Breast Cancer
R E S E A R C H

CORRECTION

Correction: An integration of complementary strategies for gene-expression analysis to reveal novel therapeutic opportunities for breast cancer

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In our previous publication [1], Figure 4 involved the analysis of chemotherapy-response signatures (as carried out independently by author AP and described in a 2006 Nature Medicine article [2,3]). It has recently been determined that the chemotherapy-response signatures in [2] are not reproducible, causing retraction of that article [3]. As such, the results presented in Figure 4 of our original paper [1] are no longer valid.

We believe that the data presented in Figures 1-3 of our article remain valid. However, as Figure 4 can no longer be considered valid, portions of [1] are no longer applicable, including the Materials and Methods section entitled "Chemosensitivity signatures", the Results section entitled "Genomic signatures that predict response to cytotoxic chemotherapeutics", and other statements in the Abstract, Introduction, Results, Discussion, and Conclusions sections that refer directly or indirectly to the integration of chemotherapy-response signatures into the analytical approach presented in the manuscript. As such, the focus of the manuscript on the utility of an integrated approach using three complementary strategies for gene expression analysis (i.e. breast cancer intrinsic subtype analysis, pathway prediction and chemotherapy-response signatures) should now be interpreted as referring exclusively to the integration of two complementary strategies.

Competing interests
The authors declare that they have no competing interests.

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