

# Report

	TARA_ASE_RAW
# contigs (>= 1000 bp)	125
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	288230
Total length (>= 5000 bp)	85069
Total length (>= 10000 bp)	40117
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	125
Largest contig	14515
Total length	288230
Reference length	5854900
GC (%)	42.55
Reference GC (%)	63.53
N50	2436
N75	1534
L50	30
L75	68
# 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	4 + 120 part
Unaligned length	276265
Genome fraction (%)	0.069
Duplication ratio	2.956
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4767.79
# indels per 100 kbp	0.00
Largest alignment	1116
Total aligned length	11278
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_ASE_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	122
# possible misassemblies	140
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	193
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

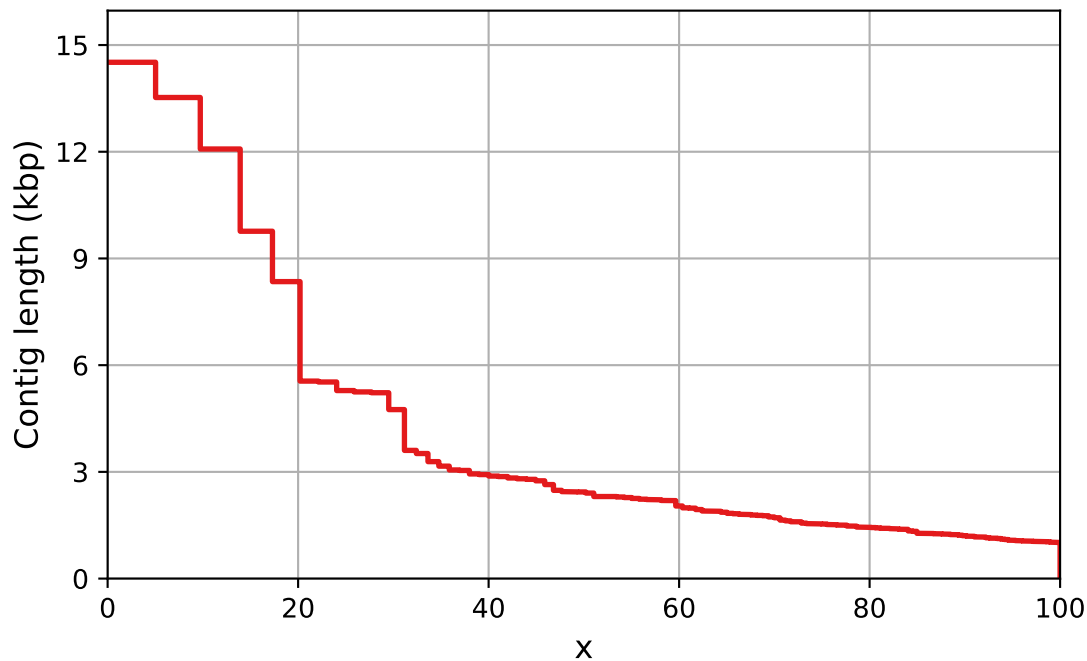
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	4
Fully unaligned length	7694
# partially unaligned contigs	120
Partially unaligned length	268571
# N's	0

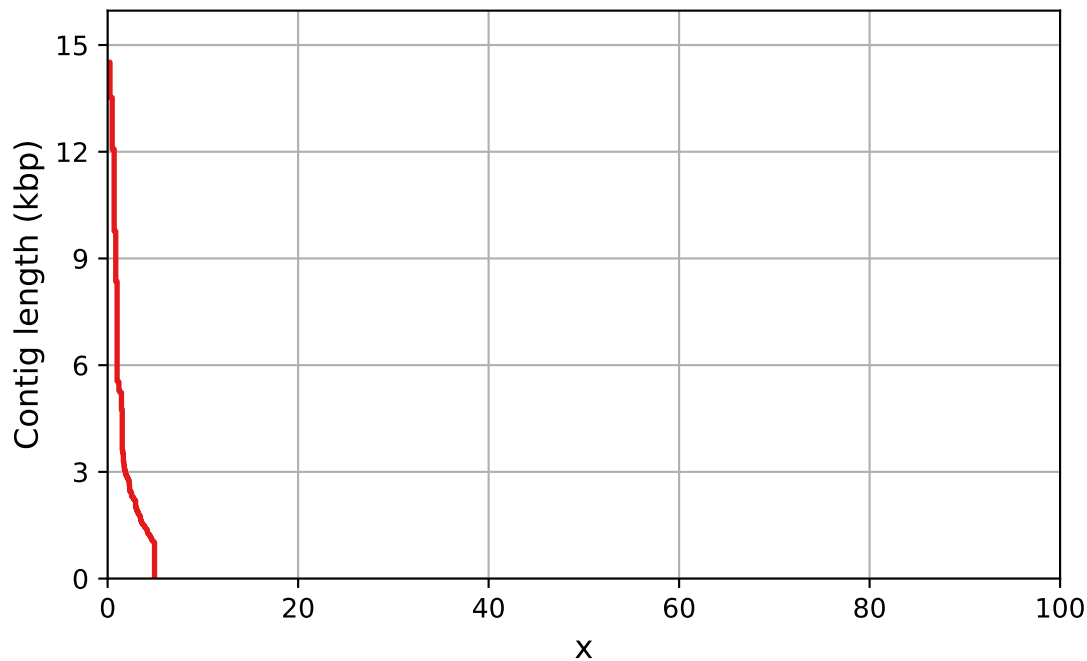
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



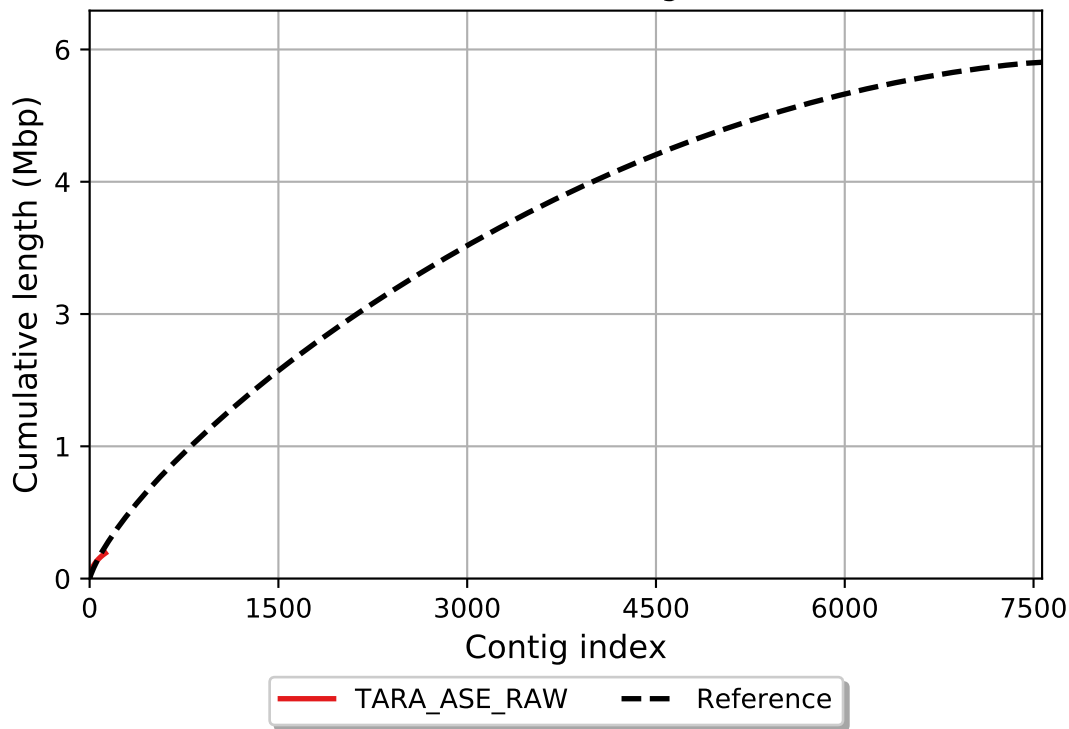
TARA\_ASE\_RAW

NGx

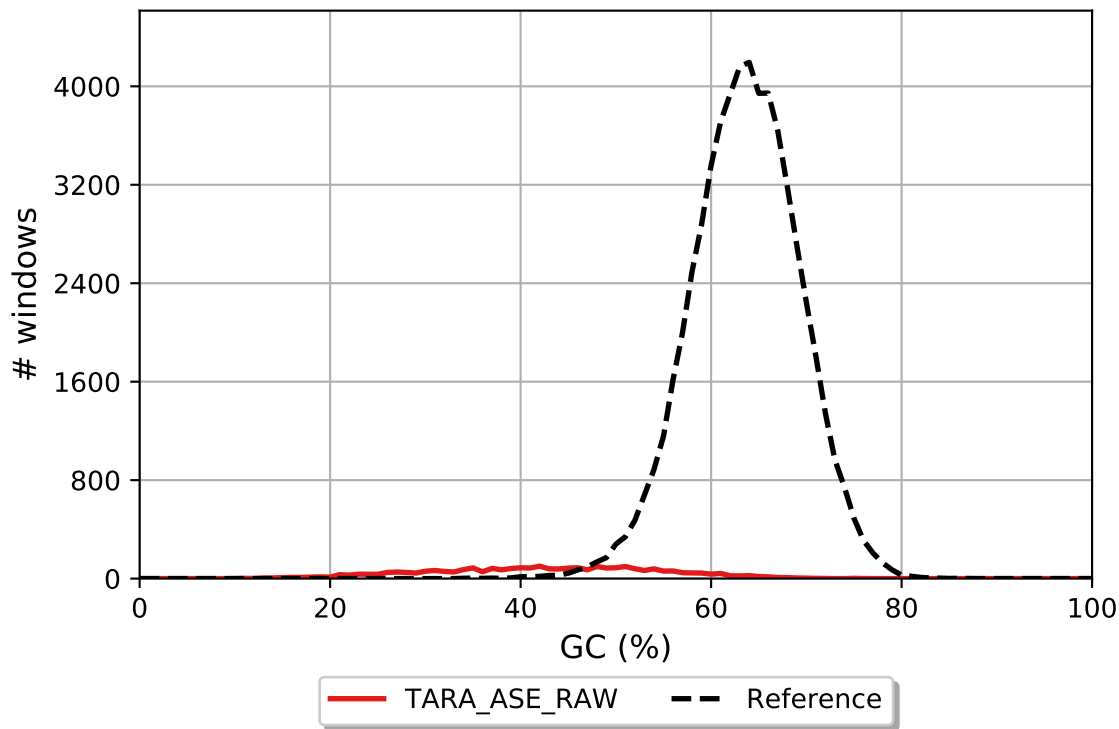


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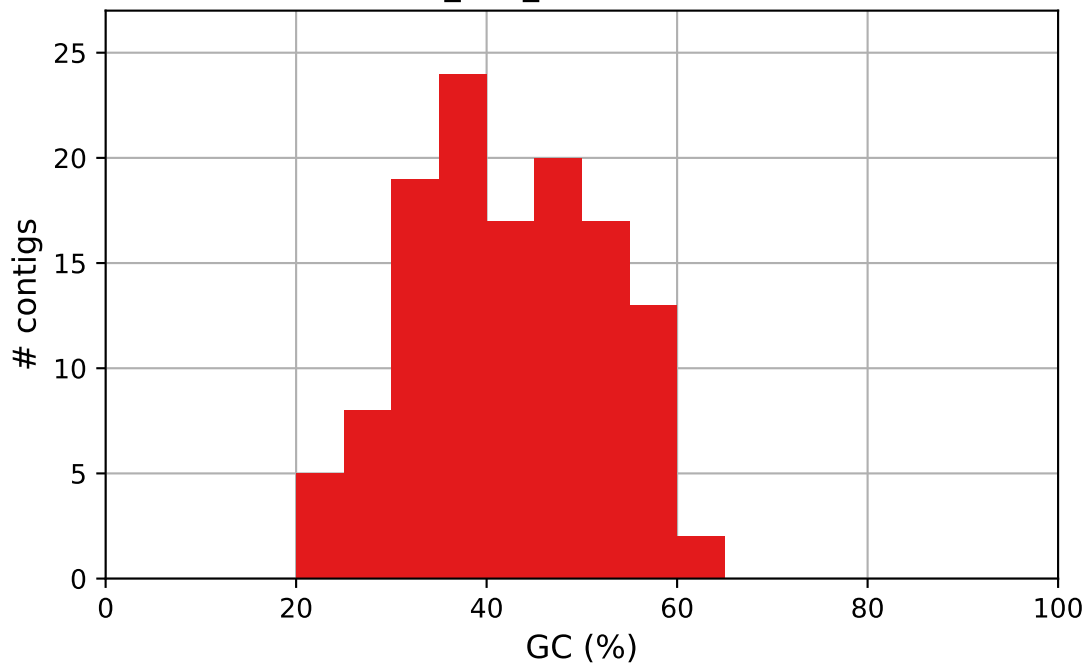
Cumulative length



## GC content



TARA\_ASE\_RAW GC content



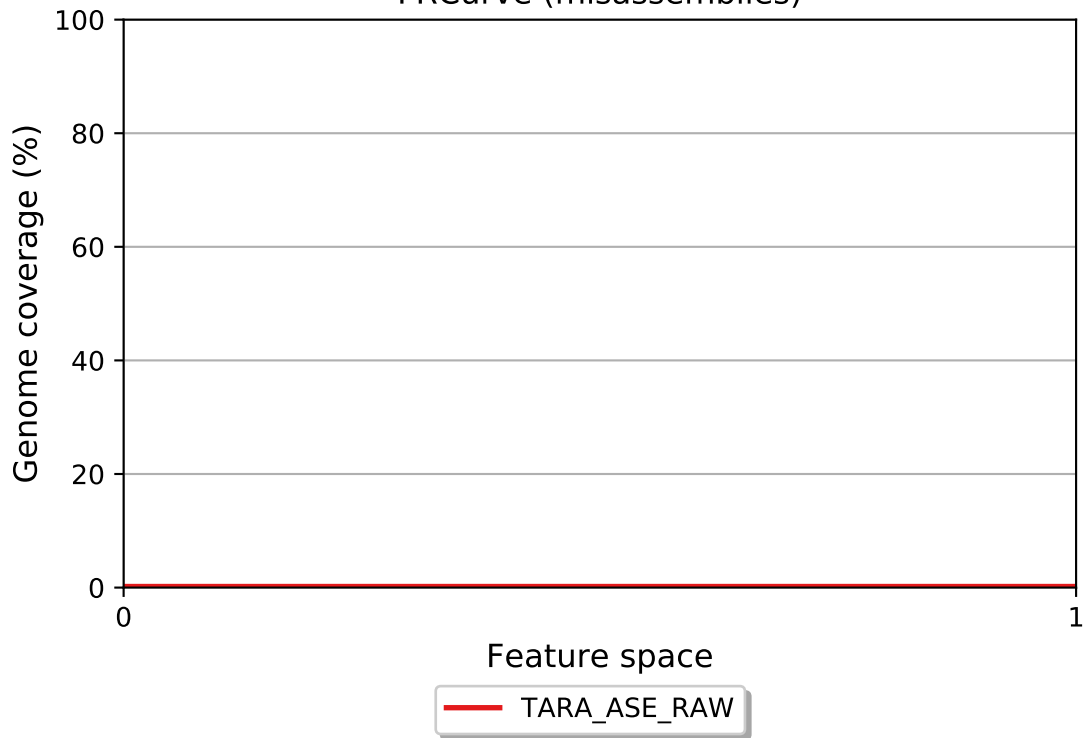
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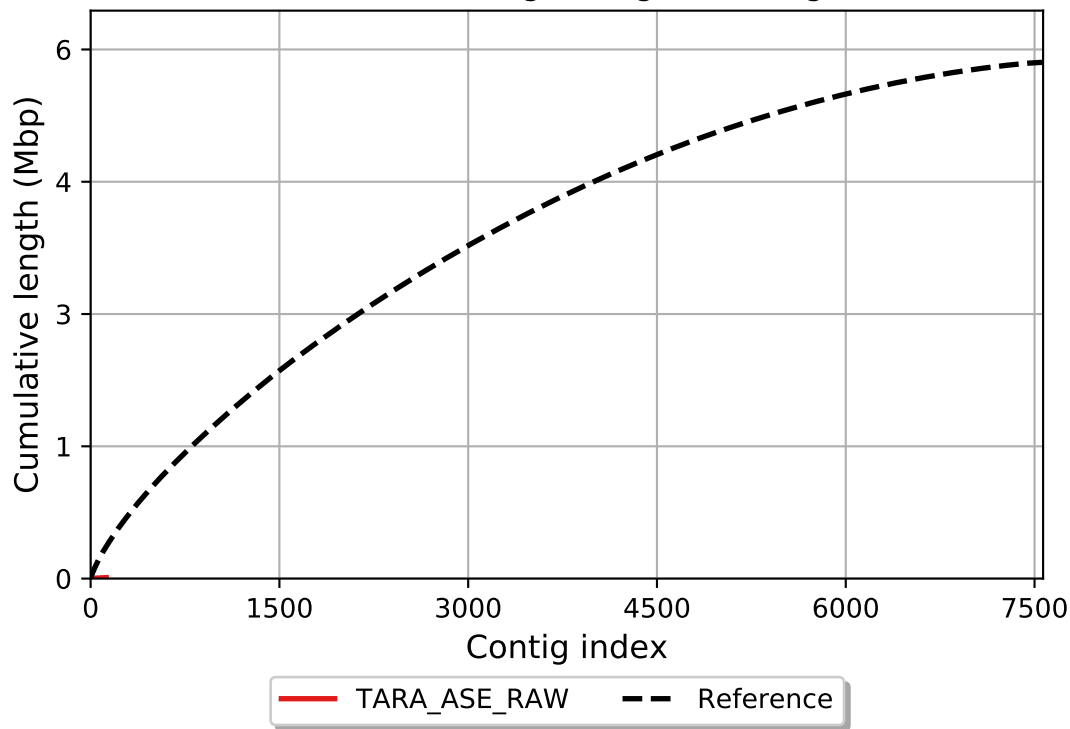
## Misassemblies



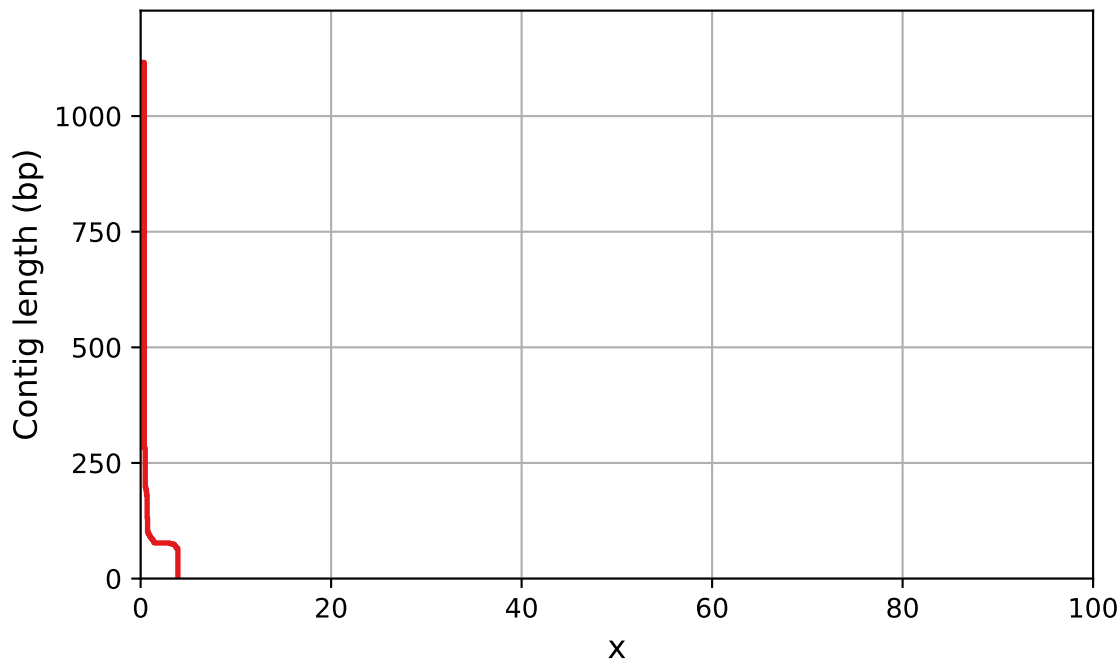
FRCurve (misassemblies)



Cumulative length (aligned contigs)

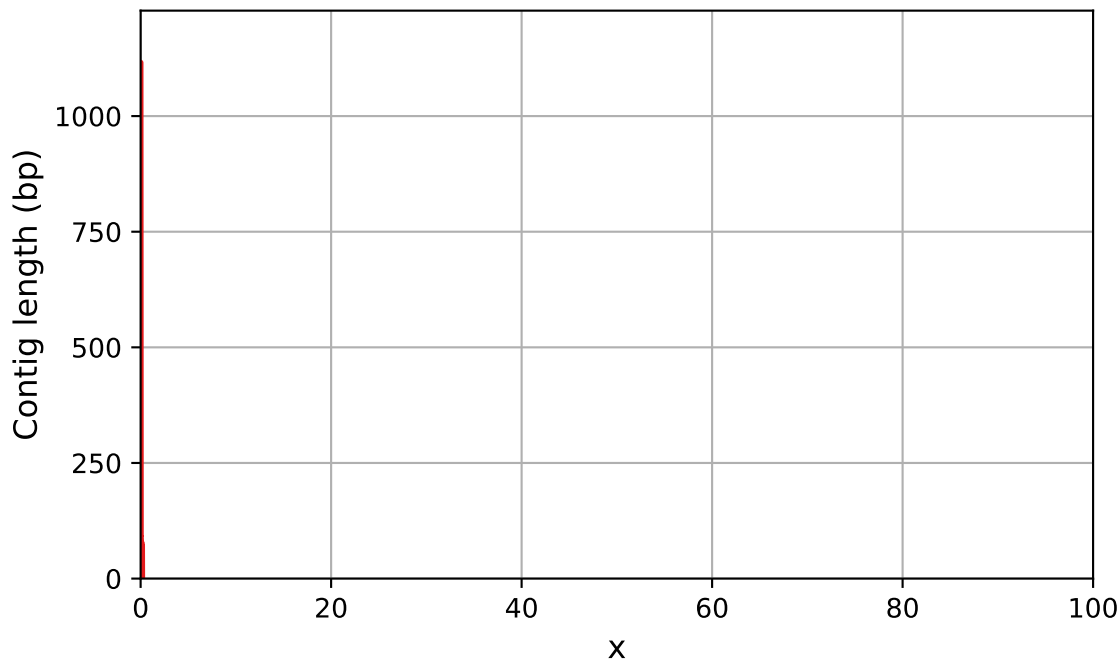


NAx



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# NGAx



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