**Supplementary Tables Legends**

**Table S1. CeL-Gen’s inferred cell-type-specificity of eQTLs in influenza-infected mice.** The table reports genes with cell-type specificity *cis* eQTLs that were identified by CeL-Gen with FDR < 0.05. For each gene (column 1), reported are its associated SNP (SNP identifier and its genomic position in columns 2,3, respectively), the inferred branch of alteration (column 4), known immune and non-immune associated disease based on GWAS studies (column 5) and based on the annotation in the Ingenuity knowledge base (columns 6).

**Table S2. Westra’s inferred cell-type-specificity of eQTLs in influenza-infected mice.** The table reports genes with cell-type specificity *cis* eQTLs that were identified by Westra with FDR < 0.05, for which the inferred set of cell types could be categorized as immune/non-immune types. For each gene (column 1), reported are its associated SNP (column 2), the inferred cell types (column 3) and their respective immune/non-immune categorization (column 4). Reported are known immune and non-immune diseases associated with the gene based on GWAS (column 5) and based on the annotation in the Ingenuity knowledge base (column 6).

**Table S3. Running time.** Running time was measured on a MacBook Pro (16-inch, 2019), 2.3 GHz 8-Core Intel Core i9, 32 GB 2667 MHz DDR4. Simulations were tested with a single SNP for each gene, using 50, 200, and 1000 genes. Reported are mean running time per gene (left) and the standard deviation among repeats (right).

**Table S4. Westra’s inferred cell-type-specificity of eQTLs in influenza-infected mice.** The table reports all genes with *cis* eQTLs that were identified by Westra with FDR < 0.05. For each gene (column 1), reported are its associated SNP (column 2), the inferred cell types (column 3) and the minimal number of switch-on/switch-off events that are consistent with the inferred cell types (column 4).