

Report

	TARA_PSW_RAW
# contigs (>= 1000 bp)	60
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	448757
Total length (>= 5000 bp)	356217
Total length (>= 10000 bp)	322655
Total length (>= 25000 bp)	289201
Total length (>= 50000 bp)	222419
# contigs	60
Largest contig	222419
Total length	448757
Reference length	4234461
GC (%)	50.36
Reference GC (%)	41.03
N50	35322
N75	7257
L50	2
L75	7
# 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	1
# unaligned contigs	13 + 46 part
Unaligned length	443072
Genome fraction (%)	0.027
Duplication ratio	4.987
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11315.79
# indels per 100 kbp	87.72
Largest alignment	201
Total aligned length	4576
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

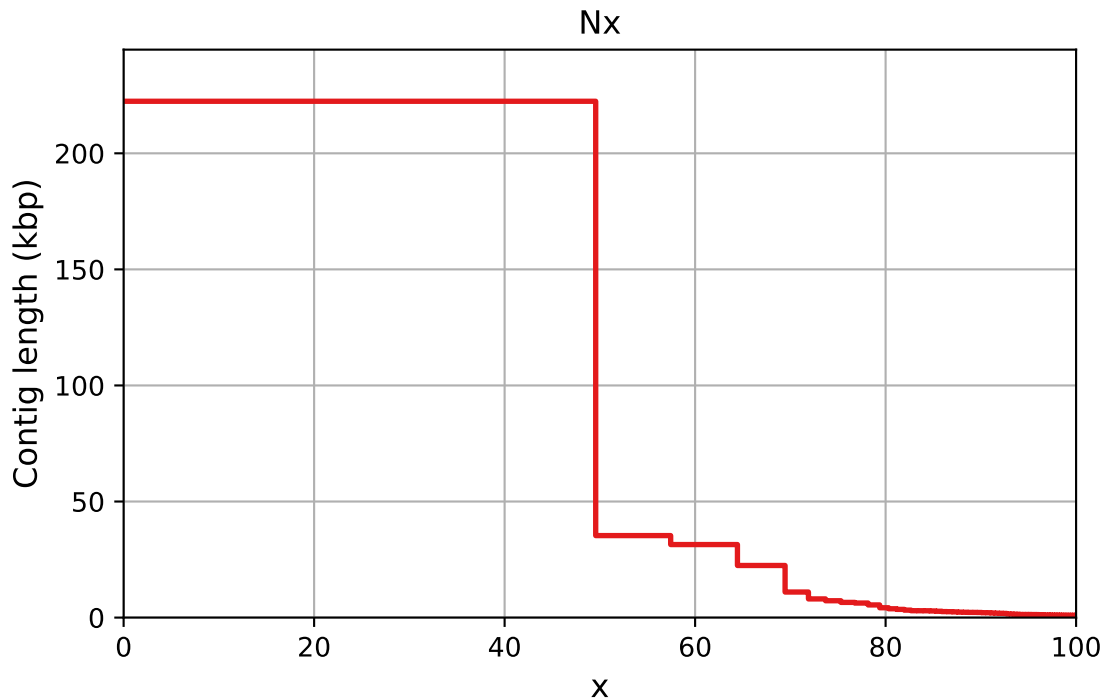
	TARA_PSW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	59
# possible misassemblies	70
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	129
# 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

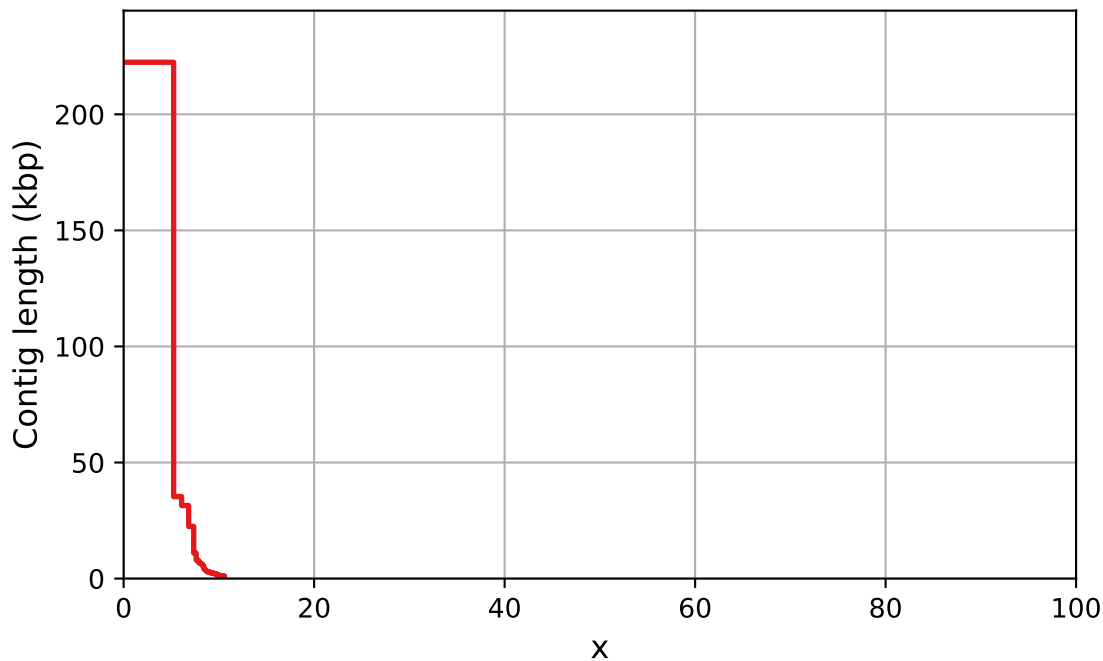
	TARA_PSW_RAW
# fully unaligned contigs	13
Fully unaligned length	252135
# partially unaligned contigs	46
Partially unaligned length	190937
# N's	0

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).

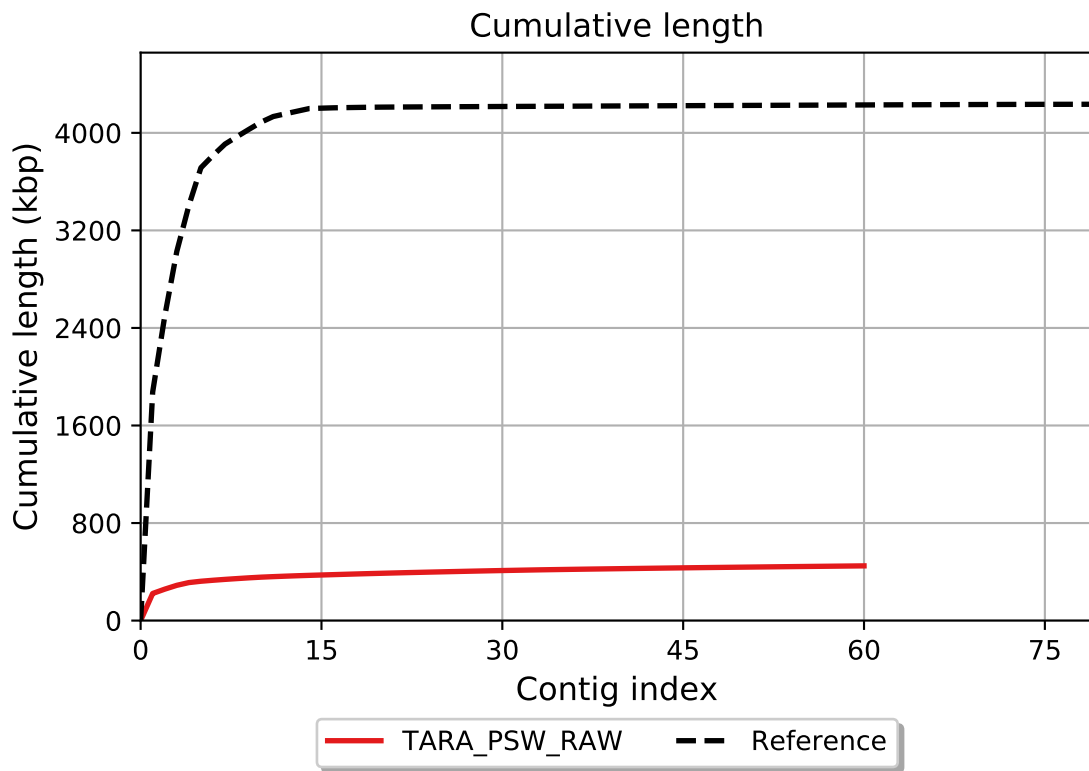


— TARA_PSW_RAW

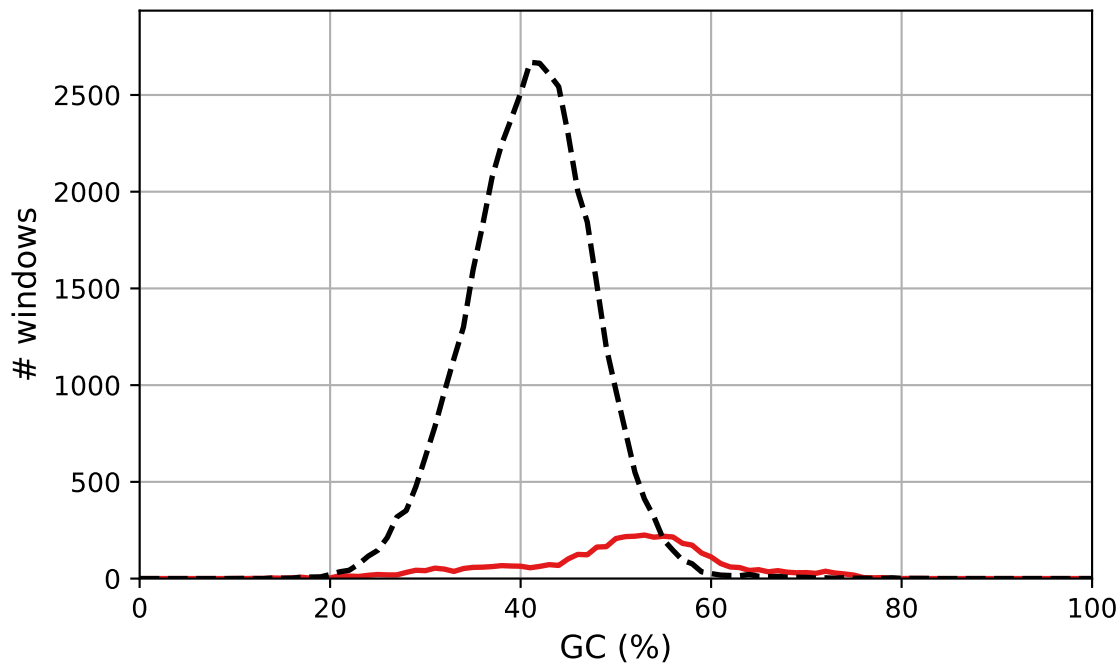
NGx



TARA_PSW_RAW

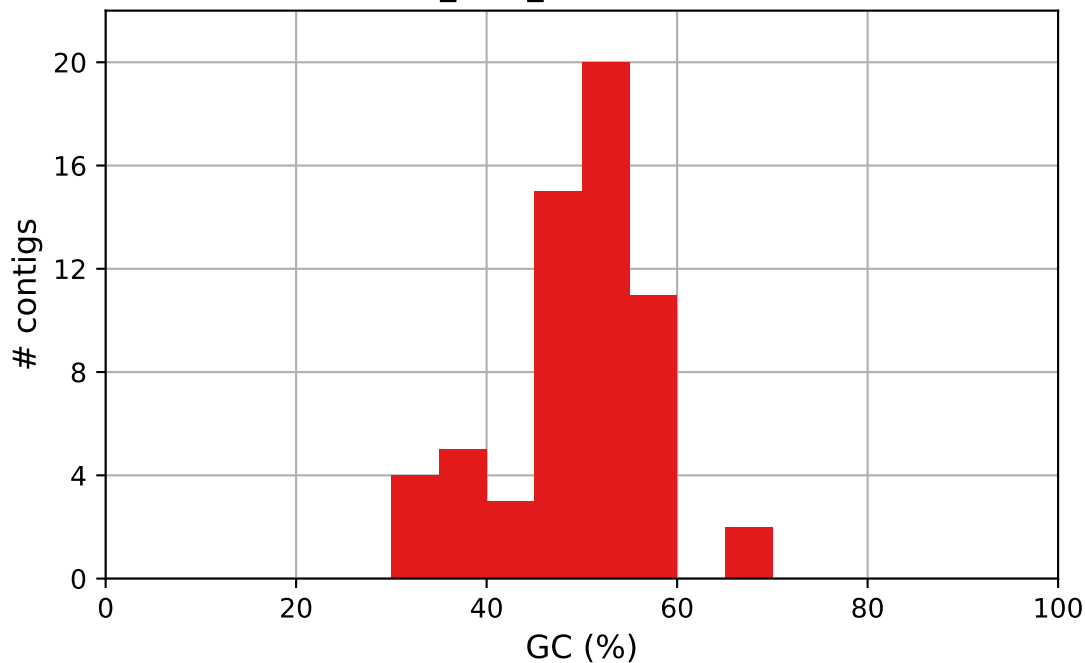


GC content



TARA_PSW_RAW Reference

TARA_PSW_RAW GC content



TARA_PSW_RAW

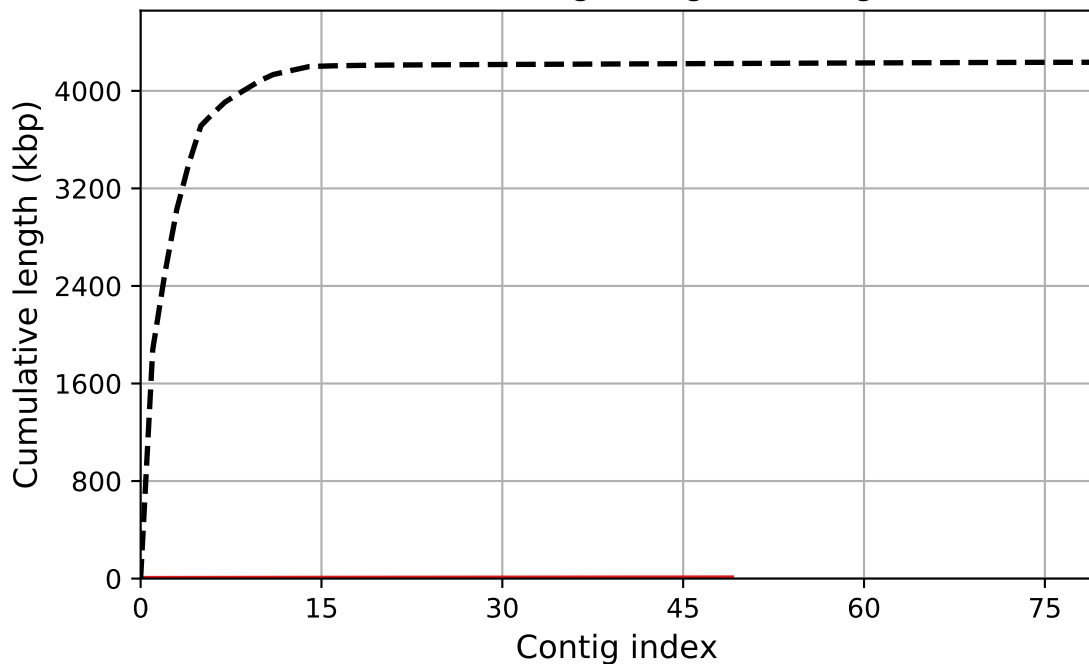
Misassemblies



FRCurve (misassemblies)

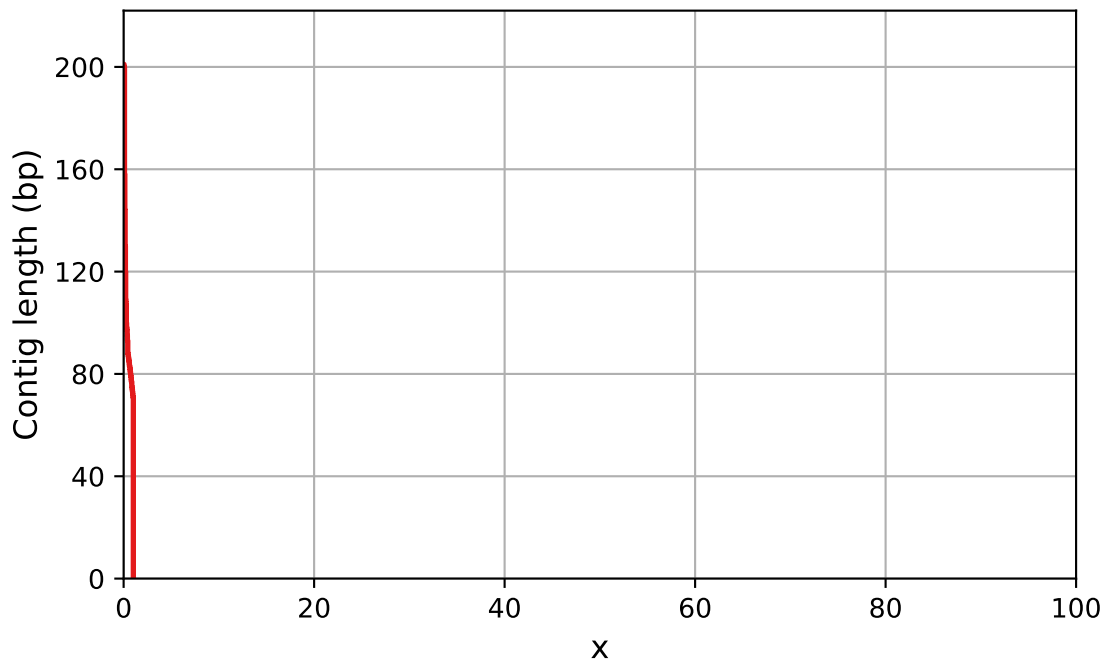


Cumulative length (aligned contigs)



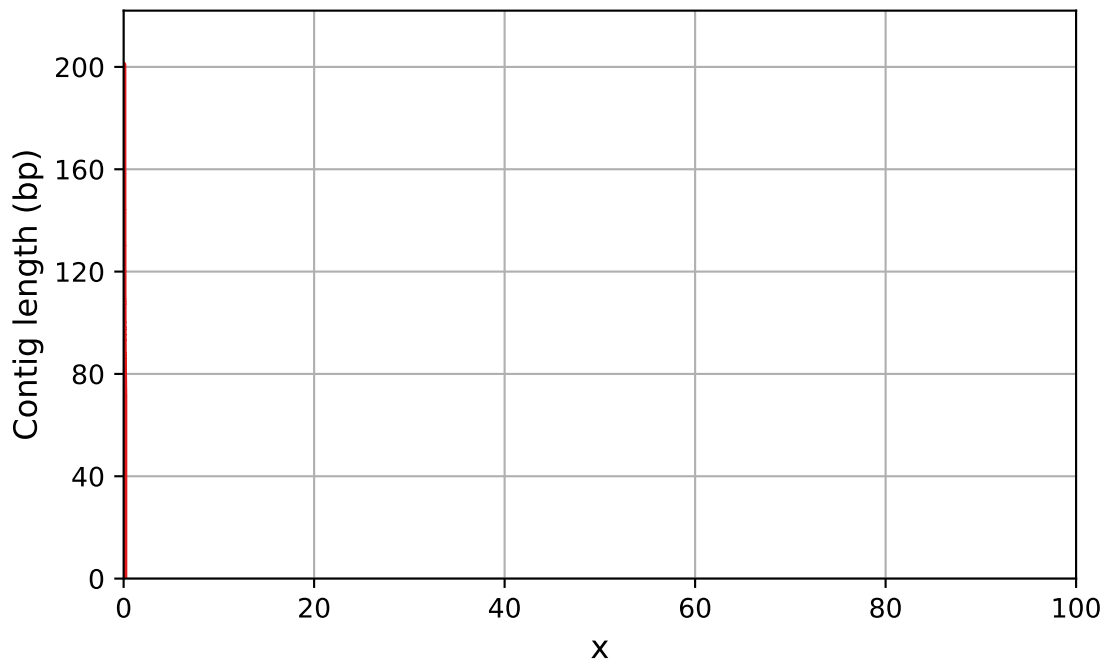
— TARA_PSW_RAW - - Reference

NAx



TARA_PSW_RAW

NGAx



TARA_PSW_RAW