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Supplementary Online Material (SOM)

## Methods

**DNA Extraction, Genotyping, and Quality Control**

DNA extraction was semiautomated to ensure high quality and sufficient quantity. All samples used in the present study were genotyped within the context of the IMAGEN study (Schumann *et al*, 2010). As described here, (ref), genome-wide genotyping of ~600 000 autosomal SNPs was performed using the Illumina Quad 610 chip (Illumina, San Diego, CA, USA). DNA purification and genotyping was performed by the Centre National de Genotypage in Paris. DNA was extracted from whole-blood samples (~10 ml) preserved in BD Vacutainer EDTA tubes (Becton Dickinson and Company, Oxford, UK) using Gentra Puregene Blood Kit (Qiagen, Valencia, CA, USA) according to the manufacturer’s instructions. Genotype information was collected at 582 982 markers using the Illumina HumanHap610 Genotyping BeadChip (Illumina). SNPs with call rates of <98%, minor allele frequency <1%, or deviation from the Hardy–Weinberg equilibrium (P<1 X 10-4) were excluded from the analyses. Individuals with an ambiguous sex code, excessive missing genotypes (failure rate 42%), and outlying heterozygosity (heterozygosity rate of 3 SDs from the mean) were also excluded. Closely related individuals with identity-by descent (IBD40.1875) were filtered out before the subsequent analysis. Population stratification for the GWAS data was examined by principal component analysis (PCA) using EIGENSTRAT software (Pritchard et al, 2000). The four HapMap II populations were used as reference groups in the PCA analysis and individuals with divergent ancestry (from CEU) were also excluded. Quality control procedure of the IMAGEN data set was done in three waves starting with N=705 in wave 1, N=1004 in wave 2, and N=394 subjects in wave 3. After quality control N=620 in wave 1, N=868 in wave 2, and N=351 in wave 3 were available.

**Schumann G, Loth E, Banaschewski T, Barbot A, Barker G, Buchel C, Conrod PJ, Dalley JW, Flor H, Gallinat J, Garavan H, Heinz A, Itterman B, Lathrop M, Mallik C, Mann K, Martinot JL, Paus T, Poline JB, Robbins TW, Rietschel M, Reed L, Smolka M, Spanagel R, Speiser C, Stephens DN, Ströhle A, Struve M, IMAGEN consortium** (2010) The IMAGEN study: reinforcement-related behaviour in normal brain function and psychopathology. *Molecular Psychiatry* **15**, 1128-1139.