

Report

	TARA_ASW_RAW
# contigs (>= 1000 bp)	36
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	136500
Total length (>= 5000 bp)	75098
Total length (>= 10000 bp)	57838
Total length (>= 25000 bp)	40866
Total length (>= 50000 bp)	0
# contigs	36
Largest contig	40866
Total length	136500
Reference length	3561038
GC (%)	40.06
Reference GC (%)	41.87
N50	5642
N75	2209
L50	4
L75	16
# 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 + 28 part
Unaligned length	133630
Genome fraction (%)	0.024
Duplication ratio	3.306
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10368.66
# indels per 100 kbp	0.00
Largest alignment	144
Total aligned length	2870
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	34
# possible misassemblies	38
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	90
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

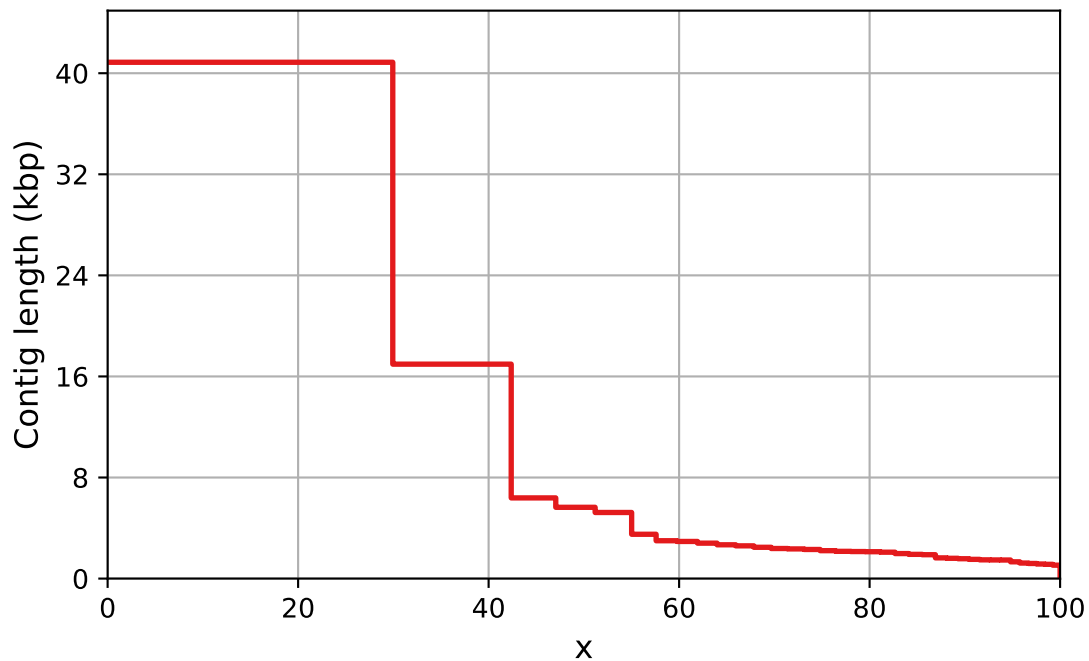
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_ASW_RAW
# fully unaligned contigs	8
Fully unaligned length	14411
# partially unaligned contigs	28
Partially unaligned length	119219
# N's	0

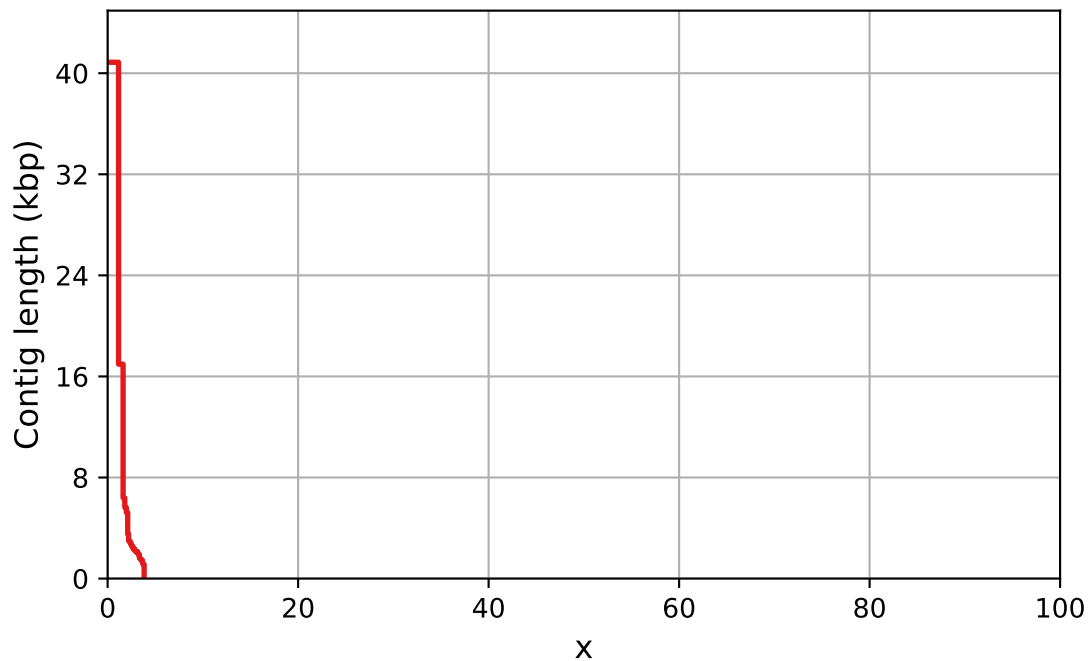
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

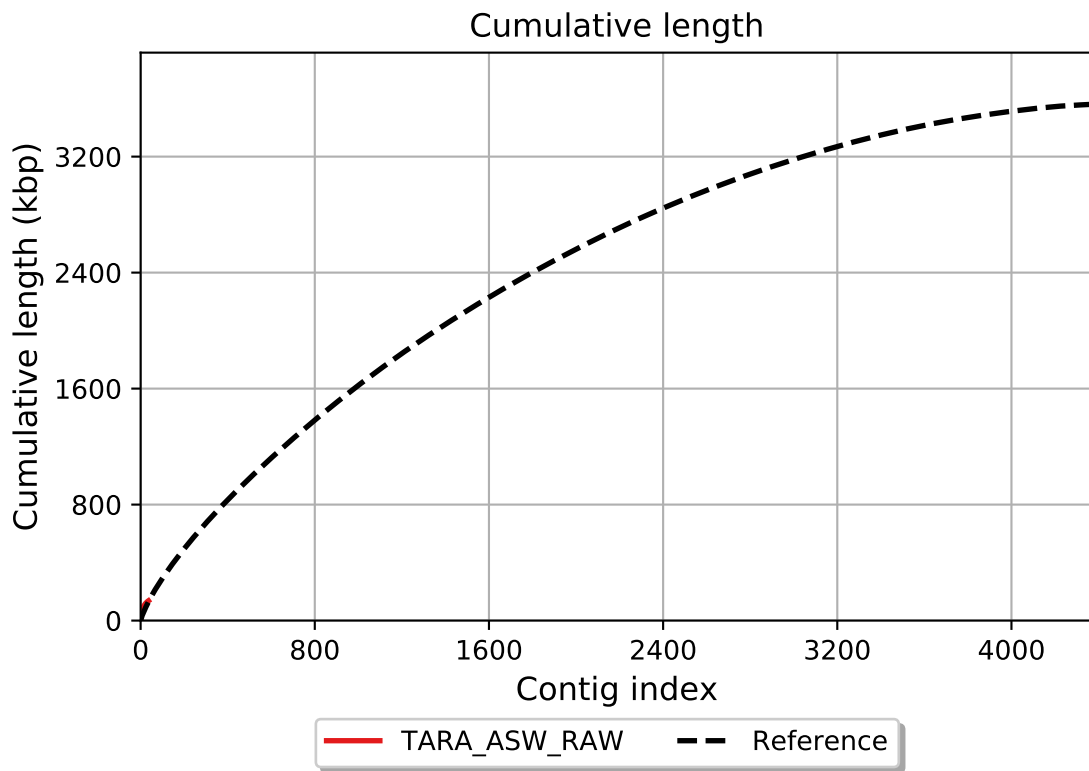


TARA_ASW_RAW

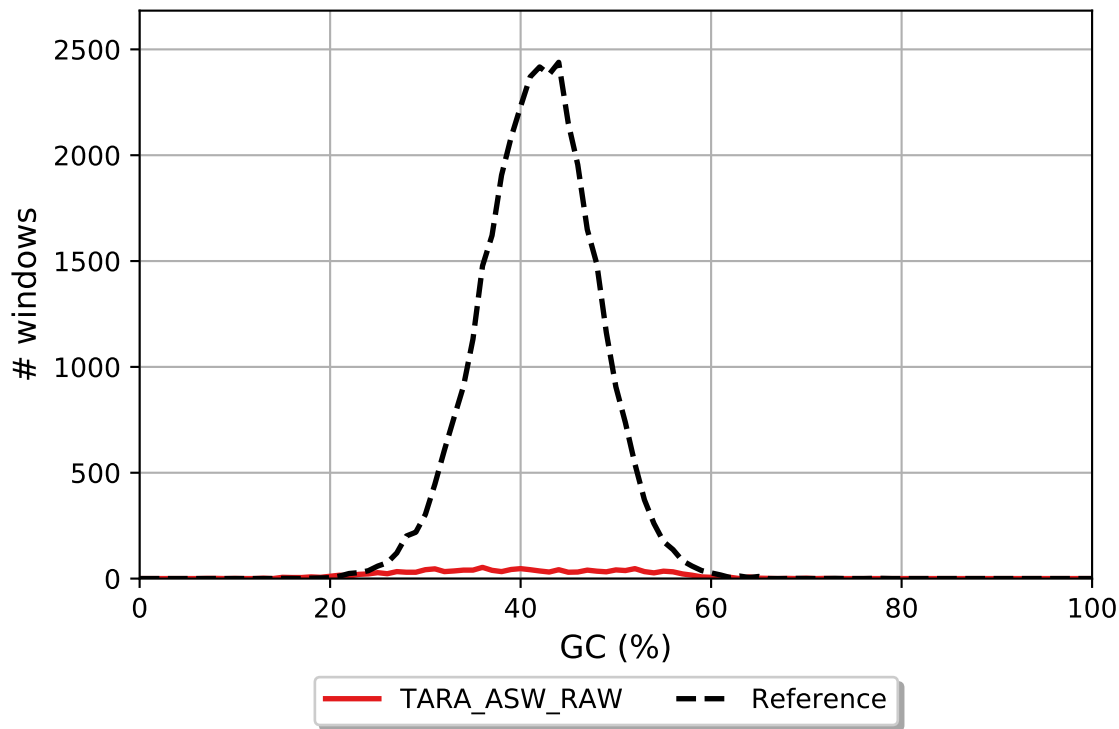
NGx



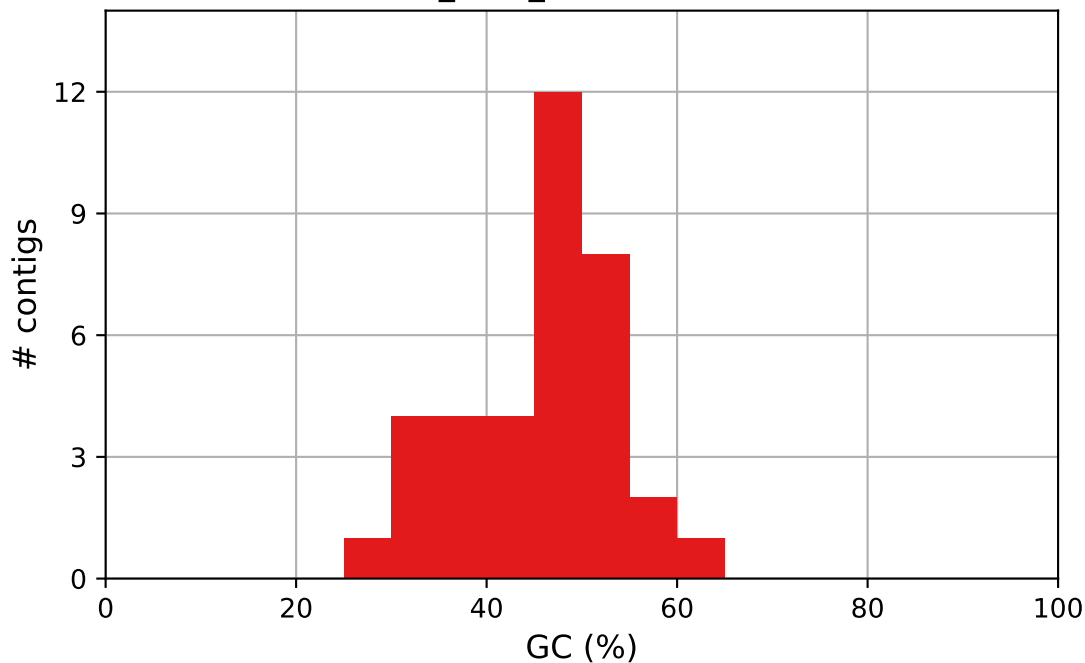
TARA_ASW_RAW



GC content



TARA_ASW_RAW GC content

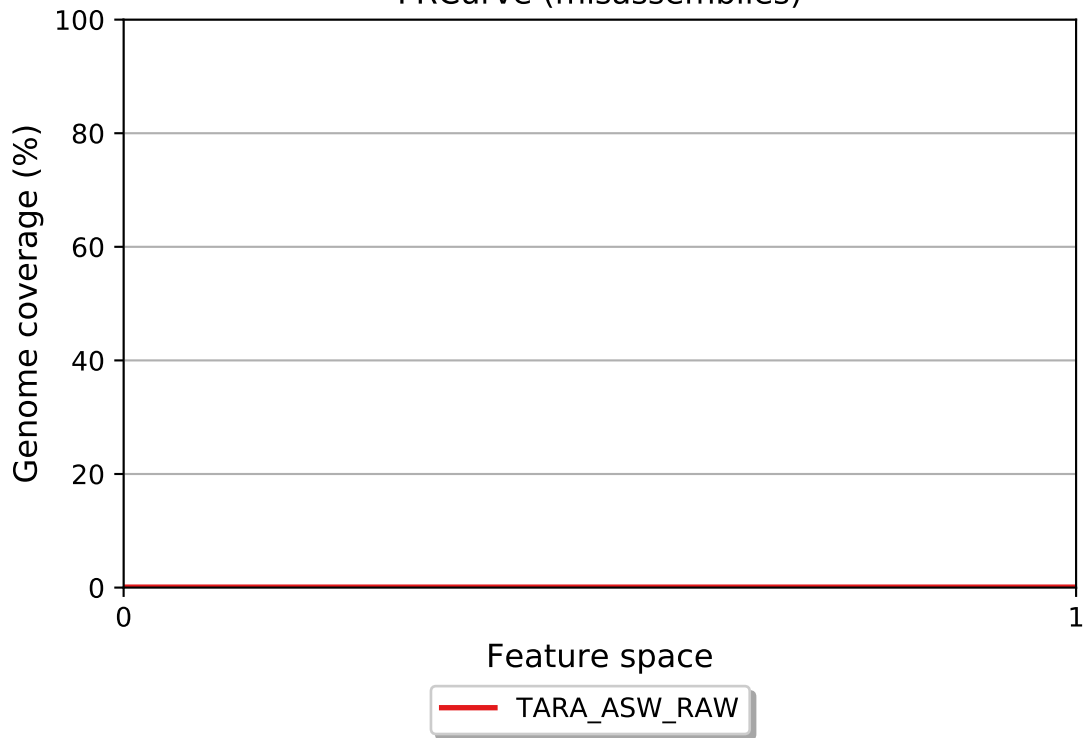


TARA_ASW_RAW

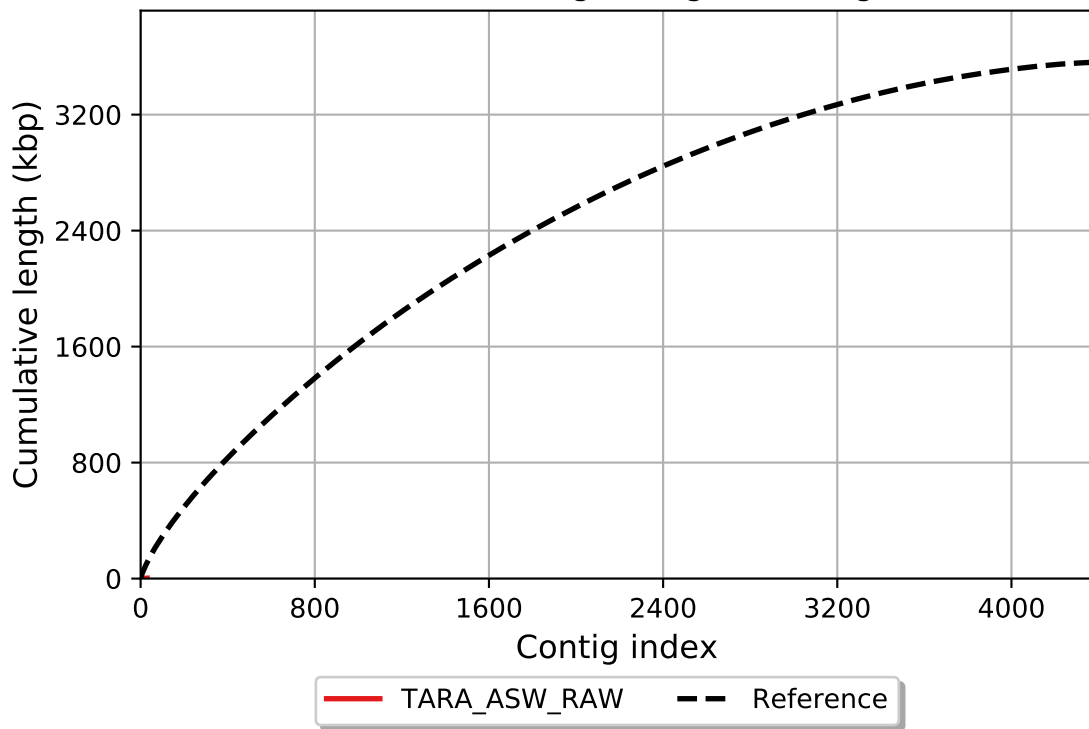
Misassemblies



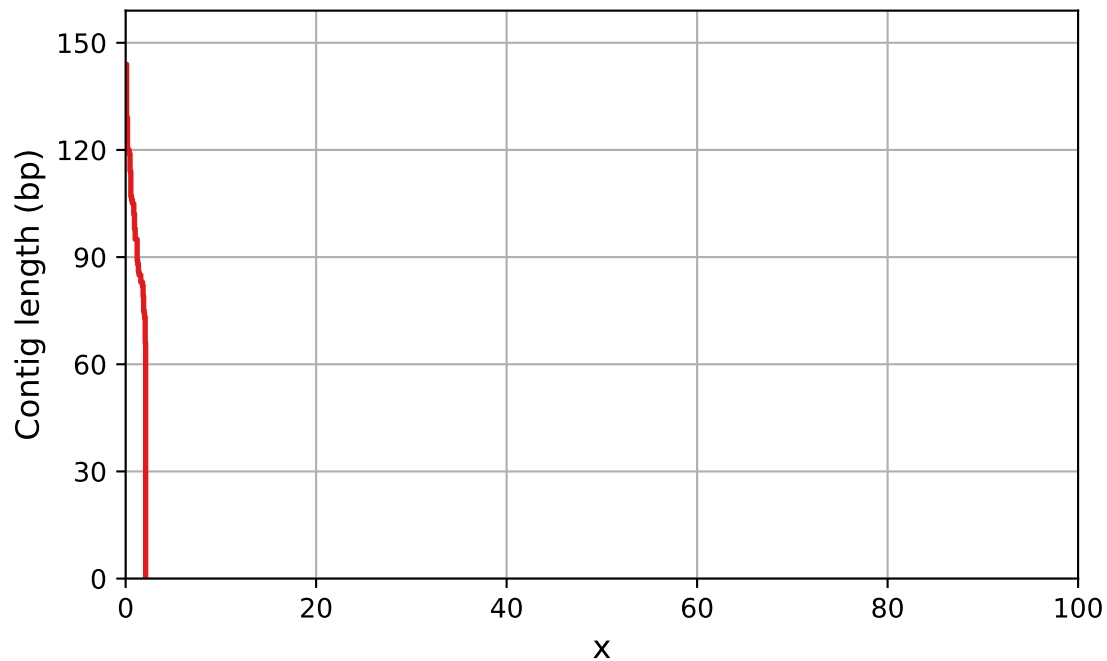
FRCurve (misassemblies)



Cumulative length (aligned contigs)

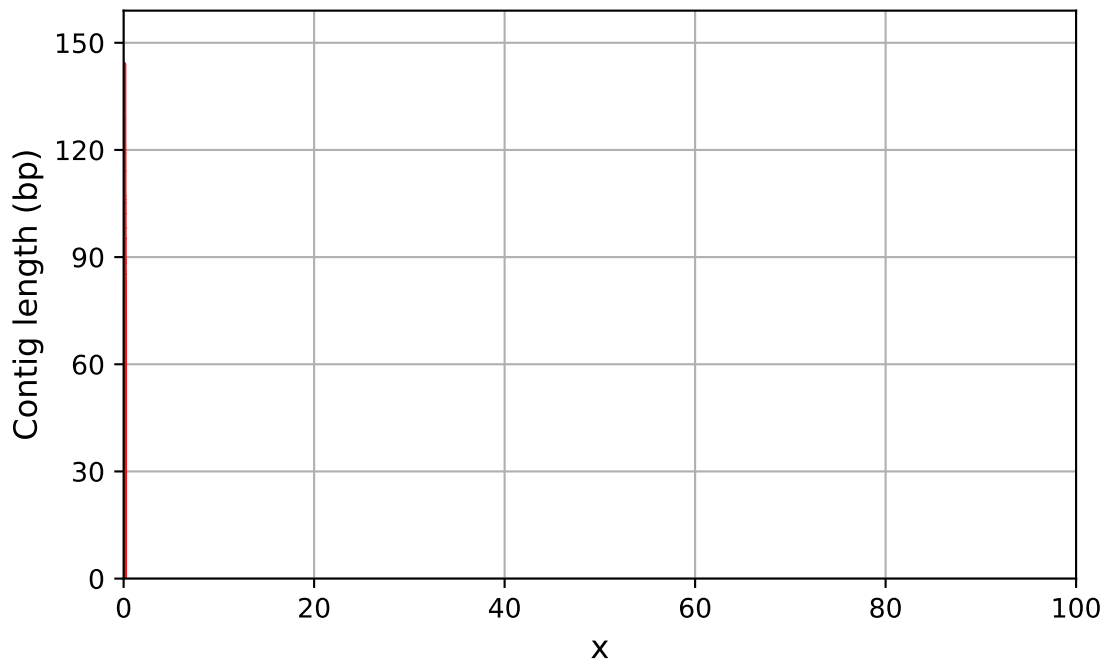


NAx



TARA_ASW_RAW

NGAx



TARA_ASW_RAW