

# Report

	TARA_RED_RAW
# contigs (>= 0 bp)	1039053
# contigs (>= 1000 bp)	1039053
# contigs (>= 5000 bp)	59693
# contigs (>= 10000 bp)	17020
# contigs (>= 25000 bp)	3375
# contigs (>= 50000 bp)	976
Total length (>= 0 bp)	2353055133
Total length (>= 1000 bp)	2353055133
Total length (>= 5000 bp)	654277328
Total length (>= 10000 bp)	367501749
Total length (>= 25000 bp)	170042350
Total length (>= 50000 bp)	89535681
# contigs	1039053
Largest contig	920255
Total length	2353055133
Reference length	3561038
N50	2414
N75	1444
L50	218504
L75	542376
# 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	1039011 + 42 part
Unaligned length	2353051206
Genome fraction (%)	0.028
Duplication ratio	3.959
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10685.48
# indels per 100 kbp	0.00
Largest alignment	129
Total aligned length	3927

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

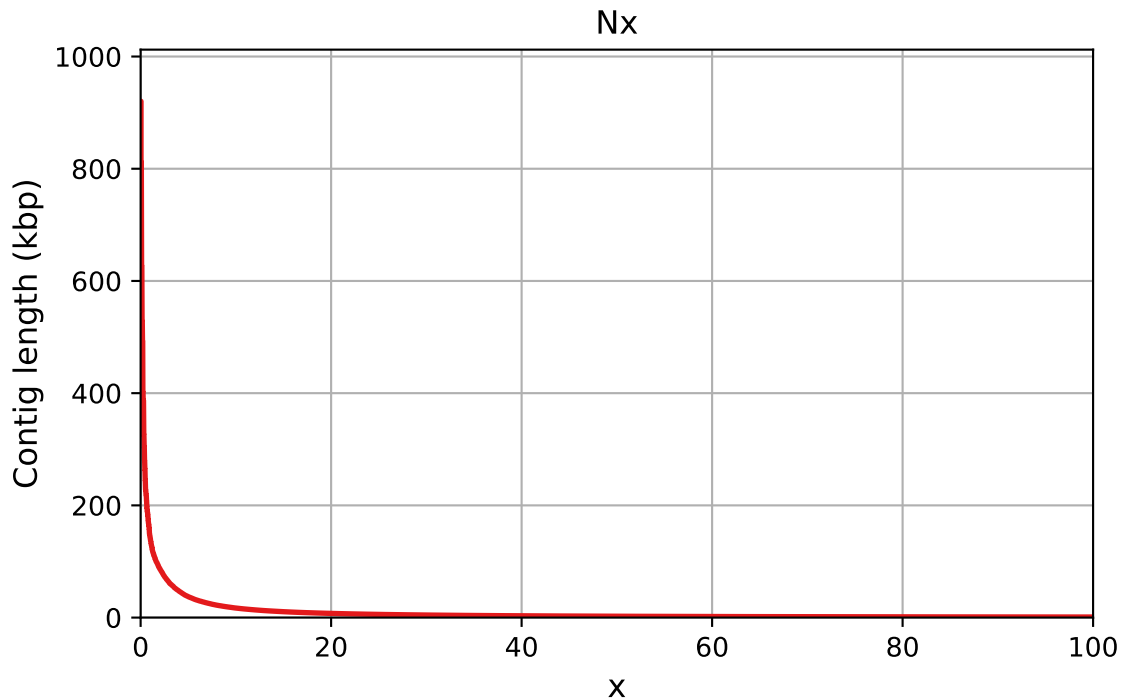
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	40
# possible misassemblies	44
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	106
# 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).

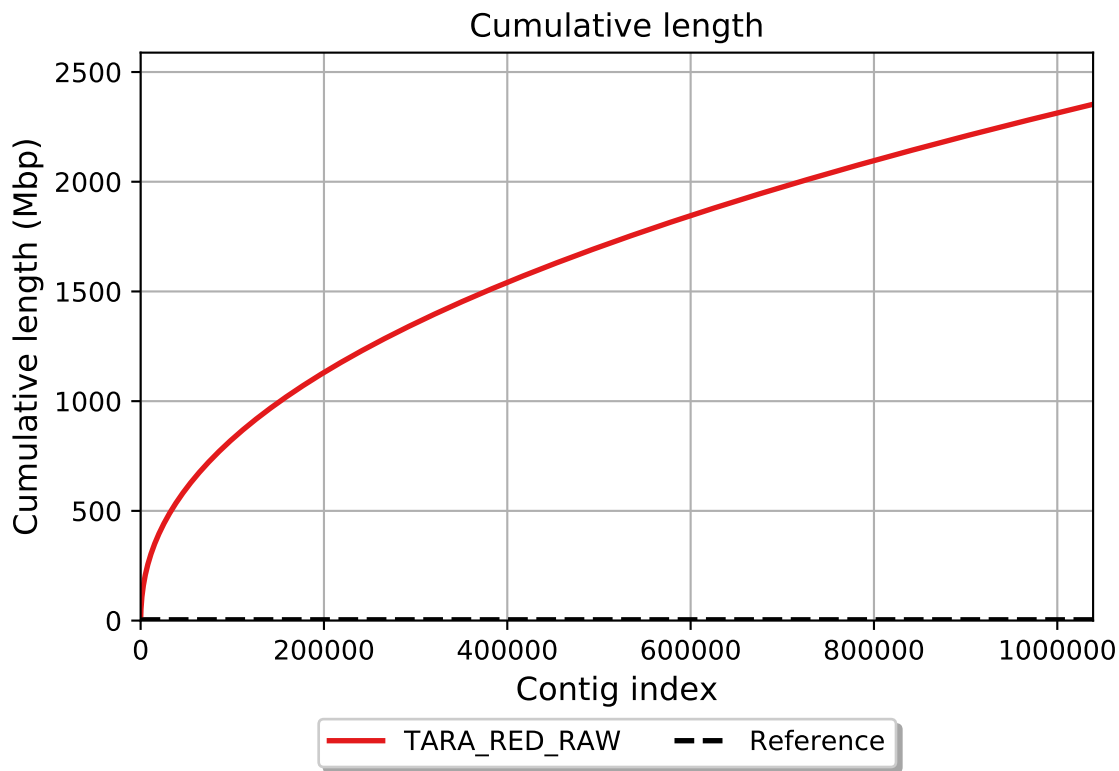
## Unaligned report

	TARA_RED_RAW
# fully unaligned contigs	1039011
Fully unaligned length	2352270145
# partially unaligned contigs	42
Partially unaligned length	781061
# N's	0

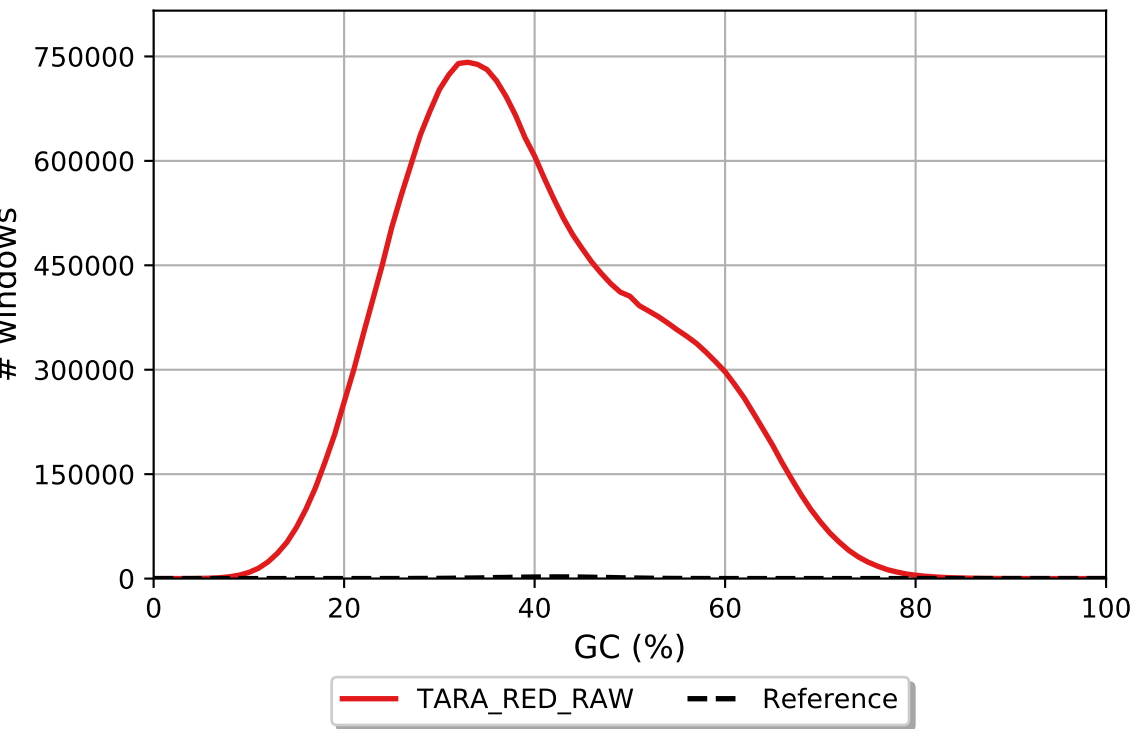
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



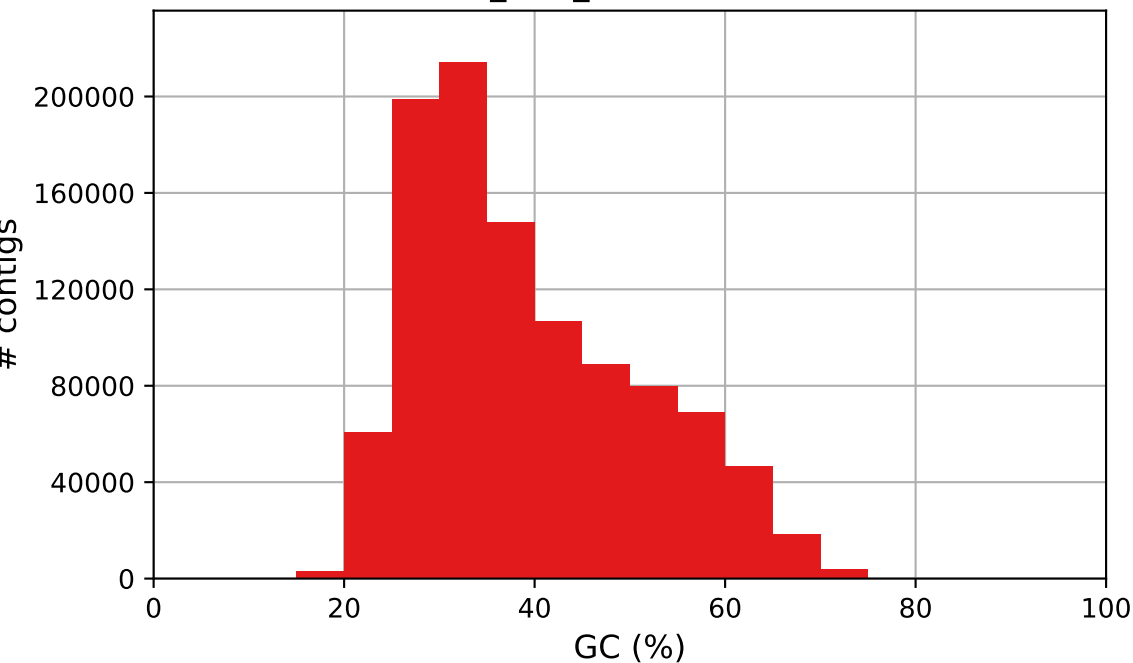
TARA\_RED\_RAW



GC content



TARA\_RED\_RAW GC content



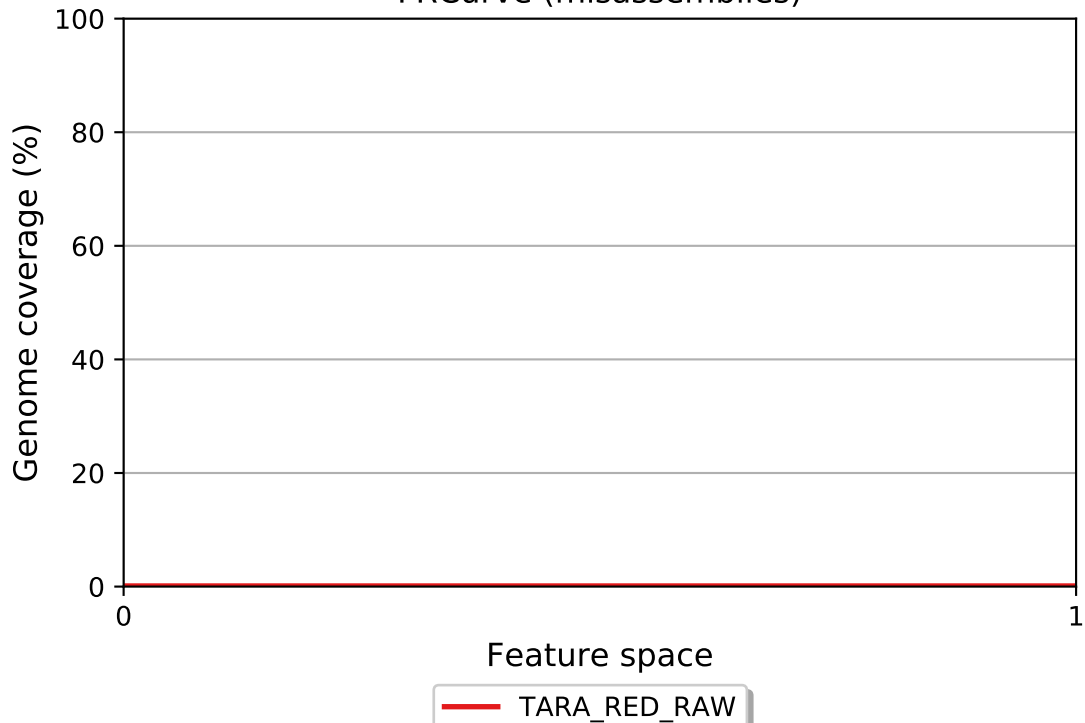
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## Misassemblies

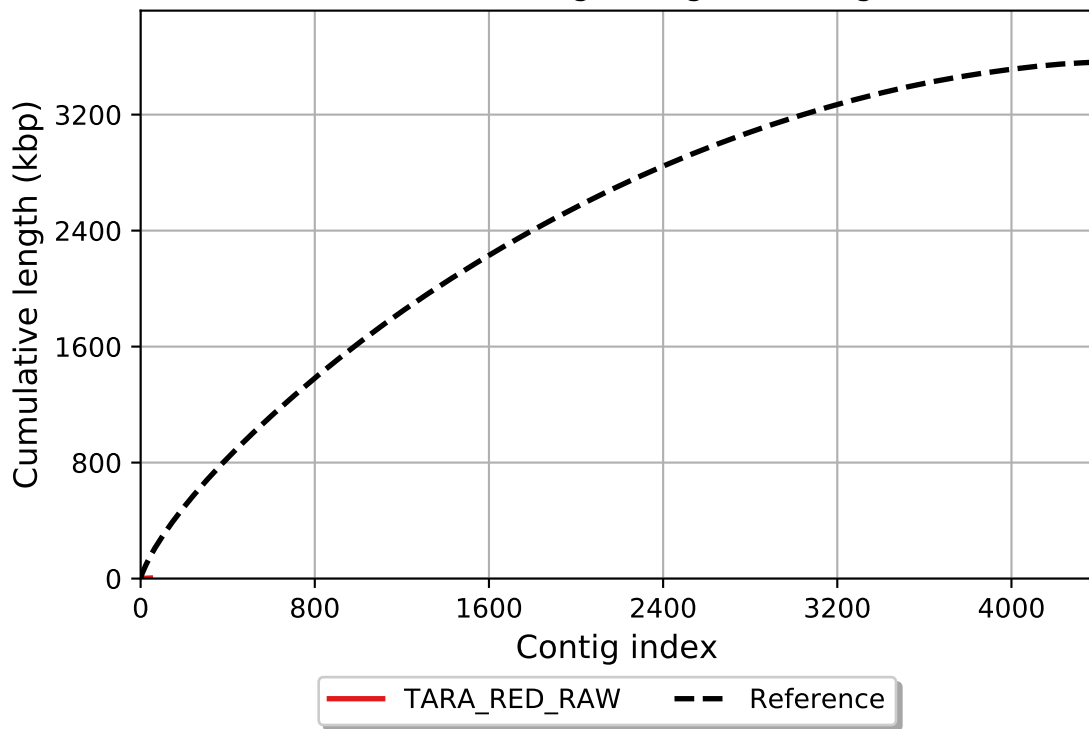




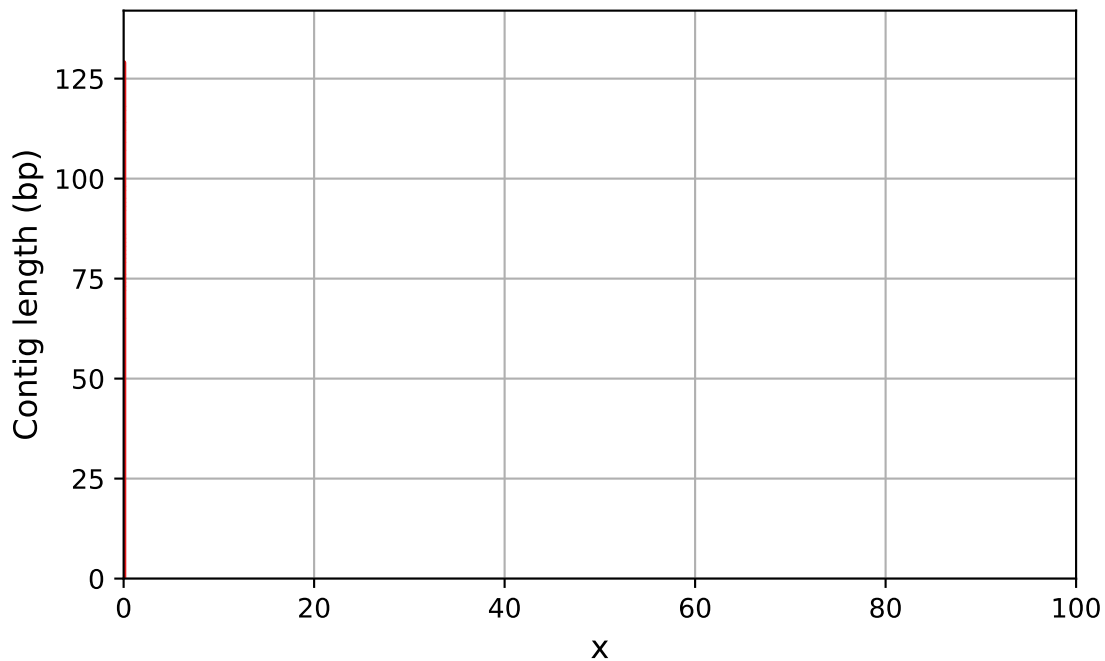
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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