

CORRECTION

Correction: Whole genome expression profiling associates activation of unfolded protein response with impaired production and release of epinephrine after recurrent hypoglycemia

Juhye Lena Kim, Edmund F. La Gamma, Todd Estabrook, Necla Kudrick, Bistra B. Nankova

The image for [Fig 6](#) is incorrect. The image should be in color. Please see the complete, correct [Fig 6](#) here.



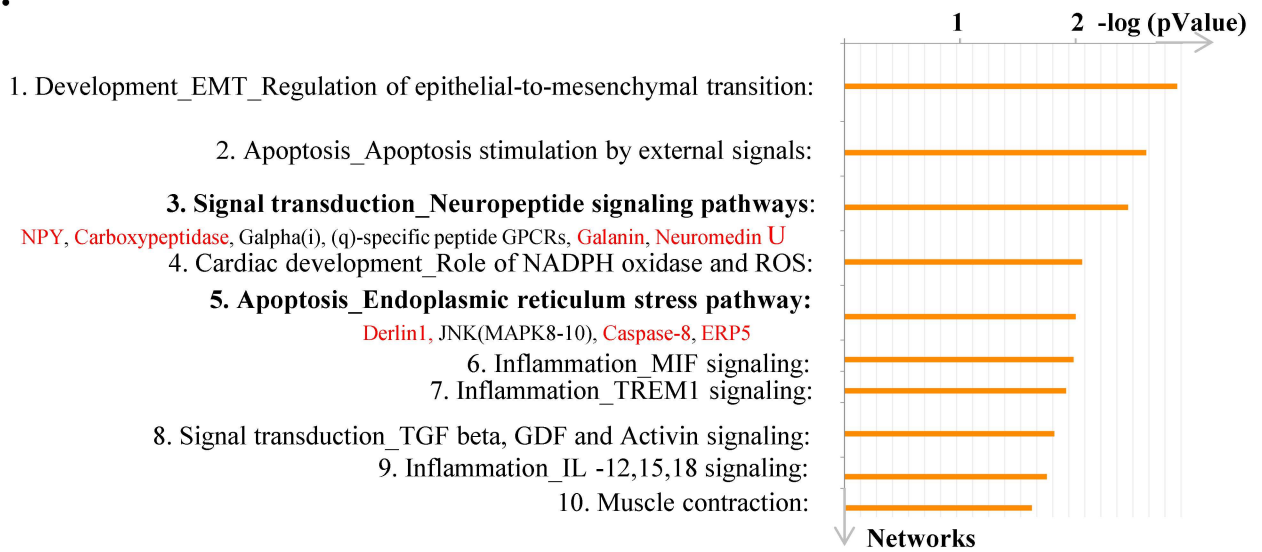
 OPEN ACCESS

Citation: Kim JL, La Gamma EF, Estabrook T, Kudrick N, Nankova BB (2017) Correction: Whole genome expression profiling associates activation of unfolded protein response with impaired production and release of epinephrine after recurrent hypoglycemia. PLoS ONE 12(3): e0173839. doi:10.1371/journal.pone.0173839

Published: March 8, 2017

Copyright: © 2017 Kim et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

A:



B:

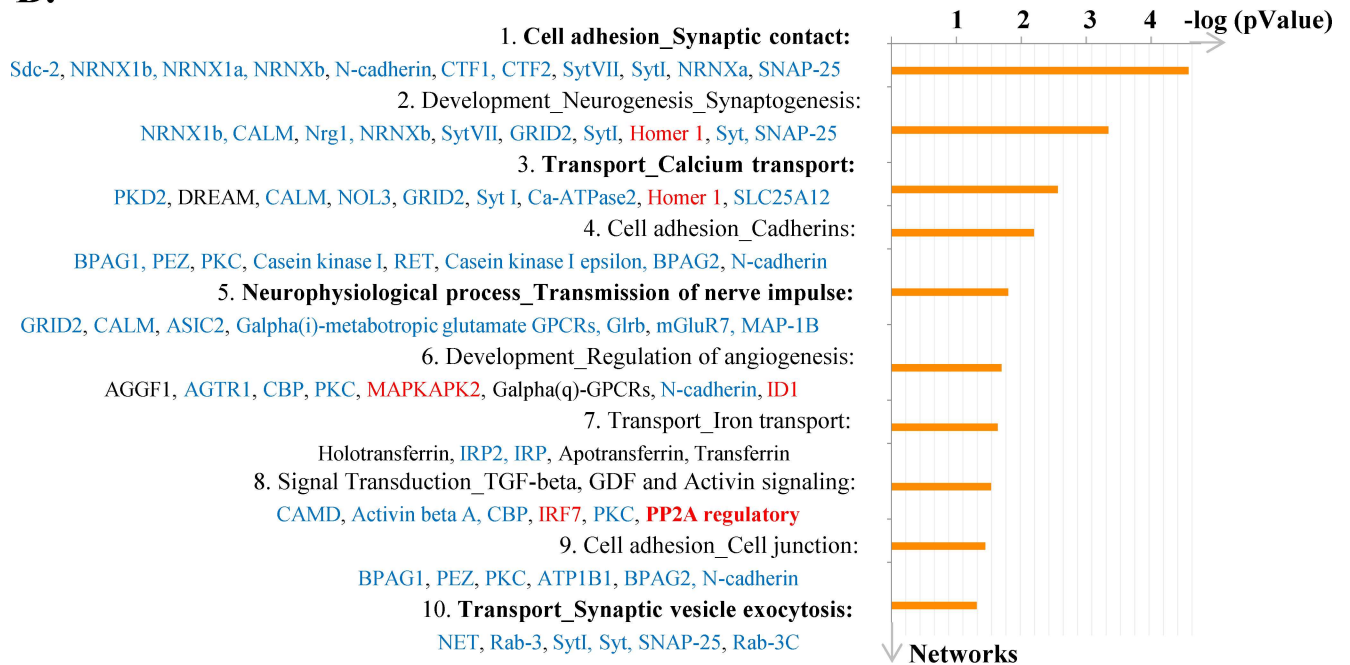


Fig 6. Enrichment analysis of DEGs in 2RH and 2RS experimental groups. A) Shown is the distribution by process networks at 0 time point (2RH0 vs. 2RS0) and B) at 60 min time point (2RH60 vs. 2RS60). Sorting is done for unique genes and both signals (induced genes—shown in red and repressed genes—in blue) included. Top 10 process networks are listed based on their—log (p-value). For list of abbreviations see supplemental file [S1 Text](#).

doi:10.1371/journal.pone.0173839.g001

Reference

1. Kim JL, La Gamma EF, Estabrook T, Kudrick N, Nankova BB (2017) Whole genome expression profiling associates activation of unfolded protein response with impaired production and release of epinephrine after recurrent hypoglycemia. PLoS ONE 12(2): e0172789. doi:[10.1371/journal.pone.0172789](https://doi.org/10.1371/journal.pone.0172789) PMID: [28234964](https://pubmed.ncbi.nlm.nih.gov/28234964/)