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## scientific reports

Published online: 14 October 2021

## **OPEN** Author Correction: Development and Evaluation of <sup>18</sup>F-IRS for Molecular Imaging Mutant EGF **Receptors in NSCLC**

Yan Song, Zunyu Xiao, Kai Wang, Xiance Wang, Chongqing Zhang, Fang Fang, Xilin Sun & **Baozhong Shen** 

Correction to: Scientific Reports https://doi.org/10.1038/s41598-017-01443-7, published online 09 June 2017

This Article contains errors.

In Figure 5A, the blots for EGFR (E746-A750del) and GAPDH band are incorrect, which affected the quantification in Figure 5B. A corrected version of Figure 5 and its accompanying legend appear below.

In Figure 7B, the image for the H358 is incorrect. The correct Figure 7 appears below with its accompanying legend.

This correction does not alter the conclusions of this study.









**Figure 7.** Quantitative analysis of QD620-IRS binding affinity by confocal imaging and flow cytometry. (**A**) Comparison of the expression levels of EGFR specific E749-A750del mutation in HCC827, H520, H1975 and H358 cell lines by immunofluorescence (Green color is from Alexa Fluor\*488 secondary antibody, blue color from DAPI). (**B**) There is little uptake of QD620 in the four cell lines. (**C**) QD620-IRS uptake in HCC827 cells expressing EGFR 19 exon deleted mutation is considerably higher than in H1975, H520 and H358 cells. The binding of QD620-IRS in HCC827 cells was inhibited by application of gefitinib (100 µmol/L) (red circle is from QD620-IRS and blue color from DAPI). All scale bars 10 µm. (**D**) Flow cytometric analysis of endocytic rates in HCC827, H1975, H520 and H358 cells incubated with QD620-IRS or QD620 1 h. In (**E**), error bars indicate the mean ± S.D. of data from three separate experiments. \*\*\**P* < 0.001 vs. HCC827 group.

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