Acta Neuropathologica Communications

CORRECTION

Open Access

Correction: Investigating genotype-phenotype correlation of limb-girdle muscular dystrophy R8: association of clinical severity, protein biological function and protein oligomerization

Xiongda Liang[1], Jiameng Si[1], Hongting Xie[1], Yuqing Guan[2,3], Wanying Lin[4], Zezhang Lin[1], Ganwei Zheng[1], Xiaofeng Wei[1], Xingbang Xiong[1], Zhengfei Zhuang[5] and Xuan Shang[1,6*]

Correction: Acta Neuropathologica Communications (2025) 13:47
https://doi.org/10.1186/s40478-025-01971-8

In this article [1], Figs. 2, 3 and 4 captions had been interchanged. Caption of Figure 2 inadvertently give in as caption for Figure 4; Caption of Figure 3 inadvertently give in as caption for Figure 2 and Caption of Figure 4 inadvertently give in as caption for Figure 3. The figure(s) should have appeared as shown below.

The original article can be found online at https://doi.org/10.1186/s40478-025-01971-8.

*Correspondence:
Xuan Shang
shangrabbit@163.com
[1] Department of Medical Genetics, School of Basic Medical Science, Southern Medical University, Guangzhou 510515, China
[2] Department of Neurology, Nanfang Hospital, Southern Medical University, Guangzhou, China
[3] Department of Neurology, Ganzhou People's Hospital, Ganzhou, China
[4] Department of Laboratory Medicine, Nanfang Hospital, Southern Medical University, Guangzhou, China
[5] College of Biophotonics, South China Normal University, Guangzhou, China
[6] Innovation Center for Diagnostics and Treatment of Thalassemia, Nanfang Hospital, Southern Medical University, Guangzhou, China

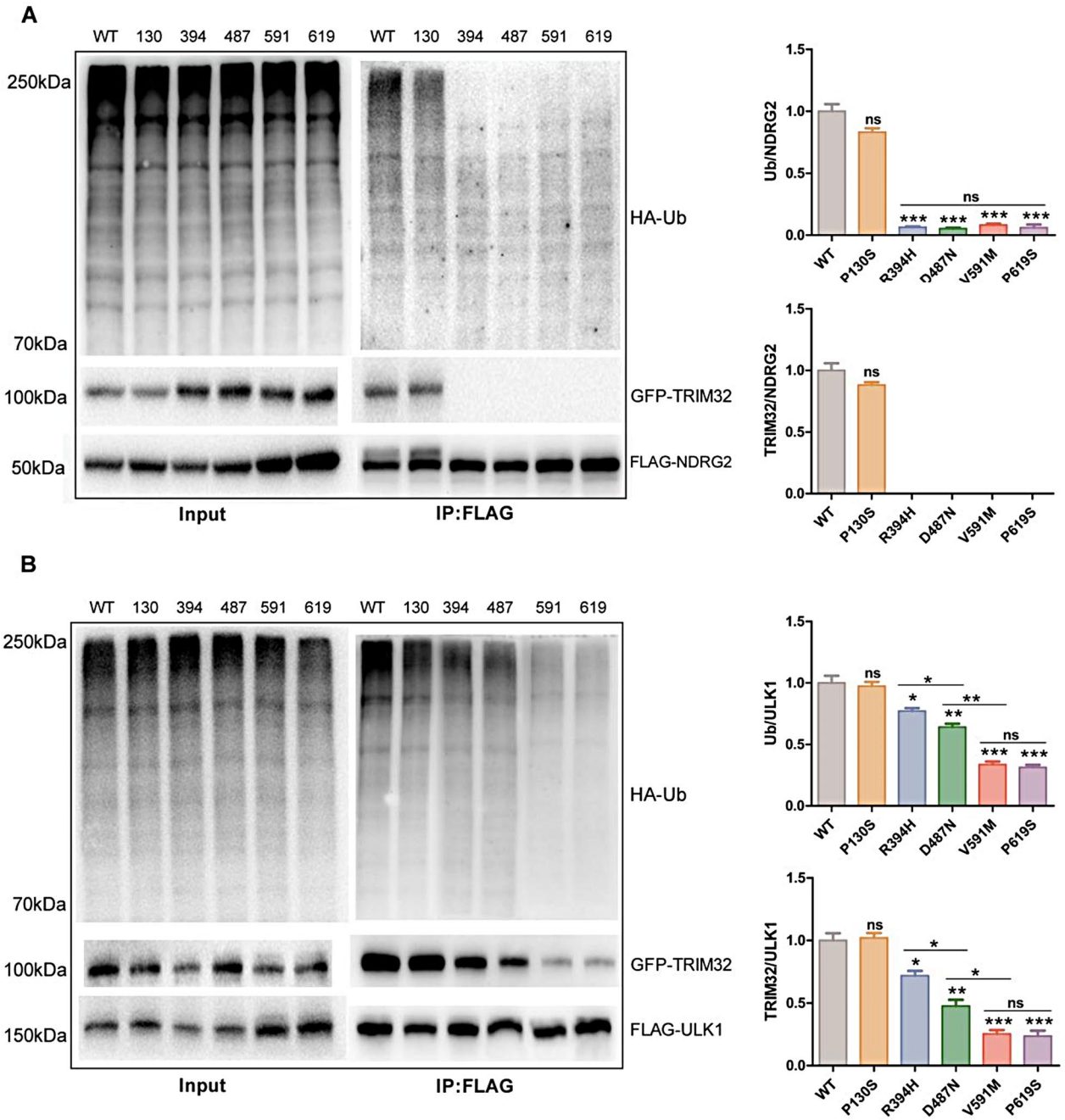

Fig. 2 Interaction and ubiquitination detection between TRIM32 and its substrate. (**A**) Left panel: Flag-NDRG2 was immunoprecipitated from HEK293T cells expressing HA-ubiquitin and either TRIM32-WT, P130S, D487N, R394H, V591M or P619S. Immunoprecipitated NDRG2 was probed for the presence of conjugated TRIM32 and HA-ubiquitin by western blot. Right panel: Protein grey value analysis performed using ImageJ, and the data are presented as means ± SEMs. (**B**) Left panel: Flag-ULK1 was immunoprecipitated from HEK293T cells expressing HA-ubiquitin and either TRIM32-WT, P130S, D487N, R394H, V591M or P619S. Immunoprecipitated ULK1 was probed for the presence of conjugated TRIM32 and HA-ubiquitin by western blot. Right panel: Protein grey value analysis performed using ImageJ, and the data are presented as means ± SEMs. A high molecular weight smear is seen on the HA blot indicative of high ubiquitination. Student's T-tests were performed to analyze the data and all data are shown as three biological replicates. "*" on the histogram columns represents the significant differences between each variant and WT; "*" on the horizontal line represents the significant differences of the variants below it. *P < 0.05; **P < 0.01; ***P < 0.001; ns, no significance

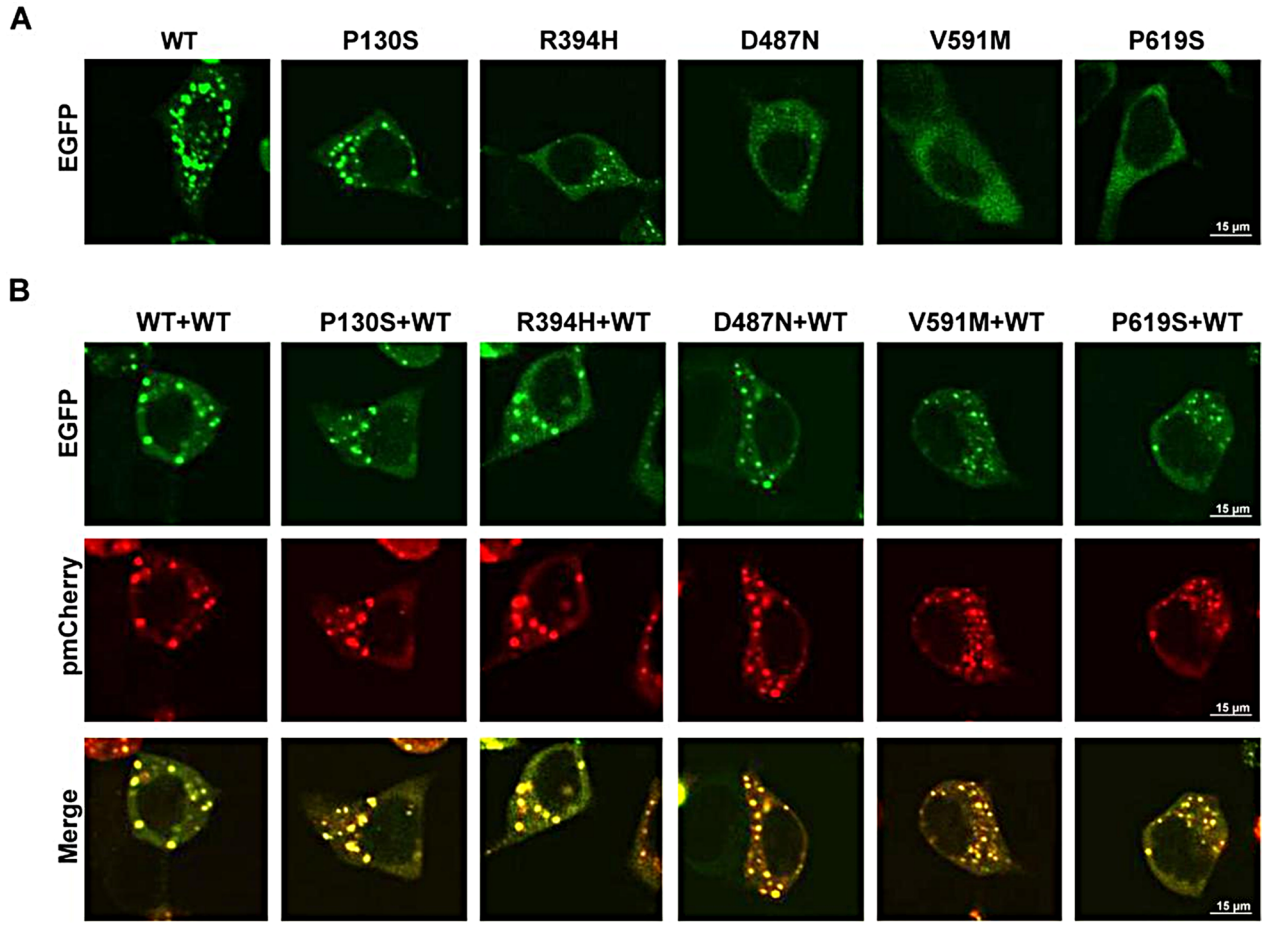

Fig. 3 Subcellular distribution of TRIM32 protein. (**A**) Localization of TRIM32-WT-EGFP and mutants in HEK-293T cell. HEK-293T cells were transfected with TRIM32-WT-EGFP, P130S-EGFP, 487N-EGFP, R394H-EGFP, V591M-EGFP and P619S-EGFP. (**B**) Co-localization of TRIM32-EGFP mutants and TRIM32-WT-pmCherry in HEK-293T cells. TRIM32-EGFP mutants and TRIM32-WT-pmCherry were transfected into HEK-293T cells. TRIM32-EGFP mutants protein can be found in aggregates that co-localize with the TRIM32-WT -pmCherry fluorescence, which appear yellow in the merged image. Scale bar = 15 μm (40 × magnification)

(See figure on next page.)

Fig. 4 Detection and FRET quantitative analysis of oligomerization of TRIM32. (**A**) Left panel: Co-IP-mediated analysis of TRIM32 self-interaction. HEK293T cells were transfected with Flag-tagged TRIM32, P130S, R394H, D487N, V591M or P619S and their EGFP-tagged counterparts. Immunoprecipitated Flag-tagged proteins were probed for the presence of conjugated EGFP-tagged proteins by western blot. Right panel: Protein grey value analysis performed using ImageJ, and the data are presented as means ± SEMs. (**B**) The fluores-cence images of representative cells and the corresponding pseudo-color ED and Rc images as well as their histograms. Scale bar = 15 μm (40 × magnification). (**C**) The corrresponding ED-Rc plot from at least 100 cells. The saturation binding curves were fitted using Origin with the function: ED = EDmax × Rc/(Kd + Rc). (**D**) Statistical analysis of ED-Vmax. ED-Vmax is the maximum ED corresponding to saturation of donor binding sites by an acceptor. Student's T-tests were performed to analyse the data of each variant and WT. all data are shown with error bars (± SEMs). "*" on the histogram columns represents the significant differences between each variant and WT; "*" on the horizontal line represents the significant differences of the variants below it. *P < 0.05; **P < 0.01; ***P < 0.001; ns, no significance

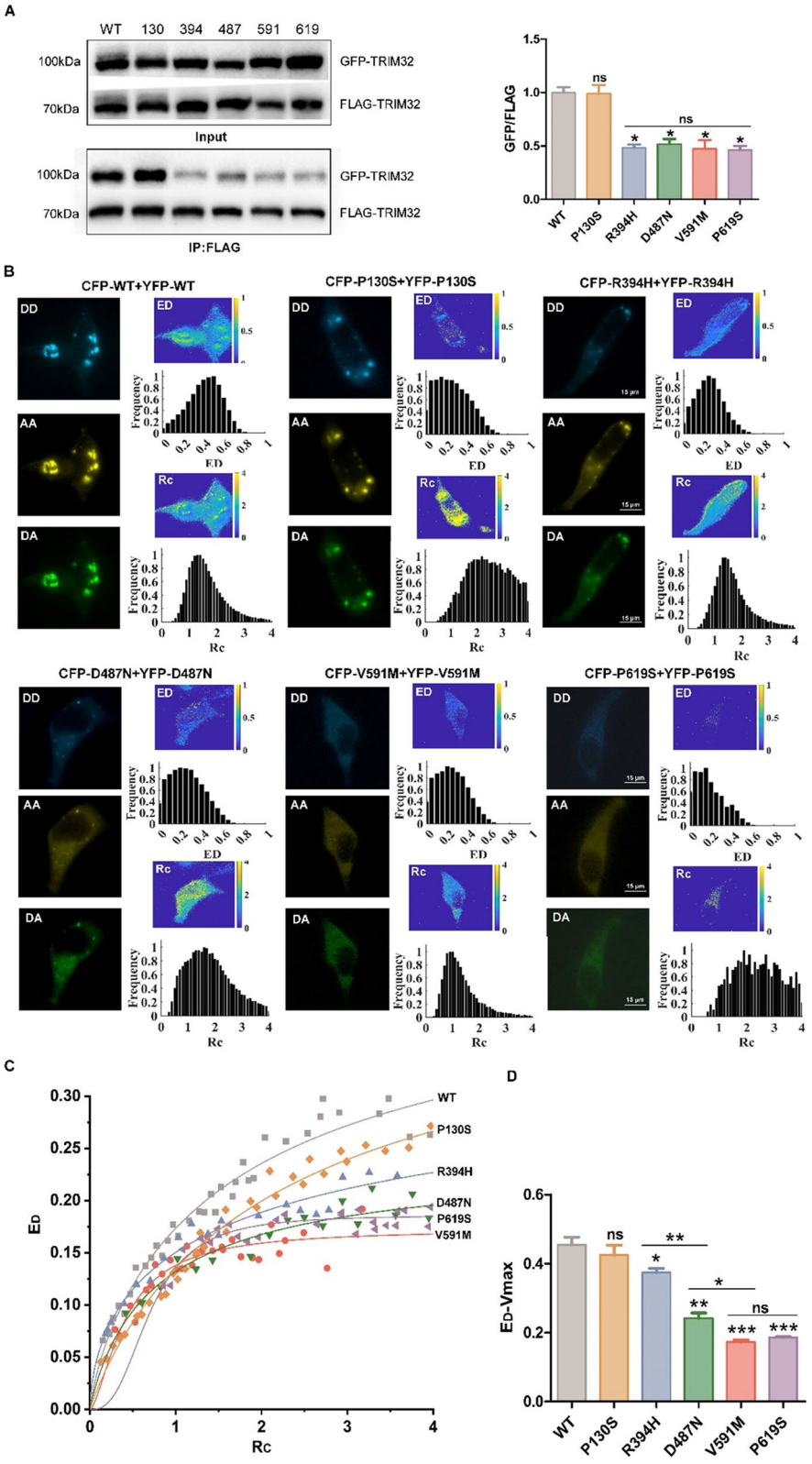

Fig. 4 (See legend on previous page.)

The original article has been corrected.

Published online: 06 May 2025

Reference

1. Liang X, Si J, Xie H, et al. Investigating genotype-phenotype correlation of limb-girdle muscular dystrophy R8: association of clinical severity, protein biological function and protein oligomerization. *Acta Neuropathol Commun* 2025;13:47. https://doi.org/10.1186/s40478-025-01971-8

Publisher's Note