

# Report

	TARA_PSE_RAW
# contigs (>= 0 bp)	2722083
# contigs (>= 1000 bp)	2722083
# contigs (>= 5000 bp)	115024
# contigs (>= 10000 bp)	29181
# contigs (>= 25000 bp)	4698
# contigs (>= 50000 bp)	1070
Total length (>= 0 bp)	5521130017
Total length (>= 1000 bp)	5521130017
Total length (>= 5000 bp)	1142936782
Total length (>= 10000 bp)	569869199
Total length (>= 25000 bp)	218853608
Total length (>= 50000 bp)	98400475
# contigs	2722083
Largest contig	711776
Total length	5521130017
Reference length	5854900
N50	2040
N75	1350
L50	672715
L75	1521496
# 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	7
# unaligned contigs	2721247 + 834 part
Unaligned length	5521061061
Genome fraction (%)	0.154
Duplication ratio	8.724
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13524.27
# indels per 100 kbp	44.23
Largest alignment	370
Total aligned length	67074

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

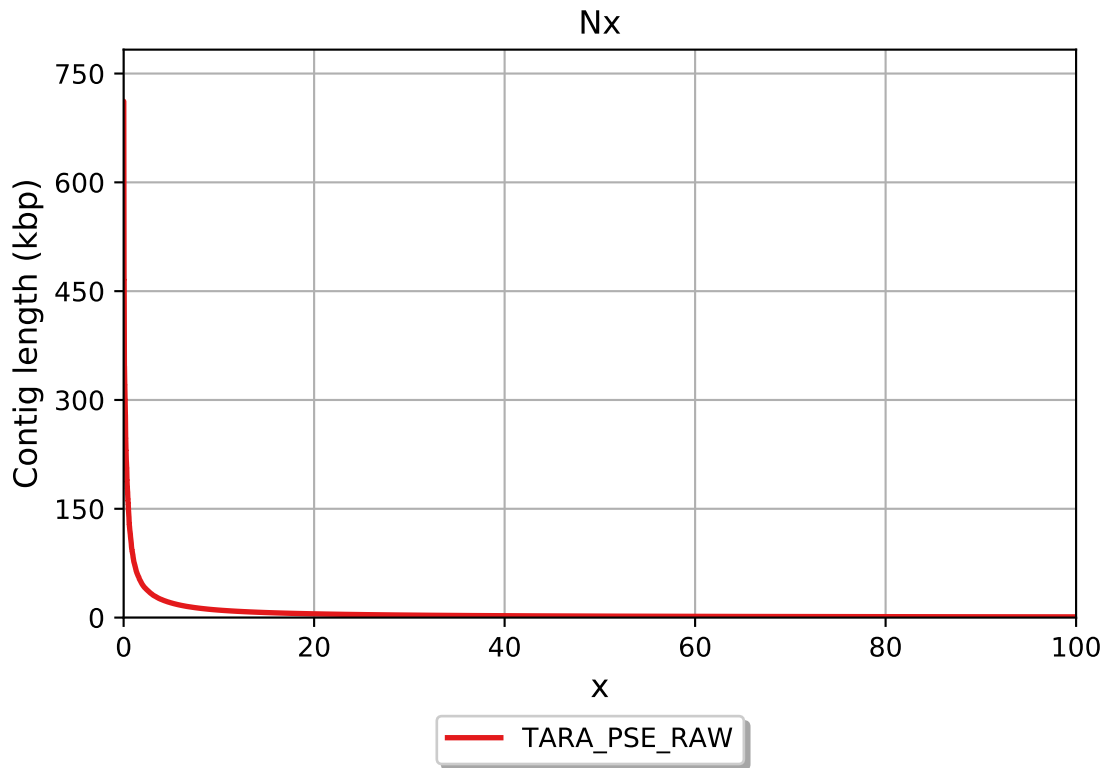
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	828
# possible misassemblies	1033
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	1223
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

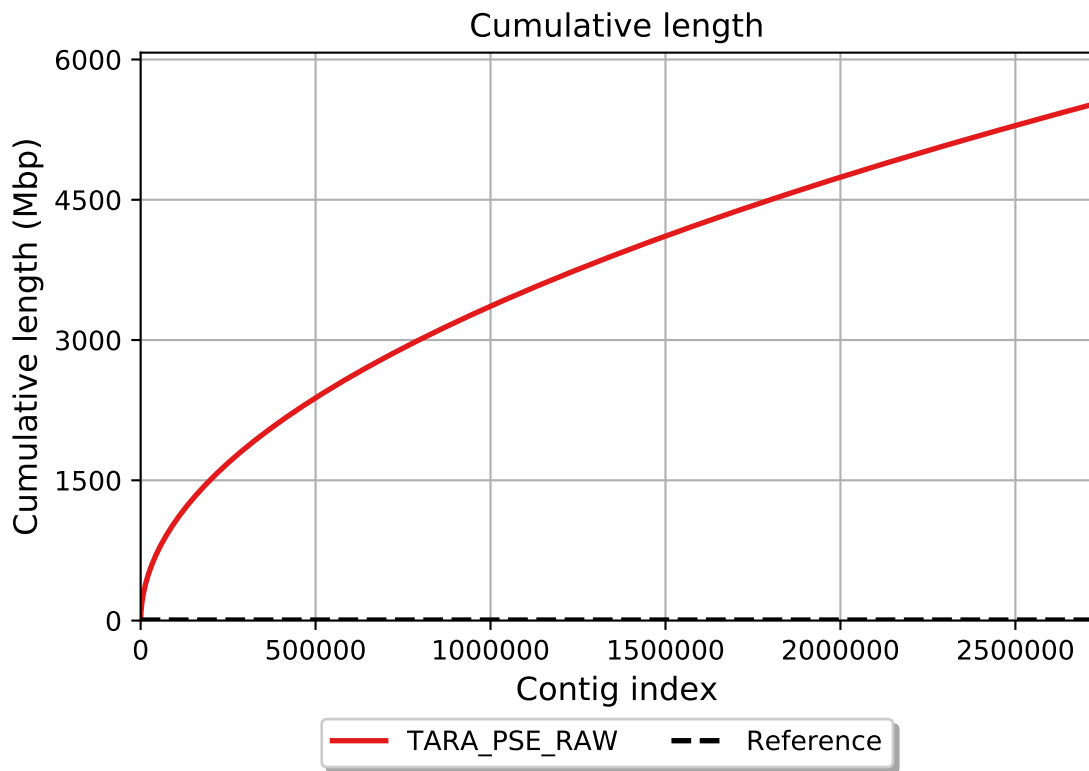
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

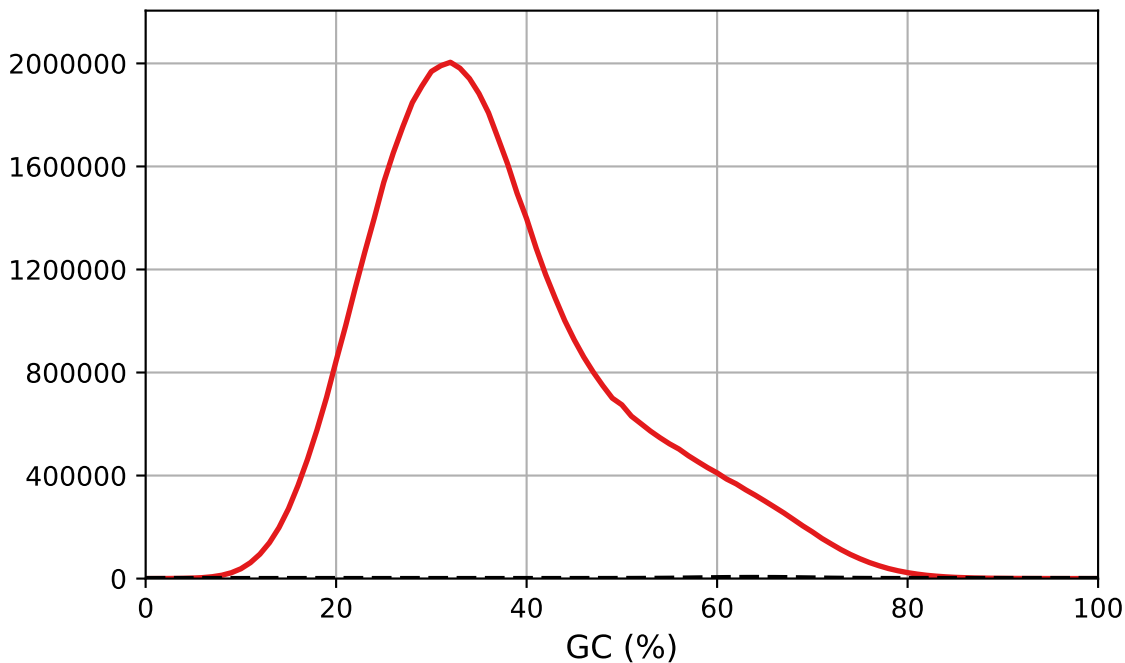
	TARA_PSE_RAW
# fully unaligned contigs	2721247
Fully unaligned length	5515196474
# partially unaligned contigs	834
Partially unaligned length	5864587
# N's	0

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).



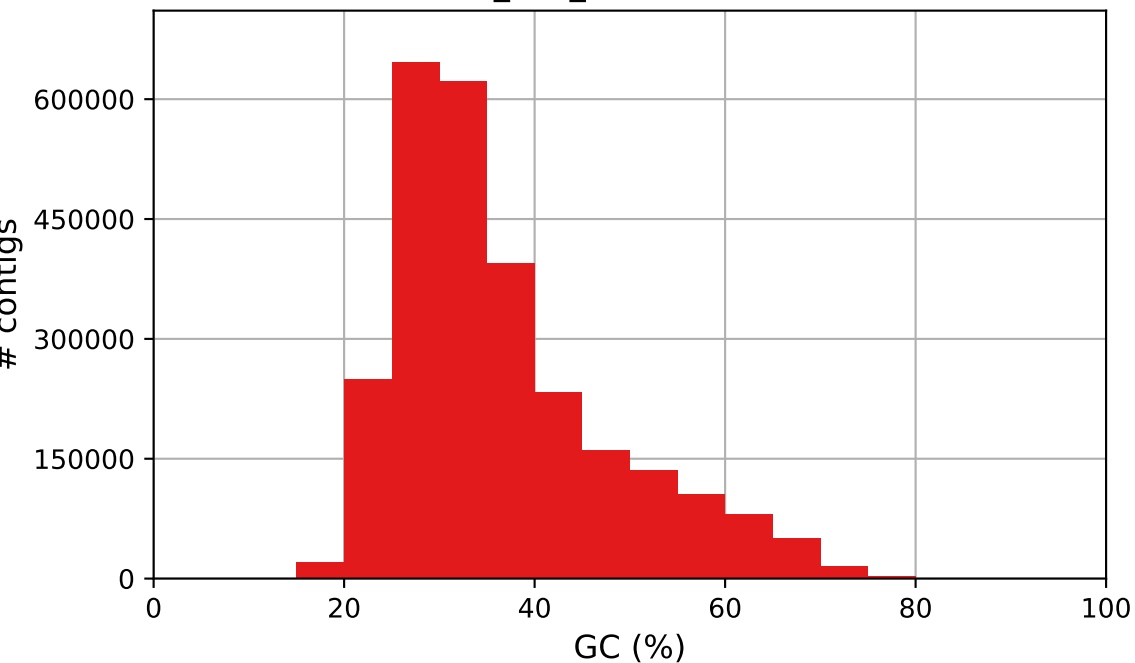


## GC content



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TARA\_PSE\_RAW GC content



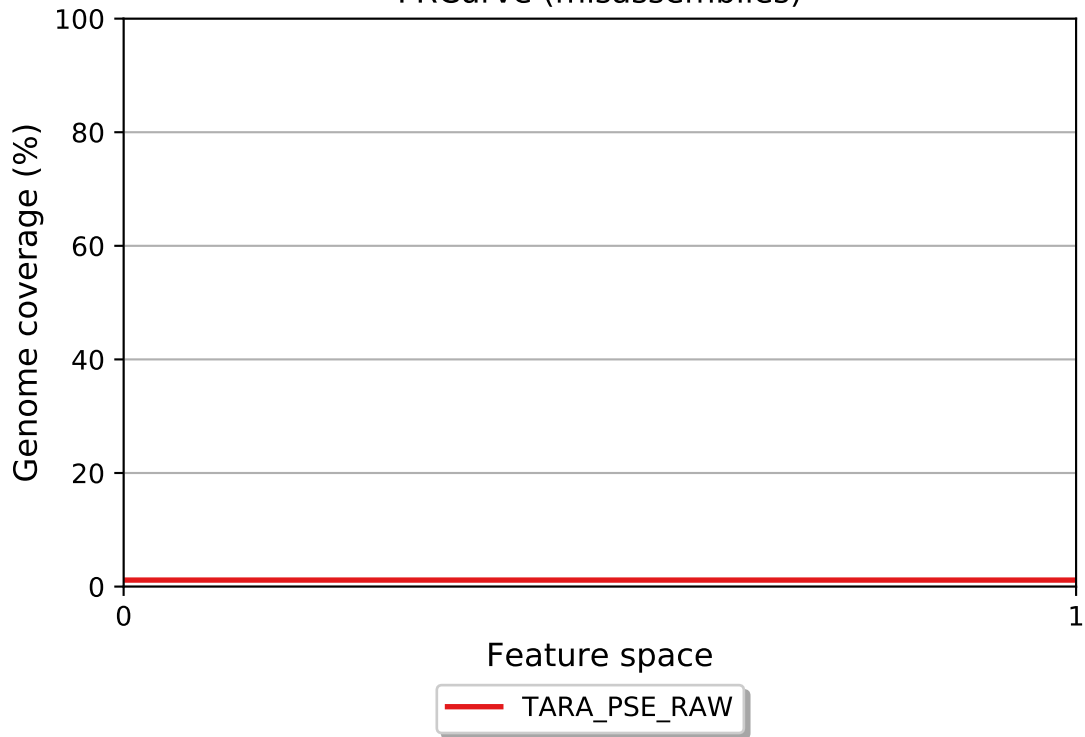
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## Misassemblies

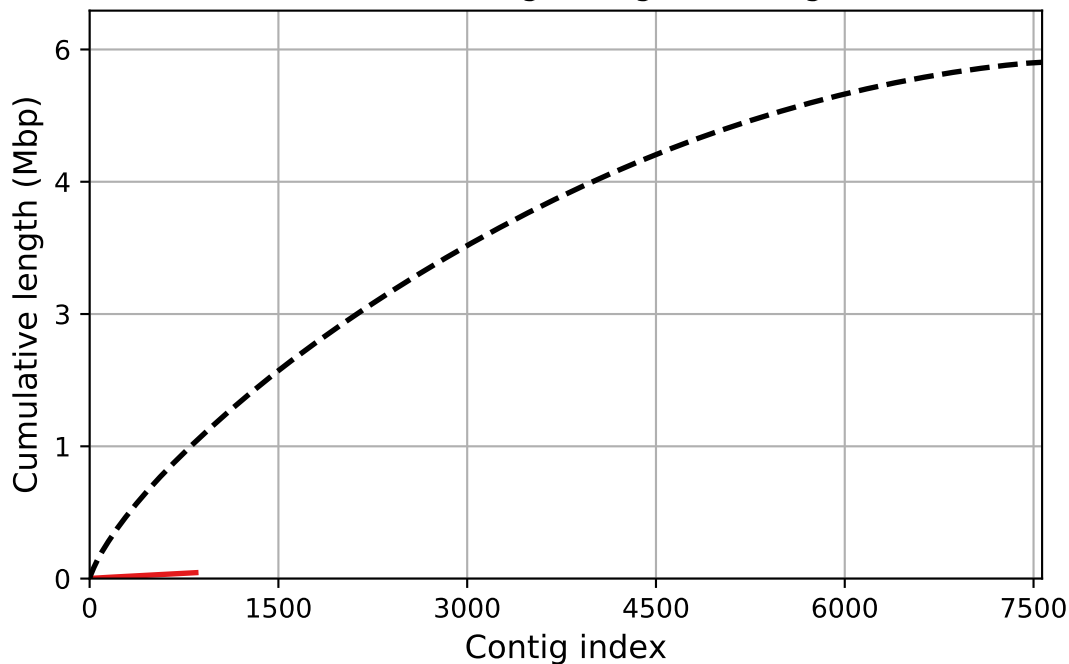




FRCurve (misassemblies)

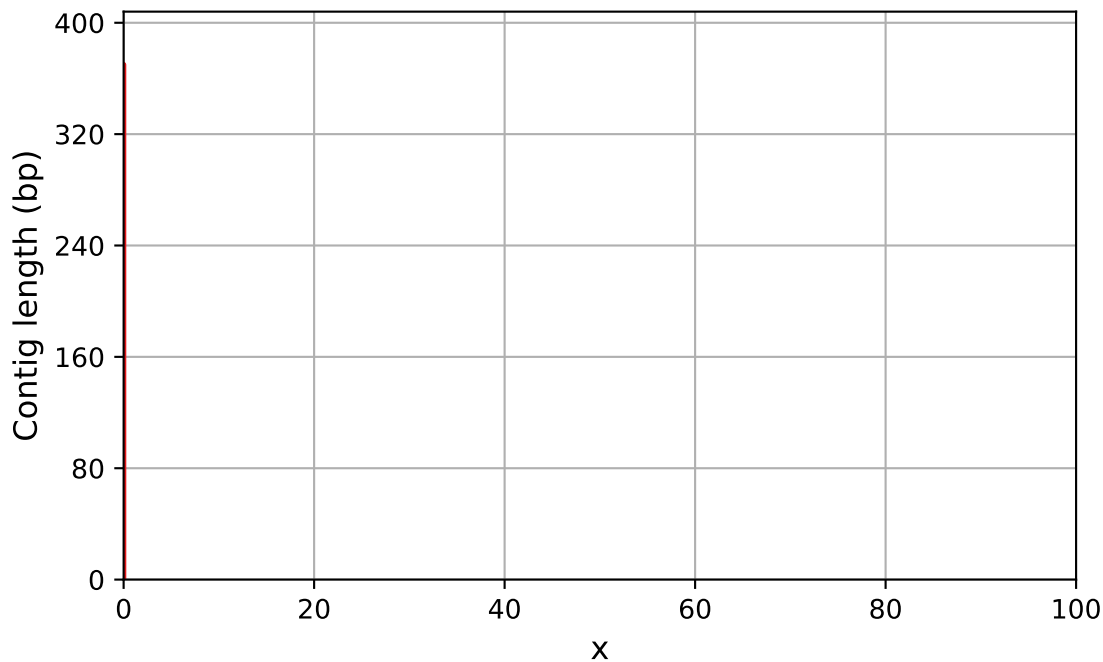


Cumulative length (aligned contigs)



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NAx



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