

Supplementary Information

| Datasets | | 16S rRNA gene amplicon sequencing details | | | |
|-------------------------|---|---|----------------|----------------|-------|
| | | # Raw reads | # Clean* reads | # Reads used** | # ESV |
| Paleomat | 16S rRNA; Metagenome: (1) whole DNA fraction MiniSeq, (2) whole DNA fraction MiSeq, (3) size-selected DNA MiSeq, (4) size-selected DNA Pacbio; RNASeq | 363,111 | 291,406 | 291,388 | 481 |
| Modern mat | 16S rRNA | 305,452 | 285,161 | 284,417 | 476 |
| Surrounding soil | 16S rRNA | 96,133 | 88,146 | 88,146 | 106 |

*trimmed, filtered, denoised, merged and non-chimera

**after removing singletons and unassigned

Table S1. Summary of datasets for each sample and sequencing details for 16S rRNA gene amplicons.

| MAG | Assembly | Lineage* | Completeness | Contamination | GC | N50 | Number of scaffolds | Number of genes |
|----------------|----------|---------------------|--------------|---------------|------|--------|---------------------|-----------------|
| bin.6 | Whole | Cytophagales | 100.0 | 1.7 | 40.5 | 42620 | 301 | 6212 |
| bin.10 | Select | algicola | 99.6 | 1.2 | 38.1 | 66238 | 128 | 3584 |
| bin.15 | Whole | Sphingomonadales | 99.5 | 0.5 | 64.6 | 489437 | 8 | 2585 |
| bin.14 | Whole | algicola | 99.4 | 0.1 | 38.3 | 160316 | 37 | 3349 |
| bin.4 | Whole | Bacilli | 99.3 | 0.7 | 40.2 | 73866 | 90 | 3026 |
| bin.12 | Whole | Cytophagales | 99.1 | 0.6 | 48.0 | 36837 | 201 | 4318 |
| bin.16 | Whole | Cytophagales | 99.1 | 0.9 | 50.2 | 37455 | 198 | 4719 |
| bin.12 | Select | Sphingomonadales | 98.8 | 1.3 | 64.8 | 116445 | 40 | 2501 |
| bin.3 | Whole | Xanthomonadaceae | 96.2 | 1.3 | 67.5 | 74478 | 69 | 2911 |
| bin.17 | Whole | Cytophagales | 96.0 | 1.5 | 49.7 | 22070 | 314 | 4628 |
| bin.42 | Select | Bacilli | 95.9 | 0.0 | 47.3 | 39197 | 134 | 3366 |
| bin.22 | Select | Xanthomonadaceae | 94.3 | 2.3 | 67.5 | 14645 | 309 | 3118 |
| bin.2 | Whole | Actinomycetales | 93.9 | 3.0 | 68.3 | 19714 | 308 | 4143 |
| bin.31 | Select | Alphaproteobacteria | 91.3 | 1.7 | 66.0 | 13589 | 299 | 3163 |
| checkm lineage | | | | | | | | |

Table S2. Metagenome Assembled Genome Summary Statistics

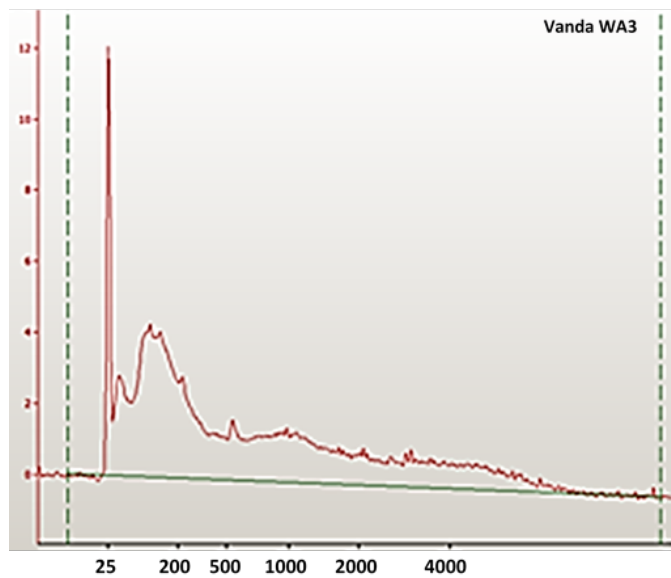


Figure S1: Agilent 2100 Bioanalyzer Trace of RNA isolated from the Lake Vanda paleomat. Total RNA was analyzed on an Agilent Pico chip 6000. The majority of total RNA is composed of mostly short degraded fragments, however, the small abundance of larger fragments suggests preserved or active RNA.

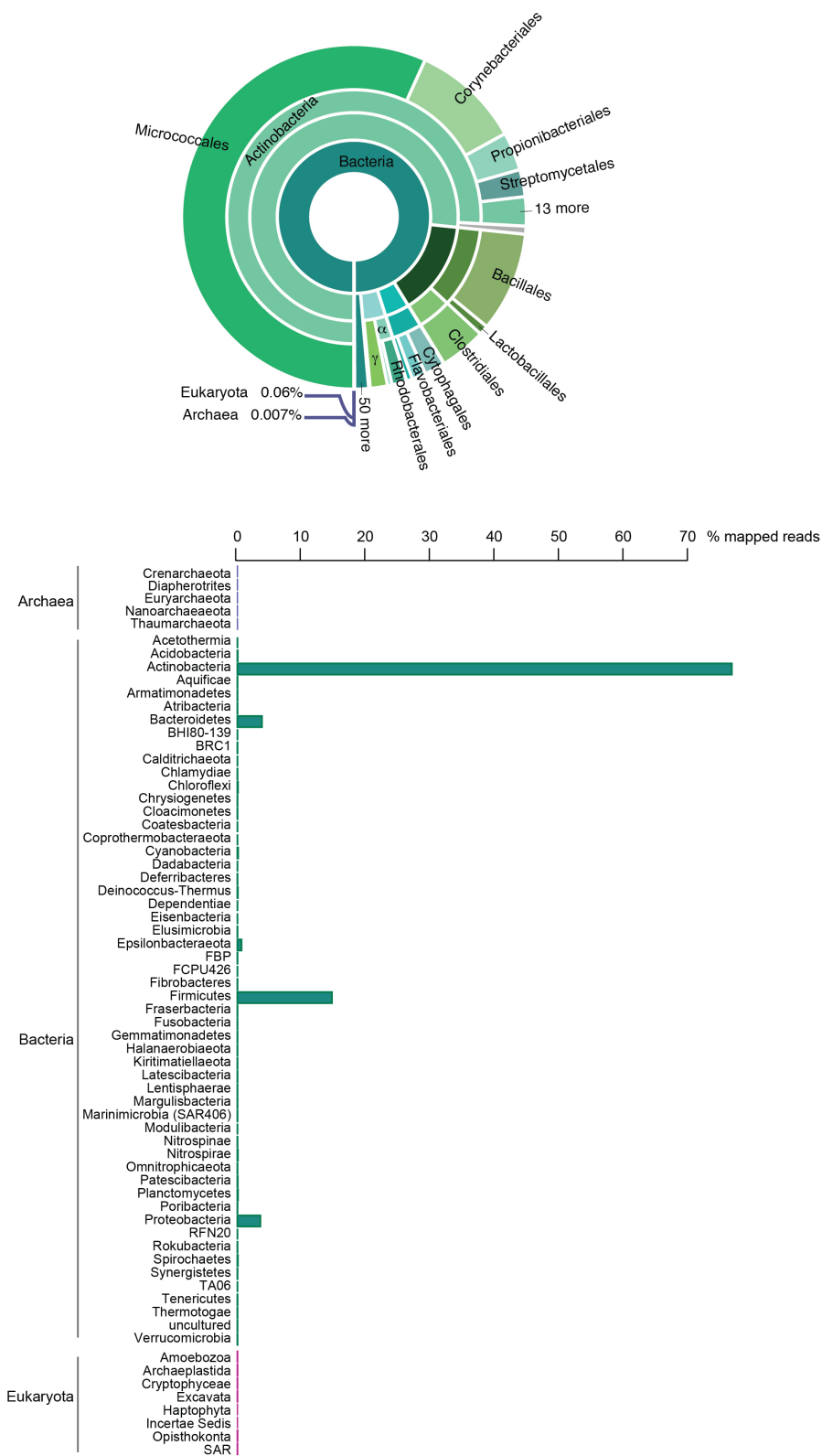


Figure S2: Taxonomic distribution of RNASeq reads from Lake Vanda paleomat mapping to Silva v 132 LSU and SSU reference sequences, with at least 10 reads/sequence.



Figure S3: Heatmap of TPM values of the 50 most highly expressed genes in the paleomat community.

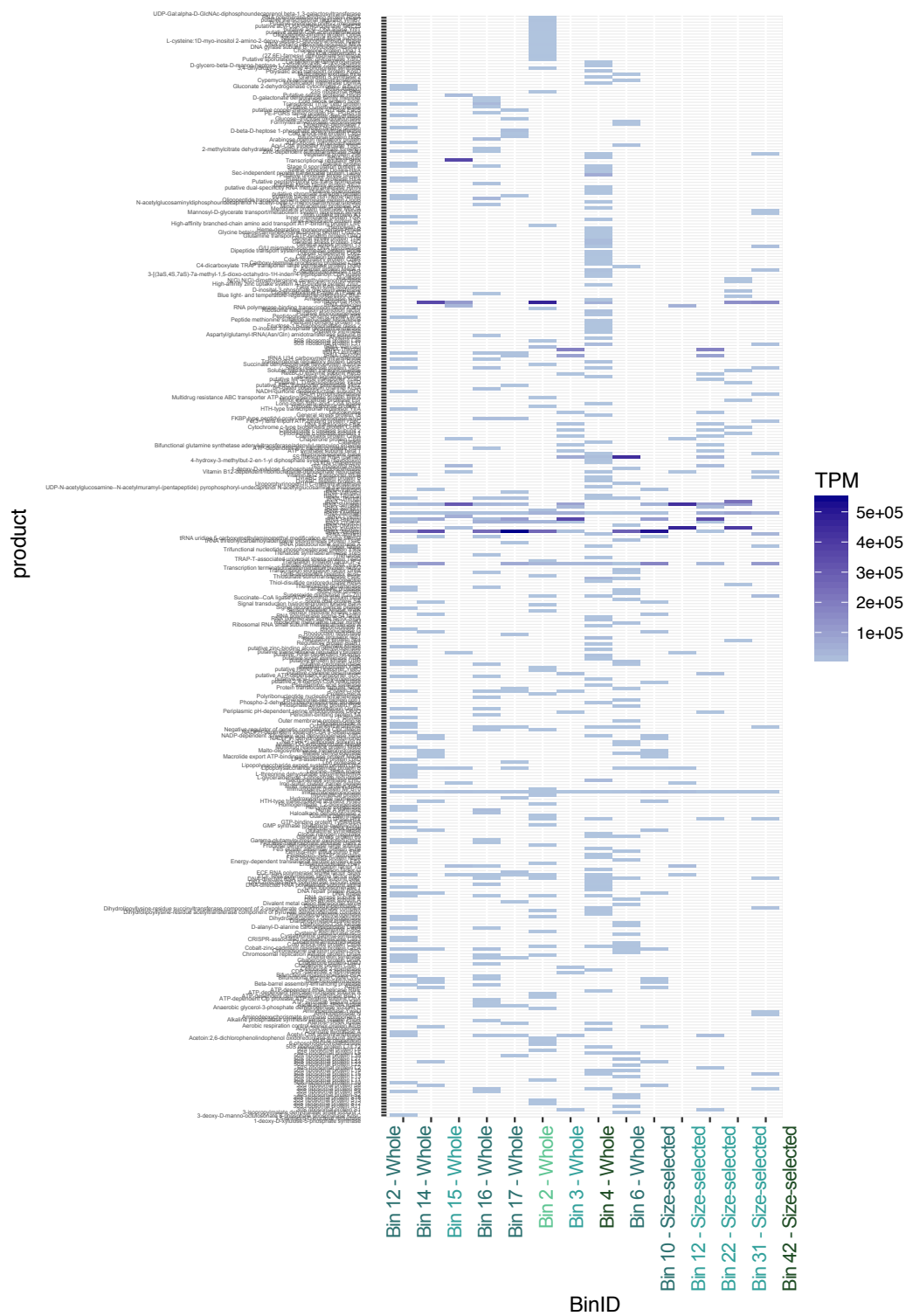


Figure S4: Heatmap of TPM values of all expressed genes in MAGs.