

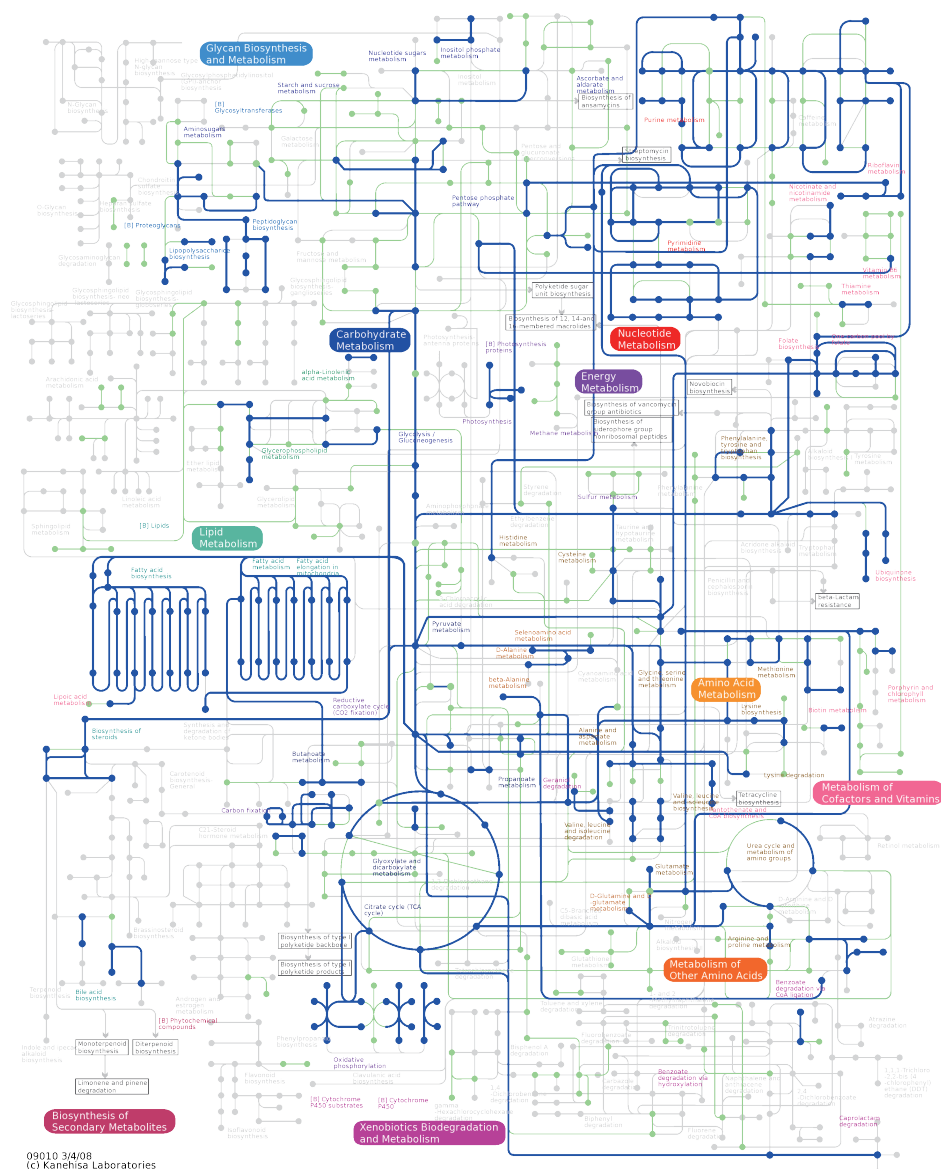


Figure S3. Global metabolic map displaying the common core genes shared between *Bacillaceae* and *Enterobacteriaceae* (CC class), which was drawn by the KEGG Atlas system (Kanehisa et al., 2008). The map was drawn based on the *E. coli* genes. The blue dots and lines indicate the pathway generated from the *E. coli* genes belonging to the common core OGs, and the green dots and lines indicate the entire *E. coli* pathway.