

Report

	TARA_ASW_RAW
# contigs (>= 1000 bp)	255
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	1015341
Total length (>= 5000 bp)	572398
Total length (>= 10000 bp)	511449
Total length (>= 25000 bp)	389463
Total length (>= 50000 bp)	360331
# contigs	255
Largest contig	142397
Total length	1015341
Reference length	7658814
GC (%)	50.67
Reference GC (%)	63.29
N50	10631
N75	2213
L50	13
L75	84
# 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	5
# unaligned contigs	6 + 247 part
Unaligned length	992444
Genome fraction (%)	0.063
Duplication ratio	4.710
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7796.75
# indels per 100 kbp	288.01
Largest alignment	326
Total aligned length	21315
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

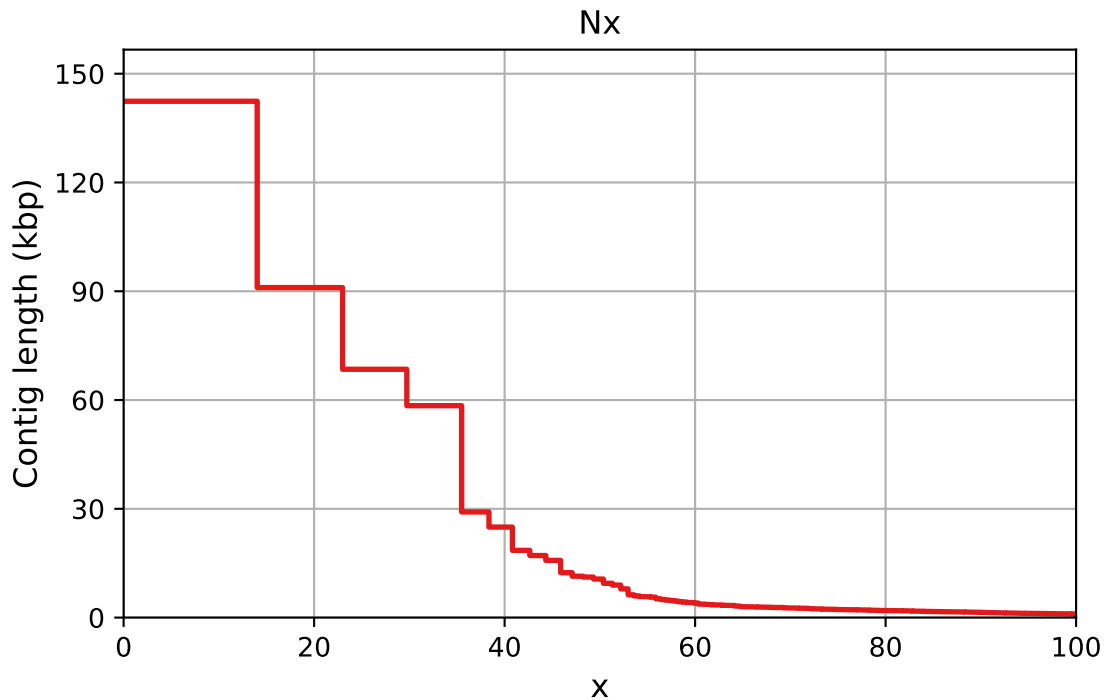
	TARA_ASW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	246
# possible misassemblies	294
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	379
# indels	14
# indels (<= 5 bp)	14
# indels (> 5 bp)	0
Indels length	21

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

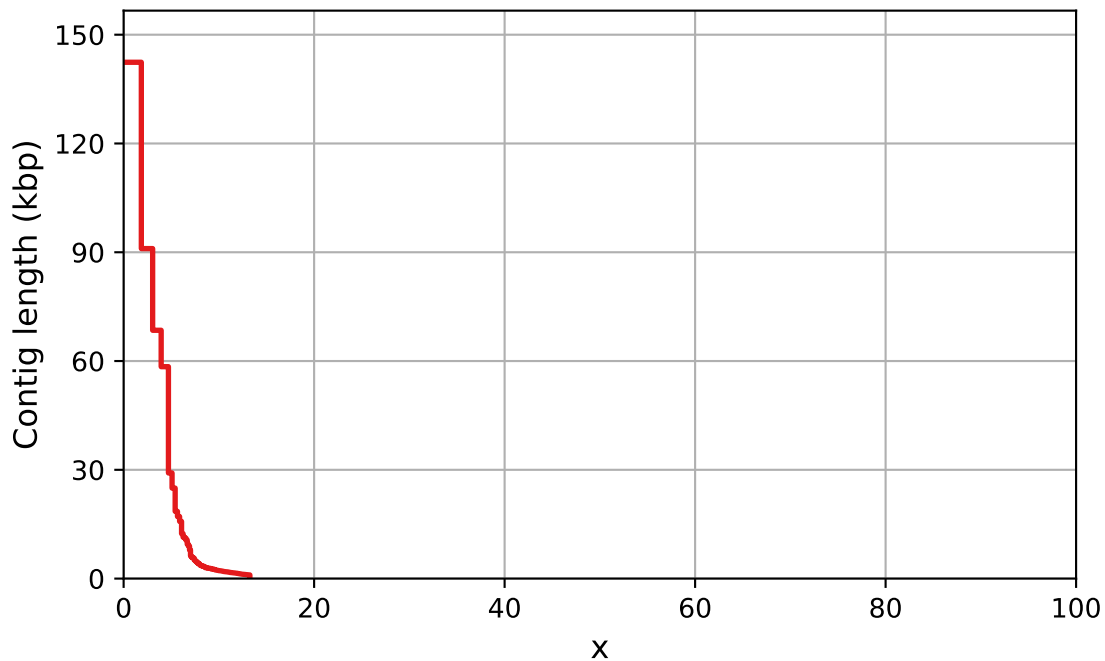
	TARA_ASW_RAW
# fully unaligned contigs	6
Fully unaligned length	27093
# partially unaligned contigs	247
Partially unaligned length	965351
# N's	0

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).



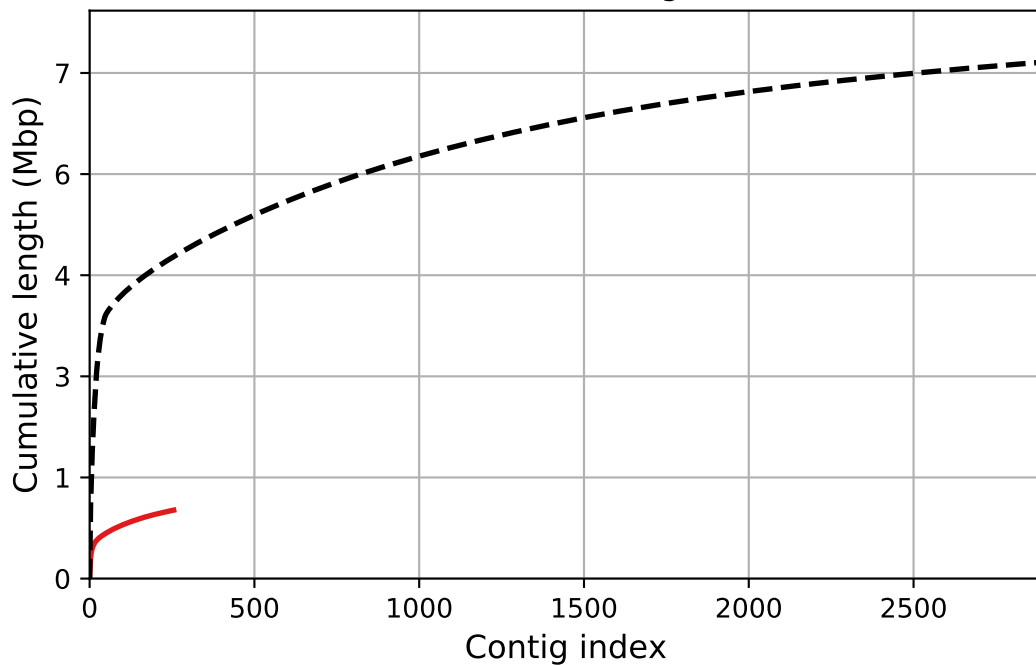
— TARA_ASW_RAW

NGx



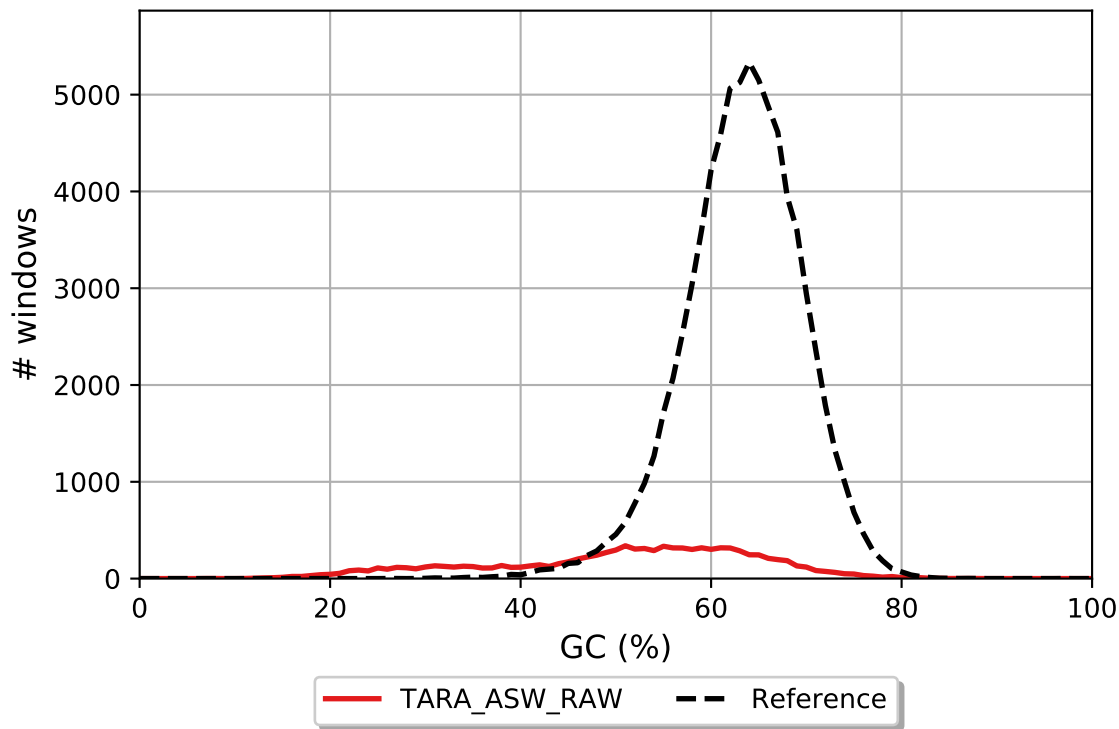
TARA_ASW_RAW

Cumulative length

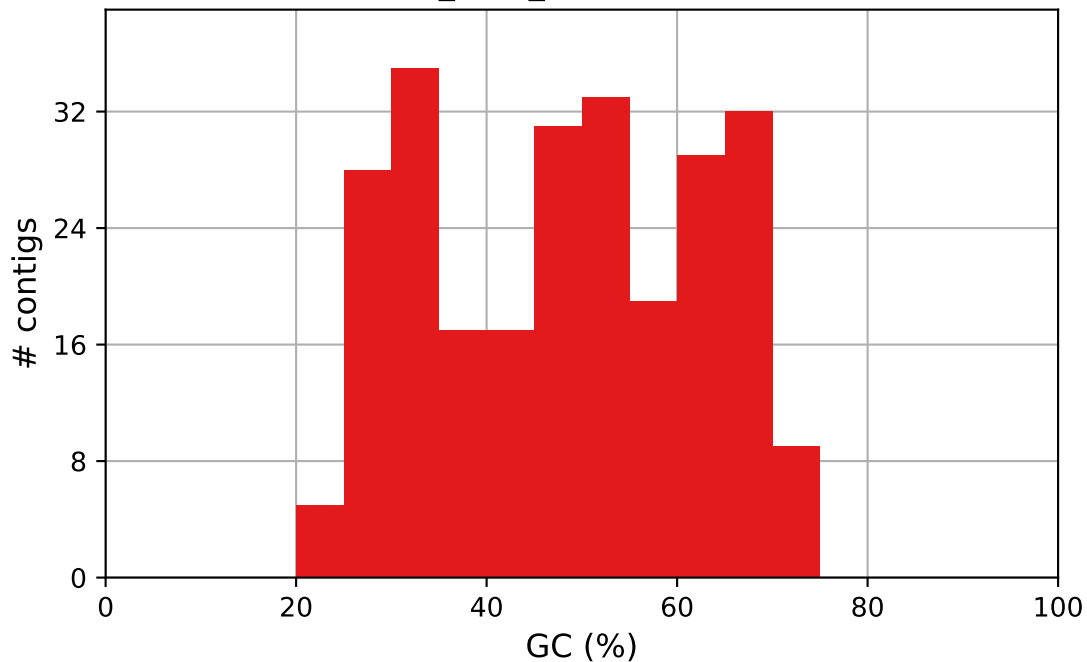


— TARA_ASW_RAW - - Reference

GC content



TARA_ASW_RAW GC content

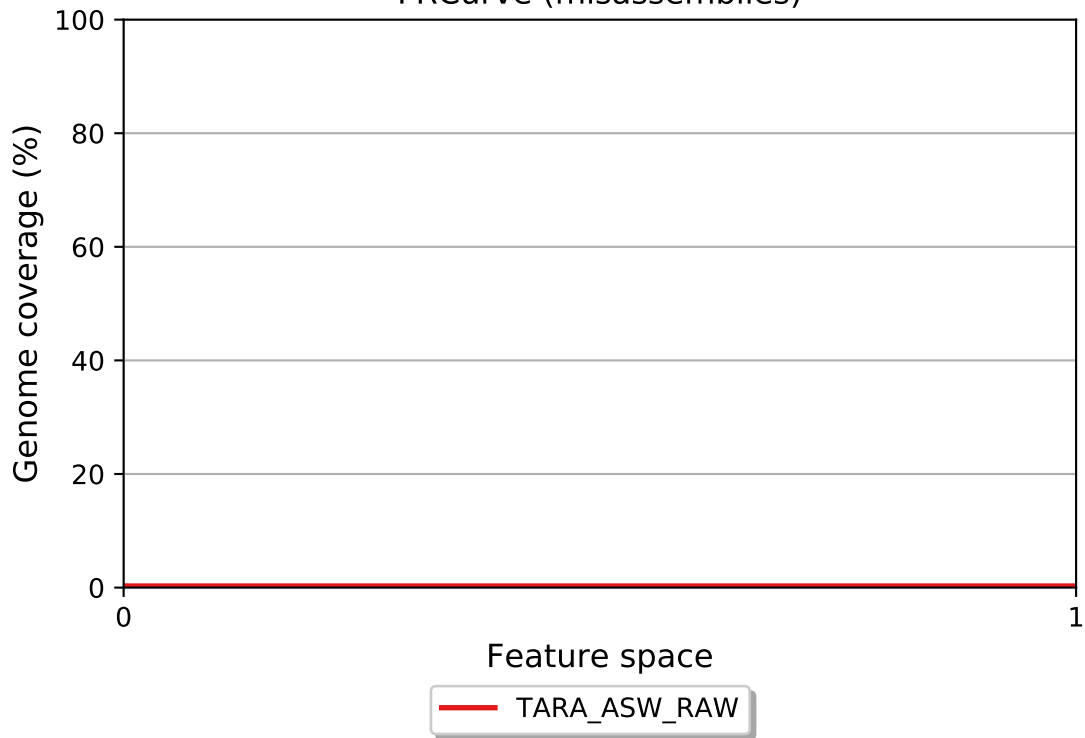


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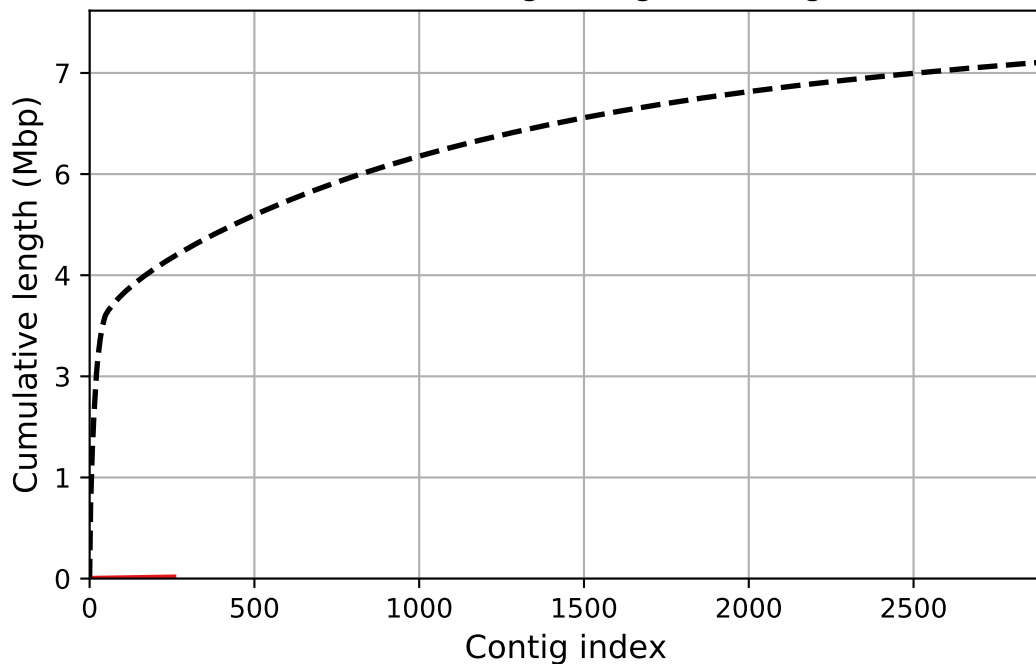
Misassemblies



FRCurve (misassemblies)

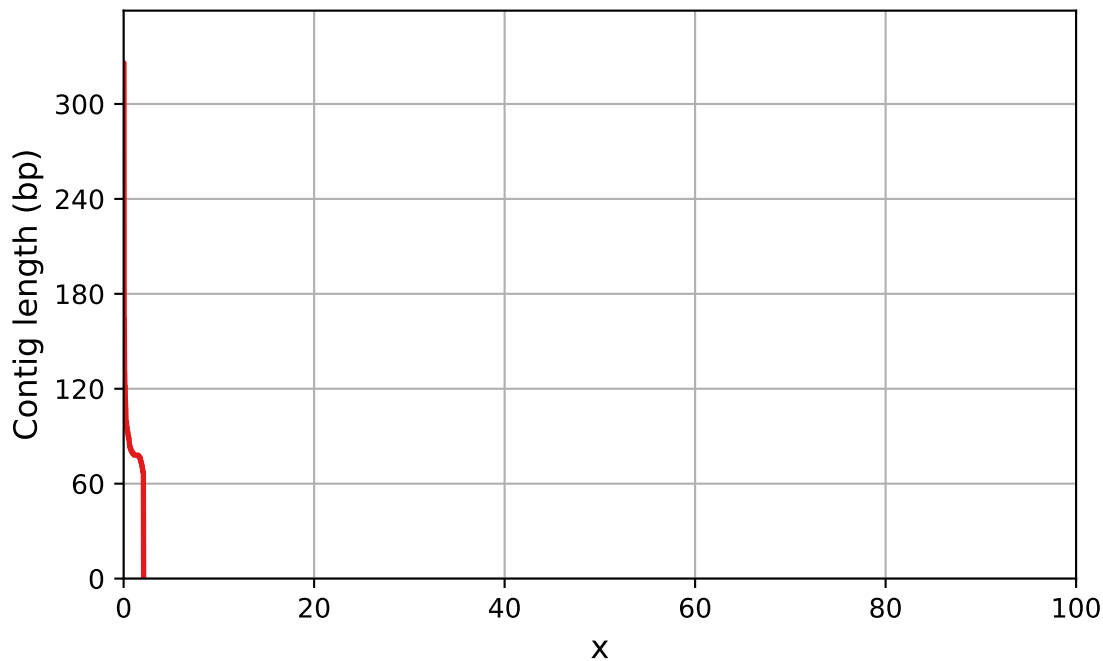


Cumulative length (aligned contigs)



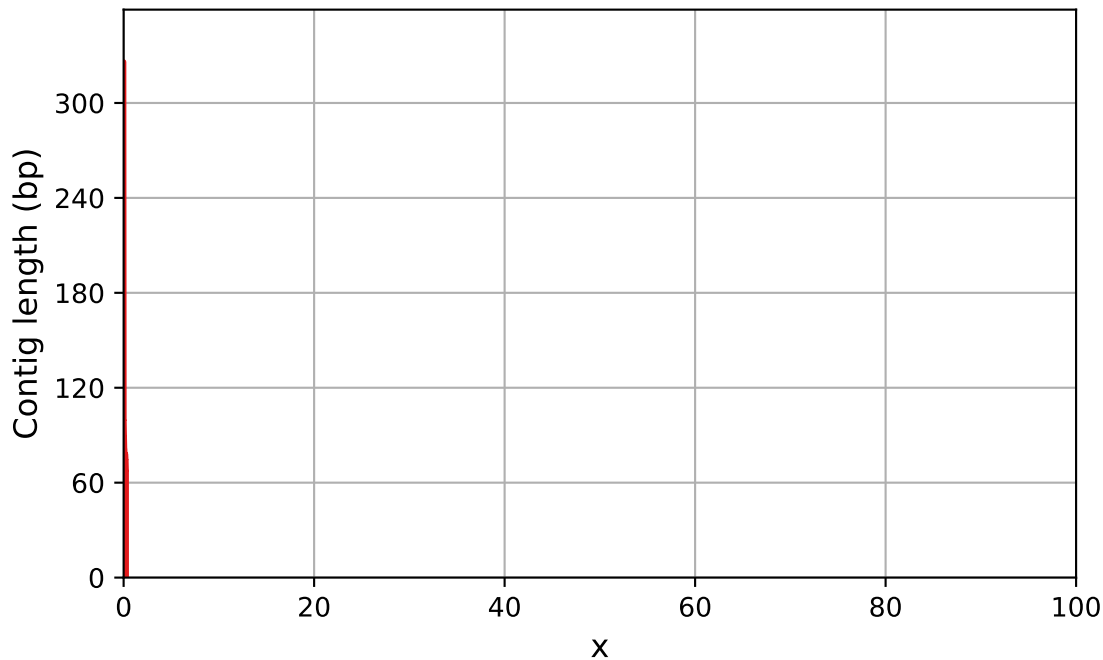
— TARA_ASW_RAW - - Reference

NAx



TARA_ASW_RAW

NGAx



TARA_ASW_RAW