

# Report

	TARA_IOS_RAW
# contigs (>= 1000 bp)	42
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	151308
Total length (>= 5000 bp)	74798
Total length (>= 10000 bp)	69496
Total length (>= 25000 bp)	58856
Total length (>= 50000 bp)	58856
# contigs	42
Largest contig	58856
Total length	151308
Reference length	4234461
GC (%)	47.74
Reference GC (%)	41.03
N50	4873
N75	2272
L50	4
L75	16
# 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	0
# unaligned contigs	3 + 38 part
Unaligned length	146616
Genome fraction (%)	0.031
Duplication ratio	3.552
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8478.43
# indels per 100 kbp	151.40
Largest alignment	208
Total aligned length	3821
NGA50	-

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_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	41
# possible misassemblies	45
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	112
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	3

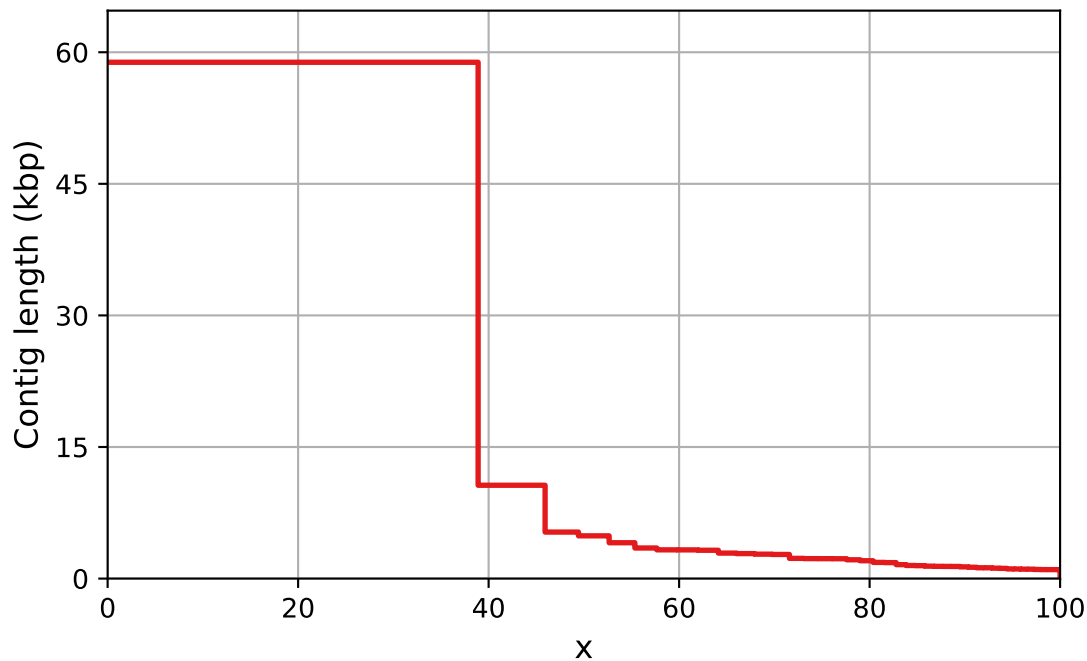
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_IOS_RAW
# fully unaligned contigs	3
Fully unaligned length	7011
# partially unaligned contigs	38
Partially unaligned length	139605
# N's	0

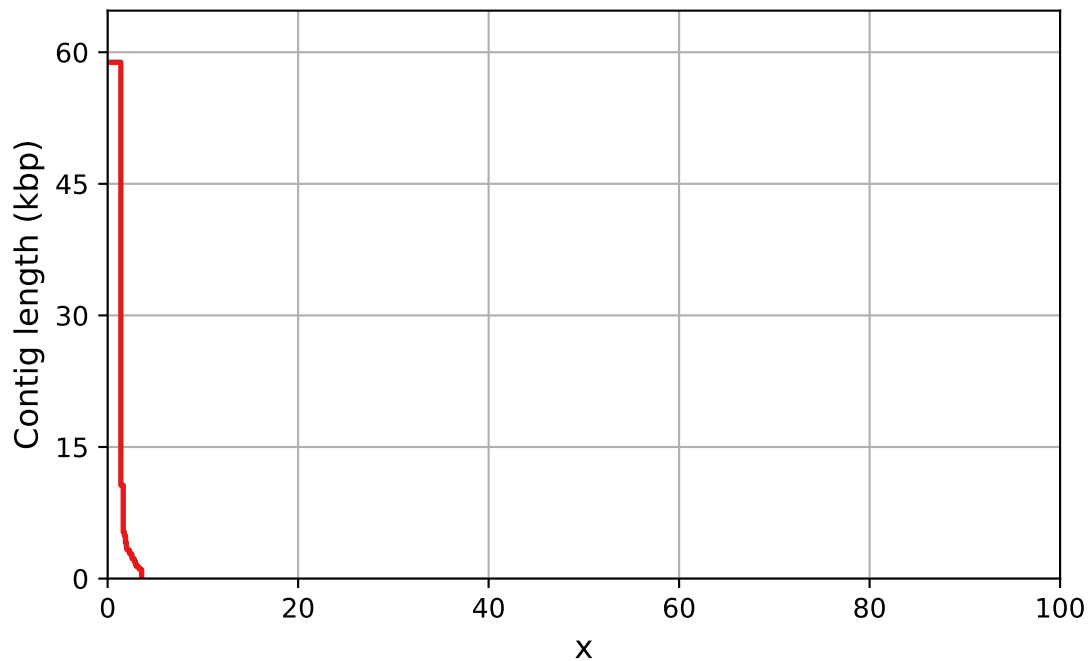
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



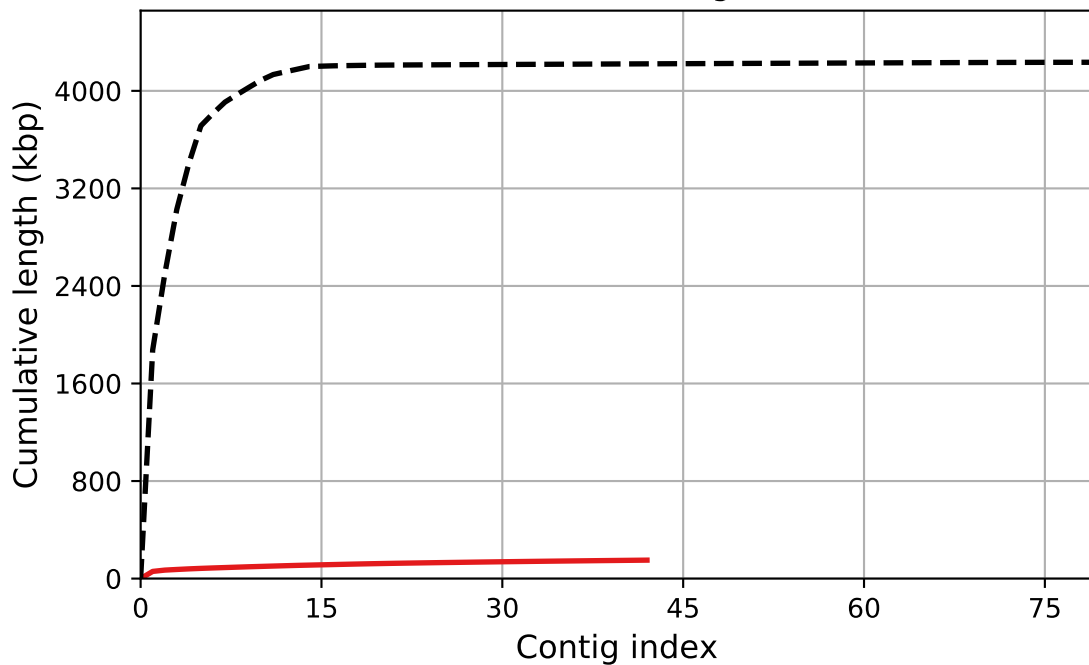
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NGx



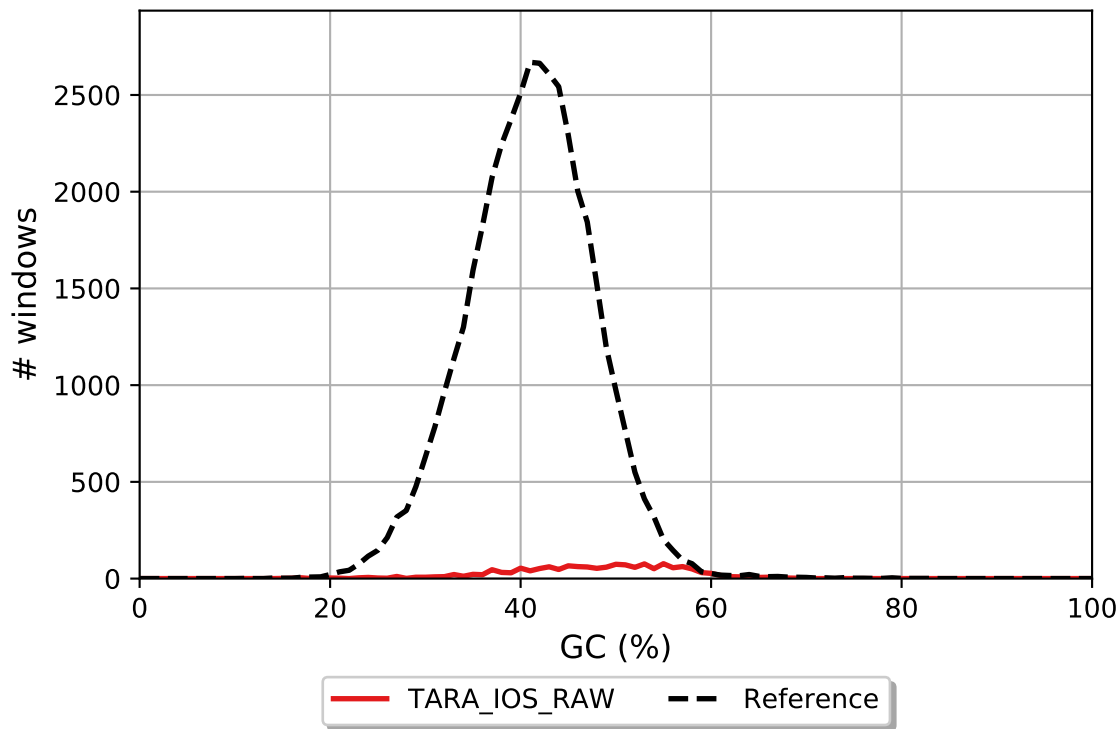
TARA\_IOS\_RAW

Cumulative length

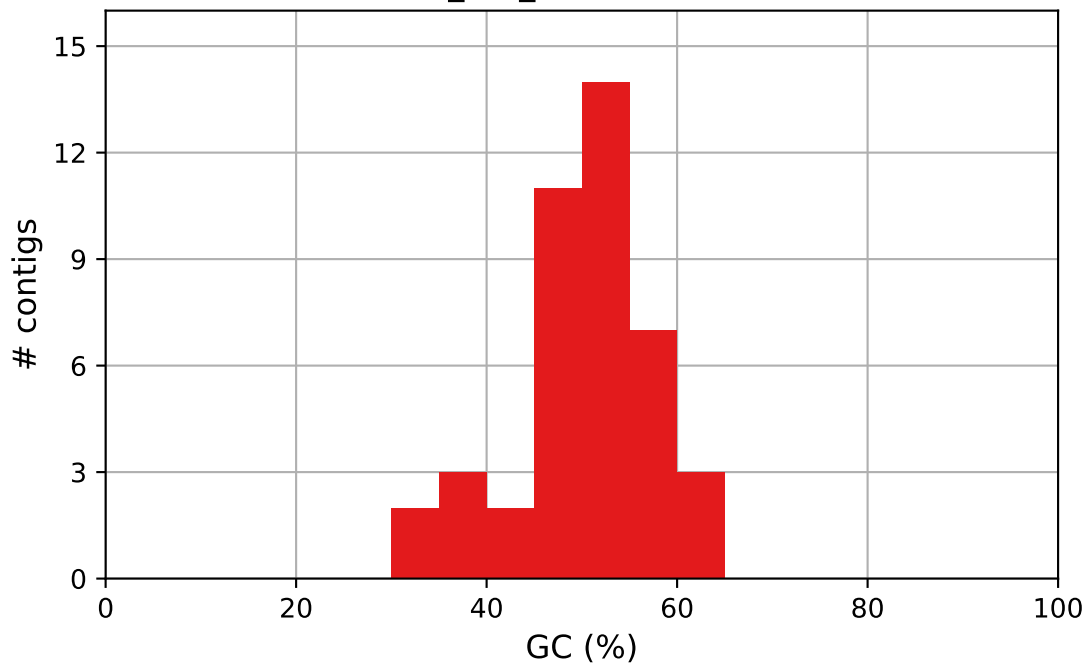


— TARA\_IOS\_RAW    - - Reference

## GC content



TARA\_IOS\_RAW GC content



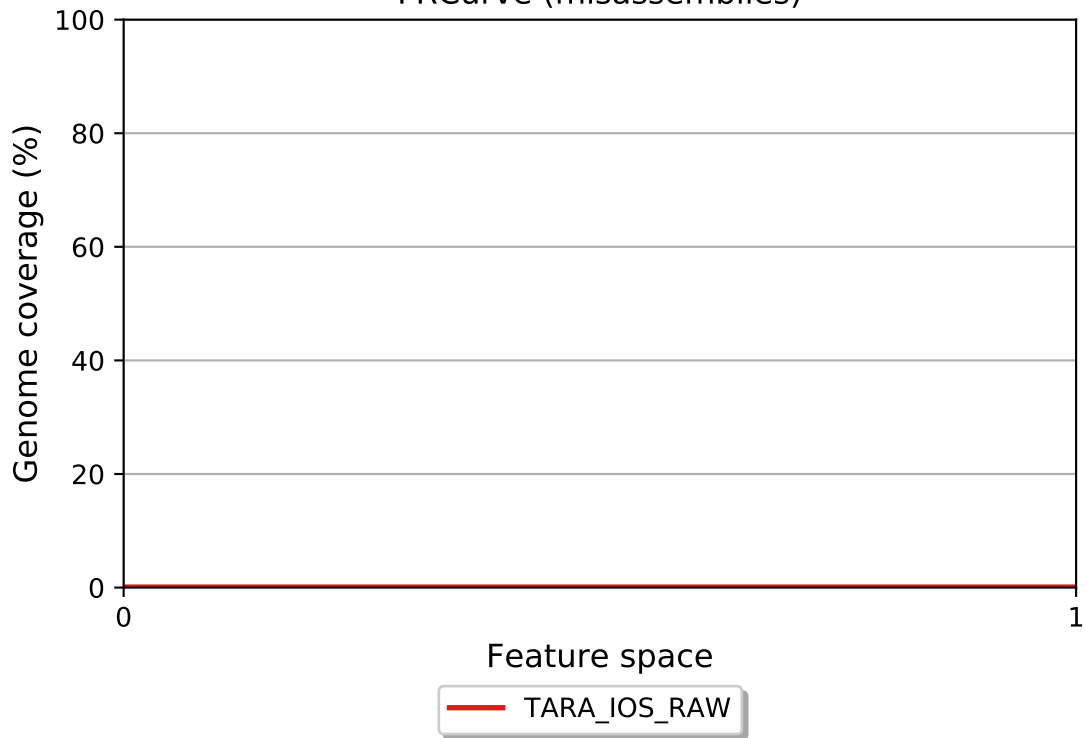
TARA\_IOS\_RAW



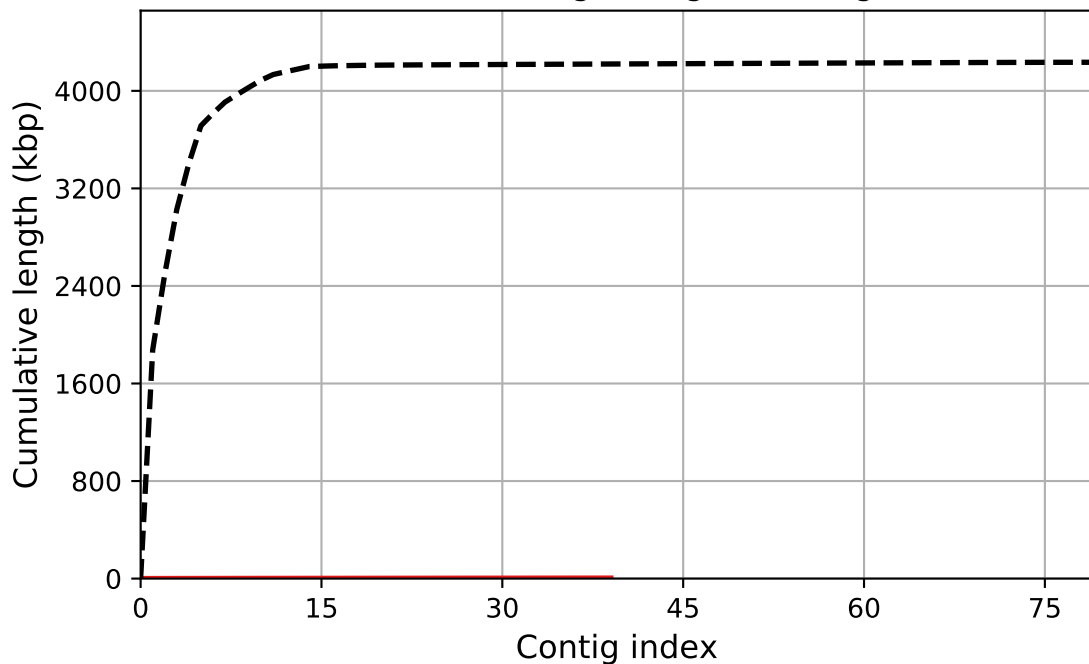
## Misassemblies



FRCurve (misassemblies)

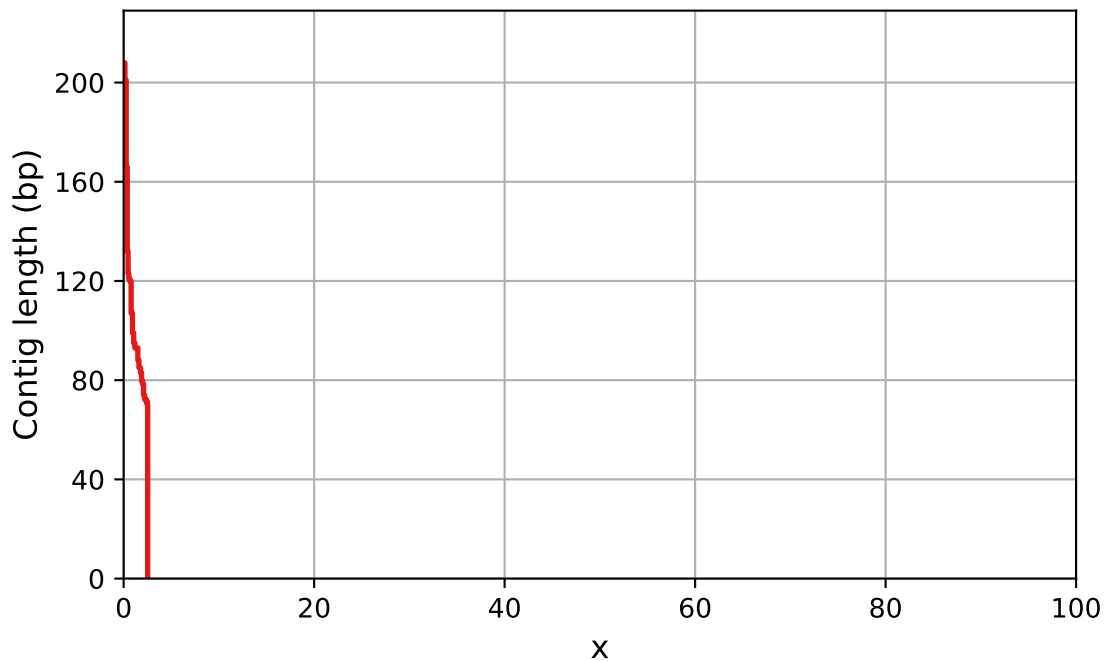


Cumulative length (aligned contigs)



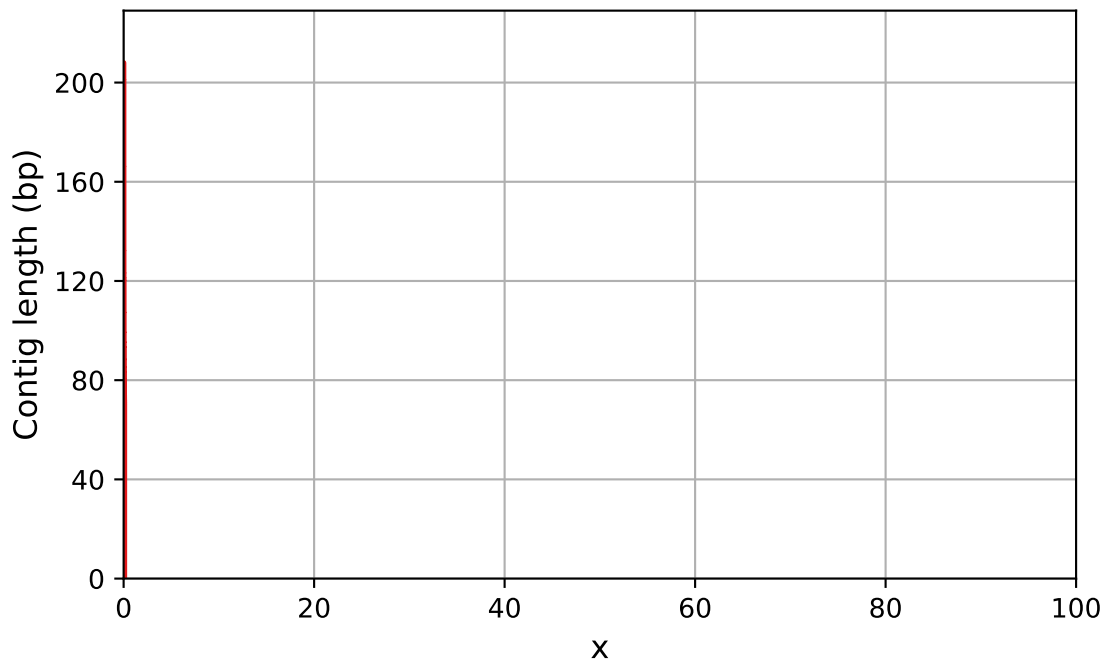
— TARA\_IOS\_RAW    - - Reference

NAx



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# NGAx



— TARA\_IOS\_RAW