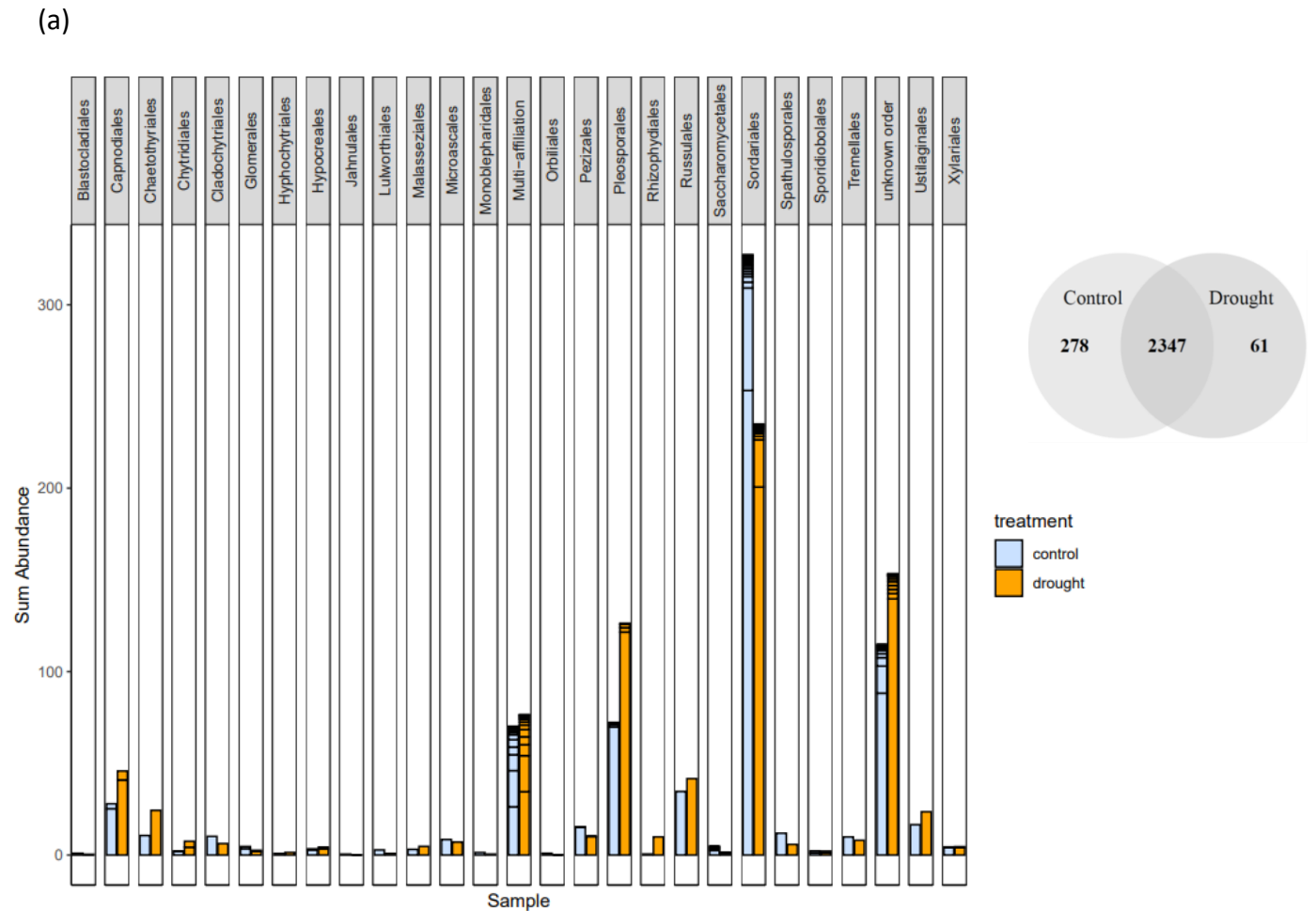
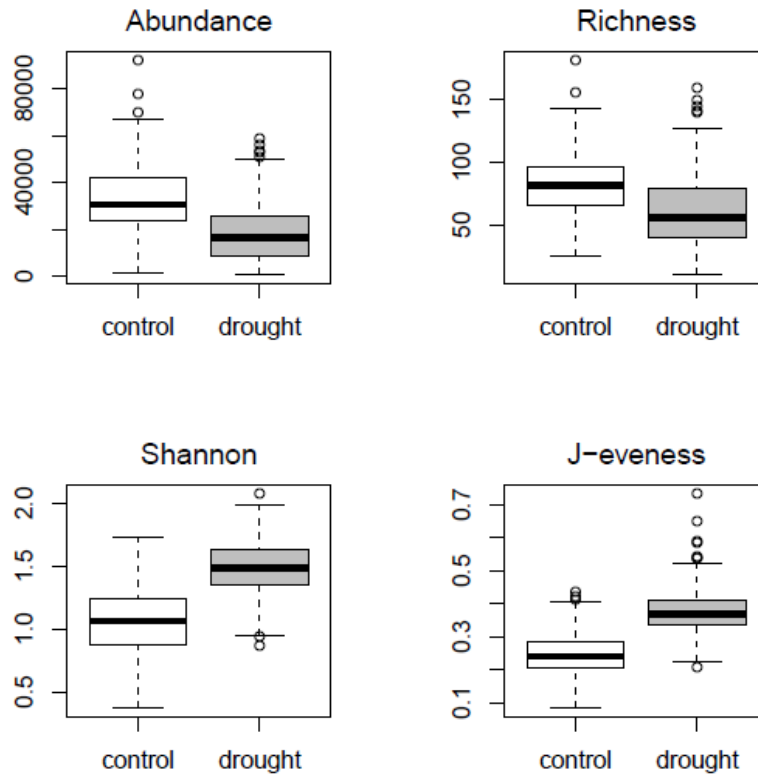


## Additional File 1

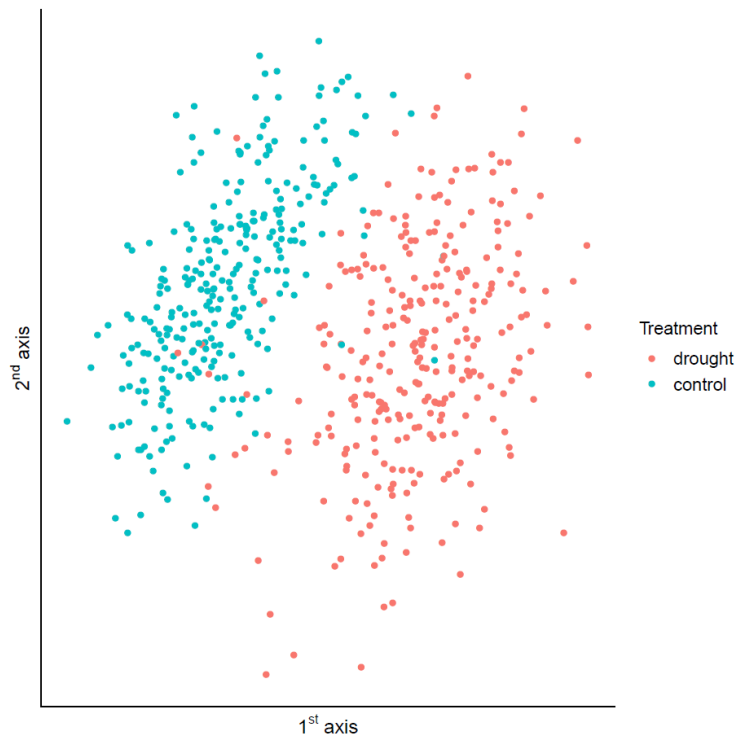
**Fig. S1** Mycobiota description. (a) Mycobiota found in the study. Bars represent total sum of abundances for each taxa. Order level is represented. Total number of sequence-clusters in each treatment is represented in the Venn diagram. (b) Description of the community per treatment. Means and SD shown. ANOVA shows that all parameters (Shannon, richness, J-evenness and abundance) are significantly different between treatments ( $P > 0.001$ ).



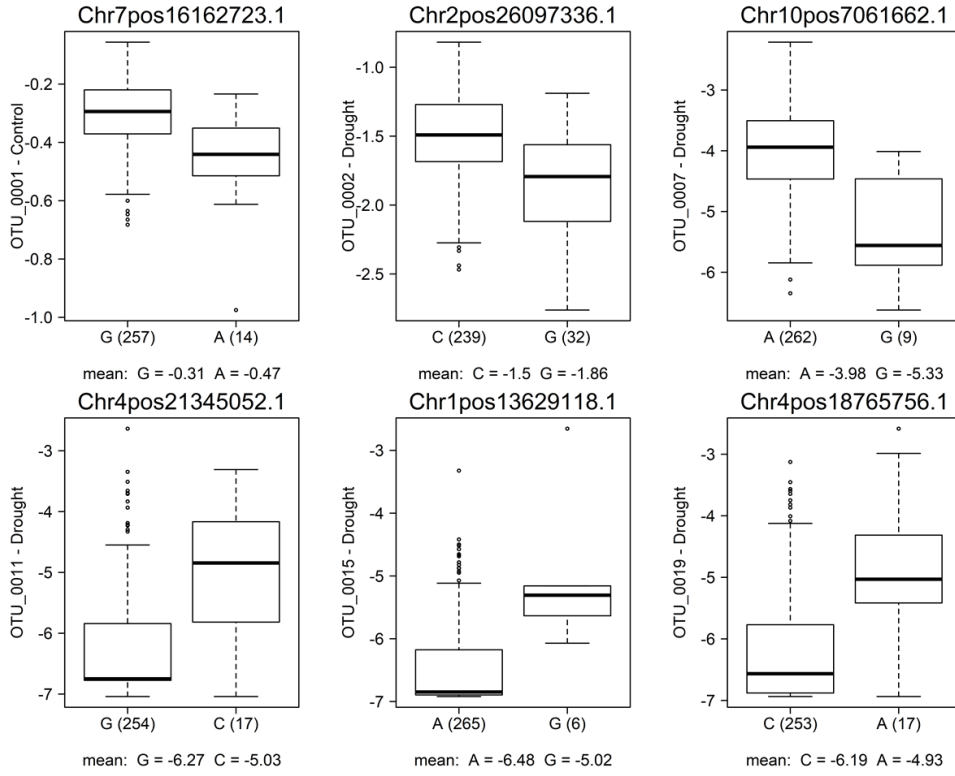
(b)



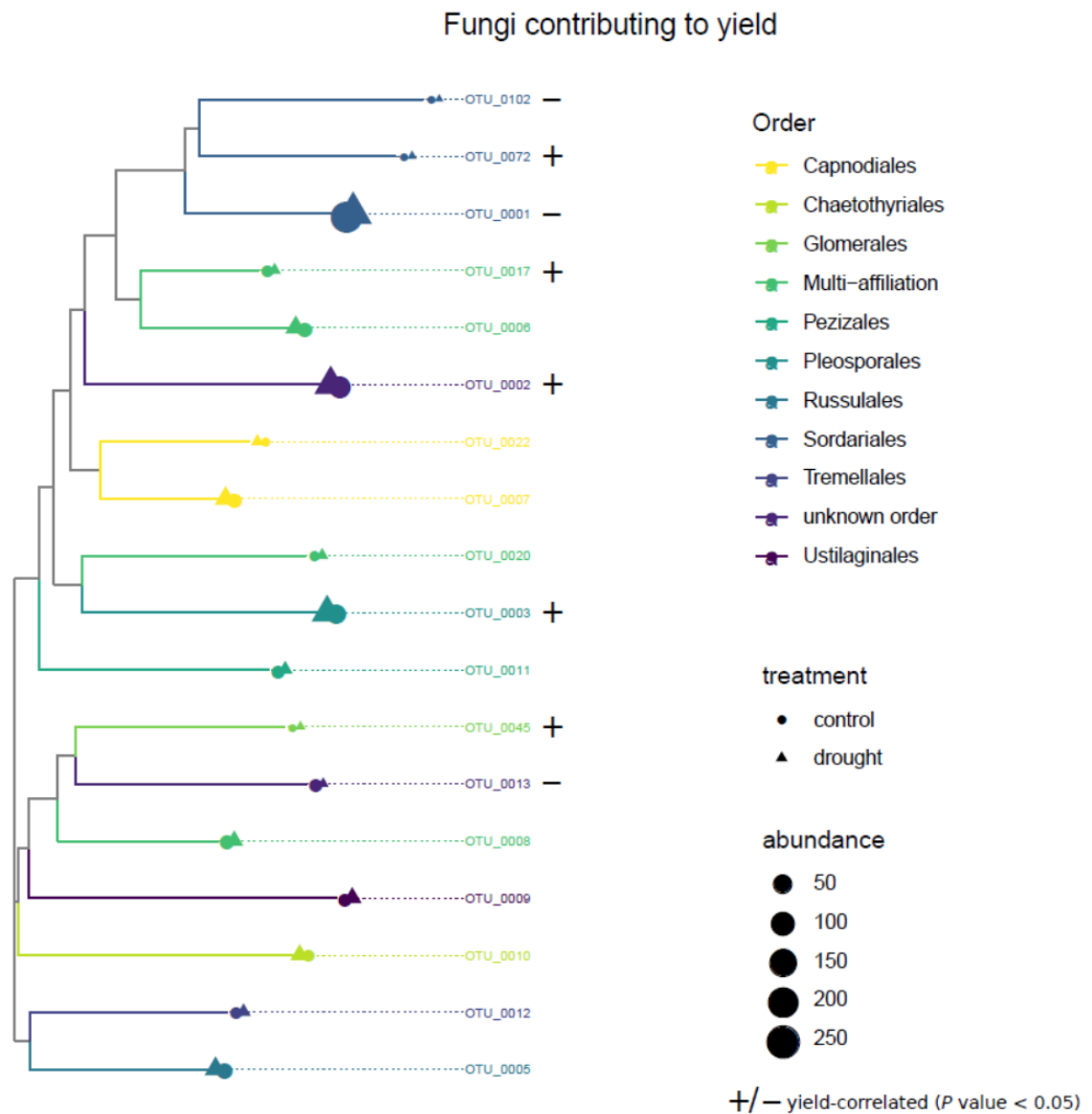
**Fig. S2** PCA of the mycobiota. Sequence-clusters community in control (blue) and drought (red). Data was transformed with log-proportions and corrected for the sequencing run plate effect before performing the PCA analysis.



**Fig. S3** Boxplots with SNP allelic effect. All SNPs found in the univariate GWAS with sequence-clusters are shown.



**Fig. S4** Sequence-clusters contributing to plant yield. Spearman correlation analysis was performed with permuted  $P$  values ( $P$  values  $< 0.05$ ) and RDA with yield as constrained axis. The top 18 sequence-clusters with the lowest  $P$  value and the higher yield contribution (RDA) are shown.



**Table S1** List of SNPs found to be associated with specific fungal-clusters abundances and with drought-related fungal-clusters.

SNP	GWAS	OTU	loci number	gene functions
Chr1pos5498898.1	RDA-C	na	28	kinase/RALFL/keratin/MADS-box/plastocyanin/xylosyltransferase/AP2 protein/HD-Zip protein/MPPN
Chr1pos5530841.1	RDA-C	na	27	kinase/RALFL/Defensin/keratin/MADS-box/plastocyanin-like/xylosyltransferase
Chr2pos26097336.1	OTU-D	OTU_0002	25	kinase/aldehyde dehydrogenase/cytochrome/homeobox associated leucine zipper/hydrolase/protease/B-box zinc finger protein/glutaredoxin/polyamine oxidase
Chr4pos21345052.1	OTU-D	OTU_0011	23	kinase/cellulose synthase/calmodulin dependent kinase/chaperone GrpE/CorA-like magnesium transporter/dehydration-responsive element/F-box protein/Leucine-rich protein/nicotinate phosphoribosyltransferase/phospholipase/subtilisin
Chr2pos26151135.1	OTU-D	OTU_0002	22	kinase/aldehyde dehydrogenase/cytochrome/homeobox associated leucine zipper/hydrolase/protease
Chr10pos15125375.1	OTU-D	OTU_0019	19	BTB/POZ protein
Chr10pos15139435.1	OTU-D	OTU_0019	19	BTB/POZ protein
Chr4pos18765756.1	OTU-D	OTU_0019	13	RALFL/Defensin/CBS protein/EMB1688/exo70 exocyst complex/SWIB MDM2/vacuolar protein
Chr10pos7061662.1	OTU-D	OTU_0007	12	kinase/ligA
Chr4pos22658643.1	OTU-D	OTU_0019	5	transporter
Chr7pos16162723.1	OTU-C	OTU_0001	5	aminotransferase/chloroplast precursor/Fb34 fiber protein/HAD phosphatase/WRKY115
Chr4pos3632808.1	RDA-D	na	4	dioxygenase/peroxidase
Chr1pos13629118.1	OTU-D	OTU_0015	3	GATA zinc finger protein/importin/TPR repeat

**Table S2** Sequence-clusters contributing to plant yield: detailed information.

OTU_ID	taxonomy	Control			Drought		
		R <sup>†</sup>	<i>P</i> value (permuted)*	RDA scores**	R <sup>†</sup>	<i>P</i> value (permuted)*	RDA scores**
OTU_0001	Chaetomiaceae fam.	-0.198	<b>0.001</b>	-5.88E-02	-0.007	0.904	-3.26E-03
OTU_0002	Ceratosphaeria spp.	0.159	<b>0.007</b>	1.64E-01	0.007	0.907	4.98E-03
OTU_0003	Paraconiothyrium spp.	0.276	<b>0</b>	<b>3.71E-01</b>	0.085	0.148	6.53E-02
OTU_0005	Russulales ord.	0.109	0.062	<b>1.62E-01</b>	0.012	0.841	<b>2.20E-02</b>
OTU_0006	Sordariomycetes class	0.051	0.381	<b>1.00E-01</b>	-0.03	0.615	<b>-6.58E-02</b>
OTU_0007	Cladosporium spp.	0.074	0.21	<b>1.35E-01</b>	0.066	0.264	<b>1.07E-01</b>
OTU_0008	Chytridiomycetes class	0.098	0.095	<b>1.68E-01</b>	0.01	0.87	<b>2.01E-02</b>
OTU_0009	Ustilaginales ord.	-0.099	0.09	<b>-1.92E-01</b>	-0.059	0.32	<b>-1.14E-01</b>
OTU_0010	Chaetothyriales ord.	0.048	0.409	<b>1.01E-01</b>	0.104	0.076	<b>2.30E-01</b>
OTU_0011	Boudiera spp.	0.121	0.039	<b>2.64E-01</b>	0.08	0.172	<b>1.66E-01</b>
OTU_0012	Tremellales ord.	-0.071	0.222	<b>-1.21E-01</b>	-0.046	0.43	<b>-7.84E-02</b>
OTU_0013	Peronosporomycetes phy.	-0.16	<b>0.006</b>	-2.44E-01	-0.038	0.513	-2.28E-02
OTU_0017	Apiosporaceae fam.	0.215	<b>0</b>	2.91E-01	0.024	0.676	2.47E-02
OTU_0020	Dothideomycetes class	0.076	0.194	<b>7.94E-02</b>	0.014	0.806	<b>1.74E-02</b>
OTU_0022	Mycosphaerellaceae fam.	0.108	0.065	7.67E-02	0.014	0.816	<b>1.79E-02</b>
OTU_0045	Glomerales ord.	0.144	<b>0.013</b>	5.80E-02	-0.054	0.36	-2.14E-02
OTU_0072	Chaetomium spp.	0.145	<b>0.014</b>	1.06E-02	na	na	na
OTU_0102	Sordariales ord.	-0.149	<b>0.01</b>	-7.35E-03	na	na	na

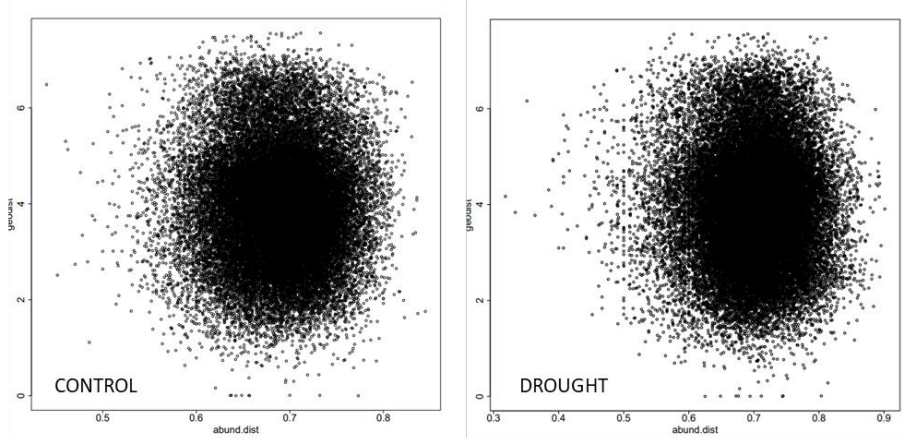
†represents Spearman correlation values between the OTU abundance and yield

\*OTUs correlated with yield shown in bold (*P* value < 0.05)

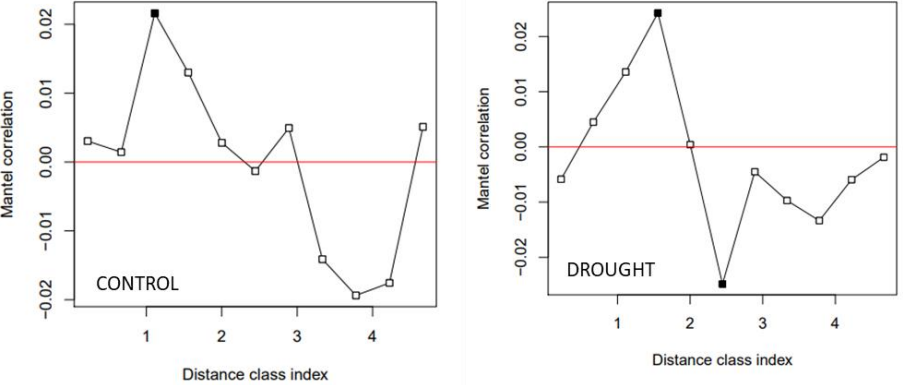
\*\*top 10 OTUs contributing to yield constrained axis in RDA analysis

**Fig. S5** Mantel test plots. We studied the field position effect on the mycobiota results. Euclidean distances between samples (a) and correlogram (b) in control and drought samples.

(a)



(b)





**Fig. S6** Mycobiota found in the study. Bars represent total sum of abundances for each taxa. Phylum level is represented.

