ERRATA

Mutations in *SLC33A1* Cause a Lethal Autosomal-Recessive Disorder with Congenital Cataracts, Hearing Loss, and Low Serum Copper and Ceruloplasmin

Peter Huppke,* Cornelia Brendel, Vera Kalscheuer, Georg Christoph Korenke, Iris Marquardt, Peter Freisinger, John Christodoulou, Merle Hillebrand, Gaele Pitelet, Callum Wilson, Ursula Gruber-Sedlmayr, Reinhard Ullmann, Stefan Haas, Orly Elpeleg, Gudrun Nürnberg, Peter Nürnberg, Shzeena Dad, Lisbeth Birk Møller, Stephen G. Kaler, and Jutta Gärtner

(The American Journal of Human Genetics, *90,* 61–68; January 12, 2012)
This paper incorrectly described one of the *SLC33A1* mutations as c.615_616insT. It should have been c.614_615insT. The authors regret the error.

*Correspondence: phuppke@med.uni-goettingen.de
DOI 10.1016/j.ajhg.2012.01.015.

Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia

Mait Metspalu,* Irene Gallego Romero, Bayazit Yunusbayev, Gyaneshwer Chaubey, Chandana Basu Mallick, Georgi Hudjashov, Mari Nelis, Reedik Mägi, Ene Metspalu, Maido Remm, Ramasamy Pitchappan, Lalji Singh, Kumarasamy Thangaraj, Richard Villems, and Toomas Kivisild

(The American Journal of Human Genetics, *90*, 731–744; December 9, 2011)
The original Table S1 is updated by this erratum. The table has been corrected online.

Our samples labeled D238 and evo_32 that were reported as belonging to Tharu and Kanjar populations are in fact a Brahmin and a Kol, respectively, from Uttar Pradesh.

Our Tharu samples D254 and D260 and Velama sample VELZ260 have been previously published and genotyped on a different platform (Affymetrix) by Reich et al.[1] as Tharu_107_R1, Tharu_108_R1, and Velama_184_R2, respectively.

There are four first-degree relatives groups in our sample: Dusadh A393, A394, and A395; Dusadh A387 and A388; Dharkar HA030 and HA039; and Kol evo_32 and 321e.

There are three second-degree relatives groups in our sample: Dusadh A392 is equally related to the three Dusadh samples A393, A394, and A395; Dharkars HA039 and HA041; Kanjar evo_37 and Dharkar HA023. The last pair needs further explanation. The Dharkar and Kanjar practice a nomadic lifestyle and were living side by side at the time of sampling. Because the ethnic border between the two is permeable, we cannot rule out neither our error during sample collection and/or subsequent labeling nor shifted self-identity.

The identified issues of mislabeling do not have any notable impact on the results as discussed in the published article.

Similarly, the few relative groups have only marginal effect on the results at a level of detail not considered in the paper. These effects include the emergence of Dusadh relatives' group-specific ancestry component starting at $K = 14$ in the Admixture analysis (Figure S4).

The mislabeling issues have also been corrected in NCBI GEO where the raw data can be accessed under Series GSE33489.

The authors regret the errors.

Reference

1. Reich, D., Thangaraj, K., Patterson, N., Price, A.L., and Singh, L. (2009). Reconstructing Indian population history. Nature *461*, 489–494.

*Correspondence: mait@ebc.ee
DOI 10.1016/j.ajhg.2012.01.001.