

# Report

	TARA_ANE_RAW
# contigs (>= 1000 bp)	436
# contigs (>= 5000 bp)	99
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	2263390
Total length (>= 5000 bp)	1575730
Total length (>= 10000 bp)	1199931
Total length (>= 25000 bp)	738786
Total length (>= 50000 bp)	116677
# contigs	436
Largest contig	58665
Total length	2263390
Reference length	7658814
GC (%)	32.68
Reference GC (%)	63.29
N50	12930
N75	4012
L50	41
L75	127
# 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	3
# unaligned contigs	10 + 425 part
Unaligned length	2227832
Genome fraction (%)	0.054
Duplication ratio	8.566
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15152.98
# indels per 100 kbp	72.27
Largest alignment	287
Total aligned length	34746
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_ANE_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	430
# possible misassemblies	532
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	629
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	4

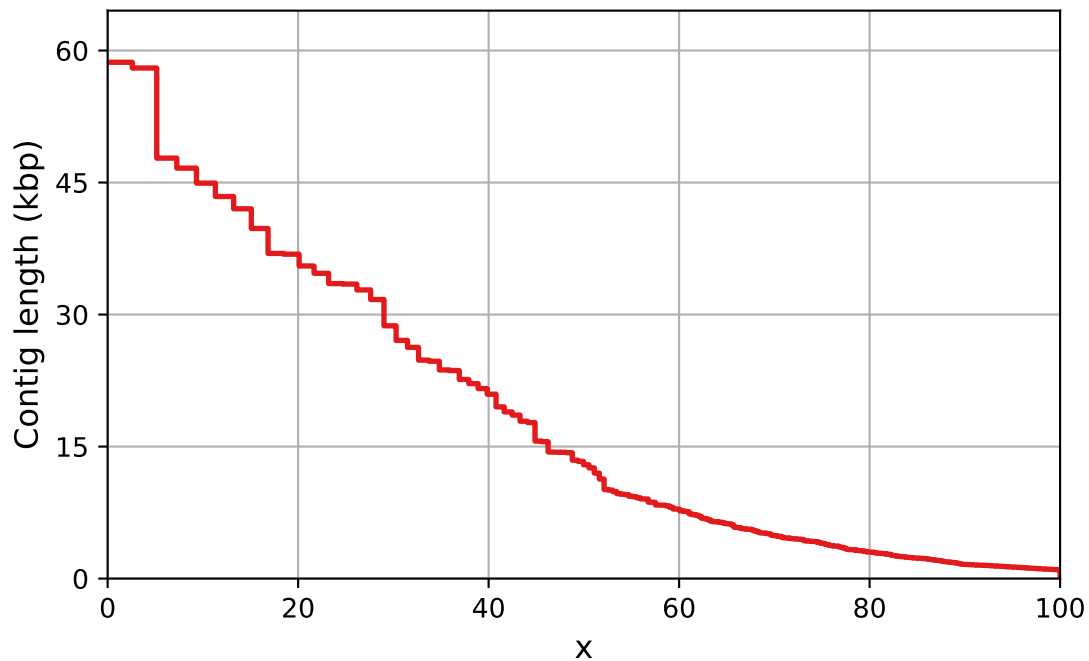
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_ANE_RAW
# fully unaligned contigs	10
Fully unaligned length	17776
# partially unaligned contigs	425
Partially unaligned length	2210056
# N's	0

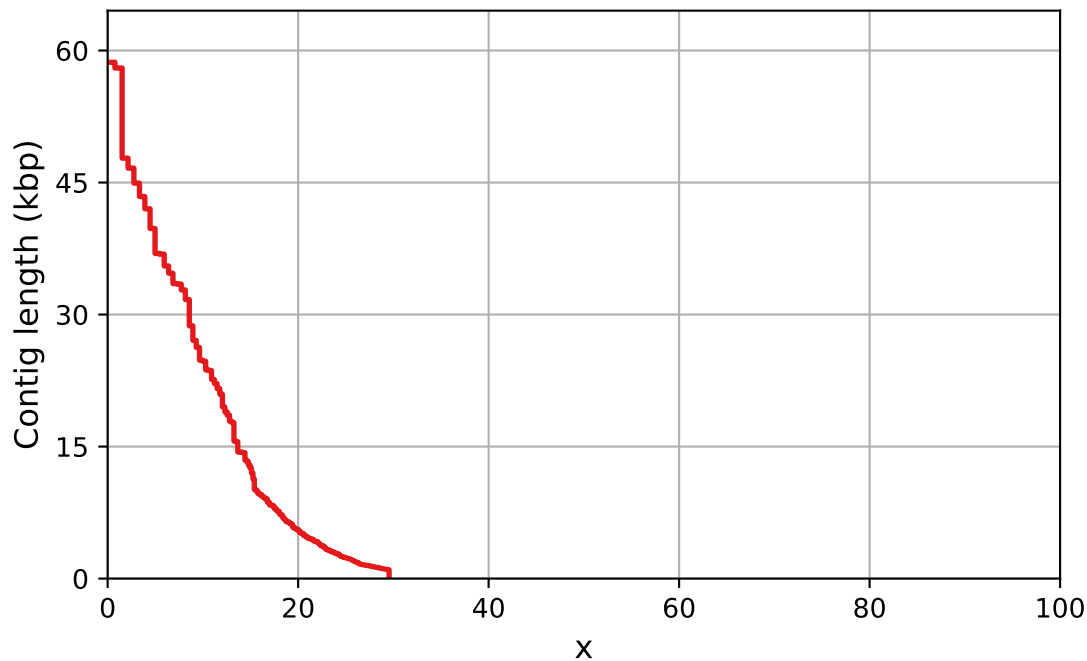
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



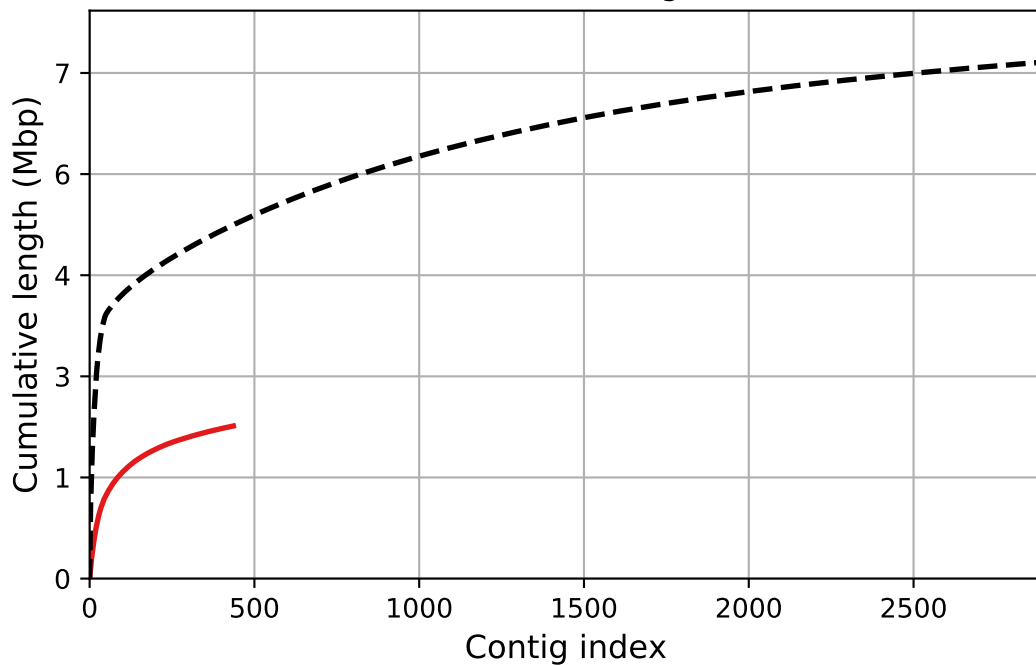
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NGx



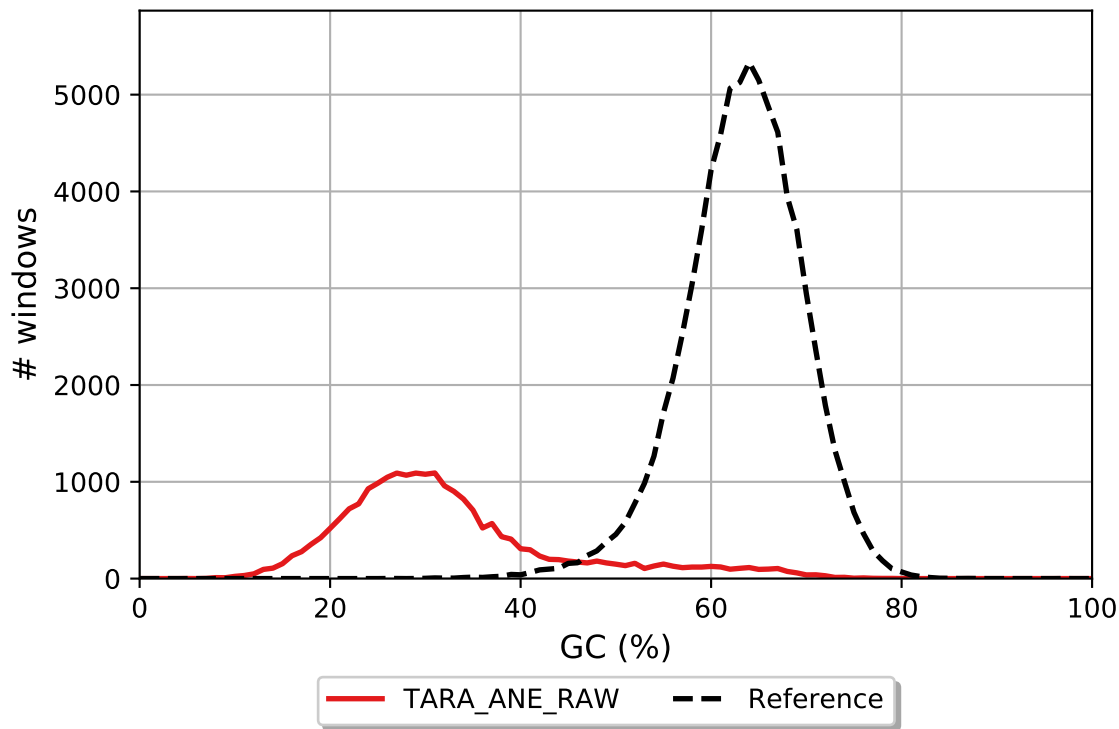
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Cumulative length

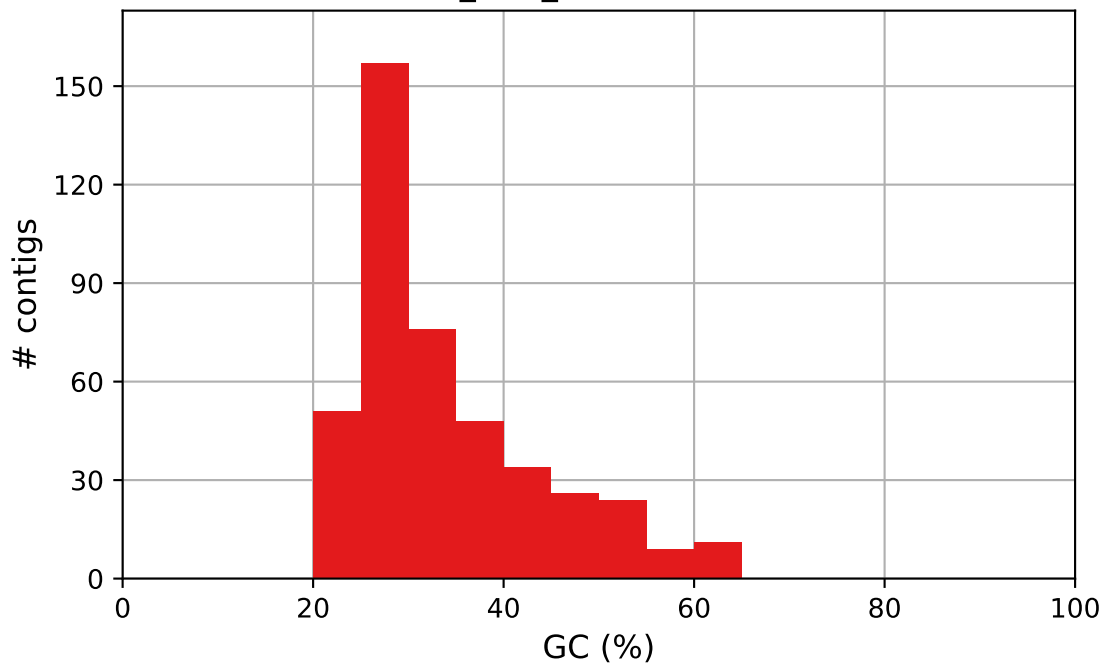


— TARA\_ANE\_RAW    - - Reference

## GC content



TARA\_ANE\_RAW GC content



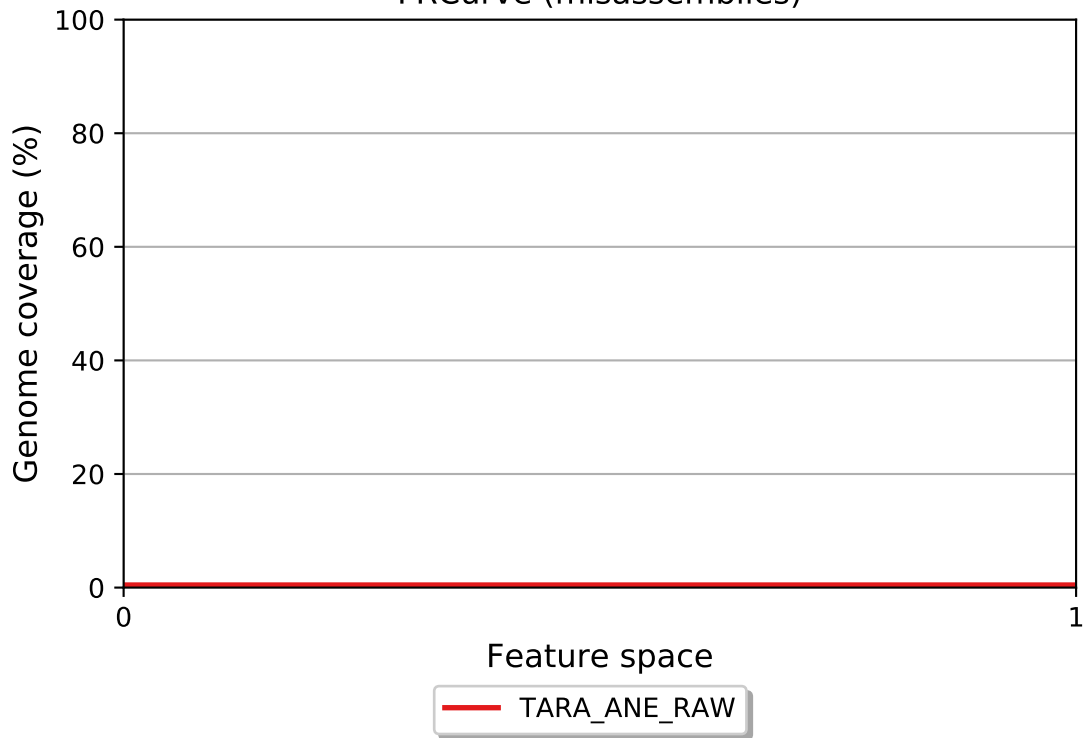
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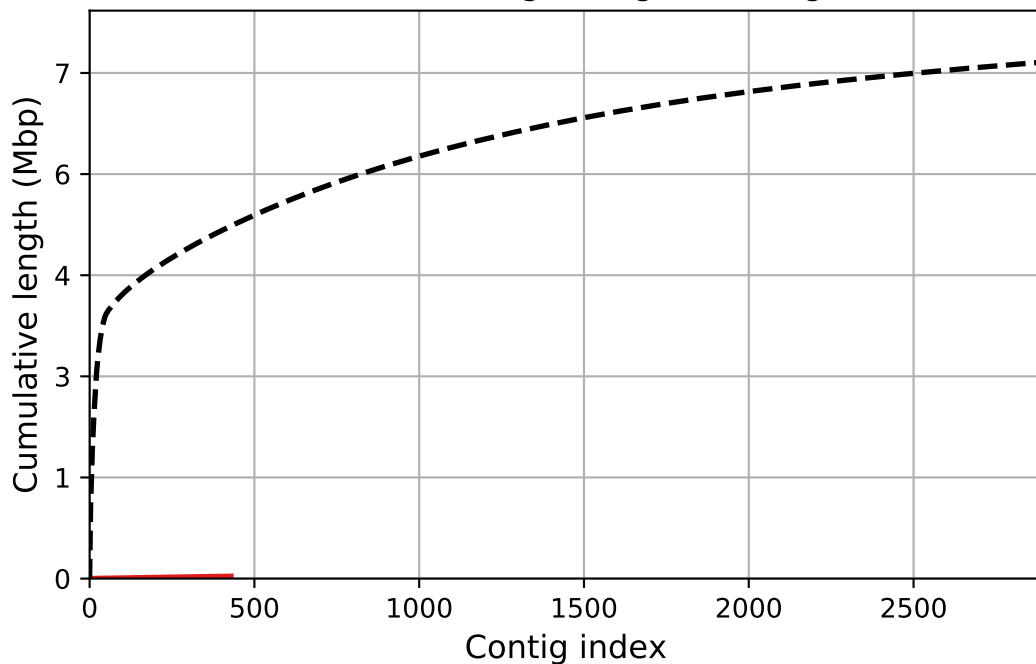
## Misassemblies



FRCurve (misassemblies)

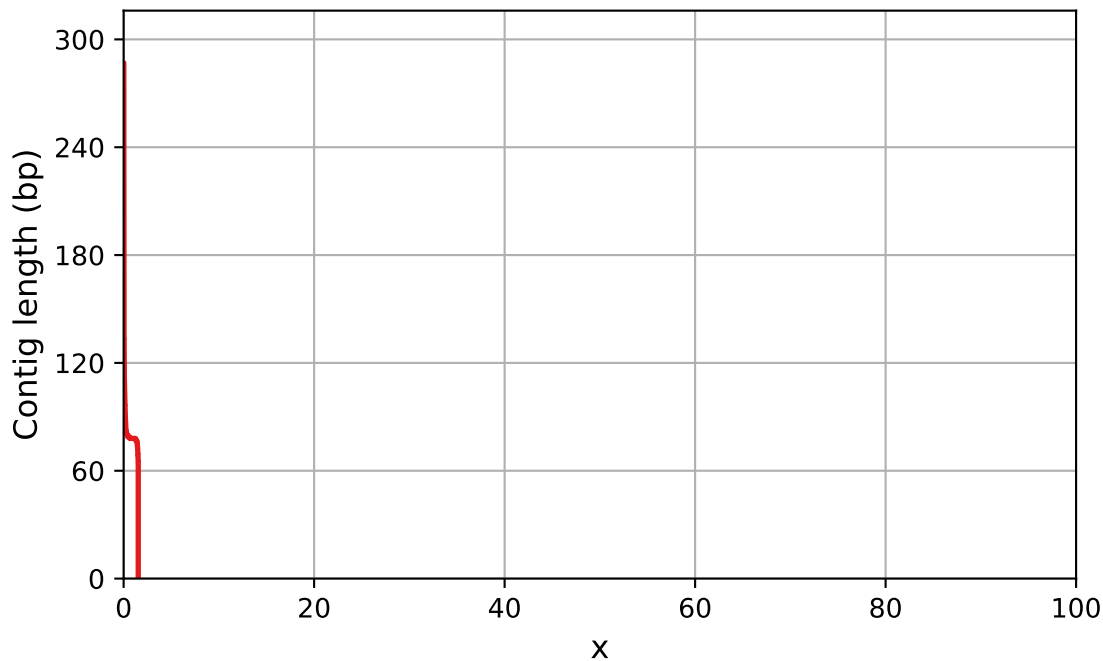


Cumulative length (aligned contigs)



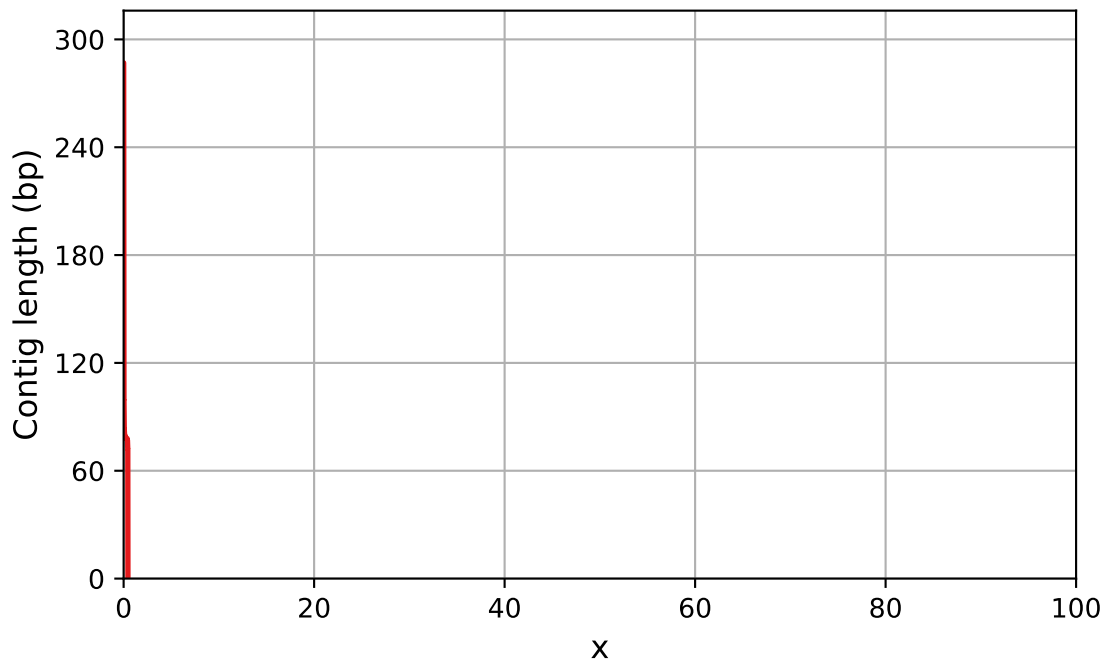
— TARA\_ANE\_RAW    - - Reference

NAx



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# NGAx



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