

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	7658814
N50	2156
N75	1382
L50	330727
L75	759418
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	1381803 + 434 part
Unaligned length	2894875576
Genome fraction (%)	0.073
Duplication ratio	7.443
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14902.03
# indels per 100 kbp	71.90
Largest alignment	645
Total aligned length	36448

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

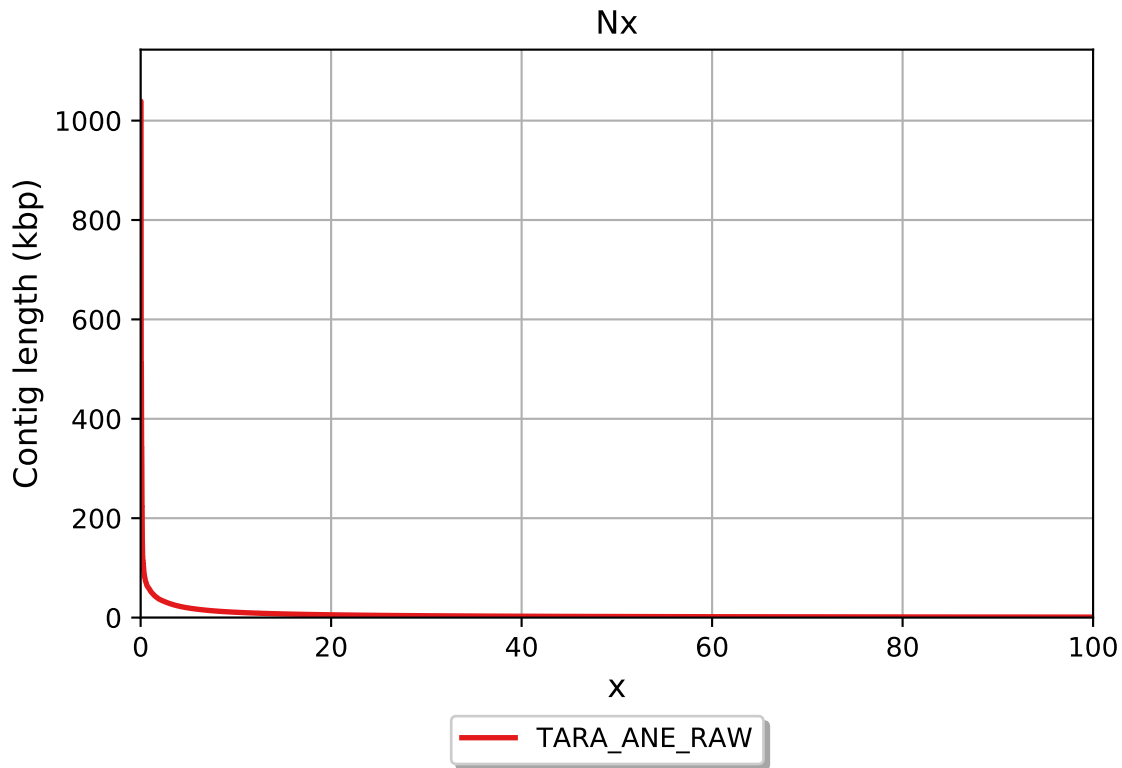
	TARA_ANE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	430
# possible misassemblies	532
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	829
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	6

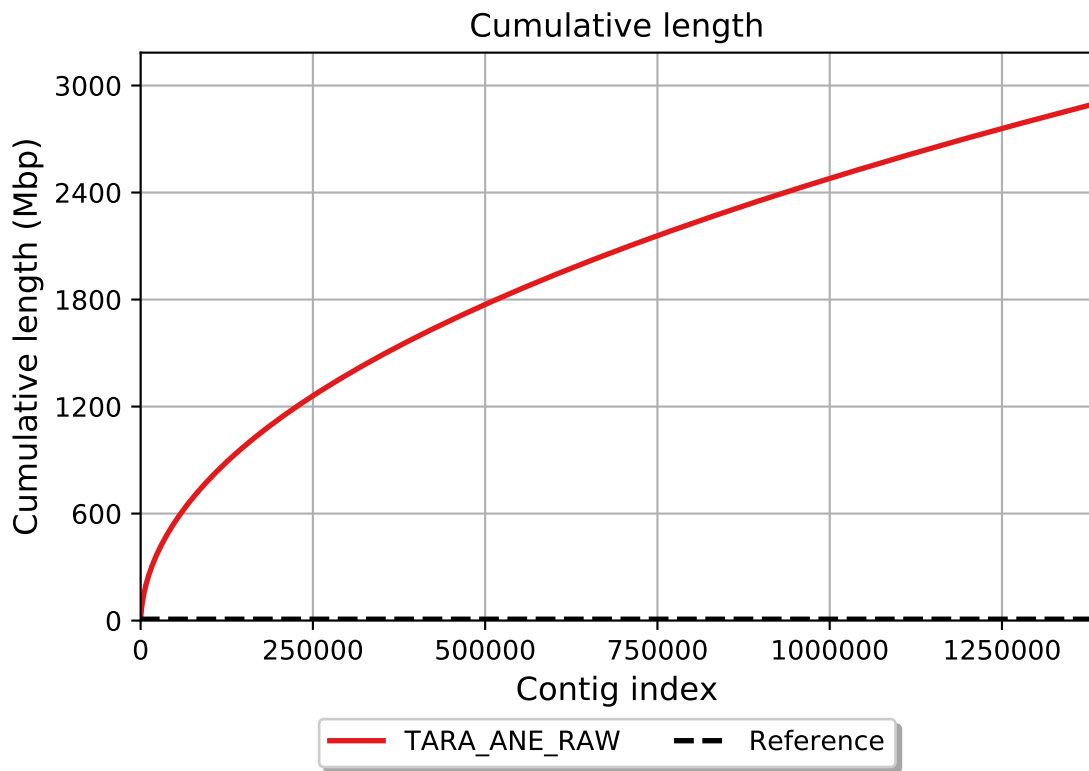
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

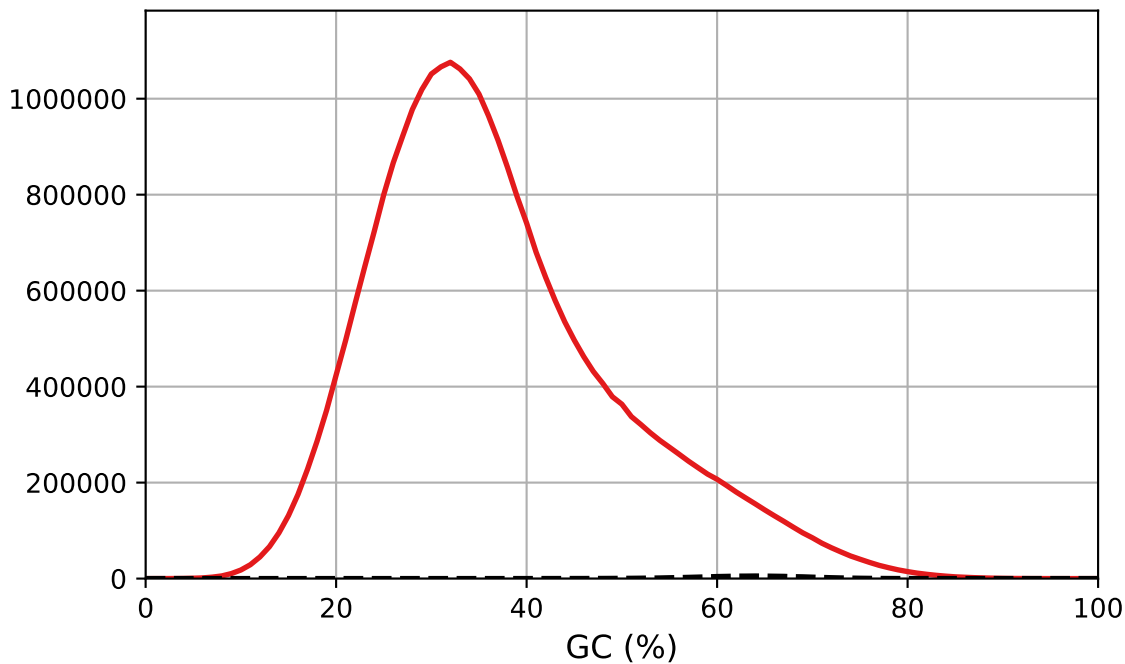
	TARA_ANE_RAW
# fully unaligned contigs	1381803
Fully unaligned length	2892649823
# partially unaligned contigs	434
Partially unaligned length	2225753
# N's	0

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).



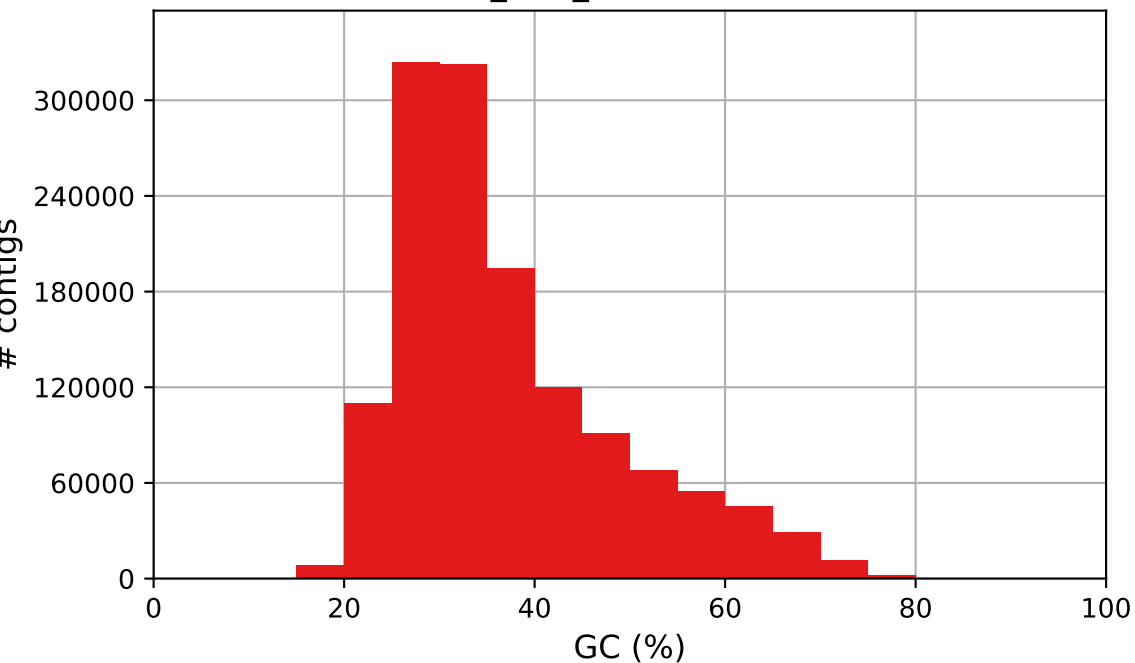


GC content



— TARA_ANE_RAW - - Reference

TARA_ANE_RAW GC content

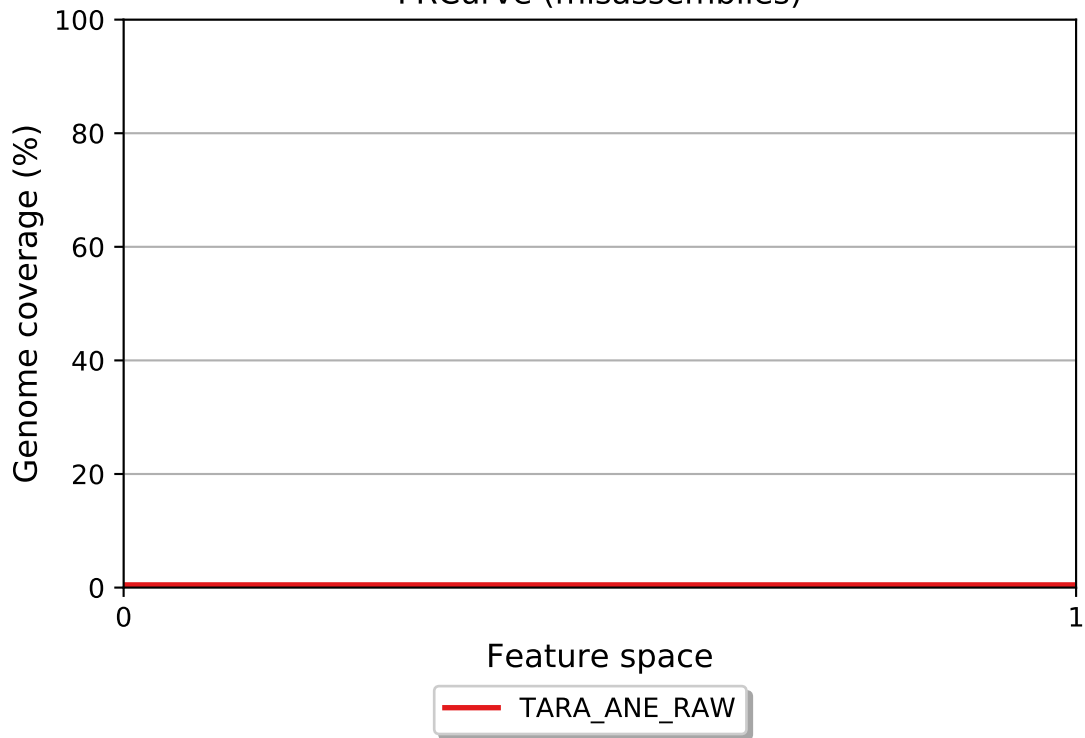


TARA_ANE_RAW

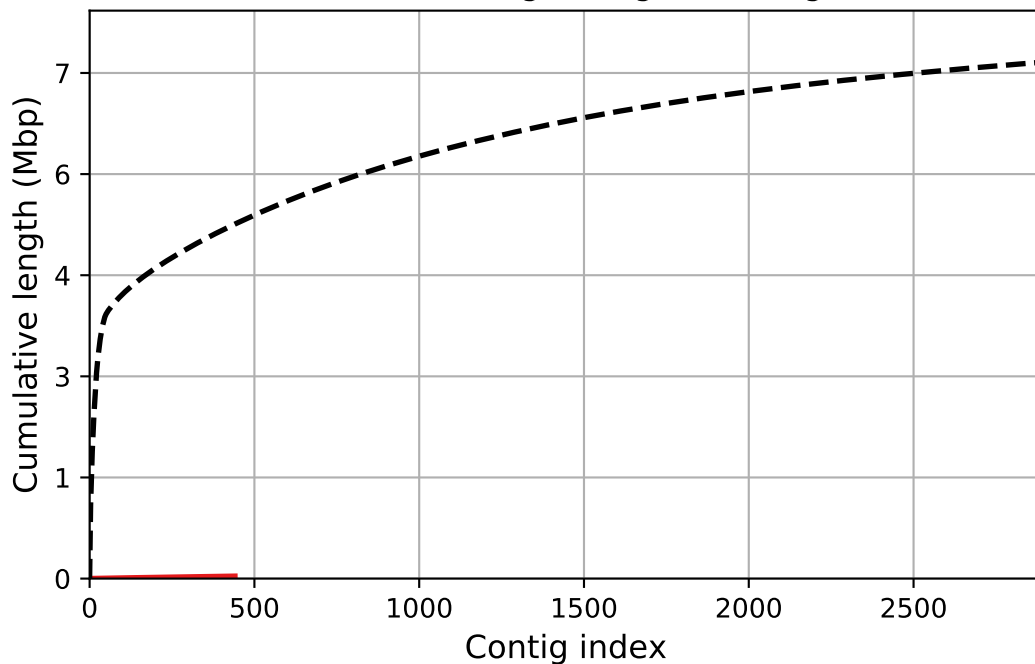
Misassemblies



FRCurve (misassemblies)

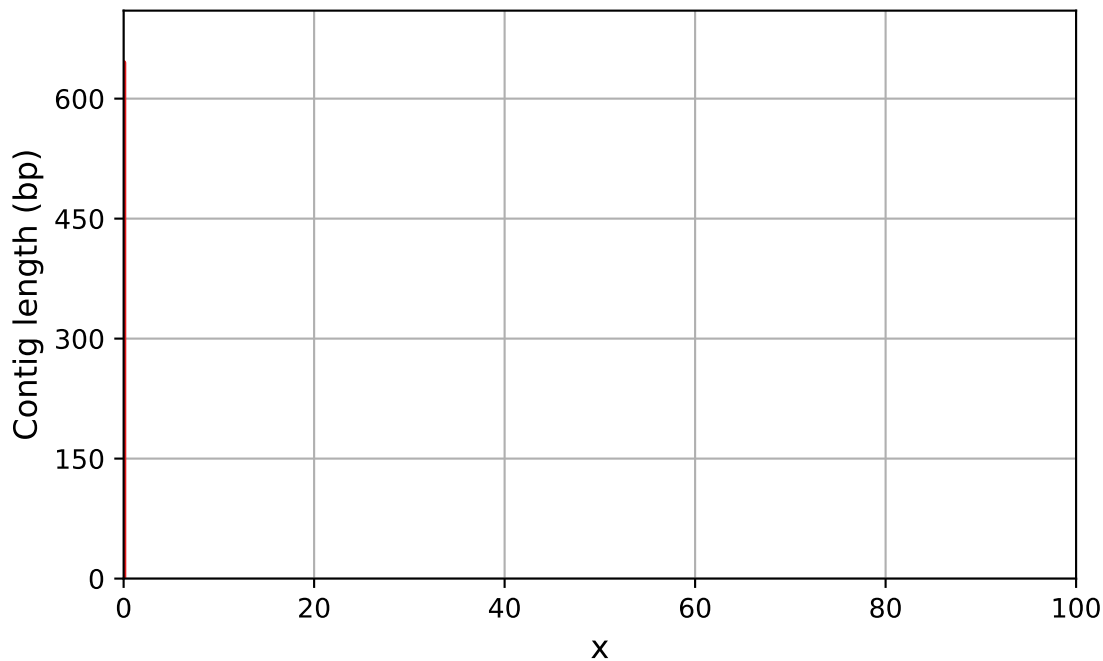


Cumulative length (aligned contigs)



— TARA_ANE_RAW - - Reference

NAx



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