

UNCOVERING THE GENOMIC LANDSCAPE OF LBCL IN LATIN AMERICA: REPORTS OF TWO CENTERS FROM BRAZIL AND CHILE



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BACKGROUND

The genomic landscape of large B-cell lymphomas (LBCL) has been extensively mapped in high-income countries, but data from low- and middle-income countries (LMICs) such as Brazil and Chile remain scarce.

Distinct demographics and ancestry-related genetic backgrounds may influence disease biology, limiting the applicability of existing risk models.

AIM

To provide a molecular characterization of a Latin American LBCL cohort using next-generation sequencing (NGS).

METHODS

Retrospective analysis of patients diagnosed with DLBCL at two centers who underwent targeted NGS.

Profiling used the TSO500 HT panel (Illumina NextSeq 500 / NovaSeq 6000) at Hospital Israelita Albert Einstein, or the Oncomine Comprehensive Assay Plus (Thermo Fisher Ion GeneStudio S5 Plus) at Clínica Alemana de Santiago.

Patients were classified by the LymphPlex system.

CONCLUSIONS

This Latin American LBCL cohort shares fundamental oncogenic drivers with global populations but is distinctly enriched for high-risk genetic features.

Risk-stratification models developed elsewhere may not fully capture this profile, underscoring the value of local genomic data to advance precision oncology in LMICs.

RESULTS

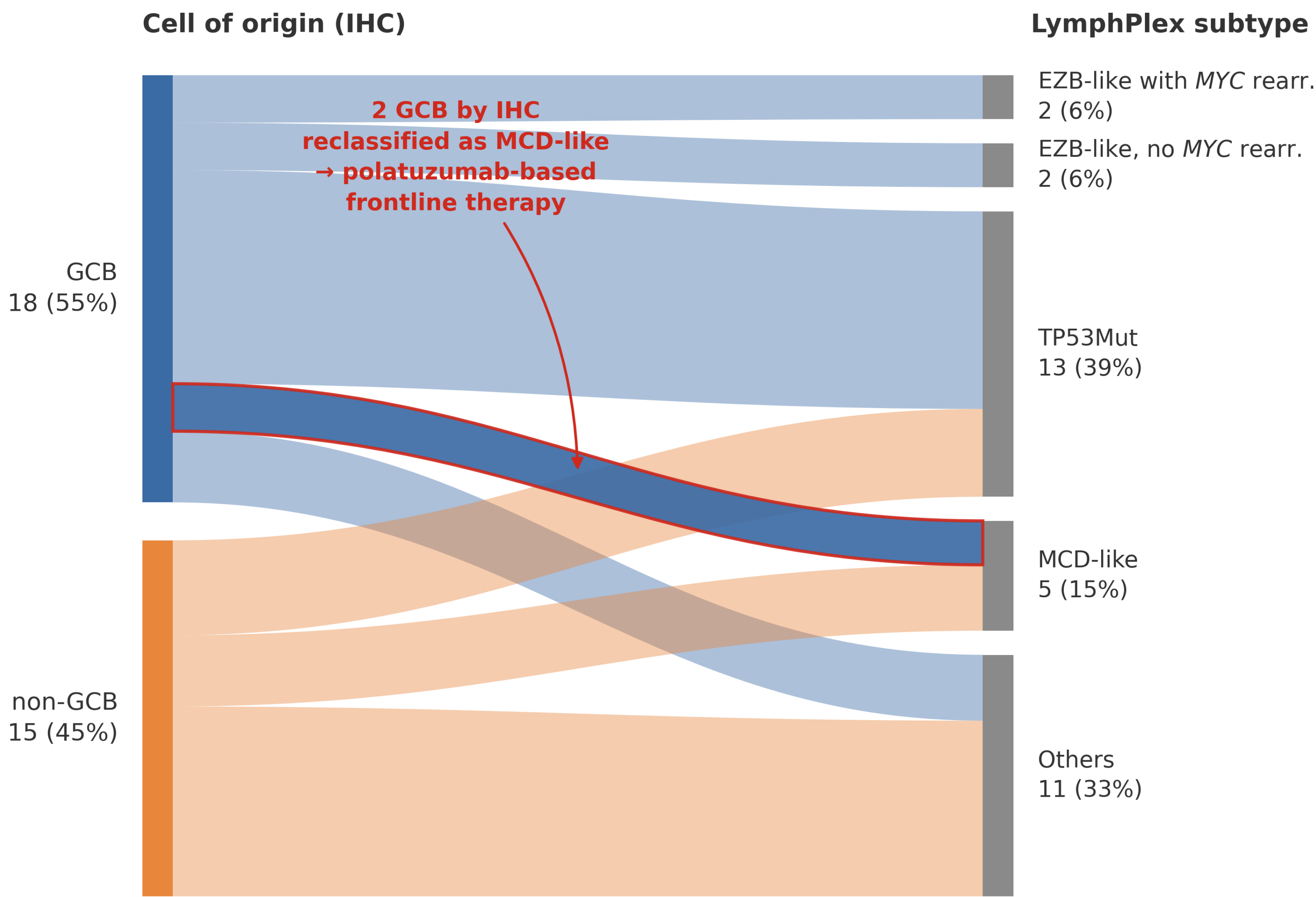
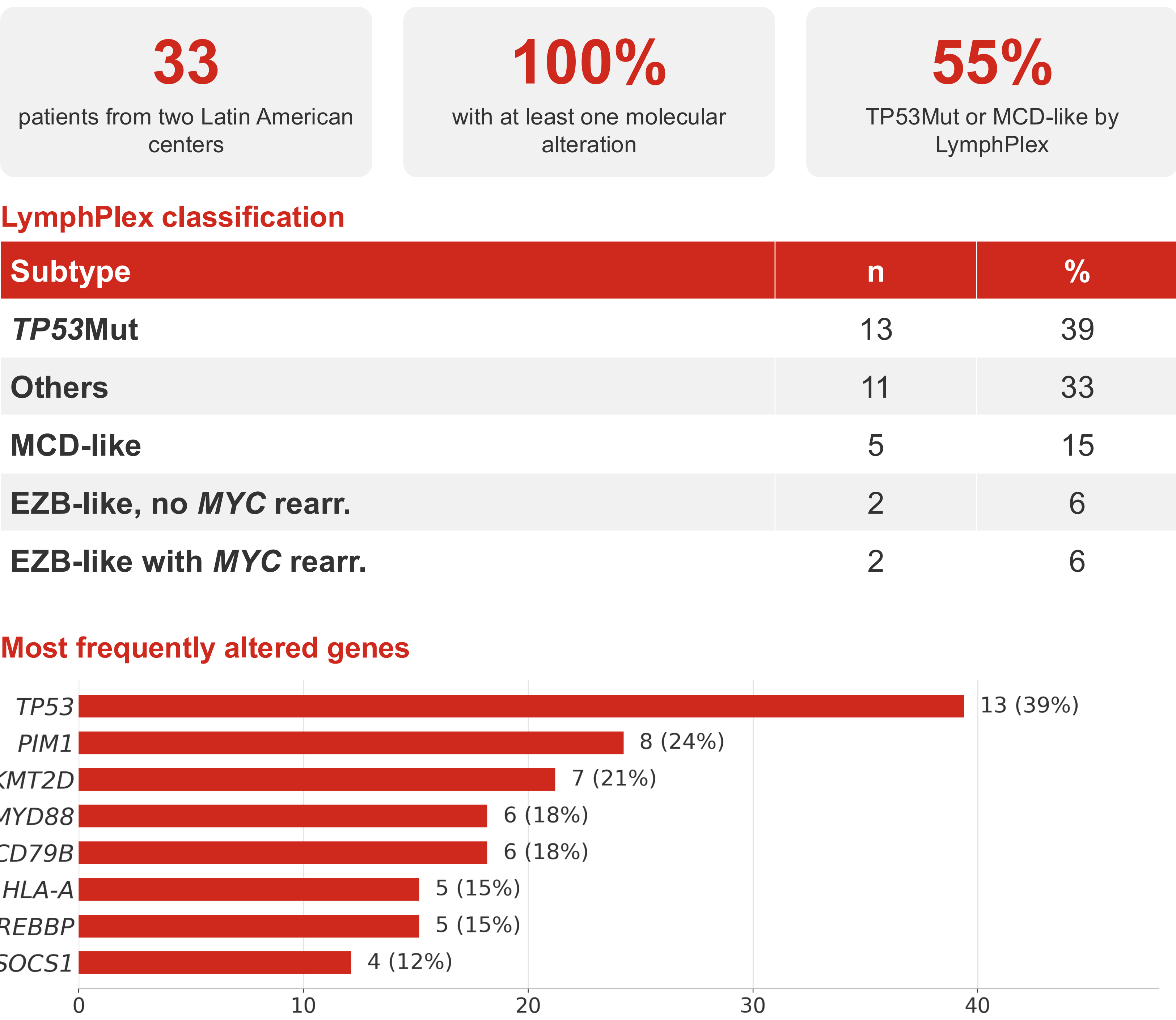


Figure 1. Cell of origin by immunohistochemistry and corresponding LymphPlex subtype (n = 33).

- Cell of origin: GCB 18 (55%), non-GCB 15 (45%);
- Median TMB 11.5 mut/Mb (range 1.6–192.7);
- MSI in 3 patients (9%).

LIMITATIONS

- Retrospective design with a limited sample size (n = 33);
- Two different NGS platforms across centers may limit direct comparability;
- Molecular findings were not correlated with clinical features and outcomes.

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