

# Report

	TARA_PSW_RAW
# contigs (>= 0 bp)	1124813
# contigs (>= 1000 bp)	1124813
# contigs (>= 5000 bp)	57961
# contigs (>= 10000 bp)	16819
# contigs (>= 25000 bp)	3454
# contigs (>= 50000 bp)	1035
Total length (>= 0 bp)	2467968766
Total length (>= 1000 bp)	2467968766
Total length (>= 5000 bp)	654697028
Total length (>= 10000 bp)	378461969
Total length (>= 25000 bp)	185100868
Total length (>= 50000 bp)	103282434
# contigs	1124813
Largest contig	952125
Total length	2467968766
Reference length	5854900
N50	2277
N75	1402
L50	241839
L75	596698
# 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	4
# unaligned contigs	1124498 + 315 part
Unaligned length	2467942002
Genome fraction (%)	0.114
Duplication ratio	4.549
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9198.15
# indels per 100 kbp	44.80
Largest alignment	339
Total aligned length	26764

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

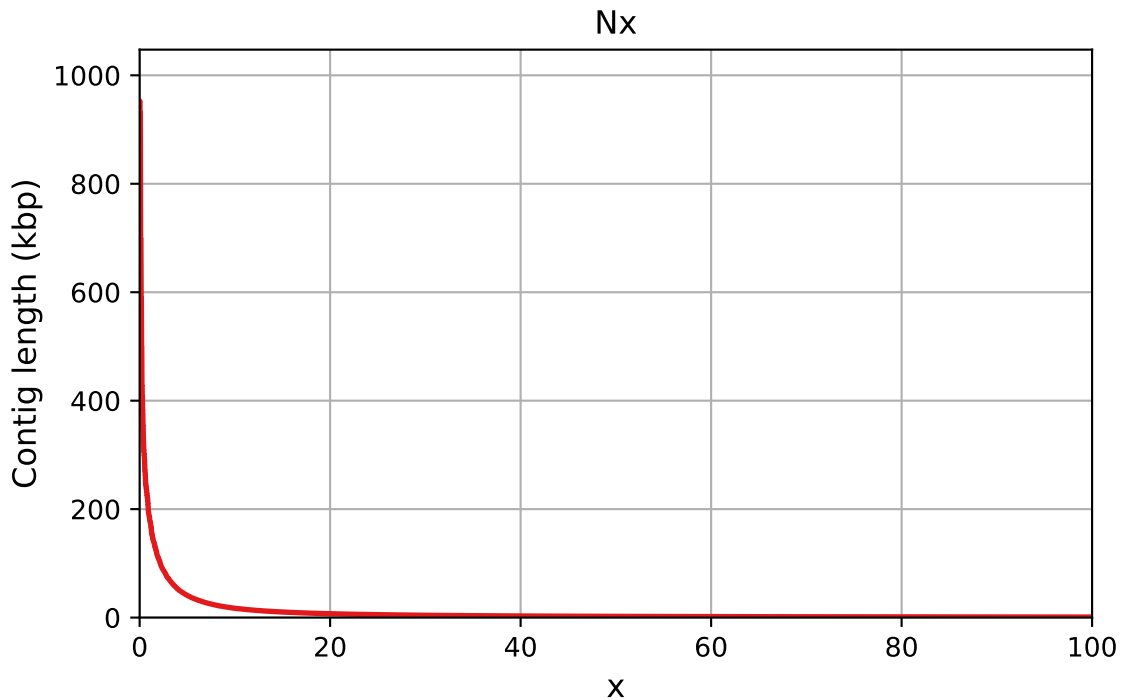
	TARA_PSW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	311
# possible misassemblies	385
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	616
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	4

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

## Unaligned report

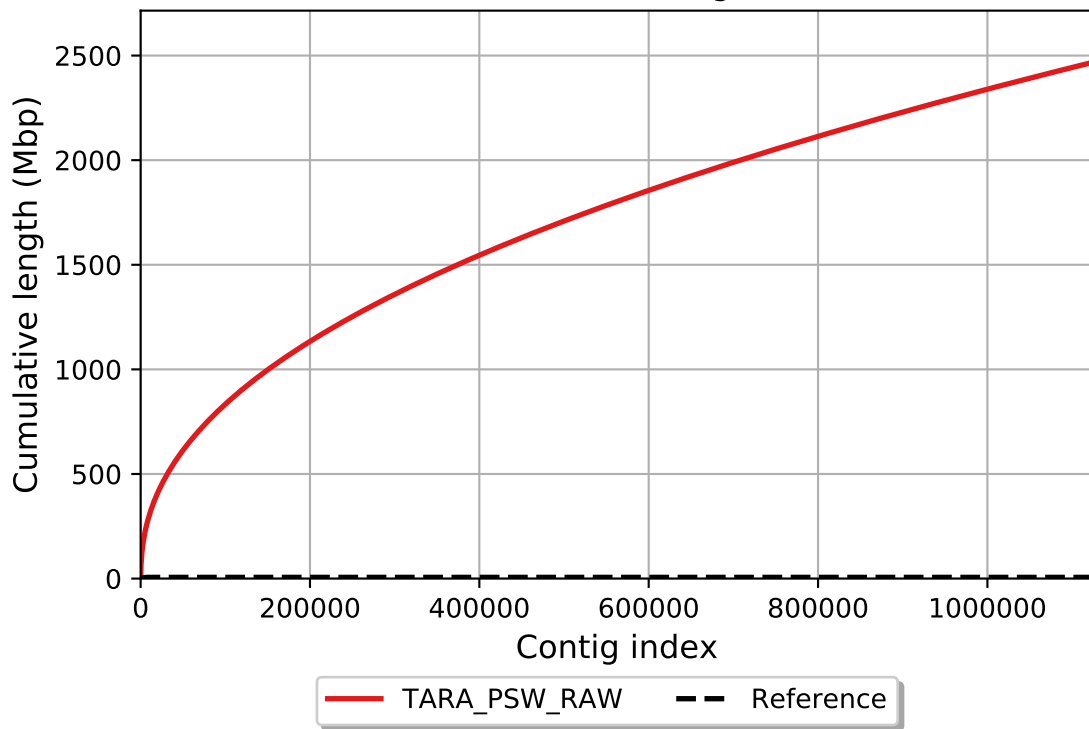
	TARA_PSW_RAW
# fully unaligned contigs	1124498
Fully unaligned length	2465477057
# partially unaligned contigs	315
Partially unaligned length	2464945
# N's	0

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

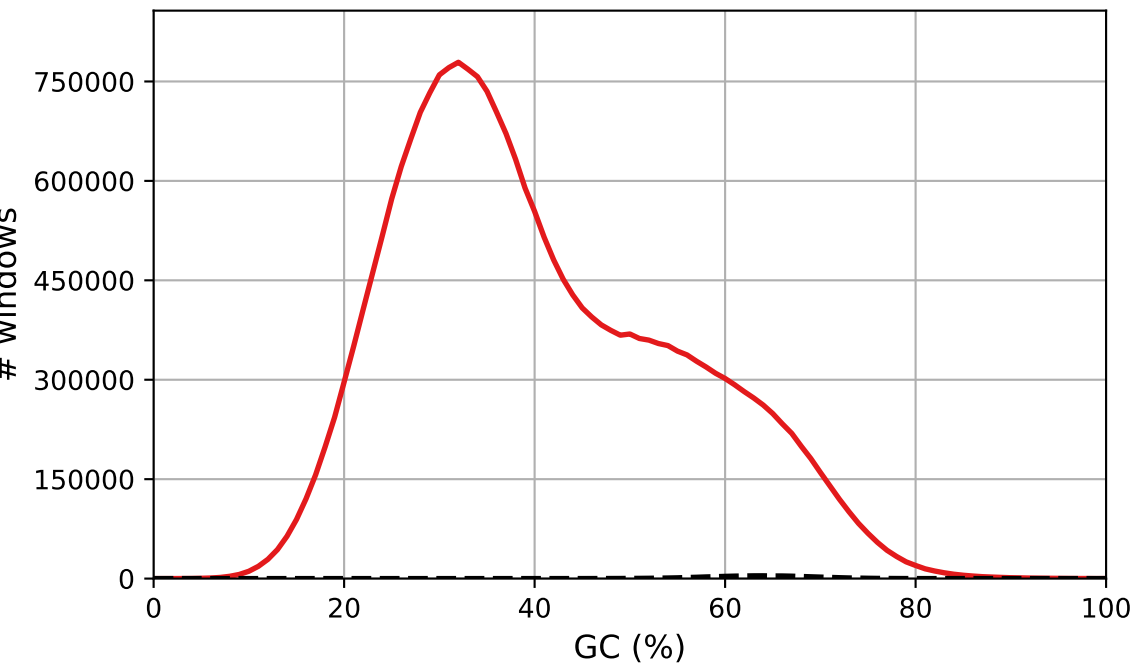


TARA\_PSW\_RAW

Cumulative length

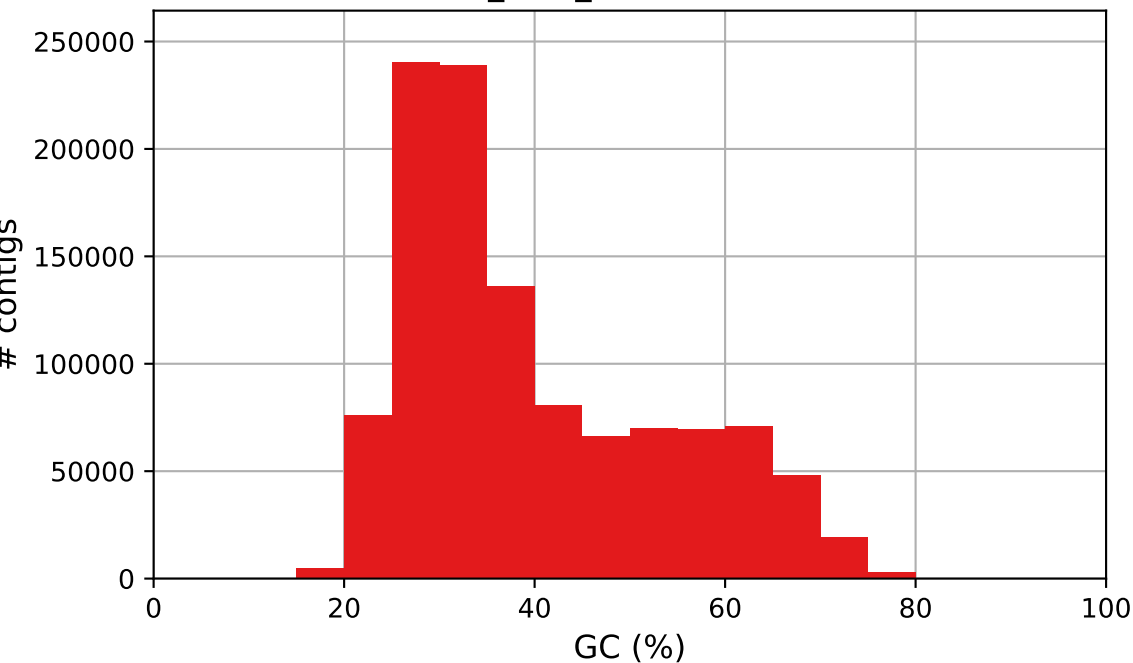


GC content



— TARA\_PSW\_RAW    - - Reference

TARA\_PSW\_RAW GC content



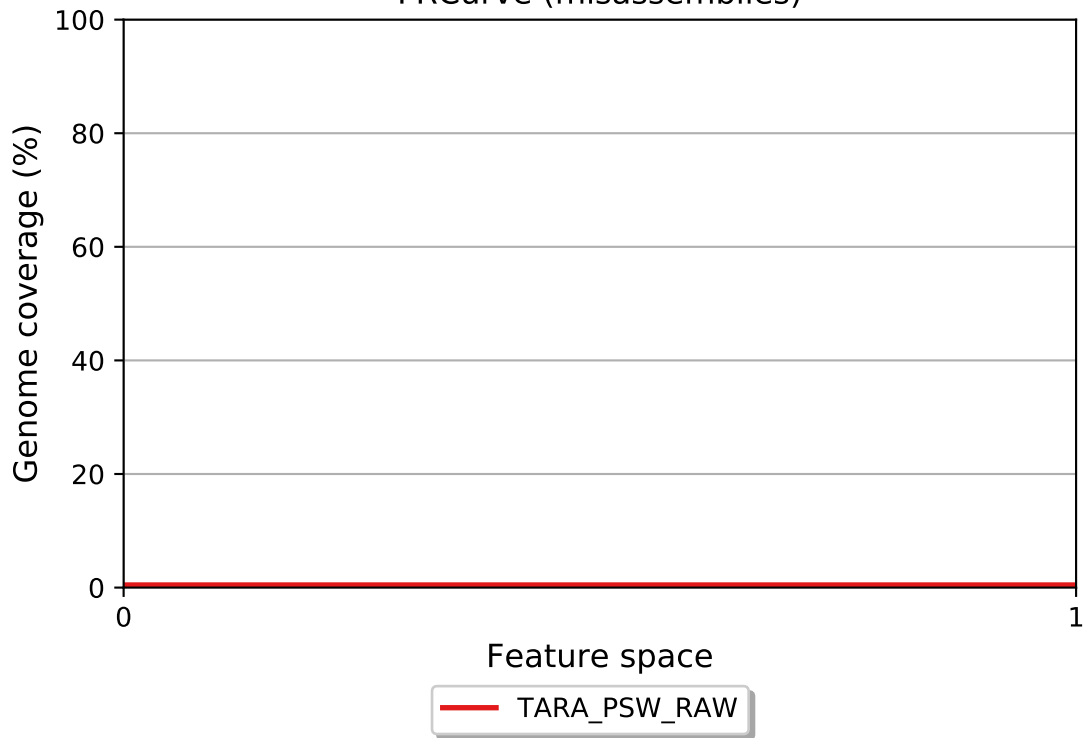
TARA\_PSW\_RAW

## Misassemblies

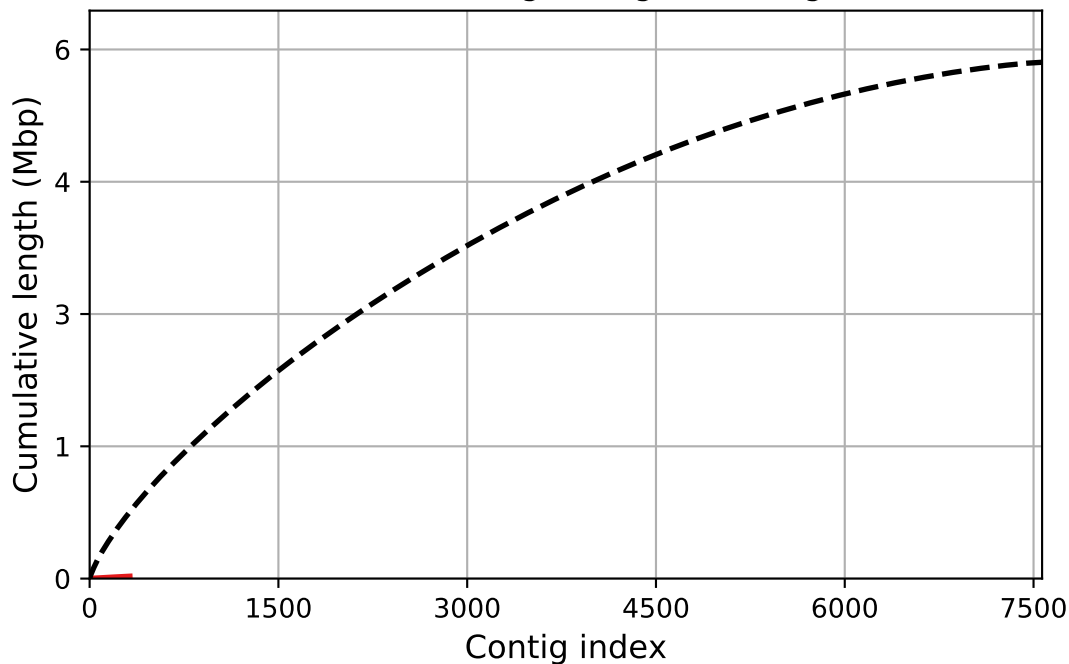




FRCurve (misassemblies)

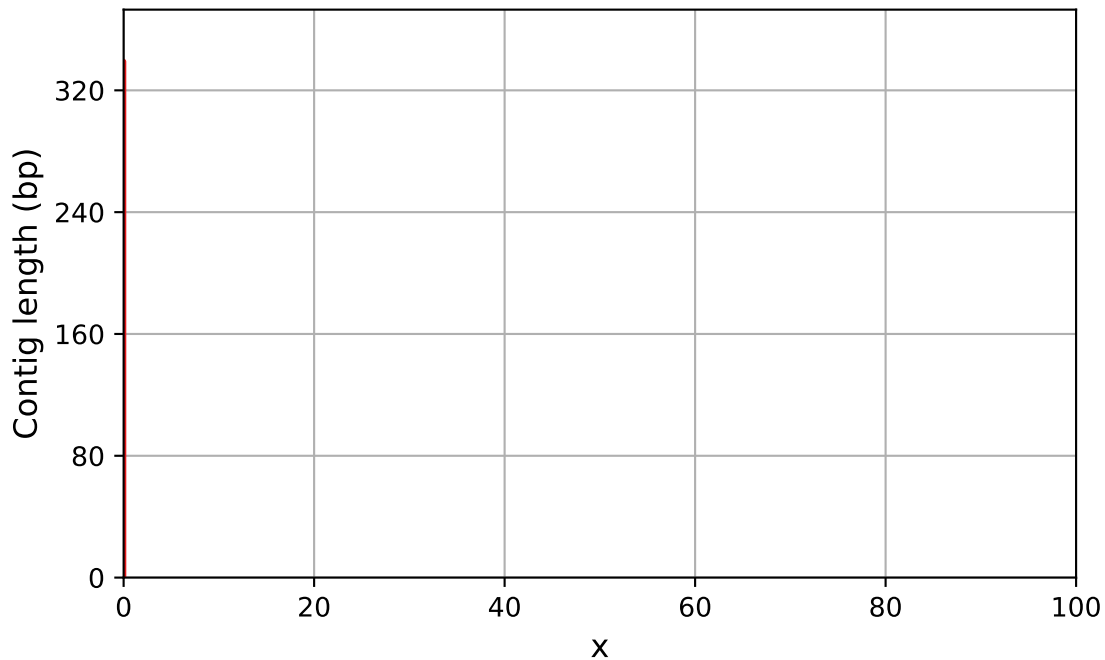


Cumulative length (aligned contigs)



— TARA\_PSW\_RAW    - - Reference

NAx



TARA\_PSW\_RAW