

Supplementary information for:

Environmental microbiome diversity and stability is a barrier to antimicrobial resistance gene accumulation

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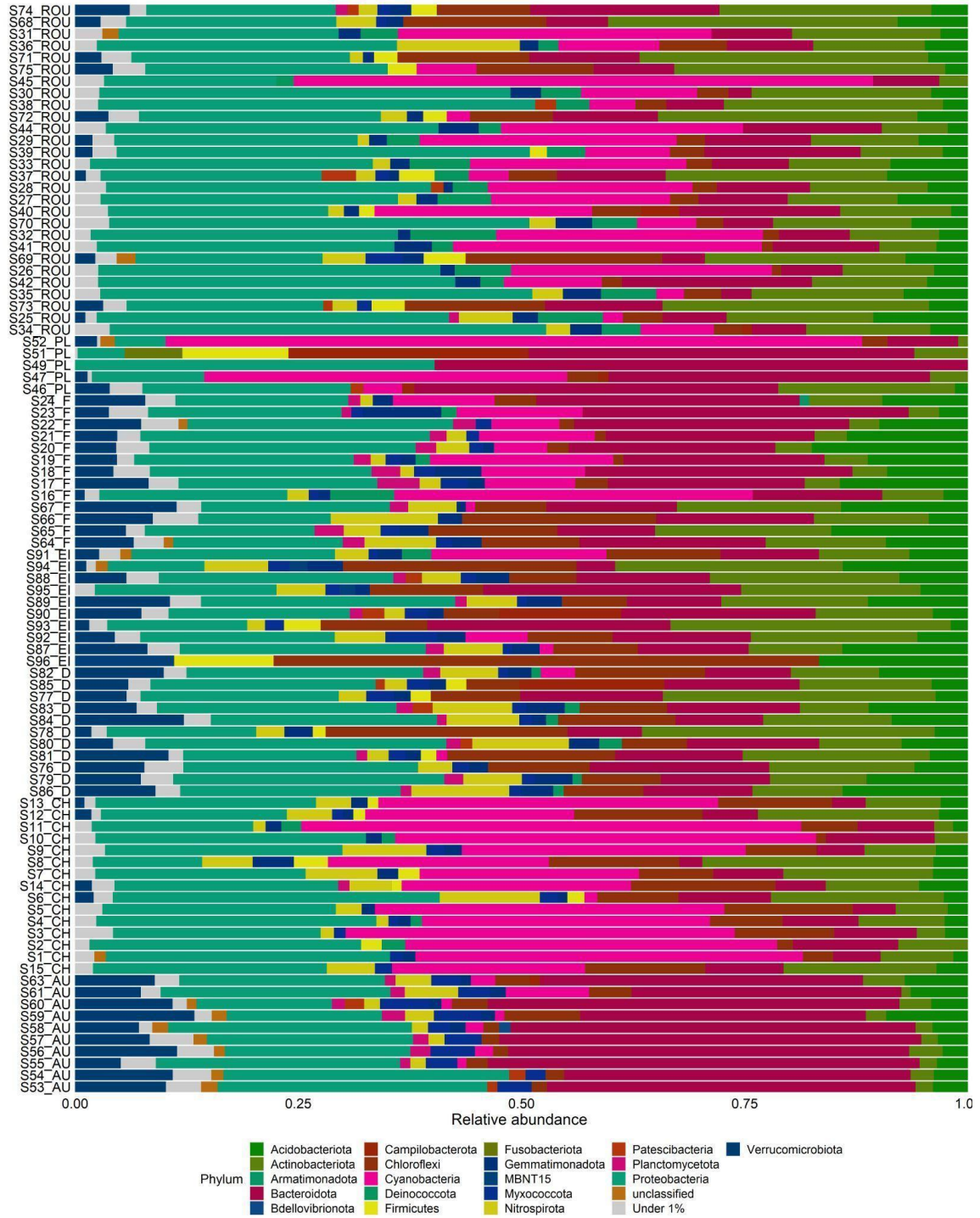
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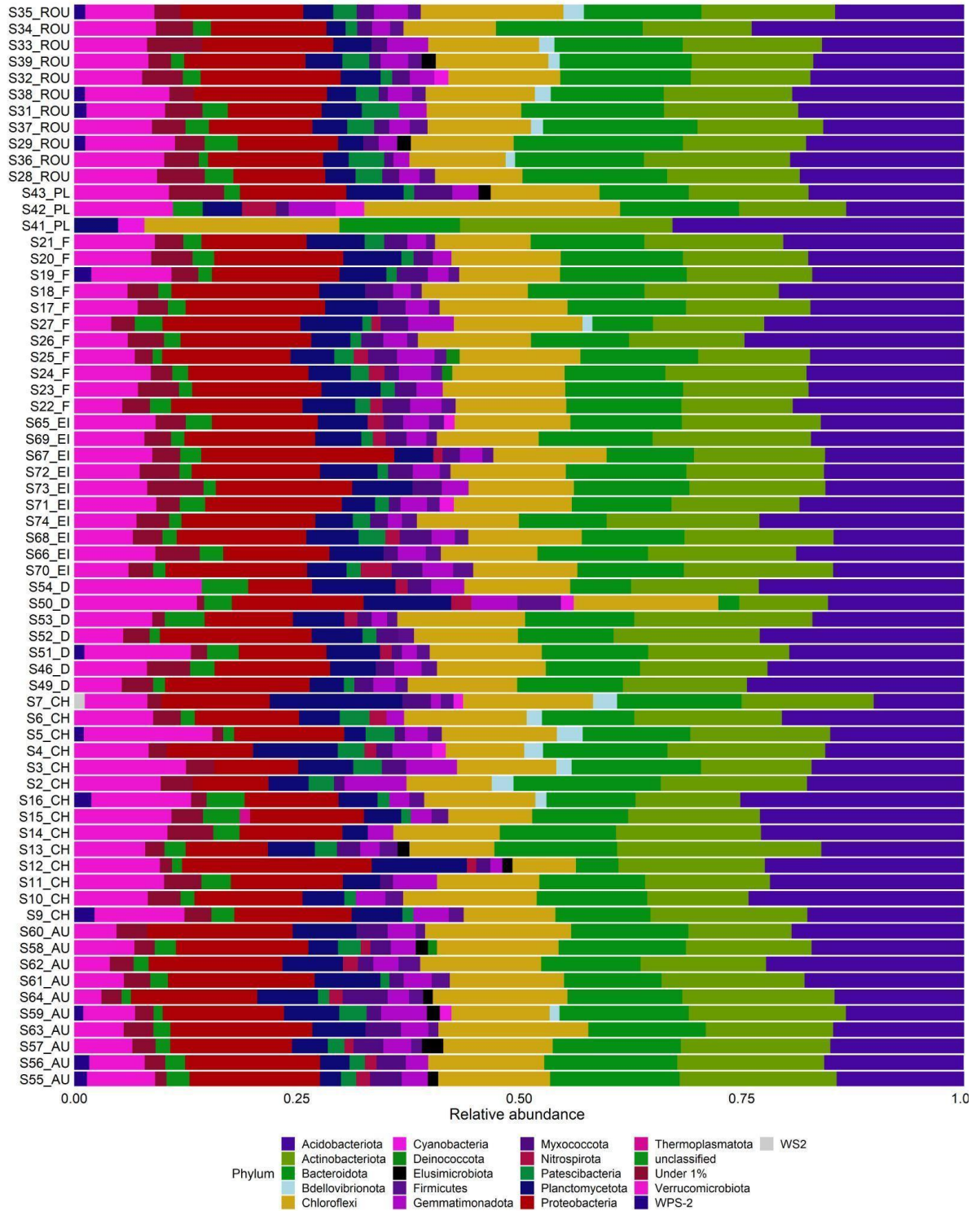
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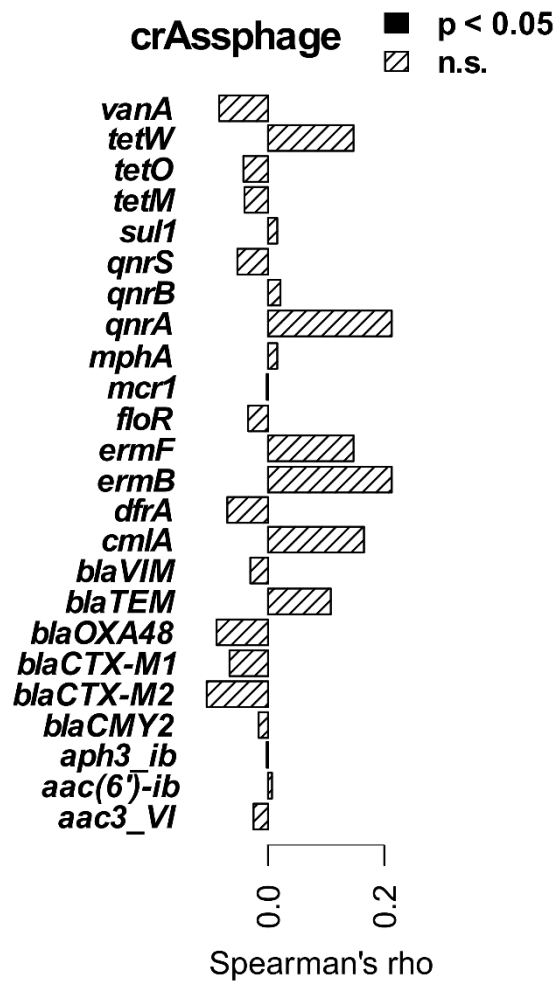
Mail thomas.berendonk@tu-dresden.de



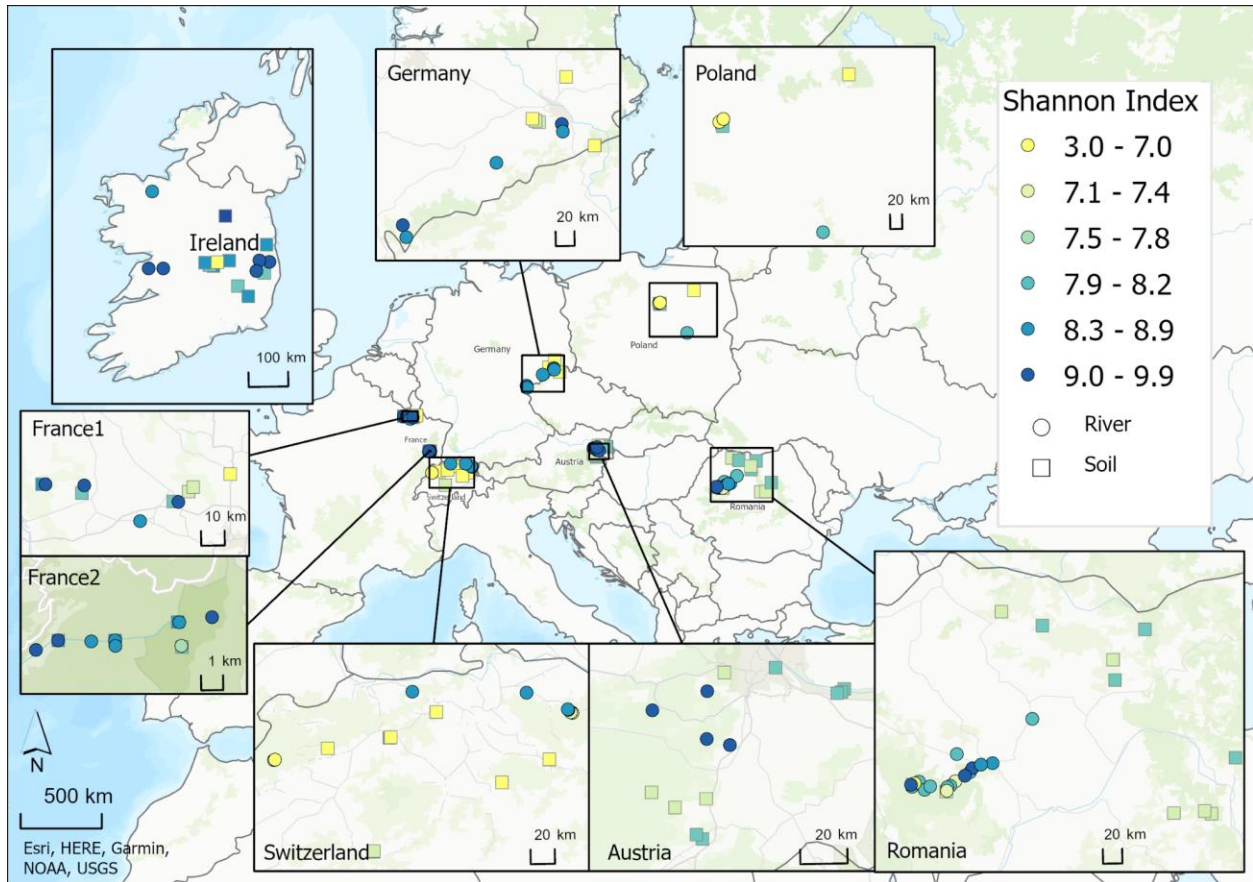
Supplementary Figure 1. Barplot of phylum diversity in all rivers sampled across 7 countries. For each sample, the phyla with less than 1% relative abundance were clustered as “Under 1%” to help with visualization.



Supplementary Figure 2. Barplot of phylum diversity in all soil sampled across 7 countries. For each sample, the phyla with less than 1% relative abundance were clustered as “Under 1%” to help with visualization.



Supplementary Figure 3. Correlation analysis of ARG abundance with observed crAssphage abundance. Spearman rank correlation with Bonferroni correction for multiple testing from river environmental samples are displayed. For soil samples no correlation was possible as crAssphage was not observed in any of the samples. Filled bars represent significant, while hatched bars represent non-significant correlations.



Supplementary Figure 4. Sampling locations across seven European countries. GIS Maps were created in ArcGIS Pro (Esri, Redlands, CA, USA) software using open-source location data. River and regional boundary open-source data was obtained from swisstopo (Swiss Federal Office of Topography) and integrated into the map. River (circle) and soil (square) samples are displayed in the map with their Shannon diversity index indicated through color coding.