Figure 3. Principal Components Analysis of the soil prokaryote community obtained by sequencing the 16S rRNA gene from soil samples collected from a) full-season soybean (June 2015) b) winter wheat (May 2016) and c) corn (June 2017). The community composition did not differ significantly between treatments in full-season soybean (PERMANOVA P=0.728, R^2=0.083), winter wheat (PERMANOVA P=0.208, R^2=0.108), or corn (PERMANOVA P=0.317, R^2=0.104).