

Heavy metal accumulation shaped presence and potential activity of sediment bacteria

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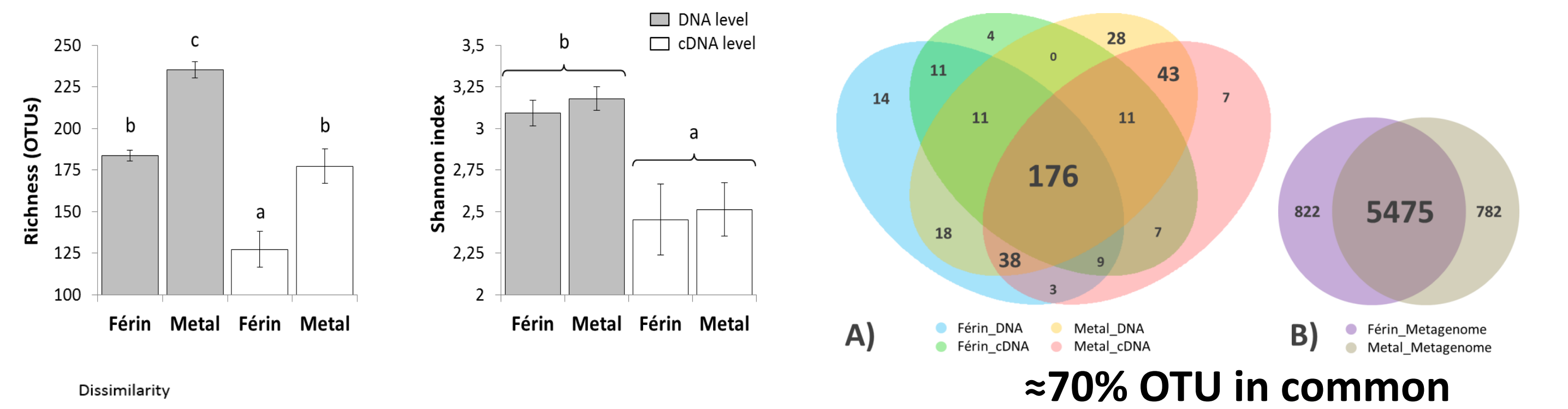


Anthropogenic metal contamination of **sediments** poses serious biotoxicity and bioaccumulation issues. Besides important ecological roles such as organic matter mineralization, bacteria play a key role in metal speciation. The **MetalEurop** foundry released **zinc, copper, cadmium** and **lead** in the “Deûle” river (France) during a century, resulting in present-day metal concentrations in sediments up to 30-fold higher than upstream (**Férin**, control site in the Sensée canal). On the basis of a shotgun metaproteogenomic approach, it was found that sediments (MetalEurop & Férin) harbored phylogenetically analogous microbial communities (Gillan *et al.*, 2015).

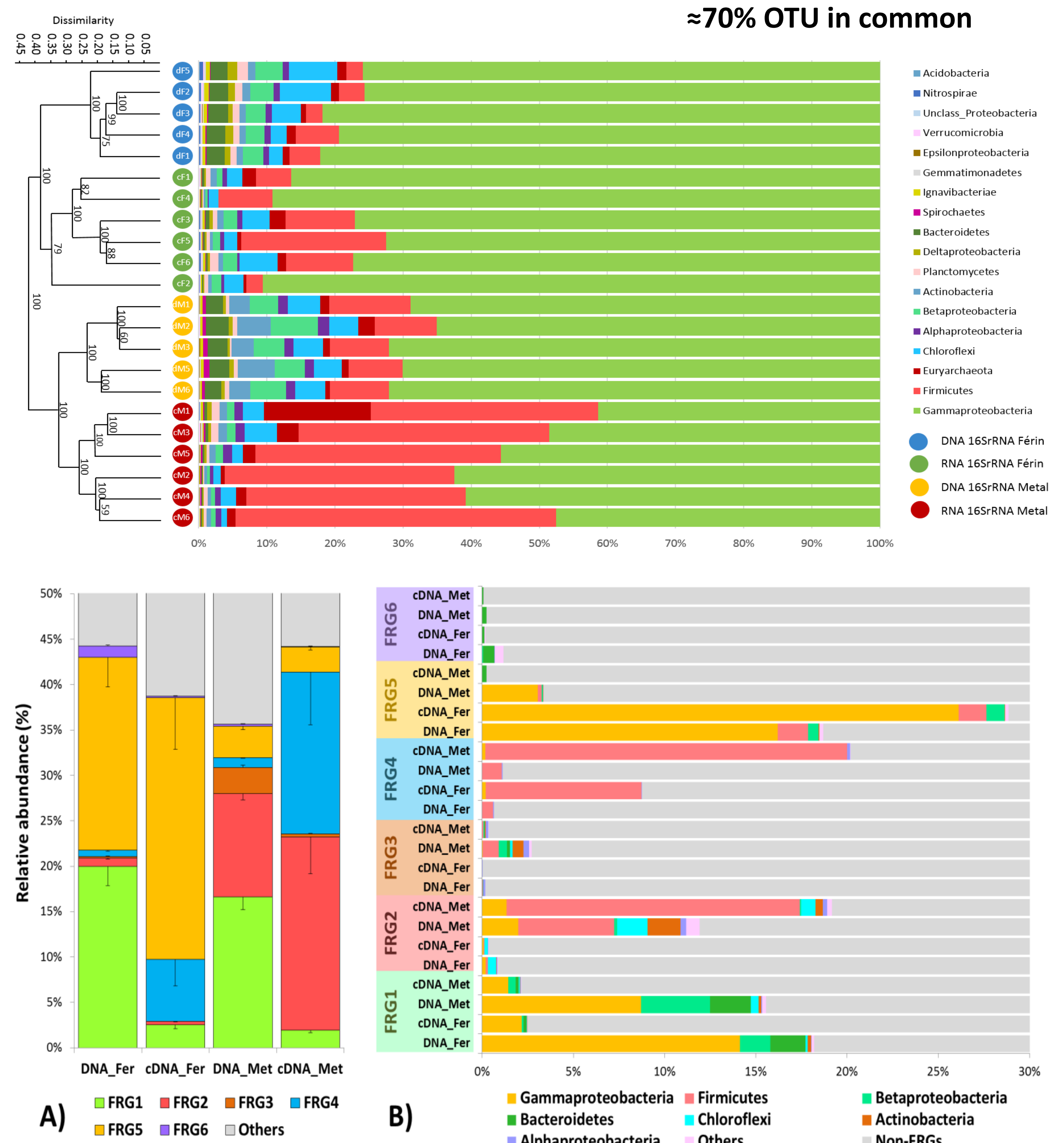
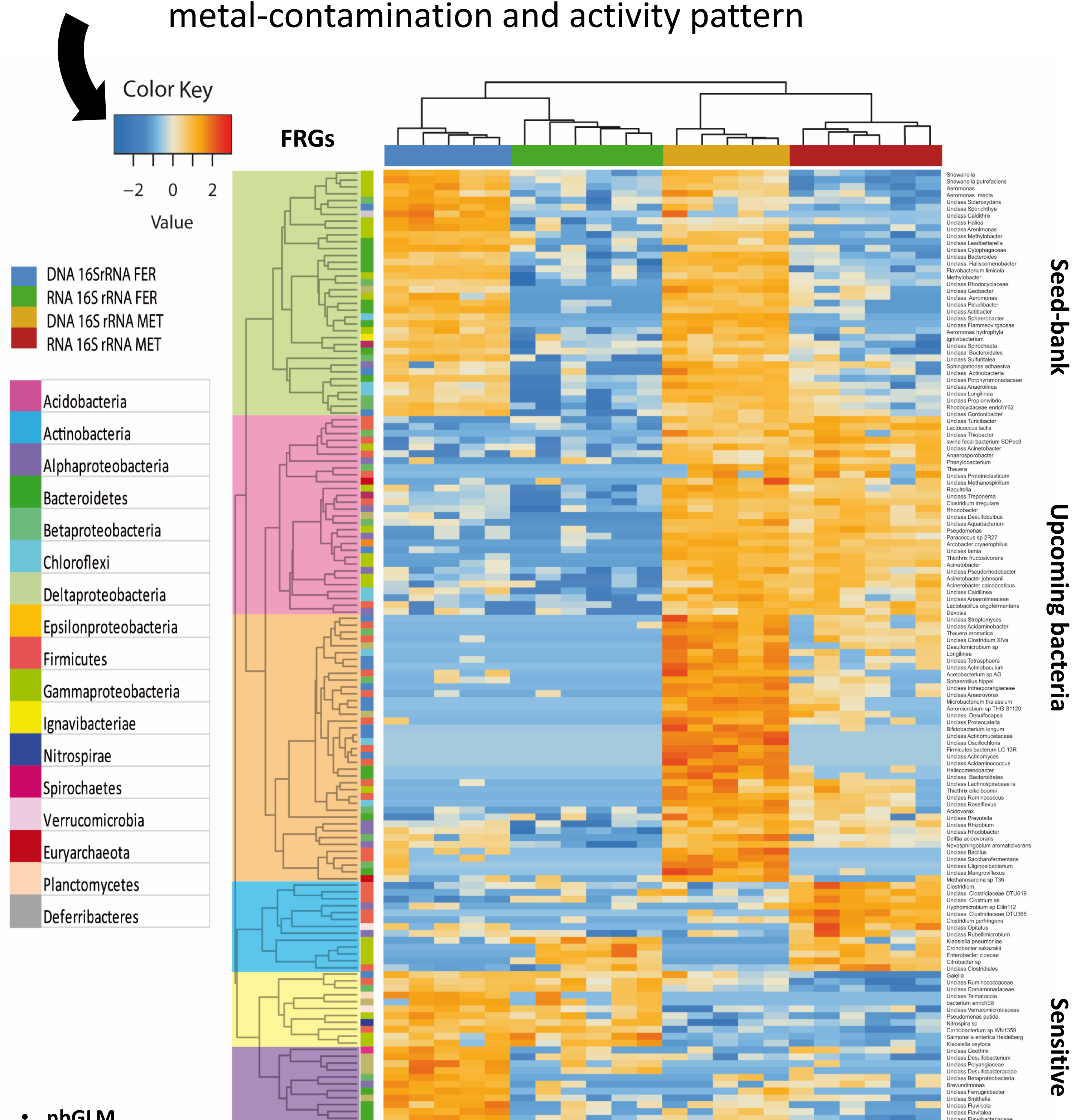


But what about bacterial activity?

This study compares taxonomic profiles of the complete (DNA) and the potentially **active** (RNA) fraction of the **sediment prokaryotic communities** present in MetalEurop and Férin via 16S rRNA **gene amplicon sequencing** (Illumina® MiSeq® 2x250 bp). The ecological concept of **Functional Response Group** was applied to highlight the tolerance and sensitivity levels in the microbial community, linked to the long-term metal pollution (Nunes *et al.*, 2016).



Using nbGLM, we found OTUs responding significantly to metal-contamination and activity pattern



- **Similar communities** dominated by Gammaproteobacteria and Firmicutes.
- **Richness** and Firmicutes activity **increased** in the metal-stressed community.
- The arrival of new bacteria (from upstream or the river banks) combined to the *in situ* metal selection seems to **drive the structure and activity** of the community.
- Anthropogenic metal contamination removes dominant bacteria permitting **specialist/ slow growing** bacteria to thrive better as Verrucomicrobia, Alphaproteobacteria, Acidobacteria
- Some species can act as “**public good**” thanks to metal precipitation contributing to the overall community richness
- In MetalEurop, the increasing richness but similar genetic diversity imply that other mechanisms could explain the previously reported metaproteogenomic functional differences as **Horizontal Gene Transfer**

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REFERENCES: D.C. Gillan *et al.*, 2015, *Environmental microbiology*, 17(6); I. Nunes, *et al.*, 2016, *FEMS Microbiology Ecology* 92(11).

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