

Report

	TARA_PSW_RAW
# contigs (>= 0 bp)	1124813
# contigs (>= 1000 bp)	1124813
# contigs (>= 5000 bp)	57961
# contigs (>= 10000 bp)	16819
# contigs (>= 25000 bp)	3454
# contigs (>= 50000 bp)	1035
Total length (>= 0 bp)	2467968766
Total length (>= 1000 bp)	2467968766
Total length (>= 5000 bp)	654697028
Total length (>= 10000 bp)	378461969
Total length (>= 25000 bp)	185100868
Total length (>= 50000 bp)	103282434
# contigs	1124813
Largest contig	952125
Total length	2467968766
Reference length	7658814
N50	2277
N75	1402
L50	241839
L75	596698
# 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	9
# unaligned contigs	1124426 + 387 part
Unaligned length	2467934864
Genome fraction (%)	0.124
Duplication ratio	6.090
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10754.38
# indels per 100 kbp	125.90
Largest alignment	427
Total aligned length	33902

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

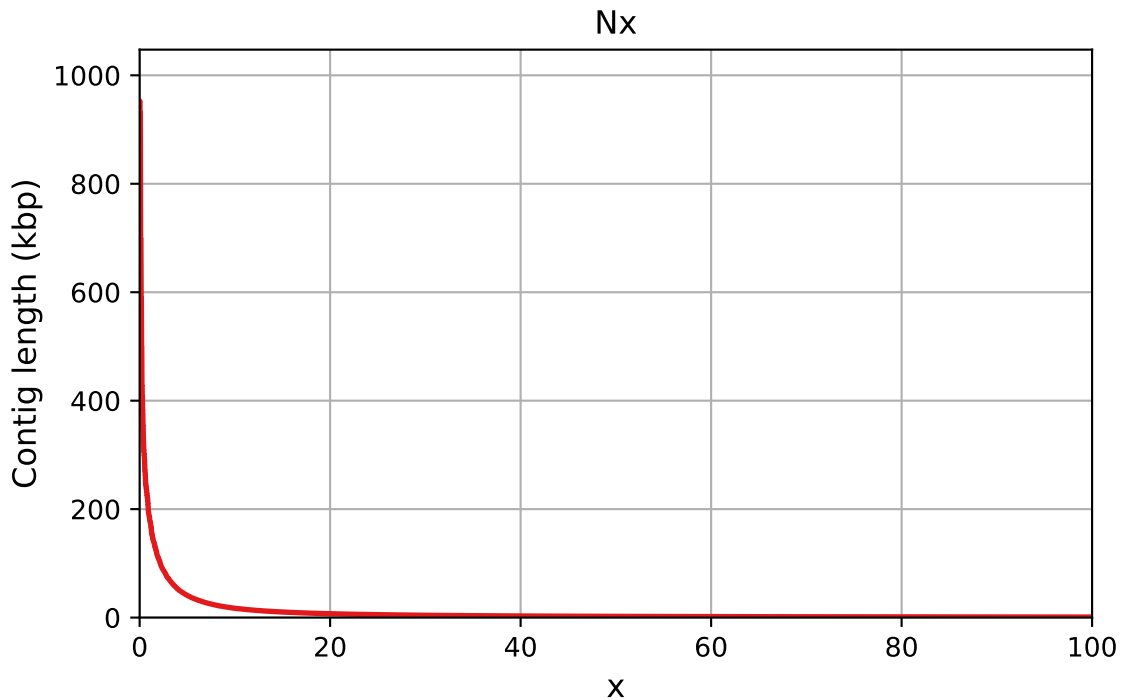
	TARA_PSW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	378
# possible misassemblies	470
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# mismatches	1025
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	15

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).

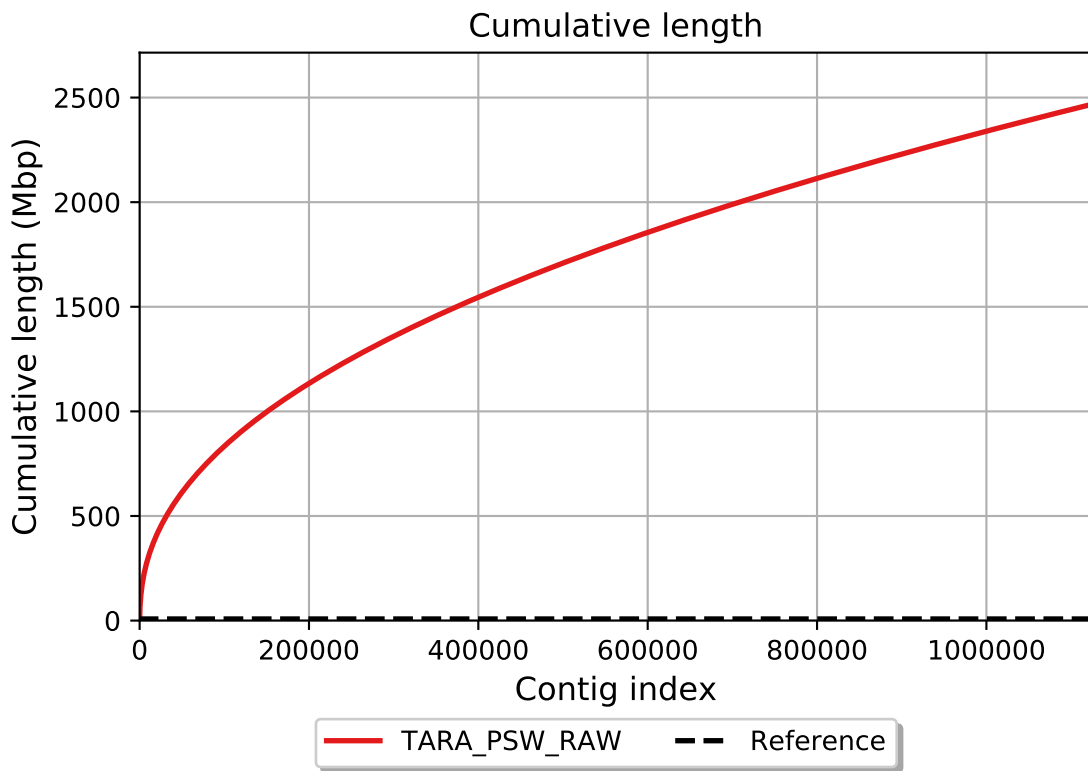
Unaligned report

	TARA_PSW_RAW
# fully unaligned contigs	1124426
Fully unaligned length	2464099817
# partially unaligned contigs	387
Partially unaligned length	3835047
# N's	0

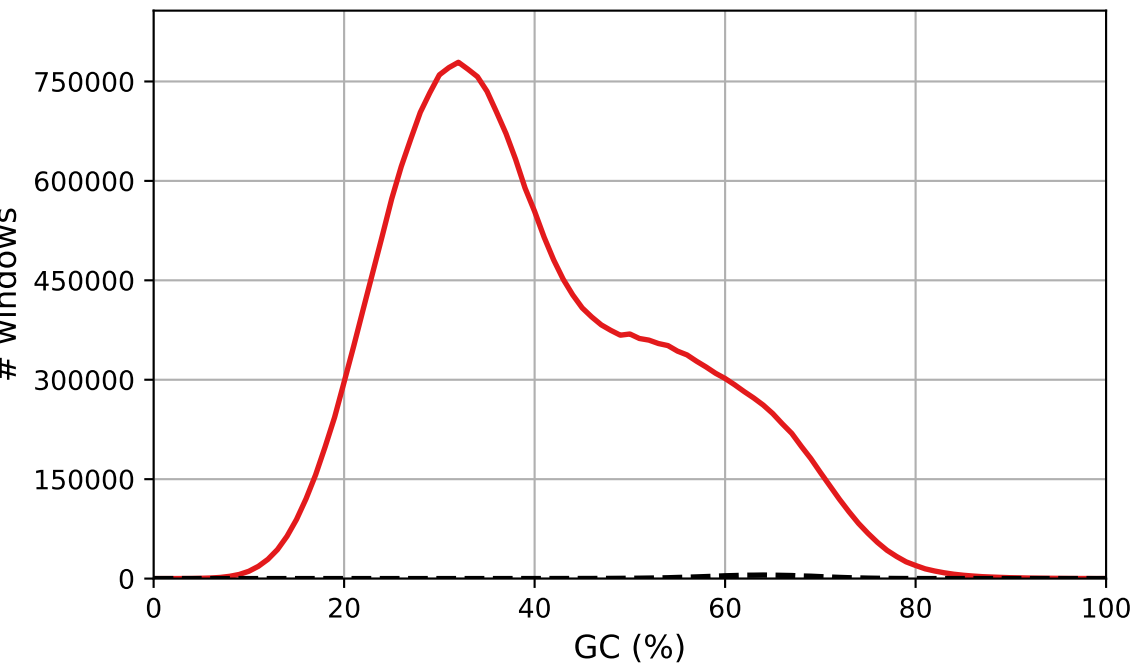
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



TARA_PSW_RAW

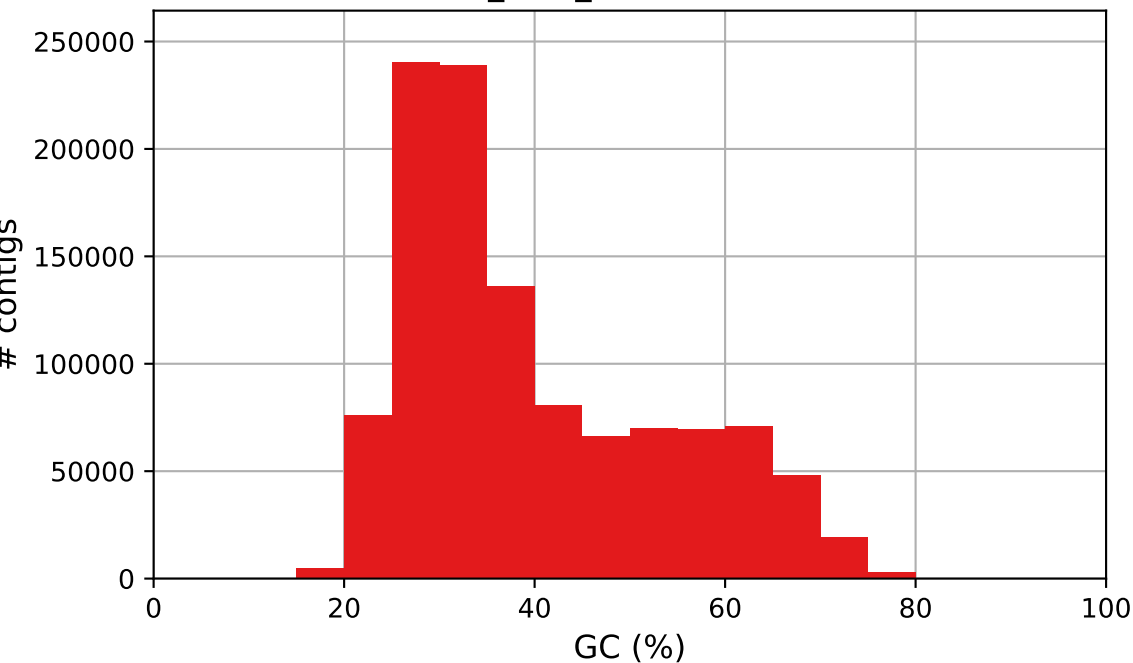


GC content



— TARA_PSW_RAW - - Reference

TARA_PSW_RAW GC content

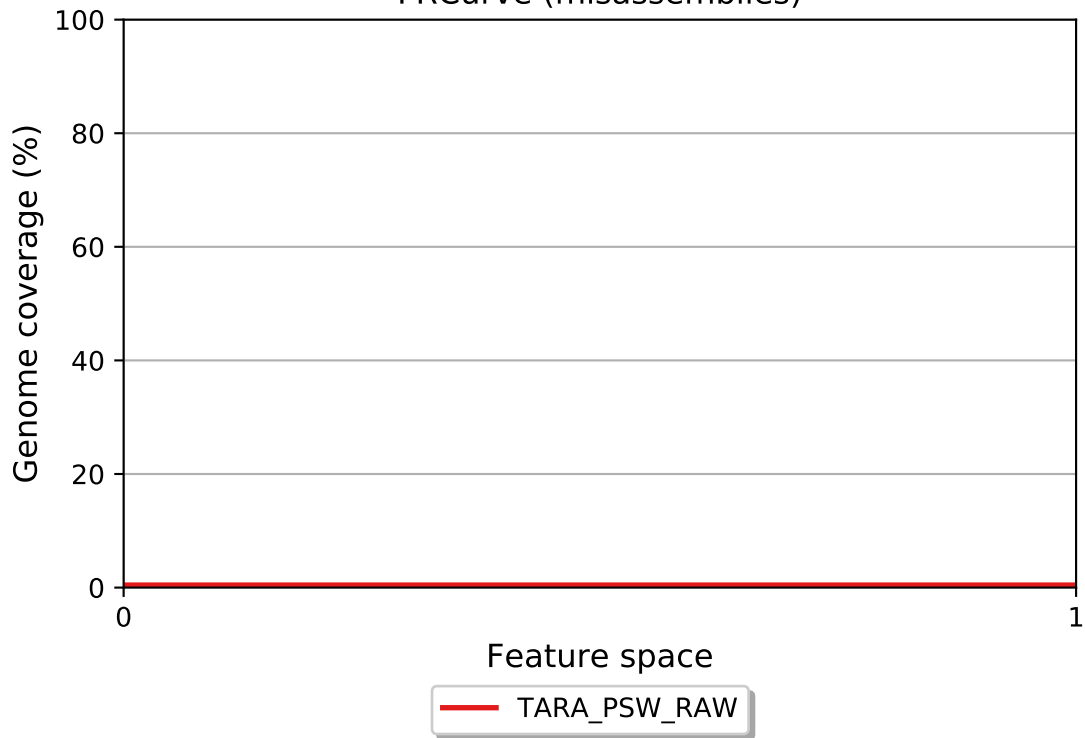


TARA_PSW_RAW

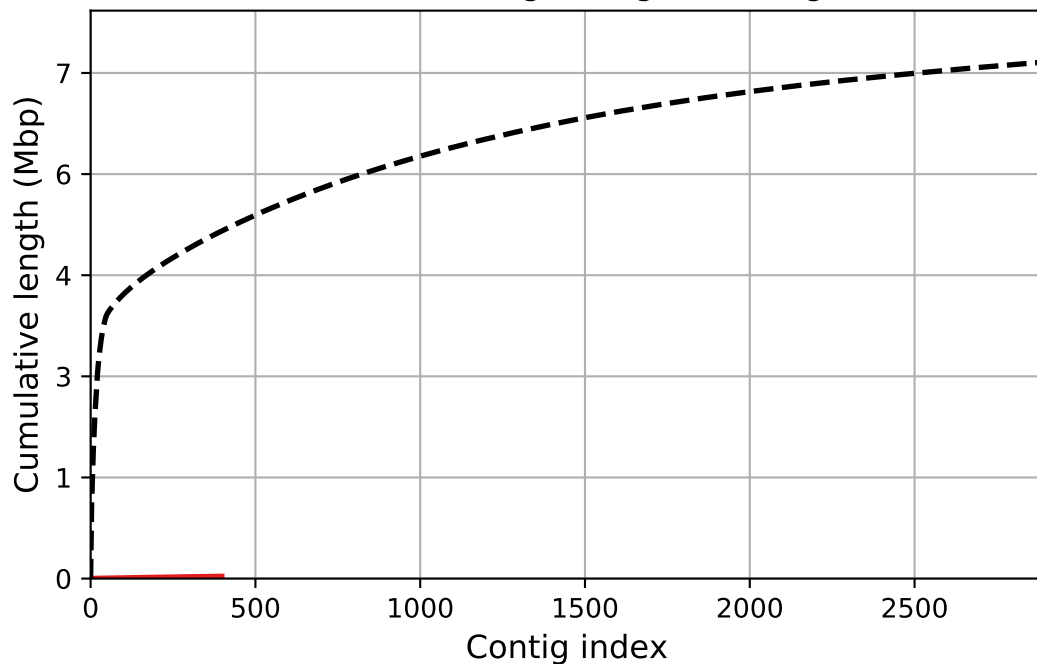
Misassemblies



FRCurve (misassemblies)

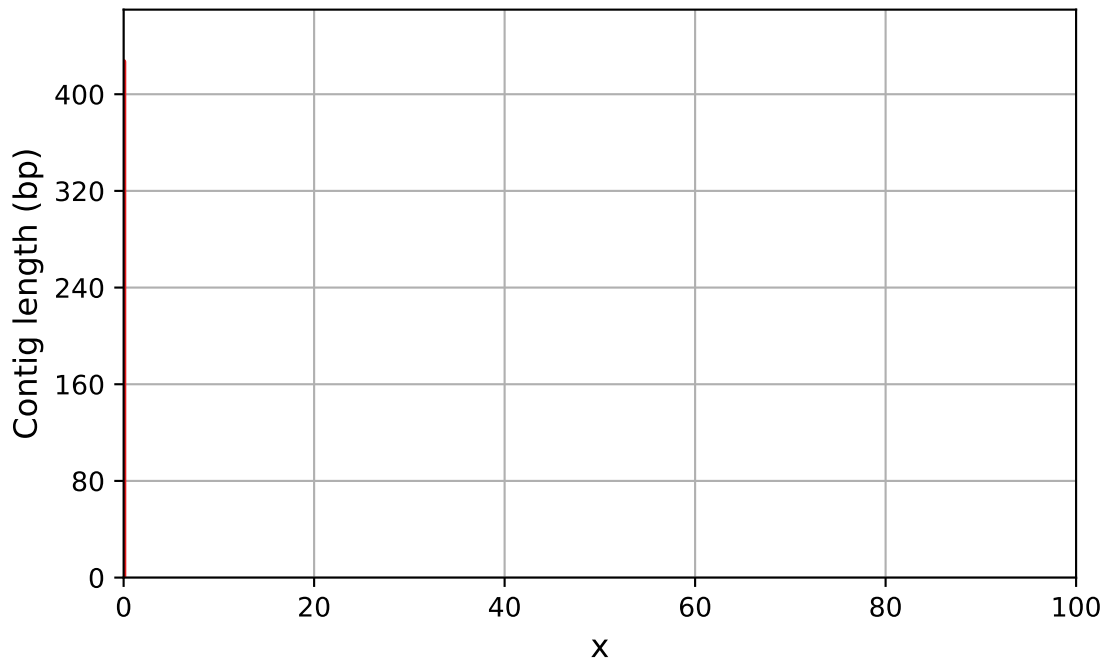


Cumulative length (aligned contigs)



— TARA_PSW_RAW - - Reference

NAx



TARA_PSW_RAW