

Supplementary Table 1. List of common enriched OTUs by ABC001 and HS2 supernatant treatment using the random forest analysis

# OTUs	Average relative abundance (%)				Taxonomy
	ABC001	HS2	Fungicides	Control	
OTU1171 ^a	0.651	0.193	0.061	0.095	p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Nitrobacteraceae; g__Pseudolabrys
OTU1430 ^a	0.387	0.074	0.000	0.000	p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Nitrosomonadaceae; g__mle1-7
OTU0144	0.253	0.252	0.522	0.135	p__Acidobacteriota; c__Blastocatellia; o__Pyrinomonadales; f__Pyrinomonadaceae; g__RB41
OTU1606 ^a	0.218	0.265	0.091	0.150	p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Piscinibacter
OTU1432	0.171	0.245	0.174	0.072	p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Rhodofera
OTU1384	0.242	0.085	0.131	0.068	p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Aquabacterium
OTU0445	0.169	0.101	0.131	0.048	p__Acidobacteriota; c__Acidobacteriae; o__Bryobacterales; f__Bryobacteraceae; g__Bryobacter
OTU1742 ^a	0.139	0.125	0.021	0.061	p__Chloroflexi; c__KD4-96; o__KD4-96; f__KD4-96; g__KD4-96; s__uncultured_bacterium
OTU1599 ^a	0.225	0.131	0.020	0.029	p__Desulfobacterota; c__Desulfuromonadia; o__Geobacterales; f__Geobacteraceae
OTU1750 ^a	0.175	0.089	0.000	0.014	p__Proteobacteria; c__Alphaproteobacteria; o__Tistrellales; f__Geminicoccaceae; g__Candidatus_Alysiosphaera; s__metagenome
OTU0507	0.050	0.110	0.099	0.014	p__Myxococcota; c__Polyangia; o__Haliangiales; f__Haliangiaceae; g__Haliangium
OTU0467	0.016	0.142	0.022	0.000	p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Chitinophagaceae
OTU1396	0.187	0.028	0.044	0.000	p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiales_Incertae_Sedis; g__Bauldia
OTU0209 ^a	0.122	0.008	0.000	0.000	p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Hydrogenophilaceae; g__uncultured
OTU1253 ^a	0.055	0.047	0.014	0.000	p__Myxococcota; c__Polyangia; o__Polyangiales; f__BIrii41; g__BIrii41; s__metagenome
OTU0742	0.040	0.065	0.051	0.000	p__Myxococcota; c__Polyangia; o__Polyangiales; f__Polyangiaceae; g__Pajaroellobacter; s__metagenome
OTU0463	0.024	0.048	0.050	0.010	p__Planctomycetota; c__OM190; o__OM190; f__OM190; g__OM190; s__uncultured_bacterium
OTU1863	0.012	0.058	0.052	0.000	p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__uncultured
OTU0059	0.019	0.098	0.028	0.000	p__Verrucomicrobiota; c__Verrucomicrobiae; o__Pedosphaerales; f__Pedosphaeraceae
OTU0554	0.004	0.077	0.042	0.000	p__Acidobacteriota; c__Subgroup_5; o__Subgroup_5; f__Subgroup_5; g__Subgroup_5; s__uncultured_bacterium

^aThe enriched operational taxonomic units (OTUs) by ABC001 and HS2 supernatant treatment compared to both control and fungicides.