

CORRECTION

Open Access



Correction to: Simulated complexes formed from a set of postsynaptic proteins suggest a localised effect of a hypomorphic Shank mutation

Marcell Miski¹, Áron Weber^{1,2}, Krisztina Fekete-Molnár¹, Bence Márk Keömley-Horváth^{1,2}, Attila Csikász-Nagy^{1,2*} and Zoltán Gáspári^{1*}

Correction to: BMC Neurosci 25, 32 (2024)

<https://doi.org/10.1186/s12868-024-00880-1>

Following publication of the original article [1], the authors identified an error in Fig. 1.

The correct figure was originally supplied, however during proofing was accidentally replaced by the authors with an incorrect version of the figure.

The online version of the original article can be found at <https://doi.org/10.1186/s12868-024-00880-1>.

*Correspondence:

Attila Csikász-Nagy
csikasznagy@gmail.com
Zoltán Gáspári
gaspari.zoltan@itk.ppke.hu

¹Faculty of Information Technology and Bionics, Pázmány Péter Catholic University, Budapest, Hungary

²Cytocast Hungary Kft, Budapest, Hungary



© The Author(s) 2024. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

The incorrect Figure 1 is given hereafter:

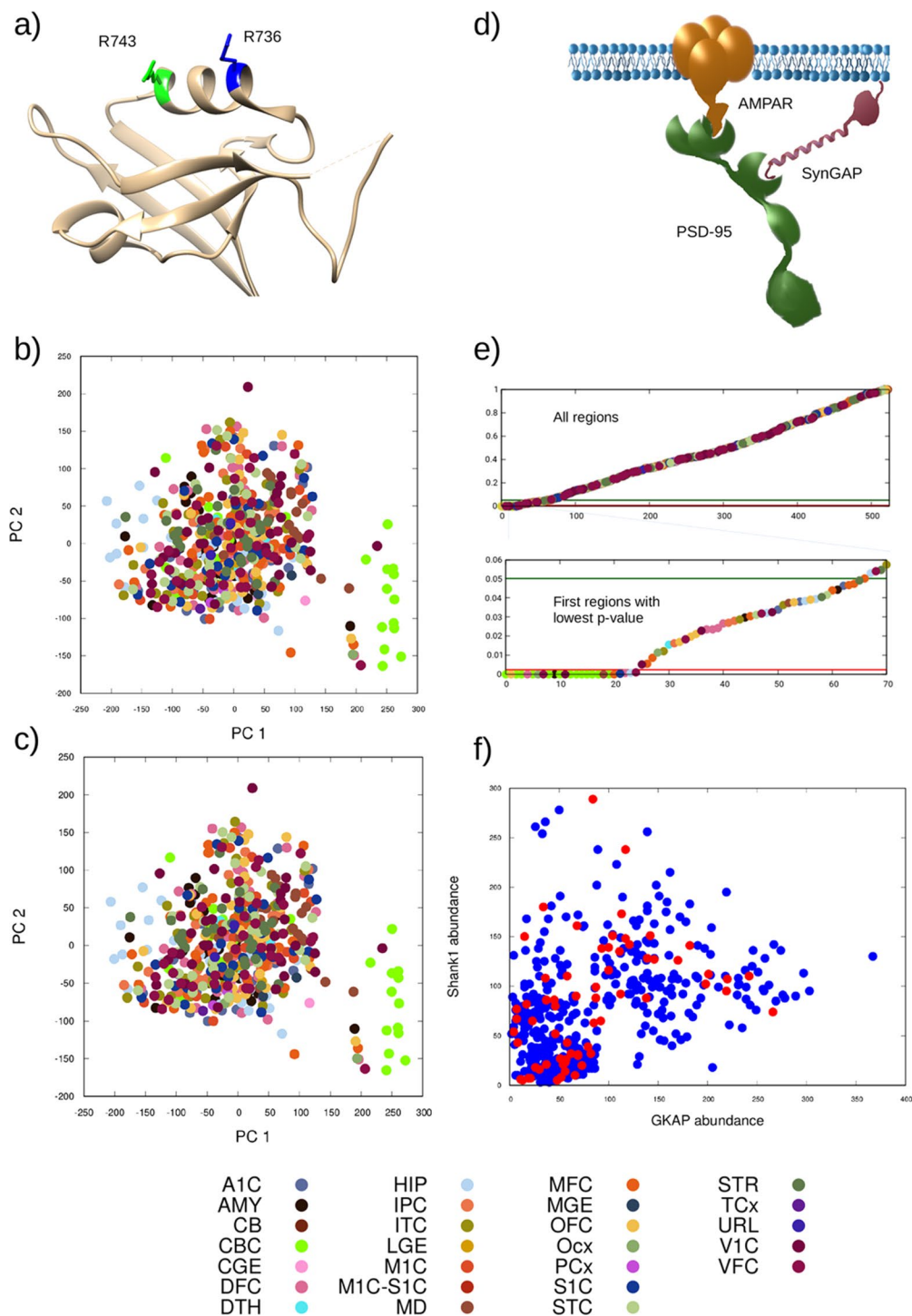


Fig. 1 (a) Position of the mutation selected (R743H, green) and a similar one reported in ASD (R736Q, blue) on the ribbon representation of the Shank1 PZ domain (PDB ID 6YWZ). Both arginines are located on the $\alpha 2$ helix flanking the ligand binding groove. Principal component analysis of the obtained protein complex distributions for (b) the wild-type and (c) the mutant scenarios investigated. Different colors denote different brain regions according to the key at the bottom. (d) Schematic depiction of the most informative complex according to the PCA (AMPA/PSD-95/SynGAP). (e) P-values describing the change upon the mutation relative to the wild-type, the value for the most informative complex is shown in increasing order from left to right, colored by the region type (key at the bottom) The green line denotes the 0.05 significance limit while the red line the limit of 0.0024 obtained using the Benjamini-Hochberg correction. (f) Abundance of Shank1 and GKAP, the two proteins in the interaction affected by the mutation, in the input data sets. Red circles indicate data sets where the abundance of the most informative complex changed significantly in the output using the Benjamini-Hochberg correction

The correct Figure 1 is given hereafter:

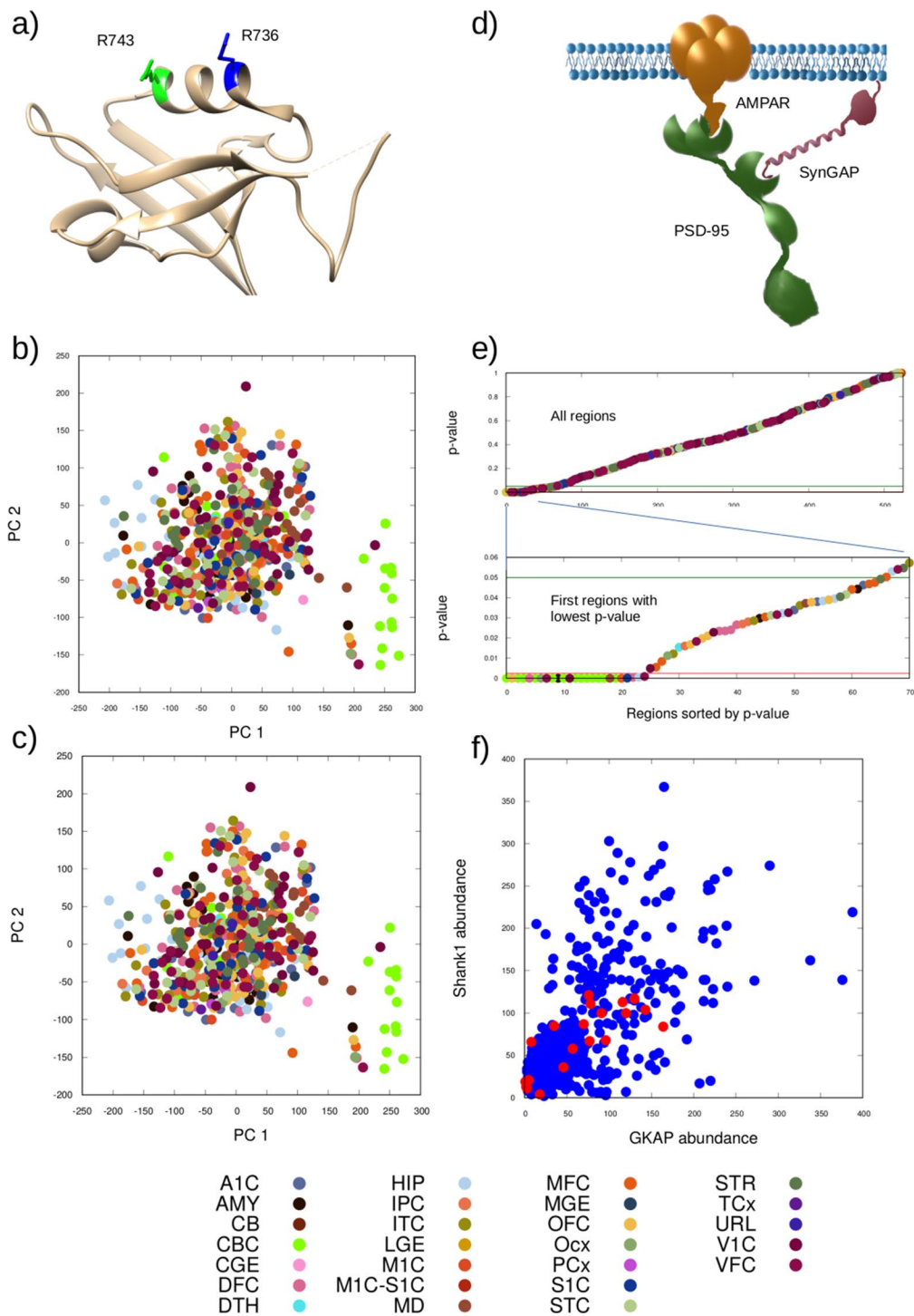


Fig. 1 (a) Position of the mutation selected (R743H, green) and a similar one reported in ASD (R736Q, blue) on the ribbon representation of the Shank1 PZ domain (PDB ID 6YWZ). Both arginines are located on the $\alpha 2$ helix flanking the ligand binding groove. Principal component analysis of the obtained protein complex distributions for (b) the wild-type and (c) the mutant scenarios investigated. Different colors denote different brain regions according to the key at the bottom. (d) Schematic depiction of the most informative complex according to the PCA (AMPA/PSD-95/SynGAP). (e) P-values describing the change upon the mutation relative to the wild-type, the value for the most informative complex is shown in increasing order from left to right, colored by the region type (key at the bottom) The green line denotes the 0.05 significance limit while the red line the limit of 0.0024 obtained using the Benjamini-Hochberg correction. (f) Abundance of Shank1 and GKAP, the two proteins in the interaction affected by the mutation, in the input data sets. Red circles indicate data sets where the abundance of the most informative complex changed significantly in the output using the Benjamini-Hochberg correction

The revised Fig. 1 has been updated in this correct article and the original article [1] has been corrected.

Publisher's note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Published online: 09 October 2024

References

1. Miski M, Weber Á, Fekete-Molnár K, et al. Simulated complexes formed from a set of postsynaptic proteins suggest a localised effect of a hypomorphic Shank mutation. *BMC Neurosci.* 2024;25:32. <https://doi.org/10.1186/s12868-024-00880-1>.