Description of additional supplementary files

Supplementary Data 1. Small molecule features impacted by infection over time. N=15 mice per group and per position. Source data are provided as a Source Data file.

Supplementary Data 2. Differentially-expressed genes based on RNA-seq. N=5/group. Source data are provided as a Source Data file. Statistical testing using likelihood-ratio test to determine if "condition" has an effect on gene counts. Pairwise Wald tests to determine which condition "levels" contribute to the difference. All tests are two-sided. P-value correction: BenjaminiHochberg False Discovery Rate (BH FDR). lfcSE, standard error of log2 fold change

Supplementary Data 3. Small molecule features impacted by treatment. N=15 mice per group and per position. Source data are provided as a Source Data file.