

Supplementary Information:

Comparison of the Microbiota and Inorganic Anion Content in the Saliva of Patients with Gastroesophageal Reflux Disease and Gastroesophageal Reflux Disease-Free Individuals

Elvira E. Ziganshina,¹ Ildar I. Sagitov,² Ramilya F. Akhmetova,¹ Gulshat T. Saleeva,² Andrey P. Kiassov,³ Natalya E. Gogoleva,⁴ Elena I. Shagimardanova,⁴ and Ayrat M. Ziganshin¹

¹Department of Microbiology, Institute of Fundamental Medicine and Biology, Kazan (Volga Region) Federal University, Kazan 420008, Russia

²Department of Orthopedic Dentistry, Kazan State Medical University, Kazan 420012, Russia

³Department of Morphology and General Pathology, Institute of Fundamental Medicine and Biology, Kazan (Volga Region) Federal University, Kazan 420008, Russia

⁴Laboratory of Extreme Biology, Institute of Fundamental Medicine and Biology, Kazan (Volga Region) Federal University, Kazan 420021, Russia

* E-mail: ayrat.ziganshin@kpfu.ru (A.M. Ziganshin).

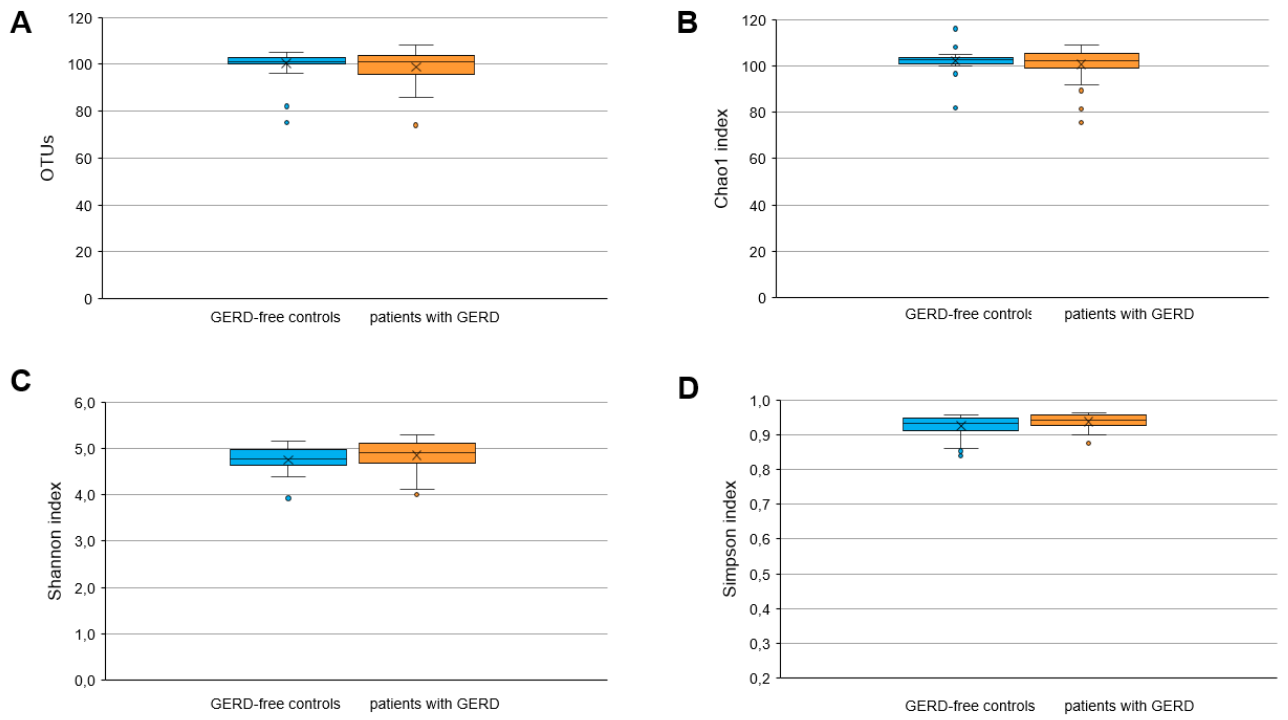


Figure S1. Calculation of the alpha diversity indices for the salivary bacterial communities associated with gastroesophageal reflux disease-free subjects and patients with gastroesophageal reflux disease (A – observed OTUs; B – Chao1 index; C – Shannon index; D – Simpson index).

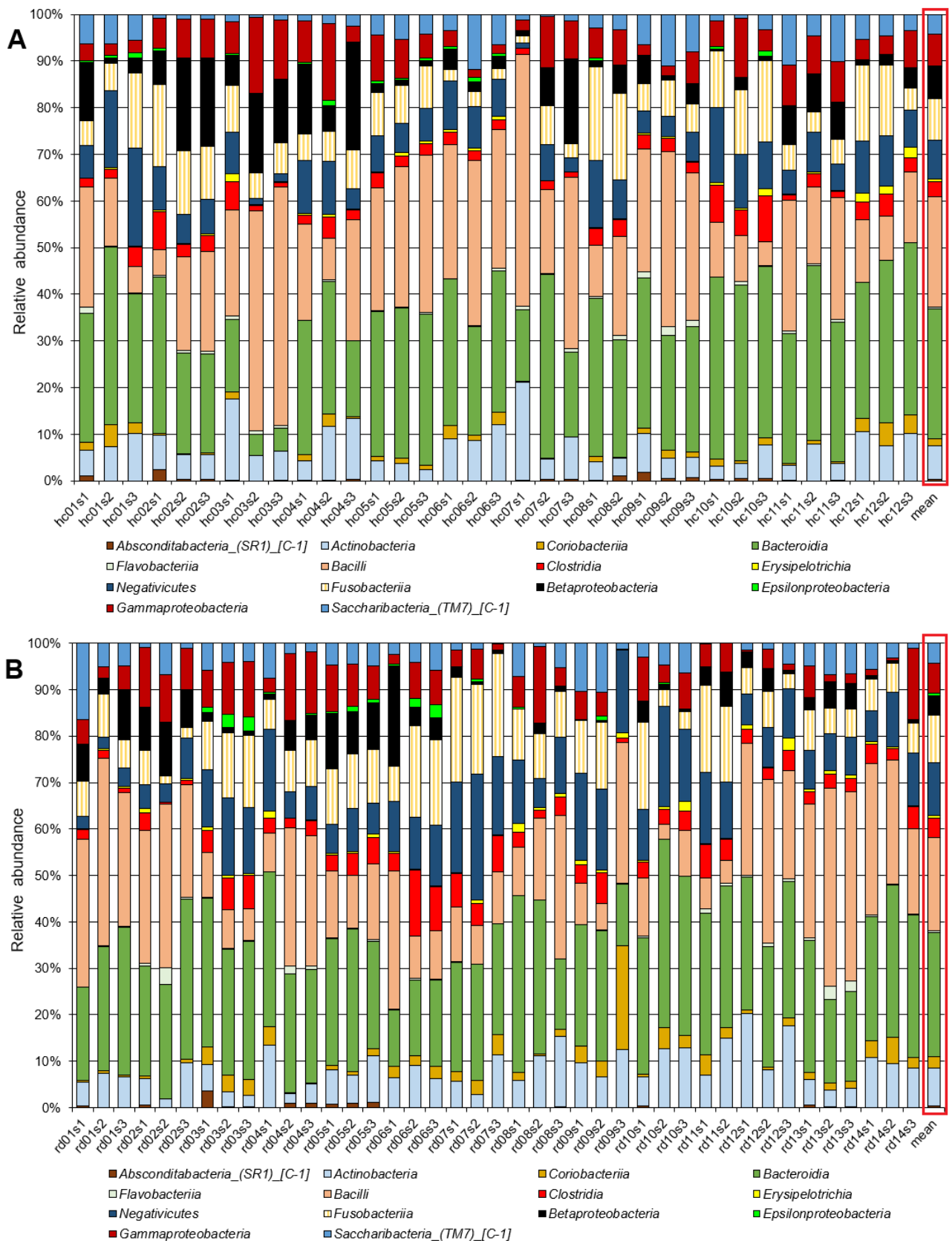


Figure S2. Taxonomic composition of the salivary bacterial communities for (A) gastroesophageal reflux disease-free subjects and (B) patients with gastroesophageal reflux disease. Bacterial community composition according to sequencing of 16S rRNA gene is shown on the class level. In the framed red box, a summary of salivary bacterial communities associated with gastroesophageal reflux disease-free controls (hc) and patients with gastroesophageal reflux disease (rd) is demonstrated.