

## Supplemental Methods Text

The following coding was used in R to determine the  $\beta$ -diversity for Bacteria and *Archaea* in this study.

### Bacteria

Call:

```
adonis(formula = umat ~ metdat$Treatment + metdat$MPP, strata = metdat$Site)
```

Blocks: strata

Permutation: free

Number of permutations: 999

Terms added sequentially (first to last)

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
metdat\$Treatment	3	0.72179	0.240596	13.7688	0.76849	0.002 **
metdat\$MPP	1	0.09512	0.095119	5.4435	0.10127	0.004 **
Residuals	7	0.12232	0.017474	0.13023		
Total	11	0.93922	1.00000			

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Archaea

Call:

```
adonis(formula = umat ~ metdat$Treatment + metdat$MPP, strata = metdat$Site)
```

Blocks: strata

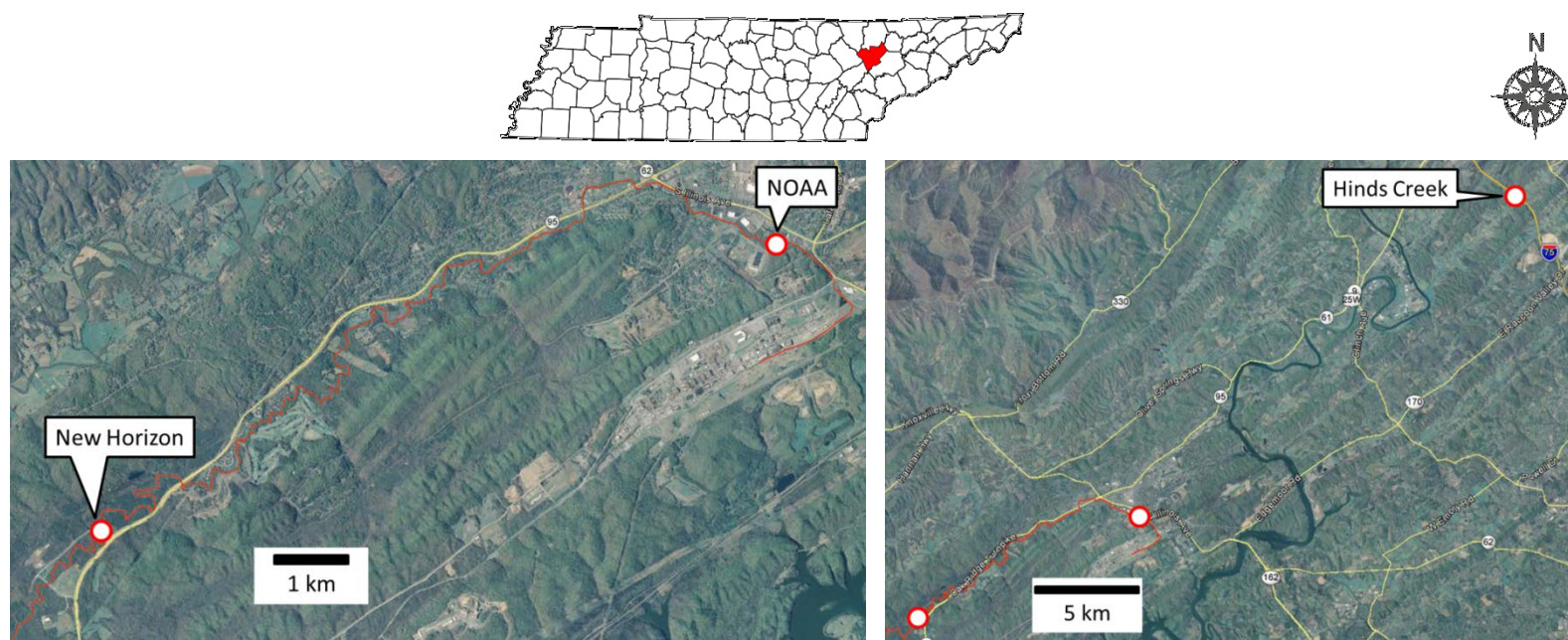
Permutation: free

Number of permutations: 999

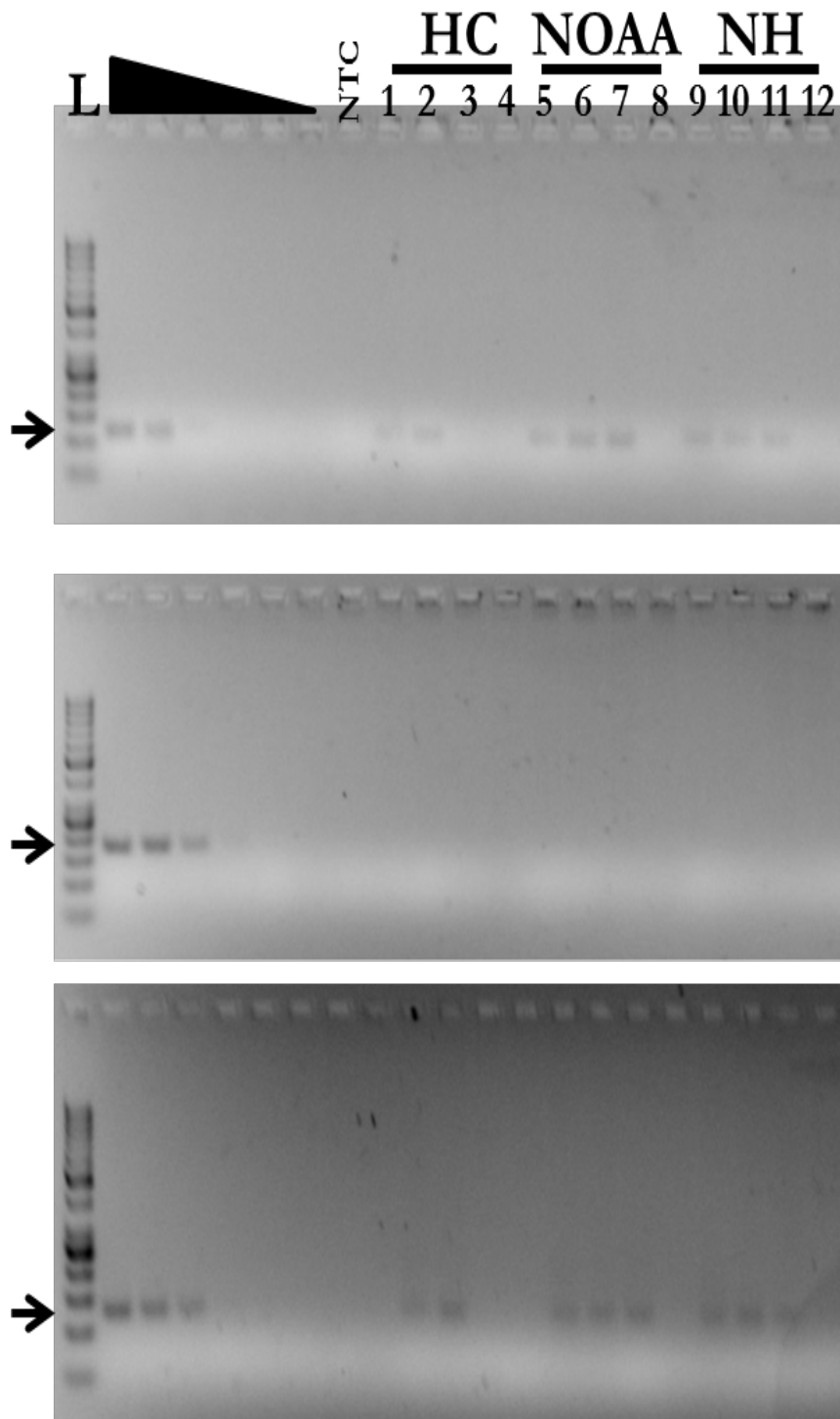
Terms added sequentially (first to last)

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
metdat\$Treatment	3	0.08631	0.028769	0.4804	0.11734	0.665
metdat\$MPP	1	0.23000	0.230005	3.8408	0.31272	0.603
Residuals	7	0.41920	0.059885	0.56994		
Total	11	0.73551	1.00000			

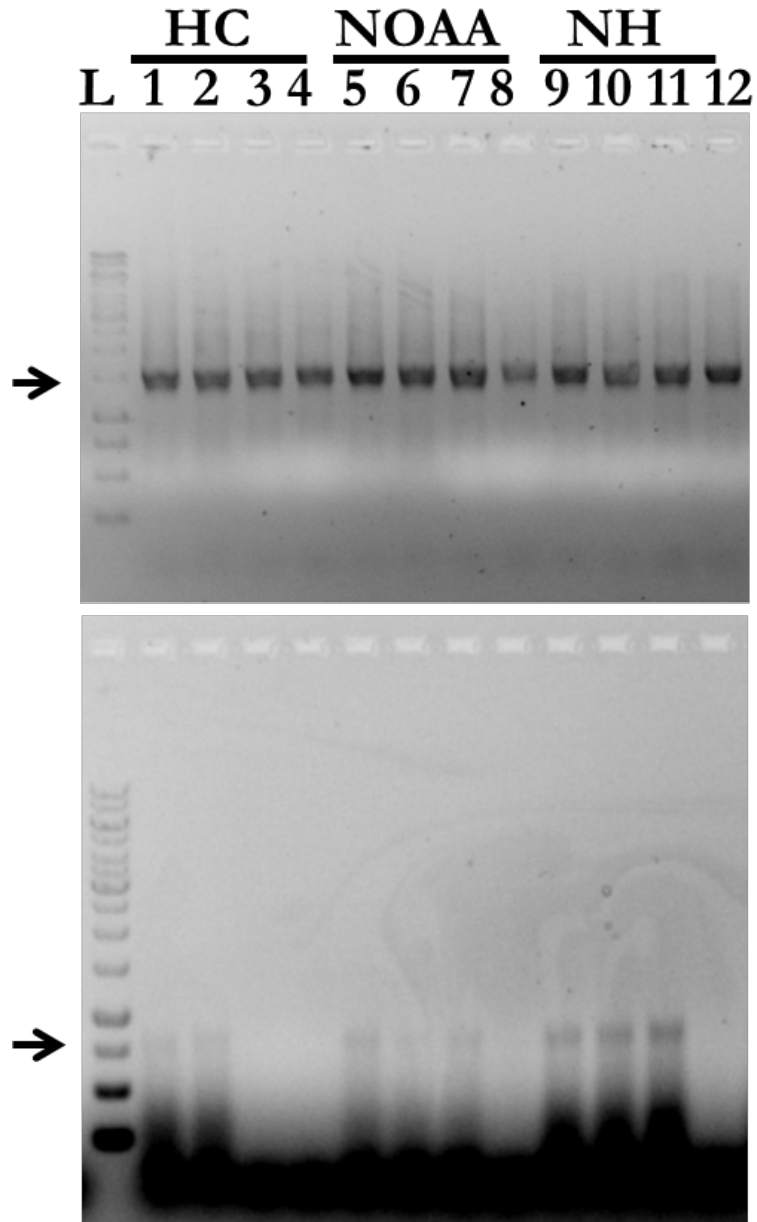
Supplemental Figures:



**Figure S1:** Sediment cores were isolated from three locations within Anderson County, TN (highlighted in red). (Left) Samples were taken from two locations from the mercury contaminated East Fork Poplar Creek (EFPC) including at the New Horizon (NH) and NOAA sites. (Right) Hinds Creek (HC), approximately 20 km northeast of EFPC, was selected as a background site with minimal THg and MeHg concentrations. Aerial views were acquired using Google Earth.



**Figure S2:** Gel electrophoresis. Cellobiose (1, 5, 9), Lactate (2, 6, 10), Ethanol (3, 7, 11) and Unamended (4, 8, 12). Ladder (L) is 50 bp from New England BioLabs. Arrow denotes expected product size specific to *Deltaproteobacteria* (107 bp), *Firmicutes* (167 bp) and *Archaea* (125 bp). The black triangle represents decreasing concentration of the standard curve (serial 10-fold dilution,  $1 \times 10^6$  -  $1 \times 10^1$ ) of *Desulfovibrio desulfuricans* ND132 (*Deltaproteobacteria*), *Desulfitobacterium metallireducens* (*Firmicutes*), and *Methanomethylovorans hollandica* (*Archaea*), respectively.



**Figure S3:** PCR for 16S rRNA gene (Top) and *hgcAB* (Bottom) of the three sites (HC, NOAA, and NH) for each of the treatments: Cellobiose (1, 5, 9), Lactate (2, 6, 10), Ethanol (3, 7, 11) and Unamended (4, 8, 12). Ladder (L) is 1kb Plus from Thermo Fisher Scientific. Arrow denotes expected product size for 16S (~1500 bp) and *hgcAB* (~750-1100 bp).