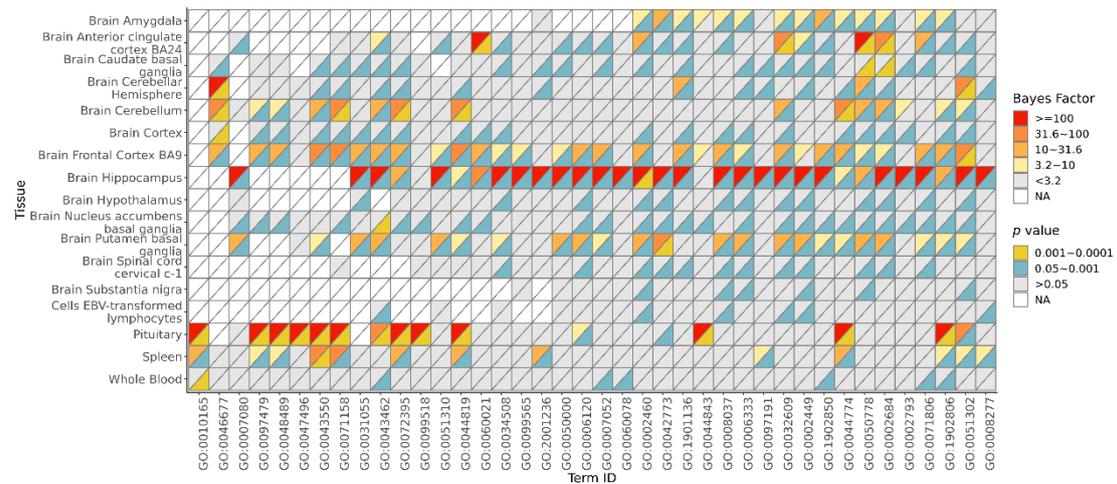


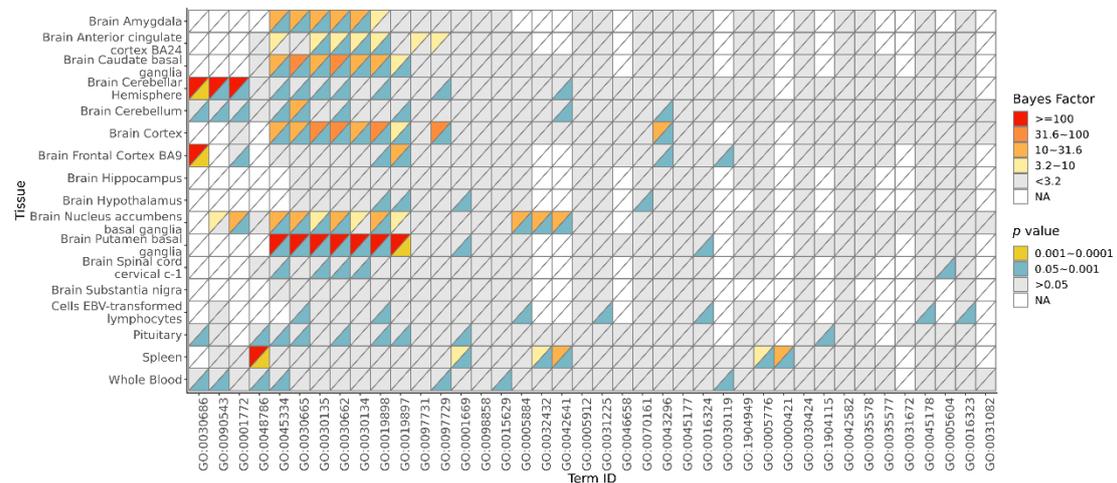
## Supplemental Figure 6. GIGSEA pathway analysis of the genes relevant to cluster headache GWAS variants.

We employed the weighted linear regression model of the GIGSEA with empirical p-values incorporating 1,000 permutations for (A-C) Gene Ontology (GO) ((A)GOBP (B)GOCC (C)GOMF), (D) Kyoto Encyclopedia of Genes and Genomes (KEGG), and (E) Reactome (REAC). The Bayes factor was used to correct the multiple hypothesis testing.

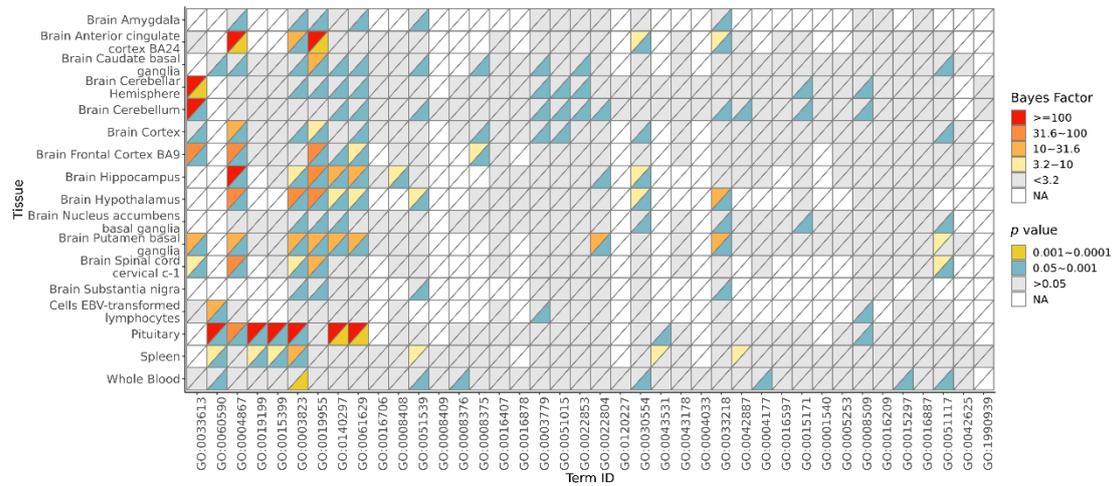
A



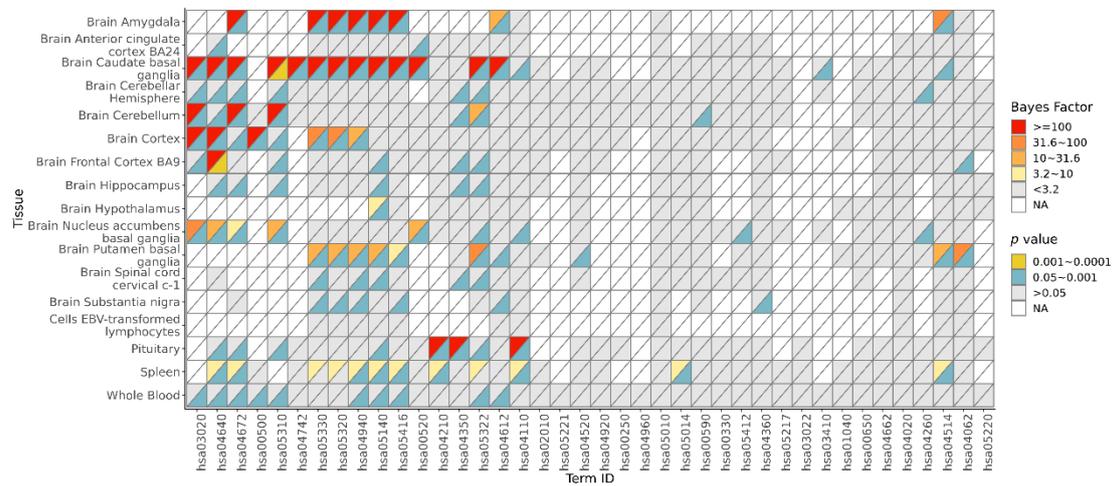
B



C



D



E

