Four datasets downloaded from GEO

Common genes extracted (6643)

FC top 100 (20 genes)

T test top 100 (10 genes)

Marginal effect (126)

Joint effect (56)

Lasso penalized estimate (56)

FDR0.001 (121 genes)

GWAS-reported susceptibility genes (91)

Overlapped genes (10)

PPI analysis

GO analysis

**S1 Fig. Flowchart of Data Processing and Data Analyses**

Note: the numbers in brackets are numbers of genes selected by the corresponding analysis methods.