

# Supplementary Material

## Genetic and neural bases of the Neuroticism general factor

We calculated genetic correlations between the Neuroticism general factor and the following traits:

- subjective well-being (Okbay et al., [2016](#))
- household income (Hill et al., [2019](#))
- risk tolerance (Linnér et al., [2019](#))
- morning person (Hu et al., [2016](#))
- Townsend Deprivation Index (Hill et al., [2019](#))
- years of education (Lee et al., [2018](#))
- IQ (i.e., cognitive performance) (Lee et al., [2018](#))
- brain volume (Jansen et al., [2020](#))
- autism spectrum disorder (ASD) (Grove et al., [2019](#))
- schizophrenia (Pardiñas et al., [2018](#))
- bipolar disorder (Mullins et al., [2021](#))
- attention deficit/hyperactivity disorder (ADHD) (Demontis et al., [2019](#))
- obsessive compulsive disorder (OCD) (International Obsessive Compulsive Disorder Foundation Genetics Collaborative & OCD Collaborative Genetics Association Studies, [2018](#))
- major depressive disorder (Howard et al., [2019](#))
- number of children (Barban et al., [2016](#))

- number of sex partners (Linnér et al., [2019](#))
- drinks per week (Linnér et al., [2019](#))
- cannabis use disorder (CUD) (Johnson et al., [2020](#))

Supplementary Fig. [S3](#) presents the genetic correlations between the Neuroticism general factor and our selected traits studied in GWAS. The pattern of results—most notably the genetic correlations of large magnitude with subjective well-being and major depression—are indeed very similar to what has been obtained with observed measures of Neuroticism (Baselmans et al., [2019](#); Luciano et al., [2018](#); Nagel et al., [2018](#); Okbay et al., [2016](#); Turley et al., [2018](#)).

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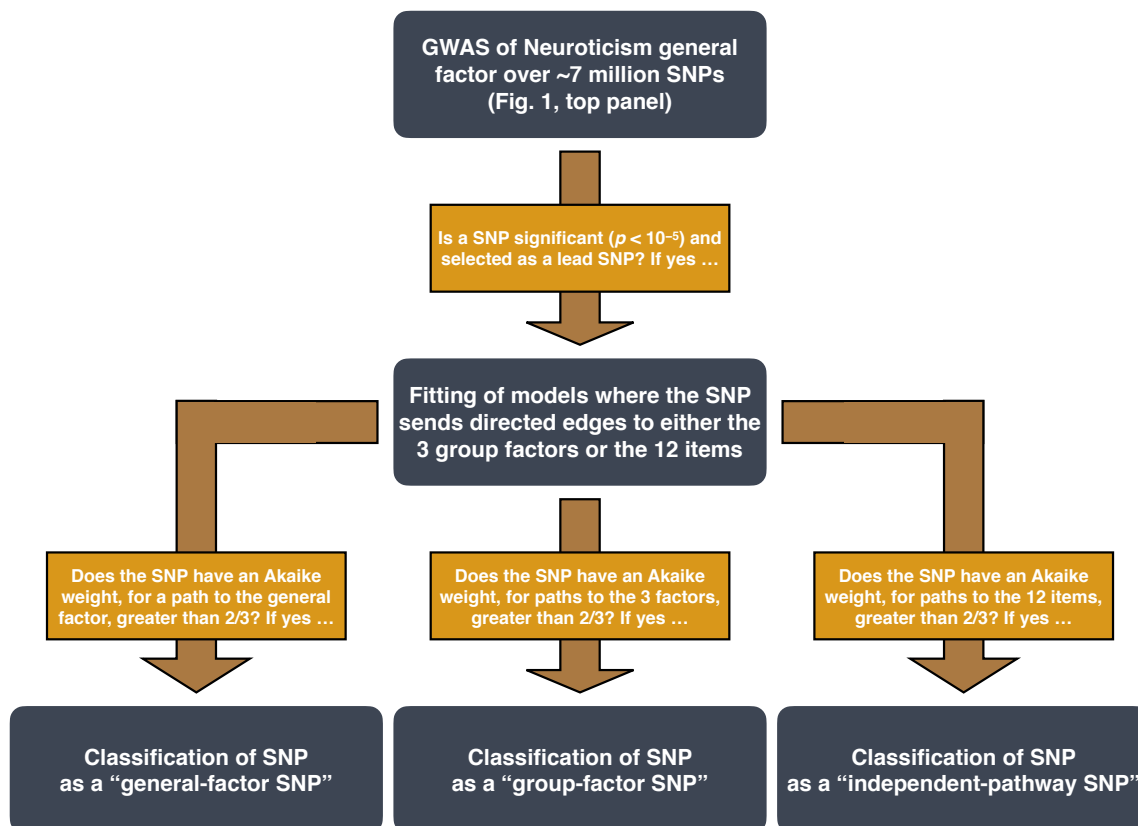


Figure S1: Flowchart of pipeline for our genome-wide association study (GWAS) of the Neuroticism general factor and subsequent classification of lead SNPs. Each gray box corresponds to an analysis step. Later steps use the output of earlier steps as input; such a relationship is represented by a gold arrow. The label of an arrow describes how the output of the prior step was filtered. Path modeling in the context of genetic association testing was conducted with Genomic SEM. Fig. 1 of the main text depicts the general-factor and independent-pathway model. Note that a SNP may not qualify for any of the three classifications in the final step.

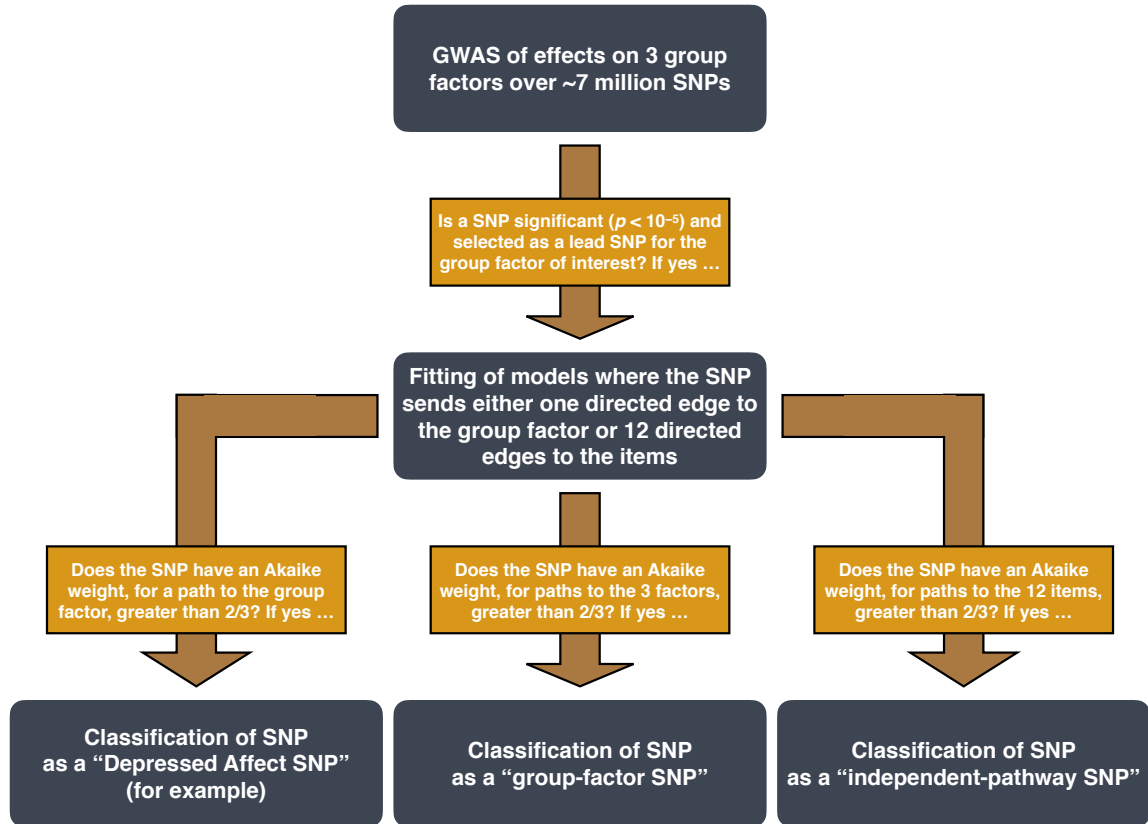


Figure S2: Flowchart of pipeline for our genome-wide association study (GWAS) of the group factors indicated by the Neuroticism items in the Eysenck Personality Questionnaire–Revised Short Form and our subsequent classification of lead SNPs. Each gray box corresponds to an analysis step. Later steps use the output of earlier steps as input; such a relationship is represented by a gold arrow. The label of an arrow describes how the output of the prior step was filtered. Path modeling in the context of genetic association testing was conducted with Genomic SEM. Fig. 1b of the main text depicts the independent-pathway model. Note that a SNP may not qualify for any of the three classifications in the final step.

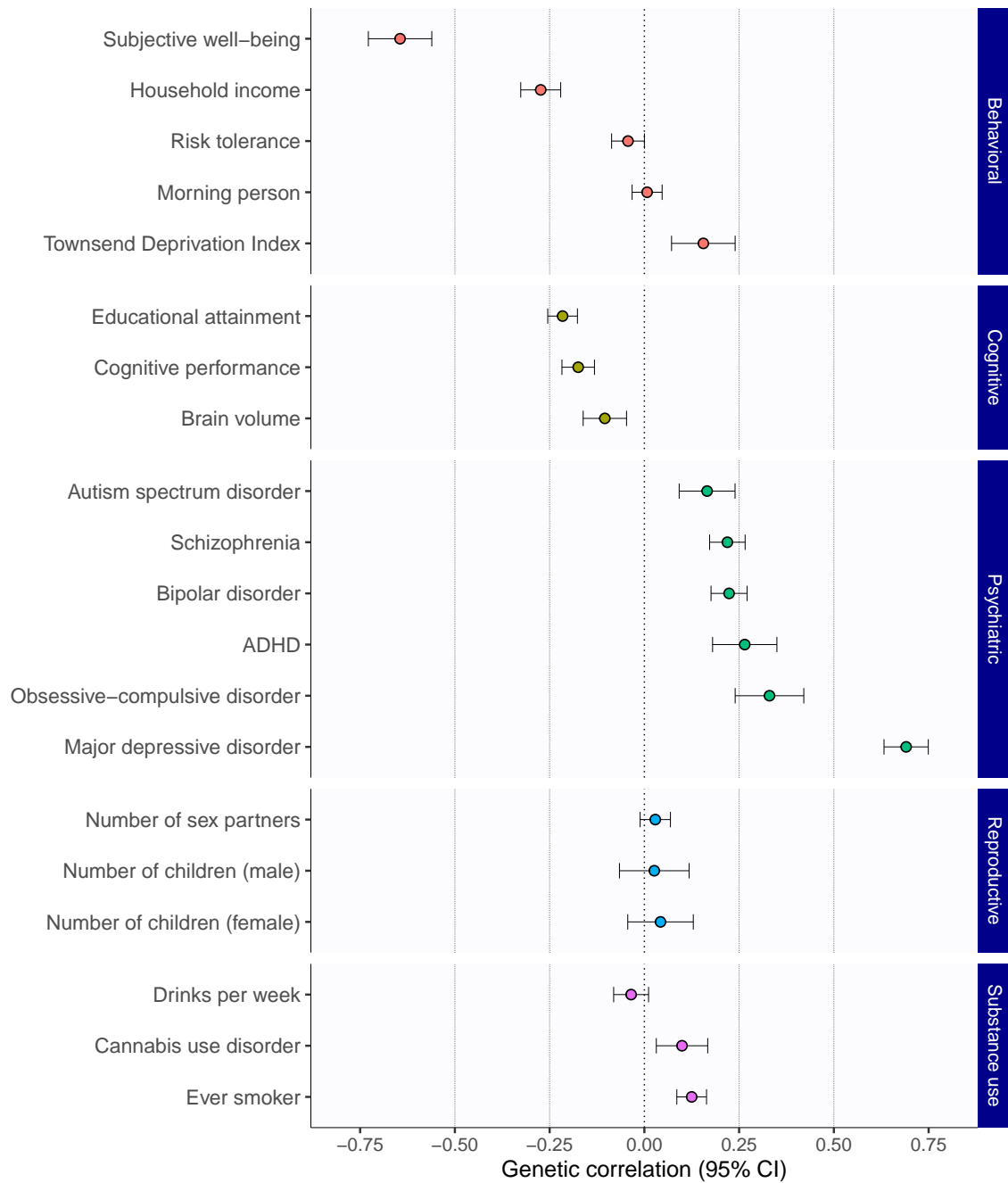


Figure S3: Estimates of the genetic correlations with the Neuroticism general factor and accompanying 95% confidence intervals were calculated with LD Score regression, as called by Genomic SEM. Supplementary Table S1 gives the results in numerical form.