

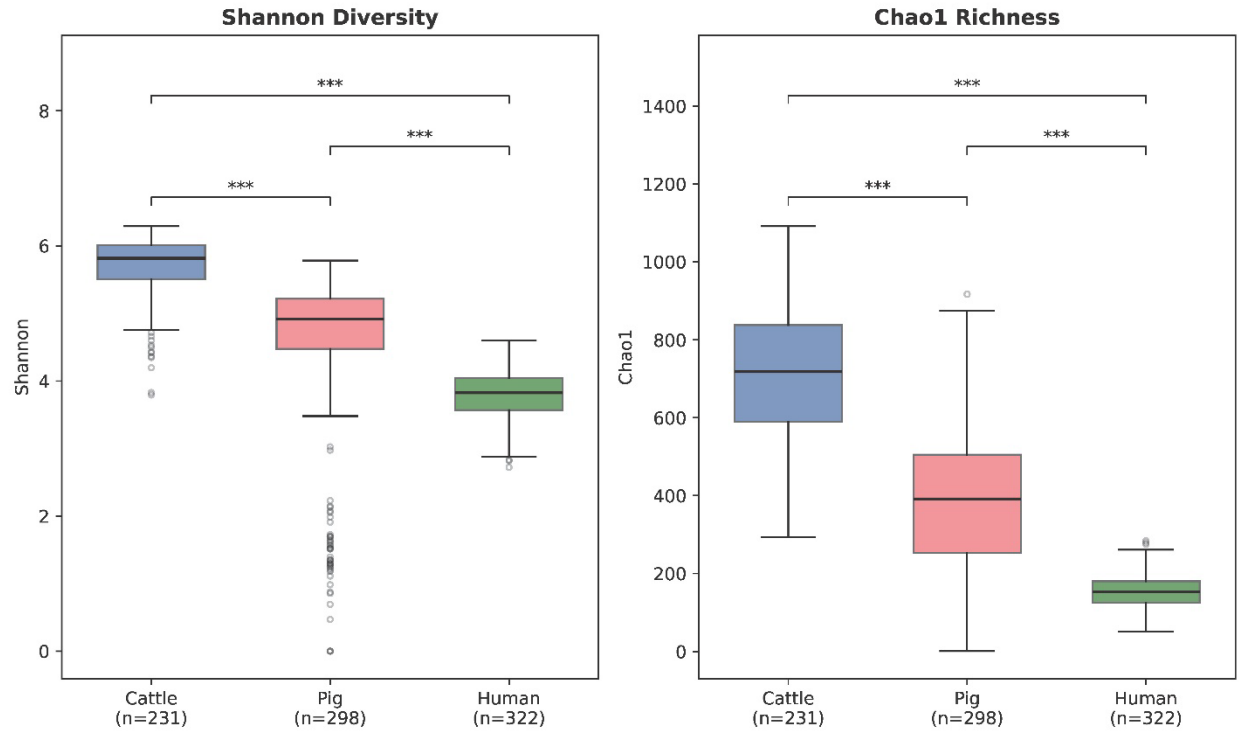


Fig. S2. Alpha-diversity comparison across host species. Box plots show Shannon diversity index (left) and Chao1 richness (right) for cattle ($n = 231$), pig ($n = 298$), and human ($n = 322$) fecal microbiomes based on 16S rRNA gene sequencing. All pairwise comparisons were significant (***, $p < 0.001$). Cattle had the highest diversity and richness, followed by pig, then human. Data from Song and Unno (2024).