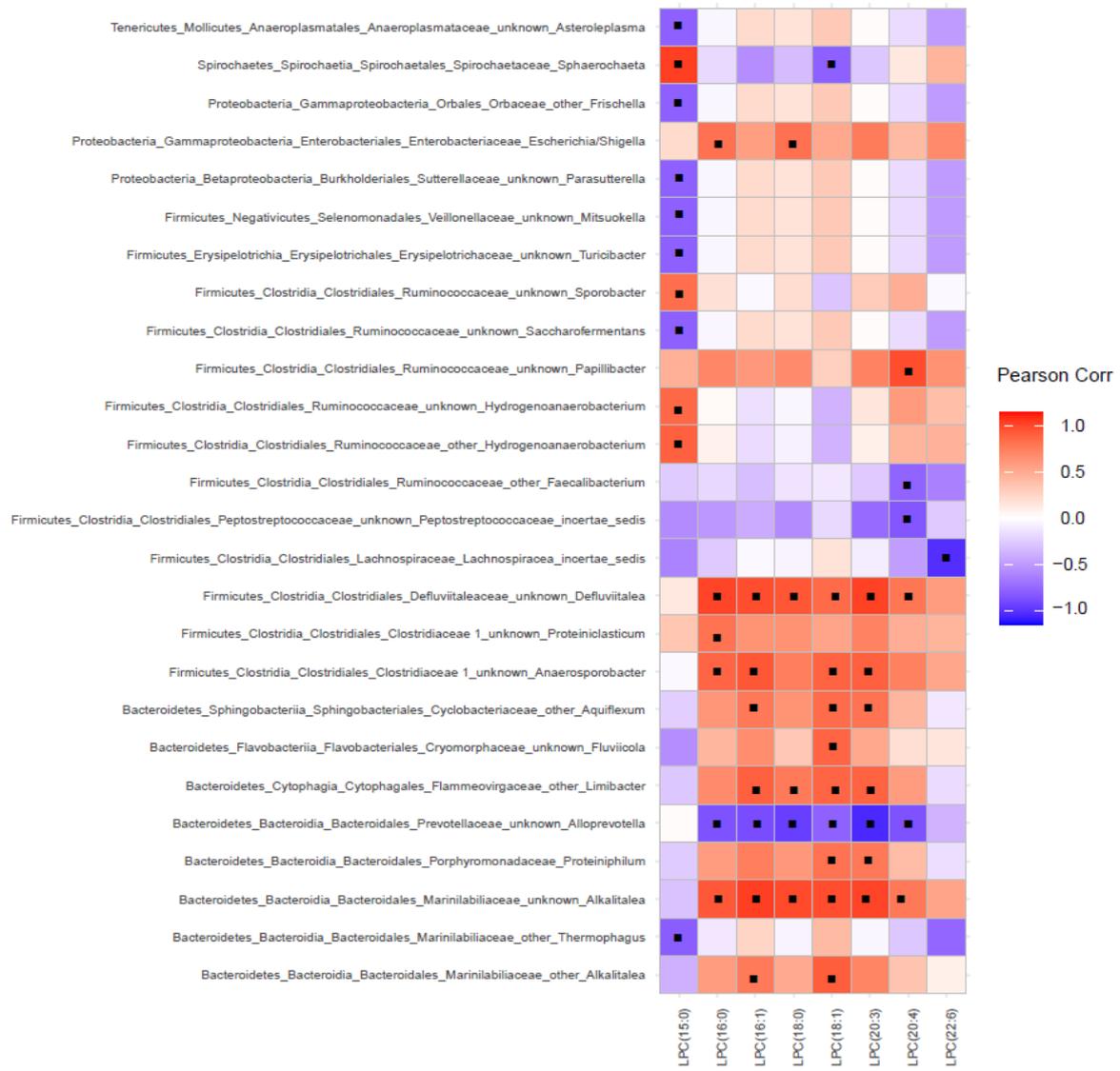
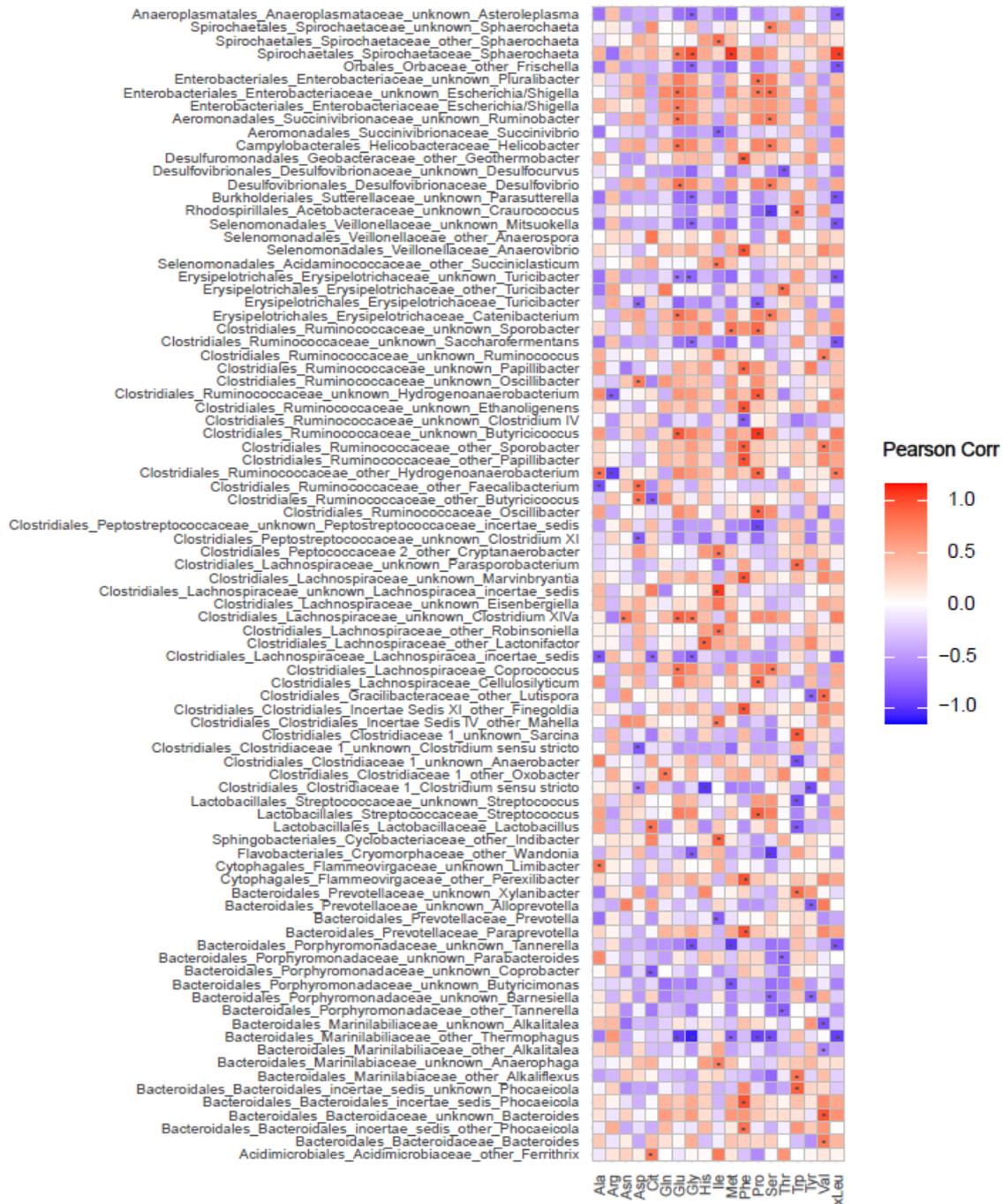


**Supplementary Figure S1. Comparisons of Univariate analysis between groups.** Three heatmaps were created to show the results of the univariate analysis. For each of the three organs, a heatmap with corrected p values were created. Each row is a compound, and each column is a pairwise comparison. The color represents the fold change value (red indicates that the metabolites is more abundant in group 1 than in group 2, and blue indicates the opposite). Asterisks indicate p-values (one asterisk indicates  $p < 0.05$ ; two asterisks indicate  $p < 0.01$ ). Metabolite class information is represented by the color displayed in the legend bar.



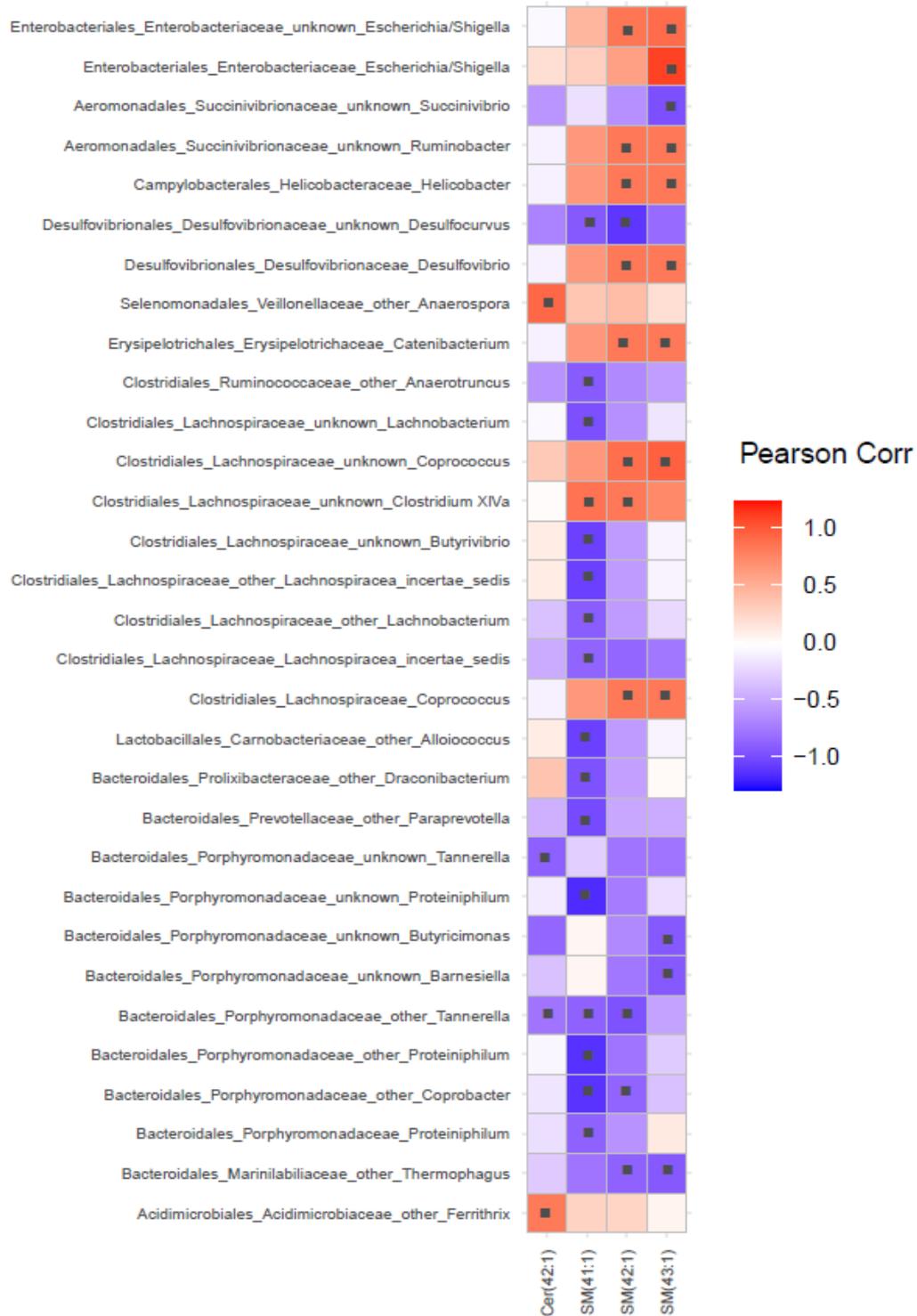




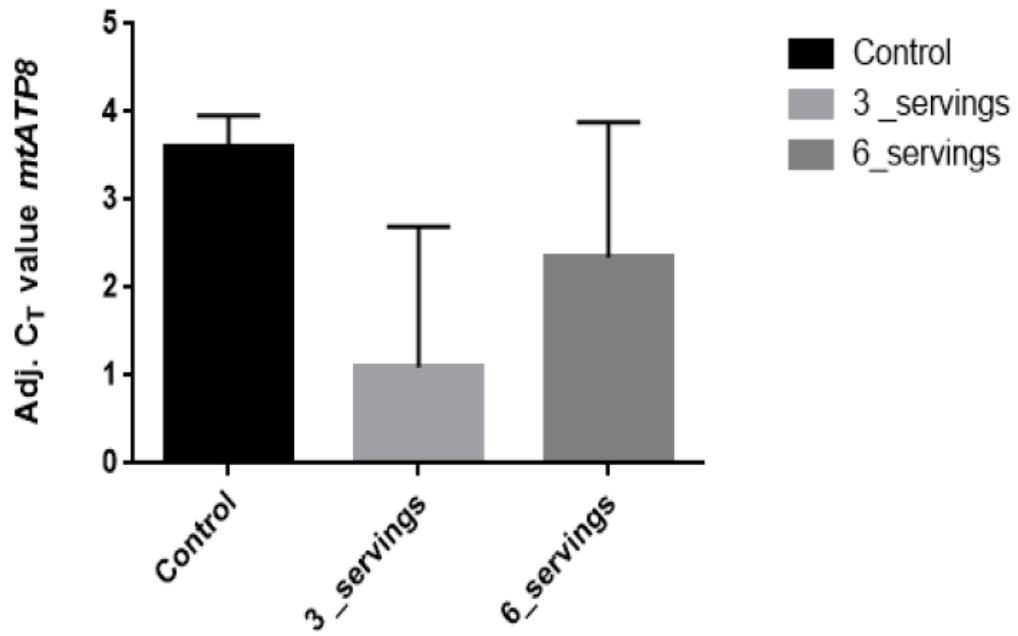


**Supplementary Figure S2. Correlation between bacteria in the fecal microbiome and metabolites in the cortex of pigs fed six-servings of a WBM supplemented diet.** Several lipid species within glycerophospholipids (alkyl-acyl-glycerol phosphocholines (PC-O)(S2-1), lyso-phosphatidylcholines (LPC)(S2-2) and phosphatidylcholines (PC)(S2-3) and amino acids (S2-4) in the cortex of pigs fed six servings of a WBM supplemented diet were correlated with bacteria in the fecal microbiome. Pearson Correlation coefficients were estimated for each pairwise comparison of bacterial taxa and metabolite with direction of correlation represented by color according to legend. Black dots within heatmap represent significant relationships ( $p$  value < 0.05).





**Supplementary Figure S3. Correlation of bacteria in the fecal microbiome and metabolites in the liver from pigs fed six servings of a WBM supplemented diet.** Most abundant metabolites classes of phosphatidylcholine (S3-1) and sphingolipids (S3-2) were correlated with bacteria in the fecal microbiome. Pearson correlation coefficients were estimated for each pairwise comparison of bacterial taxa and metabolite with direction of correlation represented by color according to legend. Black dots within heatmap represent significant relationships ( $p < 0.05$ ).



**Supplementary Figure S4. Real time PCR of mitochondrial gene *mtATP8* in the brain cortex.** Bars represent average adjusted Ct values for *mtATP8* gene expression in the cortex of pigs fed three or six servings of WBM supplemented diets compared to a control diet.