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Author Correction: The immunotherapy candidate TNFSF4 may help the induction of a promising immunological response in breast carcinomas

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The original version of this Article contained an error in Figure 6, panel E, where the labeling of the flow cytometry antibody gate and thresholds was incorrect. Additionally, the manually added scale number and the gates data have been deleted. The original Figure 6 and accompanying legend appear below.

The original Article has been corrected.

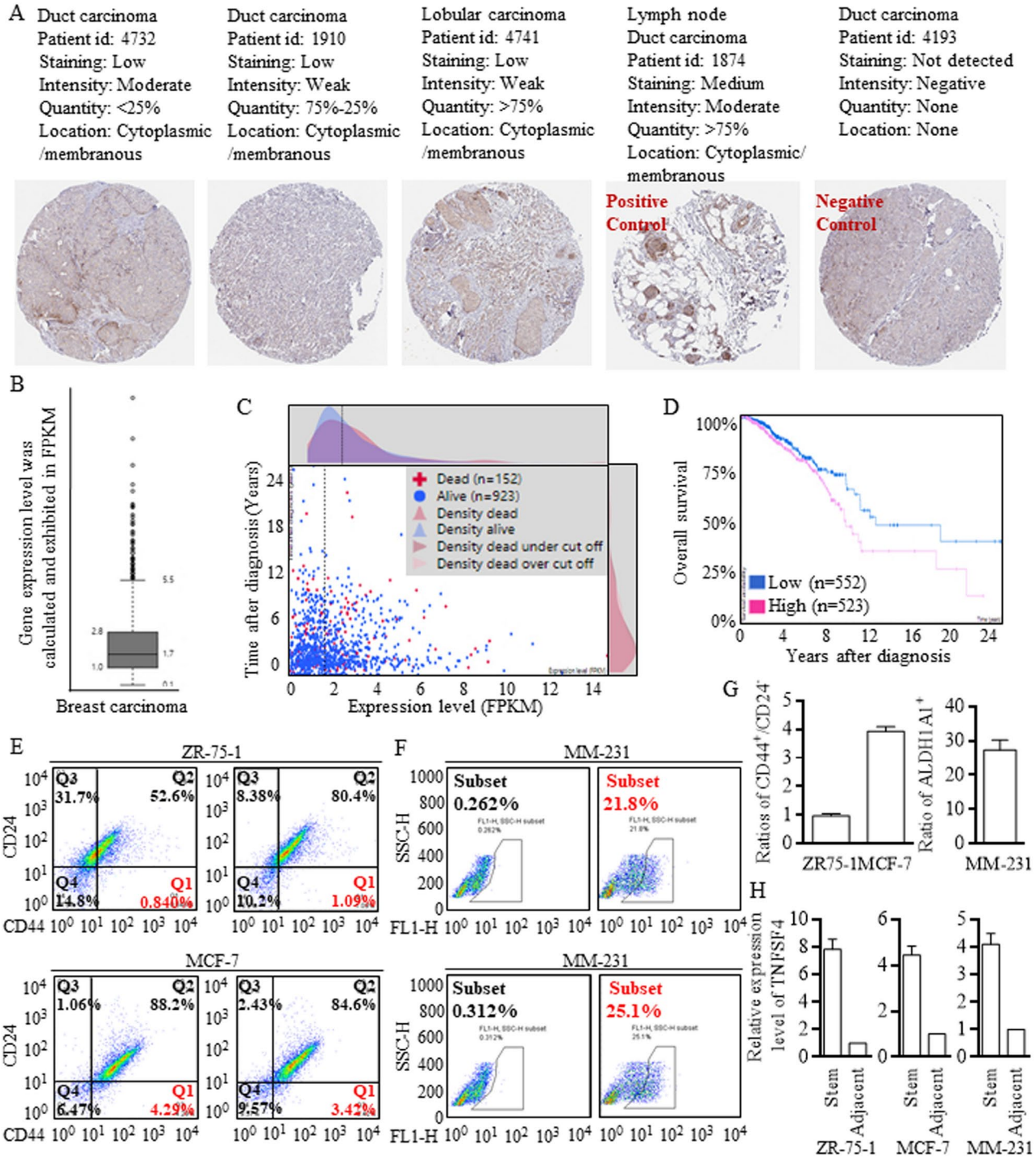

Figure 6. Exploration of the putative clinical roles of TNFSF4. (**A**) IHC staining images are shown to clarify different expression patterns (left to right, in sequence, < 25%, 25–75%, and > 75%). A lymph node slide was set as a positive control, and an unstained slide was set as a negative control. (**B**) High RNA expression of TNFSF4 was universally identified in breast carcinoma, with testing and calculation based on FPKM, and the cutoff line is labeled, which was used for clinical predictions. (**C**,**D**) Higher TNFSF4 expression pointed to poorer survival outcomes. (**E**,**F**) Flow cytometry with FACSAria sorting was applied to isolate stem cells from ZR75-1, MCF-7, and MM-231 cells. (**G**,**H**) Stem cells with a $CD44^{+}/24^{-}$ or $ALDH1A1^{+}$ phenotype were identified and isolated, and the TNFSF4 expression patterns in different cell lines were checked to illustrate the increased expression.