

Description of Additional Supplementary Files

Supplementary Data 1. Samples used in this study.

Supplementary Data 2. Correlations between N₂O emissions and the relative abundance of all genera uncovered by metagenomes.

Supplementary Data 3. List of archaeal OTUs showing strongest correlations to N₂O fluxes.

Supplementary Data 4. Correlation between N₂O fluxes and Archaeal OGs across global wetland soils.

Supplementary Data 5. Comparison between the functional gene profiles (MetaCyc and KEGG modules) of N₂O taxa (determined using PacBio metabarcoding) that showed strongest positive and negative correlations with N₂O production.

Supplementary Data 6. List of genomes that contain genes related to ammonia oxidation from a total of 91 archaeal and 116 bacterial genomes.

Supplementary Data 7. Analysis of MetaCyc nitrogen metabolism pathways in available Archaeal genomes in JGI as of 15-jul-2020.

Supplementary Data 8. Characteristics of qPCR primer pairs and programs used.