Supplementary document for:

**Response of the rare biosphere to environmental disturbance in a highly diverse ecosystem (Zodletone spring, OK, USA).**

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Table S1. Percentage abundances based on the number of sequences in each treatment condition that were affiliated with phyla in the first column. Unclassified bin denotes the number of sequences that were < 85% to any Greengenes database classified entry. Classification was done using the PyNAST pipeline (Caporaso et al. 2010).

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phylaa | Control | Salinity enrichment | | | | | Temperature enrichment | | | |
| 1% | 2% | 3% | 4% | 10% | 28 | 30 | 32 | 70 |
| Acidobacteria | 1.05 | 0.75 | 1.07 | 0.6 | 0.79 | 0.73 | 1.08 | 1.15 | 0.61 | 0.78 |
| Actinobacteria | 1.54 | 1.79 | 3.57 | 1.85 | 1.92 | 1.71 | 1.4 | 1.501 | 1.5 | 7.94 |
| Armatimonadetes | 0.014 | 0.015 | 0.012 | 0.034 | 0.016 | 0.036 | 0 | 0 | 0.061 | 0.06 |
| Bacteroidetes | 21. | 8.76 | 10.52 | 11.34 | 9.1 | 8.71 | 17.42 | 16.33 | 10.86 | 4.14 |
| Caldithrix | 0.007 | 0 | 0.06 | 0 | 0 | 0.018 | 0 | 0 | 0 | 0 |
| Chlorobi | 0.26 | 0.42 | 0.096 | 0.15 | 0.26 | 0.24 | 0.29 | 0.32 | 0.32 | 0.45 |
| Chloroflexi | 1.96 | 1.61 | 4.53 | 1.97 | 1.65 | 2.07 | 1.77 | 1.97 | 2.18 | 2.74 |
| Cyanobacteria | 0.07 | 0.03 | 0.012 | 0.017 | 0.082 | 0.036 | 0.026 | 0.059 | 0.015 | 0.06 |
| Elusimicrobia | 0.007 | 0 | 0 | 0 | 0.016 | 0 | 0.026 | 0 | 0 | 0 |
| Fibrobacteres | 0.07 | 0 | 0.048 | 0 | 0 | 0.054 | 0.053 | 0 | 0 | 0 |
| Firmicutes | 10 | 20.34 | 11.55 | 20 | 21.5 | 20.61 | 9.31 | 10.77 | 17.84 | 37.12 |
| Fusobacteria | 0.25 | 0.06 | 0.036 | 0.017 | 0.082 | 0.018 | 0.132 | 0.06 | 0.015 | 0.06 |
| Gemmatimonadetes | 0.17 | 0.18 | 0.9 | 0.19 | 0.25 | 0.47 | 0.37 | 0.41 | 0.21 | 0.28 |
| Gracilibacteria | 0.028 | 0 | 0.048 | 0.034 | 0 | 0.018 | 0.026 | 0 | 0.03 | 0 |
| Lentisphaerae | 0.007 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Marinimicrobia | 0.12 | 0.09 | 0.024 | 0.12 | 0.1 | 0.054 | 0.11 | 0.12 | 0.17 | 0.06 |
| Nitrospirae | 0.15 | 0.015 | 0.16 | 0 | 0.033 | 0.13 | 0.21 | 0.09 | 0.015 | 0.11 |
| Aminicenantes | 0.45 | 0.53 | 0.13 | 0.6 | 0.48 | 0.53 | 0.21 | 0.35 | 0.55 | 0.95 |
| Atribacteria | 0.26 | 0.12 | 0.072 | 0.14 | 0.2 | 0.13 | 0.4 | 0.18 | 0.17 | 0.73 |
| Planctomycetes | 0.085 | 0.045 | 0.012 | 0.086 | 0.033 | 0.073 | 0.079 | 0.059 | 0.06 | 0.22 |
| Proteobacteria | 23.75 | 34.12 | 29.35 | 32.67 | 33 | 35.77 | 28.07 | 25.96 | 33.79 | 17.78 |
| Parcubacteria | 0.036 | 0.03 | 0.12 | 0.034 | 0 | 0.018 | 0.026 | 0 | 0.015 | 0.45 |
| SPAM | 0.06 | 0.015 | 0.012 | 0.02 | 0.05 | 0.018 | 0.053 | 0.029 | 0.03 | 0 |
| Spirochaetes | 4.04 | 2.31 | 2.42 | 1.94 | 1.59 | 1.89 | 4.1 | 5.44 | 2.12 | 2.91 |
| Synergistetes | 0.11 | 0.045 | 0.012 | 0.051 | 0.08 | 0.054 | 0.11 | 0.29 | 0.076 | 0 |
| Thermi | 0 | 0.015 | 0 | 0 | 0 | 0 | 0.29 | 0.29 | 0.52 | 0.56 |
| Thermotogae | 0.19 | 0.750 | 0.216 | 0.531 | 0.589 | 0.71 | 0.13 | 0.18 | 0.076 | 0.11 |
| TM6 | 0.12 | 0.05 | 0.04 | 0 | 0.13 | 0.073 | 0.13 | 0.18 | 0.091 | 0.06 |
| TM7 | 0.15 | 0.030 | 0.084 | 0.051 | 0.065 | 0.091 | 0.11 | 0.15 | 0.091 | 0.06 |
| Verrucomicrobia | 0.14 | 0.05 | 0.1 | 0.051 | 0.033 | 0.04 | 0.34 | 0.47 | 0.17 | 0.06 |
| Latescibacteria | 0.31 | 0.2 | 0.23 | 0.14 | 0.18 | 0.13 | 0.026 | 0 | 0.015 | 0 |
| Other CD | 0.044 | 0.05 | 0.144 | 0 | 0 | 0.072 | 0.026 | 0.059 | 0 | 0 |
| Unclassified | 33.48 | 27.57 | 34.43 | 27.32 | 27.8 | 25.53 | 33.68 | 33.58 | 28.43 | 22.36 |

a: Gracilibacteria denotes candidate division GN02, Marinimicrobia denotes candidate division SAR406, Aminicenantes denotes candidate division OP8, Atribacteria denotes candidate division OP9, Parcubacteria denotes candidate division OD1, and Latescibacteria denotes candidate division WS3. Other CD denotes other candidate divisions including AD3, CV51, KSB3, NC10, WS6, WPS-2, OP1, and OP11.

References.

Caporaso JG, Bittinger K, Bushman FD, DeSantis TZ, Andersen GL, and Knight R. 2010. PyNAST: a flexible tool for aligning sequences to a template alignment. *Bioinformatics* 26:266-267.