

Figure S1

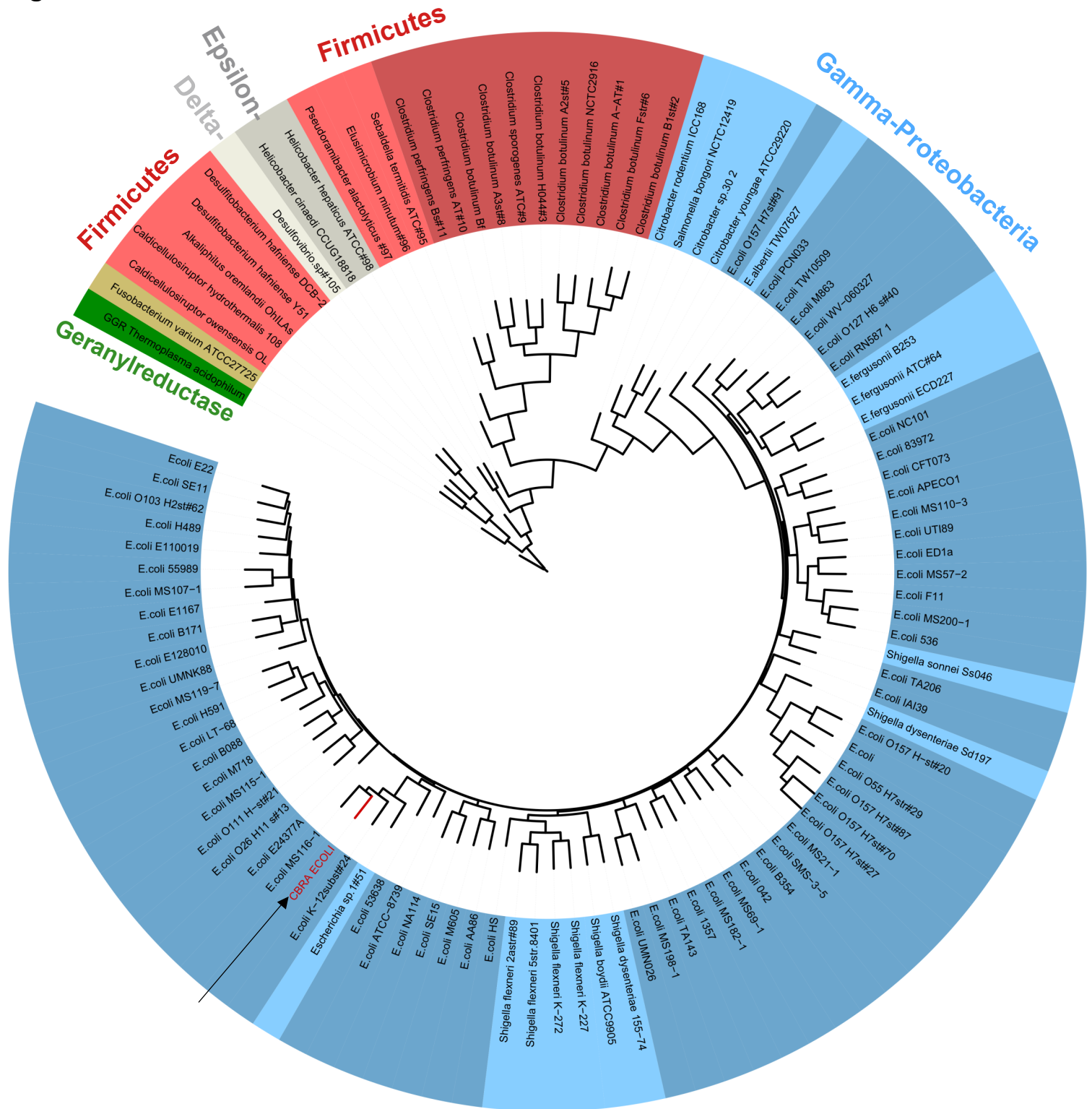


Figure S1. Phylogenetic Tree of CbrA Proteins. Multiple sequence alignments of CbrA proteins and the geranylreductase of *T. acidophilum* - used as an outgroup - for phylogenetic inference were computed with PROMALS 3D (3). Phylogenetic analysis was conducted with PHYLIP-NEIGHBOR using the JTT model (1). The arrowhead indicates the gene expressed for this study. The consensus phylogenetic tree is drawn with iTOL (<http://itol.embl.de/>) (2).

Supplementary References

1. **Felsenstein J.** 1996. Inferring phylogenies from protein sequences by parsimony, distance, and likelihood methods. *Methods Enzymol* **266**:418-427.
2. **Letunic I, Bork P.** Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. *Nucleic Acids Res* **39**:W475-478.
3. **Pei, J, Tang M, Grishin NV.** 2008. PROMALS3D web server for accurate multiple protein sequence and structure alignments. *Nucleic Acids Res* **36**:W30-34.