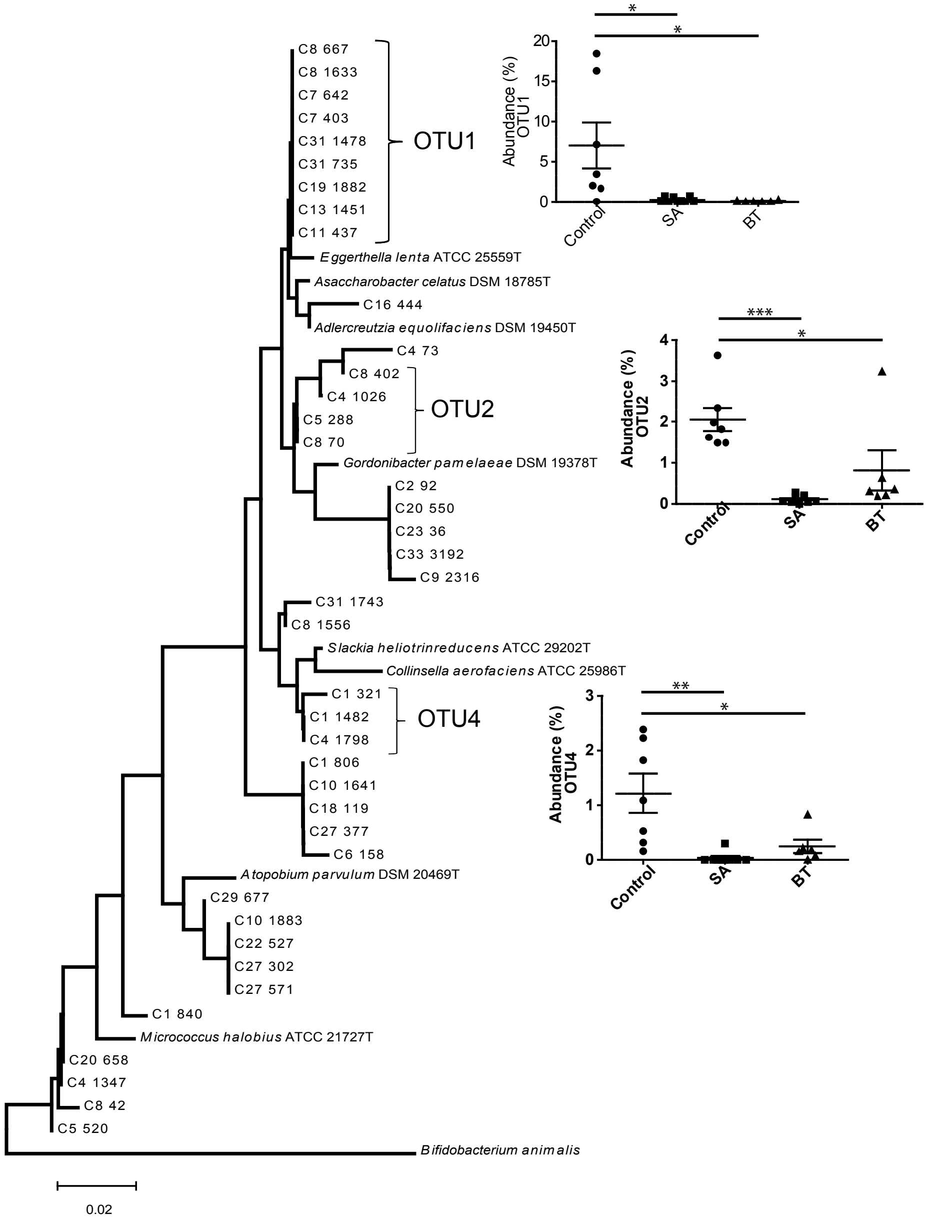
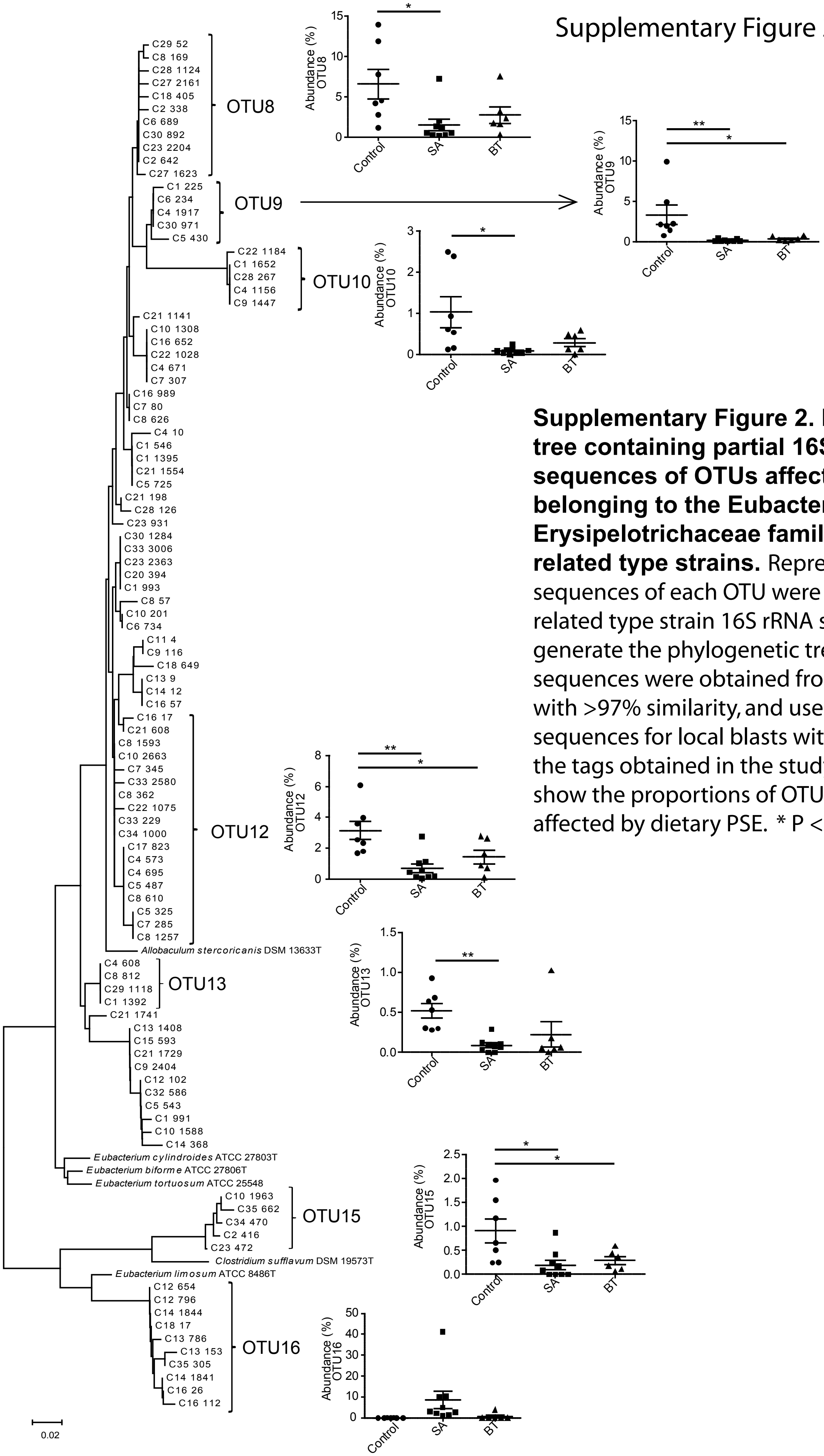
Supplementary Figure 1



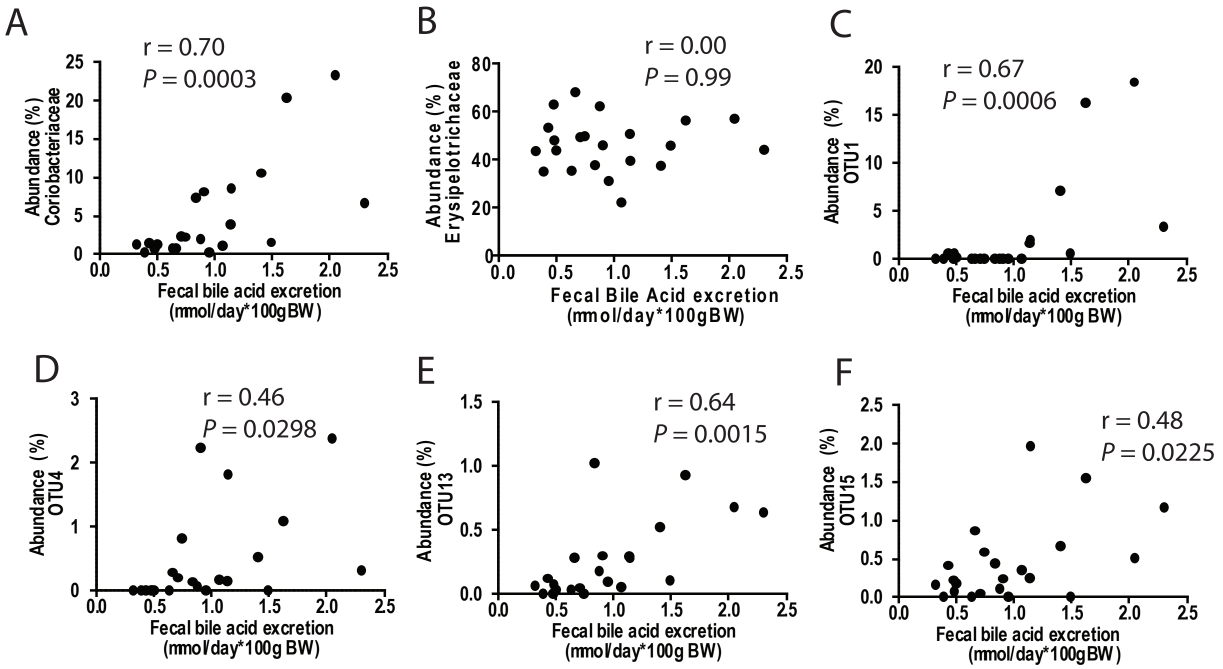
Supplementary Figure 1. Phylogenetic tree containing partial 16S rRNA gene sequences of OTUs affected by PSE belonging to the Coriobacteriaceae family and closely related type strains. Representative sequences of each OTU were aligned with related type strain 16S rRNA sequences to generate the phylogenetic tree. Consensus sequences were obtained from sequences with >97% similarity, and used as query sequences for local blasts with a database for the tags obtained in the study. The graphs show the proportions of OTUs significantly affected by dietary PSE. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Supplementary Figure 2



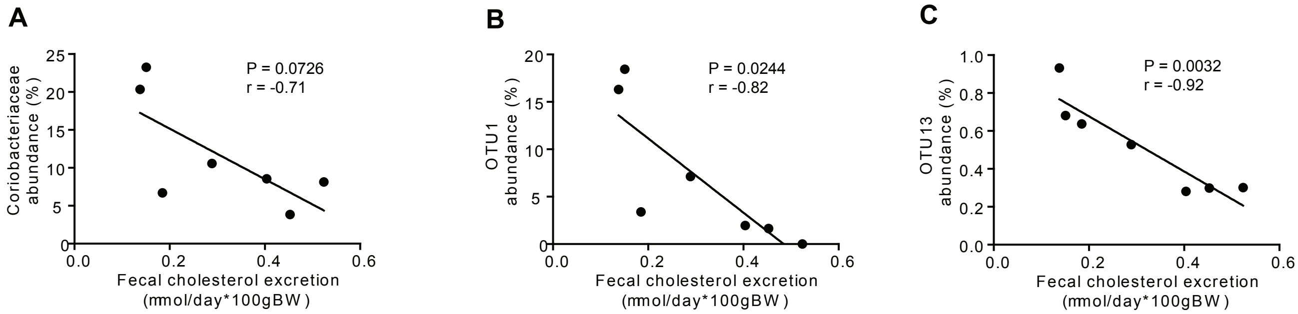
Supplementary Figure 2. Phylogenetic tree containing partial 16S rRNA gene sequences of OTUs affected by PSE belonging to the Eubacteriaceae and Erysipelotrichaceae families and closely related type strains. Representative sequences of each OTU were aligned with related type strain 16S rRNA sequences to generate the phylogenetic tree. Consensus sequences were obtained from sequences with >97% similarity, and used as query sequences for local blasts with a database for the tags obtained in the study. The graphs show the proportions of OTUs significantly affected by dietary PSE. * $P < 0.05$, ** $P < 0.01$.

Supplementary Figure 3



Supplementary Figure 3. Associations between bile acid excretion and proportions of gut bacterial populations. Correlations between bile acid excretion and the abundance of Coriobacteriaceae (A), Erysipelotrichaceae (B), OTU1 (C), OTU4 (D), OTU13 (E), and OTU15 (F).

Supplementary Figure 4



Supplementary Figure 4. Associations between fecal cholesterol excretion and proportions of gut bacterial populations in hamsters on the control diet. Correlations between fecal cholesterol excretion and abundance of Coriobacteriaceae (A), OTU1 (B), and OTU 13 (C).