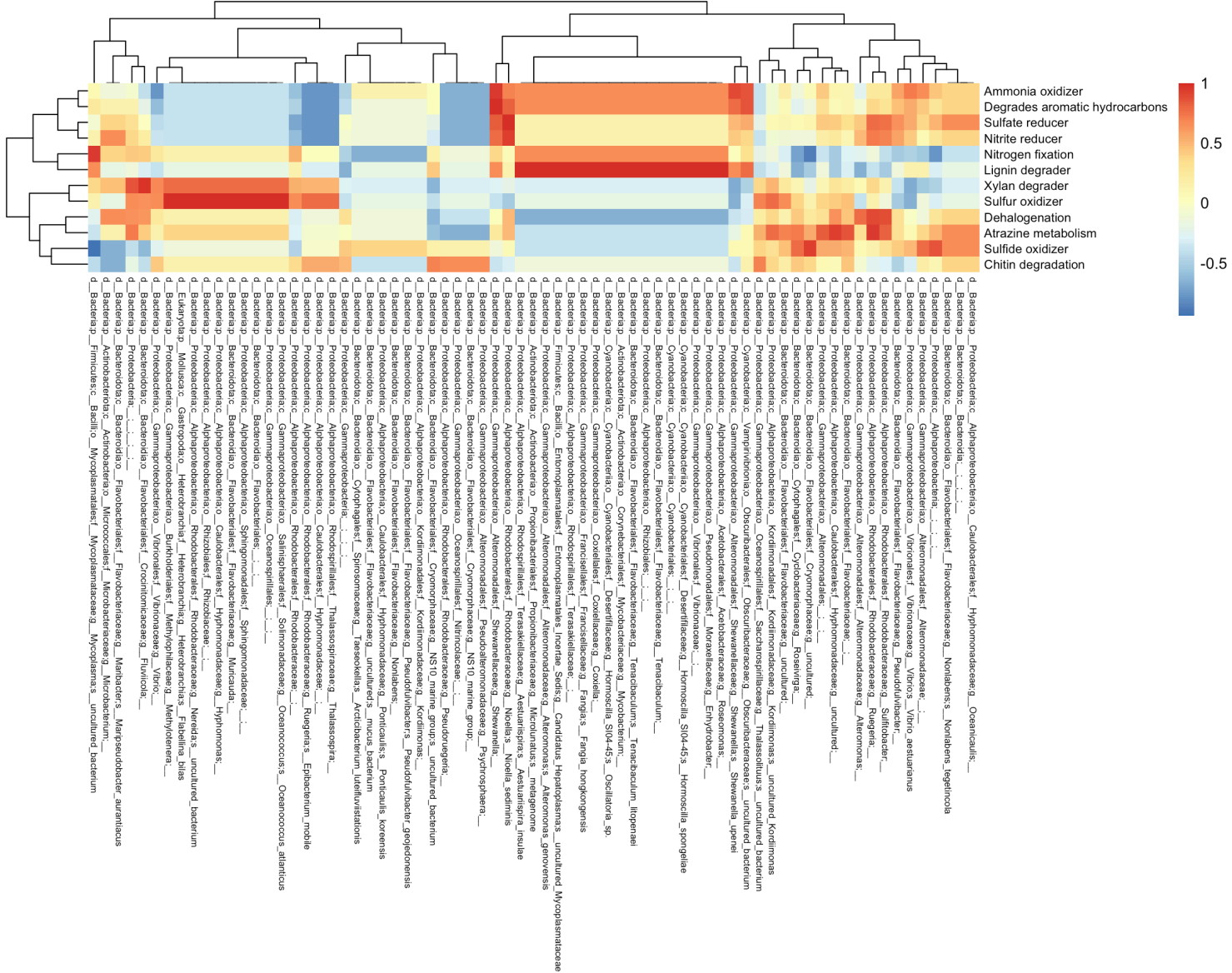


Heatmap showing the relative abundance of 16S rRNA sequences from the Sargassum microbiome across 16 functional categories. The color scale ranges from -0.5 (blue) to 1 (red). The functional categories are: Nitrogen fixation, Chitin degradation, Stores polyhydroxybutyrate, Degrades aromatic hydrocarbons, Nitrite reducer, Ammonia oxidizer, Sulfate reducer, Dehalogenation, Sulfide oxidizer, Xylan degrader, Atrazine metabolism, Denitrifying, Sulfur oxidizer, and Lignin degrader. The heatmap is divided into three main clusters of sequences, each with its own dendrogram on the left. The sequences are labeled with their taxonomic classification, including phylum, class, order, and genus.

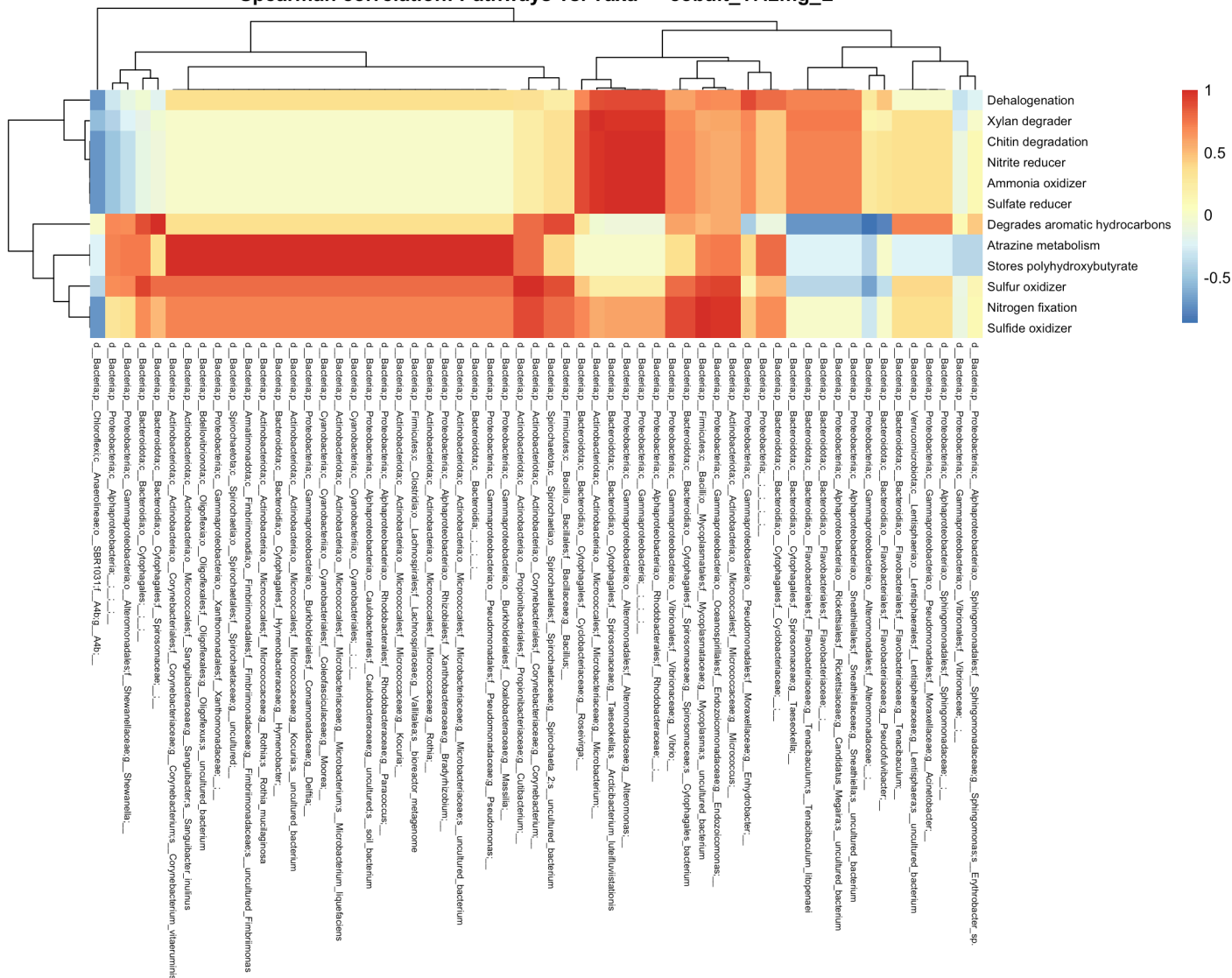
Spearman correlation: Pathways vs. Taxa — cobalt_1mg_L



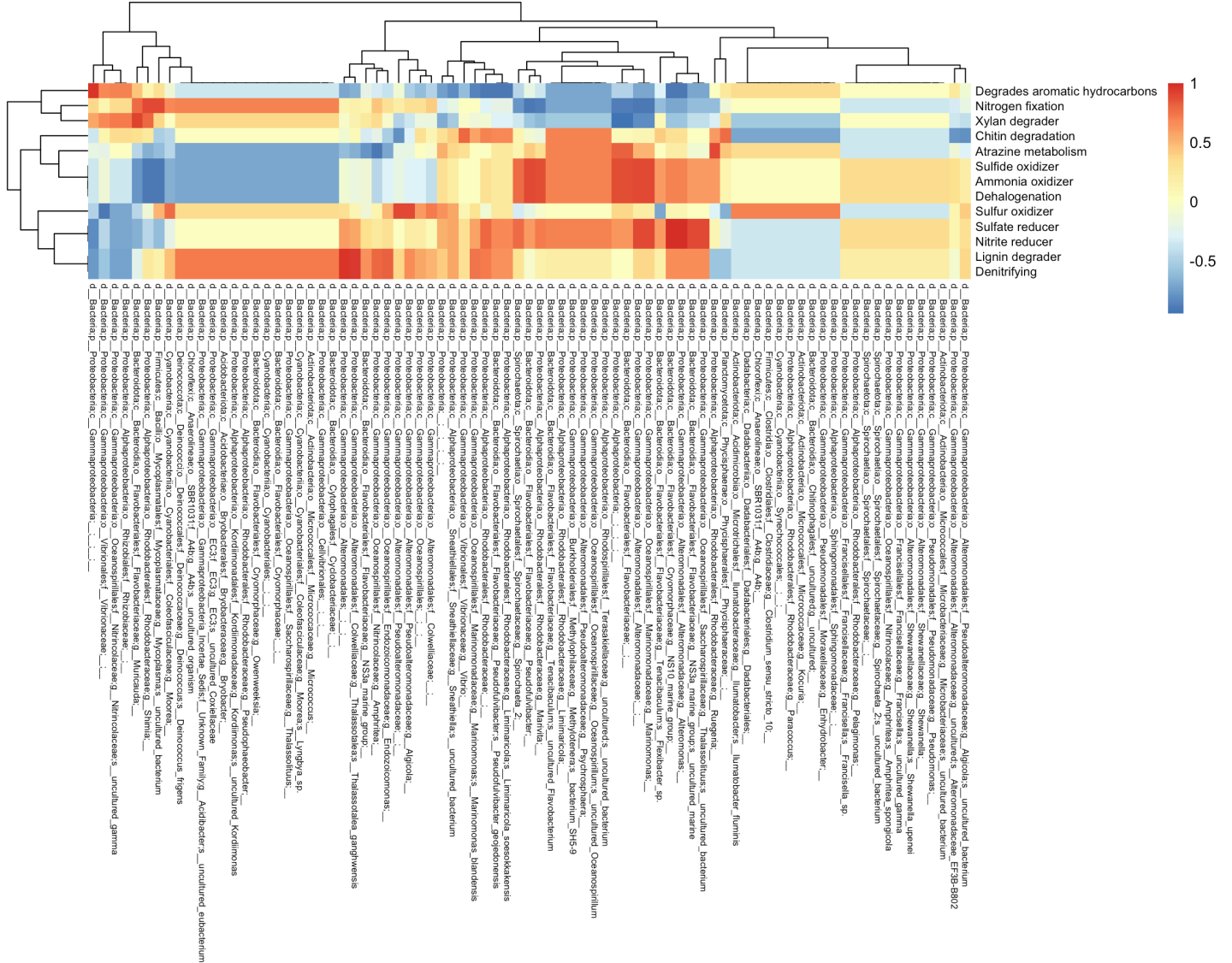
Spearman correlation: Pathways vs. Taxa — cobalt_3mg_L



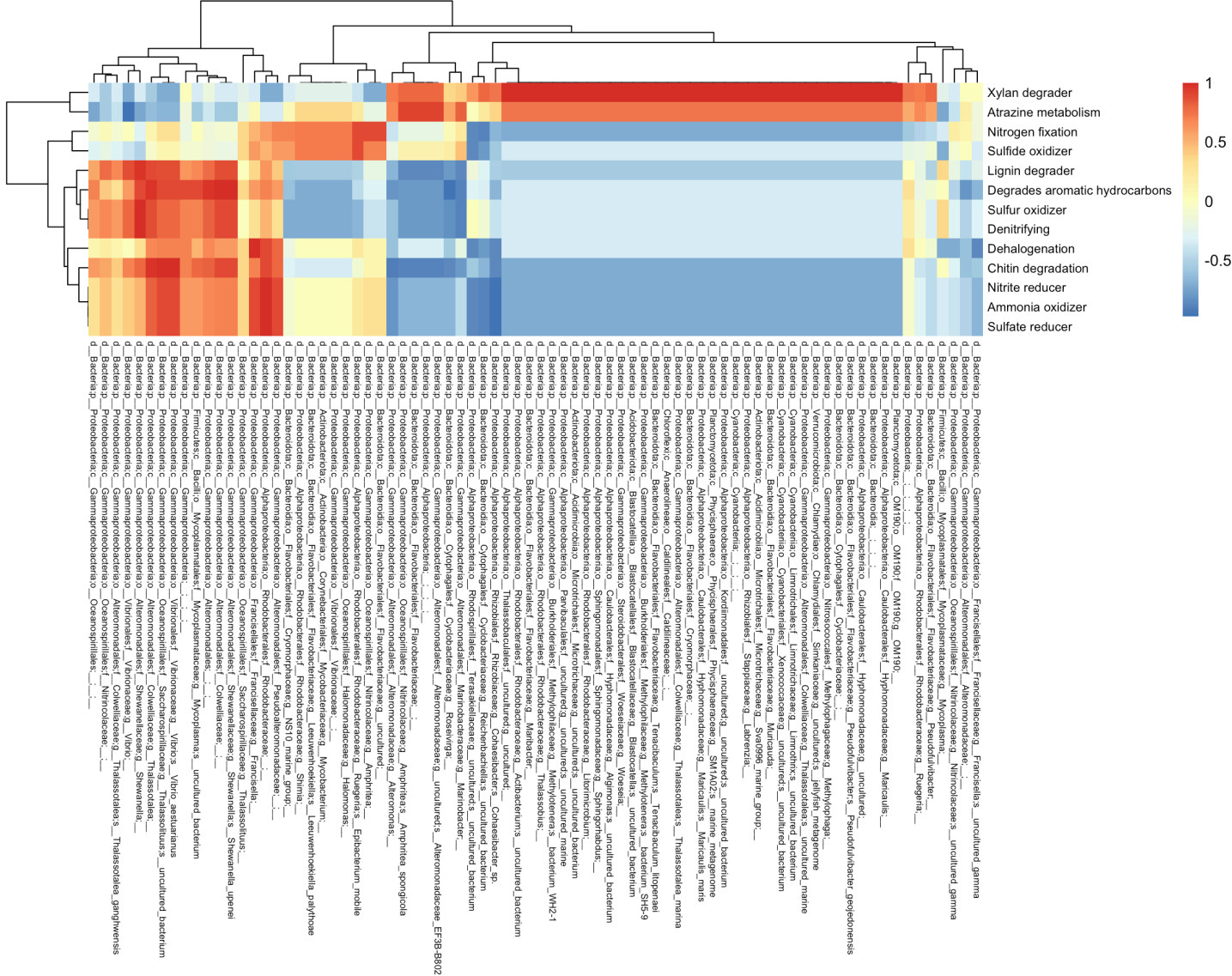
Spearman correlation: Pathways vs. Taxa — cobalt_17.2mg_L



Spearman correlation: Pathways vs. Taxa — nickel_1mg_L



Spearman correlation: Pathways vs. Taxa — nickel_3mg_L



Spearman correlation: Pathways vs. Taxa — nickel_17.2mg_L

