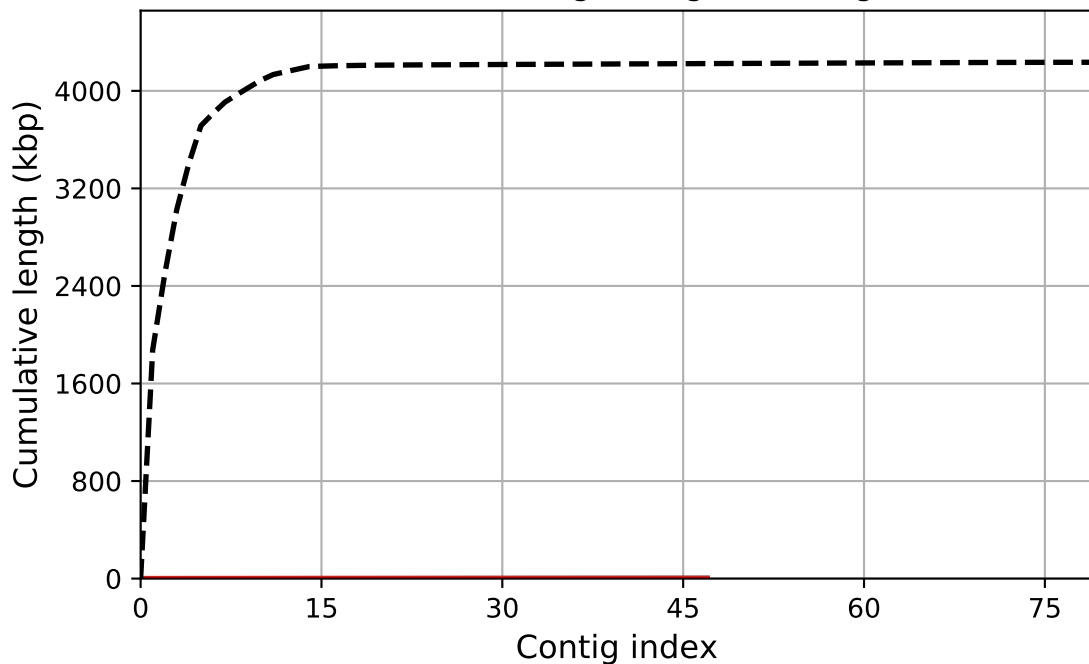




FRCurve (misassemblies)

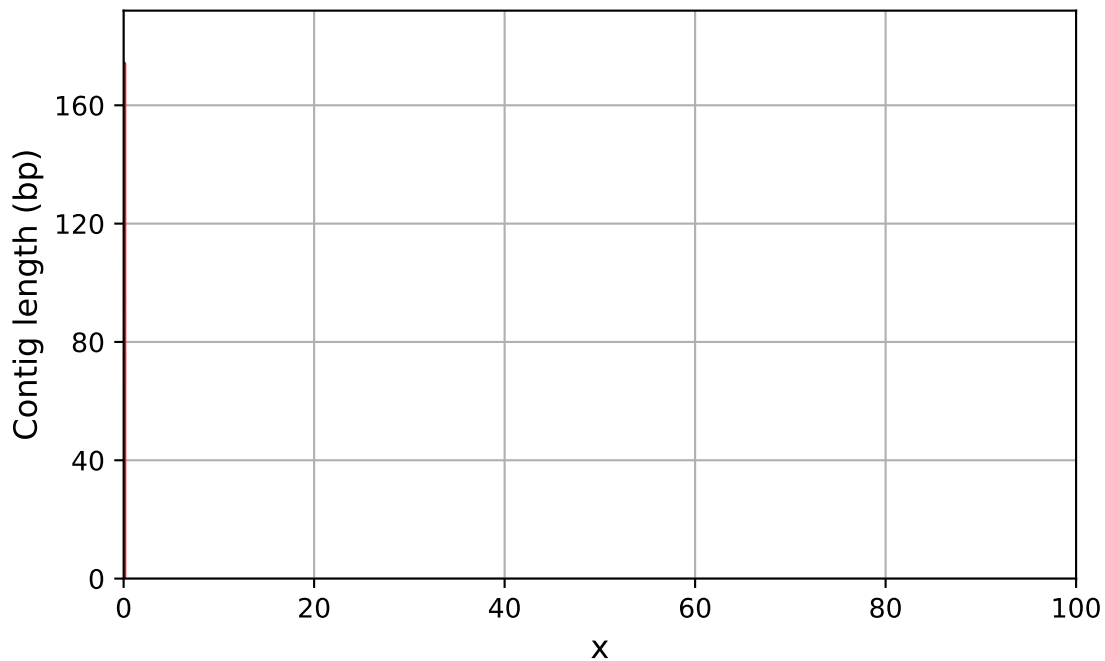


Cumulative length (aligned contigs)



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NAx



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