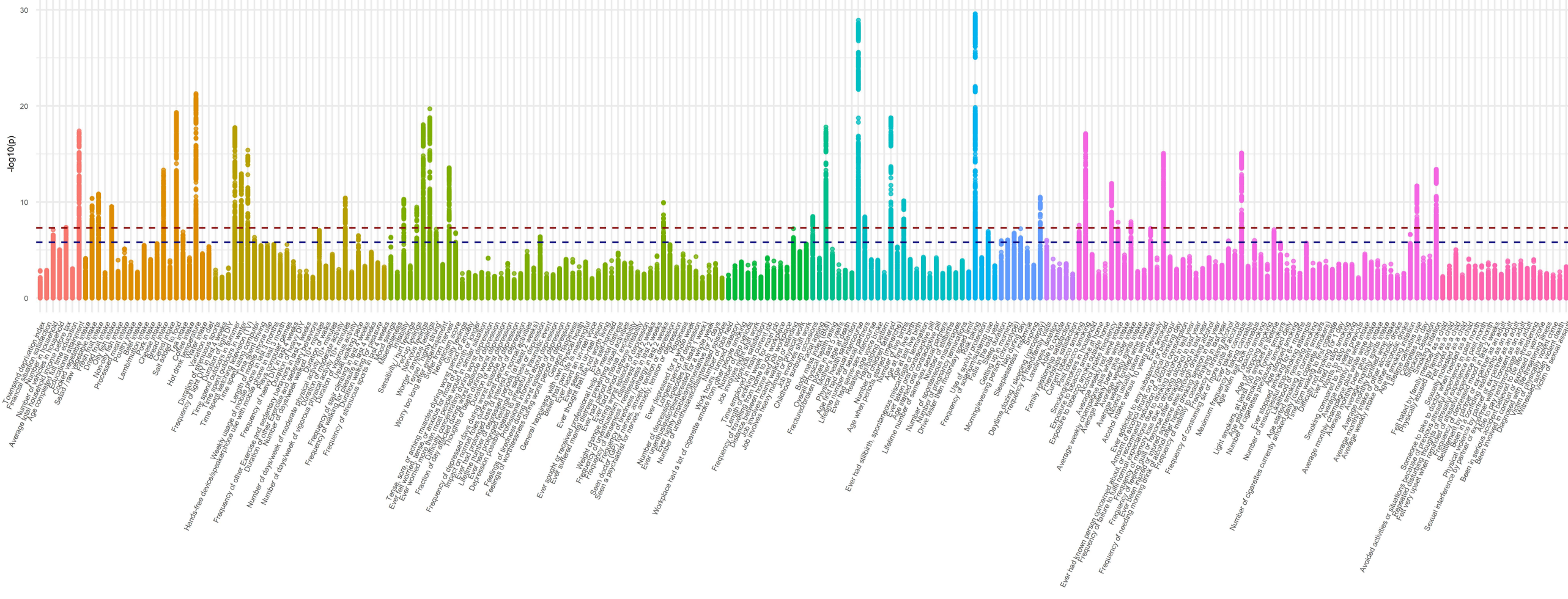


## Supplementary Figures

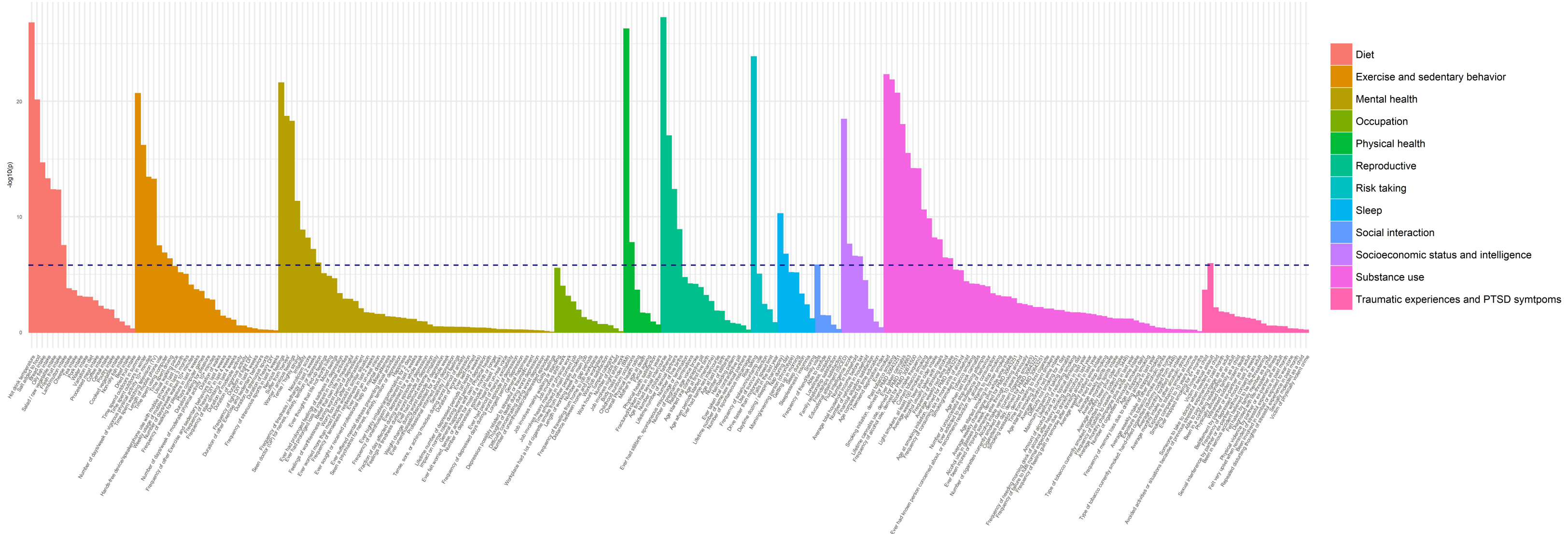
**Figure S1.** PheWAS results. Panel **a)** shows the associations of the SNP-based test for all 242 traits. The x-axis shows the traits (colored by trait category) and the y-axis the p-values of the association. Each dot represents a SNP association. SNPs exceeding the red horizontal line have a p-value significant at a genome-wide threshold of  $p=5E-08$ . The blue horizontal line represents the suggestive threshold of  $p=1.55E-06$ . Full SNP-based results are given in Supplementary Figure 1. Panel **b)** shows the results of the MAGMA gene-based test (for all 242 traits), with p-values on the y-axis. The red dotted line represents a threshold of  $p=2.62E-06$ . Panel **c)** shows the results of the MAGMA gene-based test (for all 242 traits), after additional correction for MSOA regions (birthplace and current address). p-values on the y-axis. The red dotted line represents a threshold of  $p=2.62E-06$ .

**Figure S2.** Number of significant trait associations per comparison gene (with SNP associations at  $p<5E-08$ ). On the right the CADM2 gene, the only one with more than 13 trait associations. See Tables S4 and S5 for the association results per comparison gene.

CADM2 PHEWAS - SNPs



- Cognition & SES
- Diet
- Exercise and sedentary behavior
- Mental health
- Occupation
- Physical health
- Reproductive
- Risk taking
- Sleep
- Social interaction
- Substance use
- Traumatic experiences and PTSD symptoms



- Diet
- Exercise and sedentary behavior
- Mental health
- Occupation
- Physical health
- Reproductive
- Risk taking
- Sleep
- Social interaction
- Socioeconomic status and intelligence
- Substance use
- Traumatic experiences and PTSD symptoms



