

Report

	TARA_ANW_RAW
# contigs (≥ 1000 bp)	429
# contigs (≥ 5000 bp)	107
# contigs (≥ 10000 bp)	69
# contigs (≥ 25000 bp)	32
# contigs (≥ 50000 bp)	15
Total length (≥ 1000 bp)	4367398
Total length (≥ 5000 bp)	3713385
Total length (≥ 10000 bp)	3458838
Total length (≥ 25000 bp)	2876923
Total length (≥ 50000 bp)	2250052
# contigs	429
Largest contig	1019813
Total length	4367398
Reference length	7658814
GC (%)	55.27
Reference GC (%)	63.29
N50	54820
NG50	3855
N75	13544
L50	14
LG50	134
L75	54
# 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	10
# unaligned contigs	25 + 404 part
Unaligned length	4330625
Genome fraction (%)	0.155
Duplication ratio	3.093
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6046.59
# indels per 100 kbp	42.05
Largest alignment	591
Total aligned length	36773
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

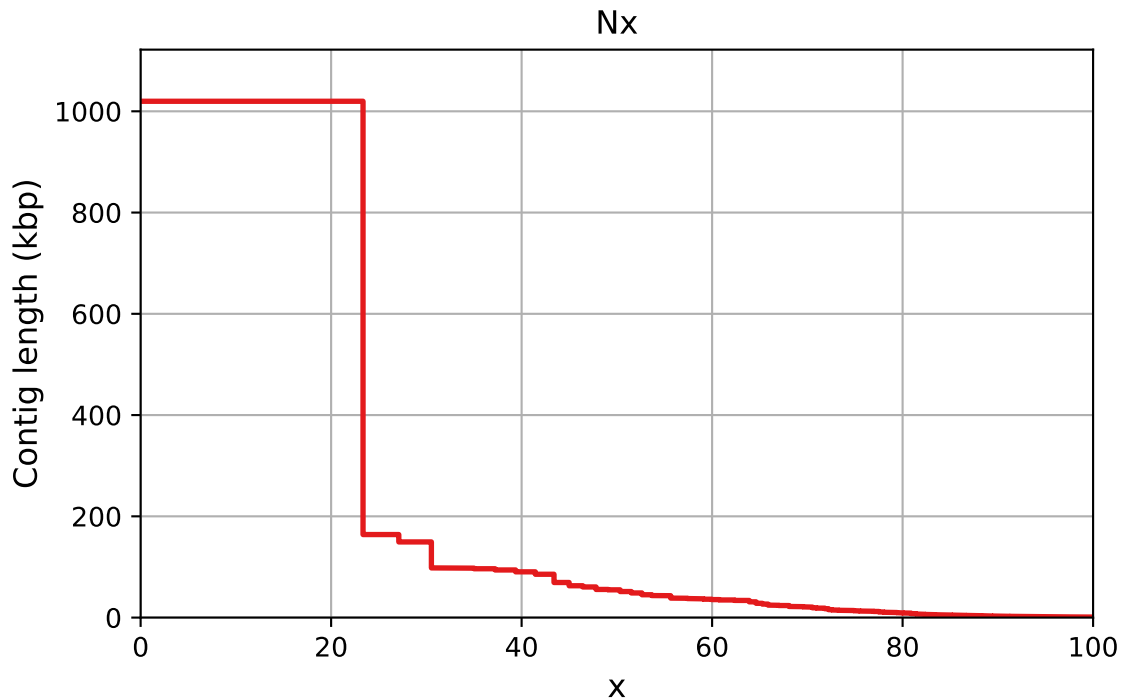
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	417
# possible misassemblies	540
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	10
# mismatches	719
# 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

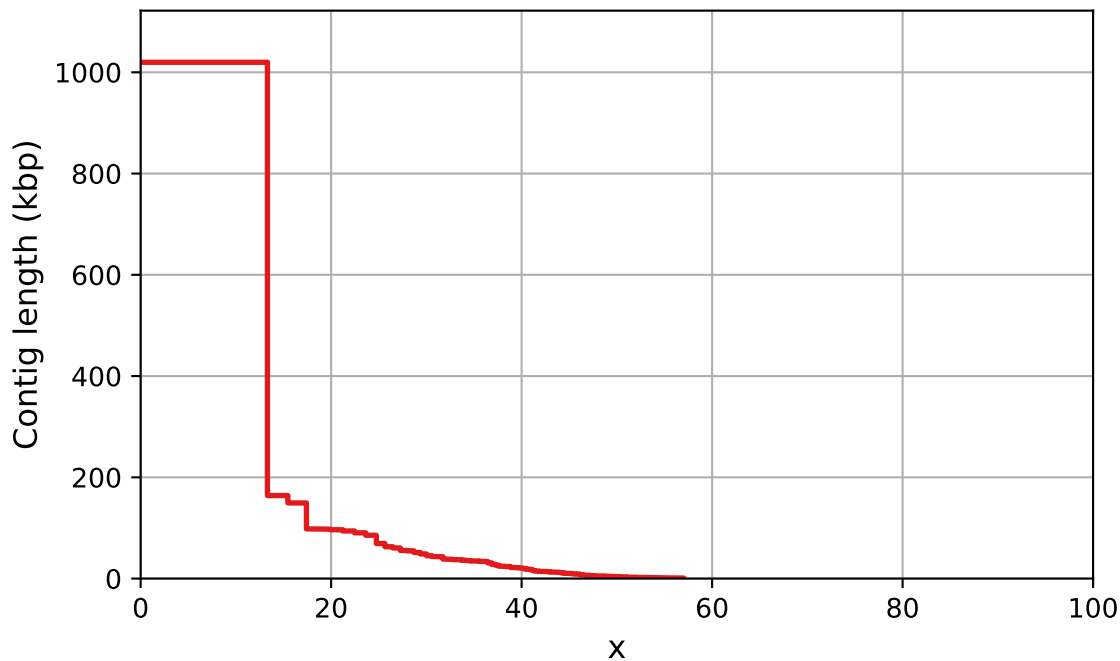
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# fully unaligned contigs	25
Fully unaligned length	558314
# partially unaligned contigs	404
Partially unaligned length	3772311
# N's	0

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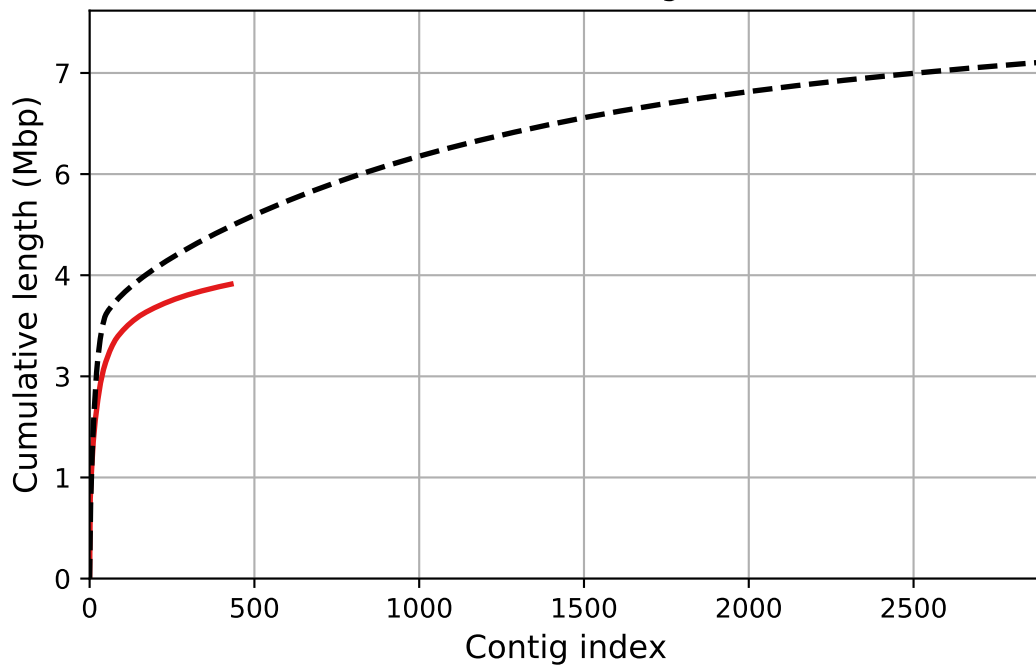
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NGx



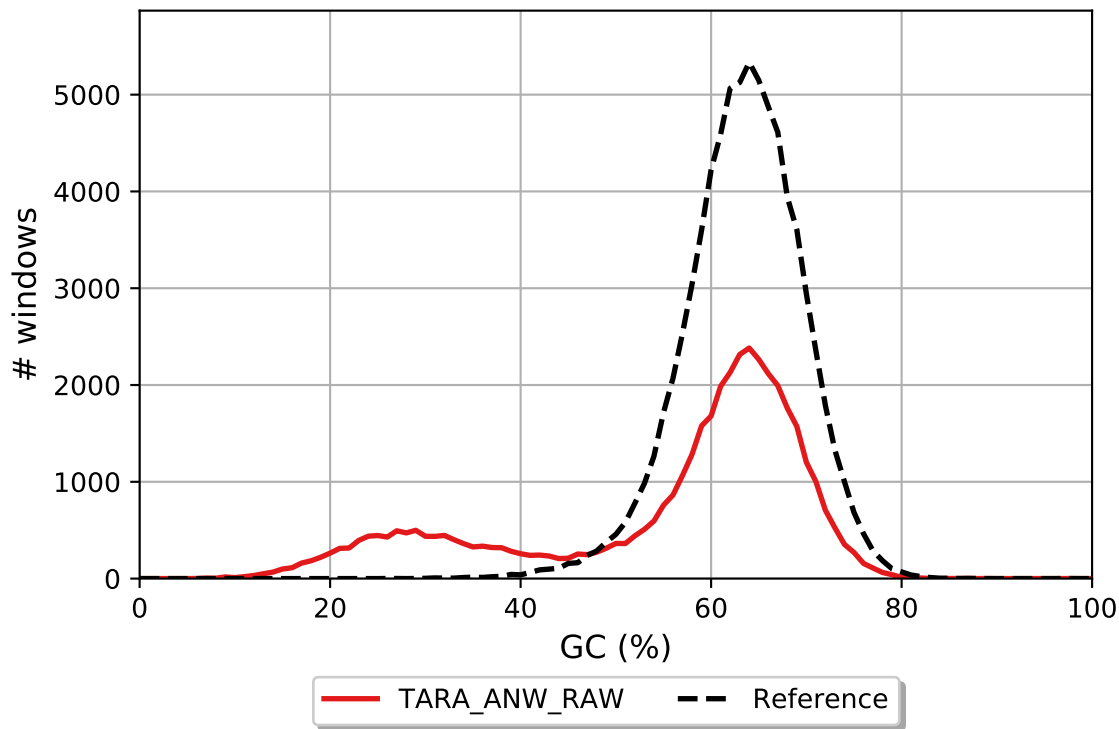
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Cumulative length

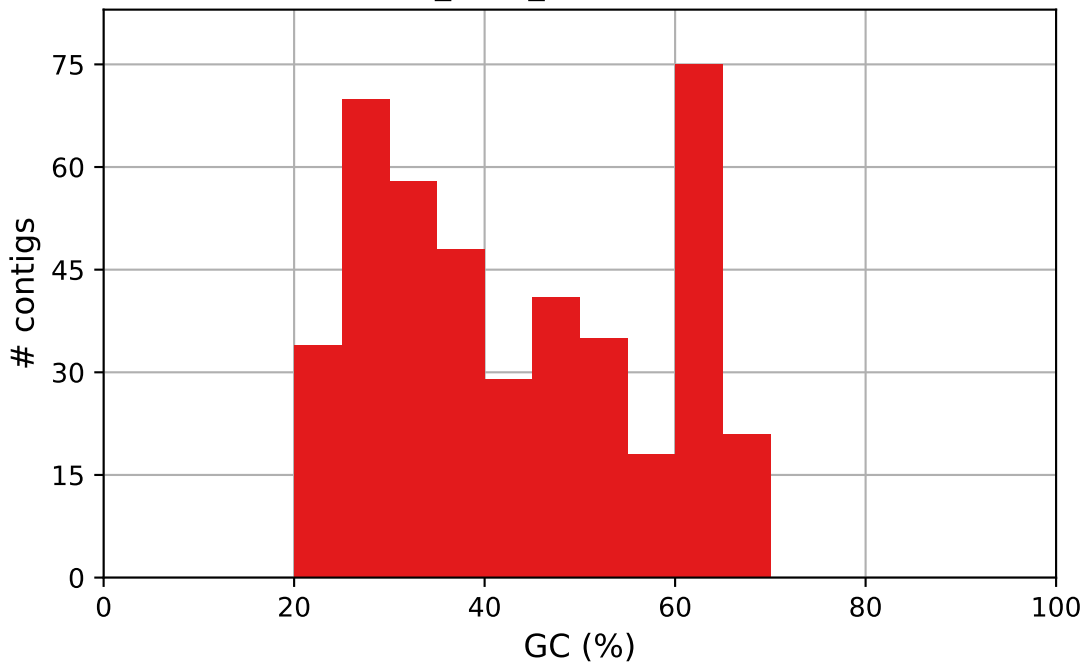


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GC content



TARA_ANW_RAW GC content

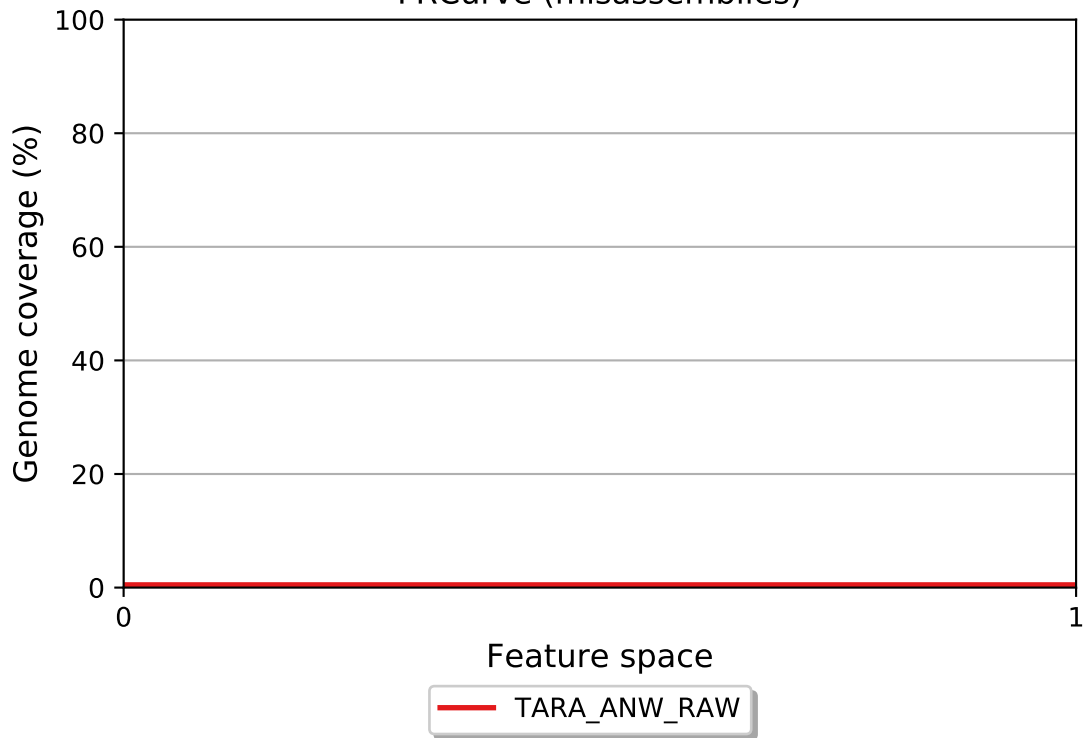


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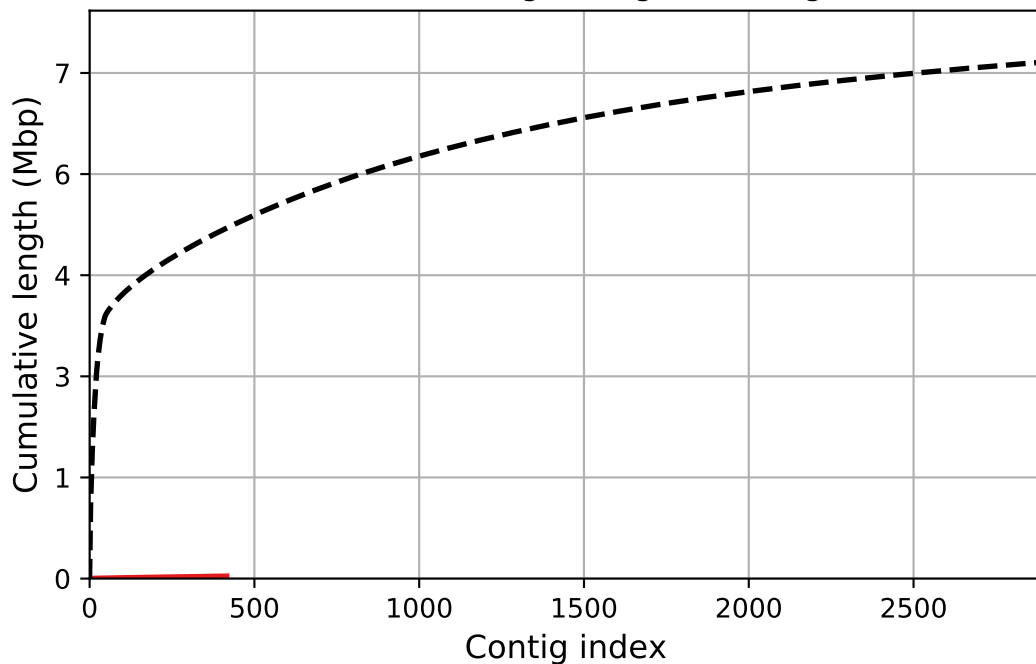
Misassemblies



FRCurve (misassemblies)

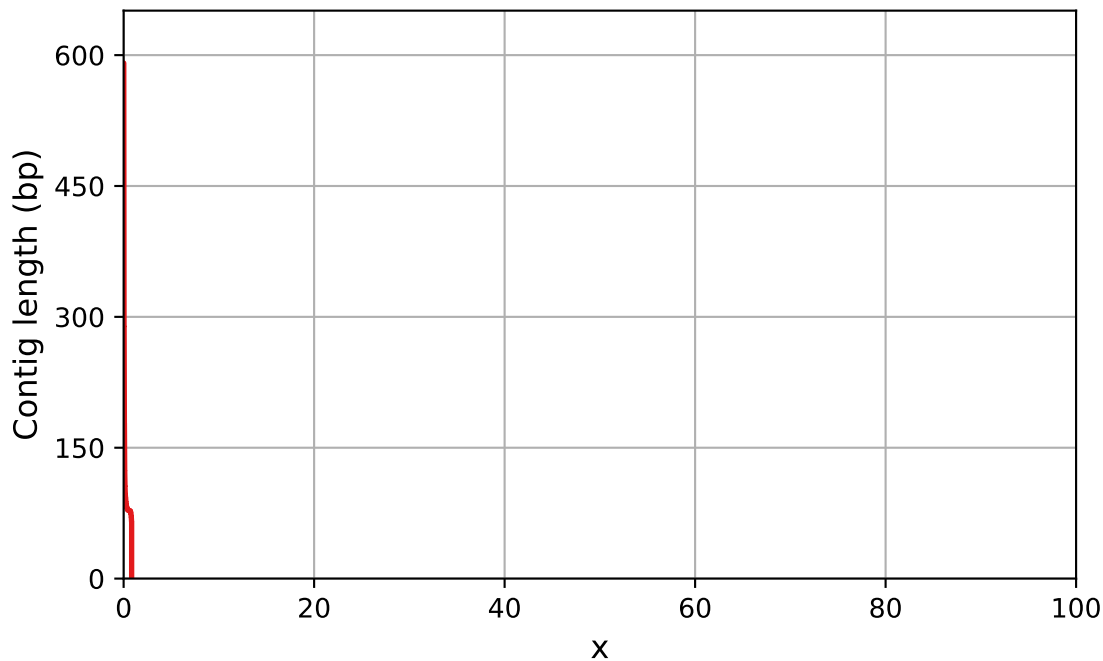


Cumulative length (aligned contigs)



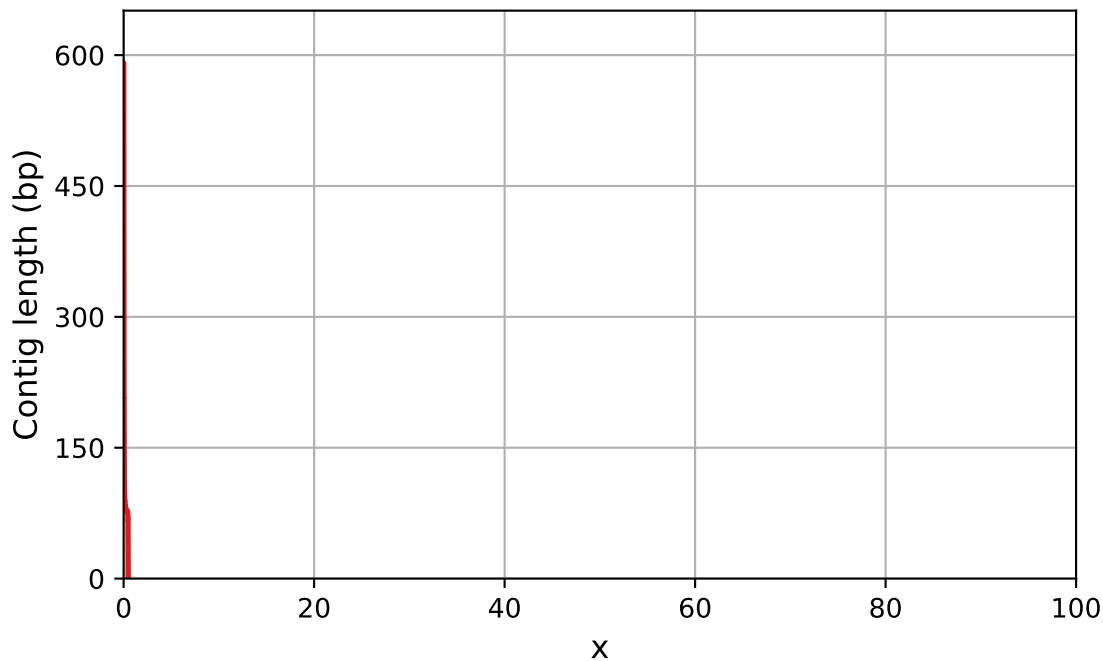
— TARA_ANW_RAW - - Reference

NAx



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NGAx



TARA_ANW_RAW