

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Psoriasis GWAS summary statistics used in this study.

File Name: Supplementary Data 2

Description: Estimated parameters of the Duffy's adjusting method for UK Biobank and 23andMe.

File Name: Supplementary Data 3

Description: List of independent significant SNP from GCTA-COJO.

File Name: Supplementary Data 4

Description: Psoriasis summary statistics of sample sizes and independent loci counts.

File Name: Supplementary Data 5

Description: Pathway enrichment of MAGMA gene-set analysis from psoriasis GWAS.

File Name: Supplementary Data 6

Description: LAVA local genetic correlation.

File Name: Supplementary Data 7

Description: Psoriasis susceptibility loci reported in previous GWAS located in LAVA-significant blocks.

File Name: Supplementary Data 8

Description: LDSC-SEG result for gene expression.

File Name: Supplementary Data 9

Description: LDSC-SEG result for chromatin modification.

File Name: Supplementary Data 10

Description: Phenotypes used in the genetic correlation analysis.

File Name: Supplementary Data 11

Description: Differential gene expression result for major cell types.

File Name: Supplementary Data 12

Description: Differential gene expression between PP, PN, and NS tissues for major cell types.

File Name: Supplementary Data 13

Description: Differential gene expression result for cell subtypes.

File Name: Supplementary Data 14

Description: scDRS result of 55 cell subtypes.

File Name: Supplementary Data 15

Description: Comparison of scDRS heterogeneity and scDRS scores between lesional and non-lesional cells.

File Name: Supplementary Data 16

Description: Gene prioritization result.

File Name: Supplementary Data 17

Description: SMR and HEIDI analysis in four eQTL datasets.

File Name: Supplementary Data 18

Description: Known drugs for prioritized genes.

File Name: Supplementary Data 19

Description: Cell subtype-specific module enrichment.

File Name: Supplementary Data 20

Description: Associated pathways with differential connectivity between normal and lesional samples in MYE-M2 module genes.

File Name: Supplementary Data 21

Description: Pairwise module correlations.

File Name: Supplementary Data 22

Description: Pathway enrichment of KER-M1 module genes.

File Name: Supplementary Data 23

Description: Pathway enrichment of KER-M3 module genes.

File Name: Supplementary Data 24

Description: Pathway enrichment of MYE-M2 module genes.

File Name: Supplementary Data 25

Description: Pathway enrichment of MYE-M5 module genes.

File Name: Supplementary Data 26

Description: Pathway enrichment of T-M1 module genes.

File Name: Supplementary Data 27

Description: Demographics of transcriptomic samples used in this study.