Report

	TARA_RED_RAW
# contigs (>= 0 bp)	1039053
# contigs (>= 1000 bp)	1039053
# contigs (>= 5000 bp)	59693
# contigs (>= 10000 bp)	17020
# contigs (>= 25000 bp)	3375
# contigs (>= 50000 bp)	976
Total length (>= 0 bp)	2353055133
Total length (>= 1000 bp)	2353055133
Total length (>= 5000 bp)	654277328
Total length (>= 10000 bp)	367501749
Total length (>= 25000 bp)	170042350
Total length (>= 50000 bp)	89535681
# contigs	1039053
Largest contig	920255
Total length	2353055133
Reference length	7658814
N50	2414
N75	1444
L50	218504
L75	542376
# 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	1038781 + 271 part
Unaligned length	2353031860
Genome fraction (%)	0.049
Duplication ratio	6.583
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13063.18
# indels per 100 kbp	26.66
Largest alignment	125
Total aligned length	22285

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).
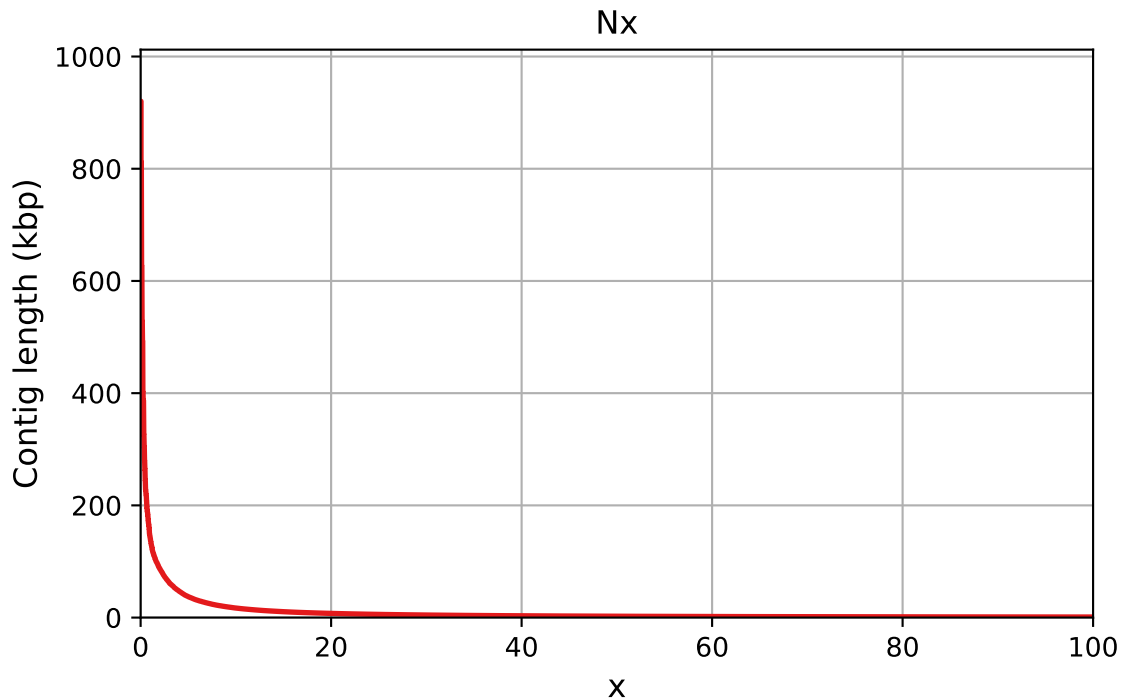
Misassemblies report

	TARA_RED_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	269
# possible misassemblies	333
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	490
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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).
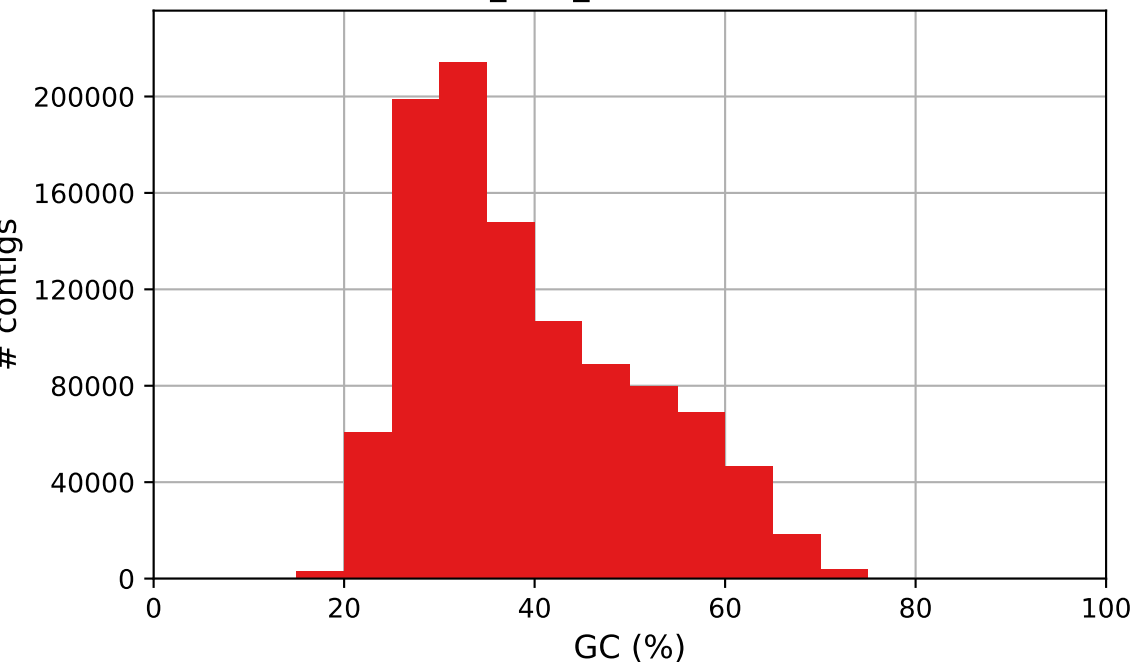
Unaligned report

	TARA_RED_RAW
# fully unaligned contigs	1038781
Fully unaligned length	2349319540
# partially unaligned contigs	271
Partially unaligned length	3712320
# 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

Cumulative length

GC content

| GC (%) | # windows |

TARA_RED_RAW ─ ─ Reference
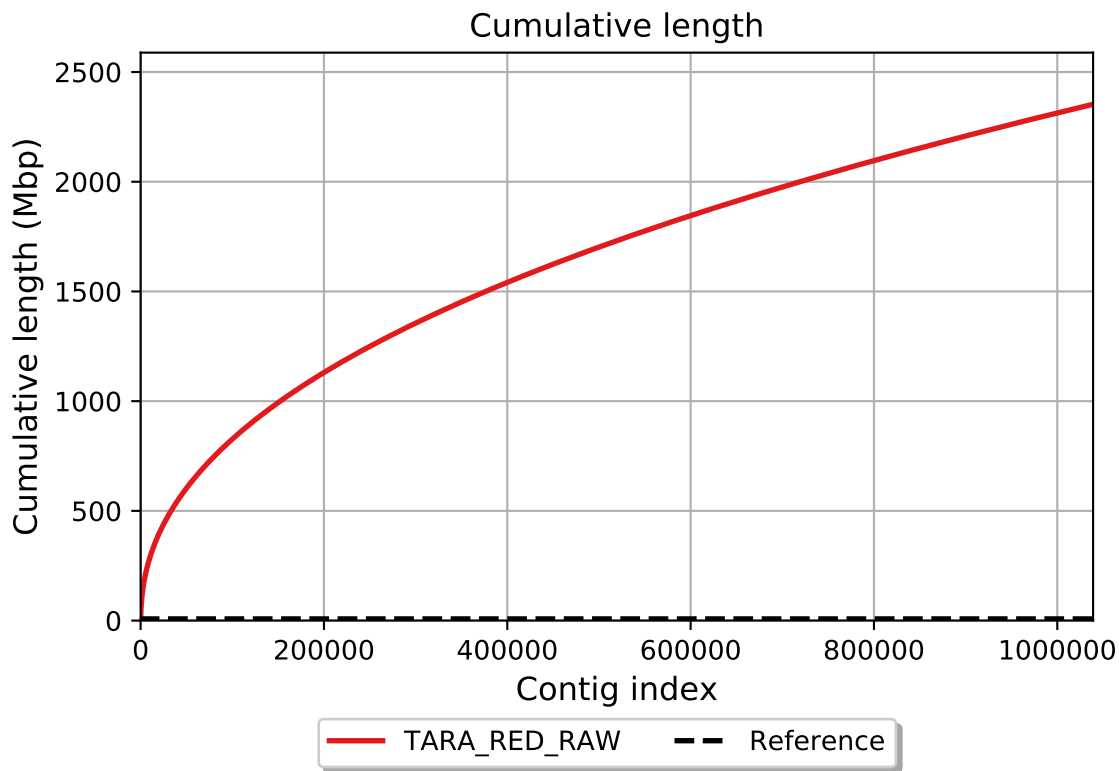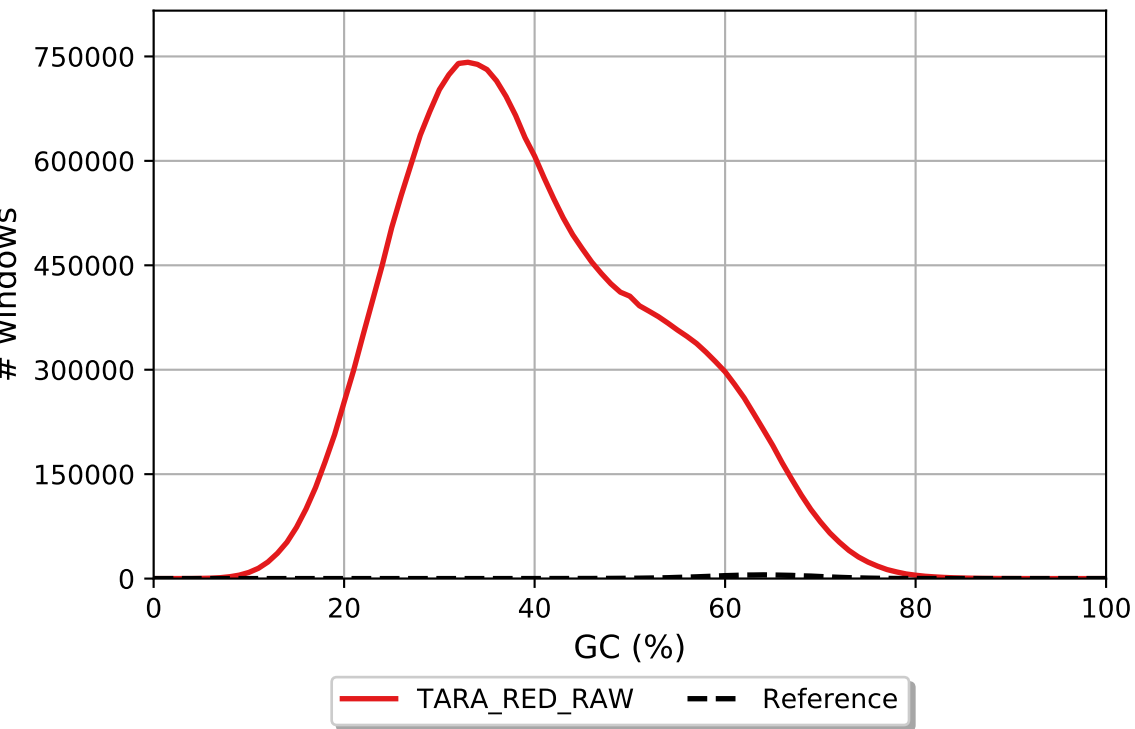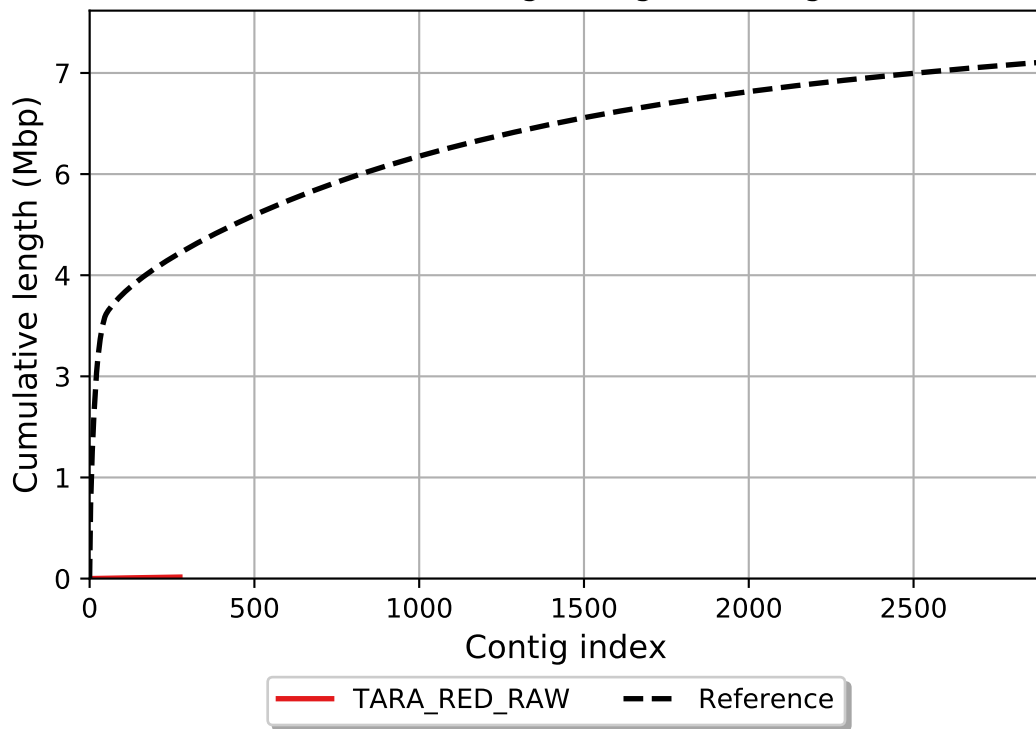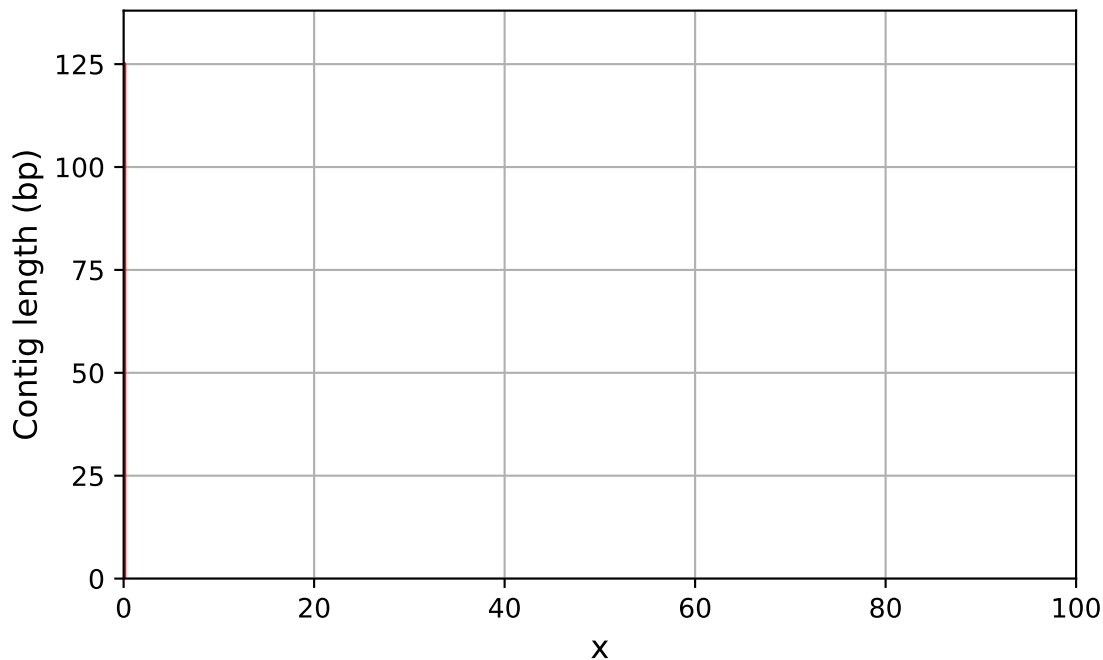
TARA_RED_RAW GC content

Misassemblies

TARA_RED_RAW

FRCurve (misassemblies)
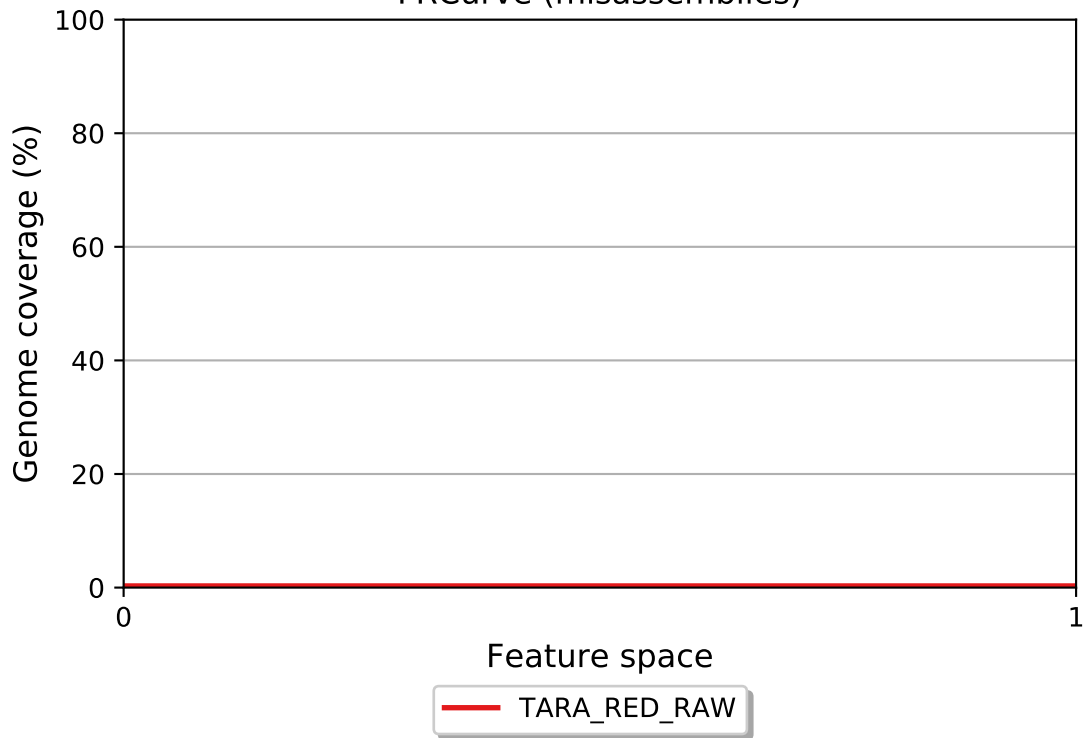
Cumulative length (aligned contigs)

NAx