

Report

	TARA_ASE_RAW
# contigs (>= 1000 bp)	37
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	82022
Total length (>= 5000 bp)	23930
Total length (>= 10000 bp)	12662
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	37
Largest contig	12662
Total length	82022
Reference length	3561038
GC (%)	46.26
Reference GC (%)	41.87
N50	2253
N75	1477
L50	9
L75	21
# 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	1
# unaligned contigs	2 + 35 part
Unaligned length	78895
Genome fraction (%)	0.019
Duplication ratio	4.709
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12801.20
# indels per 100 kbp	0.00
Largest alignment	154
Total aligned length	3127
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	36
# possible misassemblies	39
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	85
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

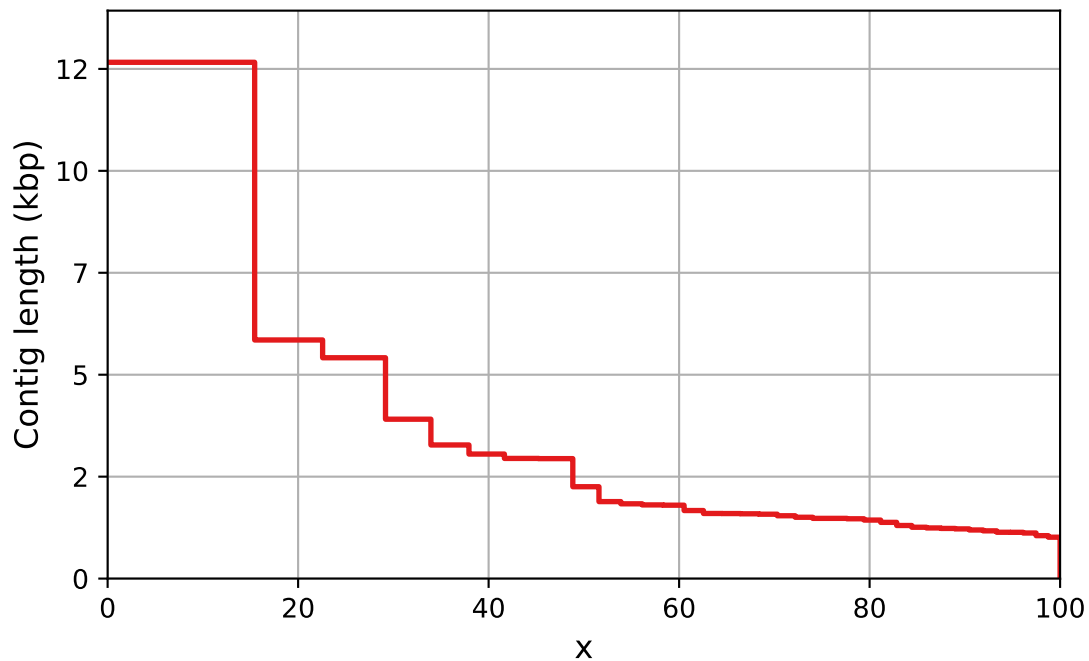
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	2
Fully unaligned length	2976
# partially unaligned contigs	35
Partially unaligned length	75919
# N's	0

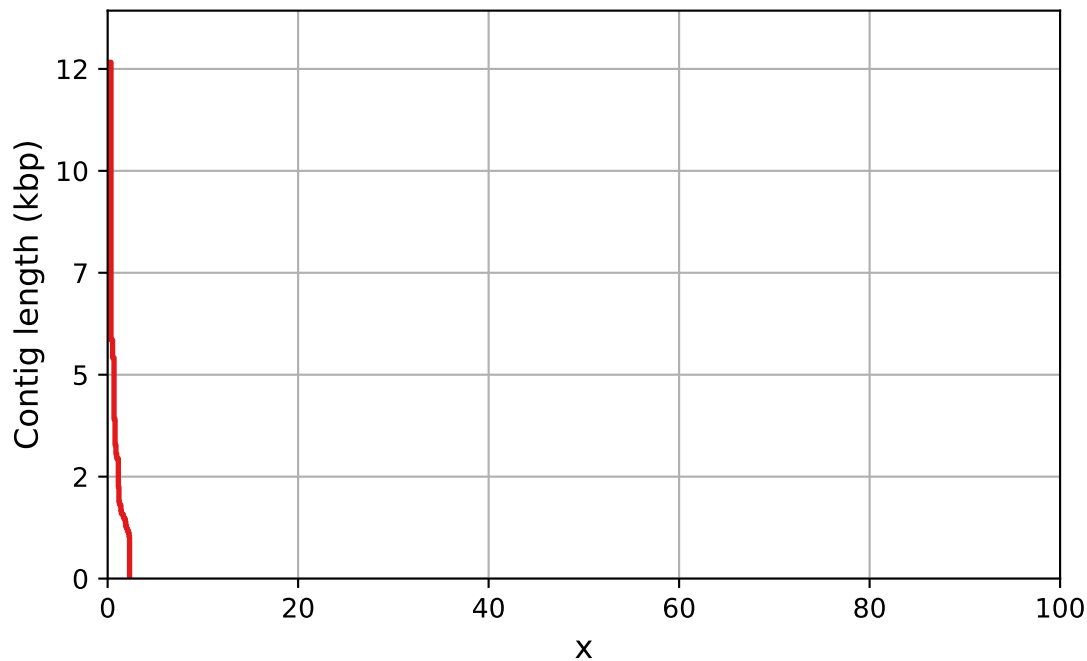
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

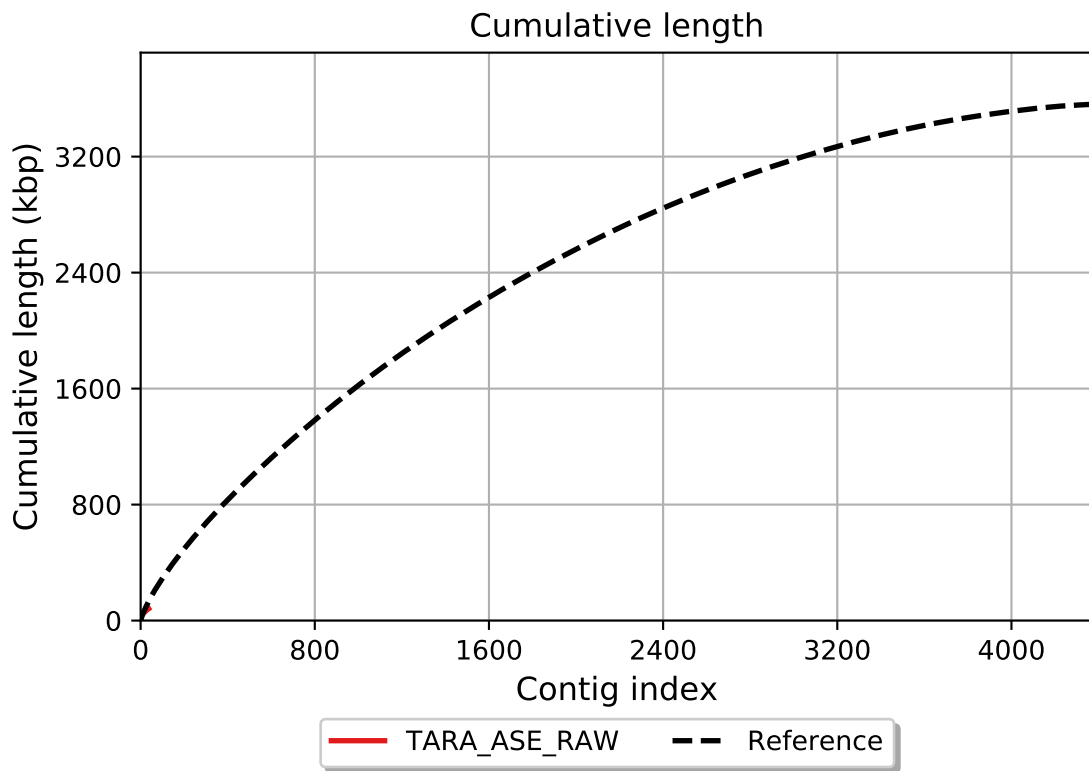


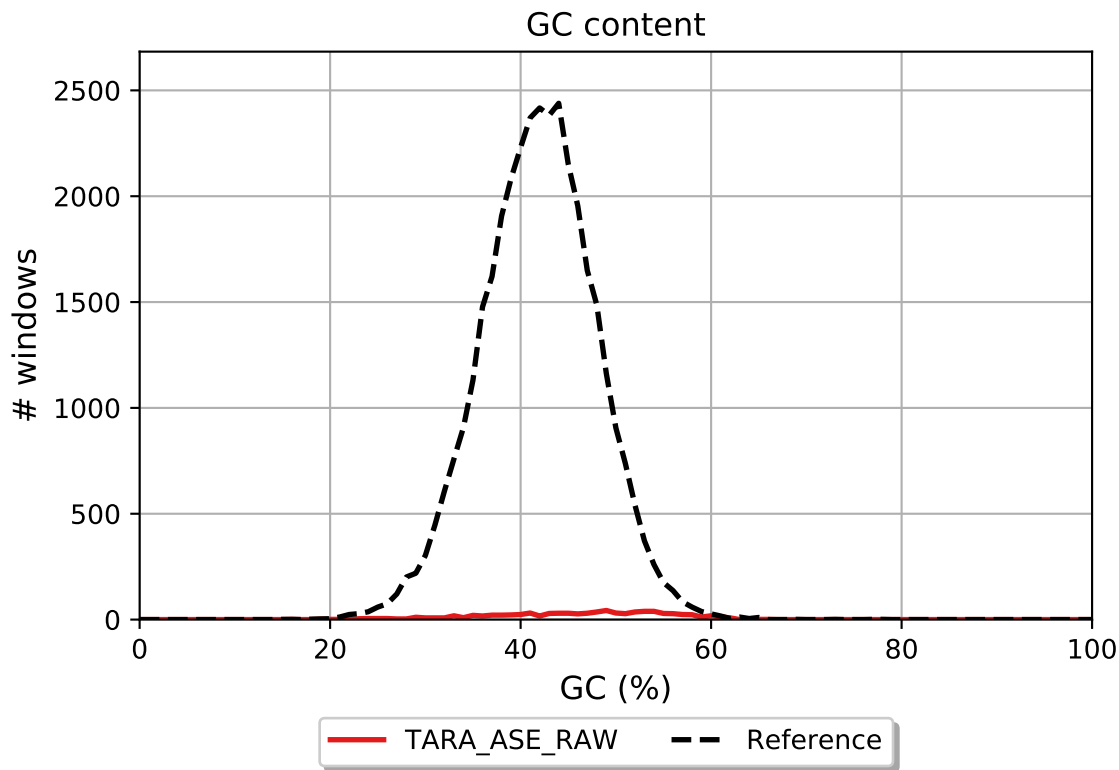
TARA_ASE_RAW

NGx

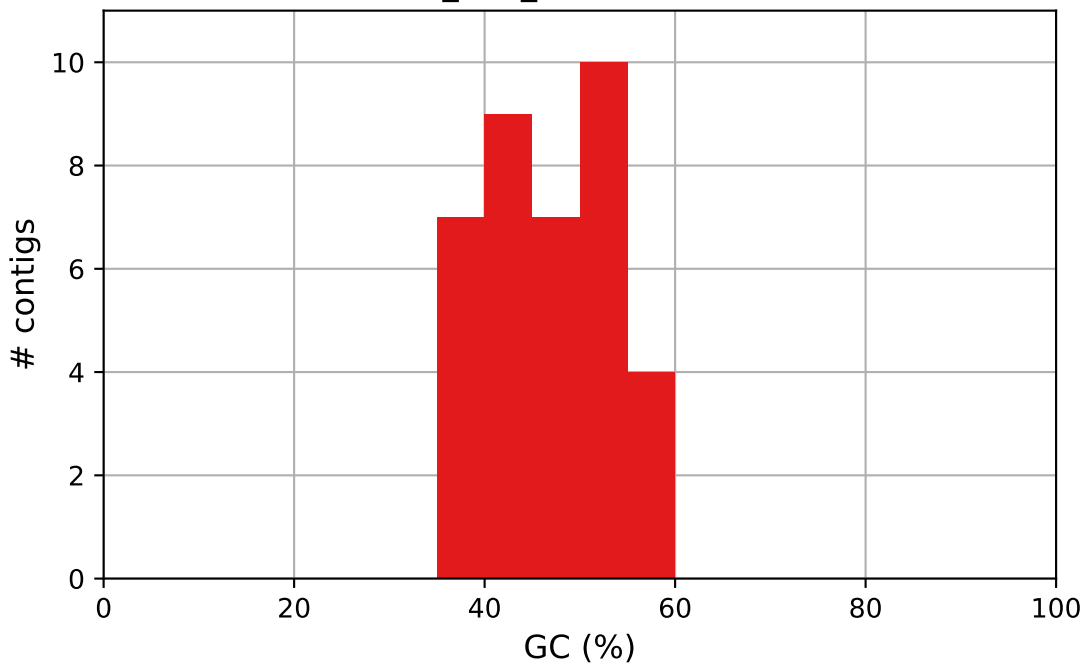


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TARA_ASE_RAW GC content

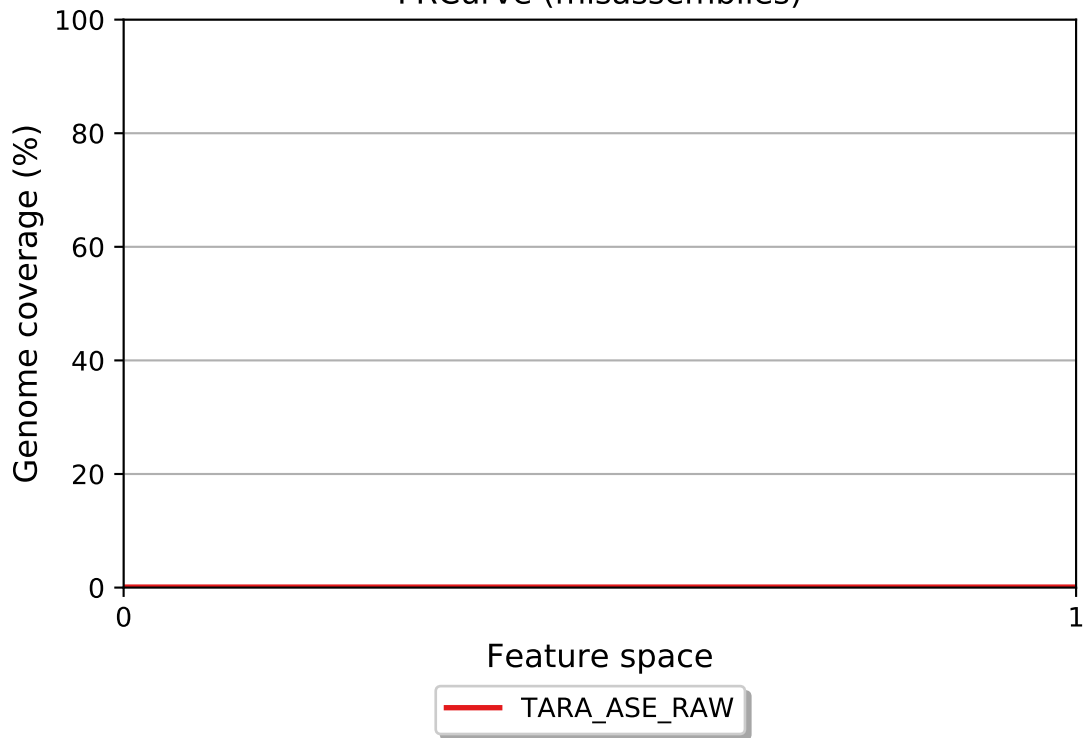


TARA_ASE_RAW

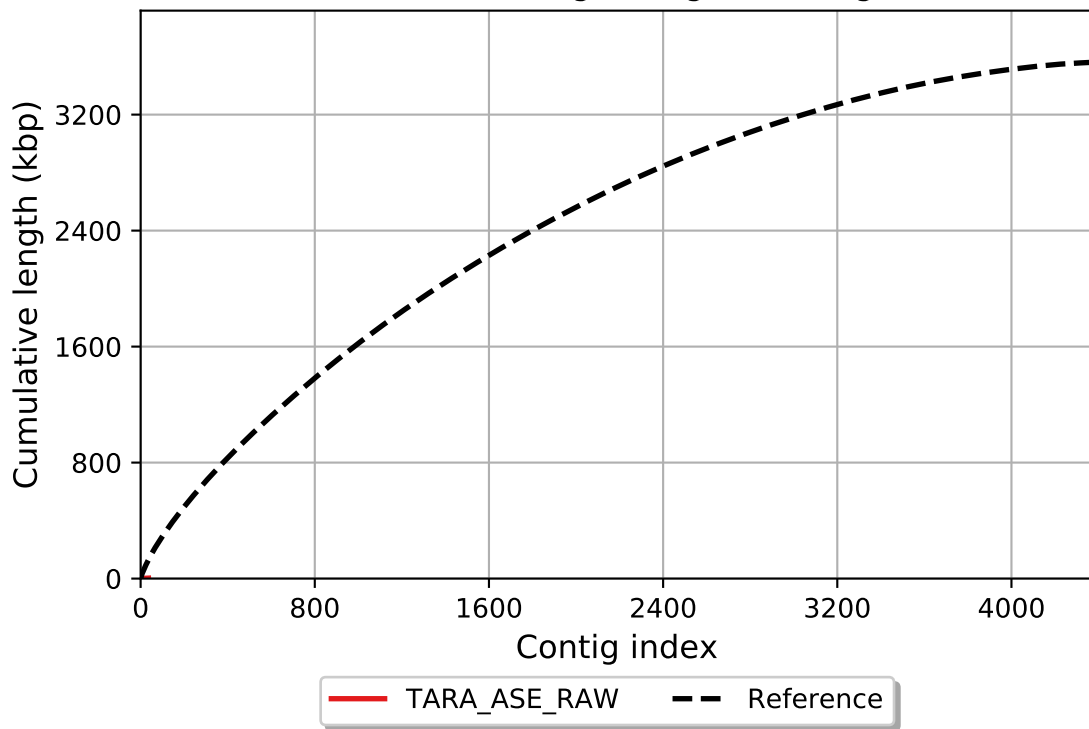
Misassemblies



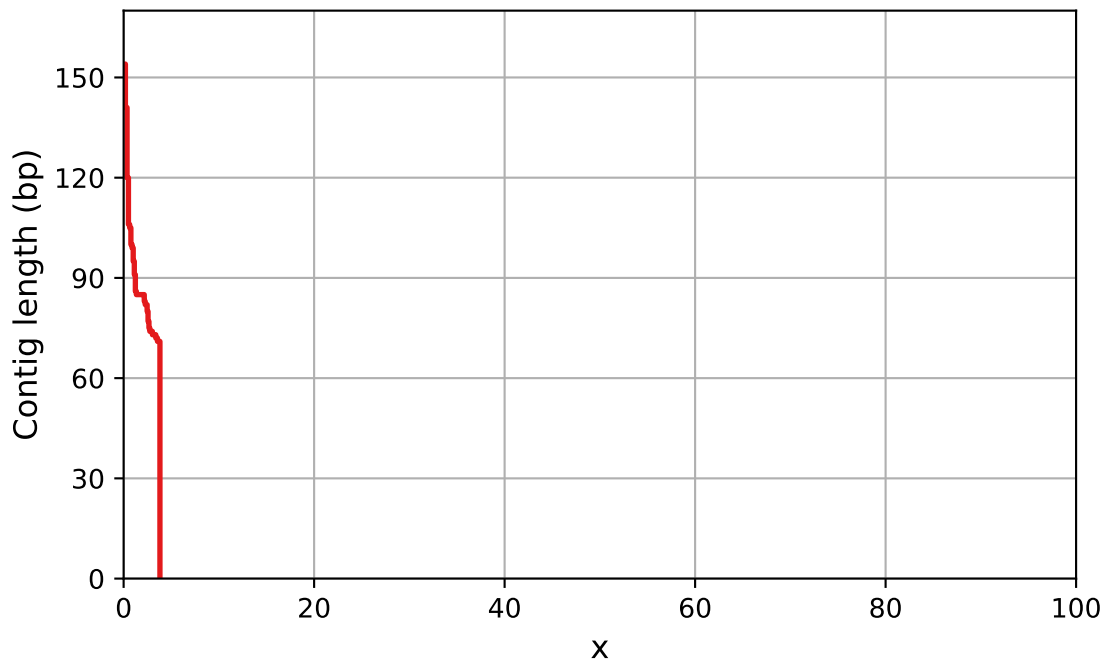
FRCurve (misassemblies)



Cumulative length (aligned contigs)

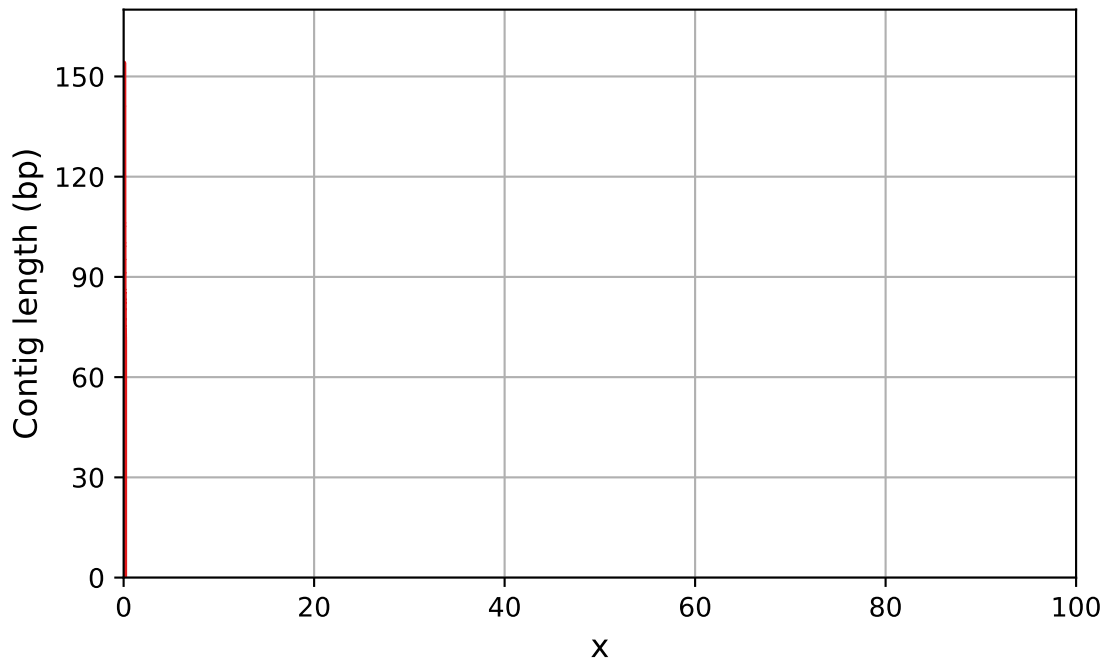


NAx



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NGAx



— TARA_ASE_RAW