

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	5854900
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	1
# unaligned contigs	1038807 + 246 part
Unaligned length	2353035294
Genome fraction (%)	0.053
Duplication ratio	6.912
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13863.93
# indels per 100 kbp	32.09
Largest alignment	125
Total aligned length	19839

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

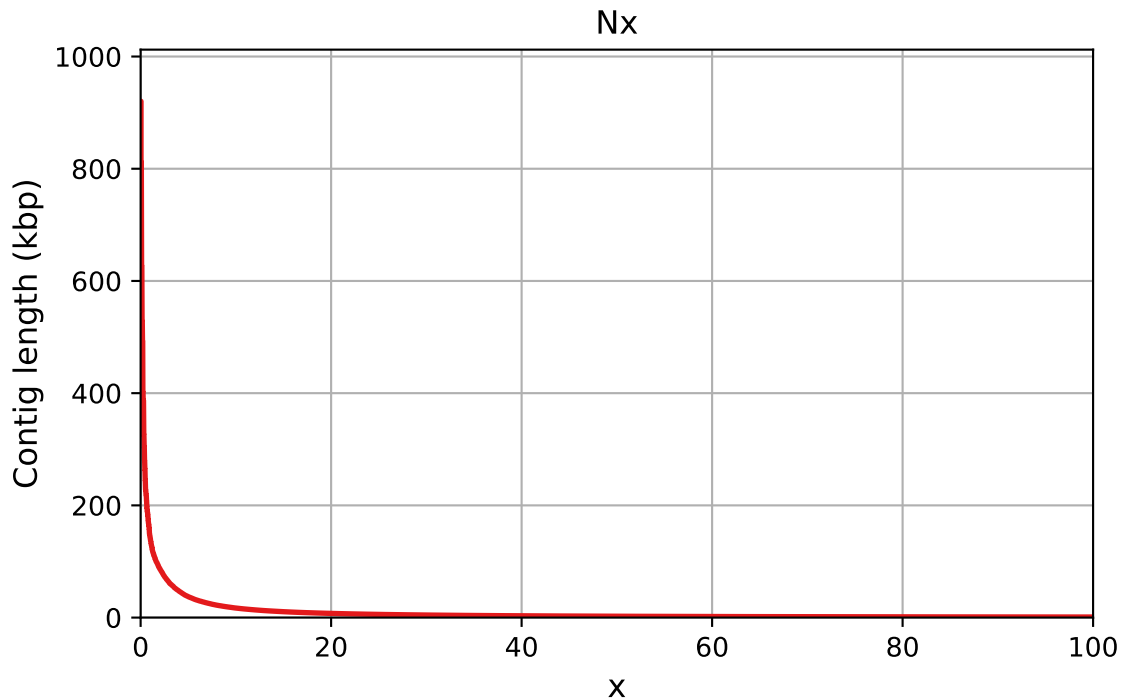
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	245
# possible misassemblies	307
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	432
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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).

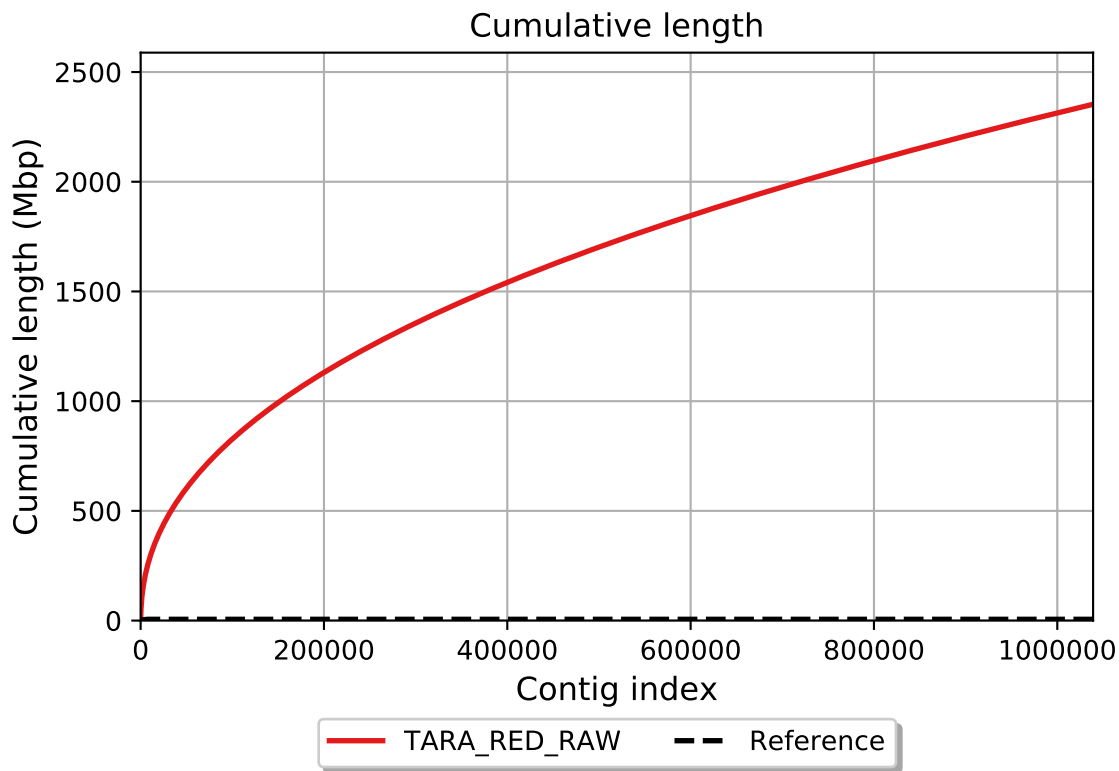
Unaligned report

	TARA_RED_RAW
# fully unaligned contigs	1038807
Fully unaligned length	2349561321
# partially unaligned contigs	246
Partially unaligned length	3473973
# N's	0

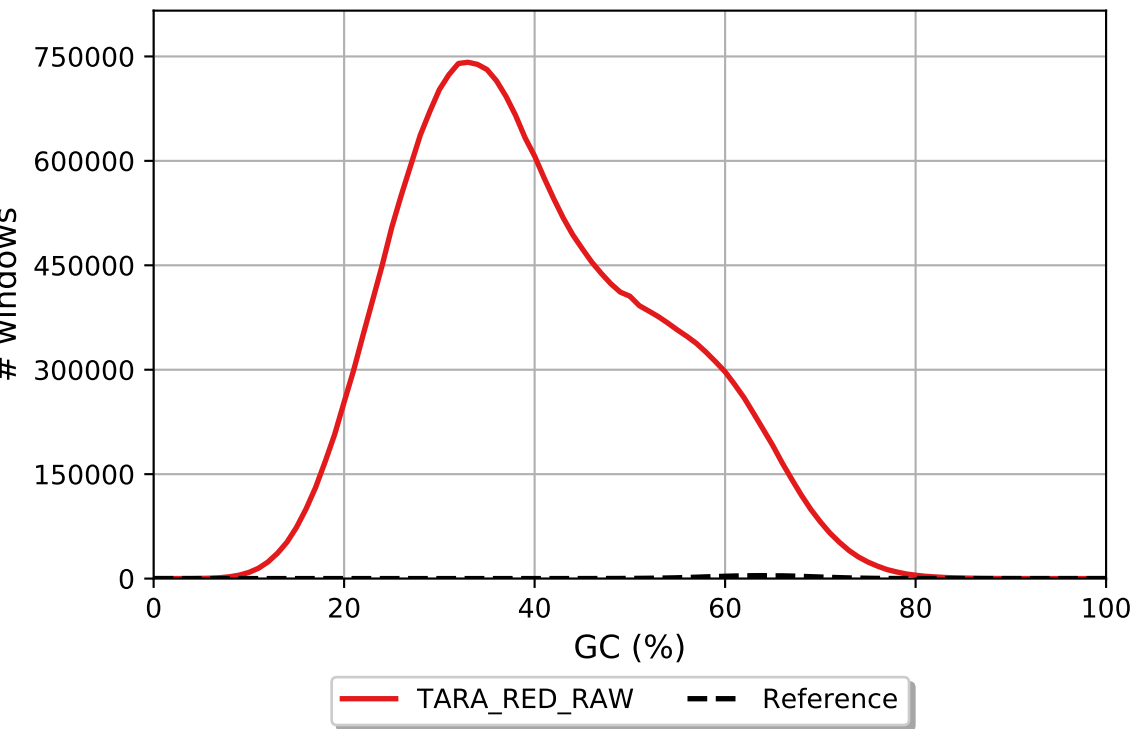
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



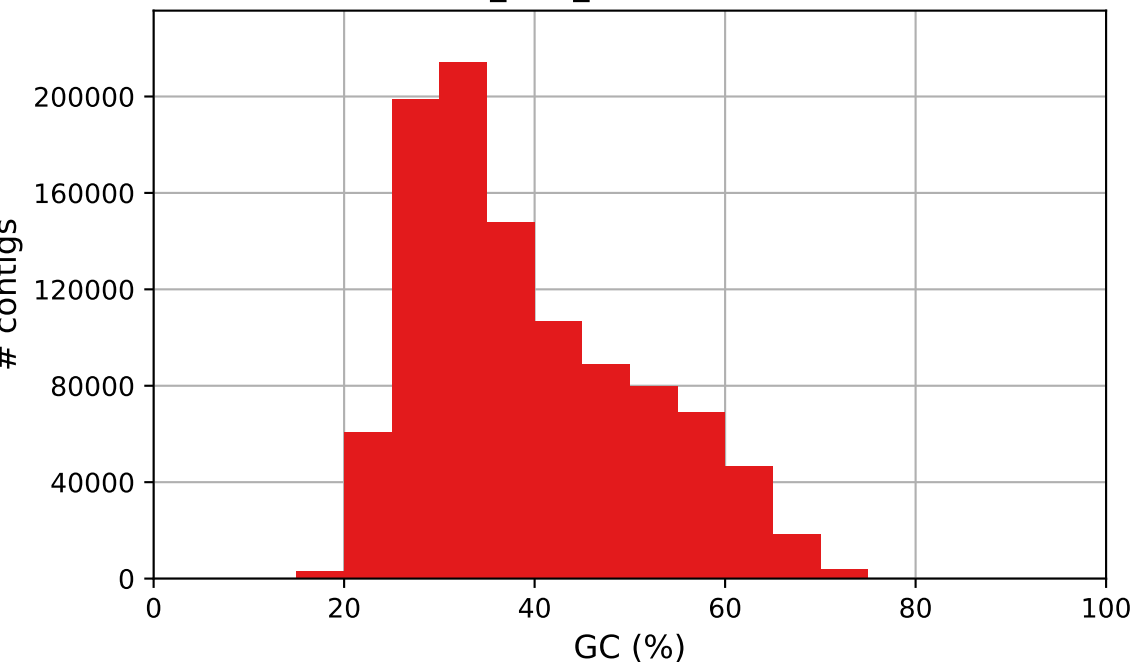
TARA_RED_RAW



GC content



TARA_RED_RAW GC content

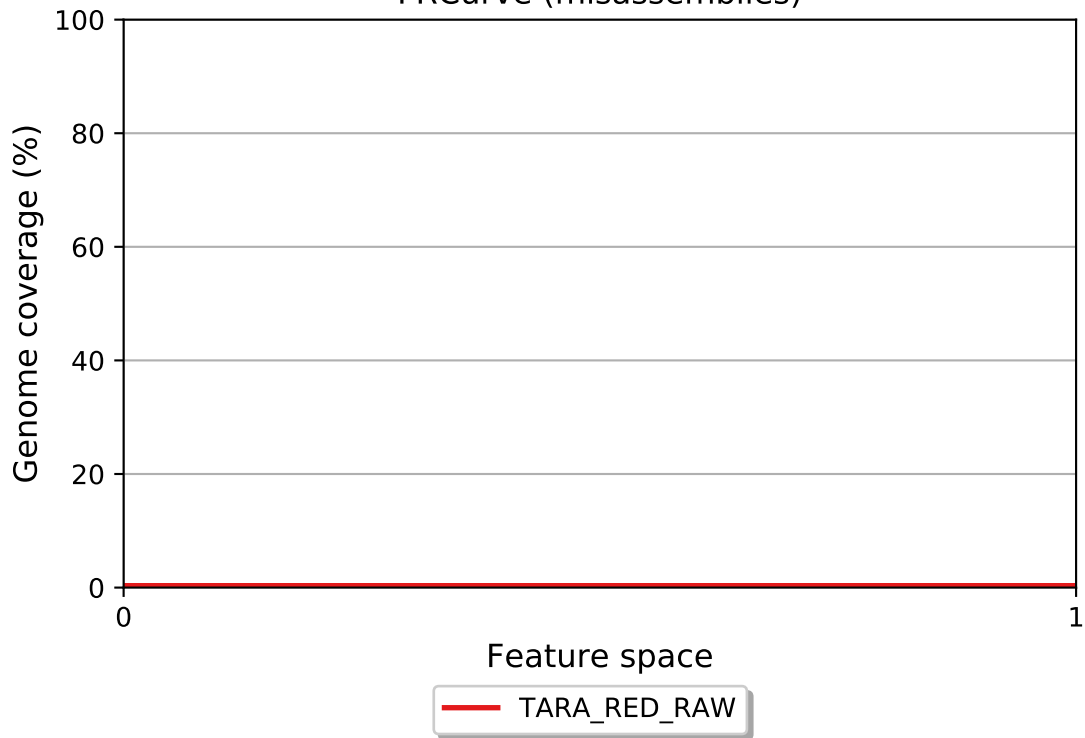


TARA_RED_RAW

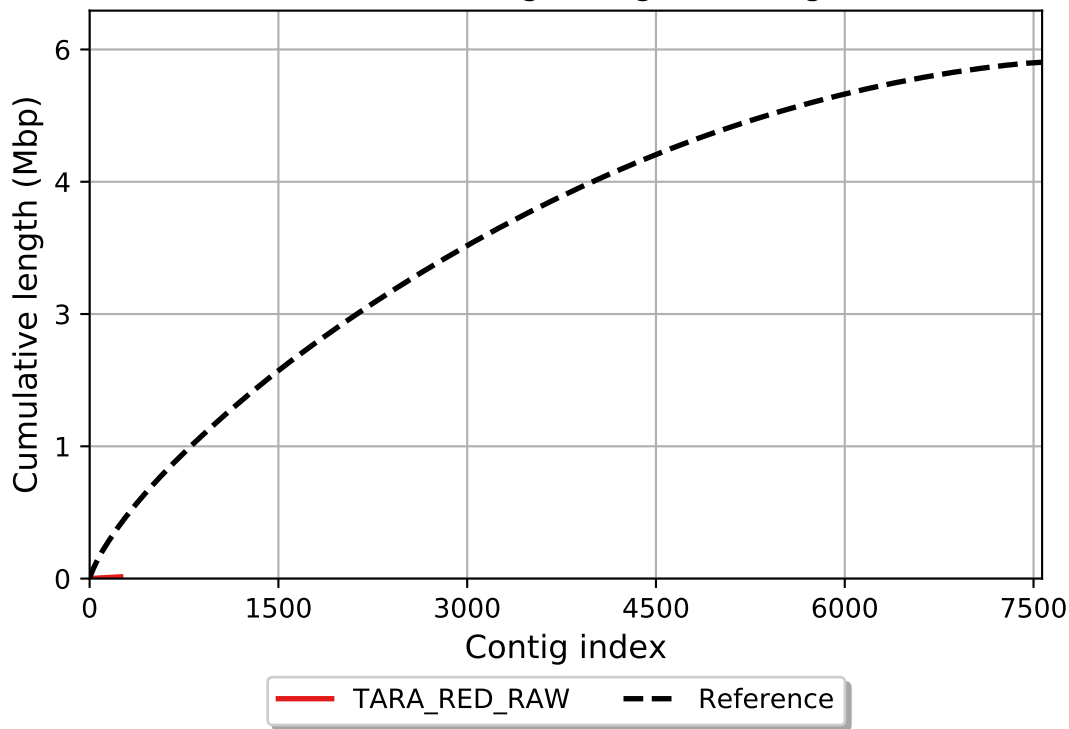
Misassemblies



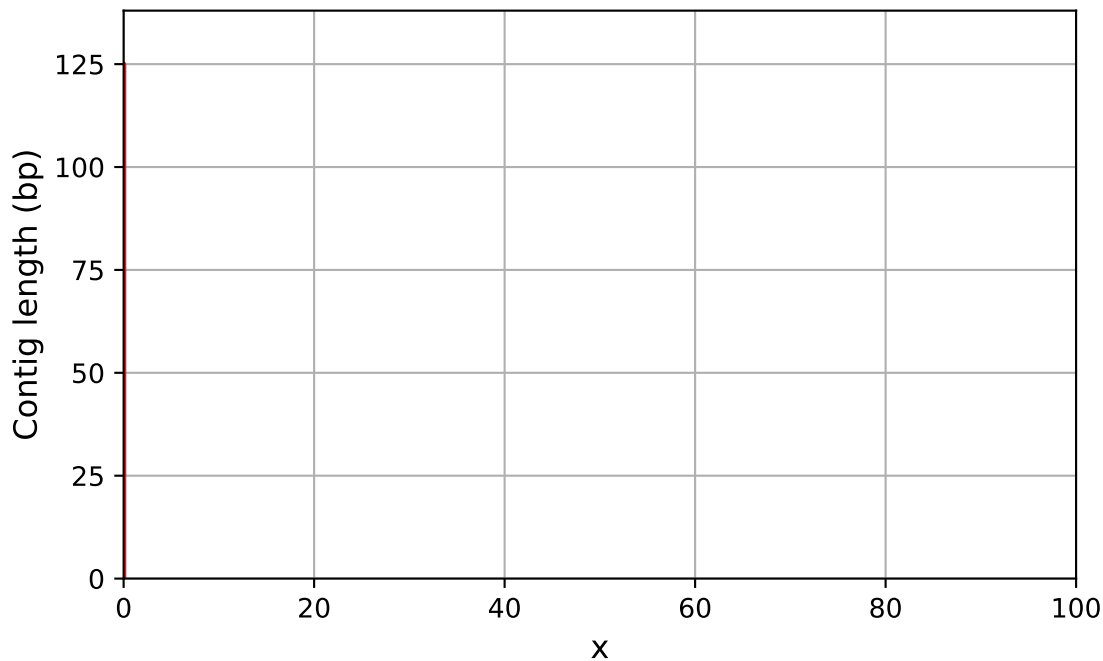
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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