

Supplementary File

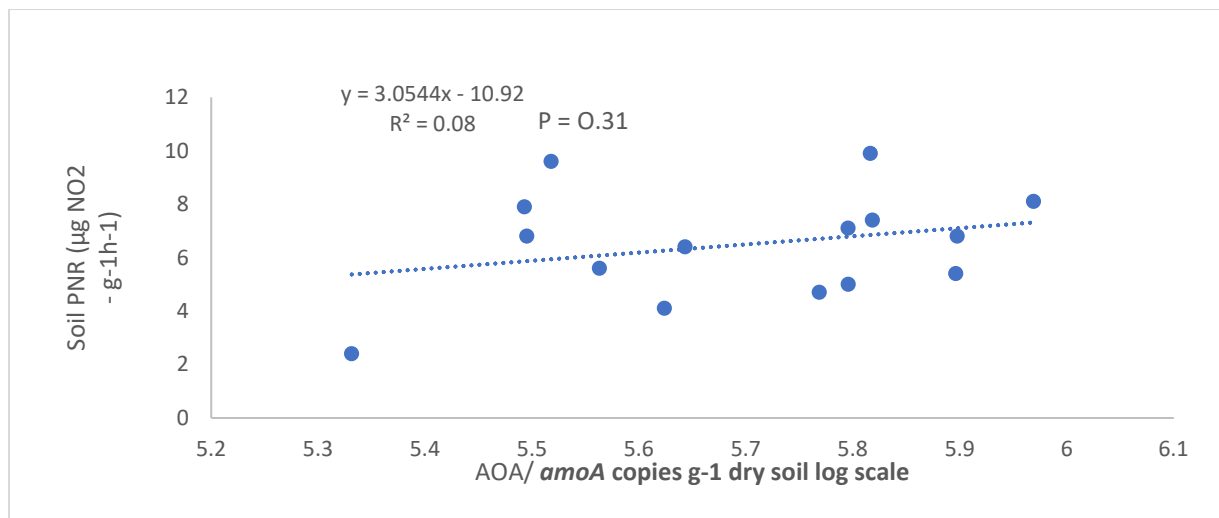
Table S1. Pearson's correlation between gene copies of the bacterial (AOB) and archaeal (AOA) amoA abundance, PNA, and soil properties.

| Soil depth | Variable | pH | TN | SOC | AP | NH ₄ ⁺ -N | NO ₃ ⁻ -N |
|------------|----------|---------|-------|-------|-------|---------------------------------|---------------------------------|
| 0-20 cm | AOA | -0.30 | 0.307 | -0.01 | 0.38 | 0.15 | 0.15 |
| | AOB | -0.71** | 0.10 | -0.26 | 0.45 | 0.02 | 0.83** |
| | PNA | -0.62* | 0.28 | -0.06 | 0.61* | 0.07 | 0.71** |

Abbreviations: Soil pH; TN= Total Nitrogen; SOC= Soil organic carbon; NO₃⁻-N= Nitrate; NH₄⁺-N= Ammonium N; AP= Available Phosphorous. PNA indicates soil potential nitrification activity.

* Significant correlations are indicated at P < 0.05, ** suggesting significant correlations at P < 0.01.

A.



B.

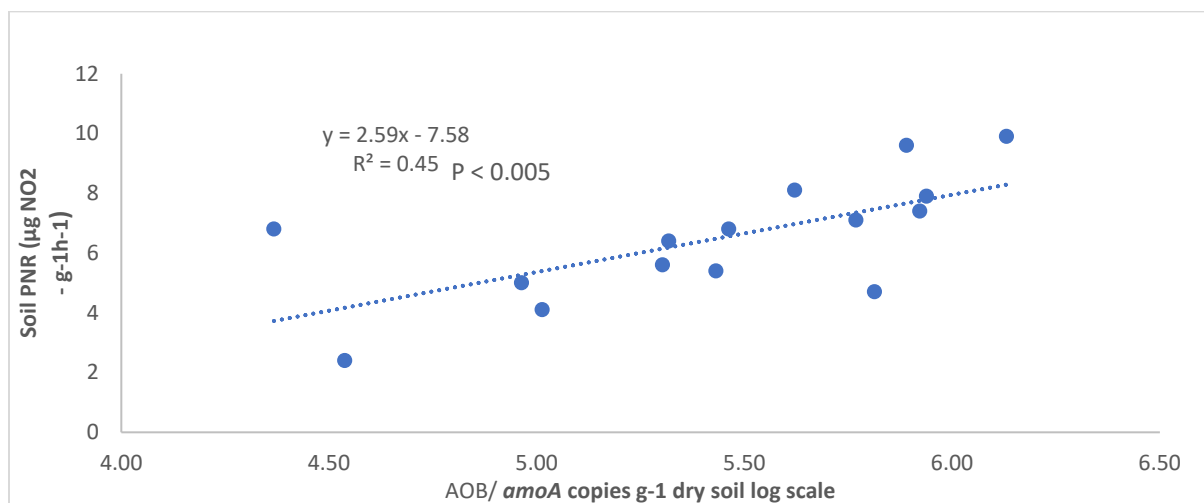


Figure S1. The potential nitrification rate (PNR) and the correlation between PNR and AOA(A) and AOB (B) gene copy numbers.

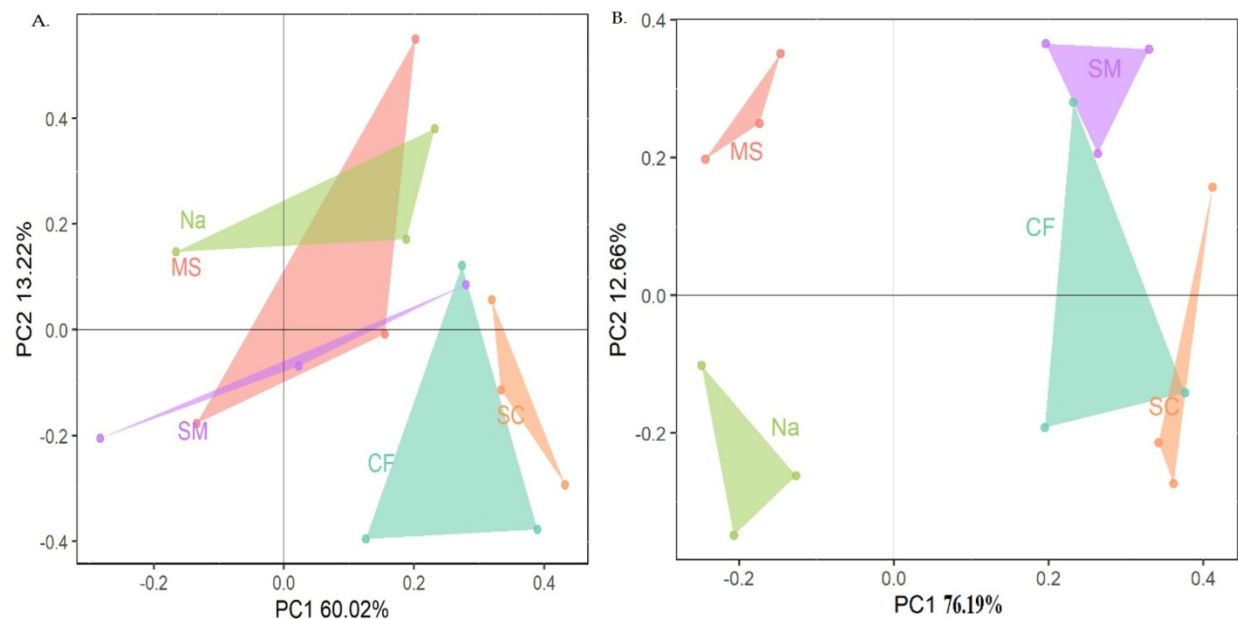
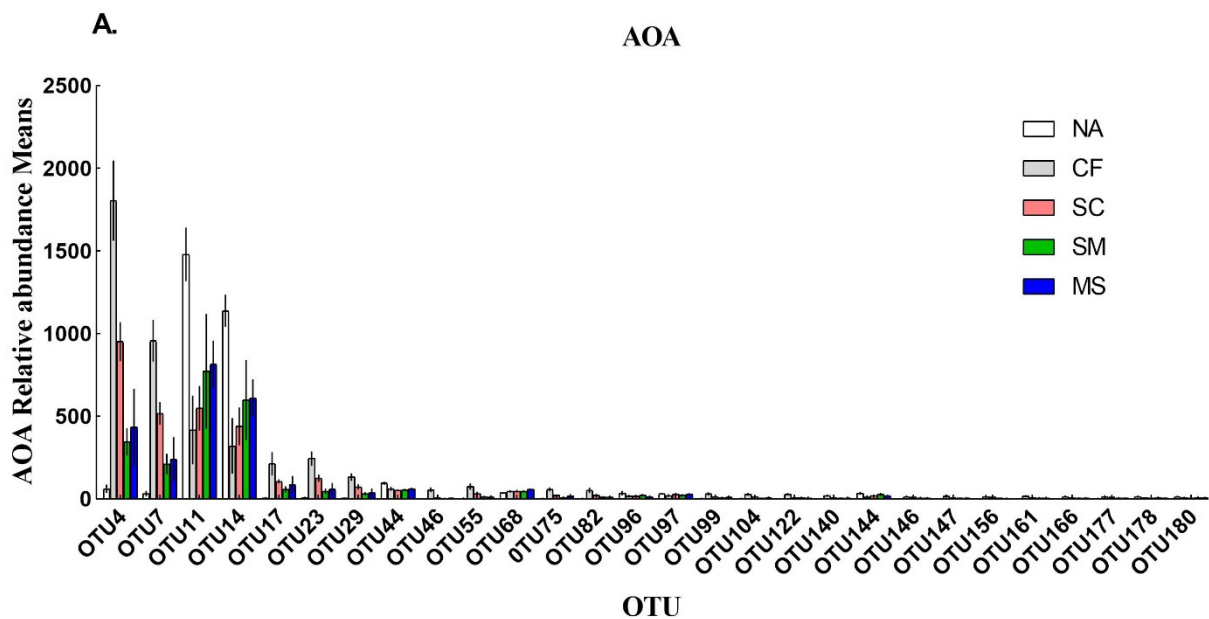


Figure S2. Principal component analysis as impacted by the fertilizer regime. (A). Ammonia-oxidizing archaea (*amoA* AOA gene) and (B). Ammonia-oxidizing bacteria (*amoA* AOB gene). NA= no fertilization; SM= cow manure; CF= chemical fertilizer; SC= chemical fertilizer + cow manure; MS= corn stalk.



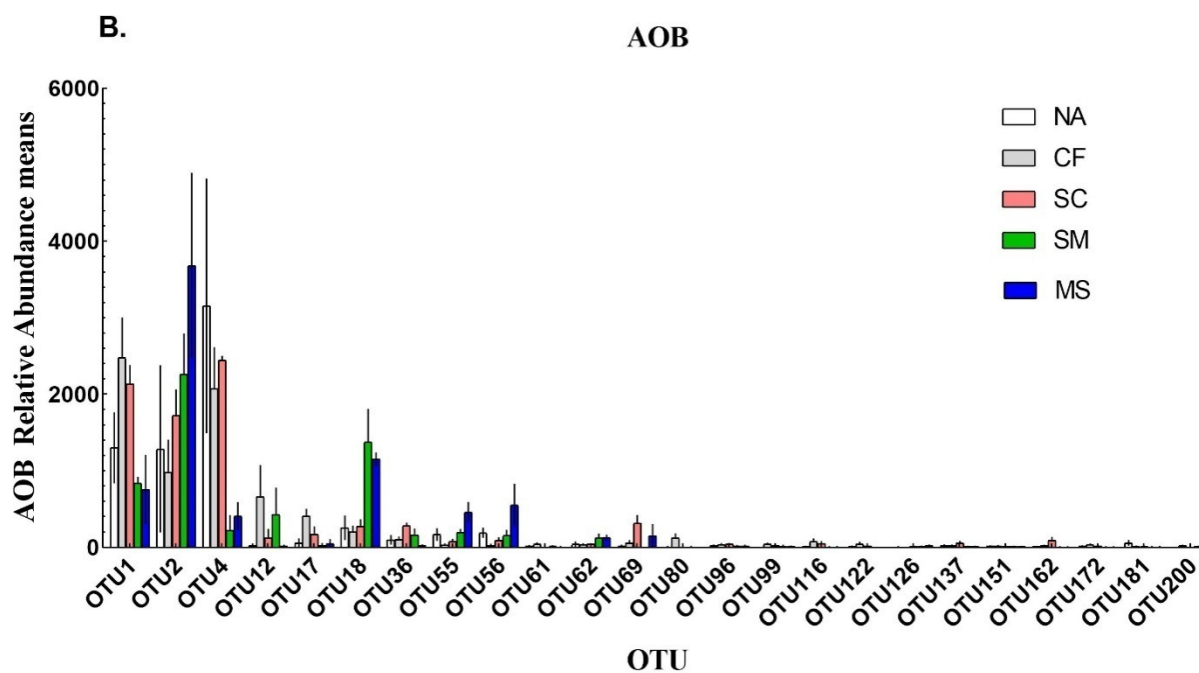


Figure S3. Relative abundances of selected Genus cluster of AOA (A) and AOB (B) among dominant 200 OTUs, which were significantly changed by N fertilization amendments. Error bars represent standard errors ($n = 4$). Relative abundance among the N amendments within an OTU ($P < 0.05$). NA= no fertilization; SM= cow manure; CF= chemical fertilizer; SC= chemical fertilizer + cow manure; MS= corn straw.