

## Supplementary Figure

**Fig. S1.** Phenotypic correlations among the 24 HASV traits.

**Fig. S2.** Density plot of HASV phenotypes and residuals.

**Fig. S3.** Manhattan plots of GWAS results for 12 left cerebral hemispheres HASVs.

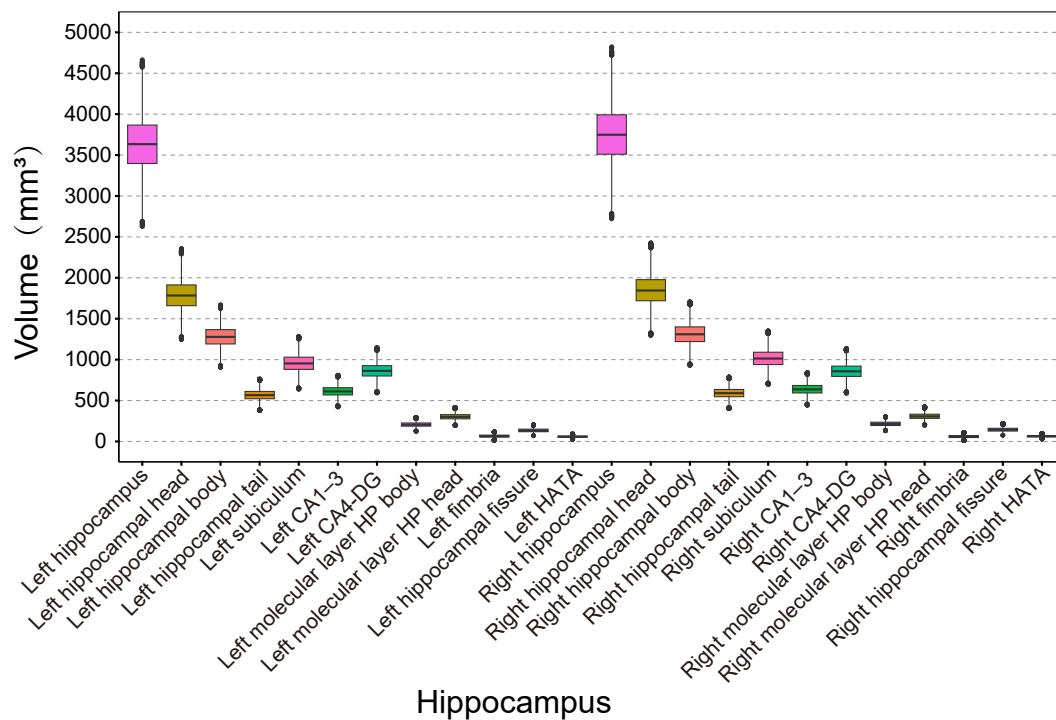
**Fig. S4.** Manhattan plots of GWAS results for 12 right cerebral hemispheres HASVs.

**Fig. S5.** Heatmap of pleiotropic gene distribution of each HASV using four methods.

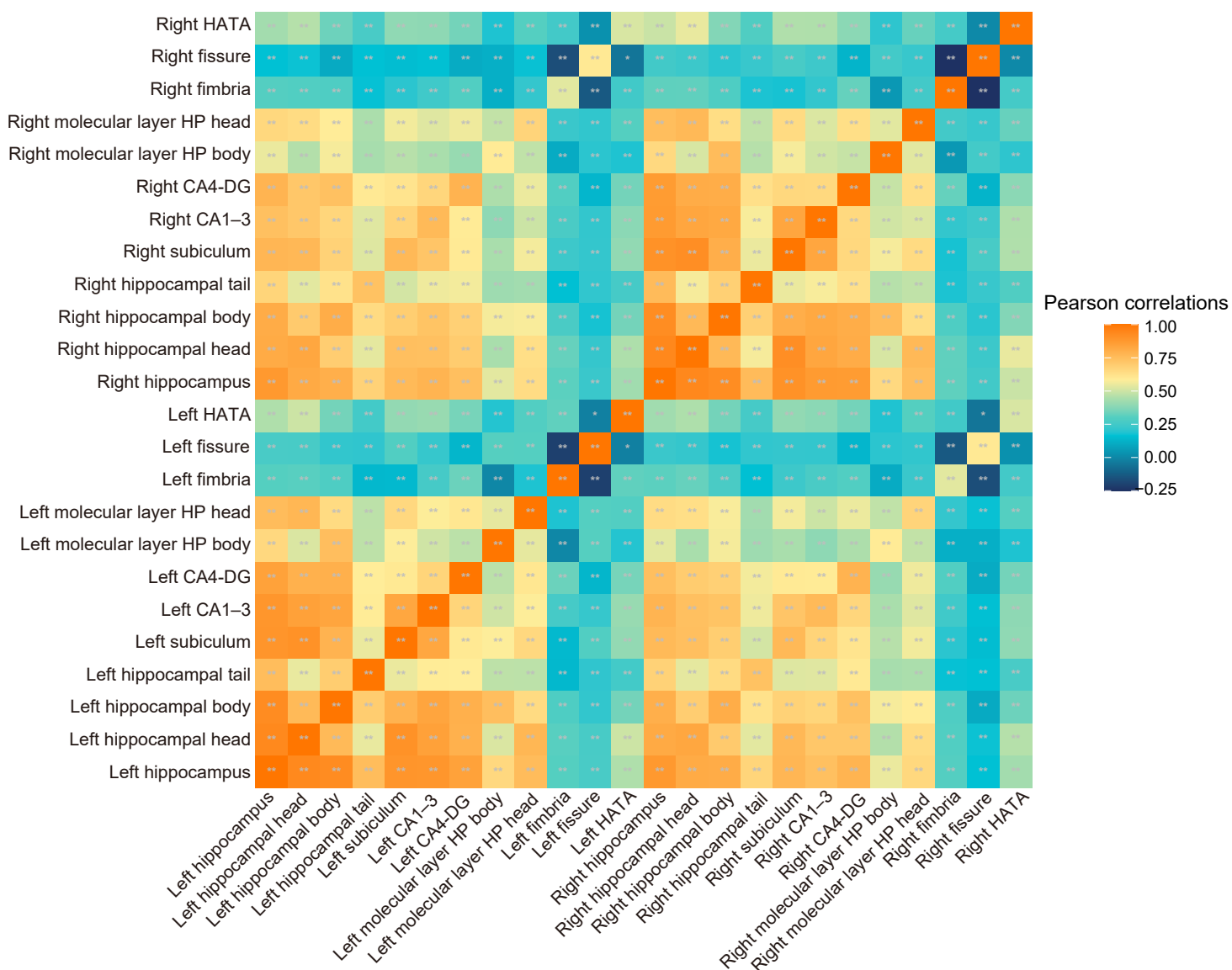
**Fig. S6.** Genetic correlations between 24 HASV traits and 97 other regional brain volumes.

Fig. S1

A



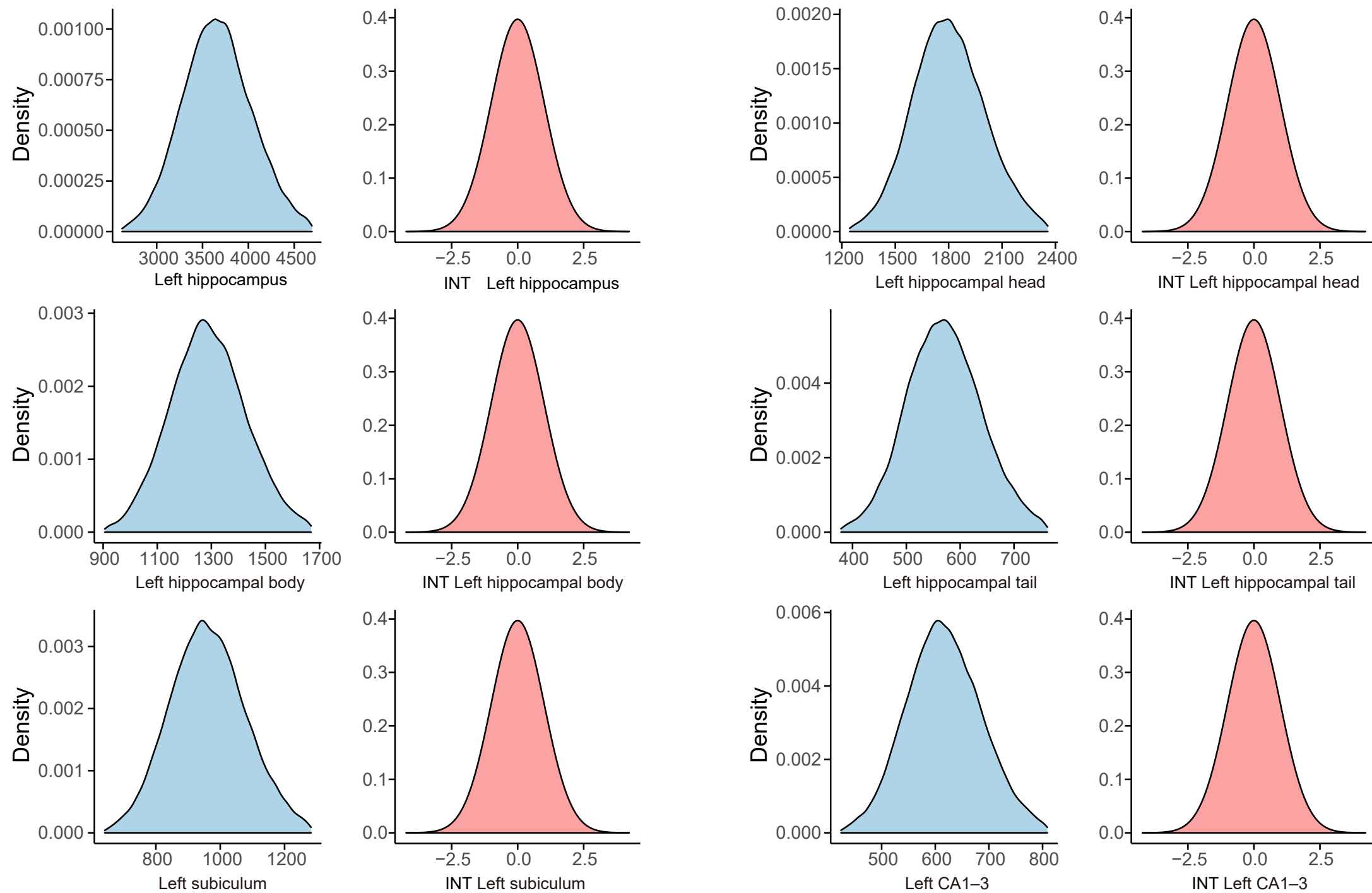
B



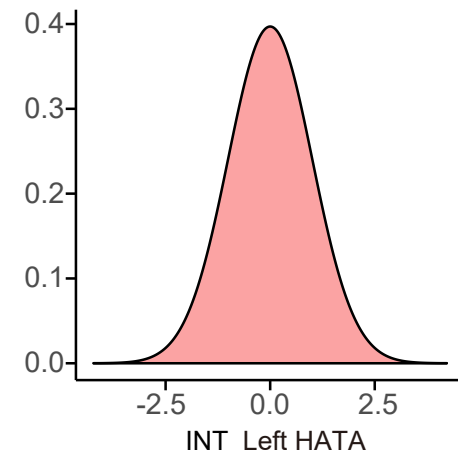
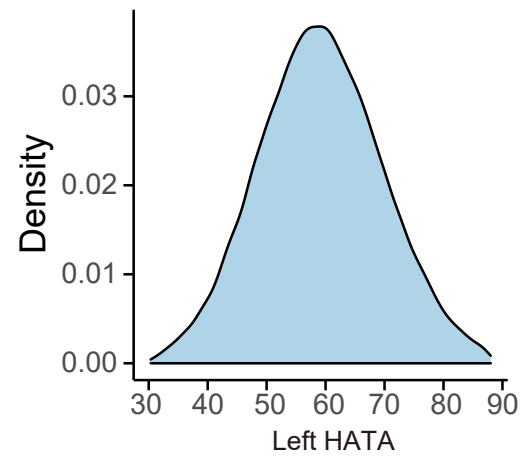
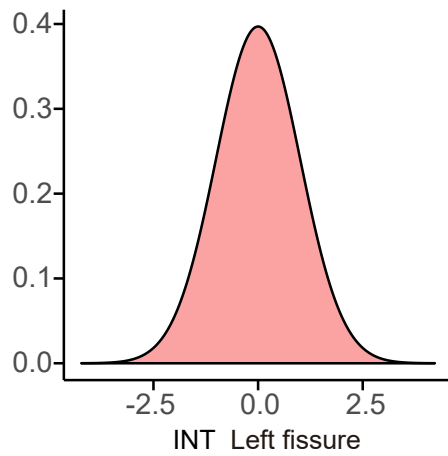
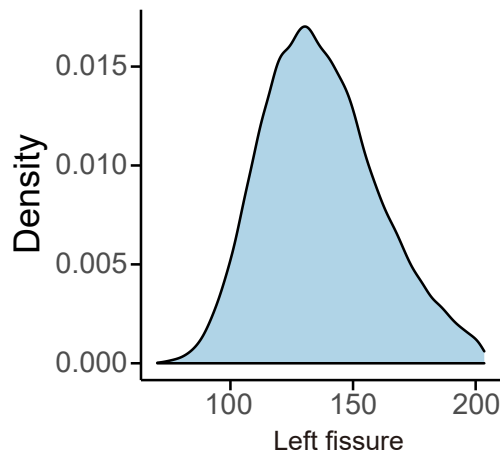
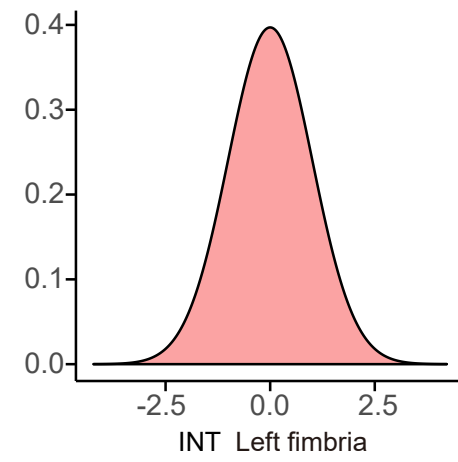
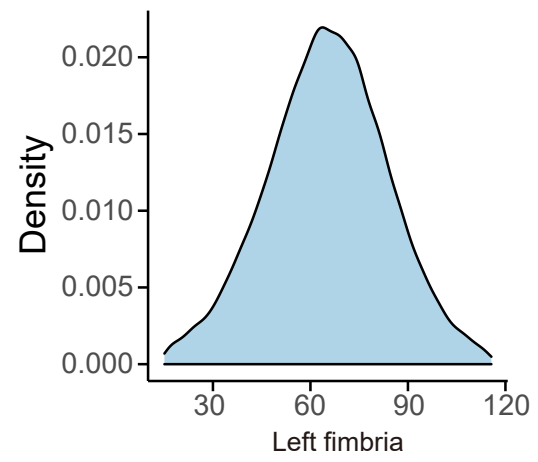
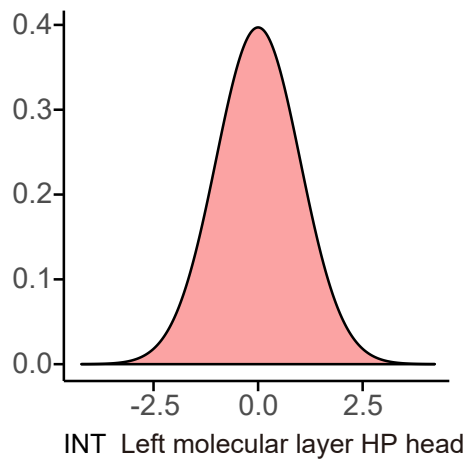
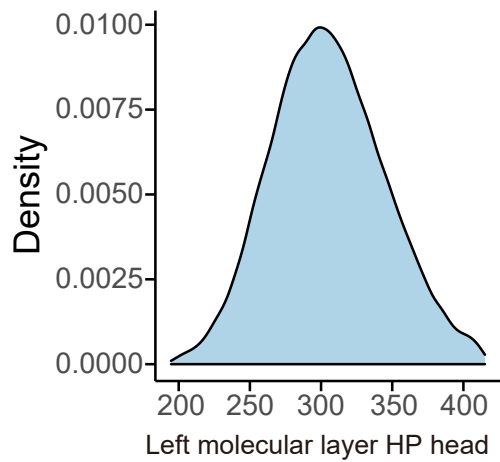
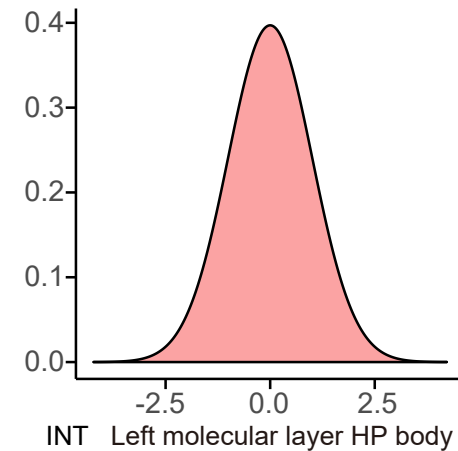
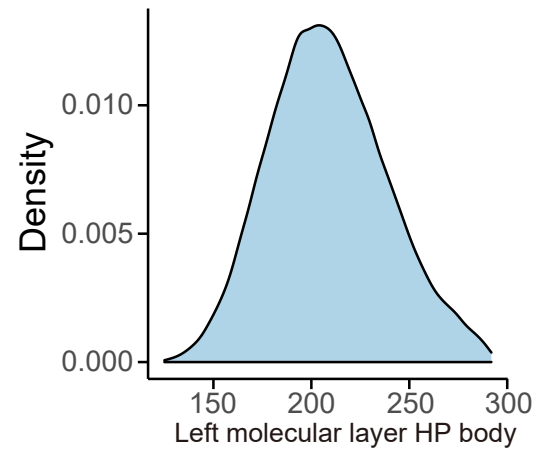
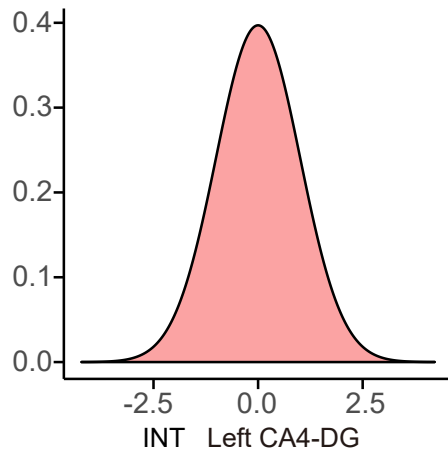
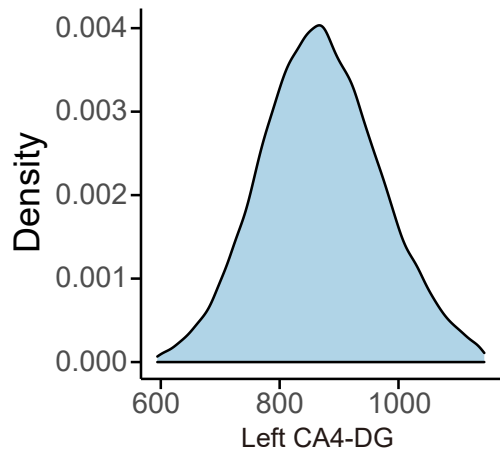
**Fig. S1. Phenotypic correlations among the 24 HASV traits**

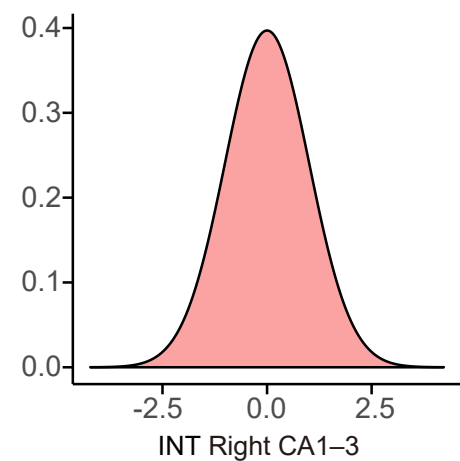
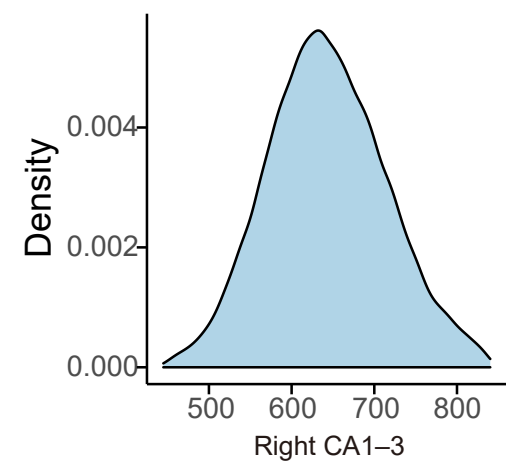
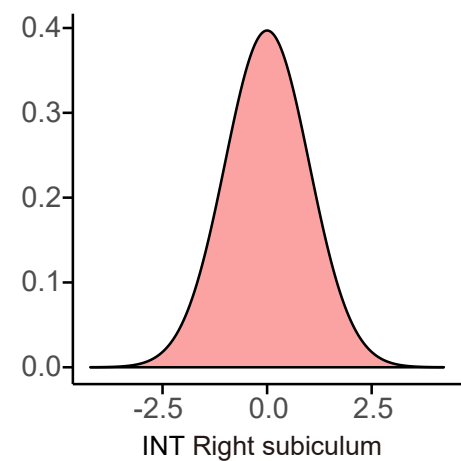
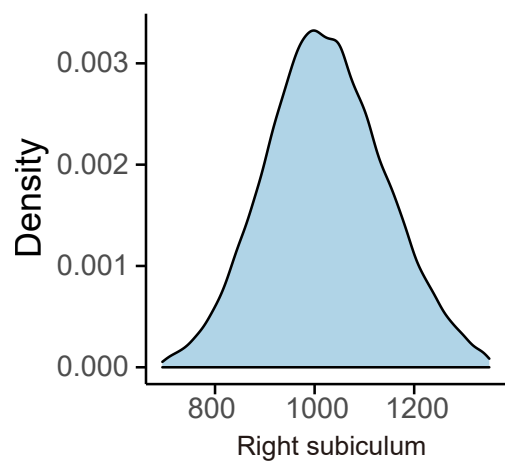
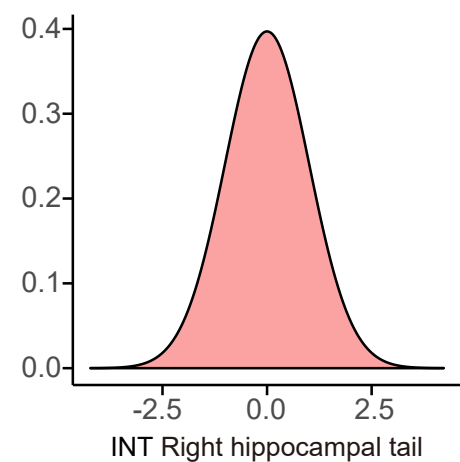
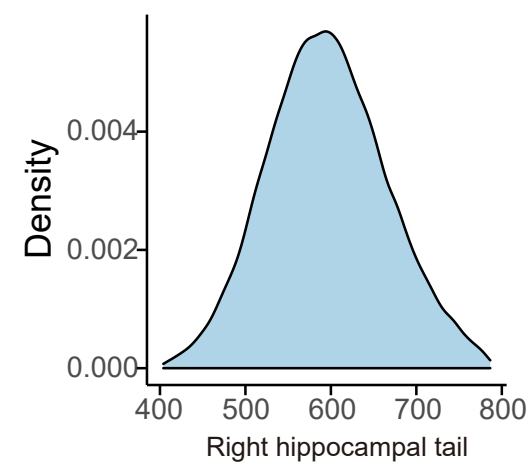
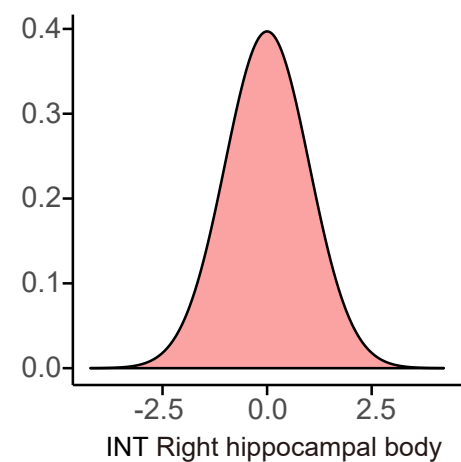
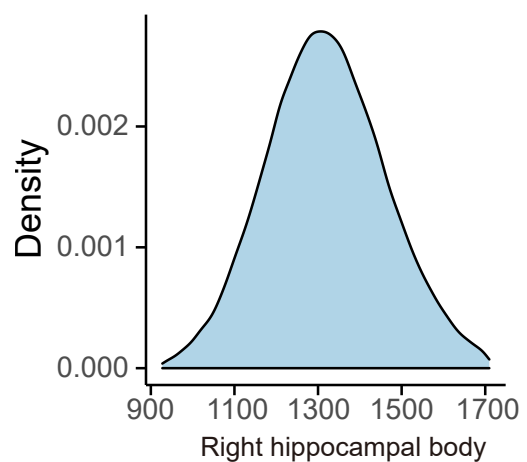
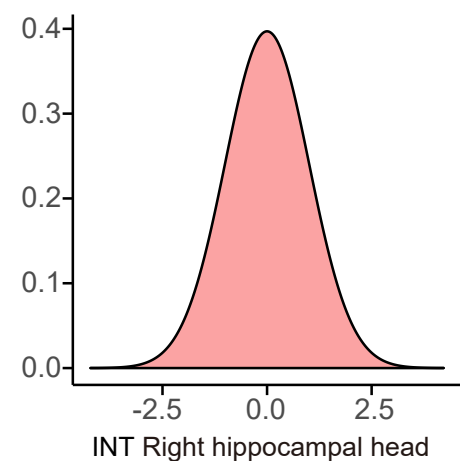
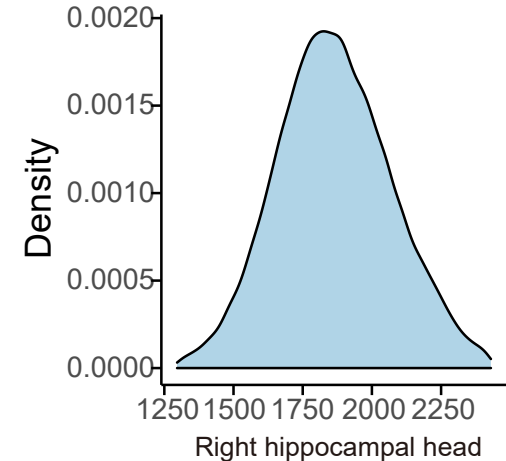
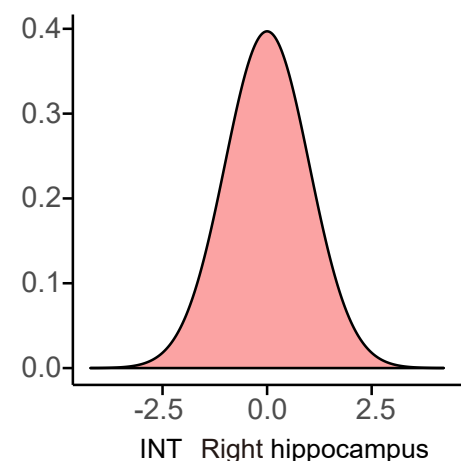
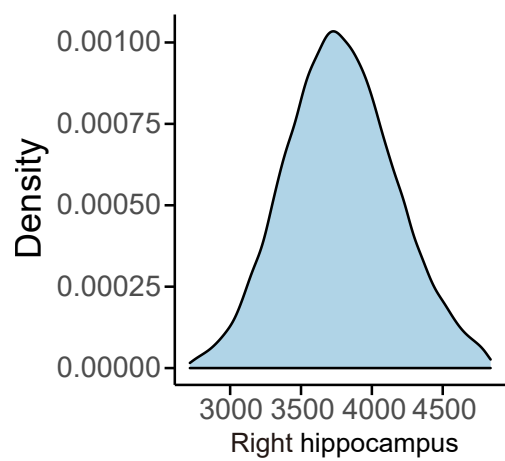
(A) These box charts illustrate the volumes ( $\text{mm}^3$ ) distribution for each of the 24 hippocampal and subfield volumes (HASV) traits. Every box shows the 25th–75th percentile; the line shows the median; the whiskers show  $1.5 \times \text{IQR}$  (interquartile range). (B) Pearson correlations between 24 HASV traits phenotypes. Degree of correlation is indicated by color legend, ranging from -1 to +1. Asterisk denotes statistically significant differences, \*  $P < 0.05$ ; \*\*  $P < 1.81 \times 10^{-4}$  ( $0.05/276$ , Bonferroni corrected).

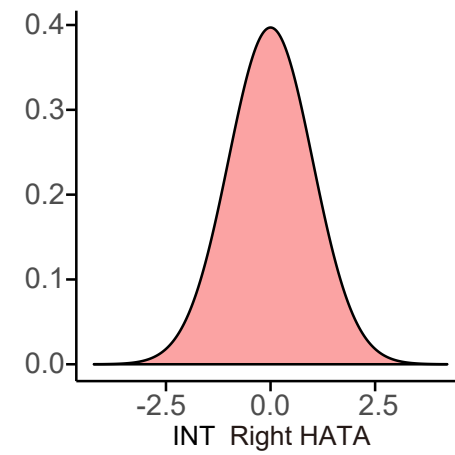
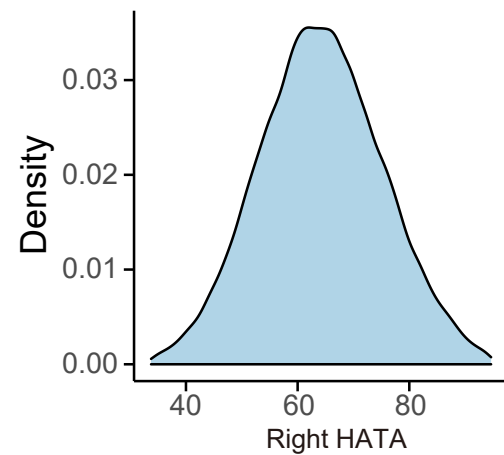
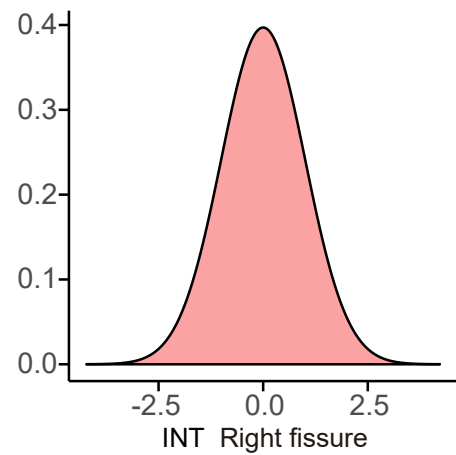
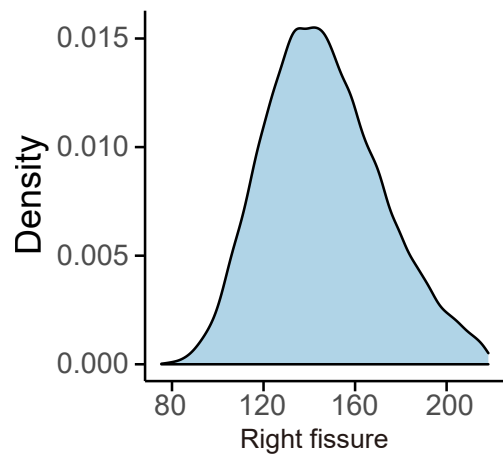
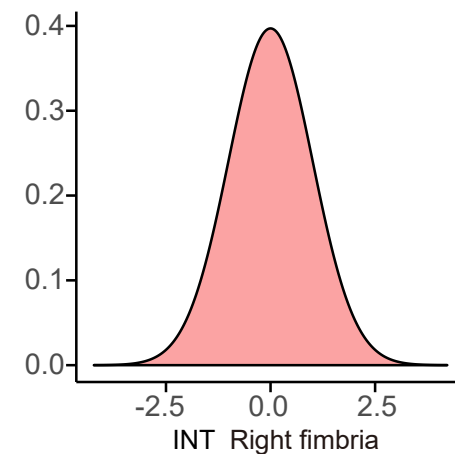
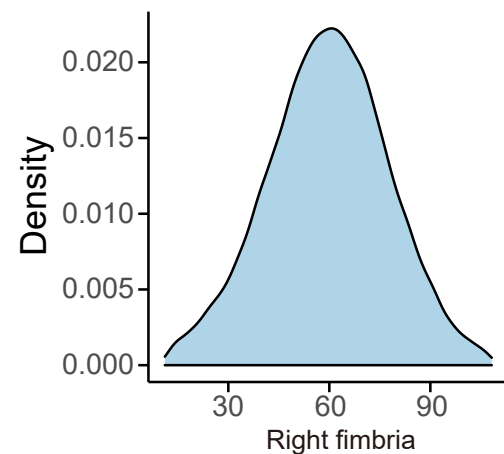
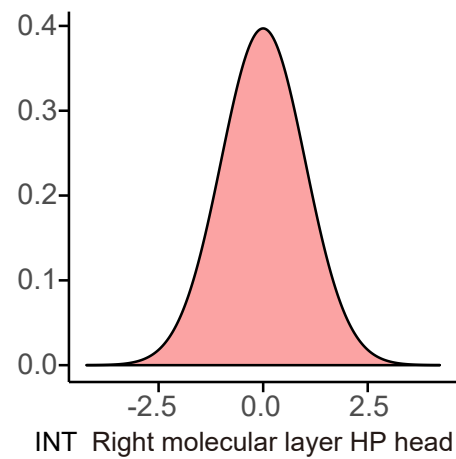
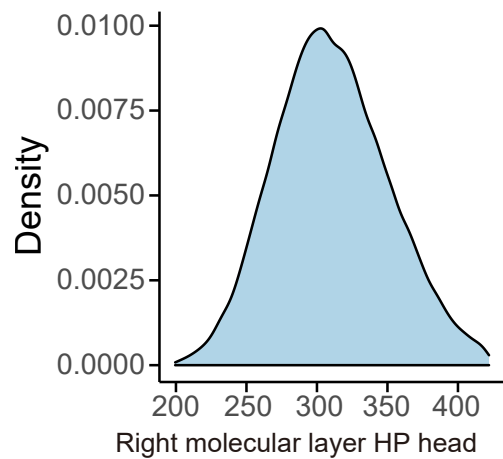
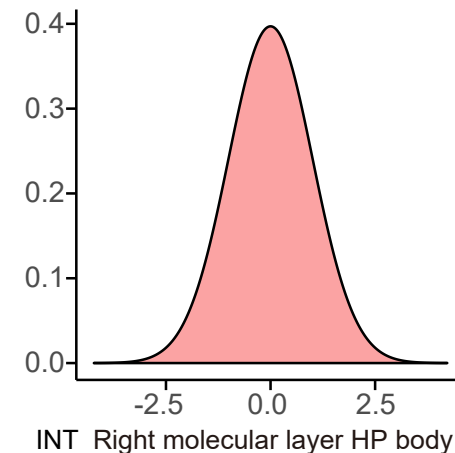
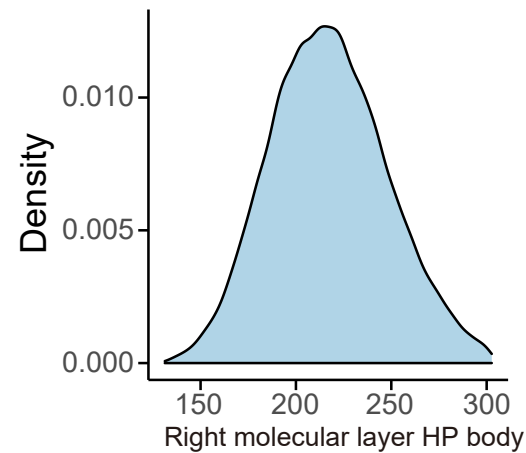
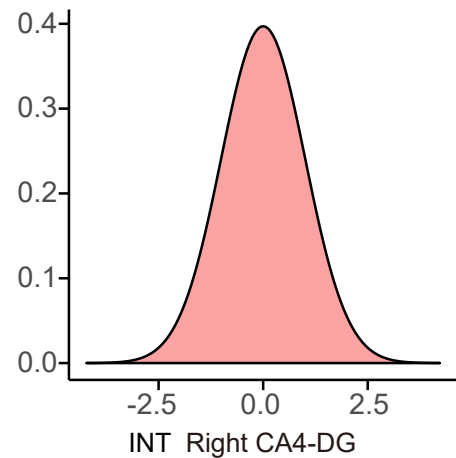
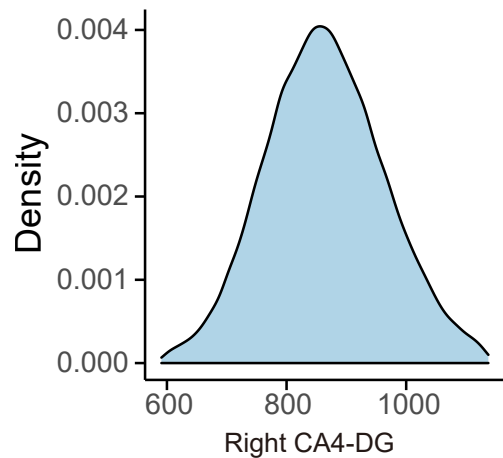
Fig. S2







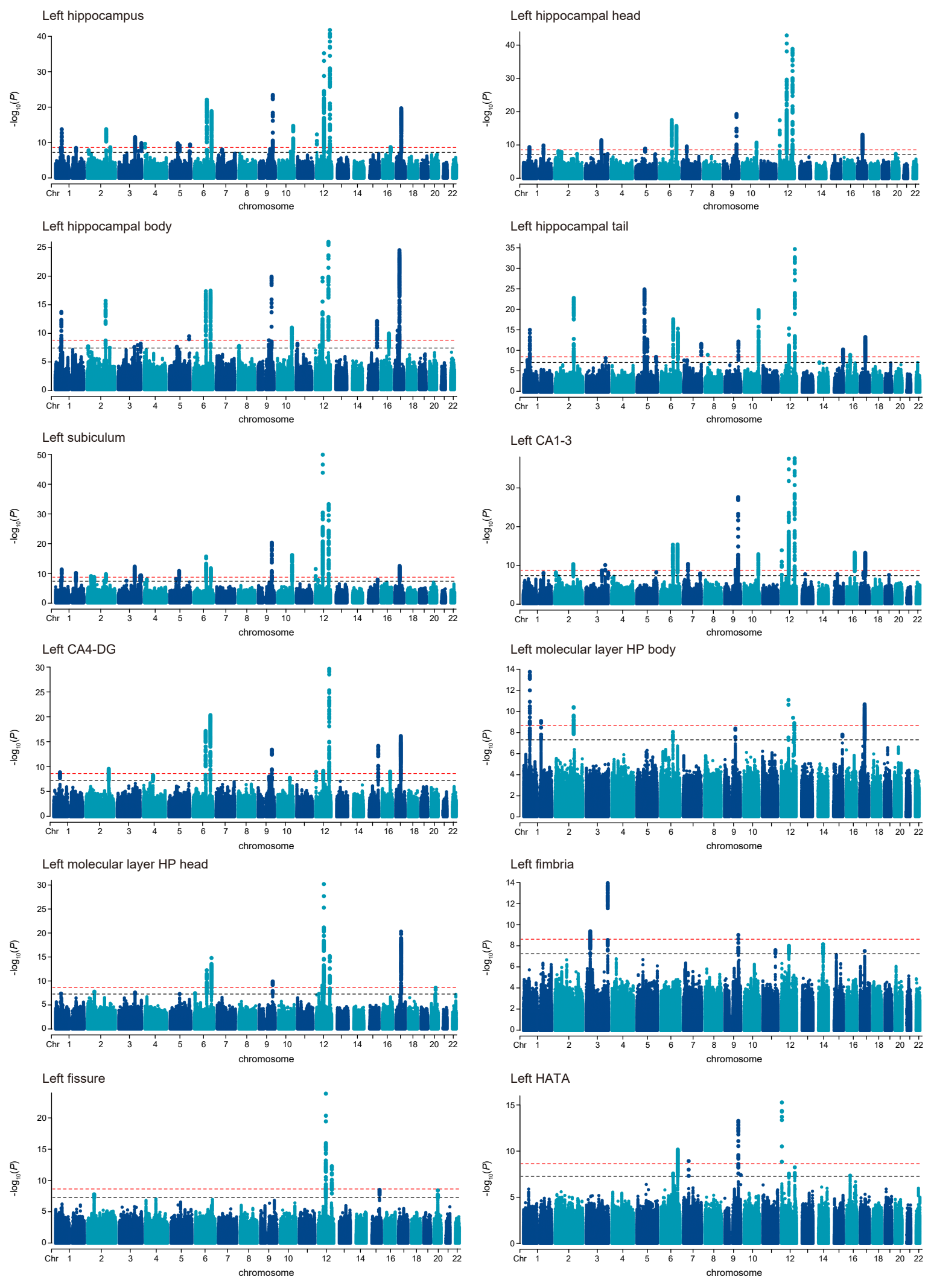




**Fig. S2. Density plot of HASV phenotypes and residuals.**

Density plot of 24 HASVs phenotypes for left and right cerebral hemispheres. The blue histograms show the distribution of HASVs phenotypes. The red histograms show the distribution of residuals which were rank-based inverse normal transformed (INT) after regressing against the variables (including sex, age, body mass index, imaging center).

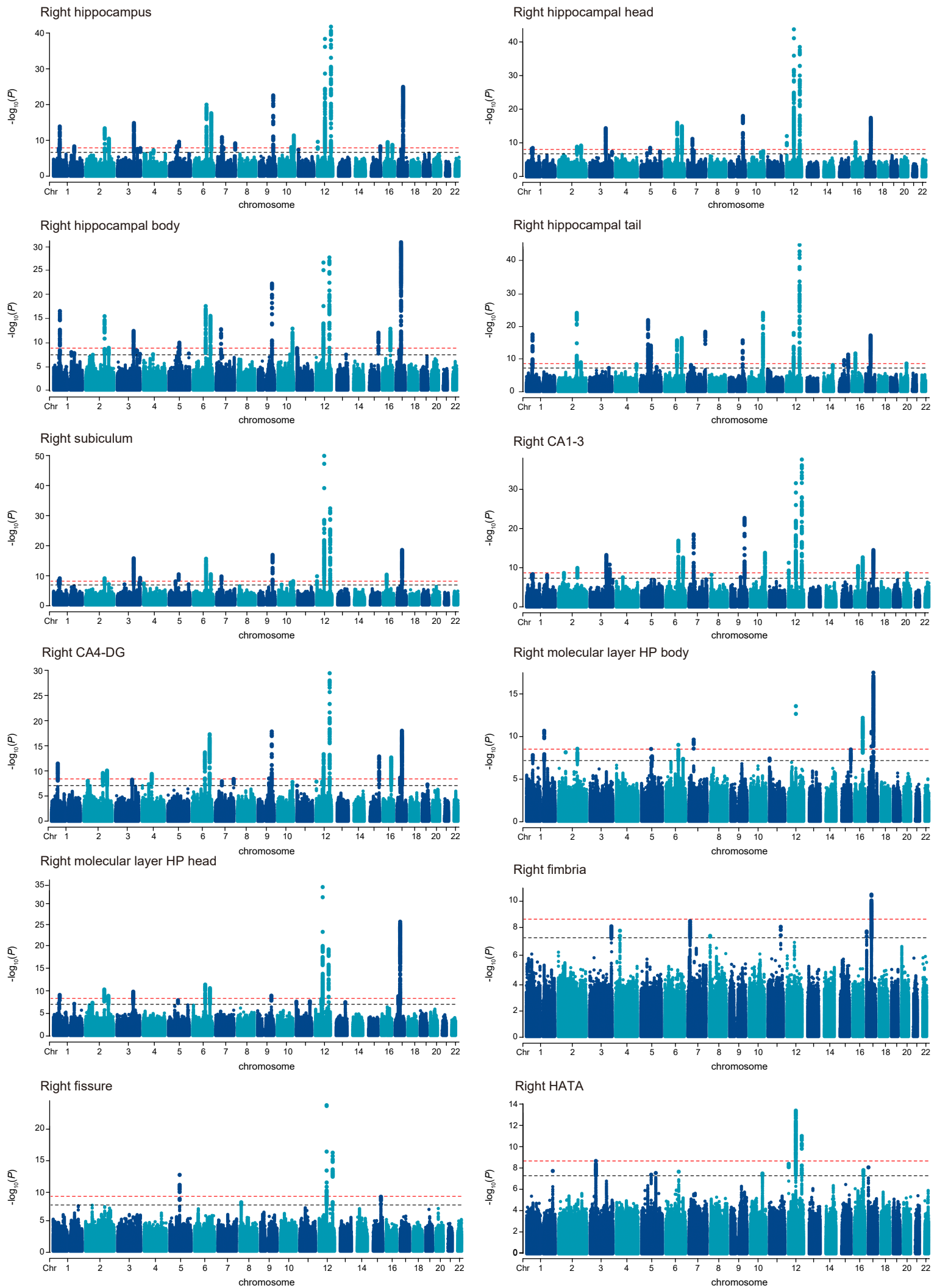
Fig. S3



**Fig. S3. Manhattan plots of GWAS results for 12 left cerebral hemispheres HASVs**

Manhattan plots show the chromosomal position on the x-axis and the  $-\log_{10}(P)$  on the y-axis for each HASV trait. The black dashed line indicates the genome-wide significance threshold at  $P < 5 \times 10^{-8}$ , while the red dashed line represents the significance level after additionally corrected for the 24 HASV traits ( $P < 2.1 \times 10^{-9}$ ).  $P$  values are two sided based on the chi-squared test statistics in BOLT-LMM software.

Fig. S4



**Fig. S4. Manhattan plots of GWAS results for 12 right cerebral hemispheres HASVs.**

Manhattan plots show the chromosomal position on the x-axis and the  $-\log_{10}(P)$  on the y-axis for each HASV trait. The black dashed line indicates the genome-wide significance threshold at  $P < 5 \times 10^{-8}$ , while the red dashed line represents the significance level after additionally corrected for the 24 HASV traits ( $P < 2.1 \times 10^{-9}$ ).  $P$  values are two sided based on the chi-squared test statistics in BOLT-LMM software.

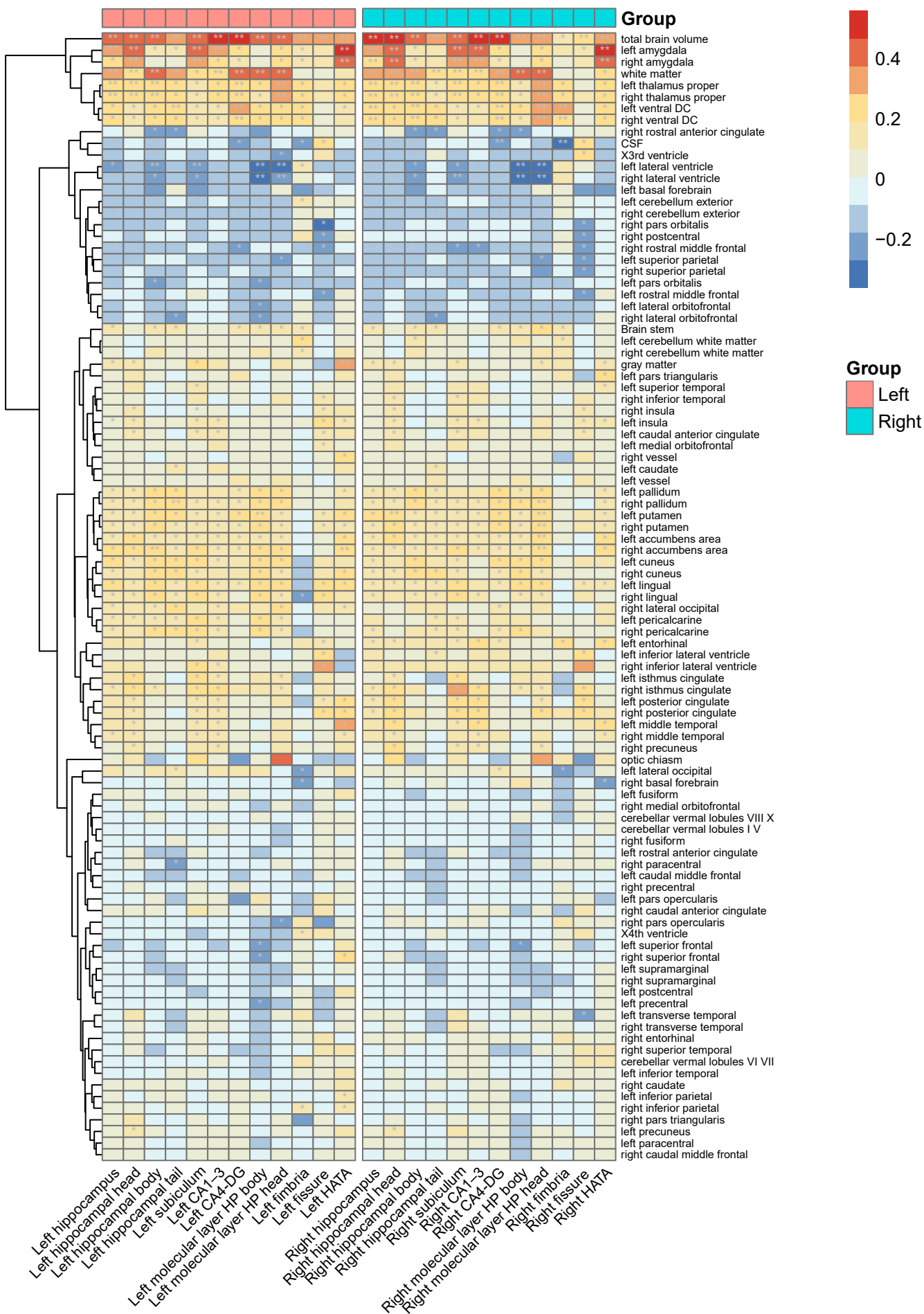




**Fig. S5. Heatmap of pleiotropic gene distribution of each HASV using four methods**

The times of the gene annotated by four methods (Nearest Gene, eQTL, MAGMA, TWAS) are indicated by the color legend. For example, the *HRK* gene can be annotated by the four methods in Left hippocampus. The maximum number of each cell is 4. Further details can see in Supplementary Table 9.

Fig. S6



**Fig. S6. Genetic correlations between 24 HASV traits and 97 other regional brain volumes.**

Genetic correlations between 24 HASV traits (X-axis) and 97 other regional brain volumes (Y-axis). Genetic correlation was estimated using the LDSC method. Asterisk denotes statistically significant differences \*  $P < 0.05$ ; \*\*  $P < 2.15 \times 10^{-5}$  (0.05/2328, Bonferroni corrected)