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CORRECTION
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# Corrigendum: To Ki or Not to Ki: Re-Evaluating the Use and Potentials of Ki-67 for T Cell Analysis

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**A Corrigendum on**

**To Ki or Not to Ki: Re-Evaluating the Use and Potentials of Ki-67 for T Cell Analysis**
*By Di Rosa F, Cossarizza A and Hayday AC (2021). Front. Immunol. 12:653974. doi: 10.3389/fimmu.2021.653974.*

In the original article, there was a mistake in the legend for **Figure 1** as published. On the Viable cells, no "dump" gate, "CD16" was written instead of "CD19". The correct legend appears below.

"HD PBMCs were stained with the viability dye eFluor 780 (eF780), the DNA dye Hoechst-33342, and fluorochrome conjugated mAbs against surface markers and Ki-67, as described (16). An example of flow cytometry analysis is shown. **(A)** Gating of viable single CD8 T cells in 6 steps: 1) DNA-A/-W singlets. Single cells having 2n≤ DNA content ≤4n were selected on the DNA-area (A) *versus (vs)* DNA-width (W) plot; 2) Time exclusion. Stable acquisition over time (seconds) was monitored on the time *vs* DNA-A plot and any events collected in case of pressure fluctuations were excluded; 3) Viable cells, no "dump". Cells expressing CD4, CD14 and CD19, and dead cells were excluded; 4) FSC-A/SSC-A "relaxed" gate. A "relaxed" gate was used on the FSC-A *vs* SSC-A plot, to include highly activated and cycling lymphocytes (15); 5) CD8 T cells. CD8 T cells were gated on the CD3 *versus* CD8 plot; 6) Refined singlets. A few remaining doublets composed by one cell sitting on top of another (so called "shadow" doublets) were excluded as Ki-67$^{int/-}$ events having > 2n DNA content (16). This gating strategy was used as a base for the subsequent gates. **(B)** The following naïve/memory subsets of CD8 T cells were identified: CD45RA$^+$ CCR7$^+$ Naïve, CD45RA$^-$ CCR7$^+$ central memory (CM), CD45RA$^-$ CCR7$^-$ effector memory (EM), and CD45RA$^+$ CCR7$^-$ (EMRA). **(C)** Cell cycle phases of each naïve/memory CD8 T cell subset were defined on DNA-A *vs* Ki67-A plot as follows: cells in $G_0$ were identified as DNA 2n/Ki67$^-$ (bottom left quadrant); cells in $G_1$ as DNA 2n/Ki67$^+$ (upper left quadrant); cells in S-$G_2$/M (or $T_{DS}$ cells) as DNA>2n/Ki67$^+$ (top right quadrant). Unpublished data in relation to (16)."

In the original article, there was also a mistake in the legend for **Supplementary Table 1** as published. The peptide- HLA-A*02 tetramer list was incorrectly formatted, there was missing information about numbers in the table (they represent average percentages); missing information about the number of mice (panel A) and number of human donors (panel B and C); and a missing citation of original references at the end. The corrected **Supplementary Material File** is linked below.

In the original article, there was also a mistake in **Figure 1** as published. **There was an incorrect y-axis label in panel A, third graph from left.** The corrected **Figure 1** appears below.

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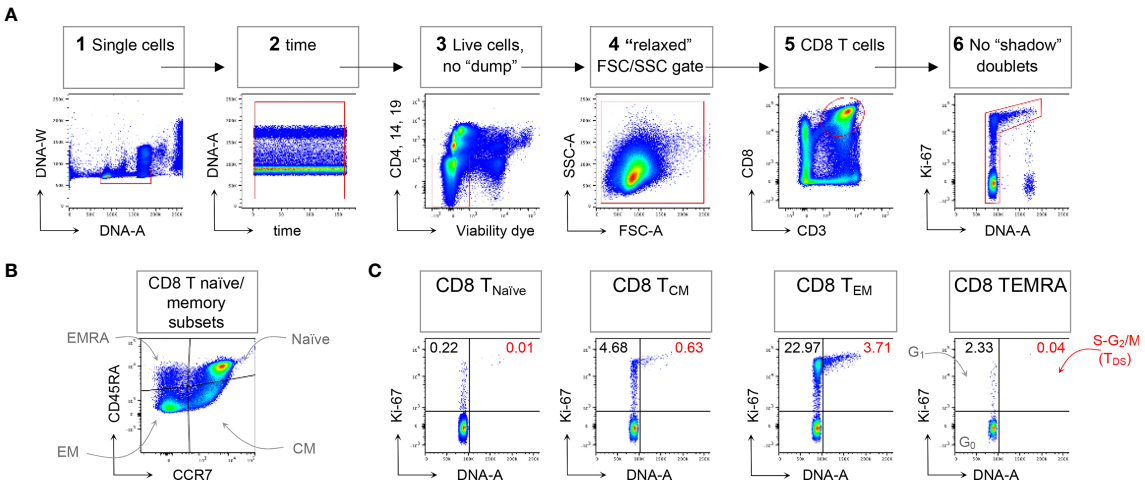


**FIGURE 1** | Example of CD8 T cell naïve/memory subset analysis by $T_{DS}$ assay. HD PBMCs were stained with the viability dye eFluor 780 (eF780), the DNA dye Hoechst-33342, and fluorochrome conjugated mAbs against surface markers and Ki-67, as described (16). An example of flow cytometry analysis is shown. **(A)** Gating of viable single CD8 T cells in 6 steps: 1) DNA-A/-W singlets. Single cells having 2n≤ DNA content ≤4n were selected on the DNA-area (A) *versus* (*vs*) DNA-width (W) plot; 2) Time exclusion. Stable acquisition over time (seconds) was monitored on the time *vs* DNA-A plot and any events collected in case of pressure fluctuations were excluded; 3) Viable cells, no "dump". Cells expressing CD4, CD14 and CD19, and dead cells were excluded; 4) FSC A/SSC-A "relaxed" gate. A "relaxed gate was used on the FSC-A *vs* SSC-A plot, to include highly activated and cycling lymphocytes (15); 5) CD8 T cells. CD8 T cells were gated on the CD3 *versus* CD8 plot; 6) Refined singlets. A few remaining doublets composed by one cell sitting on top of another (so called "shadow" doublets) were excluded as Ki-67int/$^-$ events having > 2n DNA content (16). This gating strategy was used as a base for the subsequent gates. **(B)** The following naïve/memory subsets of CD8 T cells were identified: CD45RA$^+$ CCR $^+$ Naïve, CD45RA$^-$ CCR7$^+$ central memory (CM), CD45RA$^-$ CCR7$^-$ effector memory (EM), and CD45RA$^+$ CCR7$^-$ (EMRA). **(C)** Cell cycle phases of each naïve/memory CD8 T cell subset were defined on DNA-A *vs* Ki67-A plot as follows: cells in $G_0$ were identified as DNA 2n/Ki67$^-$ (bottom left quadrant); cells in $G_1$ as DNA 2n/Ki67$^+$ (upper left quadrant); cells in S-G2/M (or TDS cells) as DNA>2n/Ki67$^+$ (top right quadrant). Unpublished data in relation to (16).

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

## SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fimmu.2021.756641/full#supplementary-material