

# Report

	TARA_ION_RAW
# contigs (>= 1000 bp)	41
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	142038
Total length (>= 5000 bp)	67500
Total length (>= 10000 bp)	62305
Total length (>= 25000 bp)	36852
Total length (>= 50000 bp)	0
# contigs	41
Largest contig	36852
Total length	142038
Reference length	4234461
GC (%)	46.09
Reference GC (%)	41.03
N50	4353
N75	2155
L50	5
L75	18
# 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	6 + 35 part
Unaligned length	138995
Genome fraction (%)	0.015
Duplication ratio	4.823
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12995.25
# indels per 100 kbp	0.00
Largest alignment	129
Total aligned length	3043
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_ION_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	39
# possible misassemblies	42
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	82
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

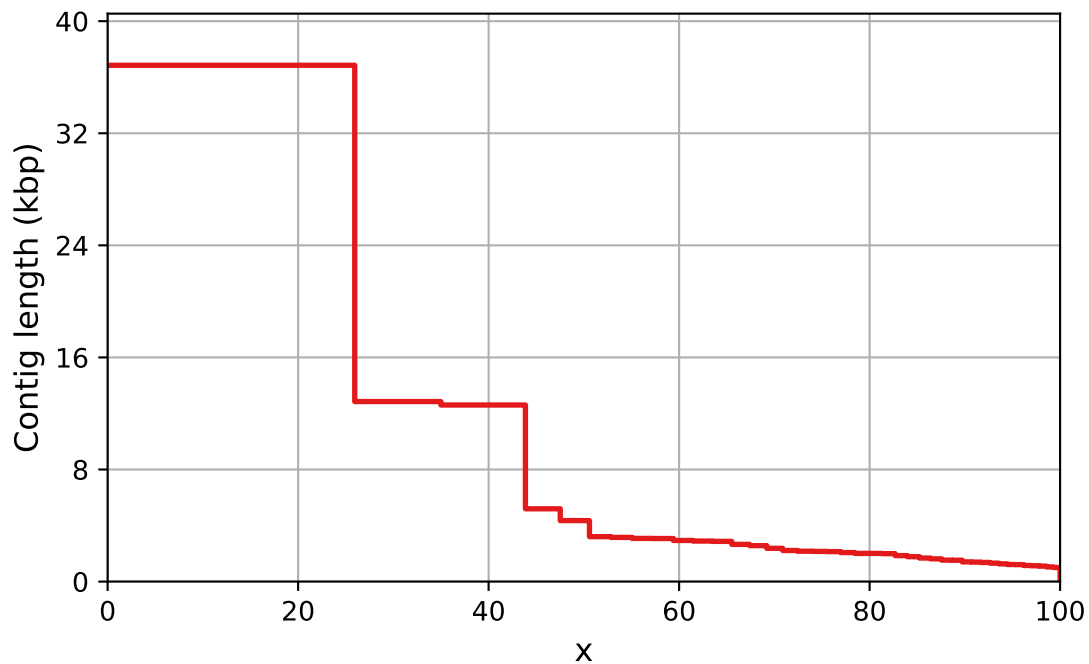
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_ION_RAW
# fully unaligned contigs	6
Fully unaligned length	16563
# partially unaligned contigs	35
Partially unaligned length	122432
# N's	0

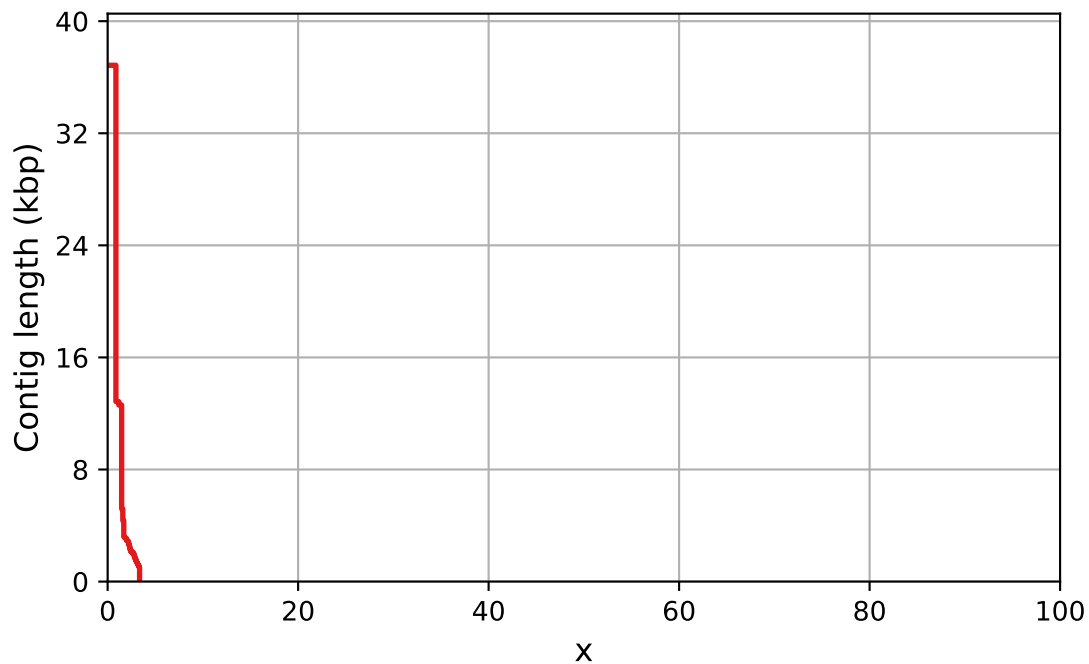
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



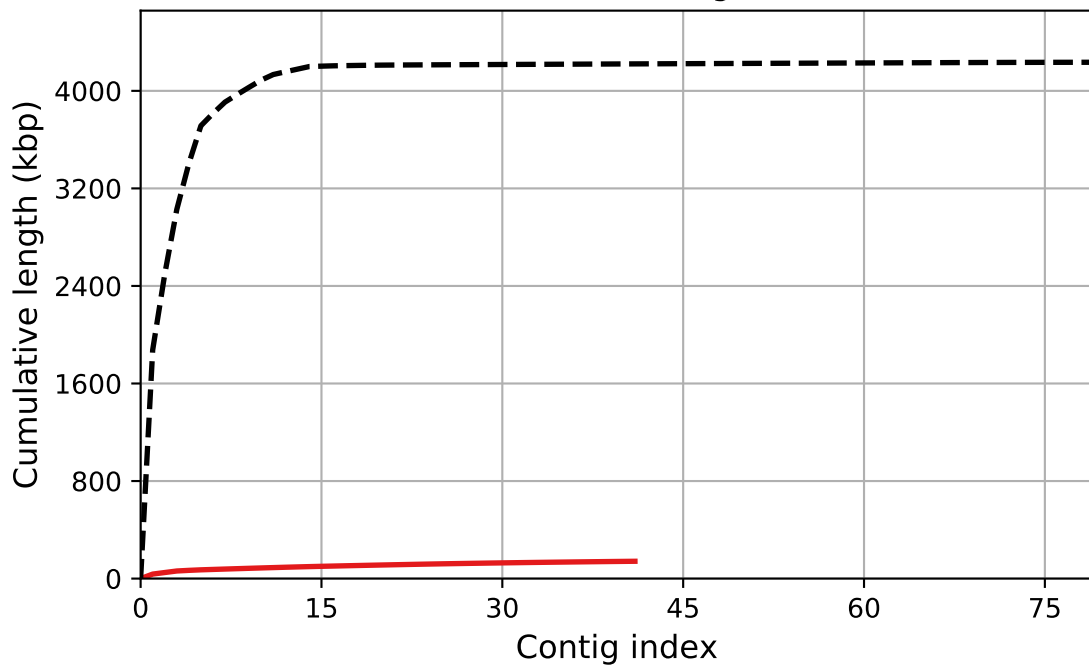
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NGx



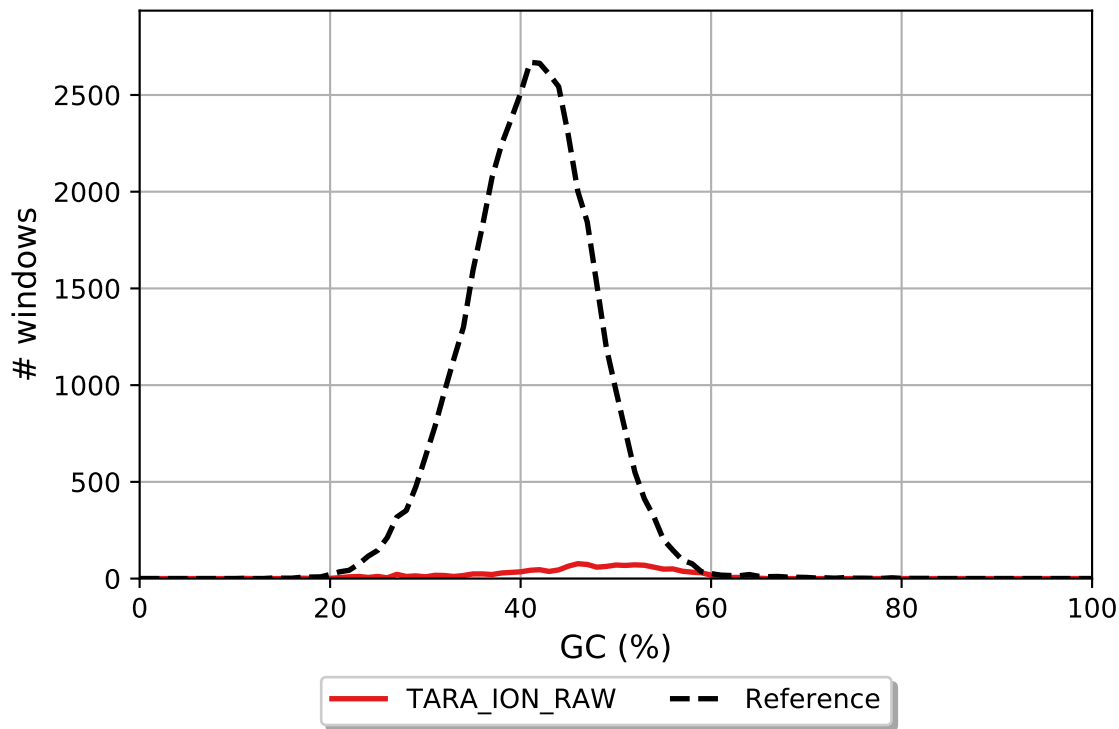
TARA\_ION\_RAW

Cumulative length

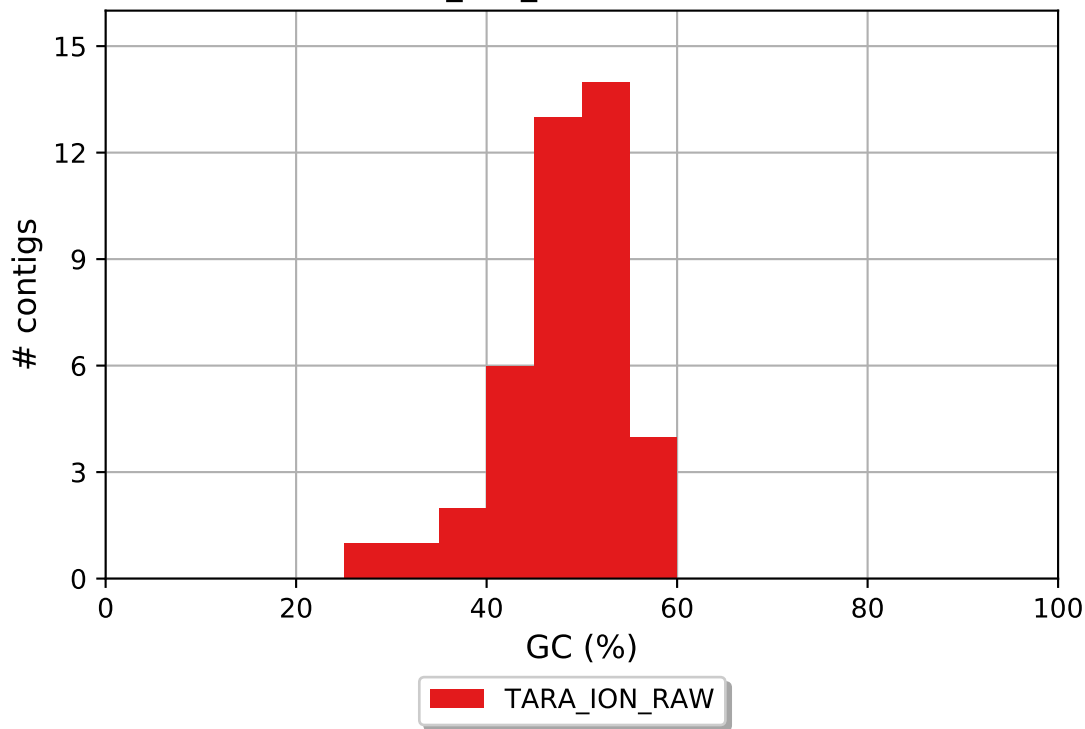


TARA\_ION\_RAW      Reference

## GC content



TARA\_ION\_RAW GC content

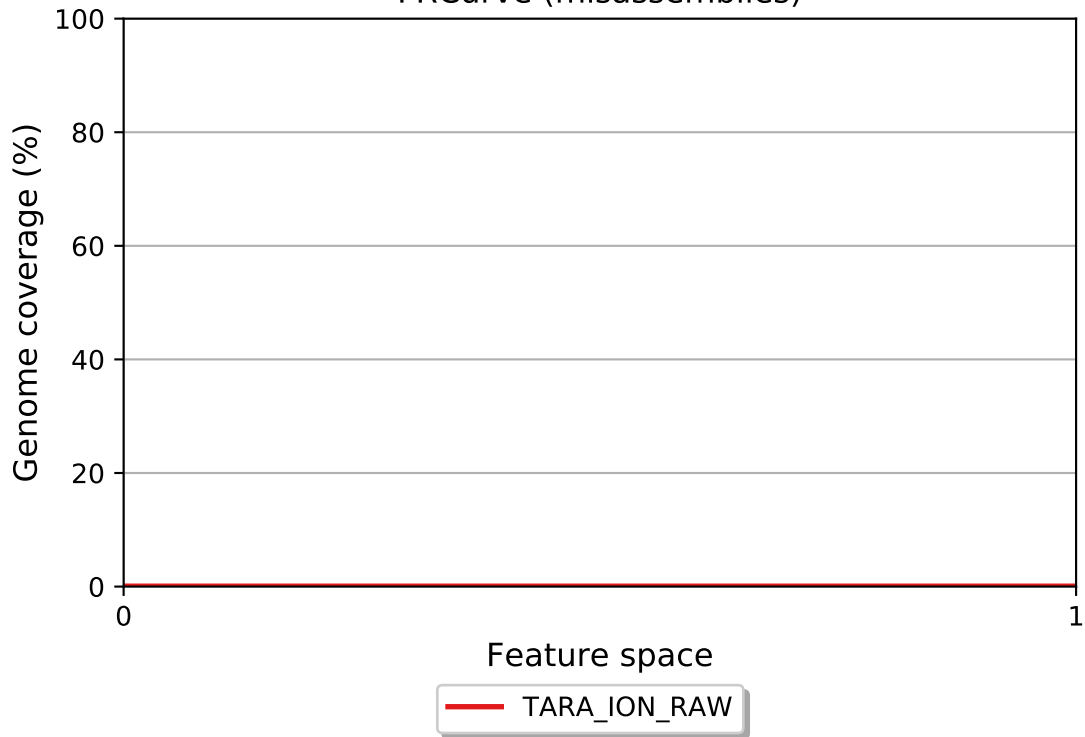




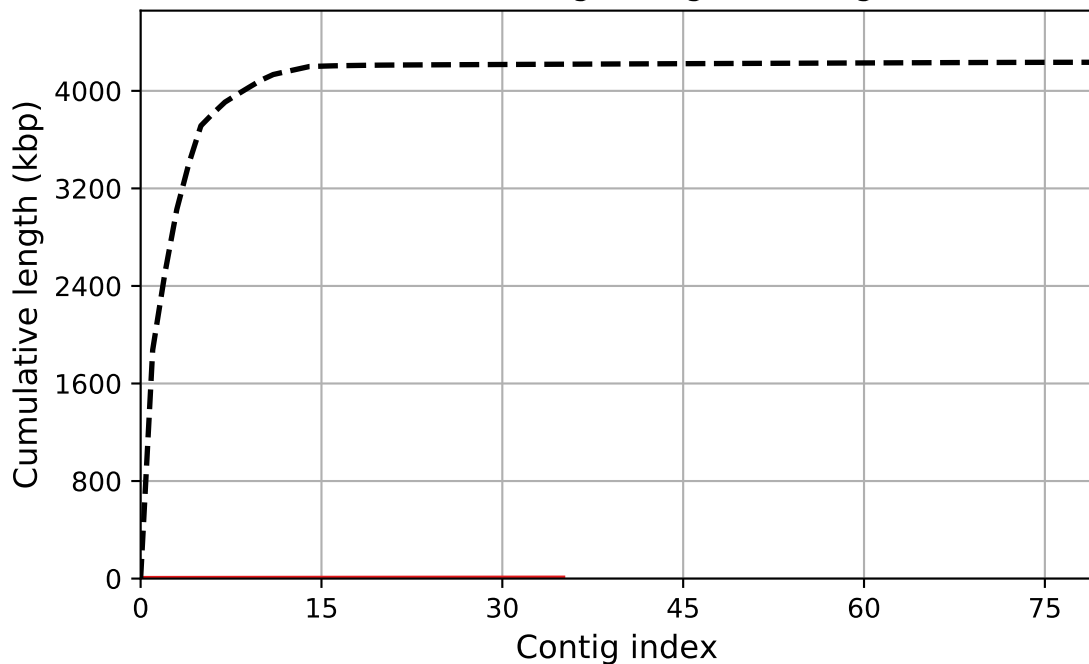
# Misassemblies



FRCurve (misassemblies)

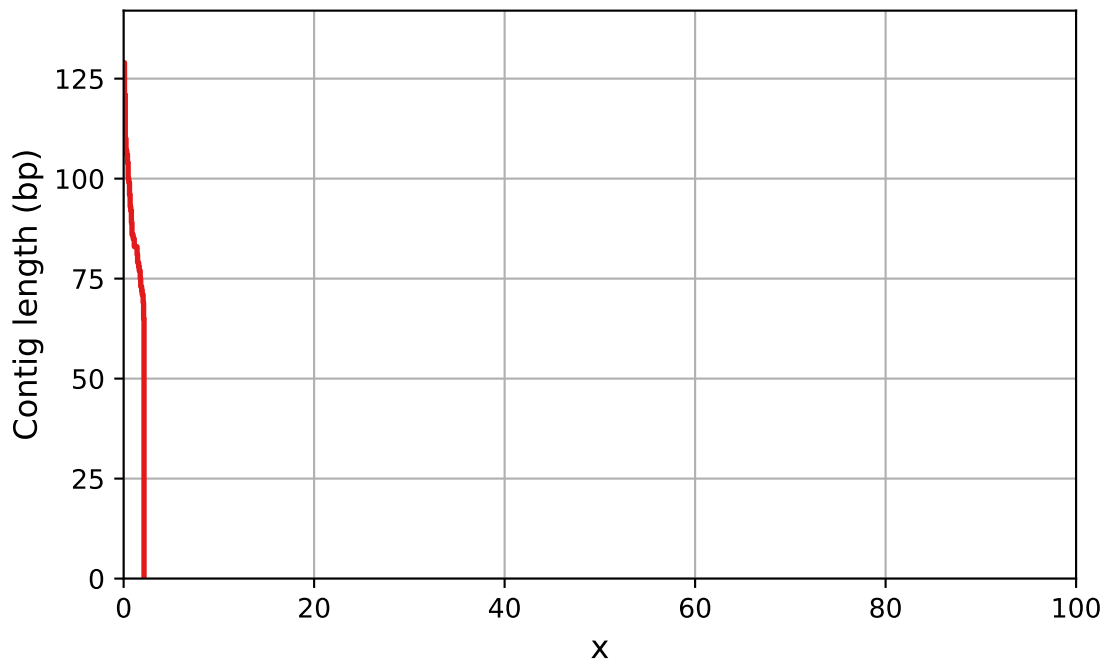


Cumulative length (aligned contigs)



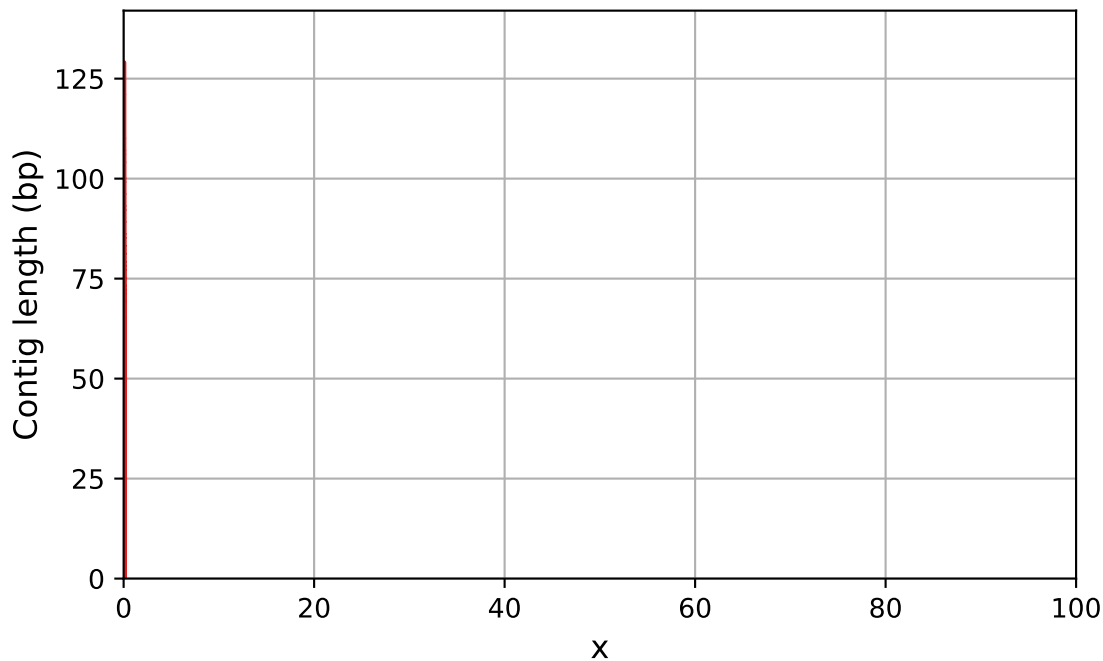
TARA\_ION\_RAW      Reference

NAx



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# NGAx



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