

Report

	TARA_PON_RAW
# contigs (>= 0 bp)	1663221
# contigs (>= 1000 bp)	1663221
# contigs (>= 5000 bp)	73322
# contigs (>= 10000 bp)	19113
# contigs (>= 25000 bp)	3249
# contigs (>= 50000 bp)	778
Total length (>= 0 bp)	3411305116
Total length (>= 1000 bp)	3411305116
Total length (>= 5000 bp)	739386287
Total length (>= 10000 bp)	376859143
Total length (>= 25000 bp)	150171410
Total length (>= 50000 bp)	67234015
# contigs	1663221
Largest contig	594166
Total length	3411305116
Reference length	4234461
N50	2072
N75	1355
L50	402266
L75	922394
# 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	1663179 + 42 part
Unaligned length	3411301314
Genome fraction (%)	0.027
Duplication ratio	3.300
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9461.81
# indels per 100 kbp	86.81
Largest alignment	201
Total aligned length	3802

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

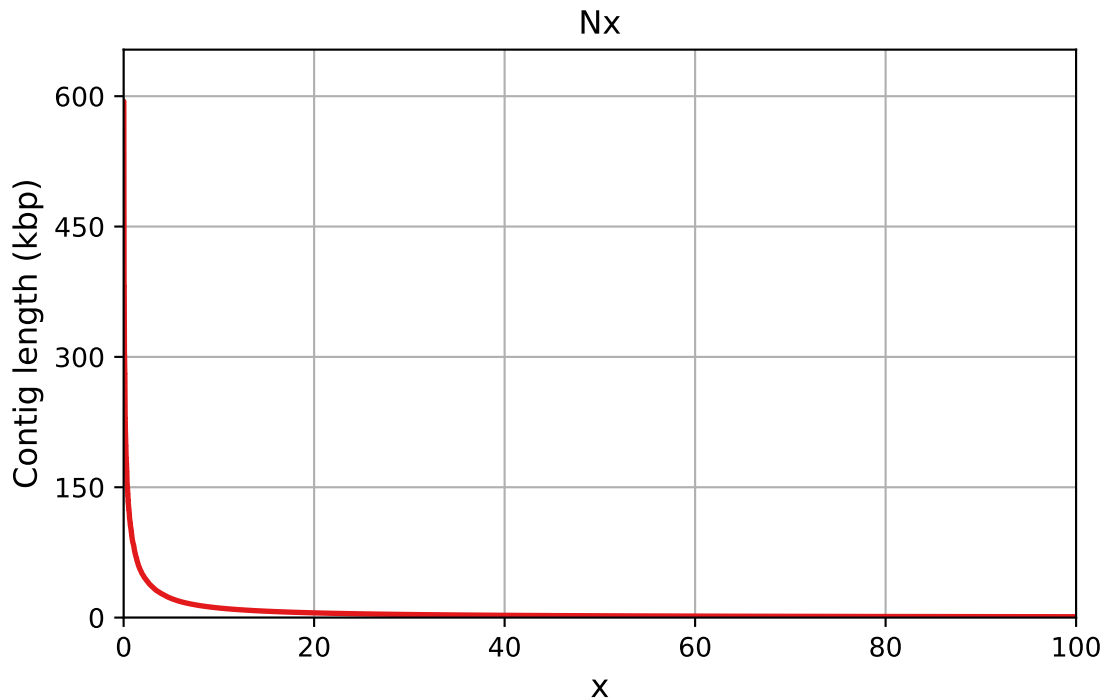
	TARA_PON_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	41
# possible misassemblies	43
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	109
# 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

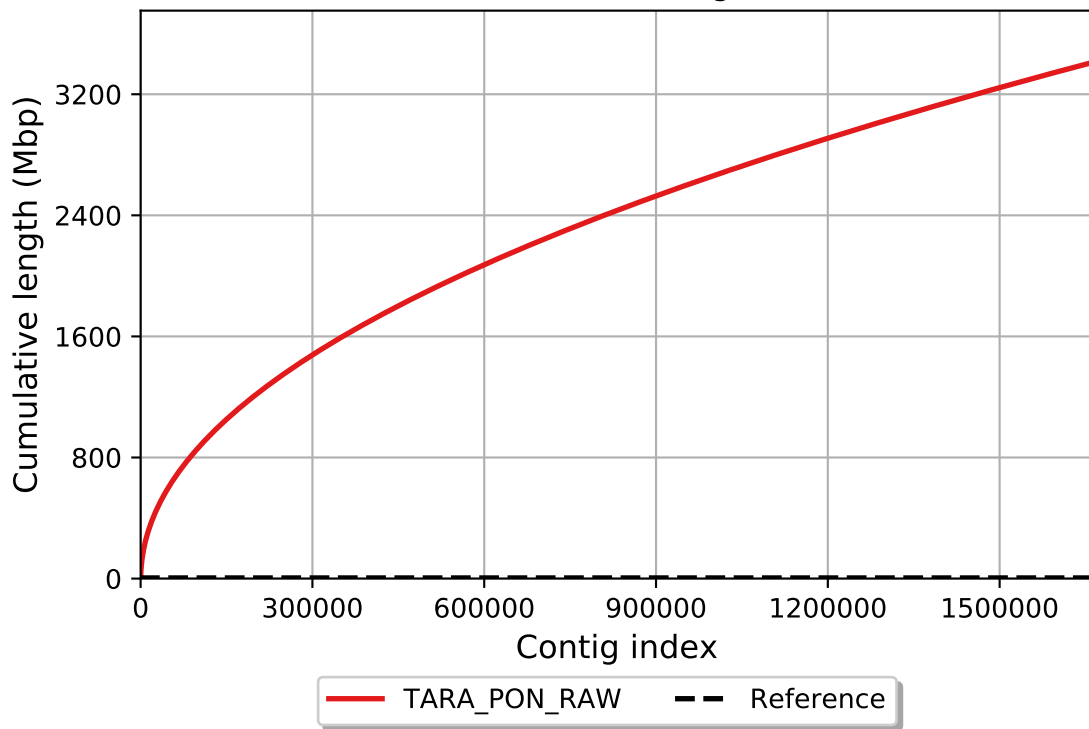
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# fully unaligned contigs	1663179
Fully unaligned length	3411212035
# partially unaligned contigs	42
Partially unaligned length	89279
# N's	0

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).

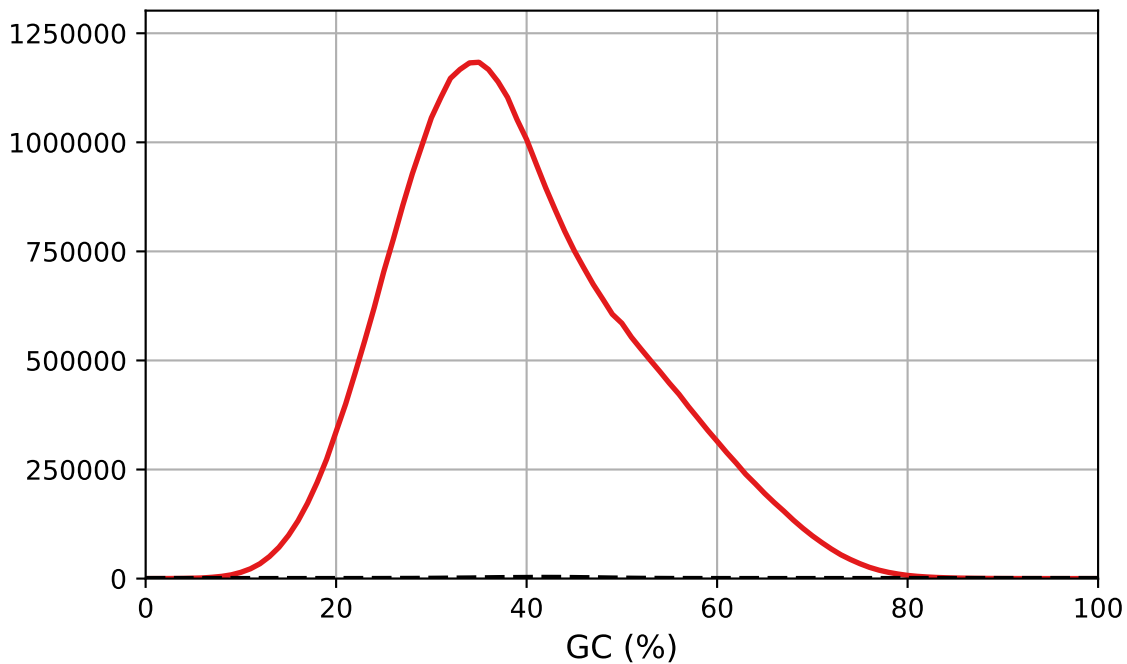


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Cumulative length

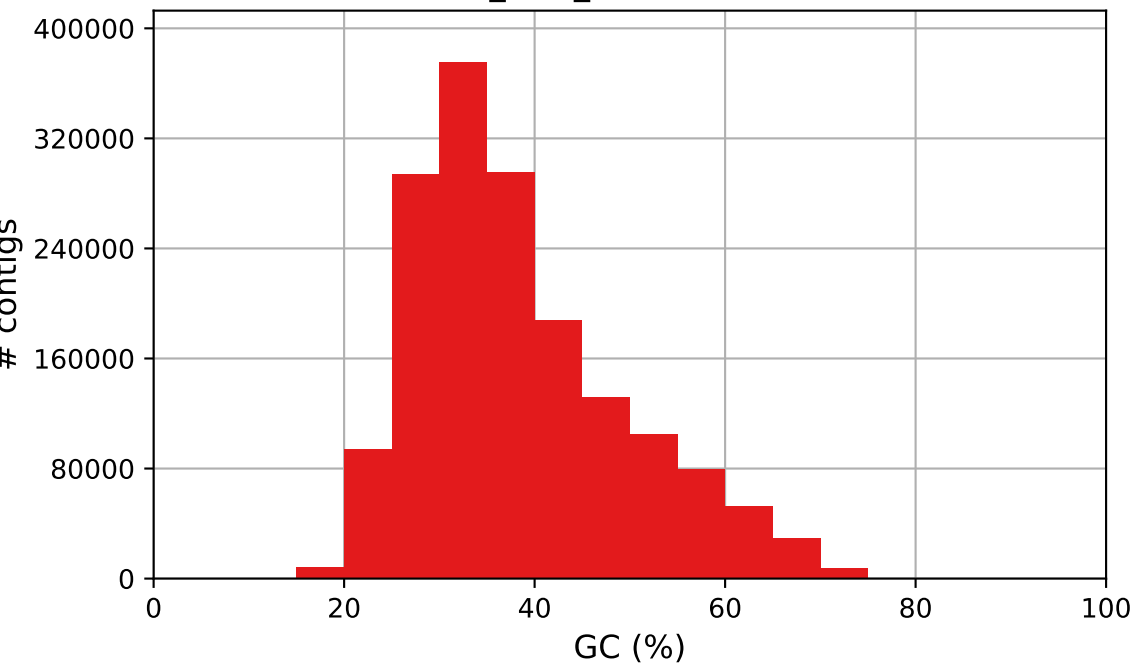


GC content



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TARA_PON_RAW GC content



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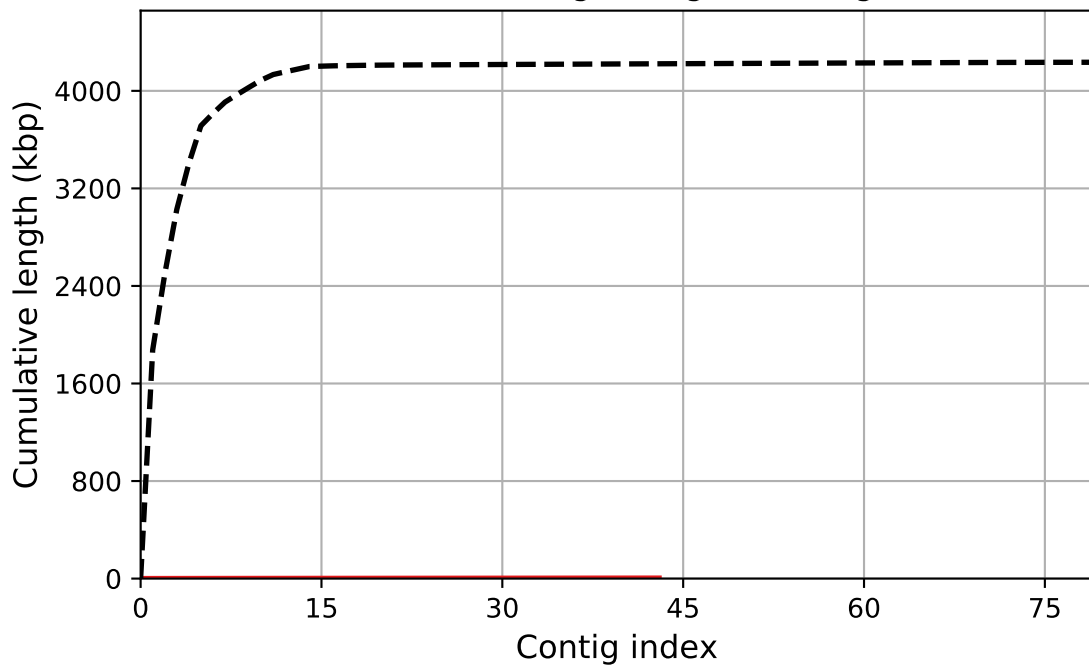
Misassemblies



FRCurve (misassemblies)

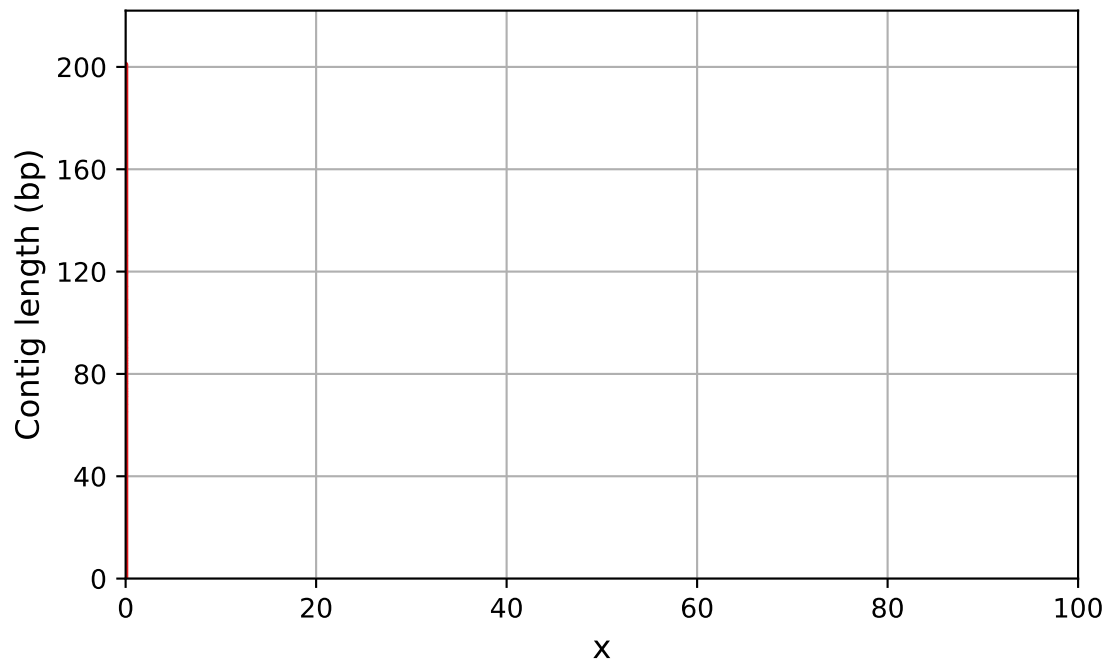


Cumulative length (aligned contigs)



— TARA_PON_RAW - - Reference

NAx



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