

Report

	TARA_ASW_RAW
# contigs (>= 1000 bp)	38
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	139442
Total length (>= 5000 bp)	75098
Total length (>= 10000 bp)	57838
Total length (>= 25000 bp)	40866
Total length (>= 50000 bp)	0
# contigs	38
Largest contig	40866
Total length	139442
Reference length	4234461
GC (%)	40.29
Reference GC (%)	41.03
N50	5642
N75	2157
L50	4
L75	17
# 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	8 + 30 part
Unaligned length	136375
Genome fraction (%)	0.021
Duplication ratio	3.450
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10798.65
# indels per 100 kbp	0.00
Largest alignment	144
Total aligned length	3067
NGA50	-

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
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	36
# possible misassemblies	41
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	96
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

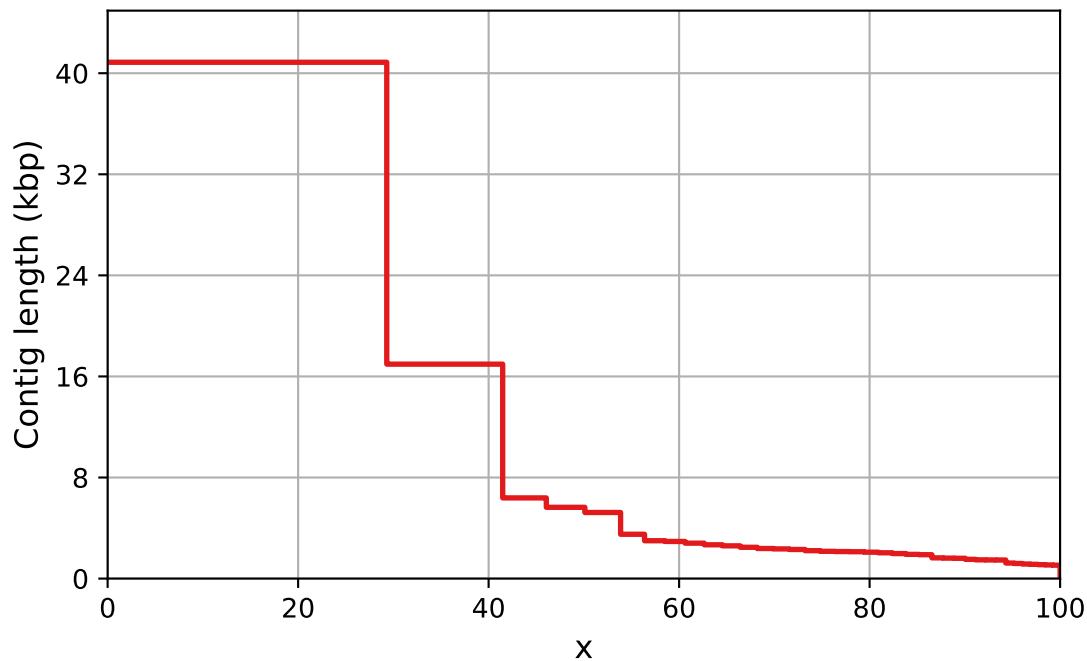
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_ASW_RAW
# fully unaligned contigs	8
Fully unaligned length	12930
# partially unaligned contigs	30
Partially unaligned length	123445
# N's	0

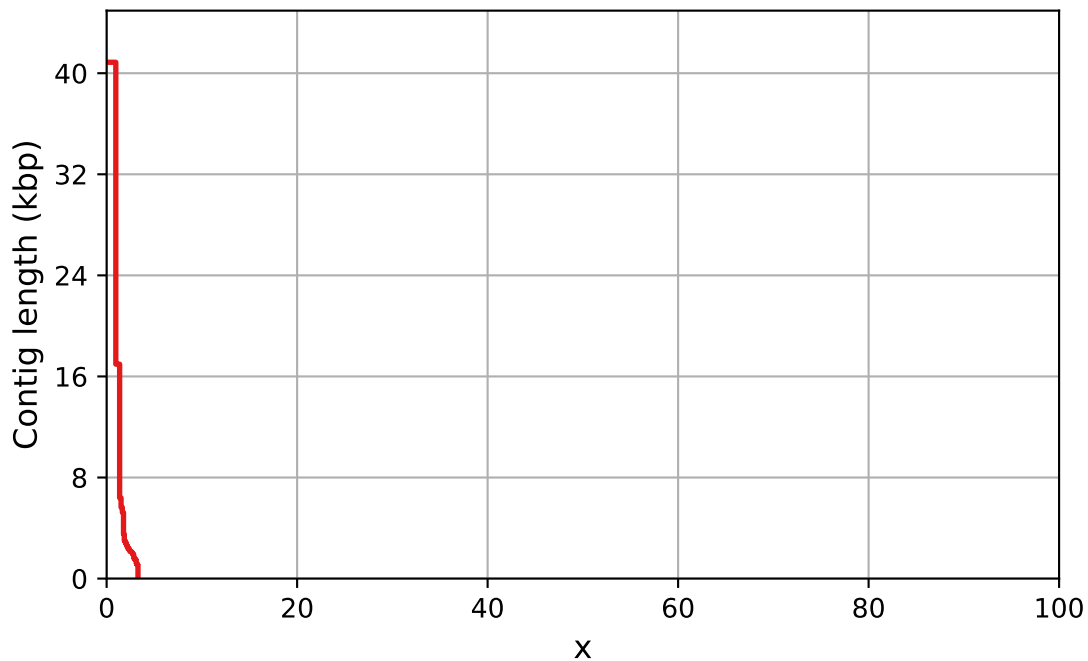
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



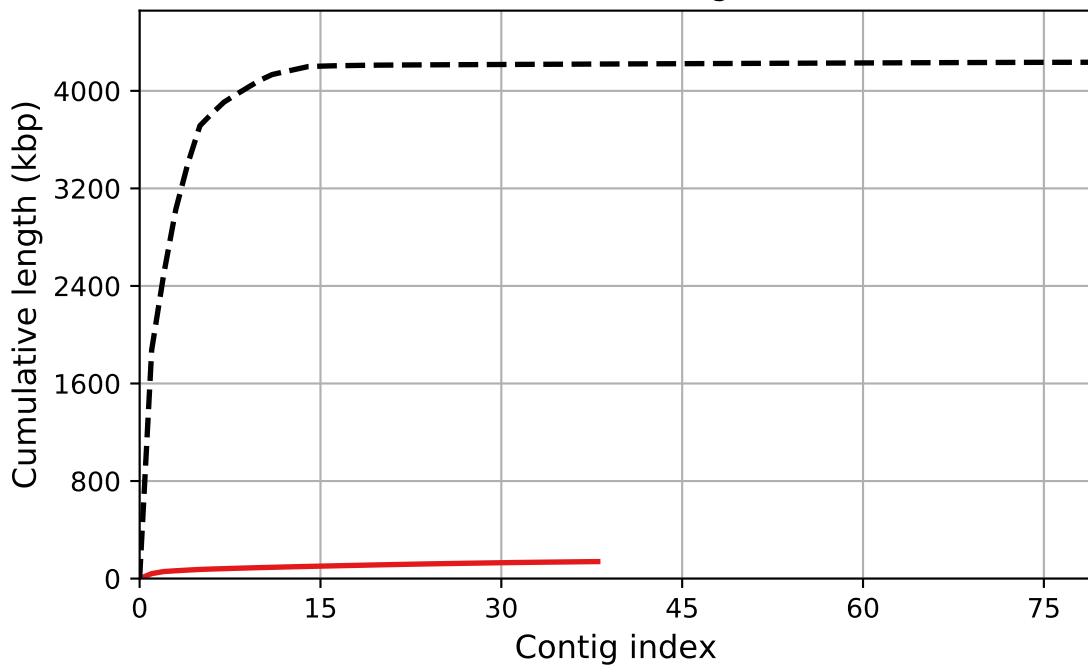
TARA_ASW_RAW

NGx



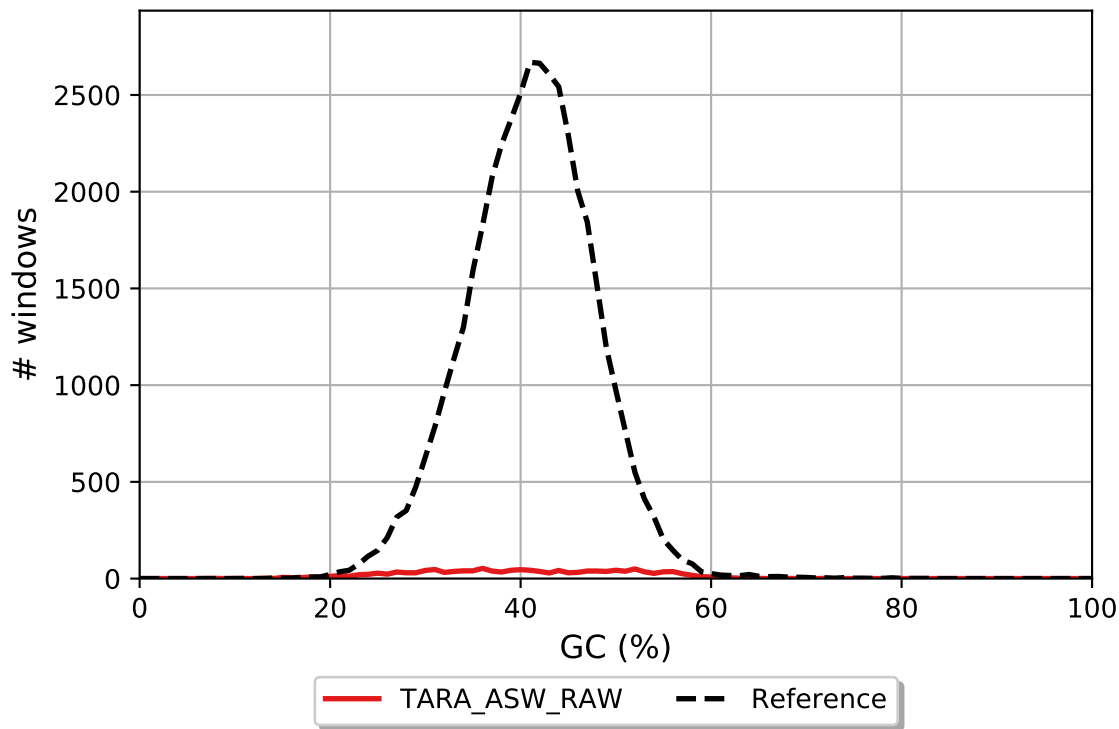
TARA_ASW_RAW

Cumulative length

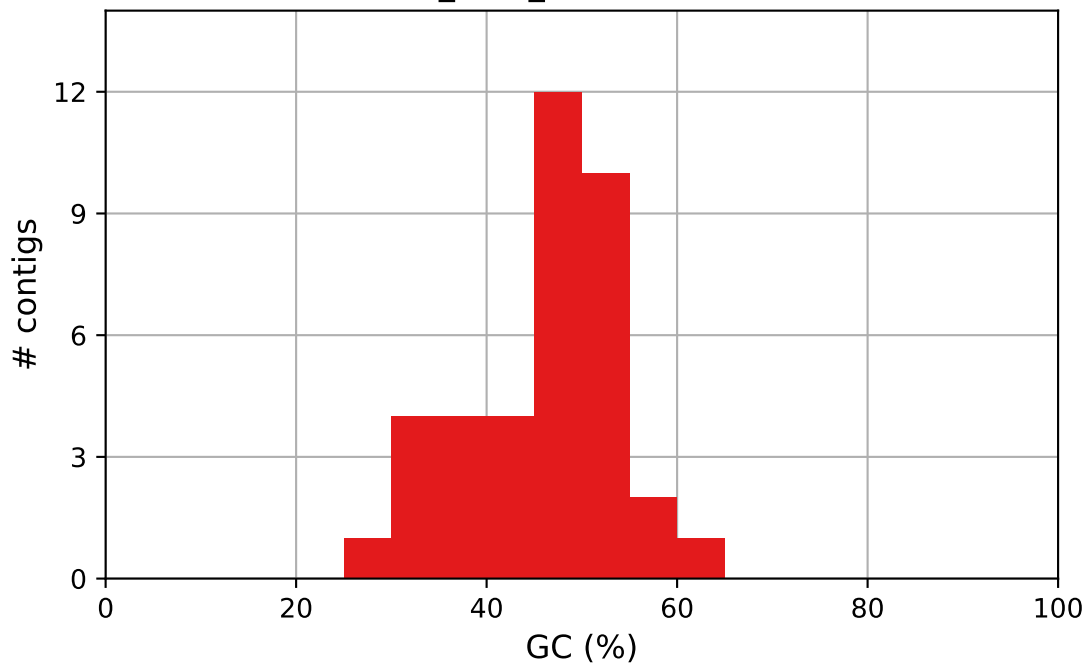


— TARA_ASW_RAW - - Reference

GC content



TARA_ASW_RAW GC content

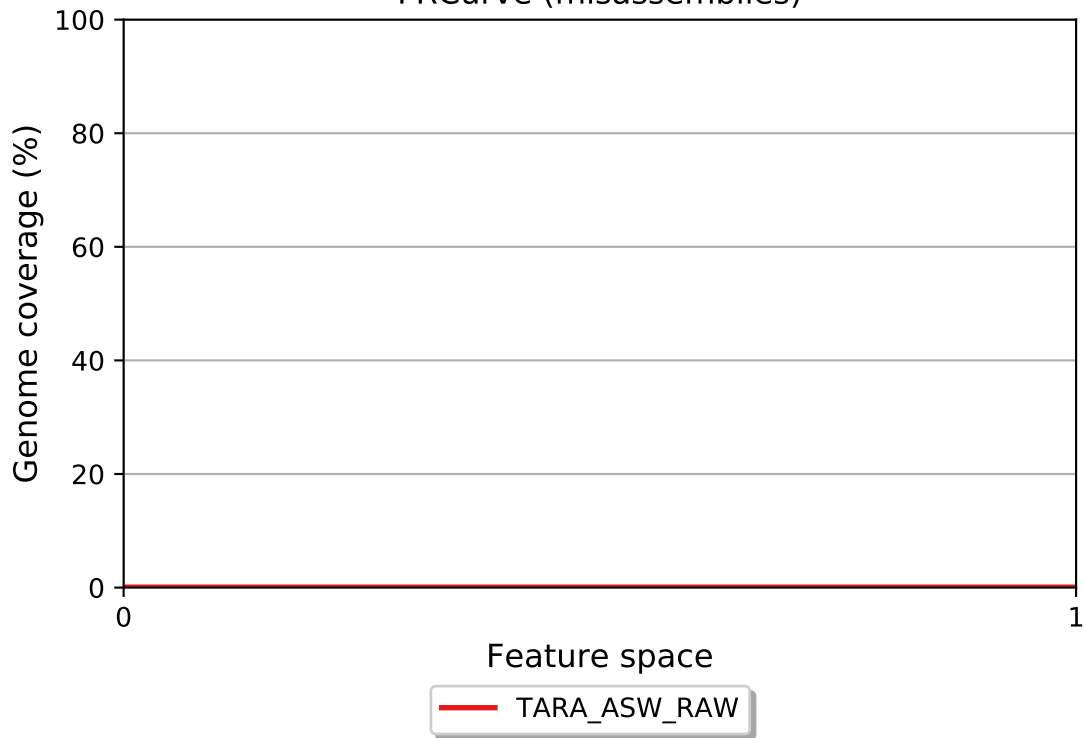


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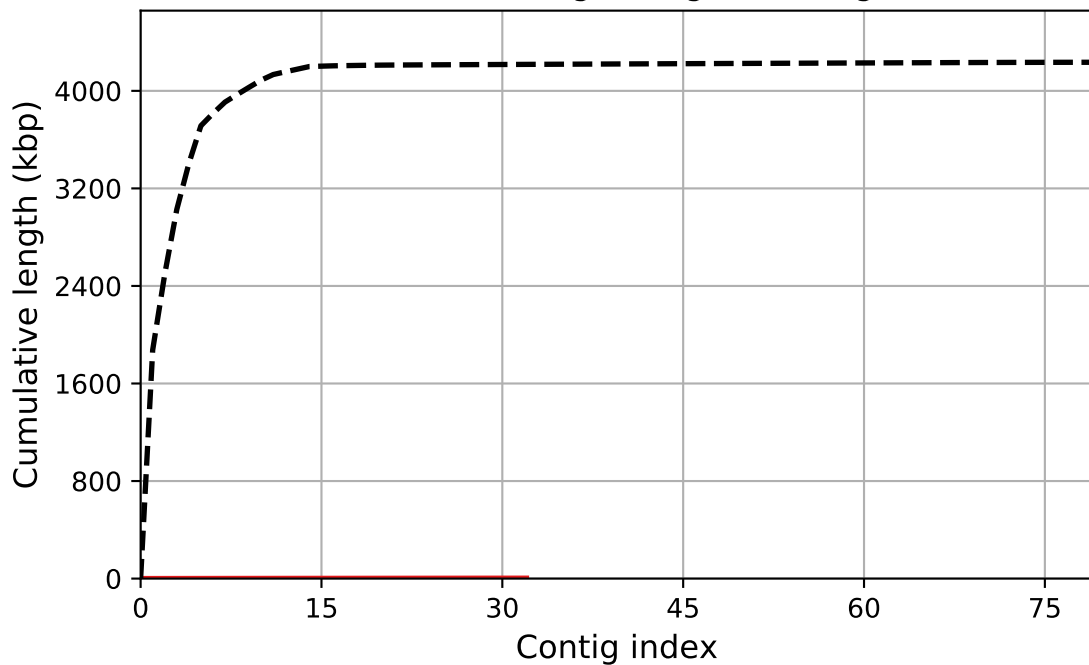
Misassemblies



FRCurve (misassemblies)

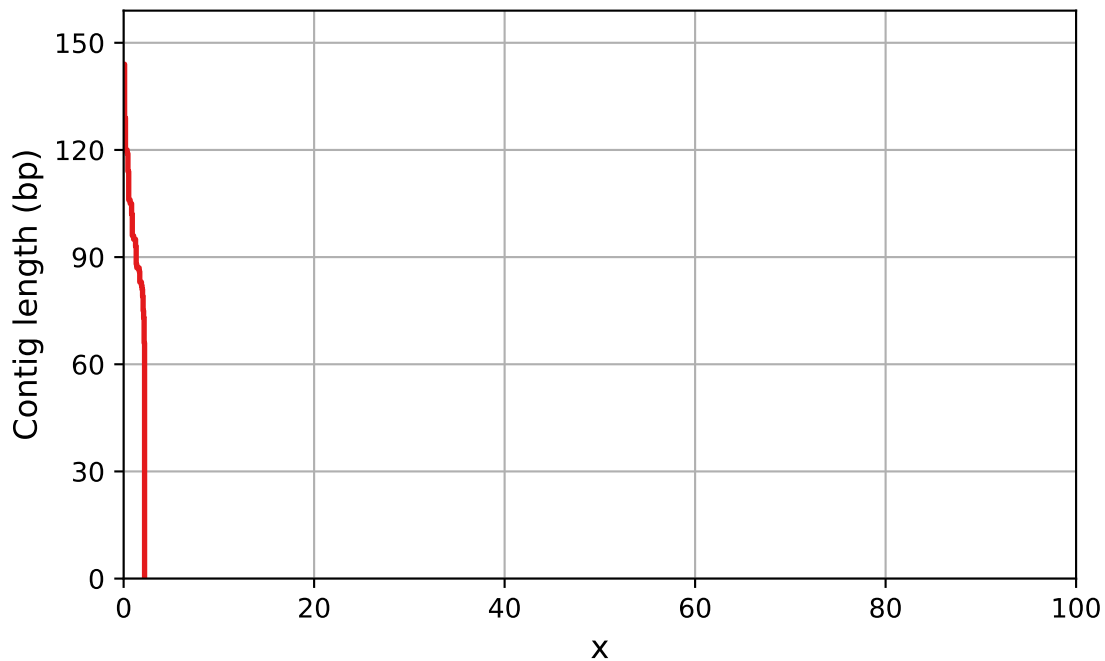


Cumulative length (aligned contigs)



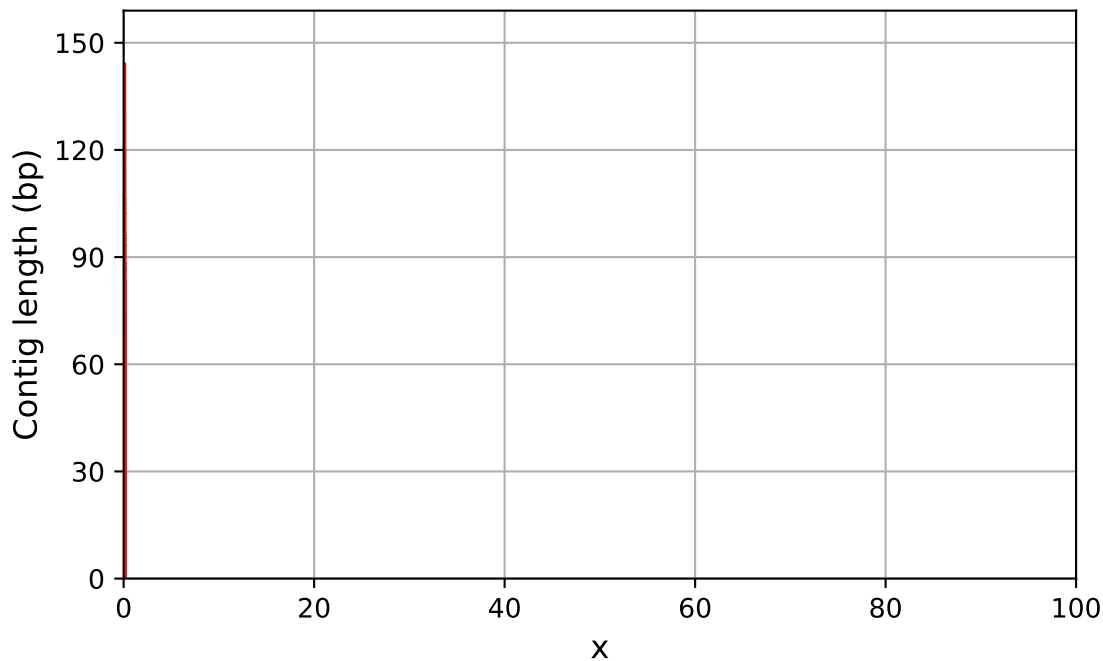
— TARA_ASW_RAW - - Reference

NAx



TARA_ASW_RAW

NGAx



TARA_ASW_RAW