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CORRECTION
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Corrigendum: Impact of NK Cell Activating Receptor Gene Variants on Receptor Expression and Outcome of Immunotherapy in Acute Myeloid Leukemia

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A Corrigendum on

Impact of NK Cell Activating Receptor Gene Variants on Receptor Expression and Outcome of Immunotherapy in Acute Myeloid Leukemia

by Hussein BA, Hallner A, Wennström L, Brune M, Martner A, Hellstrand K, et al. (2021). Front. Immunol. 12:5300. doi: 10.3389/fimmu.2021.796072

In the original article, there was an error regarding **Figure 3D** as published. For purpose of clarification, AML patients enrolled in Re:Mission trial supposed to be divided into two groups based on NKp30 rs986475 gene variants (0=No G allele or 1=G allele carriers) in this **Figure 3D** but there is a third arm in the figure which is a patient with a zero value of NKp30 MFI and this was mistakenly added in GraphPad prism. The corrected version of **Figure 3** appears below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

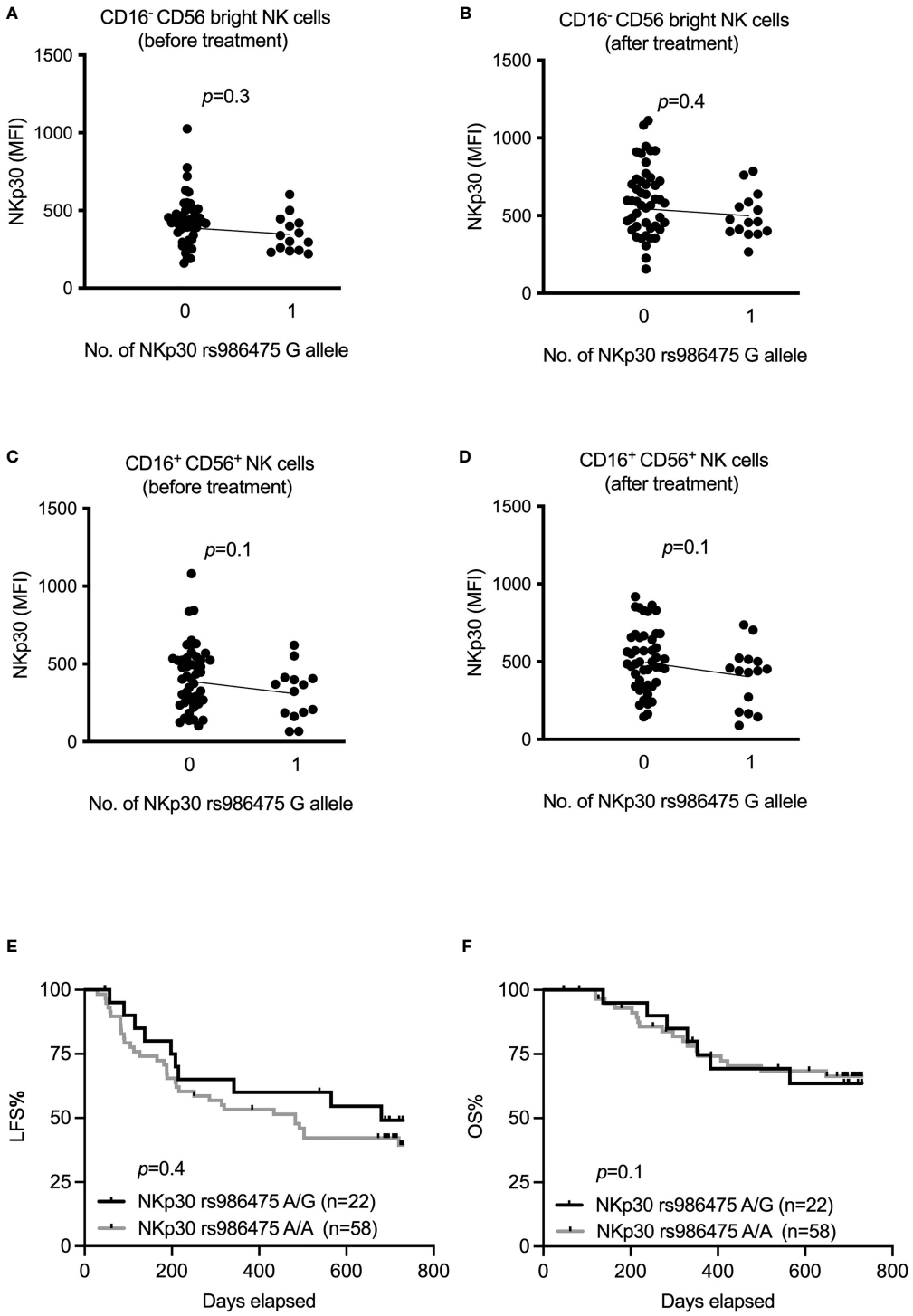

FIGURE 3 | Impact of NKp30 rs986475 gene polymorphism on expression of NKp30 and clinical outcome of AML during immunotherapy. **(A–D)** Median fluorescence intensity of NKp30 based on genotype status of NKp30 rs986475 in AML patients in both CD16$^-$ CD56^{bright} and CD16$^+$ CD56$^+$ NK cells before and after receiving one cycle of HDC/IL-2 therapy. Patients are divided according to presence (14 out of 61 before therapy, and 15 out of 62 after therapy) or absence of G allele in figures **(A–D)**. **(E, F)** Kaplan-Meier curves show impact of different NKp30 rs986475 genotypes on leukemia-free survival (LFS) and overall survival (OS) of AML patients after receiving HDC/IL-2 therapy. Simple linear regression was applied to investigate impact of NKp30 gene variants on NKp30 expression both before and after immunotherapy in various NK subsets as shown in figures **(A–D).** Logrank test was used to analyze the survival based on NKp30 gene variants in figures **(E, F)**.