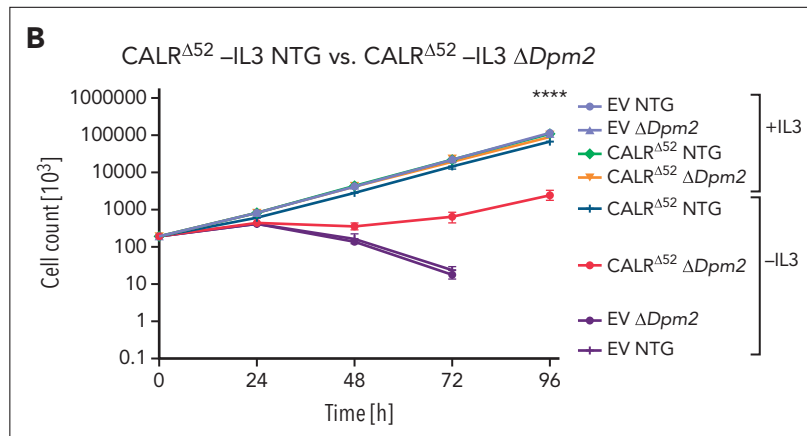




**Jutzi JS, Marneth AE, Ciboddo M, et al. Whole-genome CRISPR screening identifies N-glycosylation as a genetic and therapeutic vulnerability in CALR-mutant MPNs. *Blood*. 2022;140(11):1291-1304.**

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.

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**Boyratz 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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