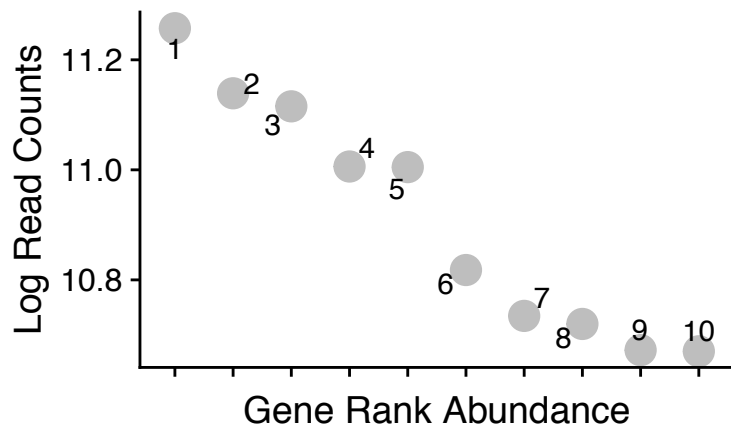
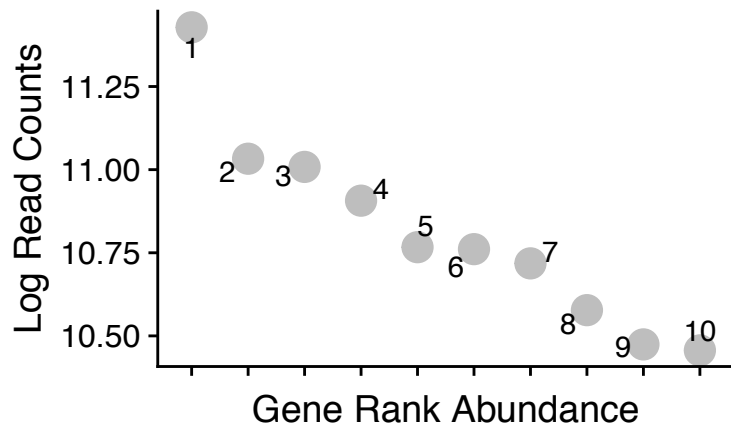


Sparkling Lake



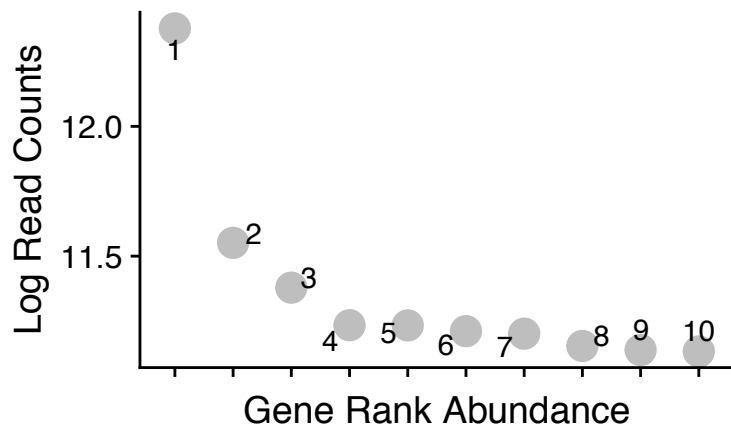
1. Hypothetical - unclassified
2. Hypothetical - unclassified
3. Photosystem II P680 - Cyanobacteria
4. Photosystem II P680 - Eukaryota
5. Photosystem II P680 - Cyanobacteria
6. Hypothetical - unclassified
7. Hypothetical - unclassified
8. Photosystem II P680 - Cyanobacteria
9. Hypothetical - unclassified
10. Hypothetical - unclassified

Lake Mendota



1. Photosystem II P680 - Cyanobacteria
2. Photosystem II P680 - unclassified
3. Photosystem II P680 - Cyanobacteria
4. Hypothetical - unclassified
5. Hypothetical - unclassified
6. RuBisCo - Cyanobacteria
7. PQQ-dependent dehydrogenase - LD28
8. Hypothetical - unclassified
9. Hypothetical - Bdellovibrio
10. RuBisCo - Cyanobacteria

Trout Bog



1. Photosystem II P680 - Cyanobacteria
2. RuBisCo - unclassified
3. Photosystem II P680 - unclassified
4. Beta-barrel porin-2 - Verrucomicrobia
5. Photosystem II P680 - Cyanobacteria
6. Photosystem I P700 - Eukaryota
7. Photosystem II CP47 - unclassified
8. Hypothetical - unclassified
9. Photosystem I P700 - Eukaryota
10. Photosystem II P680 - unclassified

Figure S1. Top 10 most expressed genes in each lake. Coding regions from reference genomes and metagenome assemblies were clustered at 97% sequence similarity, and the longest coding region was chosen as the representative sequence. Metatranscriptomic reads were mapped to these representative sequences. Annotations and classifications are derived from the sequence to which each read mapped. Read counts were summed across each lake and log transformed for visualization.