

# Report

	TARA_ANW_RAW
# contigs (>= 0 bp)	1267057
# contigs (>= 1000 bp)	1267057
# contigs (>= 5000 bp)	59397
# contigs (>= 10000 bp)	15465
# contigs (>= 25000 bp)	2423
# contigs (>= 50000 bp)	529
Total length (>= 0 bp)	2648602495
Total length (>= 1000 bp)	2648602495
Total length (>= 5000 bp)	593369101
Total length (>= 10000 bp)	299298940
Total length (>= 25000 bp)	113445149
Total length (>= 50000 bp)	50720126
# contigs	1267057
Largest contig	1019813
Total length	2648602495
Reference length	7658814
N50	2138
N75	1378
L50	302257
L75	696663
# 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	12
# unaligned contigs	1266628 + 428 part
Unaligned length	2648562087
Genome fraction (%)	0.198
Duplication ratio	3.097
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6331.29
# indels per 100 kbp	79.22
Largest alignment	594
Total aligned length	39805

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

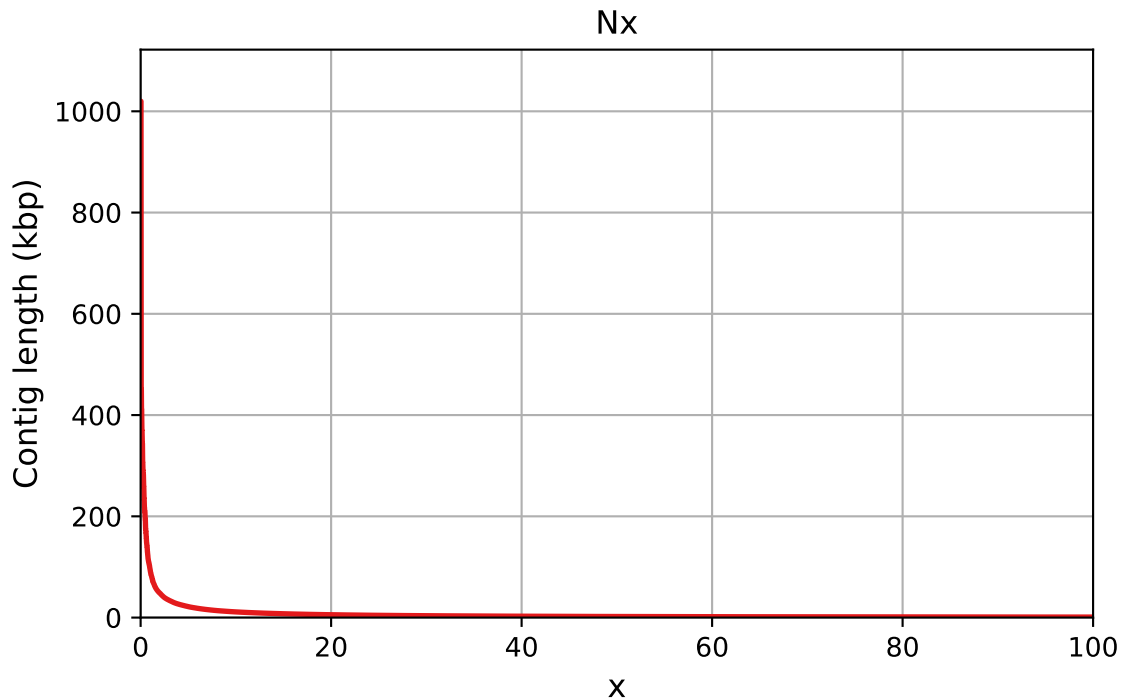
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	417
# possible misassemblies	540
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	12
# mismatches	959
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	14

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).

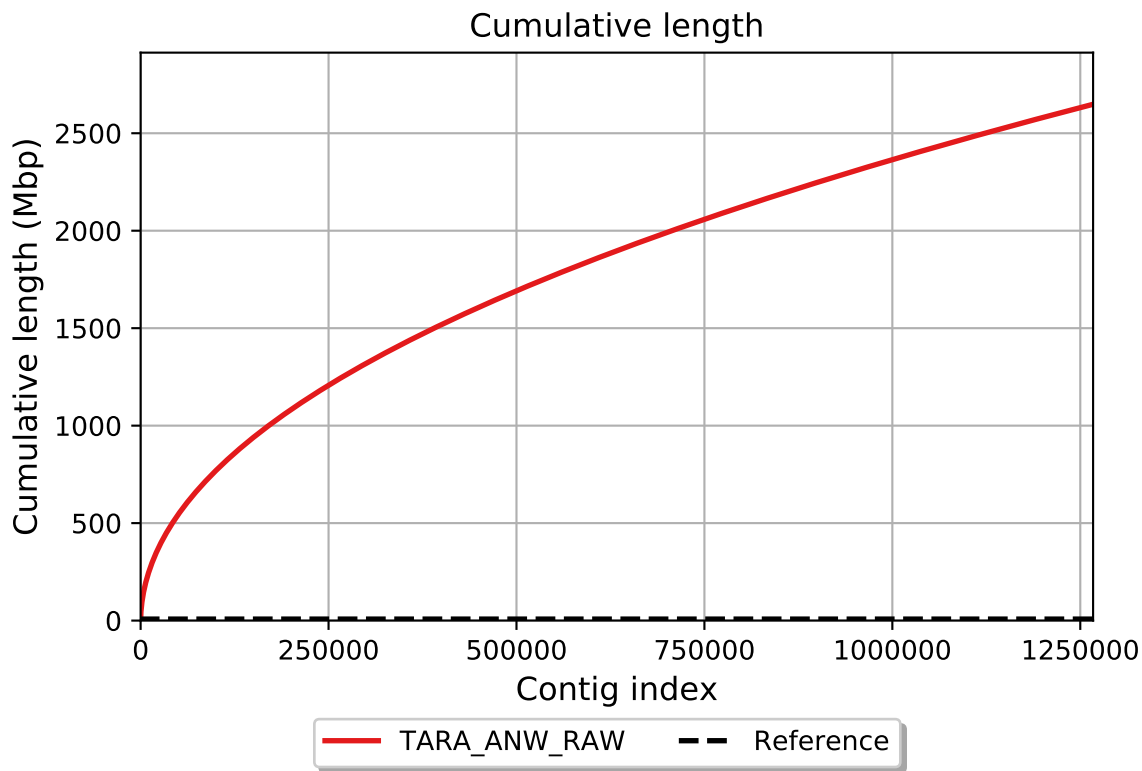
## Unaligned report

	TARA_ANW_RAW
# fully unaligned contigs	1266628
Fully unaligned length	2644235097
# partially unaligned contigs	428
Partially unaligned length	4326990
# N's	0

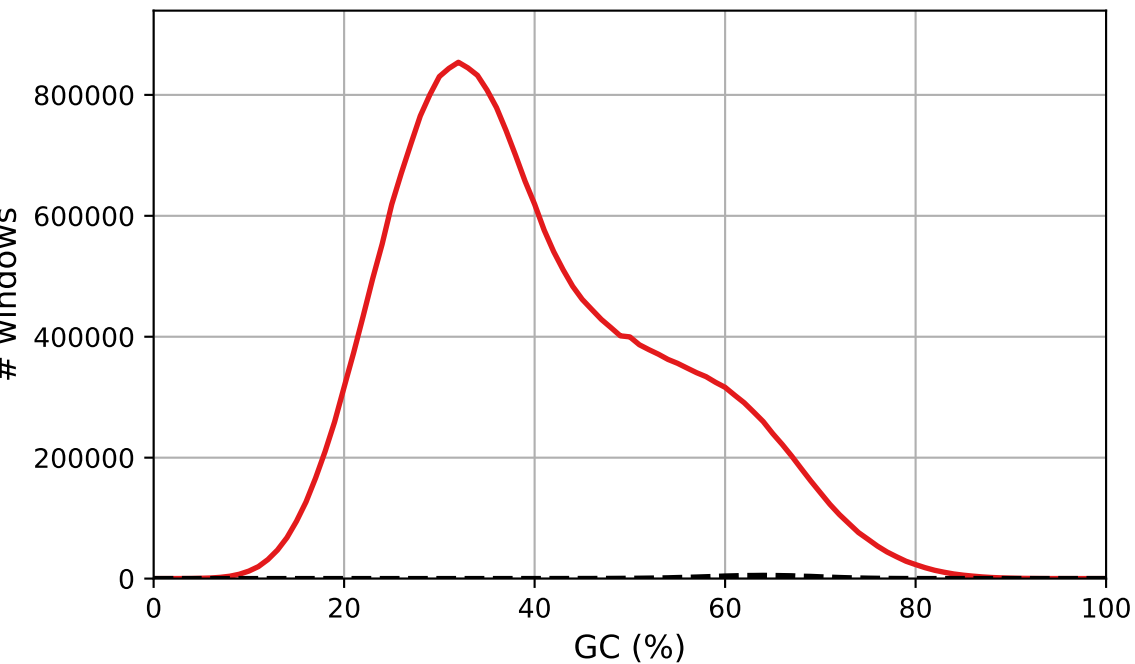
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



— TARA\_ANW\_RAW

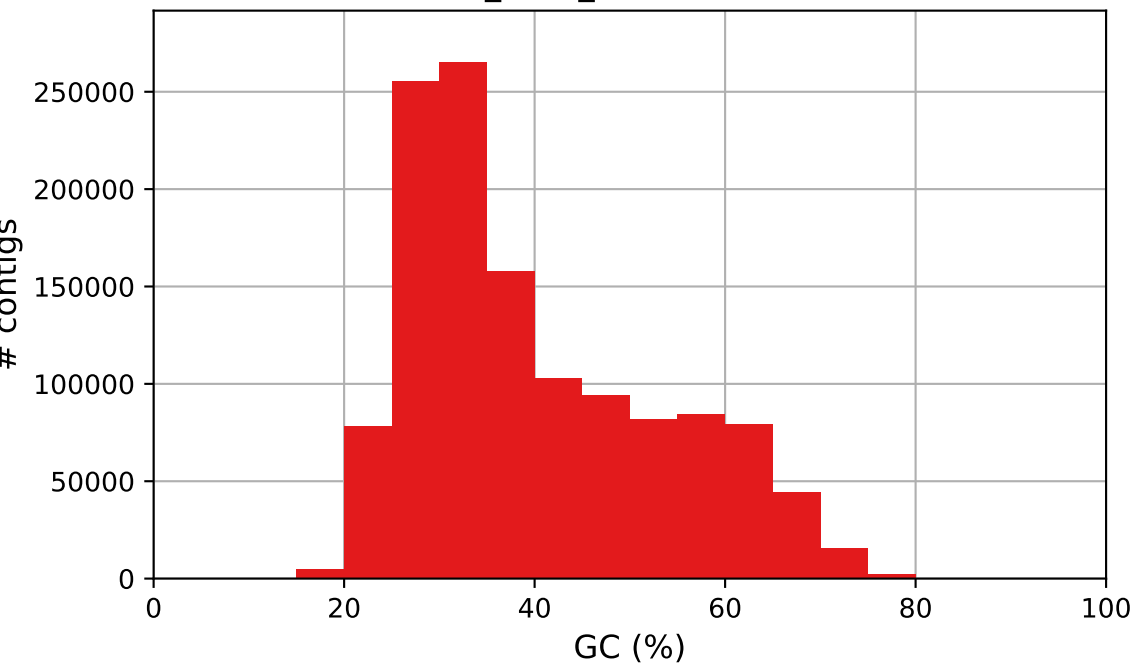


GC content



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TARA\_ANW\_RAW GC content



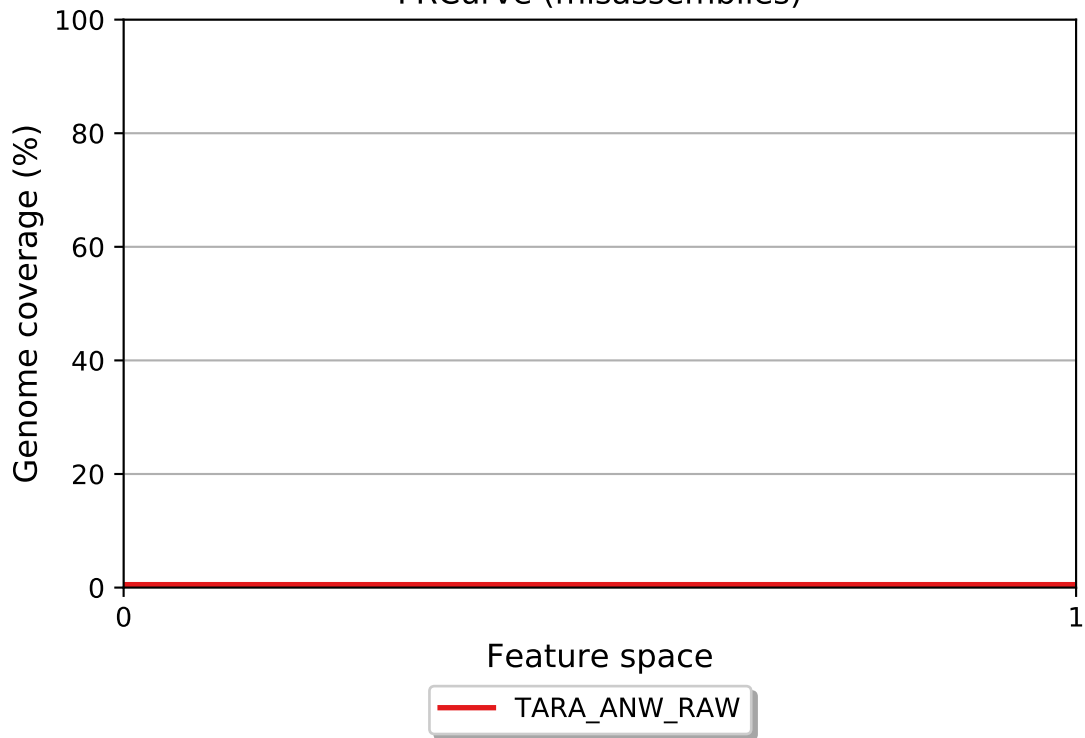
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## Misassemblies

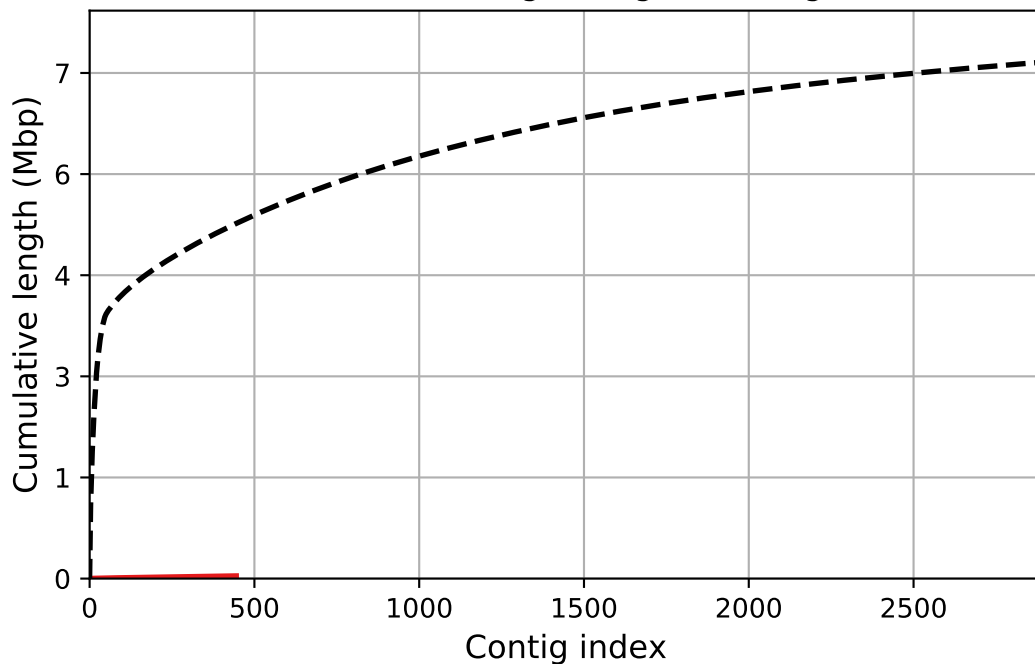




FRCurve (misassemblies)

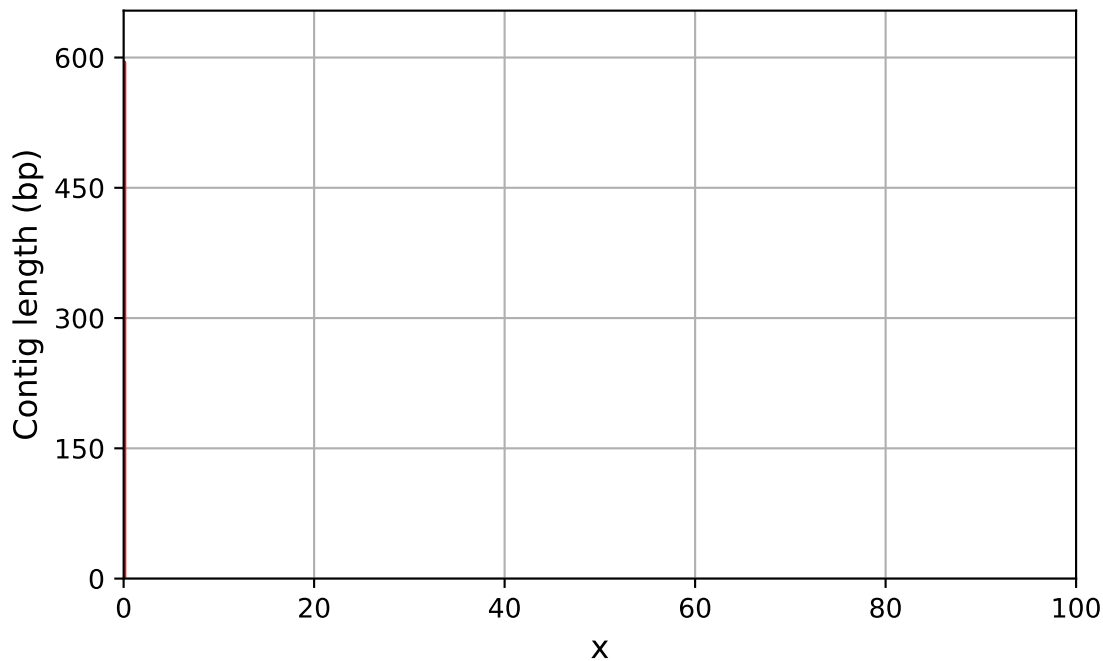


Cumulative length (aligned contigs)



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NAx



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