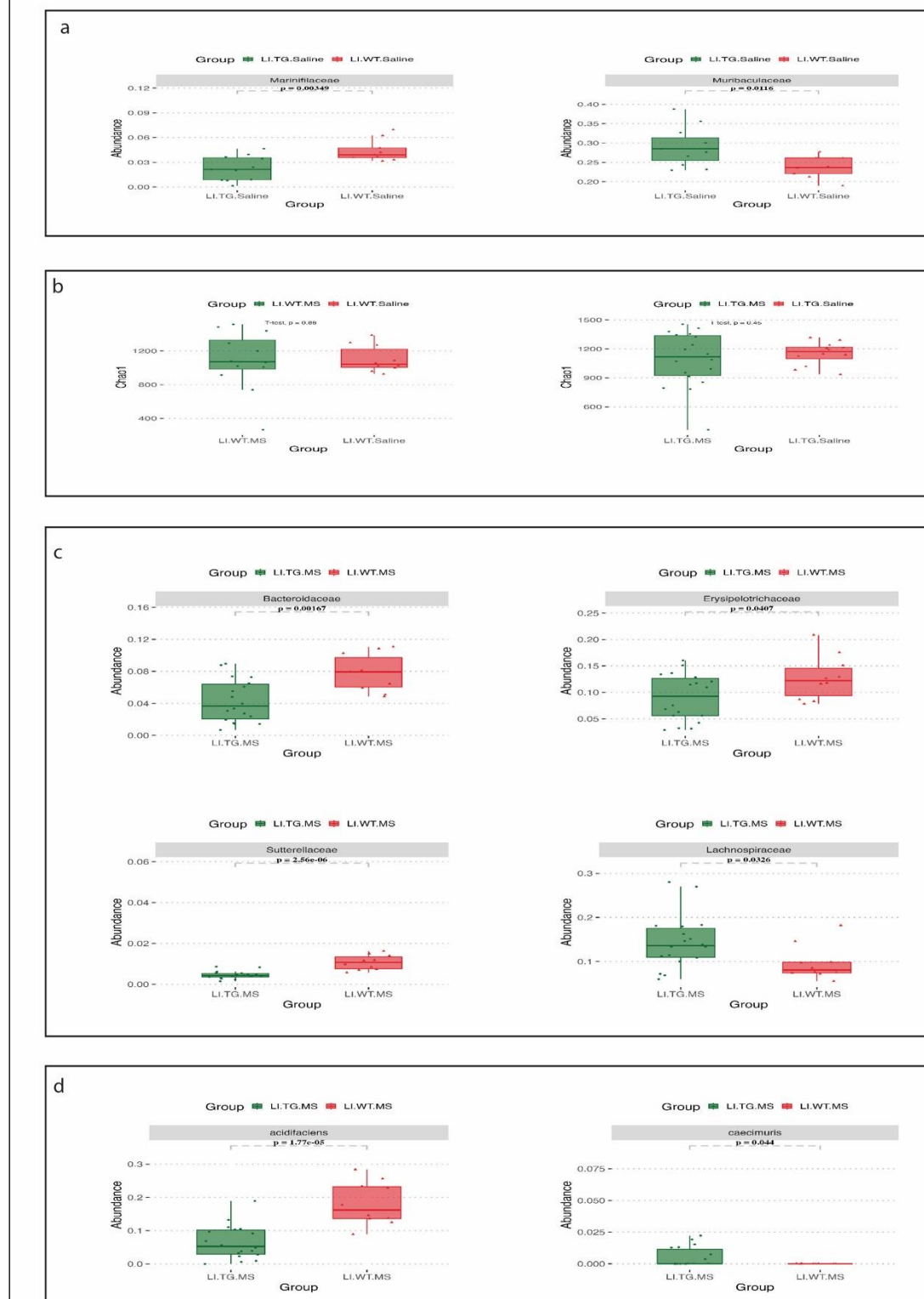


Appendix A

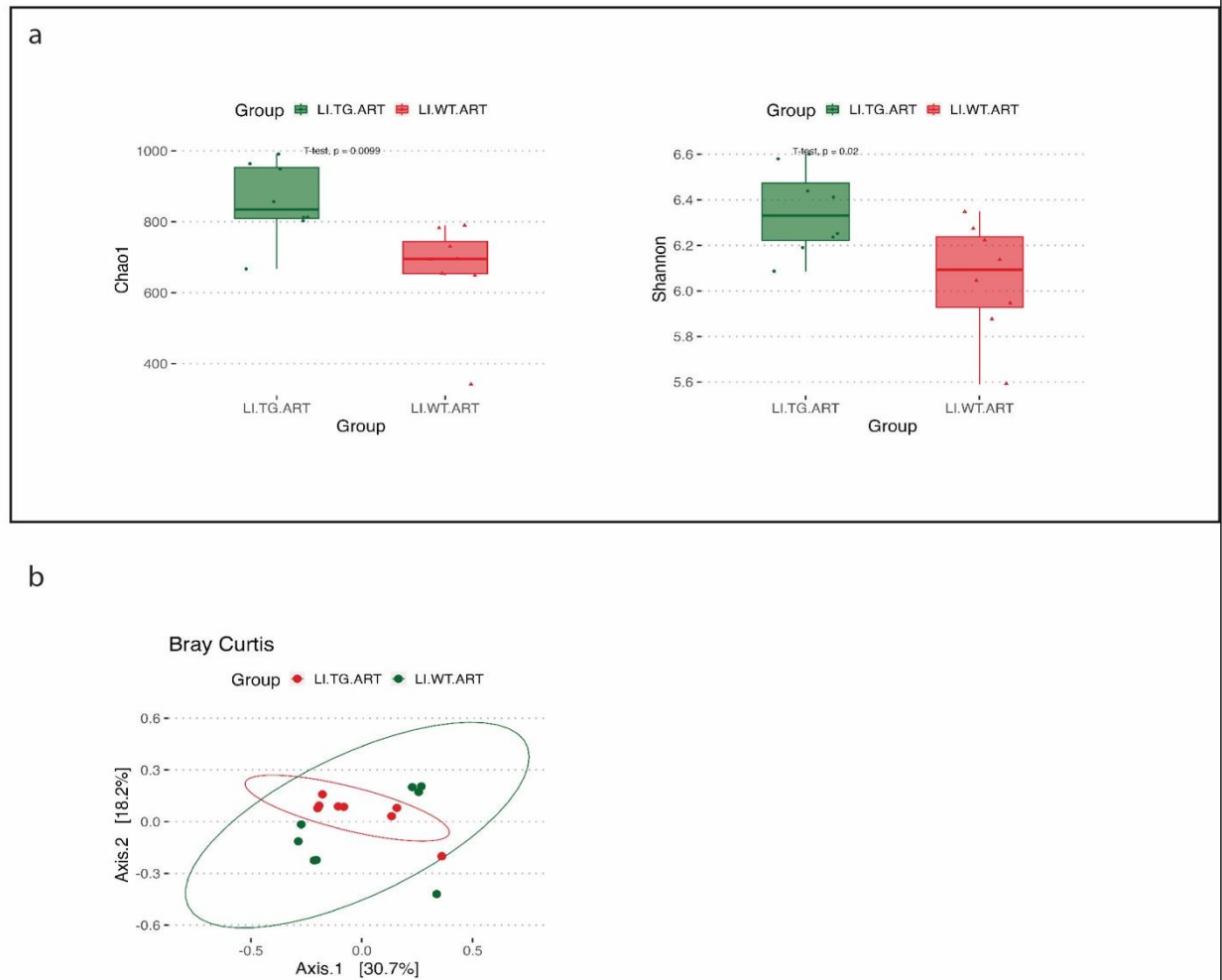
Supplementary Figure 1



Scheme 1. Distinct bacterial community are observed between WT and Tg26 mice before and after morphine treatment. (a) Box plot showing higher abundance of Muribaculaceae family and has lower abundance of Marinifilaceae family of bacteria in Tg26 mice compared to WT mice (b) Morphine treatment did not cause any significant change in alpha diversity in

WT and Tg26 mice compared to saline control. Box plots showing (c) family level and (d) species level changes observed after morphine treatment in Tg26 mice compared to morphine treated WT mice. (n=7-8 per group). Alpha diversity and abundance between the groups were analyzed using the student's t test.

Supplementary Figure 2



Scheme 2. ART treatment modulates the gut microbiome in WT and Tg26 mice. (a) Chao1 and Shannon index show a significant decrease in alpha diversity in WT mice after ART treatment compared to Tg26 mice after ART treatment (b) PCoA plot using Bray-Curtis show overlapping bacterial community in ART treated WT and Tg26 mice microbiome. (n=7-8 per group). Alpha diversity and abundance between the groups were analyzed using the student's t test and beta diversity was analyzed using the PERMANOVA.