

## CORRECTION

# Correction: A secreted proteomic footprint for stem cell pluripotency

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The datapoints, axes and trend-line of Rebl.PAT are missing in [Fig 3](#). Please see the correct [Fig 3](#) here.

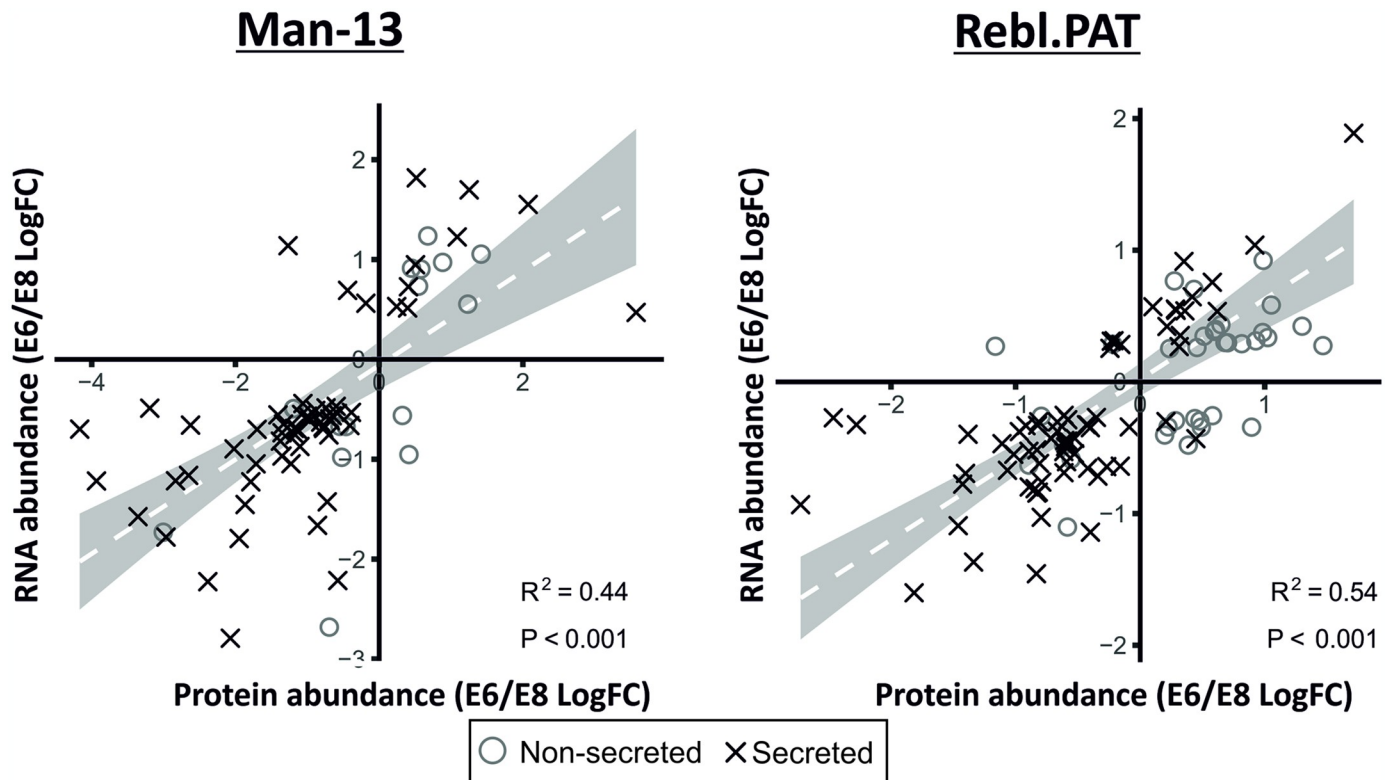


## OPEN ACCESS

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**Fig 3. Correlation between E6/E8 log fold-changes between mRNA and protein data.** Protein data was paired to RNA-Seq data using Entrez IDs retrieved from Uniprot and Bioconductor [22–24]. These data show a correlation between the changes observed in significantly changed ( $q < 0.05$ ) secreted proteins and the corresponding RNA-seq data (Man-13  $R^2 = 0.44$  & Rebl.PAT  $R^2 = 0.54$ ).

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## Reference

1. Lewis PA, Silajdžić E, Smith H, Bates N, Smith CA, Mancini FE, et al. (2024) A secreted proteomic footprint for stem cell pluripotency. *PLoS ONE* 19(6): e0299365. <https://doi.org/10.1371/journal.pone.0299365> PMID: 38875182