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*CORRESPONDENCE
Frontiers Production Office
✉ production.office@frontiersin.org

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# Erratum: Uncovering novel KCC2 regulatory motifs through a comprehensive transposon-based mutant library

Frontiers Production Office*

Frontiers Media SA, Lausanne, Switzerland

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**KCC2, SLC12A5, GABA, chloride homeostasis, Mu transposon mutagenesis, KCC2-CTD mutations**

An Erratum on
Uncovering novel KCC2 regulatory motifs through a comprehensive transposon-based mutant library

by Uvarov, P., Fudo, S., Karakus, C., Golubtsov, A., Rotondo, F., Sukhanova, T., Soni, S., Di Scala, C., Kajander, T., Rivera, C., and Ludwig, A. (2025). *Front. Mol. Neurosci.* 17:1505722. doi: 10.3389/fnmol.2024.1505722

Due to a production error, there was a mistake in the published legend of Figure 4, resulting in the incorrect use and duplication of the legend for Figure 3. The corrected Figure 4 and its legend appear below.

The publisher apologizes for this mistake.

The original article has been updated.

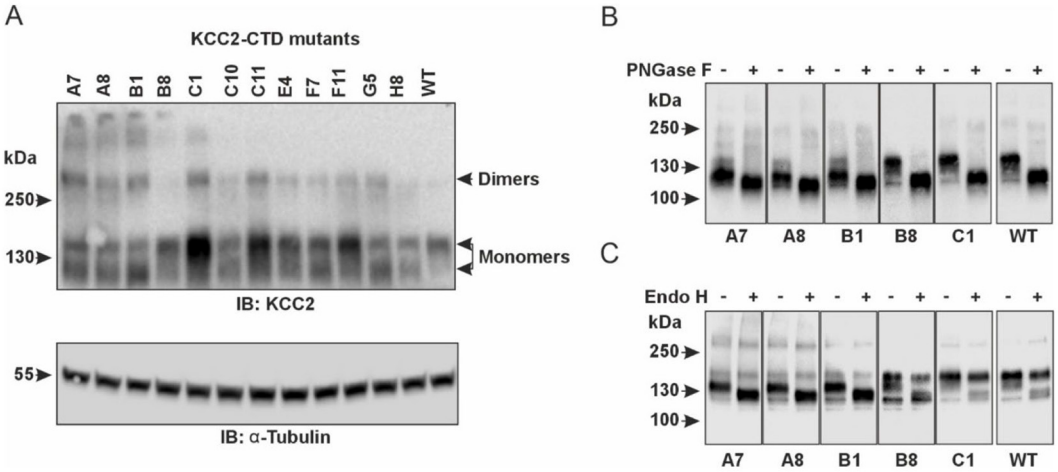


FIGURE 4
Glycosylation patterns of the KCC2-CTD mutants. **(A)** Top panel: Western blot analysis of KCC2 polypeptides in the total protein lysates of HEK293 cells expressing KCC2-CTD mutants, using a KCC2 antibody recognizing the C-terminal epitope. Two bands around 130-kDa corresponding to the putative glycosylated forms of monomeric KCC2 are observed. Bottom panel: To ensure equal amounts of total proteins loaded on SDS–PAGE, blots were analyzed with the antibody recognizing α-Tubulin. **(B)** PNGase F treatment removes all N-linked oligosaccharides from the KCC2 polypeptides, thus shifting the KCC2 bands to their predicted unglycosylated molecular weight of 123.6-kDa. **(C)** Endo H treatment shifts down the 125-kDa band corresponding to the A7, A8, and B1 KCC2 mutants, which contain mainly ER-added high-mannose glycans but leaves intact the 140-kDa KCC2 band corresponding to the B8 and C1 mutants, which contain mainly Golgi-added complex glycans.