

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Description of GWAS summary statistics used in LDSR.

File Name: Supplementary Data 2

Description: Description of GWAS summary statistics used in MTAG.

File Name: Supplementary Data 3

Description: Estimate of cross-trait genetic correlation of PSC among potential comorbid traits.

File Name: Supplementary Data 4

Description: MTAG-identified PSC-specific summary statistics for SNPs with  $P < 5 \times 10^{-8}$ .

File Name: Supplementary Data 5

Description: Genomic risk loci from MTAG-identified PSC-specific GWAS using FUMA GWAS.

File Name: Supplementary Data 6

Description: Prioritized genes from MTAG PSC-specific GWAS by functional annotation and mapping of genomic risk loci of the European panels using FUMA GWAS.

File Name: Supplementary Data 7

Description: Immune-related genes prioritized by functional annotation and mapping of genomic risk loci of the European panels from MTAG PSC-specific GWAS using InnateDB.

File Name: Supplementary Data 8

Description: Description of headers for Supplementary Table 9

File Name: Supplementary Data 9

Description: Functional annotation of independent significant SNPs in genomic risk loci of the European panels from MTAG PSC-specific GWAS using FAVOR.

File Name: Supplementary Data 10

Description: Prediction of regulatory potential for MTAG-identified PSC-specific variants using MACIE.

File Name: Supplementary Data 11

Description: Fine-mapping of PSC 7 novel risk loci and 1 new independent variant at the reported risk locus using FINEMAP and GCTA-COJO.

File Name: Supplementary Data 12

Description: Colocalization results between MTAG-identified GWAS and eQTL signals (GTEx v8) calculated by coloc ( $PP.H4 > 0.8$ ).

File Name: Supplementary Data 13

Description: Enrichment results amongst 406 prioritized genes using STRING protein-protein interaction networks.

File Name: Supplementary Data 14

Description: Enrichment results with  $FDR < 0.05$  amongst 406 prioritized genes using DAVID Bioinformatics Resources.

File Name: Supplementary Data 15

Description: Pathway enrichment results for each MTAG-identified three prioritized gene (MANBA, IRF5, NKX2-3) using STRING protein-protein interaction networks.

File Name: Supplementary Data 16

Description: PSC candidate genes for drug repurposing using network-based proximity.

File Name: Supplementary Data 17

Description: Network-based proximity between drugs and PSC candidate genes for drug repurposing.

File Name: Supplementary Data 18

Description: Gene Table mapped to DrugBank Database using 406 prioritized genes by functional annotation, position, eQTL, and chromatin interaction mapping listed in Supplementary Table 6 via FUMA.