

Report

	TARA_ANW_RAW
# contigs (>= 1000 bp)	55
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	207362
Total length (>= 5000 bp)	121401
Total length (>= 10000 bp)	105935
Total length (>= 25000 bp)	105935
Total length (>= 50000 bp)	105935
# contigs	55
Largest contig	105935
Total length	207362
Reference length	4234461
GC (%)	41.81
Reference GC (%)	41.03
N50	105935
N75	1978
L50	1
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	1
# unaligned contigs	11 + 44 part
Unaligned length	203124
Genome fraction (%)	0.028
Duplication ratio	3.549
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11139.03
# indels per 100 kbp	83.75
Largest alignment	201
Total aligned length	4238
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

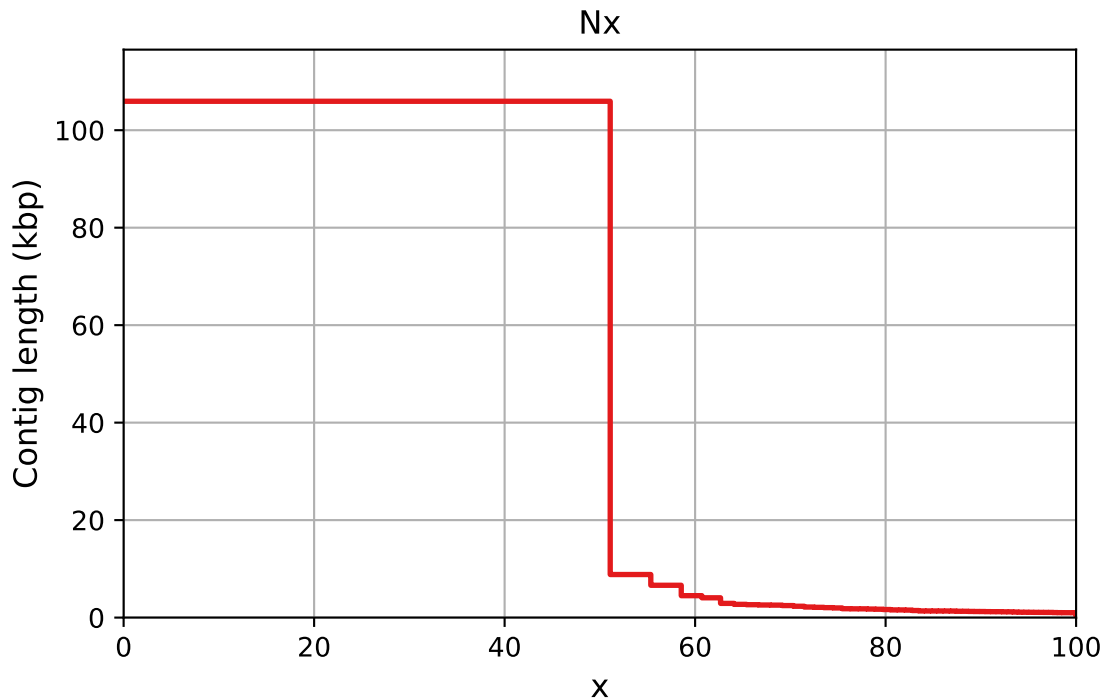
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	52
# possible misassemblies	59
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	133
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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

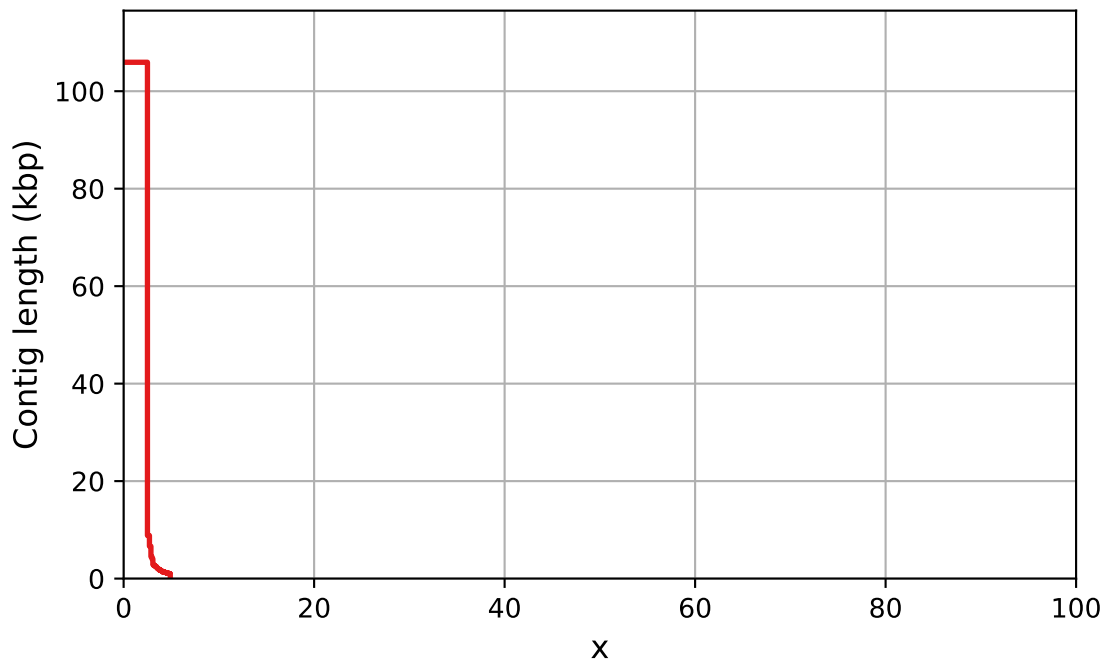
	TARA_ANW_RAW
# fully unaligned contigs	11
Fully unaligned length	23368
# partially unaligned contigs	44
Partially unaligned length	179756
# N's	0

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).



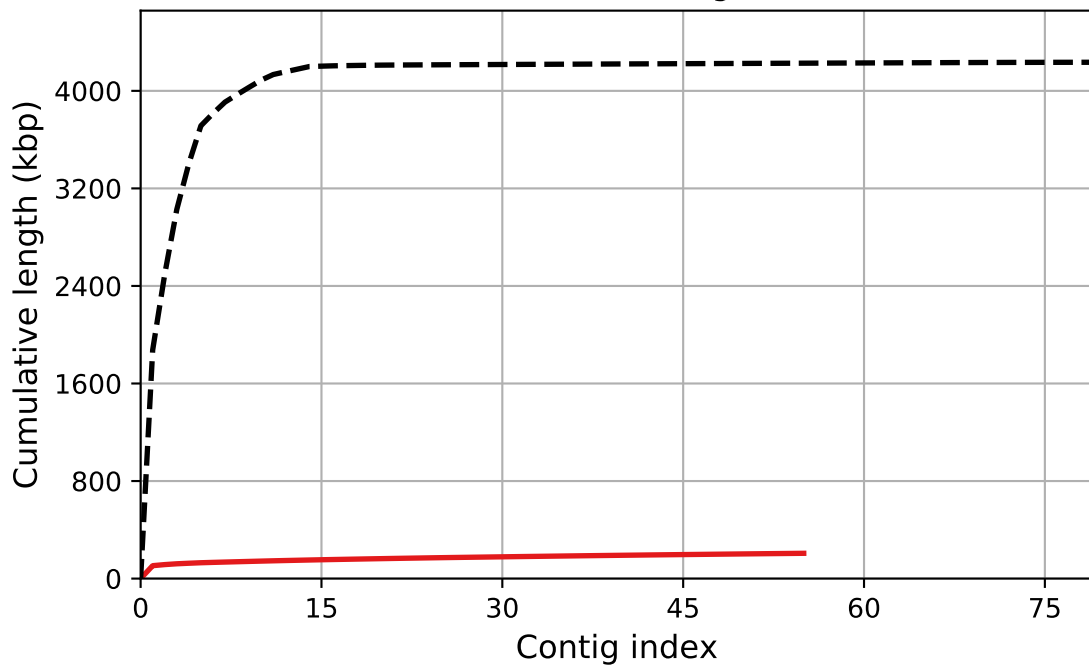
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NGx



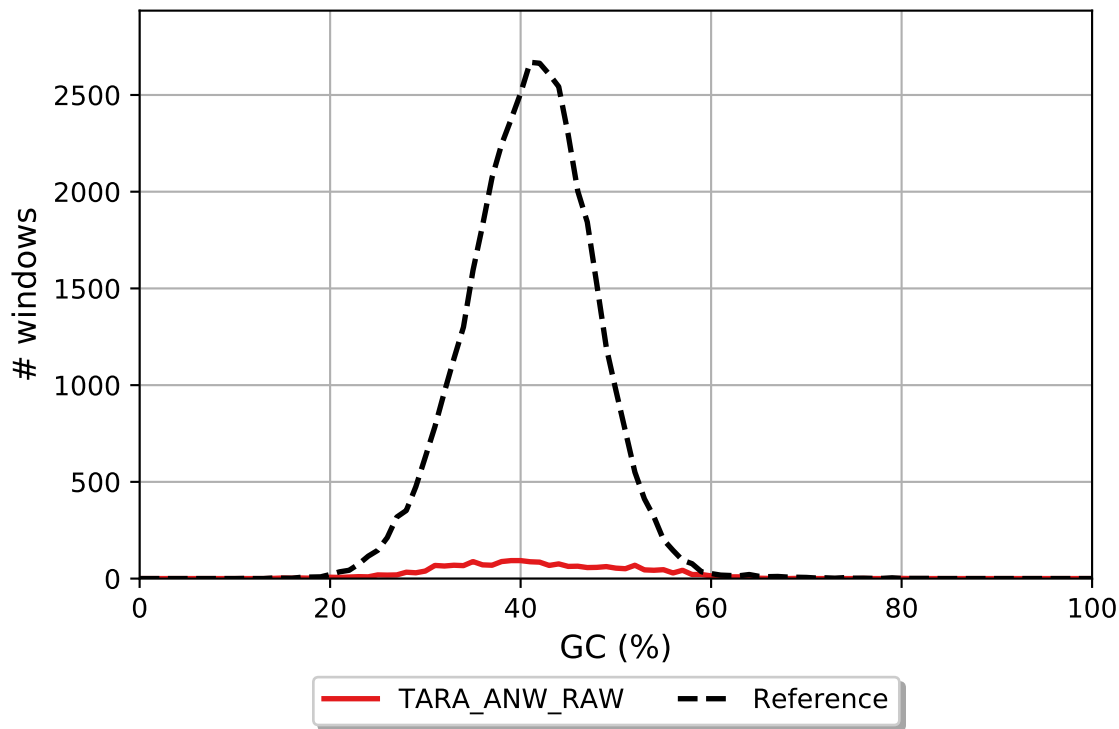
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Cumulative length

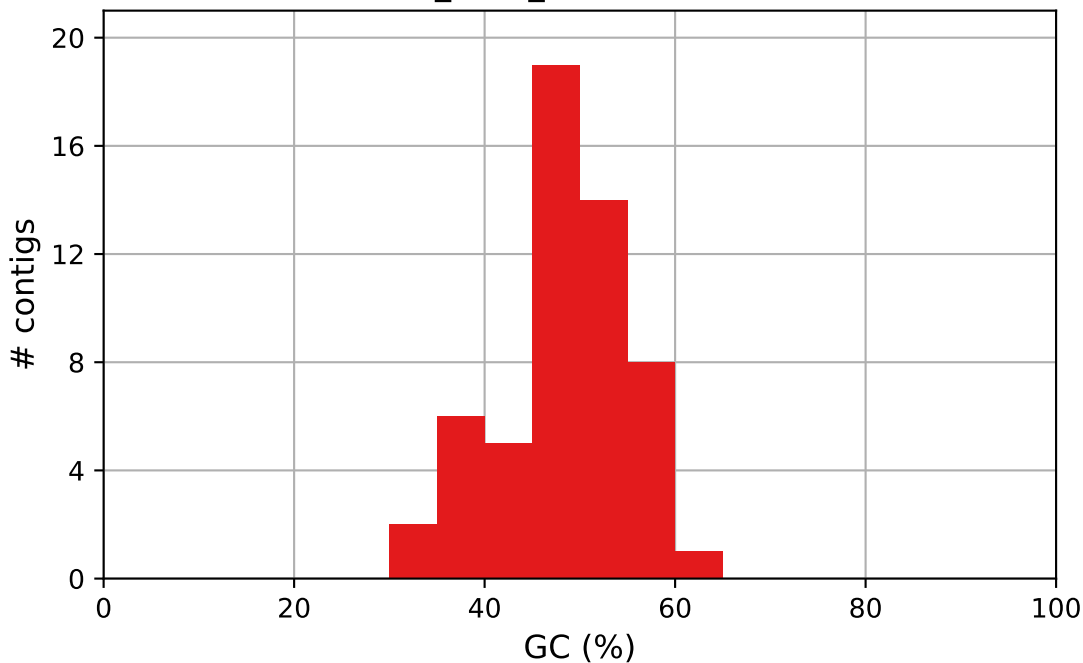


— TARA_ANW_RAW - - Reference

GC content



TARA_ANW_RAW GC content

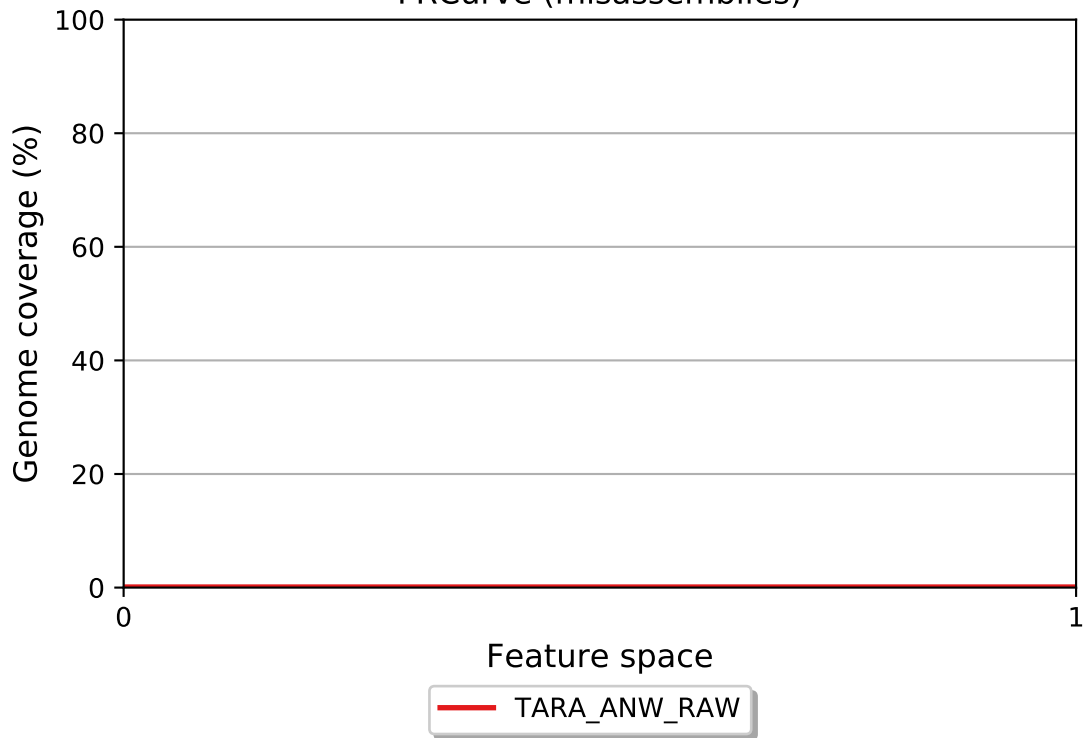


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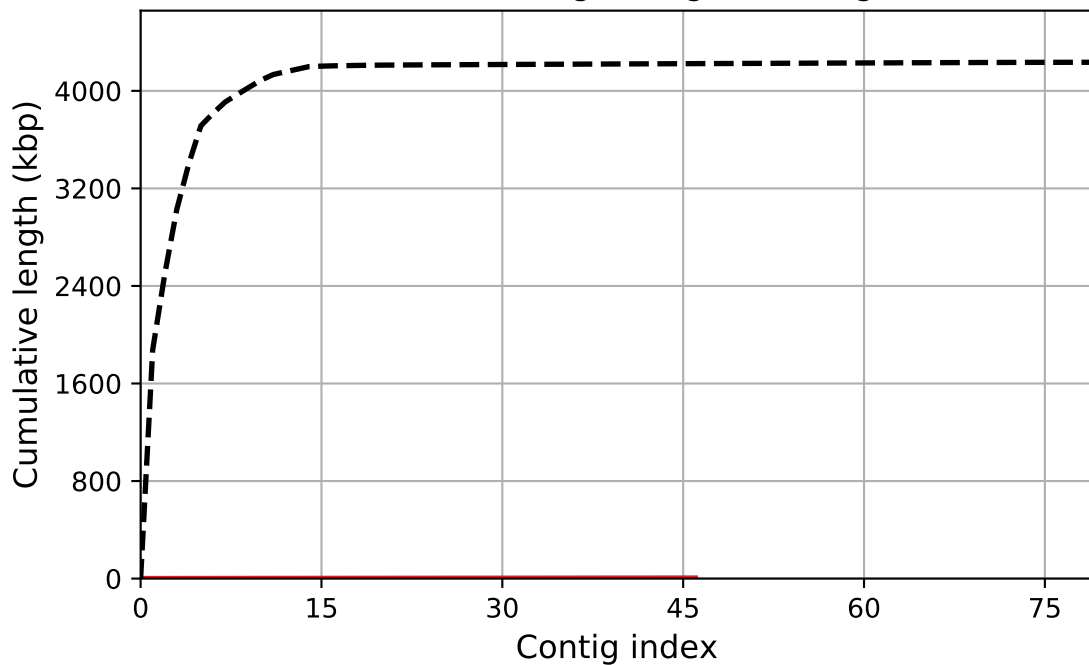
Misassemblies



FRCurve (misassemblies)

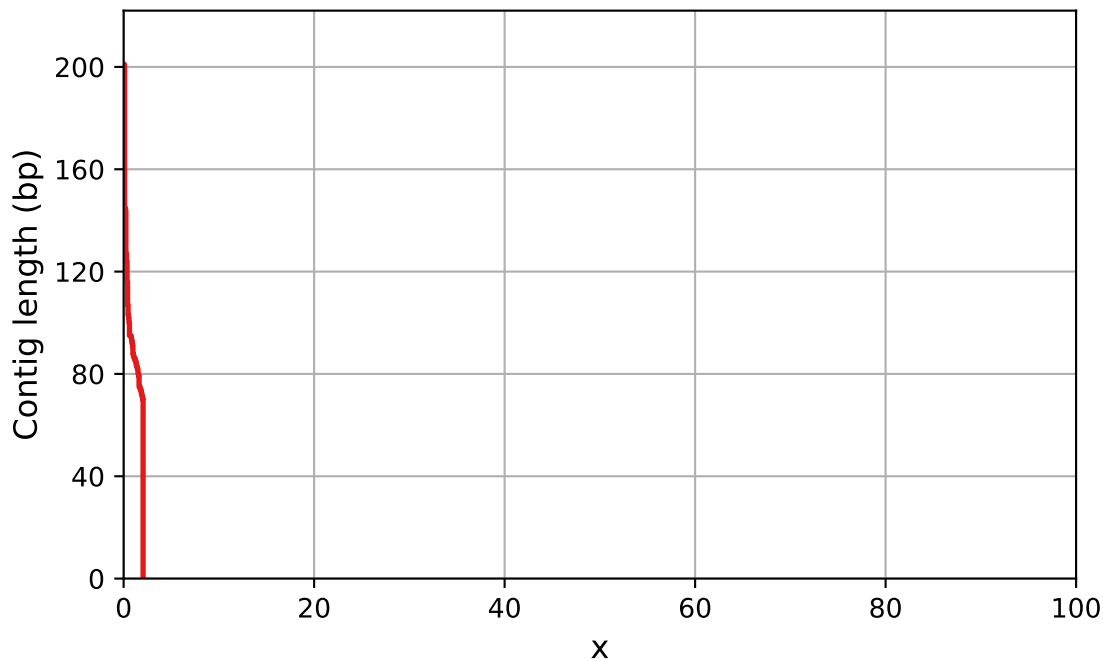


Cumulative length (aligned contigs)



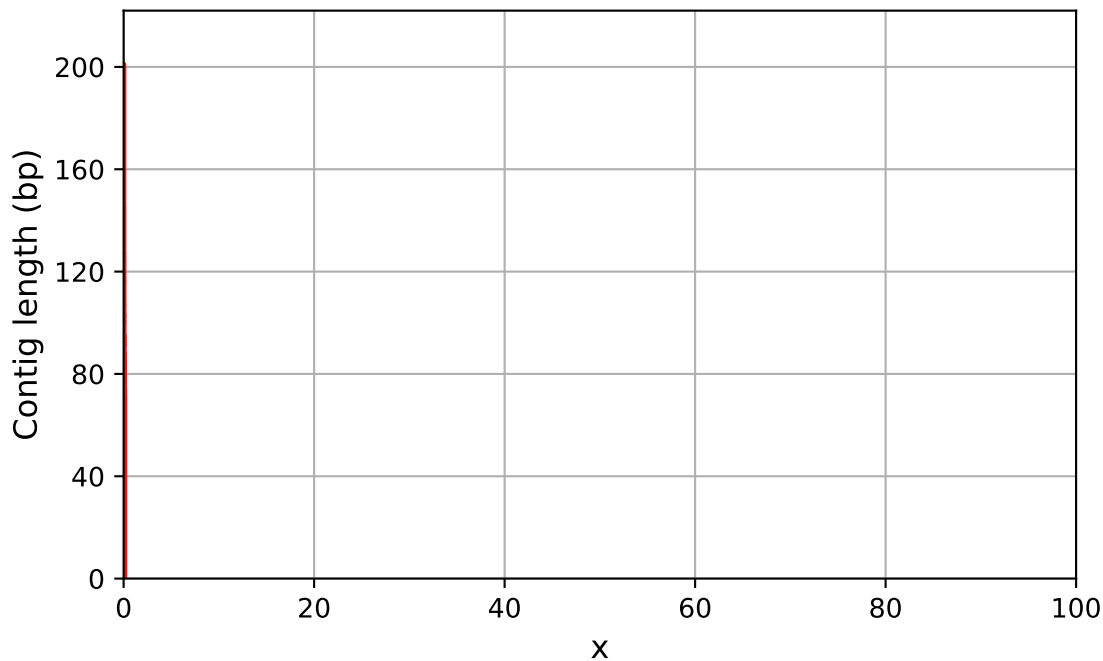
— TARA_ANW_RAW - - Reference

NAx



TARA_ANW_RAW

NGAx



TARA_ANW_RAW