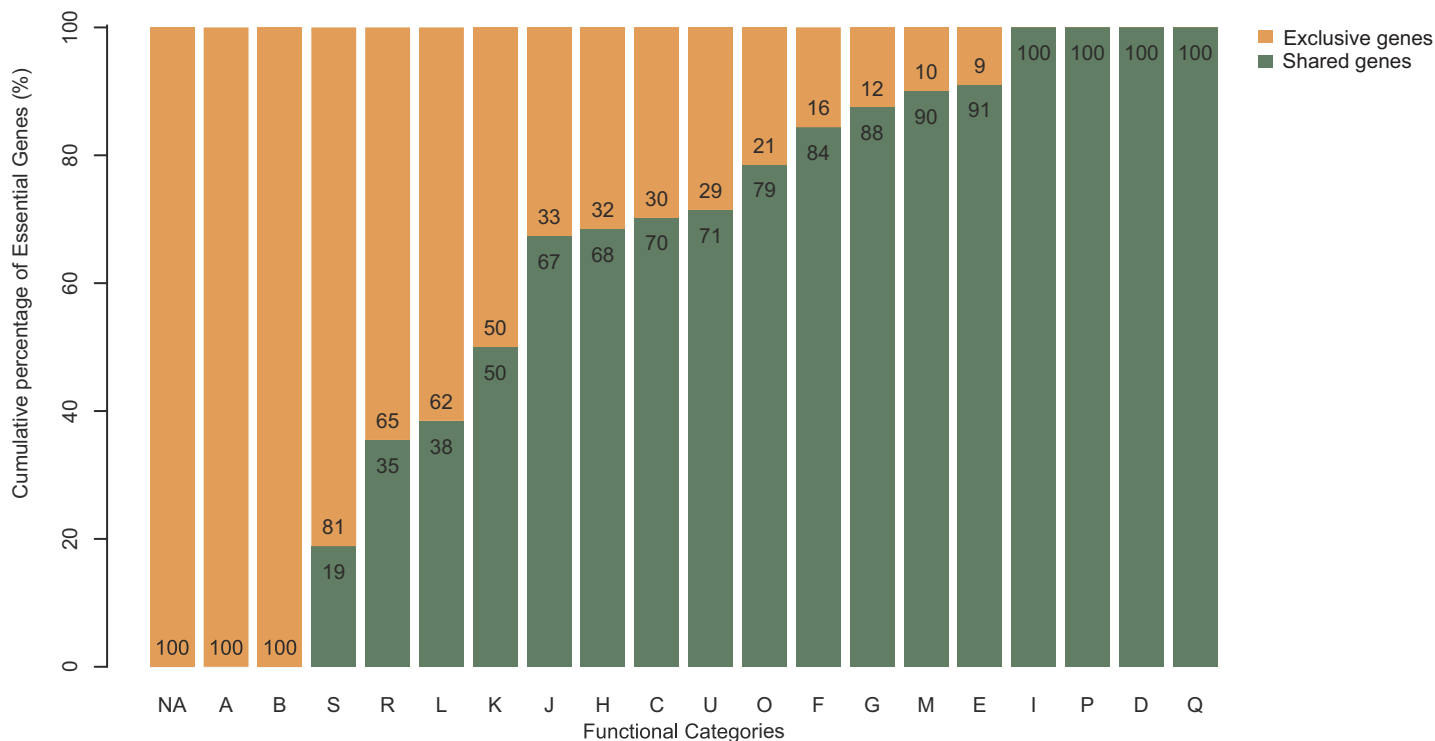
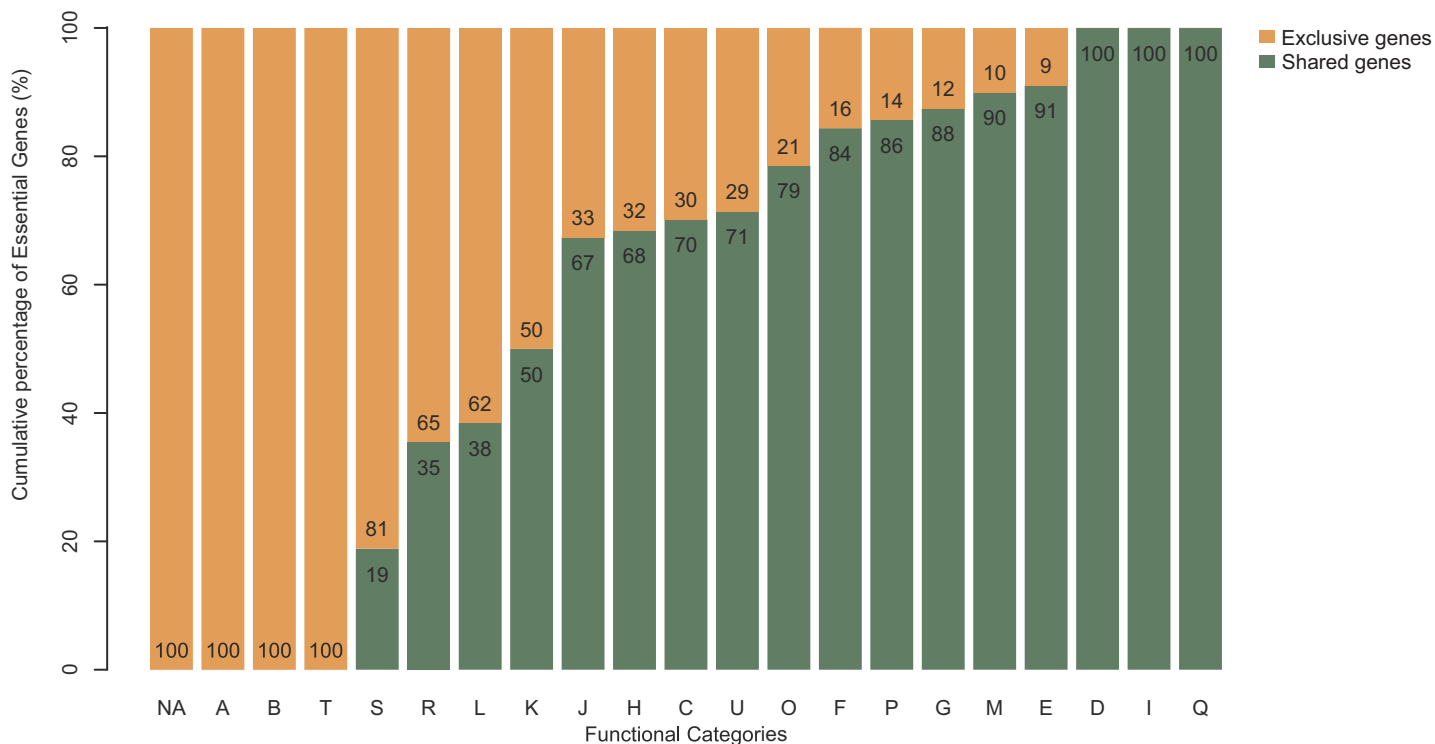


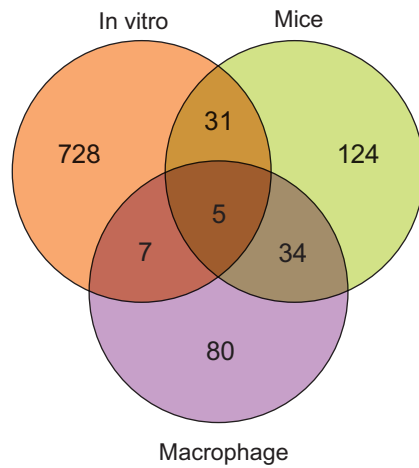
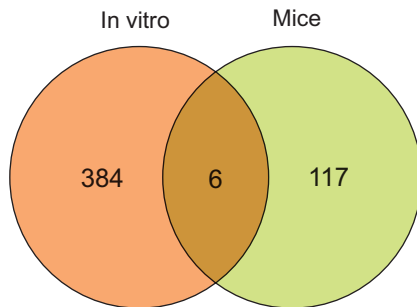
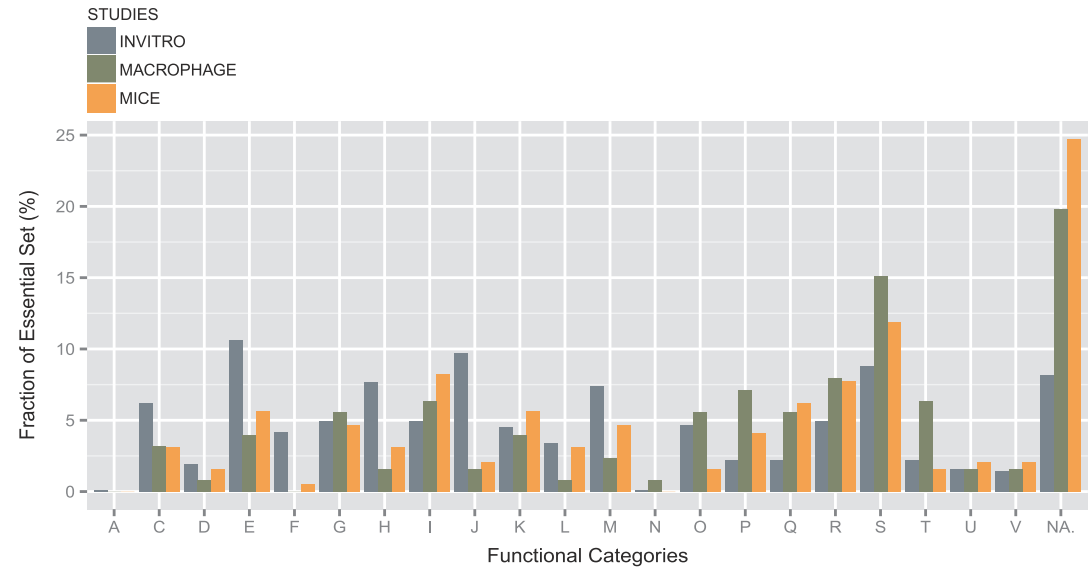
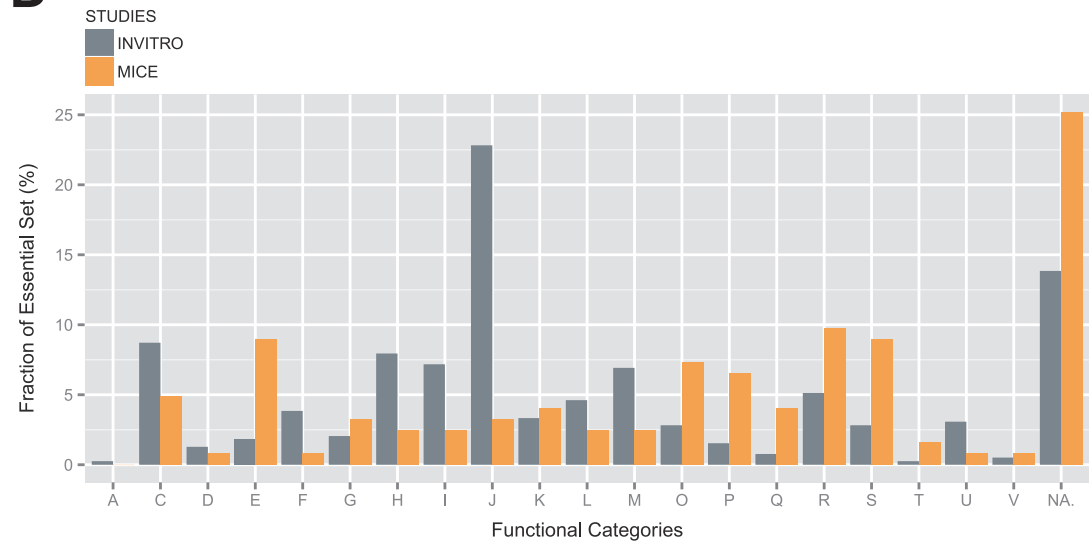
A



B



Supplementary Figure S1. Functional categorization of *Methanococcus maripaludis* S2 exclusive and shared essential genes. All COG/NOG annotations of essential genes from *M. maripaludis* were compared to 15 bacterial experimentally-determined essential gene sets. Essential archaeal COG/NOGs with no orthologs in any bacteria were considered *M. maripaludis* exclusive essential genes while COG/NOGs with at least one bacterial ortholog were considered shared genes. Distribution of functional categories of *M. maripaludis* essential genes in rich (A) and minimum (B) media are represented.

A**B****C****D**

Supplementary Figure S2. *In vitro* essential gene sets versus *in vivo* required gene sets. A) Venn diagram showing the number of shared and unique essential gene sets for *Mycobacterium tuberculosis* H37Rv experiments *in vivo* (mice and macrophage) and *in vitro* (agar medium); B) Venn diagram showing the number of shared essential gene sets for *Francisella tularensis* novicida U112 experiments *in vivo* (mice) and *in vitro* (agar medium); C) Functional categorization of essential genes for *M. tuberculosis* H37Rv experiments *in vivo* (mice and macrophage) and *in vitro* (agar medium); D) Functional categorization of essential genes for *F. tularensis* novicida U112 experiments *in vivo* (mice) and *in vitro* (agar medium).