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Attention-deficit hyperactivity disorder in adults: a systematic review and meta-analysis of genetic, pharmacogenetic and biochemical studies

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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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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-QMIR)*	*Heter* P	*Associated region*	*Genes*
rs490647	1	37 242 743	A/G	0.227	0.091 (0.017)	5.0×10^{-8}	+++	0.720	37 219 429–37 261 085	*GRIK3*
rs4653663	1	225 927 218	A/T	0.255	0.091 (0.016)	1.8×10^{-8}	+++	0.095	225 899 639–225 947 638	*ENAH, SRP9*
rs12637928	3	110 184 749	A/T	0.490	−0.077 (0.014)	4.3×10^{-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)	5.5×10^{-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)	9.0×10^{-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)	9.4×10^{-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)	1.4×10^{-8}	+++	0.318	23 291 526–23 340 616	*ELAVL2*
rs111433752	17	43 857 989	T/G	0.790	−0.121 (0.018)	6.7×10^{-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)	9.5×10^{-9}	+++	0.515	35 287 090–35 413 260	*CELF4*

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 β columns. Frequency of allele 1 is calculated in the UK Biobank data set. Chr and Position denote the location of the index SNP. β is linear regression coefficient for allele1, and s.e. is the standard error for β. 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.