

APPENDICES

Table A1: The RAW 264.7 macrophage SGL including, average logRAT2N, fold-change, COG functional category associations, and distribution of each feature in the *Enterobacteriaceae*.

Table A2: The BALB/cJ SGL and information regarding overlap of features with the macrophage SGL.

Figure A1: Comparison of the distribution of COG in the SGL and array dataset. Values are reported as percentage of either the SGL or the array dataset that fall within each respective category. The LT2 COG designations and COG Codes are as defined by on the National Center for Biotechnology Information website at <http://www.ncbi.nlm.nih.gov/sutils/coxik.cgi?cut=45&gi=202>. Categories are as follows: C, Energy production and conversion; D, Cell cycle control, mitosis and meiosis; E, Amino acid transport and metabolism; F, Nucleotide transport and metabolism; G, Carbohydrate transport and metabolism; H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; J, Translation; K, Transcription; L, Replication, recombination and repair; M, Cell wall/membrane biogenesis; N, Cell motility; O, Posttranslational modification, protein turnover, chaperones; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis, transport and catabolism; R, General function prediction only; S, Function unknown; T, Signal transduction mechanisms; U, Intracellular trafficking and secretion; and V, Defense mechanisms. The “not in COGs” category was designated by the authors as X.

Figure A1

