

## Supplementary Figures

# Insights into the bacterial profiles and resistome structures following severe 2018 flood in Kerala, South India

**Soumya Jaya Divakaran <sup>\$1</sup>, Jamiema Sara Philip<sup>\$1</sup>, Padma Chereddy<sup>1</sup>, Sai Ravi Chandra Nori<sup>1</sup>, Akshay Jaya Ganesh<sup>1</sup>, Jiffy John<sup>1</sup>, Shijulal Nelson-Sathi<sup>1\*</sup>**

<sup>1</sup>Interdisciplinary Biology, Rajiv Gandhi Centre for Biotechnology (RGCB), Thiruvananthapuram, India

\* Correspondence: [shijulalns@rgcb.res.in](mailto:shijulalns@rgcb.res.in); Shijulal Nelson-Sathi, Interdisciplinary Biology, Rajiv Gandhi Centre for Biotechnology (RGCB), Thiruvananthapuram, India, Phone: +91-4712781236

\$ These authors contributed equally to this work

**Keywords:** metagenomics; flood; antibiotic resistance; bacterial diversity

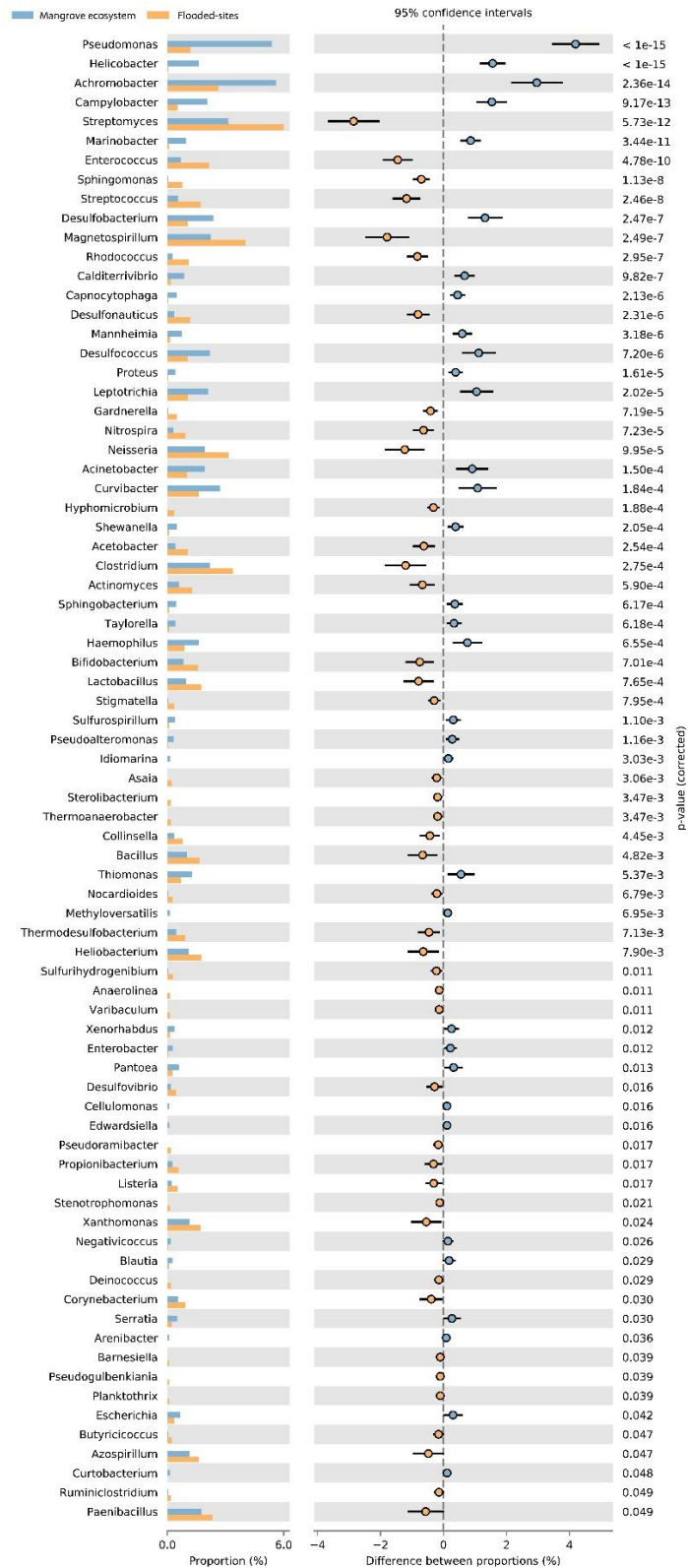


Figure S1: Distribution of 77 genera found at significantly different abundances in the metagenomics profiles of flooded and mangrove settings as identified by STAMP analysis.

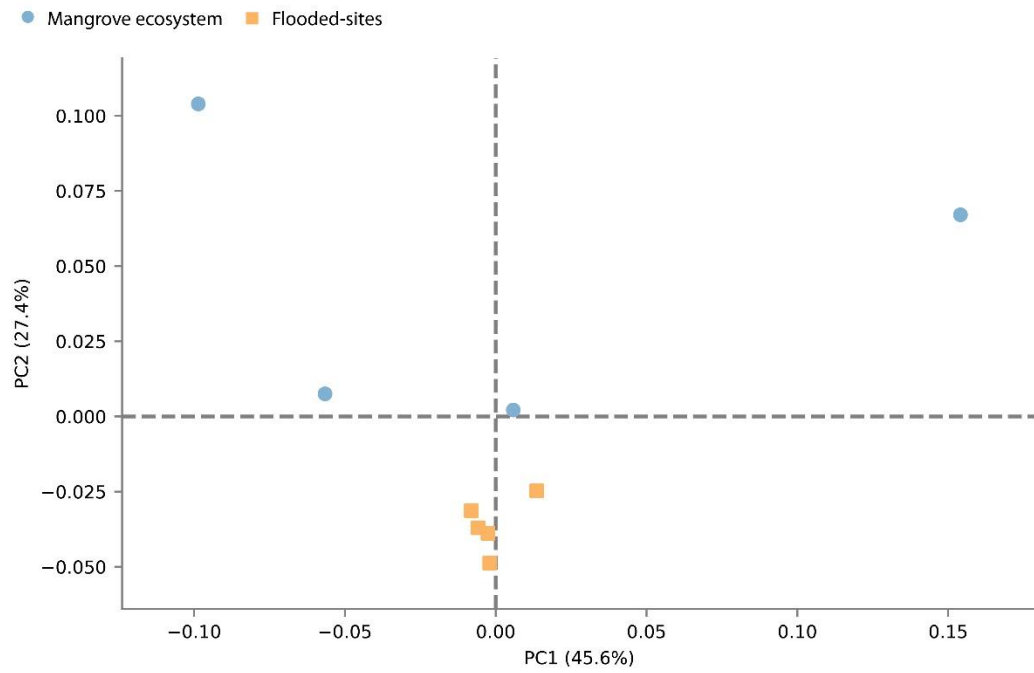


Figure S2: Principal component analysis (PCA) based on relative abundance of bacterial taxa at genus level in mangrove (blue) and flooded (orange) sites using Welch's t-test two sided ( $p < 0.05$ ).

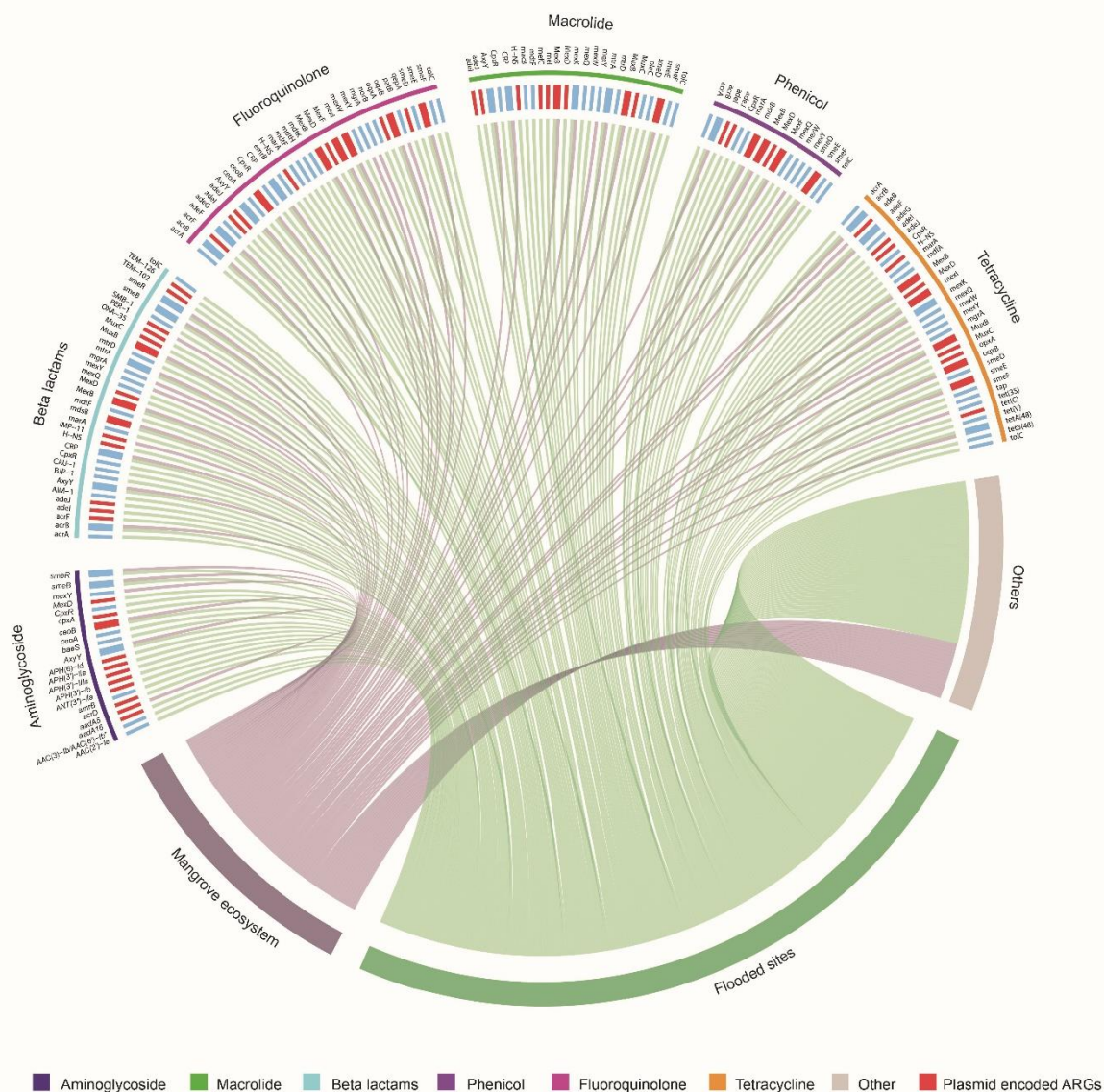


Figure S3: Chord diagram showing the presence of Antibiotic Resistant Genes (ARG) detected in flooded (green) and mangrove (grey) settings.