

# Report

	TARA_ANE_RAW
# contigs (>= 0 bp)	1382239
# contigs (>= 1000 bp)	1382239
# contigs (>= 5000 bp)	67373
# contigs (>= 10000 bp)	17109
# contigs (>= 25000 bp)	2572
# contigs (>= 50000 bp)	438
Total length (>= 0 bp)	2894913213
Total length (>= 1000 bp)	2894913213
Total length (>= 5000 bp)	647998330
Total length (>= 10000 bp)	312384860
Total length (>= 25000 bp)	104590748
Total length (>= 50000 bp)	33849995
# contigs	1382239
Largest contig	1038928
Total length	2894913213
Reference length	4234461
N50	2156
N75	1382
L50	330727
L75	759418
# 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	1382199 + 40 part
Unaligned length	2894909221
Genome fraction (%)	0.023
Duplication ratio	4.213
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13043.48
# indels per 100 kbp	0.00
Largest alignment	120
Total aligned length	3992

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

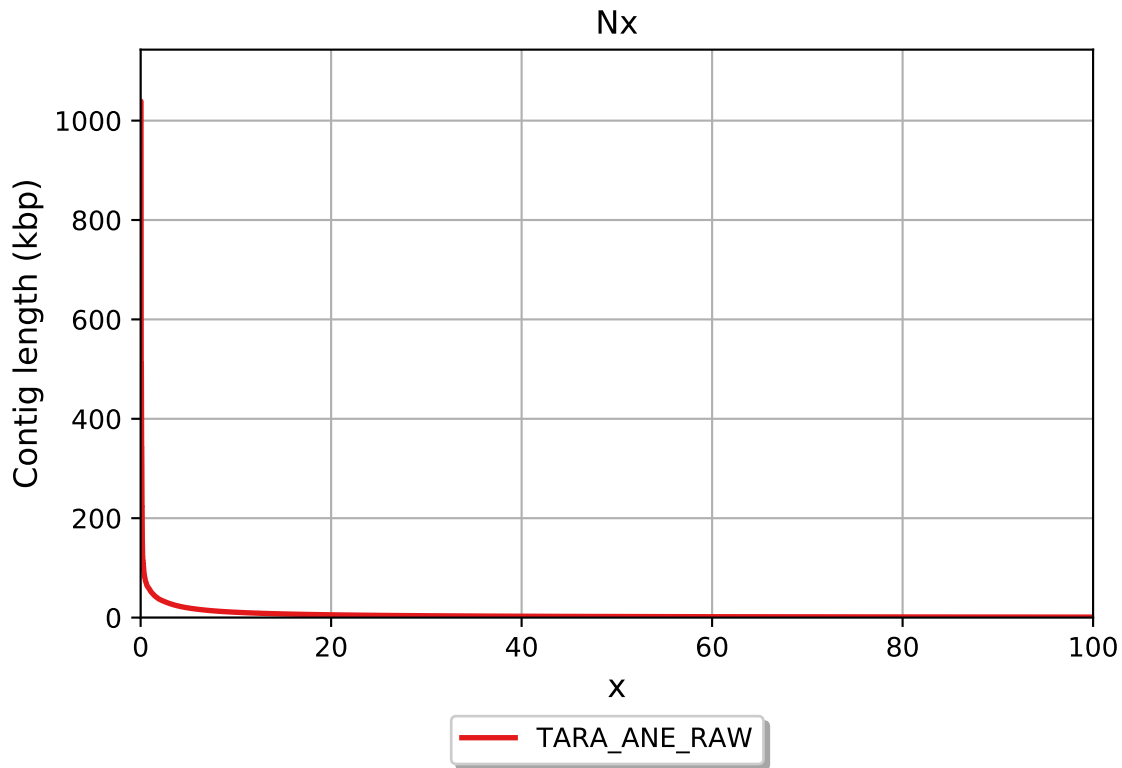
	TARA_ANE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	36
# possible misassemblies	37
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	126
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

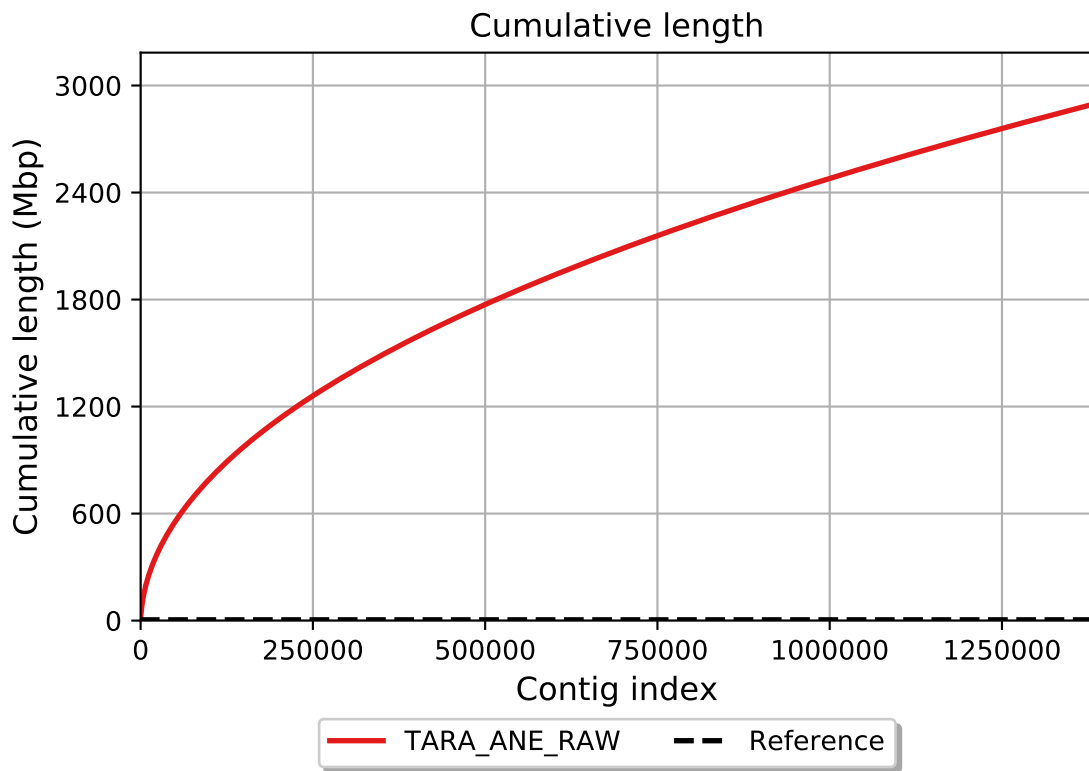
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

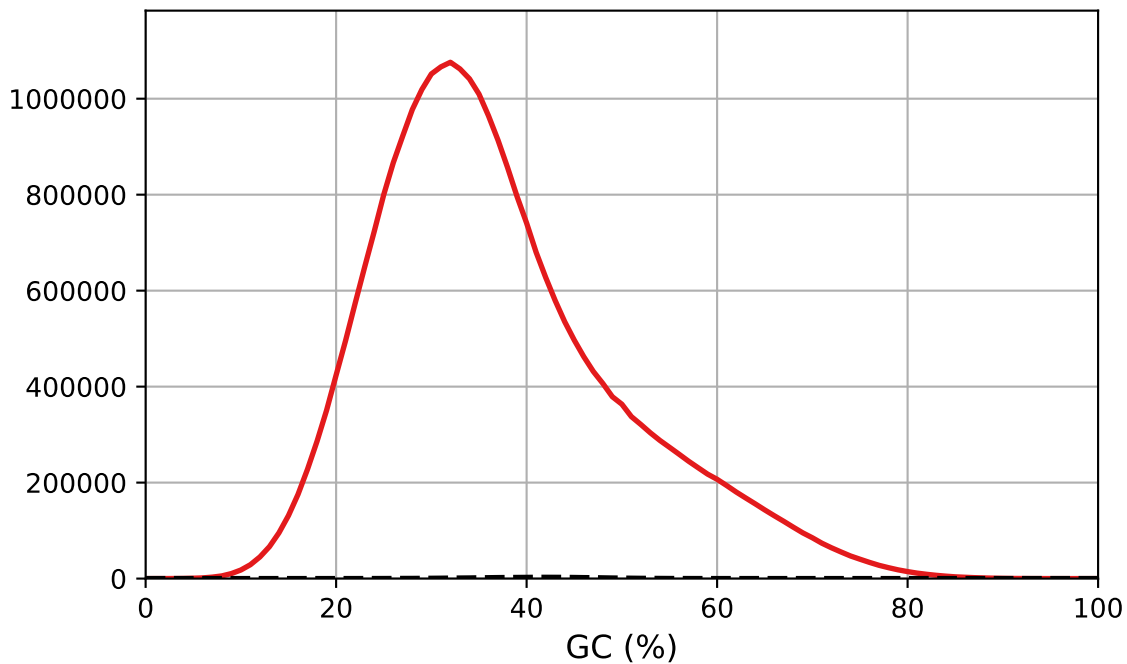
	TARA_ANE_RAW
# fully unaligned contigs	1382199
Fully unaligned length	2894799316
# partially unaligned contigs	40
Partially unaligned length	109905
# N's	0

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).



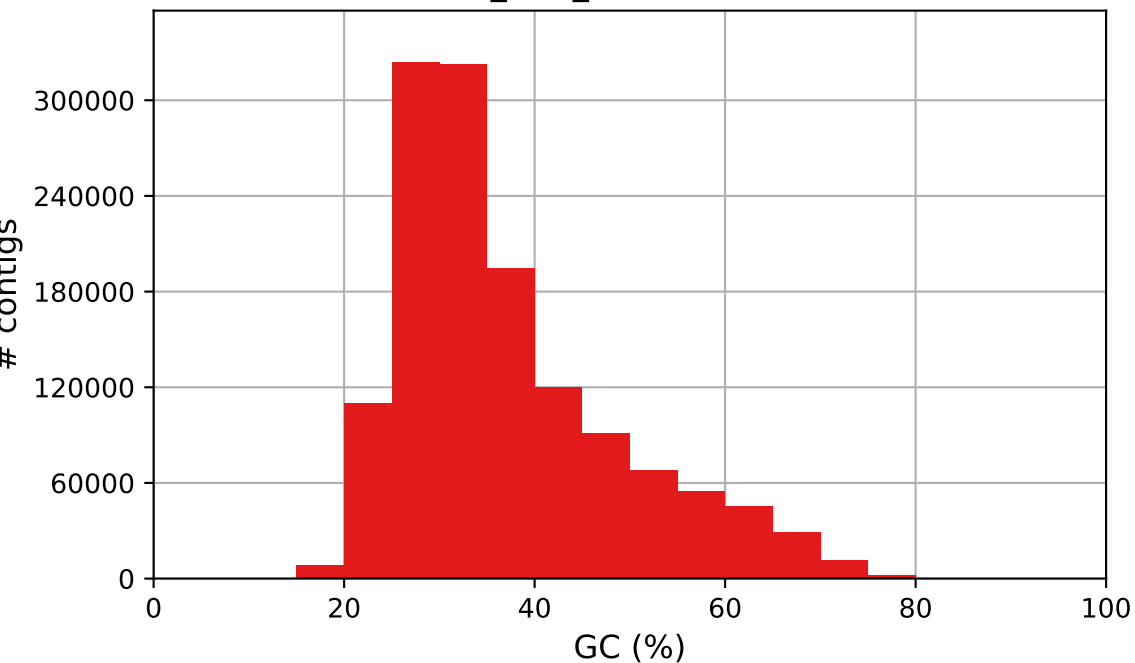


## GC content



— TARA\_ANE\_RAW    - - Reference

TARA\_ANE\_RAW GC content



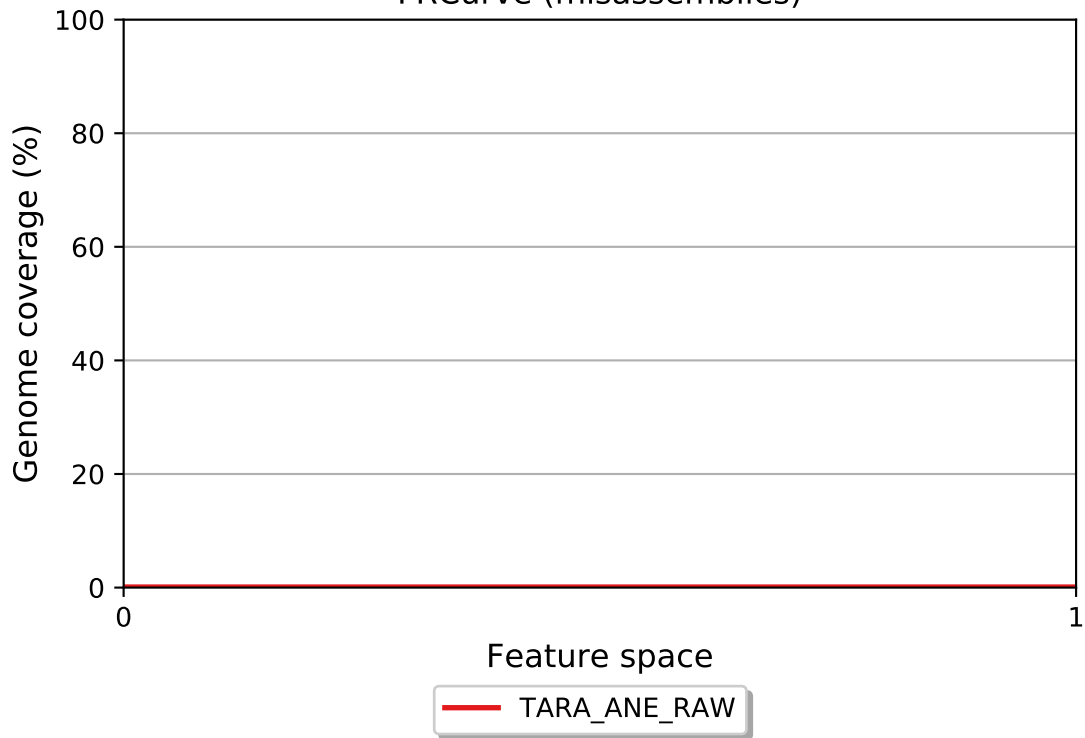
TARA\_ANE\_RAW

## Misassemblies

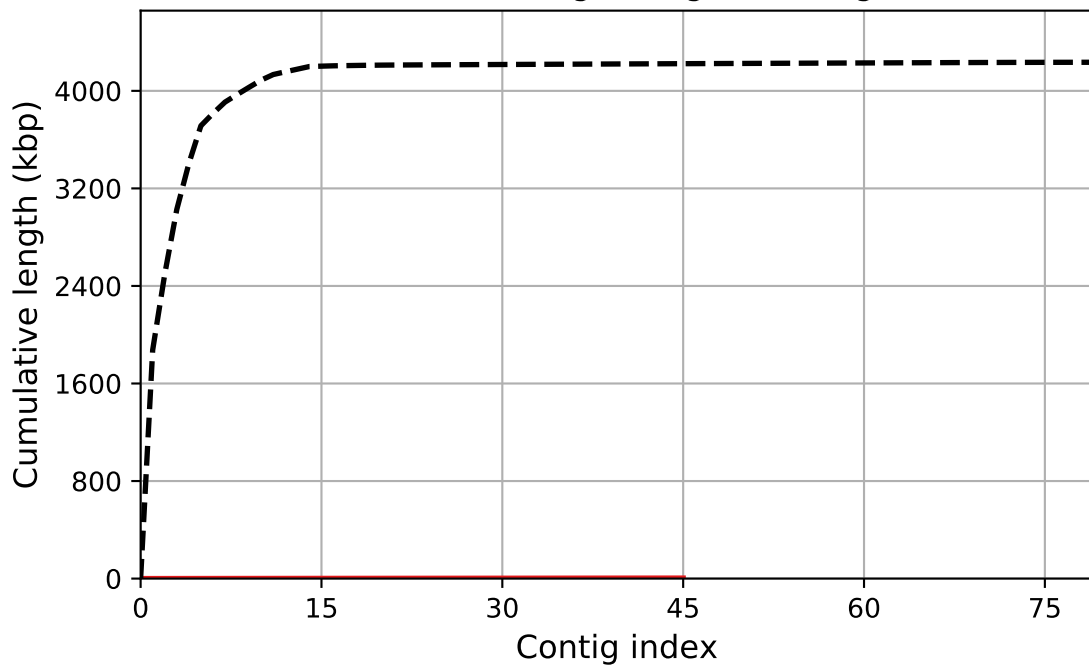




FRCurve (misassemblies)

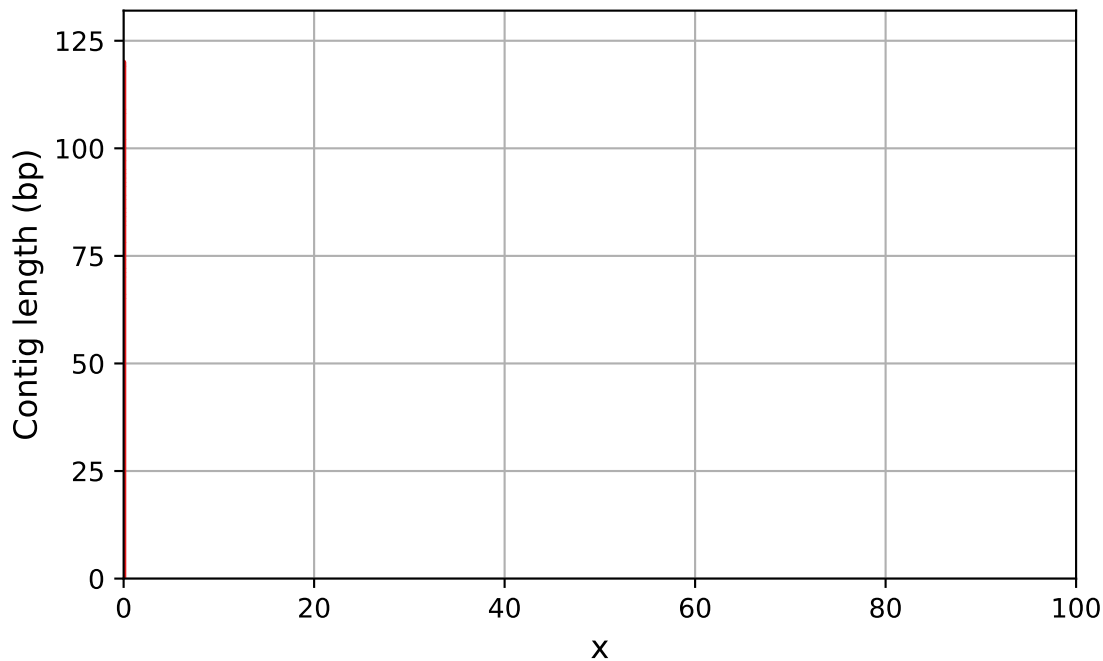


Cumulative length (aligned contigs)



— TARA\_ANE\_RAW    - - Reference

NAx



TARA\_ANE\_RAW