Molecular Psychiatry (2017) 22, 1223–1224

www.nature.com/mp

CORRIGENDA

Genome-wide association study identifies *SESTD1* as a novel risk gene for lithium-responsive bipolar disorder

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Molecular Psychiatry (2017) **22,** 1223; doi:10.1038/mp.2016.246; published online 14 February 2017

Correction to: *Molecular Psychiatry* advance online publication, 27 October 2015; doi:10.1038/mp.2015.165

The list of authors in the HTML version of the article incorrectly included all the members of the International Cohort Collection for Bipolar Disorder. The PDF version correctly lists only the primary authors, as shown above. (The cohort members are listed at the end of the published article.).

In addition, following publication, the authors discovered an error in a subset of the sample affecting the results. A database error led to mismatched phenotypes for the objective lithium-response measures in the Swedish data. This resulted in the total number of lithium responders (objective measurements) in the second wave of Swedish data changing from 159 to 223 and that of non-responders from 780 to 719 (the correct numbers are underscored in the revised Table 1 shown here). This also changed the total number of subjects entered into the meta-analysis. The numbers of responders and nonresponders were also changed in the first wave of Swedish data (Table 1), but this wave was not used in the original analyses (because the low number of subjects did not allow for an analysis) and thus did not affect the results.

As a consequence of this error, the results of the genetic analyses changed (Table 2, final section): (1) The former top hit, rs146727601, had a *P*-value of 1.33×10^{-8} (OR = 3.98), but changed to 1.22×10^{-9} (OR = 4.12) in the revised analyses. (2) The other significant association, rs116323614 in *SESTD1*, changed from $P = 2.74\times10^{-8}$ (OR = 3.14) to 1.53×10^{-6} (OR = 2.69).

Table 2 shows the corrected meta-analysis comparing lithium responders (objective assessment) with controls.

Table 1. Sample sizes by group and study [the corrected values are underscored]

Phenotype assessment	*Swedish sample*		*UK BDRN*	*Meta-analysis*
	Wave 1	*Wave 2*		
Subjective measurement				
Responders	149	588	902	1639
Nonresponders	45	338	676	1059
Controls	2215	1271	5413	8899
Objective measurement				
Responders	—	223	164	387
Nonresponders	—	719	73	792
Controls	—	1271	5413	6684

Abbreviation: BDRN, Bipolar Disorder Research Network; GWAS, genome-wide association study; OR, odds ratio. The numbers are subjects with: (1) available assessments of lithium response according to our definition (for details, see Supplementary Methods) and (2) passed genotyping quality control. Too few subjects in Sweden wave 1 had objective measures of lithium response. Therefore, a GWAS for that sample and measure was not able to be performed.

A Supplementary Corrigendum file describing all article corrections in detail, including a revised Figure 1b, is provided with the corrigendum online.

Table 2. ['Responders vs controls, objective assessments section' (changes underscored)]

Chr	*Index SNP*	*A1/A2*	*Freq*	*OR*	P-*value*	N	*Position*	*KB*	*Genes*
11	**rs146727601**	**– T/A**	**0.01**	**4.12**	**1.22×10^{-9}**	**2**	**112118590–112343856**	**225**	***PTS*,*PLET1***
2	**rs116323614**	**A/G**	**0.03**	**2.69**	**1.53×10^{-6}**	**58**	**179859406–180139219**	**280**	***SESTD1*,*CCDC141***
19	rs77866734	C/T	0.98	0.29	7.59×10^{-7}	11	1633923–1642221	8	*TCF3*, *KIR3DP1*, *KIR2DL4*
17	rs142643109	T/G	0.98	0.31	4.04×10^{-6}	3	60086587–60497572	411	*TBC1D3P2*, *MIR4315-2*, *MIR4315-1*, *METTL2A*, *MED13*, *EFCAB3*

Abbreviations: A1/A2, alternate and reference allele; Chr, chromosome; Freq, frequency of alternate allele; Index SNP, the single-nucleotide polymorphism with the strongest association in the genomic region; LD, linkage disequilibrium; MHC, major histocompatibility complex; *N*, number of SNPs in the reported region; OR, odds ratio. We used LD clumping to define regions of association. Positions are given in UCSC hg19 coordinates. Lines in bold indicate associations that were genome-wide statistically significant.