

Report

	TARA_MED_RAW
# contigs (>= 1000 bp)	494
# contigs (>= 5000 bp)	143
# contigs (>= 10000 bp)	84
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	15
Total length (>= 1000 bp)	3647818
Total length (>= 5000 bp)	2883682
Total length (>= 10000 bp)	2468238
Total length (>= 25000 bp)	1712683
Total length (>= 50000 bp)	987642
# contigs	494
Largest contig	107525
Total length	3647818
Reference length	7658814
GC (%)	34.72
Reference GC (%)	63.29
N50	22364
N75	6458
L50	40
L75	118
# 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	4
# unaligned contigs	9 + 485 part
Unaligned length	3607979
Genome fraction (%)	0.066
Duplication ratio	7.914
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16090.58
# indels per 100 kbp	19.86
Largest alignment	628
Total aligned length	39839
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

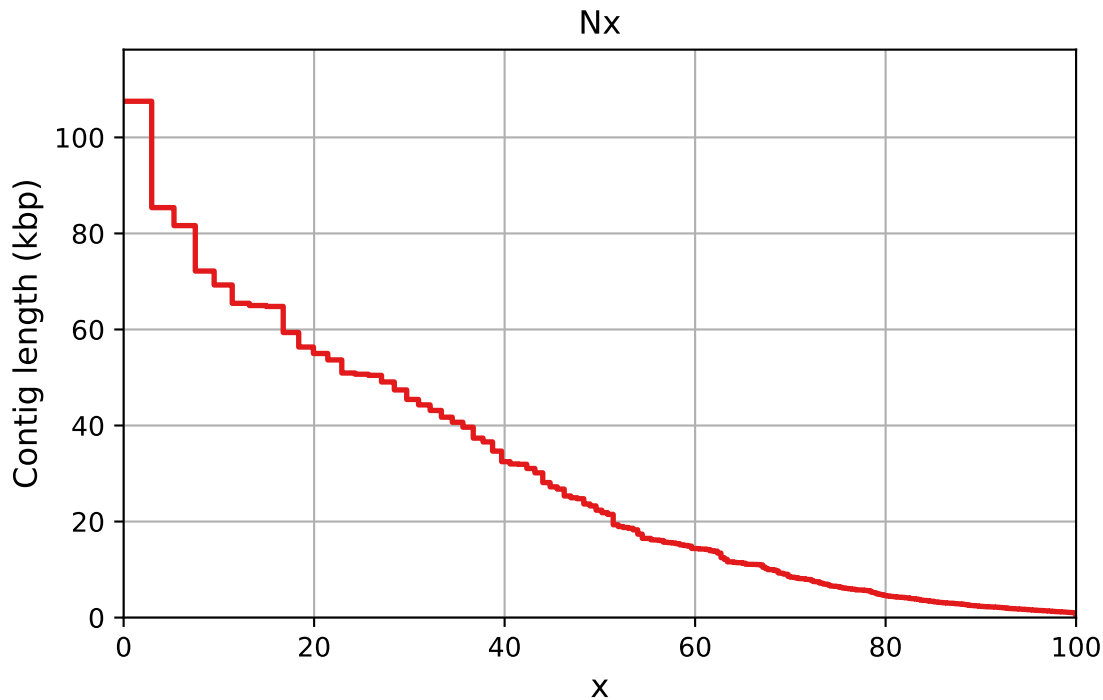
	TARA_MED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	489
# possible misassemblies	613
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	810
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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

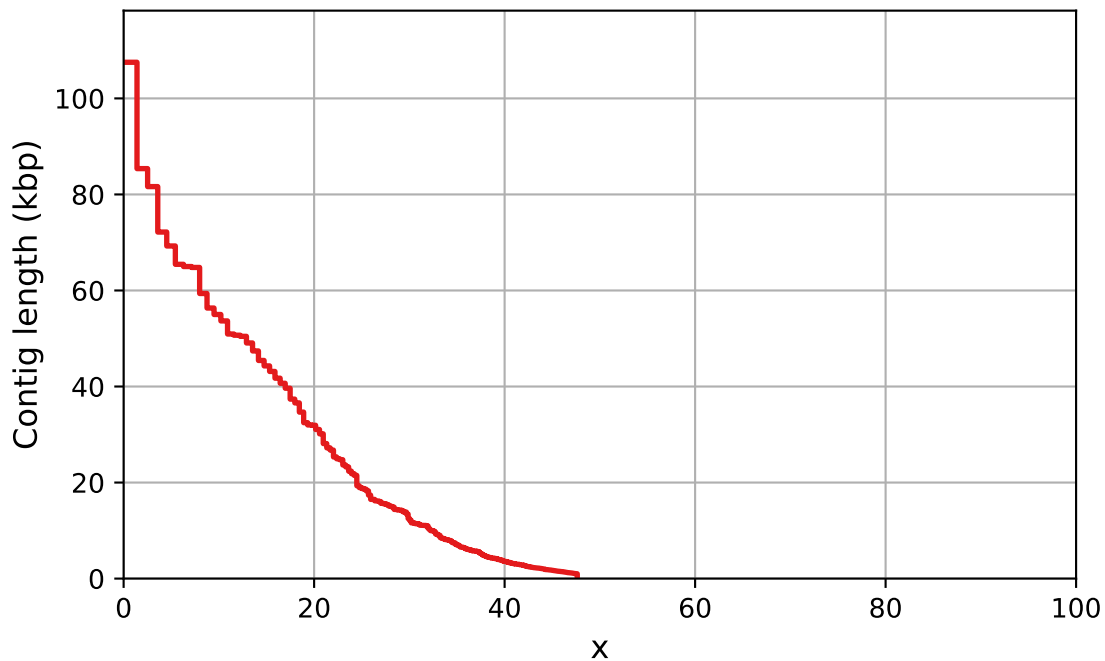
	TARA_MED_RAW
# fully unaligned contigs	9
Fully unaligned length	40875
# partially unaligned contigs	485
Partially unaligned length	3567104
# N's	0

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).



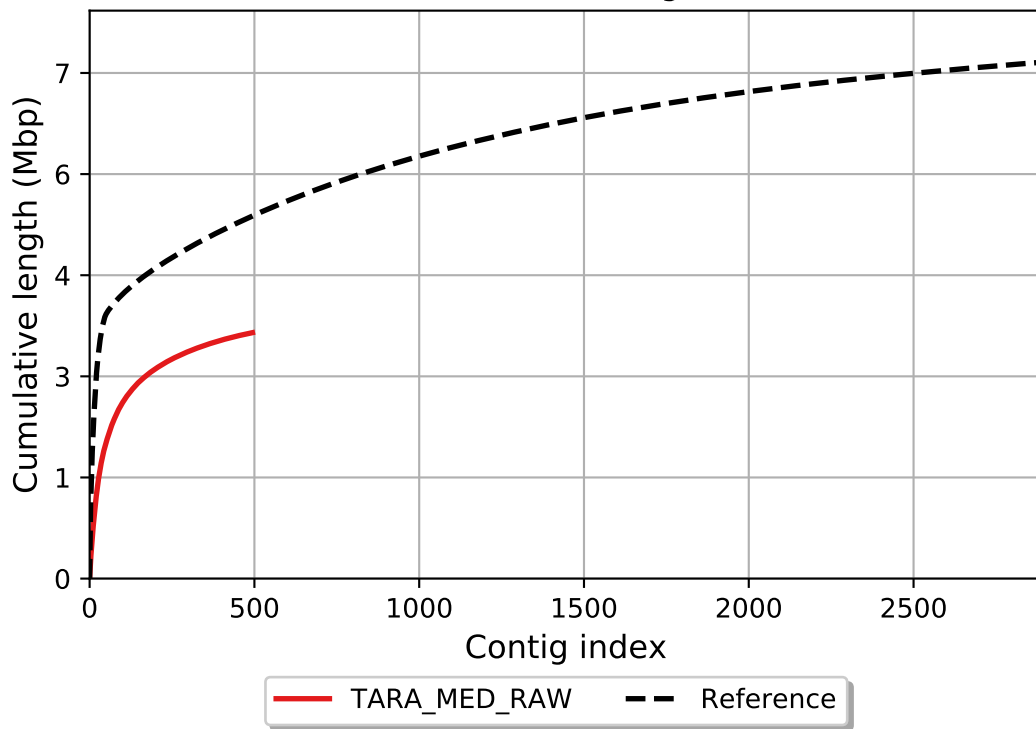
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NGx

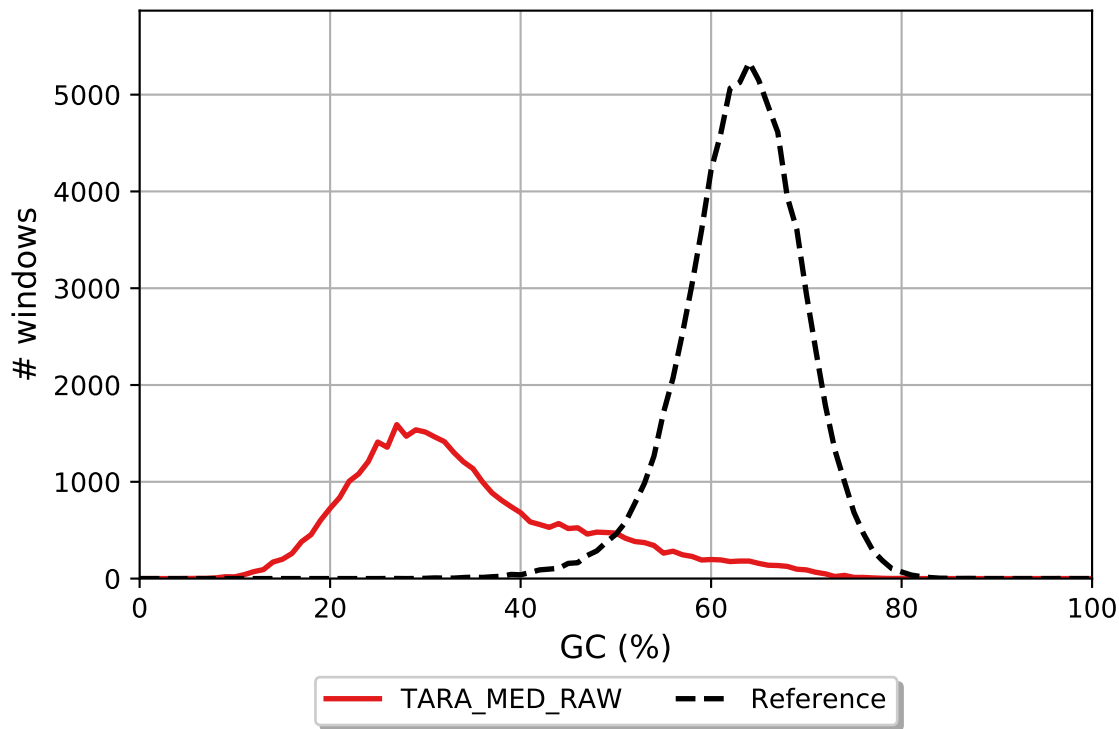


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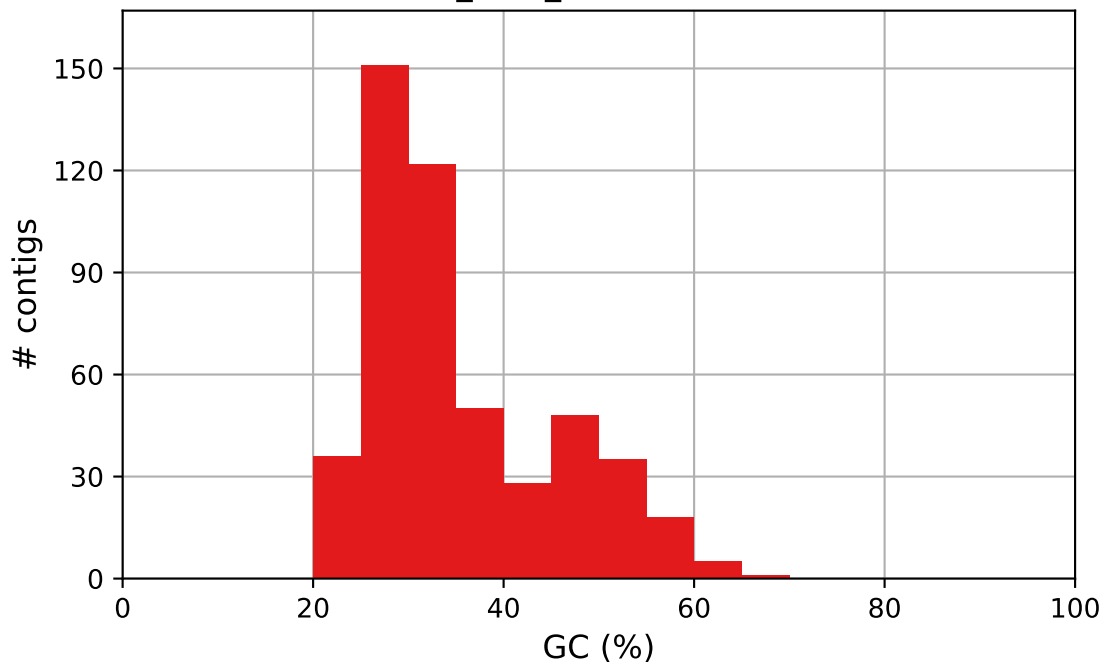
Cumulative length



GC content



TARA_MED_RAW GC content

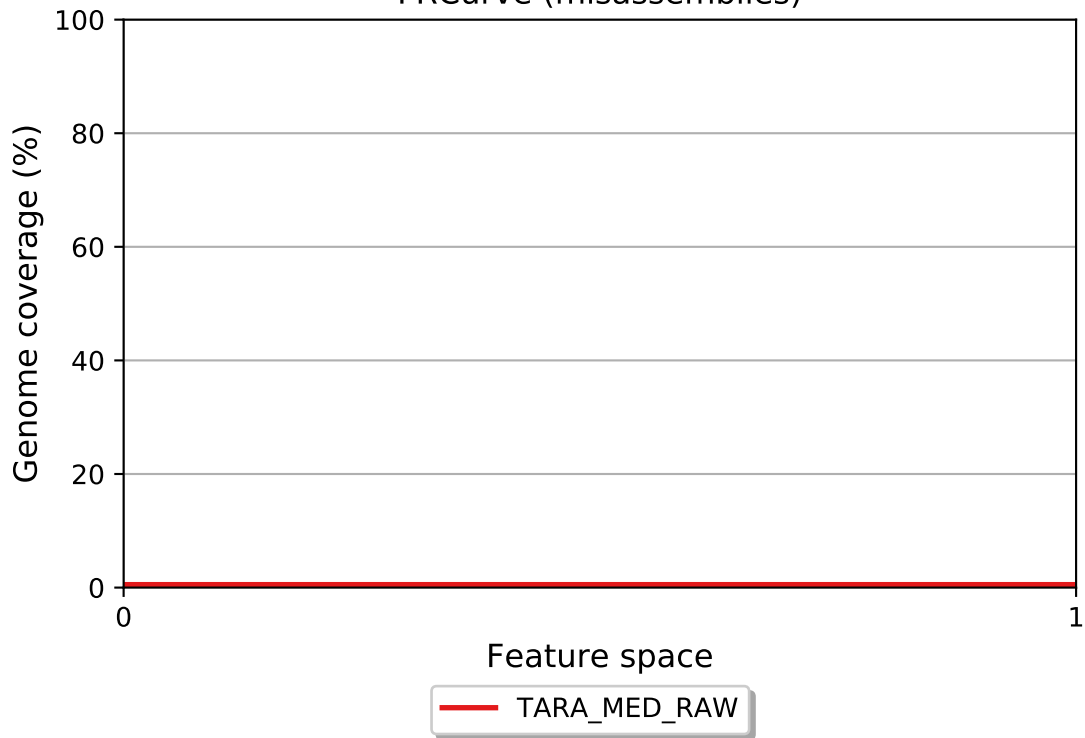


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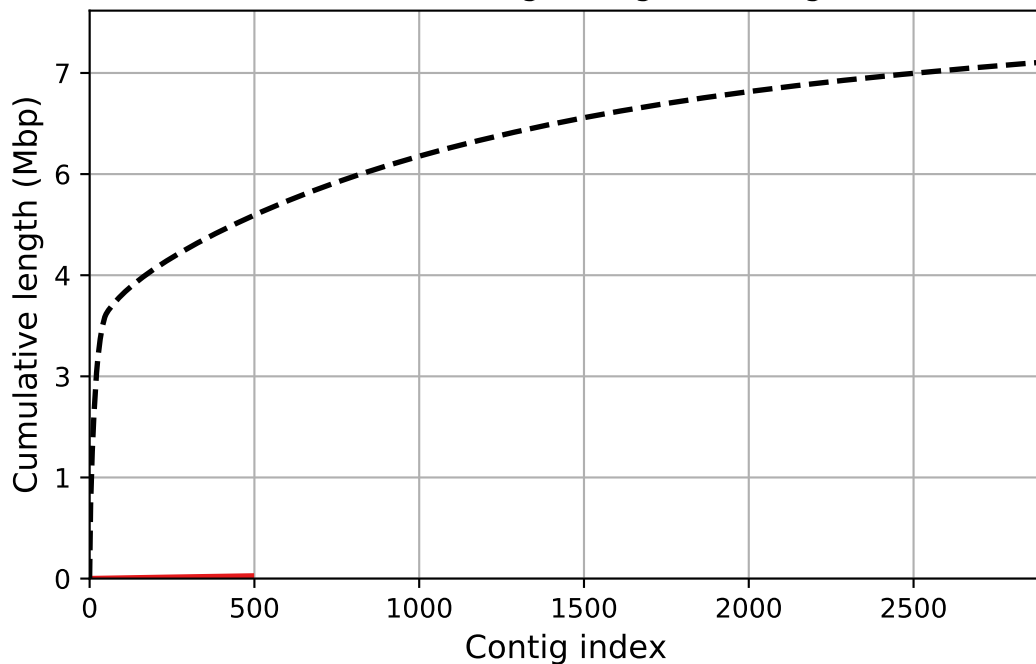
Misassemblies



FRCurve (misassemblies)

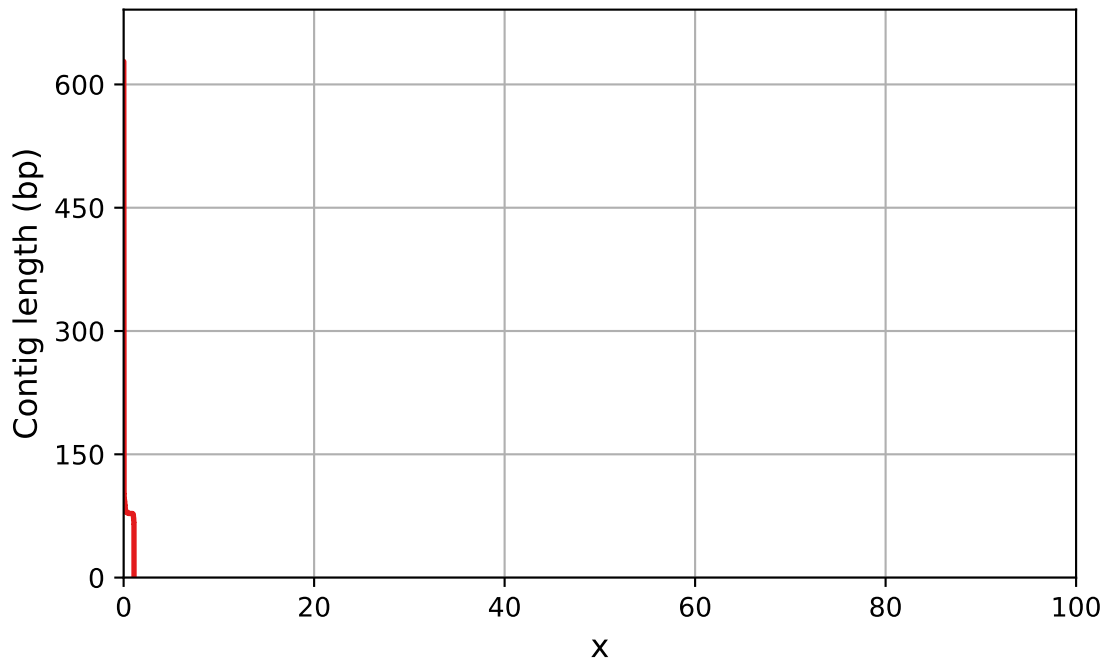


Cumulative length (aligned contigs)



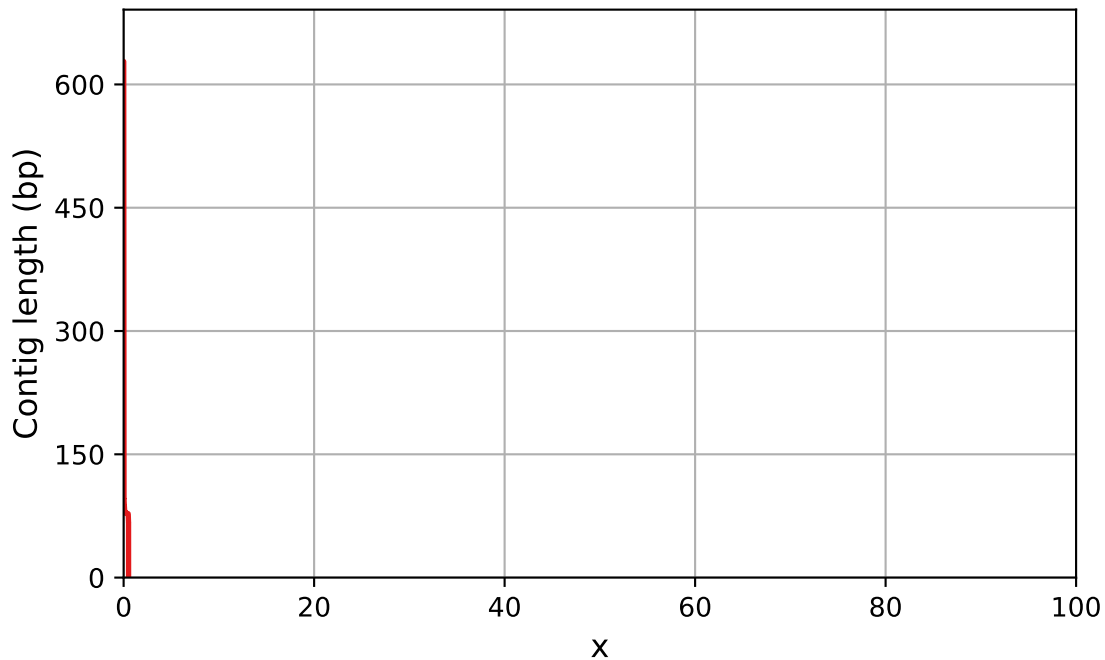
— TARA_MED_RAW - - Reference

NAx



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NGAx



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