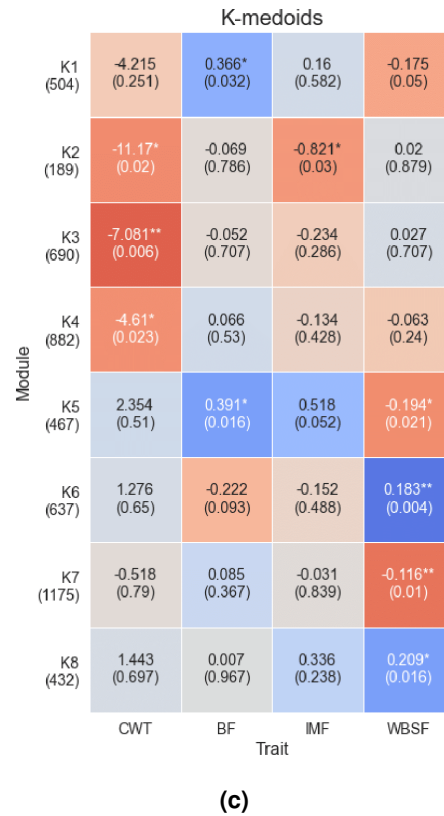
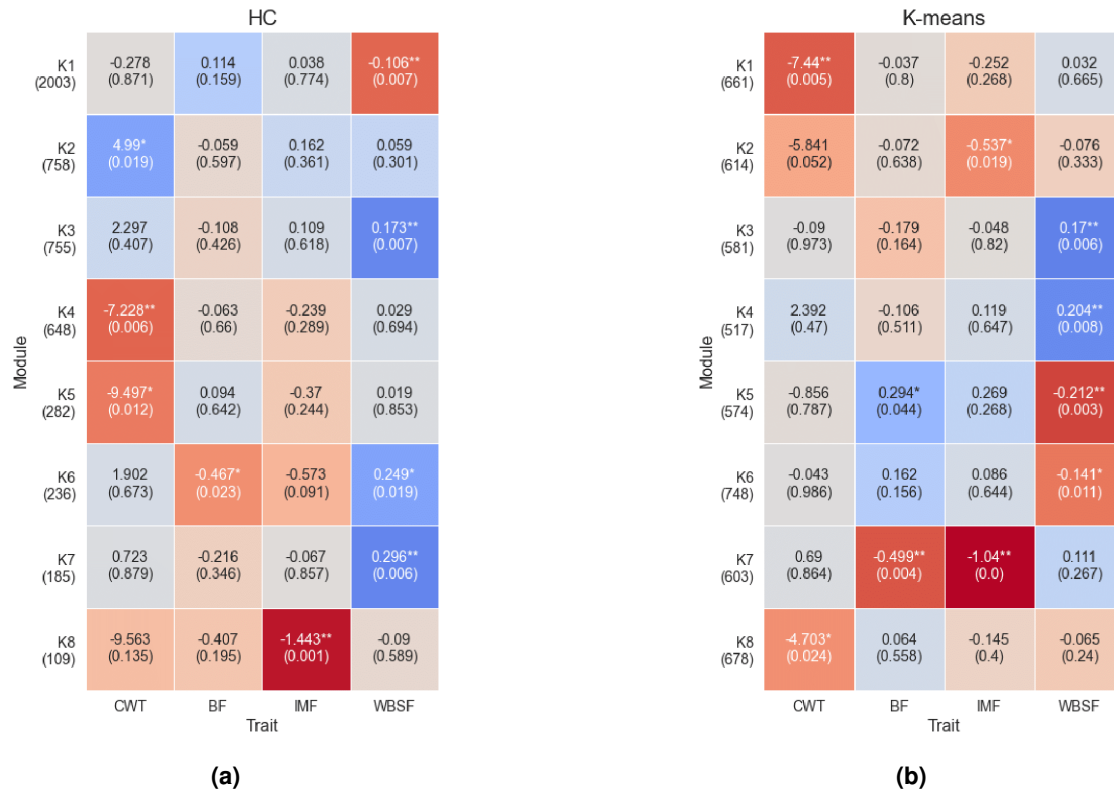




S1 Fig. The DEM signals of modules defined by baseline methods: (a) hierarchical clustering, (b) K-means, (c) K-medoids. The y-axis shows the module names and numbers of genes within each module. The x-axis shows the complex traits. The numbers in each cell are regression coefficients (no parentheses) and the regression p-values (in parentheses). Red and blue indicate negative and positive coefficients, respectively. * $p < 0.05$, ** $p < 0.01$.