

The Effect of Legacy Gold Mining On Methylmercury Cycling and Microbial Community Structure in Northern Freshwater Lakes

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Figure S1: Partial regression plots for each variable from the regression model in Table 2. Each plots shows the estimated relationship between the response and the explanatory variable after adjusting for the other variables in the model.

Figure S2: Regression plots showing relationship between K_m with respect to sulfate concentrations (A) and %MeHg (B) in water, plot only contains samples that have sulfate concentrations < 40 mg/L.

Figure S3: Boxplots of the two groups of demethylation rate constants (K_d) in lake sediments with respect to the different water chemistry measured. Lakes were categorized as following: lakes with detectable demethylation (>LOQ) and lakes with demethylation below detection limit (<LOQ). (LOQ = limit of quantification)

Figure S4: Methylation and demethylation figures for all lakes. The top panel (pink points) for each lake represents the increase in Me^{199}Hg (i.e. methylation) and the bottom panel (green points) for each lake represents the decrease in Me^{198}Hg (i.e. demethylation). The horizontal red line is the concentration of spiked MeHg at the start ($t=0$) of each incubation.

Figure S5: Relative abundance of microbial Phyla in each lake sediment sample

Table S1: Raw results from ICP-MS analysis of methylmercury isotopes in incubation sediments. For each lake two types of treatment are shown, one spiked with mercury isotopes (spiked) and one that is left unspiked (unspiked).

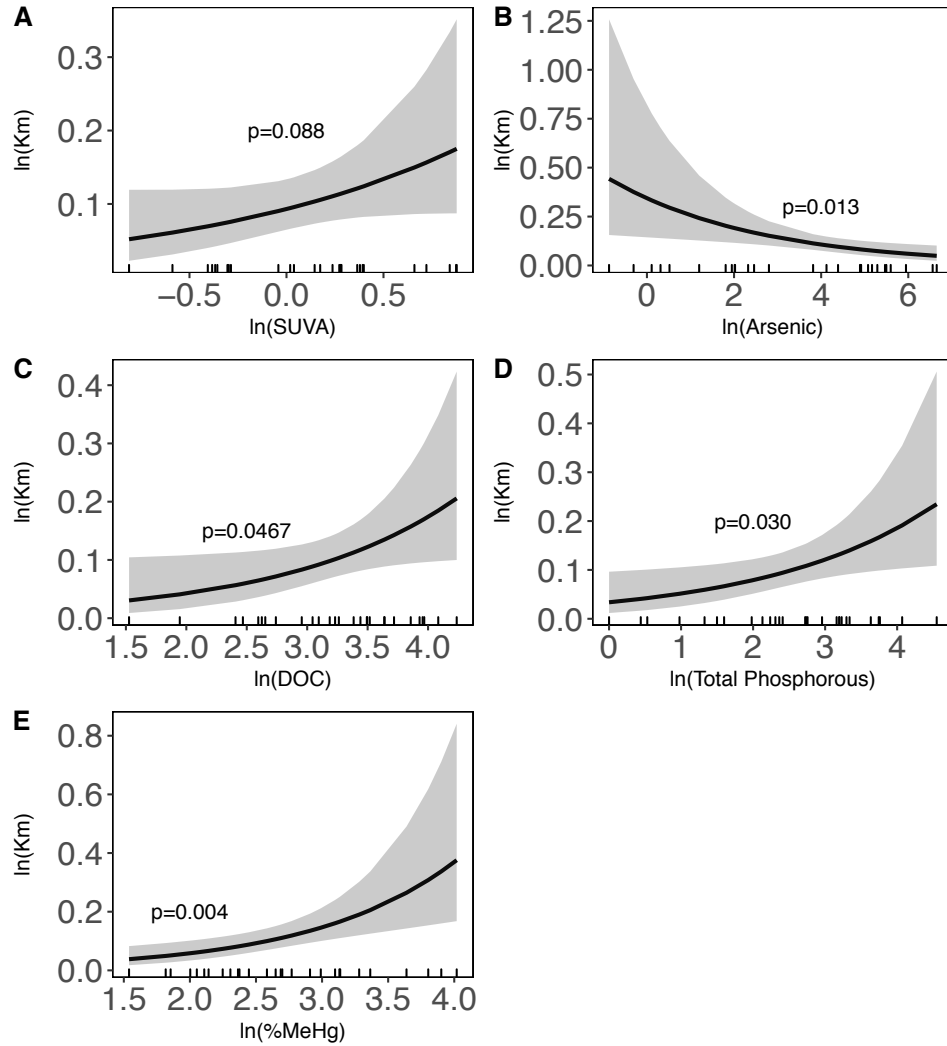


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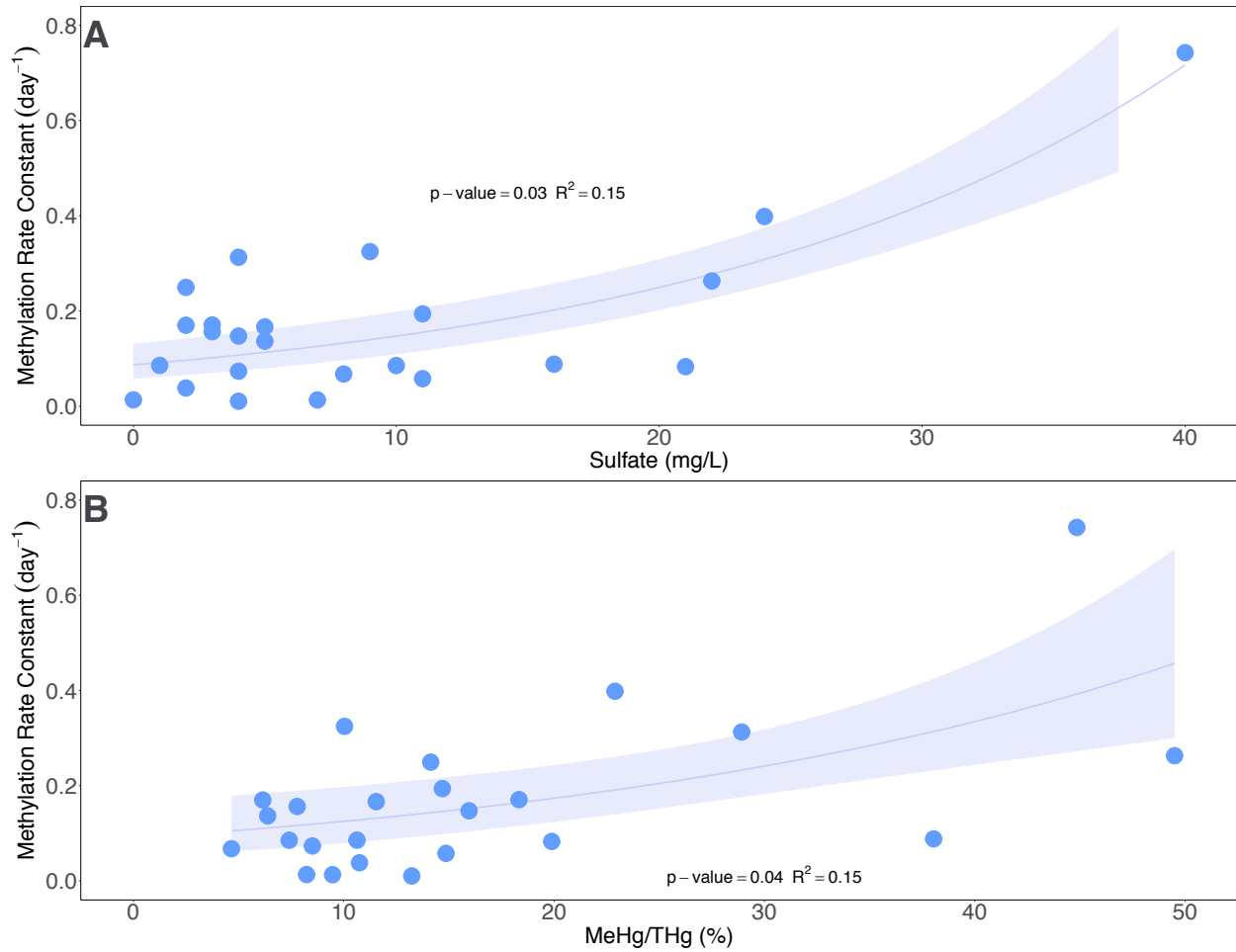


Figure S2: Regression plots showing relationship between K_m with respect to sulfate concentrations (A) and %MeHg (B) in water, plot only contains samples that have sulfate concentrations < 40 mg/L.

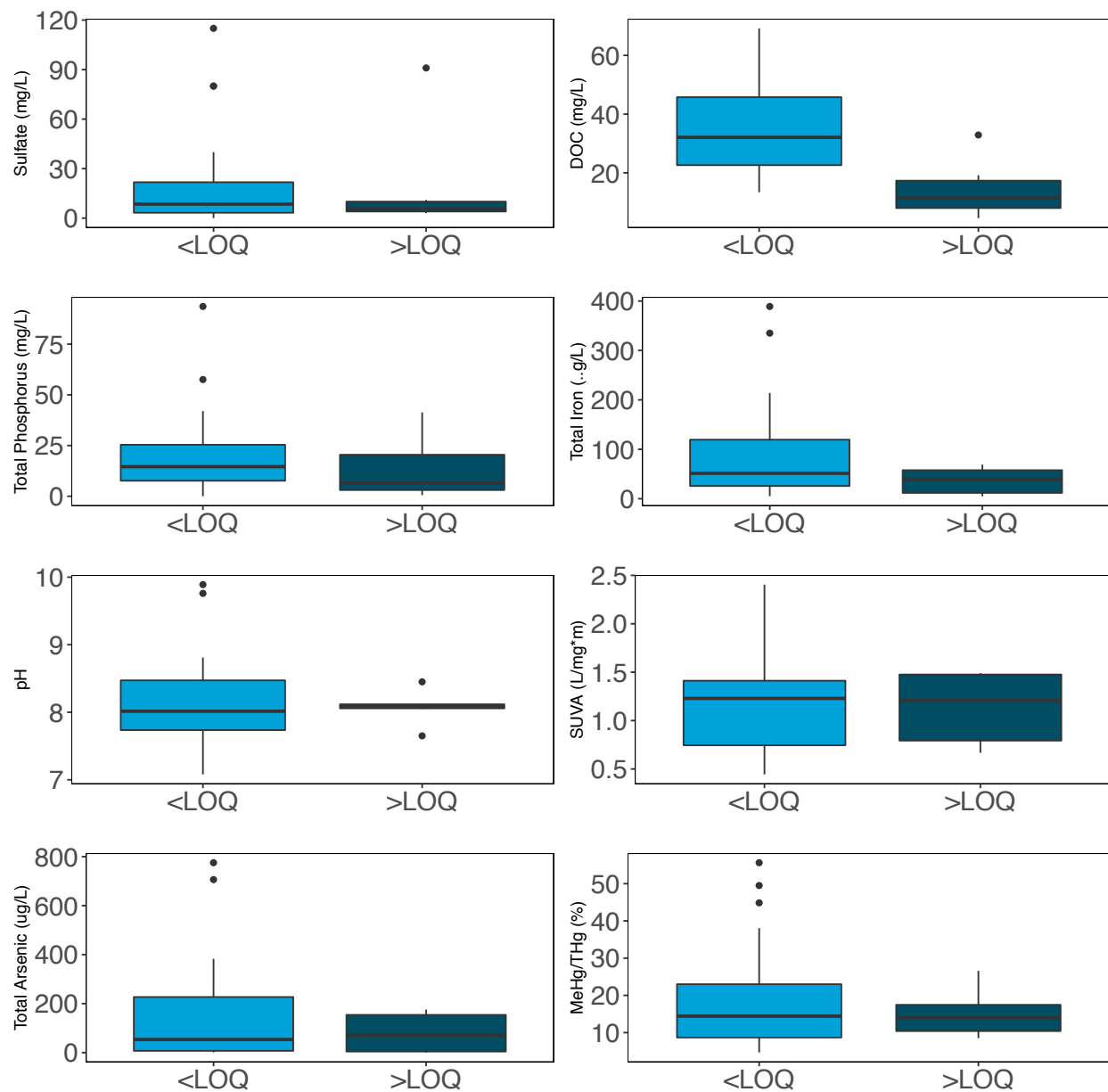
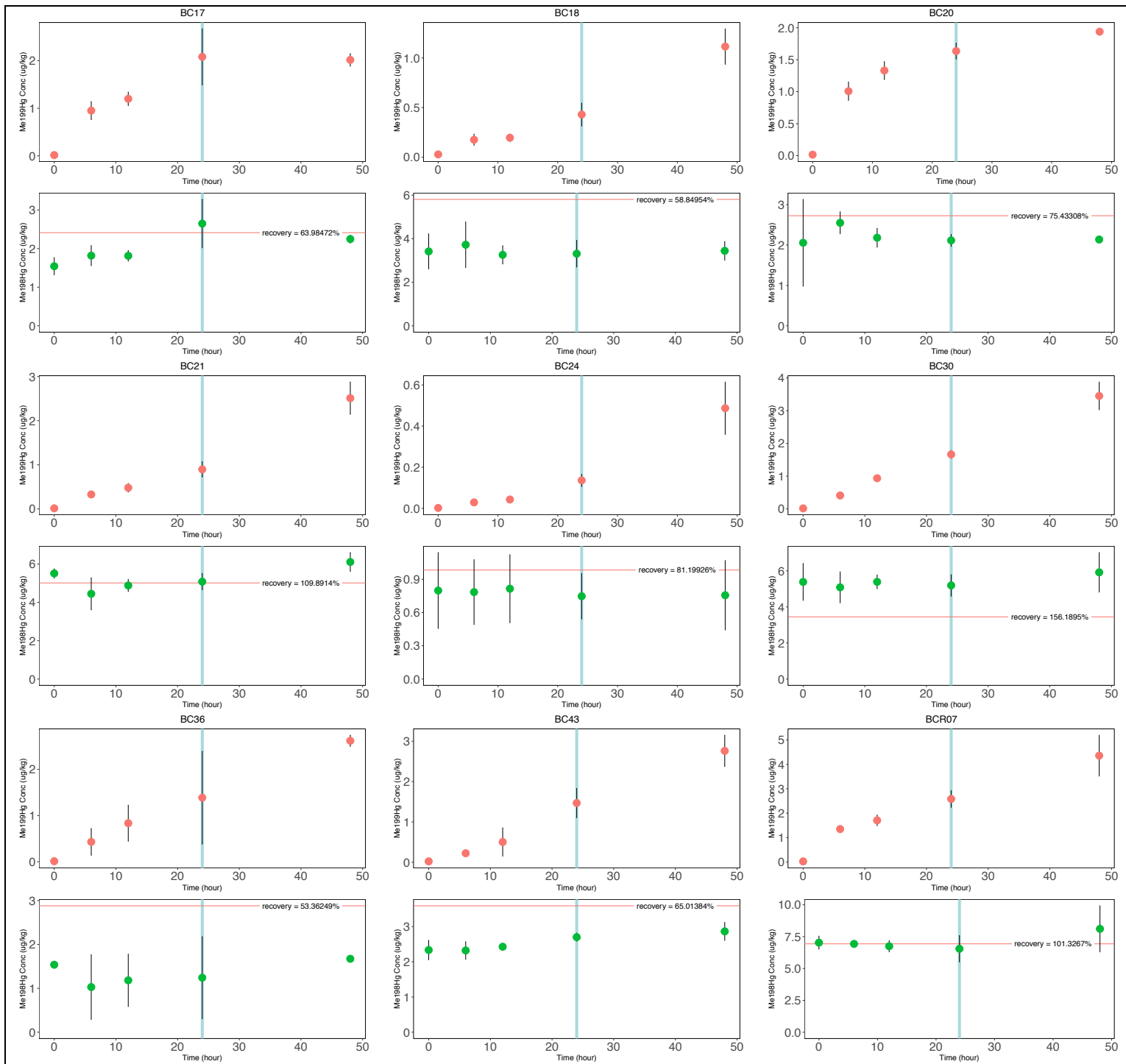
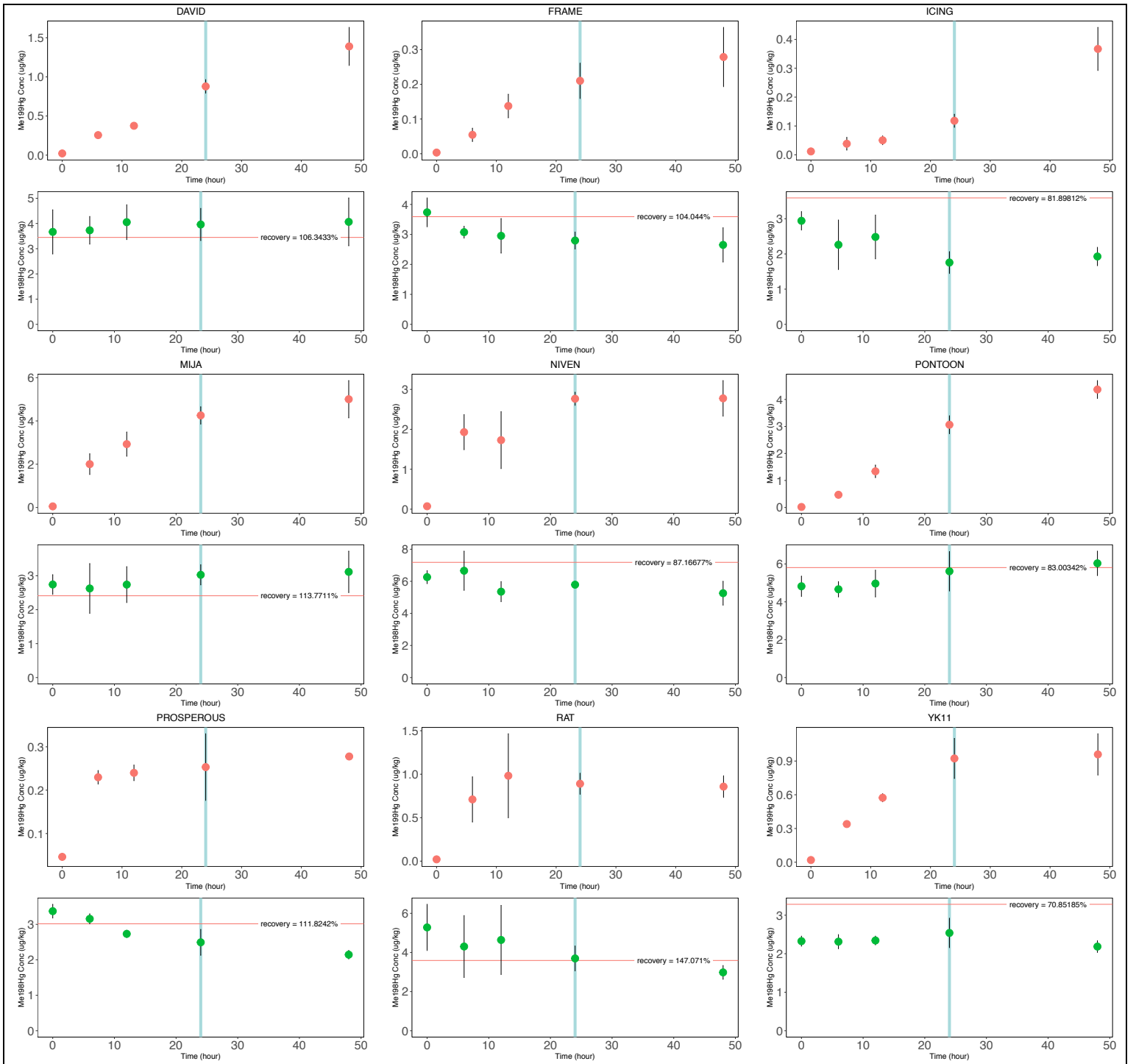


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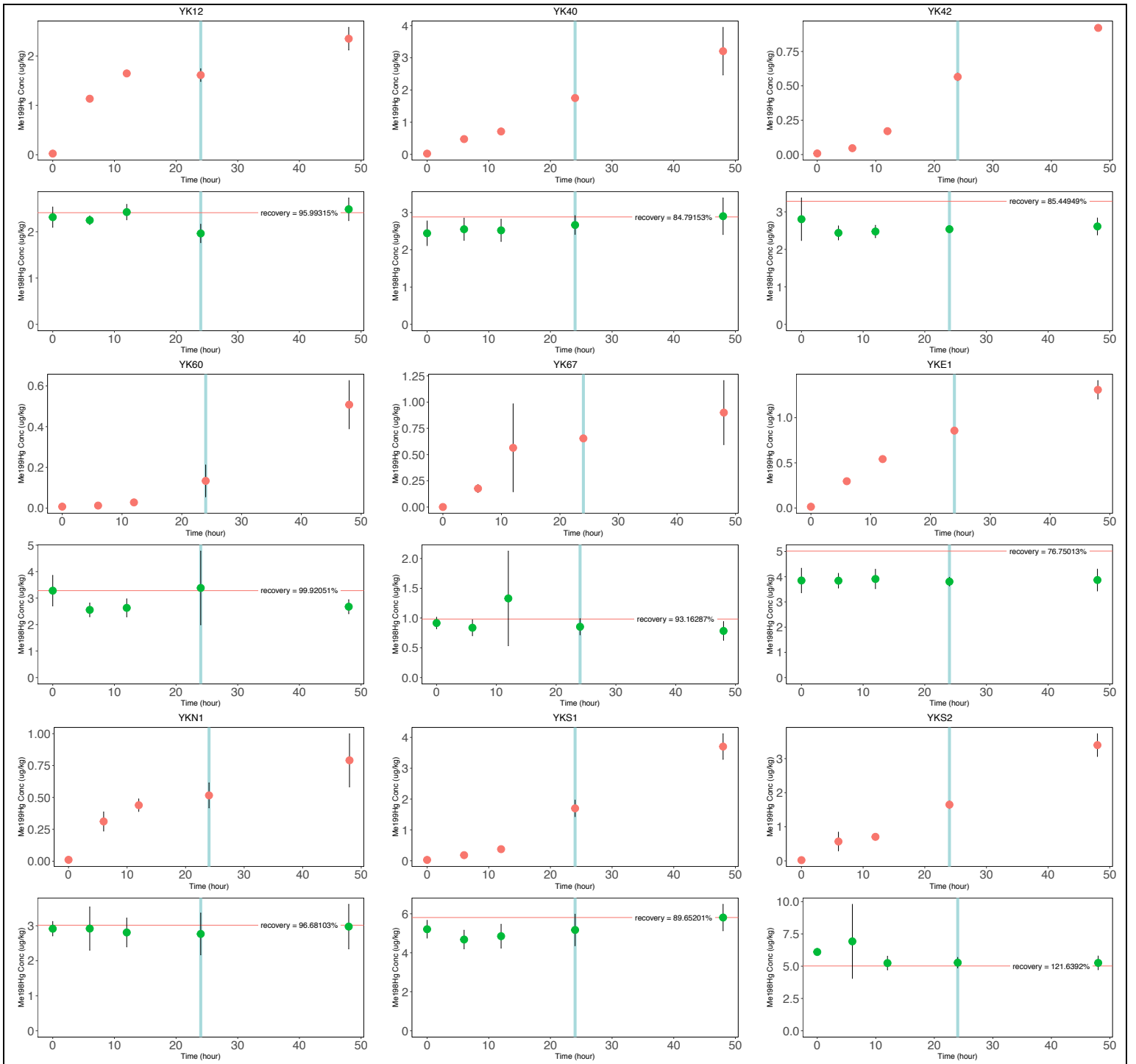




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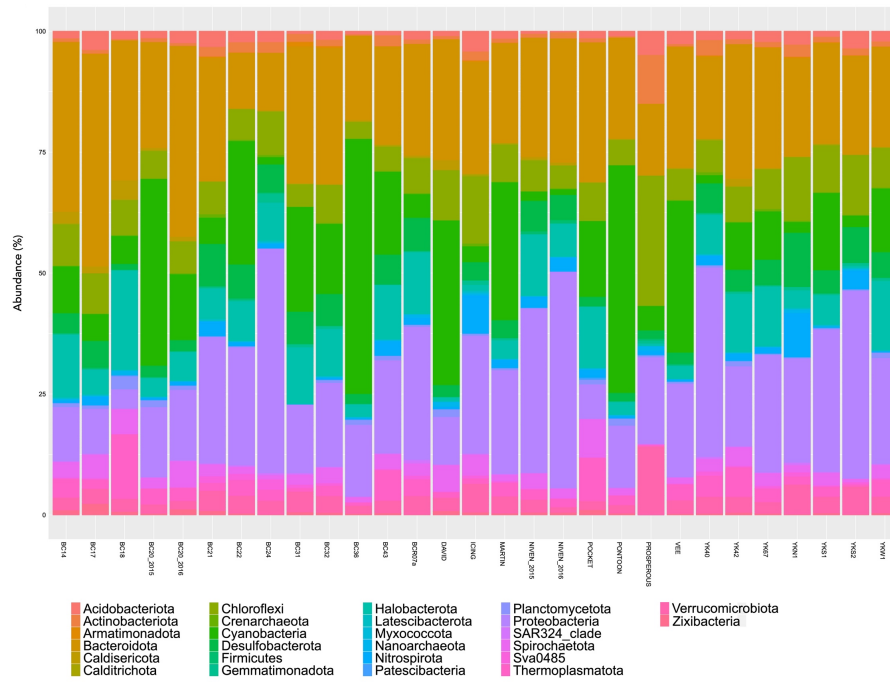


Figure S5: Relative abundance of microbial Phyla in each lake sediment sample