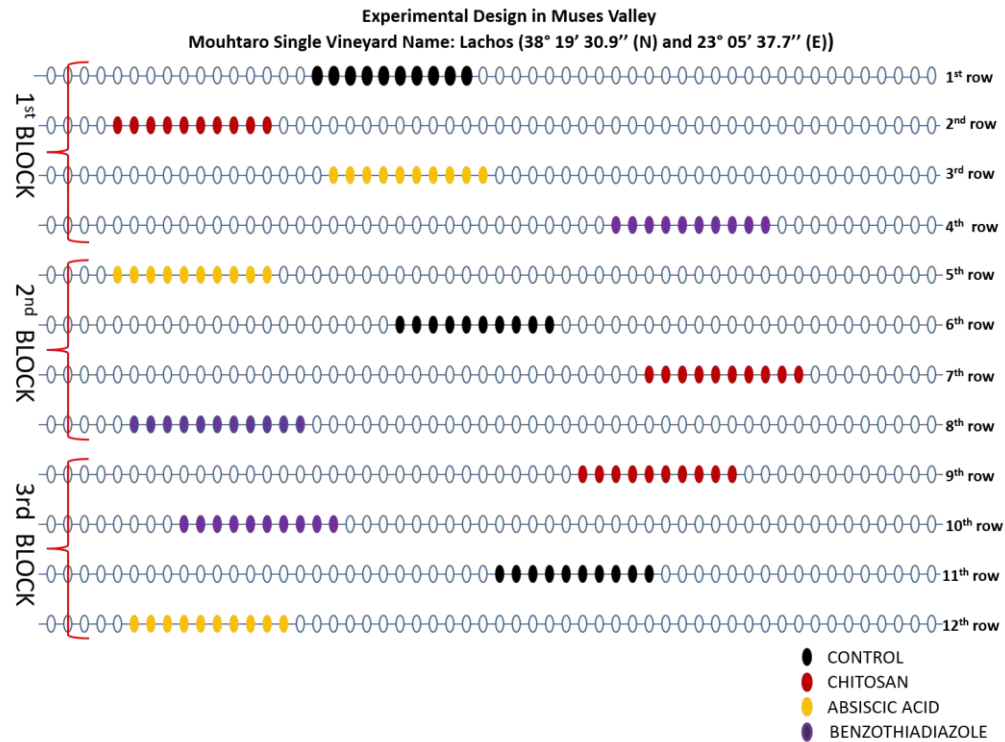
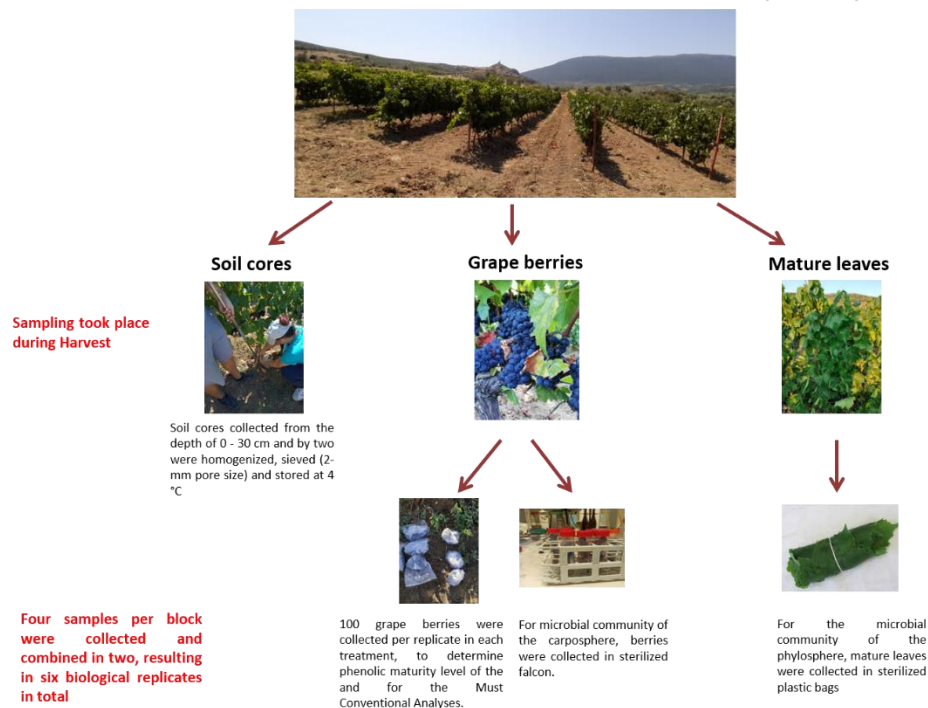


Supplementary Figures



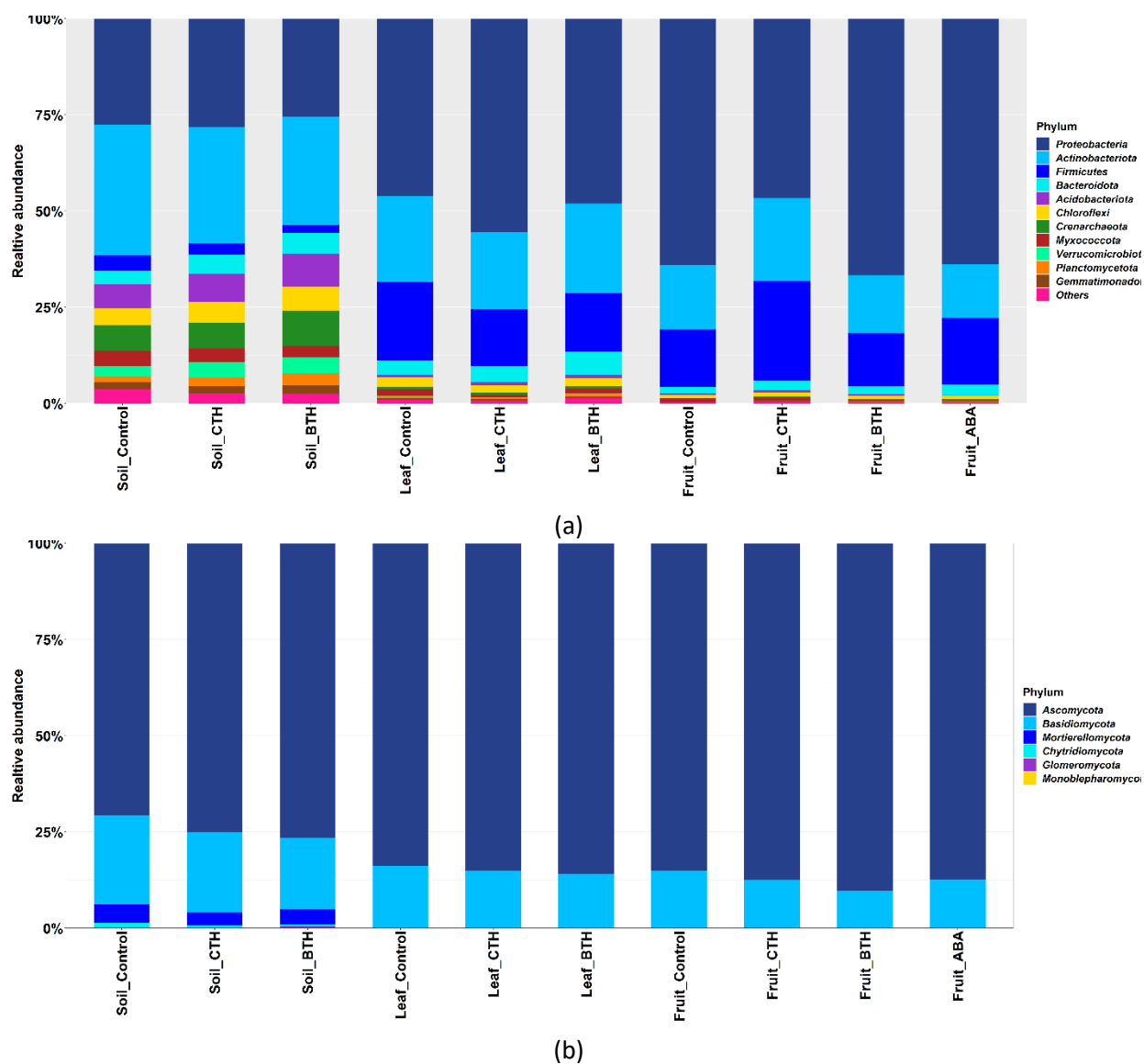
(a)

Sampling at Optimum Technological Maturity stage (Harvest)

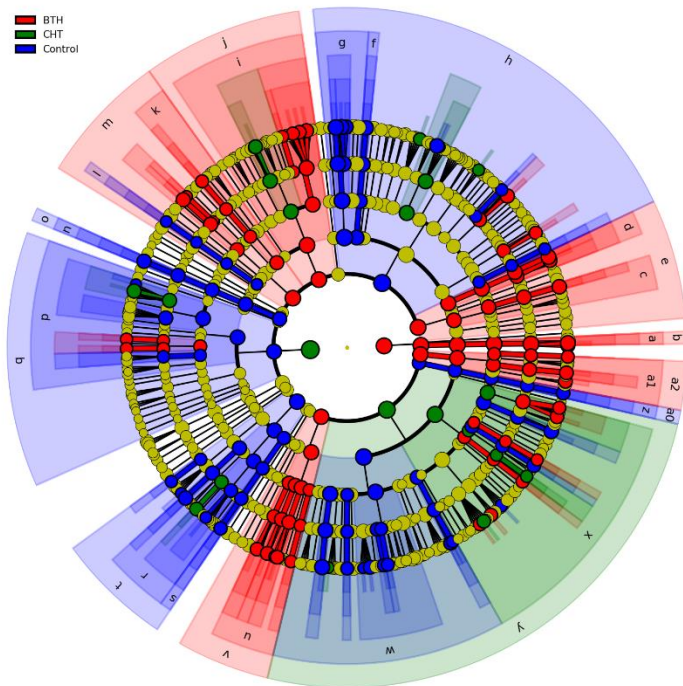


(b)

Supplementary Figure S1. (a) Graphical representation of the experimental set up. Circles represent vines and different colors correspond to the applied treatments. (b) Flowchart of the sampling procedure.



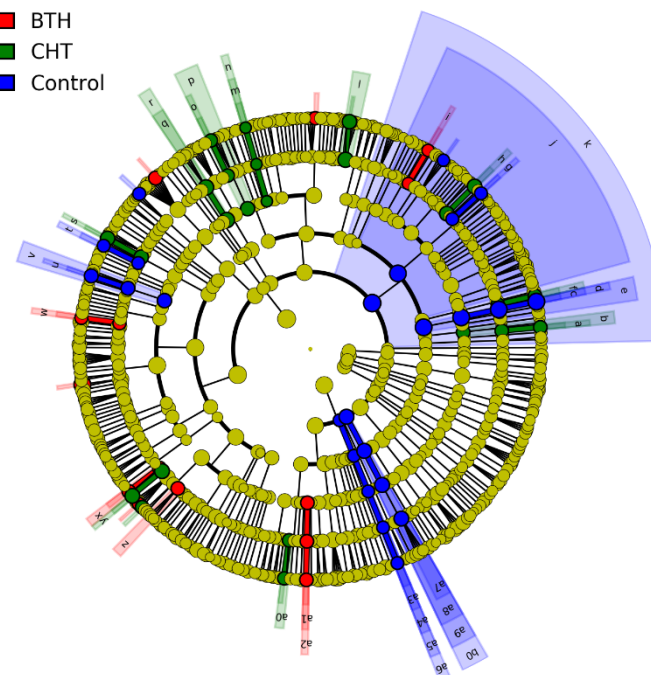
Supplementary Figure S2. (a) Prokaryotic and (b) fungal community composition at the phylum level (ten most abundant phyla shown) across habitats (rhizosphere: Soil; phyllosphere: Leaf and carposphere: Fruit) and treatments (Control, CHT, BTH, ABA). Significant differences between treatments for each habitat are shown in Supplementary Table 1.



(a)

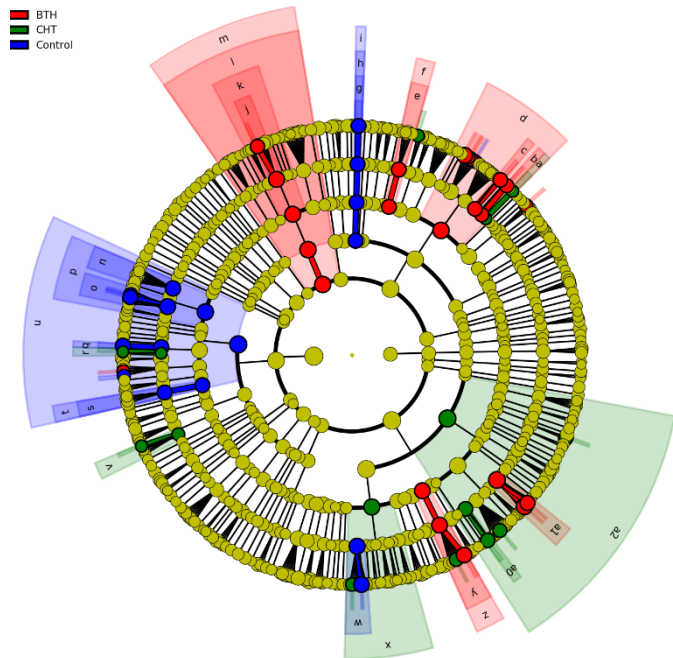
- a: Nitrososphaeria
- b: Crenarchaeota
- c: Blastocatellia
- d: Vicinamibacteria
- e: Acidobacteriota
- f: Rubrobacteria
- g: Thermoleophila
- h: Actinobacteriota
- i: Bacteroidia
- j: Bacteroidota
- k: Anaerolineae
- l: P2_11E
- m: Chloroflexi
- n: Entothionellia
- o: Entothionellaeota
- p: Bacilli
- q: Firmicutes
- r: Polyangia
- s: bacteriap25
- t: Myxococcota
- u: Planctomycetes
- v: Planctomycetota
- w: Alphaproteobacteria
- x: Gammaproteobacteria
- y: Proteobacteria
- z: RCP2_54_Unknown
- a0: RCP2_54
- a1: Verrucomicrobiae
- a2: Verrucomicrobiota

- BTH
- CHT
- Control



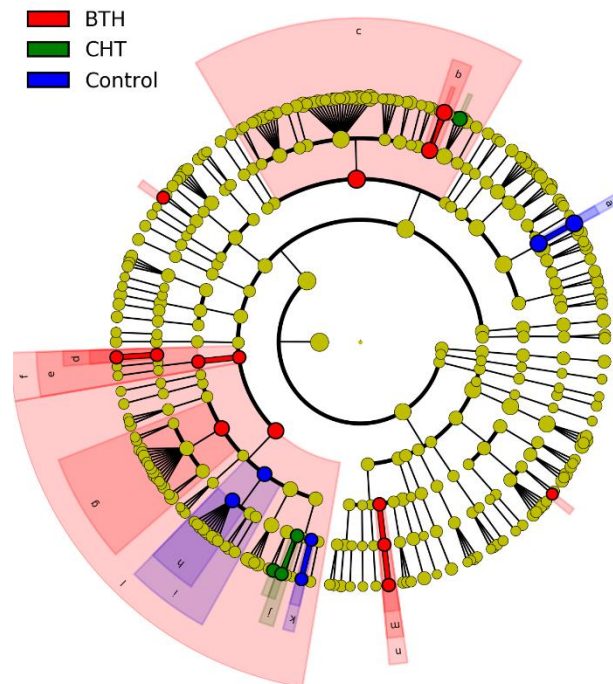
(b)

- a: Cladosporium_Unknown
- b: Cladosporiaceae
- c: Hormonemavitticola
- d: Dothioraceae
- e: Dothideales
- f: Arthrographischlamyospora
- g: Setophaeosphaeriabaddalingensis
- h: Alternariaalternata
- i: Preussiaterricola
- j: Pleosporales
- k: Dothideomycetes
- l: Aspergillus_Unknown
- m: Emmonsiiellopsicoralliformis
- n: Ajellomycetaceae
- o: Chrysosporiumspseudomeridarium
- p: Onygenales_fam_Incertae_sedis
- q: Helotiales_Unknown
- r: Helotiales_Unknown
- s: Plectosphaerella_Unknown
- t: Plectosphaerellaniemeljarum
- u: Trichoderma_Unknown
- v: Hypocreaeaceae
- w: Dactylonectriamacrodidyma
- x: Amesiaatrobrunnea
- y: Botryotrichumspirotrichum
- z: Chaetomiumangustispirale
- a0: Leucocoprinusstraminellus
- a1: Coprinellusverrucispermus
- a2: Psathyrellaceae
- a3: Basidioascuspersicus
- a4: Geminibasidiaceae
- a5: Geminibasidiaceae
- a6: Geminibasidiomycetes
- a7: Rhodotorula_Unknown
- a8: Sporidiobolaceae
- a9: Sporidiobolales
- b0: Microbotryomycetes



(c)

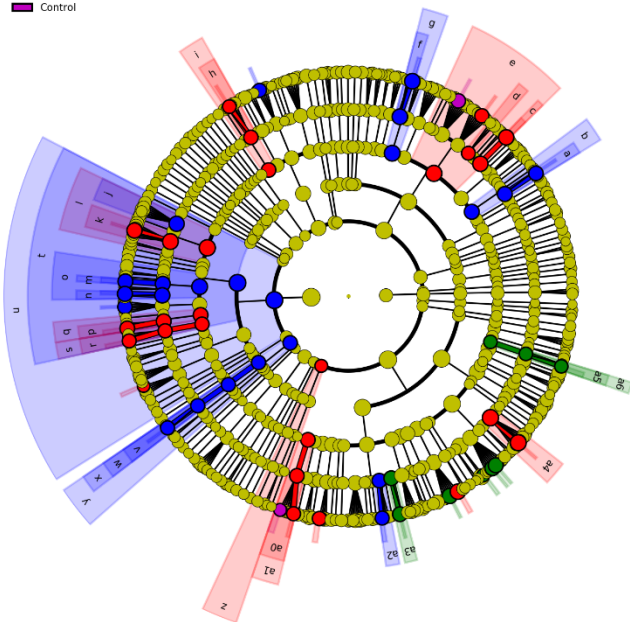
- a: Brevibacteriaceae
- b: Cellulomonadaceae
- c: Intrasporangiaceae
- d: Micrococcales
- e: Pseudonocardaceae
- f: Pseudonocardiales
- g: Rubrobacteriaceae
- h: Rubrobacterales
- i: Rubrobacteria
- j: Hymenobacteraceae
- k: Cytophagales
- l: Bacteroidia
- m: Bacteroidia
- n: Bacillaceae
- o: Planococcaceae
- p: Bacillales
- q: Lactobacillaceae
- r: Leuconostocaceae
- s: Thermoactinomycetaceae
- t: Thermoactinomycetales
- u: Bacilli
- v: Peptostreptococcales_Tissierellales_fa
- w: Beijerinckiaceae
- x: Rhizobiales
- y: Sphingomonadaceae
- z: Sphingomonadales
- aa: Burkholderiaceae
- a1: Oxalobacteraceae
- a2: Gammaproteobacteria



(d)

- a: Mycosphaerellaceae
- b: Didymosphaeriaceae
- c: Pleosporales
- d: Debaryomycetaceae
- e: Saccharomycetales
- f: Saccharomycetes
- g: Hypocreales
- h: Chaetomiaceae
- i: Sordariales
- j: Apiosporaceae
- k: Xylariaceae
- l: Sordariomycetes
- m: Ganodermataceae
- n: Polyporales

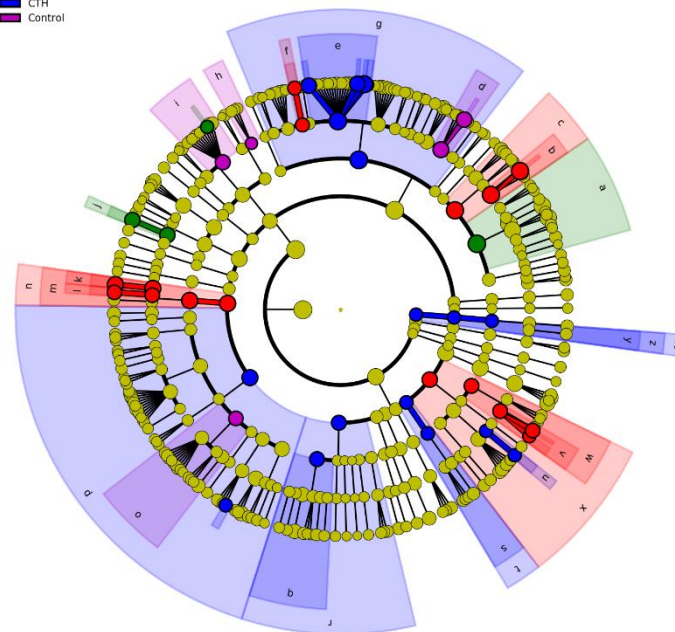
ABA
BTH
CTH
Control



(e)

a: Corynebacteriaceae
b: Corynebacteriales
c: Brevibacteriaceae
d: Intraspangliaceae
e: Micrococcales
f: Propionibacteriaceae
g: Propionibacteriales
h: Sphingobacteriaceae
i: Sphingobacteriales
j: Bacillaceae
k: Planococcaceae
l: Bacillales
m: Lactobacillaceae
n: Streptococcaceae
o: Lactobacillales
p: Staphylococcaceae
q: Staphylococcales
r: Thermoactinomycetaceae
s: Thermoactinomycetales
t: Bacilli
u: Firmicutes
v: Gemmatimonadaceae
w: Gemmatimonadales
x: Gemmatimonadetes
y: Gemmatimonadota
z: Planctomycetota
a0: Acetobacteraceae
a1: Acetobacterales
a2: Rhizobiaceae
a3: Xanthobacteraceae
a4: Oxalobacteraceae
a5: Solimonadaceae
a6: Salinisphaerales

ABA
BTH
CTH
Control



(f)

a: Capnoidiales
b: Aureobasidiaceae
c: Dothideales
d: Didymellaceae
e: Pleosporaceae
f: Pleosporales_fam_Incertae_sedis
g: Pleosporales
h: Herpotrichiellaceae
i: Aspergillaceae
j: Sclerotiniaceae
k: Debaryomycetaceae
l: Saccharomycetaceae
m: Saccharomycetales
n: Saccharomycetes
o: Sordariales
p: Sordariomycetes
q: Agaricales
r: Agaricomycetes
s: Pucciniales
t: Pucciniomycetes
u: Piskurozymaceae
v: Bulleribasidiaceae
w: Tremellales
x: Tremellomycetes
y: Mucorales
z: Mucoromycetes
a0: Mucoromycota

Supplementary Figure S3. Cladograms based on linear discriminant analysis (LDA) effect size (LEfSe) analysis of the (a, c, e) prokaryotic and (b, d, f) fungal communities among all sampling sites rhizosphere (a, b), phyllosphere (c, d) and carposphere (e, f).

Supplementary Tables

Supplementary Table S1. The prokaryotic community composition at the phylum level (ten most abundant phyla shown) across habitats and treatments (Control, CHT, BTH, ABA). Letters Significant differences between treatments within each habitat and for each phylum are indicated with different letters at $p < 0.05$ (Tukey's post hoc test).

	<i>Proteobacteria</i>	<i>Actinobacteriota</i>	<i>Firmicutes</i>	<i>Bacteroidota</i>	<i>Acidobacteriota</i>	<i>Chloroflexi</i>	<i>Chrenarchaeota</i>	<i>Myxococcota</i>	<i>Verrucomicrobiota</i>	<i>Planctomycetota</i>	<i>Gemmatimonadota</i>	Other
Rhizosphere												
Control	27.11% a	33.03% a	3.05% a	4.21% a	6.63% a	4.55% a	6.13% a	5.07% a	2.87% a	1.80% a	1.68% a	3.86%
CTH	27.35% a	31.40% a	2.92% a	6.04% b	6.27% a	5.18% a	5.45% a	3.88% b	3.95% a	2.76% a	2.14% a	2.67%
BTH	24.89% a	25.55% b	1.72% a	6.92% b	8.38% b	6.33% b	8.74% b	2.91% b	4.94% b	4.60% b	2.39% a	2.63%
Phylosphere												
Control	44.20% a	22.76% a	19.06% a	4.70% a	0.94% a	2.58% a	0.68% a	2.03% a	0.14% a	1.01% a	0.41% a	1.48%
CTH	49.92% a	23.03% a	13.85% b	5.84% a	1.09% a	2.22% a	0.82% a	1.05% a	0.10% a	0.51% a	0.43% a	1.14%
BTH	46.78% a	25.12% a	11.79% b	7.72% b	1.24% a	2.18% a	0.78% a	1.50% a	0.19% a	0.75% a	0.51% a	1.44%
Casrposphere												
Control	62.18% a	18.25% a	14.18% ab	2.67% a	0.46% a	0.71% a	0.10% a	0.94% a	0.00%	0.02% a	0.06% b	0.42%
CTH	44.50% a	22.92% a	23.39% a	4.18% a	0.70% a	0.97% a	0.15% a	0.70% a	0.00%	0.00% a	1.36% a	1.12%
BTH	68.64% a	13.18% a	11.11% b	2.54% a	0.51% a	1.26% a	0.52% a	0.51% a	0.00%	0.18% a	0.26% b	1.30%
ABA	54.64% a	17.03% a	20.24% ab	5.07% a	0.15% a	1.16% a	0.28% a	0.45% a	0.00%	0.25% a	0.17% b	0.56%

Supplementary Table S2. The fungal and community composition at the phylum level (ten most abundant phyla shown) across habitats and treatments (Control, CHT, BTH, ABA). Letters Significant differences between treatments within each habitat and for each phylum are indicated with different letters at $p < 0.05$ (Tukey's post hoc test).

	<i>Ascomycota</i>	<i>Basidiomycota</i>	<i>Mortierellomycota</i>	<i>Chytridiomycota</i>	<i>Mucoromycota</i>	<i>Glomeromycota</i>	<i>Monoblepharomycota</i>
Rhizosphere							
Control	70.42% a	23.09% a	4.68% a	1.19% a	0.39% a	0.15% a	0.08% a
CTH	74.65% a	20.65% a	3.36% a	0.59% a	0.55% a	0.12% a	0.06% a
BTH	76.30% a	18.56% a	3.89% a	0.53% a	0.24% a	0.32% a	0.16% a
Phylosphere							
Control	83.59% a	16.09% a	0.01% a	0.02% a	0.29% a	0.00%	0.00%
CTH	85.00% a	14.88% a	0.01% a	0.00% a	0.11% a	0.00%	0.00%
BTH	85.81% a	14.03% a	0.01% a	0.03% a	0.11% a	0.00%	0.00%
Casrposphere							
Control	84.83% a	14.85% a	0.04% a	0.00%	0.21% a	0.00%	0.00%
CTH	87.20% a	12.39% a	0.11% a	0.00%	0.29% a	0.00%	0.00%
BTH	90.12% a	9.78% a	0.00% b	0.00%	0.10% a	0.00%	0.00%
ABA	87.27% a	12.69% a	0.00% b	0.00%	0.03% a	0.00%	0.00%

Supplementary Table S3. The prokaryotic community members at the rhizosphere that emerged from LefSe analysis as discriminant for BTH and CHT treatments.

Soil_16S									Mean abundance		Relative
BTH							LDA score	p value	BTH	CHT	Control
Archaea	Crenarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus_Nitrososphaera	ASV13	3.688497	0.03211	2.12%	1.17%	1.37%
Bacteria	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	ASV44	3.613742	0.009683	1.26%	0.69%	0.46%
Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	ASV5	3.523651	0.028733	1.25%	0.89%	0.59%
Archaea	Crenarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaeraceae_Unknown	ASV42	3.541284	0.007486	1.19%	0.53%	0.60%
Archaea	Crenarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus_Nitrocosmicus	ASV41	3.43638	0.003399	1.13%	0.62%	0.61%
Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30_KF_CM45	JG30_KF_CM45_Unknown	ASV26	3.548619	0.017997	1.06%	0.58%	0.37%
Bacteria	Chloroflexi	KD4_96	KD4_96_Unknown	KD4_97_Unknown	KD4_98_Unknown	ASV20	3.041047	0.031367	1.04%	1.02%	0.83%
Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	ASV8	3.454029	0.011951	1.01%	0.70%	0.46%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Chitinophagaceae_Unknown	ASV100	3.540811	0.005089	0.98%	0.43%	0.29%
Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacterales_Unknown	Vicinamibacterales_Unknown	ASV69	3.304356	0.022085	0.83%	0.54%	0.42%
Archaea	Crenarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus_Nitrososphaera	ASV81	3.138729	0.048921	0.62%	0.36%	0.53%
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	ASV118	3.194191	0.013278	0.59%	0.46%	0.28%
Bacteria	Planctomycetota	Planctomycetes	Isosphaerales	Isosphaeraceae	Isosphaeraceae_Unknown	ASV132	3.322537	0.010757	0.57%	0.27%	0.17%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	ASV304	3.399283	0.047408	0.52%	0.23%	0.00%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter	ASV97	2.889544	0.02411	0.51%	0.46%	0.38%
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	ASV137	3.170183	0.0035	0.49%	0.30%	0.22%

Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Parasegetibacter	ASV152	2.829784	0.049787	0.37%	0.29%	0.25%
Bacteria	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus	ASV325	3.239043	0.042991	0.36%	0.22%	0.07%
Bacteria	Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Pedosphaeraceae_Unknown	ASV225	3.063478	0.023086	0.35%	0.27%	0.14%
Bacteria	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	ASV221	3.066737	0.018859	0.35%	0.14%	0.14%
Bacteria	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter	ASV327	3.149858	0.004171	0.32%	0.16%	0.07%
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Luteolibacter	ASV269	3.134102	0.002436	0.31%	0.22%	0.06%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	TRA3_20	TRA3_20_Unknown	ASV513	3.114609	0.0287	0.27%	0.12%	0.02%
Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonadaceae_Unknown	ASV399	3.012533	0.00542	0.26%	0.11%	0.08%
Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	ASV501	3.070692	0.006462	0.25%	0.11%	0.04%
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pir4_lineage	ASV512	3.142727	0.004106	0.25%	0.08%	0.01%
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	Gemmata	ASV323	2.857857	0.017892	0.24%	0.14%	0.12%
Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardaceae	Pseudonocardia	ASV126	3.026997	0.047408	0.20%	0.09%	0.00%
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter	ASV423	2.951536	0.009498	0.20%	0.13%	0.03%
Bacteria	Planctomycetota	Planctomycetes	Planctomycetes_Unknown	Planctomycetes_Unknown	Planctomycetes_Unknown	ASV607	2.893751	0.015824	0.18%	0.09%	0.05%
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Thermomonas	ASV1050	2.927059	0.040323	0.16%	0.05%	0.00%
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	ASV187	2.90287	0.040323	0.14%	0.05%	0.00%
Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	BIyi10	ASV680	2.754287	0.036023	0.11%	0.10%	0.04%
Bacteria	Acidobacteriota	Acidobacteriae	Solibacterales	Solibacteraceae	Candidatus_Solibacter	ASV613	2.757125	0.047408	0.11%	0.00%	0.10%
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	Gemmata	ASV1575	2.781776	0.03277	0.10%	0.00%	0.01%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Saprospiraceae	Saprospiraceae_Unknown	ASV1624	2.826352	0.040323	0.08%	0.02%	0.00%
Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	AKYG1722_Unknown	ASV592	2.709215	0.044681	0.08%	0.05%	0.00%
									Mean abundance	Relative	

CHT							LDA score	p value	BT H	CH T	Contr ol
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	ASV7	3.6254 42	0.0246 8	0.31 %	1.27 %	0.93%
Bacteria	Actinobacterio ta	Thermoleophilia	Solirubrobacterales	Solirubrobacterales_Un know	Solirubrobacterales_Unkn onw	ASV14 0	3.2844 39	0.0260 04	0.05 %	0.43 %	0.32%
Bacteria	Proteobacteria	Gammaproteobac teria	Burkholderiales	Comamonadaceae	Ramlibacter	ASV12 3	3.1901 6	0.0020 41	0.00 %	0.27 %	0.23%
Bacteria	Proteobacteria	Alphaproteobacte ria	Rhizobiales	Beijerinckiaceae	Microvirga	ASV53 26	3.1539 26	0.0142 4	0.00 %	0.27 %	0.16%
Bacteria	Proteobacteria	Alphaproteobacte ria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	ASV28 1	3.0426 14	0.0418 61	0.05 %	0.26 %	0.04%
Bacteria	Actinobacterio ta	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	ASV36 9	3.0797 72	0.0139 14	0.06 %	0.24 %	0.00%
Bacteria	Actinobacterio ta	Actinobacteria	Pseudonocardiales	Pseudonocardaceae	Actinophytocola	ASV32 4	2.9080 12	0.0440 28	0.04 %	0.19 %	0.16%
Bacteria	Actinobacterio ta	Thermoleophilia	Solirubrobacterales	Solirubrobacterales_Un know	Solirubrobacterales_Unkn onw	ASV28 9	3.0584 86	0.0131 88	0.00 %	0.19 %	0.19%
Bacteria	Proteobacteria	Alphaproteobacte ria	Reyranellales	Reyranellaceae	Reyranella	ASV40 4	2.8058 2	0.0281 71	0.16 %	0.17 %	0.07%
Bacteria	Entotheonellae ota	Entotheonellia	Entotheonellales	Entotheonellaceae	Entotheonellaceae_Unkno wn	ASV29 8	2.9691 72	0.0218 88	0.00 %	0.16 %	0.11%
Bacteria	Proteobacteria	Gammaproteobac teria	Enterobacterales	Enterobacteriaceae	Klebsiella	ASV14 3	2.8956 07	0.0218 88	0.07 %	0.14 %	0.00%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Chitinophagaceae_Unkno wn	ASV47 0	2.8624 04	0.0062	0.00 %	0.12 %	0.10%
Bacteria	Proteobacteria	Gammaproteobac teria	Xanthomonadales	Xanthomonadaceae	Arenimonas	ASV71 0	2.8696 76	0.0291 28	0.01 %	0.09 %	0.05%
Bacteria	Actinobacterio ta	Actinobacteria	Micrococcales	Microbacteriaceae	Galbitalea	ASV71 4	2.7848 56	0.0369 38	0.00 %	0.09 %	0.05%
Bacteria	Actinobacterio ta	Thermoleophilia	Gaiellales	Gaiellales_Unknown	Gaiellales_Unknown	ASV88 9	2.7721 11	0.0476 4	0.00 %	0.08 %	0.03%
Bacteria	Proteobacteria	Alphaproteobacte ria	Caulobacterales	Caulobacteraceae	Brevundimonas	ASV88 7	2.6008 03	0.0413 73	0.04 %	0.06 %	0.00%

Supplementary Table S4. The fungal community members at the rhizosphere that emerged from LefSe analysis as discriminant for BTH and CHT treatments.

Soil ITS								Mean abundance		Relative		
BTH								LDA score	p value	BTH	CH T	Contr ol
Ascomy cota	Sordariom ycetes	Hypocreales	Nectriaceae	Gibberella intricans	ASV 6	5.126 251	BTH	4.445 159	0.045 34	13.37 %	9.75 %	7.42%
Ascomy cota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus_Unknown	ASV 137	3.701 854	BTH	3.542 22	0.021 691	0.50 %	0.02 %	0.00%
Ascomy cota	Sordariom ycetes	Sordariales	Chaetomiaceae	Amesia atrobrunnea	ASV 121	3.593 128	BTH	3.315 422	0.003 143	0.39 %	0.00 %	0.14%
Basidio mycota	Agaricom ycetes	Agaricales	Psathyrellaceae	Coprinellus verrucispermus	ASV 183	3.535 954	BTH	3.315 109	0.019 618	0.34 %	0.00 %	0.15%
Ascomy cota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium_Unknown	ASV 182	3.382 32	BTH	3.296 914	0.033 912	0.24 %	0.14 %	0.01%
Ascomy cota	Sordariom ycetes	Hypocreales	Nectriaceae	Dactylonectria macrodidyma	ASV 134	3.294 956	BTH	3.119 48	0.041 23	0.20 %	0.05 %	0.15%
Ascomy cota	Dothideo mycetes	Pleosporales	Sporormiaceae	Preussia terricola	ASV 226	2.926 681	BTH	3.305 502	0.032 77	0.08 %	0.00 %	0.01%
CHT								Mean abundance		Relative		
								LDA score	p value	BTH	CH T	Contr ol
Ascomy cota	Sordariom ycetes	Sordariales	Chaetomiaceae	Botryotrichum spirotrichum	ASV 35	4.144 331	CHT	3.668 629	0.010 948	1.27 %	1.39 %	0.49%
Ascomy cota	Dothideo mycetes	Pleosporales	Pleosporaceae	Alternaria alternata	ASV 1	4.036 844	CHT	3.698 623	0.009 226	0.25 %	1.09 %	0.13%
Ascomy cota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus_Unknown	ASV 46	3.974 609	CHT	3.676 987	0.037 916	0.94 %	0.94 %	0.14%
Ascomy cota	Sordariom ycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella_Unknown	ASV 69	3.951 072	CHT	3.581 059	0.018 175	0.35 %	0.89 %	0.11%
Ascomy cota	Sordariom ycetes	Sordariales	Chaetomiaceae	Chaetomiaceae_Unknown	ASV 96	3.569 568	CHT	3.369 105	0.025 622	0.00 %	0.37 %	0.32%
Ascomy cota	Dothideo mycetes	Capnodiales	Cladosporiaceae	Cladosporium_Unknown	ASV 3	3.525 124	CHT	3.256 162	0.027 144	0.04 %	0.34 %	0.20%
Ascomy cota	Dothideo mycetes	Dothideomycetes_ord_Incertae_sedis	Eremomycetaceae	Arthrographis chlamydospora	ASV 141	3.491 241	CHT	3.241 251	0.010 54	0.00 %	0.31 %	0.27%
Ascomy cota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Chrysosporium pseudomerdarium	ASV 175	3.359 948	CHT	3.165 351	0.020 287	0.06 %	0.23 %	0.02%

Basidio mycota	Agaricom ycetes	Agaricales	Agaricaceae	Leucocoprinuss traminellus	ASV 197	3.357 015	CHT	3.232 349	0.036 938	0.00 %	0.23 %	0.08%
Ascomy cota	Eurotiomy cetes	Onygenales	Ajellomycetaceae	Emmonsiiellopsis coralliformis	ASV 506	2.494 663	CHT	3.157 444	0.047 408	0.00 %	0.03 %	0.02%

Supplementary Table S5 The prokaryotic community members at the phyllosphere that emerged from LefSe analysis as discriminant for BTH and CHT treatments.

Leaf_1 6S BTH									LDA score	p value	Mean abundance		Relative
											BTH	CHT	Contr ol
Bacteri a	Proteobac teria	Gammaproteo bacteria	Burkholderi ales	Oxalobactera ceae	Massilia	ASV 1	4.787 605	BTH	3.970 77	0.024 971	6.13 %	4.42 %	4.44%
Bacteri a	Actinoba cteriota	Actinobacteri a	Micrococca les	Micrococcace ae	Pseudarthrobacter	ASV 2	4.655 994	BTH	3.855 903	0.024 11	4.53 %	3.13 %	3.49%
Bacteri a	Actinoba cteriota	Actinobacteri a	Micrococca les	Intrasporangi aceae	Intrasporangiaceae_Unknown	ASV 176	3.757 611	BTH	3.157 748	0.046 367	0.57 %	0.27 %	0.33%
Bacteri a	Actinoba cteriota	Actinobacteri a	Micrococca les	Micrococcace ae	Kocuria	ASV 133	3.755 498	BTH	3.306 226	0.025 765	0.57 %	0.48 %	0.26%
Bacteri a	Bacteroid ota	Bacteroidia	Cytophagal es	Hymenobacte raceae	Rufibacter	ASV 138	3.754 207	BTH	3.386 81	0.019 453	0.57 %	0.44 %	0.17%
Bacteri a	Chlorofle xi	KD4_96	KD4_96_U nknown	KD4_97_Unk nown	KD4_98_Unknown	ASV 20	3.734 18	BTH	3.287 302	0.011 897	0.54 %	0.19 %	0.39%
Bacteri a	Proteobac teria	Gammaproteo bacteria	Burkholderi ales	Oxalobactera ceae	Massilia	ASV 455	3.382 371	BTH	3.193 658	0.047 64	0.24 %	0.08 %	0.00%
Bacteri a	Actinoba cteriota	Actinobacteri a	Frankiales	Geodermatop hilaceae	Modestobacter	ASV 722	3.314 889	BTH	3.254 846	0.013 3	0.21 %	0.06 %	0.00%
Bacteri a	Actinoba cteriota	Actinobacteri a	Frankiales	Geodermatop hilaceae	Blastococcus	ASV 820	3.226 052	BTH	3.216 145	0.021 691	0.17 %	0.00 %	0.02%
Bacteri a	Firmicute s	Bacilli	Paenibacill ales	Paenibacillac eae	Paenibacillaceae_Unknown	ASV 256	3.045 303	BTH	3.183 165	0.041 373	0.11 %	0.06 %	0.00%
Bacteri a	Bacteroid ota	Bacteroidia	Cytophagal es	Hymenobacte raceae	Adhaeribacter	ASV 1309	3.006 18	BTH	3.413 66	0.002 48	0.10 %	0.00 %	0.02%
Bacteri a	Proteobac teria	Alphaproteob acteria	Sphingomo nadales	Sphingomona daceae	Altererythrobacter	ASV 1056	2.966 398	BTH	3.358 309	0.046 284	0.09 %	0.06 %	0.00%
Bacteri a	Firmicute s	Bacilli	Paenibacill ales	Paenibacillac eae	Paenibacillaceae_Unknown	ASV 651	2.789 865	BTH	3.326 376	0.028 729	0.06 %	0.00 %	0.01%
CHT									LDA score	p value	Mean abundance		Relative
											BTH	CHT	Contr ol
Bacteri a	Proteobac teria	Alphaproteob acteria	Azospirillal es	Azospirillace ae	Skermanella	ASV 8	4.393 678	CHT	3.709 064	0.046 413	1.46 %	2.48 %	1.96%
Bacteri a	Proteobac teria	Gammaproteo bacteria	Pseudomon adales	Moraxellacea e	Enhydrobacter	ASV 94	3.851 484	CHT	3.481 227	0.021 893	0.10 %	0.71 %	0.04%
Bacteri a	Proteobac teria	Gammaproteo bacteria	Burkholderi ales	Burkholderia ceae	Burkholderia_Caballeronia_P araburkholderia	ASV 3	3.846 222	CHT	3.572 232	0.015 709	0.02 %	0.70 %	0.01%

Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	ASV 36	3.649 164	CHT	3.151 043	0.023 74	0.15 %	0.45 %	0.37%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaeae	Microvirga	ASV 187	3.644 12	CHT	3.144 445	0.021 867	0.16 %	0.44 %	0.38%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobiaceae_Unknown	ASV 415	3.407 648	CHT	3.206 678	0.021 691	0.00 %	0.26 %	0.03%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaeae	Beijerinckiaeae_Unknown	ASV 348	3.331 4	CHT	3.132 502	0.022 689	0.03 %	0.21 %	0.16%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Paucibacter	ASV 87	3.317 841	CHT	3.267 621	0.021 691	0.00 %	0.21 %	0.03%
Bacteria	Actinobacteria	Actinobacteriia	Propionibacteriales	Propionibacteriaceae	Microlunatus	ASV 467	3.147 277	CHT	3.083 994	0.018 144	0.00 %	0.14 %	0.04%
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonadaceae_Unknown	ASV 658	3.139 237	CHT	3.078 166	0.046 284	0.12 %	0.14 %	0.00%
Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacteriales	Acetobacteraceae	Craurococcus_Caldovatus	ASV 691	3.091 531	CHT	2.994 357	0.017 868	0.00 %	0.12 %	0.10%

Supplementary Table S6. The fungal community members at the phyllosphere that emerged from LefSe analysis as discriminant for BTH and CHT treatments.

Leaf ITS										Mean abundance		Relative
BTH								LDA score	p value	BTH	CH T	Contr ol
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces rosae	ASV22	4.60211	BTH	3.975854	0.003006	4.00%	2.95%	2.18%
Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Dothiora_Unknown	ASV171	3.71065	BTH	3.506373	0.011607	0.51%	0.08%	0.04%
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma_Unknown	ASV294	3.423727	BTH	3.453198	0.004093	0.27%	0.08%	0.12%
Ascomycota	Saccharomyces	Saccharomycetales	Debaryomycetaceae	Debaryomyces hansenii	ASV33	3.415451	BTH	3.345142	0.03836	0.26%	0.19%	0.02%
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Thermomyces lanuginosus	ASV192	3.221209	BTH	3.445059	0.015458	0.17%	0.06%	0.04%
CHT										Mean abundance		Relative
								LDA score	p value	BTH	CH T	Contr ol
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum_Unknown	ASV32	4.257883	CHT	3.732387	0.038044	1.74%	1.81%	0.88%
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Seimatosporium vitis	ASV31	3.571163	CHT	3.267057	0.034906	0.05%	0.37%	0.36%

Supplementary Table S7 The prokaryotic community members at the carposphere that emerged from LefSe analysis as discriminant for ABA, BTH and CHT treatments.

Fruit_16S											Mean abundance		Relative	
ABA									LDA score	p value	CT H	BT H	AB A	Control
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Brevibacteriaceae	Brevibacterium	ASV 155	4.499 43	AB	4.173 66	0.000 49	0.0 9%	0.0 8%	3.1 6%	0.00 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	ASV 35	4.412 976	AB	4.141 981	0.000 656	0.2 3%	0.1 7%	2.5 9%	0.00 %
Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planococcaceae_Unknown	ASV 17	4.394 677	AB	3.943 188	0.037 253	1.5 1%	0.7 8%	2.4 8%	0.77 %
Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Domibacillus	ASV 76	4.129 545	AB	3.751 479	0.043 157	0.4 7%	0.2 9%	1.3 5%	0.20 %
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Curtobacterium	ASV 200	3.965 899	AB	3.762 708	0.046 103	0.1 5%	0.1 3%	0.9 2%	0.00 %
Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Thermoactinomyces	ASV 60	3.918 923	AB	3.807 628	0.001 495	0.1 1%	0.3 6%	0.8 3%	0.04 %
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	ASV 335	3.895 873	AB	3.800 176	0.001 459	0.0 0%	0.1 0%	0.7 9%	0.09 %
Bacteria	Firmicutes	Clostridia	Peptostreptococcales_Tissierellales	Peptostreptococcales_Tissierellales_fa	Anaerococcus	ASV 742	3.134 625	AB	3.810 795	0.027 693	0.0 0%	0.0 7%	0.1 4%	0.04 %
											Mean abundance		Relative	
BTH									LDA score	p value	CT H	BT H	AB A	Control
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia_Caballeronia_Paraburkholderia	ASV 9	4.761 234	BTH	4.483 75	0.046 045	0.5 5%	5.7 7%	1.6 2%	5.52 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Curvibacter	ASV 46	4.507 572	BTH	4.192 75	0.035 449	0.0 0%	3.2 2%	1.0 3%	1.28 %

Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospirillaceae	Magnetospirillaceae_Unknown	ASV 54	4.342 525	BTH	4.034 23	0.036 239	0.0 0%	2.2 0%	1.1 9%	1.24 %
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	ASV 43	4.338 039	BTH	4.027 18	0.042 406	0.0 0%	2.1 8%	0.6 9%	1.58 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Paucibacter	ASV 67	4.142 174	BTH	3.842 425	0.019 769	0.0 0%	1.3 9%	0.3 5%	0.62 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Paucibacter	ASV 87	4.126 812	BTH	3.834 999	0.038 926	0.0 0%	1.3 4%	0.7 6%	0.69 %
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	ASV 195	4.103 683	BTH	3.797 368	0.037 856	0.0 0%	1.2 7%	0.2 9%	0.20 %
Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	ASV 16	3.890 153	BTH	3.600 567	0.044 656	0.4 6%	0.7 8%	0.3 2%	0.00 %
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium	ASV 23	3.764 835	BTH	3.528 894	0.029 117	0.0 0%	0.5 8%	0.4 1%	0.26 %
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	ASV 394	3.757 652	BTH	3.544 203	0.029 681	0.0 0%	0.5 7%	0.0 9%	0.30 %
Bacteria	Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	Nevskia	ASV 497	3.646 011	BTH	3.496 415	0.014 912	0.0 0%	0.4 4%	0.0 2%	0.22 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Ralstonia	ASV 478	3.478 468	BTH	3.250 139	0.026 962	0.1 3%	0.3 0%	0.1 3%	0.00 %
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Microbacterium	ASV 1013	3.286 839	BTH	3.573 928	0.047 385	0.0 0%	0.1 9%	0.0 4%	0.02 %
CHT									LDA score	p value	Mean abundance		Relative	
											CT H	BT H	AB A	Control
Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Cutibacterium	ASV 19	4.738 796	CTH	4.379 759	0.007 225	5.4 8%	2.3 9%	0.7 8%	4.68 %
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	ASV 1	4.627 941	CTH	4.176 592	0.031 56	4.2 5%	1.5 4%	4.2 4%	1.11 %

Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus	ASV 4	4.486 086	C T H	4.193 571	0.018 078	3.0 6%	0.5 2%	0.0 4%	1.85 %
Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Lawsonella	ASV 164	4.222 079	C T H	3.937 821	0.012 792	1.6 7%	0.3 0%	0.0 5%	0.62 %
Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Staphylococcus	ASV 61	4.188 454	C T H	3.744 597	0.019 401	1.5 4%	0.5 2%	0.4 1%	1.47 %
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	ASV 18	4.146 885	C T H	3.847 389	0.022 689	1.4 0%	0.6 4%	0.0 0%	0.96 %
Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Paenibacillaceae_Unknown	ASV 256	4.062 384	C T H	3.777 604	0.026 292	1.1 5%	0.2 9%	0.3 4%	0.00 %

Supplementary Table S8. The fungal community members at the carposphere that emerged from LefSe analysis as discriminant for BTH, CHT and ABA treatments.

ABA									LDA score	p value	CT H	BT H	AB A	Control
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium pullulans	ASV 4	Aureobasidium pullulans(ASV4)	5.369 023	A B A	4.963 875	0.010 116	5.15 %	7.88 %	23.3 9%	5.17 %
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Debaryomyces hansenii	ASV 33	Debaryomyces hansenii(ASV33)	4.870 322	A B A	4.523 488	0.008 942	0.94 %	0.62 %	7.42 %	0.66 %
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Saccharomyces _Unknown	ASV 199	Saccharomyces _Unknown(ASV199)	4.144 138	A B A	3.848 425	0.032 555	0.00 %	0.01 %	1.39 %	0.03 %
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma foliicola	ASV 208	Vishniacozyma foliicola(ASV208)	4.142 343	A B A	3.837 641	0.000 436	0.06 %	0.02 %	1.39 %	0.00 %
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Foliophoma fallens	ASV 327	Foliophoma fallens(ASV327)	3.833 675	A B A	3.633 916	0.024 276	0.02 %	0.01 %	0.68 %	0.02 %
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma carnescens	ASV 205	Vishniacozyma carnescens(ASV205)	3.361 968	A B A	3.550 39	0.038 303	0.00 %	0.04 %	0.23 %	0.07 %
BTH											Mean Relative abundance			
									LDA score	p value	CT H	BT H	AB A	Control
Ascomycota	Leotiomyces	Helotiales	Sclerotiniaceae	Sclerotiniaceae _Unknown	ASV 51	Sclerotiniaceae _Unknown(ASV51)	4.516 295	BT H	4.258 39	0.042 158	0.13 %	3.28 %	0.38 %	0.01 %
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus carbonarius	ASV 92	Aspergillus carbonarius(ASV92)	3.458 271	BT H	3.315 684	0.011 816	0.01 %	0.29 %	0.00 %	0.04 %
CHT											Mean Relative abundance			
									LDA score	p value	CT H	BT H	AB A	Control
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria alternata	ASV 1	Alternaria alternata(ASV1)	5.378 932	CT H	4.593 128	0.018 566	23.9 3%	17.3 7%	16.1 5%	20.0 9%
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Stemphylium _Unknown	ASV 9	Stemphylium _Unknown(ASV9)	4.641 127	CT H	4.113 807	0.016 531	4.38 %	3.67 %	1.84 %	4.01 %
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymellaceae _Unknown	ASV 40	Didymellaceae _Unknown(ASV40)	4.028 552	CT H	3.776 784	0.001 621	1.07 %	0.47 %	0.00 %	0.54 %

Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora oryzae	ASV87	Nigrospora oryzae(ASV87)	3.564512	CTH	3.620798	0.0168	0.37%	0.11%	0.13%	0.10%
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria_Unknown	ASV115	Alternaria_Unknown(ASV115)	3.549621	CTH	3.658485	0.000726	0.35%	0.06%	0.00%	0.24%
Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae	Solicoccozyma_Unknown	ASV13	Solicoccozyma_Unknown(ASV13)	3.343636	CTH	3.490115	0.026962	0.22%	0.03%	0.01%	0.03%
Basidiomycota	Pucciniales	Pucciniales	Pucciniales_Unknown	Pucciniales_Unknown	ASV256	Pucciniales_Unknown(ASV256)	3.231668	CTH	3.654385	0.039884	0.17%	0.01%	0.00%	0.04%