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# Corrigendum: Identification of m6A modification patterns and development of m6A–hypoxia prognostic signature to characterize tumor microenvironment in triple-negative breast cancer

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## KEYWORDS

Triple-negative breast cancer, m6A RNA methylation, m6A-hypoxia signature, tumor microenvironment, immune cell infiltration

## A Corrigendum on

**Identification of m6A modification patterns and development of m6A–hypoxia prognostic signature to characterize tumor microenvironment in triple-negative breast cancer**

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In the published article, there was an error in **Figure 9F** as published. After checking the original paper, the images of **Figure 9F** were mistakenly included. The corrected **Figure 9** and its caption **Figure 9** Nomogram and detection of MHPS gene expression. appear 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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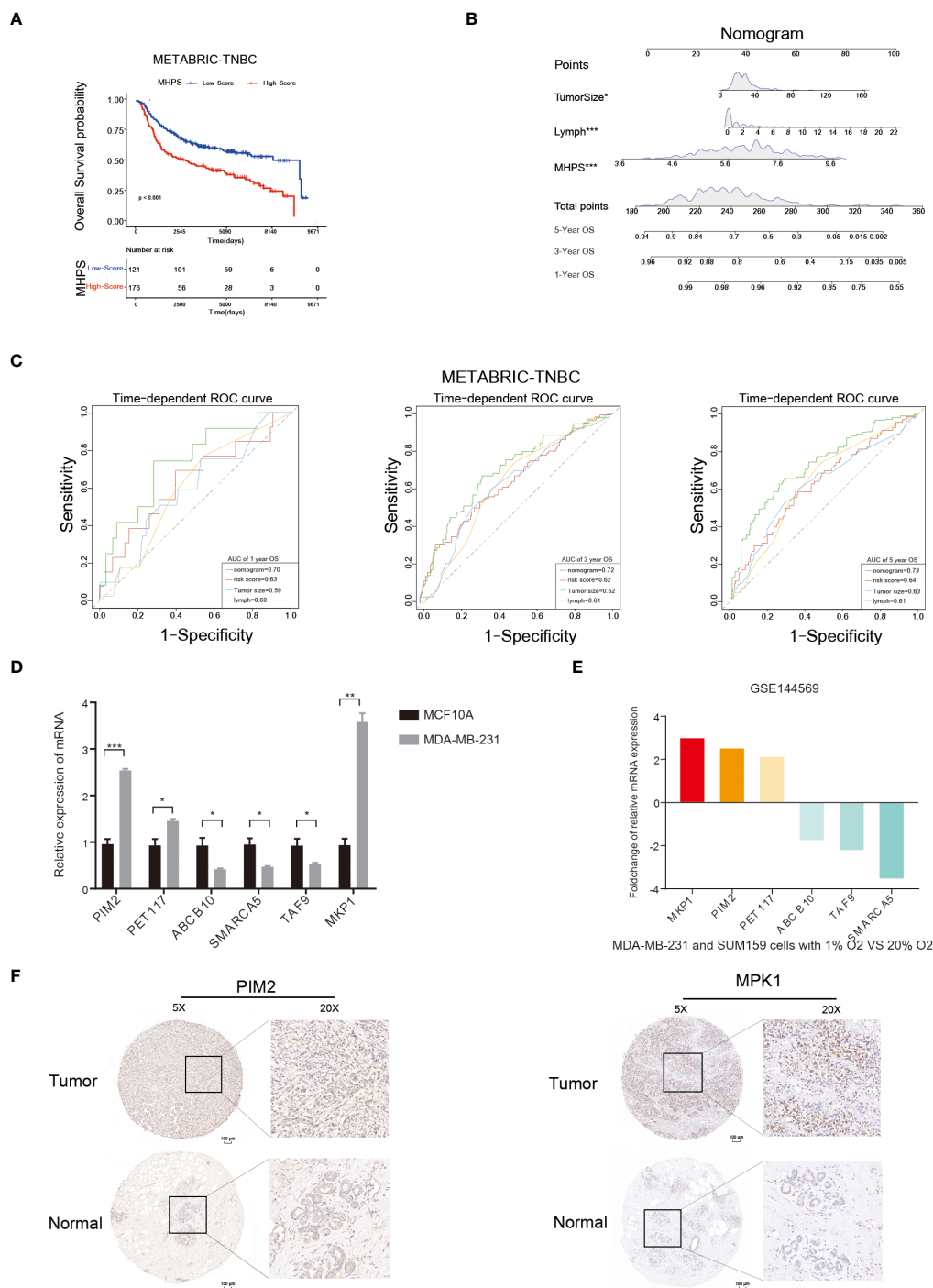


FIGURE 9

Nomogram and detection of MHPs gene expression. (A) Kaplan-Meier analysis of patients with high or low MHPs risk score in METABRIC-TNBC cohort. (B) Construction of nomogram scoring system to predict patient survival at 1-, 3- and 5- years. Each clinical factor in the nomogram system corresponds to a score, and all scores are summed to obtain a total point, which can predict the survival rate of patients at 1-, 3- and 5- years. (C) Time-dependent ROC for the nomogram, MHPs, tumor size, lymph node in the METABRIC cohort (for predicting 1-, 3- and 5-years OS). (D) Comparison of mRNA expression of hub genes in normal breast and TNBC cell lines. (E) Different expression of hub genes in normoxia and hypoxia cultured TNBC cells based on GSE144569 dataset. (F) IHC staining to detect protein expression of PIM2 and MKP1 in normal and tumor tissues. Scale bar:100µm. (\*P< 0.05,\*\*P< 0.01, and \*\*\*P< 0.001). ns, not significant.