

# Report

	TARA_PON_RAW
# contigs (>= 1000 bp)	301
# contigs (>= 5000 bp)	40
# contigs (>= 10000 bp)	25
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	1283134
Total length (>= 5000 bp)	768051
Total length (>= 10000 bp)	669062
Total length (>= 25000 bp)	456871
Total length (>= 50000 bp)	172950
# contigs	301
Largest contig	61783
Total length	1283134
Reference length	5854900
GC (%)	35.64
Reference GC (%)	63.53
N50	11720
N75	2585
L50	23
L75	96
# 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	7 + 292 part
Unaligned length	1257380
Genome fraction (%)	0.058
Duplication ratio	7.550
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12547.64
# indels per 100 kbp	146.58
Largest alignment	335
Total aligned length	23959
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_PON_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	294
# possible misassemblies	352
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	428
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

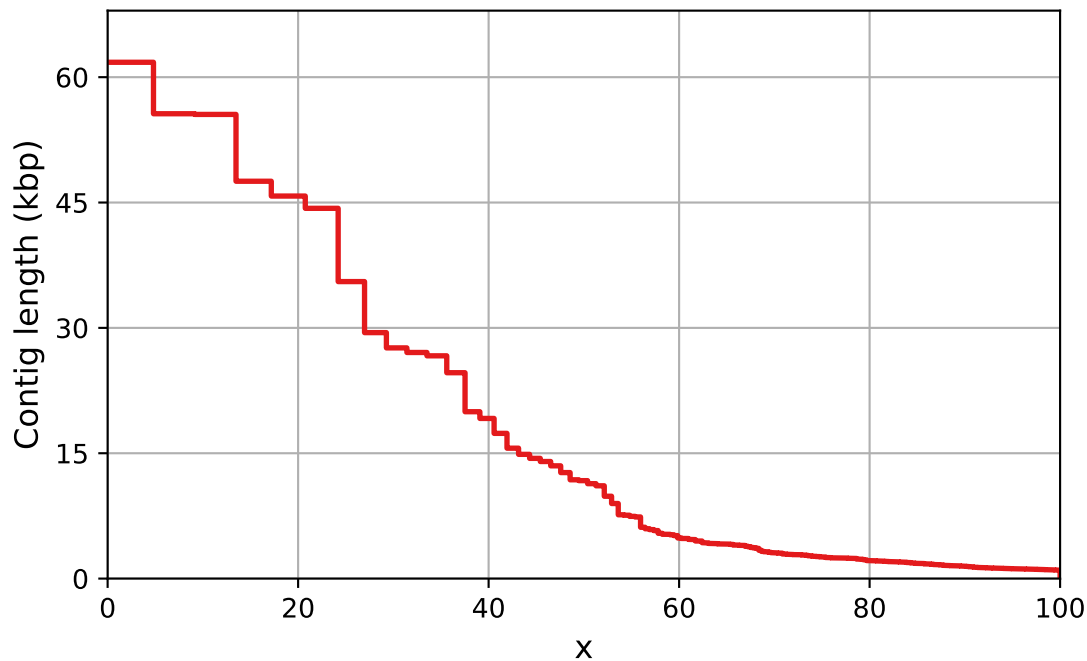
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_PON_RAW
# fully unaligned contigs	7
Fully unaligned length	13259
# partially unaligned contigs	292
Partially unaligned length	1244121
# N's	0

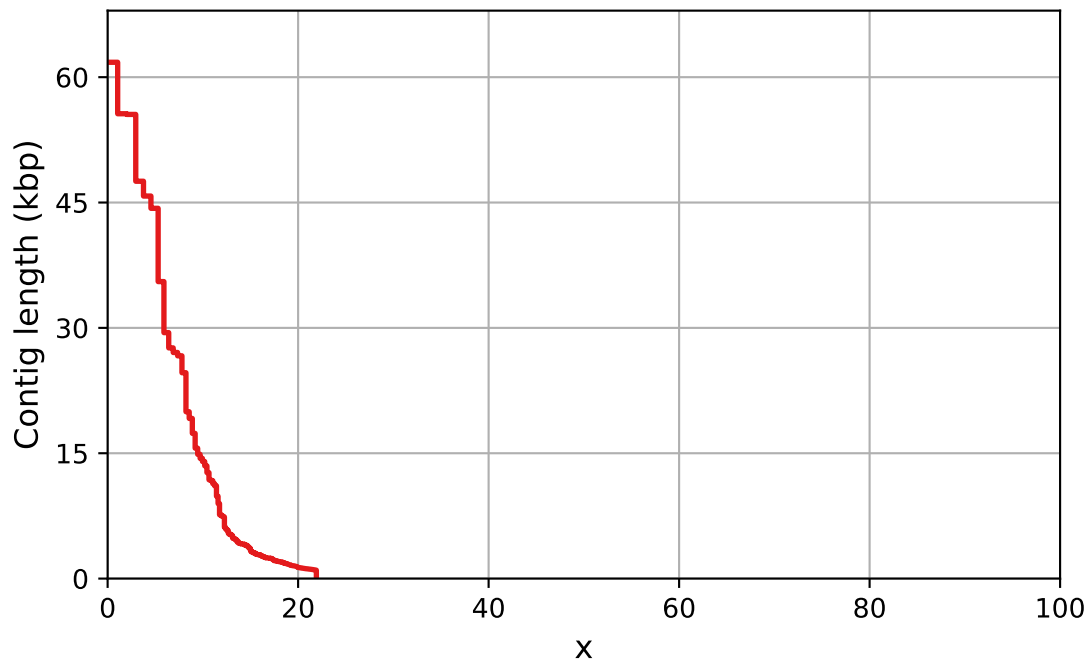
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



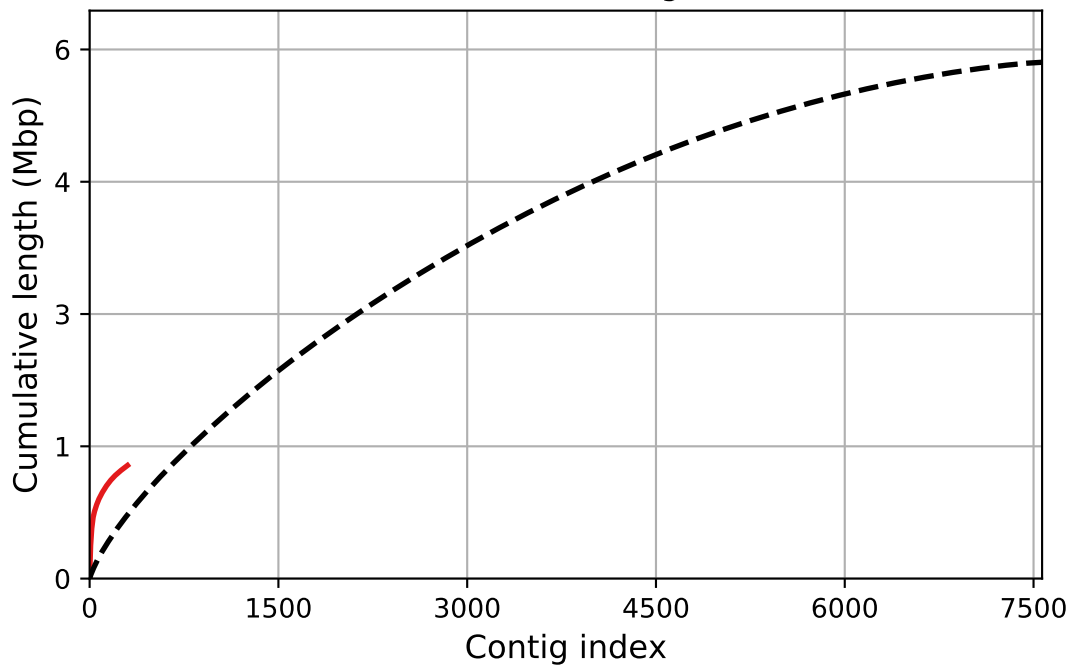
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NGx



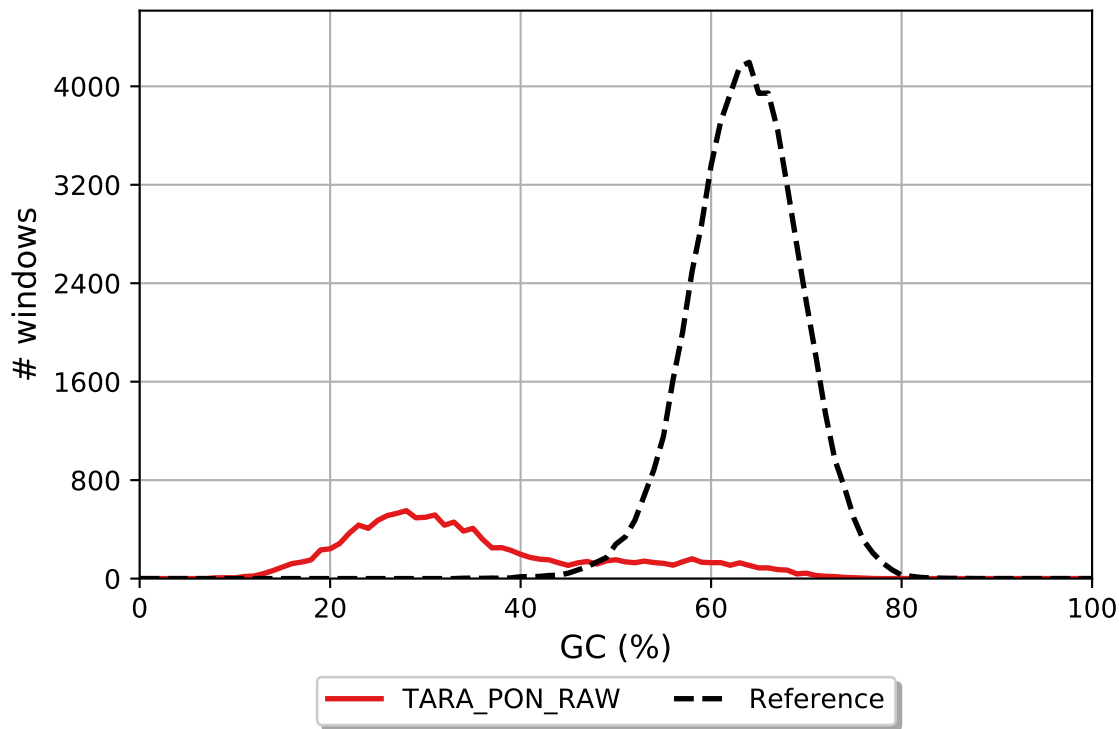
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Cumulative length

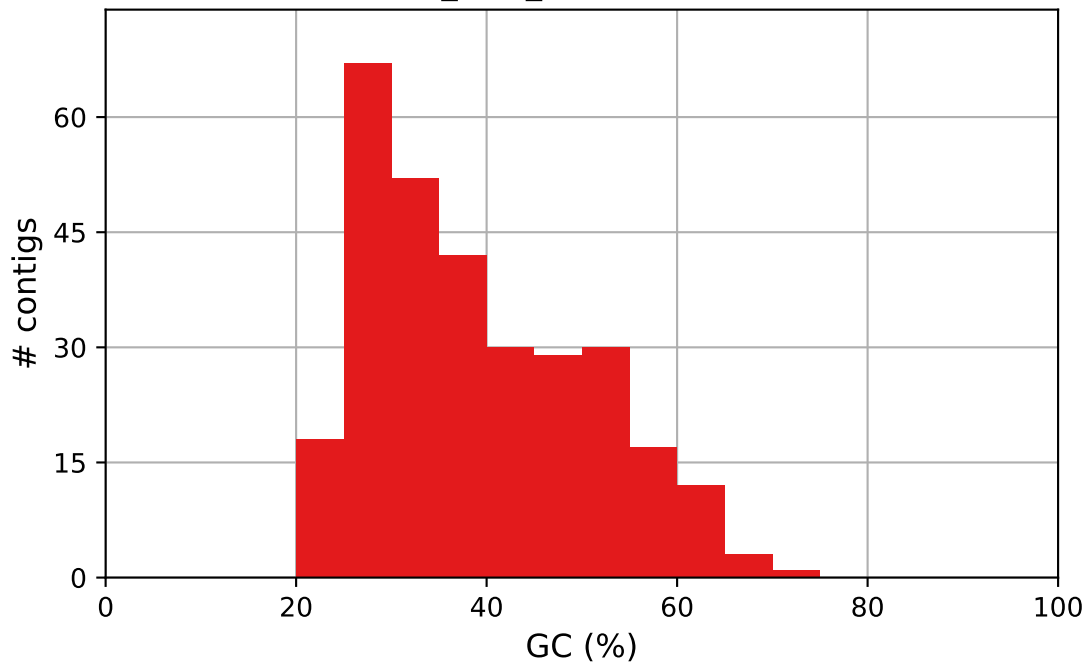


— TARA\_PON\_RAW    - - Reference

## GC content



TARA\_PON\_RAW GC content



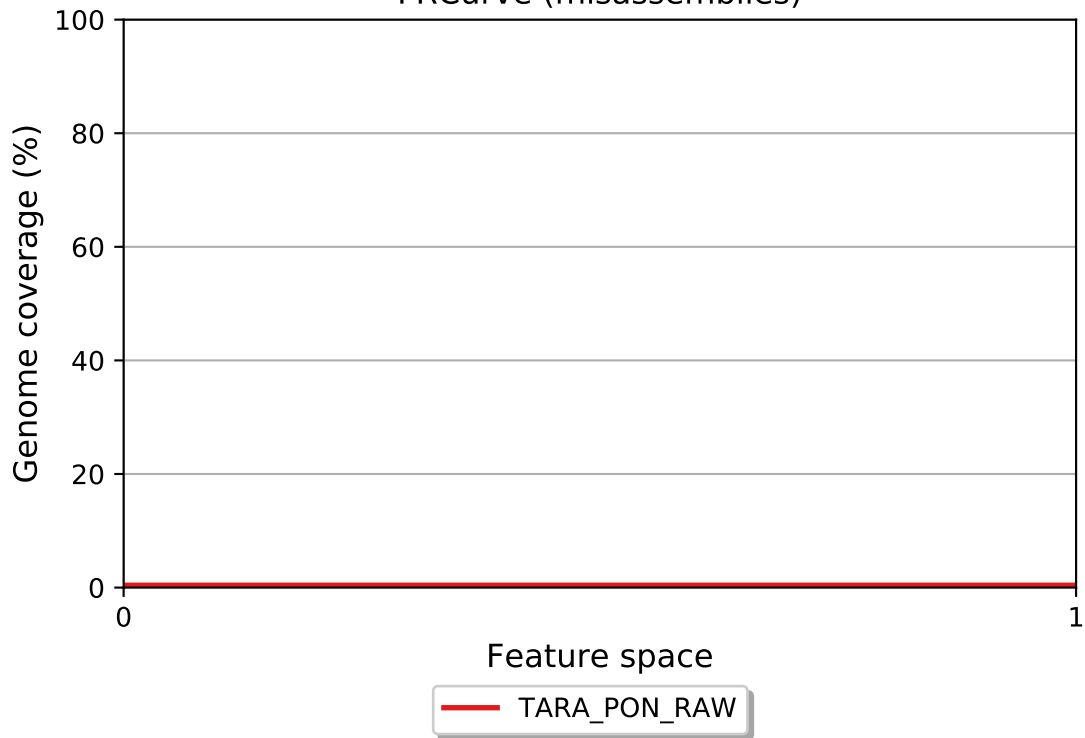
TARA\_PON\_RAW



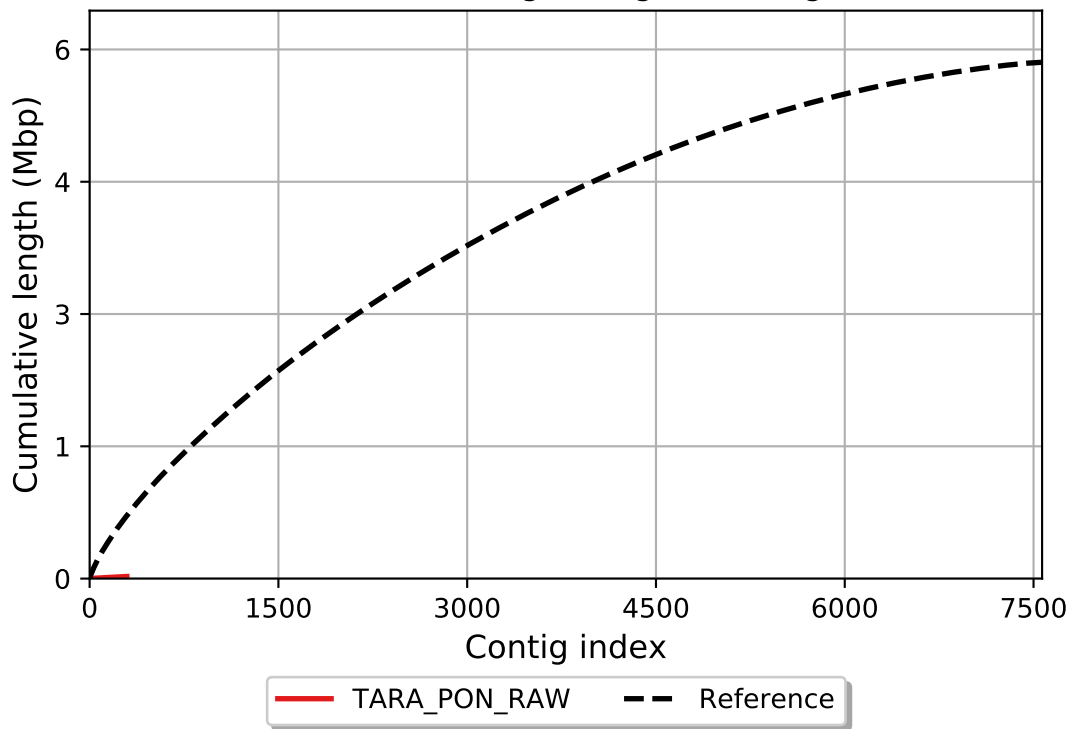
## Misassemblies



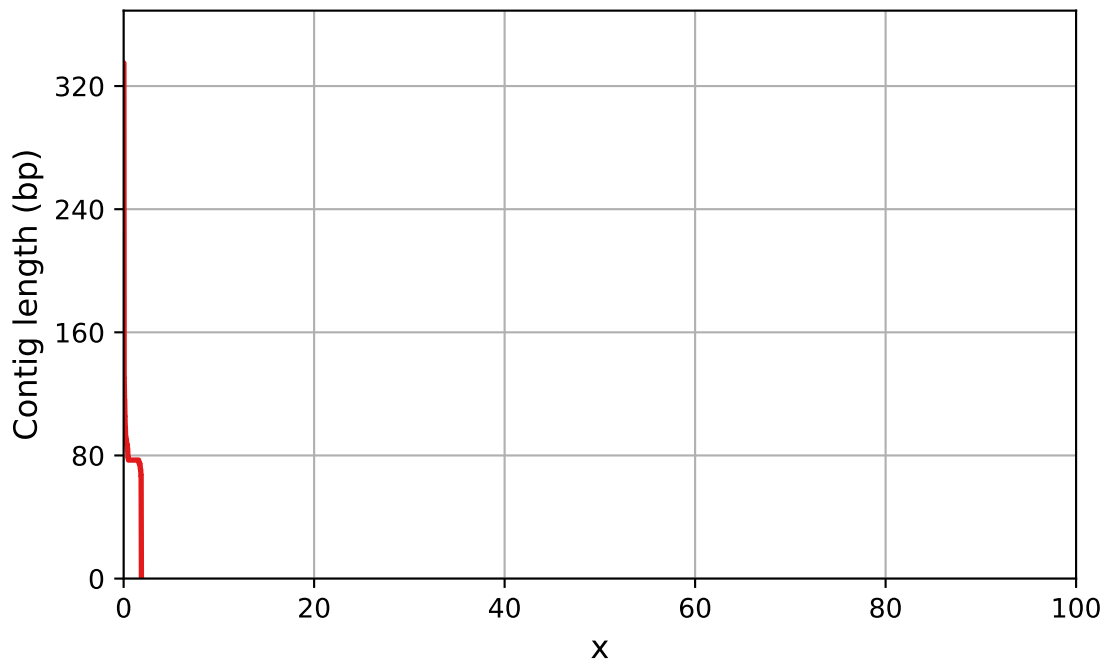
FRCurve (misassemblies)



Cumulative length (aligned contigs)

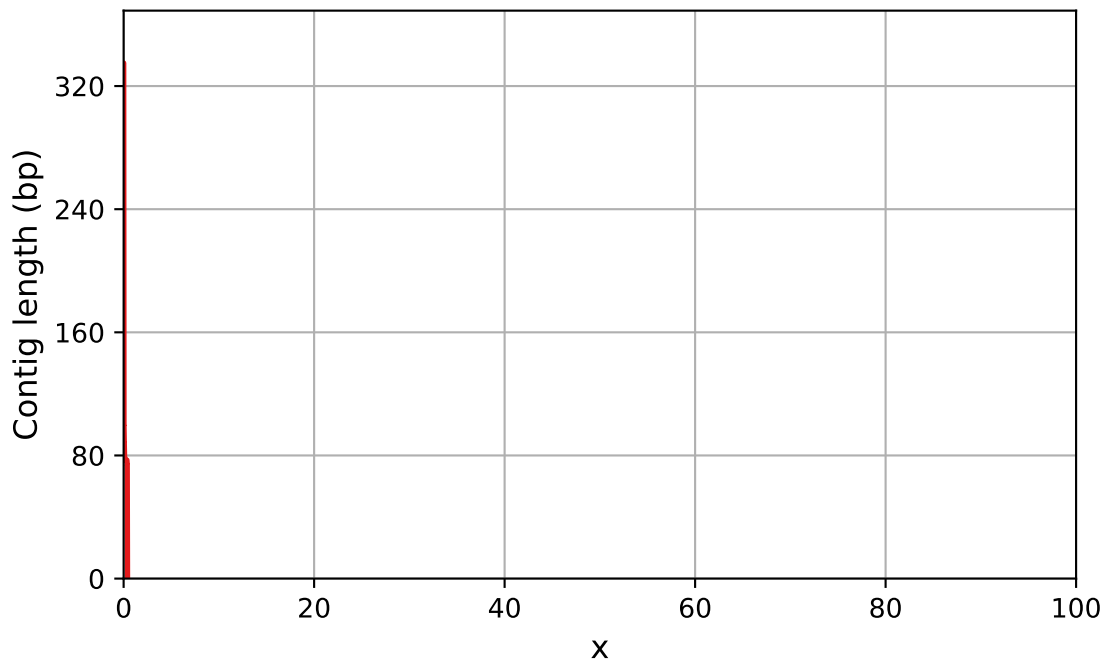


NAx



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# NGAx



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