Supplementary Figure 2. Analysis of CFM-associated variants in the *SHROOM3* region. This figure illustrates the variants linked to CFM within the *SHROOM3* gene region. The logistic regression *P*-values have been adjusted for population stratification, utilizing the first 20 eigenvectors from principal component analysis as covariates. The plot specifically focuses on variants exhibiting a minor allele frequency greater than 0.05.