

Title: Supplementary Table 1

Description: Genome-wide sepsis eQTLs showing interaction with neutrophil-to-lymphocyte ratio (NLR).

Title: Supplementary Table 2

Description: Colocalisation results between the MTOR sepsis eQTL and eQTLs across different cell types and treatment conditions.

Title: Supplementary Table 3

Description: GWAS traits significantly associated with rs4845987 or linked variants in strong linkage disequilibrium.

Title: Supplementary Table 4

Description: Summary data-based Mendelian randomisation results linking MTOR expression to type 2 diabetes risk across cell types.

Title: Supplementary Table 5

Description: Differentially expressed cytokine genes in activated CD4⁺ and CD8⁺ T cells following anti-CD3/CD28 stimulation.

Title: Supplementary Table 6

Description: Epigenomic datasets used to assess chromatin accessibility and regulatory features at the MTOR locus.

Title: Supplementary Table 7

Description: ENCODE histone modification and CTCF ChIP-seq datasets analysed at the MTOR locus.

Title: Supplementary Table 8

Description: sgRNA, primer and oligonucleotide sequences used for qRT-PCR, Sanger sequencing, RNAi, CRISPR-based epigenetic editing and base-editing experiments.