

Climate oscillations reflected within the microbiome of Arabian Sea sediments

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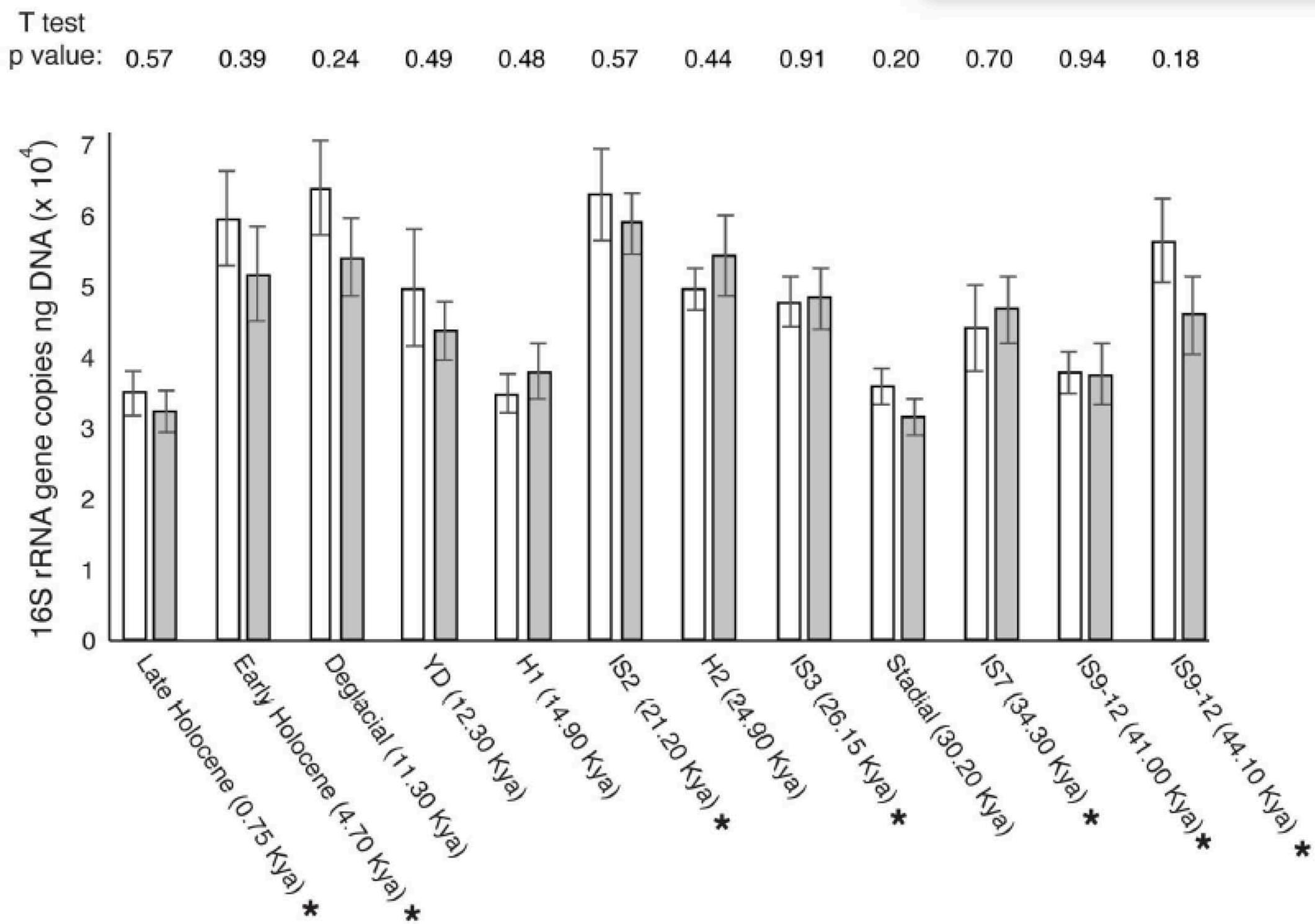


Figure S1: Estimates of microbial biomass in Arabian Sea sediment samples stored at ± 4 °C for 2 years (white) was compared to storage at ± 4 °C for 6 years (grey). Histograms represent the average value across 5 replicates, and error bars represent standard deviations. If storage at ± 4 °C caused significant bacterial growth, it is expected that samples stored for longer periods of time at ± 4 °C would have significantly higher microbial biomass. However, no samples show a significant increase or decrease in the quantity of 16S rRNA genes between the different storage conditions, even in TOC rich samples. Asterisks mark sediment intervals with TOC content greater than 0.5 wt% that were deposited under suboxic conditions.

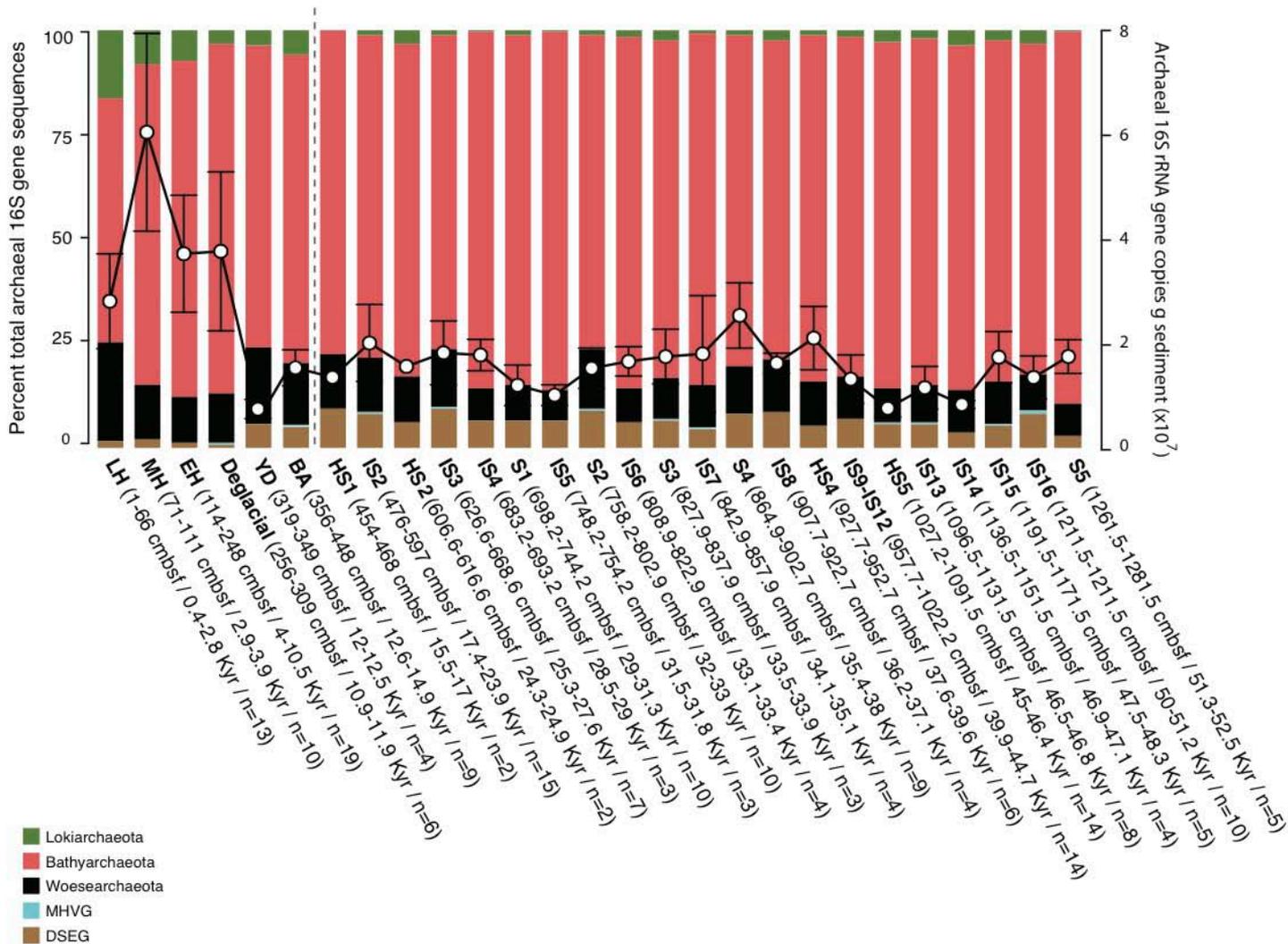


Fig S2. Taxonomic distributions of Archaea in each of the climate intervals. Climate intervals are denoted below panel B with the number of samples in each depth interval / time period / number of samples listed in brackets. The dotted line marks the Glacial Interglacial transition. Superimposed are average rRNA gene copy numbers for each climate interval. Error bars indicate the standard deviations (see bottom of Figure for number of samples in each interval, sediment depth, and time period spanned).

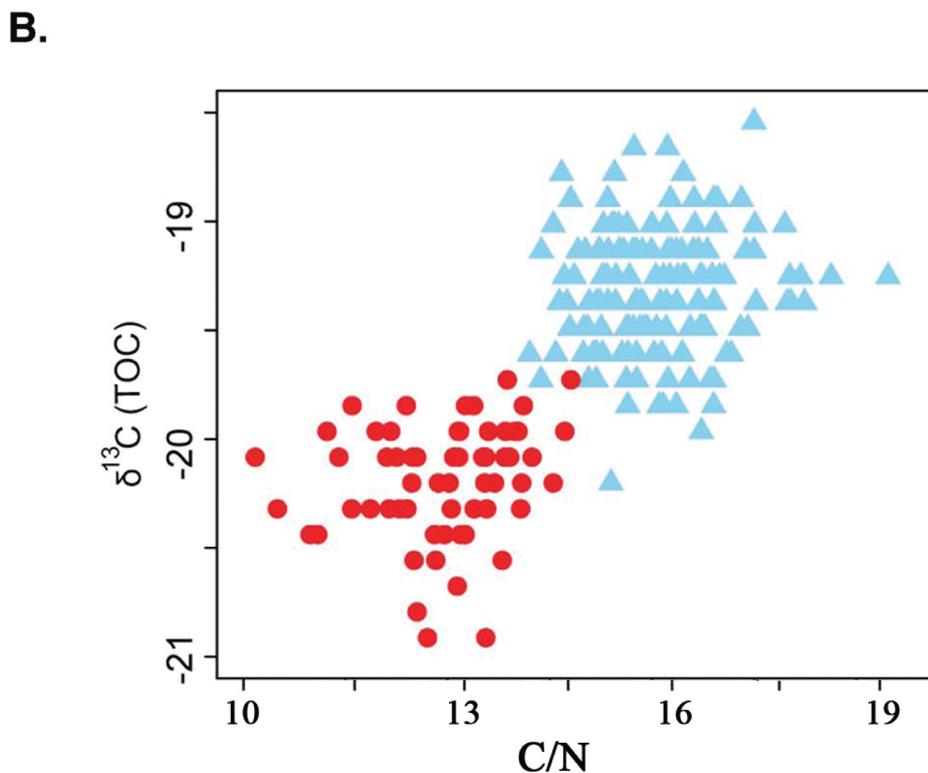
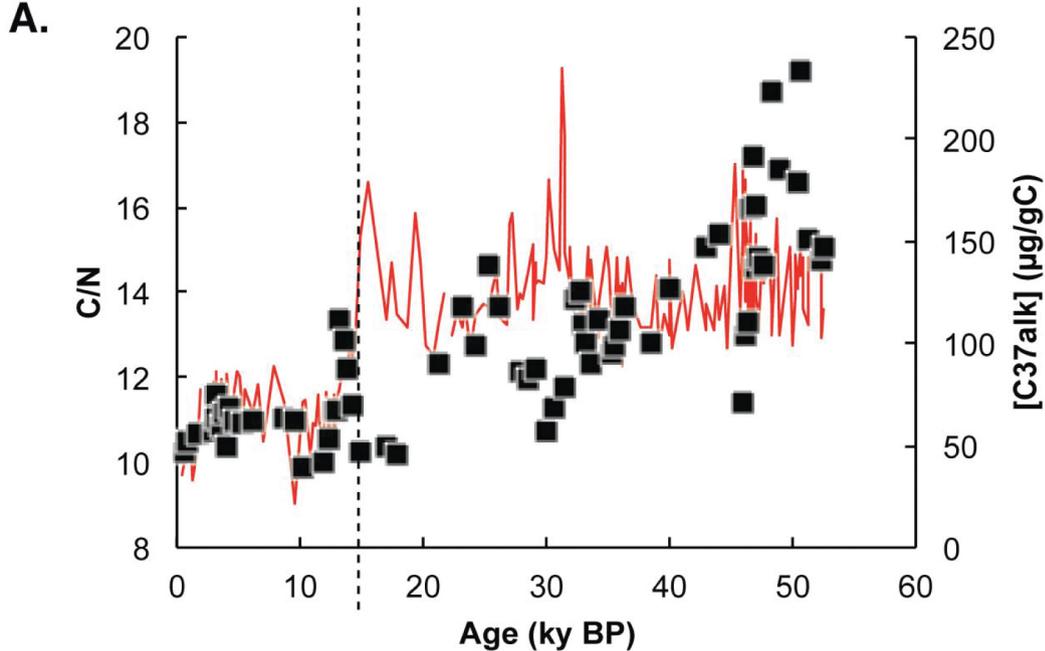


Fig. S3. (A) Abundance of alkenones (squares) and C/N ratios (red line). Note the relatively higher abundance of alkenones during the glacial period relative to the interglacial period. Dotted line marks the deglaciation. **(B)** OM in glacial (triangles) versus interglacial (circles) samples are chemically distinct, as evidenced by unique $\delta^{13}\text{C}$ and C/N values.

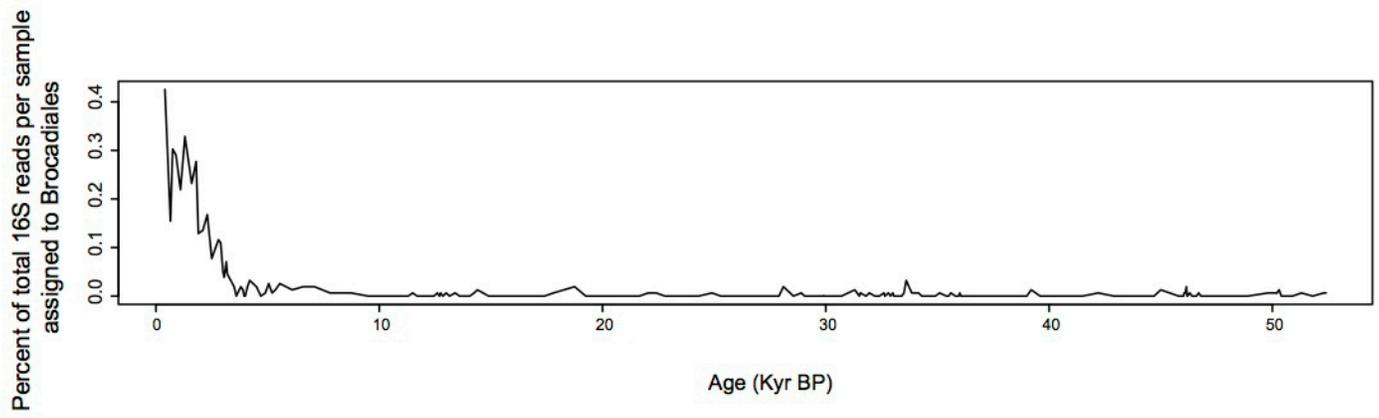


Fig. S4: Relative abundance of anammox bacteria affiliated with the Brocadiales order in the 16S rRNA gene libraries down core.

| Lab No. | Depth (cm) | Species | Radiocarbon Age (¹⁴ C years) | Error (¹⁴ C years) | Calibrated Age* (cal years BP) | Median Age (cal years BP) |
|-----------|------------|--------------------------|--|--------------------------------|--------------------------------|---------------------------|
| OS-112414 | 13 | mixed planktonics | 1470 | 20 | 745-930 | 848 |
| OS-111794 | 73 | <i>Orbulina universa</i> | 3270 | 20 | 2762-2992 | 2877 |
| OS-111793 | 87 | <i>Orbulina universa</i> | 3530 | 20 | 3106 - 3345 | 3229 |
| OS-110013 | 125 | <i>Orbulina universa</i> | 4280 | 20 | 4043 - 4333 | 4172 |
| OS-111792 | 176 | <i>Orbulina universa</i> | 5800 | 20 | 5925 - 6167 | 6037 |
| OS-111795 | 231 | <i>Orbulina universa</i> | 9380 | 25 | 9879 - 10165 | 10030 |

*2 sigma error rate

Table S1: Radiocarbon dates for core 64PE300-11C.

| Technique | Depth (cm) | Age cal kyr BP |
|-------------------|------------|----------------|
| Radiocarbon date | 13 | 0.8 |
| Radiocarbon date | 73 | 2.9 |
| Radiocarbon date | 87 | 3.2 |
| Radiocarbon date | 125 | 4.2 |
| Radiocarbon date | 176 | 6.0 |
| Radiocarbon date | 231 | 10.0 |
| Tie to SO90-136KL | 307 | 12.0 |
| Tie to SO90-136KL | 374 | 12.8 |
| Tie to SO90-136KL | 436 | 14.5 |
| Tie to SO90-136KL | 453 | 15.4 |
| Tie to SO90-136KL | 463 | 16.8 |
| Tie to SO90-136KL | 599 | 24.0 |
| Tie to SO90-136KL | 623 | 25.2 |
| Tie to SO90-136KL | 674 | 27.8 |
| Tie to SO90-136KL | 685 | 28.7 |
| Tie to SO90-136KL | 703 | 29.2 |
| Tie to SO90-136KL | 724 | 30.3 |
| Tie to SO90-136KL | 760 | 32.1 |
| Tie to SO90-136KL | 833 | 33.8 |
| Tie to SO90-136KL | 869 | 35.5 |
| Tie to SO90-136KL | 917 | 36.6 |
| Tie to SO90-136KL | 935 | 38.5 |
| Tie to SO90-136KL | 951 | 39.6 |
| Tie to SO90-136KL | 970 | 40.4 |
| Tie to SO90-136KL | 980 | 41.5 |
| Tie to SO90-136KL | 995 | 42.8 |
| Tie to SO90-136KL | 1038 | 45.7 |
| Tie to SO90-136KL | 1128 | 46.7 |
| Tie to SO90-136KL | 1161 | 46.9 |
| Tie to SO90-136KL | 1177 | 47.6 |
| Tie to SO90-136KL | 1204 | 48.9 |
| Tie to SO90-136KL | 1217 | 50.2 |
| Tie to SO90-136KL | 1259 | 51.3 |
| Tie to SO90-136KL | 1276 | 52.4 |
| Tie to SO90-136KL | 1294 | 52.9 |

Table S2: Age model for core 64PE300-11C.

| Variable | Bacteria | | | Archaea | | |
|-----------------------|-------------|-------------|-------------|-------------|-------------|-------------|
| | P-value | RDA1 scores | RDA2 scores | P-value | RDA1 scores | RDA2 scores |
| Br | 0.01 | -0.5466 | -0.5594 | 0.01 | -0.6405 | 0.48078 |
| %TOC | 0.27 | -0.4762 | -0.3365 | 0.12 | -0.4625 | 0.50388 |
| %N | 0.01 | -0.5057 | -0.5328 | 0.01 | -0.6413 | 0.50305 |
| C:N | 0.01 | -0.3143 | 0.6936 | 0.01 | 0.5972 | 0.53697 |
| $\delta^{13}\text{C}$ | 0.02 | 0.3405 | 0.7366 | 0.01 | 0.8750 | 0.12247 |
| $\delta^{15}\text{N}$ | 0.01 | -0.5801 | -0.1810 | 0.20 | -0.4329 | 0.13044 |

Table S3: Redundancy analysis (RDA) for bacteria and archaea, with the significance probability value for each paleoenvironmental variable, tested using 200 permutations, and RDA scores for the first two axis. Bold font indicates significant ($P < 0.05$) correlations.

| Age Kyr BP | Number of contigs | Reads mapping to contigs | Average coverage | Average length (kb) | Max contig length (kb) |
|------------|-------------------|--------------------------|------------------|---------------------|------------------------|
| 0.65 | 18756 | 3388046 | 8.4 | 1.99 | 90 |
| 0.75 | 16142 | 2249446 | 7.6 | 1.868 | 105 |
| 1.60 | 24316 | 2642774 | 7.4 | 1.644 | 76 |
| 2.10 | 18451 | 3289249 | 8.5 | 1.923 | 115 |
| 2.50 | 19395 | 2613206 | 7.8 | 1.631 | 196 |
| 2.90 | 26001 | 3628145 | 8.6 | 1.637 | 122 |
| 3.10 | 25522 | 2975222 | 7.8 | 1.364 | 360 |
| 3.20 | 27306 | 2550554 | 7.7 | 1.274 | 238 |
| 3.50 | 26011 | 3127282 | 8.2 | 1.369 | 143 |
| 3.80 | 31304 | 4849967 | 9.6 | 1.619 | 223 |
| 4.00 | 23165 | 3669695 | 8.7 | 1.793 | 305 |
| 4.20 | 30922 | 3977837 | 8.5 | 1.583 | 160 |
| 4.70 | 21929 | 3908680 | 8.6 | 1.899 | 302 |
| 5.35 | 13767 | 4302749 | 10.1 | 2.424 | 628 |
| 6.10 | 31907 | 3442006 | 7.6 | 1.249 | 134 |
| 7.10 | 33570 | 4786439 | 7.6 | 1.534 | 271 |
| 8.75 | 28954 | 4541919 | 8.3 | 1.603 | 302 |
| 9.50 | 24719 | 3722457 | 8 | 1.416 | 425 |
| 10.20 | 28864 | 4993428 | 8.5 | 1.517 | 291 |
| 11.30 | 26256 | 5143107 | 8.2 | 1.4 | 491 |
| 11.90 | 16081 | 4807483 | 6.7 | 1.11 | 912 |
| 12.30 | 12224 | 5549052 | 7.1 | 1.575 | 503 |
| 12.70 | 21385 | 3836208 | 8.6 | 1.406 | 320 |
| 13.00 | 24956 | 7128154 | 8.6 | 1.777 | 444 |
| 13.15 | 12113 | 4371610 | 7.8 | 1.982 | 642 |
| 13.60 | 13327 | 5395632 | 8 | 1.959 | 1301 |
| 13.80 | 14218 | 4493735 | 7.7 | 1.701 | 444 |
| 14.25 | 18705 | 5147831 | 8.7 | 2.069 | 330 |
| 14.90 | 18943 | 4721712 | 7.7 | 1.491 | 445 |
| 16.95 | 18547 | 6581895 | 7.9 | 1.521 | 535 |
| 17.80 | 32698 | 4217451 | 9.7 | 1.568 | 133 |
| 21.20 | 21107 | 5363136 | 9.2 | 1.731 | 402 |
| 22.05 | 35722 | 6209491 | 9.6 | 1.512 | 187 |
| 23.10 | 20818 | 6465918 | 8.8 | 1.538 | 655 |
| 24.30 | 50724 | 19991574 | 10.3 | 1.2 | 641 |
| 25.30 | 9425 | 6518373 | 7.7 | 1.615 | 1250 |
| 26.15 | 11030 | 4611130 | 8.1 | 1.379 | 885 |
| 27.90 | 17753 | 6900444 | 7.5 | 1.389 | 979 |
| 28.55 | 7389 | 6305016 | 9.2 | 1.86 | 980 |
| 29.10 | 20307 | 4072797 | 9.3 | 1.64 | 329 |
| 29.90 | 13984 | 5700651 | 8.5 | 1.67 | 655 |
| 30.70 | 14691 | 5658677 | 10.1 | 1.64 | 418 |
| 31.55 | 36299 | 5343263 | 10 | 1.25 | 106 |
| 32.30 | 15583 | 6038014 | 9.2 | 1.8 | 535 |
| 32.65 | 34319 | 4218744 | 15 | 0.8 | 11 |
| 32.90 | 28142 | 5079237 | 13 | 0.96 | 504 |
| 33.10 | 17861 | 4286556 | 25 | 0.78 | 11 |
| 33.50 | 14068 | 5950118 | 13.8 | 1.1 | 68 |
| 34.30 | 16536 | 3863372 | 8.8 | 1.4 | 359 |
| 35.40 | 6681 | 7088076 | 12.7 | 3 | 628 |
| 35.60 | 59024 | 11838869 | 11 | 1.1 | 1160 |
| 35.95 | 17446 | 6071020 | 9.9 | 1.9 | 366 |
| 36.35 | 25024 | 5972118 | 9.6 | 1.7 | 284 |
| 38.50 | 21766 | 6164173 | 9.9 | 1.9 | 628 |
| 39.90 | 8826 | 5526455 | 15.5 | 2.5 | 402 |
| 42.90 | 9892 | 4599427 | 9.4 | 2.2 | 473 |
| 44.10 | 15213 | 7230125 | 11.2 | 1.8 | 881 |
| 45.95 | 28313 | 5230241 | 9.8 | 1.4 | 210 |
| 46.15 | 28912 | 5185324 | 12.2 | 1.2 | 155 |
| 46.40 | 25127 | 7002873 | 11.1 | 1.6 | 210 |
| 46.55 | 17783 | 7071887 | 12.4 | 1.9 | 291 |
| 46.80 | 12182 | 5020128 | 11.3 | 1.9 | 458 |
| 47.00 | 11494 | 7687592 | 9.8 | 1.7 | 642 |
| 47.05 | 8226 | 6787807 | 12 | 2.7 | 554 |
| 47.20 | 7219 | 6436040 | 7.3 | 1.6 | 1177 |
| 47.60 | 8763 | 5648347 | 11.6 | 2.8 | 519 |
| 48.20 | 21691 | 4754413 | 10 | 1.7 | 476 |
| 48.90 | 25046 | 5848677 | 8.4 | 1.3 | 322 |
| 50.40 | 16408 | 6073314 | 11.7 | 2.1 | 574 |
| 50.70 | 15556 | 5300105 | 10.5 | 2.1 | 673 |
| 51.20 | 12885 | 6211942 | 11.1 | 1.9 | 411 |
| 52.50 | 15588 | 5543548 | 10 | 1.9 | 350 |

Table S4: Assembly summary statistics for the 72 metagenomes.

| Metric | Interglacial TOC | | Glacial TOC | |
|---|------------------|--------------------|-------------|---------|
| | R-squared | P value | R-squared | P value |
| Methanogenesis | 0.38 | 0.0007 | 0.07 | 0.5 |
| Archaeal protein degradation | 0.5 | <0.00001 | -0.01 | 0.46 |
| Bacterial protein degradation | 0.38 | 0.0002 | -0.02 | 0.54 |
| Bacterial FA degradation regulons | 0.42 | <0.00001 | -0.02 | 0.54 |
| Bacterial central aromatic cleavage pathway | 0.5 | <0.00001 | -0.011 | 0.4 |
| Bacterial murein hydrolases | 0.4 | 0.0001 | 0.04 | 0.12 |

Table S5: Correlations of bacterial and archaeal SEED catabolic gene categories with TOC in the interglacial and glacial stages (Fig. 3B). Bold font indicates significant ($P < 0.05$) correlations.