

Report

	TARA_RED_RAW
# contigs (>= 1000 bp)	48
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	836956
Total length (>= 5000 bp)	758017
Total length (>= 10000 bp)	752323
Total length (>= 25000 bp)	675208
Total length (>= 50000 bp)	603011
# contigs	48
Largest contig	527714
Total length	836956
Reference length	4234461
GC (%)	42.95
Reference GC (%)	41.03
N50	527714
N75	43067
L50	1
L75	3
# 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	2
# unaligned contigs	6 + 42 part
Unaligned length	833059
Genome fraction (%)	0.029
Duplication ratio	3.161
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8353.61
# indels per 100 kbp	162.21
Largest alignment	201
Total aligned length	3897
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

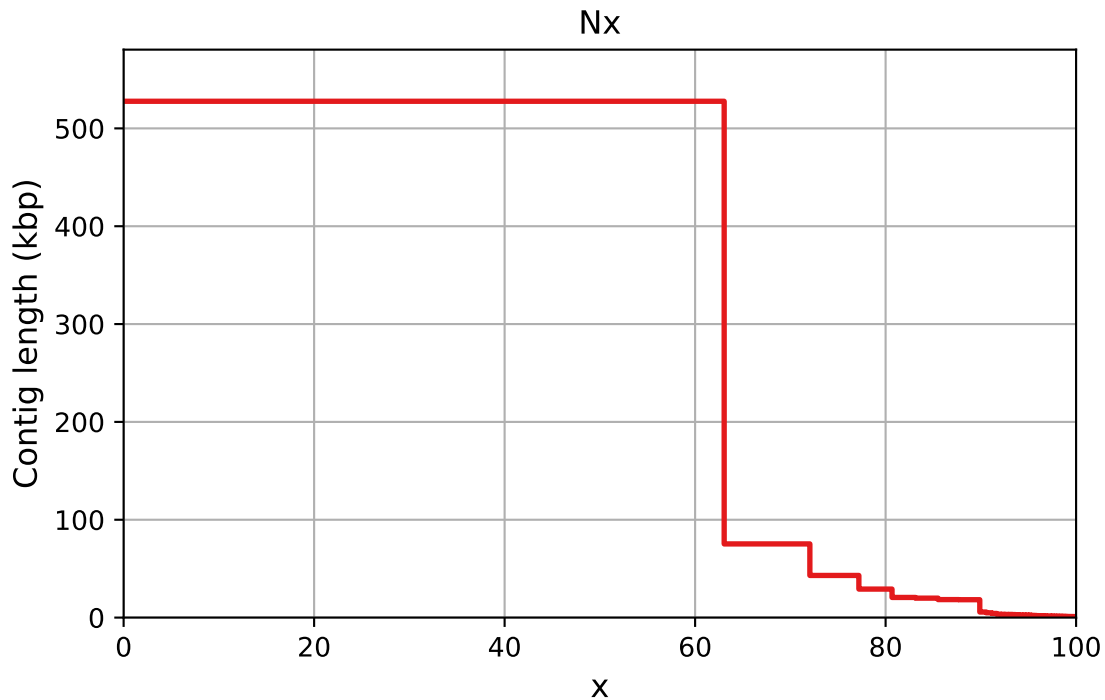
	TARA_RED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	46
# possible misassemblies	52
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	103
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	3

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

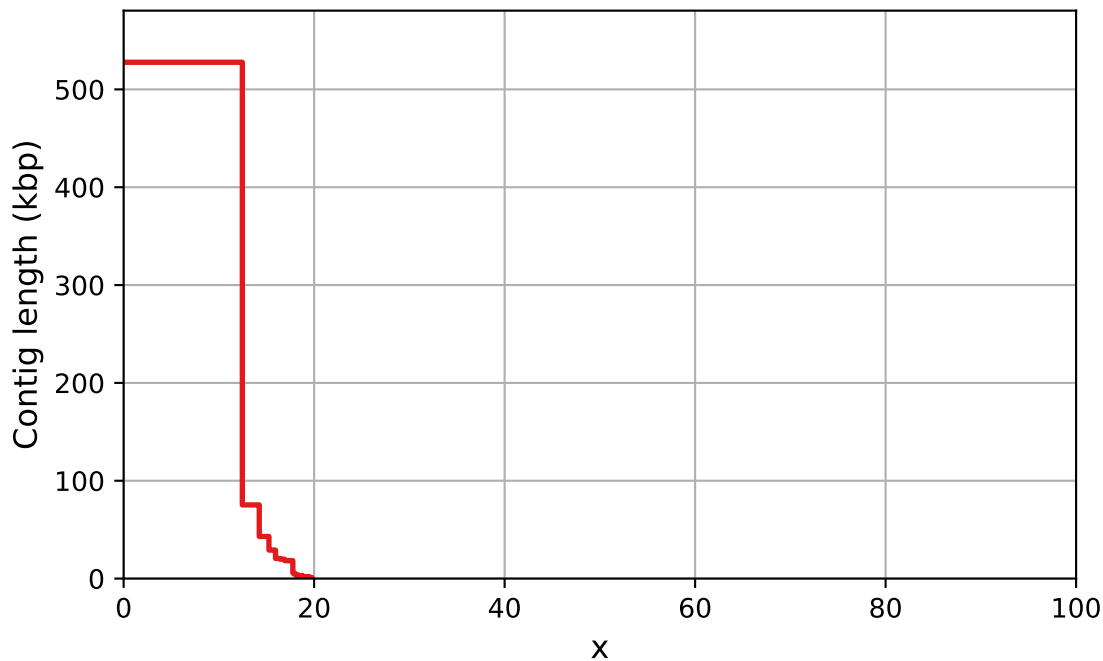
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# fully unaligned contigs	6
Fully unaligned length	53688
# partially unaligned contigs	42
Partially unaligned length	779371
# N's	0

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).



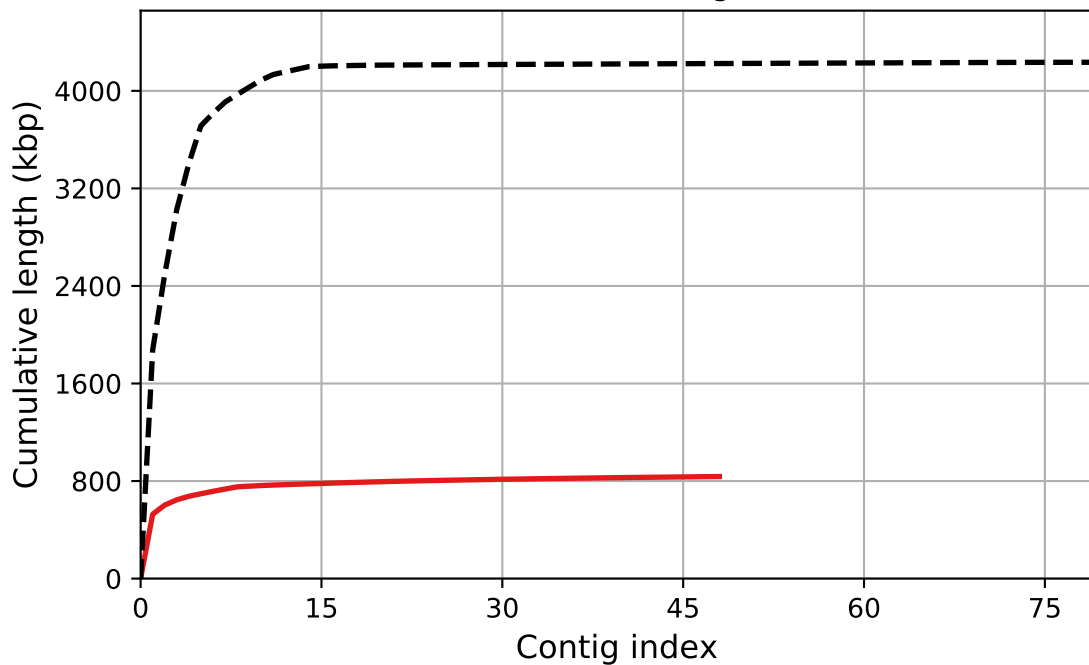
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NGx



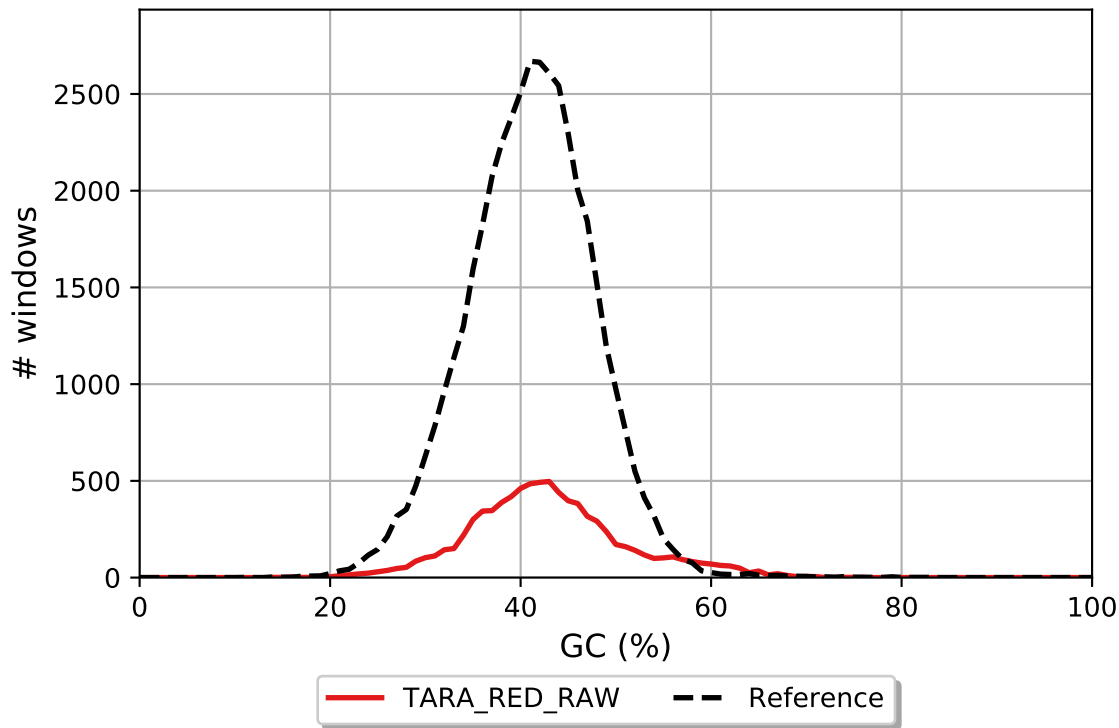
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Cumulative length

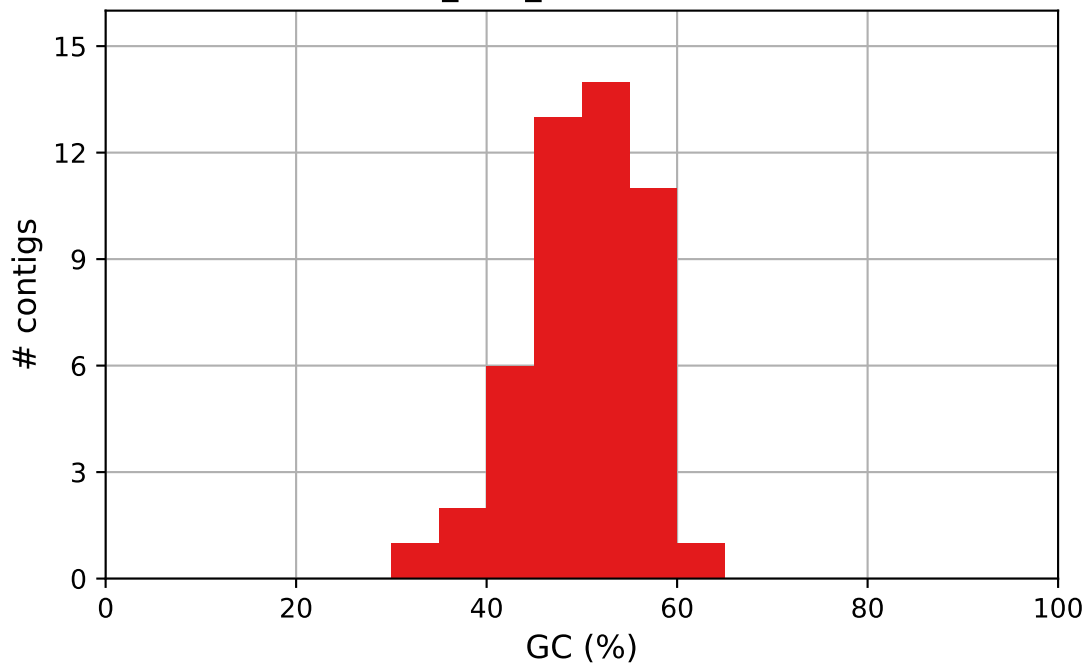


TARA_RED_RAW Reference

GC content



TARA_RED_RAW GC content

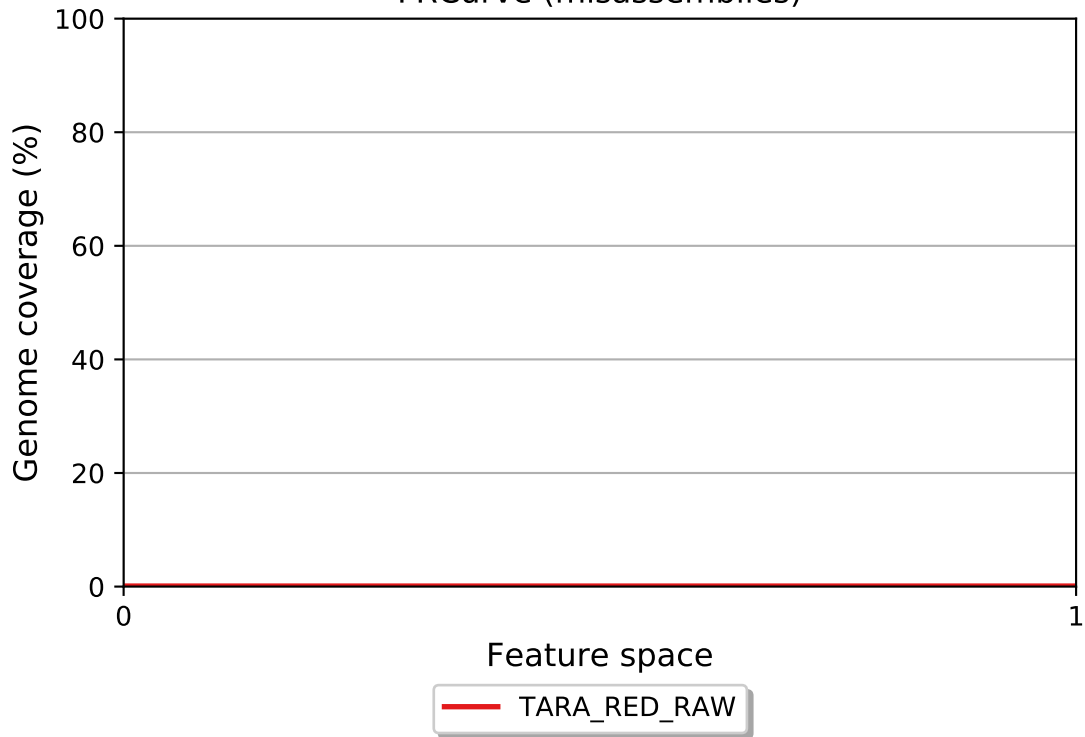


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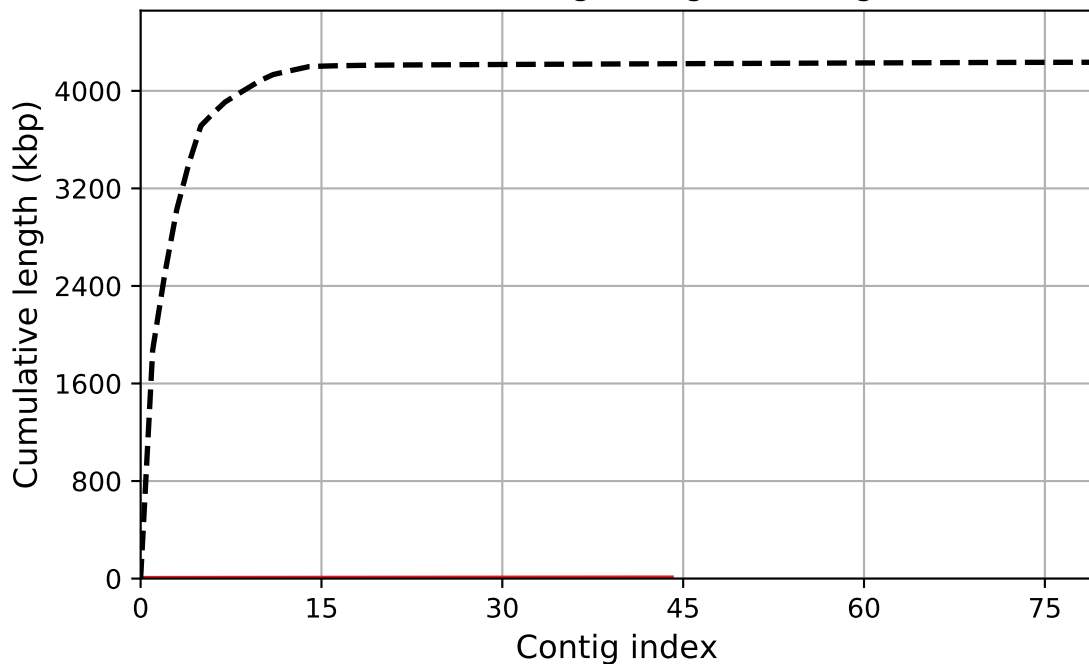
Misassemblies



FRCurve (misassemblies)

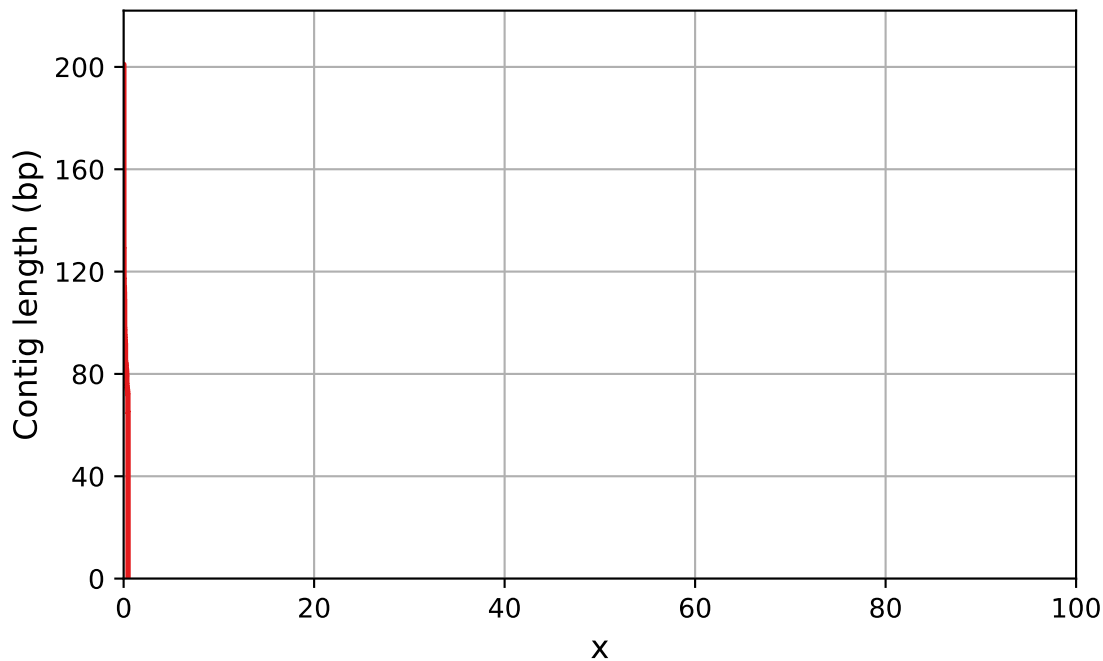


Cumulative length (aligned contigs)



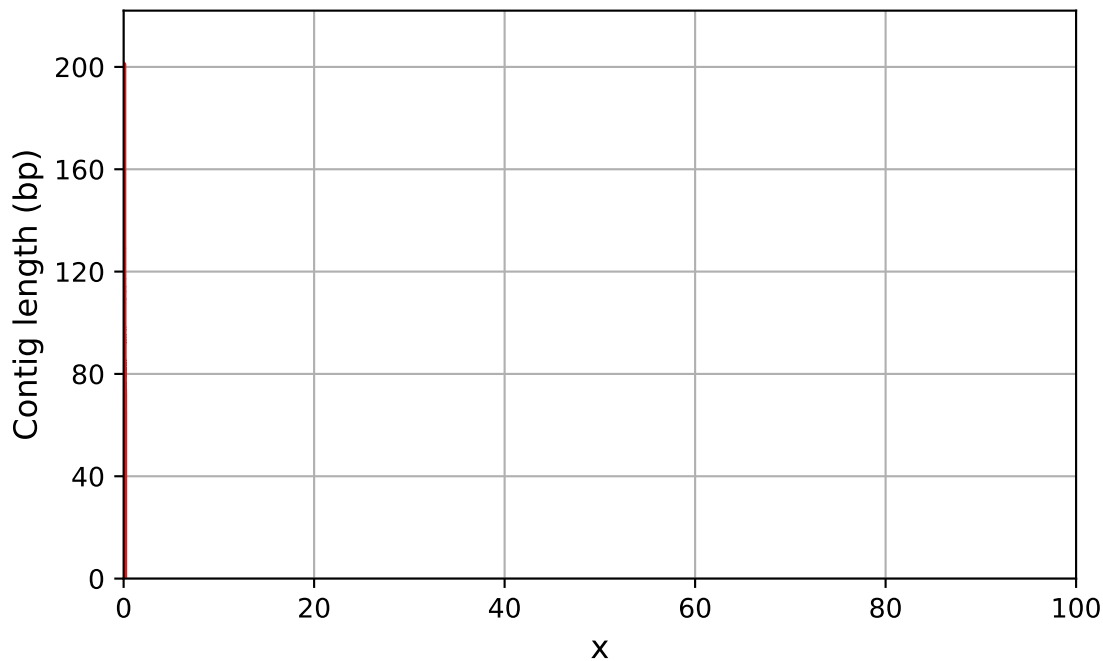
— TARA_RED_RAW - - Reference

NAx



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NGAx



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