

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	5854900
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	6
# unaligned contigs	1662920 + 299 part
Unaligned length	3411278300
Genome fraction (%)	0.072
Duplication ratio	6.987
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12199.15
# indels per 100 kbp	117.98
Largest alignment	335
Total aligned length	25021

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

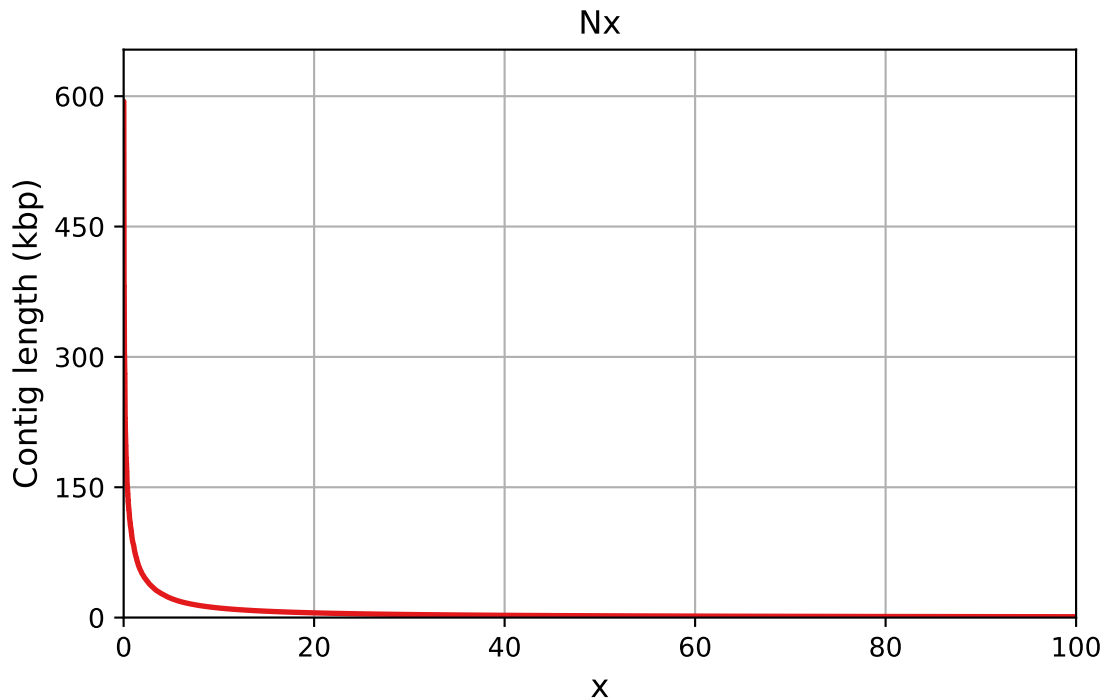
	TARA_PON_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	294
# possible misassemblies	352
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	517
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

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

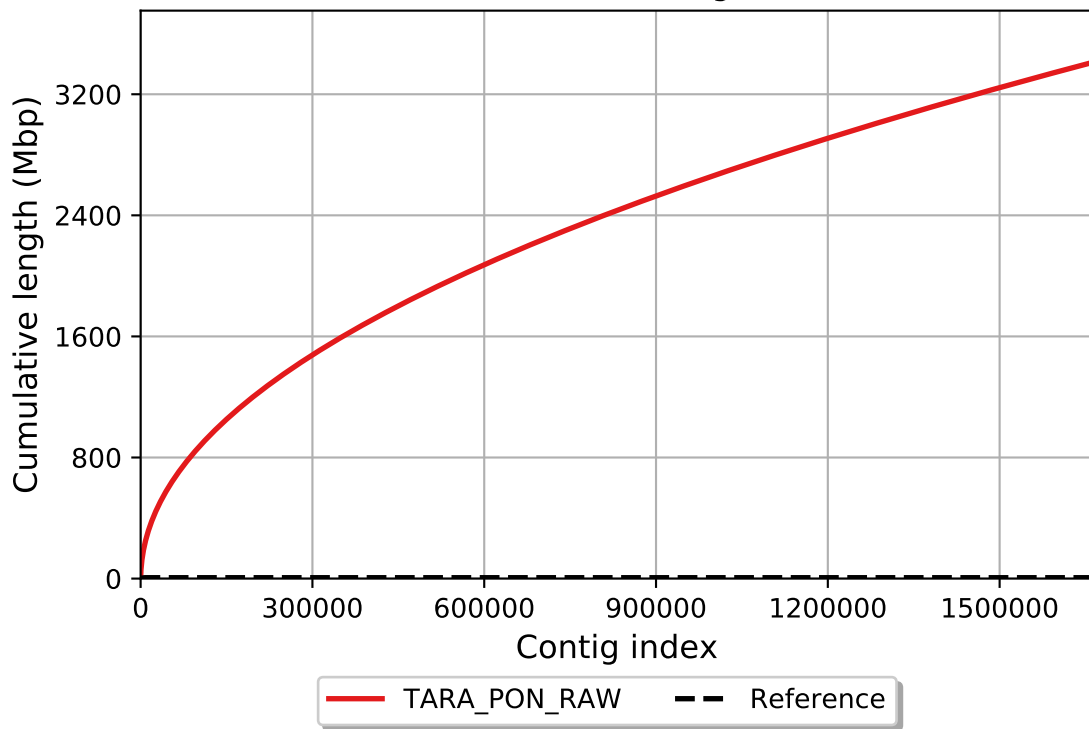
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# fully unaligned contigs	1662920
Fully unaligned length	3410021982
# partially unaligned contigs	299
Partially unaligned length	1256318
# N's	0

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).

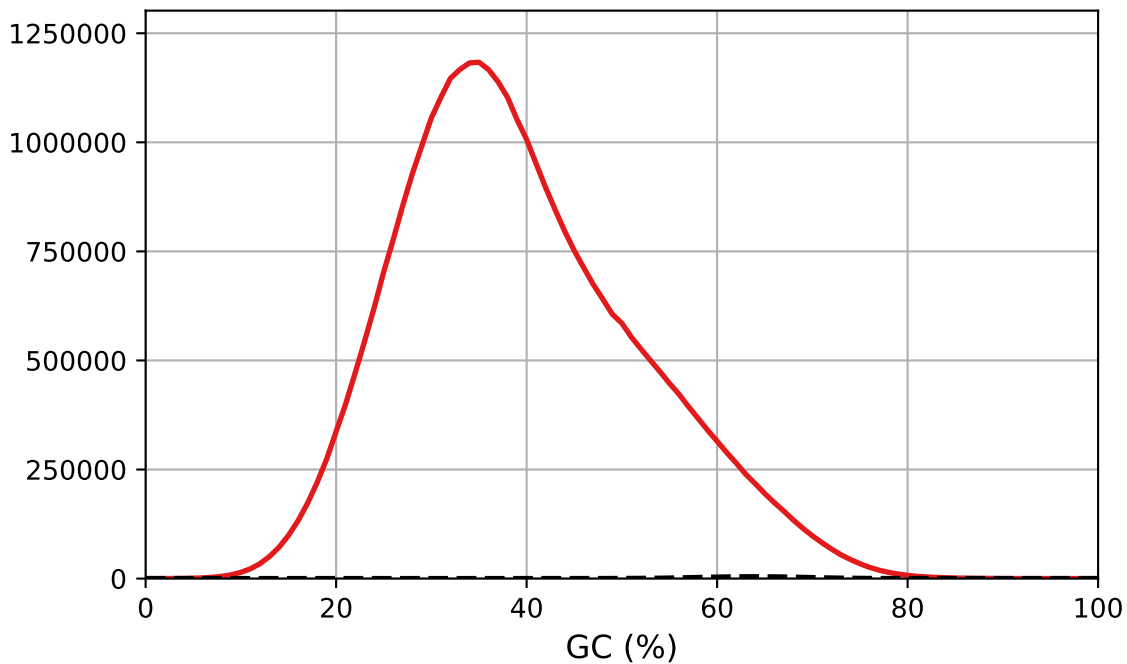


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Cumulative length

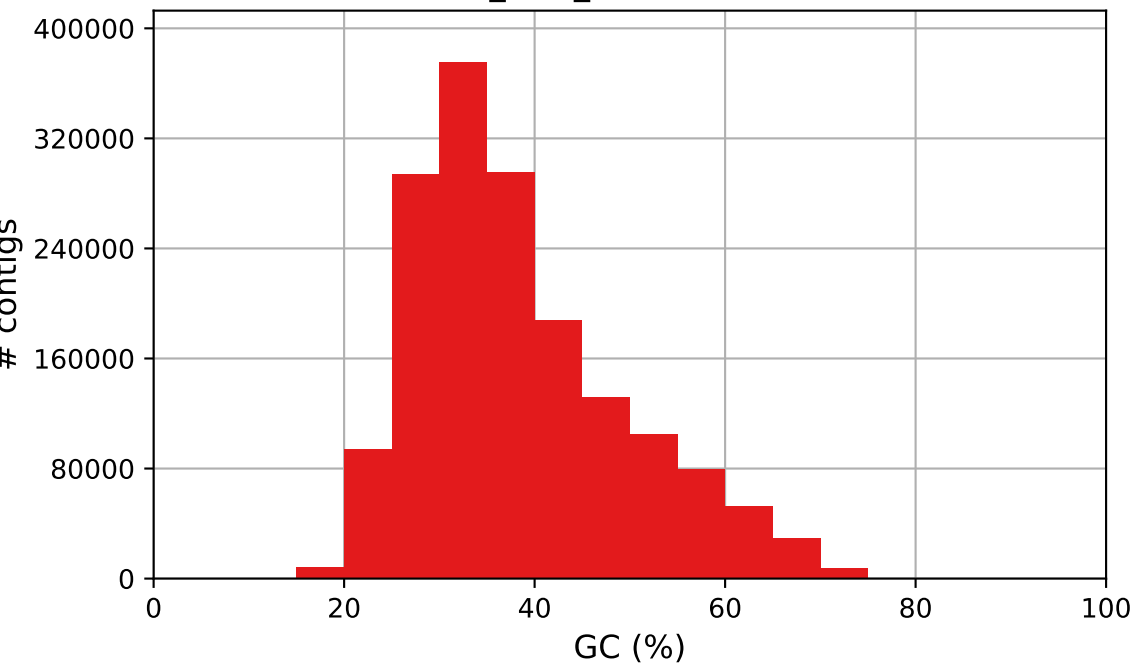


GC content



— TARA_PON_RAW - - Reference

TARA_PON_RAW GC content

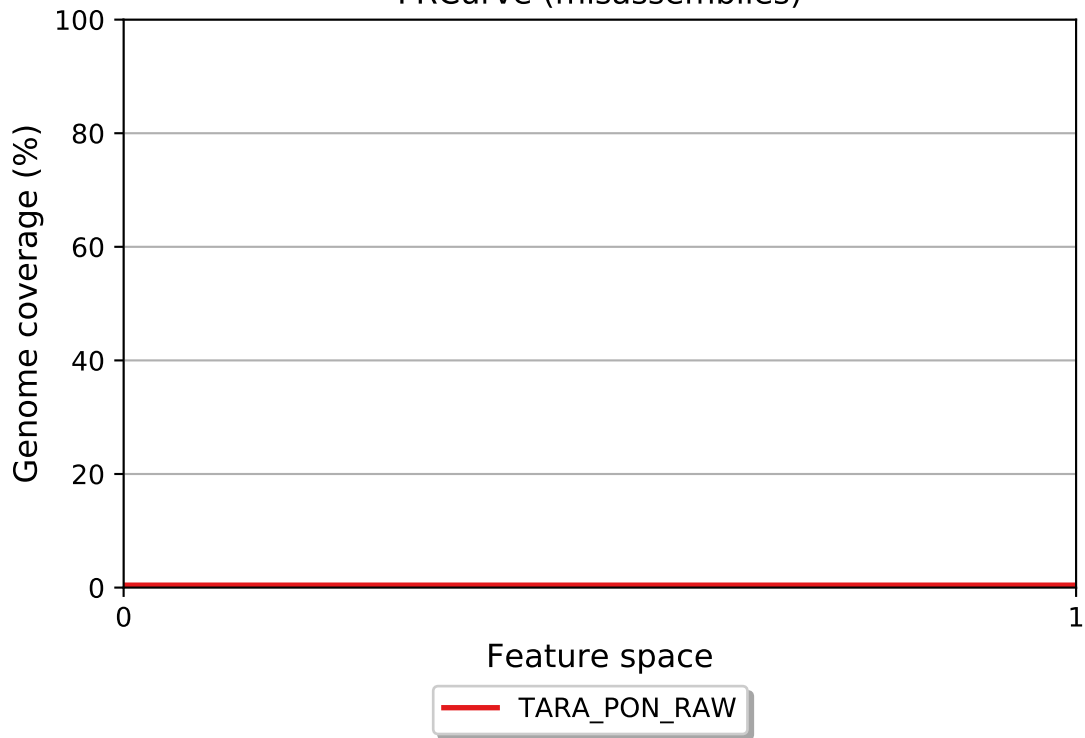


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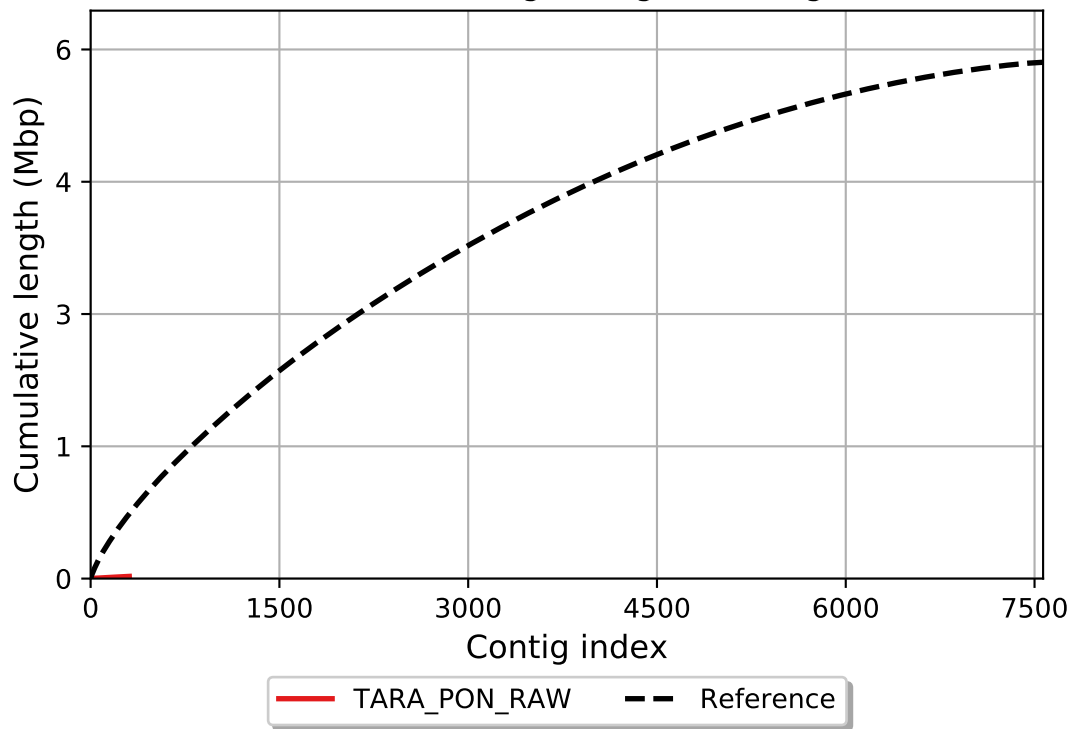
Misassemblies



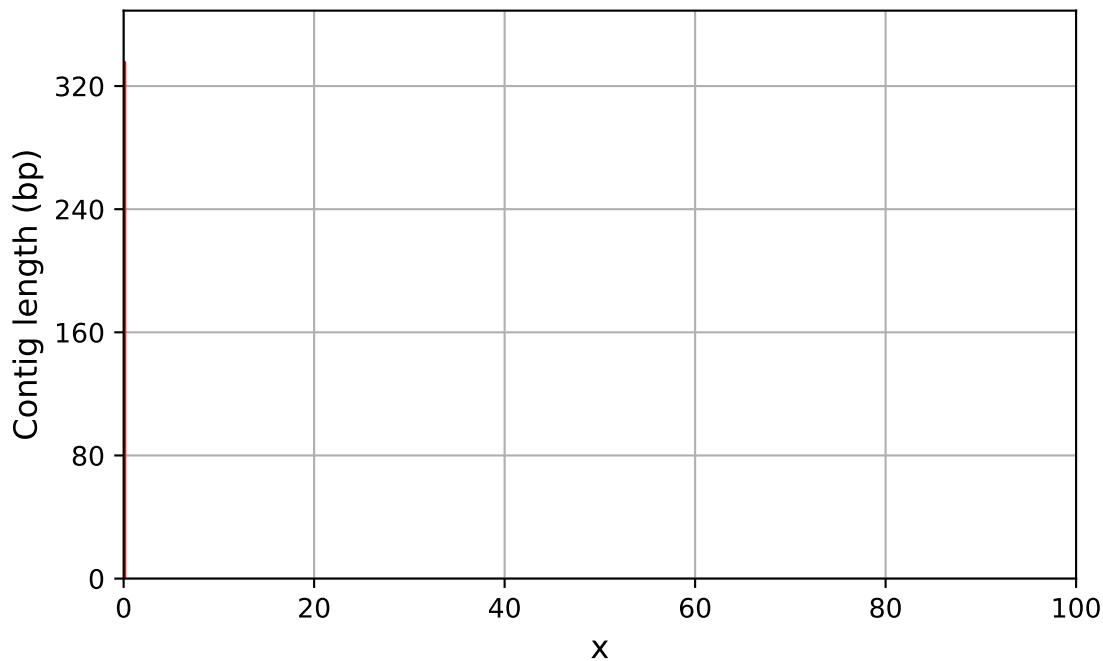
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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