

Report

	TARA_PON_RAW
# contigs (>= 1000 bp)	331
# contigs (>= 5000 bp)	43
# contigs (>= 10000 bp)	26
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	1360775
Total length (>= 5000 bp)	796992
Total length (>= 10000 bp)	680737
Total length (>= 25000 bp)	456871
Total length (>= 50000 bp)	172950
# contigs	331
Largest contig	61783
Total length	1360775
Reference length	7658814
GC (%)	36.30
Reference GC (%)	63.29
N50	10152
N75	2466
L50	26
L75	110
# 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	8 + 321 part
Unaligned length	1331721
Genome fraction (%)	0.063
Duplication ratio	5.976
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10798.03
# indels per 100 kbp	205.68
Largest alignment	573
Total aligned length	27390
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_PON_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	322
# possible misassemblies	384
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	525
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	11

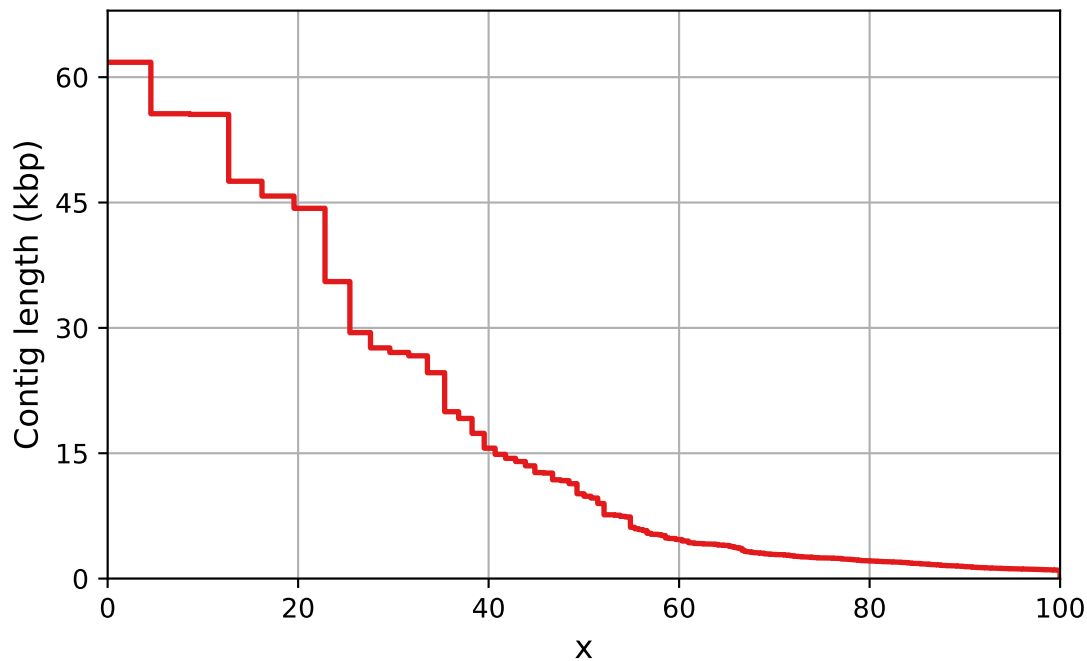
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_PON_RAW
# fully unaligned contigs	8
Fully unaligned length	14597
# partially unaligned contigs	321
Partially unaligned length	1317124
# N's	0

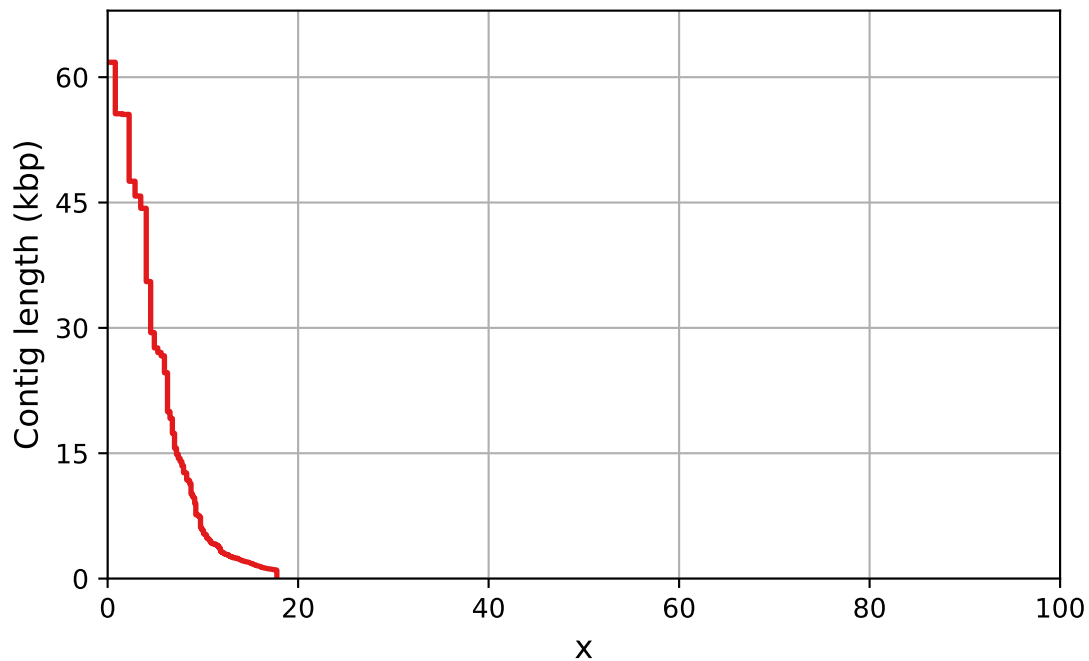
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



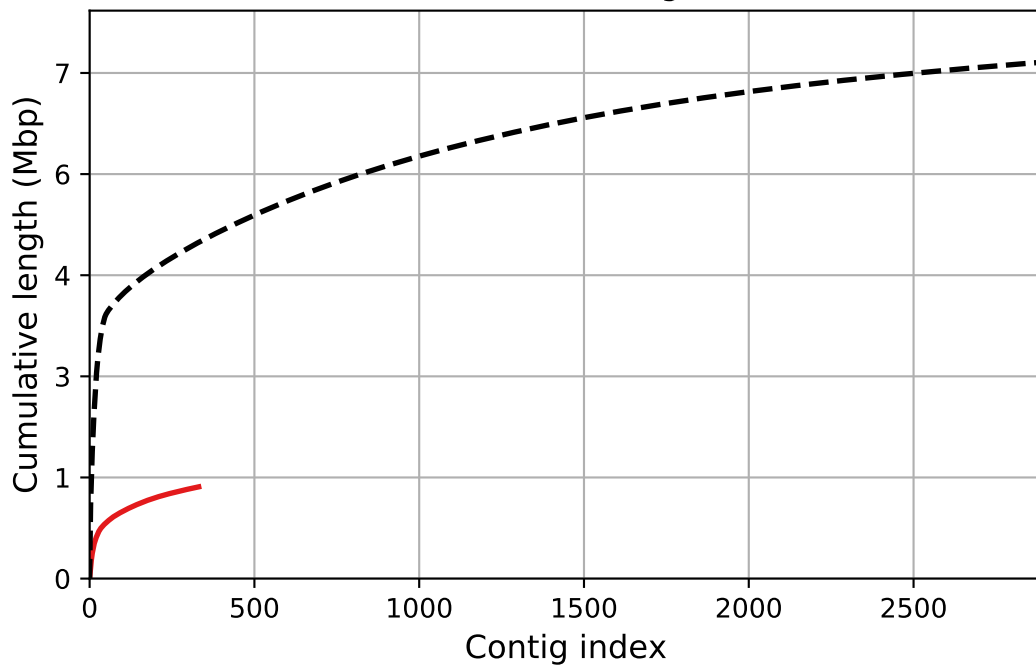
TARA_PON_RAW

NGx



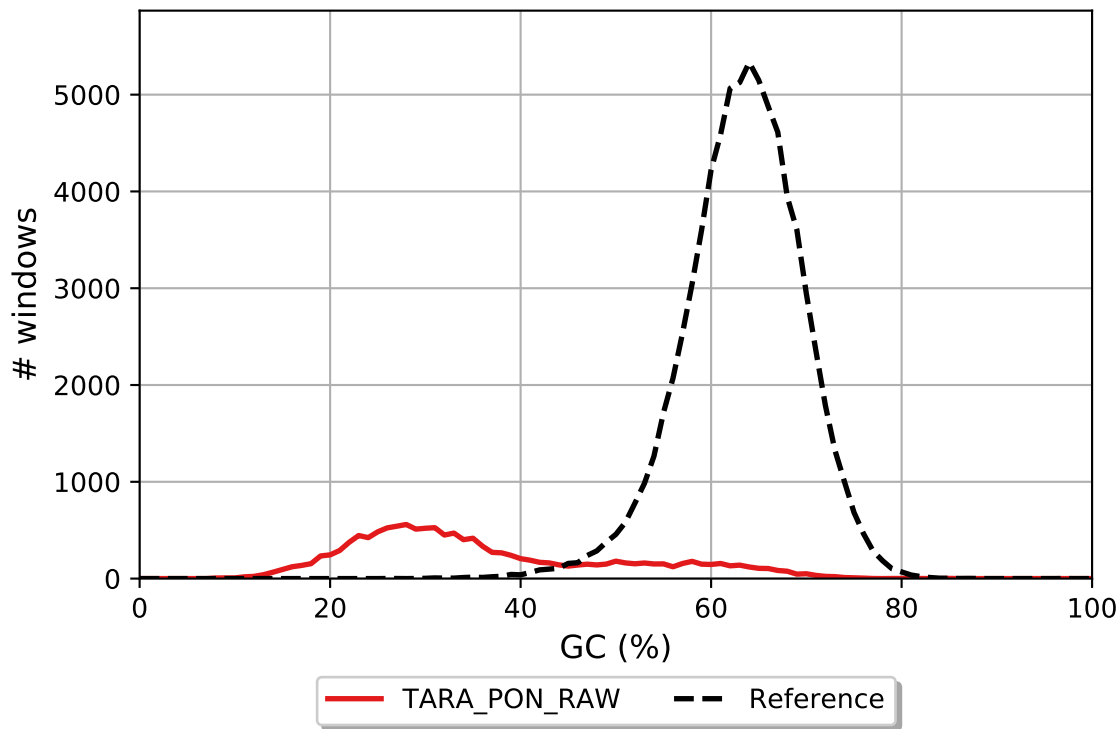
TARA_PON_RAW

Cumulative length

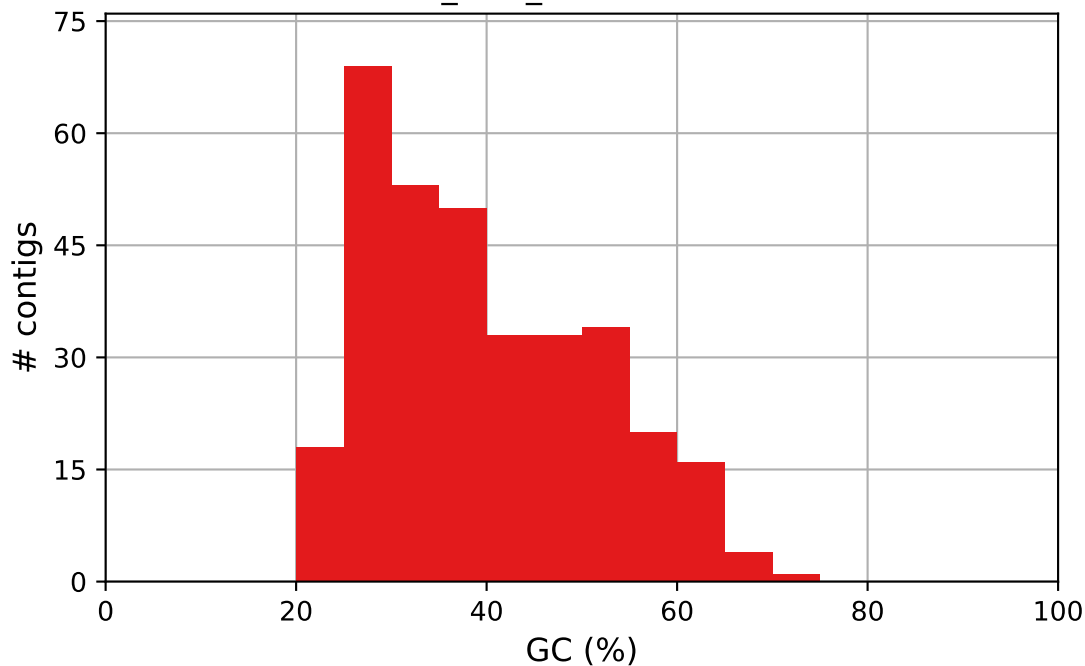


— TARA_PON_RAW - - Reference

GC content



TARA_PON_RAW GC content

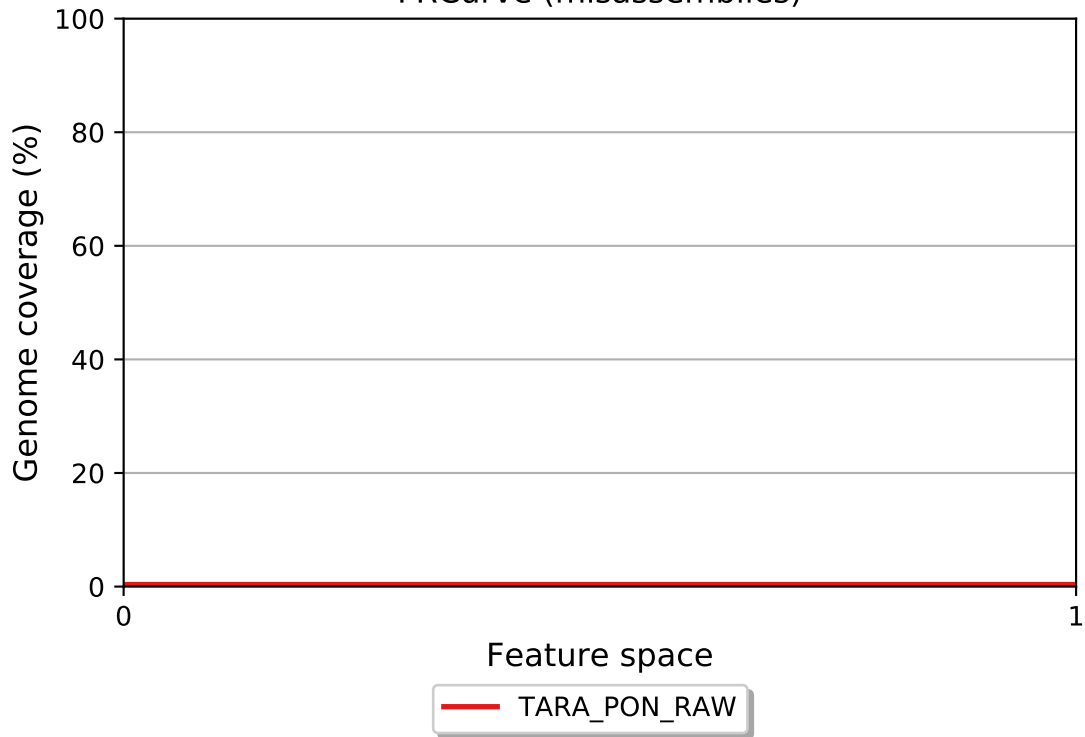


TARA_PON_RAW

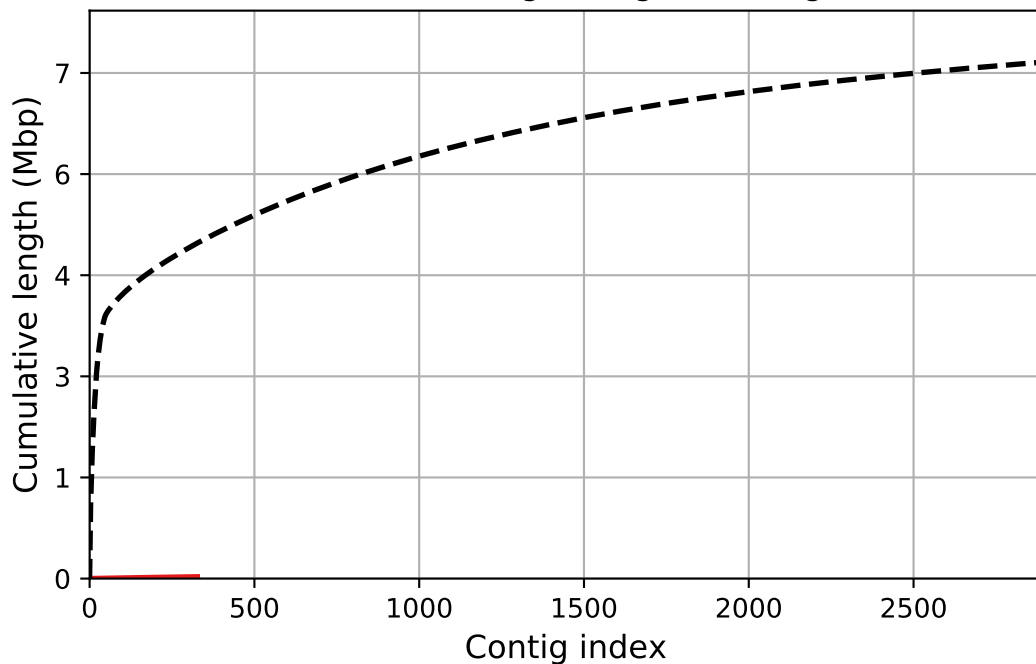
Misassemblies



FRCurve (misassemblies)

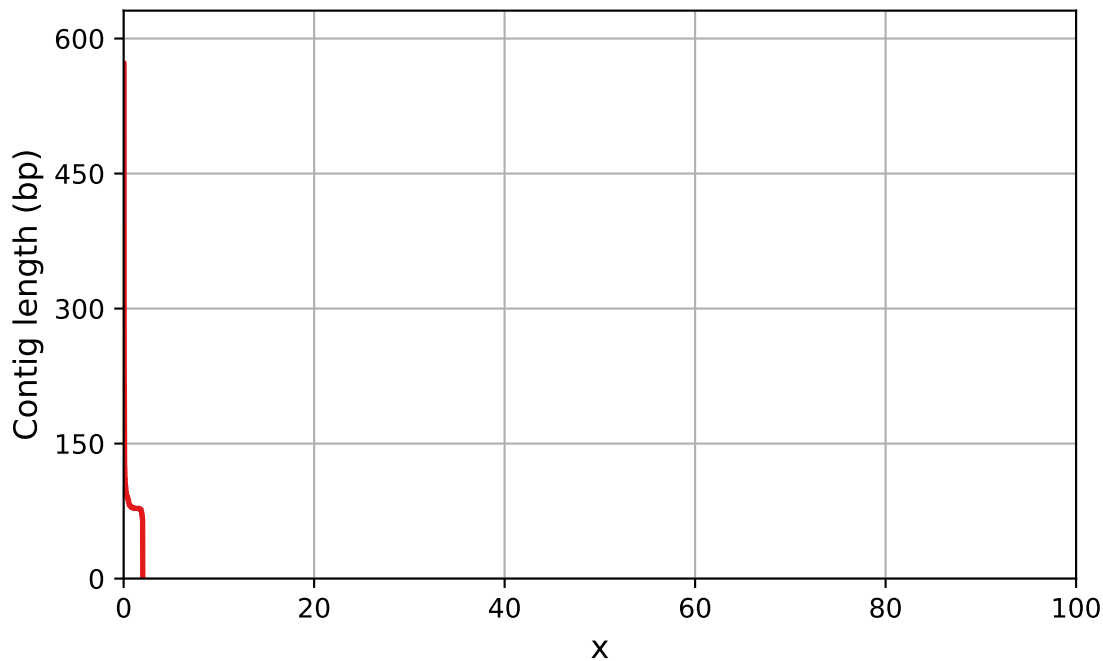


Cumulative length (aligned contigs)



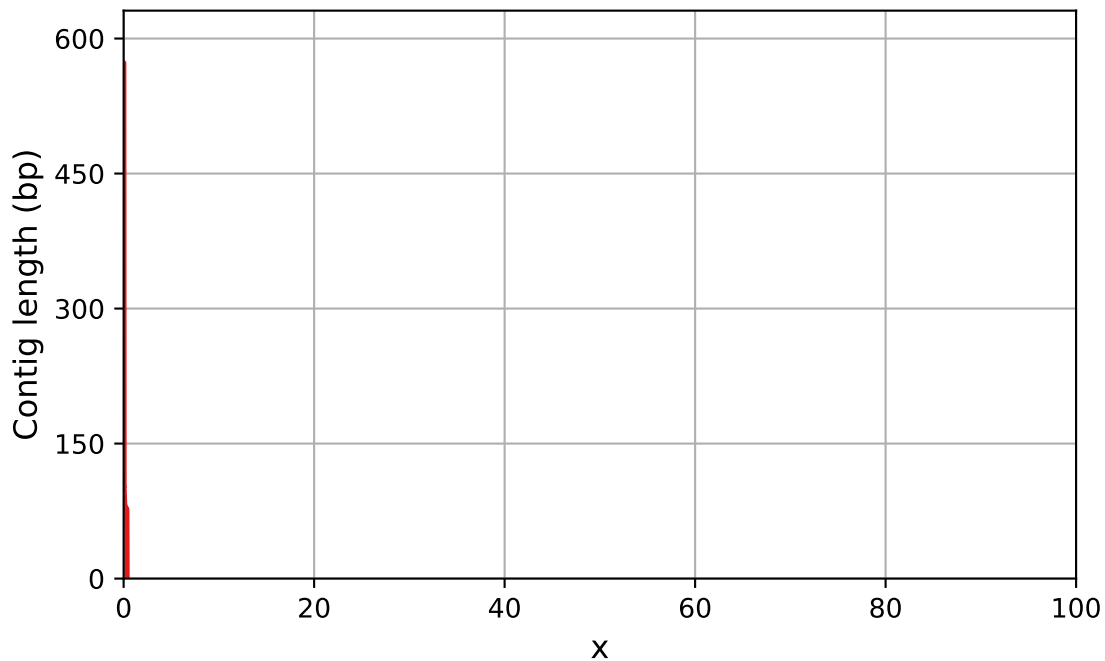
— TARA_PON_RAW - - Reference

NAx



TARA_PON_RAW

NGAx



TARA_PON_RAW