



Figure S2 Abundance variations in the ten dominant genera (>1% of total sequences), *Escherichia/Shigella* (A), *Klebsiella* (B), *Streptococcus* (C), *Lactococcus* (D), *Lactobacillus* (E), *Weissella* (F), *Enterococcus* (G), *Clostridium sensu stricto* (H), *Clostridium XI* (I) and *Turicibacter* (J) across seasons, compared by paired sample Wilcoxon signed rank test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ (with Bonferroni post-hoc test). Only the 33 individuals that were sampled in all three seasons are included. See Figure 2 for definition of box and whisker plot.