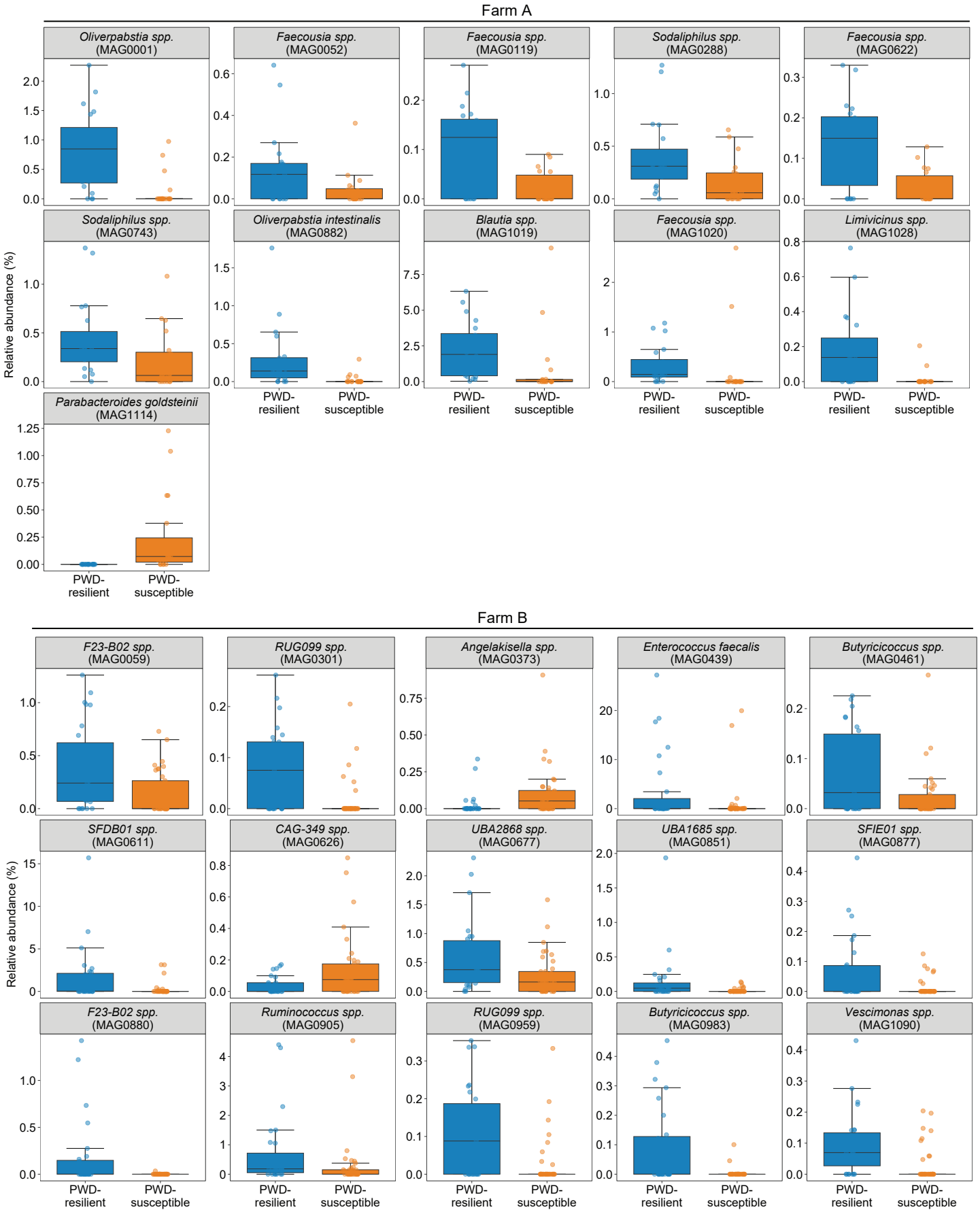

Figure S5. Boxplots illustrating the relative abundance of metagenome-assembled genomes (MAGs) identified by the Random Forest model as significantly associated with piglet health status.