CORRECTION

Correction: Comparison of the Prognostic Utility of Diverse Molecular Data among lncRNA, DNA Methylation, microRNA and mRNA across Five Human Cancers

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The Funding information is missing from the published article. The corrected funding information is as follows:

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[S1 File](#) contains errors. The correct [S1 File](#) and its caption can be viewed below.

Supporting Information

S1 File. Supplementary files. Model performance with different threshold of feature numbers across four molecular data (Figure A). K-M curves and bar-plot of lncRNA predictors confirmed in literature (Figure B). Overview of tumor samples in four molecular data profiles across five TCGA cancers (Table A). Model performance of diverse molecular data in five TCGA cancers (Table B). The test set accuracies of the 20 integrated molecular models (Table C). Survival analysis of IDFO predictors in five cancers (Table D). Comparison of the prognostic power of molecular data associate with additional clinical variables using clinical models (Table E). List of 22 IDFO—lncRNAs confirmed in literature (Table F). Supplementary Methods. (DOC)

Reference

1. Xu L, Fengji L, Changning L, Liangcai Z, Yinghui L, Yu L, et al. (2015) Comparison of the Prognostic Utility of the Diverse Molecular Data among lncRNA, DNA Methylation, microRNA, and mRNA across Five Human Cancers. PLoS ONE 10(11): e0142433. doi: [10.1371/journal.pone.0142433](https://doi.org/10.1371/journal.pone.0142433) PMID: [26606135](https://pubmed.ncbi.nlm.nih.gov/26606135/)

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