

# 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	3561038
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	2
# unaligned contigs	1267006 + 51 part
Unaligned length	2648597822
Genome fraction (%)	0.025
Duplication ratio	5.353
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17182.13
# indels per 100 kbp	0.00
Largest alignment	145
Total aligned length	4673

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

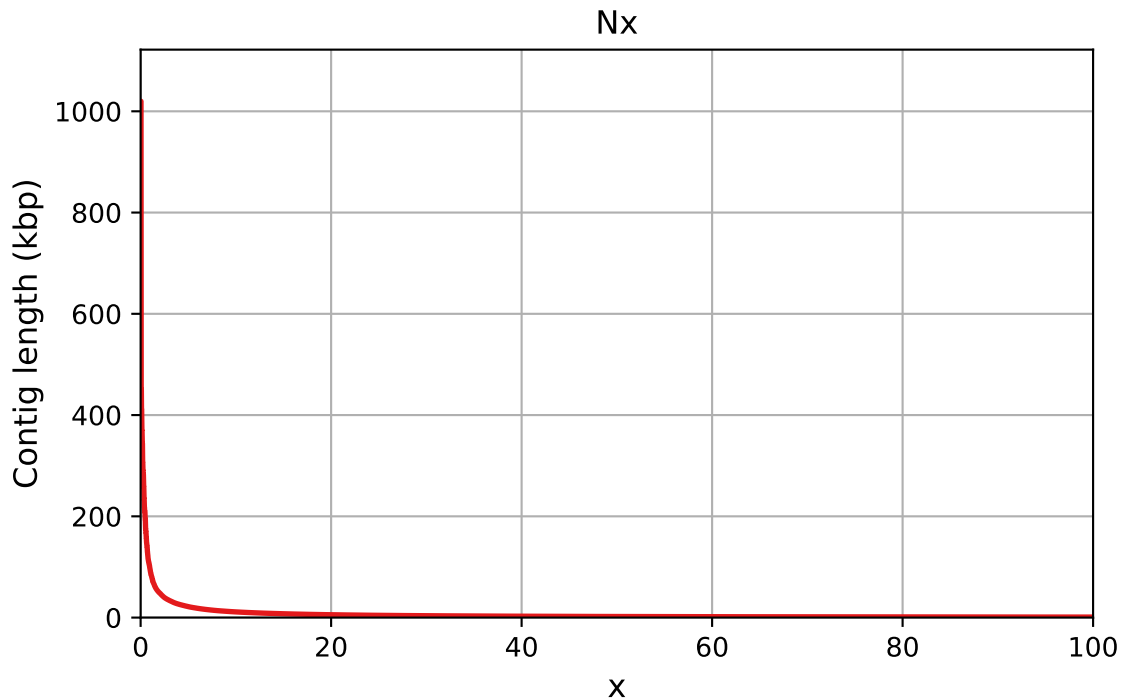
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	49
# possible misassemblies	56
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	150
# 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

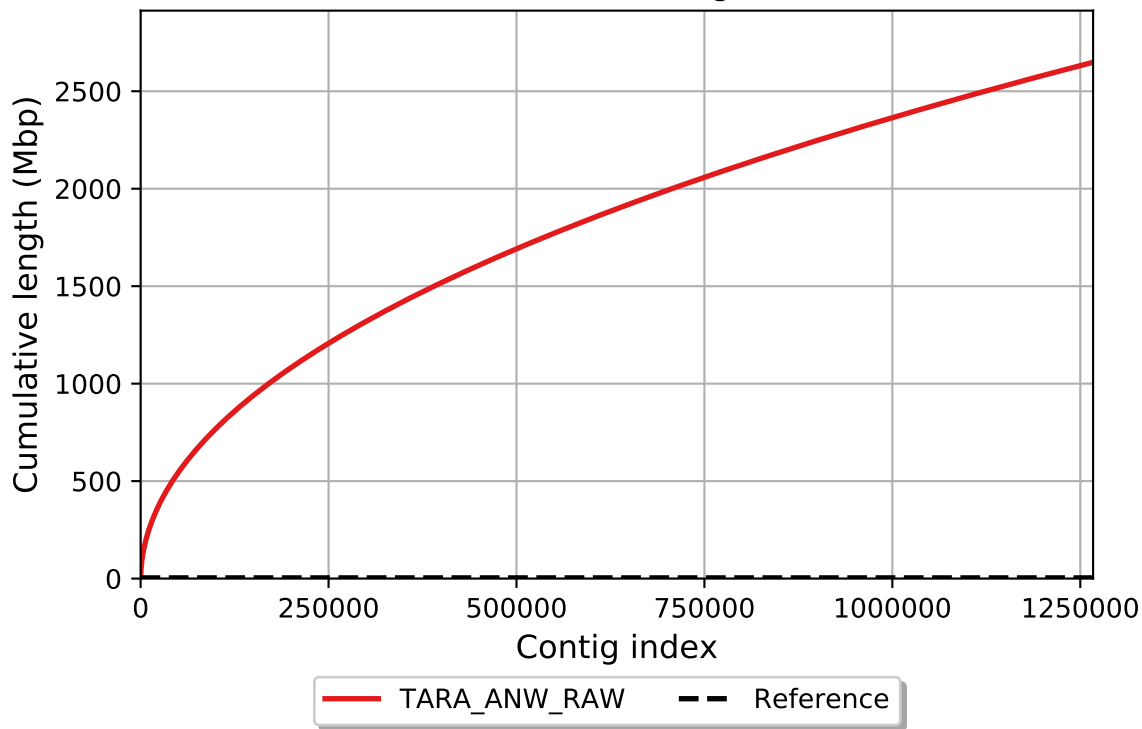
	TARA_ANW_RAW
# fully unaligned contigs	1267006
Fully unaligned length	2648402274
# partially unaligned contigs	51
Partially unaligned length	195548
# N's	0

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).

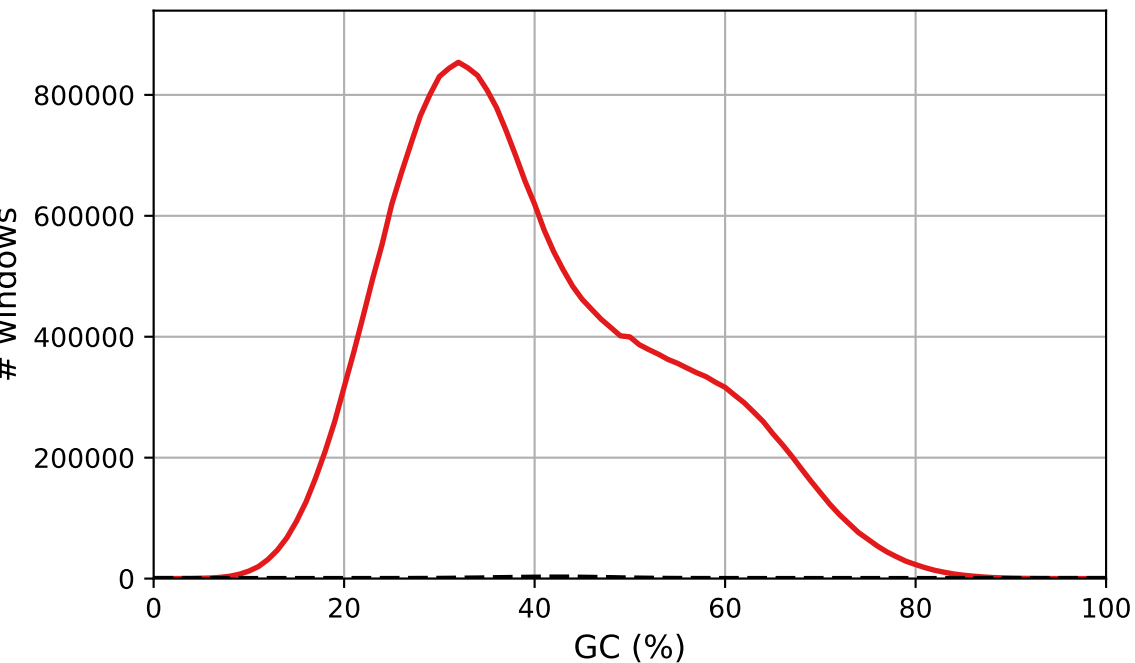


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Cumulative length

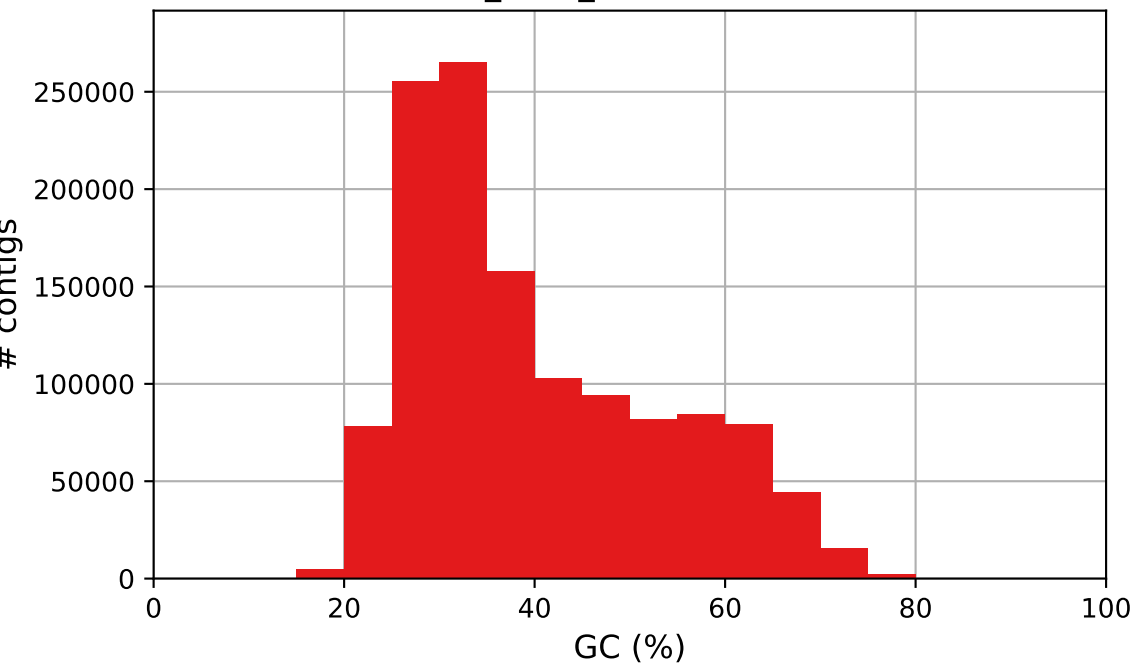


GC content



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TARA\_ANW\_RAW GC content



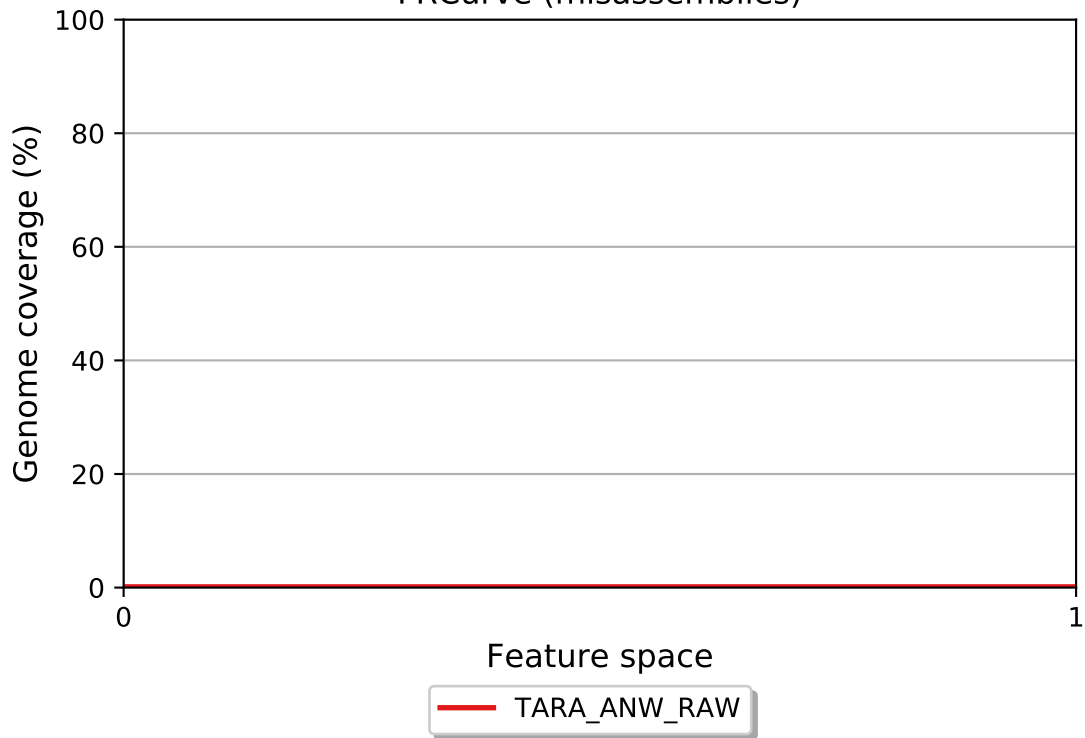
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## Misassemblies

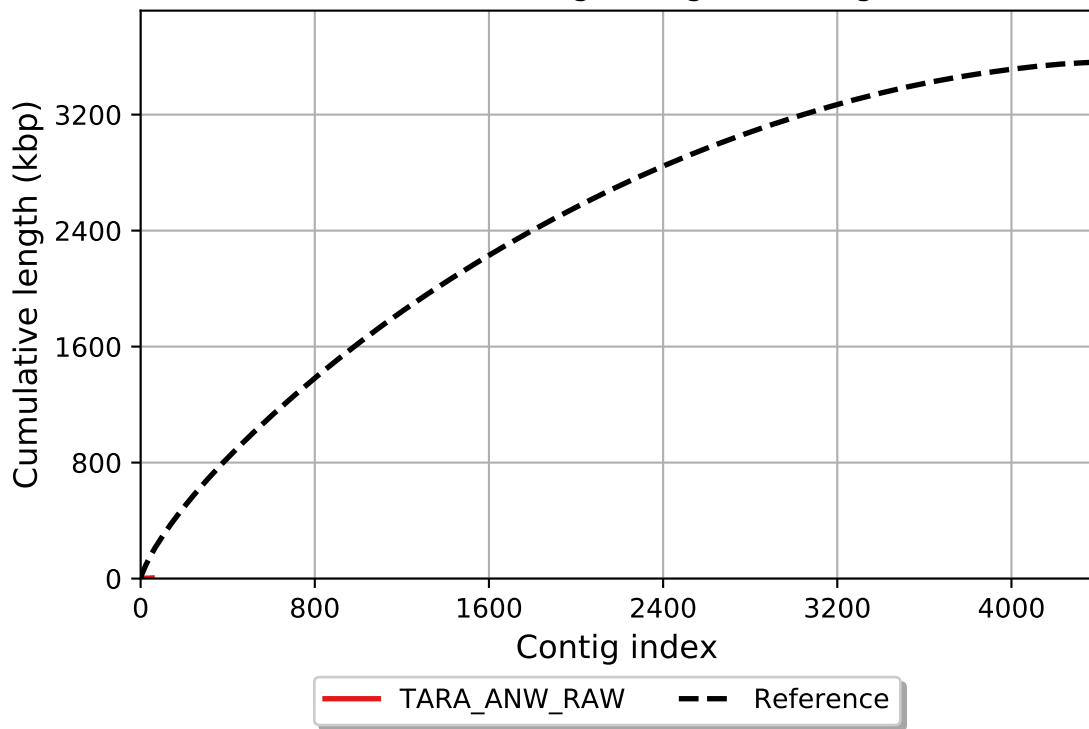




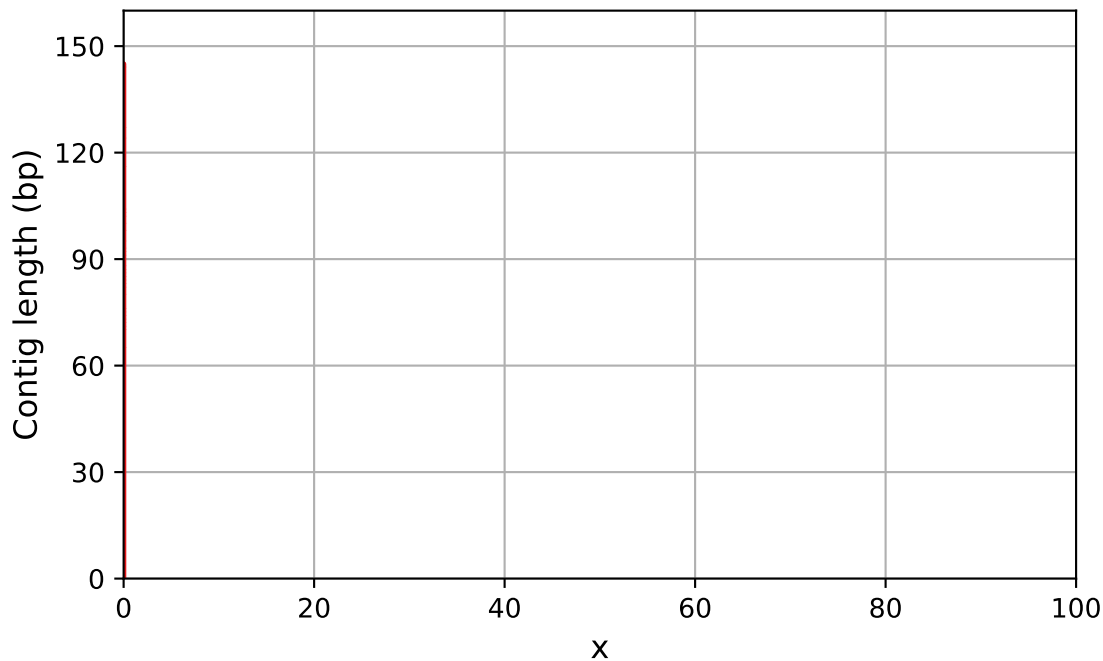
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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