# Figure Legends

**Figure 1:** Fraction of dissolved nitrogen species (NO3-, NO2-, and NH4+) removed between input water and the deepest piezometer in the native soil (beige) and woodchip-amended plots (brown) at the three field sites (HSP= Harkins Slough, KTR= Kelly Thompson Ranch, KTYA= Kitayama Ranch). A positive fraction indicates that N was removed from the system while a negative fraction indicates addition of dissolved N species. The median is the bold line in the middle of the box, the upper and lower edges of the box represent the 25th and 75th percentiles. The whiskers extend to give the 90th percentile. Each point represents a chemical data from an infiltration day during the experiment. \*=p<0.01 \*\*\*=p<0.0001, \*\*\*\*= p<0.00001.

**Figure 2:** Non-metric multidimensional scales (NMDS) of the before infiltration samples (n=30, replicates were not included) from the different plots with Total Carbon, Total Nitrogen, and percent sand, silt, and clay as inputs. Samples from Harkins Slough (HSP) are blue squares (■), Kelly Thompson Ranch (KTR) are brown triangles (△), and Kitayama Ranch (KTYA) are green circles (●). The ellipses show the locations with a multivariate t-distribution of 95%.

**Figure 3:** First two constrained axes (12.8% and 11.2% of variance respectively) of the Constrained Correspondence Analysis (CCA) of each initial sample's microbial community (n=38). The constraints were Total Carbon, Total Nitrogen, and percent sand, silt, and clay. Samples from Harkins Slough (HSP) are blue squares (■), Kelly Thompson Ranch (KTR) are brown triangles (△), and Kitayama Ranch (KTYA) are green circles (●). The ellipses show the locations with a multivariate t-distribution of 95%.

**Figure 4:** (a) Relative abundances of the top 10 phyla in soil samples (n=92) pooled by infiltration timing and treatment from Harkins Slough (HSP), Kelly Thompson Ranch (KTR), and Kitayama Ranch (KTYA). The top row shows before infiltration and the bottom show after infiltration. Samples are split by treatment type: either native soil (NS) or a wood chip PRB (WC). (b) Shannon- Weaver diversity index for the samples at all three sites before and after infiltration. The median is the bold line in the middle of the box, the upper and lower edges of the box represent the 25th and 75th percentiles. The whiskers extend to give the 90th percentile. Data that extends outside the whiskers are represented as points. \*\*\*=p<0.0001, \*\*\*\*= p<0.00001. (c) Non-metric dimensional scaling (NMDS) of the microbial communities. Each ● represents samples before infiltration (n=38) and each × (n=54) represents samples after infiltration. Colored ellipses show each location with a multivariate t-distribution of 95%.

**Figure 5:** Significant (p<0.05) genera which had changes in differential abundance between before (n=17) and after (n=25) infiltration samples in native soil samples. Analysis of Composition of Microbiomes with Bias Correction (ANCOM-BC) was used to calculate log 2-fold changes. A positive fold change indicates that abundance was high in post-infiltration samples. Error bars show standard errors. Color indicates the assigned Phylum of the sequence.

**Figure 6**: Significant (p<0.05) genera which had differential abundance between samples treated with a wood chip PRB (n=29) compared to samples with no treatment (n=25). Analysis of Composition of Microbiomes with Bias Correction (ANCOM-BC) was used to calculate log 2-fold changes. A positive fold change indicates that abundance was higher in treated samples. Error bars show standard errors. Color indicates the assigned Phylum of the sequence.

**Figure 7:** Constrained Correspondence Analysis (CCA) using NO3-. Mn, Fe, and DOC concentrations from the infiltrating water as constraints to explain the variance among the top 20 genera. Axis 1 explains 43.9% of the variance among species while axis 2 explains 3%. After infiltration samples (n=32) with profession water quality panel data were used for analysis.

**Figure 8**: Phylogenetic tree of sequenced clade I *nosZ* reads with reference *nosZ* sequences and their relative abundance. Samples are from 30cm below the plot surface at either Kelly Thompson Ranch (KTR) or Kitayama Ranch (KTYA) before or after infiltration in native soil (NS) or wood chip (WC) amended plots. The tip points indicate the Family assigned to the sequences.