Supplemental methods

Monte Carlo sampling approach

We used LD-score regression implemented in Genomic SEM to obtain a 5x5 r_G matrix constructed from the two traits of interest plus the three SES indicators. This r_G matrix served as basis for the Genomic SEM models as shown in the main text figure 1. The unique elements of the r_G matrix are stored in a vector *mu*. In genomic SEM, variance of all estimates (factor loadings, residual variances, regression paths and correlations) are based on the variability of the r_G matrix. This variability is calculated duding LD score regression with the leave-one-chromosome-out jacknife method. That is, multivariate LD score regression r_G matrix is not only calculated for the full set of SNPs, but also 22 times each time leaving the SNPs on one chromosome out. Each of these rg matrices varies slightly around the full, 22 chromosome estimate. From these genetic (co)variance matrices the standard error of all h^2 and r_G estimates are calculated. In addition, the covariance between all estimates is calculated. Since a symmetric 5x5 matrix holds 5(5+1)/2=15 unique estimates, this means the it creates a 15x15 matrix with variance of the 15 estimates on the diagonal, and covariance between estimates on the off-diagonals. This 15x15 matrix is called *sigma*. Note that the covariance between estimates tends to be substantial. It is important to include this covariance in the modelling, because assuming that r_G estimation errors are independent will lead to substantial loss of statistical power and incorrect inference. Supplementary Figure 1 shows a graphical depiction of the estimated matrices and their elements, and the sampling procedure.

Armed with the point estimate vector *mu* and the covariance in matrix *sigma*, we used R function mvrnorm (MASS package) to create random samples that keeps all dependencies intact. Restructuring each sample back to an r_G matrix, we refitted the two models (that is, either with or without regressing out SES variance; see main text figure 1) and compared the estimates of h^2 and r_G between these two models. To establish significance of effects we counted the proportion of times an estimate was larger in the first compared to the second model (i.e., before and after partialling out SES variance).

Statistical source data for all figures, of the main text and Extended Data, can be found in the Supplementary Tables file.

$$\begin{bmatrix} h^2_{t1} & & & & \\ rg_{(t2,t1)} & h^2_{t2} & & & \\ rg_{(EA,t1)} & rg_{(EA,t2)} & h^2_{EA} & & \\ rg_{(TI,t1)} & rg_{(TI/,t1)} & rg_{(TI/,EA)} & h^2_{TI} & \\ rg_{(HI,t1)} & rg_{(HI,t1)} & rg_{(HI/,EA)} & rg_{(HI/,TI)} & h^2_{HI} \end{bmatrix}$$

$$\begin{bmatrix} h^2_{t1} & rg_{(t2,t1)} & rg_{(EA,t1)} & \dots & h^2_{HI} \end{bmatrix} = mu$$

$$\begin{bmatrix} \sigma^2_{h^2_{t1}} & & & & \\ \sigma^2_{rg_{(t2,t1)}h^2_{t1}} & \sigma^2_{rg_{(t2,t1)}} & & & \\ \sigma^2_{rg_{(EA,t1)}h^2_{t1}} & \sigma^2_{rg_{(EA,t1)}rg_{(t2,t1)}} & \sigma^2_{rg_{(EA,t1)}} & & \\ \vdots & \vdots & \vdots & \ddots & \\ \sigma^2_{h^2_{HI}h^2_{t1}} & \sigma^2_{h^2_{HI}rg_{(t2,t1)}} & \sigma^2_{h^2_{HI}rg_{(EA,t1)}} & \sigma^2_{rg_{(HI,t1)}h^2_{t1}} & \sigma^2_{h^2_{HI}} \end{bmatrix} = \text{sigma}$$

$$\begin{array}{cccccc} 1 & \sim h^2_{t1} & \sim rg_{(t2,t1)} & \sim rg_{(EA,t1)} & \dots & \sim h^2_{HI} \\ 2 & \sim h^2_{t1} & \sim rg_{(t2,t1)} & \sim rg_{(EA,t1)} & \dots & \sim h^2_{HI} \\ 3 & \vdots & \vdots & \vdots & \vdots & \vdots \end{array}$$

$$\begin{bmatrix} \sim h^2_{t1} & & & & \\ \sim rg_{(t2,t1)} & \sim h^2_{t2} & & & \\ \sim rg_{(EA,t1)} & \sim rg_{(EA,t2)} & \sim h^2_{EA} & & \\ \sim rg_{(TI,t1)} & \sim rg_{(TI/,t1)} & \sim rg_{(TI/,EA)} & \sim h^2_{TI} & \\ \sim rg_{(HI,t1)} & \sim rg_{(HI,t1)} & \sim rg_{(HI/,EA)} & \sim rg_{(HI/,TI)} & \sim h^2_{HI} \end{bmatrix}$$

Supplementary Figure 1. Steps in producing random samplings of the LD-score regression SNP-h^2 and r_G matrix. The 5x5 r_G matrix is restructured into 1x15 vector mu. Variability of the estimates as obtained in LD-score regression using a leave-one-chromosome-out jackknife method are restructured into 15x15 matrix sigma, which holds the standard error of the 15 unique estimates in h^2 and r_G on the diagonal, and the covariance between these estimates on the off-diagonals. These are entered into mvrnorm to obtain 1000 row vectors. Finally, each row of 120 correlated samples is restructured back into a symmetric 15x15 r_G matrix, representing a resampled version of the matrix. This matrix is then used in the same analyses as described in the methods.