



Author Correction: Integrating microarray-based spatial transcriptomics and single-cell RNA-seq reveals tissue architecture in pancreatic ductal adenocarcinomas

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In the version of this article initially published, Fig. 5d reported the analysis of 183 pancreatic ductal adenocarcinoma (PDAC) RNA-seq transcriptomes from The Cancer Genome Atlas (TCGA) to compute the correlation between the identified cancer gene modules and the inflammatory fibroblast signature. Upon closer inspection, only 142 of these datasets are annotated as PDAC tumors; the rest originate from other pancreatic adenomas. Repeating the analysis using only the 142 PDAC RNA-seq datasets resulted in a nearly identical set of patterns that does not change the interpretation: the expression of the stress-response module is most significantly correlated with the expression of the inflammatory fibroblast gene signature. Figure 5d has been replaced with an image reflecting the reanalysis, and the number of TCGA tumors analyzed has been changed from 183 to 142 in the Fig. 5d legend and the main text. The error has been corrected in the PDF and HTML versions of the article.

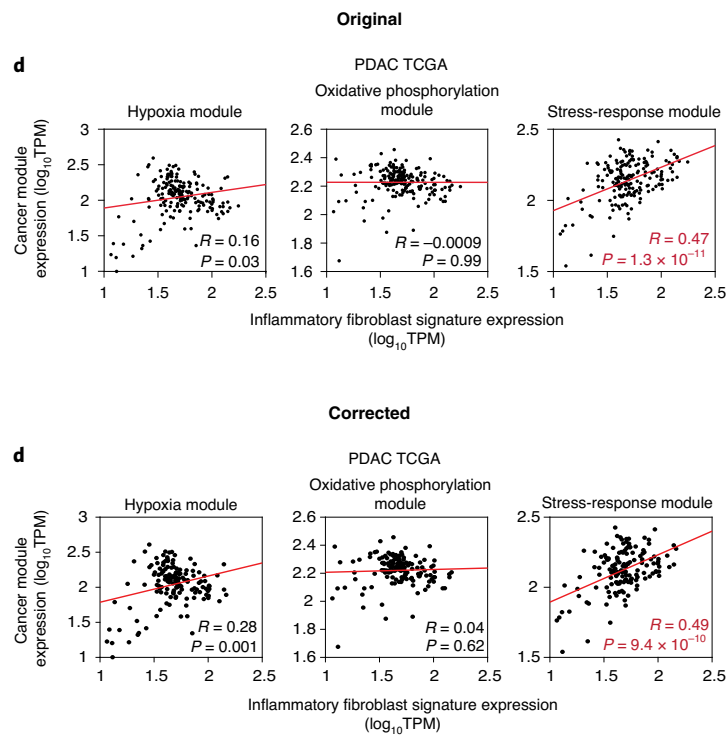


Fig. 5 | Original and corrected.

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