



**University of Dundee**

## **Corrigendum to Genome-wide analysis of over 106 000 individuals identifies 9 neuroticism-associated loci**

Smith, D. J.; Escott-Price, V.; Davies, G.; Bailey, M. E. S.; Colodro-Conde, L.; Ward, J.; Vedernikov, A.; Marioni, R.; Cullen, B.; Lyall, D.; Hagenaars, S. P.; Liewald, D. C. M.; Luciano, M.; Gale, C. R.; Ritchie, S. J.; Hayward, C.; Nicholl, B.; Bulik-Sullivan, B.; Adams, M.; Couvy-Duchesne, B.; Graham, N.; Mackay, D.; Evans, J.; Smith, Blair; Porteous, D. J.; Medland, S. E.; Martin, N. G.; Holmans, P.; McIntosh, A. M.; Pell, J. P.; Deary, I. J.; O'Donovan, M. C.

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## CORRIGENDUM

## Genome-wide analysis of over 106 000 individuals identifies 9 neuroticism-associated loci

DJ Smith, V Escott-Price, G Davies, MES Bailey, L Colodro-Conde, J Ward, A Vedernikov, R Marioni, B Cullen, D Lyall, SP Hagenaars, DCM Liewald, M Luciano, CR Gale, SJ Ritchie, C Hayward, B Nicholl, B Bulik-Sullivan, M Adams, B Couvy-Duchesne, N Graham, D Mackay, J Evans, BH Smith, DJ Porteous, SE Medland, NG Martin, P Holmans, AM McIntosh, JP Pell, IJ Deary and MC O'Donovan

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The GWAS of neuroticism conducted within the Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute cohort did not include covariates of age, sex, genotyping batch and 10 principal components. Adding these covariates does

not substantially change the pattern of results within the meta-analysis, but *P*-values for the nine reported loci have changed slightly (please see revised Figure 2, Table 2A and Table 2B). Of note is that, the *P*-value for the index SNP rs490647 on chromosome one is now  $5.0 \times 10^{-8}$  (previously  $3.8 \times 10^{-8}$ ) and the *P*-value for the index SNP rs62353264 on chromosome four is now  $5.5 \times 10^{-8}$  (previously  $3.7 \times 10^{-8}$ ).

**Table 2A.** Genome-wide significant index SNPs. Combined meta-analysis of UK Biobank, GS:SFHS and QIMR data sets

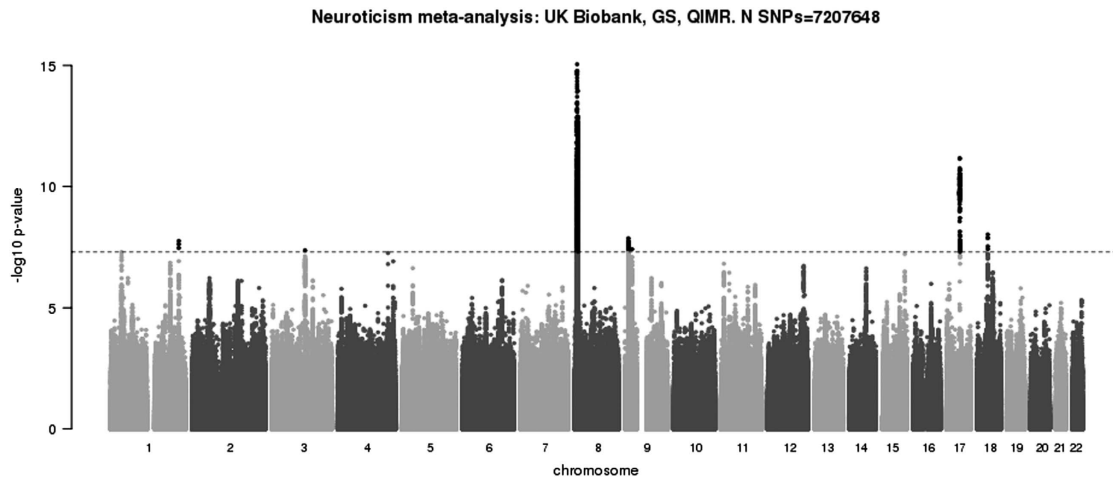
Index SNP	Chr	Position	A1/A2	Freq	BETA (SE)	P	Direction (UKBB-GS-QIMR)	Heter P	Associated region	Genes
rs490647	1	37 242 743	A/G	0.227	0.091 (0.017)	$5.0 \times 10^{-8}$	+++	0.720	37 219 429–37 261 085	GRIK3
rs4653663	1	225 927 218	A/T	0.255	0.091 (0.016)	$1.8 \times 10^{-8}$	+++	0.095	225 899 639–225 947 638	ENAH, SRP9
rs12637928	3	110 184 749	A/T	0.490	−0.077 (0.014)	$4.3 \times 10^{-8}$	---	0.695	110 103 126–110 299 632	PVRL3 (579KB distal)
rs62353264	4	166 085 805	A/T	0.986	−0.330 (0.061)	$5.5 \times 10^{-8}$	---+	0.158	166 063 134–166 198 156	TMEM192, KLHL2, MSMO1
rs12682352	8	8 646 246	T/C	0.525	0.115 (0.014)	$9.0 \times 10^{-15}$	+++	0.433	8 301 794–10 831 868	More than 10 genes
rs12378446	9	11 369 213	T/C	0.791	0.099 (0.017)	$9.4 \times 10^{-9}$	+++	0.831	11 131 371–11 880 898	PTRD (650KB distal)
rs4977844	9	23 295 899	C/G	0.358	0.083 (0.015)	$1.4 \times 10^{-8}$	+++	0.318	23 291 526–23 340 616	ELAVL2
rs111433752	17	43 857 989	T/G	0.790	−0.121 (0.018)	$6.7 \times 10^{-12}$	---	0.053	43 463 493–44 865 603	More than 10 genes
rs1187264	18	35 289 647	C/G	0.136	0.118 (0.021)	$9.5 \times 10^{-9}$	+++	0.515	35 287 090–35 413 260	CELFA

Abbreviations: Chr, chromosome; Freq, frequency; GS:SFHS, Generation Scotland: Scottish Family Health Study; Heter, heterogeneity; QIMR, Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute; SNP, single-nucleotide polymorphism. Shown are linkage disequilibrium (LD)-independent genome-wide significant SNP associations for neuroticism (sorted by genomic position according to UCSC hg19/NCBI Build 37). Column A1/A2 has the SNP alleles, with the first allele (A1) the reference allele for the frequency and  $\beta$  columns. Frequency of allele 1 is calculated in the UK Biobank data set. Chr and Position denote the location of the index SNP.  $\beta$  is linear regression coefficient for allele1, and s.e. is the standard error for  $\beta$ . Associated region indicates range positions of SNPs with  $r^2 > 0.6$  with the index and any other genome-wide association study (GWAS) significant SNP at the locus. The final column indicates protein-coding reference sequence genes at the associated loci (see region plots in Supplementary Information) or where there are no genes at the associated locus, the nearest gene if  $< 1$  Mb from the locus.

**Table 2B.** Association results for genome-wide significant index SNPs in UK Biobank, GS:SFHS and QIMR datasets separately

Index SNP	Chr	Position	UK Biobank				GS:SFHS				QIMR			
			BETA	s.e.	P	FRQ	BETA	s.e.	P	FRQ	BETA	s.e.	P	FRQ
rs490647	1	37 242 743	0.088	0.018	$7.79 \times 10^{-7}$	0.227	0.073	0.065	0.257	0.234	0.139	0.065	0.031	0.243
rs4653663	1	225 927 218	0.079	0.017	$5.12 \times 10^{-6}$	0.255	0.117	0.062	0.060	0.260	0.217	0.062	0.0005	0.259
rs12637928	3	110 184 749	−0.074	0.015	$8.76 \times 10^{-7}$	0.490	−0.073	0.055	0.186	0.506	−0.123	0.056	0.028	0.491
rs62353264	4	166 085 805	−0.335	0.065	$2.36 \times 10^{-7}$	0.986	−0.547	0.219	0.012	0.984	0.147	0.291	0.612	0.988
rs12682352	8	8 646 246	0.120	0.015	$1.02 \times 10^{-15}$	0.525	0.0005	0.111	0.997	0.539	0.076	0.055	0.169	0.528
rs12378446	9	11 369 213	0.100	0.019	$9.69 \times 10^{-8}$	0.791	0.123	0.068	0.071	0.793	0.065	0.068	0.342	0.784
rs4977844	9	23 295 899	0.083	0.016	$2.02 \times 10^{-7}$	0.358	0.136	0.058	0.019	0.351	0.012	0.059	0.837	0.352
rs111433752	17	43 857 989	−0.109	0.019	$5.19 \times 10^{-9}$	0.790	−0.143	0.073	0.050	0.806	−0.301	0.078	0.0001	0.788
rs1187264	18	35 289 647	0.123	0.022	$2.36 \times 10^{-8}$	0.136	0.029	0.081	0.720	0.136	0.139	0.081	0.086	0.132

Abbreviations: Chr, chromosome; FRQ, frequency; GS:SFHS, Generation Scotland: Scottish Family Health Study; QIMR, Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute; SNP, single-nucleotide polymorphism.



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