

Report

	contigs_olc_min20
# contigs (>= 0 bp)	53
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	11793
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	53
Largest contig	323
Total length	11793
Reference length	30119
GC (%)	41.93
Reference GC (%)	41.24
N50	227
NG50	-
N90	214
NG90	-
auN	225.2
auNG	88.2
L50	26
LG50	-
L90	47
LG90	-
# 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	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	32.375
Duplication ratio	1.208
# N's per 100 kbp	0.00
# mismatches per 100 kbp	712.83
# indels per 100 kbp	0.00
Largest alignment	320
Total aligned length	11784
NA50	227
NGA50	-
NA90	214
NGA90	-
auNA	224.8
auNGA	88.0
LA50	26
LGA50	-
LA90	47
LGA90	-

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

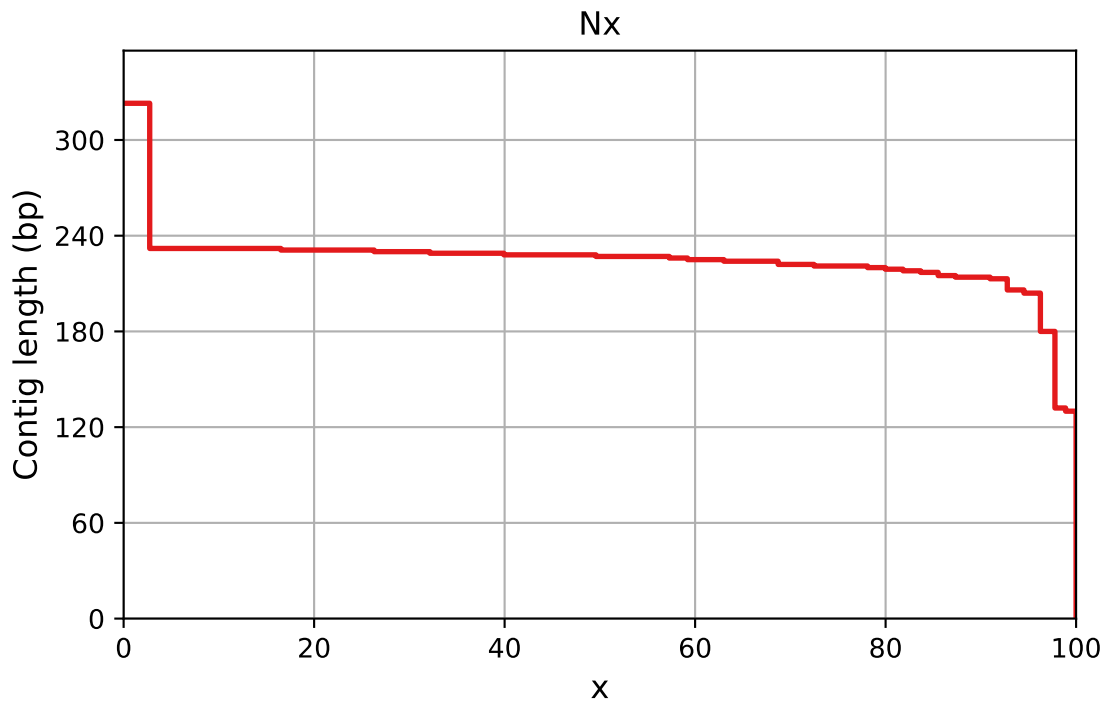
	contigs_olc_min20
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	84
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

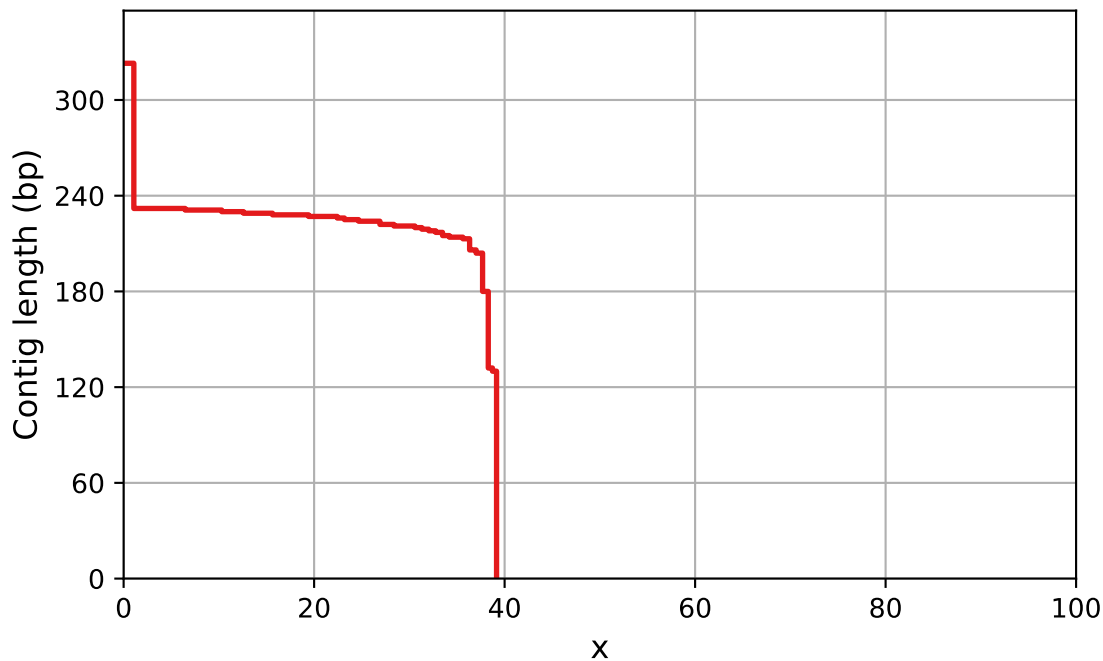
	contigs_olc_min20
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



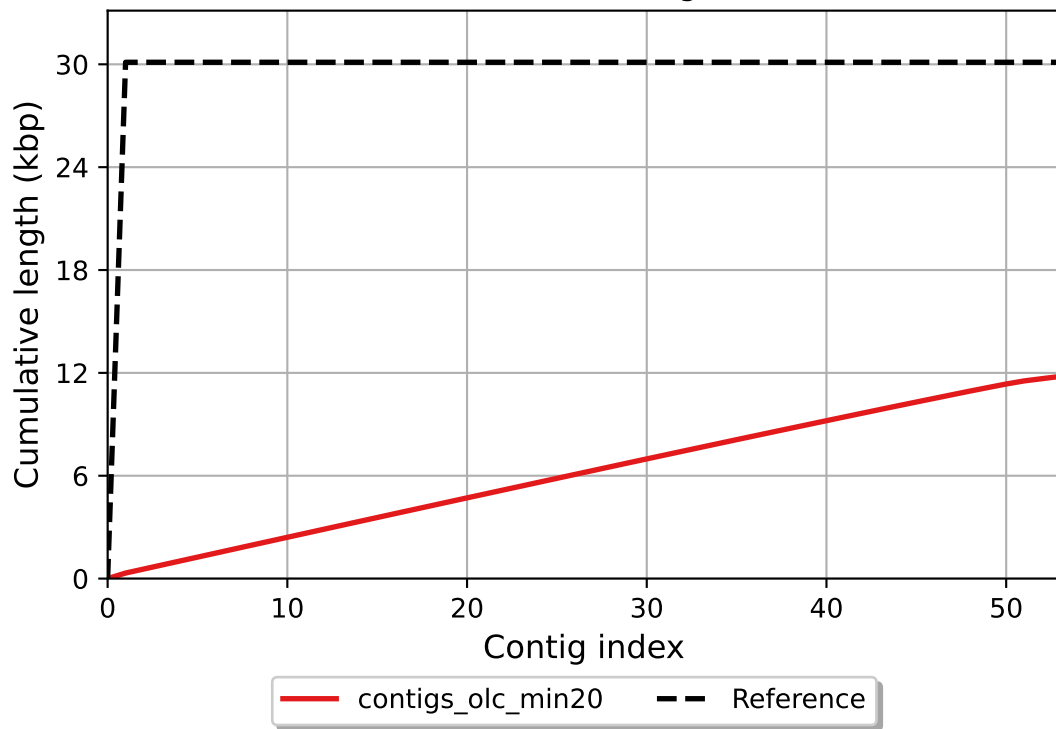
— contigs_olc_min20

NGx

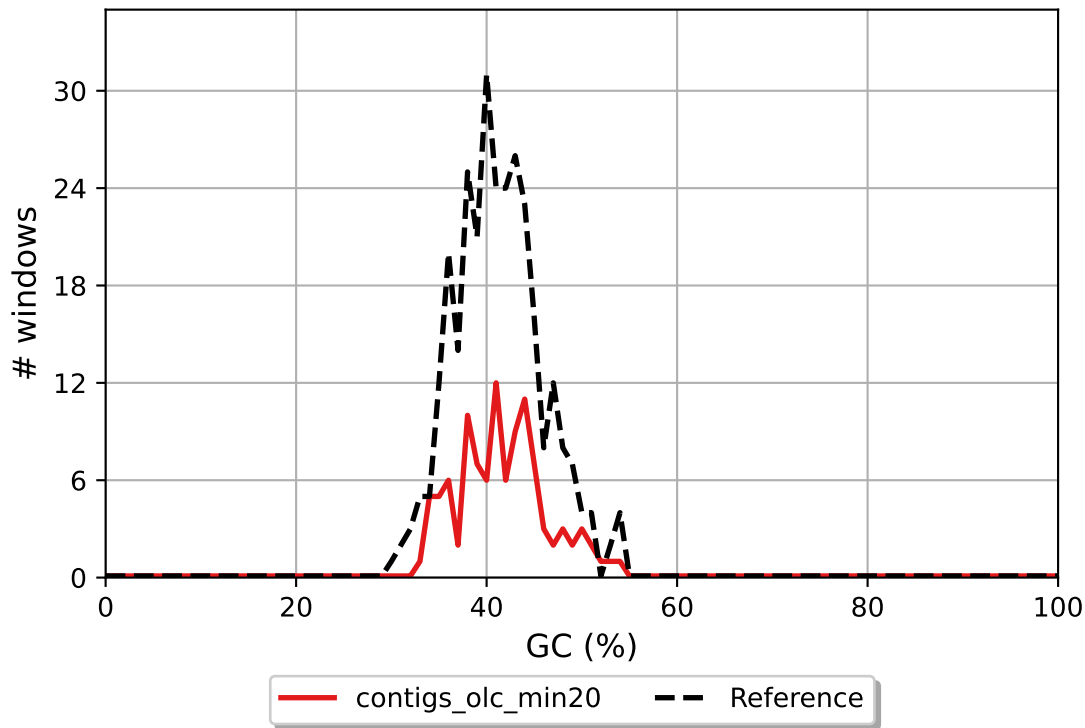


— contigs_olc_min20

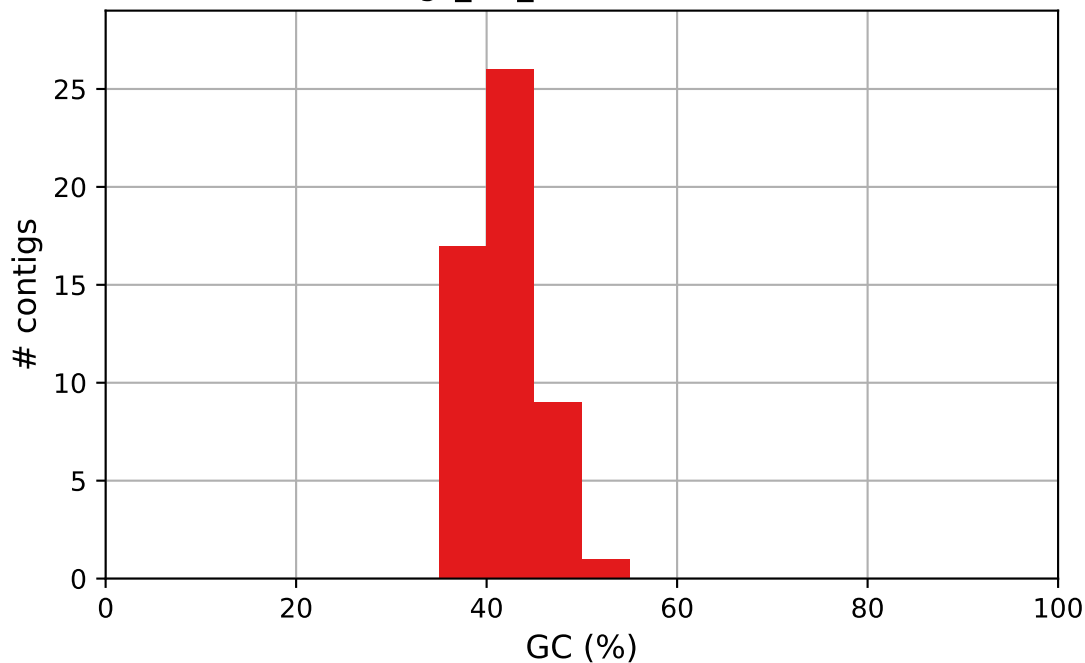
Cumulative length



GC content



contigs_olc_min20 GC content

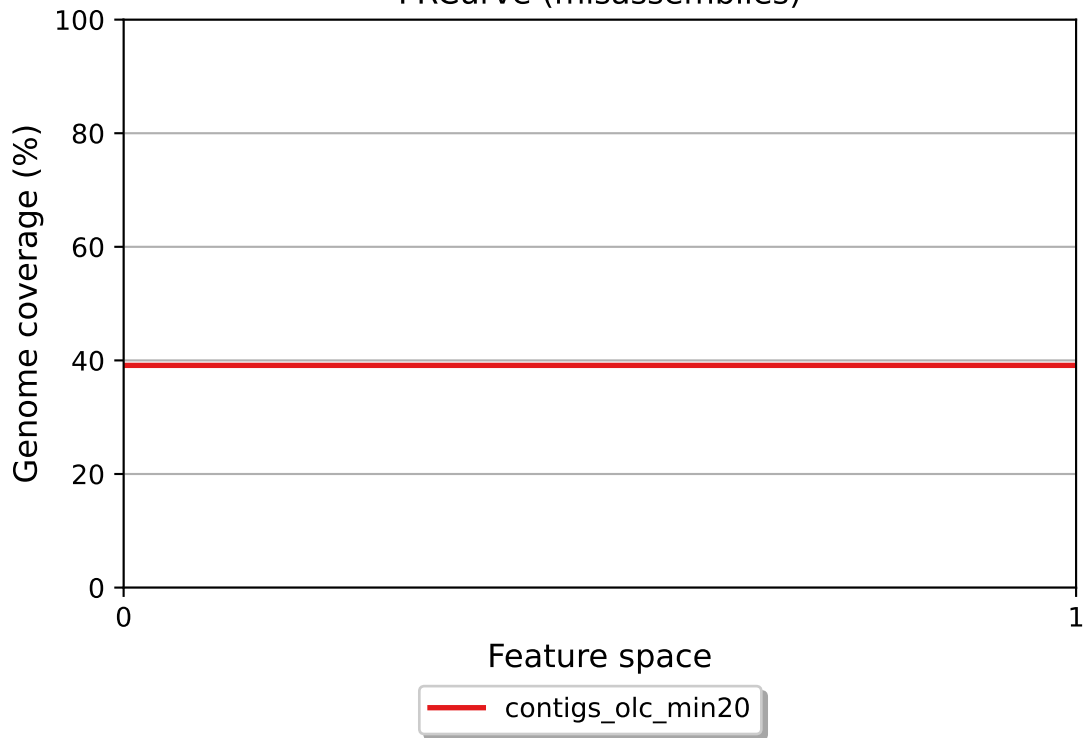


contigs_olc_min20

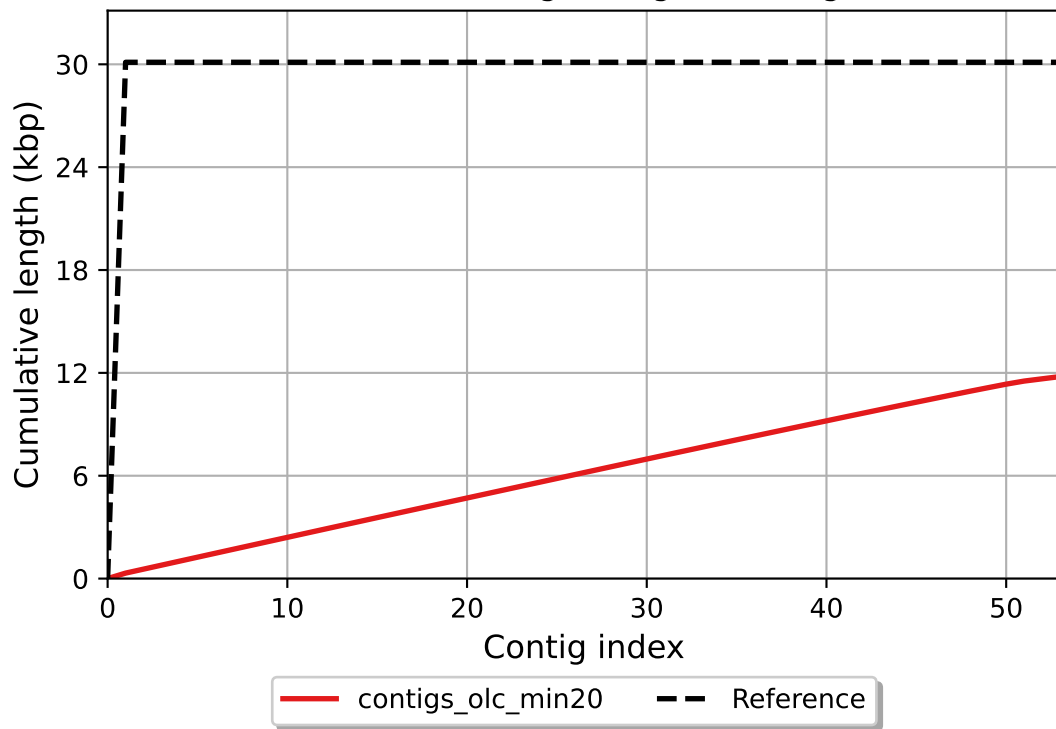
Misassemblies



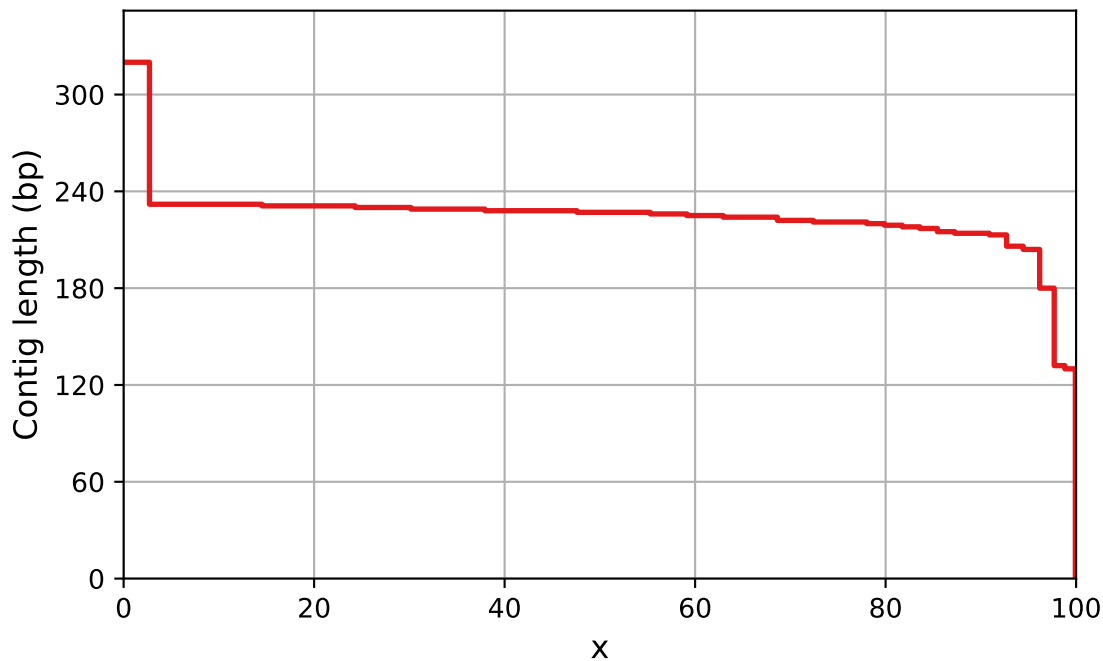
FRCurve (misassemblies)



Cumulative length (aligned contigs)

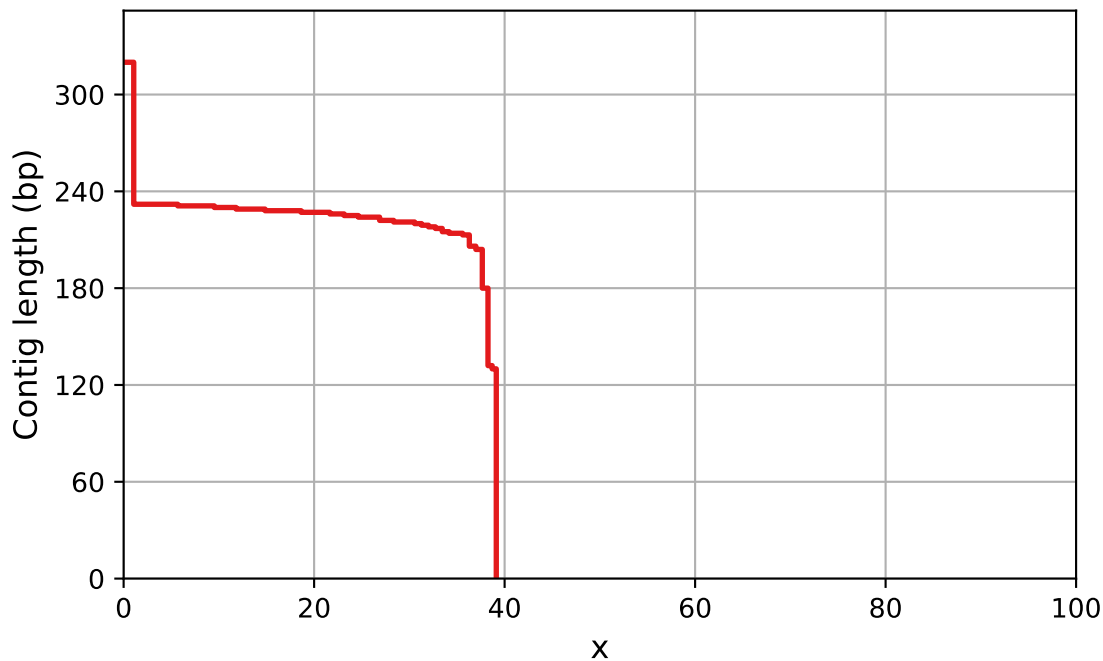


NAx



contigs_olc_min20

NGAx



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