

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	4234461
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	3
# unaligned contigs	2722032 + 51 part
Unaligned length	5521124920
Genome fraction (%)	0.028
Duplication ratio	4.345
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13725.49
# indels per 100 kbp	85.25
Largest alignment	200
Total aligned length	5097

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

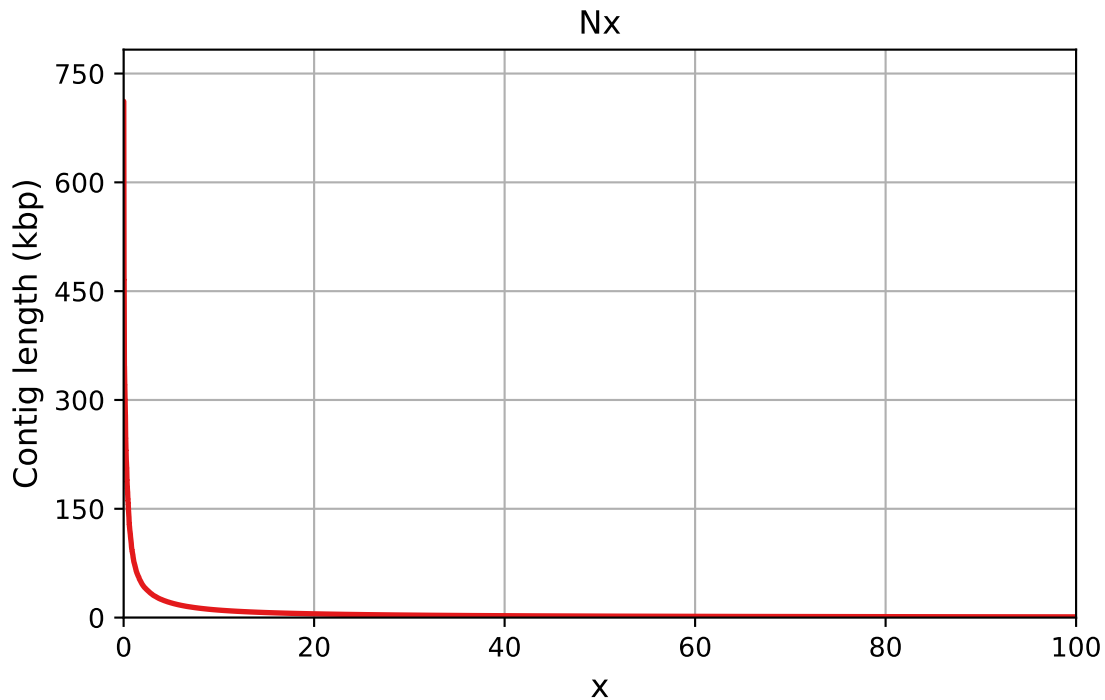
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	48
# possible misassemblies	57
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	161
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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).

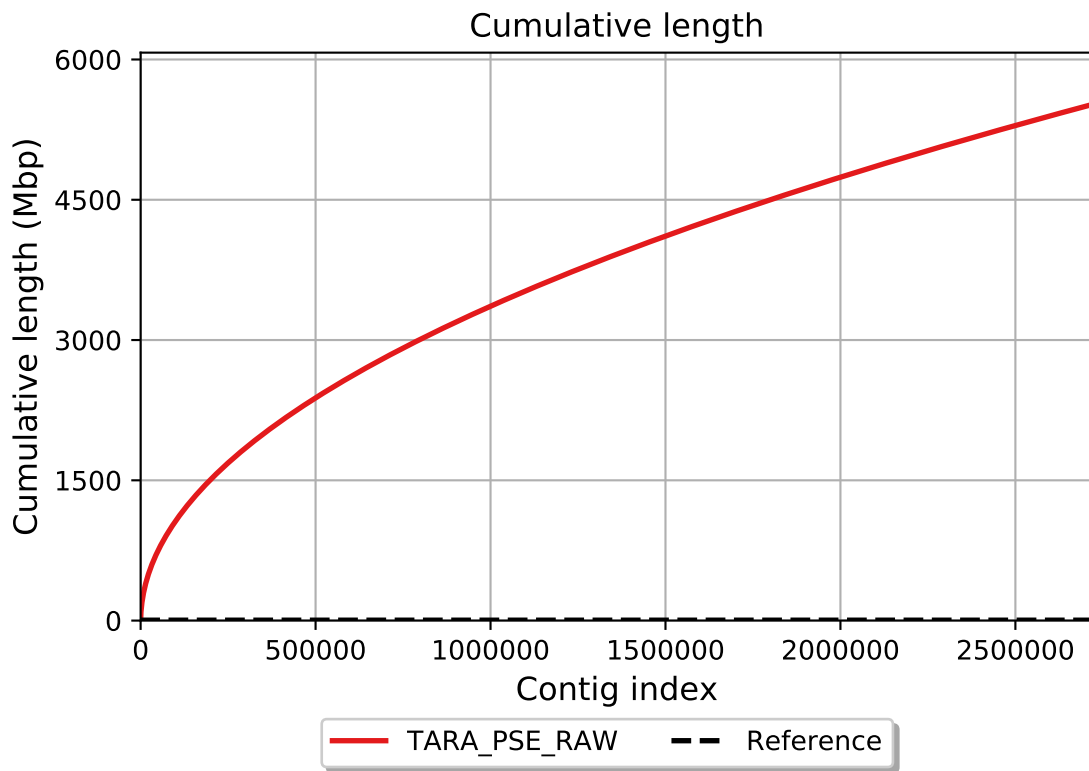
Unaligned report

	TARA_PSE_RAW
# fully unaligned contigs	2722032
Fully unaligned length	5520916900
# partially unaligned contigs	51
Partially unaligned length	208020
# N's	0

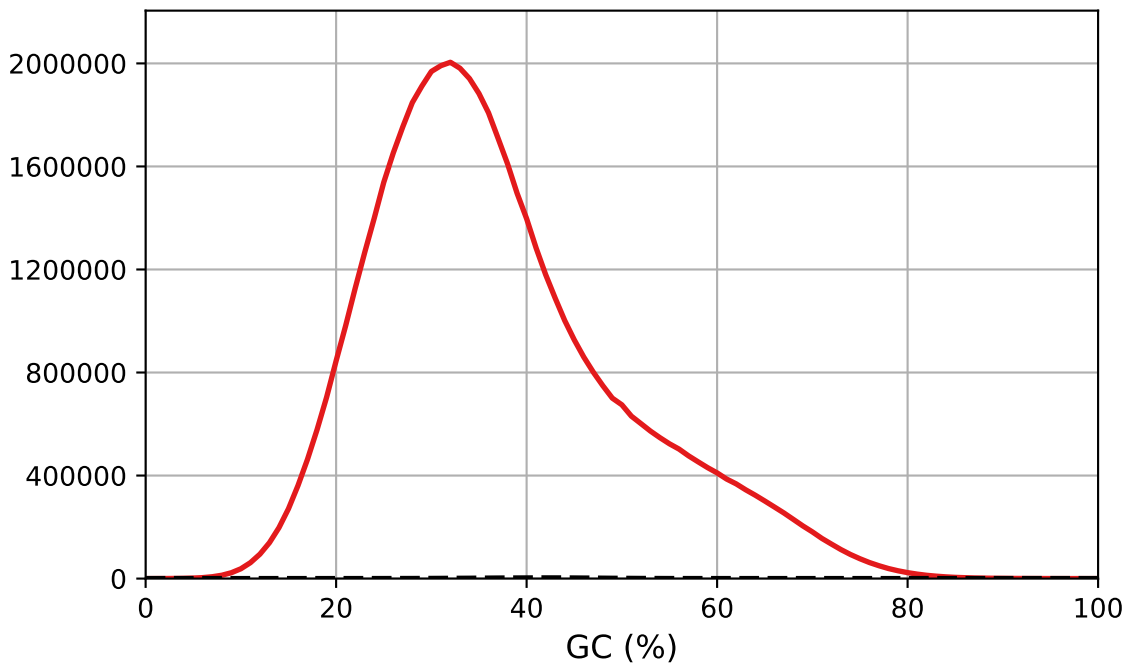
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



TARA_PSE_RAW

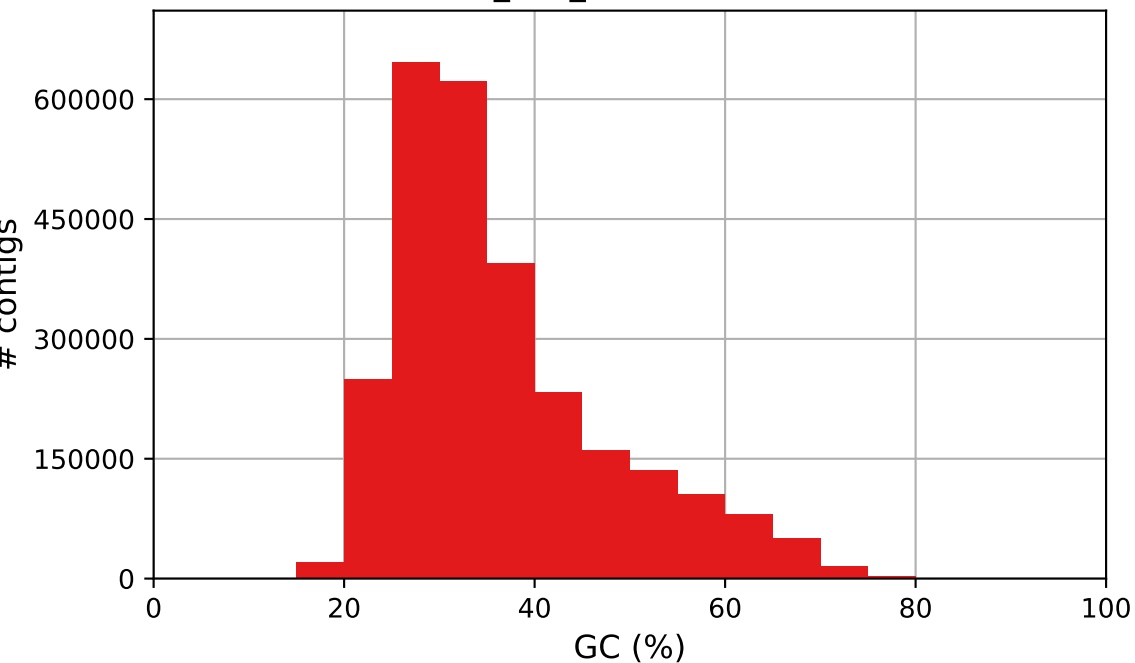


GC content



— TARA_PSE_RAW - - Reference

TARA_PSE_RAW GC content

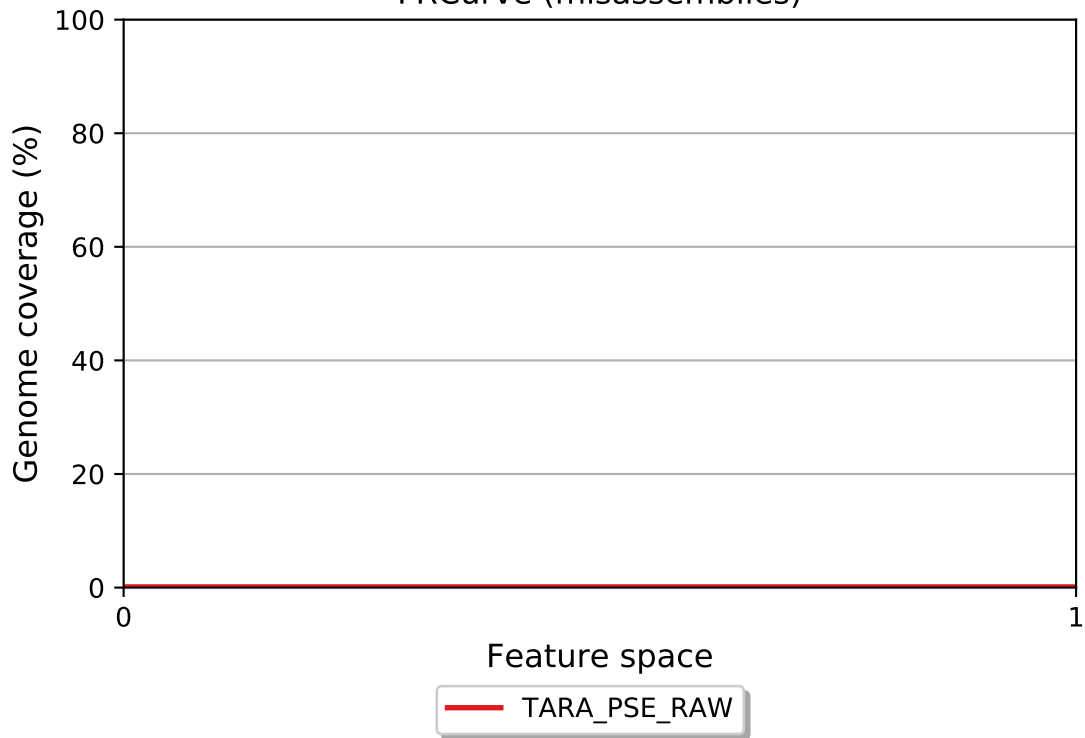


TARA_PSE_RAW

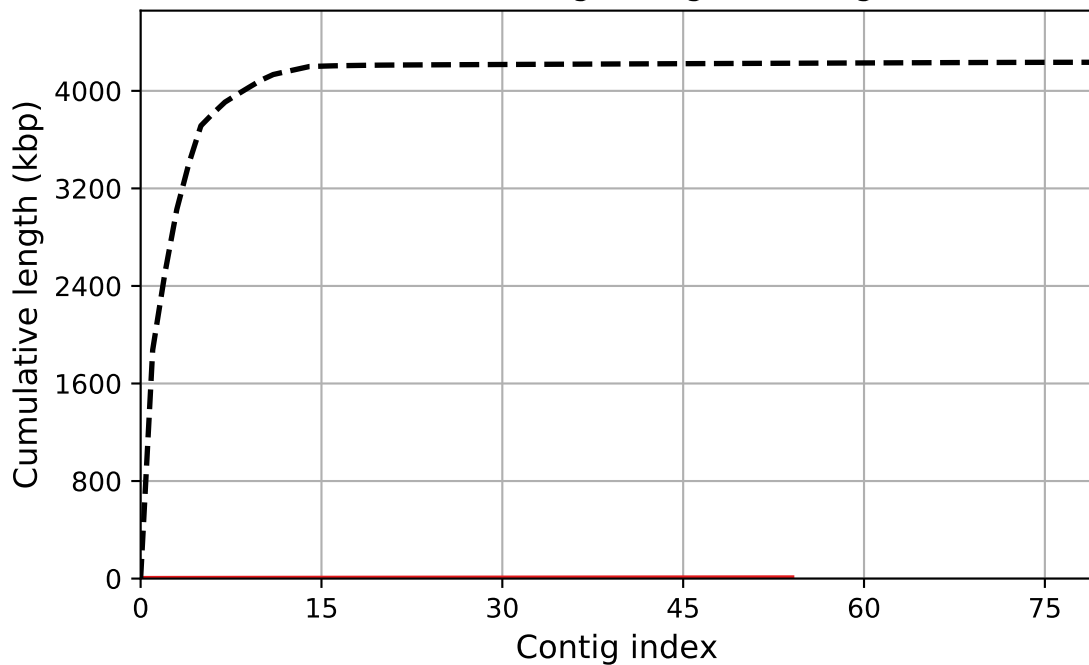
Misassemblies



FRCurve (misassemblies)

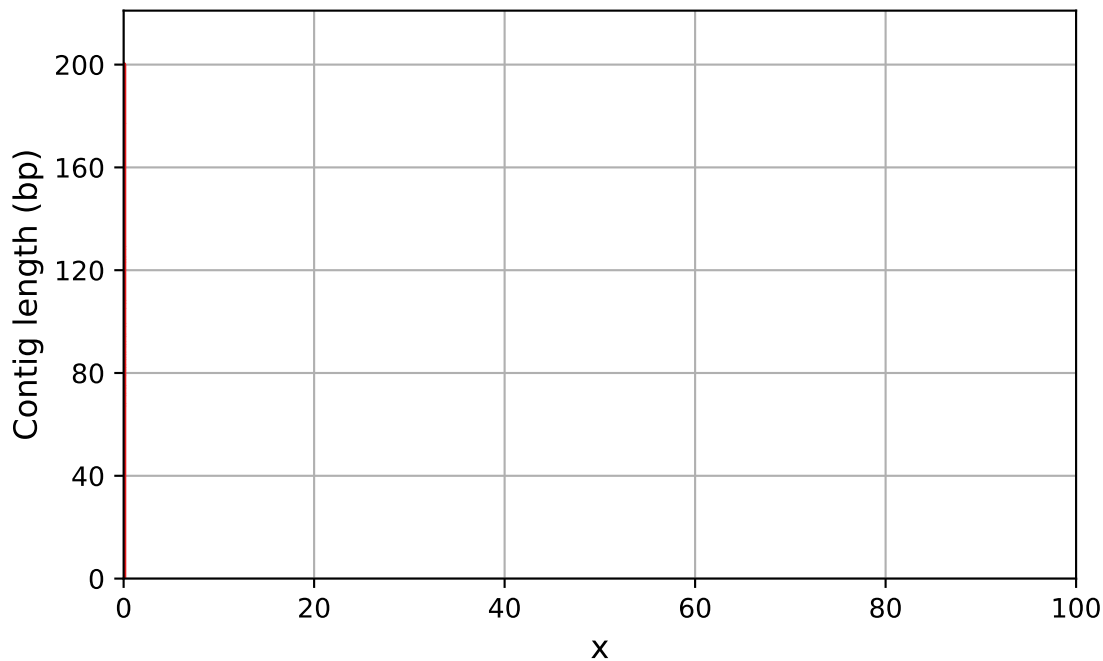


Cumulative length (aligned contigs)



— TARA_PSE_RAW - - Reference

NAx



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