



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

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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.

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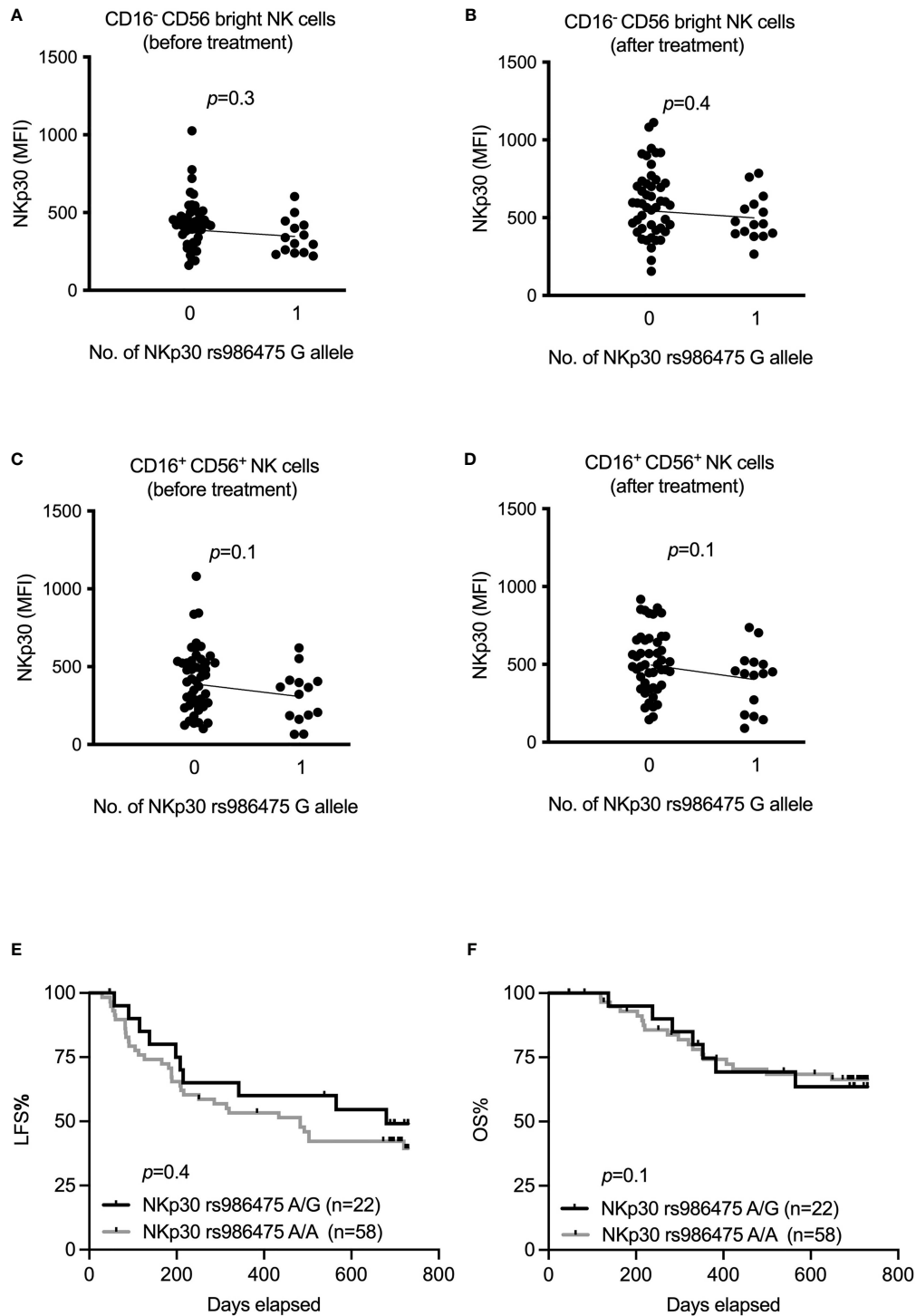


FIGURE 3 | Impact of NKp30 rs986475 gene polymorphism on expression of NKp30 and clinical outcome of AML during immunotherapy. **(A–D)** Median fluorescence intensity of NKp30 based on genotype status of NKp30 rs986475 in AML patients in both CD16⁻ CD56^{bright} and CD16⁺ CD56⁺ NK cells before and after 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)**.