

Figure S1: Relative abundances of fungal classes detected in composting sites by amplicon-based (ITS1 and ITS2) HTS method.

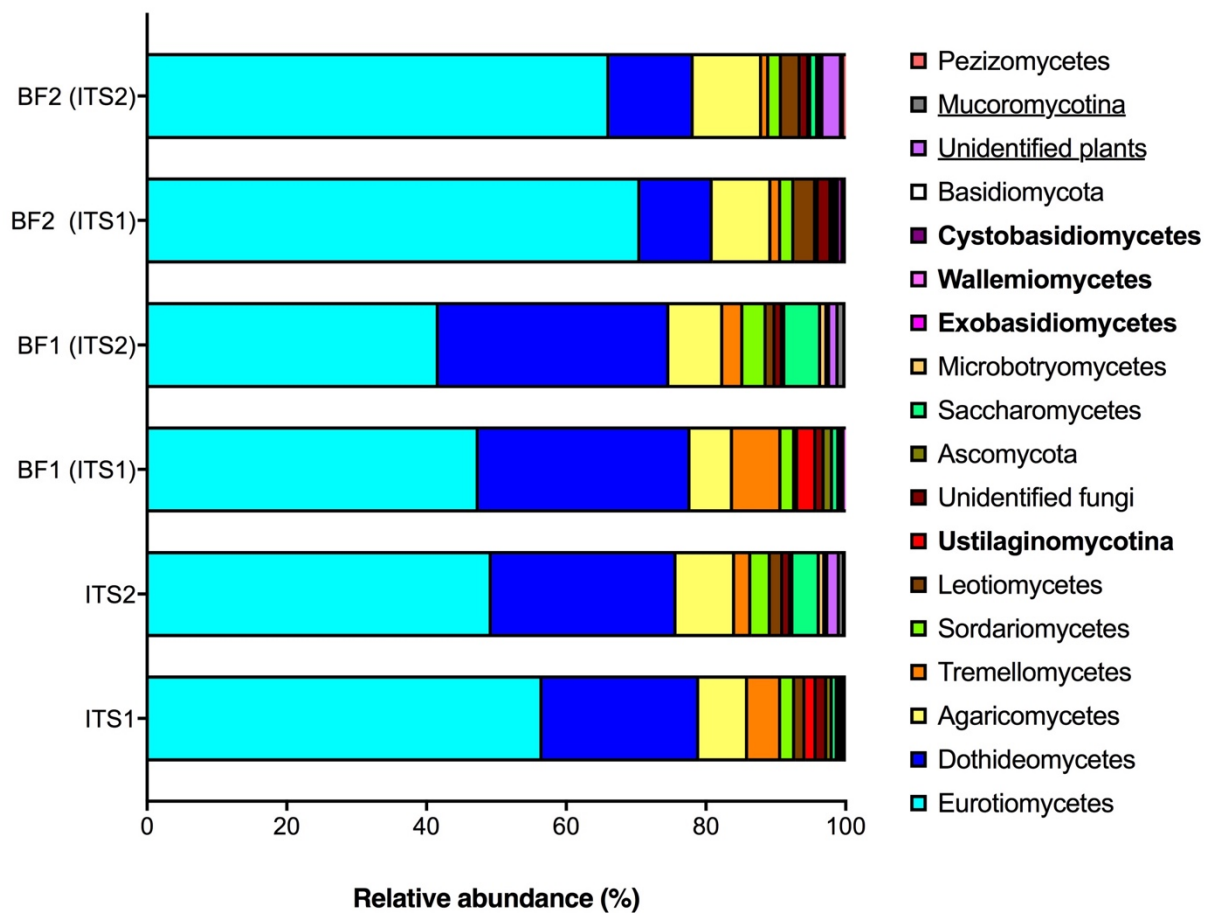


Figure S2: Relative abundances of fungal classes detected in biomethanization facilities by amplicon-based (ITS1 and ITS2) HTS method.

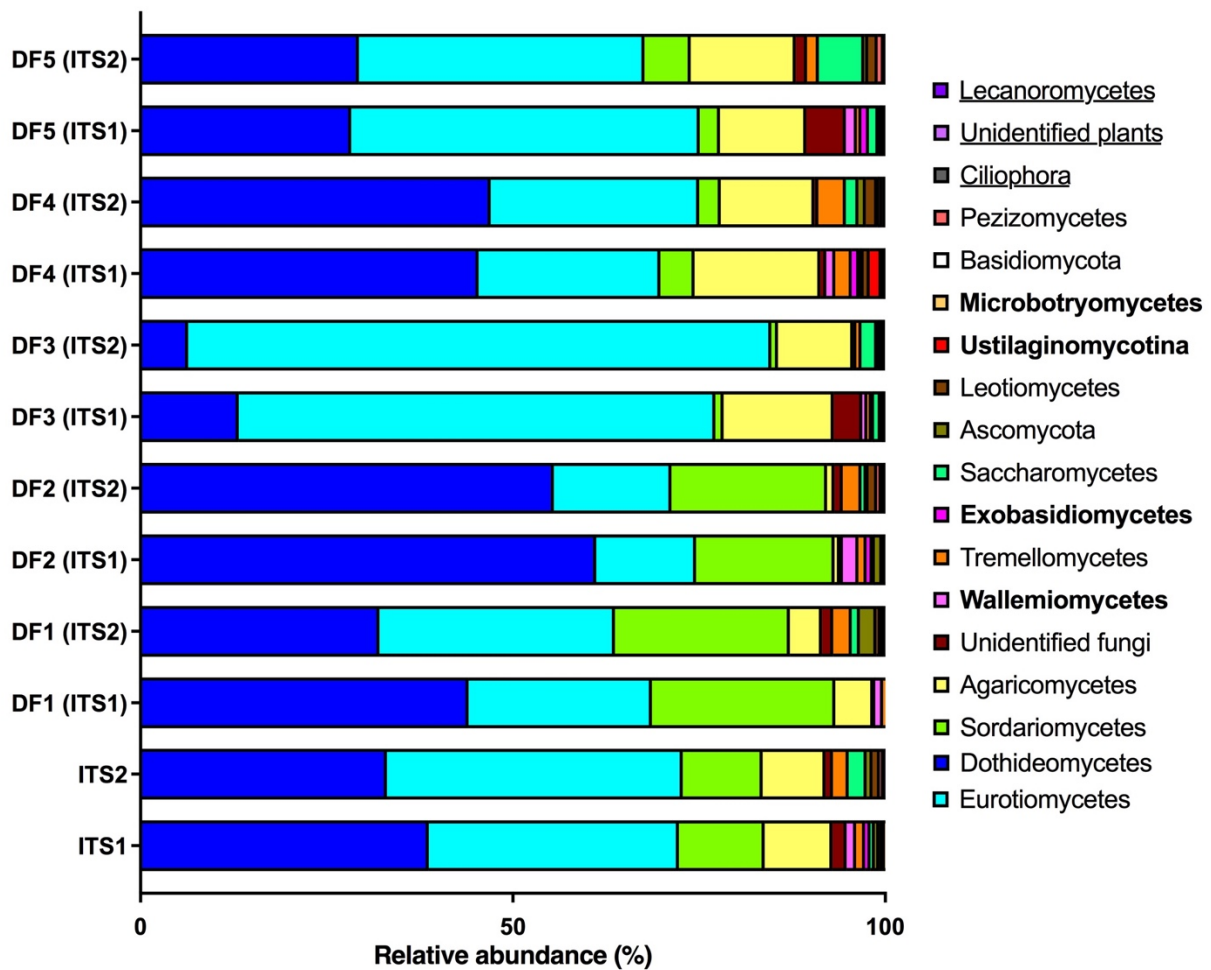


Figure S3: Relative abundances of fungal classes detected in dairy farms by amplicon-based (ITS1 and ITS2) HTS method.

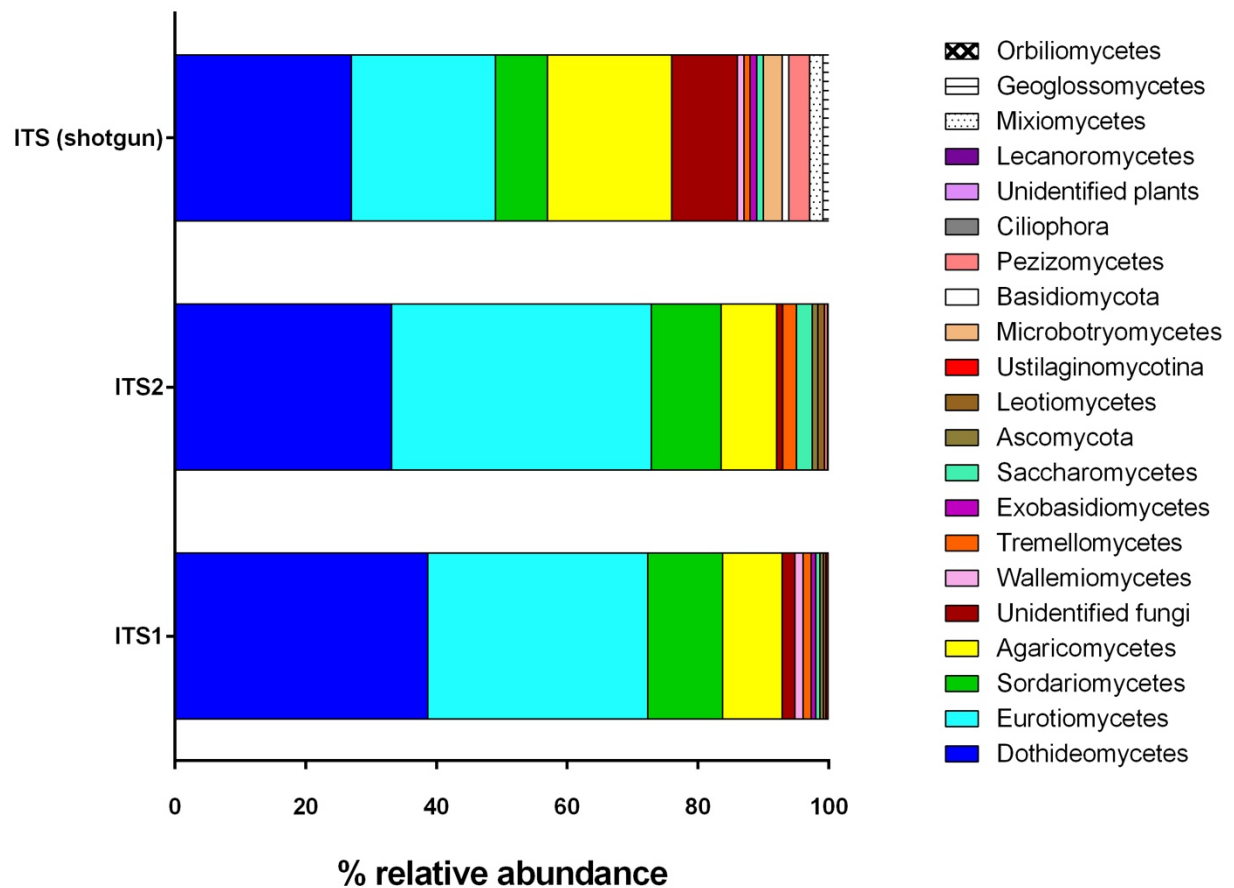


Figure S4: Relative abundances of fungal classes detected in dairy farms by shotgun and amplicon-based (ITS1 and ITS2) HTS. The whole ITS region (ITS1-5.8S-ITS2) was extracted from the shotgun metagenomes (ITS-shotgun) and relative abundance was recalculated based on the representative number of sequences.