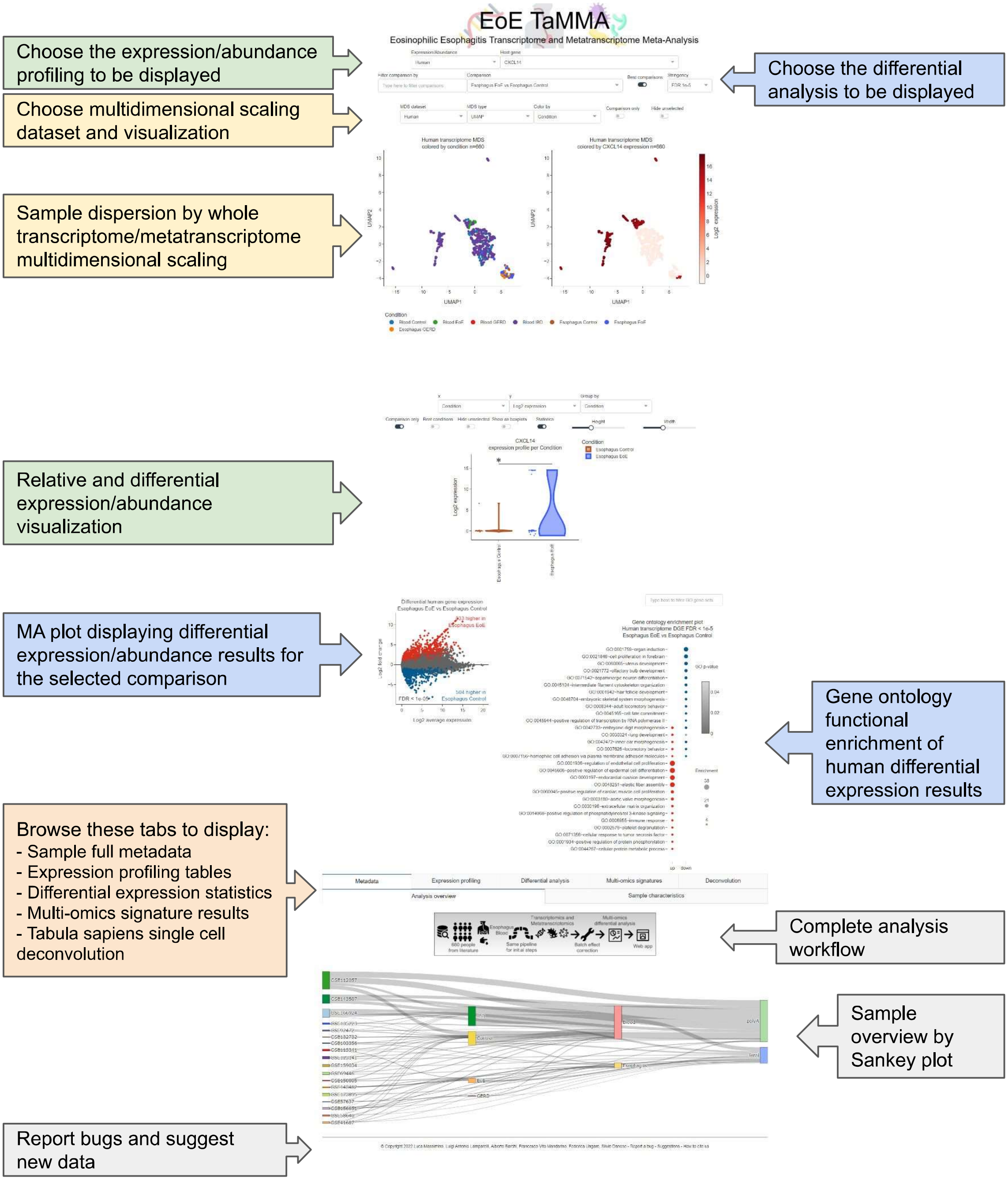
Figure S1



Choose the expression/abundance profiling to be displayed

Choose multidimensional scaling dataset and visualization

Sample dispersion by whole transcriptome/metatranscriptome multidimensional scaling

Choose the differential analysis to be displayed

Relative and differential expression/abundance visualization

MA plot displaying differential expression/abundance results for the selected comparison

Gene ontology functional enrichment of human differential expression results

Browse these tabs to display:
- Sample full metadata
- Expression profiling tables
- Differential expression statistics
- Multi-omics signature results
- Tabula sapiens single cell deconvolution

Complete analysis workflow

Sample overview by Sankey plot

Report bugs and suggest new data

Figure S1. Web app user interface. Global overview of the web app user interface where info boxes are color-coded by category or section, with represents expression profiling in green , multidimensional scaling in yellow , differential analysis and functional enrichment in blue, multi tab panel in orange, and general specification in grey.

Figure S2

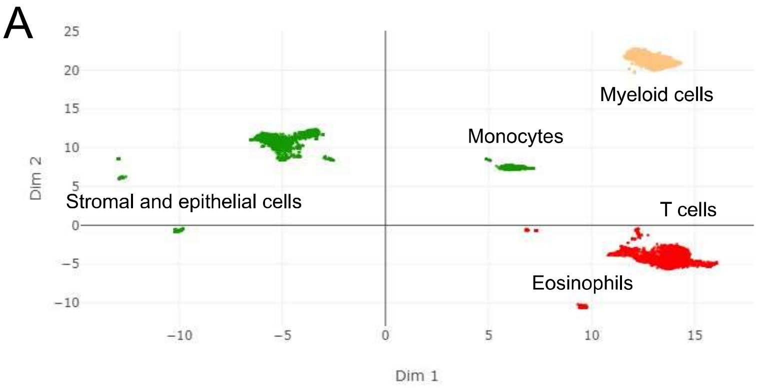


Figure S2. Esophageal mucosa-derived cell populations. (A) UMAP showing color-coded cell populations colonizinf esophageal mucosa according to a single-cell analysis by of Morgan et al., 2021.

Figure S3

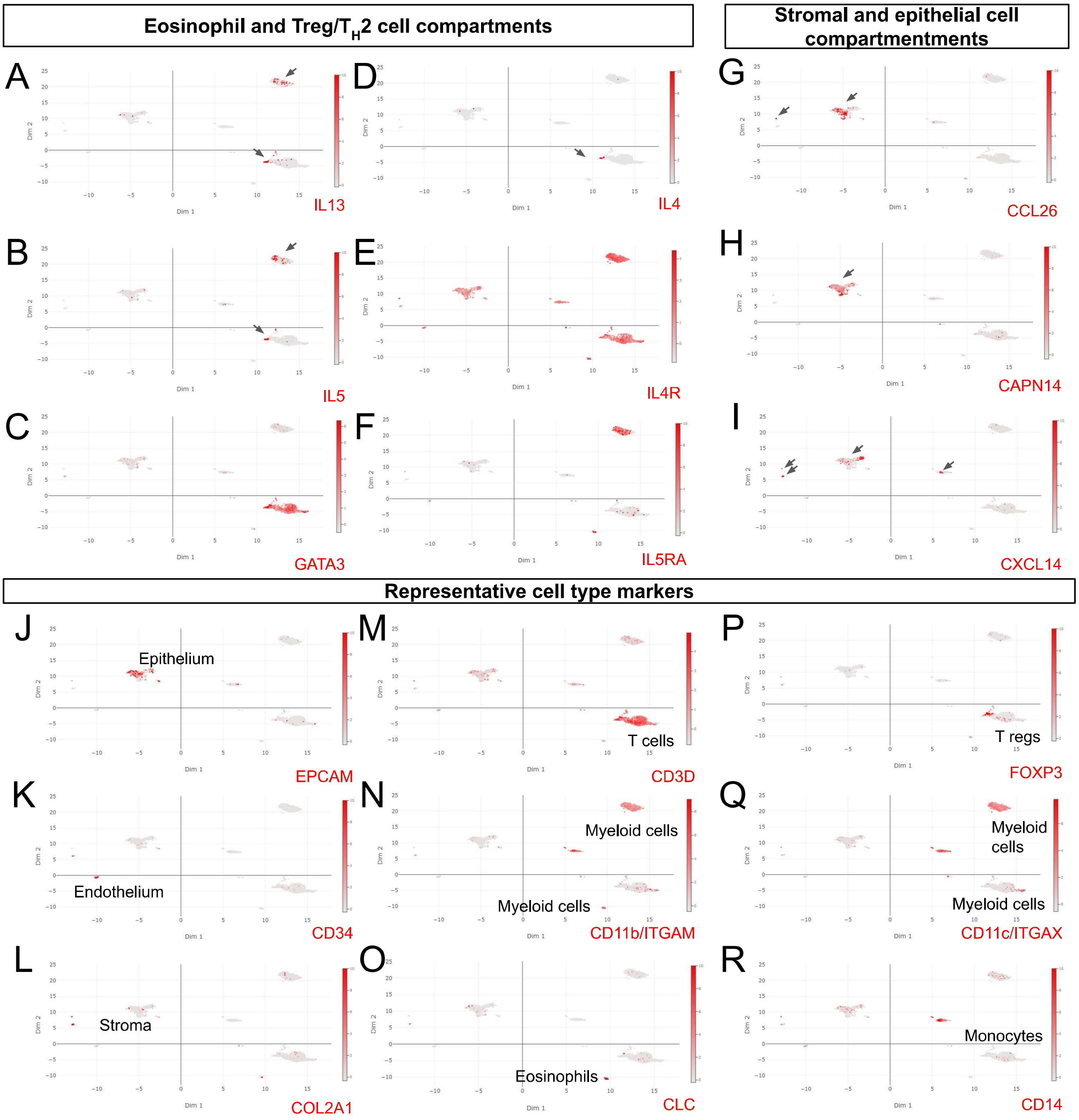


Figure S3. Single-cell analysis of esophageal mucosa. (A-R) UMAP plots showing relative gene expression profiles at a single-cell resolution of Morgan et al., 2021 data. (A-I) Expression profiles of genes found to be differentially expressed in EoE TaMMA. Arrows indicate the clusters with the highest gene expression. (J-N) Expression profiles of representative cell type markers are labeled in black.

Figure S4

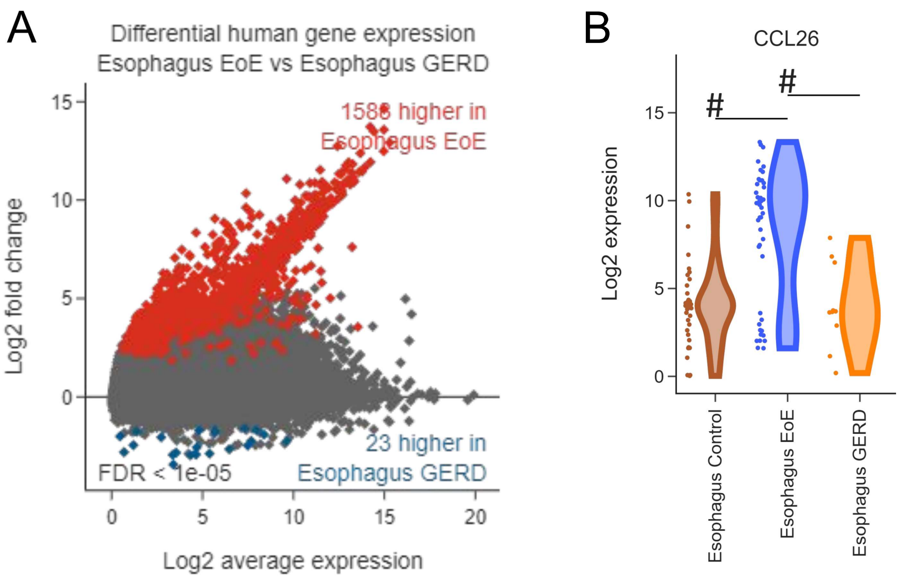


Figure S4. Gene expression profile of EoE and GERD esophagi. (A) MA plot showing the differential gene expression results expressed between the indicated comparisons as a function of log2(average gene expression). Red dots represent genes being differentially expressed with high statistical significance (false discovery rate (FDR) < 1 × 10−5). The number of differentially expressed genes and their trends are red and blue for the up and down-regulated genes, respectively. (**B**) Violin plots showing the differential CCL26 expression among the EoE GERD and control samples. The hashtags indicate FDR < 1 × 10−5.

Figure S5

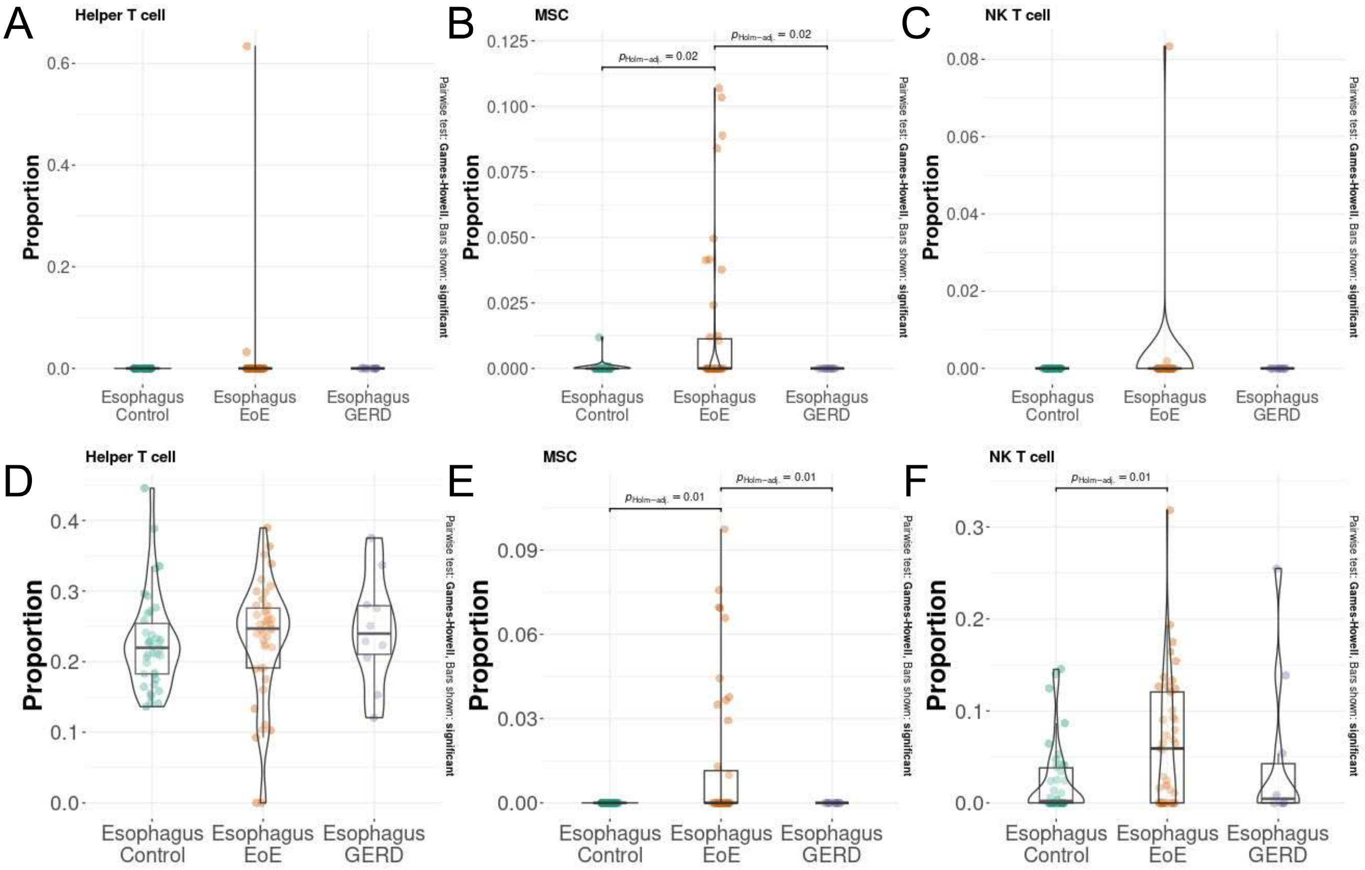


Figure S5. Deconvolution differential analysis. (A-F) Violin/box plots showing the proportions of helper T cells (A,D), mesenchymal stem cells, MSC (B,E), and natural killer, NK cells (C,F) in EoE, GERD, and control esophagi, exploiting MuSiC (A-C) or CIBERSORTx (D-F)..

Figure S6

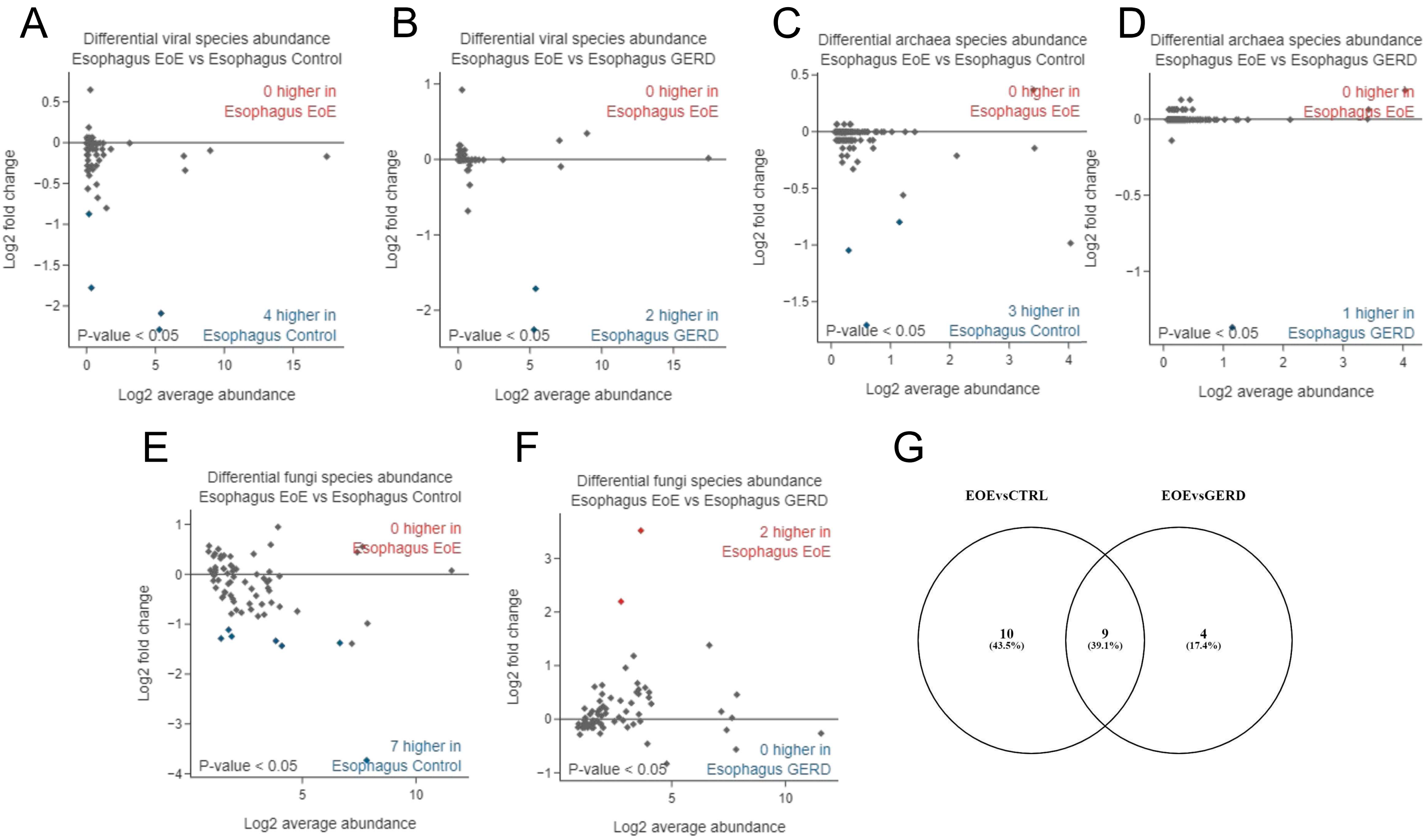


Figure S6. Microbiota profiling of EoE (A-F) MA-plot showing the relative differential abundance of viral (A, B), archaeal (C, D), and fungal (E, F) species between EoE and control and EoE and GERD. Red dots represent microbial species being differentially abundant with high statistical significance ($P < 0.05$). (**G**) Venn diagram intersecting highly upregulated bacterial species of EoE and GERD.

Figure S7

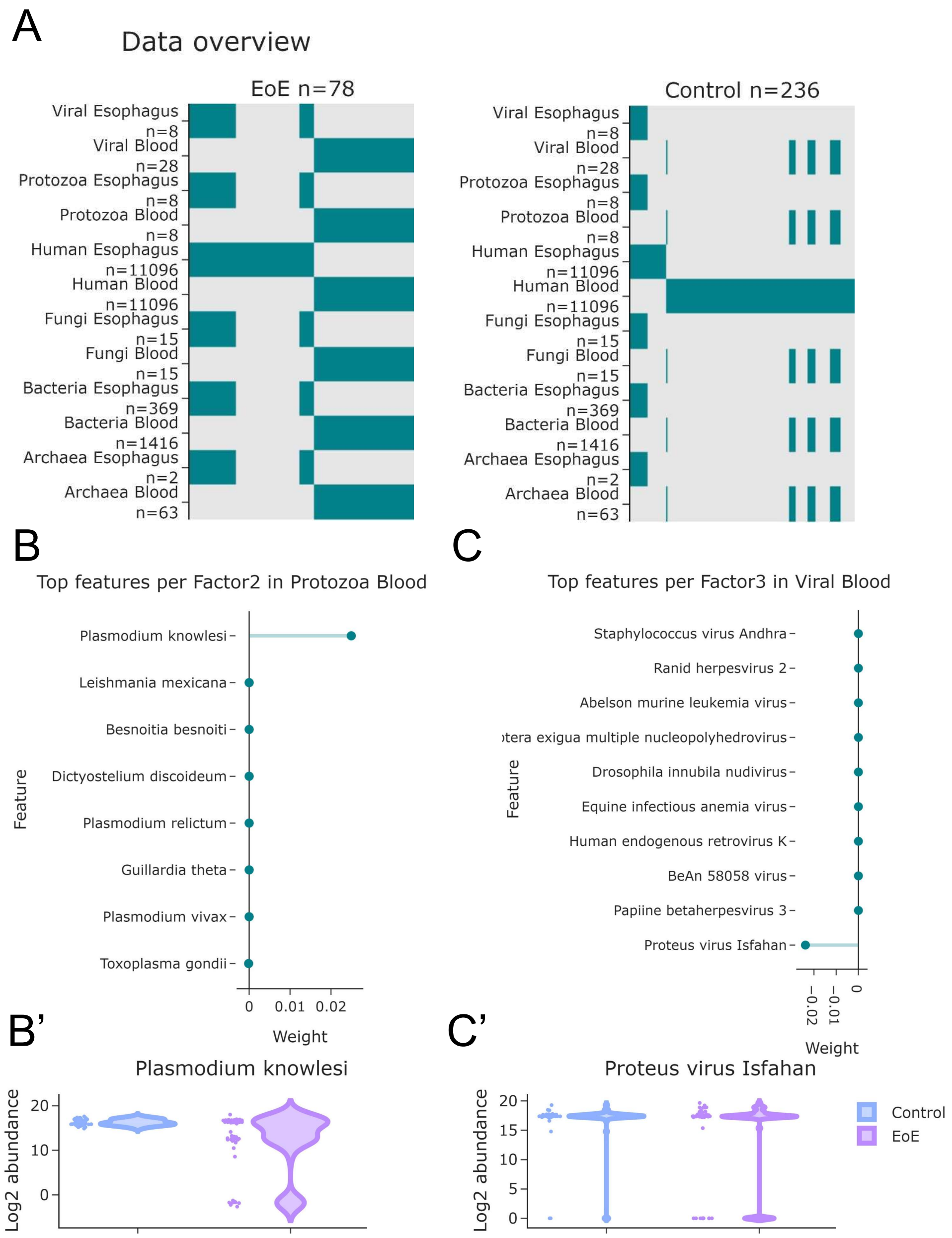


Figure S7. Multi-omic analysis in EoE TaMMA. (**A**) Data overview of MOFA analysis in EoE and control samples, shown as a heatmap where the presence and the absence of data are represented as indigo or light grey cell, respectively. (**B-C**) Needle plots showing weights representing the variance explained by each feature for the indicated factors and layers (B,C) and violin plots showing the relative abundance of top features within conditions (B’,C’).