



Fig. A1. Repeatability of the 16S rDNA pyrosequencing methodology. Each of the day 0 samples from untreated and treated sausage were used as technical repeats to estimate the repeatability of the pyrosequencing methodology. In panel A, the relative abundances for the dominant taxa are plotted from each treatment and color-coded according to the key on the right. In panel B, data from these same 20 taxa were plotted in dot-plots for all pair-wise combinations of day 0 samples. The R^2 value was derived by linear regression on the pair-wise matrix.

