Supplementary Figures

Table of Contents

PER ENVIRONMENT

This section contains relevant analysis plots organized by environment. For all environments, there are Manhattan plots for the GWEIS and gene-analysis, and for those with any genome-wide significant SNPs form the GWEIS (i.e. not corrected across environments), there are also annotated locus plots and interaction plots.

GWEIS Manhattan plot

Shows the -log10 *p*-values for the SNP interaction with the environment in question. Gene names have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest *p*-value.

Locus plot

Shows all SNPs in the genome-wide significant loci with CADD and RegulomeDB score annotations (obtained from FUMA[1]).

Interaction plots

These plots show the average predicted neuroticism at any given combination of alleles and environmental exposure. To illustrate the components that are specific to the SNP-environment interaction of interest, we plotted neuroticism predicted from the full model (as analysed in the GWEIS, i.e. with the SNP-environment interaction term, SNP/environment/covariate main effects, and covariate-SNP/environment interaction effects) as well as using the same model but excluding the SNP-environment interaction term.

Gene analysis Manhattan plot

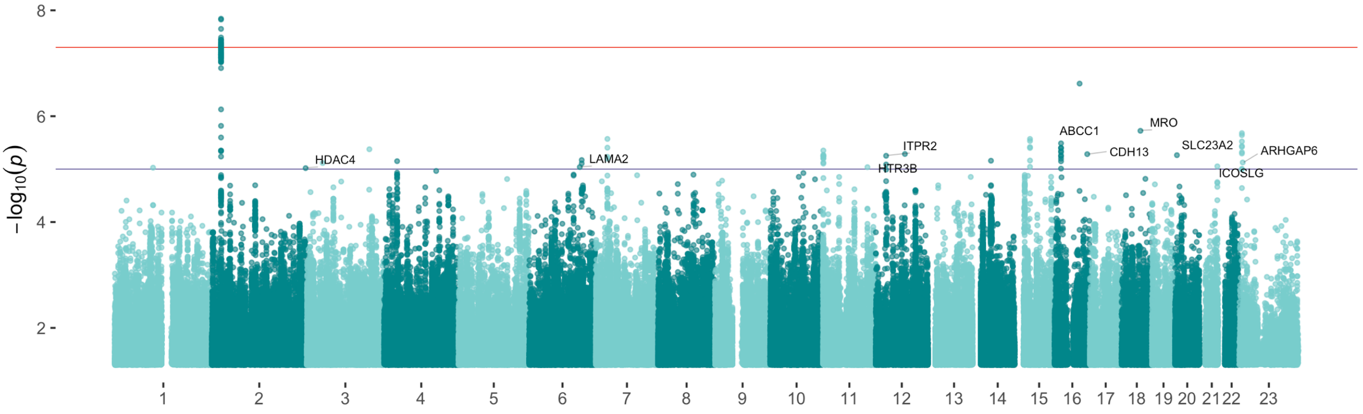
Shows the -log10 *p*-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.

1. *Watanabe, K., Taskesen, E., van Bochoven, A. & Posthuma, D. Functional mapping and annotation of genetic associations with FUMA.* Nat. Commun. ***8****, 1826 (2017).*

Work Satisfaction

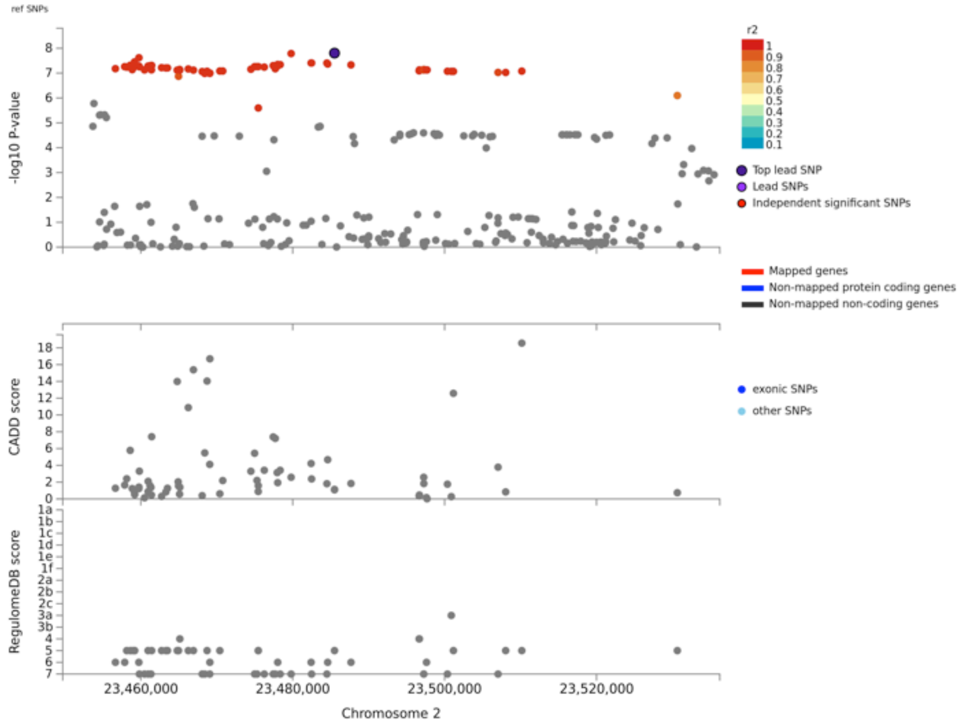
GWEIS

Manhattan plot



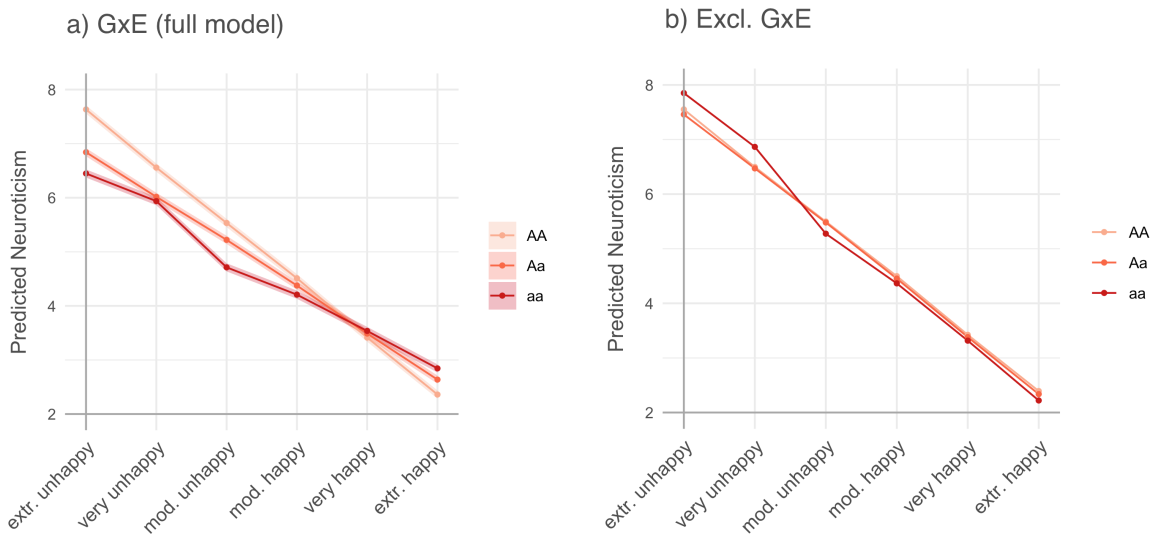
Supplementary Figure 1.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot (rs4461224)



Supplementary Figure 1.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

Interaction Plots (rs4461224)

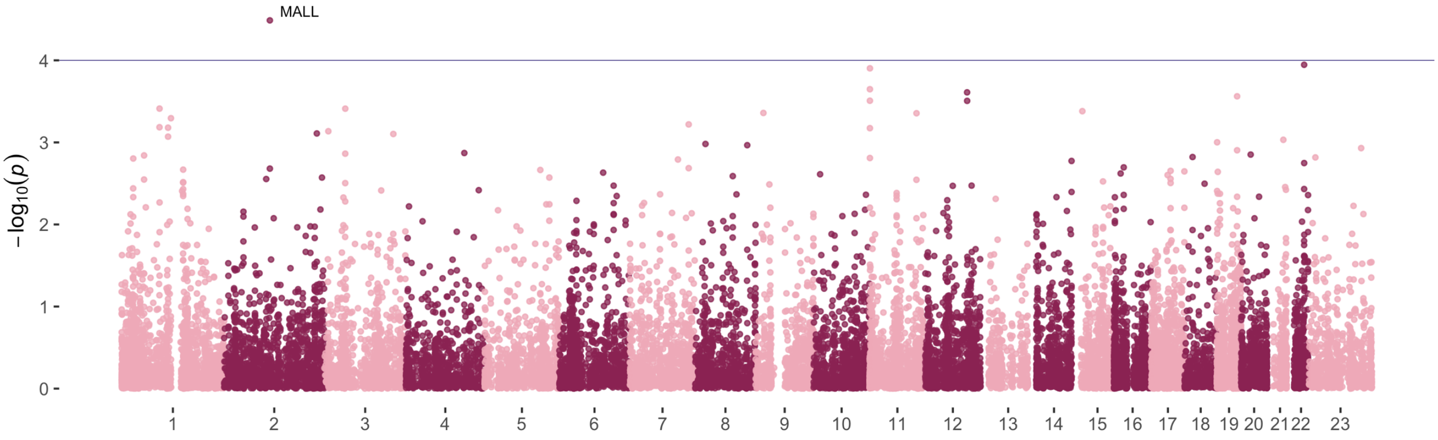

a) GxE (full model)

b) Excl. GxE

Supplementary Figure 1.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

Gene Analysis

Manhattan Plot

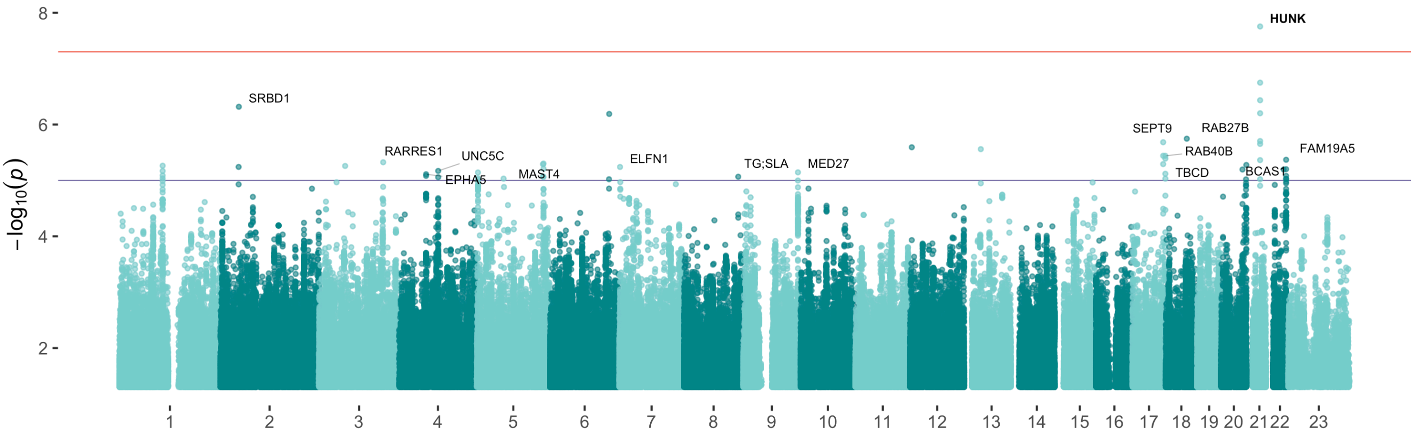


Supplementary Figure 1.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Townsend Deprivation Index (TDI)

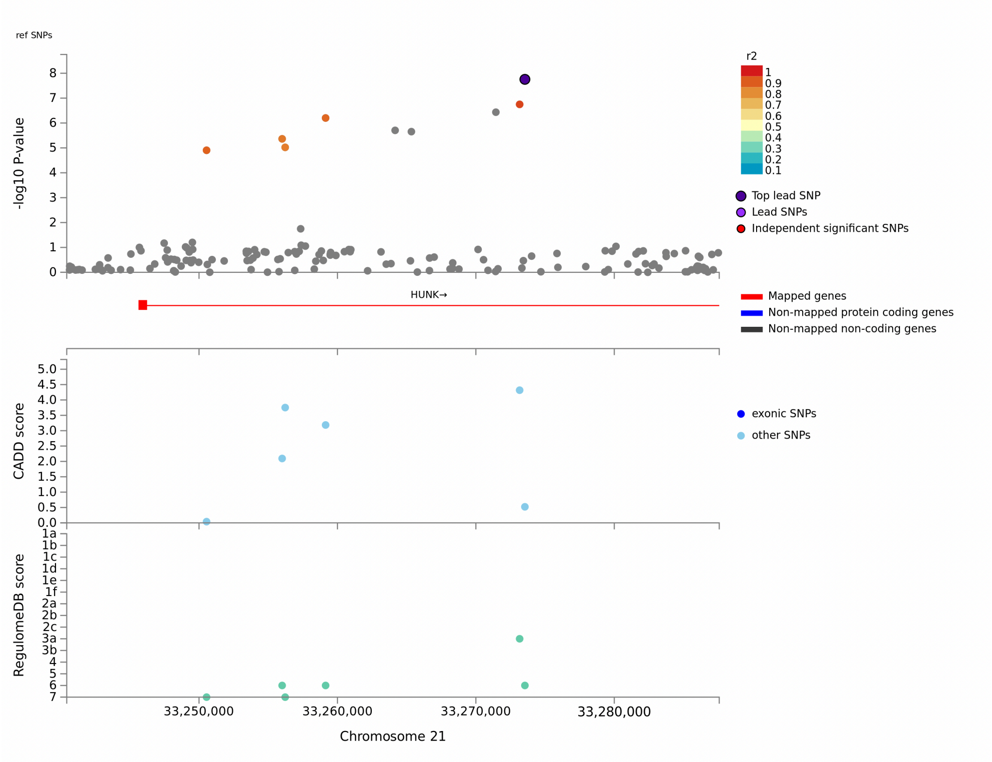
GWEIS

Manhattan Plot



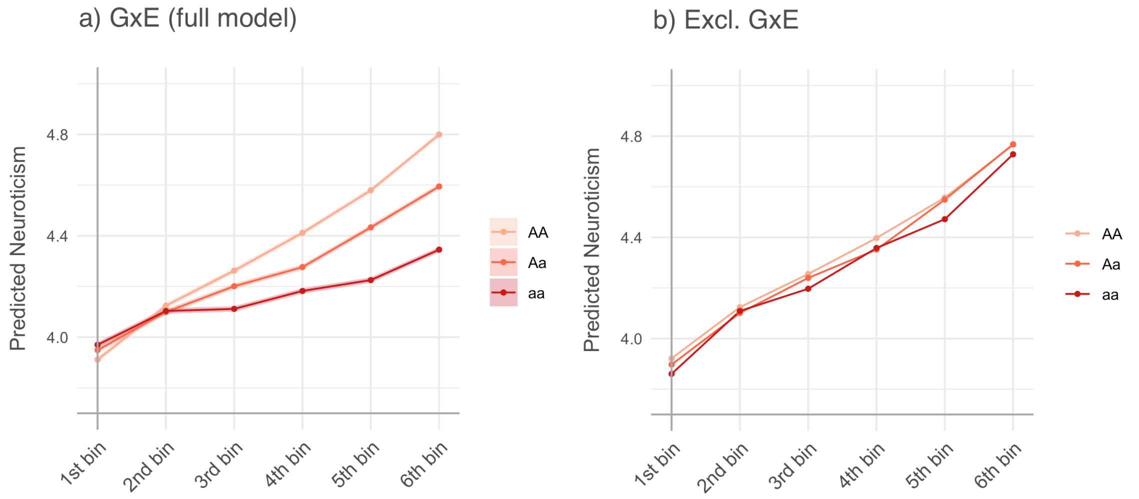
Supplementary Figure 2.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot (rs11700517)



Supplementary Figure 2.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

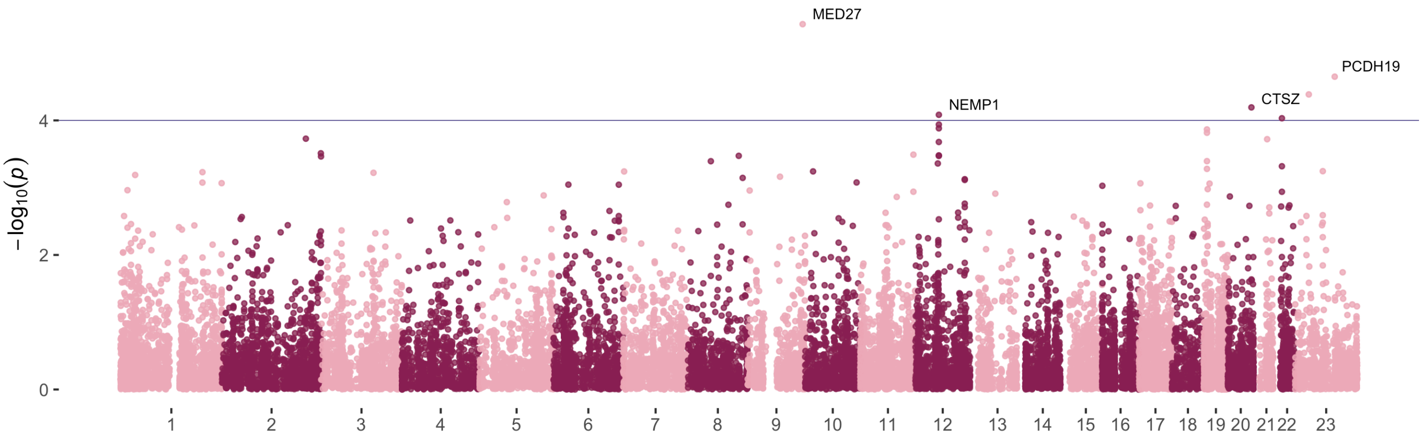
Interaction Plots (rs11700517)



Supplementary Figure 2.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates. (For plotting purposes, TDI was split into six bins).*

Gene Analysis

Manhattan plot

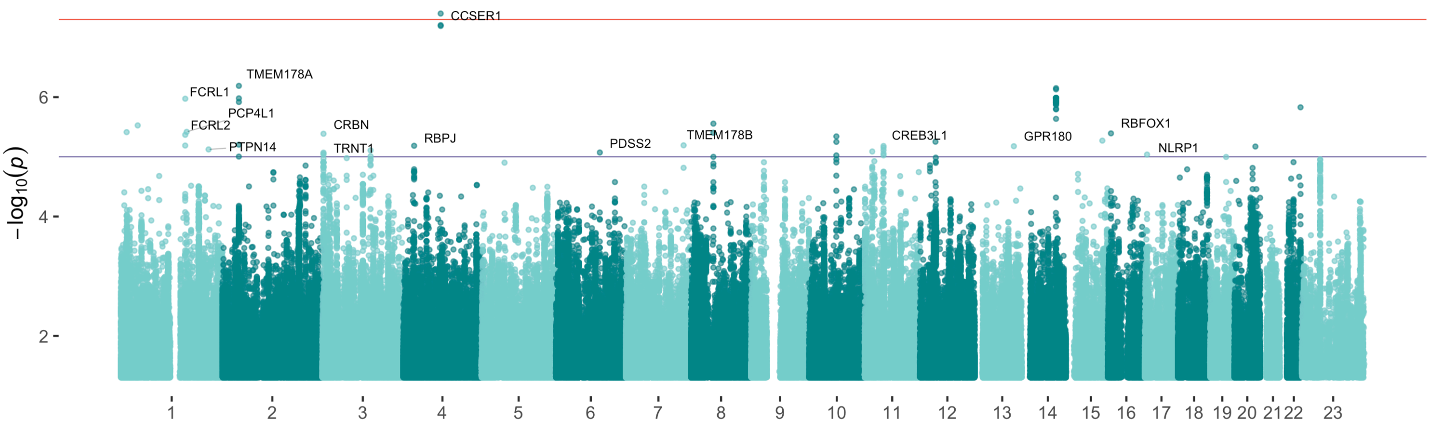


Supplementary Figure 2.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Social Activities

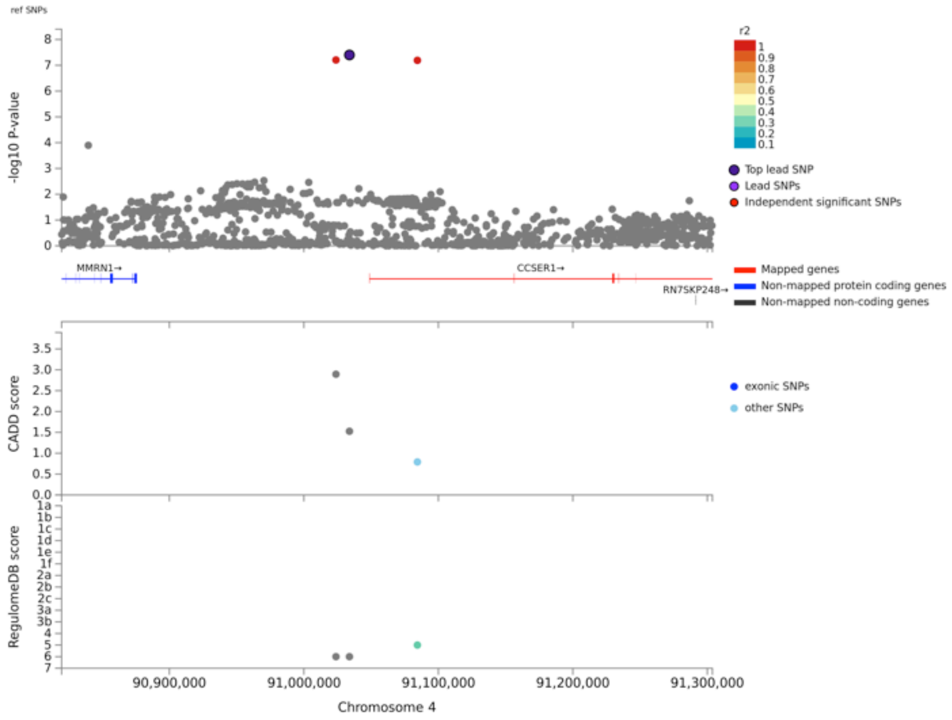
GWEIS

Manhattan Plot



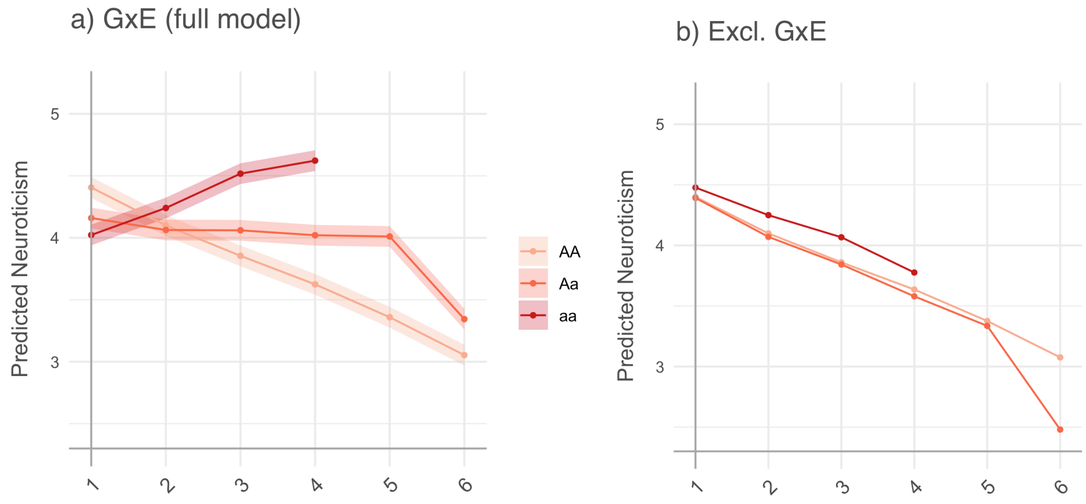
Supplementary Figure 3.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot (rs111497581)



Supplementary Figure 3.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

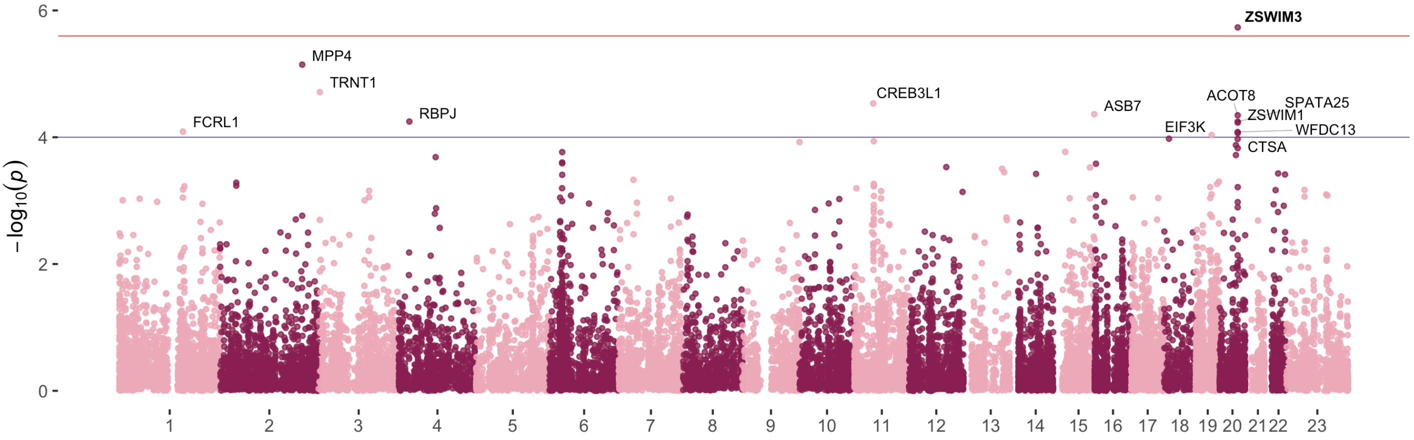
Interaction Plots (rs111497581)



Supplementary Figure 3.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

Gene Analysis

Manhattan Plot

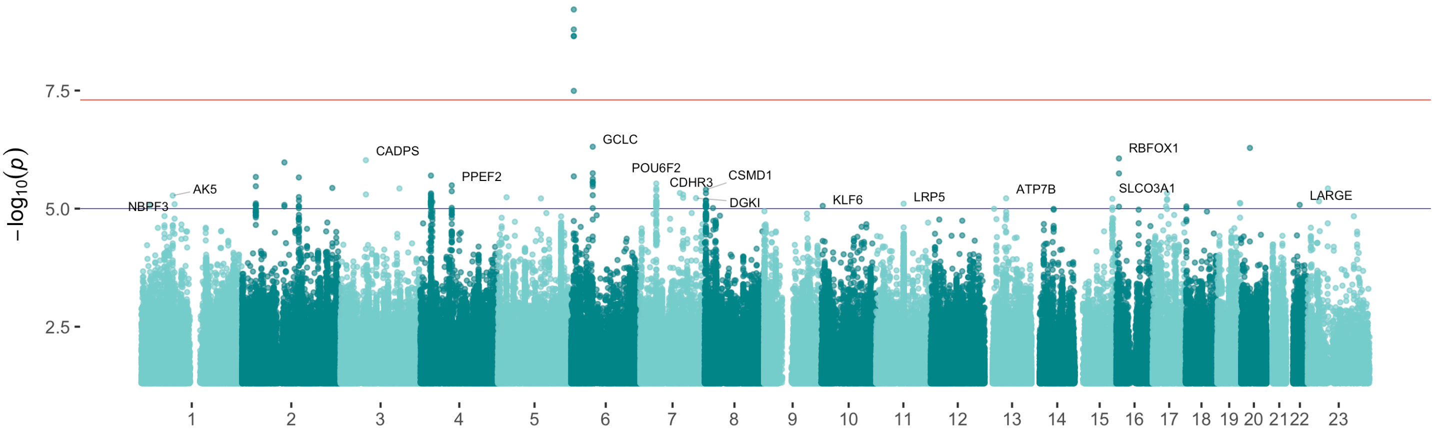


Supplementary Figure 3.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Felt Hated by Family Member as a Child

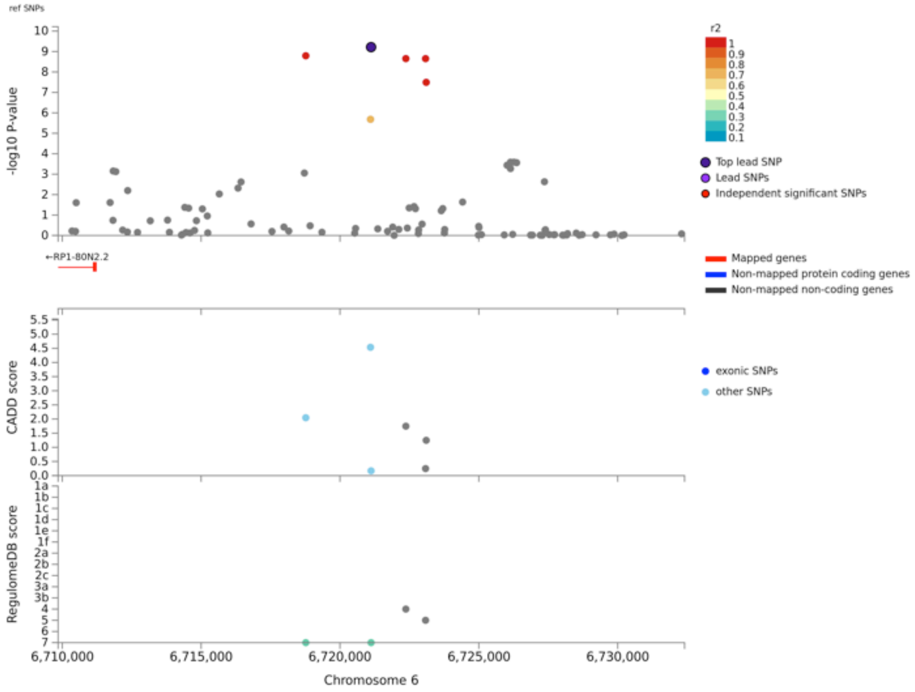
GWEIS

Manhattan Plot



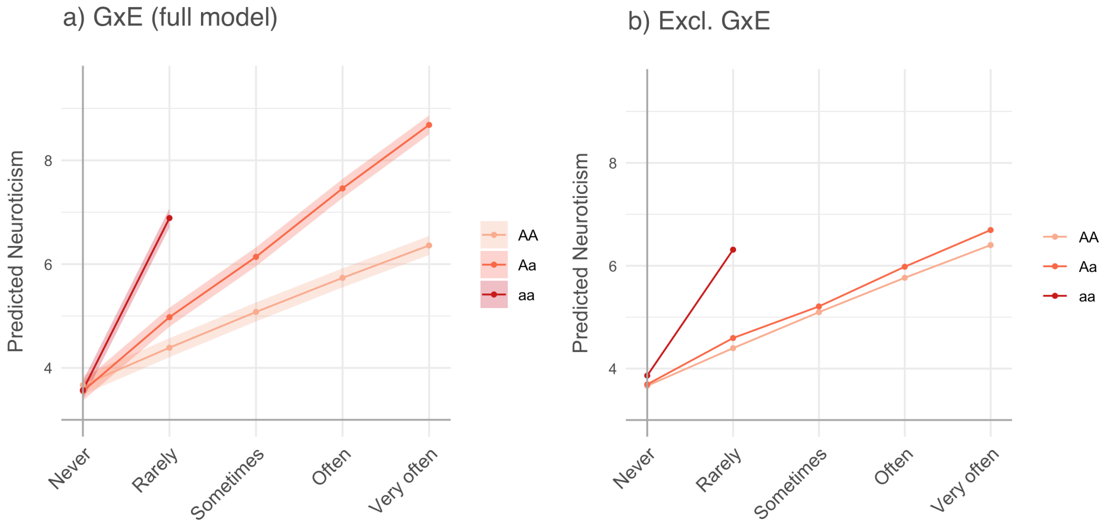
Supplementary Figure 4.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot (rs115385310)



Supplementary Figure 4.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

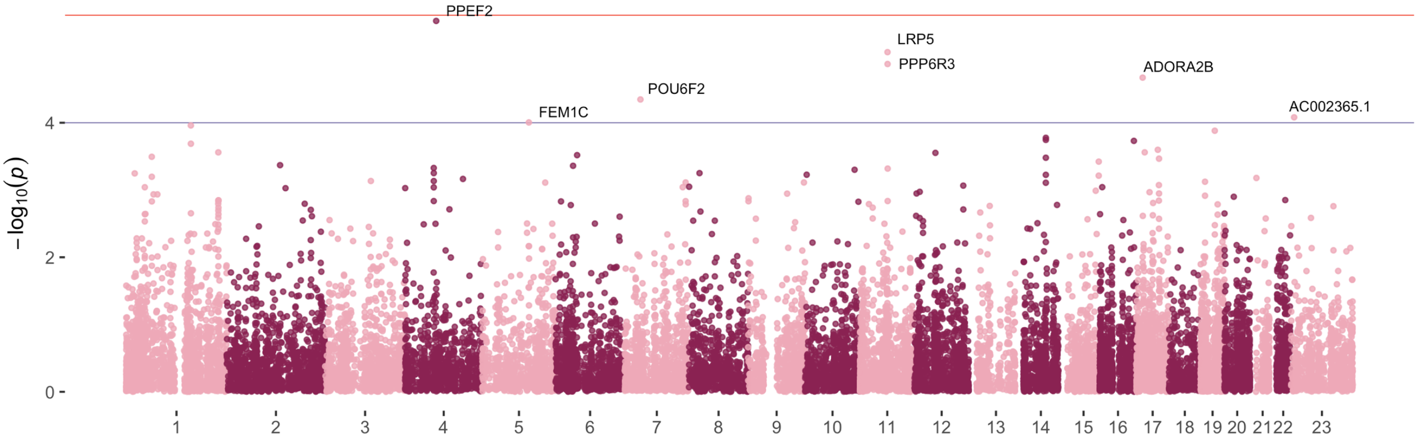
Interaction Plots (rs115385310)



Supplementary Figure 4.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

Gene Analysis

Manhattan Plot

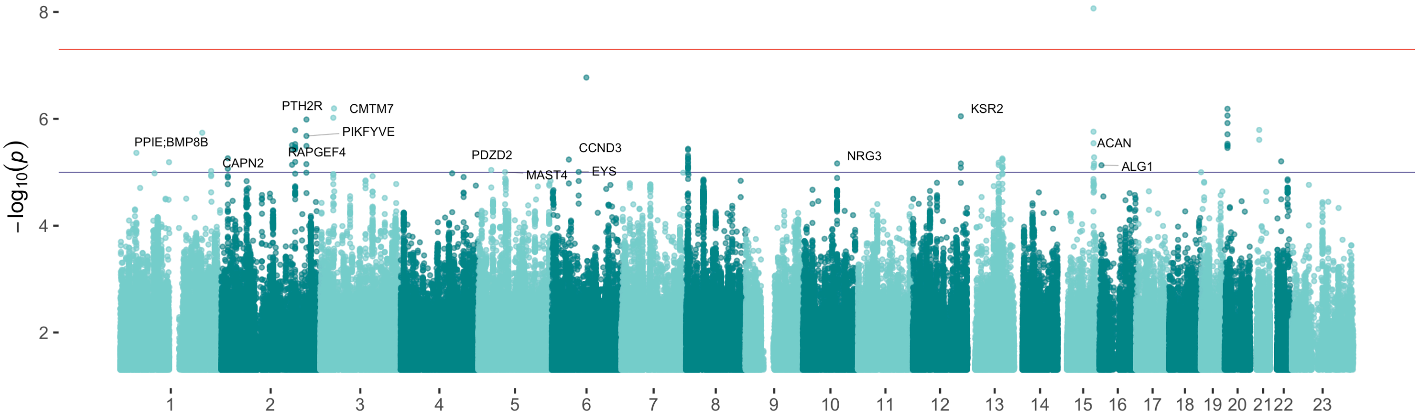


Supplementary Figure 4.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Able to Confide

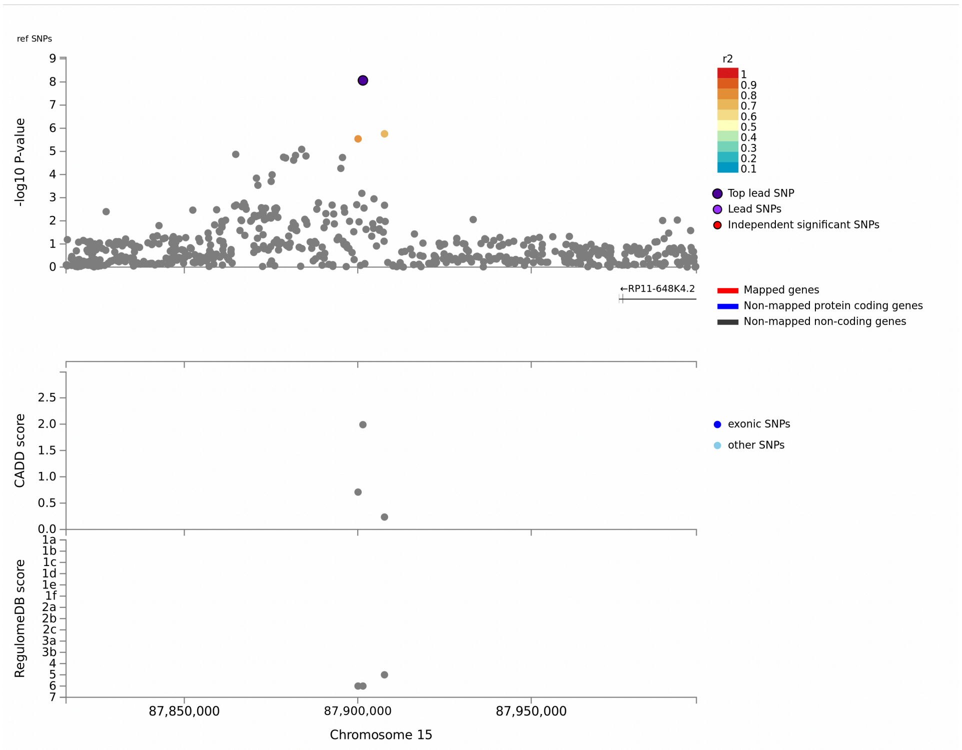
GWEIS

Manhattan Plot



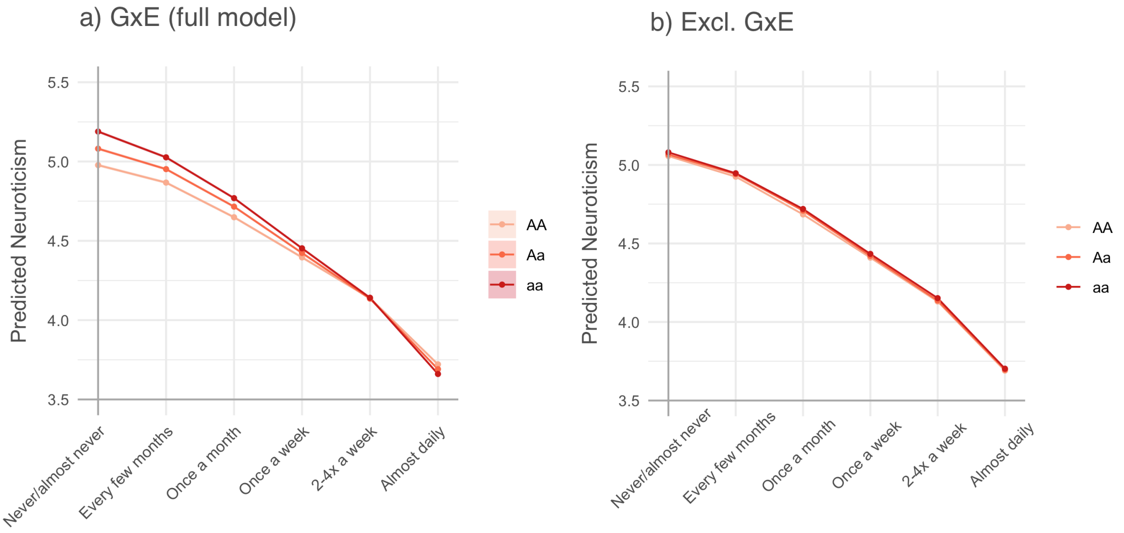
Supplementary Figure 5.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot (rs874616)



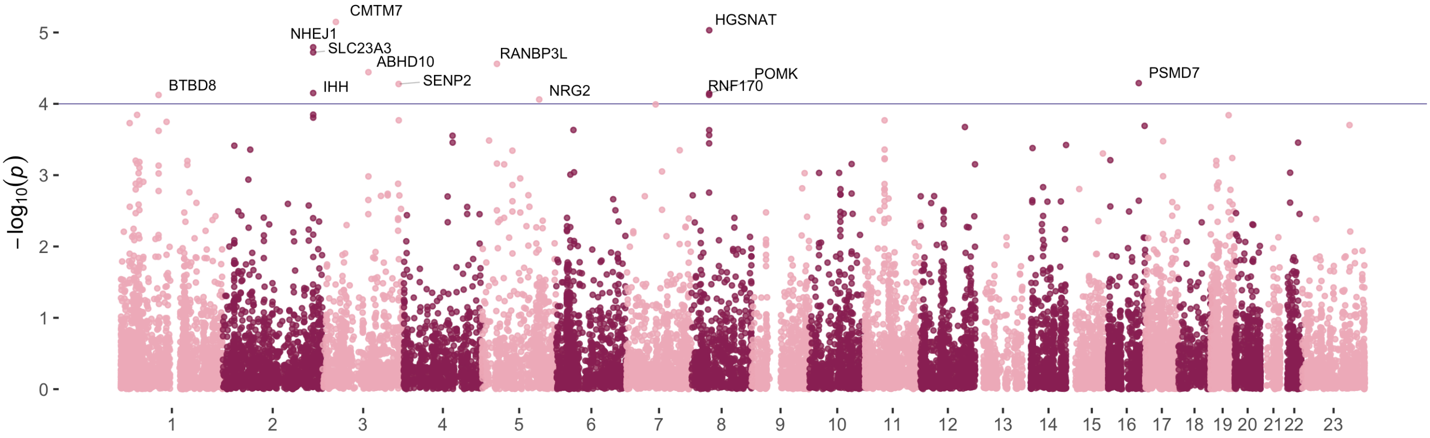
Supplementary Figure 5.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

Interaction Plots (rs874616)



Supplementary Figure 5.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

Gene Analysis

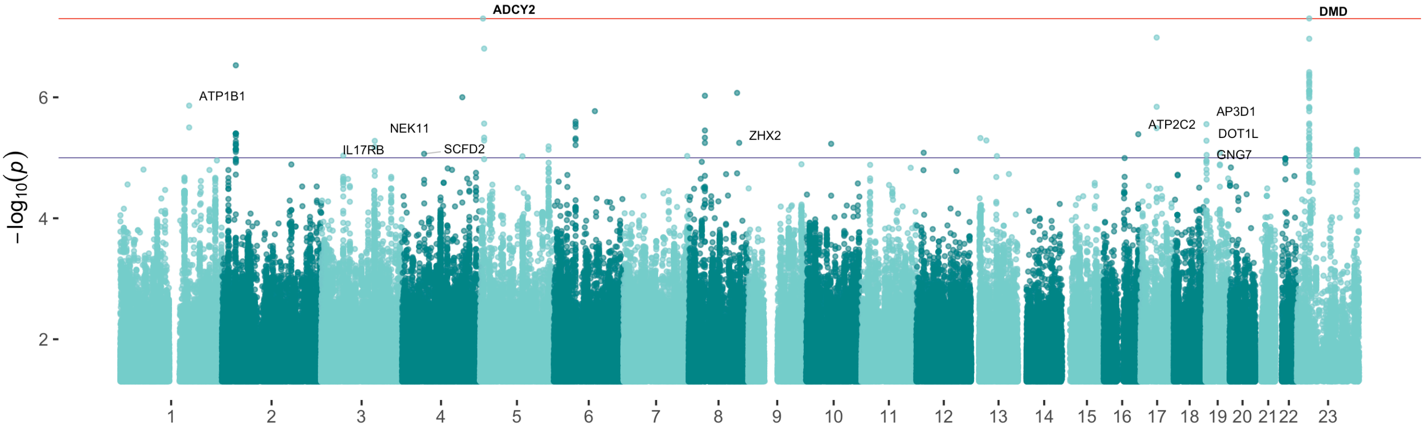


Supplementary Figure 5.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Diagnosed with Life-Threatening Illness

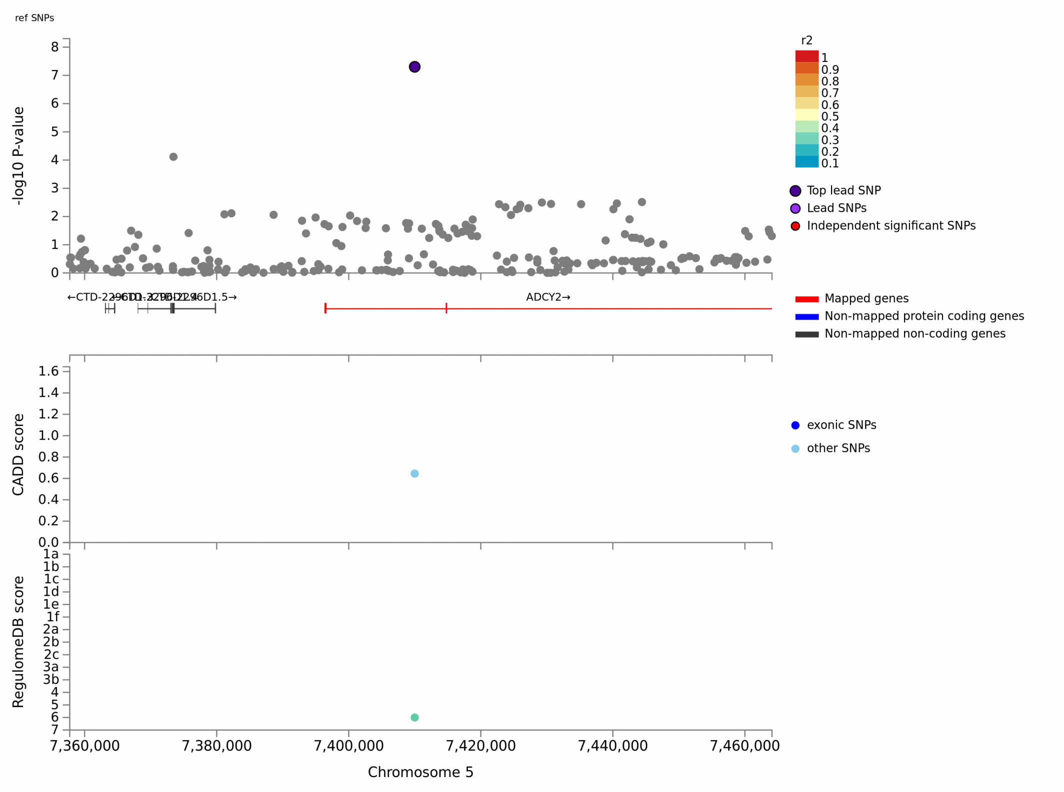
GWEIS

Manhattan Plot



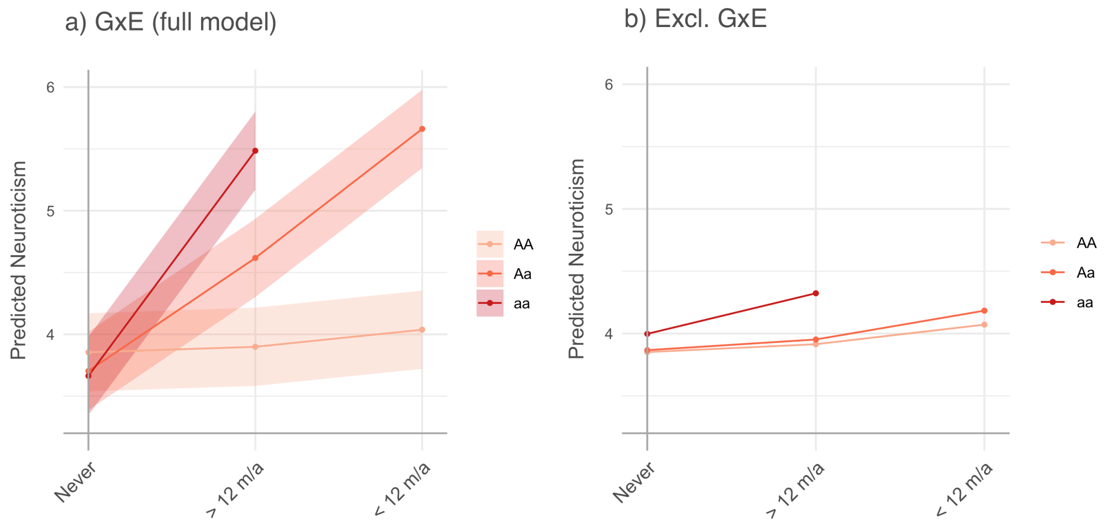
Supplementary Figure 6.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plots (rs185839186, ADCY2)



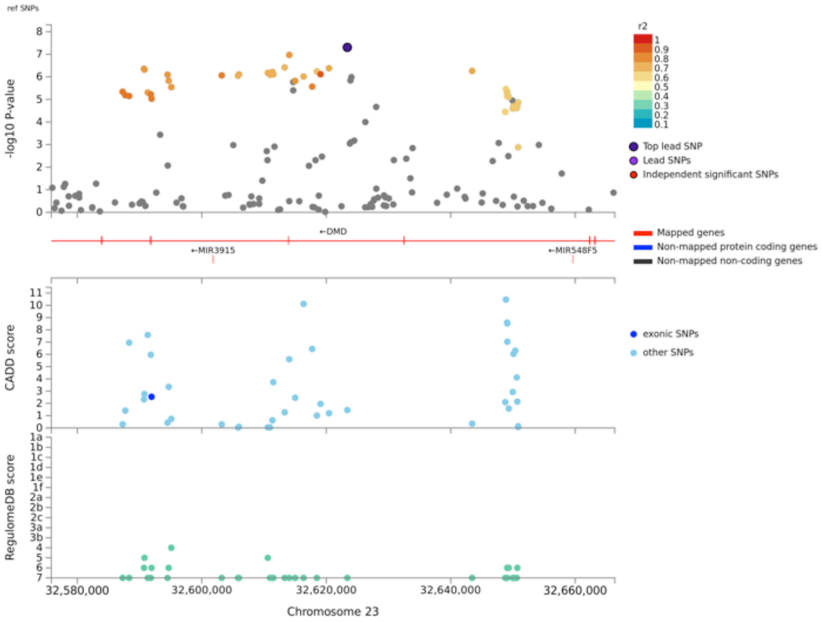
Supplementary Figure 6.2 *Annotated locus plot showing the CADD and RegulomeDB scores for one of the SNPs that reached standard genome-wide significance (p < 5e-8).*

Interaction Plots (rs185839186, ADCY2)



Supplementary Figure 6.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

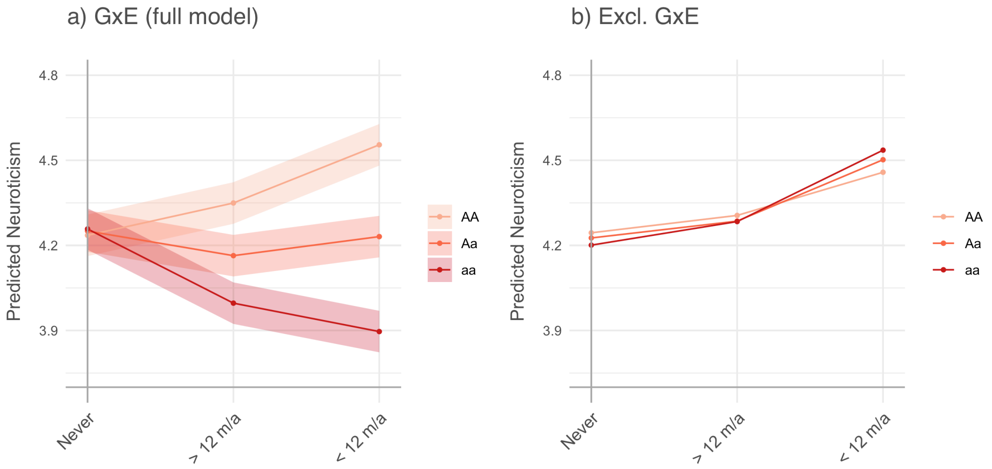
Locus Plot (rs5928040, DMD)



Supplementary Figure 6.4 *Annotated locus plot showing the CADD and RegulomeDB scores for one of the SNPs that reached standard genome-wide significance (p < 5e-8).*

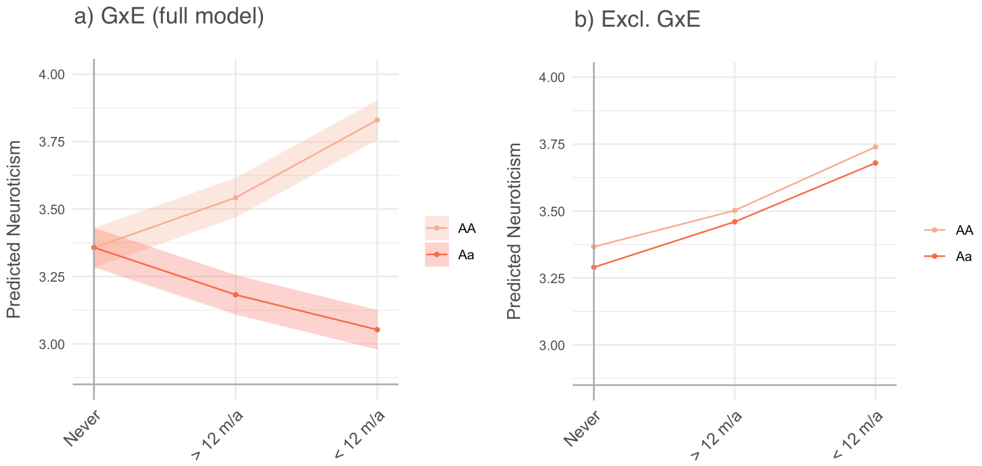
Interaction Plot (rs5928040, DMD)

Females



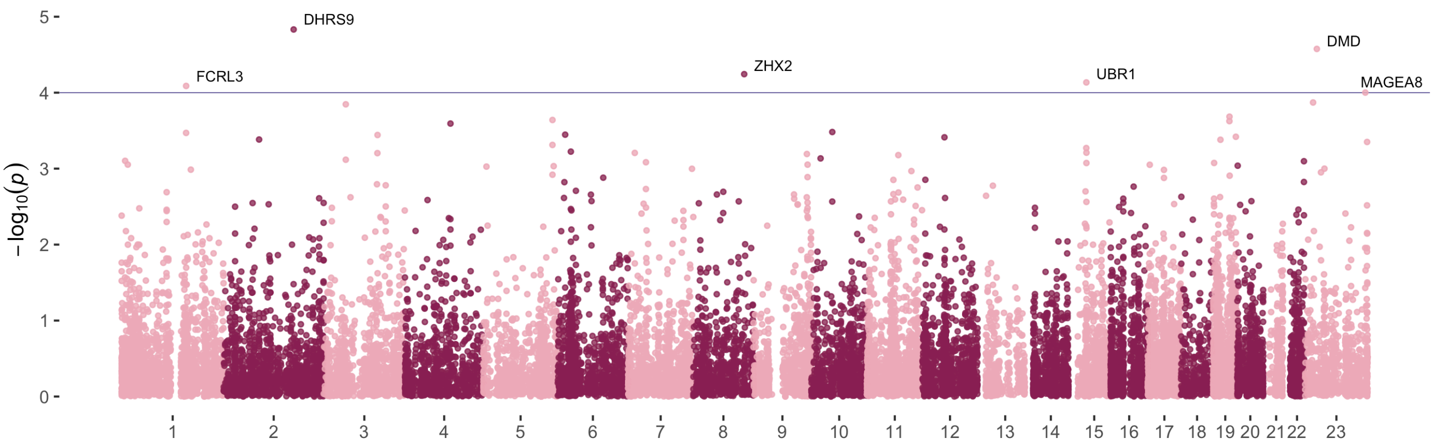
Supplementary Figure 6.5 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates. (NOTE: Males and females were analysed together, but to do differences in the number alleles they were plotted separately).*

Males



Supplementary Figure 6.6 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates. (NOTE: Males and females were analysed together, but to do differences in the number alleles they were plotted separately).*

Gene Analysis

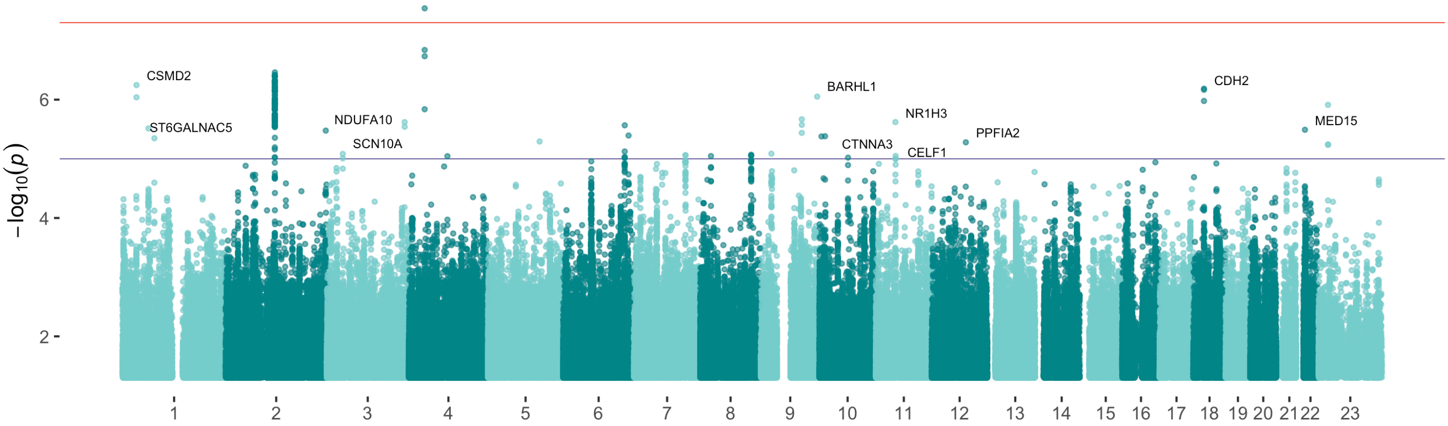


Supplementary Figure 6.7 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

Been in a Confiding Relationship as an Adult

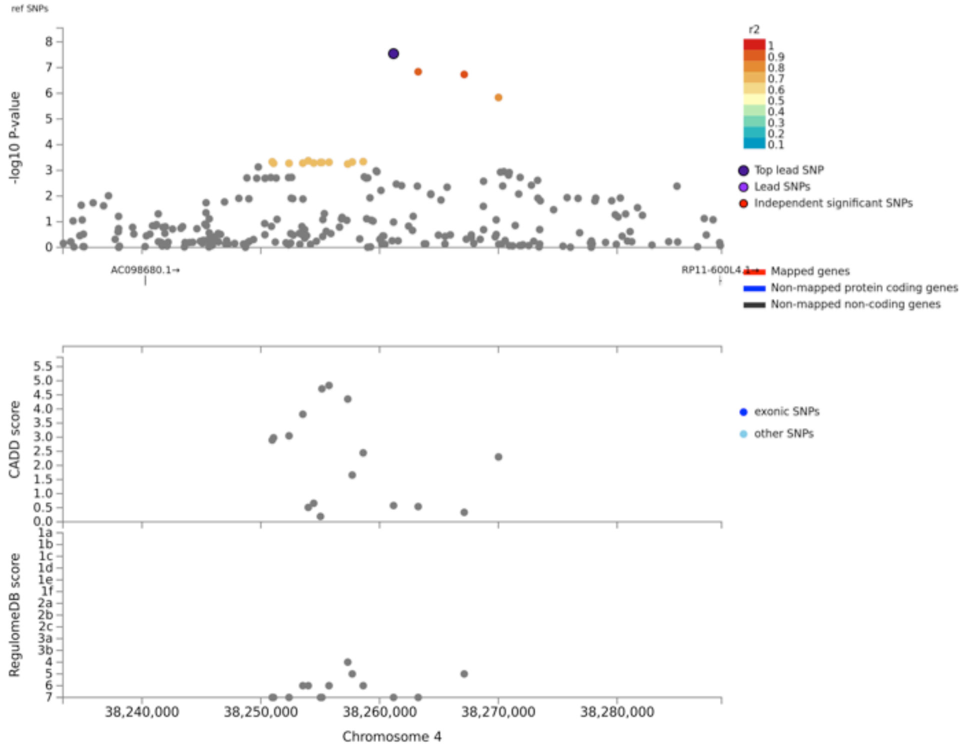
GWEIS

Manhattan Plot



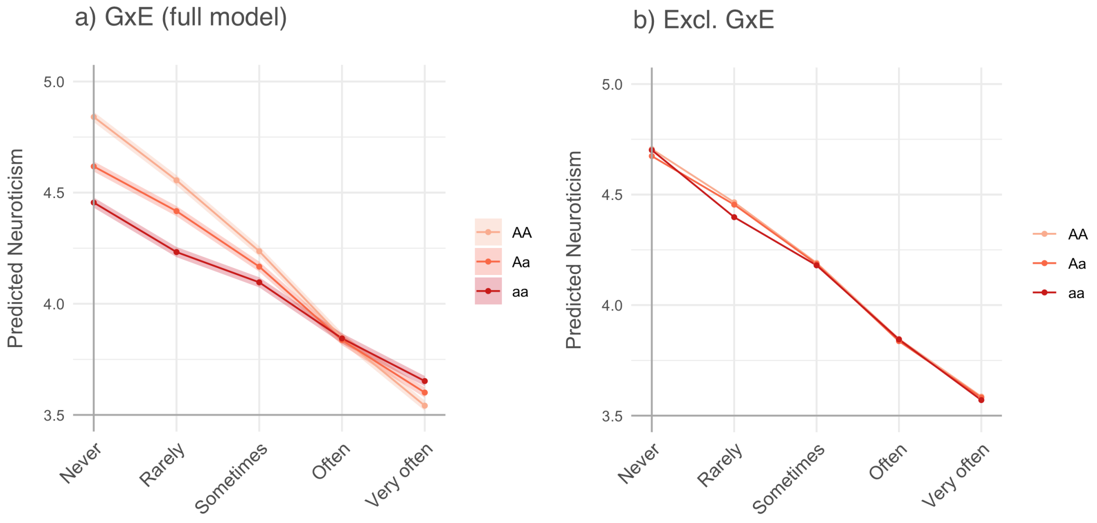
Supplementary Figure 7.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Locus Plot



Supplementary Figure 7.2 *Annotated locus plot showing the CADD and RegulomeDB scores for the SNP that reached standard genome-wide significance (p < 5e-8).*

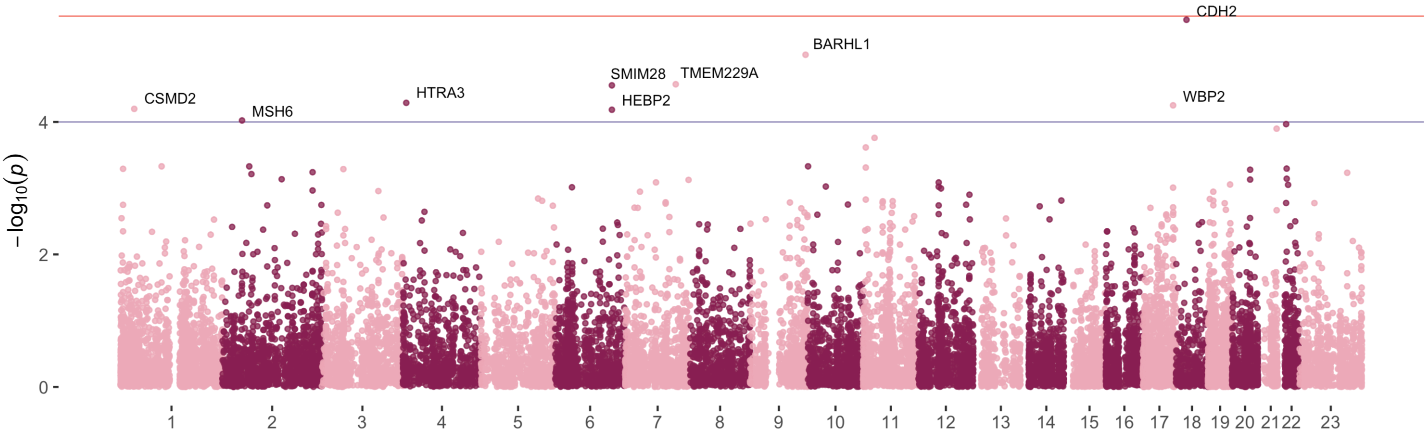
Interaction Plots



Supplementary Figure 7.3 *Average predicted neuroticism based on a) the full model (i.e., all main and interaction effects), with 95% confidence intervals for the GxE term, or b) everything except the SNP-environment interaction of interest (incl. all main effects and covariate interaction effects). Plot b will show any potential interaction effect captured by the covariates.*

Gene Analysis

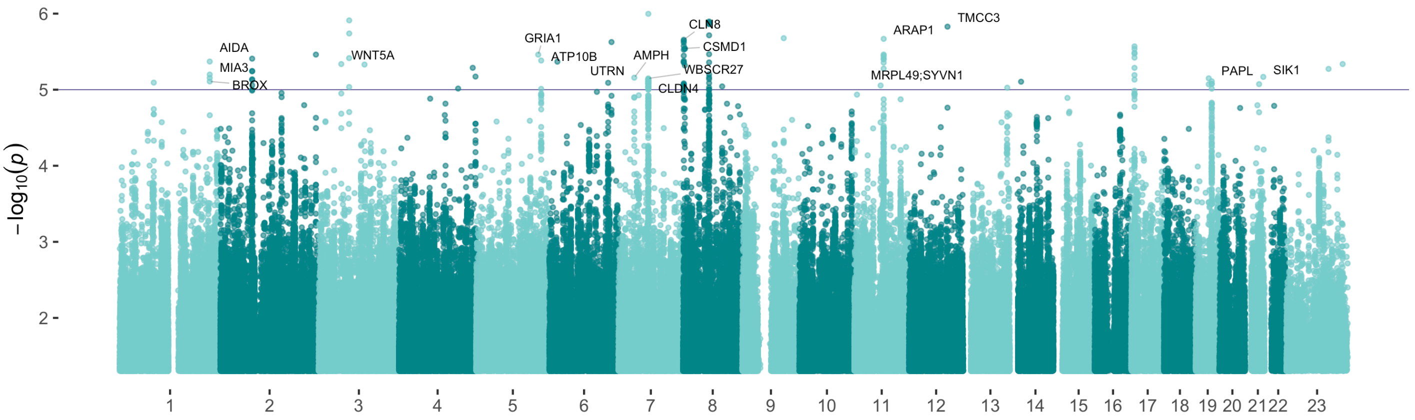
Manhattan Plot



Supplementary Figure 7.4 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

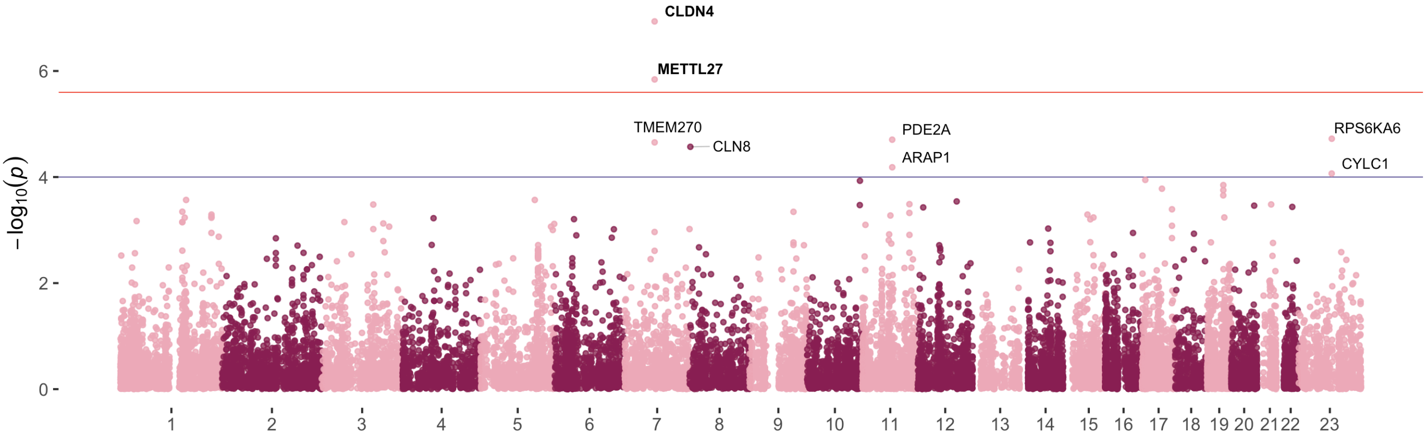
Alcohol Intake Frequency

GWEIS



Supplementary Figure 8.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

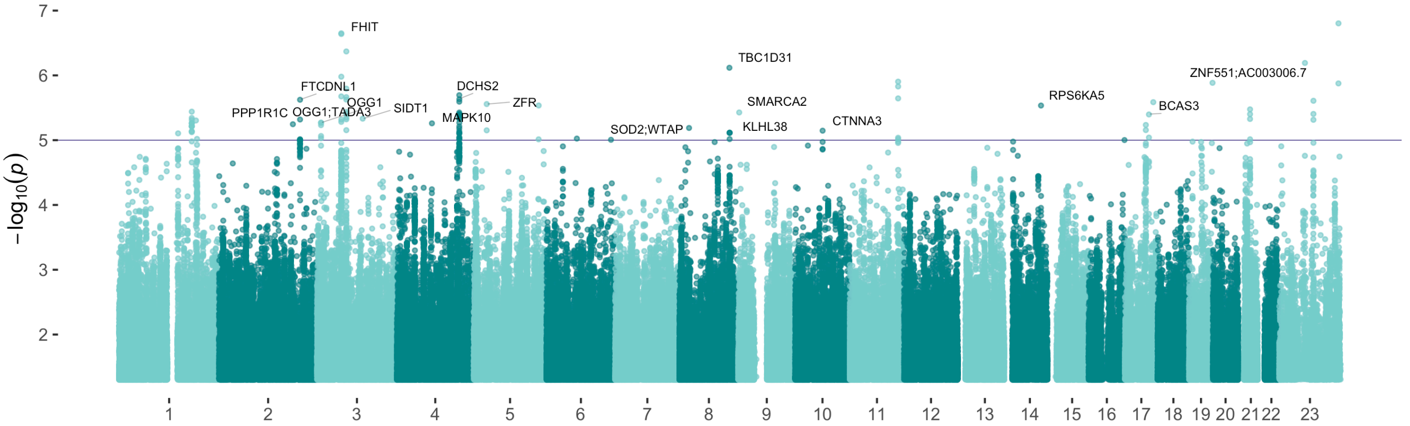
Gene Analysis



Supplementary Figure 8.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

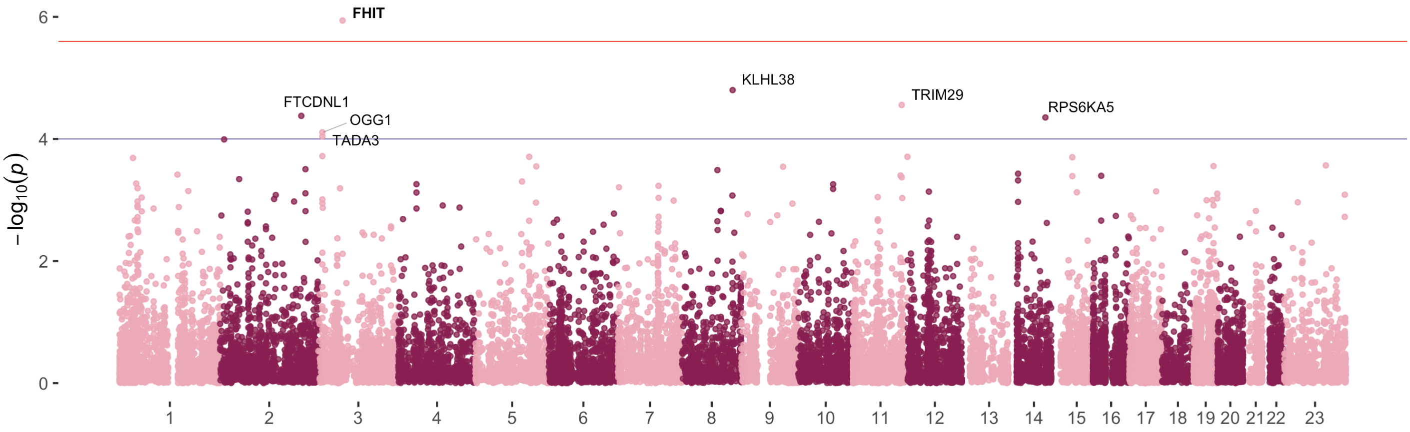
Victim of Sexual Assault

GWEIS



Supplementary Figure 9.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

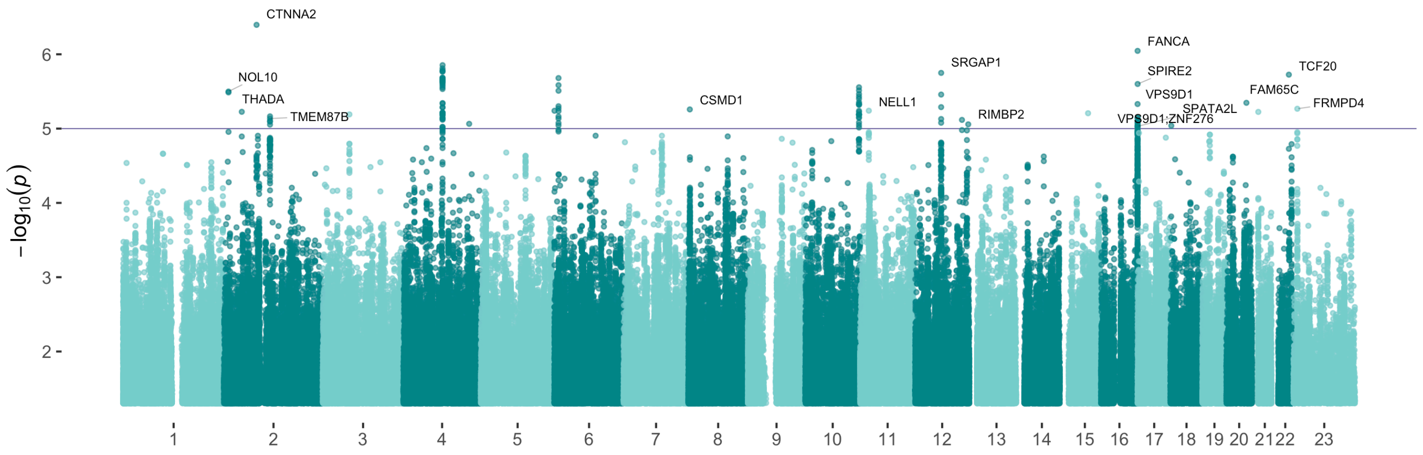
Gene Analysis



Supplementary Figure 9.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

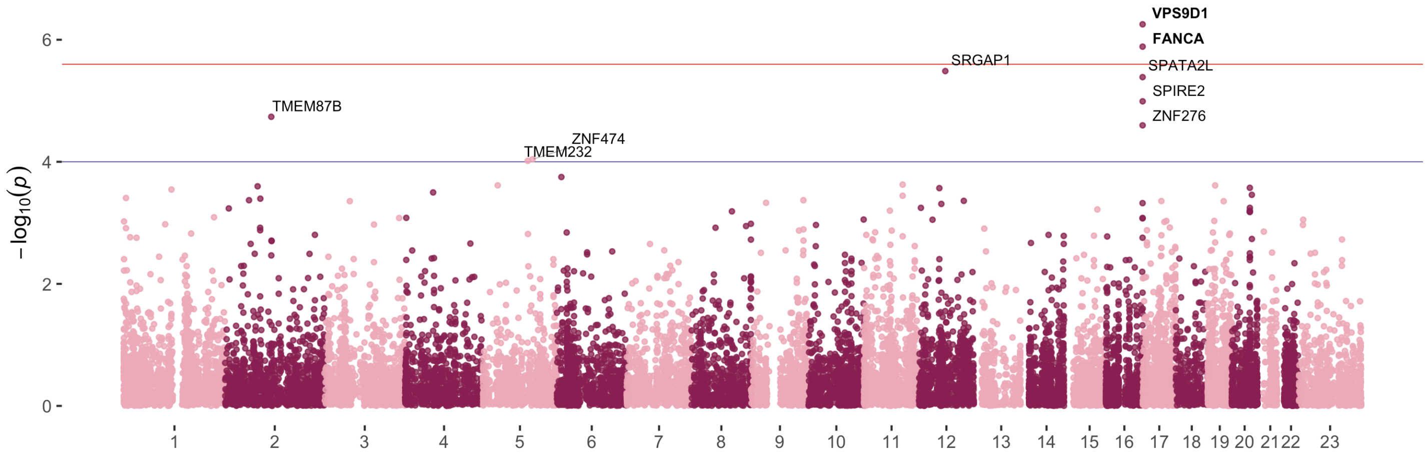
Chronic Pain

GWEIS



***Supplementary Figure 10.1** Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

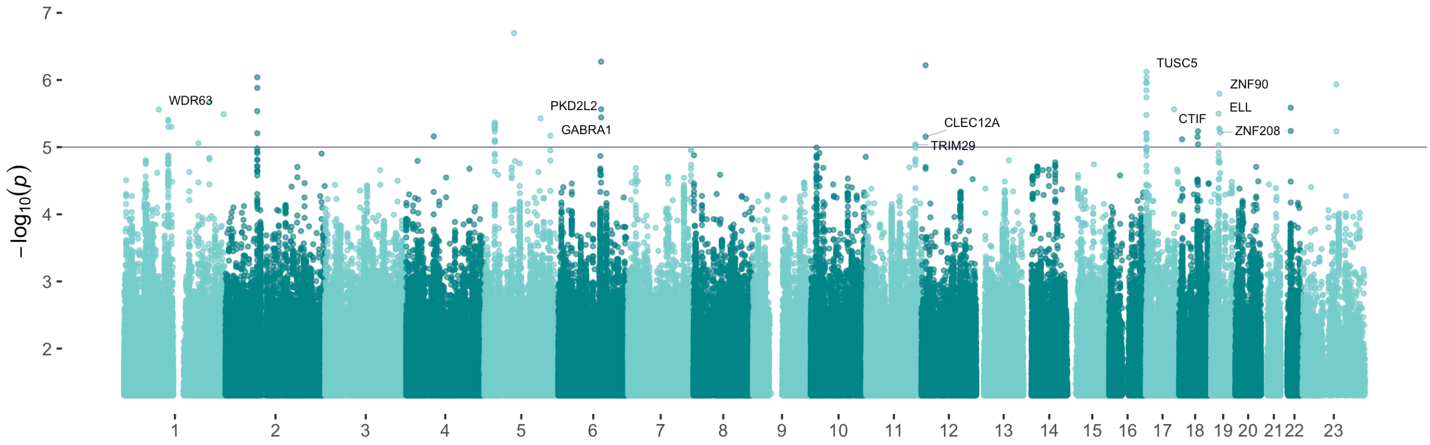
Gene Analysis



***Supplementary Figure 10.2** Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

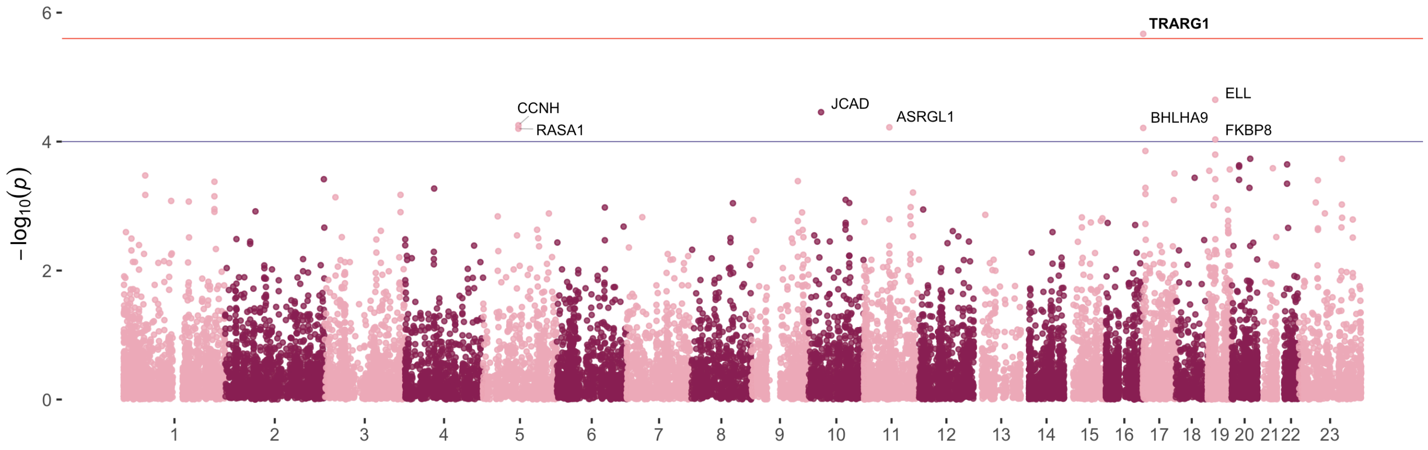
Age Completed Full-Time Education

GWEIS



***Supplementary Figure 11.1**: Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

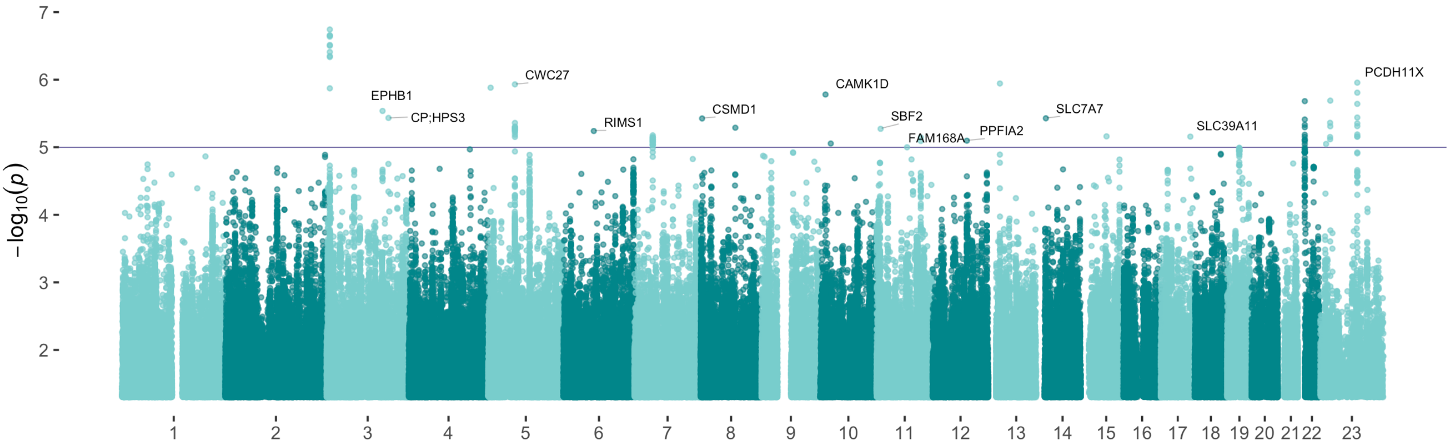
Gene Analysis



***Supplementary Figure 11.2** Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

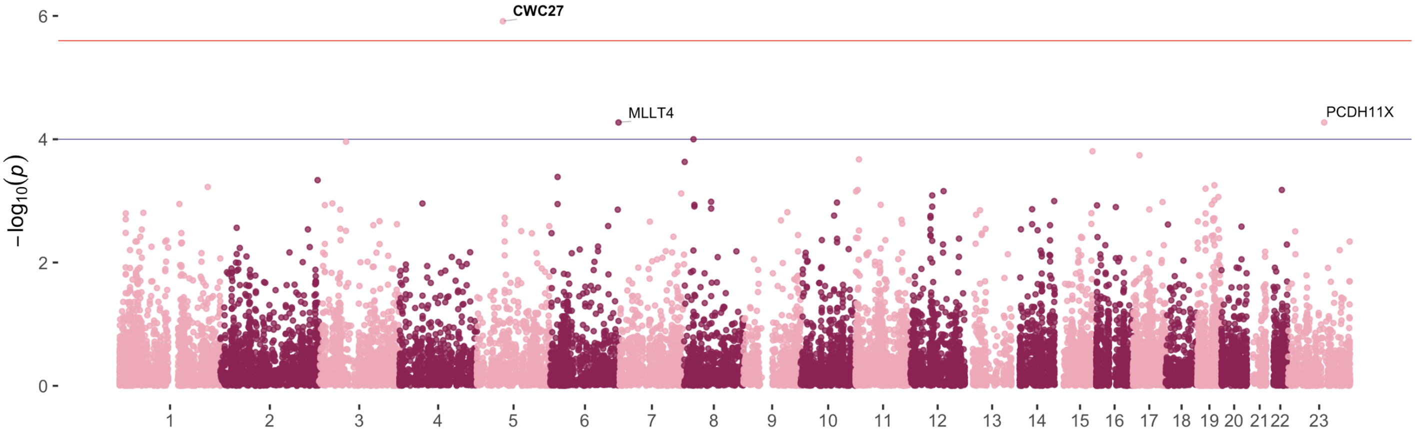
Family Relationship Satisfaction

GWEIS



Supplementary Figure 12.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

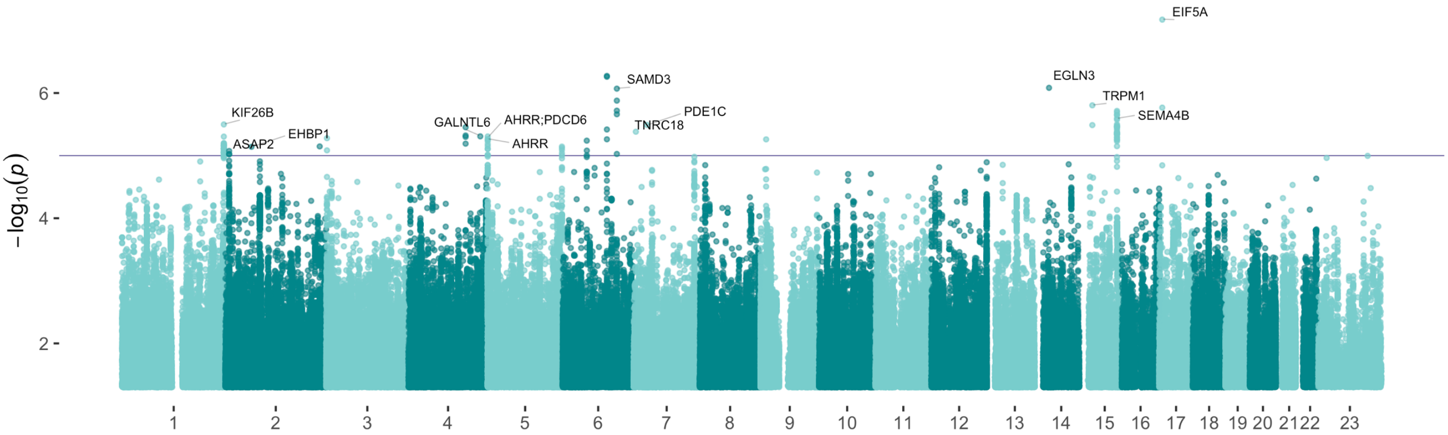
Gene Analysis



Supplementary Figure 12.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

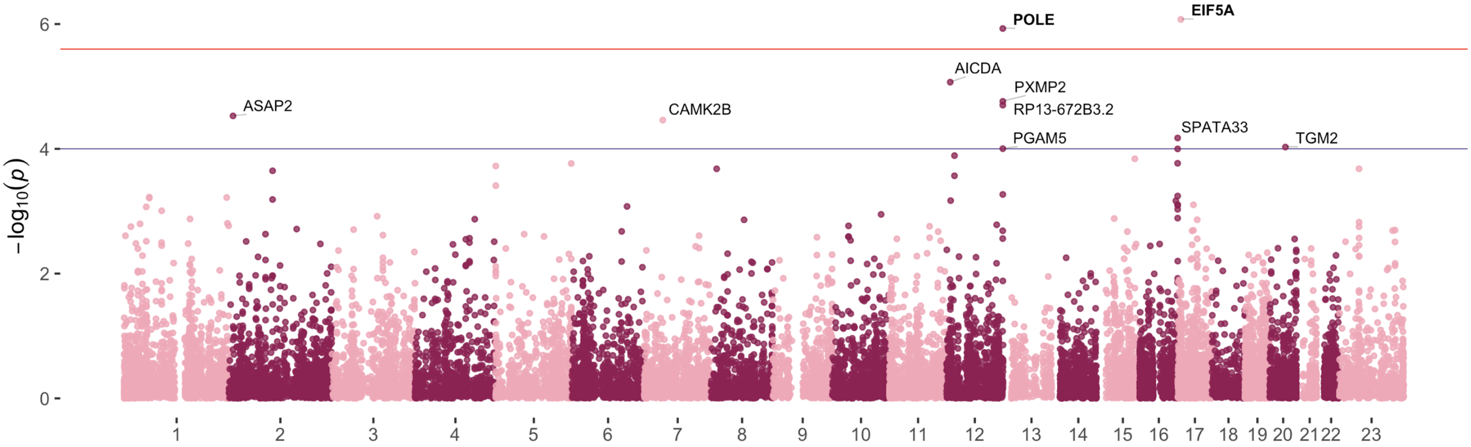
Fluid Intelligence Score

GWEIS



Supplementary Figure 13.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

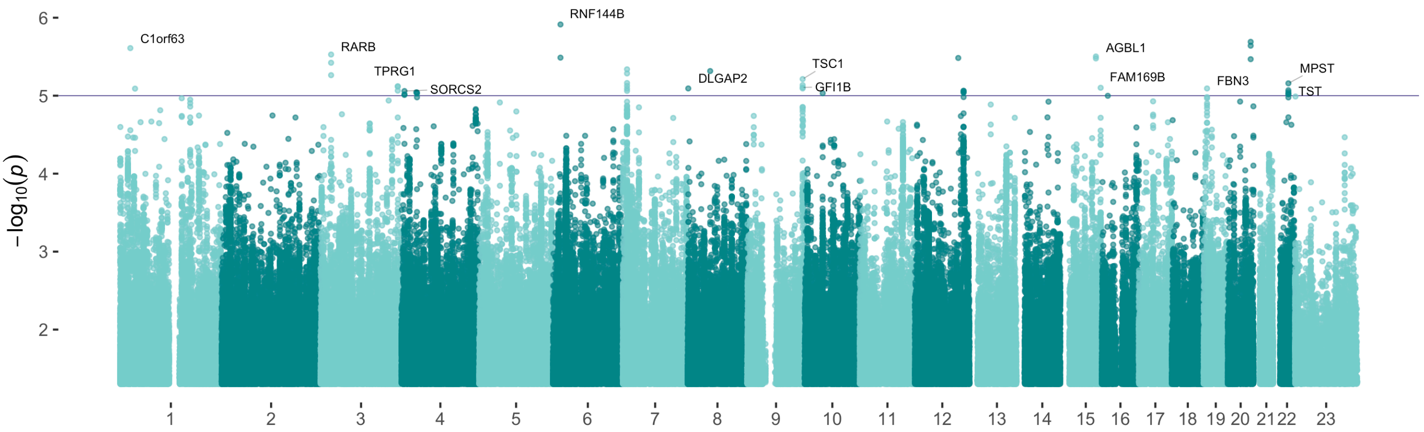
Gene Analysis



Supplementary Figure 13.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

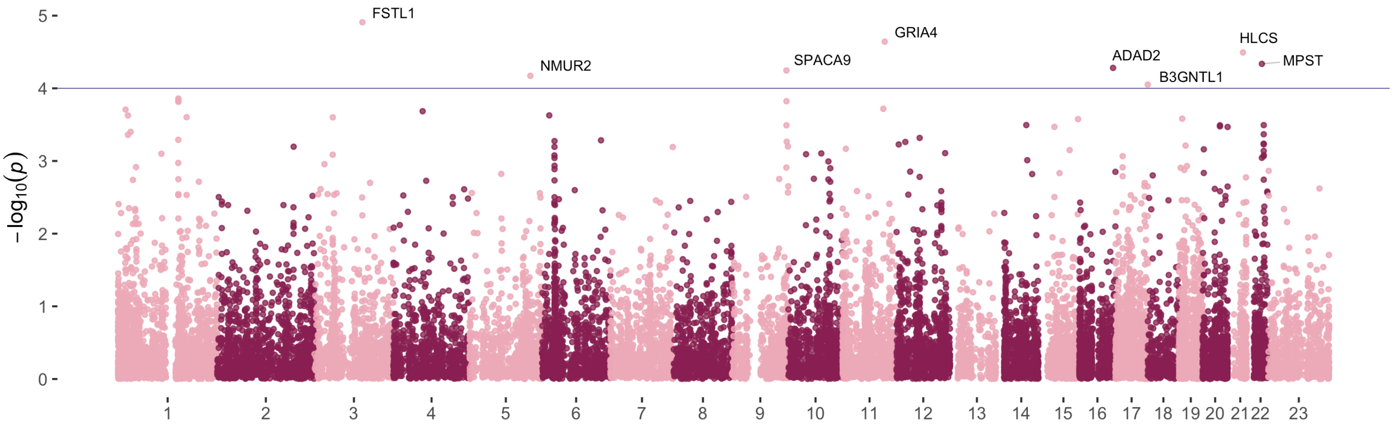
Frequency of Friend/Family Visits

GWEIS



Supplementary Figure 14.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

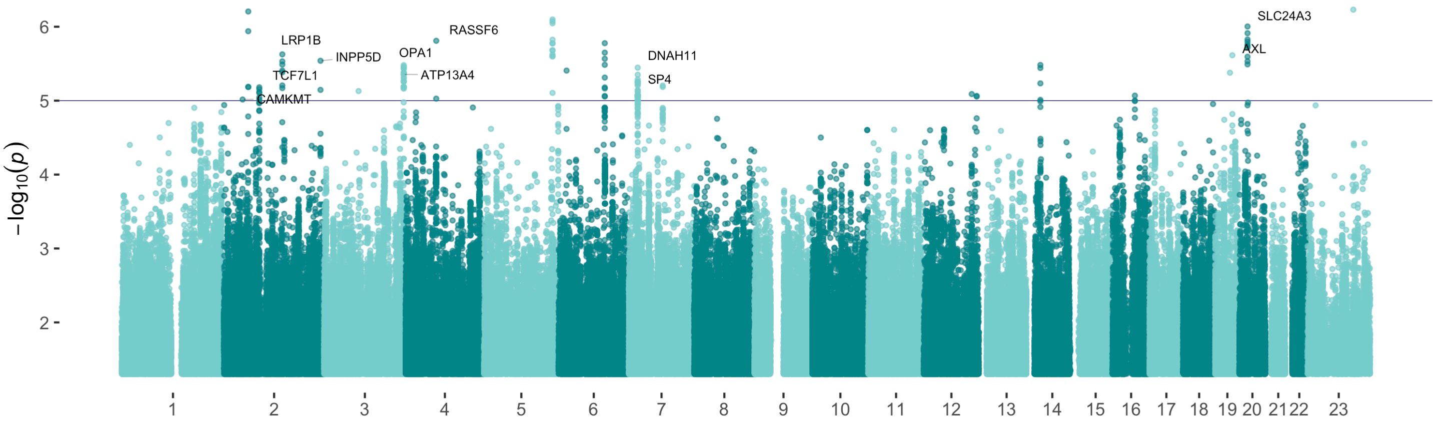
Gene Analysis



Supplementary Figure 14.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

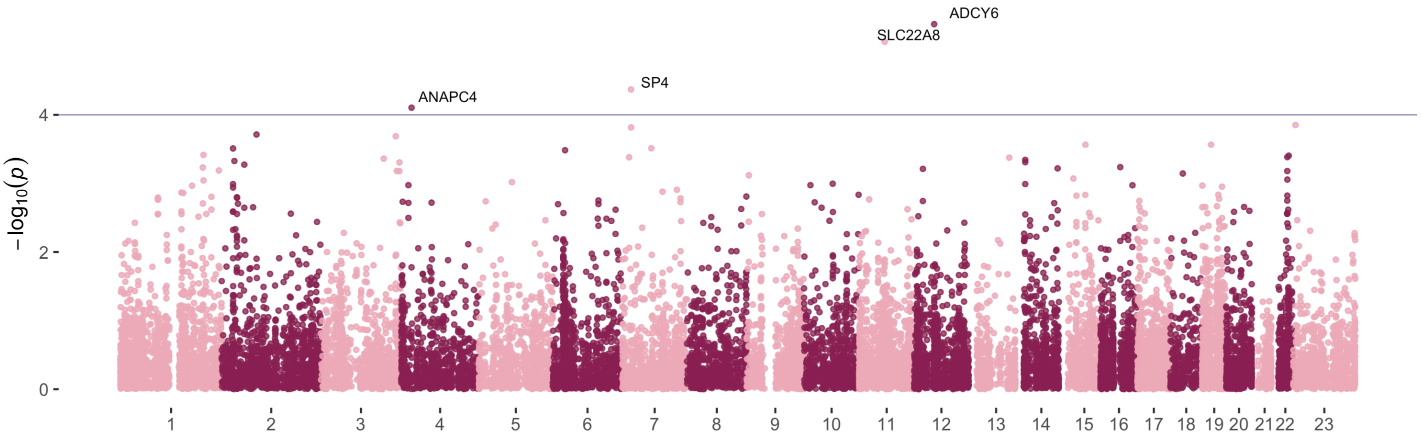
Sleeplessness / Insomnia

GWEIS



Supplementary Figure 15.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

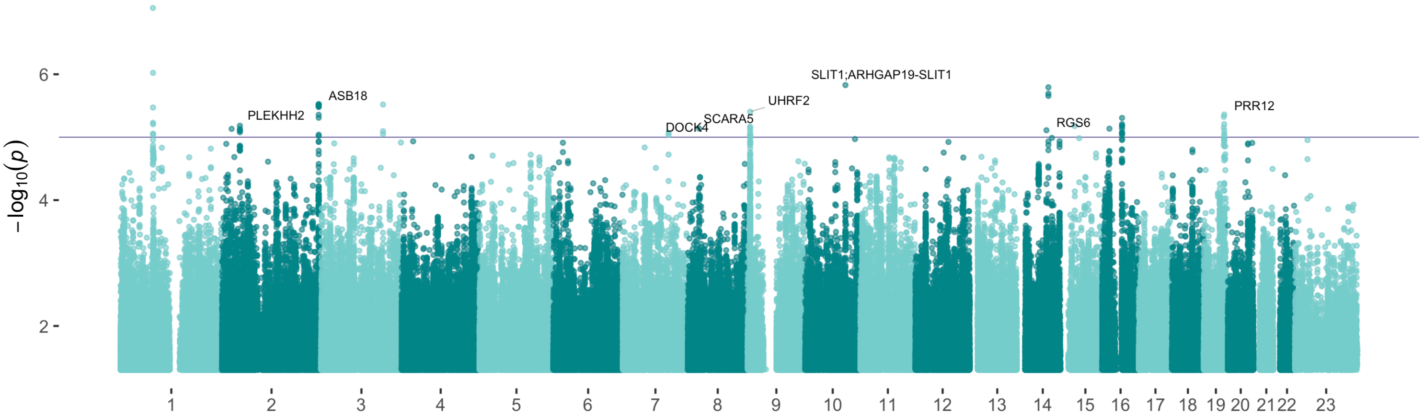
Gene Analysis



Supplementary Figure 15.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

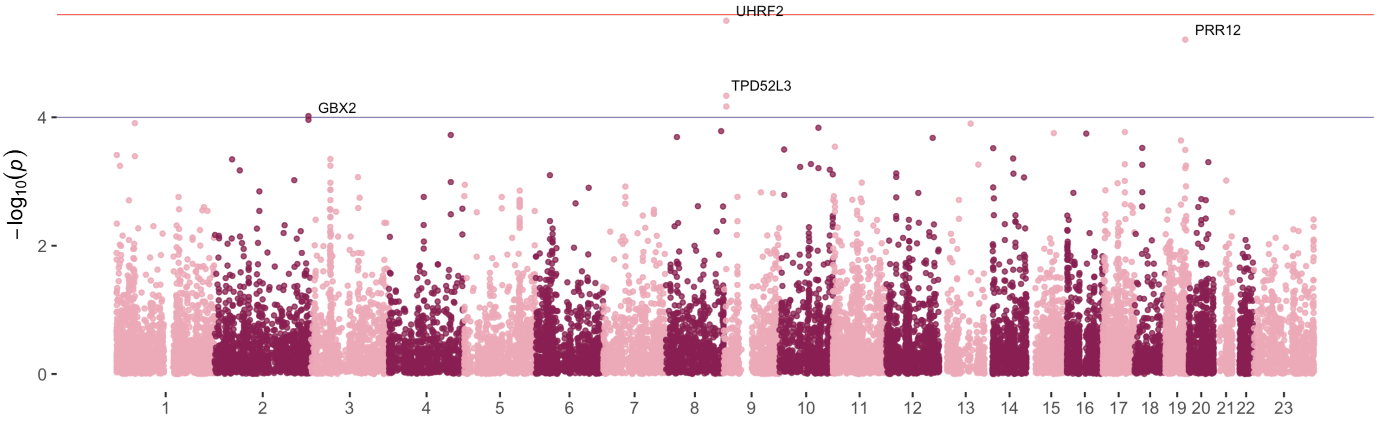
Long-Standing Illness, Disability, or Infirmity

GWEIS



Supplementary Figure 16.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

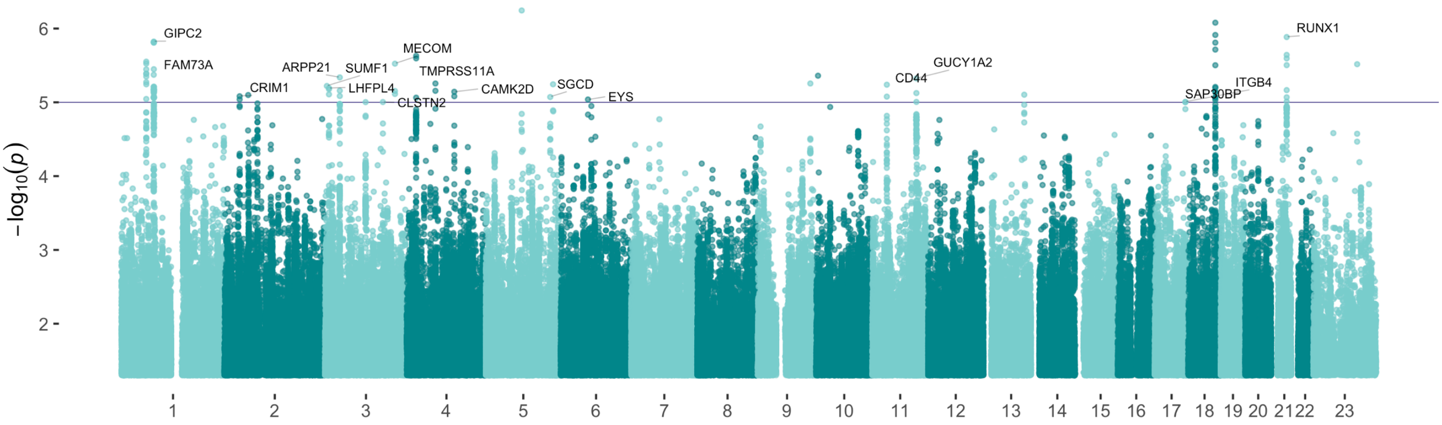
Gene Analysis



Supplementary Figure 16.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

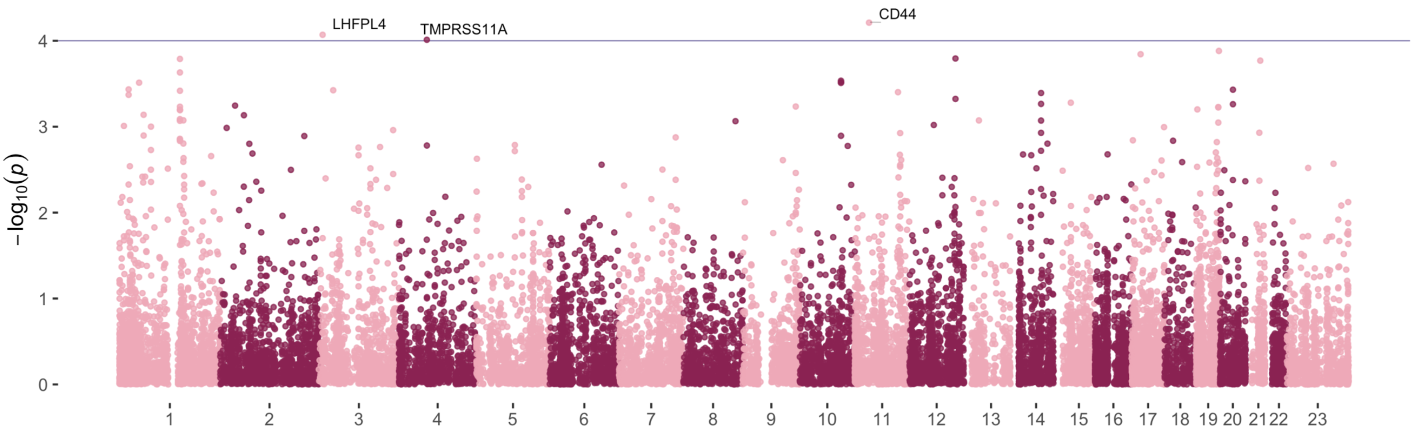
Health Satisfaction

GWEIS



Supplementary Figure 17.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

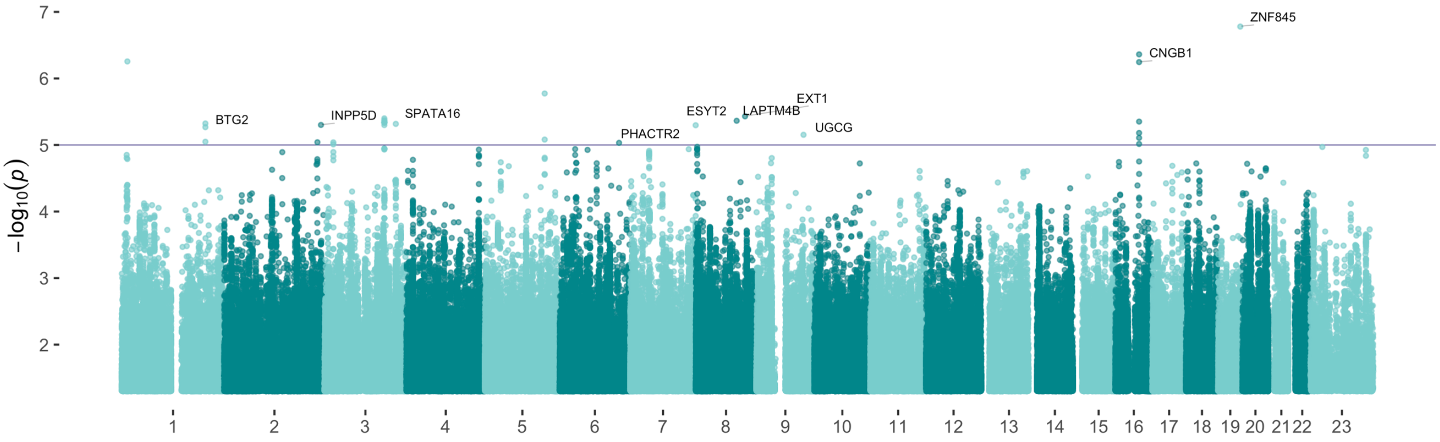
Gene Analysis



Supplementary Figure 17.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.).*

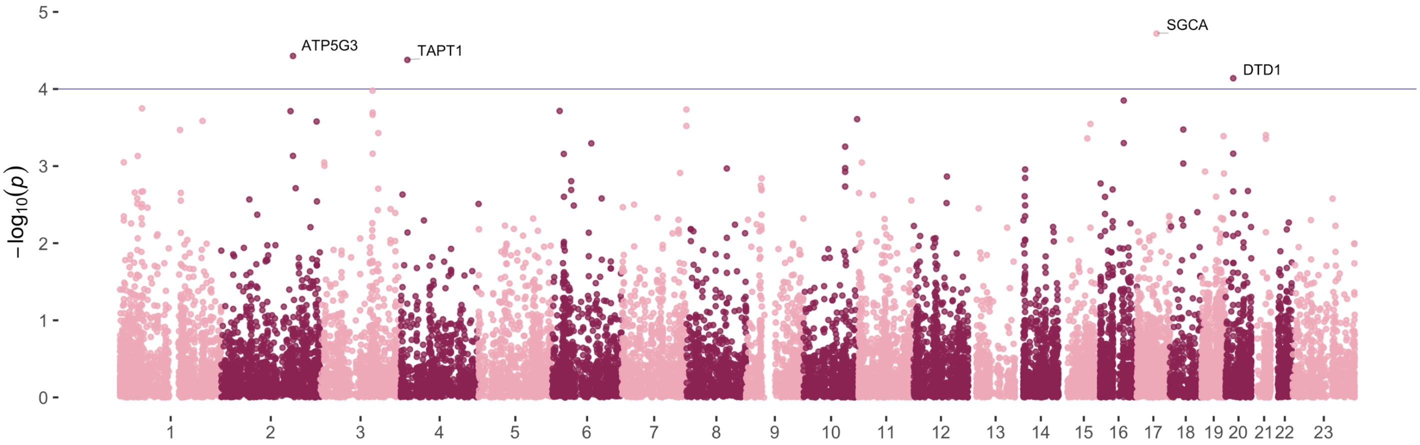
Friendships Satisfaction

GWEIS



Supplementary Figure 18.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

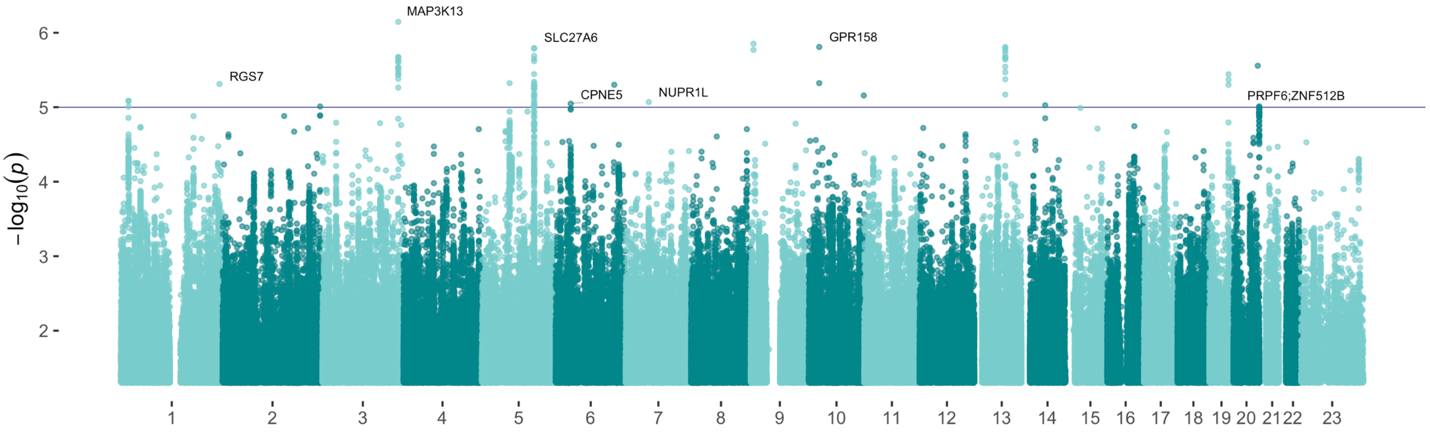
Gene Analysis



Supplementary Figure 18.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

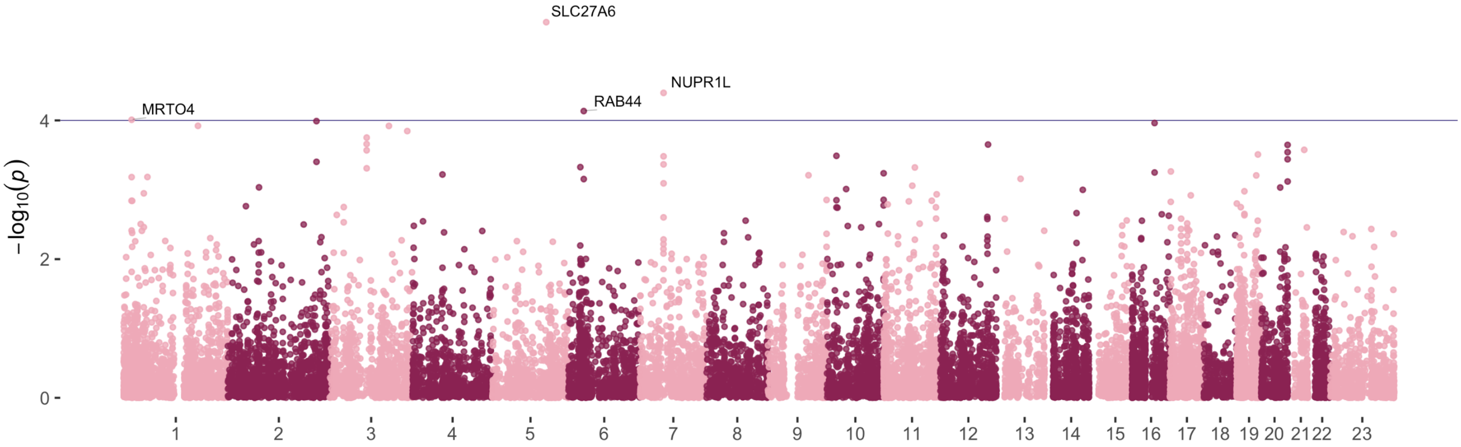
Financial Situation Satisfaction

GWEIS



Supplementary Figure 19.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

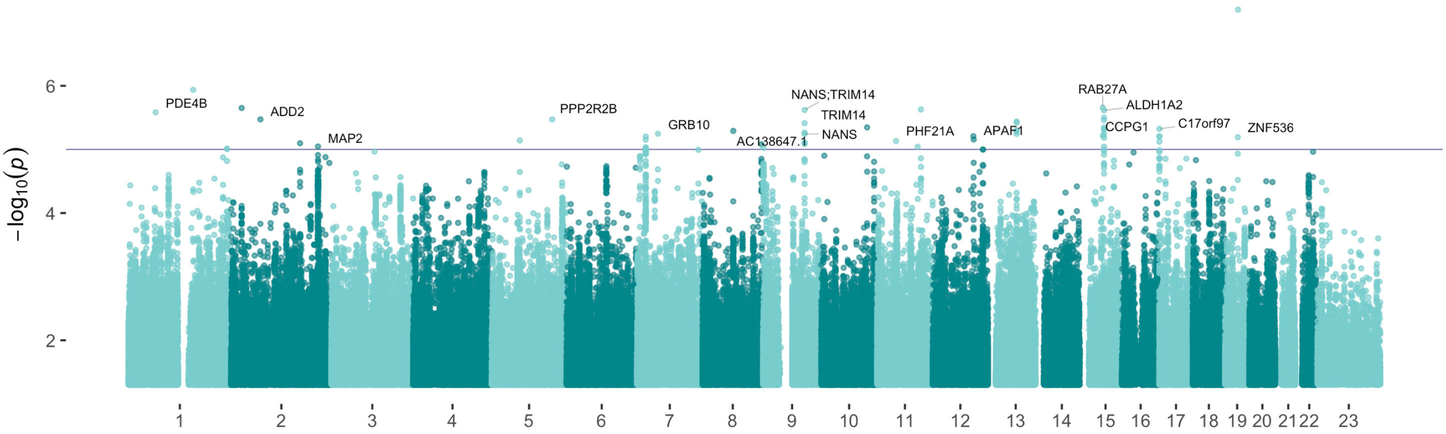
Gene Analysis



Supplementary Figure 19.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

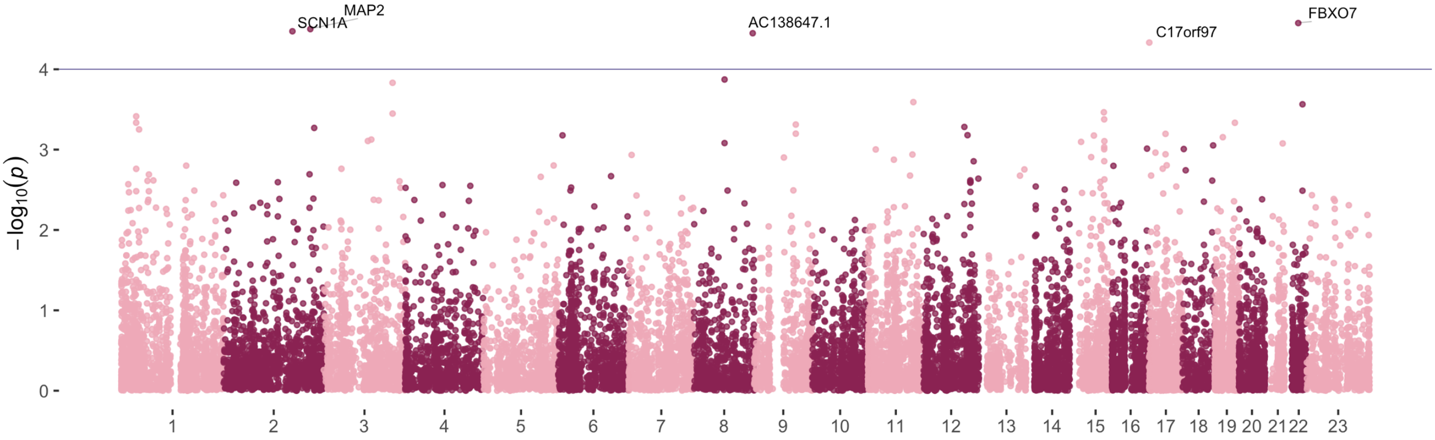
Illness, Injury, Bereavement, Stress in the Last 2 years

GWEIS



Supplementary Figure 20.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

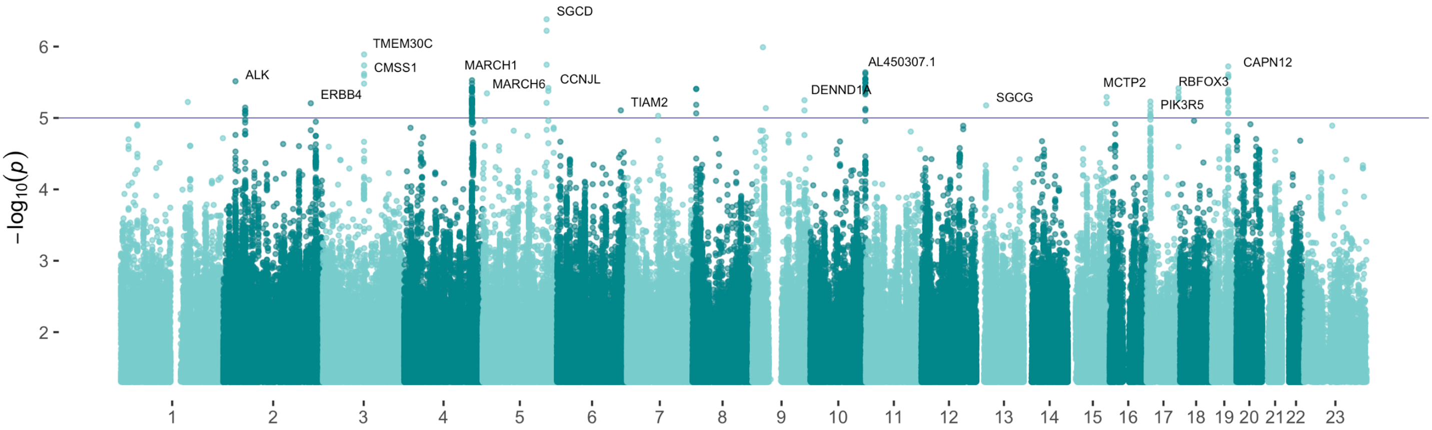
Gene Analysis



Supplementary Figure 20.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

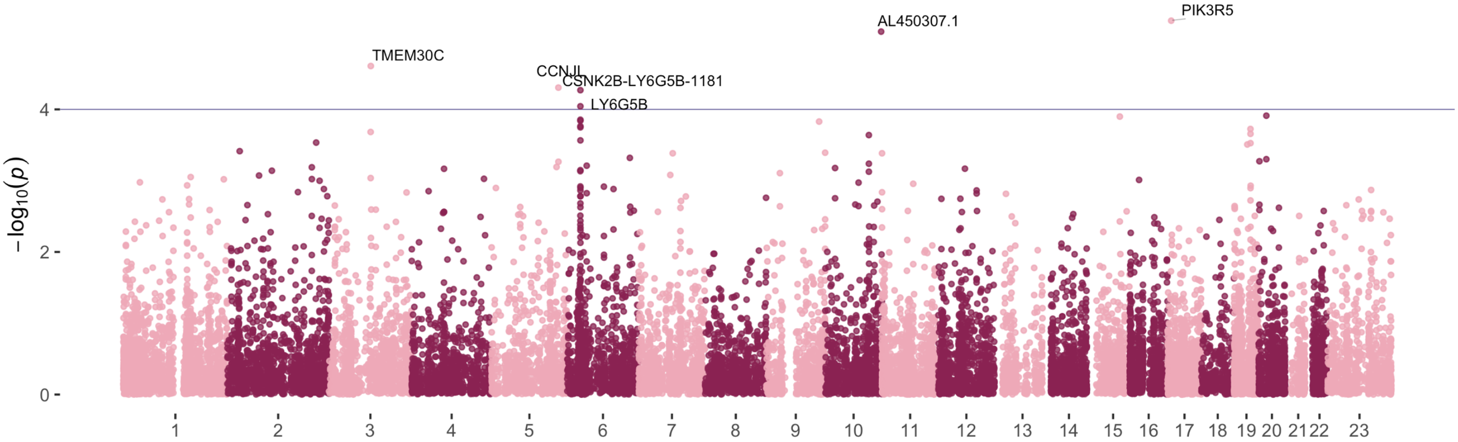
Smoking Status

GWEIS



Supplementary Figure 21.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

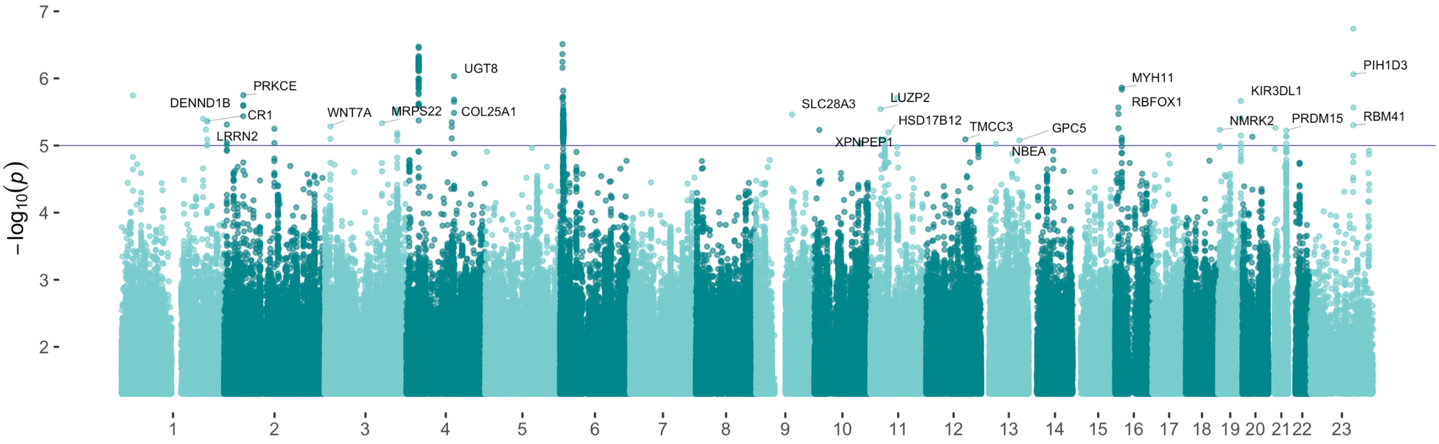
Gene Analysis



Supplementary Figure 21.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

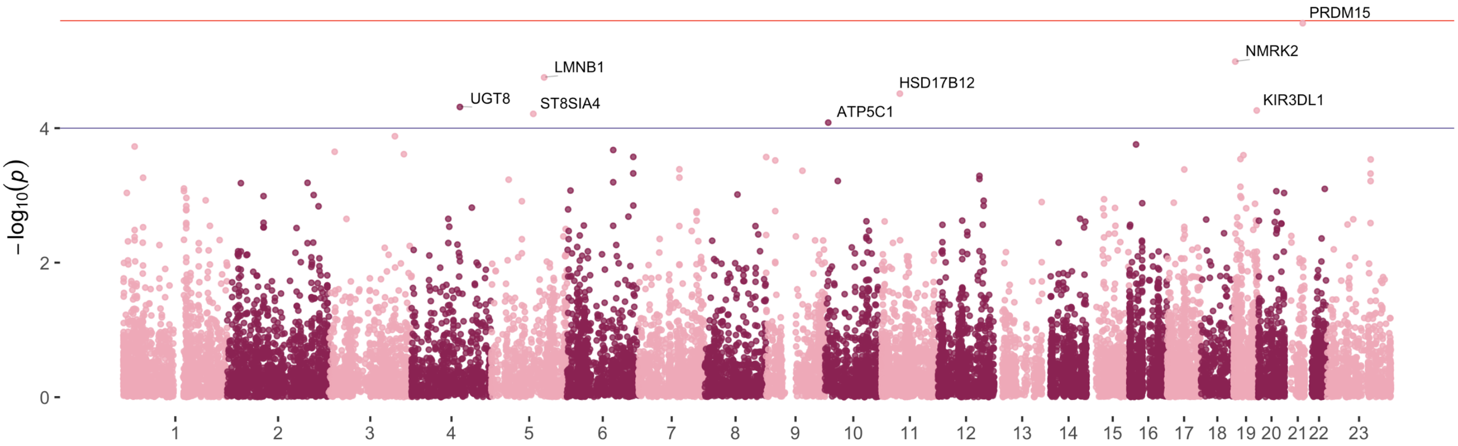
Physically Abused by Family as a Child

GWEIS



Supplementary Figure 22.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

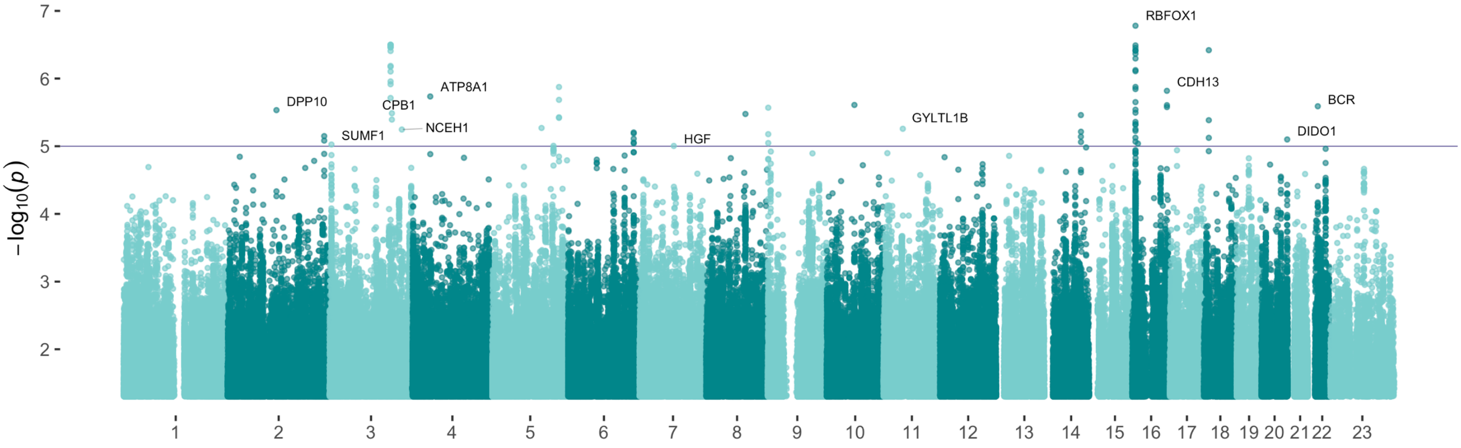
Gene Analysis



Supplementary Figure 22.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

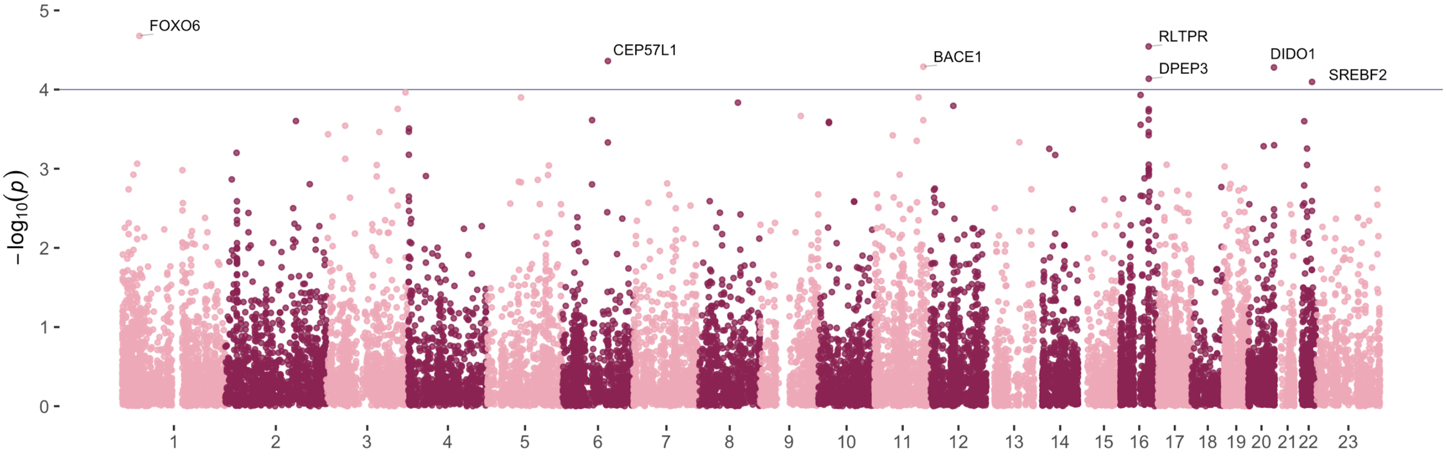
Felt Loved as a Child

GWEIS



Supplementary Figure 23.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

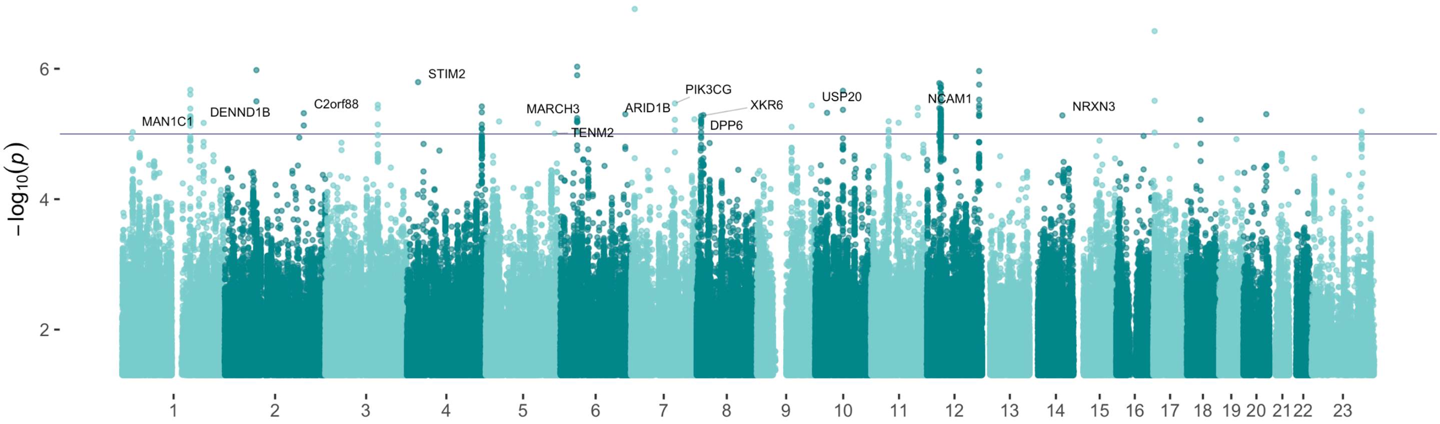
Gene Analysis



Supplementary Figure 23.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

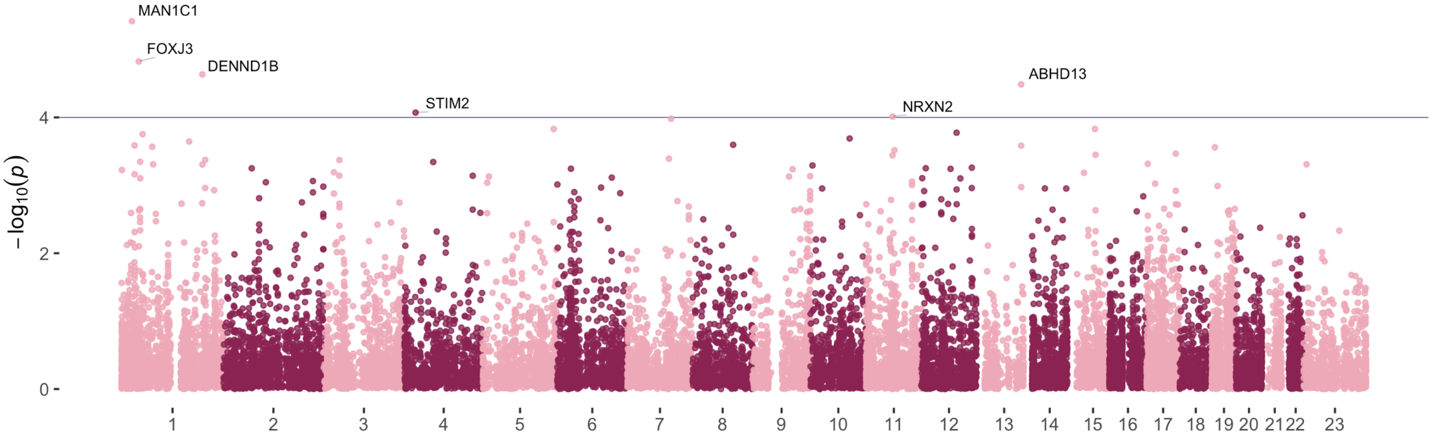
Victim of Physically Violent Crime

GWEIS



Supplementary Figure 24.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

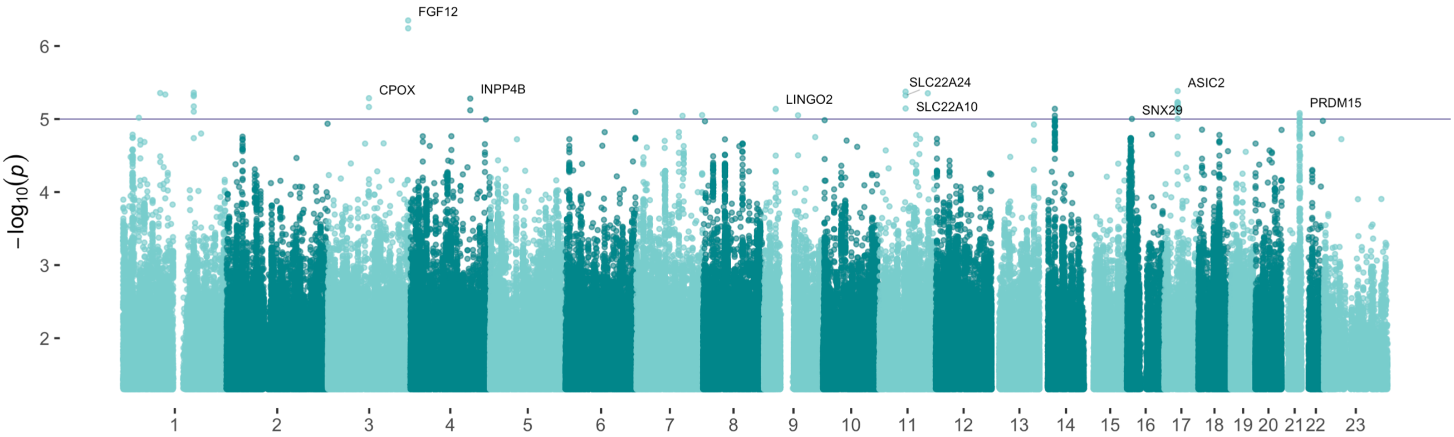
Gene Analysis



Supplementary Figure 24.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

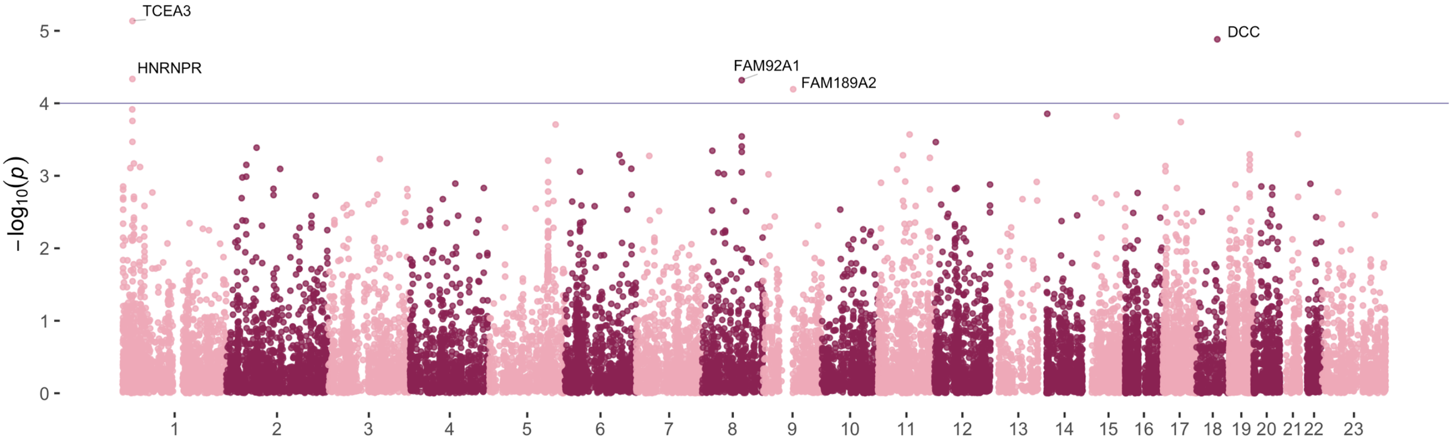
Body Mass Index (BMI)

GWEIS



Supplementary Figure 25.1 *Manhattan plot showing the -log10 SNP-environment interaction p-values from the GWEIS. Gene labels have been annotated to suggestively significant (p < 1e-5) intragenic SNPs with the lowest p-value. (Only SNPs with p < .05 were plotted).*

Gene Analysis

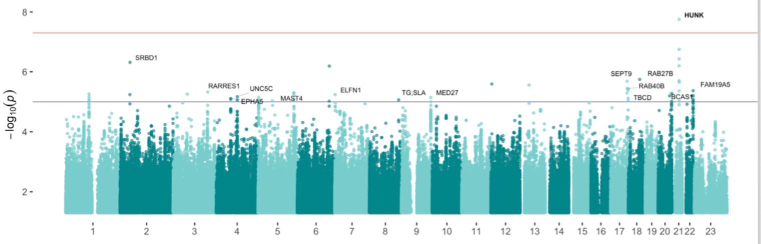


Supplementary Figure 25.2 *Manhattan plot showing the -log10 p-values for the MAGMA gene analysis (based on the GWEIS SNP-environment interaction results). Suggestively significant genes (p < 1e-4) have been annotated.*

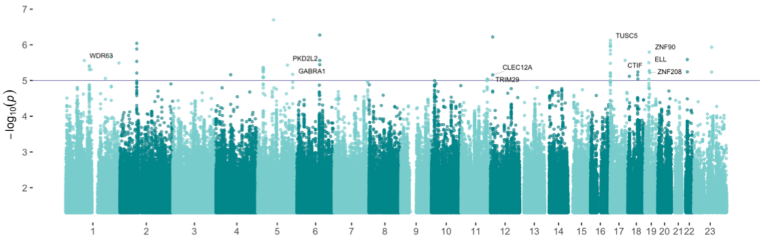
MANHATTAN PLOTS (grouped)

This section contains all Manhattan plots from the GWEIS and gene analyses grouped together

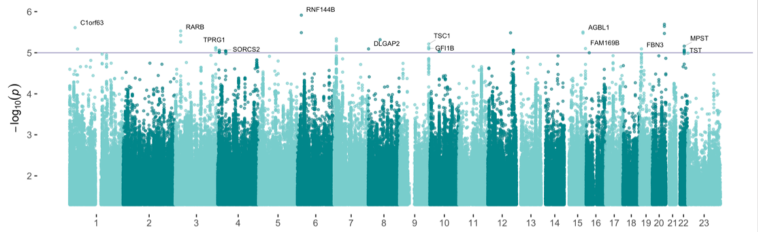
GWEIS



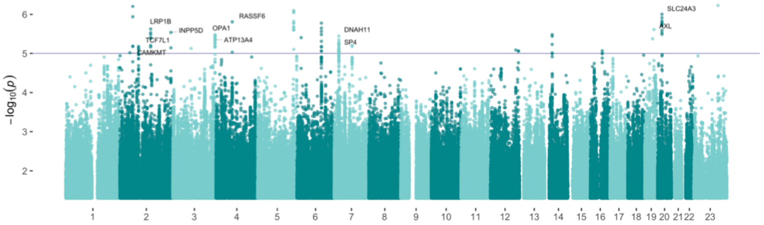
Townsend deprivation index at recruitment



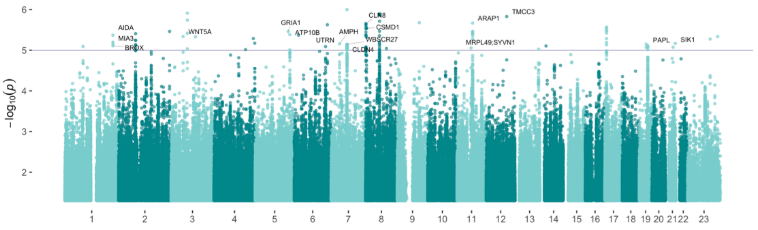
Age completed full time education



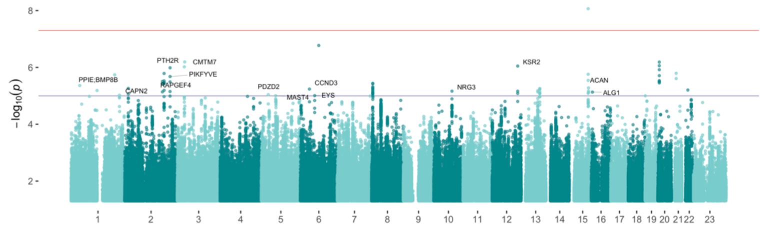
Frequency of friend/family visits



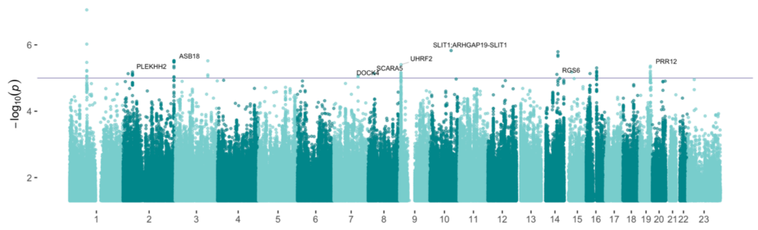
Sleeplessness / insomnia



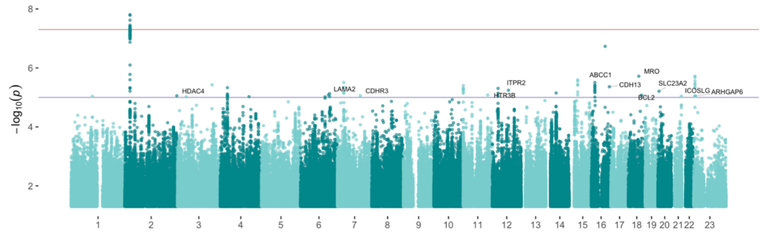
Alcohol intake frequency



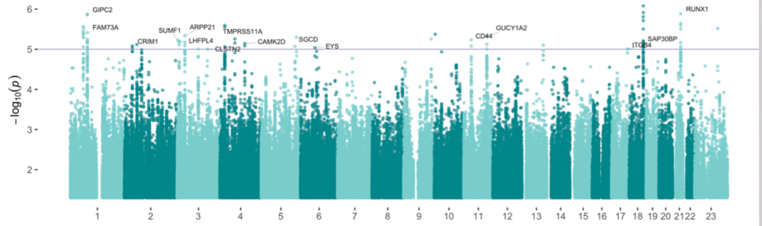
Able to confide



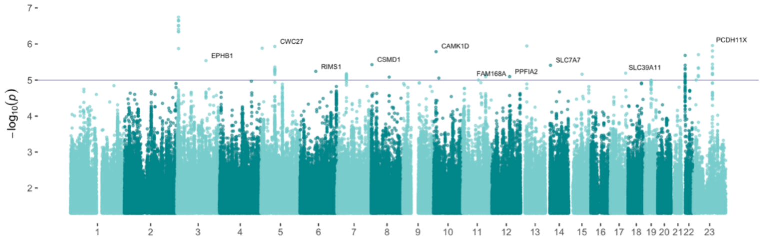
Long-standing illness, disability or infirmity



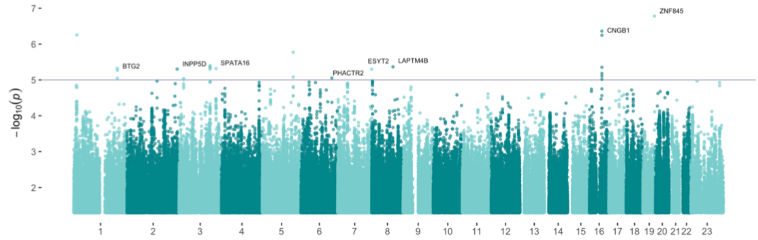
Work/job satisfaction



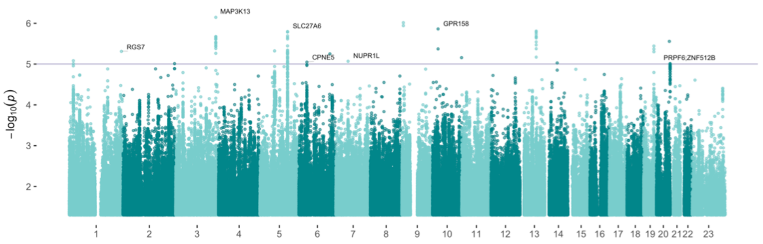
Health satisfaction



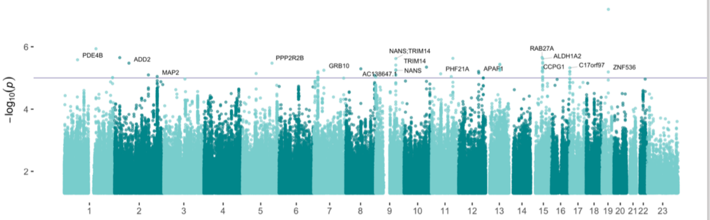
Family relationship satisfaction



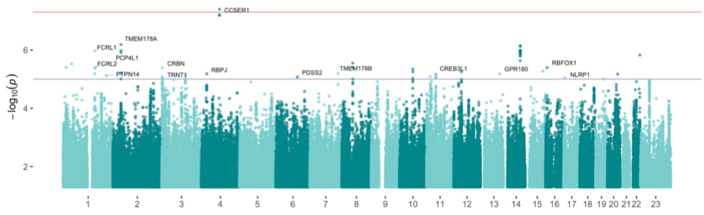
Friendships satisfaction



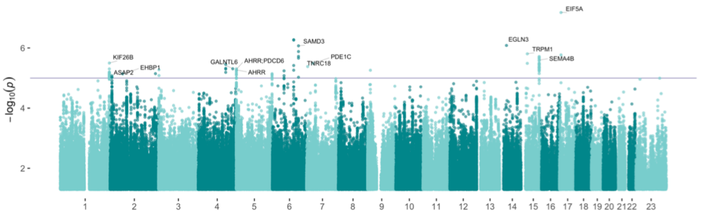
Financial situation satisfaction



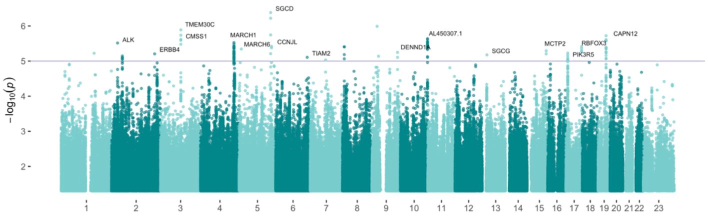
Illness, injury, bereavment, stress in the last 2 years



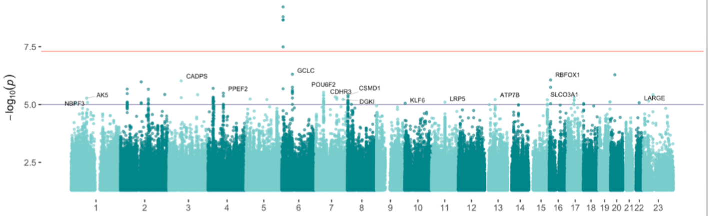
Leisure/social activities



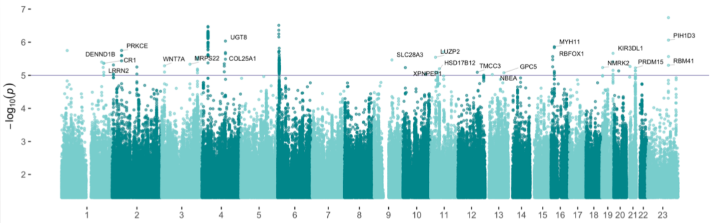
Fluid intelligence score



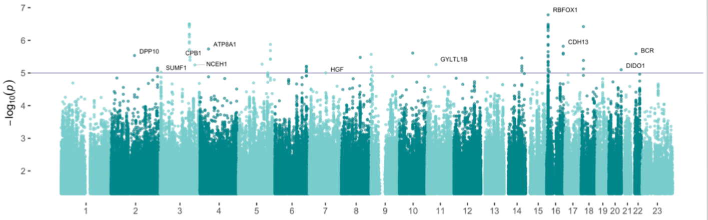
Smoking status



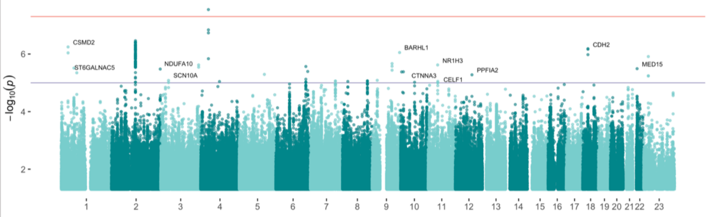
Felt hated by family member as a child



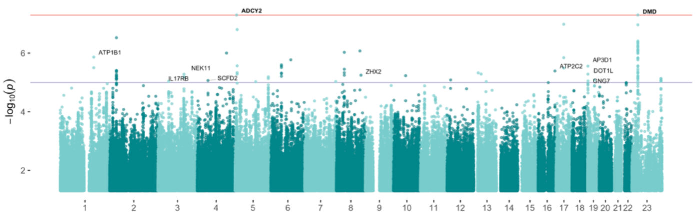
Physically abused by family as a child



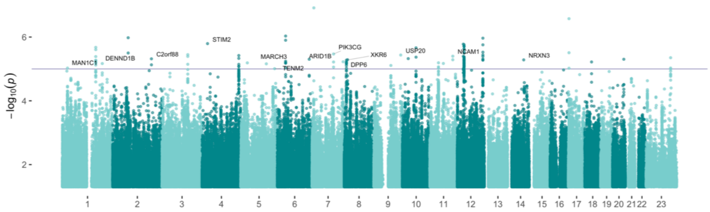
Felt loved as a child



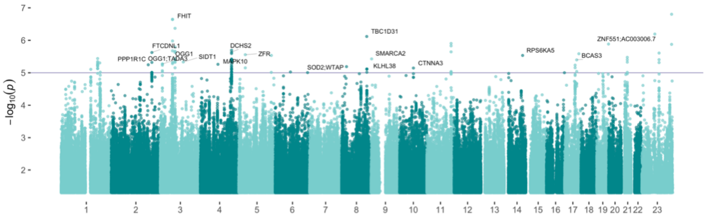
Been in a confiding relationship as an adult



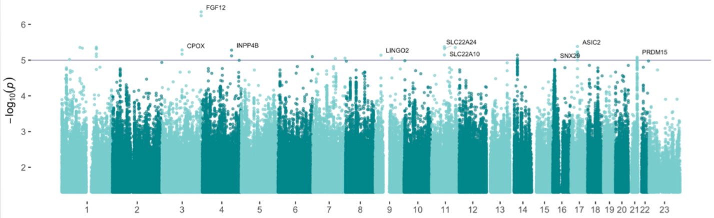
Diagnosed with life-threatening illness



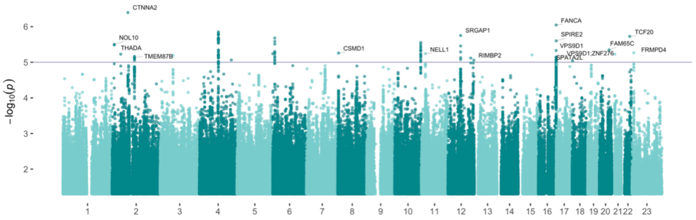
Victim of physically violent crime



Victim of sexual assault

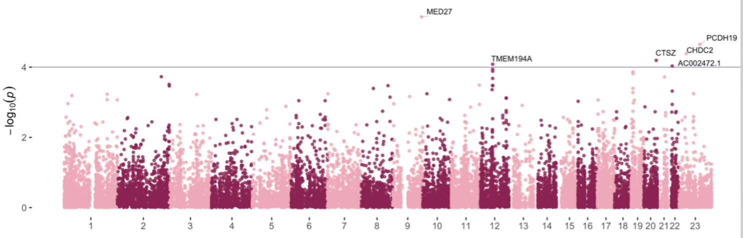


Body mass index (BMI)

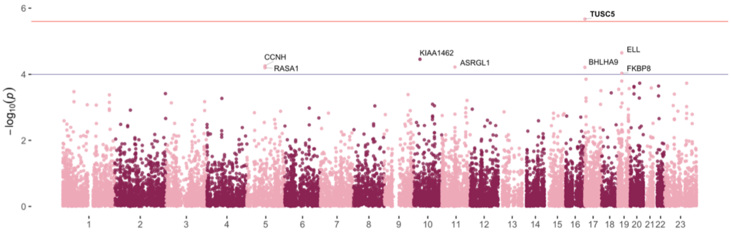


Pain for 3+ months

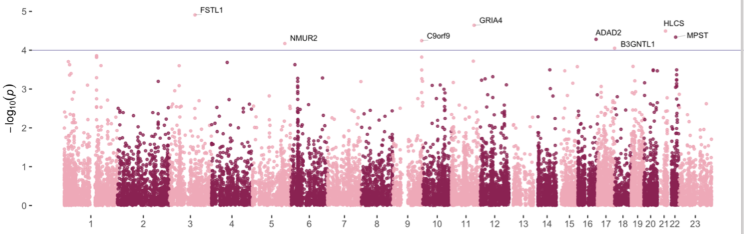
Gene Analysis



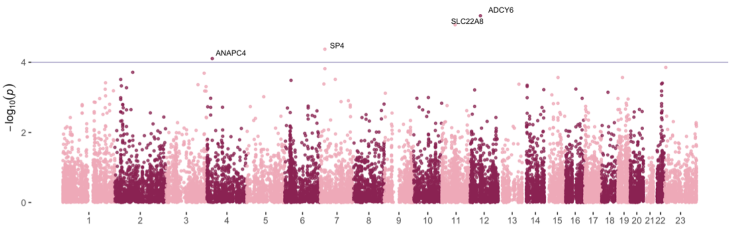
Townsend deprivation index at recruitment



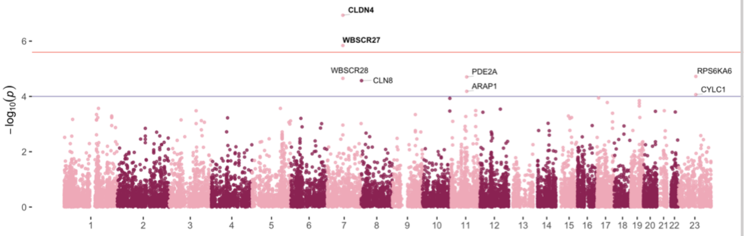
Age completed full time education



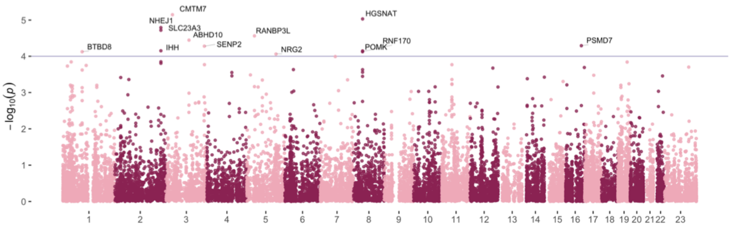
Frequency of friend/family visits



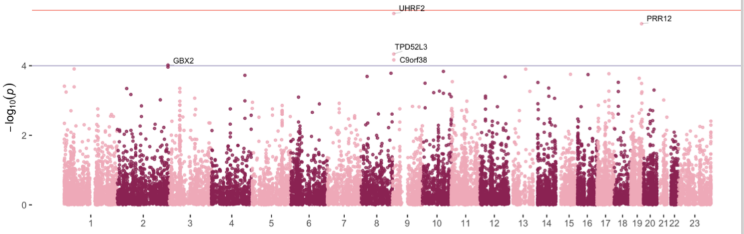
Sleeplessness / insomnia



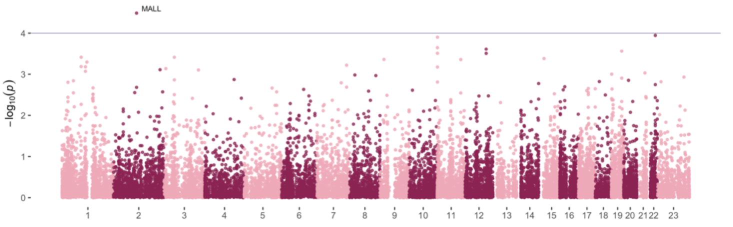
Alcohol intake frequency



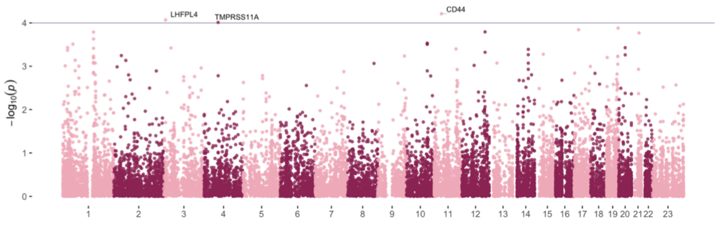
Able to confide



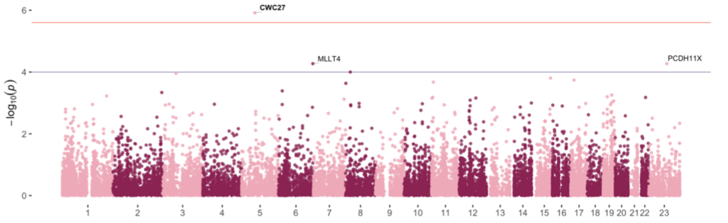
Long-standing illness, disability or infirmity



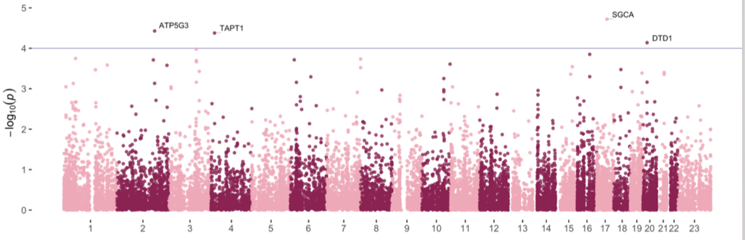
Work/job satisfaction



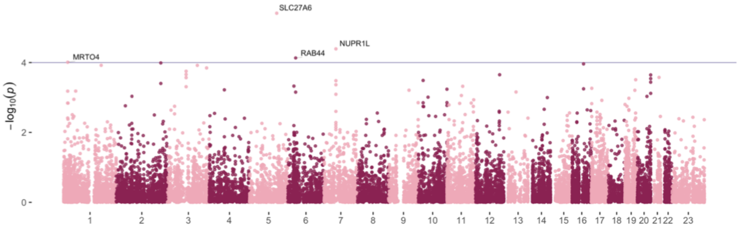
Health satisfaction



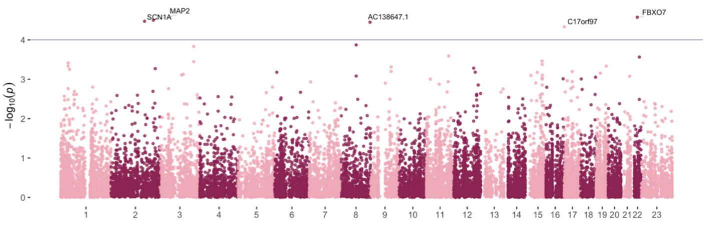
Family relationship satisfaction



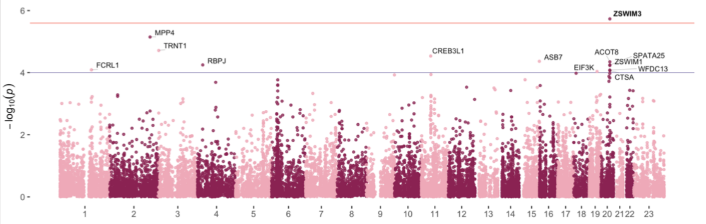
Friendships satisfaction



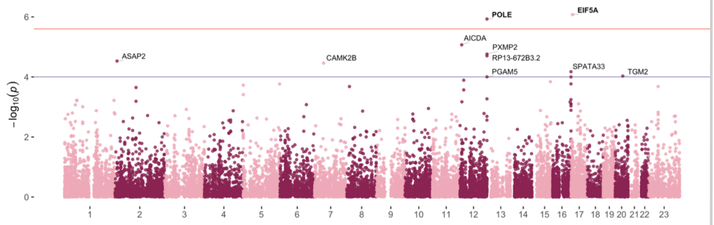
Financial situation satisfaction



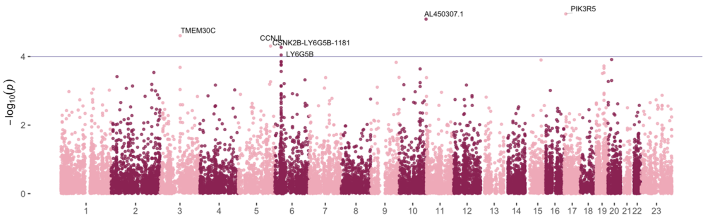
Illness injury bereavment stress



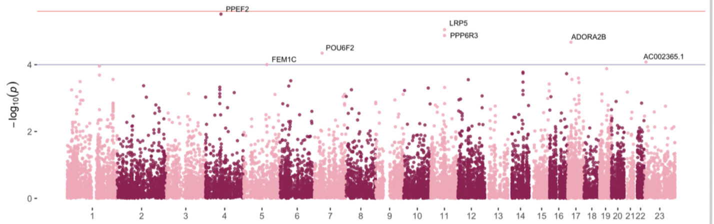
Leisure/social activities



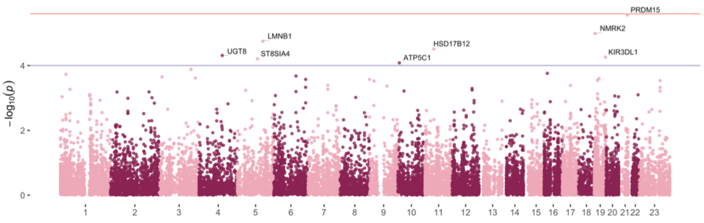
Fluid intelligence score



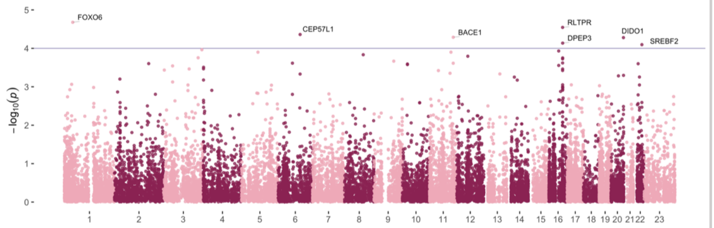
Smoking status



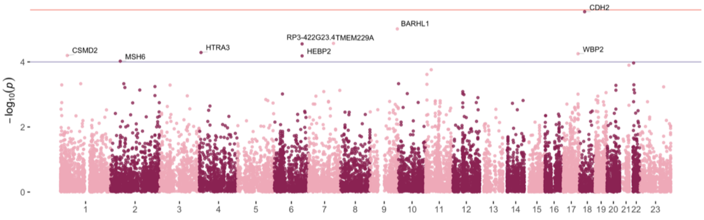
Felt hated by family member as a child



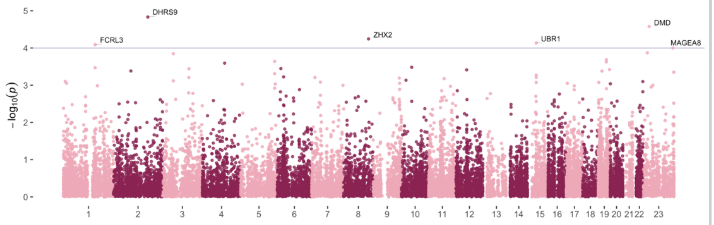
Physically abused by family as a child



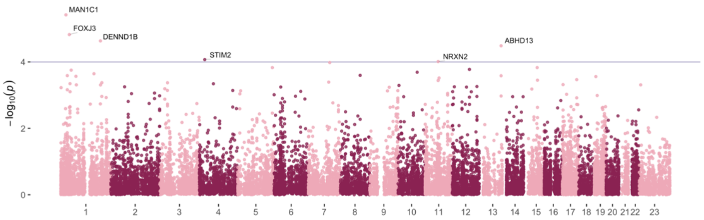
Felt loved as a child



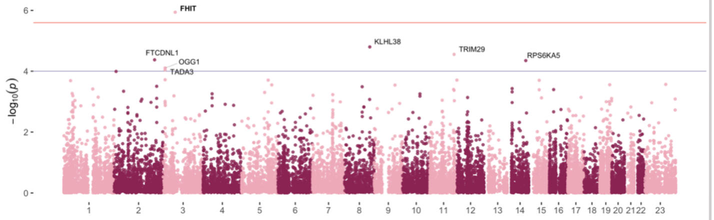
Been in a confiding relationship as an adult



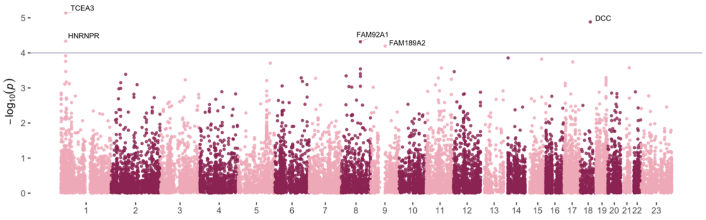
Diagnosed with life-threatening illness



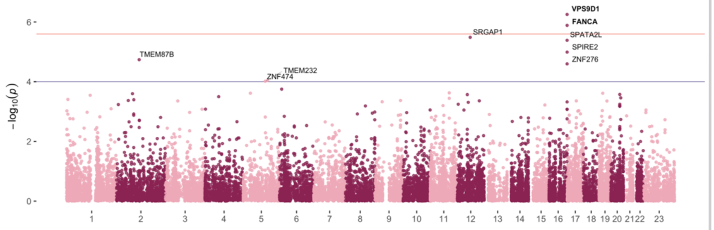
Victim of physically violent crime



Victim of sexual assault



Body mass index (BMI)



Pain for 3+ months