

Additional File 4. RNA-seq exploratory analyses. (A) Cluster analysis. Protein-coding gene expression profiles were averaged across replicates and clustered (average linkage and Euclidean distance). (B, C) Spearman correlations between expression profiles in (B) males and (C) females. (D) The 28 sex-strain-treatment combinations were plotted with respect to the first two principal components. (E) Variable importance. Linear models were generated for each gene with strain, treatment and sex as explanatory factors. Importance of each factor was assessed using likelihood ratio tests (LRTs). Boxes span the middle 50% of $-\log_{10}$ -transformed p-values from LRTs for each factor (whiskers: 10th and 90th percentiles).

