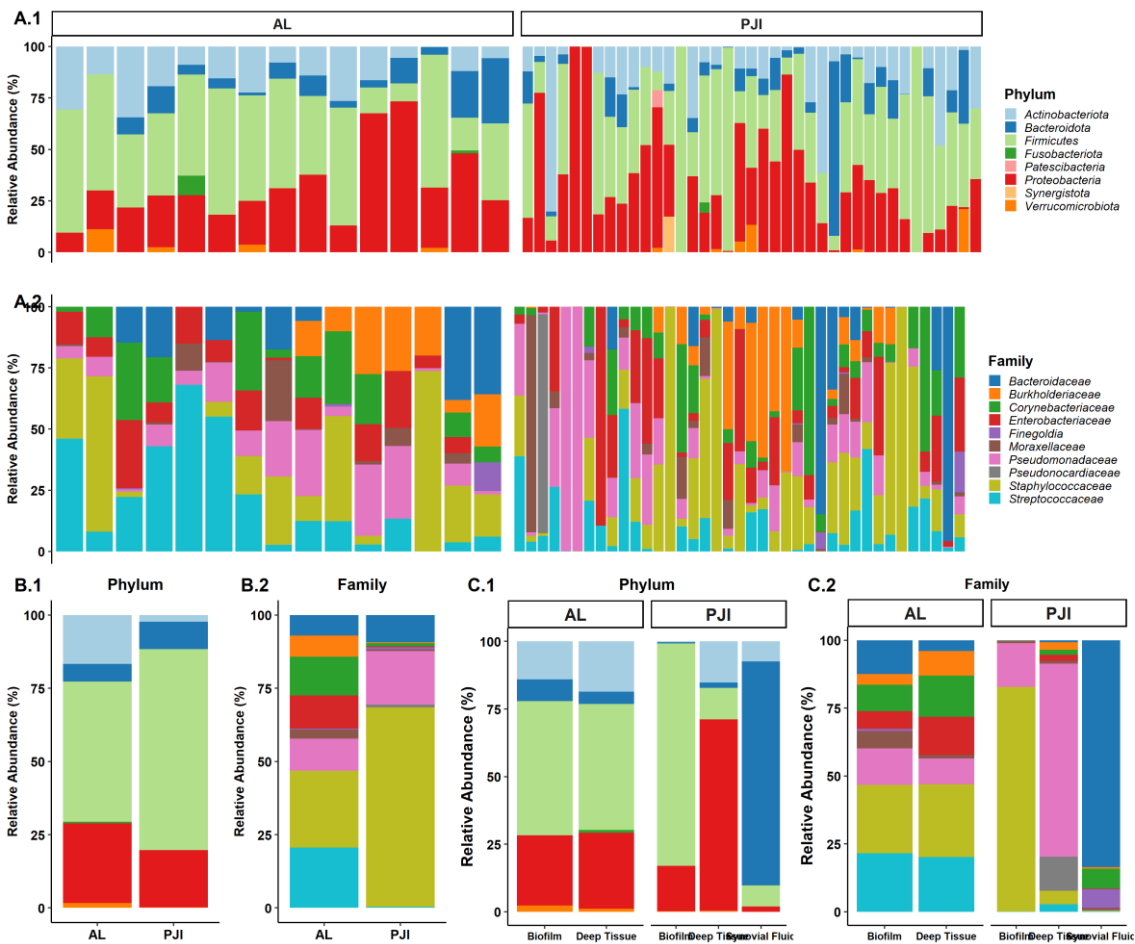
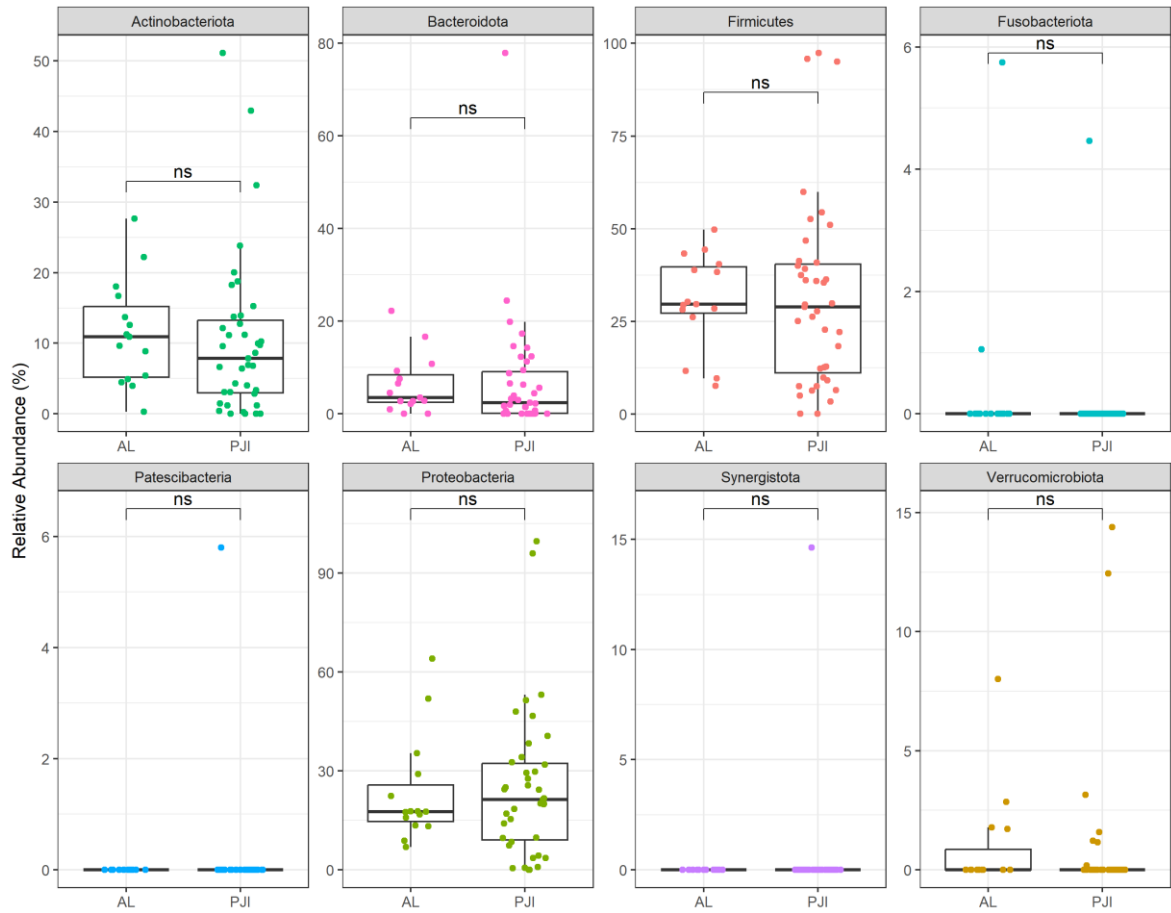


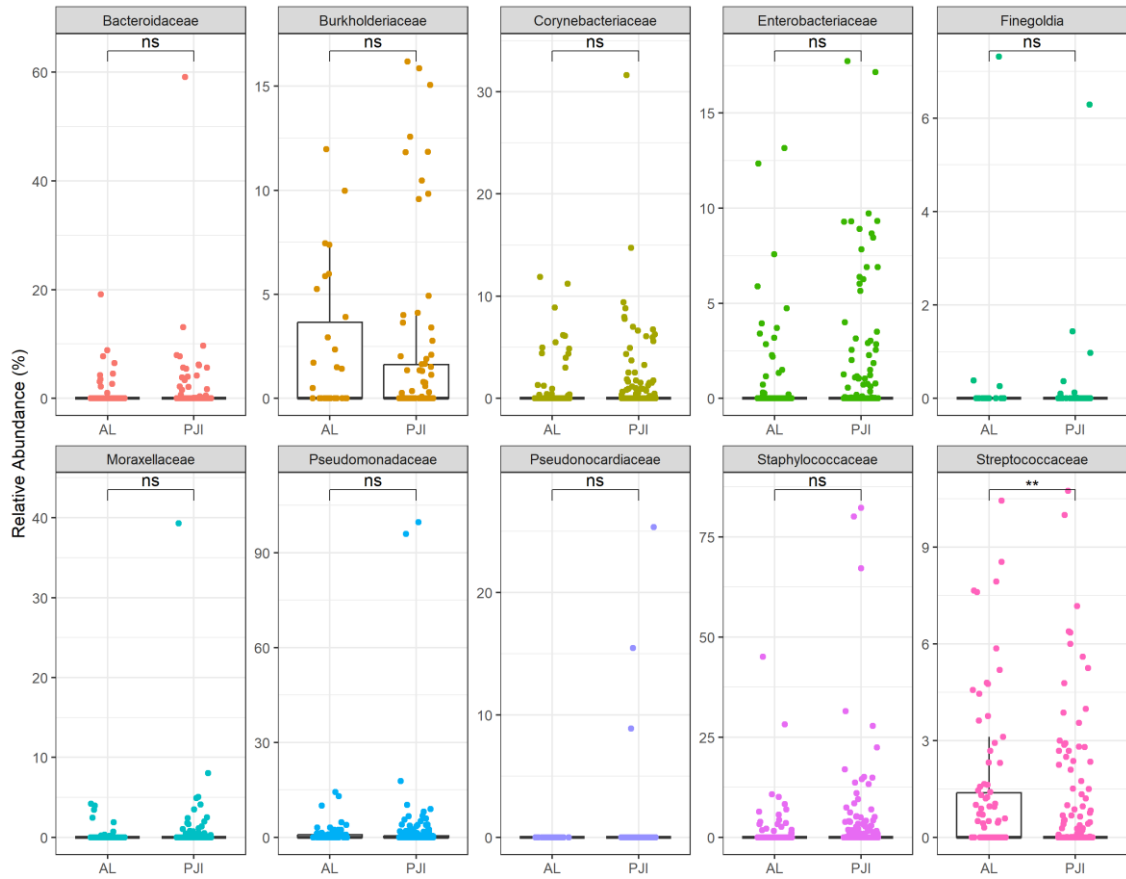
Supplementary File 1



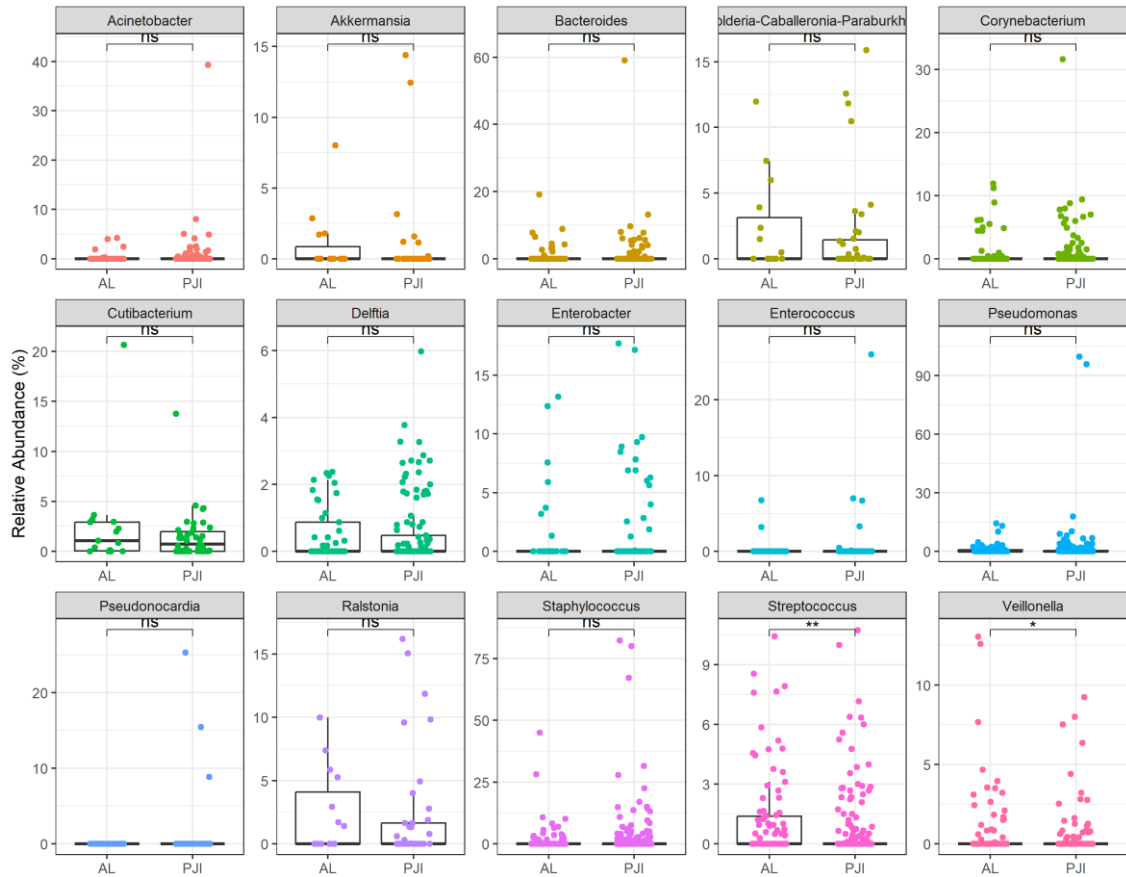
Supp. Figure 1. Stacked bar plots showing the percentage of relative abundance of (A) overall phylum and family distribution, (B) phylum and family distribution grouped by diagnosis, and (C) phylum and family distribution stratified by diagnosis status, along with sample collection sites. The most 10 dominant family taxa were demonstrated for easy interpretation.



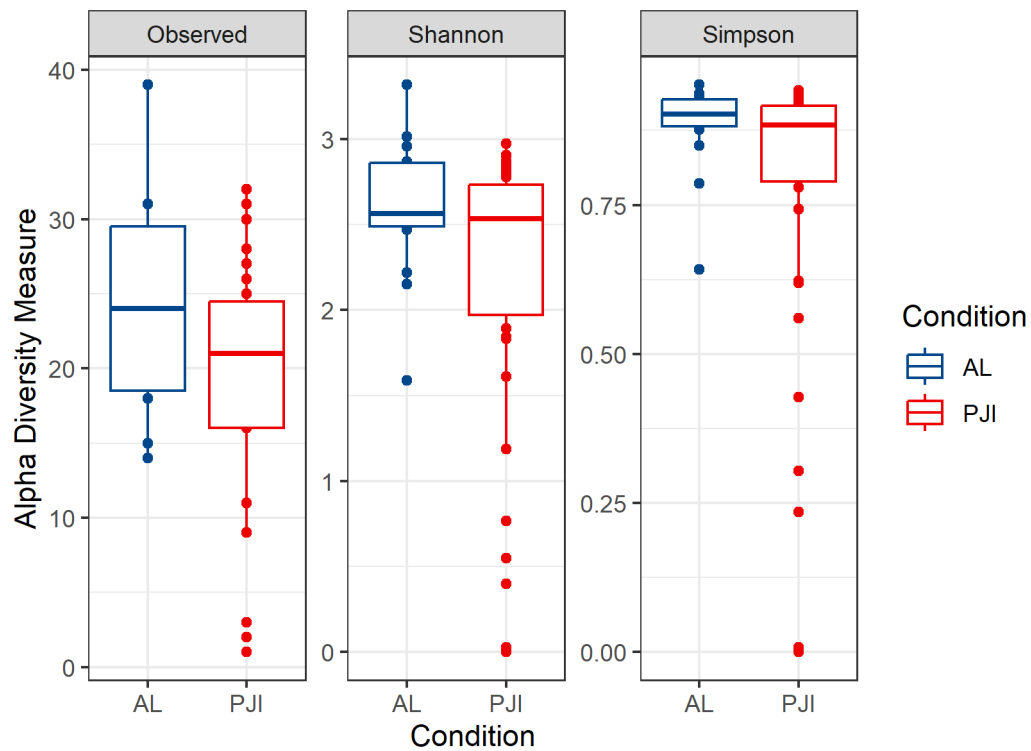
Supp. Figure 2. Distribution of relative abundance of all phyla by AL (aseptic loosening) and PJI (prosthetic joint infection) groups. The relative abundance of given phyla was not significant between groups when tested by Wilcoxon. (ns: $p > 0.05$)



Supp. Figure 3. Distribution of relative abundance of most dominant 10 family taxa by PJI (prosthetic joint infection) and AL (aseptic loosening) groups. The relative abundance of *Streptococcaceae* was significantly higher in AL group ($p < 0.05$; Wilcoxon test). (ns: $p > 0.05$)



Supp. Figure 4. Distribution of relative abundance of most dominant 15 genera by PJI (prosthetic joint infection) and AL (aseptic loosening) groups. The relative abundances of *Streptococcus* and *Veillonella* were significantly higher in AL group ($p < 0.05$; Wilcoxon test). (ns: $p > 0.05$)



Supp. Figure 5. Stacked bar plots showing the percentage of relative abundance of (A) overall phylum distribution, (B) most 10 dominant family taxa, and (C) most 15 dominant genera stratified by diagnosis status, along with sample collection sites. The x-axis represents the sample collection sites.