

Report

	TARA_PSE_RAW
# contigs (>= 1000 bp)	51
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	213117
Total length (>= 5000 bp)	120515
Total length (>= 10000 bp)	114251
Total length (>= 25000 bp)	104193
Total length (>= 50000 bp)	104193
# contigs	51
Largest contig	104193
Total length	213117
Reference length	4234461
GC (%)	48.73
Reference GC (%)	41.03
N50	10058
N75	2401
L50	2
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	3 + 48 part
Unaligned length	208446
Genome fraction (%)	0.028
Duplication ratio	3.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11986.30
# indels per 100 kbp	0.00
Largest alignment	200
Total aligned length	4671
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

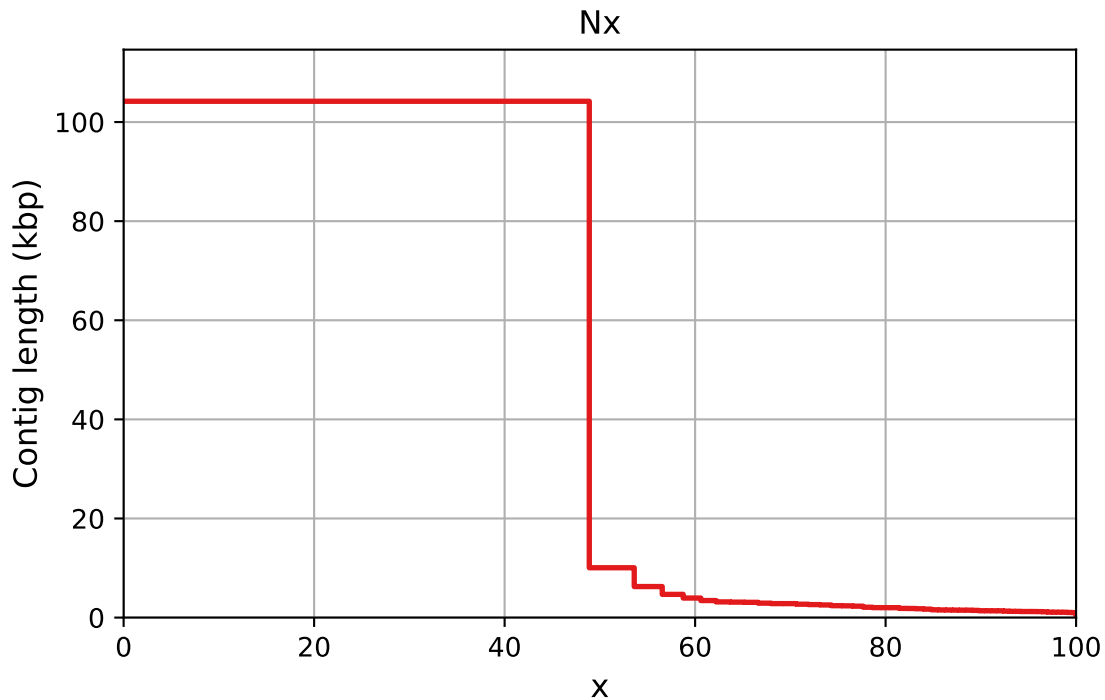
	TARA_PSE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	48
# possible misassemblies	57
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	140
# 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

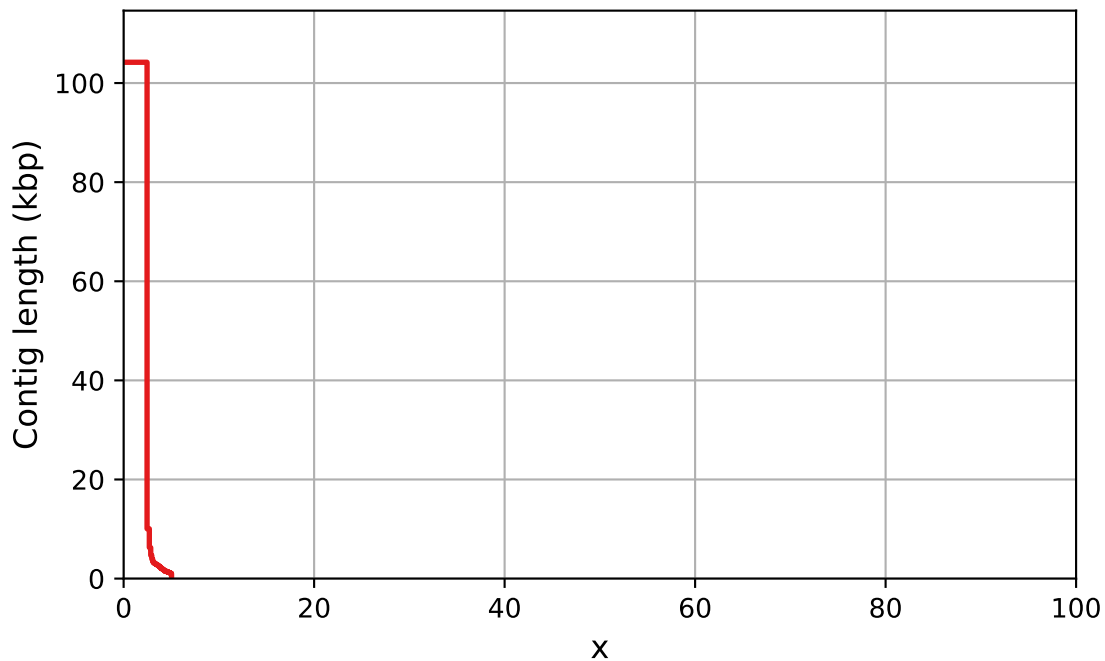
	TARA_PSE_RAW
# fully unaligned contigs	3
Fully unaligned length	7074
# partially unaligned contigs	48
Partially unaligned length	201372
# N's	0

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).



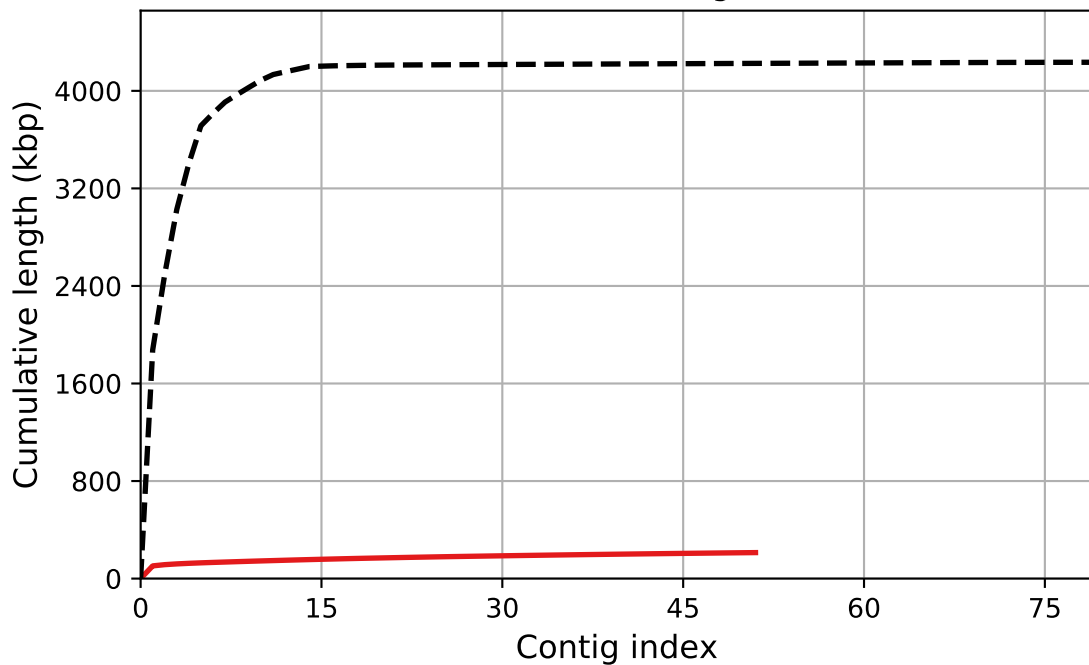
TARA_PSE_RAW

NGx



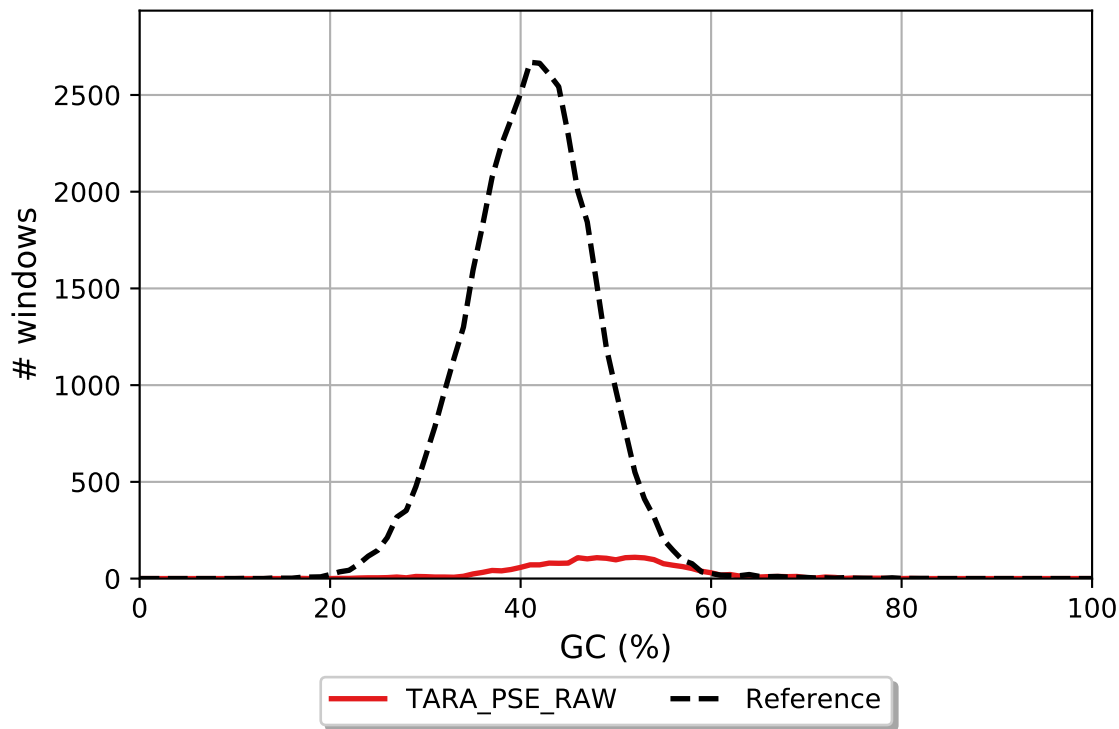
TARA_PSE_RAW

Cumulative length

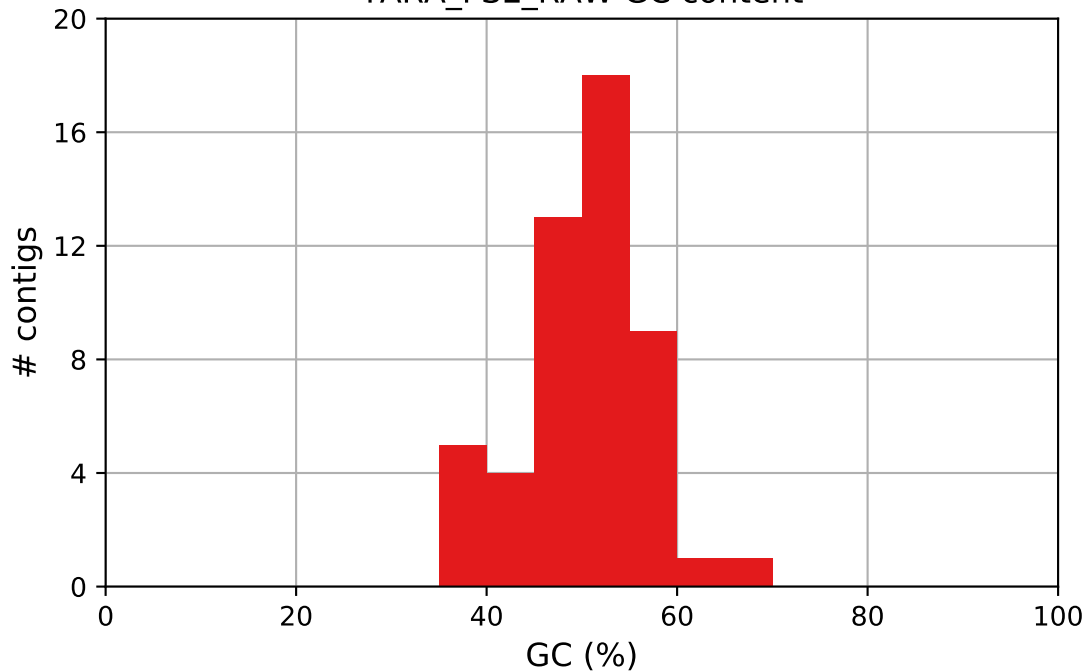


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GC content



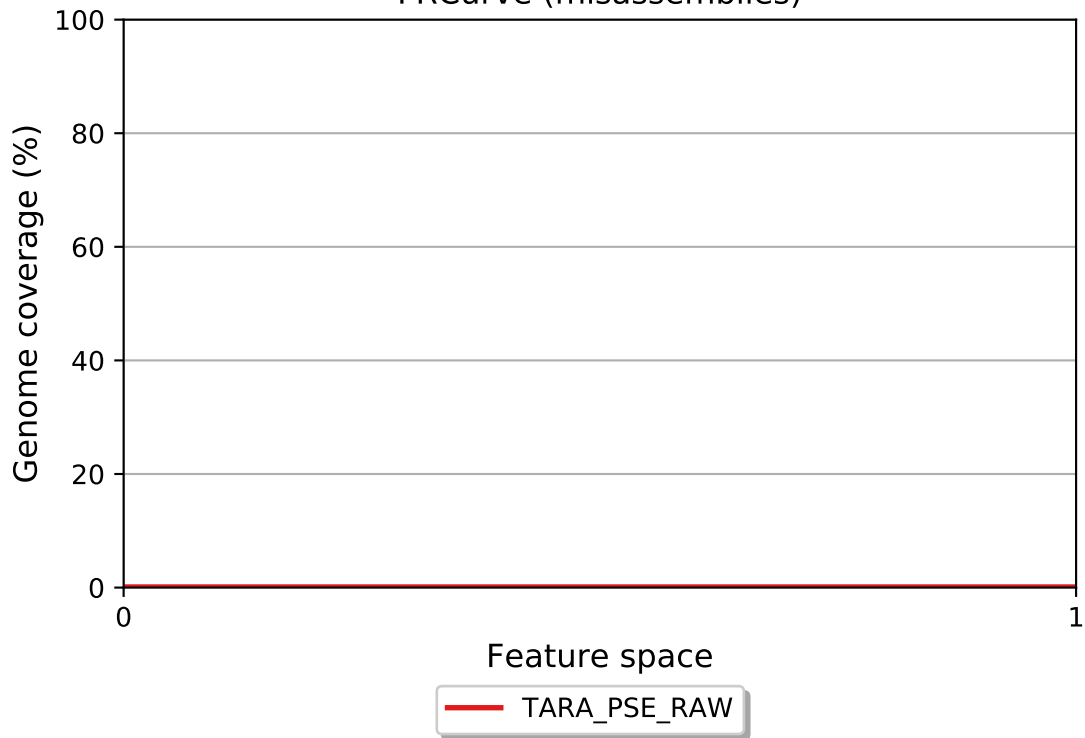
TARA_PSE_RAW GC content



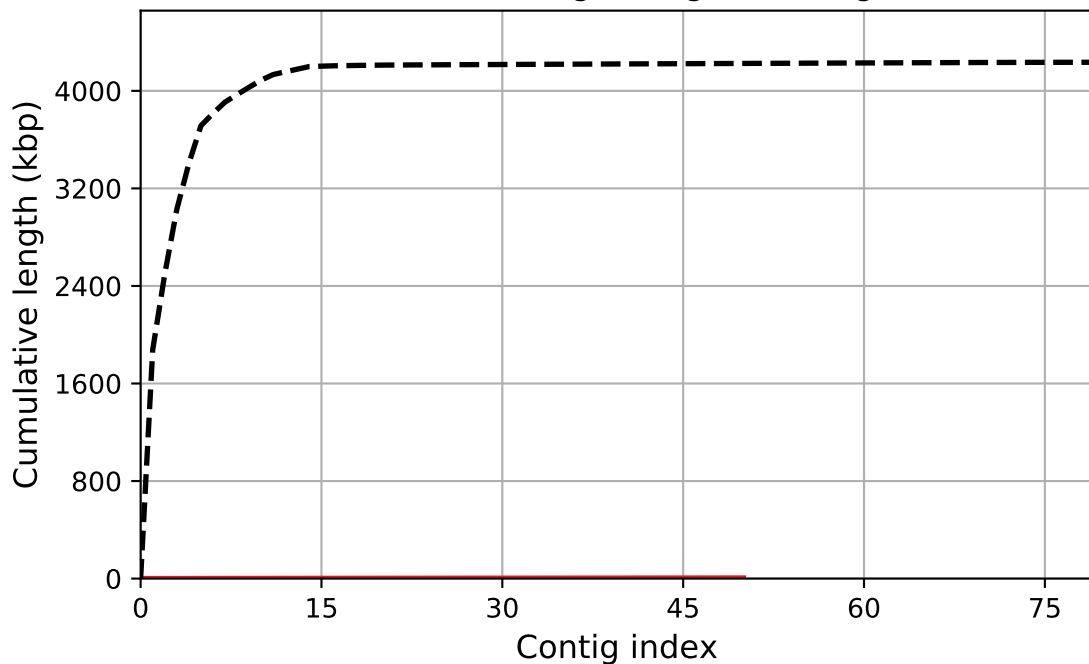
TARA_PSE_RAW

TARA_PSE_RAW

FRCurve (misassemblies)

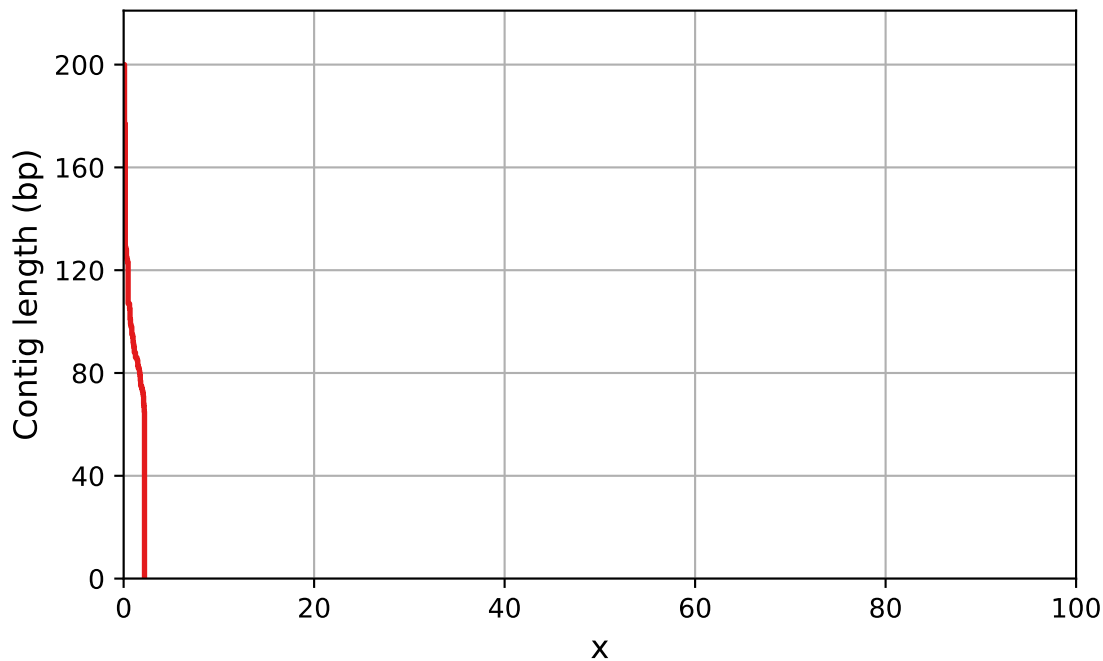


Cumulative length (aligned contigs)



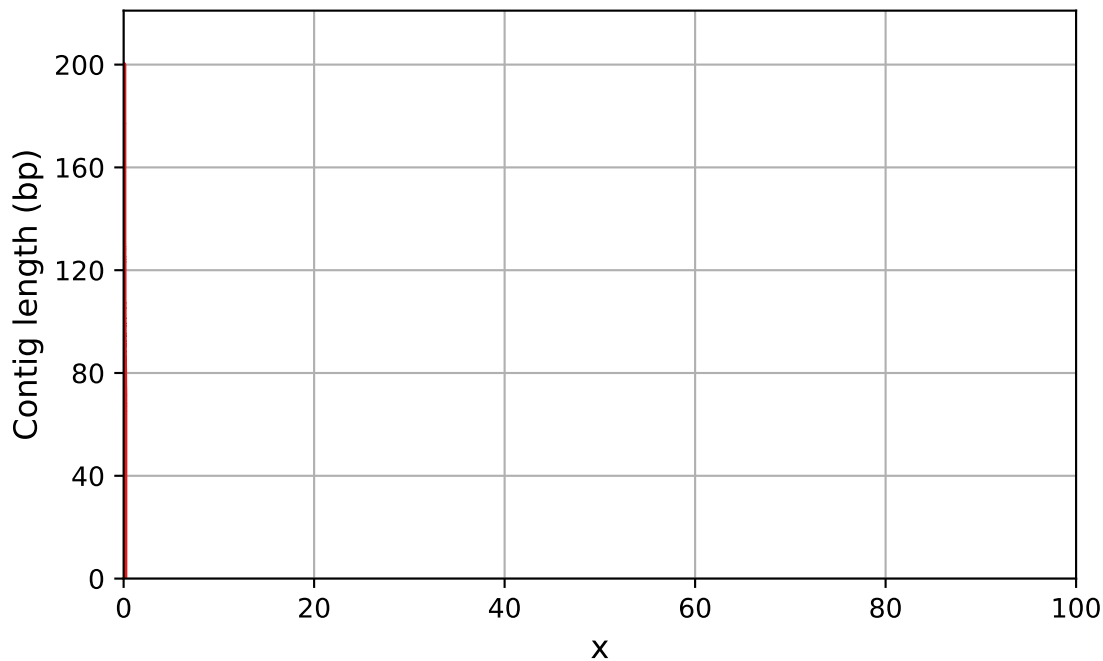
TARA_PSE_RAW Reference

NAx



TARA_PSE_RAW

NGAx



TARA_PSE_RAW