Supporting Information

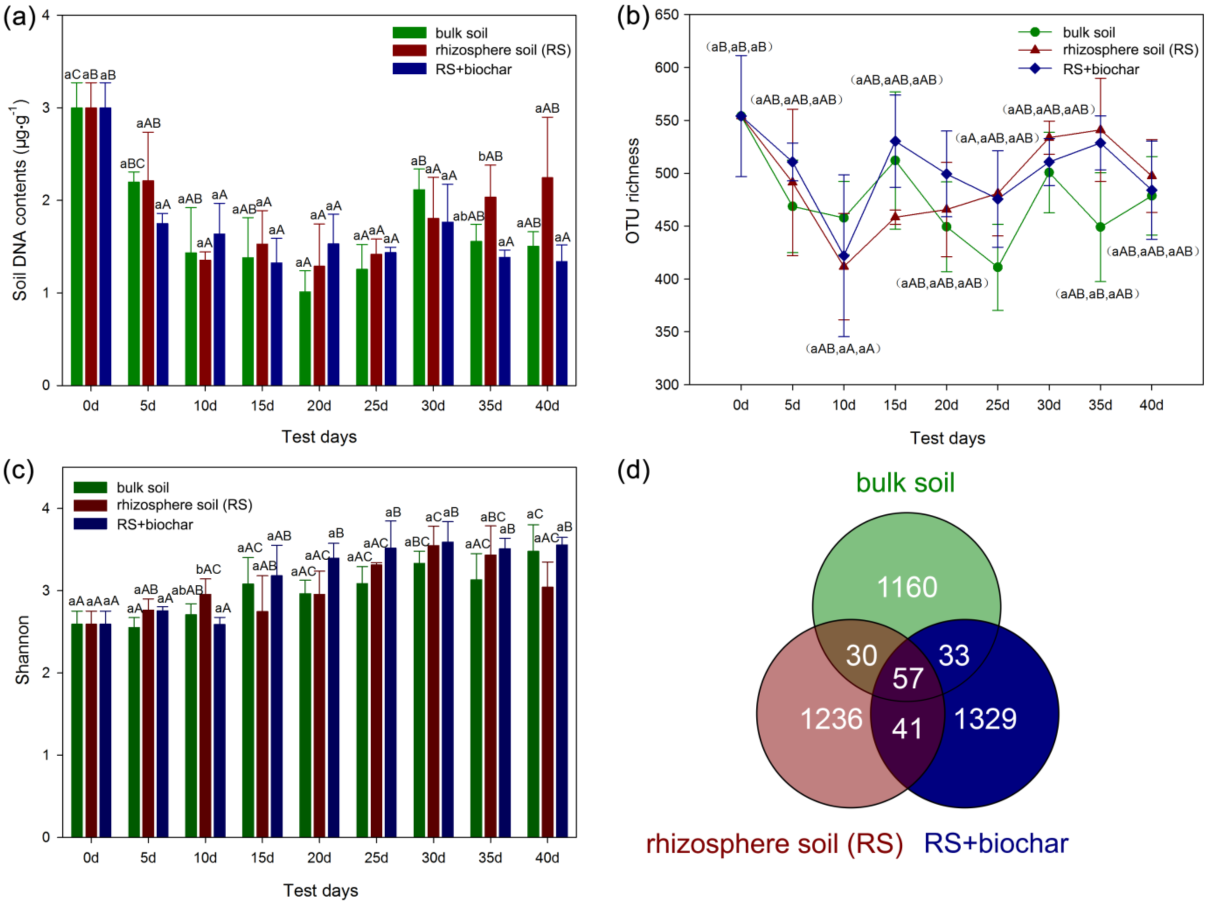

Fig. S1 Changes in the soil DNA contents (a) and fungal OTU richness (b) over time. The Shannon index of the soil fungal communities (c) and a Venn diagram showing the number of unique and overlapping OTUs in the three treatments (d). Error bars represent the standard deviation. Different lowercase letters indicate significant differences in samples from different treatments during the same period (p < 0.05). Different uppercase letters indicate significant differences among different periods in the same treatments (p < 0.05)

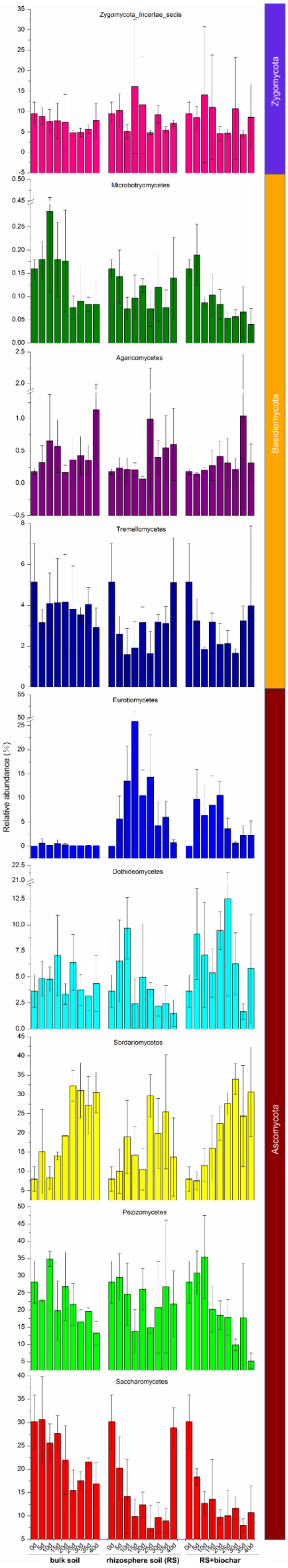

Fig. S2 Taxonomic compositions of the soil fungal communities by different treatments at the class level

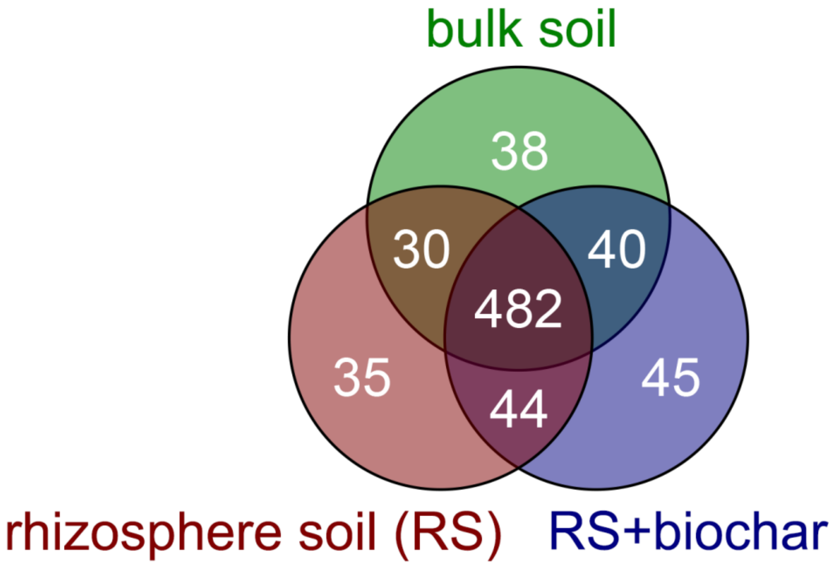

Fig. S3 Venn diagrams showing the distribution of identifiable fungi in life strategies among three treatments

Table S1 Taxonomic information for the key nodes

	OTU	Phylum	Class	Order	Family	Genus	Species	FUNGuild
bulk soil	OTU24	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU120	NA	NA	NA	NA	NA	NA	
	OTU148	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU217	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	NA	
	OTU266	NA	NA	NA	NA	NA	NA	
	OTU321	Ascomycota	Saccharomycetes	Saccharomycetales	Incertae_sedis	Candida	Candida_catenulata	Undefined saprotroph
	OTU327	NA	NA	NA	NA	NA	NA	
	OTU335	NA	NA	NA	NA	NA	NA	
	OTU338	NA	NA	NA	NA	NA	NA	
	OTU352	NA	NA	NA	NA	NA	NA	
	OTU368	NA	NA	NA	NA	NA	NA	
	OTU386	Ascomycota	Saccharomycetes	Saccharomycetales	NA	NA	NA	
	OTU404	NA	NA	NA	NA	NA	NA	
	OTU405	NA	NA	NA	NA	NA	NA	
	OTU431	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Schizothecium	NA	
	OTU780	Basidiomycota	Tremellomycetes	Tremellales	Incertae_sedis	Cryptococcus	NA	Mycoparasite/

								undefined saprotroph
rhizosphere soil (RS)	OTU37	Ascomycota	Leotiomycetes	Thelebolales	Thelebolaceae	Thelebolus	Thelebolus_sp_UFMGCB_3735	Undefined saprotroph
	OTU120	NA	NA	NA	NA	NA	NA	
	OTU182	NA	NA	NA	NA	NA	NA	
	OTU217	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	NA	
	OTU242	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU258	NA	NA	NA	NA	NA	NA	
	OTU266	NA	NA	NA	NA	NA	NA	
	OTU298	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU327	NA	NA	NA	NA	NA	NA	
	OTU335	NA	NA	NA	NA	NA	NA	
	OTU338	NA	NA	NA	NA	NA	NA	
	OTU404	NA	NA	NA	NA	NA	NA	
	OTU405	NA	NA	NA	NA	NA	NA	
	OTU415	Ascomycota	Saccharomycetes	Saccharomycetales	Pichiaceae	Pichia	Pichia_norvegensis	Animal symbiont/ saprotroph
	OTU433	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU523	Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Scutellinia	NA	

	OTU620	Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	NA	NA	
RS+biochar	OTU24	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU61	Ascomycota	Incertae_sedis	Incertae_sedis	Incertae_sedis	Cleistothelebolus	Cleistothelebolus_nipigonensis	
	OTU120	NA	NA	NA	NA	NA	NA	
	OTU131	Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	Ascobolus_crenulatus	Dung saprotroph/ wood saprotroph
	OTU138	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Schizothecium	Schizothecium_inaequale	Dung saprotroph
	OTU182	NA	NA	NA	NA	NA	NA	
	OTU217	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	NA	
	OTU266	NA	NA	NA	NA	NA	NA	
	OTU272	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	
	OTU327	NA	NA	NA	NA	NA	NA	
	OTU335	NA	NA	NA	NA	NA	NA	
	OTU338	NA	NA	NA	NA	NA	NA	
	OTU342	NA	NA	NA	NA	NA	NA	
	OTU404	NA	NA	NA	NA	NA	NA	
	OTU405	NA	NA	NA	NA	NA	NA	
	OTU424	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	unclassified_Fungi	uncultured_fungus	

Table S2 BLAST results of the key nodes (only the top three total scores are shown)

OTU	Subject	% identity	E-value	Total score
OTU24	*Alternaria alternata*	100%	1E-179	640
	Alternaria alternata	100%	1E-179	640
	Alternaria burnsii	100%	1E-179	640
OTU37	*Chlorella sp.* KU211	94%	2E-178	636
	Tetradesmus obliquus	93%	4E-175	625
	Scenedesmus quadricauda	93%	4E-175	625
OTU61	*Cephaliophora tropica*	100%	0	643
	Cephaliophora tropica	99%	4E-174	621
	Cephaliophora irregularis	99%	3E-170	608
OTU120	*Fungal endophyte*	99%	2E-172	616
	Fungal sp. D2	99%	2E-172	616
	uncultured Fungus	99%	8E-171	610
OTU131	*Chlamydomonas sp.* KNUA040	100%	0	741
	Chlamydomonadaceae sp. MCWWS36	99%	0	736
	Chlamydomonadaceae sp. MCWWS26	99%	0	736
OTU138	*uncultured Fungus*	99%	0	658
	Acremonium sp. EN13	99%	2E-162	582
	Acremonium sp. 95a	99%	3E-160	575
OTU148	*uncultured Fungus*	98%	0	713
	uncultured Fungus	98%	0	713
	uncultured Basidiomycota	98%	0	688
OTU182	*Plectosphaerella cucumerina*	100%	0	658
	Plectosphaerella cucumerina	100%	0	658
	Plectosphaerella cucumerina	100%	0	658
OTU217	*uncultured Fungus*	87%	9E-137	497
	uncultured Fungus	86%	4E-120	442

	uncultured Chytridiomycota	84%	2E-119	440
OTU242	*Chlamydomonas reinhardtii*	94%	8E-147	531
	Gonium pectorale	88%	2E-133	486
	Chlamydomonas sp. KU111	88%	4E-130	475
OTU258	*uncultured Sordariales*	96%	7E-152	547
	Podospora pyriformis	96%	8E-151	544
	Fungal endophyte	94%	1E-144	523
OTU266	*Saccharomyces cerevisiae*	93%	4E-26	130
	uncultured Fungus	93%	1E-25	128
	Elaphomyces mutabilis	93%	1E-25	128
OTU272	*Chlorella sorokiniana*	94%	1E-179	640
	Chlorella sp. IOAC1179S	94%	1E-179	640
	Chlorella sorokiniana	94%	2E-177	632
OTU298	*uncultured Fungus*	94%	5E-143	518
	uncultured Fungus	94%	7E-142	514
	uncultured Fungus	92%	6E-93	351
OTU321	*uncultured Fungus*	99%	0	664
	Mucor odoratus	99%	1E-169	606
	Mucor odoratus	99%	1E-169	606
OTU327	*uncultured Fungus*	94%	4E-56	230
	uncultured Fungus	94%	4E-56	318
	uncultured Fungus	94%	2E-53	306
OTU335	*uncultured Fungus*	99%	0	697
	Coprinellus sp. 4 LGN-2011	99%	0	695
	Coprinellus callinus	99%	0	691
OTU338	*uncultured Fungus*	99%	0	689
	uncultured Fungus	99%	0	676
	uncultured Fungus	99%	1E-179	640

OTU342	*Desmodesmus sp.* S3	99%	0	795
	Desmodesmus sp. S7	99%	0	791
	Desmodesmus sp. 1 MAT-2008	99%	0	763
OTU352	*uncultured Fungus*	94%	1E-149	540
	Homalogastra setosa	94%	5E-148	534
	Homalogastra setosa	94%	5E-148	534
OTU368	*uncultured Fungus*	87%	1E-15	159
	uncultured Basidiomycota	94%	1E-14	91.6
	uncultured Eukaryote	95%	5E-14	89.8
OTU386	*uncultured Fungus*	100%	0	656
	uncultured Glomerales	99%	1E-169	606
	uncultured Agaricales	97%	8E-162	580
OTU404	*uncultured Fungus*	100%	0	662
	uncultured Myrothecium	97%	2E-166	595
	uncultured Fungus	100%	4E-164	588
OTU405	*uncultured Fungus*	100%	0	662
	Acremonium sp.	100%	0	662
	Sarocladium strictum	100%	0	662
OTU415	*Fusarium delphinoides*	100%	0	651
	uncultured Fungus	100%	0	651
	Fusarium delphinoides	100%	0	651
OTU424	*uncultured Fungus*	99%	0	721
	uncultured Basidiomycota	99%	0	673
	Coprinopsis pseudofriesii	98%	0	667
OTU431	*Cryptococcus sp.*	100%	0	756
	Cryptococcus sp.	100%	0	756
	Goffeauzyma gilvescens	100%	0	756
OTU433	*uncultured Fungus*	96%	9E-166	593

	uncultured Fungus	94%	2E-148	536
	Homalogastra setosa	91%	3E-135	492
OTU523	*uncultured Fungus*	100%	3E-180	641
	uncultured Fungus	99%	1E-178	636
	Septoriella oudemansii	100%	1E-178	636
OTU620	*Fungal endophyte*	100%	0	665
	Sordariomycetidae sp. N133	100%	0	665
	uncultured Fungus	99%	0	660
OTU780	*uncultured Zopfiella*	96%	6E-152	547
	uncultured Zopfiella	95%	4E-149	538
	uncultured Fungus	96%	1E-148	536

Table S3 Mantel test and partial Mantel test results to discern the correlation between the fungal community similarity and either the soil geochemical variables (pH, NO_3^--N, NH_4^+-N, available phosphorous, trace elements and soil surface structural parameters), ryegrass root surface characteristics and antibiotics

Correlation between fungal community similarity and:	Controlling for:	Earlier stage	Middle stage	Later stage
all samples				
all variables		**0.498****	**0.220****	**0.160***
soil geochemical variables	root and antibiotics	**0.334****	0.107	0.146
ryegrass root	soil and antibiotics	**0.233****	0.080	-0.075
antibiotics	soil and root	0.111	-0.049	0.002
bulk soil				
all variables		0.082	**0.331***	0.335
soil geochemical variables	antibiotics	0.111	**0.434***	0.289
antibiotics	soil	0.018	-0.226	0.270
rhizosphere soil (RS)				
all variables		**0.392****	0.191	-0.307
soil geochemical variables	root and antibiotics	**0.422***	0.045	-0.284
ryegrass root	soil and antibiotics	0.048	-0.004	0.018
antibiotics	soil and root	0.272	0.243	-0.078
RS+biochar				
all variables		**0.431****	0.052	0.206
soil geochemical variables	root and antibiotics	**0.323***	-0.046	0.234
ryegrass root	soil and antibiotics	**0.428***	0.115	-0.188
antibiotics	soil and root	-0.068	-0.176	0.018

* < 0.05, ** < 0.01

Table S4 Correlation analysis between antibiotics and fungal taxa

		CTC	DC	TC	SM2	ENR	LOM	CIP	NOR
OTU richness	r	0.057	0.017	-0.043	0.022	-0.003	-0.211	-0.206	-0.087
	p	0.630	0.883	0.714	0.854	0.978	0.069	0.076	0.460
Ascomycota	r	0.102	0.063	0.201	-0.073	0.163	**0.333****	**0.315****	**0.280***
	p	0.385	0.591	0.083	0.534	0.162	0.004	0.006	0.015
Basidiomycota	r	-0.214	-0.207	-0.108	**-0.295***	-0.120	-0.026	-0.111	-0.121
	p	0.065	0.074	0.357	0.010	0.307	0.828	0.341	0.300
Blastocladiomycota	r	0.008	-0.069	-0.028	-0.054	-0.001	-0.119	-0.123	-0.042
	p	0.947	0.559	0.810	0.647	0.990	0.307	0.294	0.720
Chytridiomycota	r	-0.176	-0.072	0.022	0.075	-0.050	-0.118	-0.125	-0.041
	p	0.131	0.541	0.853	0.520	0.671	0.313	0.287	0.725
Glomeromycota	r	0.105	0.027	-0.002	0.053	0.042	0.040	-0.132	0.048
	p	0.368	0.817	0.989	0.652	0.718	0.730	0.260	0.680
Zygomycota	r	0.080	0.050	0.038	0.037	-0.008	0.074	0.110	0.109
	p	0.495	0.670	0.748	0.755	0.945	0.529	0.349	0.352
unclassified_Fungi	r	-0.146	-0.104	**-0.283***	0.075	-0.198	**-0.434****	**-0.418****	**-0.410****
	p	0.211	0.377	0.014	0.520	0.088	0.000	0.000	0.000
No_Rank	r	-0.045	0.026	-0.061	0.129	-0.010	**-0.239***	**-0.244***	-0.169
	p	0.704	0.823	0.602	0.269	0.931	0.039	0.035	0.147

CTC, chlortetracycline; DC, doxycycline; TC, tetracycline; SM2, sulfamethazine; ENR, enrofloxacin; LOM, lomefloxacin; CIP, ciprofloxacin; NOR, norfloxacin

The r value indicated the Pearson correlation coefficient. The significant ones were bolded

* Correlation is significant at the 0.05 level (2-tailed). ** Correlation is significant at the 0.01 level (2-tailed)

Table S5 Changes in life strategy of the 482 fungal species present in three treatments

bulk soil	rhizosphere soil (RS)			RS+biochar		
Changed from	To	Species	Percent	To	Species	Percent
Slowly acclimate	Slowly acclimate	31	6.4%	Slowly acclimate	24	5.0%
Slowly acclimate	Fast acclimate	42	8.7%	Fast acclimate	36	7.4%
Slowly acclimate	Sensitive	52	10.8%	Sensitive	65	13.5%
Fast acclimate	Slowly acclimate	41	8.5%	Slowly acclimate	24	5.0%
Fast acclimate	Fast acclimate	38	7.9%	Fast acclimate	45	9.3%
Fast acclimate	Sensitive	42	8.7%	Sensitive	52	10.8%
Sensitive	Slowly acclimate	21	4.4%	Slowly acclimate	21	4.4%
Sensitive	Fast acclimate	53	11.0%	Fast acclimate	42	8.7%
Sensitive	Sensitive	162	33.6%	Sensitive	173	35.9%