

# Report

	TARA_ASE_RAW
# contigs (>= 0 bp)	766472
# contigs (>= 1000 bp)	766472
# contigs (>= 5000 bp)	23509
# contigs (>= 10000 bp)	5257
# contigs (>= 25000 bp)	699
# contigs (>= 50000 bp)	146
Total length (>= 0 bp)	1430179911
Total length (>= 1000 bp)	1430179911
Total length (>= 5000 bp)	214871738
Total length (>= 10000 bp)	94359835
Total length (>= 25000 bp)	29656132
Total length (>= 50000 bp)	11639915
# contigs	766472
Largest contig	387648
Total length	1430179911
Reference length	3561038
N50	1830
N75	1291
L50	212842
L75	449143
# 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	766435 + 37 part
Unaligned length	1430176629
Genome fraction (%)	0.019
Duplication ratio	4.965
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13615.73
# indels per 100 kbp	0.00
Largest alignment	154
Total aligned length	3282

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

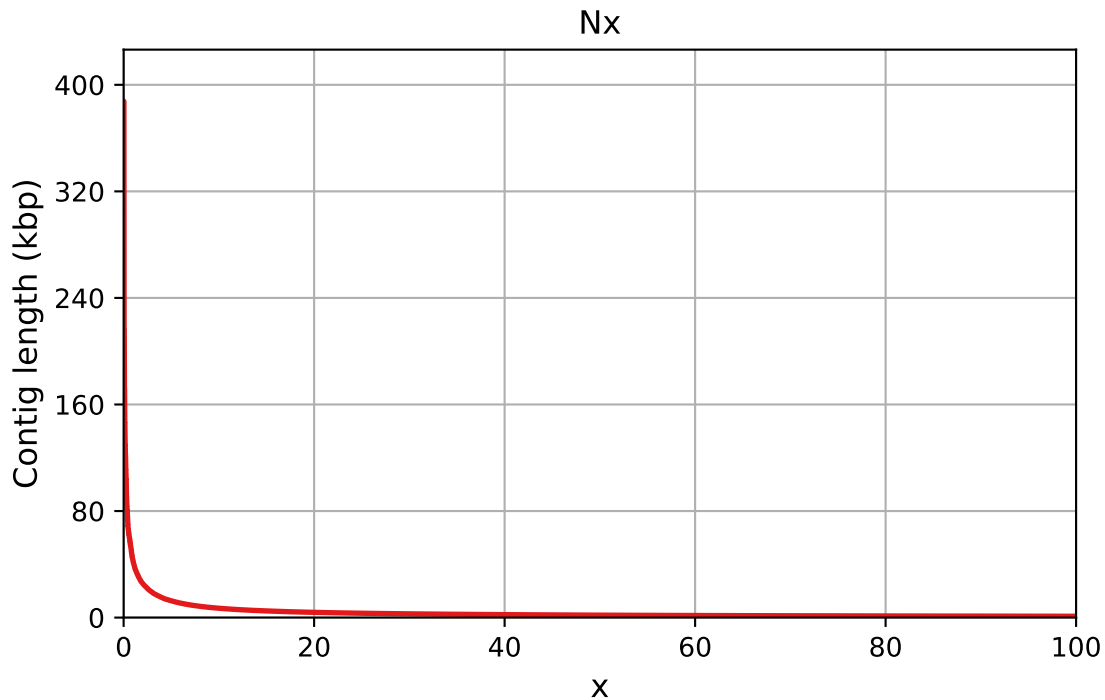
	TARA_ASE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	36
# possible misassemblies	39
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	90
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

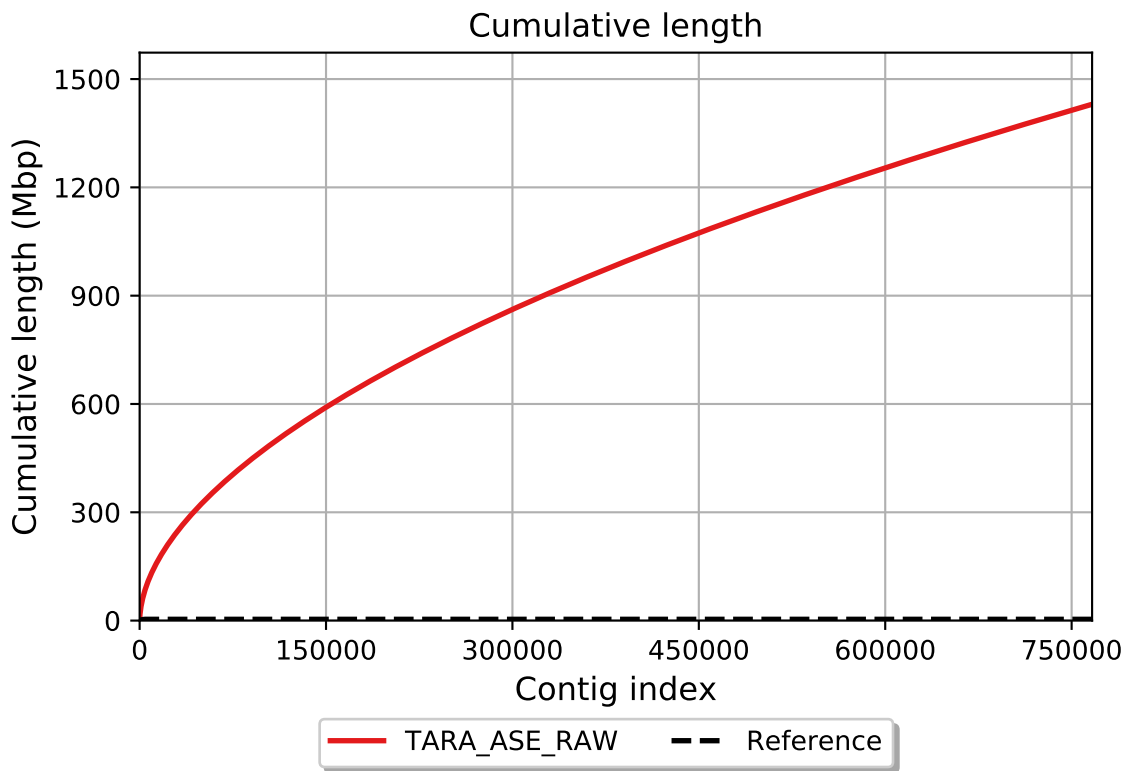
## Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	766435
Fully unaligned length	1430097889
# partially unaligned contigs	37
Partially unaligned length	78740
# 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).

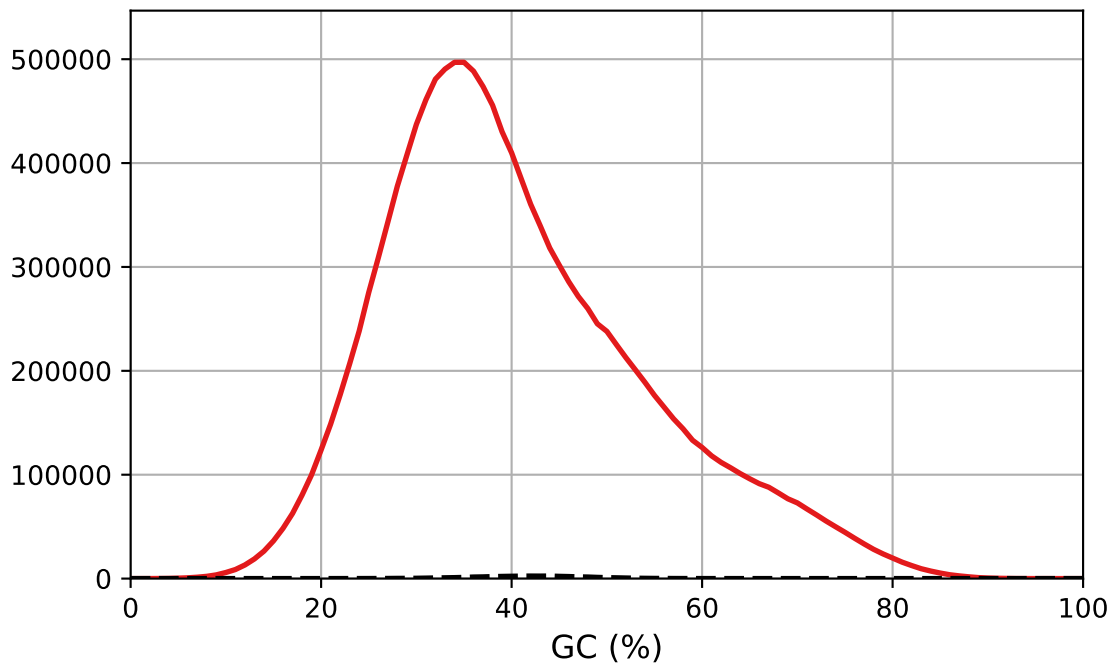


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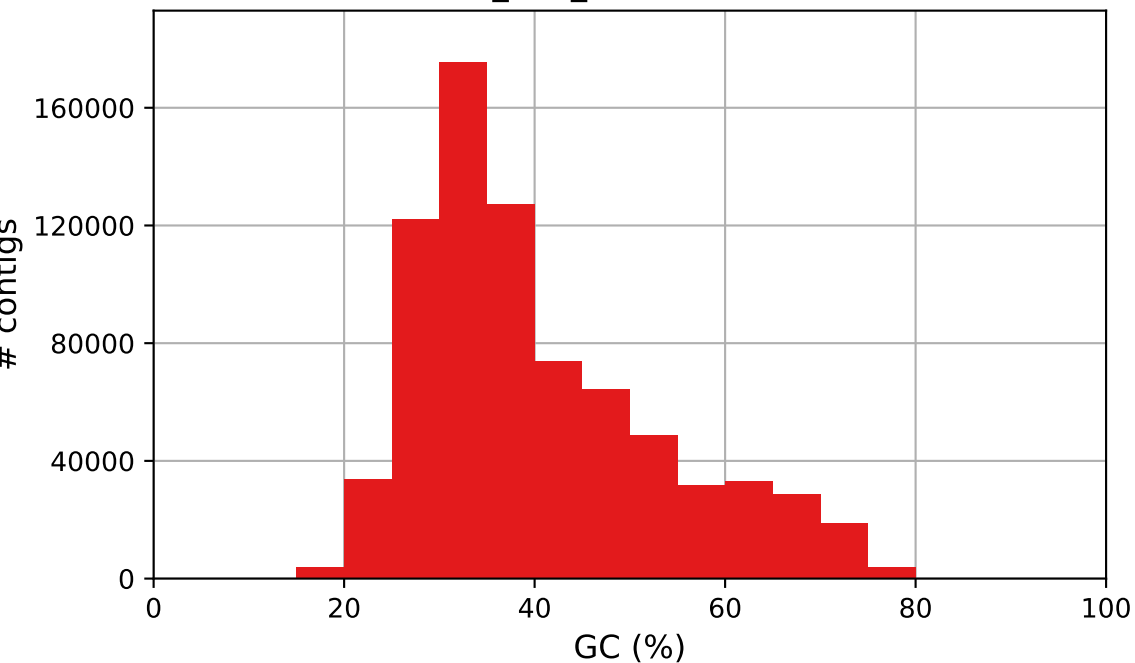
# GC content

# windows



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TARA\_ASE\_RAW GC content



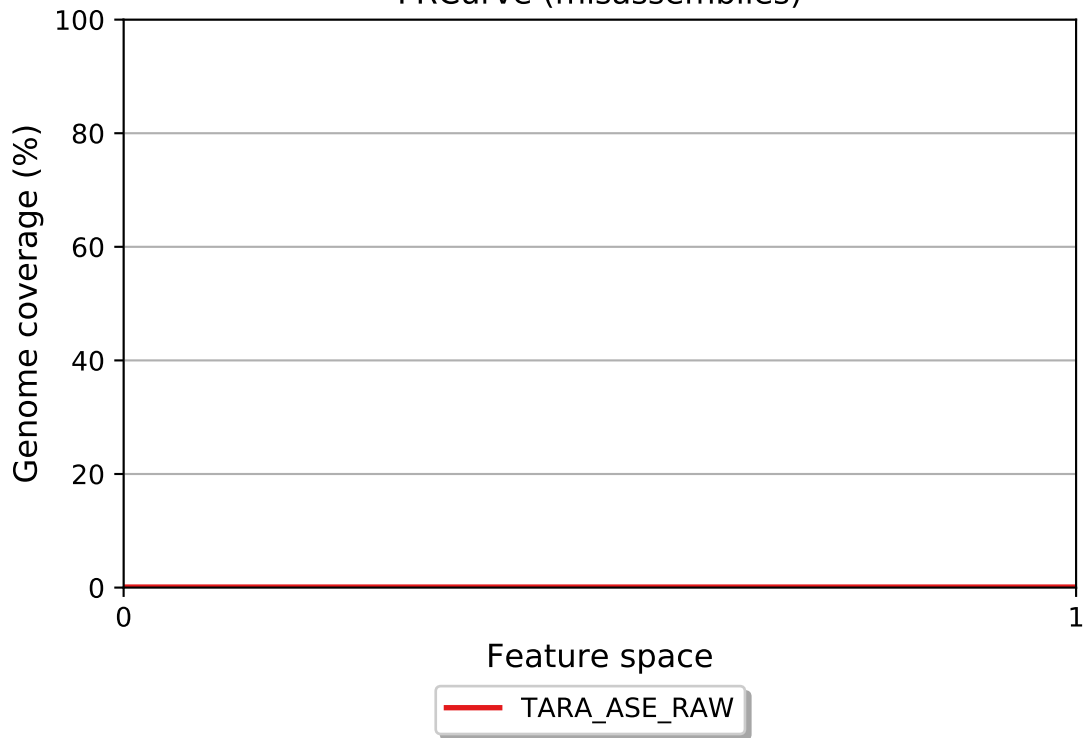
TARA\_ASE\_RAW

## Misassemblies

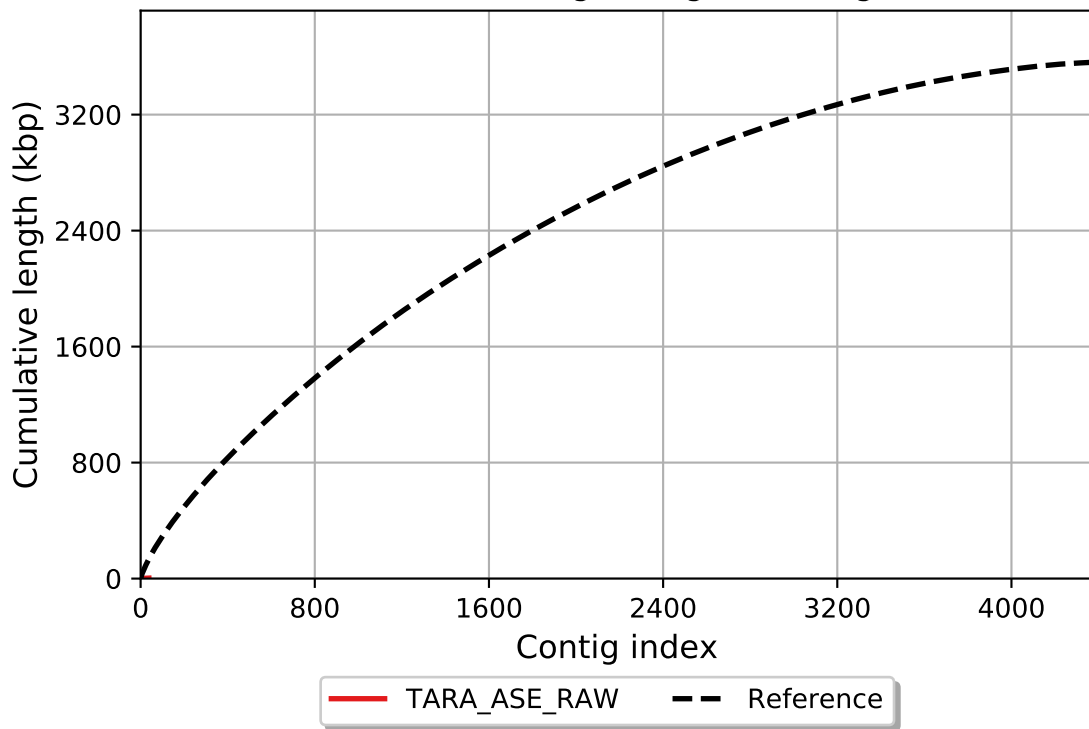




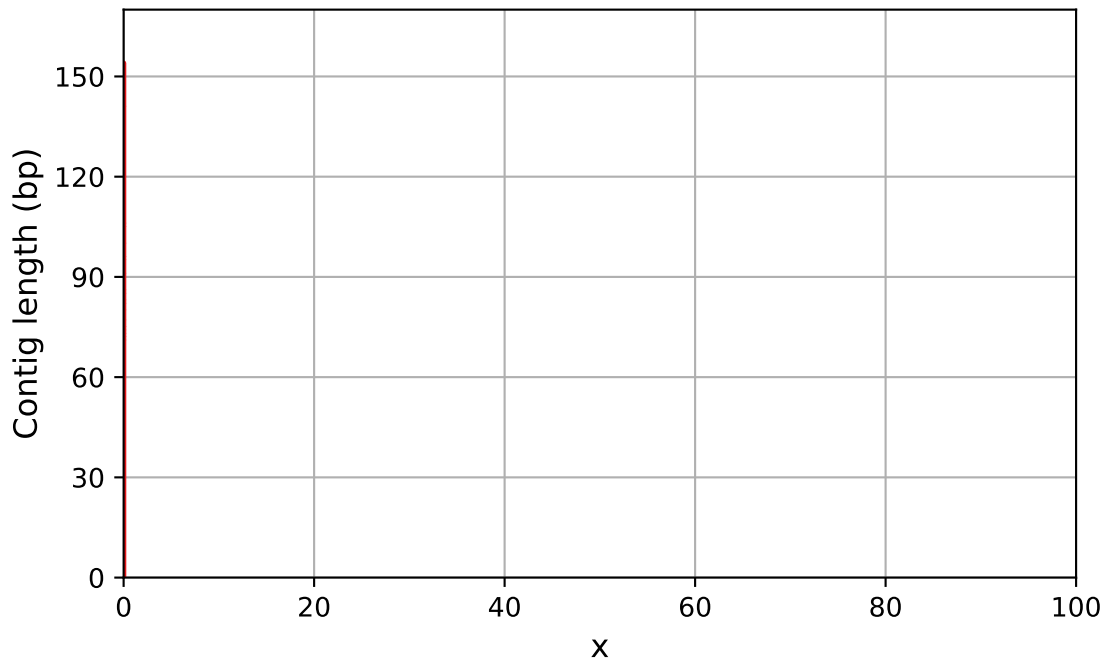
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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