

Supplementary Table S1a: Differentially abundant bacterial genera between Leaf and Berries

<u>OTUs</u>	<u>Genus</u>	<u>Corrected P-values</u>	<u>FDRs</u>
OTU94	<i>Geodermatophilus</i>	0.0060	0.00066
OTU428	<i>Kineococcus</i>	0.0060	0.00066
OTU903	<i>Hymenobacter</i>	0.0060	0.00066
OTU152	<i>Arthrobacter</i>	0.0060	0.00066
OTU39	<i>Paenisporosarcina</i>	0.0060	0.00066
OTU288	<i>Paenibacillus</i>	0.0060	0.00066
OTU101	<i>Microbacterium</i>	0.0060	0.00066
OTU460	<i>Planifilum</i>	0.0060	0.00066
OTU200	<i>Methylobacterium</i>	0.0060	0.00066
OTU72	<i>Cutibacterium</i>	0.0060	0.00066
OTU134	<i>Nocardioides</i>	0.0060	0.00066
OTU415	<i>Noviherbaspirillum</i>	0.0060	0.00066
OTU56	<i>Massilia</i>	0.0060	0.00066
OTU374	<i>Adhaeribacter</i>	0.0060	0.00066
OTU26	<i>Gluconobacter</i>	0.0060	0.00066
OTU451	<i>Roseomonas</i>	0.0117	0.00123
OTU897	<i>Streptococcus</i>	0.0172	0.00174
OTU193	<i>Domibacillus</i>	0.0278	0.00275
OTU849	<i>Tumebacillus</i>	0.0329	0.00312
OTU211	<i>Actinomycetospora</i>	0.0426	0.00396

Supplementary Table S1b: Differentially abundant fungal genera between Leaf and Berries

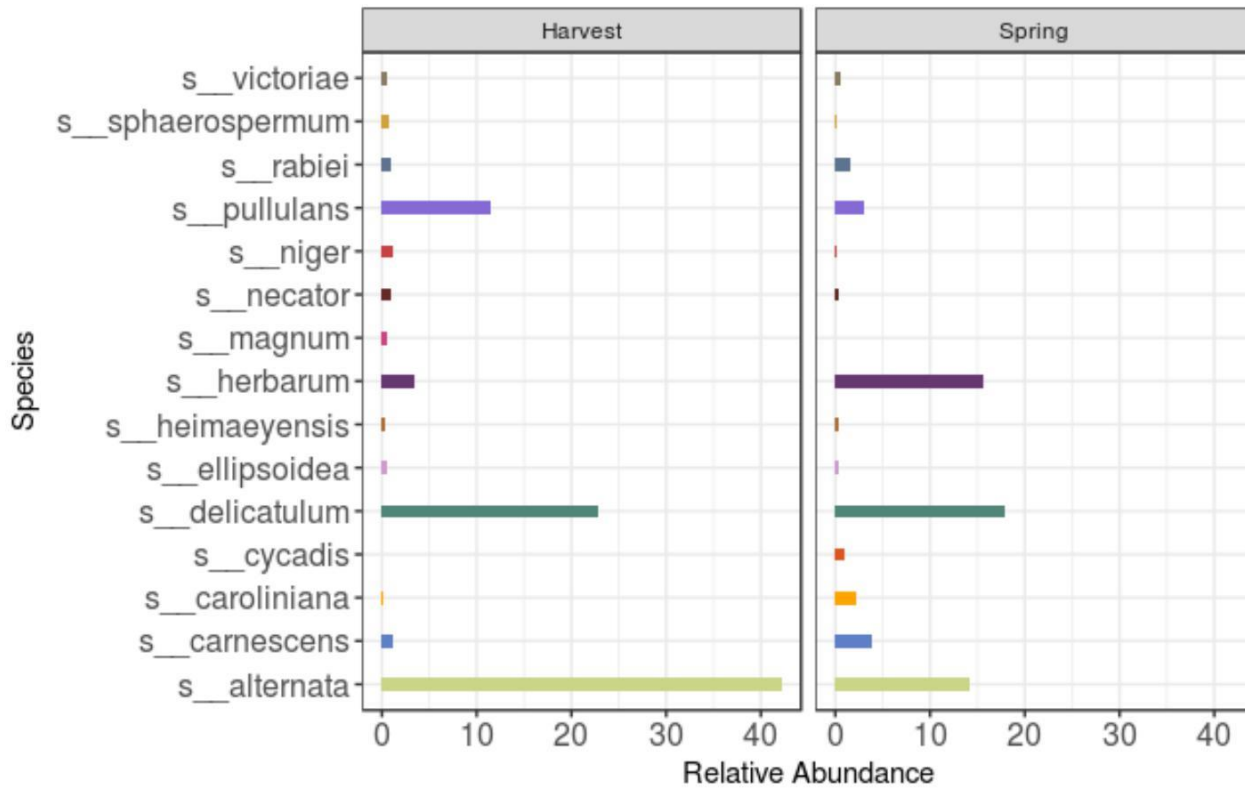
OTUs	Genus	Species	Corrected P-values	FDRs
OTU2	<i>g_Alternaria</i>	<i>s_alternata</i>	0.0021	0.0003764706
OTU4	<i>g_Cladosporium</i>	<i>s_delicatulum</i>	0.0021	0.0003764706
OTU33	<i>g_Sporobolomyces</i>	<i>s_roseus</i>	0.0021	0.0003764706
OTU18	<i>g_Sporobolomyces</i>	<i>s_roseus</i>	0.0021	0.0003764706
OTU62	<i>g_Aureobasidium</i>	<i>s_pullulans</i>	0.0021	0.0003764706
OTU49	<i>g_Rhodotorula</i>	<i>s_babjevae</i>	0.0021	0.0003764706
OTU11	<i>g_Filobasidium</i>	<i>s_magnum</i>	0.0021	0.0003764706
OTU12	<i>g_Alternaria</i>	<i>s_alternata</i>	0.0021	0.0003764706
OTU32	<i>g_Sporormia</i>	NA	0.0021	0.0003764706
OTU19	<i>g_Alternaria</i>	<i>s_alternata</i>	0.0021	0.0003764706
OTU79	<i>g_Rhodotorula</i>	<i>s_babjevae</i>	0.0021	0.0003764706
OTU61	<i>g_Quambalaria</i>	<i>s_cyanescens</i>	0.0021	0.0003764706
OTU83	<i>g_Metschnikowia</i>	<i>s_pulcherrima</i>	0.0021	0.0003764706
OTU73	<i>g_Metschnikowia</i>	<i>s_pulcherrima</i>	0.0021	0.0003764706
OTU96	<i>g_Metschnikowia</i>	<i>s_pulcherrima</i>	0.0021	0.0003764706
OTU35	<i>g_Citeromyces</i>	<i>s_matritensis</i>	0.0021	0.0003764706
OTU70	<i>g_Acaromyces</i>	<i>s_ingoldii</i>	0.0021	0.0003764706
OTU5	<i>g_Aureobasidium</i>	<i>s_pullulans</i>	0.0041	0.0006736842
OTU97	<i>g_Metschnikowia</i>	<i>s_pulcherrima</i>	0.0041	0.0006736842
OTU136	<i>g_Cryptococcus</i>	<i>s_heimaeyensis</i>	0.0123	0.00192
OTU71	<i>g_Filobasidium</i>	<i>s_stepposum</i>	0.0154	0.0024380952
OTU108	<i>g_Metschnikowia</i>	<i>s_pulcherrima</i>	0.0176	0.0026181818
OTU51	<i>g_Filobasidium</i>	<i>s_magnum</i>	0.0187	0.0027826087
OTU85	<i>g_Saccharomycopsis</i>	<i>s_vini</i>	0.0243	0.0034666667
OTU34	<i>g_Botrytis</i>	<i>s_caroliniana</i>	0.0337	0.0044307692
OTU52	<i>g_Rhizopus</i>	<i>s_arrhizus</i>	0.0337	0.0044307692

Supplementary Table S2a: Differentially abundant bacterial genera among three climate zones

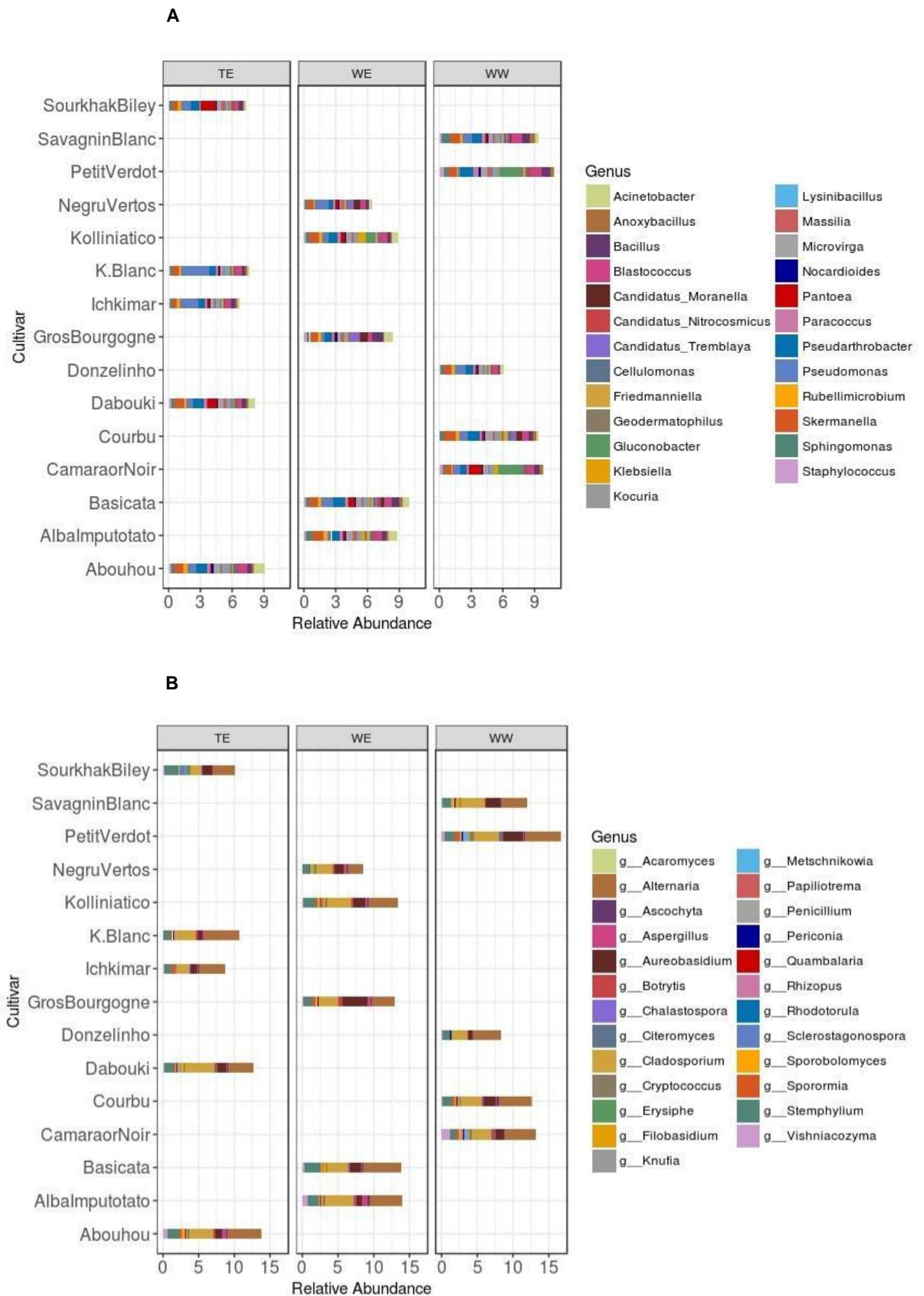
OTUs	Genus	Corrected <i>P</i> -values	FDRs
OTU29	<i>Modestobacter</i>	0.0032	0.003833333
OTU87	<i>Microvirga</i>	0.0032	0.003833333
OTU114	<i>Rubellimicrobium</i>	0.0032	0.003833333
OTU66	<i>Friedmanniella</i>	0.0032	0.003833333
OTU161	<i>Craurococcus</i>	0.0032	0.003833333
OTU271	<i>Neorhizobium</i>	0.0032	0.003833333
OTU55	<i>Paracoccus</i>	0.0063	0.0046
OTU50	<i>Blastococcus</i>	0.0063	0.0046
OTU61	<i>Kocuria</i>	0.0063	0.0046
OTU113	<i>Rathayibacter</i>	0.0063	0.0046
OTU1	<i>Sphingomonas</i>	0.0114	0.008363636
OTU218	<i>Paenisporosarcina</i>	0.0143	0.009583333
OTU7	<i>Ralstonia</i>	0.0246	0.012266667
OTU124	<i>Kocuria</i>	0.0246	0.012266667
OTU250	<i>Deinococcus</i>	0.0246	0.012266667
OTU279	<i>Devosia</i>	0.0269	0.0129375
OTU45	<i>Methylobacterium</i>	0.029	0.013529412
OTU11	<i>Rickettsiella</i>	0.0358	0.016611111
OTU14	<i>Pseudoarthobacter</i>	0.0032	0.00328
OTU171	<i>Acinetobacter</i>	0.0032	0.00328
OTU262	<i>Chamaesiphon_PCC-7430</i>	0.0032	0.00328
OTU102	<i>Rubellimicrobium</i>	0.0032	0.003285714
OTU152	<i>Pleurocapsa_PCC-7319</i>	0.0058	0.00575
OTU333	<i>Aliterella_CENA595</i>	0.0111	0.010222222
OTU57	<i>Methylobacterium</i>	0.0033	0.003833333
OTU30	<i>Skermanella</i>	0.0054	0.00575
OTU42	<i>1174-901-12</i>	0.012	0.0115
OTU72	<i>Staphylococcus</i>	0.012	0.0115
OTU95	<i>Snodgrassella</i>	0.0112	0.012545455
OTU29	<i>Modestobacter</i>	0.019	0.013416667
OTU55	<i>Paracoccus</i>	0.0237	0.015923077

Supplementary Table S2b: Differentially abundant fungal genera among three climate zones

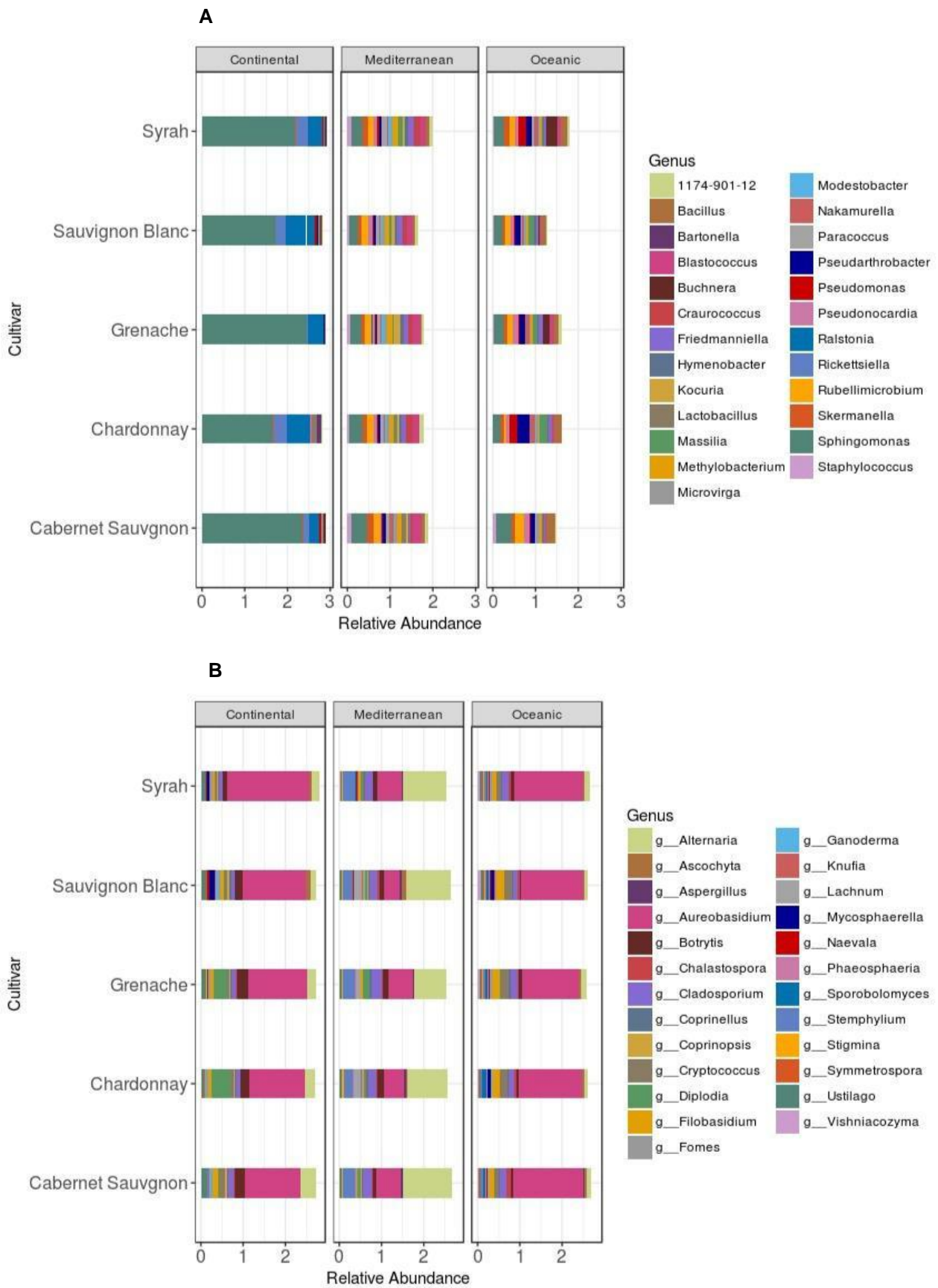
OTUs	Genus	Corrected P-values	FDRs
OTU30	<i>g__Sporobolomyces</i>	0.0019	0.00158
OTU3	<i>g__Alternaria</i>	0.0019	0.00158
OTU54	<i>g__Sporobolomyces</i>	0.0019	0.00158
OTU34	<i>g__Ascochyta</i>	0.0019	0.00158
OTU9	<i>g__Cryptococcus</i>	0.0019	0.00158
OTU66	<i>g__Hyperphyscia</i>	0.0084	0.005266667
OTU1	<i>g__Aureobasidium</i>	0.0166	0.0079
OTU8	<i>g__Stemphylium</i>	0.0231	0.009875
OTU37	<i>g__Filobasidium</i>	0.0285	0.011411111
OTU61	<i>g__Ganoderma</i>	0.0313	0.01185
OTU9	<i>g__Cryptococcus</i>	0.0014	0.0009875
OTU31	<i>g__Stigmina</i>	0.0014	0.0009875
OTU6	<i>g__Cladosporium</i>	0.0014	0.0009875
OTU73	<i>g__Aureobasidium</i>	0.0014	0.0009875
OTU39	<i>g__Symmetrospora</i>	0.0047	0.002633333
OTU56	<i>g__Coprinopsis</i>	0.0097	0.004253846
OTU62	<i>g__Aspergillus</i>	0.0138	0.004253846
OTU115	<i>g__Exophiala</i>	0.0138	0.004253846
OTU21	<i>g__Ustilago</i>	0.0165	0.005078571
OTU16	<i>g__Alternaria</i>	0.0159	0.0069125
OTU17	<i>g__Chalastospora</i>	0.0286	0.010772727



Supplementary Figure S1. Relative Abundance major species between two season, displaying the uniqueness of the fungal microbiome structure at Spring and Harvest season.



Supplementary Fig S2. Relative abundances of major (A) bacterial and (B) fungal taxa (top 25, at genus level) of each cultivar (grouped in three genetic pools). Set1. N = 213.



Supplementary Fig S3. Relative abundances of major (A) bacterial and (B) fungal taxa (top 25, at genus level) of each cultivar (grouped in three geographic locations). Set2. N = 45.