

Report

	TARA_IOS_RAW
# contigs (>= 1000 bp)	38
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	146596
Total length (>= 5000 bp)	74798
Total length (>= 10000 bp)	69496
Total length (>= 25000 bp)	58856
Total length (>= 50000 bp)	58856
# contigs	38
Largest contig	58856
Total length	146596
Reference length	3561038
GC (%)	47.71
Reference GC (%)	41.87
N50	5302
N75	2304
L50	3
L75	14
# 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	2 + 36 part
Unaligned length	143265
Genome fraction (%)	0.021
Duplication ratio	4.430
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13962.77
# indels per 100 kbp	0.00
Largest alignment	166
Total aligned length	3331
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_IOS_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	38
# possible misassemblies	42
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	105
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

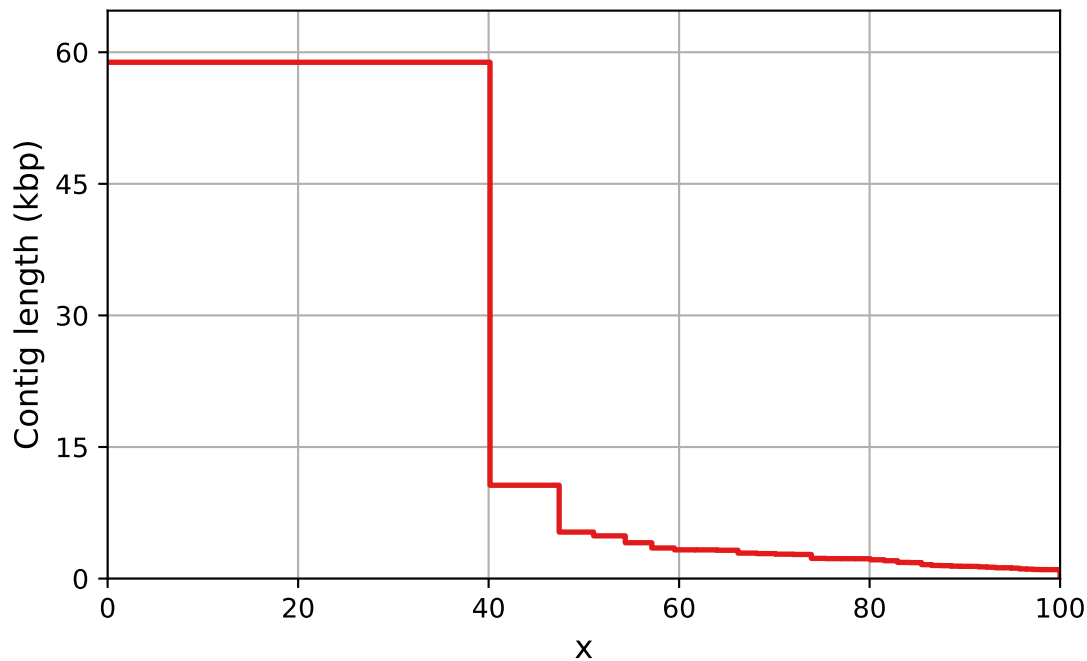
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_IOS_RAW
# fully unaligned contigs	2
Fully unaligned length	5630
# partially unaligned contigs	36
Partially unaligned length	137635
# N's	0

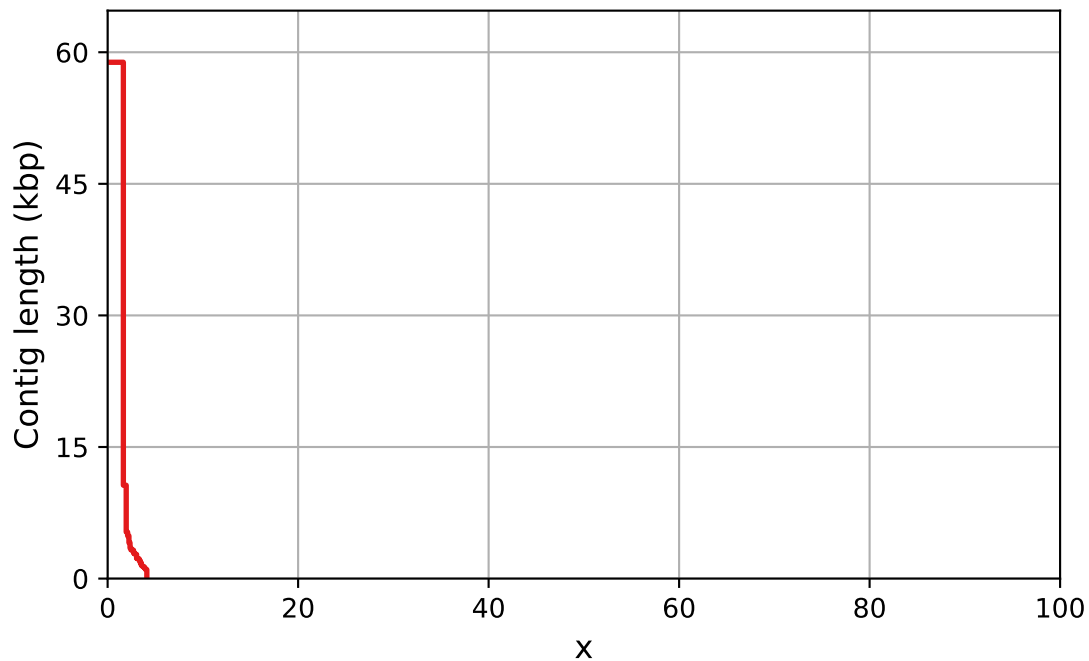
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

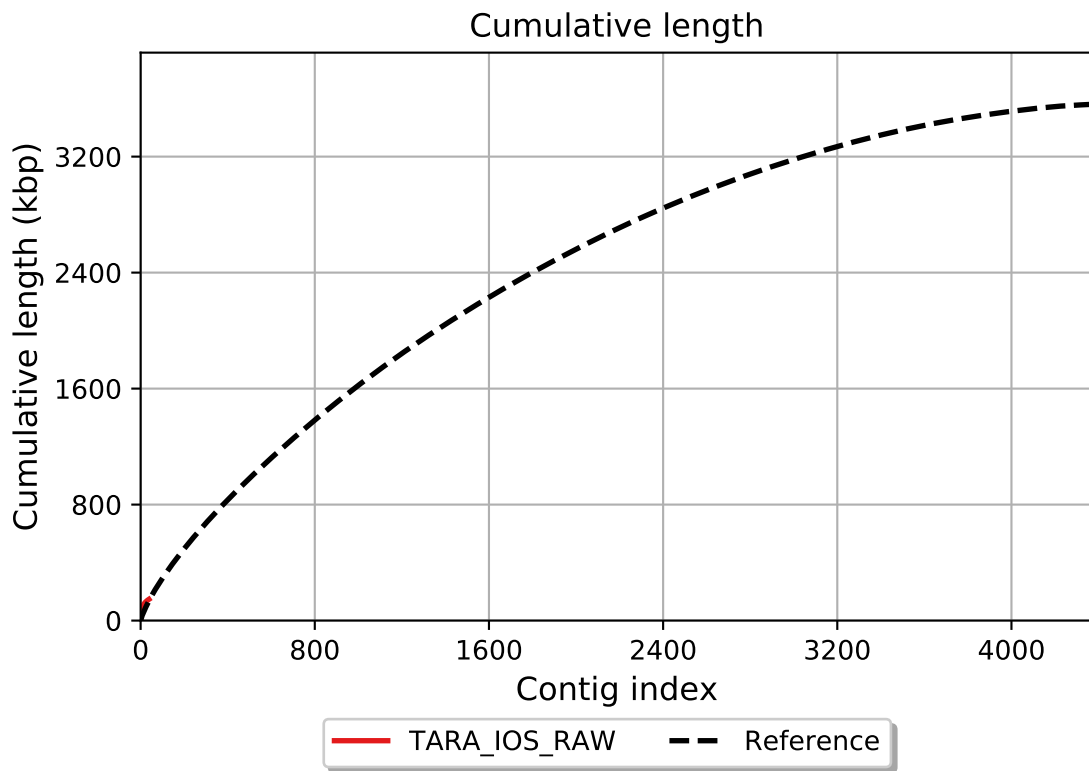


TARA_IOS_RAW

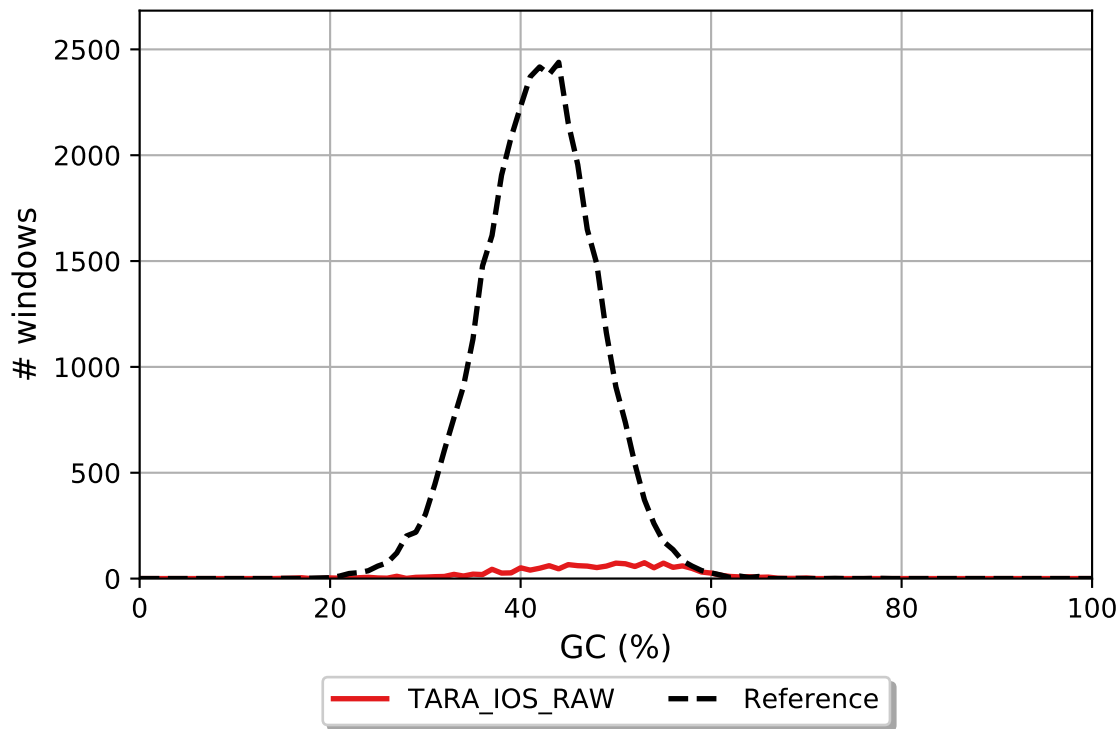
NGx



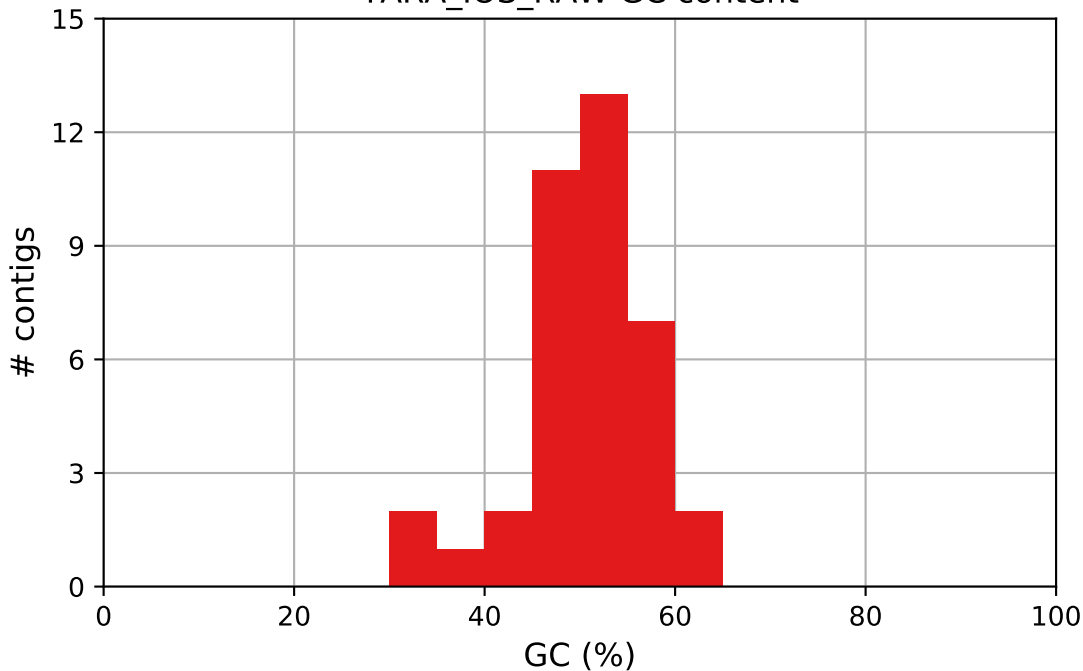
TARA_IOS_RAW



GC content



TARA_IOS_RAW GC content

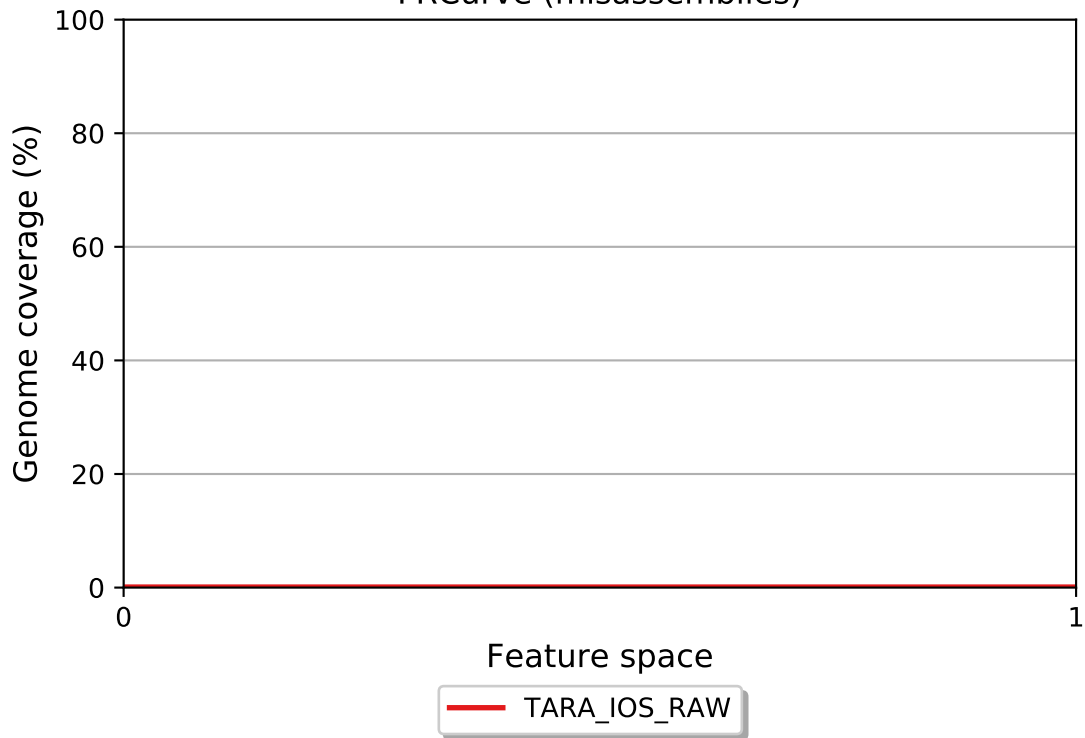


TARA_IOS_RAW

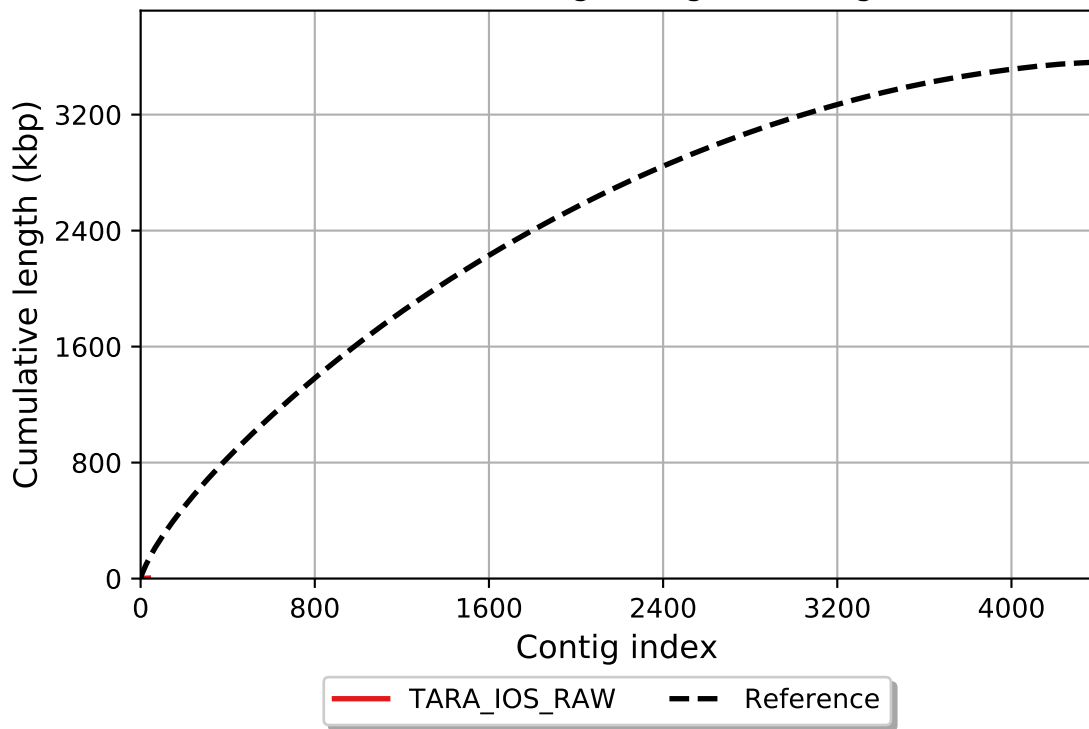
Misassemblies



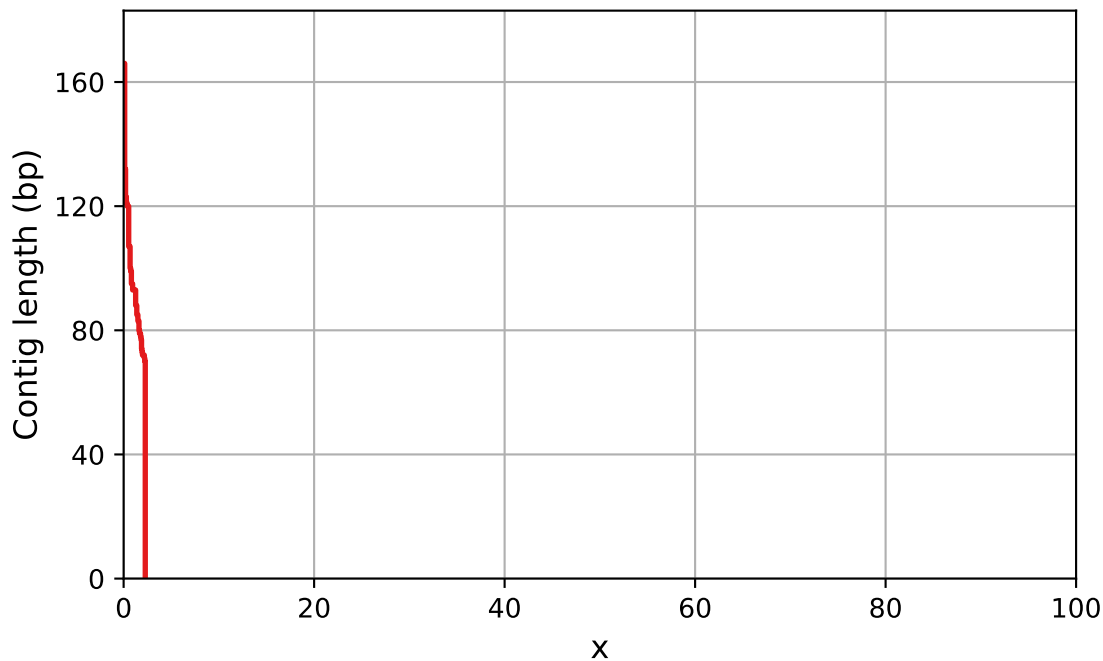
FRCurve (misassemblies)



Cumulative length (aligned contigs)

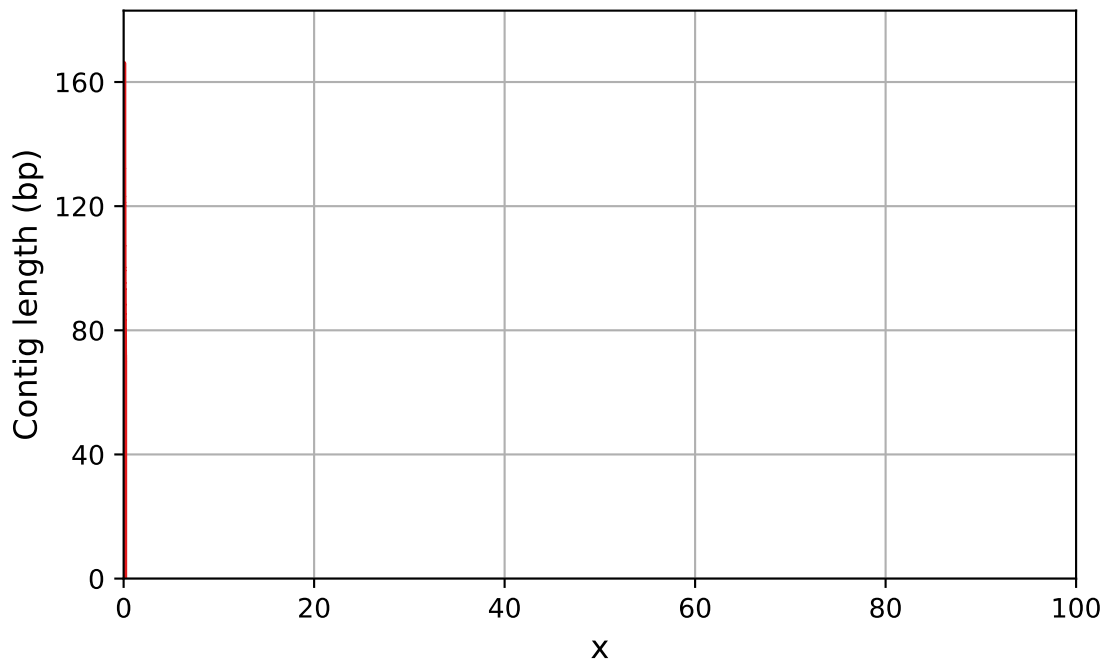


NAx



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NGAx



— TARA_IOS_RAW