## **Description of Additional Supplementary Files**

File Name: Supplementary Data 1 Description: **GWAS studies used in the analysis.** 

File Name: Supplementary Data 2

Description: **LD score regression results.** Genetic correlation p-values (two-sided) from LD score regression genetic correlation analysis. Standard errors of LD score regression genetic correlations. LDscore regression covariance matrix (on the liability scale).

File Name: Supplementary Data 3

Description: **Significant genomic regions in latent factors and traits GWAS.** Genomic SEM (WLS estimation method) was used to conduct the GWAS.

File Name: Supplementary Data 4 Description: **Conditionally independent loci.** 

File Name: Supplementary Data 5 Description: Colocalization of loci among factors and immune diseases GWAS.

File Name: Supplementary Data 6

Description: **Significant KEGG pathways enriched in latent factors.** P-values were calculated with the hypergeometric test and corrected for multiple testing with the gprofiler-g:SCS method.

File Name: Supplementary Data 7

Description: **Significant GO terms enriched in latent factors.** P-values were calculated with the hypergeometric test and corrected for multiple testing with the gprofiler-g:SCS method.

File Name: Supplementary Data 8 Description: Colocalization results between immune latent factors and eQTLs.

File Name: Supplementary Data 9 Description: **Mendelian Randomization Results of colocalizing eQTL.** Mendelian Randomization with the Wald ratio method was used to estimate the p-values (two-sided).

File Name: Supplementary Data 10 Description: Colocalisation results between immune latent factors and pQTL.

File Name: Supplementary Data 11

Description: **Mendelian Randomization results of colocalizing pQTL.** Mendelian Randomization with Wald ratio method was used to estimate the p-values (two-sided).