

Supplementary Figures

Effect of an antibiotic and probiotic on phage communities in the swine gut microbiota

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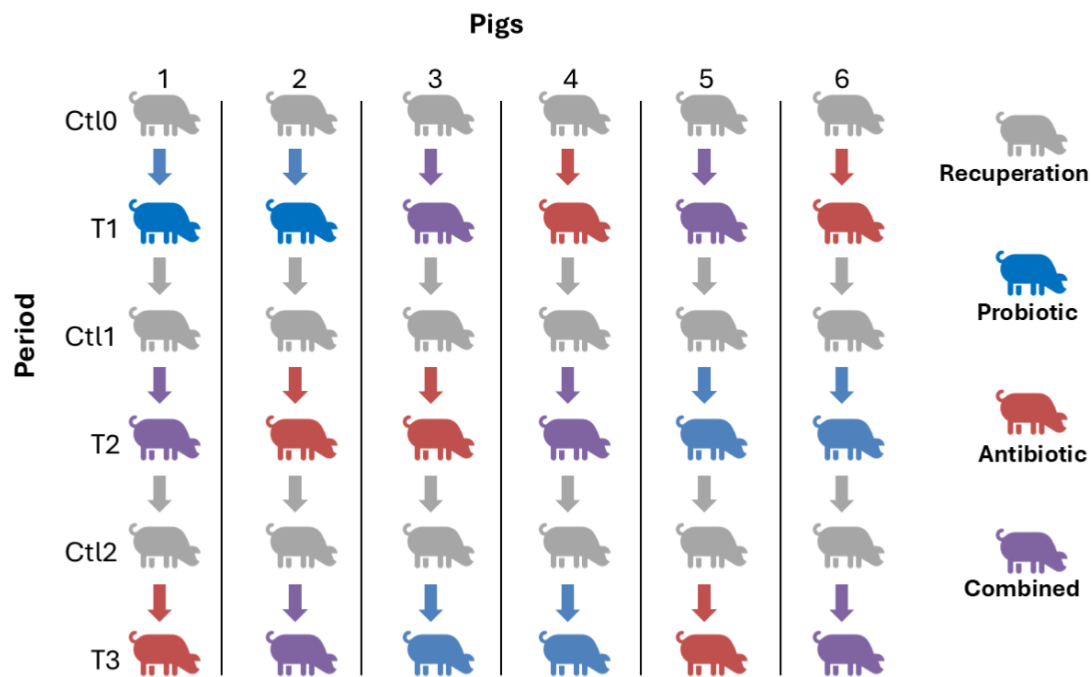


Figure S1. Experimental design. The study had a double crossover design with three treatments. Resting periods (in gray) were included prior to and between each set of treatments (T1, T2, T3; supplemented diet). Treatment sets and resting periods (Ctl0, Ctl1, Ctl2; control diet) were three weeks long. The treatments were an antibiotic (tylvalosin; 250 g/tonne of feed) in blue, a probiotic (*Pediococcus acidilactici* MA18/5M; 108 CFU/day) in red, and the combination treatment in purple.

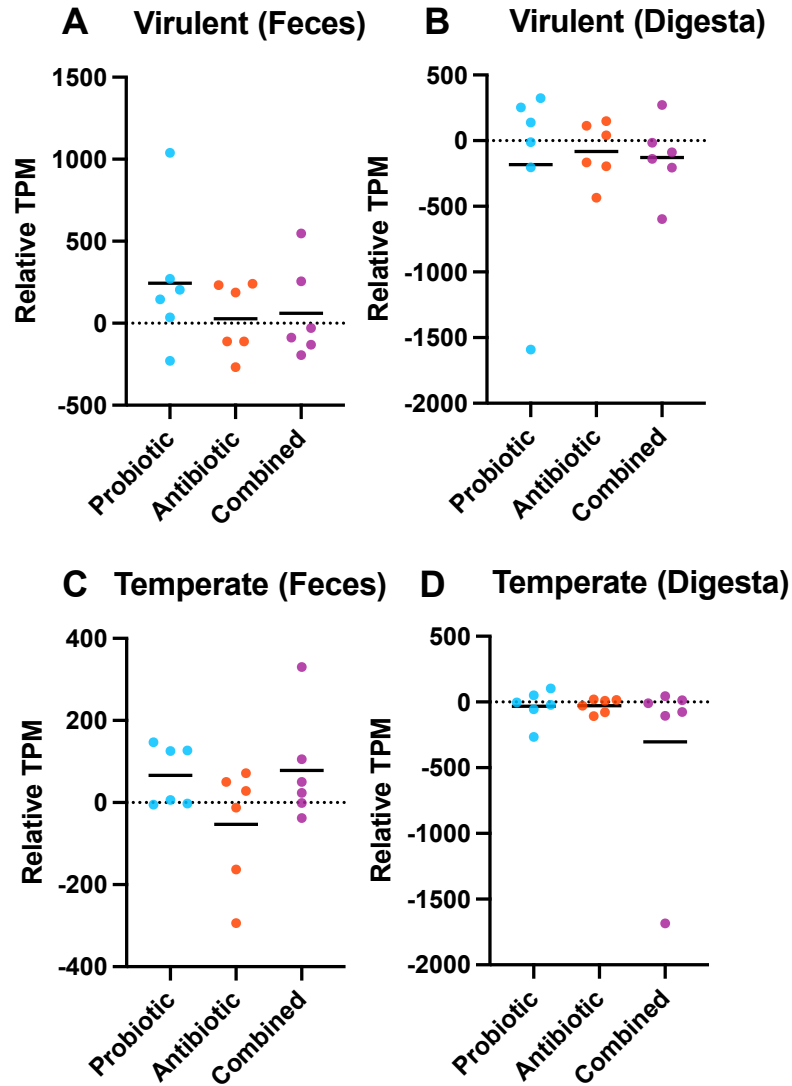


Figure S2. Variations of phage populations separated by lifestyle for each treatment in each sample type (digesta and feces). The lifestyles, predicted by BACPHLIP, were virulent (A and B) and temperate (C and D); the sample types were feces (A and C) and digesta (B and D). The treatments were probiotic (blue), antibiotic (red), and combination (purple).

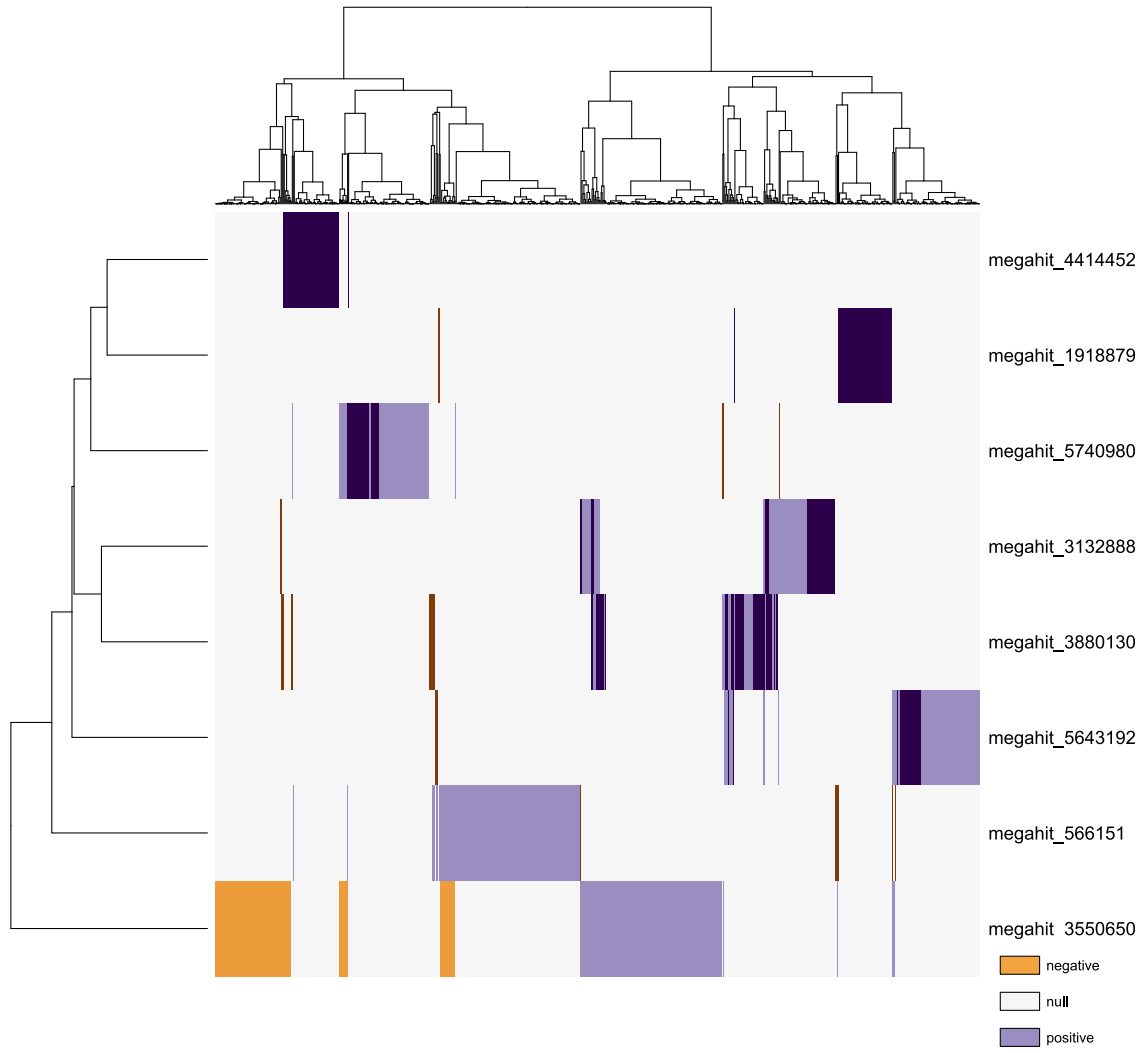


Figure S3. Heatmap showing the correlations between the relative abundances of the 8 marker phages and those of bacterial taxa.