

## *Supplementary Material*

### **Ageing-dependent genetic effects associated to ADHD predict longitudinal changes of ventricular volumes in adulthood**

#### **1 Supplementary Tables and Figures**

##### **1.1 Supplementary Tables**

**Table S1.** Full summary statistics for all SNPs tested. SNPs are LD independent ( $r^2 < 0.1$ ), and are merged into one locus when located with a distance less than 400kb. The location (chromosome [Chr] and base position [BP]), alleles (A1, A2), allele frequency (A1 freq), odds ratio (OR) of the effect with respect to A1, and association P-value of the index variant are given, along with genes within 50kb of the credible set for the locus.

**Table S2.** Full summary descriptive of brain structures included in the study. Means, standard deviations (SD), Median, and ranges values are shown.

**Table S3.** Results longitudinal design. Model: SNP\*Age. Sample: All sample (N=3,200 individuals, 8,468 observations). Date and time of computation, outcome, model adjusted, as well as, effects (Beta1, Beta2), standard deviation (SE1, SE2), T-statistics (T1, T2) and p-values (P1, P2) are shown for each spline.

**Table S4.** Results longitudinal design. Model: Genetic main effects. Sample: All sample (N=3,200 individuals, 8,468 observations). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

**Table S5.** Results longitudinal design. Model: SNP\*Age. Sample:  $\geq 70$  years old (N=900 individuals, 2,084 observations). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

**Table S6.** Results longitudinal design. Model: Genetic main effects. Sample:  $\geq 70$  years old (N=900 individuals, 2,084 observations). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

**Table S7.** Results cross-sectional design. Model: SNP\*Age. Sample: All sample (N=3,200 individuals). Date and time of computation, outcome, model adjusted, as well as, effects (Beta1, Beta2), standard deviation (SE1, SE2), T-statistics (T1, T2) and p-values (P1, P2) are shown for each spline.

**Table S8.** Results cross-sectional design. Model: Genetic main effects. Sample: All sample (N=3,200 individuals). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

**Table S9.** Results cross-sectional design. Model: SNP\*Age. Sample:  $\geq 70$  years old (N=900 individuals). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

**Table S10.** Results cross-sectional design. Model: Genetic main effects. Sample:  $\geq 70$  years old (N=900 individuals). Date and time of computation, outcome, model adjusted, as well as, effect (Beta), standard deviation (SE), T-statistic (T) and p-value (P) are shown.

## 1.2 Supplementary Figures

**Supplementary Figure 1.** Heatmap showing pair correlations across brain structures, with blue color indicating positive correlations and red color indicating negative correlations.