

1 **Supplementary Methods**

2 Sample exclusions and imputation were performed using the following steps:

3 For the genetic analyses of immune cells, a genetic map based on 6,602 samples was
4 used, genotyped using four Illumina arrays (OmniExpress, ImmunoChip, Cardio-
5 MetaboChip, and ExomeChip). Pre-phased genotypes were imputed genome-wide
6 using a reference panel of 3,514 individuals and the Minimac58 software. After
7 imputation, only SNPs with an $RSQR > 0.3$ (estimated minor allele frequency (MAF)
8 $\geq 1\%$) or > 0.6 (MAF $< 1\%$) were retained for association analyses, resulting in
9 approximately 22 million variants.

10 For SCZ, two meta-analyses were conducted, including a first-stage analysis of cohorts
11 with case-control phenotypes (the IGAP, ADSP, and PGC-ALZ datasets) and a proxy
12 phenotype in the UKB cohort included in the third stage.