

Report

	TARA_ION_RAW
# contigs (>= 1000 bp)	346
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	24
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	1517832
Total length (>= 5000 bp)	913991
Total length (>= 10000 bp)	739301
Total length (>= 25000 bp)	479082
Total length (>= 50000 bp)	371739
# contigs	346
Largest contig	154464
Total length	1517832
Reference length	5854900
GC (%)	42.40
Reference GC (%)	63.53
N50	8573
N75	2794
L50	27
L75	112
# 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	0
# unaligned contigs	5 + 340 part
Unaligned length	1490073
Genome fraction (%)	0.054
Duplication ratio	8.846
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14563.42
# indels per 100 kbp	31.87
Largest alignment	159
Total aligned length	26820
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

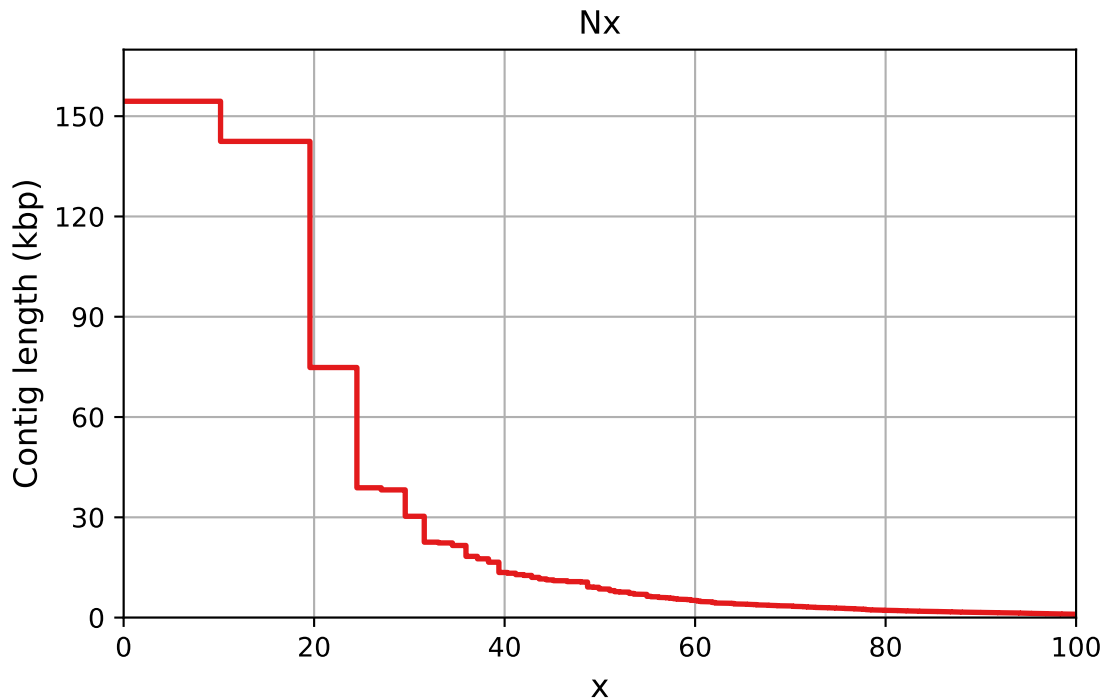
	TARA_ION_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	344
# possible misassemblies	414
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	457
# 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

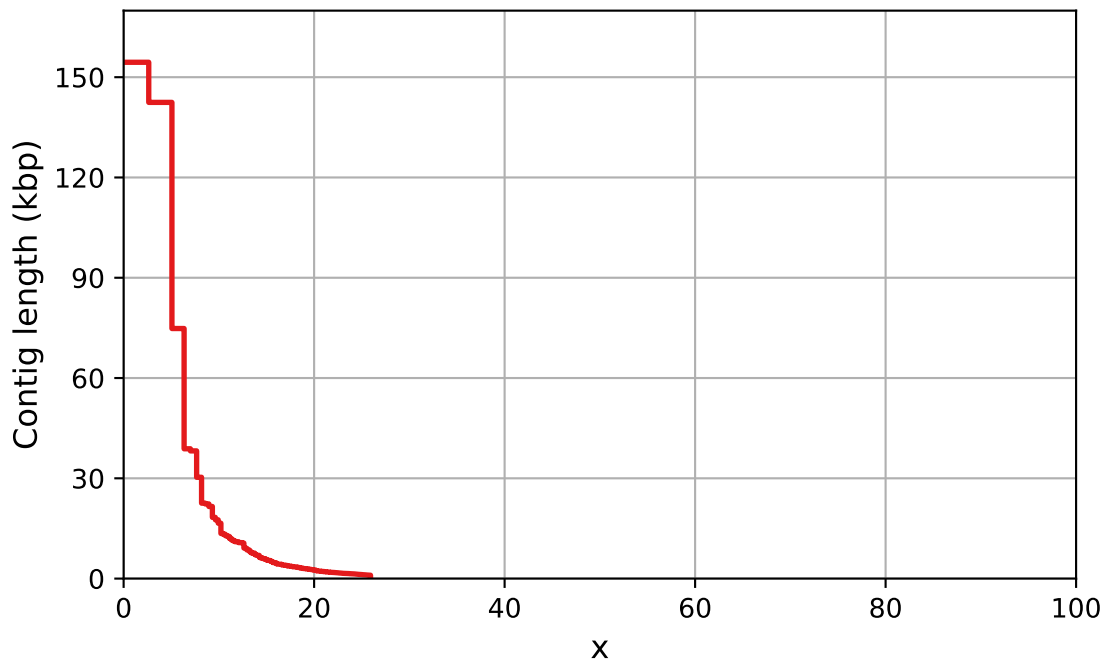
	TARA_ION_RAW
# fully unaligned contigs	5
Fully unaligned length	66005
# partially unaligned contigs	340
Partially unaligned length	1424068
# N's	0

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).



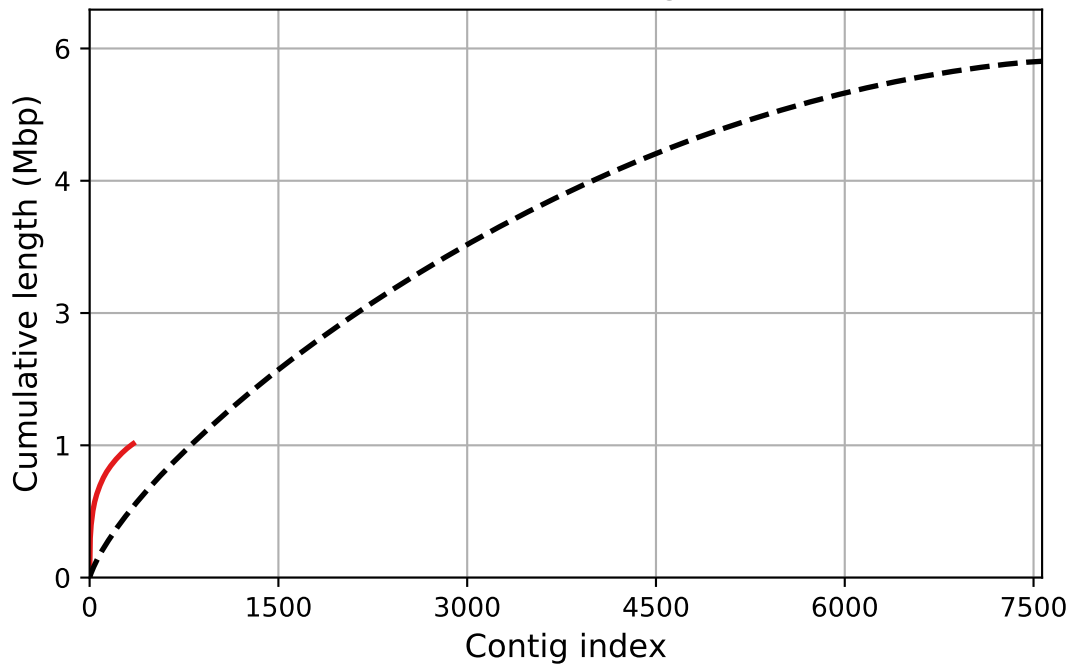
TARA_ION_RAW

NGx



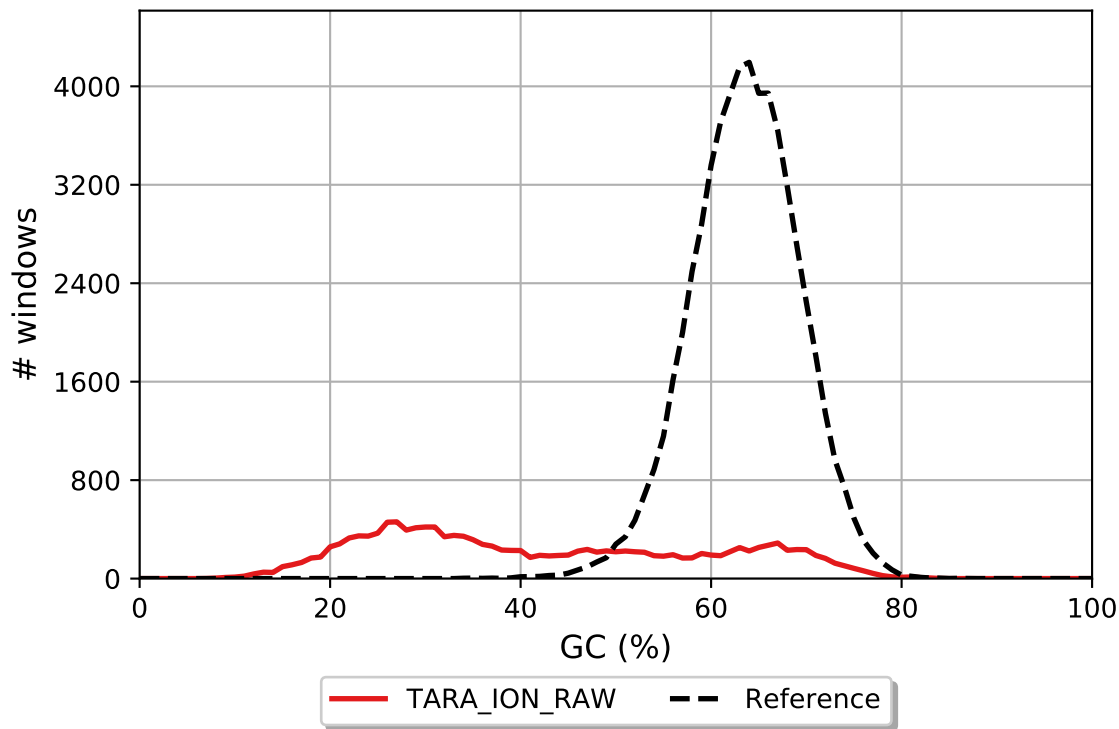
TARA_ION_RAW

Cumulative length

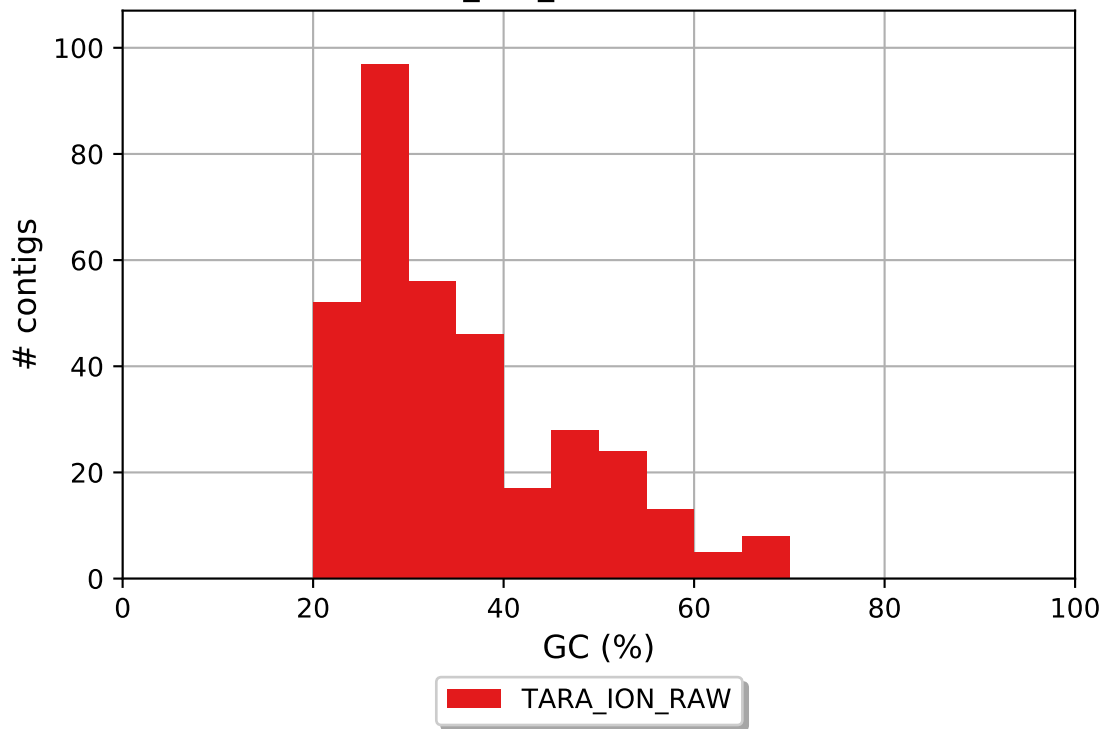


— TARA_ION_RAW - - Reference

GC content



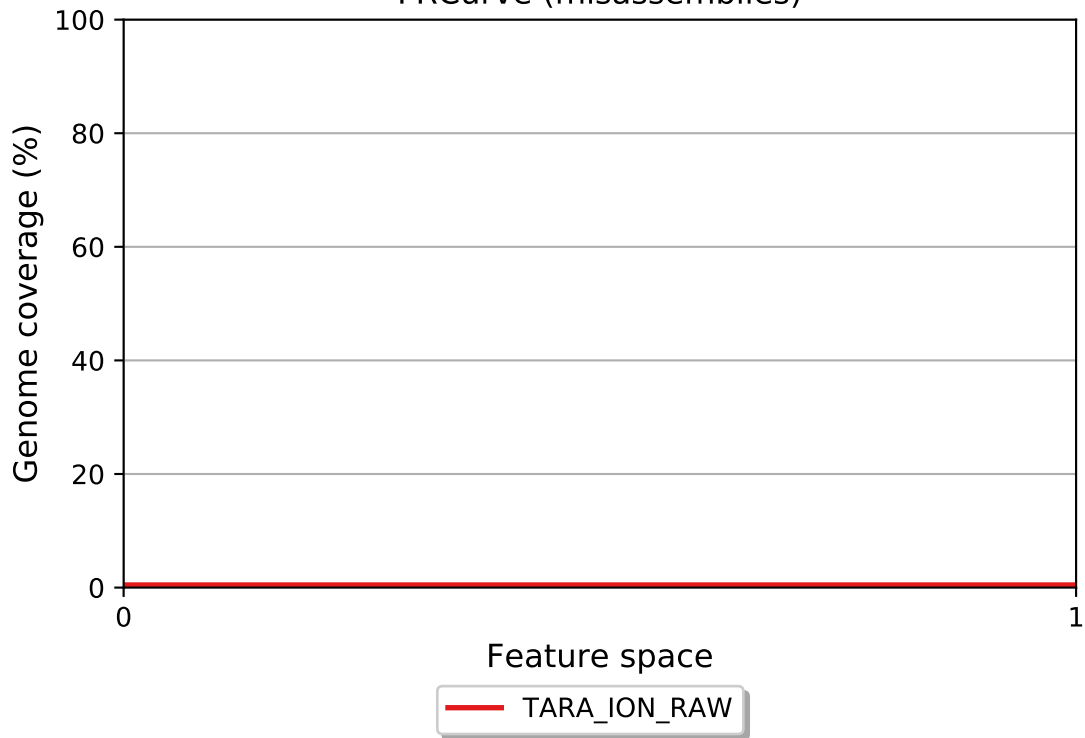
TARA_ION_RAW GC content



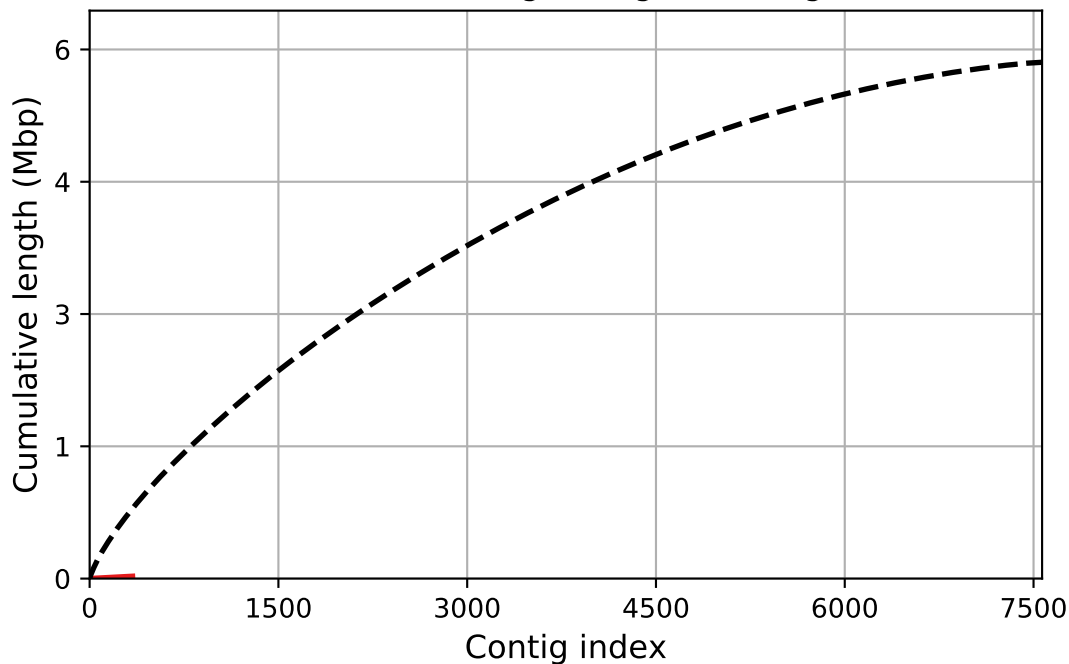
Misassemblies



FRCurve (misassemblies)

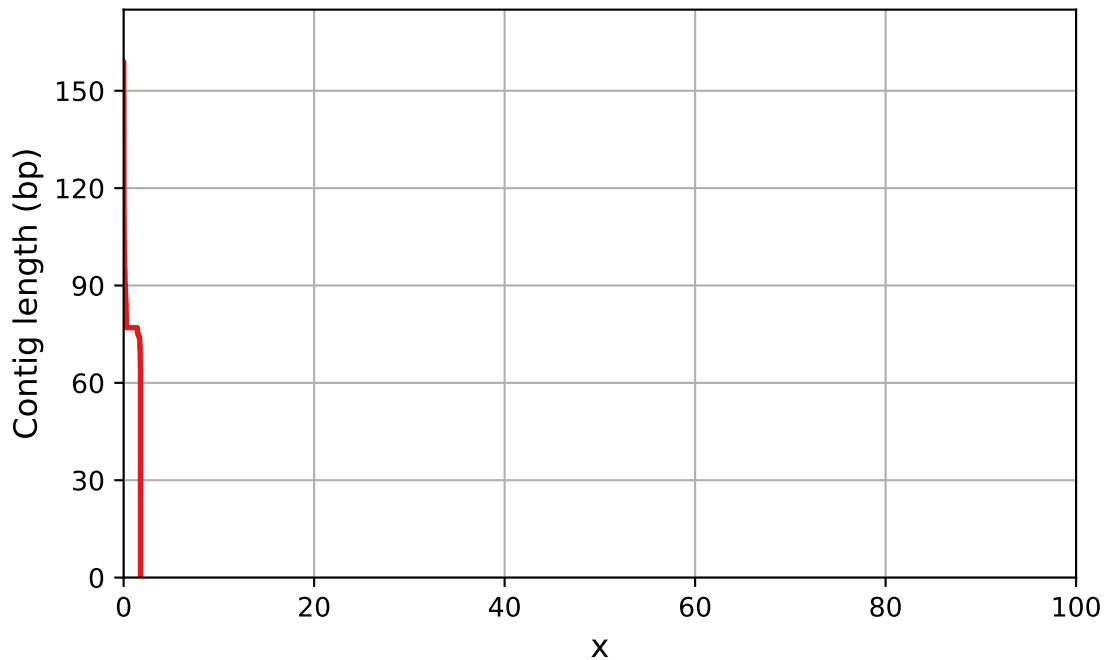


Cumulative length (aligned contigs)



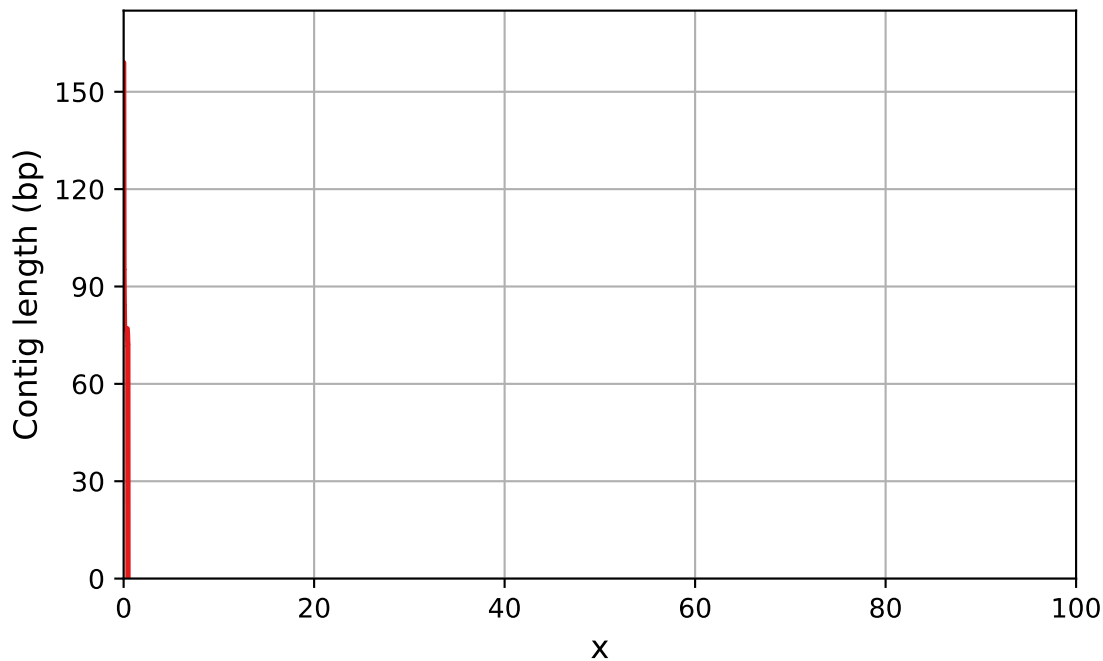
TARA_ION_RAW Reference

NAx



TARA_ION_RAW

NGAx



TARA_ION_RAW