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CORRIGENDA

Genome-wide supported variant *MIR137* and severe negative symptoms predict membership of an impaired cognitive subtype of schizophrenia

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Correction to: *Molecular Psychiatry* advance online publication, 26 June 2012; doi:10.1038/mp.2012.84

Following publication of the above article, it came to the authors' attention that they had incorrectly referred to the minor allele (G) carriers in the study sample as 'risk genotypes,' with respect to putative risk for schizophrenia. However, according to the genome-wide association study reported by Ripke *et al.*,[5] it is the major (T) allele that shows association with schizophrenia caseness. The error appears in the Results section in two places: under 'MIR137 genotype' (second sentence) and under 'Prediction of GoM-derived clinical phenotypes' (last sentence).

Genome-wide association study of obsessive-compulsive disorder

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The name of coauthor LK Davis was omitted from the author line. Dr Davis should have been listed as the tenth author (between ER Gamazon and L Osiecki). Her affiliation is as follows: Department of Medicine, University of Chicago, Chicago, IL, USA.