

Report

	TARA_MED_RAW
# contigs (>= 0 bp)	1146485
# contigs (>= 1000 bp)	1146485
# contigs (>= 5000 bp)	75053
# contigs (>= 10000 bp)	21465
# contigs (>= 25000 bp)	3865
# contigs (>= 50000 bp)	899
Total length (>= 0 bp)	2674153874
Total length (>= 1000 bp)	2674153874
Total length (>= 5000 bp)	788856372
Total length (>= 10000 bp)	427670459
Total length (>= 25000 bp)	173275639
Total length (>= 50000 bp)	73958586
# contigs	1146485
Largest contig	743739
Total length	2674153874
Reference length	7658814
N50	2548
N75	1484
L50	235584
L75	589432
# 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	5
# unaligned contigs	1145991 + 494 part
Unaligned length	2674112949
Genome fraction (%)	0.074
Duplication ratio	8.078
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16117.61
# indels per 100 kbp	17.71
Largest alignment	628
Total aligned length	40925

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

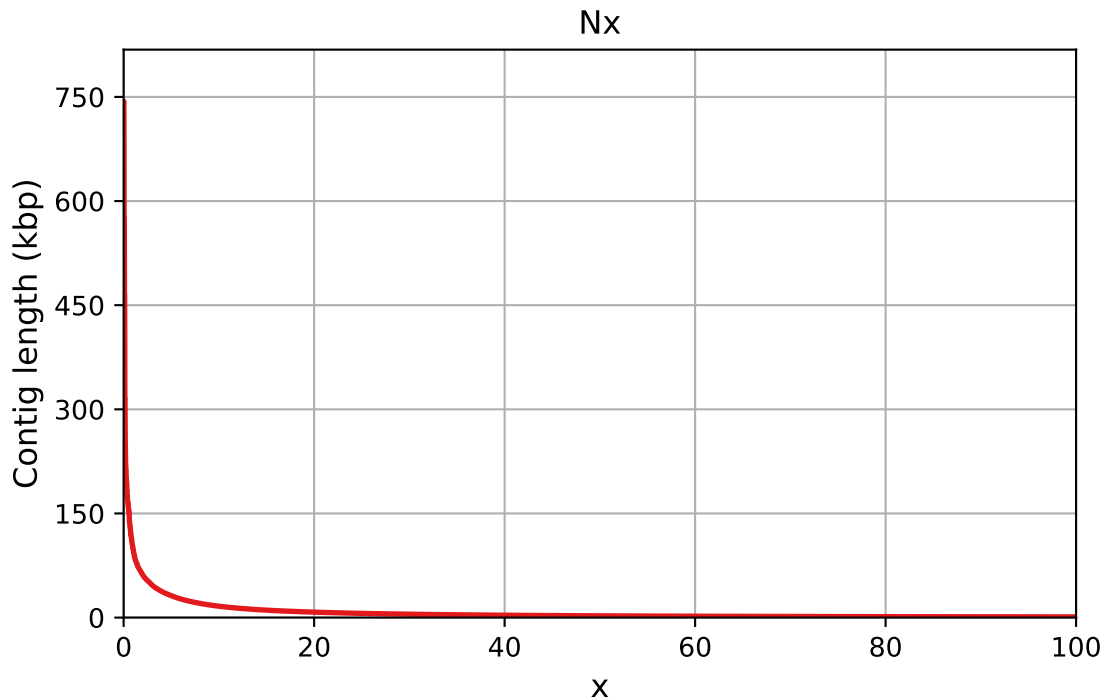
	TARA_MED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled 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	5
# mismatches	910
# 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

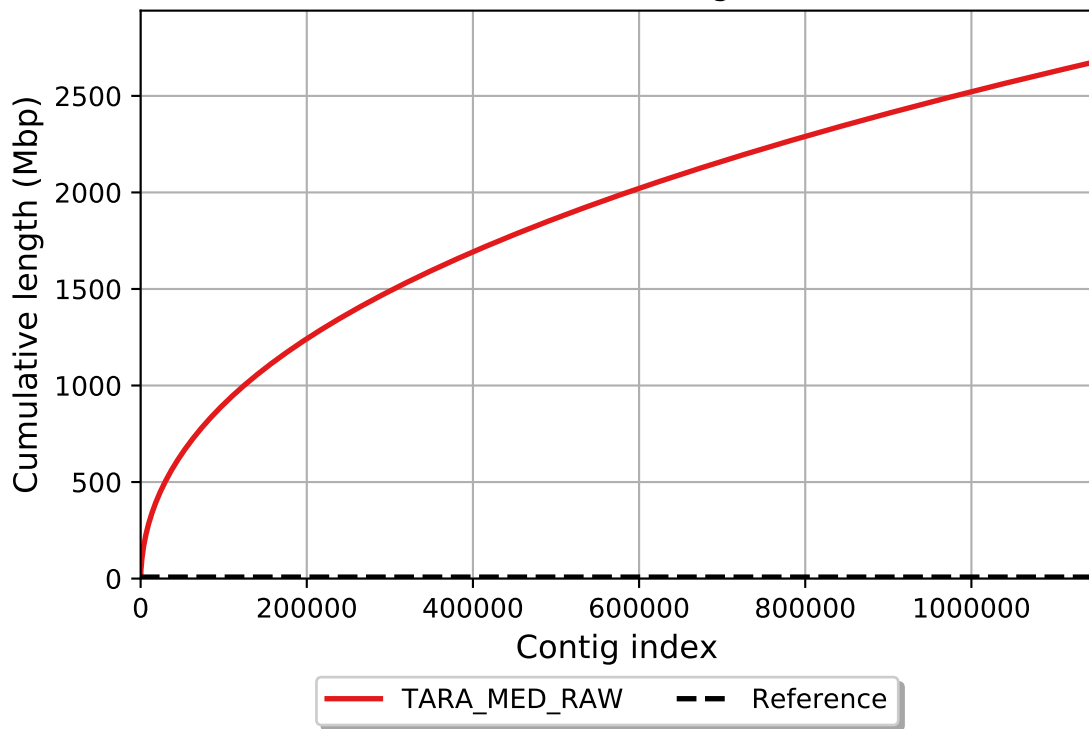
	TARA_MED_RAW
# fully unaligned contigs	1145991
Fully unaligned length	2670506056
# partially unaligned contigs	494
Partially unaligned length	3606893
# N's	0

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).

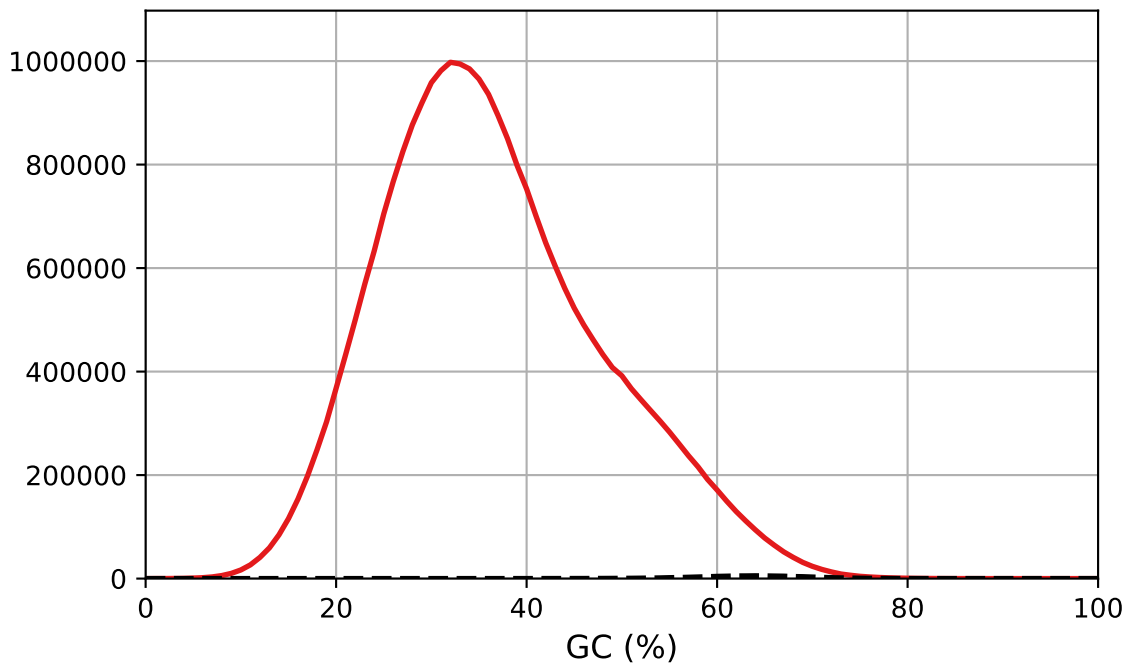


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Cumulative length

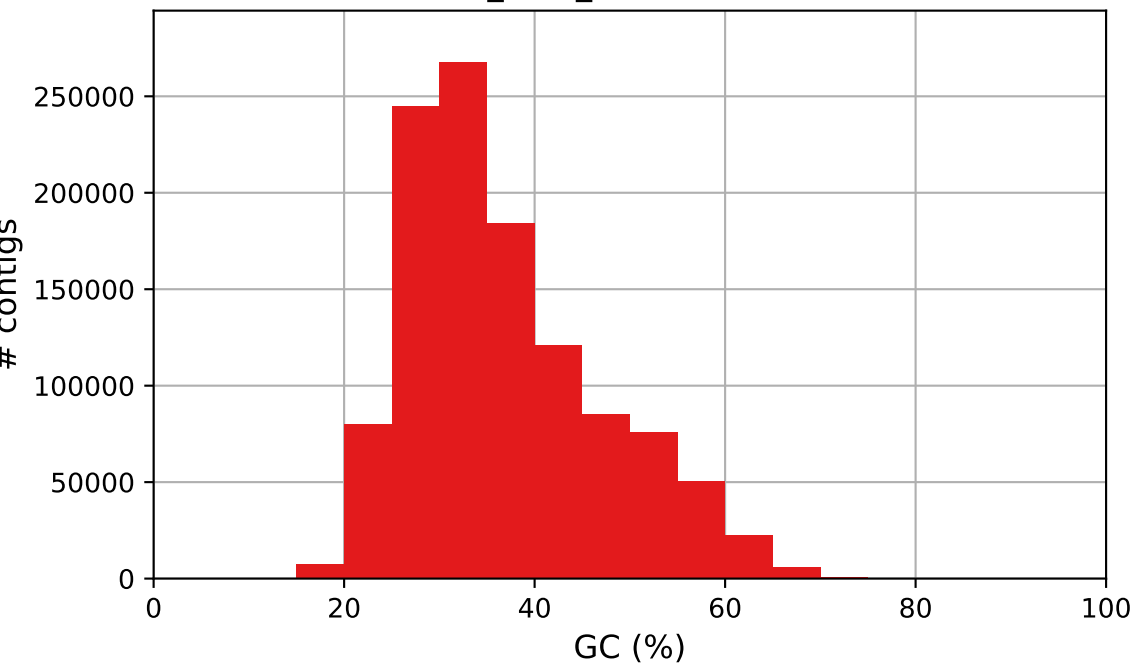


GC content



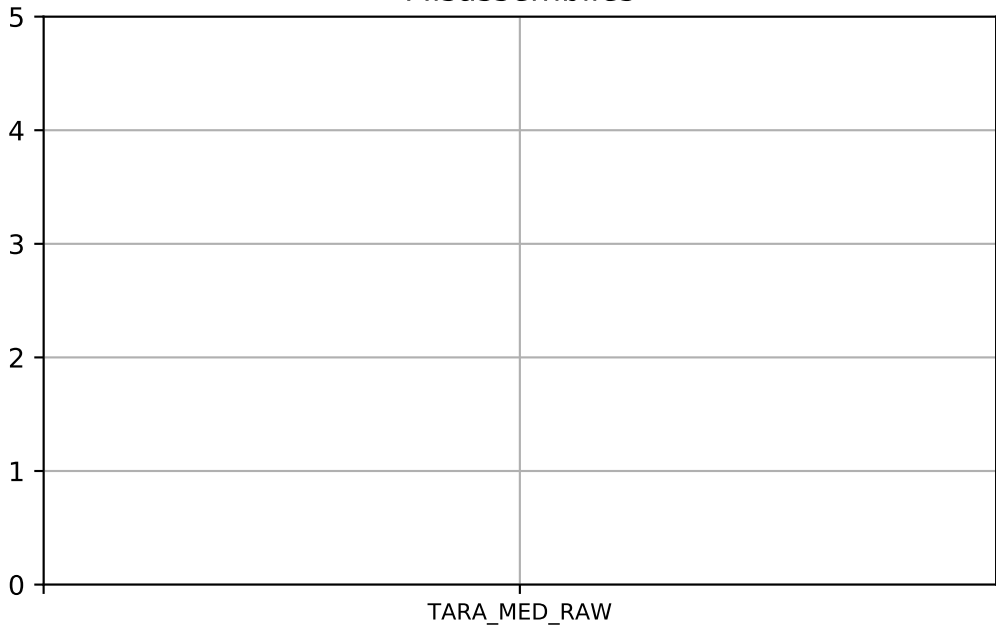
— TARA_MED_RAW - - Reference

TARA_MED_RAW GC content

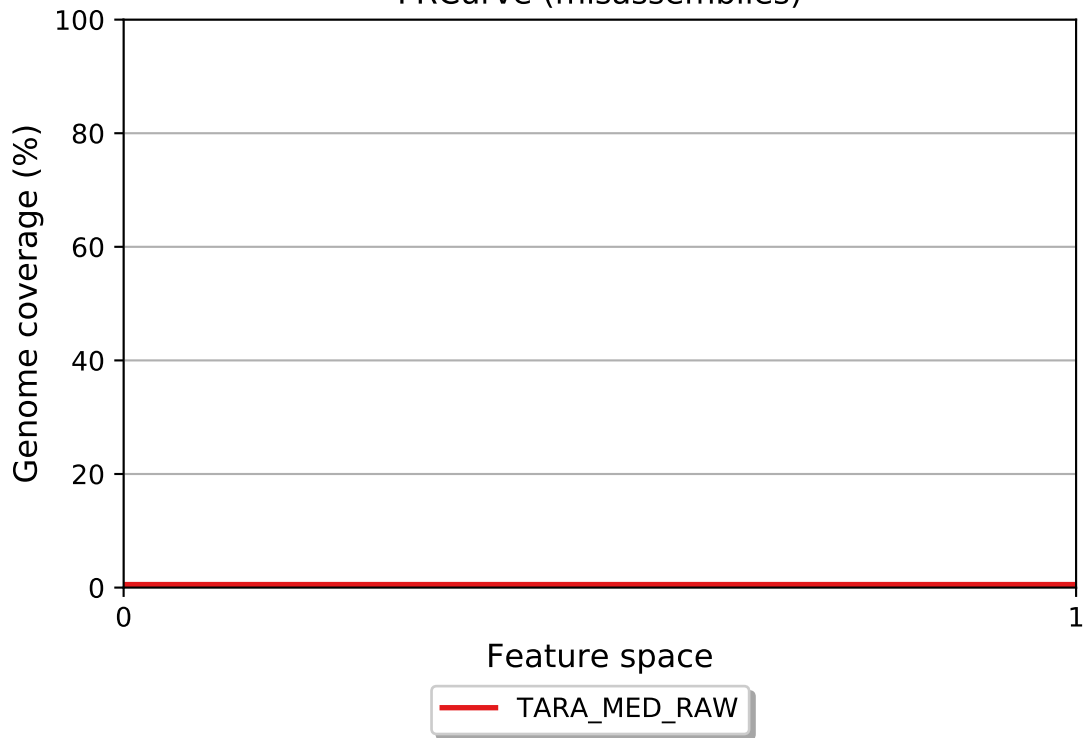


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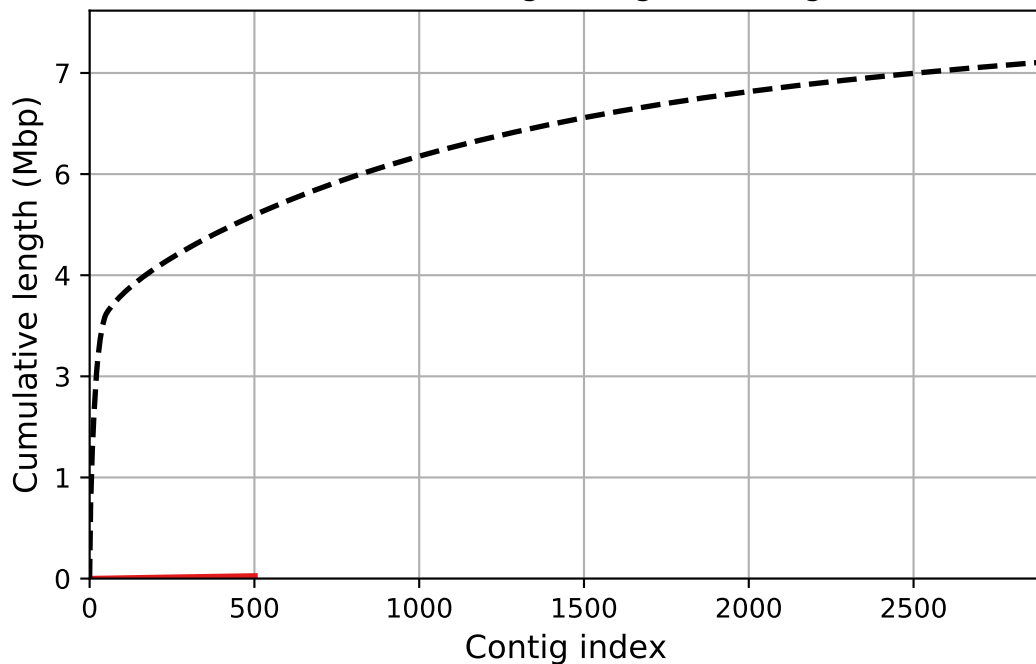
Misassemblies



FRCurve (misassemblies)

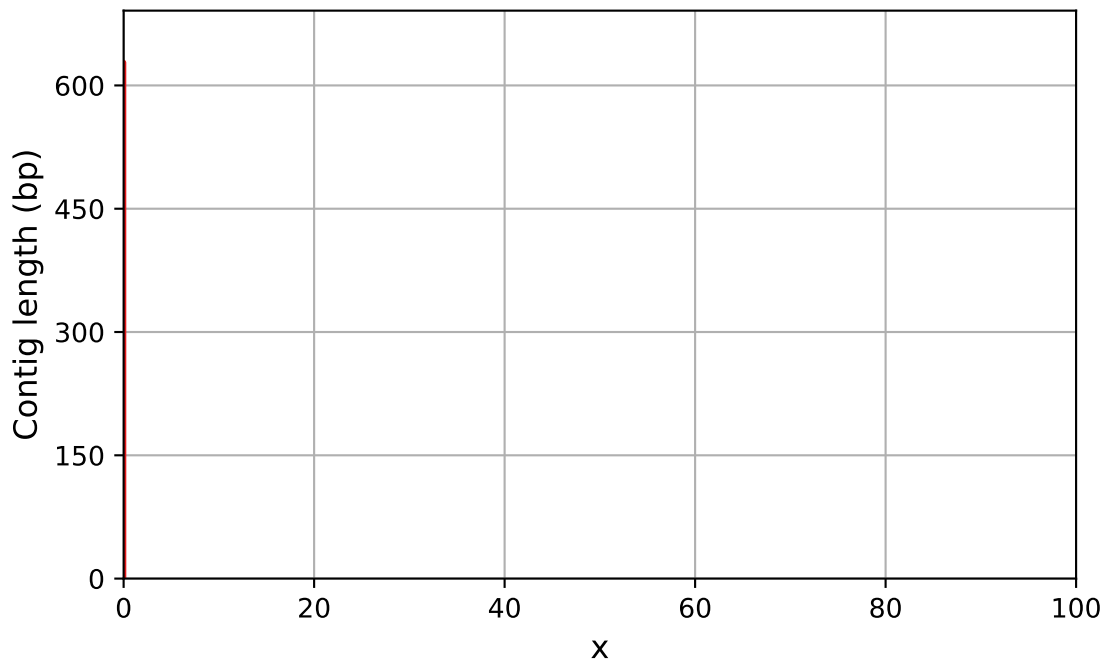


Cumulative length (aligned contigs)



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NAx



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