

Leveraging Functional-Annotation Data in Trans-ethnic Fine-Mapping Studies

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The original version of this article, published online July 16, 2015, unfortunately contained two mistakes. In the first paragraph on page 263, equation $\sigma_{e,p}^2 = (\sigma_{g,p}^2 - h_g^2 * \sigma_{g,p}^2 / h_g^2)$ should have been $\sigma_{e,p}^2 = (\sigma_{g,p}^2 - h_g^2 * \sigma_{g,p}^2) / h_g^2$. Also, in the first Results paragraph, “do incorporate” should have been “do not incorporate” in the following sentence: “For example, MANTRA meta-analysis requires 1.9 and 96.8 SNPs per locus in order to identify 50% and 90% of the causal variants, respectively, whereas methods that allow multiple causal variants but do incorporate functional data require 1.2 and 7.0 SNPs per locus to identify 50% and 90% of the causal variants, respectively.”⁴⁶ These errors have now been corrected online and in print.

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Mutations in *KIAA0586* Cause Lethal Ciliopathies Ranging from a Hydrolethalus Phenotype to Short-Rib Polydactyly Syndrome

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In the original version of this article, published online July 9, 2015, Sophie Saunier was unfortunately omitted from the author list. Her name appears correctly here and in the article online and in print. In addition, Georges Abi-Tayeh’s last name has been updated online and in print as shown here. The authors apologize for the oversights.

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