ERRATUM

Reciprocal expression of the endocytic protein HIP1R and its repressor FOXP1 predicts outcome in R-CHOP-treated diffuse large B-cell lymphoma patients

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Leukemia (2014) 28, 470; doi:10.1038/leu.2013.276

Correction to: *Leukemia* (2014) 28, 362–372; doi:10.1038/leu.2013.224; published online 13 August 2013

Since the publication of this article, the authors have identified an error contained in Figure 6 (panel c).

$FOXP1^{hi}/HIP1R^{lo}$ has been incorrectly listed as $FOXP1^{hi}/HIP1R^{hi}$.

The correct figure appears below.

The error has now been rectified, and the correct article appears in this issue. The html and online pdf versions have also been rectified, and now carry the correct paper.

The Publisher would like to apologize for any inconvenience this may have caused.

Figure 6. OS of DLBCL cases ($n = 233$) according to $HIP1R$, $FOXP1$ or combined $HIP1R/FOXP1$ transcript levels. Data were reanalyzed from the Lenz *et al.*⁶ data set (Gene Expression Omnibus accession no. GSE10846). Kaplan–Meier curves in (a) and (b) were grouped on the basis of the lower quartile Q_1 of $HIP1R$ or higher-than-median $FOXP1$ transcript values, and both cohorts showed significantly worse outcome, $P = 0.0044$ and $P = 0.0113$, respectively. (c) The $FOXP1^{hi}/HIP1R^{lo}$ subgroup ($FOXP1 \geq \text{median}/HIP1R \leq Q_1$) showed a significantly inferior outcome ($P = 0.0004$).