Syndrome of Hepatic Cirrhosis, Dystonia, Polycythemia, and Hypermanganesemia Caused by Mutations in *SLC30A10*, a Manganese Transporter in Man

Karin Tuschl,* Peter T. Clayton, Sidney M. Gospe Jr., Shamshad Gulab, Shahnaz Ibrahim, Pratibha Singhi, Roosy Aulakh, Reinaldo T. Ribeiro, Orlando G. Barsottini, Maha S. Zaki, Maria Luz Del Rosario, Sarah Dyack, Victoria Price, Andrea Rideout, Kevin Gordon, Ron A. Wevers, W.K. "Kling" Chong, and Philippa B. Mills

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In this article, Figure 1 contained an error regarding the position of the deletion detected in the affected individuals of family A. The no-call SNPs between the coordinates 218,057,426 and 218,158,564 (GRCh36) suggest that exons 3 and 4 of *SLC30A10* are deleted, whereas the original figure showed that exons 1 and 2 were deleted. The corrected Figure 1 and its legend are shown here. The authors regret the error.

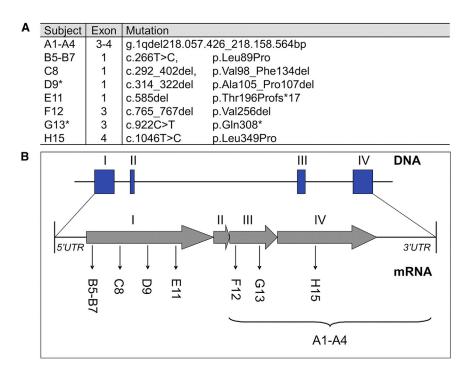
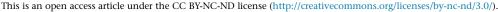


Figure 1. SLC30A10 Mutations in Affected Families with a Syndrome of Hepatic Cirrhosis, Dystonia, Polycythemia, and Hypermanganesemia



*Correspondence: k.tuschl@ucl.ac.uk





⁽A) Mutations in *SLC30A10* identified by DNA sequencing. (For families D and G no DNA was available for analysis of deceased siblings D-II-3 and G-II-1.)

⁽B) Genomic structure of the exons encoding *SLC30A10* and positions of identified mutations. The large deletion spanning exons 3 and 4 in family A is indicated by a bracket.