Report

	TARA_ANE_RAW
# contigs (>= 0 bp)	1382239
# contigs (>= 1000 bp)	1382239
# contigs (>= 5000 bp)	67373
# contigs (>= 10000 bp)	17109
# contigs (>= 25000 bp)	2572
# contigs (>= 50000 bp)	438
Total length (>= 0 bp)	2894913213
Total length (>= 1000 bp)	2894913213
Total length (>= 5000 bp)	647998330
Total length (>= 10000 bp)	312384860
Total length (>= 25000 bp)	104590748
Total length (>= 50000 bp)	33849995
# contigs	1382239
Largest contig	1038928
Total length	2894913213
Reference length	5854900
N50	2156
N75	1382
L50	330727
L75	759418
# 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	1381847 + 391 part
Unaligned length	2894880901
Genome fraction (%)	0.062
Duplication ratio	9.308
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16877.41
# indels per 100 kbp	0.00
Largest alignment	287
Total aligned length	31477

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).
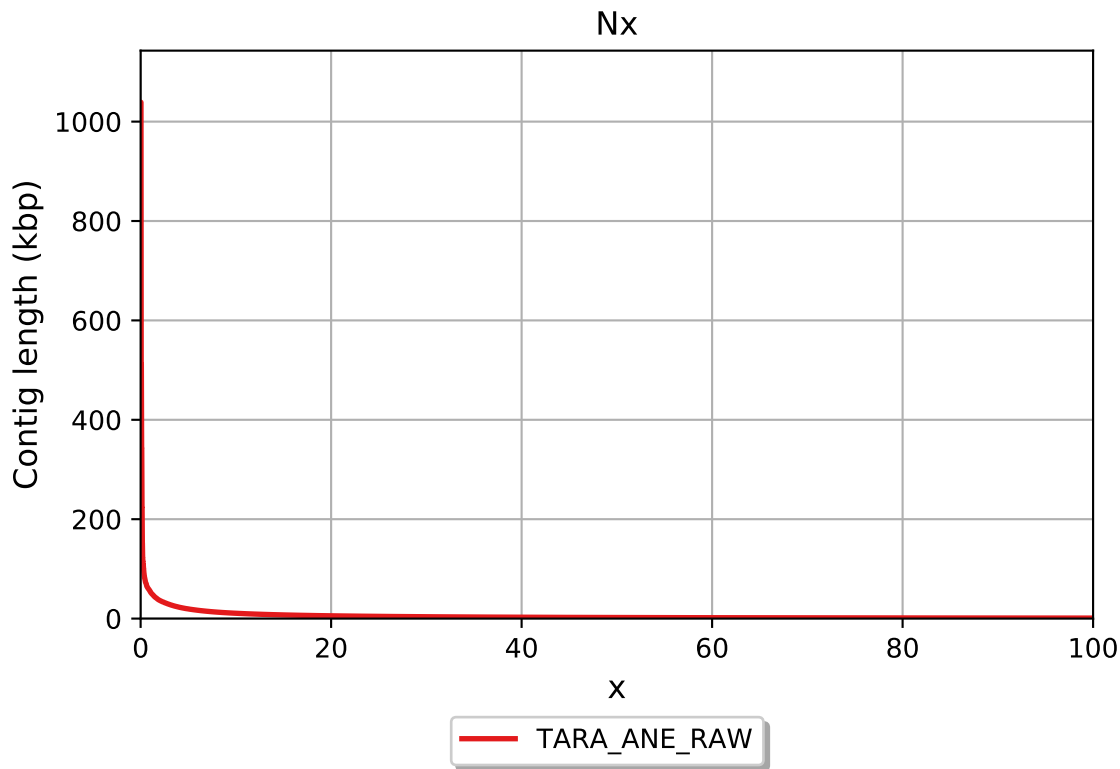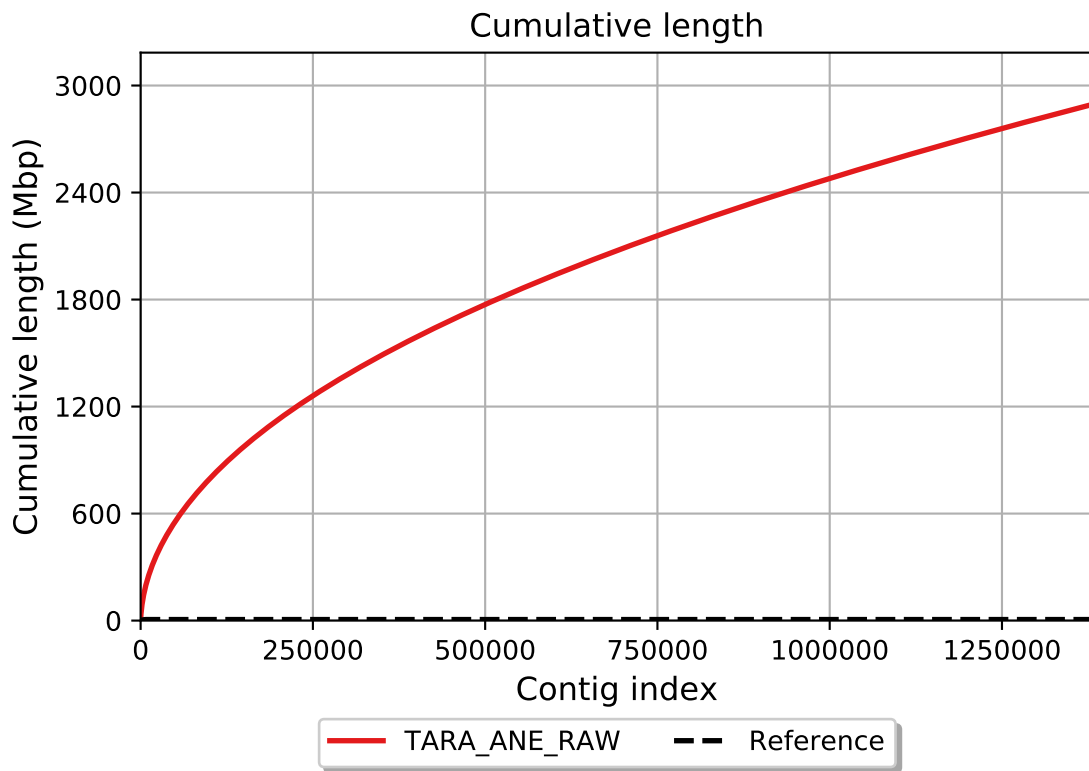
Misassemblies report

	TARA_ANE_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	390
# possible misassemblies	488
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	614
# 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).
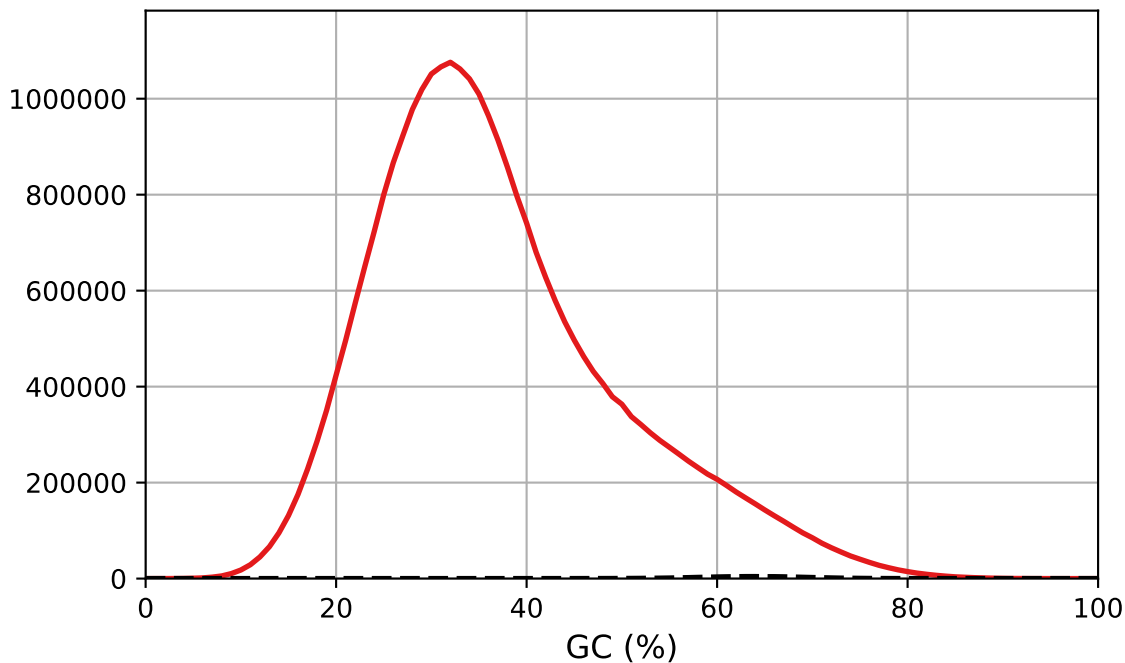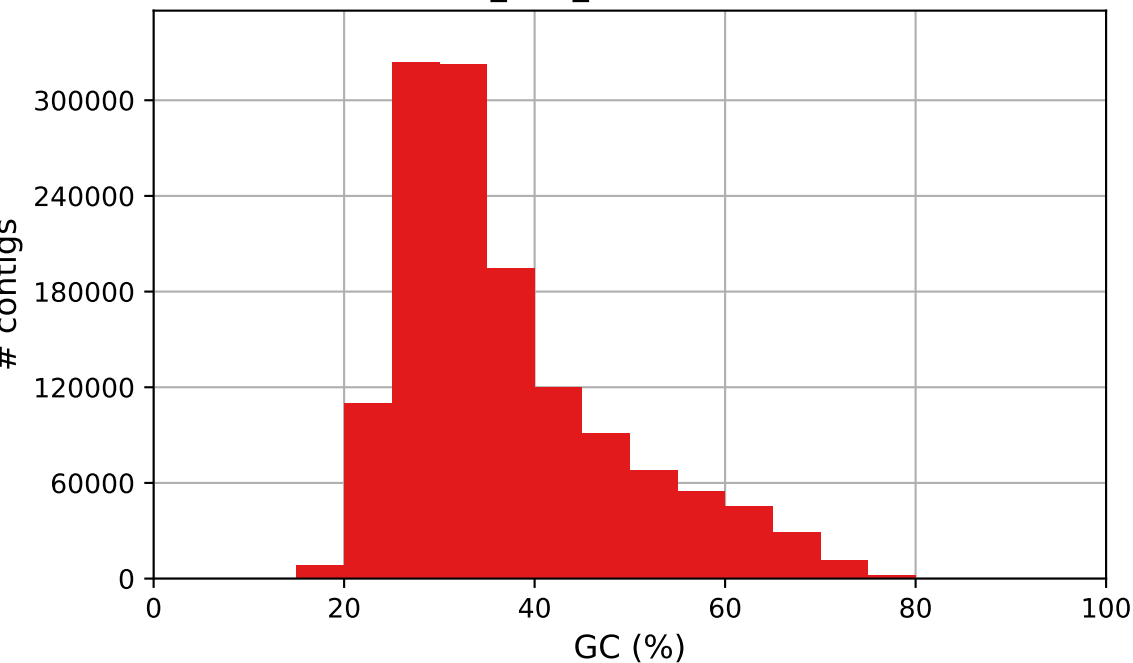
Unaligned report

	TARA_ANE_RAW
# fully unaligned contigs	1381847
Fully unaligned length	2892794232
# partially unaligned contigs	391
Partially unaligned length	2086669
# 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

Contig length (kbp) vs x

TARA_ANE_RAW

Cumulative length

Cumulative length (Mbp) vs Contig index

TARA_ANE_RAW — Reference

GC content

TARA_ANE_RAW GC content

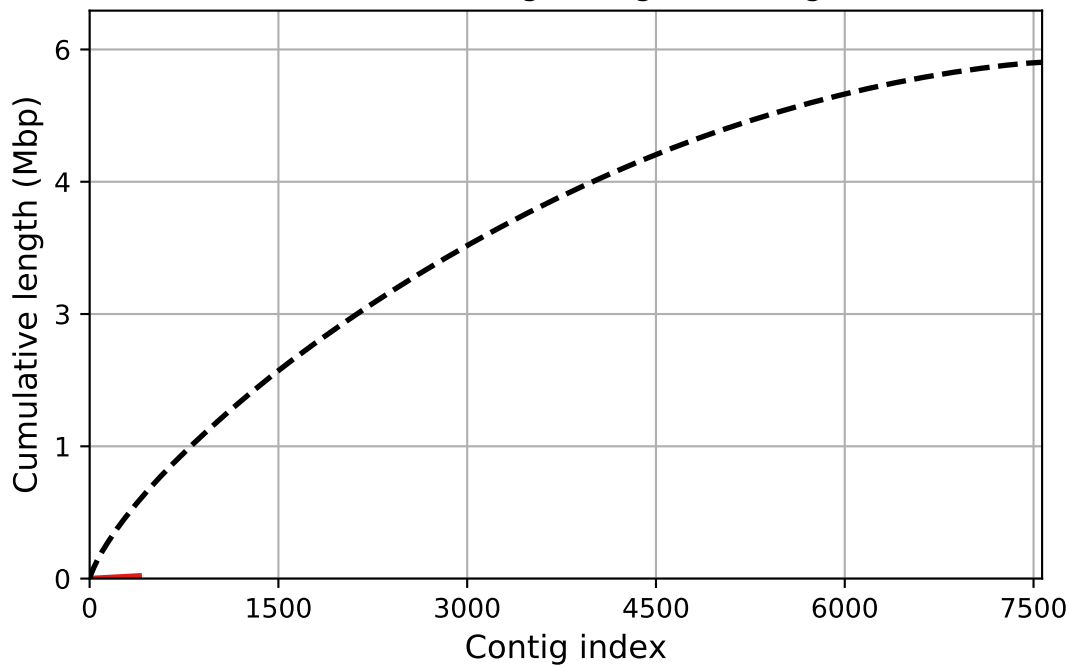# Misassemblies

TARA_ANE_RAW

FRCurve (misassemblies)
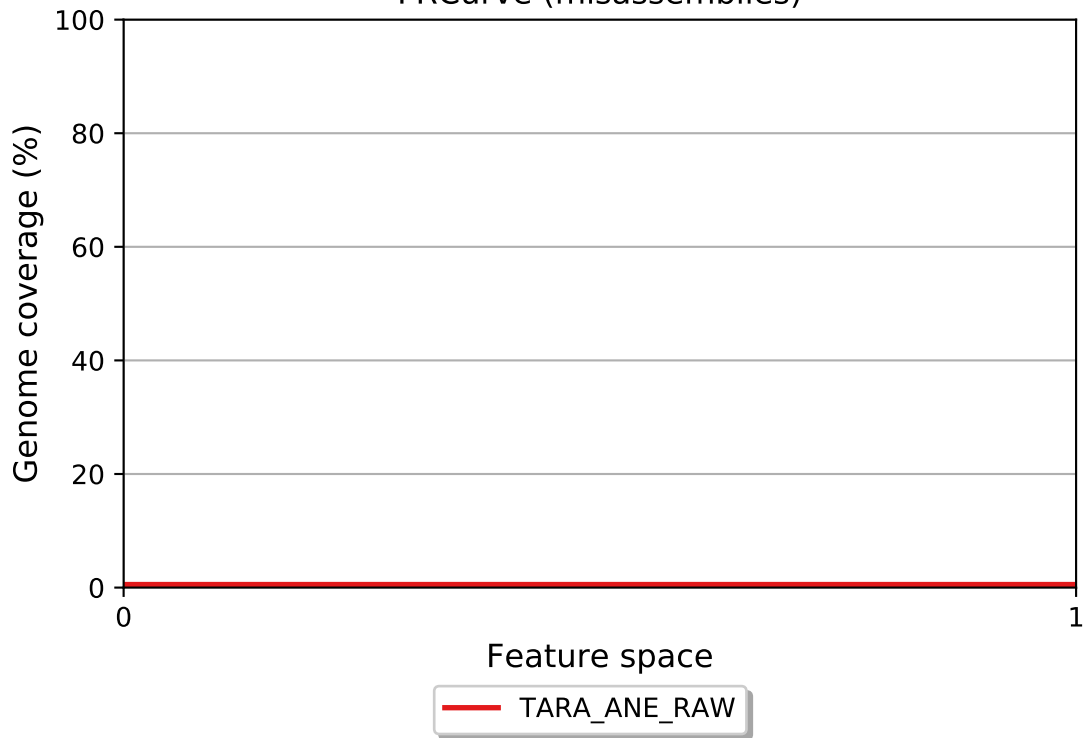
Cumulative length (aligned contigs)