

Report

	TARA_SOC_RAW
# contigs (>= 0 bp)	415693
# contigs (>= 1000 bp)	415693
# contigs (>= 5000 bp)	19160
# contigs (>= 10000 bp)	4878
# contigs (>= 25000 bp)	753
# contigs (>= 50000 bp)	146
Total length (>= 0 bp)	867144156
Total length (>= 1000 bp)	867144156
Total length (>= 5000 bp)	185494017
Total length (>= 10000 bp)	90542706
Total length (>= 25000 bp)	31376935
Total length (>= 50000 bp)	11333585
# contigs	415693
Largest contig	377717
Total length	867144156
Reference length	5854900
N50	2133
N75	1393
L50	101886
L75	230070
# 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	3
# unaligned contigs	415586 + 107 part
Unaligned length	867134988
Genome fraction (%)	0.062
Duplication ratio	3.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6699.62
# indels per 100 kbp	0.00
Largest alignment	266
Total aligned length	9168

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

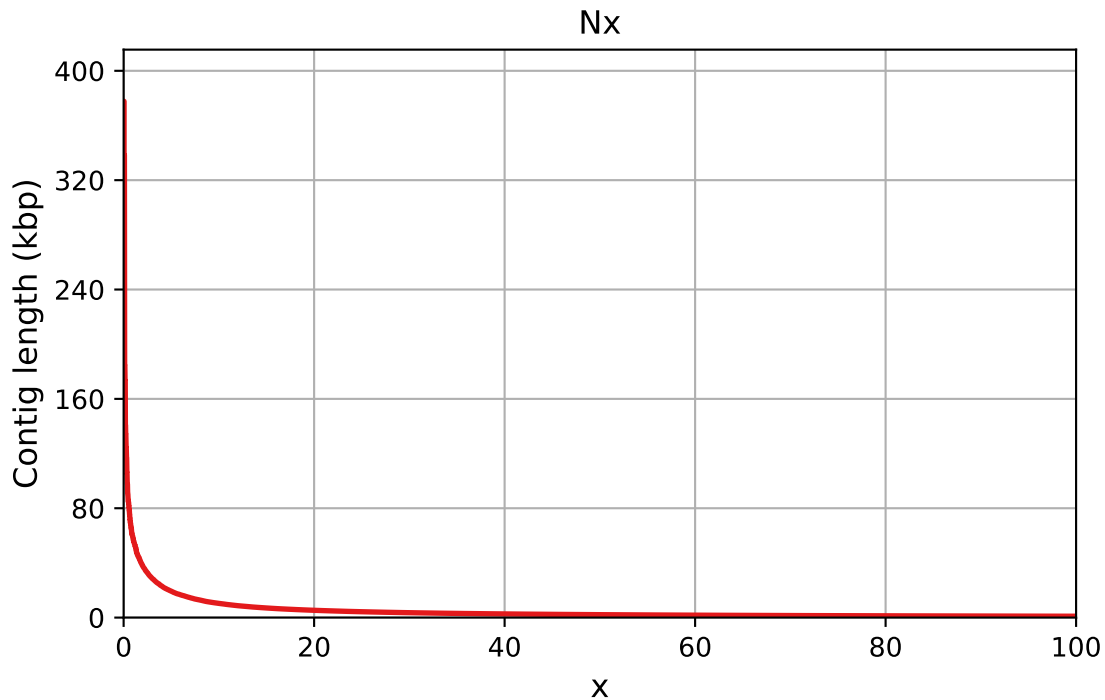
	TARA_SOC_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	104
# possible misassemblies	130
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	244
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

Unaligned report

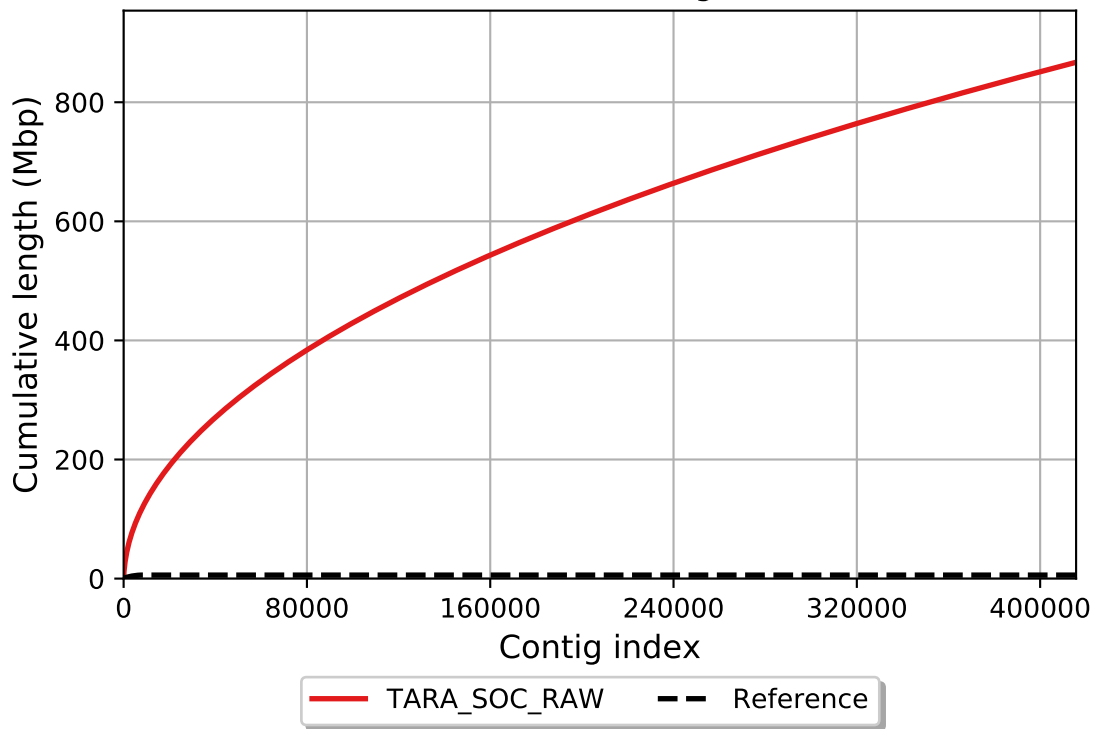
	TARA_SOC_RAW
# fully unaligned contigs	415586
Fully unaligned length	866533402
# partially unaligned contigs	107
Partially unaligned length	601586
# N's	0

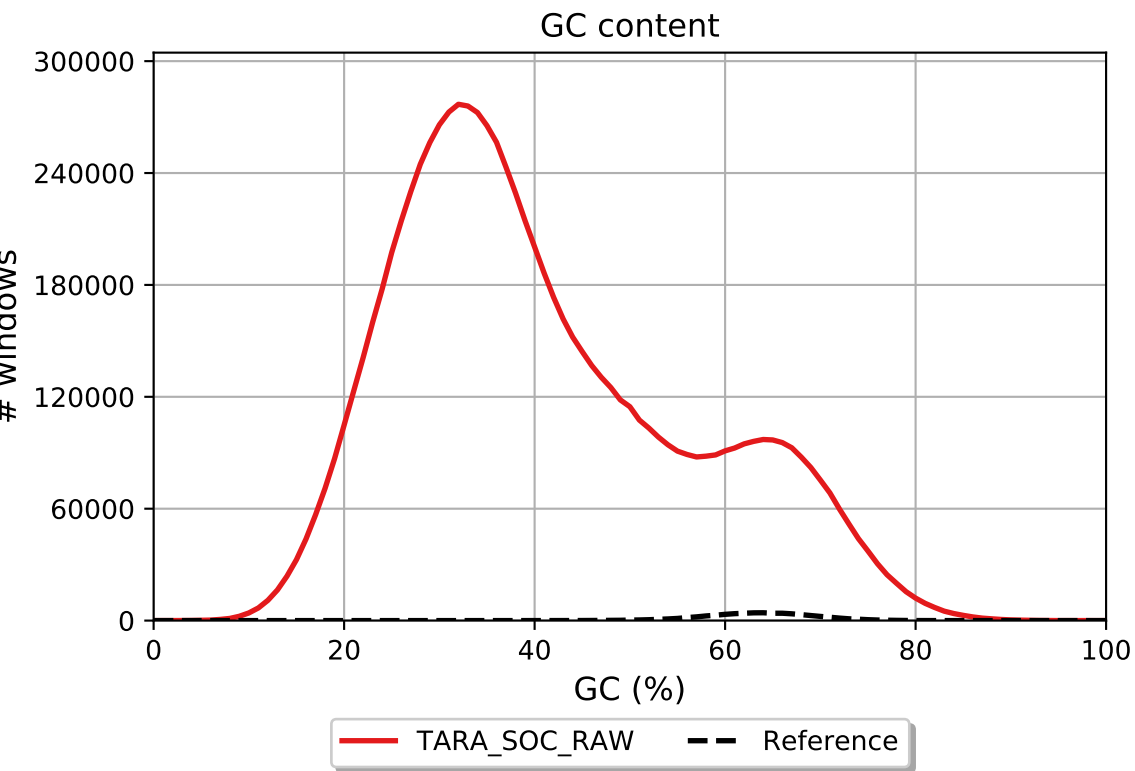
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



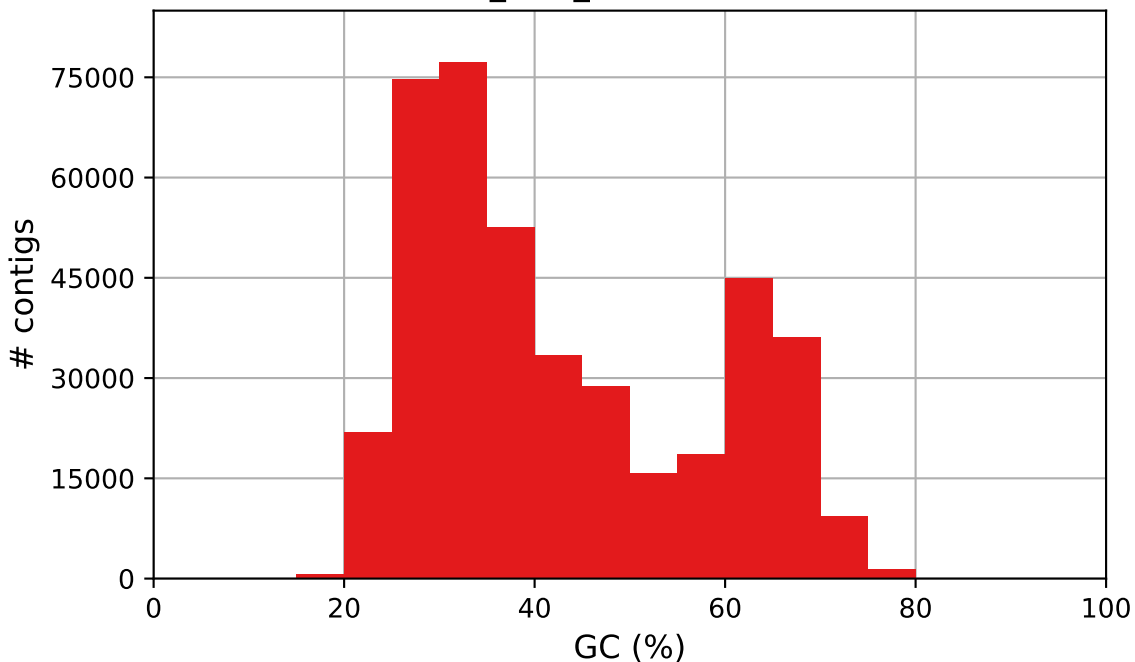
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Cumulative length





TARA_SOC_RAW GC content

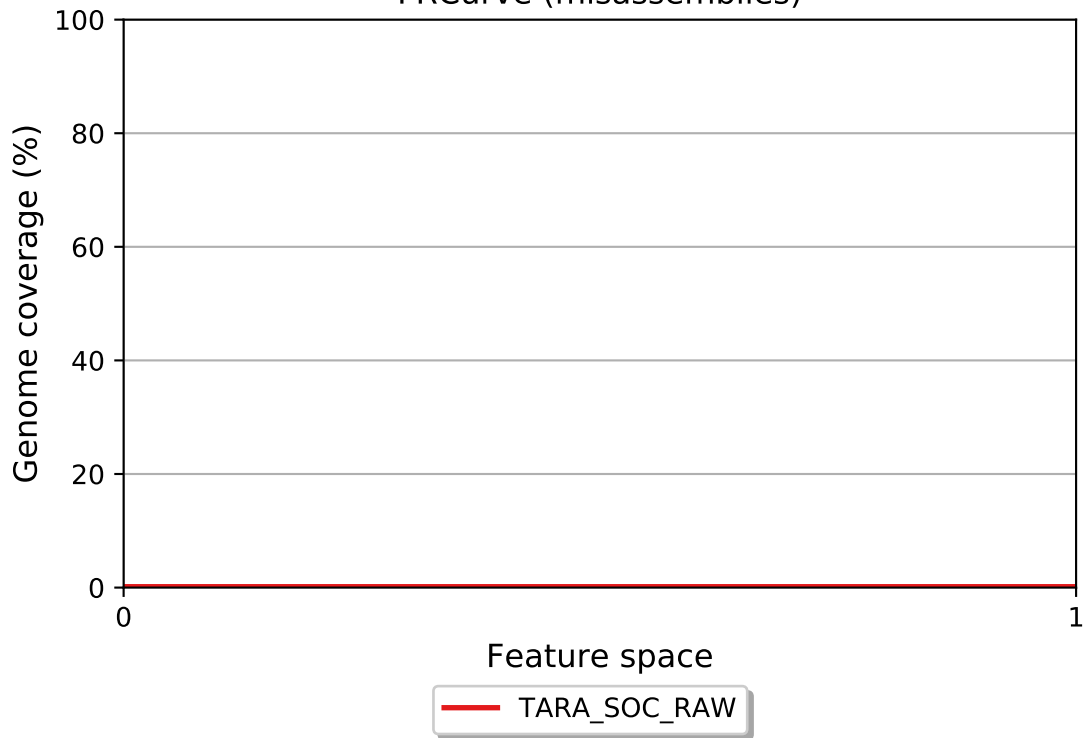


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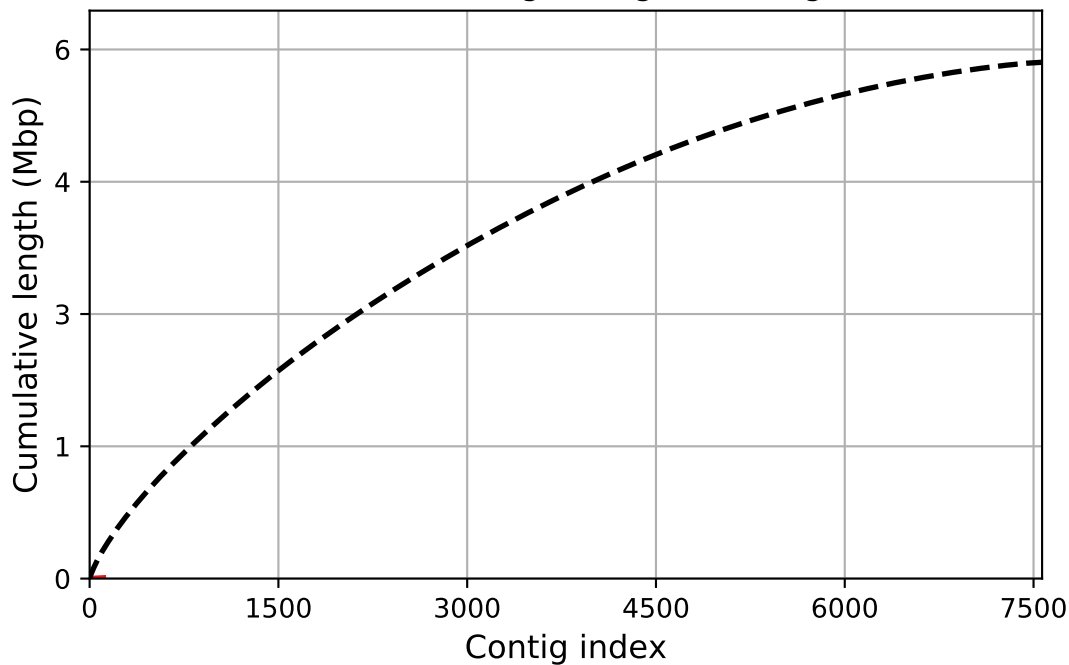
Misassemblies



FRCurve (misassemblies)

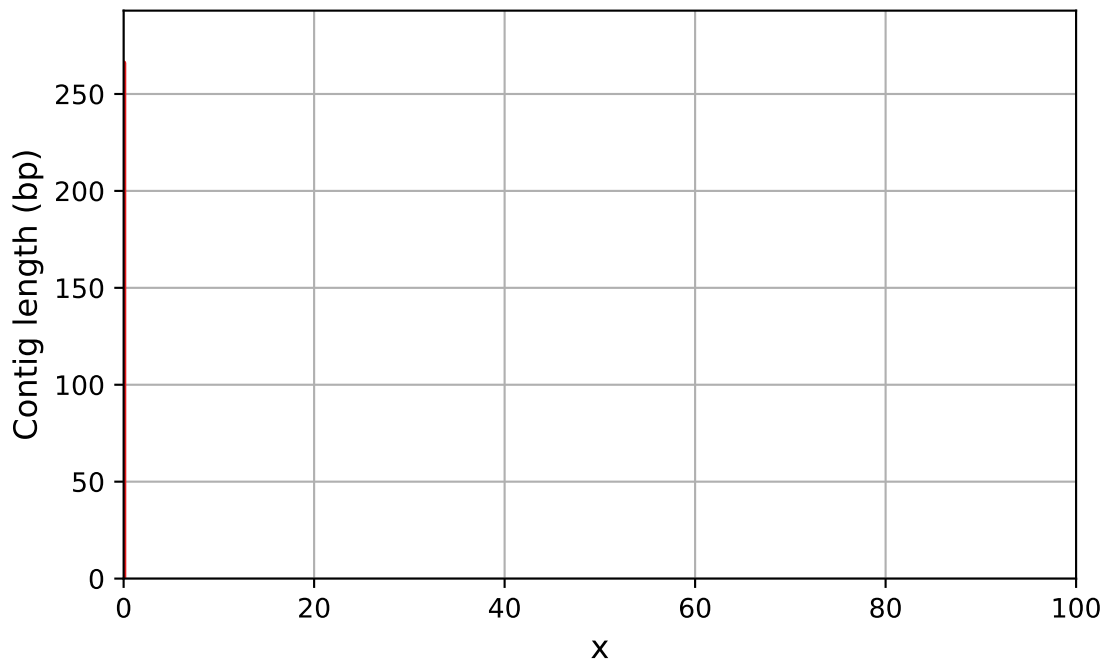


Cumulative length (aligned contigs)



— TARA_SOC_RAW - - Reference

NAx



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