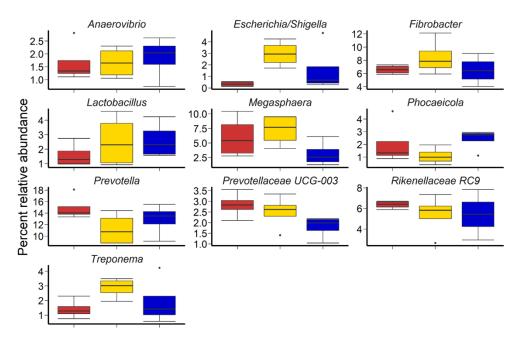
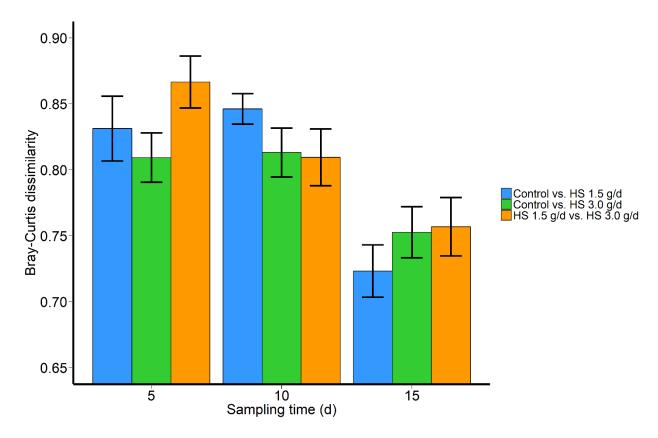


■Control
■Humic substances 1.5 g/d
■Humic substances 3.0 g/d
■

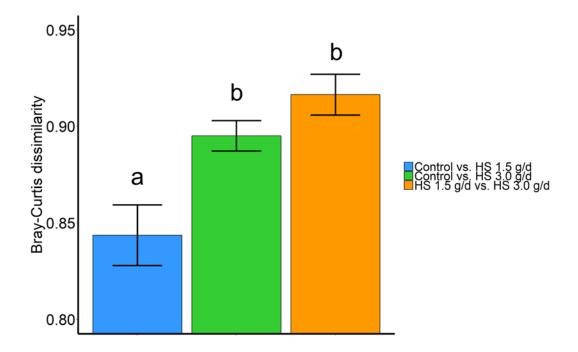
- 2 Supplementary Fig. S1. Relative abundance (%) of the ten most abundant genera in the solid-
- 3 associated microbe (SAM) samples by treatment and sampling time. Points represent outlier
- 4 samples.



- ■Control
  ■Humic substances 1.5 g/d
  ■Humic substances 3.0 g/d
- 7 Supplementary Fig. S2. Relative abundance (%) of the ten most abundant genera in the liquid-
- 8 associated microbe (LAM) samples by treatment (d 15). Points represent outlier samples.



**Supplementary Fig. S3**. Bray-Curtis dissimilarities for pairwise treatment comparisons of solid-associated microbe (SAM) samples by sampling time. Error bars represent standard error of the mean (n = 16 comparisons). HS = humic substances.



**Supplementary Fig. S4**. Bray-Curtis dissimilarities for pairwise treatment comparisons of liquid-associated microbe (LAM) samples taken at d 15. Error bars represent standard error of the mean (n = 16 comparisons). Different lowercase letters indicate significantly different means (P < 0.05). HS = humic substances.