

Report

	TARA_ASW_RAW
# contigs (>= 0 bp)	989154
# contigs (>= 1000 bp)	989154
# contigs (>= 5000 bp)	38869
# contigs (>= 10000 bp)	9877
# contigs (>= 25000 bp)	1638
# contigs (>= 50000 bp)	333
Total length (>= 0 bp)	1970794888
Total length (>= 1000 bp)	1970794888
Total length (>= 5000 bp)	382484797
Total length (>= 10000 bp)	189227956
Total length (>= 25000 bp)	69982681
Total length (>= 50000 bp)	26580787
# contigs	989154
Largest contig	414653
Total length	1970794888
Reference length	3561038
N50	1994
N75	1336
L50	250870
L75	558634
# 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	2
# unaligned contigs	989118 + 36 part
Unaligned length	1970791353
Genome fraction (%)	0.029
Duplication ratio	3.432
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11262.14
# indels per 100 kbp	0.00
Largest alignment	144
Total aligned length	3535

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

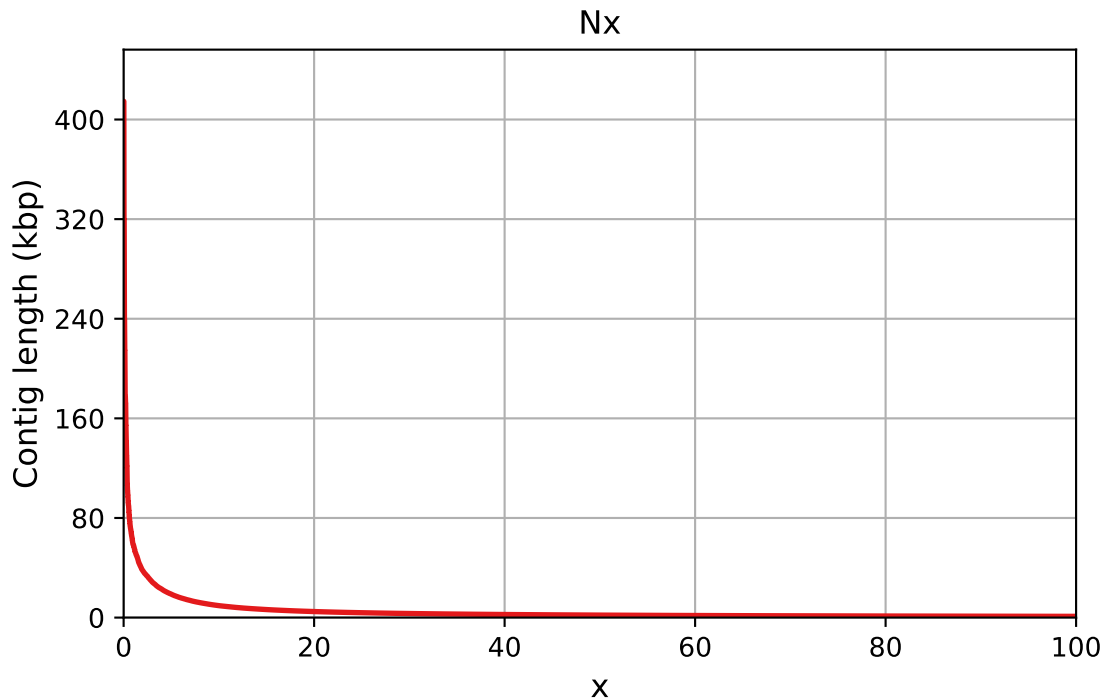
	TARA_ASW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	34
# possible misassemblies	38
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	116
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

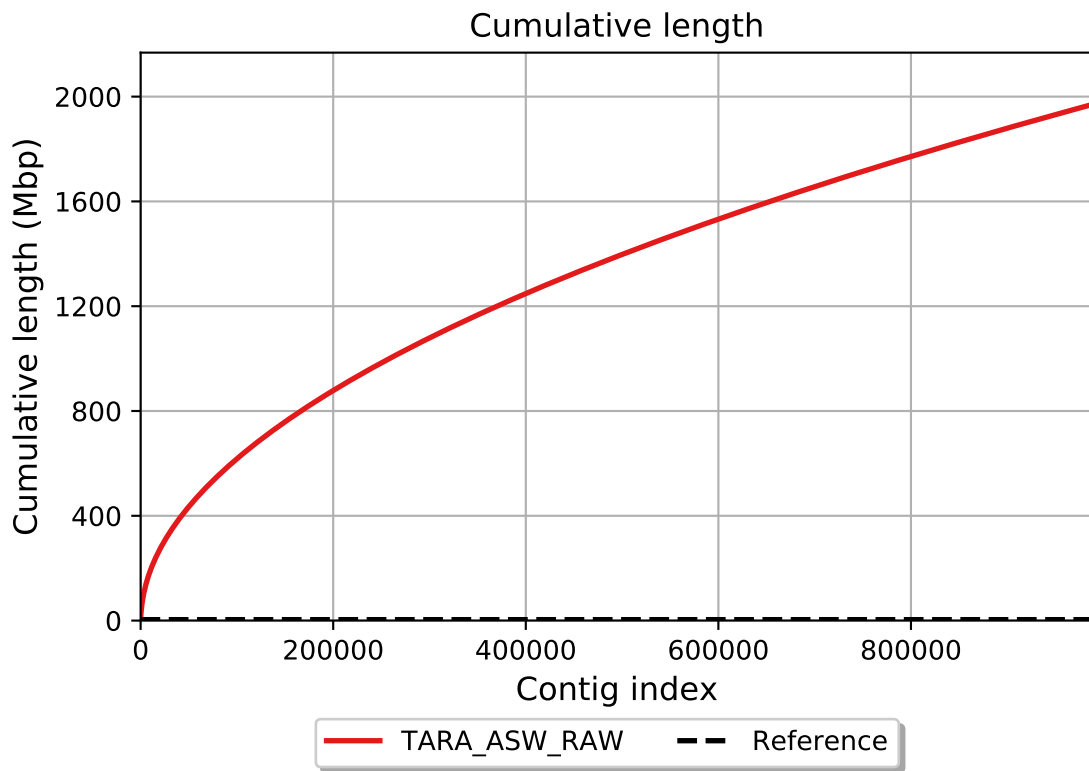
Unaligned report

	TARA_ASW_RAW
# fully unaligned contigs	989118
Fully unaligned length	1970658388
# partially unaligned contigs	36
Partially unaligned length	132965
# N's	0

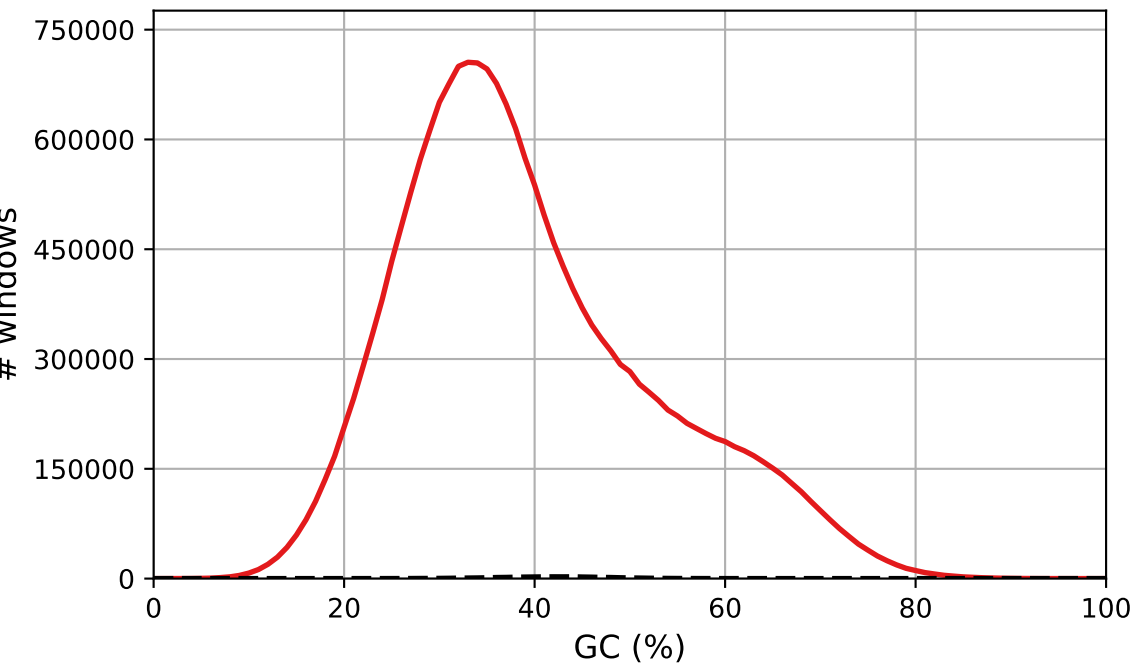
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— TARA_ASW_RAW

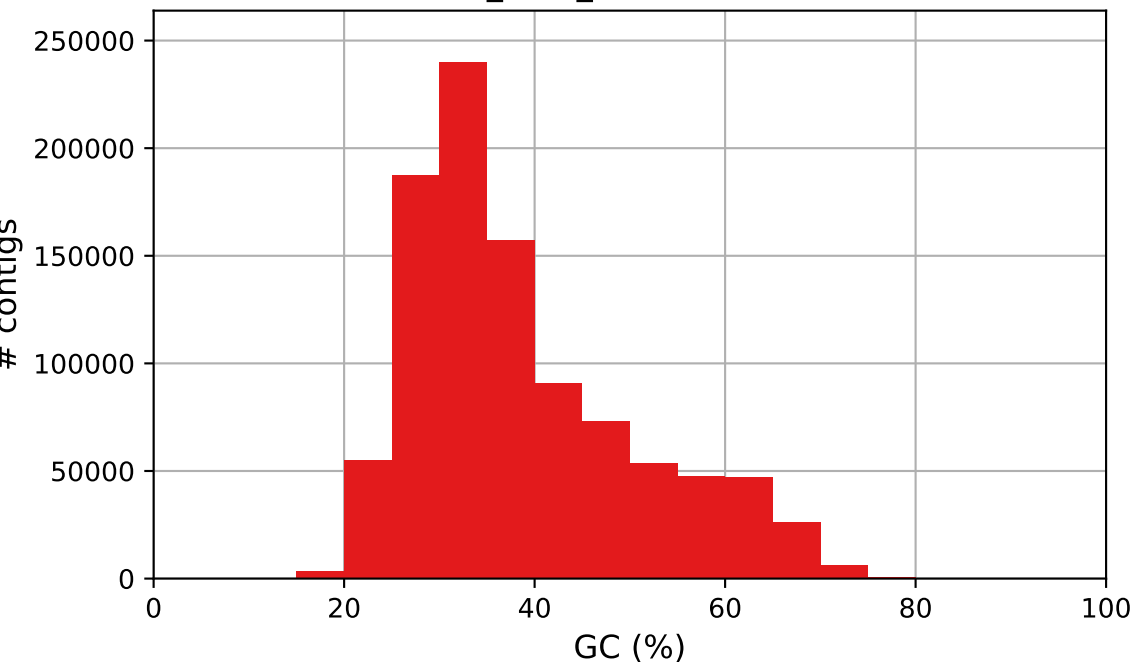


GC content



— TARA_ASW_RAW - - Reference

TARA_ASW_RAW GC content



TARA_ASW_RAW

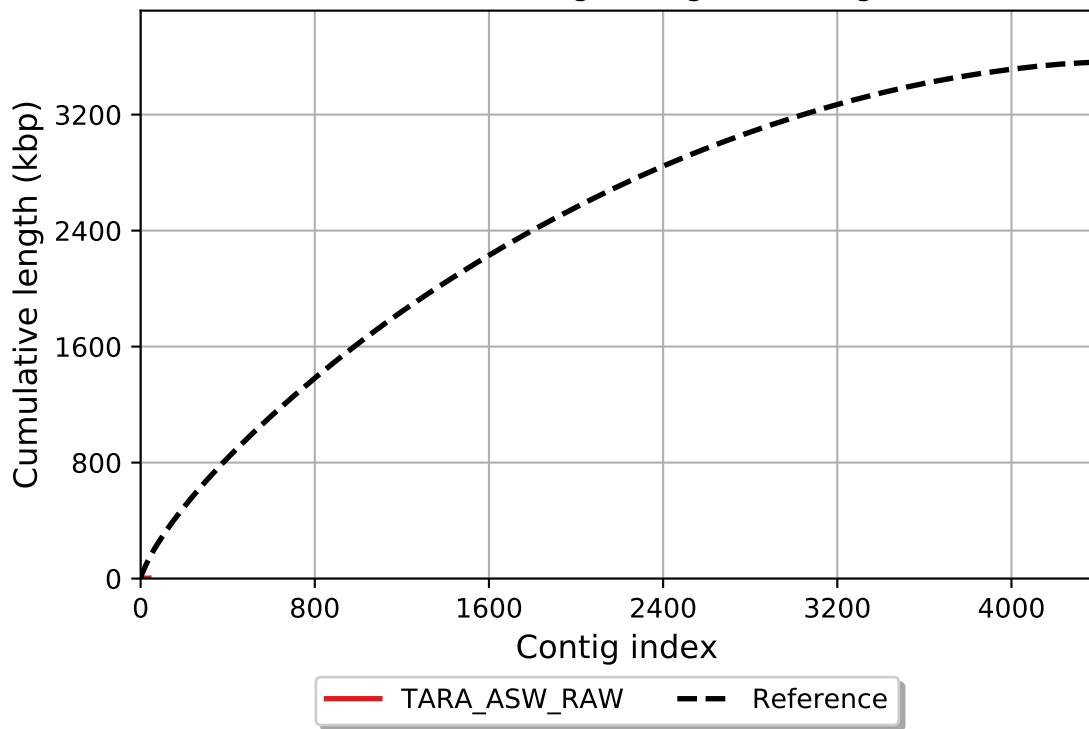
Misassemblies



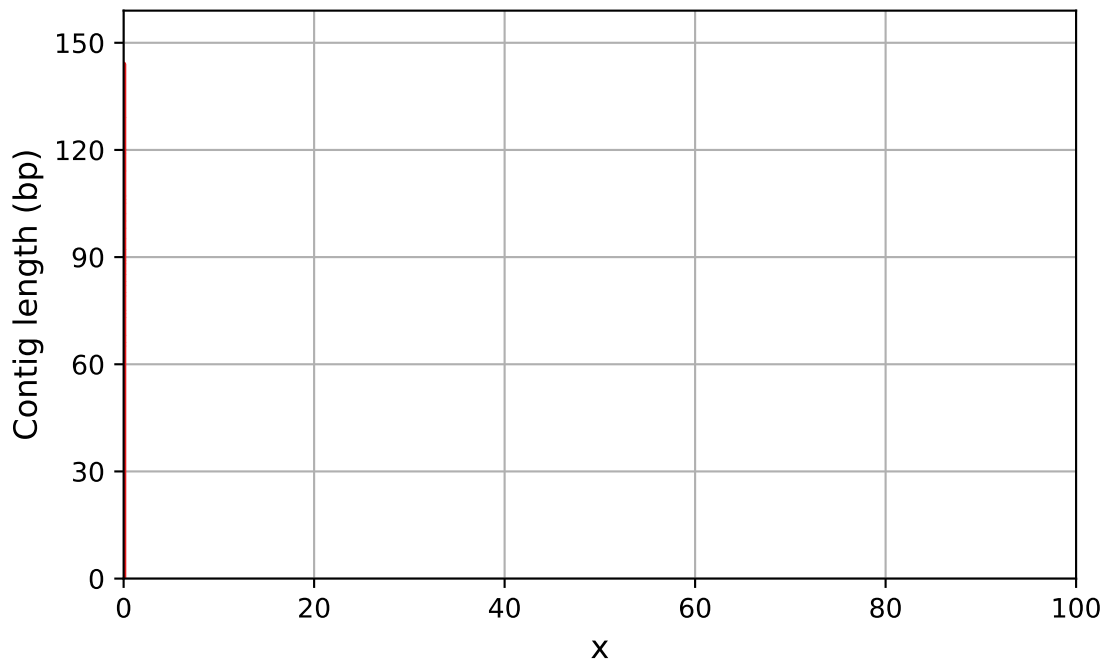
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



TARA_ASW_RAW