Report

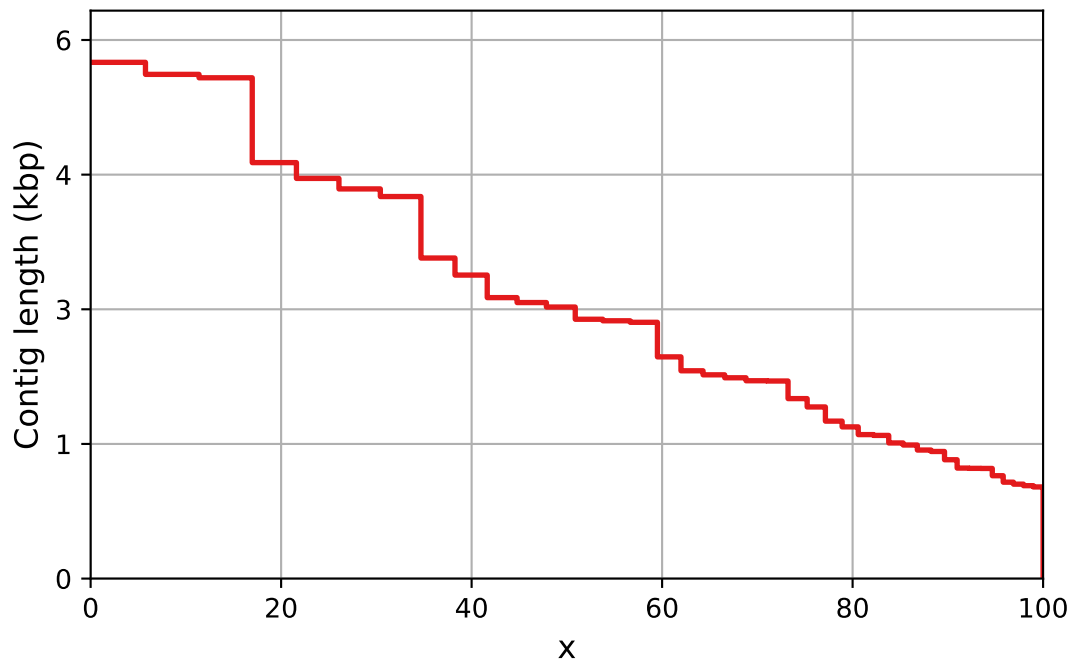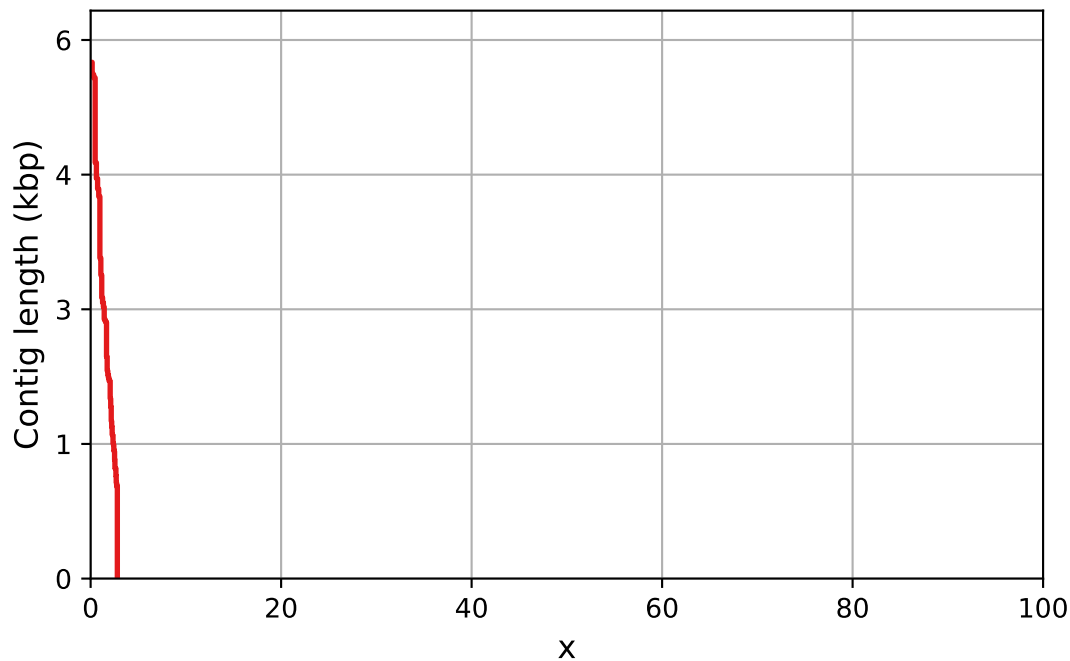|	TARA_MED_RAW
# contigs (>= 1000 bp)	40
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	99876
Total length (>= 5000 bp)	16947
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	40
Largest contig	5751
Total length	99876
Reference length	3561038
GC (%)	48.26
Reference GC (%)	41.87
N50	3025
N75	2005
L50	12
L75	22
# 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	3
# unaligned contigs	3 + 37 part
Unaligned length	96140
Genome fraction (%)	0.033
Duplication ratio	3.193
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9230.77
# indels per 100 kbp	0.00
Largest alignment	230
Total aligned length	3736
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_MED_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	37
# possible misassemblies	44
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	108
# 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).
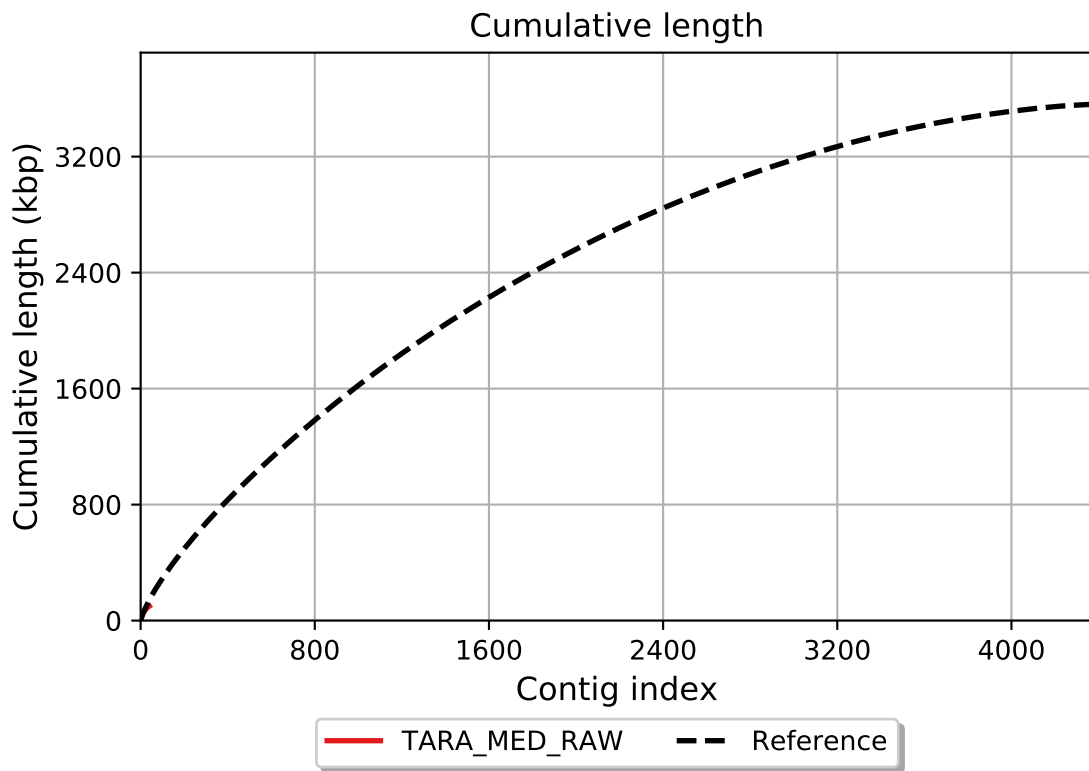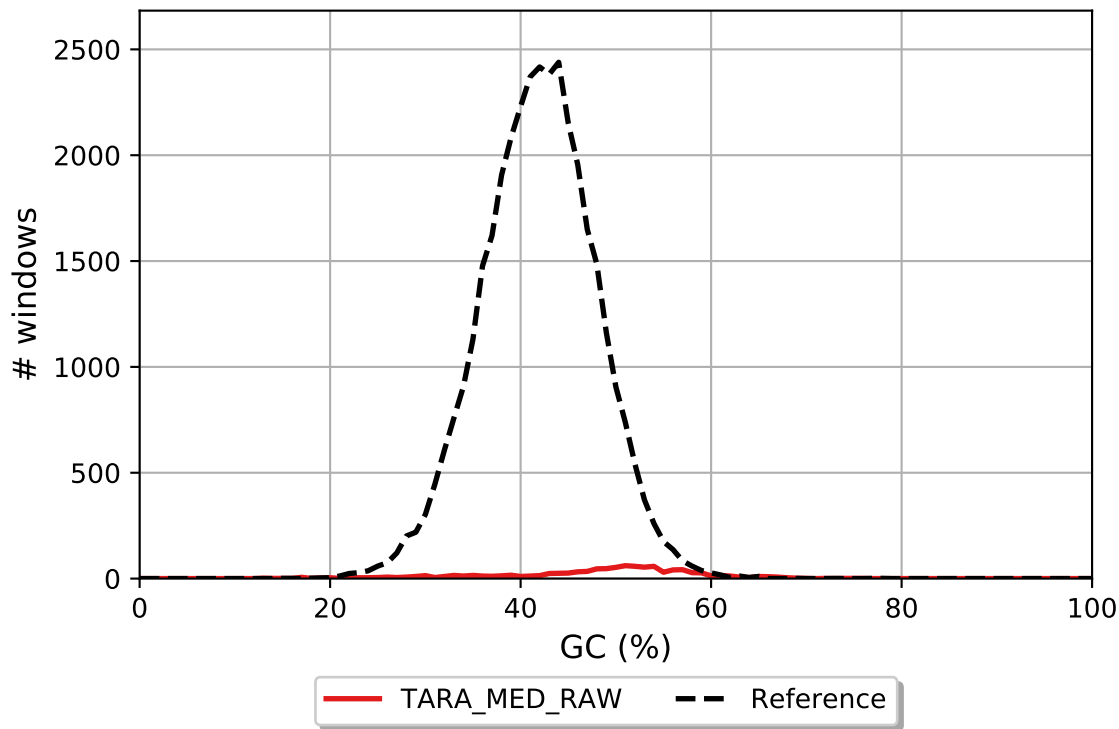
Unaligned report

	TARA_MED_RAW
# fully unaligned contigs	3
Fully unaligned length	5096
# partially unaligned contigs	37
Partially unaligned length	91044
# 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).
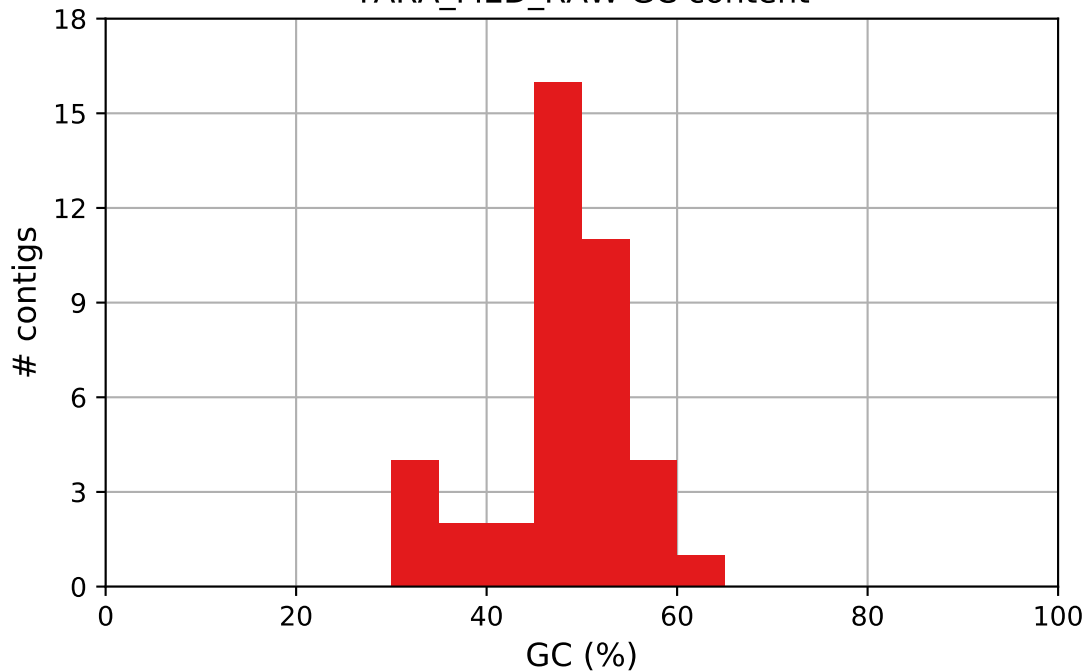
Nx

NGx

TARA_MED_RAW

Cumulative length

GC content

TARA_MED_RAW — — Reference

TARA_MED_RAW GC content

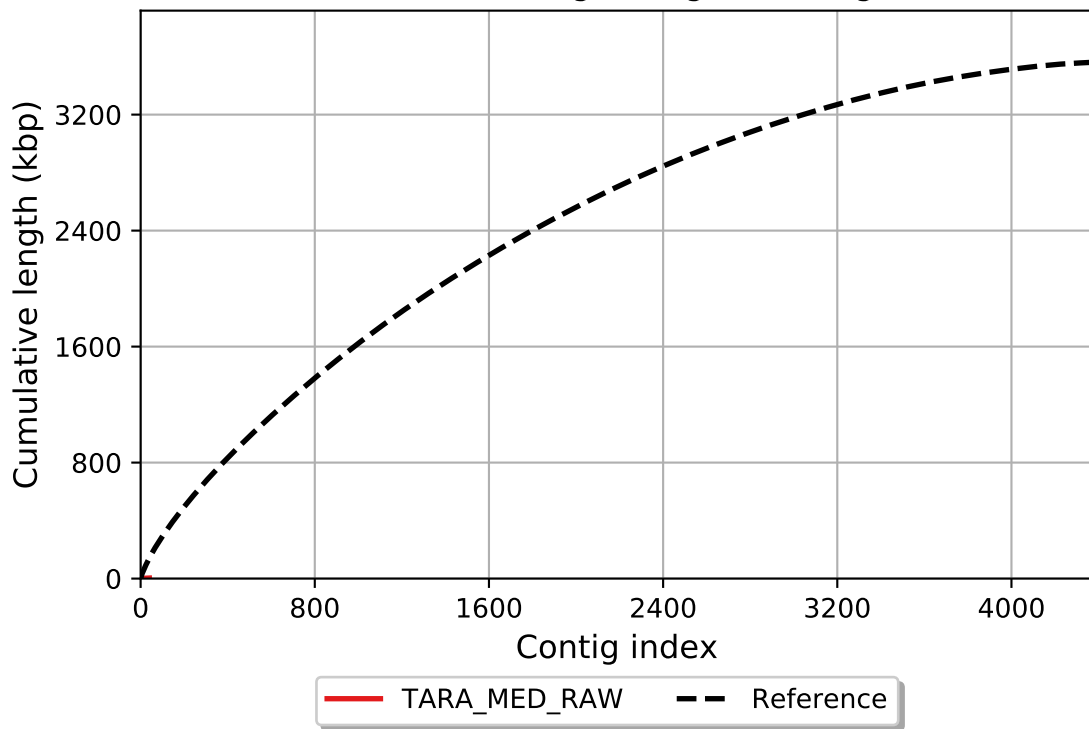# Misassemblies

TARA_MED_RAW

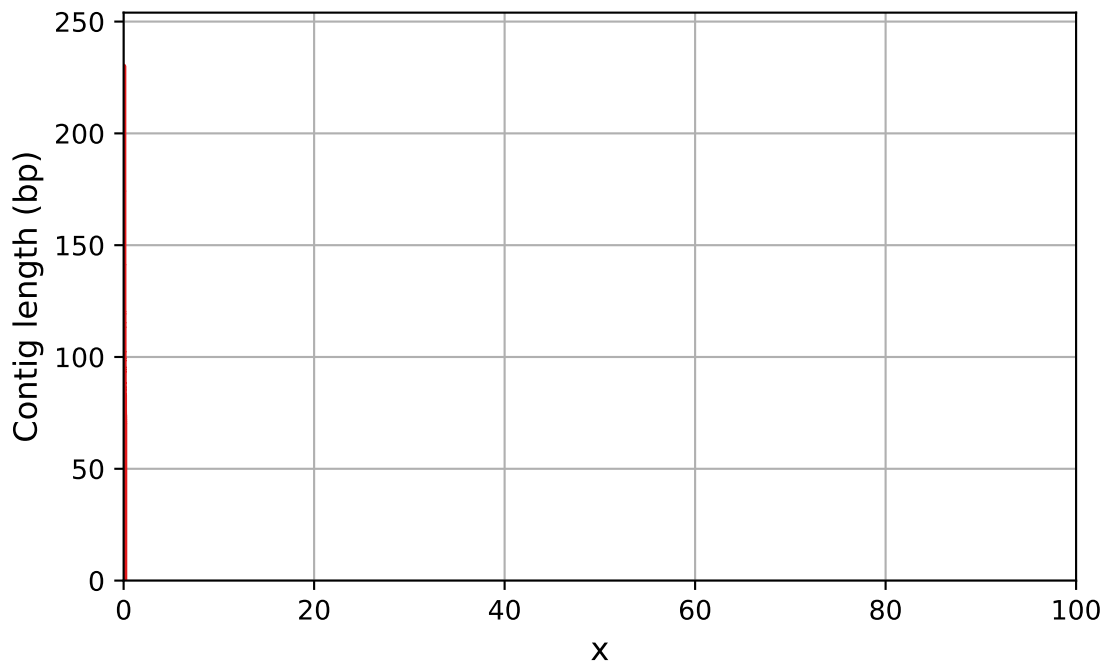FRCurve (misassemblies)
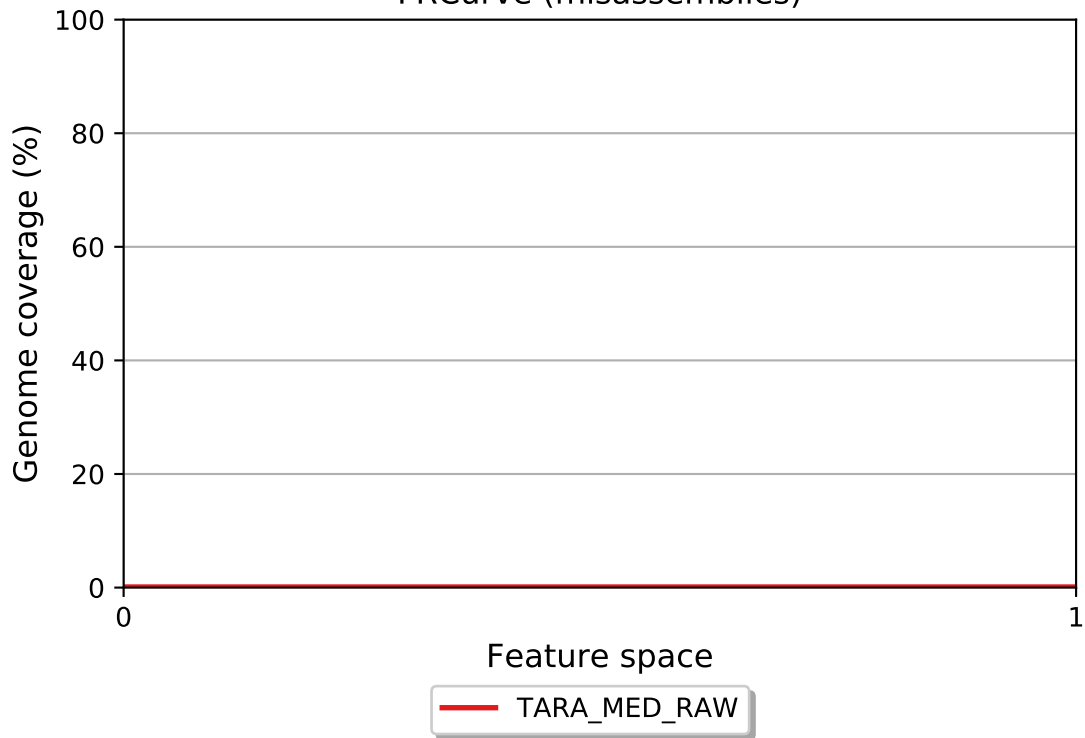
Cumulative length (aligned contigs)

NAx

NGAx