IMPACT OF THE BACTERIAL NASOPHARYNGEAL MICROBIOTA ON THE SEVERITY OF GENUS ENTEROVIRUS LOWER RESPIRATORY TRACT INFECTION IN CHILDREN: A CASE-CONTROL STUDY

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Abstract

Introduction Rhinoviruses (RV) and Enteroviruses (EV) are among the main causative etiologies of Lower Respiratory Tract Infection (LRTI) in children. The clinical spectrum of RV/EV infection is wide, which could be explained by diverse environmental, pathogen-, and host-related factors. Little is known about the nasopharyngeal microbiota as a risk factor or disease modifier for RV/EV infection in pediatric patients. This study describes distinct nasopharyngeal microbiota profiles according to RV/EV LRTI status in children. **Methods** Cross-sectional case-control study, conducted at Hospital Sant de Déu (Barcelona, Spain) from 2017 to 2020. Three groups of children <5 years were included: healthy controls without viral detection (Group A), mild or asymptomatic controls with RV/EV infection (Group B), and cases with severe RV/EV infection admitted to the pediatric intensive care unit (PICU) (Group C). Nasopharyngeal samples were collected from participants for viral DNA/RNA detection by multiplex-PCR and bacterial microbiota characterization by 16S rRNA gene sequencing. **Results** A total of 104 subjects were recruited (A=17, B=34, C=53). Children's nasopharyngeal microbiota composition varied according to their RV/EV infection status. Richness and diversity were decreased among children with severe infection. Nasopharyngeal microbiota profiles enriched in genus *Dolosigranulum* were related to respiratory health, while genus *Haemophilus*was specifically predominant in children with severe RV/EV LRTI. Children with mild or asymptomatic RV/EV infection showed an intermediate profile. **Conclusions** These results suggest a close relationship between the nasopharyngeal microbiota and different clinical presentations of RV/EV infection.

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Figure 1. Alpha diversity metrics (Observed richness, Chao1 estimator and Shannon diversity index) between study groups.

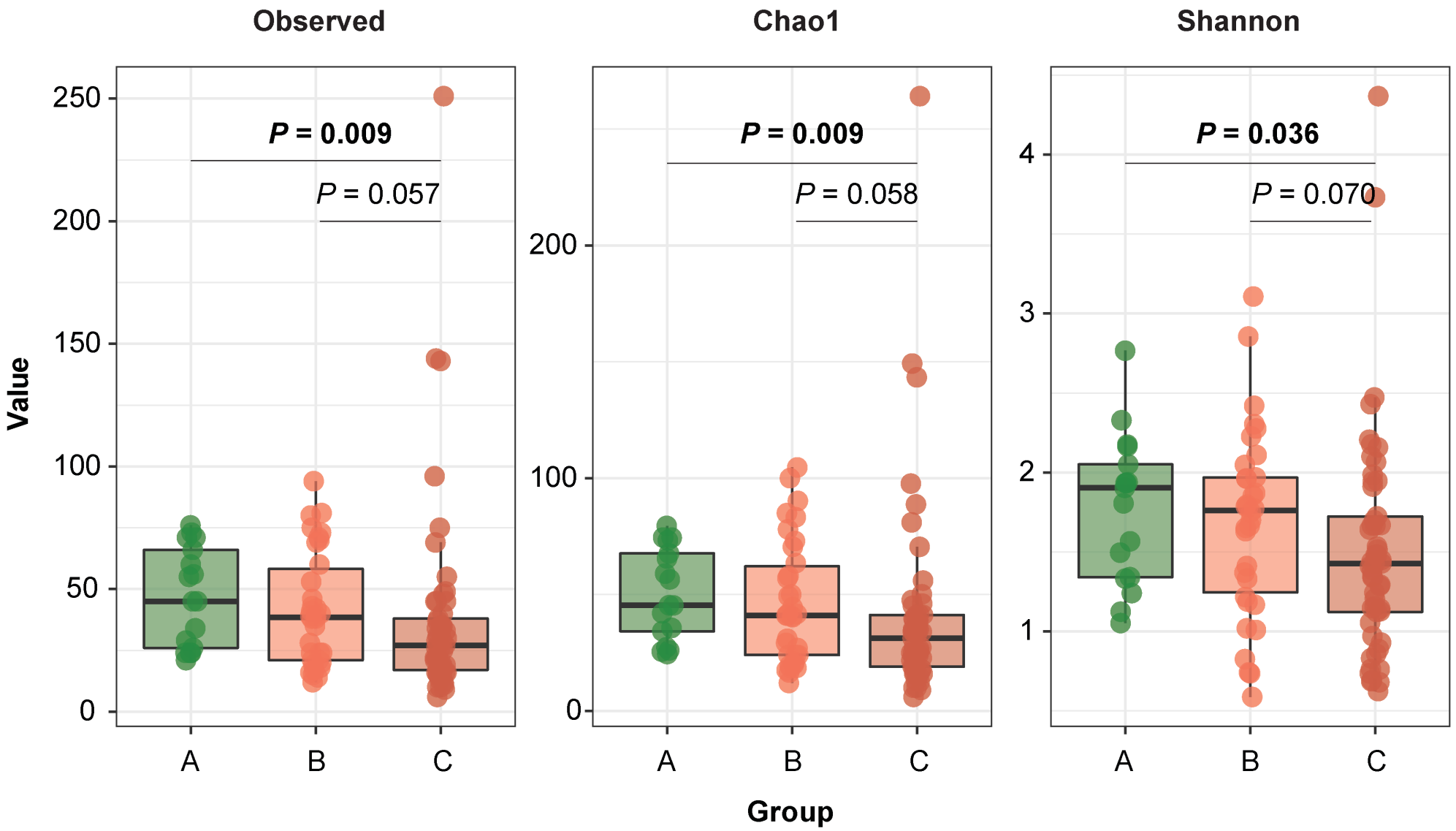


Figure 2. Overall nasopharyngeal bacterial genera composition between study groups.

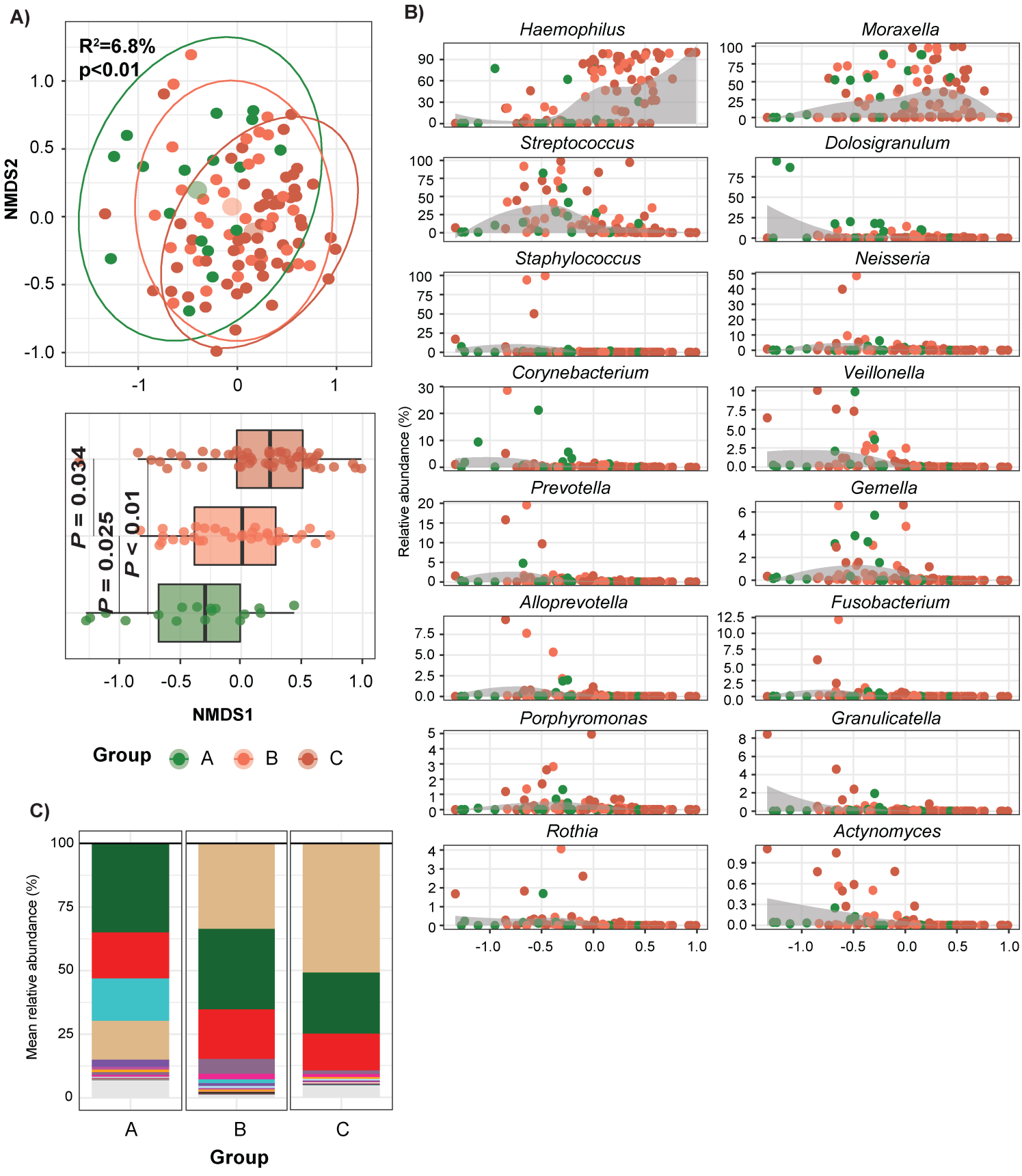
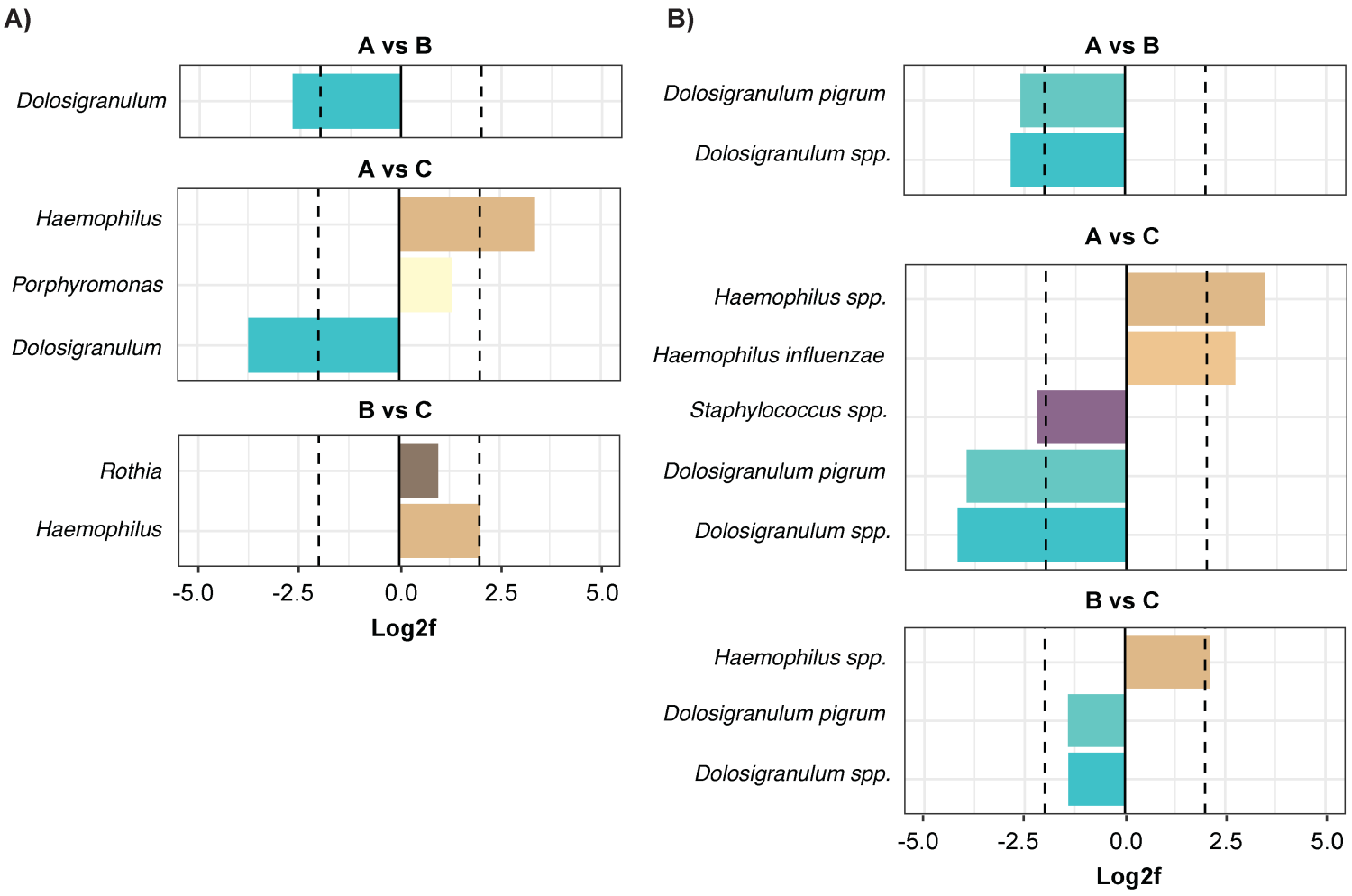
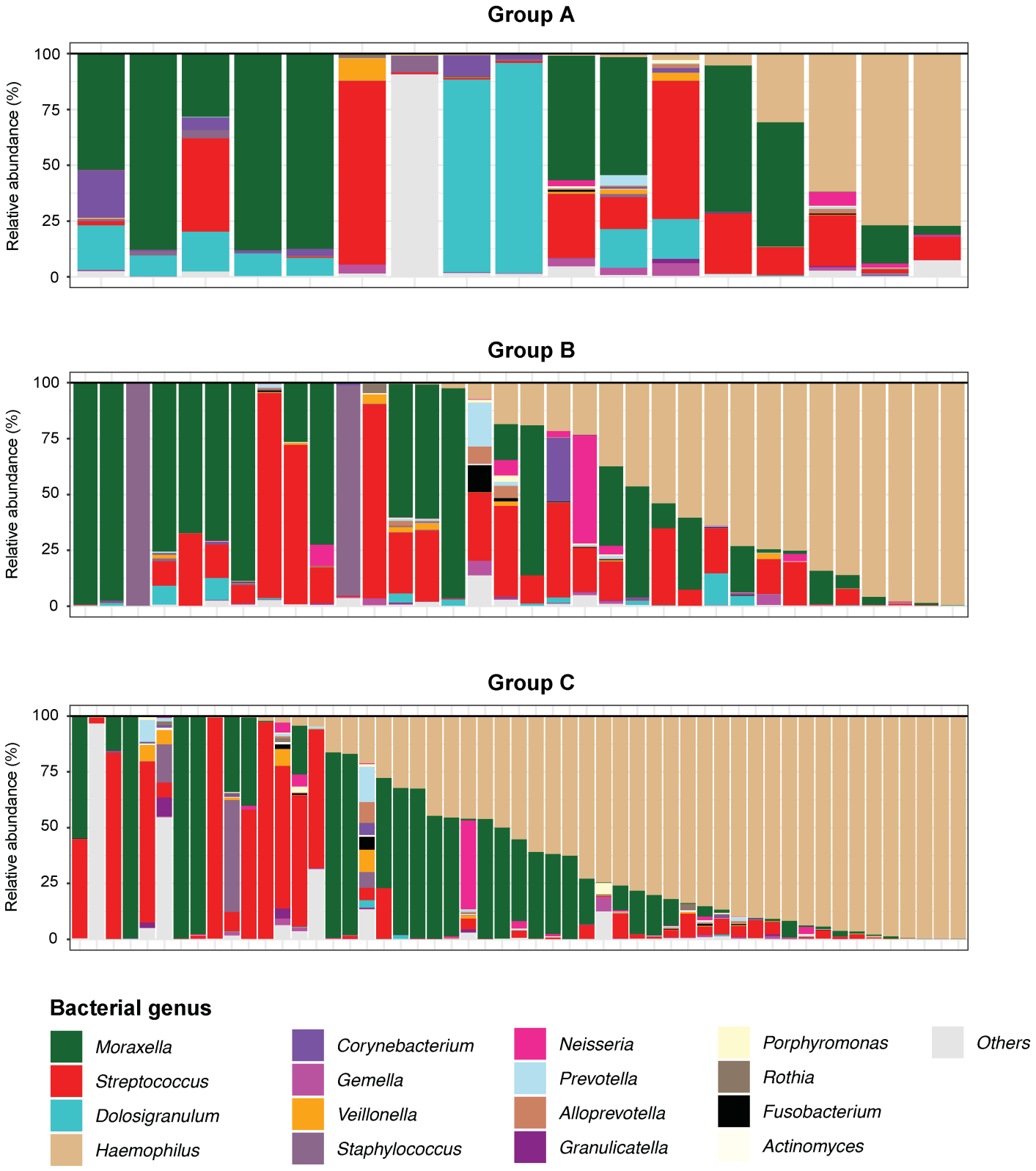


Figure 3. Differentially abundant bacterial taxa by RV/EV infection status and severity.



e-Figure1. Bacterial genera microbiota profiling by subject.



e-Figure2. Spearman correlations between bacterial genera.