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Errata

Jutzi JS, Marneth AE, Ciboddo M, et al. Whole-genome CRISPR screening identifies *N*-glycosylation as a genetic and therapeutic vulnerability in *CALR*-mutant MPNs. *Blood.* 2022;140(11):1291-1304.

Page 1295: In Figure 3B, the brackets on the right side of the graph were drawn incorrectly during the publication process. The upper bracket should end after the fourth entry in the color/symbol key, not after the third. The corrected Figure 3B is shown below.

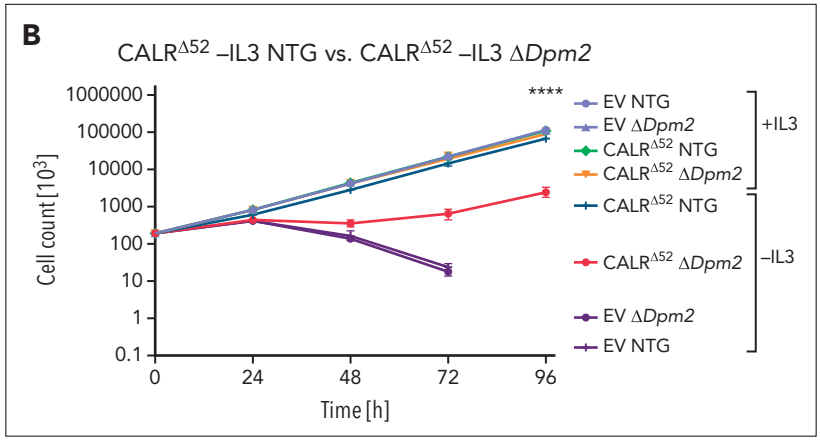

Figure 3. In-depth validation of the *N*-glycan biosynthesis pathway as an essential pathway for growth of mutant CALR-expressing hematopoietic cells. (B) Growth curves of independent biological replicates and the 2 different sgRNAs were combined in the analysis. Cells were assayed either in the presence or absence of IL3 (+IL3/−IL3) for up to 96 hours. The assay was performed n = 3 for all 4 biological replicates of both genotypes. Statistical significance was determined by 2-way analysis of variance (ANOVA). Mean plus and minus standard error of the mean (SEM). ****$P < .00001$. The most important statistical analysis is highlighted.

https://doi.org/10.1182/blood.2023022676

Boyraz B, Bellomo CM, Fleming MD, Cutler CS, Agarwal S. A novel TERC CR4/CR5 domain mutation causes telomere disease via decreased TERT binding. *Blood.* 2016;128(16):2089-2092.

The supplemental file is missing from the online version of the article. It is available in the HTML version of this erratum.

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