

## CORRIGENDUM

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### ***FUCA1* is induced by wild-type *p53* and expressed at different levels in thyroid cancers depending on *p53* status**

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Subsequent to the publication of the above paper, the authors noted that: 1) there was an error on Fig. 4, page 2046, in which the symbols of  $\alpha$ -L-fucosidase 1 (*FUCA1*) and fucosyltransferase 8 (*FUT8*) had been mistakenly labelled the wrong way around (*FUCA1* should have been represented by the blue bars, and *FUT8* by the red), and 2) the sentence 'Average levels of *FUCA1* mRNA were low in ATCs while expression levels in PTC samples were comparable or slightly higher than those present in normal thyroid tissues (Fig. 4)', page 2046, left column, 4th line from the bottom, was not appropriate to explain the result of Fig. 4. Therefore, this sentence is replaced by: '*FUCA1* RNA expression levels were found to be lower in anaplastic thyroid cancer samples (ATCs), while they were higher in papillary thyroid cancer samples (PTCs) and in normal thyroid tissues (Fig. 4)'.

The corrected version of Fig. 4 is shown below, which now accurately shows how *FUCA1* RNA expression levels were found to be lower in anaplastic thyroid cancer samples (ATCs), while they were higher in papillary thyroid cancer samples (PTCs) and in normal thyroid tissues. We sincerely apologize for the mistake and the inappropriate explanation in the text, and thank the reader of our article who drew this matter to our attention. Furthermore, we regret any inconvenience these changes have caused.

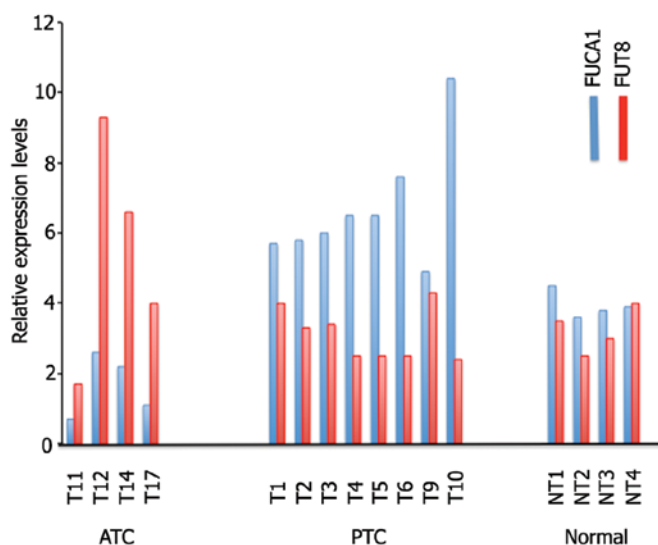


Figure 4. Microarray analyses of *FUT8* (red) and *FUCA1* (blue) expression. Four ATC samples (T11, T12, T14, T17), 8 PTC samples (T1, T2, T3, T4, T5, T6, T9, T10), and 4 normal thyroid tissues (NT1, NT2, NT3, NT4) are shown.