

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	5854900
N50	2138
N75	1378
L50	302257
L75	696663
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	1200
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	1266675 + 381 part
Unaligned length	2648567221
Genome fraction (%)	0.215
Duplication ratio	3.156
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6612.16
# indels per 100 kbp	15.88
Largest alignment	556
Total aligned length	34708

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

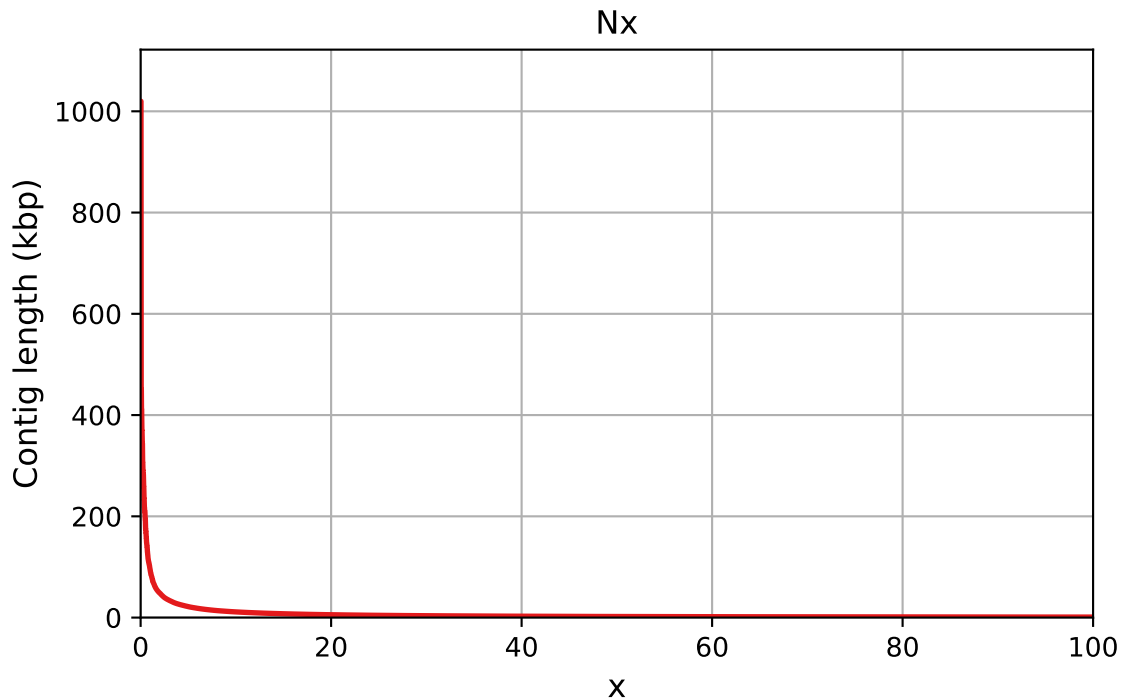
	TARA_ANW_RAW
# misassemblies	2
# contig misassemblies	2
# c. relocations	0
# c. translocations	2
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	1
Misassembled contigs length	1200
# possibly misassembled contigs	375
# possible misassemblies	496
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	833
# indels	2
# indels (<= 5 bp)	1
# indels (> 5 bp)	1
Indels length	25

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

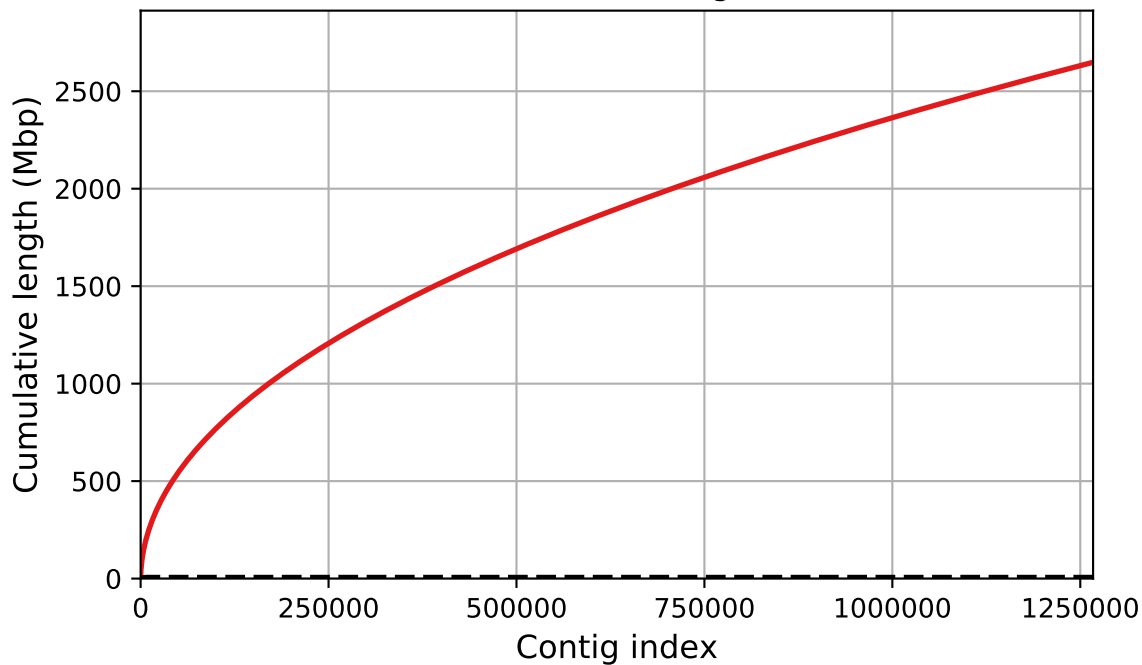
	TARA_ANW_RAW
# fully unaligned contigs	1266675
Fully unaligned length	2645288956
# partially unaligned contigs	381
Partially unaligned length	3278265
# N's	0

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).



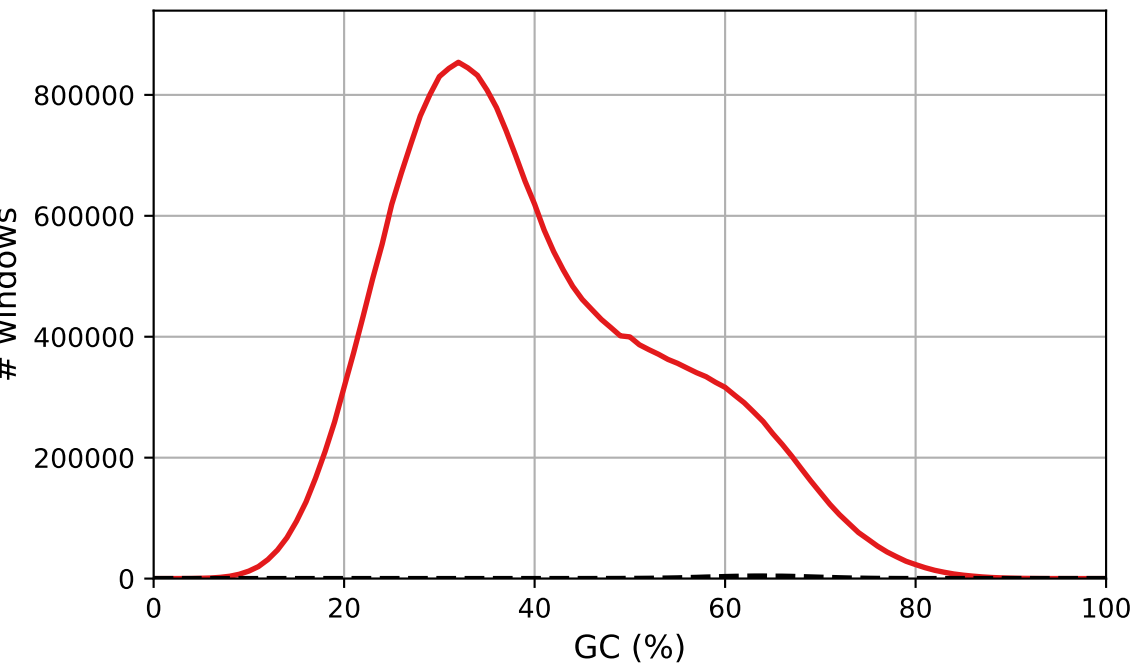
— TARA_ANW_RAW

Cumulative length



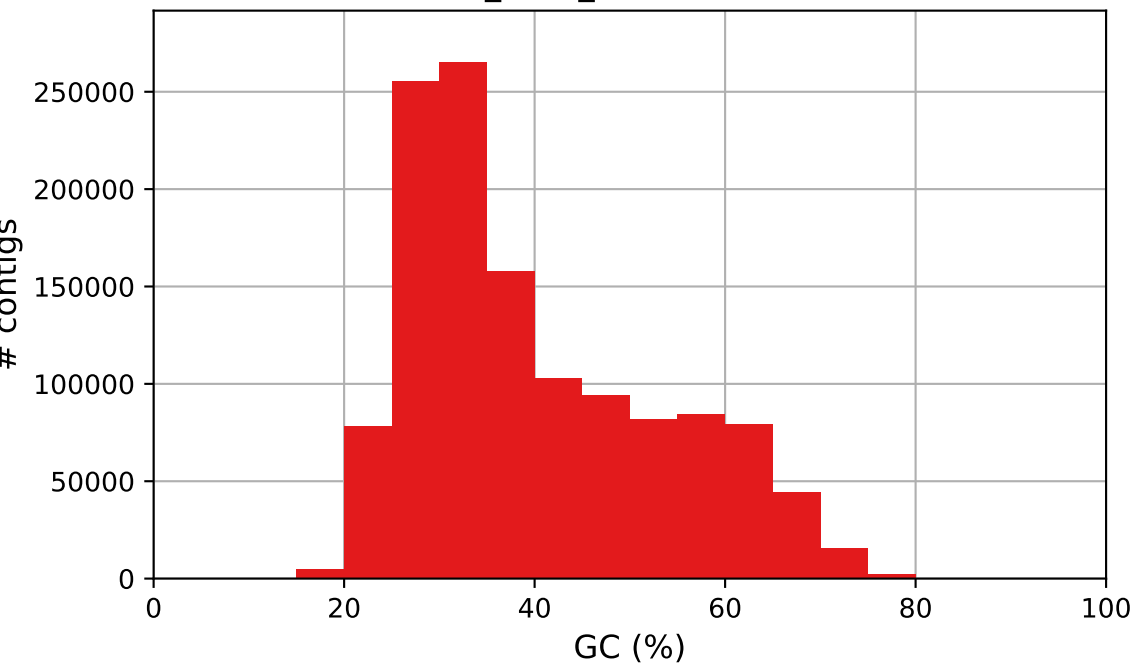
— TARA_ANW_RAW - - Reference

GC content



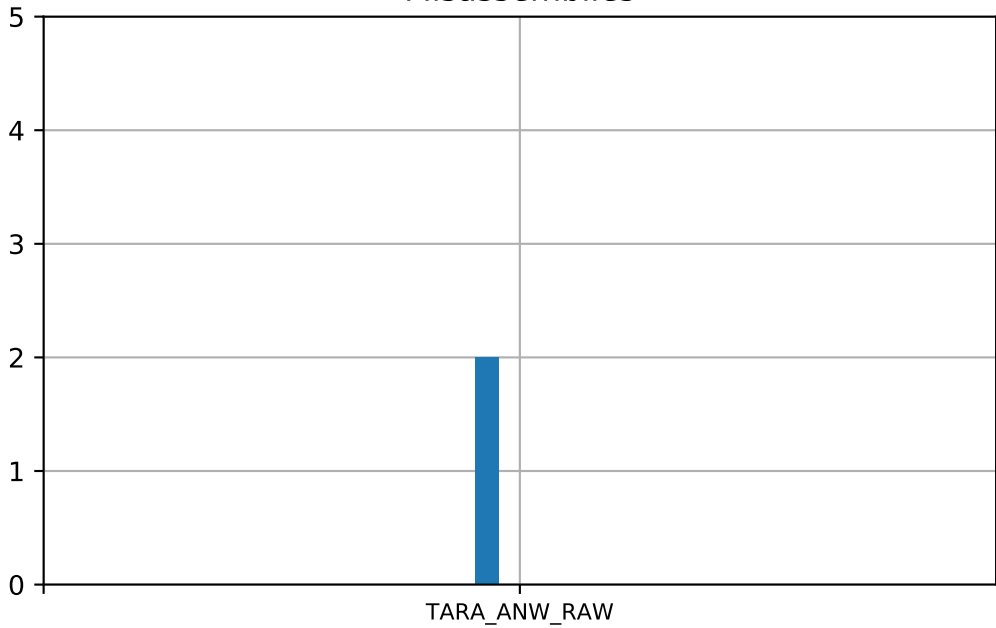
— TARA_ANW_RAW - - Reference

TARA_ANW_RAW GC content



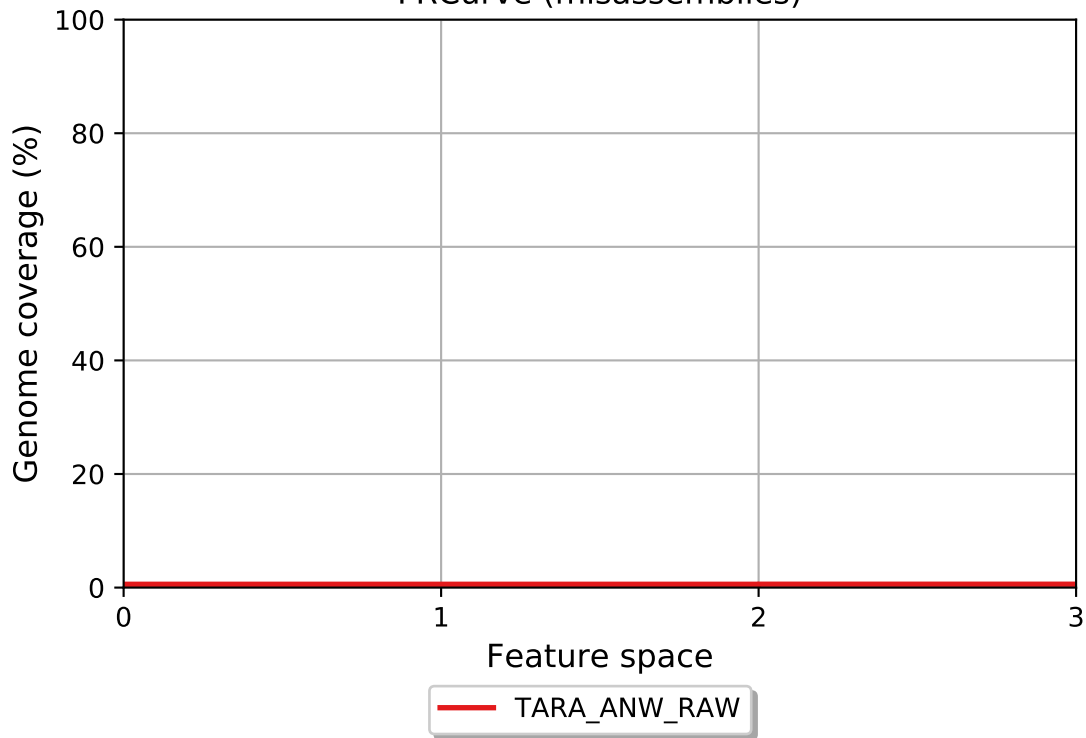
TARA_ANW_RAW

Misassemblies

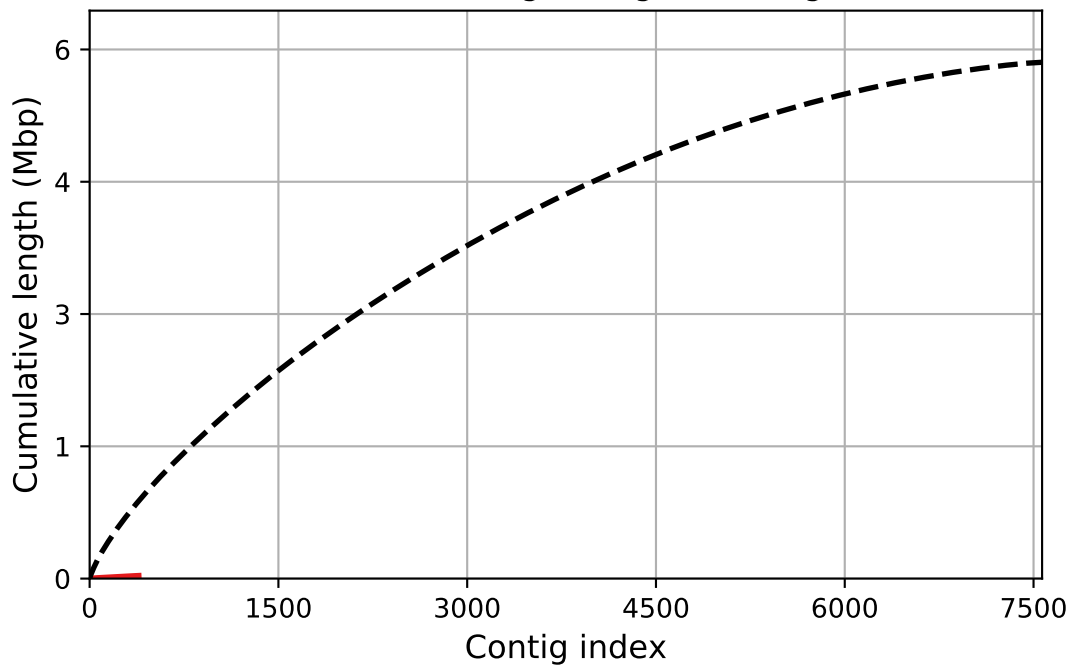


 # translocations

FRCurve (misassemblies)

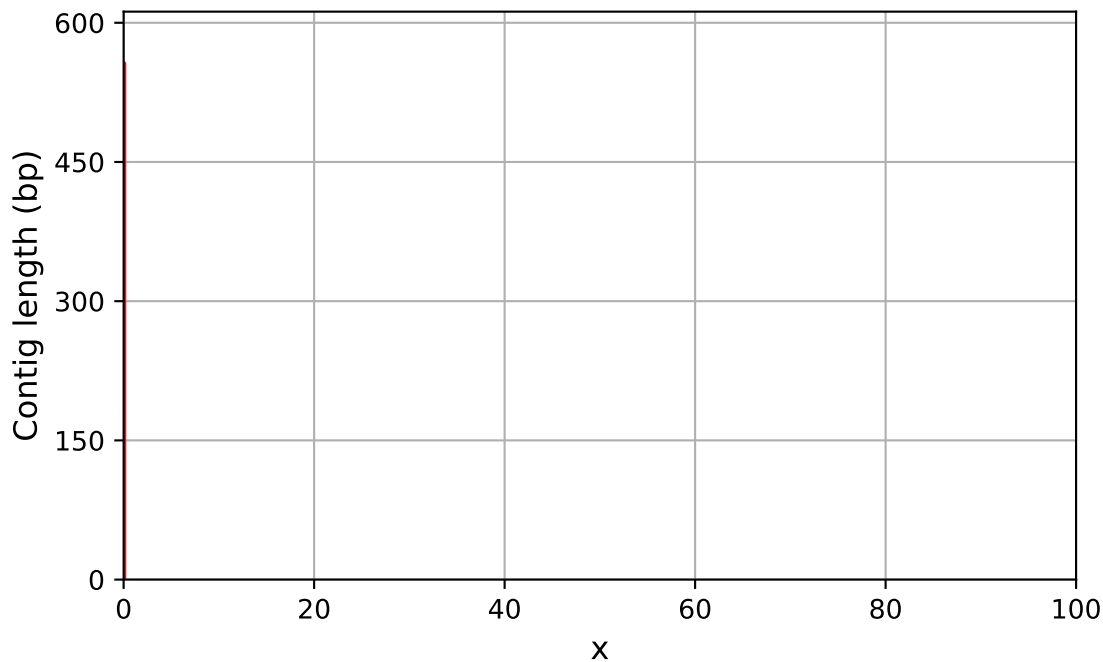


Cumulative length (aligned contigs)



— TARA_ANW_RAW - - Reference

NAx



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