

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	4234461
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	1039005 + 48 part
Unaligned length	2353050518
Genome fraction (%)	0.032
Duplication ratio	3.543
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10072.99
# indels per 100 kbp	364.96
Largest alignment	201
Total aligned length	4615

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

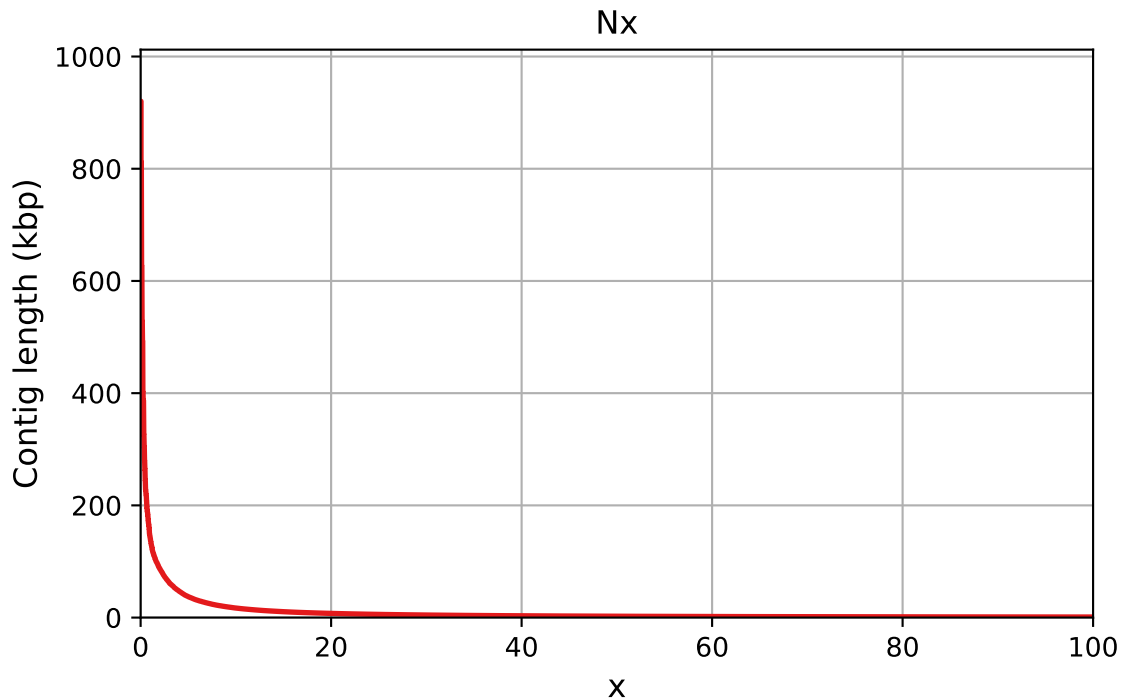
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	46
# possible misassemblies	52
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	138
# indels	5
# indels (<= 5 bp)	5
# 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).

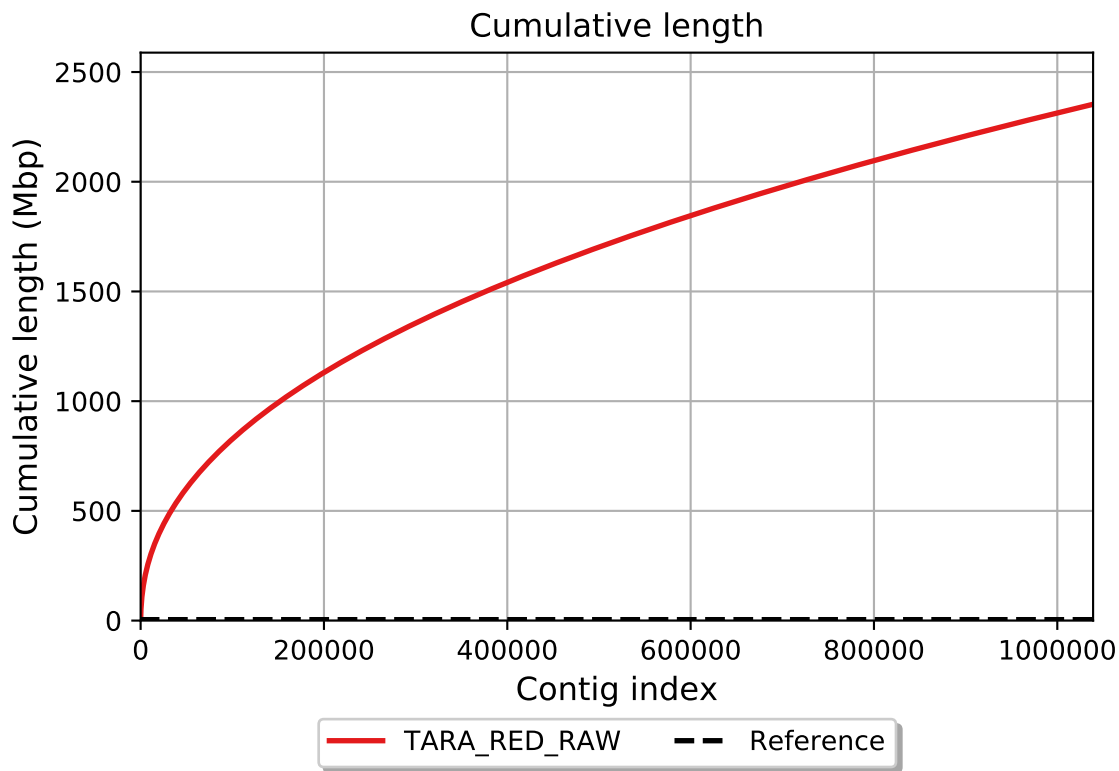
Unaligned report

	TARA_RED_RAW
# fully unaligned contigs	1039005
Fully unaligned length	2352218177
# partially unaligned contigs	48
Partially unaligned length	832341
# N's	0

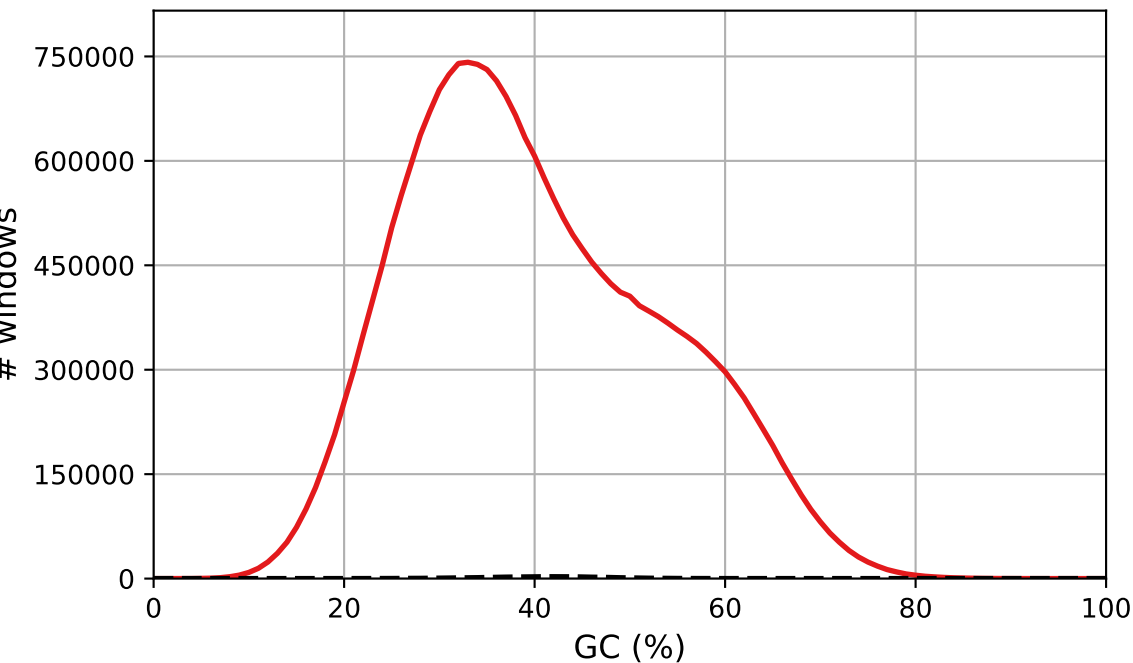
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



TARA_RED_RAW

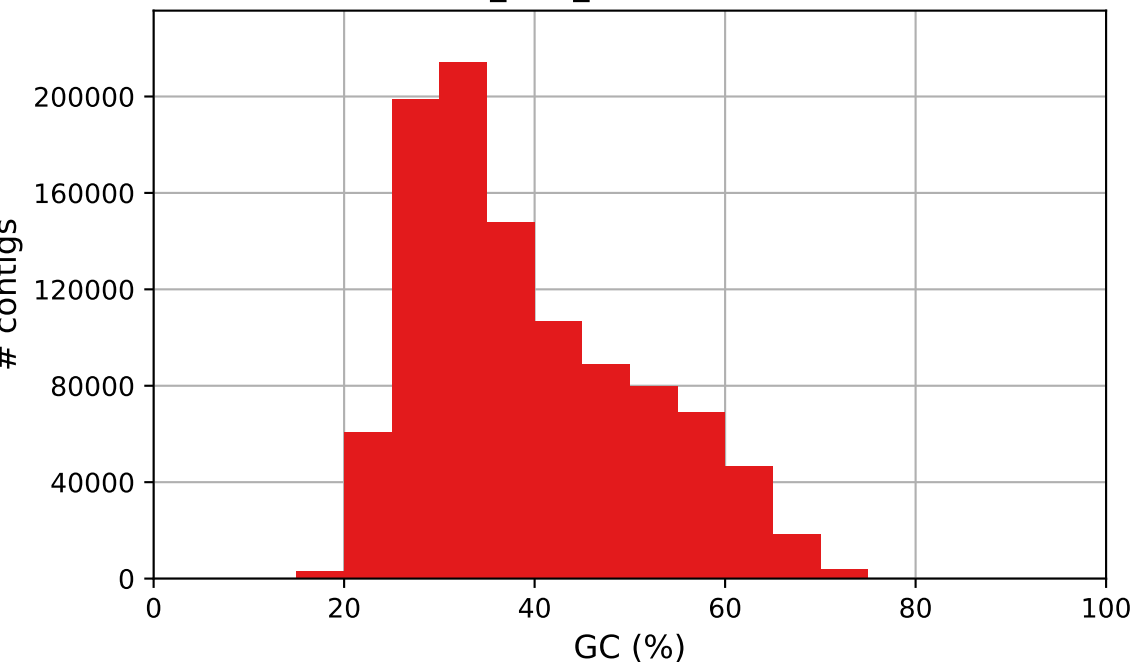


GC content



— TARA_RED_RAW - - Reference

TARA_RED_RAW GC content

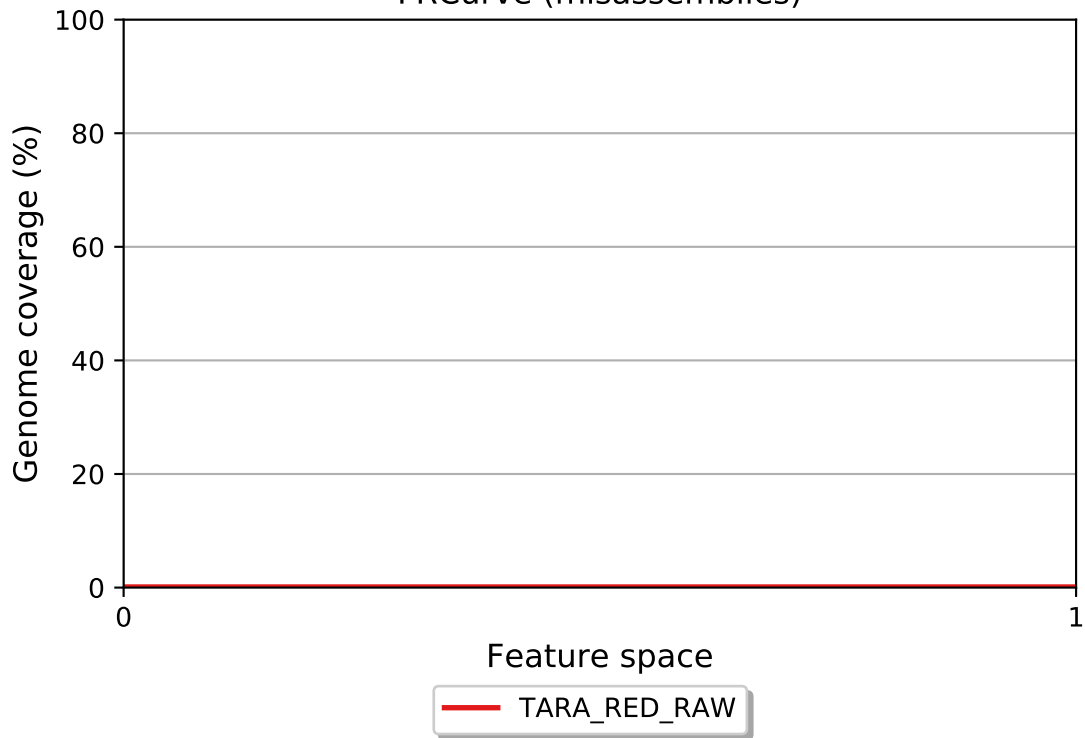


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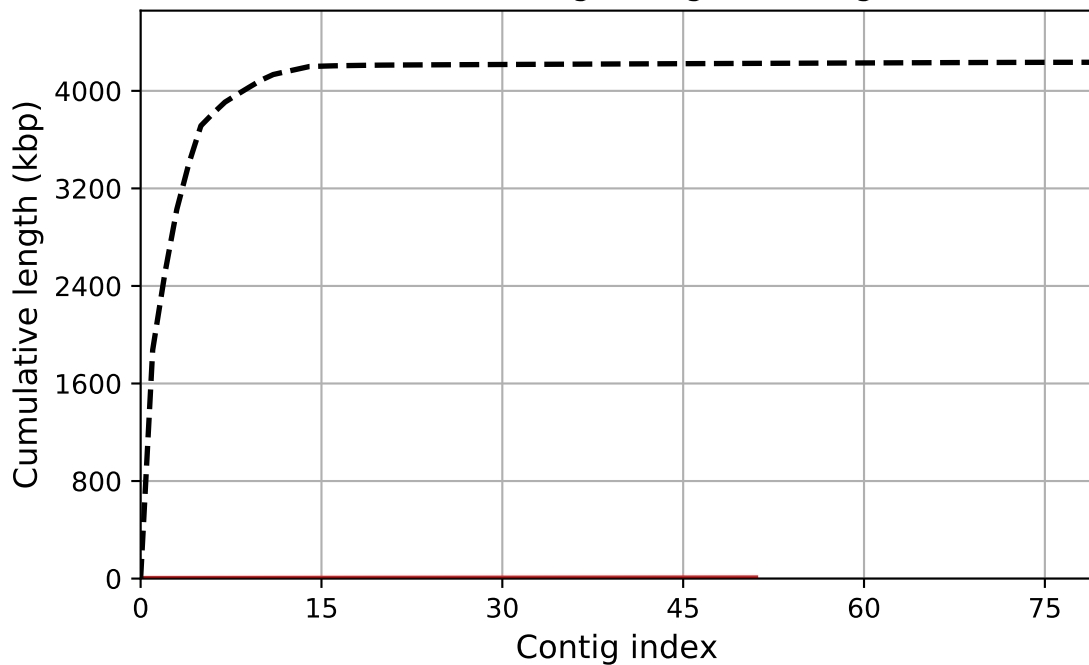
Misassemblies



FRCurve (misassemblies)

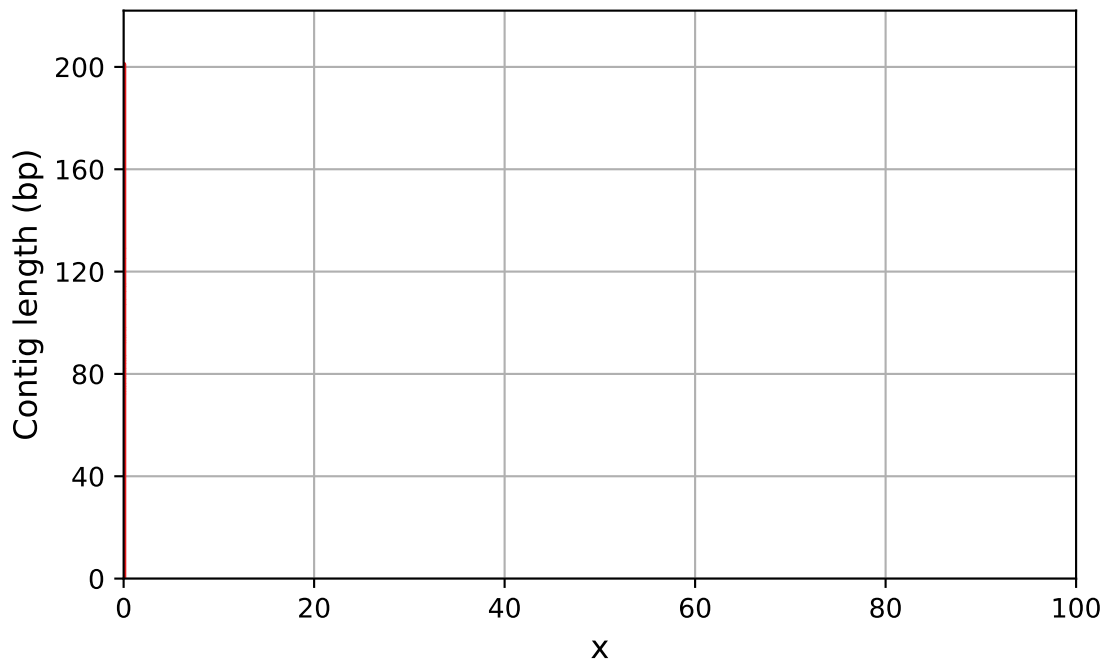


Cumulative length (aligned contigs)



— TARA_RED_RAW - - Reference

NAx



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