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Title

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Permalink

https://escholarship.org/uc/item/8xs8r7xn

Journal

Clinical Proteomics, 15(1)

ISSN

1542-6416

Authors

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Publication Date

2018-12-01

DOI

10.1186/s12014-018-9210-4

Peer reviewed

CORRECTION Open Access



Correction to: Quantitative phosphoproteomic analysis reveals reciprocal activation of receptor tyrosine kinases between cancer epithelial cells and stromal fibroblasts

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Correction to: Clin Proteom (2018) 15:21

https://doi.org/10.1186/s12014-018-9197-x

Unfortunately, after publication of this article [1], errors were noticed in Figs. 3 and 4. The "T" in the word "pTyr" was missing in Fig. 3. The word "change" was missing

after the word "Fold" in the label of y axis in Fig. 4a. The "e" in the word "Co-culture" was missing in Fig. 4a. The correct figures are presented in this correction. The original article has also been updated.

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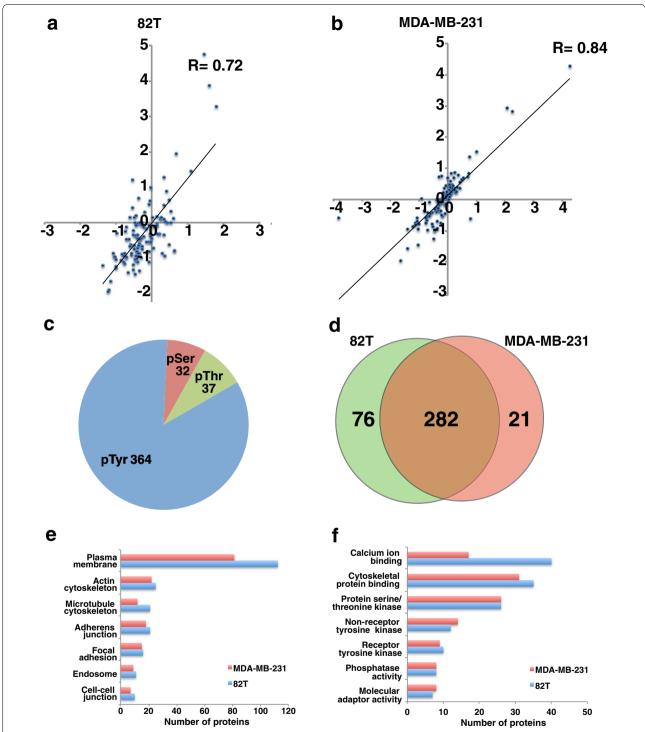


Fig. 3 Phosphotyrosine profiling of cancer epithelial cells and interacting CAFs. **a, b** Density scatter plot of log₂-transformed phosphopeptide intensity ratios (82T-co-cultured vs. 82T (A) and MDA-MB-231-co-cultured vs. MDA-MB-231) from two SILAC biological experiments. **c** Pie chart showing the composition of pTyr and pSer/Thr peptides identified in the phosphoproteomic analysis. **d** Venn diagram showing overlap of phosphopeptides identified in MDA-MB-231 and 82T cells. **e, f** Gene ontology analysis of phosphoproteins in cancer epithelium and CAFs. **e** Cellular component; **f** molecular functions

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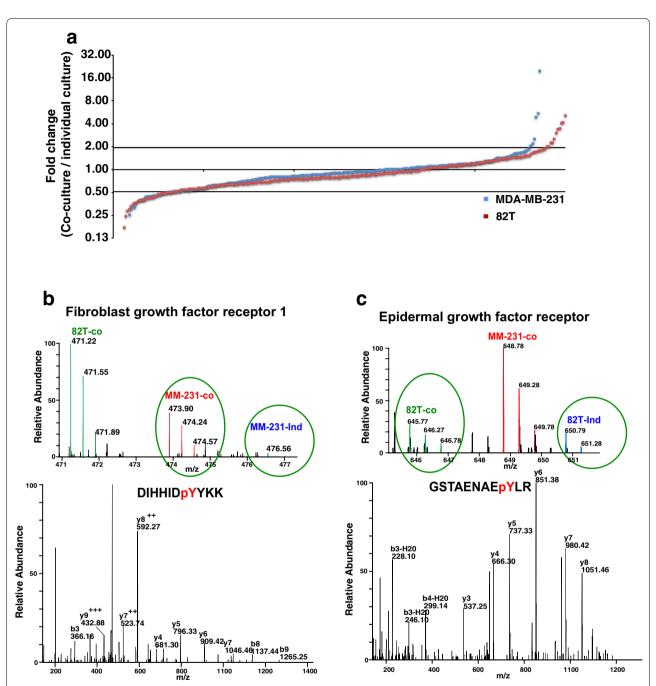


Fig. 4 Reciprocal activation of receptor tyrosine kinases induced by the crosstalk. **a** Distribution of phosphorylation ratio of pY peptides. Blue dots: log₂-transformed ratio of MDA-MB-231-co-cultured versus MDA-MB-231; red dots: log₂-transformed ratio of 82T-co-cultured versus 82T. **b, c** Representative spectrum of FGFR1 (**b**) and EGFR (**c**) identified in cancer epithelium and CAFs. Top panels: MS spectra and bottom panels: MS/MS spectra for phosphotyrosine-containing peptides identified for FGFR1 and EGFR

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The original article can be found online at https://doi.org/10.1186/s1201 4-018-9197-x.

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Publisher's Note

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Received: 23 October 2018 Accepted: 23 October 2018

Published online: 17 November 2018

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 Wu X, Zahari MS, Renuse S, Sahasrabuddhe NA, Chaerkady R, Kim M, Fackler MJ, Stampfer M, Gabrielson E, Sukumar S, Pandey A. Quantitative phosphoproteomic analysis reveals reciprocal activation of receptor tyrosine kinases between cancer epithelial cells and stromal fibroblasts. Clin Proteom. 2018;15:21. https://doi.org/10.1186/s12014-018-9197-x.