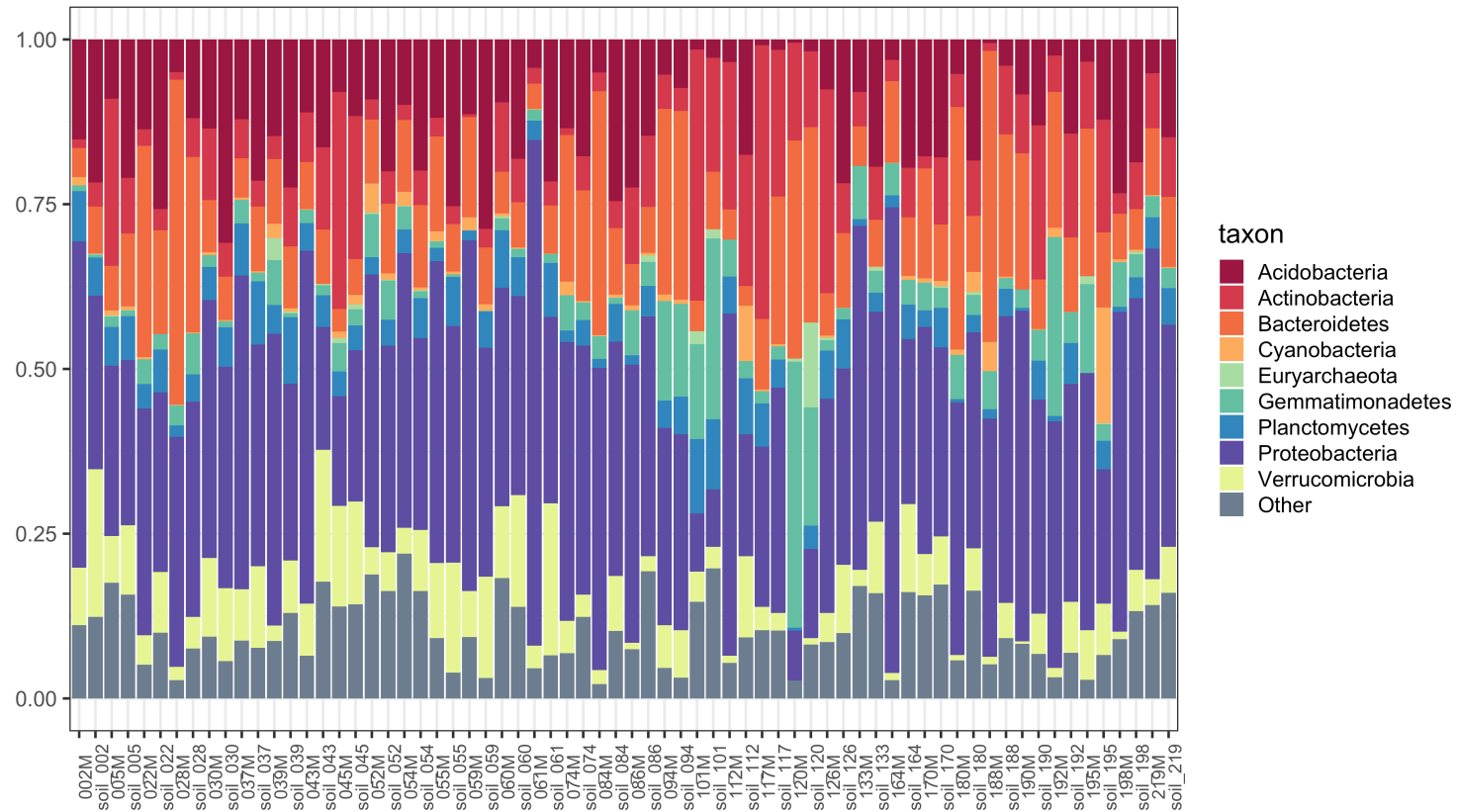
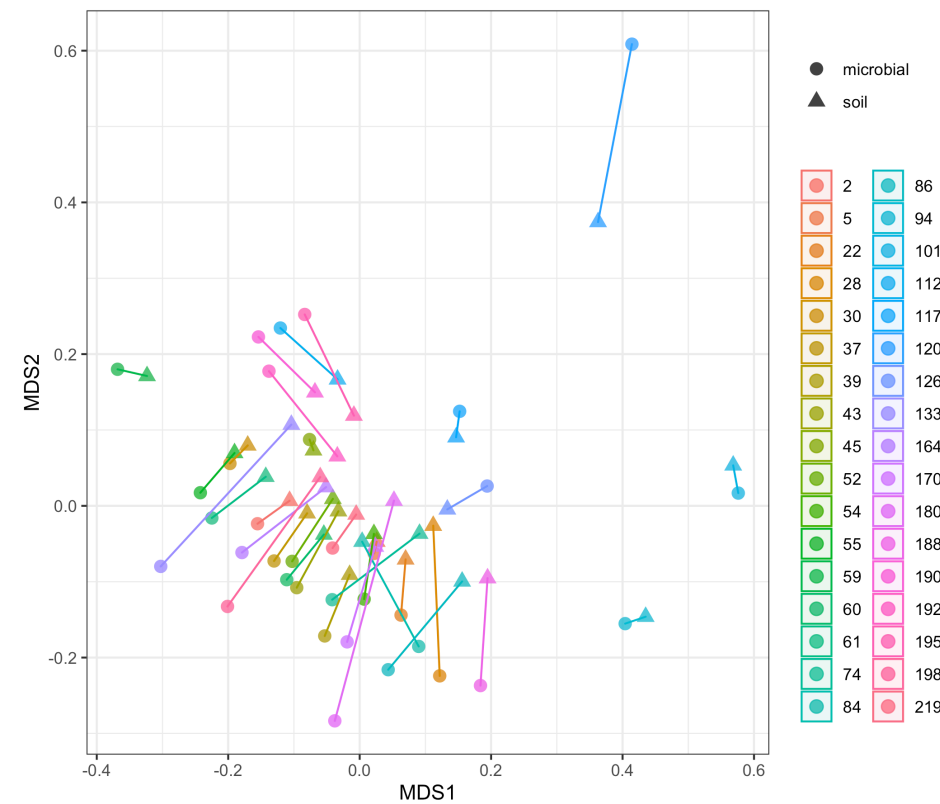


Figure S1

A



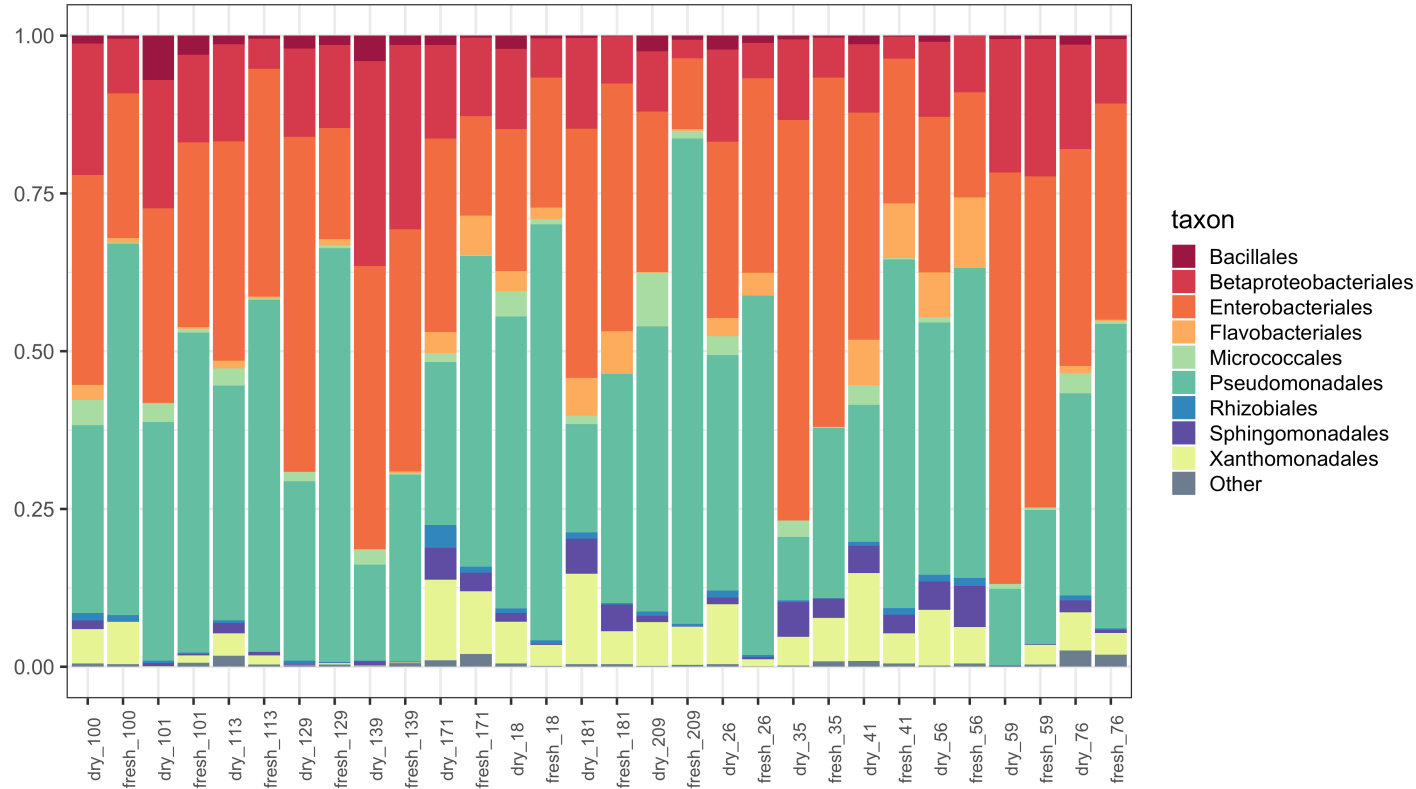
B



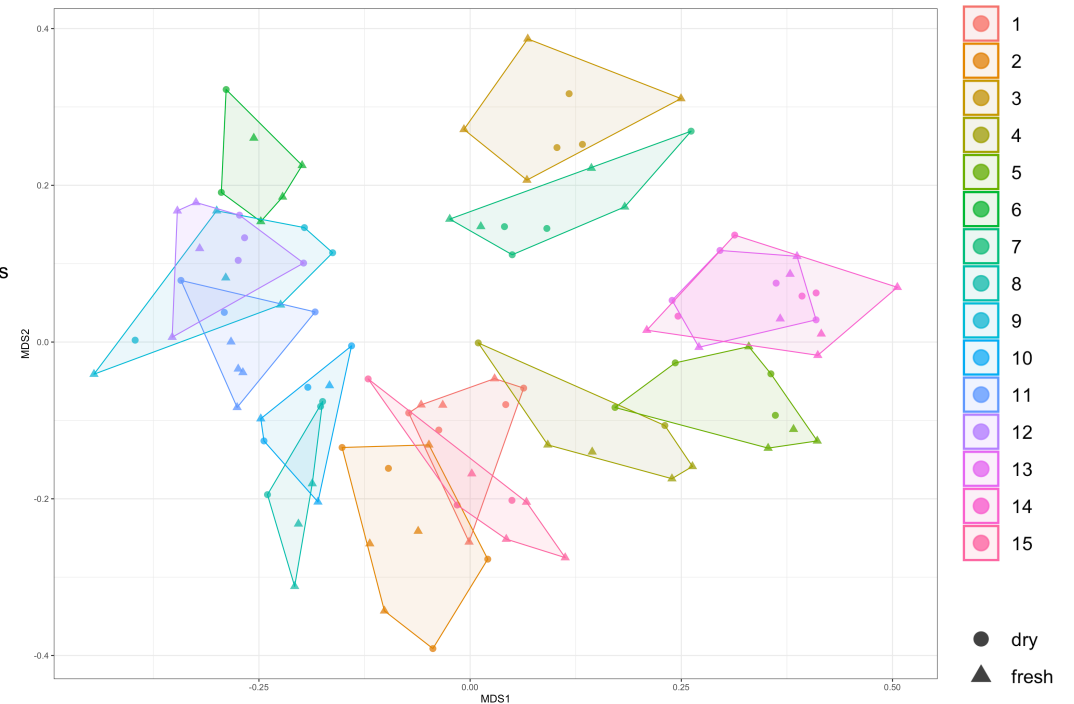
**Figure S1:** Bacterial communities in soils and soil slurries. A) The proportional abundance of major phyla in paired soils and soil slurries. Soil slurries (“M”) made from the paired soil (“soil\_”) are adjacent along the x-axis. B) NMDS ordination plot (stress = 0.18) of soil and soil slurry bacterial communities. The bulk soil sample and the corresponding soil slurry sample generated from the same soil are connected by a line.

Figure S2

A

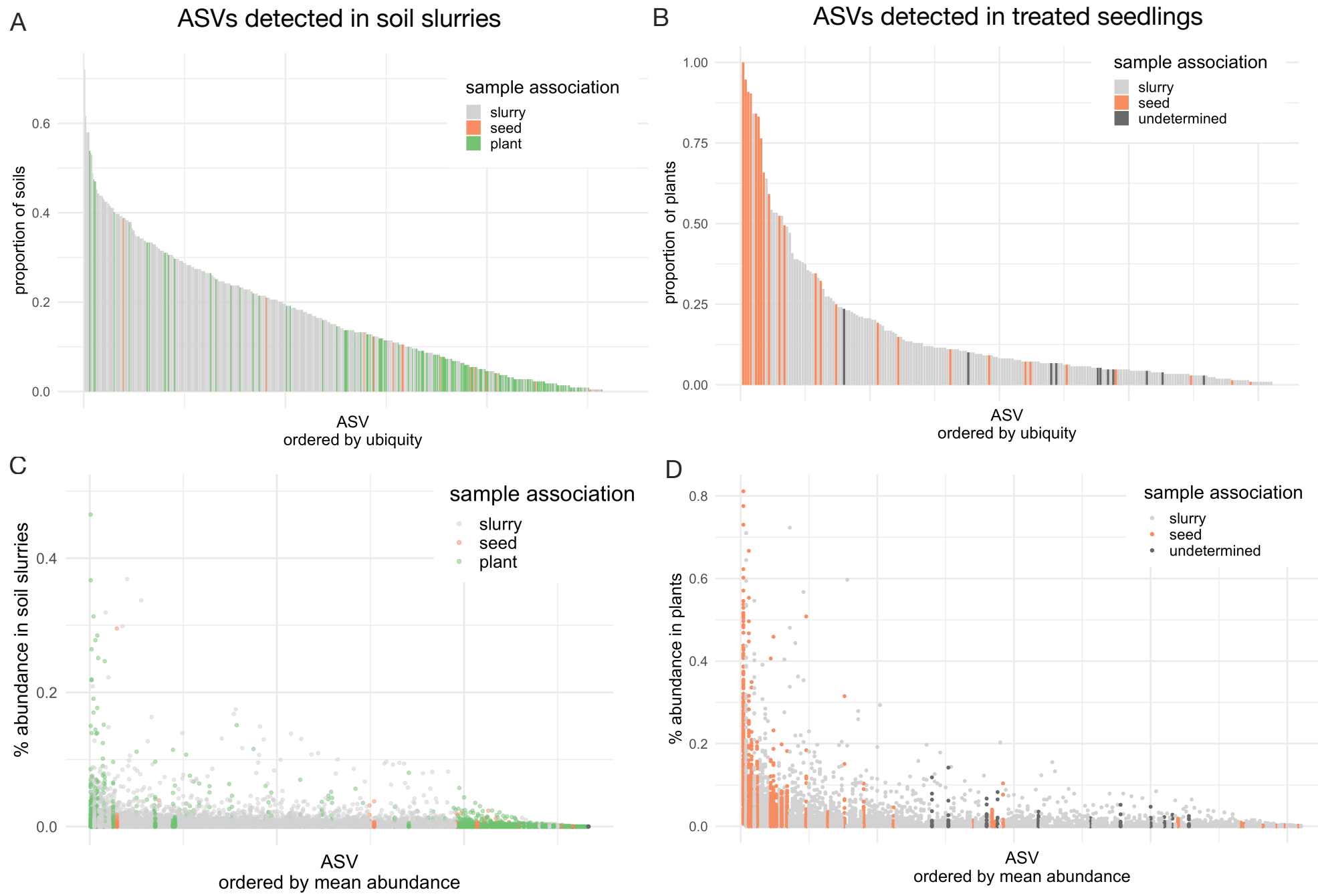


B



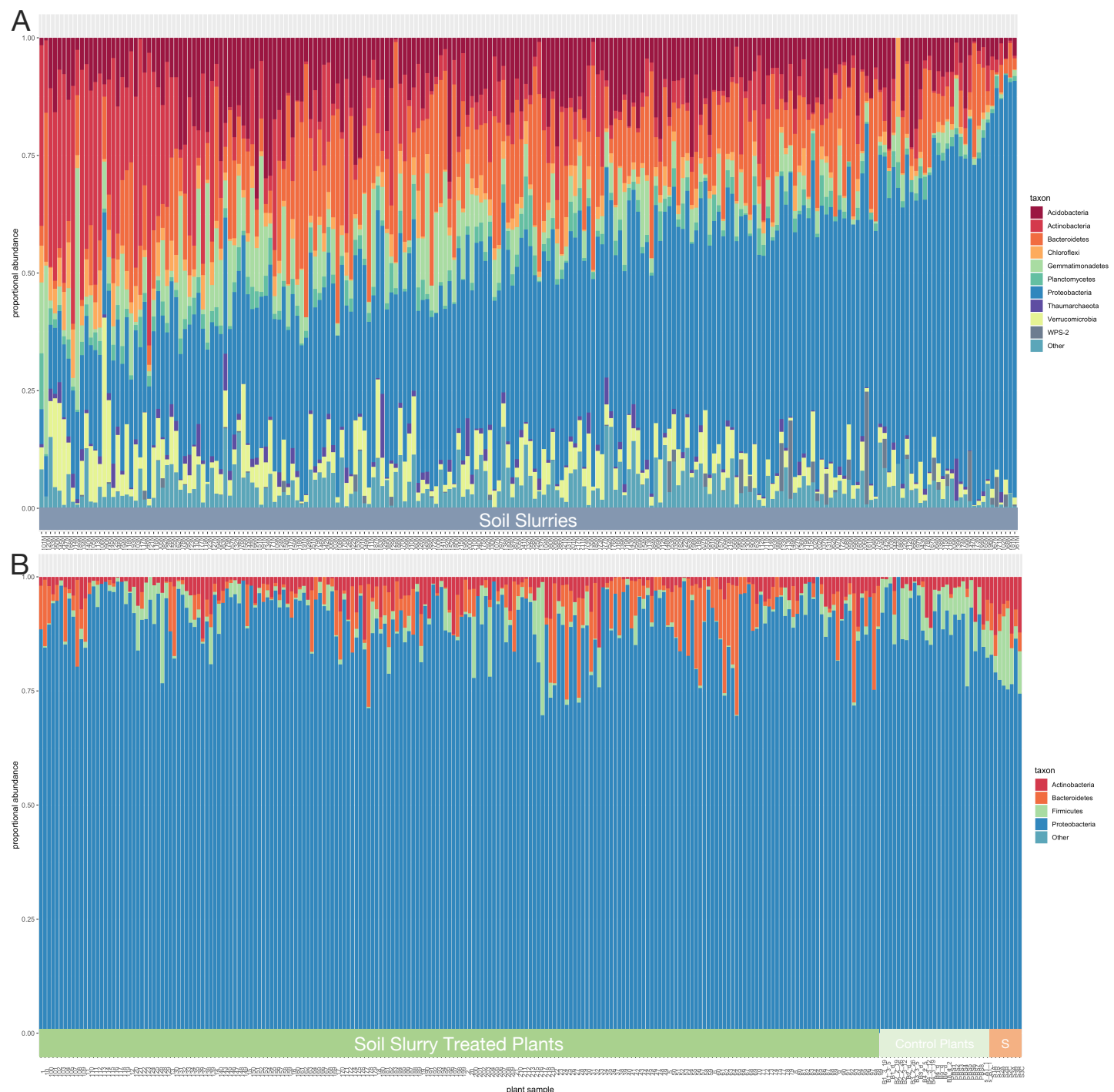
**Figure S2:** Bacterial communities in fresh frozen and dry frozen wheat seedlings. A) The proportional abundance of major taxa in seedlings frozen after drying or frozen fresh. Dried and fresh seedlings from the same treatment plate are adjacent along the x-axis. B) NMDS ordination plot (stress = 0.19) of fresh and dried replicate wheat seedlings bacterial communities. Replicates generated from the same slurry treatment are noted by color and hull, and shape represents seedling processing procedure (fresh or dry).

**Figure S3**



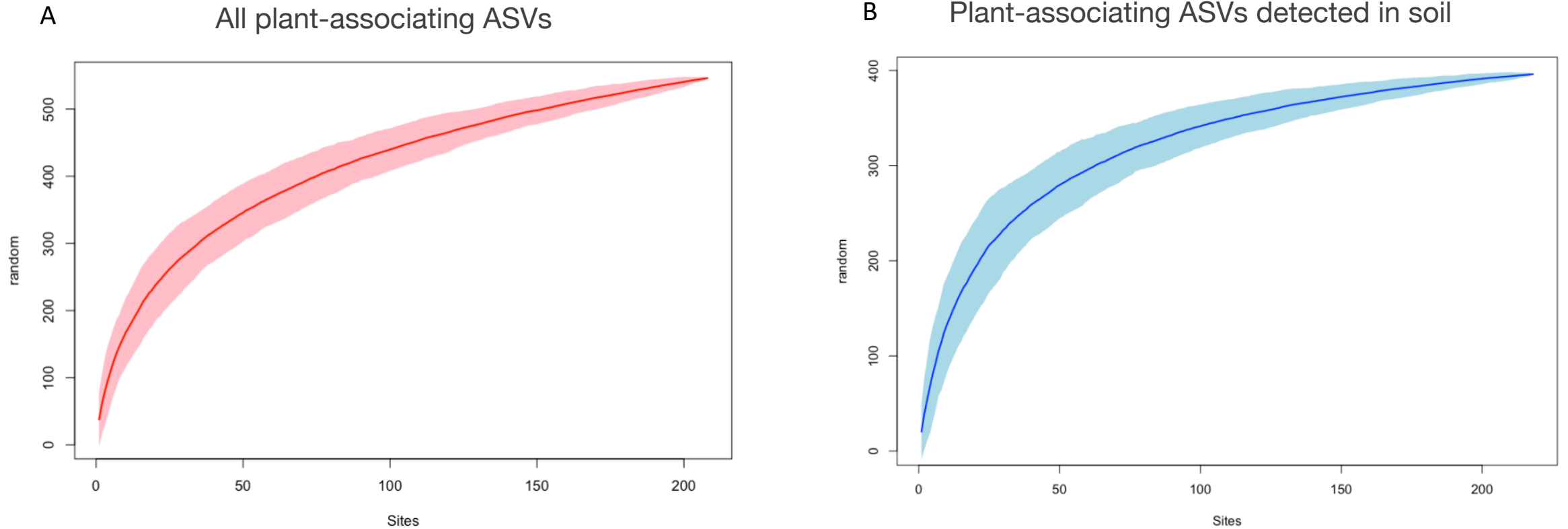
**Figure S3:** The prevalence and relative abundance of bacterial ASVs in soil slurries and wheat seedlings. Colors correspond to whether the ASV was predominantly detected in seedlings (green, A and C only), seeds (orange), soil slurries (light grey), or undetermined (dark grey). See Methods for “Sample Association” determination rules. A) Prevalence of ASVs detected across soil slurry samples (out of 219 soil slurries), B) Prevalence of ASVs detected across wheat seedling samples (out of 208 seedlings). C) Percent relative abundance of ASVs detected in soil slurry samples. D) Percent relative abundance of ASVs detected across wheat seedling samples. In each panel, the x-axes are ordered by y-axis value, and are not consistently ordered across panels.

Figure S4

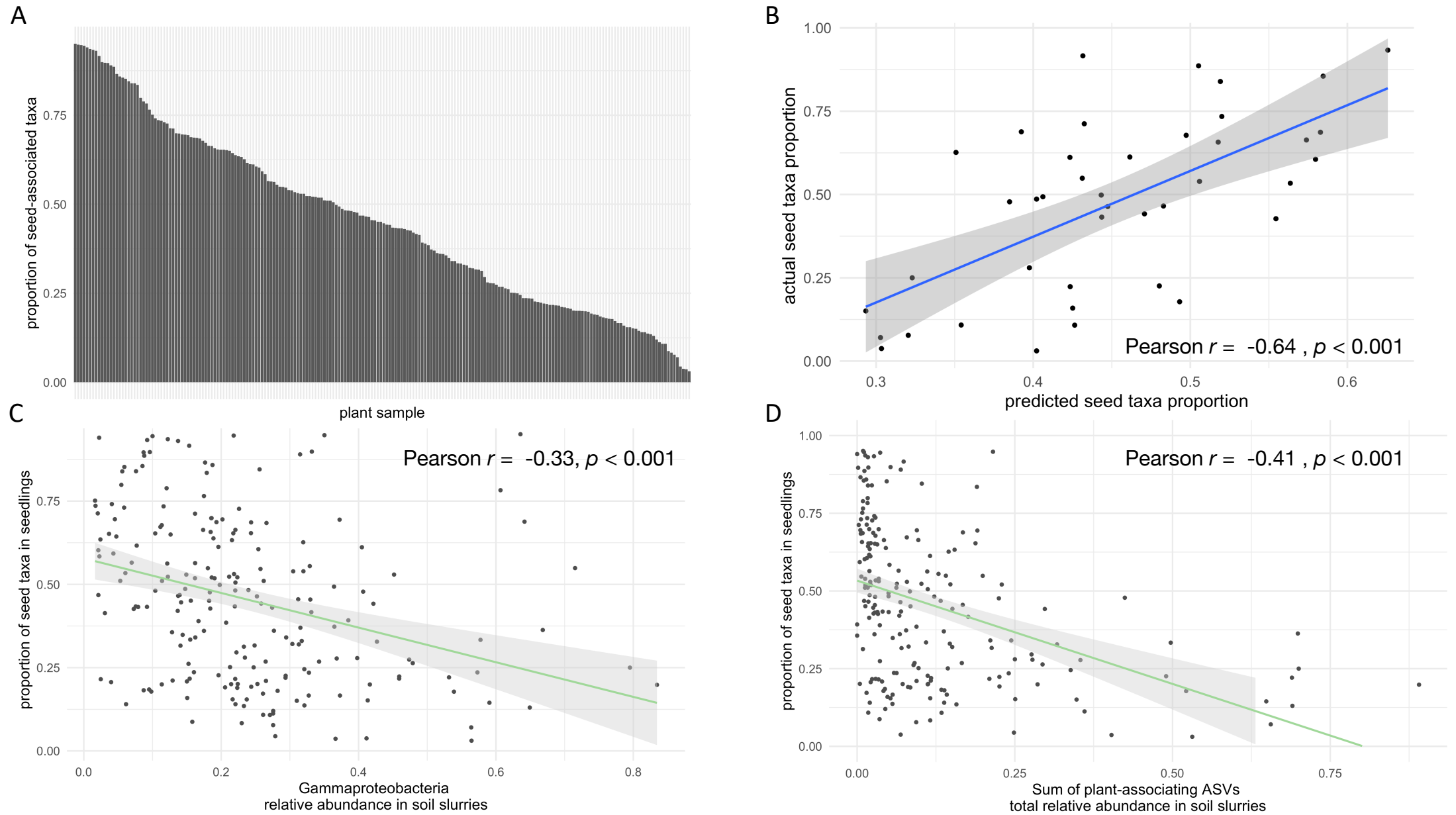


**Figure S4:** The proportional abundance of major phyla in soil slurries, wheat seedlings, and seeds. A) Soil slurry samples, ordered by increasing relative abundance of Proteobacteria. B) Soil slurry-treated seedlings, control-treated seedlings, and seeds, ordered by sample type.

**Figure S5**

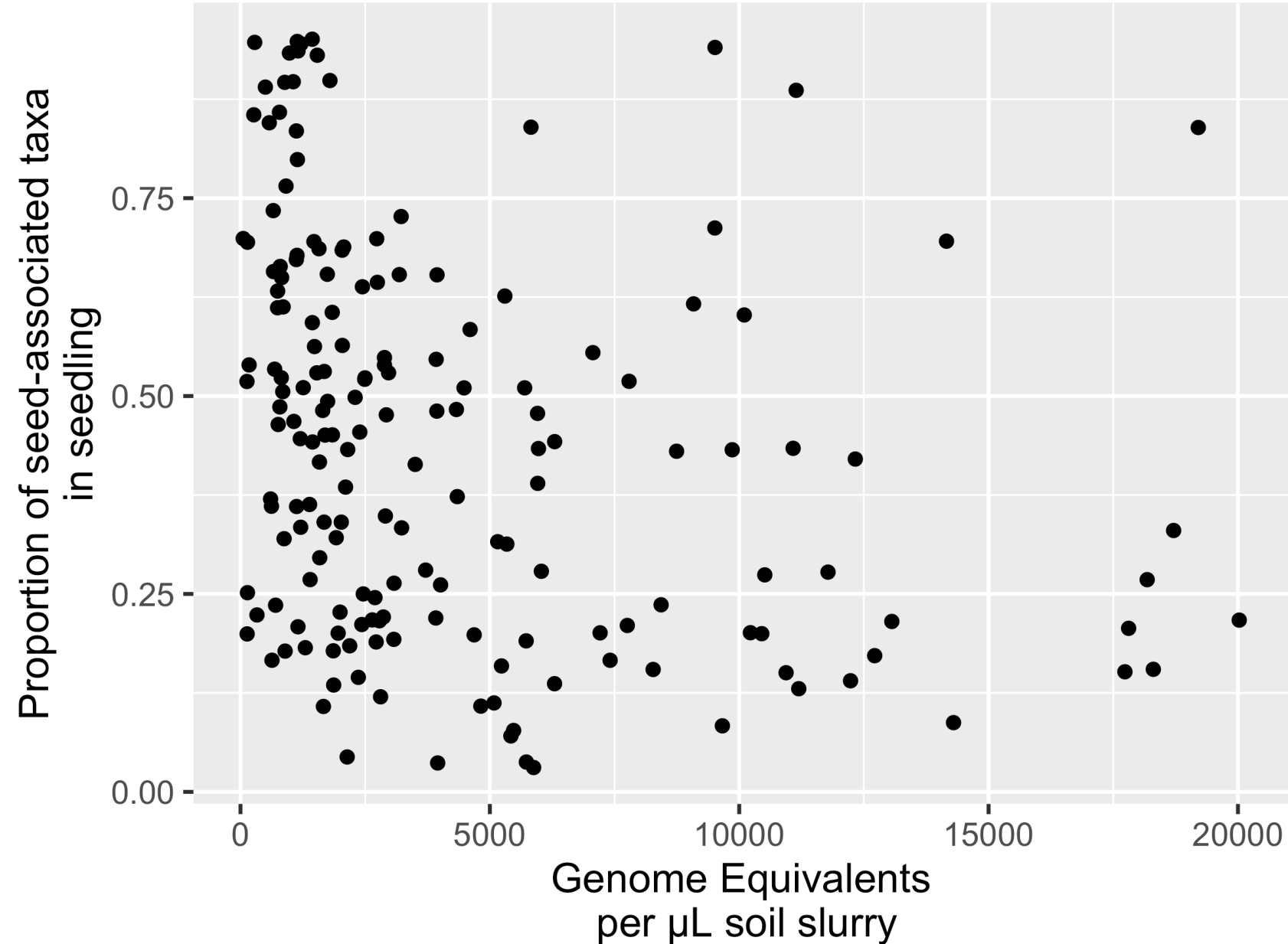


**Figure S5:** The number of bacterial ASVs detected increases with number of seedling samples tested. A) Rarefaction curve of all ASVs detected in seedling samples. B) Rarefaction curve of those plant-associating ASVs detected in soil slurry samples.



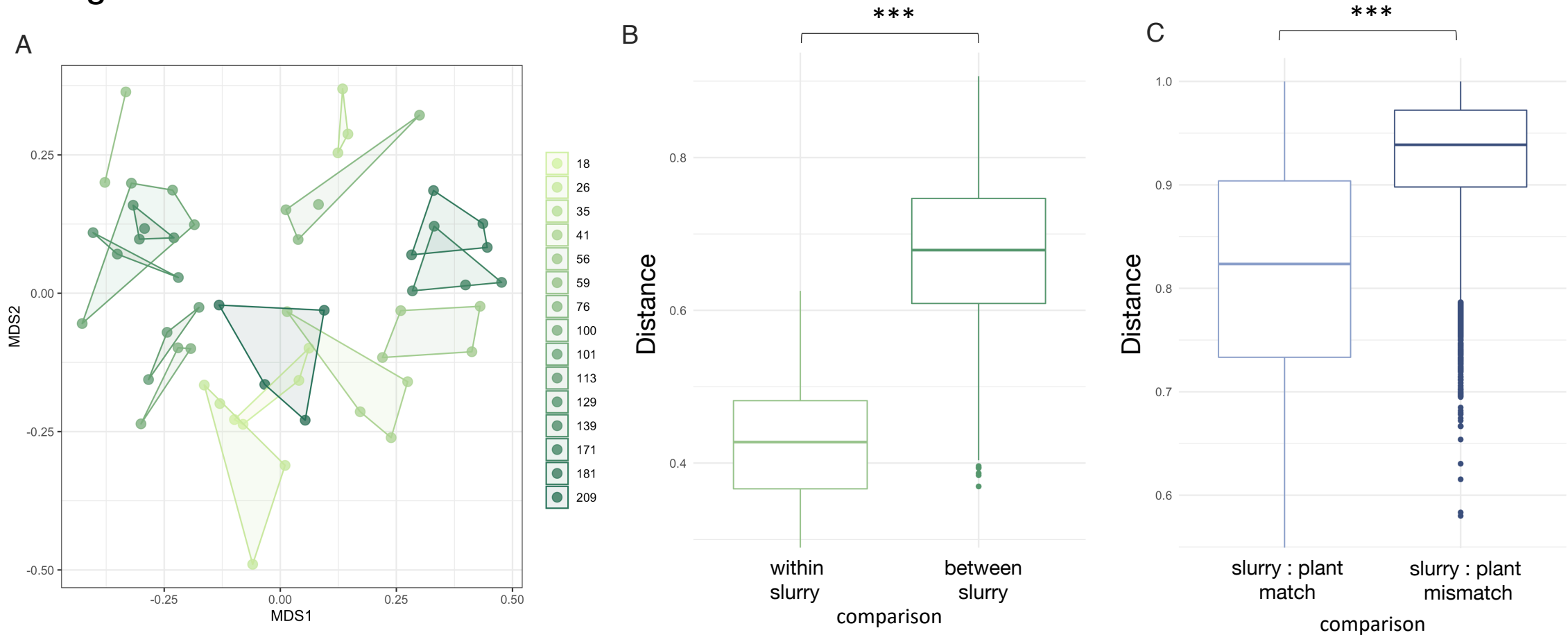
**Figure S6:** Variation in the proportion of seed-associated taxa across seedlings. A) The proportion of seed-associated taxa (ASVs found in > 3 seed samples) detected in each seedling sample. B) A Random Forest model was built to predict the proportion of seed taxa in seedlings from family level bacterial composition in soil slurry inocula. The predicted model values correlate with the true values in the test dataset (blue line = best linear fit; Pearson  $r = 0.64$ ,  $p < 0.001$ ). C) The proportion of seed-associated taxa in seedlings is negatively correlated with the proportion of Gammaproteobacteria in the soil slurry inocula (Pearson  $r = -0.33$ ,  $p < 0.001$ ). D) The proportion of seed-associated taxa in seedlings is negatively correlated with the proportion of plant-associating ASVs in soil slurries (ASVs found in >1 plants,  $n=373$ ; Pearson  $r = -0.41$ ,  $p < 0.001$ ).

Figure S7



**Figure S7:** Relationship between soil slurry bacterial biomass and proportion of seed taxa detected in seedlings. Estimate of bacterial biomass in soil slurries obtained by quantitative PCR analyses of the 16S rRNA gene, presented in *E. coli* genome equivalents. Beta regression  $\phi = 3.4$ , pseudo  $R^2 = 0.08$ ,  $p < 0.001$ , Pearson  $r = -0.29$ ,  $p < 0.001$ .

# Figure S8



**Figure S8:** Seedling bacterial community similarity of replicate soil slurry inoculations. A) NMDS ordination of seedling bacterial communities treated with distinct soil slurries, each replicated 4 times (stress = 0.17). Shades of green correspond to different soil slurry inocula (PERMANOVA  $F = 6.4$ ,  $R^2 = 0.70$ ,  $p < 0.001$ ). B) Bray-Curtis community distance of treated seedlings is lower within replicate soil slurry treatments than between replicate soil slurry treatments (within slurry treatment mean distance 0.43, between slurry treatment mean distance 0.67, Welch's t-test  $p < 0.0001^{***}$ ). C) Bray-Curtis community distance is lower between soil slurry inocula and corresponding "matched" inoculated seedling than between "mismatched" slurry-seedling comparisons (slurry: plant match mean distance 0.82, slurry: plant mismatch mean distance = 0.93, Welch's t-test  $p < 0.0001^{***}$ ). For C) the bacterial community was filtered to include only those ASVs with the potential to associate with plants, defined as being detected in  $>1$  plant across the dataset.