

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	4234461
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	4
# unaligned contigs	766433 + 39 part
Unaligned length	1430176102
Genome fraction (%)	0.024
Duplication ratio	3.814
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10893.03
# indels per 100 kbp	98.14
Largest alignment	180
Total aligned length	3809

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

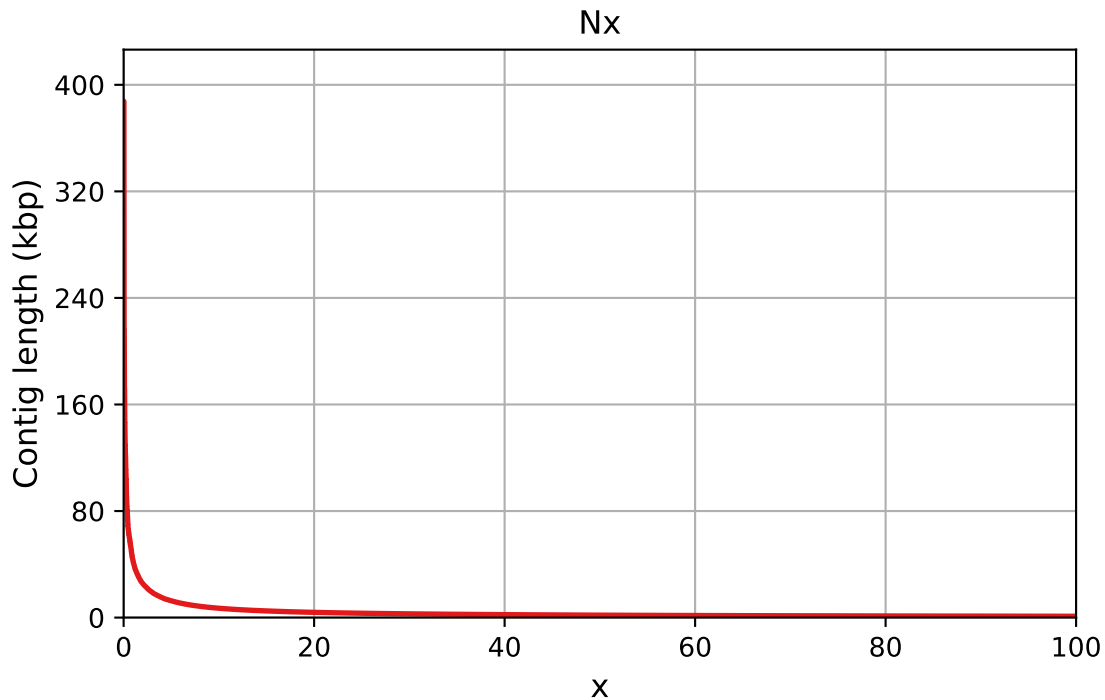
	TARA_ASE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	35
# possible misassemblies	38
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	111
# 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).

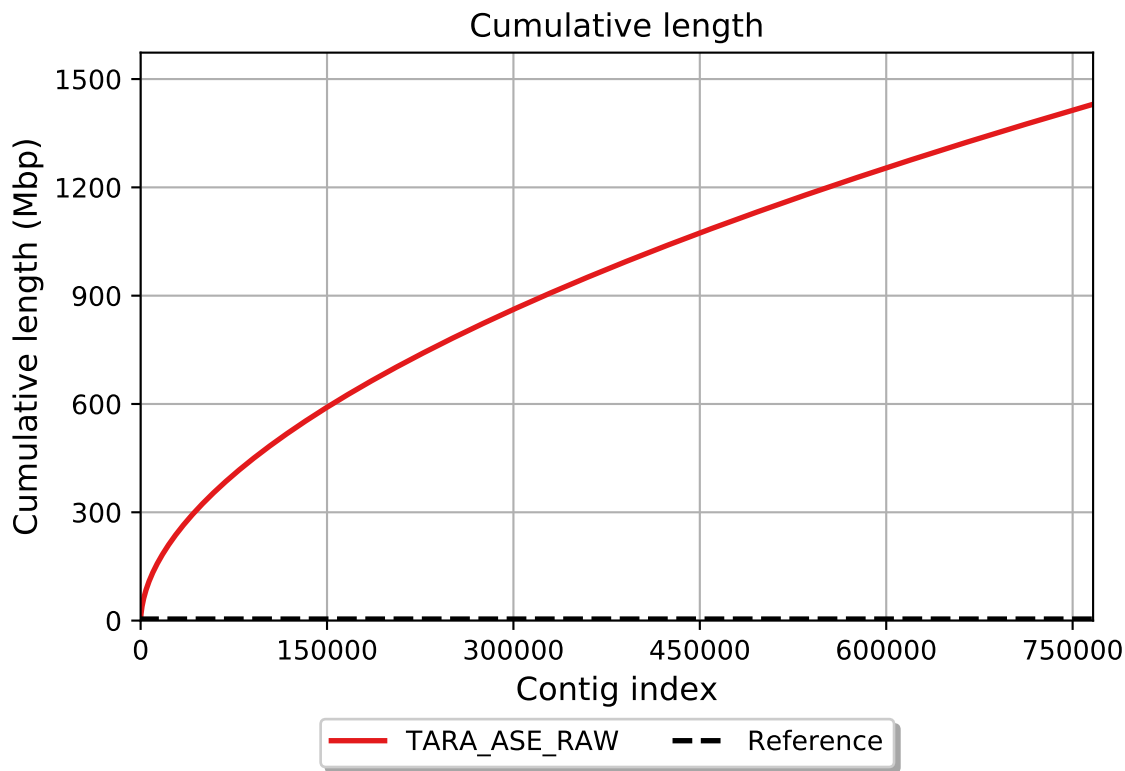
Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	766433
Fully unaligned length	1430095224
# partially unaligned contigs	39
Partially unaligned length	80878
# N's	0

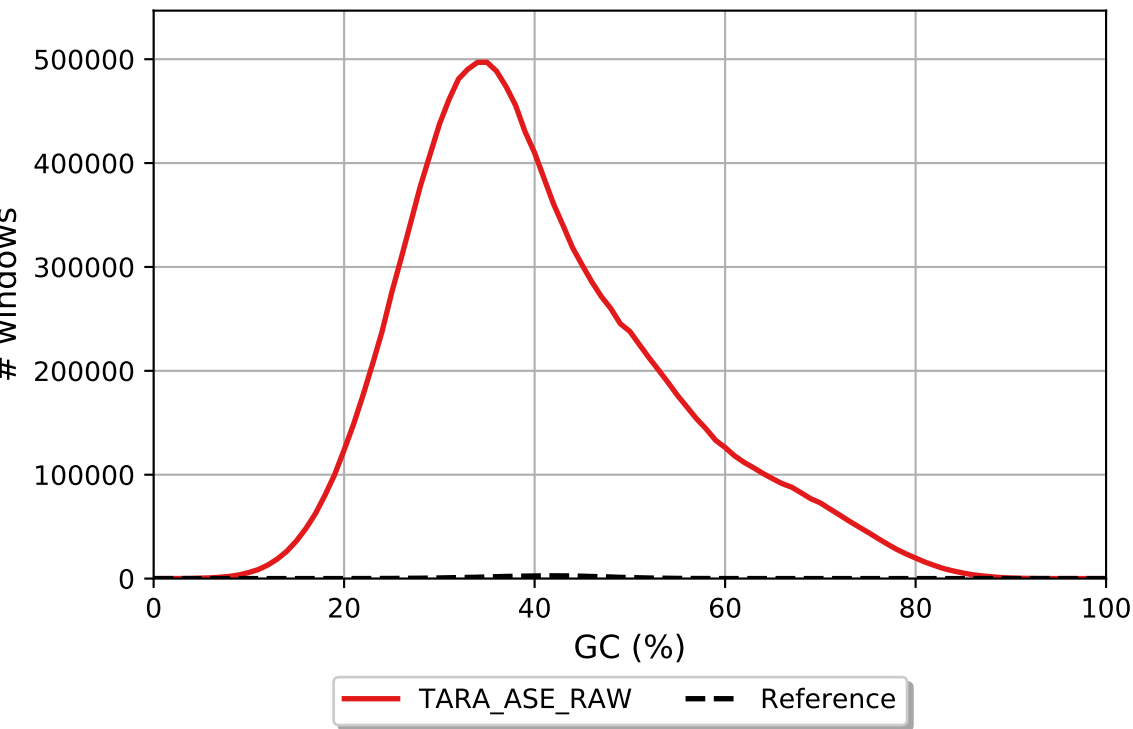
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



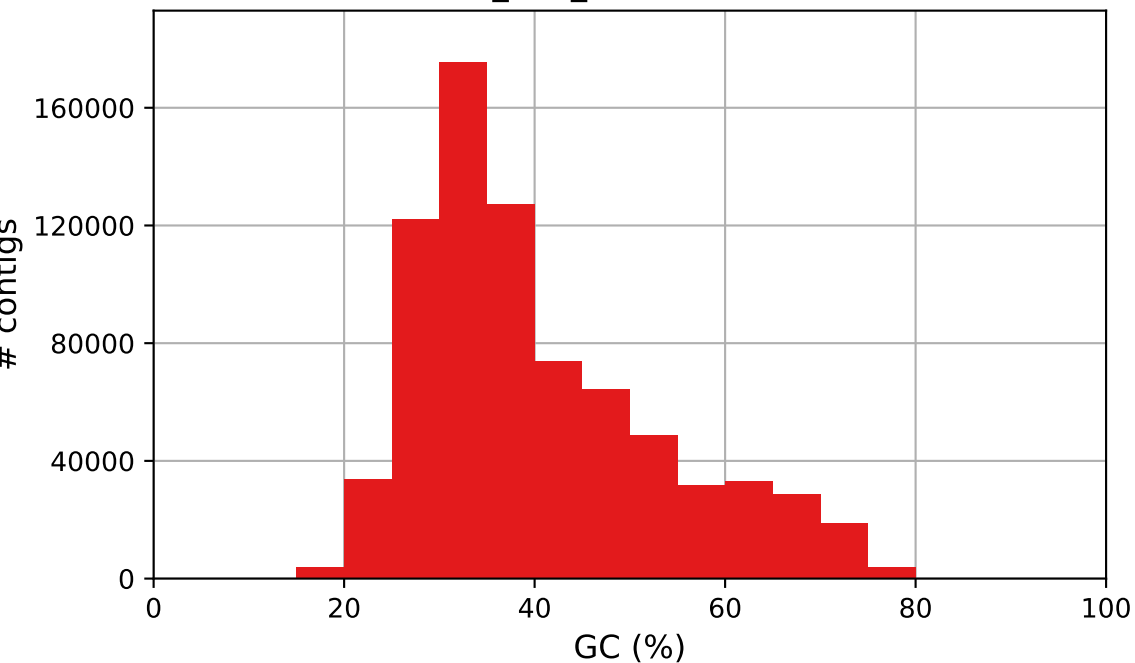
TARA_ASE_RAW



GC content



TARA_ASE_RAW GC content

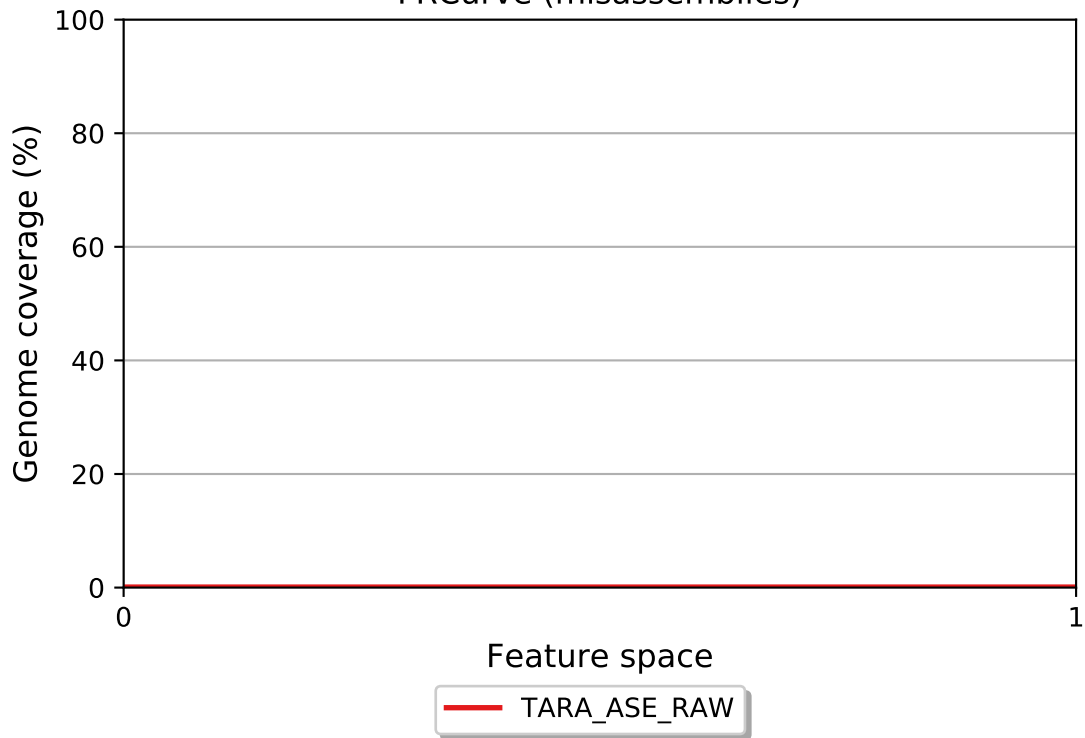


TARA_ASE_RAW

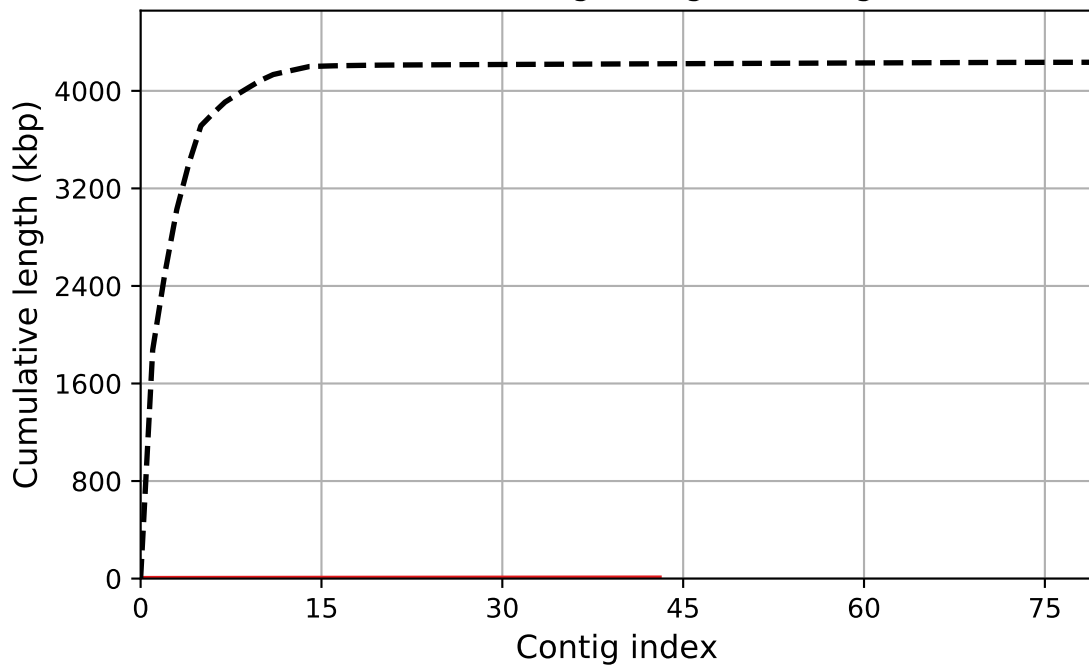
Misassemblies



FRCurve (misassemblies)

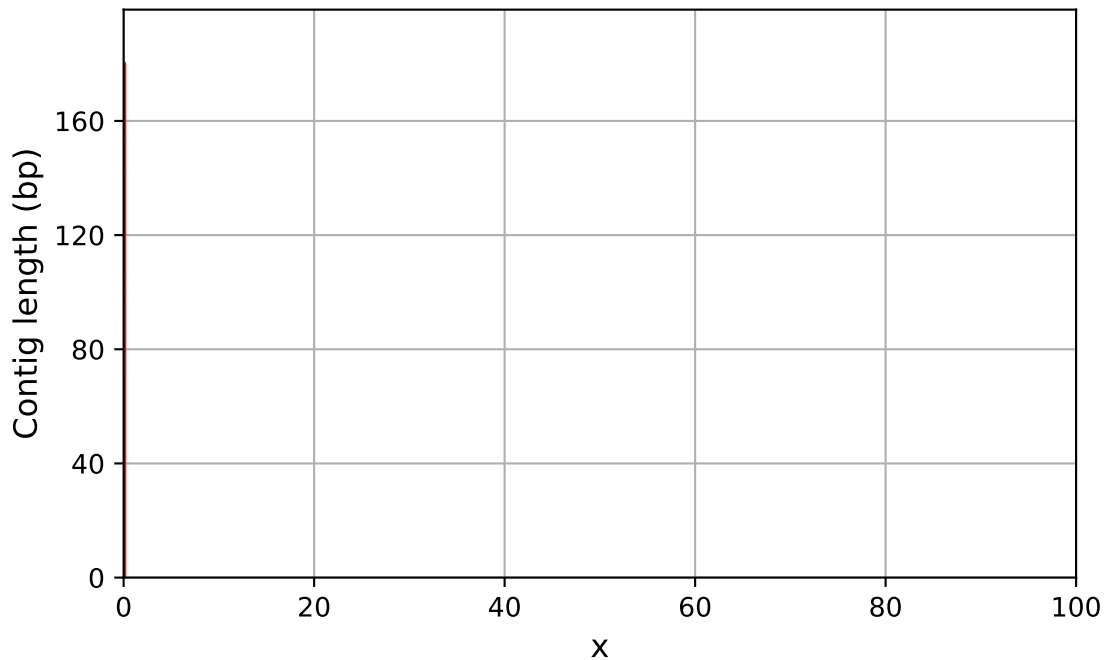


Cumulative length (aligned contigs)



— TARA_ASE_RAW - - Reference

NAx



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