

Report

	TARA_ANE_RAW
# contigs (>= 1000 bp)	40
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	113897
Total length (>= 5000 bp)	43563
Total length (>= 10000 bp)	43563
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	40
Largest contig	24659
Total length	113897
Reference length	4234461
GC (%)	47.65
Reference GC (%)	41.03
N50	3076
N75	1925
L50	6
L75	17
# 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	8 + 32 part
Unaligned length	110697
Genome fraction (%)	0.019
Duplication ratio	3.941
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11083.74
# indels per 100 kbp	0.00
Largest alignment	120
Total aligned length	3200
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_ANE_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	36
# possible misassemblies	37
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	90
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

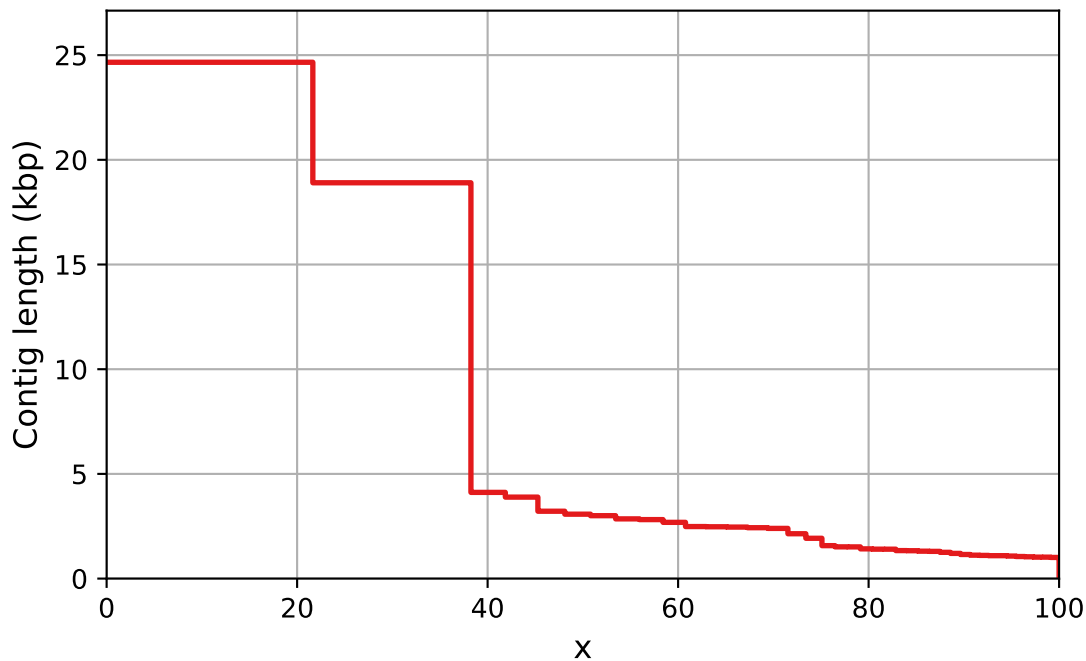
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_ANE_RAW
# fully unaligned contigs	8
Fully unaligned length	14039
# partially unaligned contigs	32
Partially unaligned length	96658
# N's	0

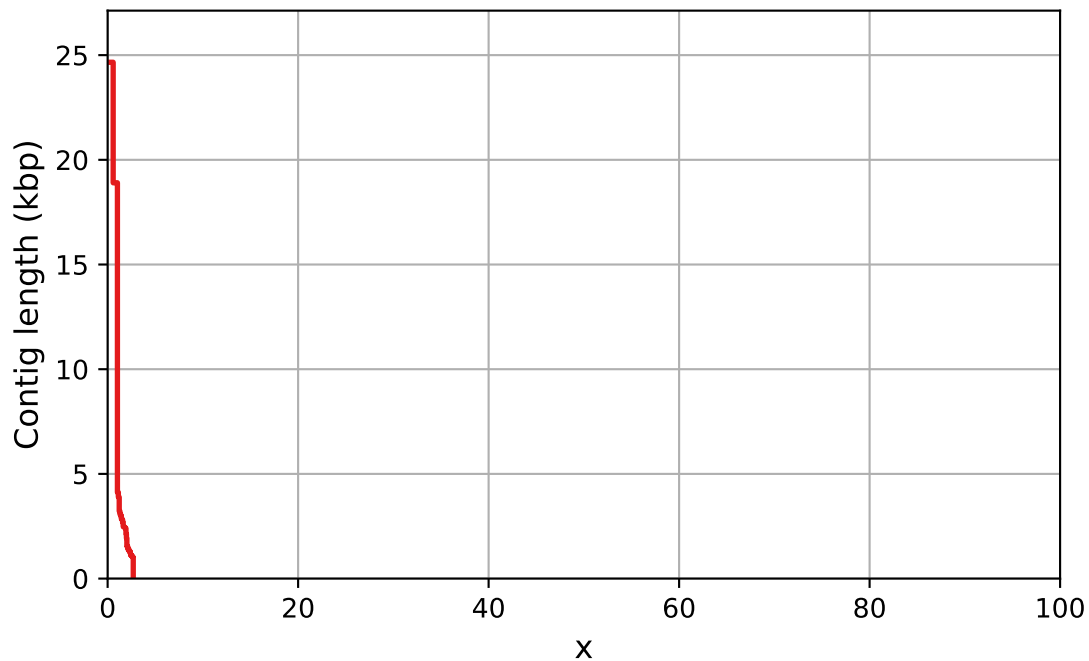
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

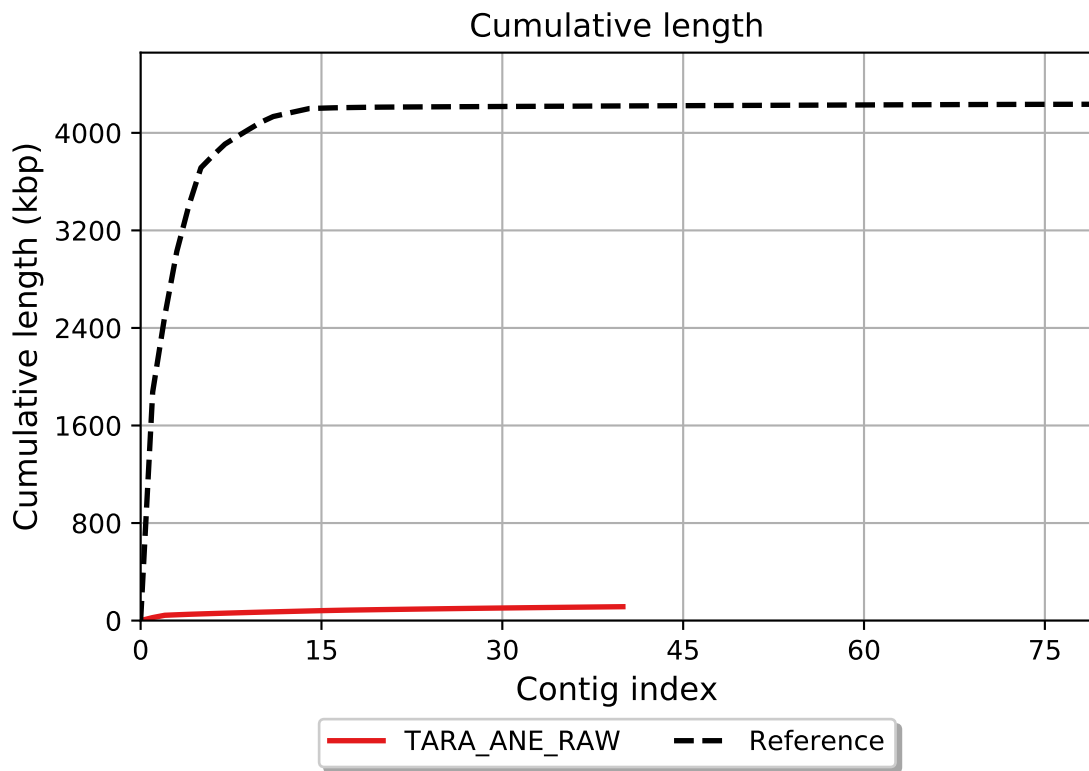


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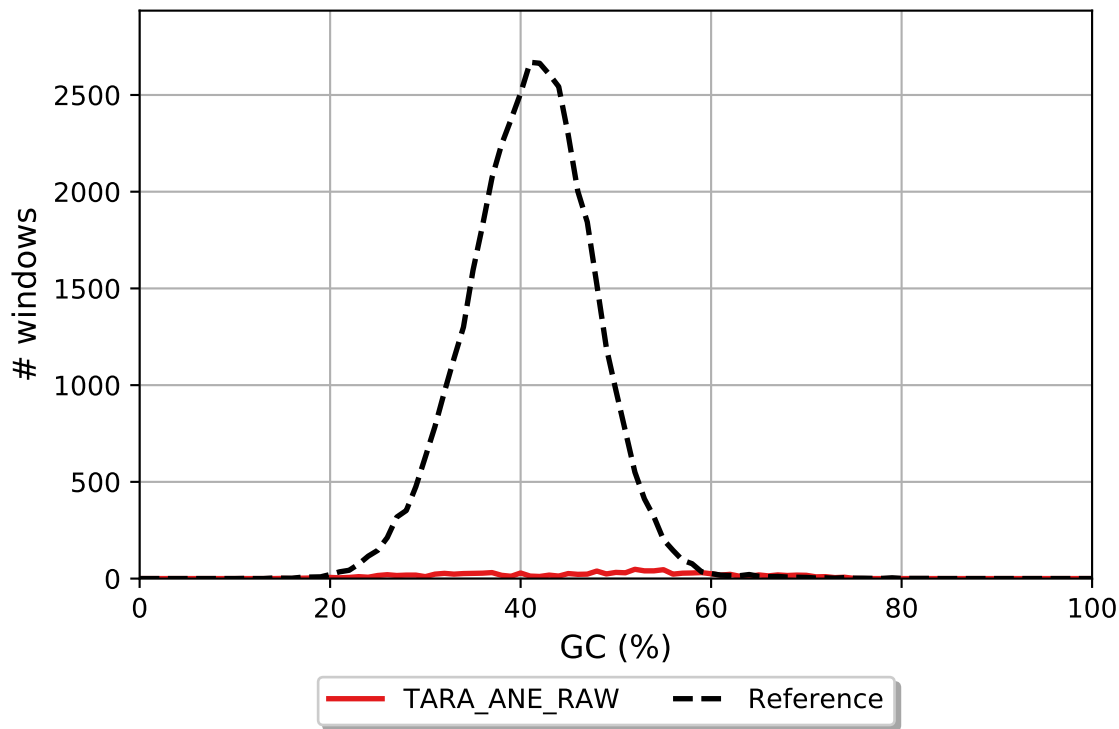
NGx



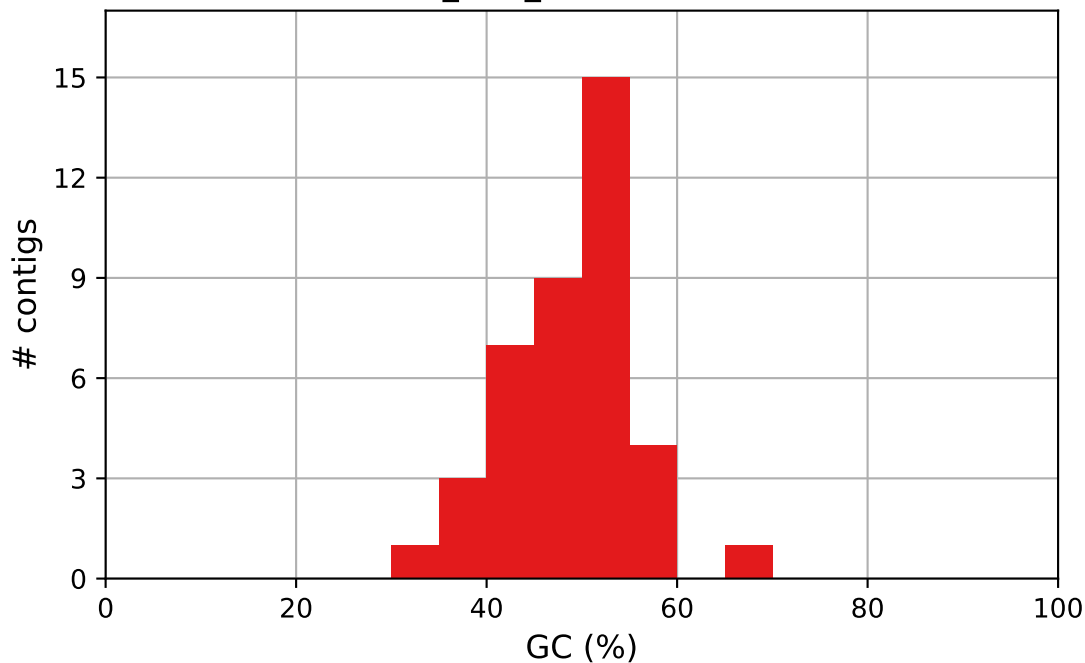
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GC content



TARA_ANE_RAW GC content

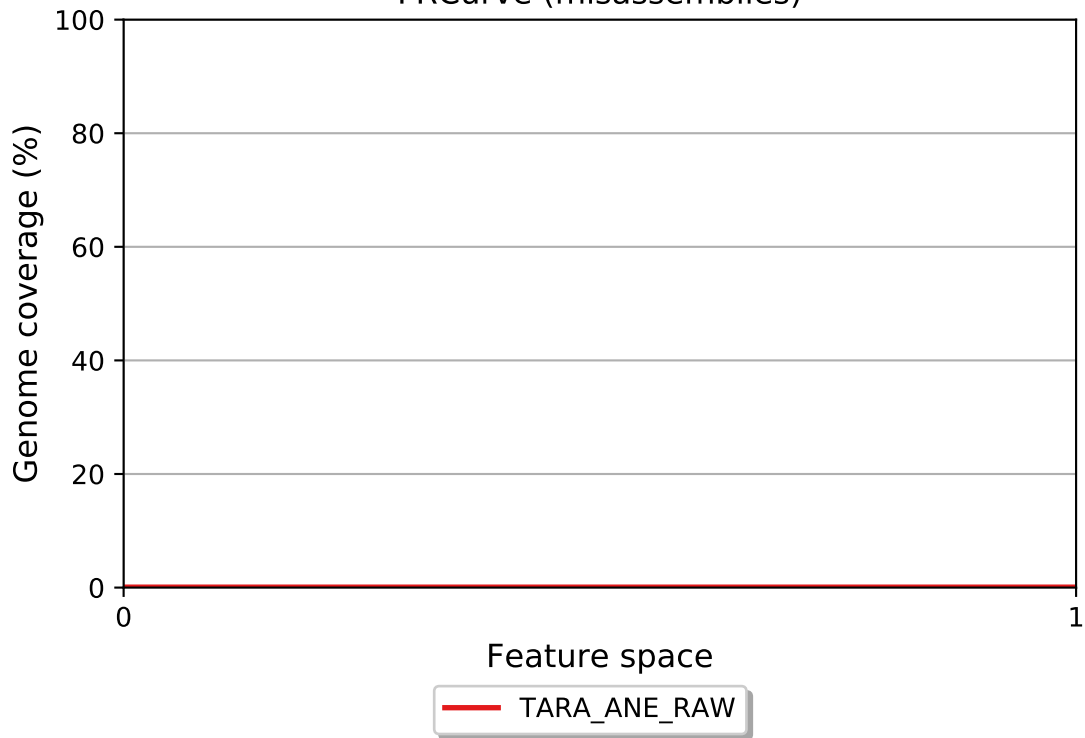


TARA_ANE_RAW

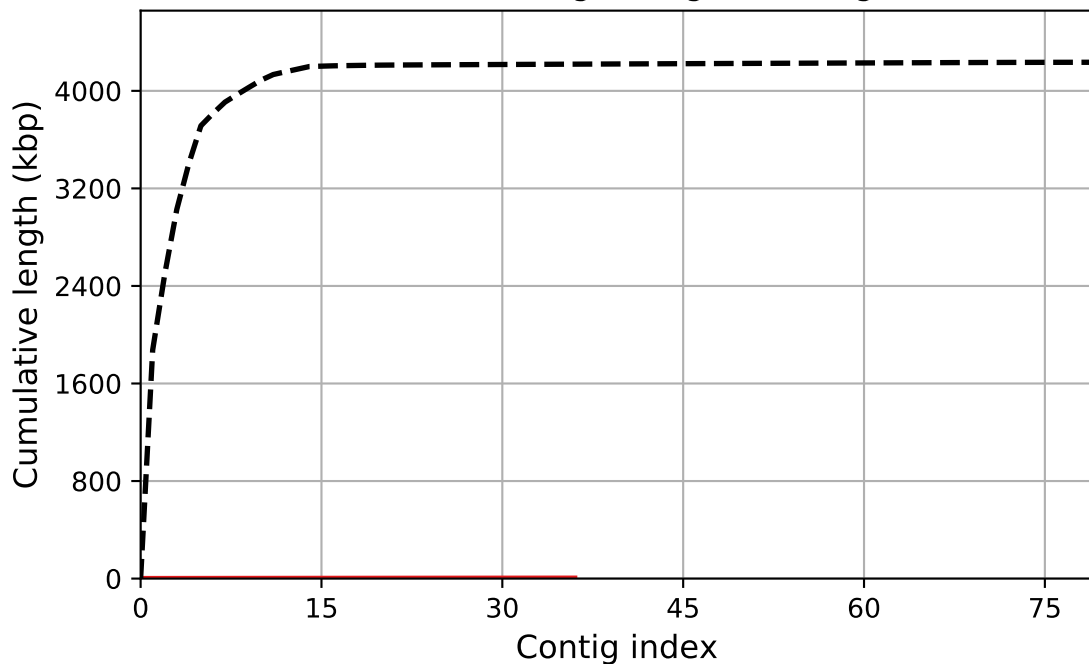
Misassemblies



FRCurve (misassemblies)

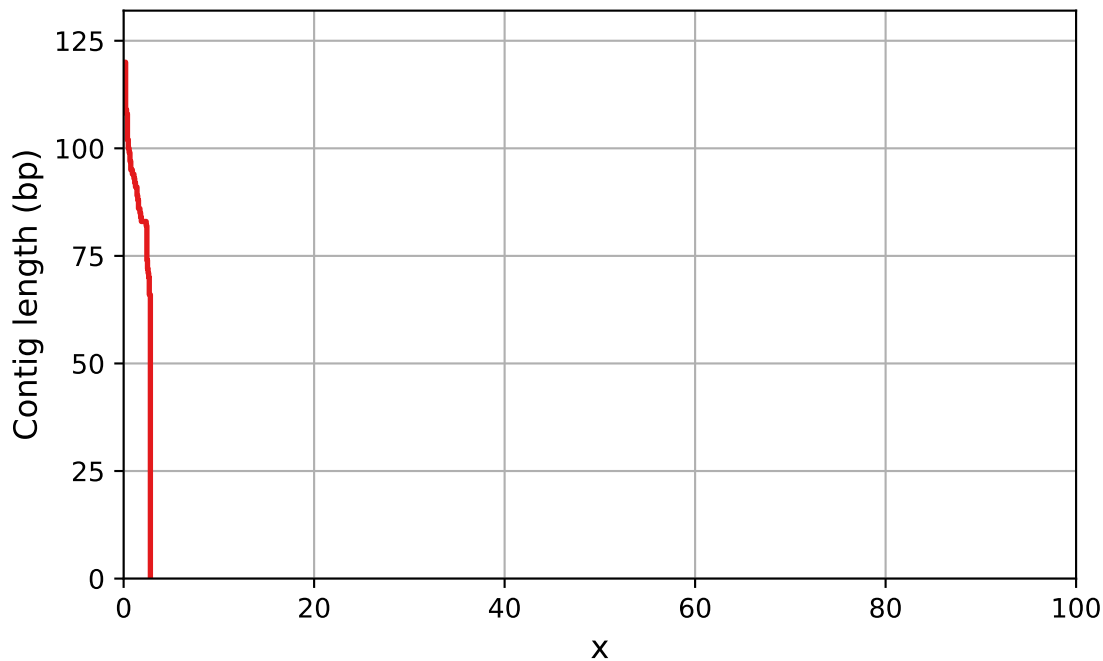


Cumulative length (aligned contigs)



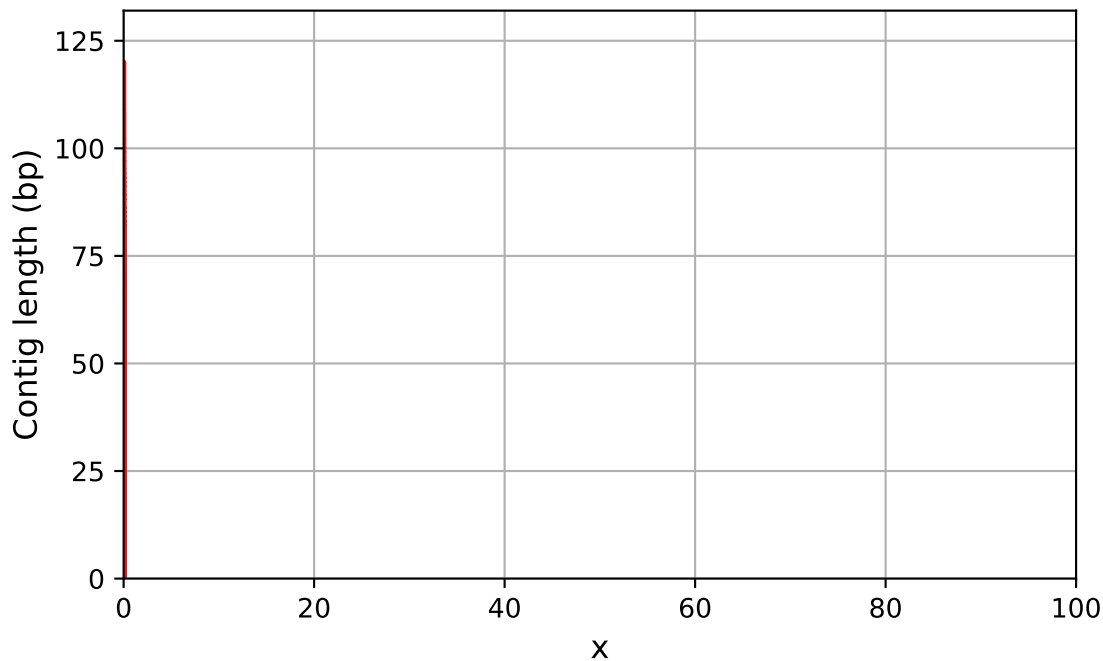
TARA_ANE_RAW Reference

NAx



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NGAx



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