CORRECTION

Correction to: MicroRNA gene expression during retinoic acid-induced differentiation of human acute promyelocytic leukemia

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Following the publication of this article, it was noted that the U6 Northern Blotting control was used more than once in Figs. 2a and 2e. The authors have carried out repeat experiments and results are consistent with the initial result reported and validated independently by other groups. The corrected version of Figs. 2a and 2e are provided below.

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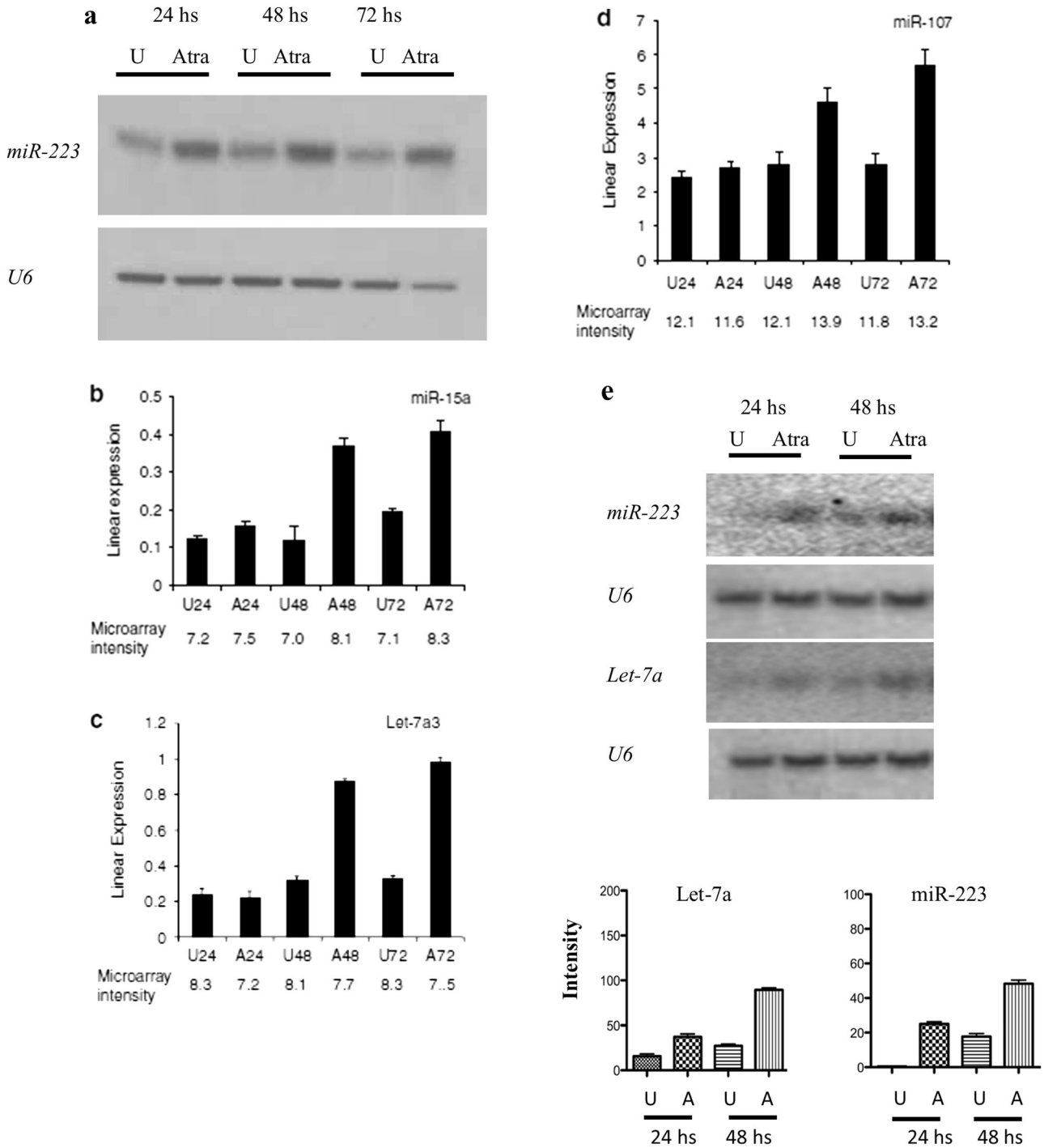

Fig. 2 Microarray data confirmation. a Northern blots were performed as described previously (Liu et al., 2004) using probes with perfect complementarities to the mature sequence of miR-223 in NB4 cells. Loading control was performed with U6. QRT–PCR of miR-15a (**b**), let-7a (**c**) and miR-107 (**d**) during granulocytic differentiation of NB4 cells induced by ATRA. The miRNA expression is shown in untreated (U) and ATRA-treated cells (A) during the time course after 2(_D-Ct) calculations with 18S normalization. Below each bar there is the normalized miRNA signal intensity (2 logged) for each sample obtained by microarrays. **e** Representative Northern blots for miR-223 and let-7a in HL-60 cells untreated or treated with ATRA for 48 h. The treatment of HL-60 was performed as described previously in the text for NB4 cells. Loading control was performed with U6. Immediately below we showed the densitometry calculations for Northern blot data shown in Fig. 2e. We calculated the intensities of bands using ImageJ, verifying for non-saturation and subtracting background. Values are expressed as the integrals (area * mean density) of each band normalized to the corresponding U6 intensity.