# Supplementary information

Tables S1-S5, Figures S1-S5

# Planting increases the abundance and structure complexity of soil core functional genes relevant to carbon and nitrogen cycling

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**Table S1**

Dissimilarity tests (adonis) of effects of planting on functional gene community structure and environmental variables among three sites

| | *Functional gene community* | | | *Environment variables* * | | |
|---|---|---|---|---|---|---|
| | N | M | S | N | M | S |
| $R^2$ | 0.738 | 0.798 | 0.913 | 0.928 | 0.975 | 0.999 |
| $P$ | 0.048 | 0.040 | <0.001 | 0.059 | 0.035 | 0.012 |

* Environment variables included soil (pH, SOM, TN, TP, TK, AN, AP, AK, $NH_4$-N, $NO_3$-N, mean soil temperature, mean soil moisture) and plant variables (aboveground biomass, SPAD). The distance was calculated by Bray-Curtis method in permutational multivariate analysis of variance.

# Table S2

## Core functional genes involving in carbon degradataion attributed to planting effects

| **Genbank. ID** | **Gene** | **Sub-category** | **Organism** |
|---|---|---|---|
| 118462569 | CDH | Cellulose | Mycobacterium avium 104 |
| 110825410 | CDH | Cellulose | Rhodococcus sp. RHA1 |
| 304359 | bgl | Cellulose | Cellulomonas fimi |
| 151362421 | bgl | Cellulose | Kineococcus radiotolerans SRS30216 |
| 116671523 | bgl | Cellulose | Arthrobacter sp. FB24 |
| 73698632 | bgl | Cellulose | Alicyclobacillus acidocaldarius |
| 58337637 | bgl | Cellulose | Lactobacillus acidophilus NCFM |
| 142230 | bgl | Cellulose | Agrobacterium sp. |
| 99078285 | bgl | Cellulose | Silicibacter sp. TM1040 |
| 153892922 | bgl | Cellulose | Opitutaceae bacterium TAV2 |
| 15023816 | bcsG | Cellulose | Clostridium acetobutylicum ATCC 824 |
| 31747164 | bcsG | Cellulose | Hypocrea jecorina |
| 7804883 | exoglucanase | Cellulose | Leptosphaeria maculans |
| 7107367 | exoglucanase | Cellulose | Trichoderma harzianum |
| 29160303 | exoglucanase | Cellulose | Acremonium thermophilum |
| 157362170 | exoglucanase | Cellulose | Polyporus arcularius |
| 25990955 | exoglucanase | Cellulose | Piromyces sp. E2 |
| 108764717 | acetylglucosaminidase | Chitin | Rubrobacter xylanophilus DSM 9941 |
| 85831632 | acetylglucosaminidase | Chitin | Leeuwenhoekiella blandensis MED217 |
| 83815976 | acetylglucosaminidase | Chitin | Salinibacter ruber DSM 13855 |
| 116253959 | acetylglucosaminidase | Chitin | Rhizobium leguminosarum bv. viciae 3841 |
| 119774080 | acetylglucosaminidase | Chitin | Shewanella amazonensis SB2B |
| 118071251 | acetylglucosaminidase | Chitin | Shewanella woodyi ATCC 51908 |
| 46912654 | acetylglucosaminidase | Chitin | Photobacterium profundum SS9 |
| 133778506 | chi | Chitin | uncultured bacterium |
| 133778504 | chi | Chitin | uncultured bacterium |
| 113945922 | chi | Chitin | Salinispora tropica CNB-440 |
| 145595773 | chi | Chitin | Salinispora tropica CNB-440 |
| 145595484 | chi | Chitin | Salinispora tropica CNB-440 |
| 85813892 | chi | Chitin | Streptomyces rimosus subsp. paromomycinus |
| 149279875 | chi | Chitin | Pedobacter sp. BAL39 |

| | | | |
|---|---|---|---|
| 142688 | chi | Chitin | Bacillus circulans |
| 46881385 | chi | Chitin | Listeria monocytogenes str. 4b F2365 |
| 111617776 | chi | Chitin | Acidovorax avenae subsp. citrulli AAC00-1 |
| 120590559 | chi | Chitin | Acidovorax avenae subsp. citrulli AAC00-1 |
| 115375191 | chi | Chitin | Stigmatella aurantiaca DW4/3-1 |
| 108460873 | chi | Chitin | Myxococcus xanthus DK 1622 |
| 108760660 | chi | Chitin | Myxococcus xanthus DK 1622 |
| 88778030 | chi | Chitin | Reinekea sp. MED297 |
| 142852981 | chi | Chitin | Aeromonas salmonicida subsp. salmonicida A449 |
| 18143418 | chi | Chitin | Alteromonas sp. O-7 |
| 83631795 | chi | Chitin | Hahella chejuensis KCTC 2396 |
| 70729461 | chi | Chitin | Pseudomonas fluorescens Pf-5 |
| 66048001 | chi | Chitin | Pseudomonas syringae pv. syringae B728a |
| 151939785 | chi | Chitin | Vibrio sp. Ex25 |
| 90580479 | chi | Chitin | Vibrio angustum S14 |
| 156529061 | chi | Chitin | Vibrio harveyi ATCC BAA-1116 |
| 145229305 | chi | Chitin | Aspergillus niger |
| 145257729 | chi | Chitin | Aspergillus niger |
| 119189427 | chi | Chitin | Coccidioides immitis RS |
| 113129062 | chi | Chitin | Hypocrea virens |
| 21223376 | exochitinase | Chitin | Streptomyces coelicolor A3(2) |
| 116623106 | ara | Hemicellulose | Solibacter usitatus Ellin6076 |
| 116621213 | ara | Hemicellulose | Solibacter usitatus Ellin6076 |
| 69284222 | ara | Hemicellulose | Kineococcus radiotolerans SRS30216 |
| 116608903 | ara | Hemicellulose | Arthrobacter sp. FB24 |
| 23326899 | ara | Hemicellulose | Bifidobacterium longum NCC2705 |
| 149936337 | ara | Hemicellulose | Parabacteroides distasonis ATCC 8503 |
| 85831189 | ara | Hemicellulose | Leeuwenhoekiella blandensis MED217 |
| 106889690 | ara | Hemicellulose | Roseiflexus sp. RS-1 |
| 156869730 | ara | Hemicellulose | Clostridium leptum DSM 753 |
| 150385878 | ara | Hemicellulose | Victivallis vadensis ATCC BAA-548 |
| 46205560 | ara | Hemicellulose | Magnetospirillum magnetotacticum MS-1 |
| 156934116 | ara | Hemicellulose | Enterobacter sakazakii ATCC BAA-894 |
| 21242039 | ara | Hemicellulose | Xanthomonas axonopodis pv. citri str. 306 |
| 1244586 | ara_fungi | Hemicellulose | Aspergillus niger |

|  |  |  |  |
|---|---|---|---|
| 120577985 | ara_fungi | Hemicellulose | Penicillium capsulatum |
| 154304204 | ara_fungi | Hemicellulose | Botryotinia fuckeliana B05.10 |
| 154297971 | ara_fungi | Hemicellulose | Botryotinia fuckeliana B05.10 |
| 60416980 | ara_fungi | Hemicellulose | Fusarium oxysporum f. sp. dianthi |
| 116208630 | ara_fungi | Hemicellulose | Chaetomium globosum CBS 148.51 |
| 106885867 | mannanase | Hemicellulose | Clostridium phytofermentans ISDg |
| 88814399 | xylA | Hemicellulose | marine actinobacterium PHSC20C1 |
| 50950653 | xylA | Hemicellulose | Leifsonia xyli subsp. xyli str. CTCB07 |
| 141994 | xylA | Hemicellulose | Actinoplanes sp. ATCC 31351 |
| 145596104 | xylA | Hemicellulose | Salinispora tropica CNB-440 |
| 71368759 | xylA | Hemicellulose | Nocardioides sp. JS614 |
| 88710156 | xylA | Hemicellulose | Flavobacteriales bacterium HTCC2170 |
| 156742580 | xylA | Hemicellulose | Roseiflexus castenholzii DSM 13941 |
| 94554210 | xylA | Hemicellulose | Deinococcus geothermalis DSM 11300 |
| 114706526 | xylA | Hemicellulose | Fulvimarina pelagi HTCC2506 |
| 37526188 | xylA | Hemicellulose | Photorhabdus luminescens subsp. laumondii TTO1 |
| 23304849 | xyn | Hemicellulose | Clostridium stercorarium |
| 106887012 | xyn | Hemicellulose | Clostridium phytofermentans ISDg |
| 113935746 | xyn | Hemicellulose | Caulobacter sp. K31 |
| 13422062 | xyn | Hemicellulose | Caulobacter crescentus CB15 |
| 86282167 | xyn | Hemicellulose | Rhizobium etli CFN 42 |
| 113876349 | xyn | Hemicellulose | Sinorhizobium medicae WSM419 |
| 103488518 | xyn | Hemicellulose | Sphingopyxis alaskensis RB2256 |
| 89950900 | xyn | Hemicellulose | Saccharophagus degradans 2-40 |
| 70986823 | xyn | Hemicellulose | Aspergillus fumigatus Af293 |
| 154299780 | glx | Lignin | Botryotinia fuckeliana B05.10 |
| 89113933 | glx | Lignin | Phanerochaete chrysosporium |
| 58268820 | glx | Lignin | Cryptococcus neoformans var. neoformans JEC21 |
| 46096440 | glx | Lignin | Ustilago maydis 521 |
| 598355 | lip | Lignin | Phanerochaete chrysosporium |
| 5616325 | lip | Lignin | Ceriporiopsis subvermispora |
| 40714547 | lip | Lignin | Trametes versicolor |
| 126105557 | phenol_oxidase | Lignin | uncultured fungus |
| 126105533 | phenol_oxidase | Lignin | uncultured fungus |
| 126035159 | phenol_oxidase | Lignin | uncultured fungus |

| | | | |
|---|---|---|---|
| 126105519 | phenol_oxidase | Lignin | uncultured fungus |
| 145236308 | phenol_oxidase | Lignin | Aspergillus niger |
| 120431228 | phenol_oxidase | Lignin | Sclerotinia minor |
| 152013640 | phenol_oxidase | Lignin | Fusarium oxysporum |
| 37703775 | phenol_oxidase | Lignin | Coprinopsis cinerea |
| 115371535 | phenol_oxidase | Lignin | Coprinopsis cinerea okayama7#130 |
| 56785440 | phenol_oxidase | Lignin | Trametes sp. AH28-2 |
| 2264396 | phenol_oxidase | Lignin | basidiomycete CECT 20197 |
| 121495873 | phenol_oxidase | Lignin | Ganoderma lucidum |
| 124495022 | phenol_oxidase | Lignin | Polyporus brumalis |
| 114228535 | phenol_oxidase | Lignin | Cryptococcus neoformans var. grubii |
| 88815516 | aceA | Others | marine actinobacterium PHSC20C1 |
| 119692341 | aceA | Others | Mycobacterium sp. KMS |
| 222527412 | aceA | Others | Chloroflexus sp. Y-400-fl |
| 6458545 | aceA | Others | Deinococcus radiodurans R1 |
| 10175298 | aceA | Others | Bacillus halodurans C-125 |
| 74422036 | aceA | Others | Nitrobacter winogradskyi Nb-255 |
| 150395535 | aceA | Others | Sinorhizobium medicae WSM419 |
| 124267078 | aceA | Others | Methylibium petroleiphilum PM1 |
| 197123496 | aceA | Others | Anaeromyxobacter sp. K |
| 121589589 | aceA | Others | Halorhodospira halophila SL1 |
| 121998184 | aceA | Others | Halorhodospira halophila SL1 |
| 88789809 | aceA | Others | Nitrococcus mobilis Nb-231 |
| 88812887 | aceA | Others | Nitrococcus mobilis Nb-231 |
| 195941139 | aceA | Others | Escherichia coli O157:H7 str. EC4024 |
| 50122910 | aceA | Others | Pectobacterium atrosepticum SCRI1043 |
| 161505331 | aceA | Others | Salmonella enterica subsp. arizonae serovar 62:z4,z23:-- |
| 90440222 | aceA | Others | Vibrio angustum S14 |
| 194347636 | aceA | Others | Stenotrophomonas maltophilia R551-3 |
| 121703954 | aceA | Others | Aspergillus clavatus NRRL 1 |
| 70993266 | aceA | Others | Aspergillus fumigatus Af293 |
| 212534768 | aceA | Others | Penicillium marneffei ATCC 18224 |
| 49651987 | aceA | Others | Yarrowia lipolytica CLIB122 |
| 1314081 | aceA | Others | Saccharomyces cerevisiae |
| 145702065 | aceB | Others | Metallosphaera sedula DSM 5348 |

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|---|---|---|---|
| 228009109 | aceB | Others | Sulfolobus islandicus Y.G.57.14 |
| 18312527 | aceB | Others | Pyrobaculum aerophilum str. IM2 |
| 126249557 | aceB | Others | Pyrobaculum calidifontis JCM 11548 |
| 226870051 | aceB | Others | Actinosynnema mirum DSM 43827 |
| 25028787 | aceB | Others | Corynebacterium efficiens YS-314 |
| 227079376 | aceB | Others | Corynebacterium lipophiloflavum DSM 44291 |
| 119949946 | aceB | Others | Arthrobacter aurescens TC1 |
| 54312035 | aceB | Others | Mycobacterium sp. P101 |
| 145216439 | aceB | Others | Mycobacterium gilvum PYR-GCK |
| 197703172 | aceB | Others | Streptomyces clavuligerus ATCC 27064 |
| 178463953 | aceB | Others | Streptomyces griseus subsp. griseus NBRC 13350 |
| 108766127 | aceB | Others | Rubrobacter xylanophilus DSM 9941 |
| 156744289 | aceB | Others | Roseiflexus castenholzii DSM 13941 |
| 159897545 | aceB | Others | Herpetosiphon aurantiacus ATCC 23779 |
| 15806175 | aceB | Others | Deinococcus radiodurans R1 |
| 46196060 | aceB | Others | Thermus thermophilus HB27 |
| 221089232 | aceB | Others | Geobacillus sp. Y412MC61 |
| 220706797 | aceB | Others | Geobacillus sp. Y412MC61 |
| 196248380 | aceB | Others | Geobacillus sp. G11MC16 |
| 51855416 | aceB | Others | Symbiobacterium thermophilum IAM 14863 |
| 16126009 | aceB | Others | Caulobacter crescentus CB15 |
| 84704542 | aceB | Others | Parvularcula bermudensis HTCC2503 |
| 84689378 | aceB | Others | Parvularcula bermudensis HTCC2503 |
| 182678865 | aceB | Others | Beijerinckia indica subsp. indica ATCC 9039 |
| 182634735 | aceB | Others | Beijerinckia indica subsp. indica ATCC 9039 |
| 209874700 | aceB | Others | Oligotropha carboxidovorans OM5 |
| 14024664 | aceB | Others | Mesorhizobium loti MAFF303099 |
| 190694973 | aceB | Others | Rhizobium etli CIAT 652 |
| 86355720 | aceB | Others | Rhizobium etli CFN 42 |
| 150398462 | aceB | Others | Sinorhizobium medicae WSM419 |
| 84516932 | aceB | Others | Loktanella vestfoldensis SKA53 |
| 84391670 | aceB | Others | Oceanicola batsensis HTCC2597 |
| 89067960 | aceB | Others | Oceanicola granulosus HTCC2516 |
| 77462527 | aceB | Others | Rhodobacter sphaeroides 2.4.1 |
| 126740332 | aceB | Others | Roseobacter sp. SK209-2-6 |

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|---|---|---|---|
| 225133279 | aceB | Others | Roseobacter sp. GAI101 |
| 109456619 | aceB | Others | Roseobacter denitrificans OCh 114 |
| 85703610 | aceB | Others | Roseovarius sp. 217 |
| 114540602 | aceB | Others | Roseovarius sp. HTCC2601 |
| 56679414 | aceB | Others | Ruegeria pomeroyi DSS-3 |
| 170142908 | aceB | Others | Burkholderia graminis C4D1M |
| 120587575 | aceB | Others | Acidovorax avenae subsp. citrulli AAC00-1 |
| 91699574 | aceB | Others | Polaromonas sp. JS666 |
| 133738798 | aceB | Others | Herminiimonas arsenicoxydans |
| 78218626 | aceB | Others | Desulfovibrio desulfuricans G20 |
| 218758227 | aceB | Others | Desulfovibrio vulgaris str. 'Miyazaki F' |
| 153005821 | aceB | Others | Anaeromyxobacter sp. Fw109-5 |
| 225085216 | aceB | Others | gamma proteobacterium NOR51-B |
| 88799326 | aceB | Others | Reinekea sp. MED297 |
| 90413673 | aceB | Others | Photobacterium profundum 3TCK |
| 151938860 | aceB | Others | Vibrio sp. Ex25 |
| 225142176 | aceB | Others | Stenotrophomonas sp. SKA14 |
| 212527146 | aceB | Others | Penicillium marneffei ATCC 18224 |
| 154277552 | aceB | Others | Ajellomyces capsulatus NAm1 |
| 114228552 | aceB | Others | Paracoccidioides brasiliensis |
| 145609990 | aceB | Others | Magnaporthe grisea 70-15 |
| 16308743 | aceB | Others | Laccaria bicolor |
| 58270612 | aceB | Others | Cryptococcus neoformans var. neoformans JEC21 |
| 111609818 | AssA | Others | sulfate-reducing bacterium AK-01 |
| iegAssA27 | AssA | Others | Unknown |
| iegAssA7 | AssA | Others | Unknown |
| 118470516 | limEH | Aromatics | Mycobacterium smegmatis str. MC2 155 |
| 90195860 | limEH | Aromatics | Mycobacterium vanbaalenii PYR-1 |
| 54026163 | limEH | Aromatics | Nocardia farcinica IFM 10152 |
| 113731798 | limEH | Aromatics | Caulobacter sp. K31 |
| 114050057 | vanA | Aromatics | Streptomyces ambofaciens |
| 75701251 | vanA | Aromatics | Anabaena variabilis ATCC 29413 |
| 113733254 | vanA | Aromatics | Caulobacter sp. K31 |
| 27350645 | vanA | Aromatics | Bradyrhizobium japonicum USDA 110 |
| 109455731 | vanA | Aromatics | Roseobacter denitrificans OCh 114 |

| | | | |
|---|---|---|---|
| 148501358 | vanA | Aromatics | Sphingomonas wittichii RW1 |
| 148502944 | vanA | Aromatics | Sphingomonas wittichii RW1 |
| 110831199 | vanA | Aromatics | Verminephrobacter eiseniae EF01-2 |
| 149814105 | vanA | Aromatics | Plesiocystis pacifica SIR-1 |
| 119459477 | vanA | Aromatics | marine gamma proteobacterium HTCC2080 |
| 91795559 | vanA | Aromatics | Chromohalobacter salexigens DSM 3043 |
| 119816076 | vanA | Aromatics | Pseudomonas putida W619 |
| 120592900 | vdh | Aromatics | Polaromonas naphthalenivorans CJ2 |
| 10184710 | vdh | Aromatics | Pseudomonas sp. HR199 |
| 66847744 | vdh | Aromatics | Aspergillus fumigatus Af293 |
| 59044731 | pectinase | Pectin | uncultured bacterium |
| 166516 | pectinase | Pectin | Aspergillus niger |
| 2251108 | amyA | Starch | Pyrococcus sp. |
| 48306 | amyA | Starch | unidentified bacterium |
| 68234636 | amyA | Starch | Frankia sp. EAN1pec |
| 86566918 | amyA | Starch | Frankia sp. CcI3 |
| 92441508 | amyA | Starch | Mycobacterium sp. KMS |
| 72161237 | amyA | Starch | Thermobifida fusca YX |
| 72162290 | amyA | Starch | Thermobifida fusca YX |
| 50842594 | amyA | Starch | Propionibacterium acnes KPA171202 |
| 119026577 | amyA | Starch | Bifidobacterium adolescentis ATCC 15703 |
| 156861181 | amyA | Starch | Bacteroides uniformis ATCC 8492 |
| 7190353 | amyA | Starch | Chlamydia muridarum Nigg |
| 76164999 | amyA | Starch | Chloroflexus aurantiacus J-10-fl |
| 76260074 | amyA | Starch | Chloroflexus aurantiacus J-10-fl |
| 87303008 | amyA | Starch | Synechococcus sp. WH 5701 |
| 75907651 | amyA | Starch | Anabaena variabilis ATCC 29413 |
| 119465693 | amyA | Starch | Nodularia spumigena CCY9414 |
| 119493471 | amyA | Starch | Lyngbya sp. PCC 8106 |
| 33238381 | amyA | Starch | Prochlorococcus marinus subsp. marinus str. CCMP1375 |
| 6457937 | amyA | Starch | Deinococcus radiodurans R1 |
| 89098045 | amyA | Starch | Bacillus sp. NRRL B-14911 |
| 46487401 | amyA | Starch | Bacillus halodurans |
| 52784460 | amyA | Starch | Bacillus licheniformis ATCC 14580 |
| 29343376 | amyA | Starch | Enterococcus faecalis V583 |

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|---|---|---|---|
| 28270020 | amyA | Starch | Lactobacillus plantarum WCFS1 |
| 90821679 | amyA | Starch | Lactobacillus salivarius subsp. salivarius UCC118 |
| 82744605 | amyA | Starch | Clostridium beijerinckii NCIMB 8052 |
| 89210693 | amyA | Starch | Halothermothrix orenii H 168 |
| 27376012 | amyA | Starch | Bradyrhizobium japonicum USDA 110 |
| 91977680 | amyA | Starch | Rhodopseudomonas palustris BisB5 |
| 86572402 | amyA | Starch | Rhodopseudomonas palustris HaA2 |
| 157408057 | amyA | Starch | Methylobacterium populi BJ001 |
| 85373461 | amyA | Starch | Erythrobacter litoralis HTCC2594 |
| 88936984 | amyA | Starch | Geobacter uraniumreducens Rf4 |
| 85777065 | amyA | Starch | Anaeromyxobacter dehalogenans 2CP-C |
| 88798833 | amyA | Starch | Reinekea sp. MED297 |
| 119768086 | amyA | Starch | Shewanella amazonensis SB2B |
| 49613597 | amyA | Starch | Erwinia carotovora subsp. atroseptica SCRI1043 |
| 50121937 | amyA | Starch | Erwinia carotovora subsp. atroseptica SCRI1043 |
| 77963046 | amyA | Starch | Yersinia mollaretii ATCC 43969 |
| 1177849 | amyA | Starch | Pseudomonas sp. KFCC10818 |
| 156528074 | amyA | Starch | Vibrio harveyi ATCC BAA-1116 |
| 85104727 | amyA | Starch | Neurospora crassa OR74A |
| 10175887 | amyX | Starch | Bacillus halodurans C-125 |
| 2788 | glucoamylase | Starch | Amorphotheca resinae |
| 1905759 | isopullulanase | Starch | Aspergillus niger |
| 29605797 | pulA | Starch | Streptomyces avermitilis MA-4680 |
| 153808537 | pulA | Starch | Bacteroides caccae ATCC 43185 |
| 125497235 | pulA | Starch | Streptococcus sanguinis SK36 |
| 15966601 | pulA | Starch | Sinorhizobium meliloti 1021 |
| 83312163 | pulA | Starch | Magnetospirillum magneticum AMB-1 |
| 67535763 | pulA | Starch | Burkholderia vietnamiensis G4 |
| 116749778 | pulA | Starch | Syntrophobacter fumaroxidans MPOB |
| 119468775 | pulA | Starch | Alteromonadales bacterium TW-7 |
| 4836215 | pulA | Starch | Fervidobacterium pennivorans |

# Table S3

## Core functional genes involving in nitrogen cycling attributed to planting effects

| Genbank. ID | Gene | Sub-category | Organism |
|---|---|---|---|
| 124007002 | gdh | Ammonification | Microscilla marina ATCC 23134 |
| 146192311 | gdh | Ammonification | Bradyrhizobium sp. ORS278 |
| 34494872 | ureC | Ammonification | Haloarcula vallismortis |
| 76557515 | ureC | Ammonification | Natronomonas pharaonis DSM 2160 |
| 158317443 | ureC | Ammonification | Frankia sp. EAN1pec |
| 152964803 | ureC | Ammonification | Kineococcus radiotolerans SRS30216 |
| 67985209 | ureC | Ammonification | Kineococcus radiotolerans SRS30216 |
| 118618420 | ureC | Ammonification | Mycobacterium ulcerans Agy99 |
| 113941017 | ureC | Ammonification | Herpetosiphon aurantiacus ATCC 23779 |
| 158338215 | ureC | Ammonification | Acaryochloris marina MBIC11017 |
| 42782712 | ureC | Ammonification | Bacillus cereus ATCC 10987 |
| 21435824 | ureC | Ammonification | Streptococcus alactolyticus |
| 125714545 | ureC | Ammonification | Clostridium thermocellum ATCC 27405 |
| 39650578 | ureC | Ammonification | Rhodopseudomonas palustris CGA009 |
| 113725650 | ureC | Ammonification | Sinorhizobium medicae WSM419 |
| 150029098 | ureC | Ammonification | Sinorhizobium medicae WSM419 |
| 119383953 | ureC | Ammonification | Paracoccus denitrificans PD1222 |
| 85669952 | ureC | Ammonification | Roseovarius sp. 217 |
| 126708478 | ureC | Ammonification | Sagittula stellata E-37 |
| 145047781 | ureC | Ammonification | Polynucleobacter sp. QLW-P1DMWA-1 |
| 151575999 | ureC | Ammonification | Ralstonia pickettii 12D |
| 84693457 | ureC | Ammonification | Polaromonas naphthalenivorans CJ2 |
| 37731823 | ureC | Ammonification | Nitrosomonas cryotolerans |
| 77166331 | ureC | Ammonification | Nitrosococcus oceani ATCC 19707 |
| 77380811 | ureC | Ammonification | Pseudomonas fluorescens PfO-1 |
| 121702879 | ureC | Ammonification | Aspergillus clavatus NRRL 1 |
| ieghzo270 | hzo | Anammox | Unknown |
| 71383860 | nasA | Assimilatory N reduction | uncultured bacterium |
| 155964459 | nasA | Assimilatory N reduction | uncultured marine bacterium |
| 116804538 | nasA | Assimilatory N reduction | uncultured prokaryote |
| 116804542 | nasA | Assimilatory N reduction | uncultured prokaryote |

| | | | |
|---|---|---|---|
| 227069639 | nirA | Assimilatory N reduction | uncultured archaeon |
| 227069699 | nirA | Assimilatory N reduction | uncultured archaeon |
| 227069643 | nirA | Assimilatory N reduction | uncultured archaeon |
| 172036138 | nirA | Assimilatory N reduction | Cyanothece sp. ATCC 51142 |
| 171697592 | nirA | Assimilatory N reduction | Cyanothece sp. ATCC 51142 |
| 166363013 | nirA | Assimilatory N reduction | Microcystis aeruginosa NIES-843 |
| 86556078 | nirA | Assimilatory N reduction | Synechococcus sp. JA-2-3B'a(2-13) |
| 148255520 | nirA | Assimilatory N reduction | Bradyrhizobium sp. BTAi1 |
| 182413555 | nirA | Assimilatory N reduction | Opitutus terrae PB90-1 |
| 134101441 | NirB | Assimilatory N reduction | Saccharopolyspora erythraea NRRL 2338 |
| 29832204 | NirB | Assimilatory N reduction | Streptomyces avermitilis MA-4680 |
| 32471653 | NirB | Assimilatory N reduction | Rhodopirellula baltica SH 1 |
| 209874150 | NirB | Assimilatory N reduction | Oligotropha carboxidovorans OM5 |
| 213925440 | NirB | Assimilatory N reduction | Pseudomonas syringae pv. tomato T1 |
| 94471203 | narG | Denitrification | uncultured bacterium |
| 38427020 | narG | Denitrification | uncultured bacterium |
| 158138839 | narG | Denitrification | uncultured bacterium |
| 157285559 | narG | Denitrification | uncultured bacterium |
| 124488337 | narG | Denitrification | uncultured bacterium |
| 26278828 | narG | Denitrification | uncultured bacterium |
| 94471271 | narG | Denitrification | uncultured bacterium |
| 45386161 | narG | Denitrification | unidentified bacterium |
| 62003549 | narG | Denitrification | uncultured bacterium |
| 26278922 | narG | Denitrification | uncultured bacterium |
| 32308029 | narG | Denitrification | uncultured bacterium |
| 94471277 | narG | Denitrification | uncultured bacterium |
| 45386181 | narG | Denitrification | unidentified bacterium |
| 94471349 | narG | Denitrification | uncultured bacterium |
| 119391415 | narG | Denitrification | uncultured bacterium |
| 62003537 | narG | Denitrification | uncultured bacterium |
| 121495608 | narG | Denitrification | uncultured bacterium |
| 94471237 | narG | Denitrification | uncultured bacterium |
| 29652532 | narG | Denitrification | uncultured bacterium |
| 32307929 | narG | Denitrification | uncultured bacterium |
| 45386179 | narG | Denitrification | unidentified bacterium |

| | | | |
|---|---|---|---|
| 29652552 | narG | Denitrification | uncultured bacterium |
| 76056963 | narG | Denitrification | uncultured bacterium |
| 66801911 | narG | Denitrification | unidentified bacterium |
| 94471133 | narG | Denitrification | uncultured bacterium |
| 26278800 | narG | Denitrification | uncultured bacterium |
| 26278878 | narG | Denitrification | uncultured bacterium |
| 45386203 | narG | Denitrification | unidentified bacterium |
| 158138865 | narG | Denitrification | uncultured bacterium |
| 78093554 | narG | Denitrification | uncultured bacterium |
| 119391597 | narG | Denitrification | uncultured bacterium |
| 28378213 | narG | Denitrification | Lactobacillus plantarum WCFS1 |
| 34332835 | narG | Denitrification | Chromobacterium violaceum ATCC 12472 |
| 56798123 | narG | Denitrification | Pseudomonas sp. MT-1 |
| 112462695 | nirK | Denitrification | uncultured bacterium |
| 46409941 | nirK | Denitrification | uncultured bacterium |
| 112462135 | nirK | Denitrification | uncultured bacterium |
| 125971537 | nirK | Denitrification | uncultured denitrifying bacterium |
| 83316998 | nirK | Denitrification | uncultured bacterium |
| 87281050 | nirK | Denitrification | uncultured bacterium |
| 112463925 | nirK | Denitrification | uncultured bacterium |
| 73762870 | nirK | Denitrification | uncultured bacterium |
| 112463277 | nirK | Denitrification | uncultured bacterium |
| 83316708 | nirK | Denitrification | uncultured bacterium |
| 112462455 | nirK | Denitrification | uncultured bacterium |
| 73762890 | nirK | Denitrification | uncultured bacterium |
| 87281165 | nirK | Denitrification | uncultured bacterium |
| 112463637 | nirK | Denitrification | uncultured bacterium |
| 109632807 | nirK | Denitrification | uncultured bacterium |
| 17742853 | nirK | Denitrification | Agrobacterium tumefaciens str. C58 |
| 28542629 | nirS | Denitrification | uncultured bacterium |
| 76577396 | nirS | Denitrification | uncultured bacterium |
| 74038408 | nirS | Denitrification | uncultured bacterium |
| 57335474 | nirS | Denitrification | uncultured bacterium |
| 51534865 | nirS | Denitrification | uncultured bacterium |
| 87281376 | nirS | Denitrification | uncultured bacterium |

| | | | |
|---|---|---|---|
| 68510354 | nirS | Denitrification | uncultured bacterium |
| 74038370 | nirS | Denitrification | uncultured bacterium |
| 116013320 | nirS | Denitrification | uncultured bacterium |
| 87281183 | nirS | Denitrification | uncultured bacterium |
| 28542625 | nirS | Denitrification | uncultured bacterium |
| 46850218 | nirS | Denitrification | uncultured bacterium |
| 83318864 | nirS | Denitrification | uncultured bacterium |
| 87281302 | nirS | Denitrification | uncultured bacterium |
| 28542639 | nirS | Denitrification | uncultured bacterium |
| 81251653 | nirS | Denitrification | uncultured organism |
| 81251657 | nirS | Denitrification | uncultured organism |
| 29466008 | norB | Denitrification | uncultured bacterium |
| 29466064 | norB | Denitrification | uncultured bacterium |
| 29466090 | norB | Denitrification | uncultured bacterium |
| 29466006 | norB | Denitrification | uncultured bacterium |
| 29466024 | norB | Denitrification | uncultured bacterium |
| 29466086 | norB | Denitrification | uncultured bacterium |
| 4454060 | norB | Denitrification | Bradyrhizobium japonicum |
| 34391456 | norB | Denitrification | Nitrosomonas marina |
| 119671792 | norB | Denitrification | Azoarcus sp. BH72 |
| 11344614 | norB | Denitrification | Pseudomonas fluorescens |
| 29125948 | nosZ | Denitrification | uncultured soil bacterium |
| 4633560 | nosZ | Denitrification | uncultured bacterium 696W |
| 4633558 | nosZ | Denitrification | uncultured bacterium ProE |
| 29125958 | nosZ | Denitrification | uncultured soil bacterium |
| 12744271 | nosZ | Denitrification | uncultured temperate forest soil bacterium CZ1441 |
| 76058152 | nosZ | Denitrification | uncultured bacterium |
| 156446963 | nosZ | Denitrification | uncultured bacterium |
| 4633565 | nosZ | Denitrification | uncultured bacterium ProI |
| 156446925 | nosZ | Denitrification | uncultured bacterium |
| 4633583 | nosZ | Denitrification | uncultured bacterium 696G |
| 83972352 | nosZ | Denitrification | uncultured alpha proteobacterium |
| 69938258 | nosZ | Denitrification | Paracoccus denitrificans PD1222 |
| 74056902 | nosZ | Denitrification | Thiobacillus denitrificans ATCC 25259 |
| 119863768 | nosZ | Denitrification | Psychromonas ingrahamii 37 |

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|---|---|---|---|
| 124488109 | napA | Dissimilatory N reduction | uncultured bacterium |
| 148474840 | napA | Dissimilatory N reduction | uncultured bacterium |
| 124488145 | napA | Dissimilatory N reduction | uncultured bacterium |
| 158138747 | napA | Dissimilatory N reduction | uncultured bacterium |
| 146195550 | napA | Dissimilatory N reduction | Bradyrhizobium sp. ORS278 |
| 146406446 | napA | Dissimilatory N reduction | Bradyrhizobium sp. BTAi1 |
| 38637875 | napA | Dissimilatory N reduction | Cupriavidus necator |
| 156255109 | napA | Dissimilatory N reduction | Pseudomonas sp. MT-1 |
| 149196318 | nrfA | Dissimilatory N reduction | Lentisphaera araneosa HTCC2155 |
| 94265724 | nrfA | Dissimilatory N reduction | delta proteobacterium MLMS-1 |
| 95133480 | nrfA | Dissimilatory N reduction | Desulfuromonas acetoxidans DSM 684 |
| 144945974 | nrfA | Dissimilatory N reduction | Geobacter bemidjiensis Bem |
| 77920456 | nrfA | Dissimilatory N reduction | Pelobacter carbinolicus DSM 2380 |
| 86152755 | nrfA | Dissimilatory N reduction | Campylobacter jejuni subsp. jejuni HB93-13 |
| 78365334 | nrfA | Dissimilatory N reduction | Shewanella sp. PV-4 |
| 149191083 | nrfA | Dissimilatory N reduction | Vibrio shilonii AK1 |
| 73697438 | amoA | Nitrification | uncultured crenarchaeote |
| 73697250 | amoA | Nitrification | uncultured crenarchaeote |
| 7595786 | amoA | Nitrification | uncultured bacterium |
| 71361353 | amoA | Nitrification | uncultured bacterium |
| 150014349 | nifH | Nitrogen fixation | Methanococcus aeolicus Nankai-3 |
| 150400783 | nifH | Nitrogen fixation | Methanococcus aeolicus Nankai-3 |
| 157401497 | nifH | Nitrogen fixation | Methanococcus maripaludis C6 |
| 150399896 | nifH | Nitrogen fixation | Methanococcus vannielii SB |
| 154151622 | nifH | Nitrogen fixation | Candidatus Methanoregula boonei 6A8 |
| 19917684 | nifH | Nitrogen fixation | Methanosarcina acetivorans C2A |
| 72394883 | nifH | Nitrogen fixation | Methanosarcina barkeri str. fusaro |
| 76667545 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 1255482 | nifH | Nitrogen fixation | unidentified bacterium |
| 29293450 | nifH | Nitrogen fixation | uncultured bacterium |
| 44829093 | nifH | Nitrogen fixation | uncultured bacterium |
| 139003462 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 3157524 | nifH | Nitrogen fixation | unidentified nitrogen-fixing bacteria |
| 60100873 | nifH | Nitrogen fixation | uncultured bacterium |
| 68135537 | nifH | Nitrogen fixation | uncultured bacterium |

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|---|---|---|---|
| 99083279 | nifH | Nitrogen fixation | uncultured bacterium |
| 60100879 | nifH | Nitrogen fixation | uncultured bacterium |
| 3157614 | nifH | Nitrogen fixation | unidentified nitrogen-fixing bacteria |
| 110931976 | nifH | Nitrogen fixation | uncultured marine bacterium |
| 780709 | nifH | Nitrogen fixation | unidentified marine eubacterium |
| 148756010 | nifH | Nitrogen fixation | uncultured bacterium |
| 139004122 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 89512768 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 497884 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 62149130 | nifH | Nitrogen fixation | uncultured bacterium |
| 139003137 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 85069178 | nifH | Nitrogen fixation | uncultured bacterium |
| 99082987 | nifH | Nitrogen fixation | uncultured bacterium |
| 139003556 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 139003319 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 112280450 | nifH | Nitrogen fixation | uncultured bacterium |
| 76667400 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 156600794 | nifH | Nitrogen fixation | uncultured bacterium |
| 99083269 | nifH | Nitrogen fixation | uncultured bacterium |
| 73534169 | nifH | Nitrogen fixation | uncultured bacterium |
| 94470897 | nifH | Nitrogen fixation | uncultured bacterium |
| 60326762 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 89512616 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 56809495 | nifH | Nitrogen fixation | uncultured bacterium |
| 139003172 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 139004179 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 1255504 | nifH | Nitrogen fixation | unidentified bacterium |
| 76667453 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 148342406 | nifH | Nitrogen fixation | uncultured bacterium |
| 76667345 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 1255480 | nifH | Nitrogen fixation | unidentified bacterium |
| 10863143 | nifH | Nitrogen fixation | marine stromatolite eubacterium HB(0697) A101A |
| 139002666 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 99083075 | nifH | Nitrogen fixation | uncultured bacterium |
| 99083367 | nifH | Nitrogen fixation | uncultured bacterium |

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|---|---|---|---|
| 99083095 | nifH | Nitrogen fixation | uncultured bacterium |
| 139003470 | nifH | Nitrogen fixation | uncultured bacterium |
| 37548710 | nifH | Nitrogen fixation | uncultured bacterium |
| 19070155 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 37925029 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 139003062 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 139003446 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 3157590 | nifH | Nitrogen fixation | unidentified nitrogen-fixing bacteria |
| 89512372 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 56809455 | nifH | Nitrogen fixation | uncultured bacterium |
| 29293252 | nifH | Nitrogen fixation | uncultured bacterium |
| 50919564 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 15186893 | nifH | Nitrogen fixation | uncultured bacterium |
| 89512930 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 151361599 | nifH | Nitrogen fixation | Kineococcus radiotolerans SRS30216 |
| 147832086 | nifH | Nitrogen fixation | Clavibacter michiganensis subsp. michiganensis NCPPB 382 |
| 78167184 | nifH | Nitrogen fixation | Pelodictyon luteolum DSM 273 |
| 148567463 | nifH | Nitrogen fixation | Roseiflexus sp. RS-1 |
| 16332205 | nifH | Nitrogen fixation | Synechocystis sp. PCC 6803 |
| 138897063 | nifH | Nitrogen fixation | Geobacillus thermodenitrificans NG80-2 |
| 2897667 | nifH | Nitrogen fixation | Paenibacillus macerans |
| 116812179 | nifH | Nitrogen fixation | Clostridium sp. Sukashi-1 |
| 116812183 | nifH | Nitrogen fixation | Clostridium sp. Kas107-2 |
| 33385703 | nifH | Nitrogen fixation | Desulfotomaculum nigrificans |
| 312237 | nifH | Nitrogen fixation | Rhodobacter capsulatus |
| 146278697 | nifH | Nitrogen fixation | Rhodobacter sphaeroides ATCC 17025 |
| 85672433 | nifH | Nitrogen fixation | Roseovarius sp. 217 |
| 158510468 | nifH | Nitrogen fixation | Candidatus Desulfococcus oleovorans Hxd3 |
| 46562231 | nifH | Nitrogen fixation | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough |
| 118746565 | nifH | Nitrogen fixation | Geobacter lovleyi SZ |
| 116697525 | nifH | Nitrogen fixation | Syntrophobacter fumaroxidans MPOB |
| 34483462 | nifH | Nitrogen fixation | Wolinella succinogenes |
| 118072158 | nifH | Nitrogen fixation | Shewanella woodyi ATCC 51908 |
| 12659200 | nifH | Nitrogen fixation | Treponema sp. ZAS-9 |
| 12659196 | nifH | Nitrogen fixation | Treponema primitia ZAS-2 |

**Table S4.** Core functional genes involving in carbon degradation and nitrogen cycling significantly (*P* < 0.01) correlated with aboveground biomass

| **Genbank. ID** | **Gene** | **Category** | **Organism** |
|---|---|---|---|
| 156529061 | chi | Chitin degradation | Vibrio harveyi ATCC BAA-1116 |
| 145229305 | chi | Chitin degradation | Aspergillus niger |
| 145257729 | chi | Chitin degradation | Aspergillus niger |
| 113129062 | chi | Chitin degradation | Hypocrea virens |
| 113935746 | xyn | Hemicellulose degradation | Caulobacter sp. K31 |
| 126105519 | phox | Lignin degradation | uncultured fungus |
| 156744289 | aceB | Others degradation | Roseiflexus castenholzii DSM 13941 |
| 133738798 | aceB | Others degradation | Herminiimonas arsenicoxydans |
| 6457937 | amyA | Starch degradation | Deinococcus radiodurans R1 |
| 67535763 | pulA | Starch degradation | Burkholderia vietnamiensis G4 |
| 150029098 | ureC | Ammonification | Sinorhizobium medicae WSM419 |
| 124488109 | napA | Dissimilatory N reduction | uncultured bacterium |
| 95133480 | nrfA | Dissimilatory N reduction | Desulfuromonas acetoxidans DSM 684 |
| 3157614 | nifH | Nitrogen fixation | unidentified nitrogen-fixing bacteria |
| 148756010 | nifH | Nitrogen fixation | uncultured bacterium |
| 148342406 | nifH | Nitrogen fixation | uncultured bacterium |
| 19070155 | nifH | Nitrogen fixation | uncultured nitrogen-fixing bacterium |
| 2897667 | nifH | Nitrogen fixation | Paenibacillus macerans |

## Table S5

Climate and soil conditions in three research sites

| **Site** | **Location** | **Climate type** | **MAT (°C)** * | **MAP (mm)** | **Soil type** | **Soil texture** |
|---|---|---|---|---|---|---|
| North site: Hailun (N) | 47°26' N, 126°38' E | cold temperate | 3.0 | 530 | Black soil (Phaeozem) | silty clay loam |
| Middle site: Fenqiu (M) | 35°00' N, 114°24' E | warm temperate | 13.9 | 605 | Chao soil (Cambisol) | sandy loam |
| South site: Yingtan (S) | 28°15N', 116°55' E | subtropical | 17.6 | 1795 | Red soil (Acrisol) | silty clay |

*MAT (mean annual temperature) and MAP (mean precipitation data) were calculated from meteorological observation data from each experiment stations (1996-2006).

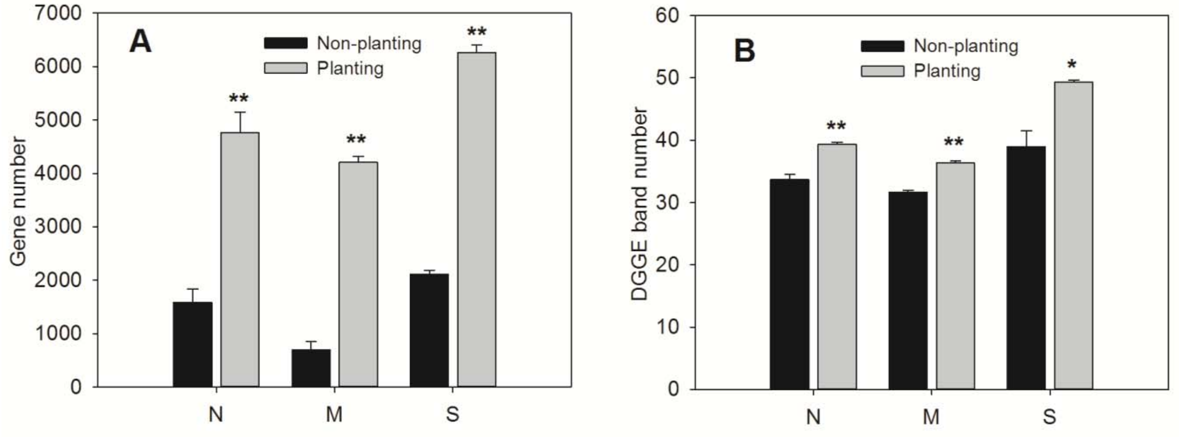

**Figure S1.** Total gene number detected by GeoChip 3.0 (A) and total DGGE band number (B) in three soilsunder non-planting and planting treatments.All data are presented as mean ± SE. The asterisk (*) and double asterisk (**) denote significant differences at $P< 0.05$ and $P <0.01$, respectively, which were assessed using two-tailed t test. N, north site in Hailun with cold temperate climate; M, middle site in Fengqiu with warm temperate climate; S, South site in Yingtan with subtropical climate.

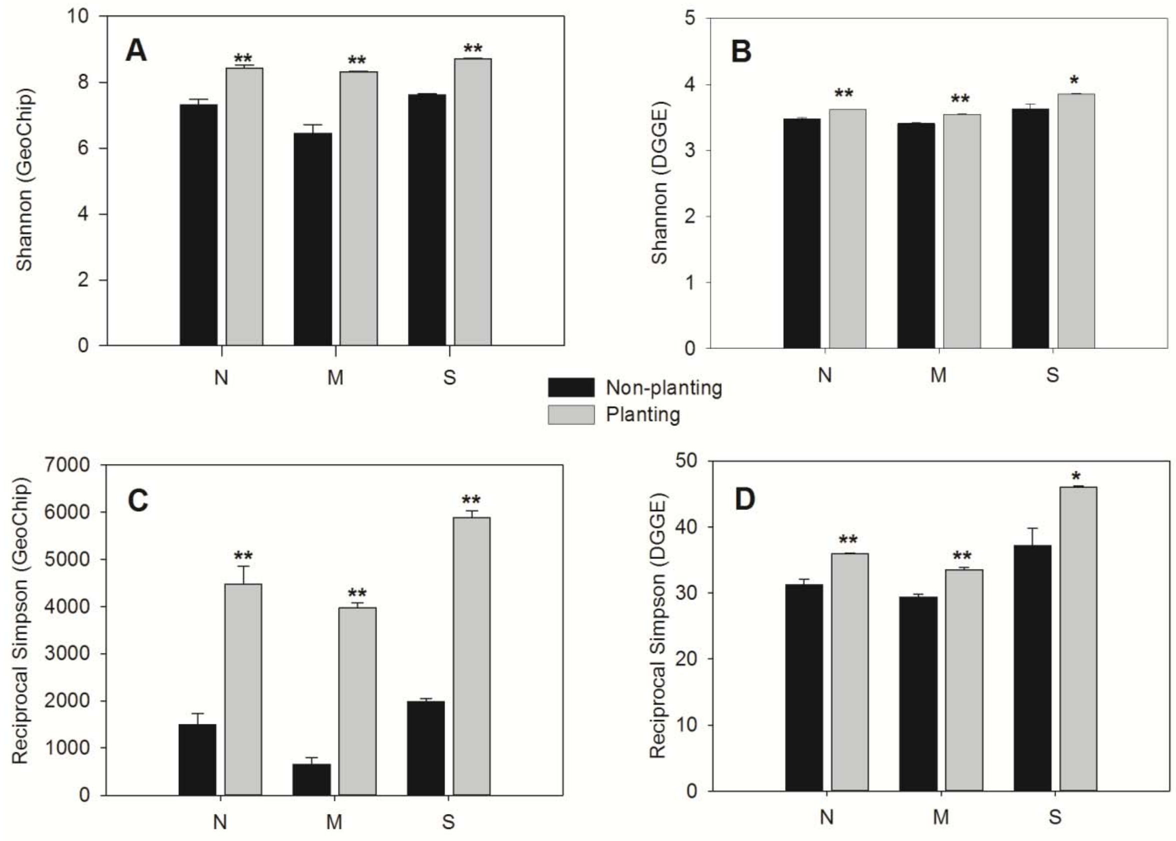

**Figure S2.** Shannon's and Simpson'sindexes of soil microbial community based on GeoChip and DGGE analysis in three soils under non-planting and planting treatments.All data are presented as mean ± SE. The asterisk (*) and double asterisk (**) denote significant differences at *P*< 0.05 and *P* <0.01, respectively, which was assessed using two-tailed t test. N, north site in Hailun with cold temperate climate; M, middle site in Fengqiu with warm temperate climate; S, South site in Yingtan with subtropical climate.

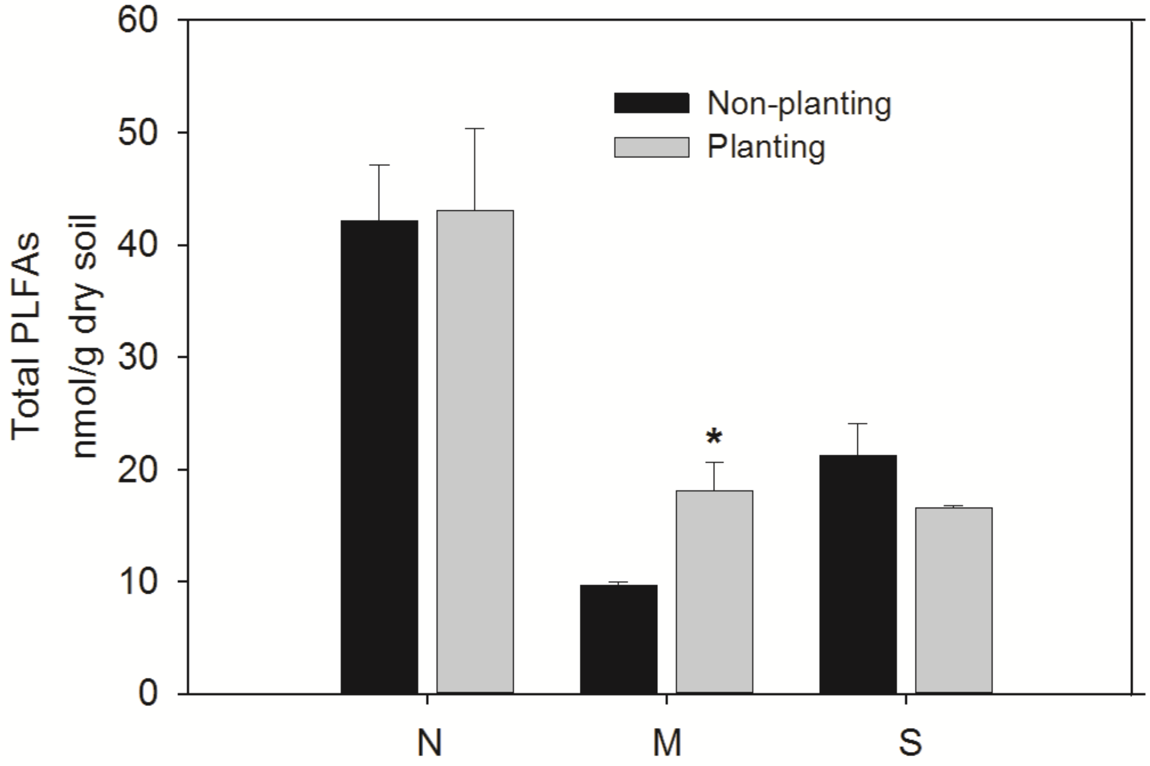

**Figure S3.** Total amounts of PLFAs in three soils under non-planting and planting treatments. All data are presented as mean±SE. The asterisk (*) denotes a significant differences at *P*< 0.05 which was assessed using two-tailed t test. N, north site in Hailun with cold temperate climate; M, middle site in Fengqiu with warm temperate climate; S, South site in Yingtan with subtropical climate.

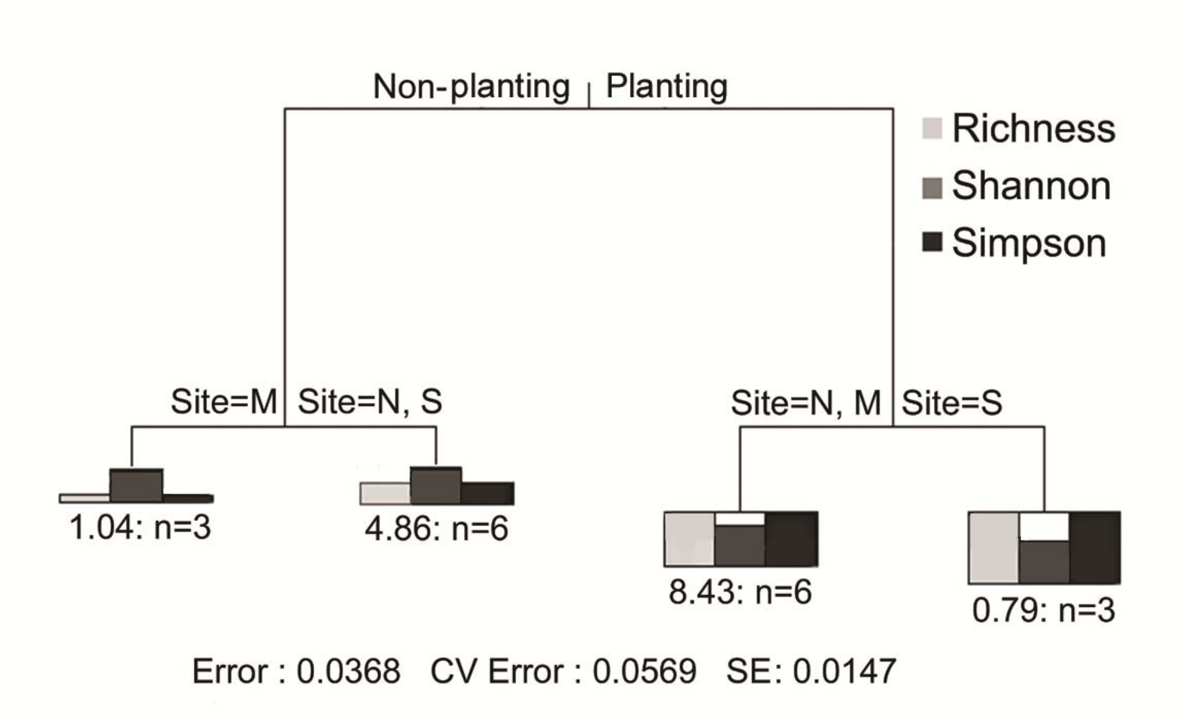

**Figure S4.** Multivariate regression tree (MRT) analysis for associations between α-diversities of soil functional genes and different treatments and locations. Bar plots show the multivariate means of diversity estimates at each branch, and the numbers of soil samples included in that splits are shown under bar plots. Error, relative error (it gives an over-optimistic estimate of how accurately a tree will predict for data); CV Error, cross-validated relative error (predictive accuracy is better estimated from the CV Error, which varies from zero for a perfect predictor to close to one for a poor predictor); SE, standard error. N, north site in Hailun with cold temperate climate; M, middle site in Fengqiu with warm temperate climate; S, South site in Yingtan with subtropical climate.

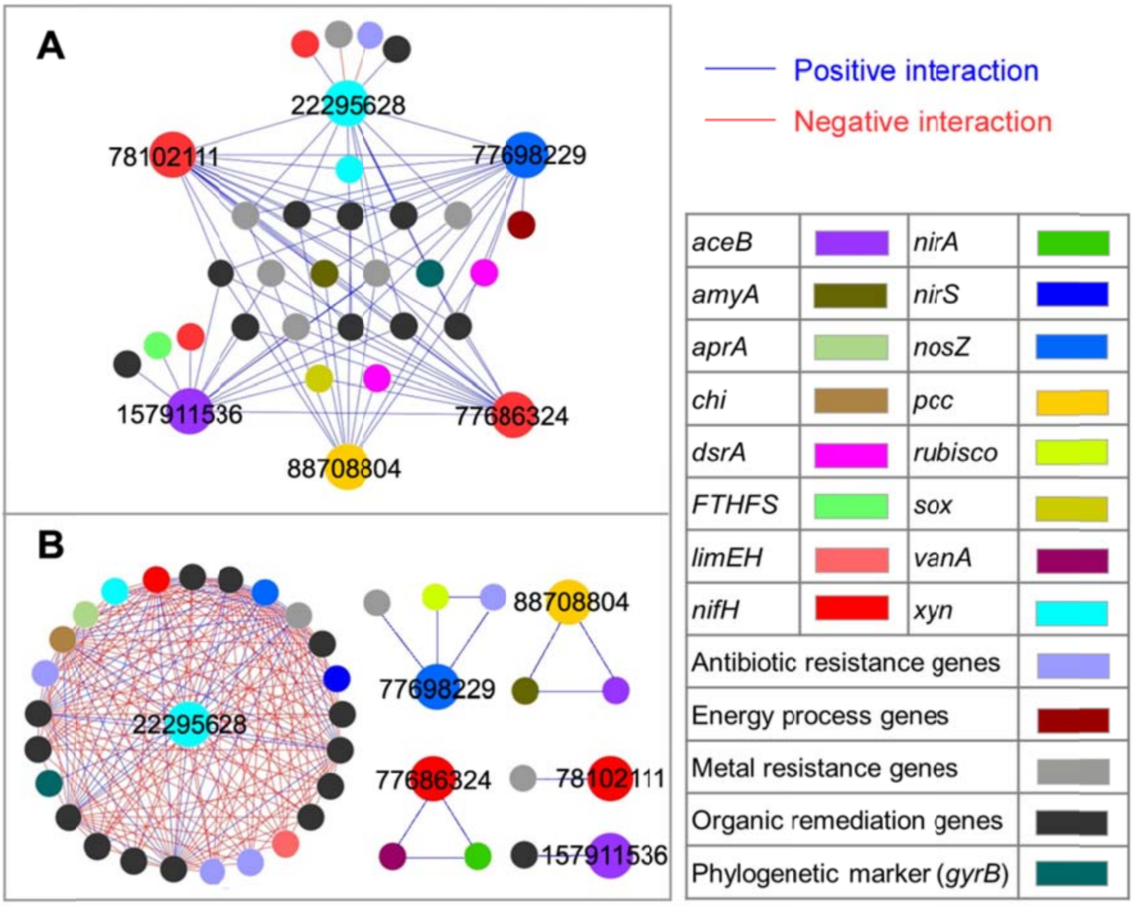

**Figure S5.** Network interactions of the top six functional genes with the highest connectivity under non-planting (A) and planting treatments (B). Each node signifies a functional gene/groups. Colors of the nodes indicate different functional genes/groups. A blue line indicates a positive interaction between two individual nodes, while a red line indicates a negative interaction. The listed genes in two networks under non-planting and planting treatments include *aceB* (malate synthase), *amyA* (alpha amylase), *chi* (endochitinase), *FTHFS* (tetrahydrofolate formylase), *limEH* (limonene epoxide hydrolase), *pcc* (propionyl-CoA carboxylase), *rubisco* (ribulose-l, 5-bisphosphate carboxylase/oxygenase), *vanA* (vanillate monooxygenase) and *xyn* (xylanase) for C cycling; *nifH* (nitrogenase reductase), *nirA* (nitrite reductase), *nirS* (nitrite reductase) and *nosZ* (nitrous oxide reductase) for N cyxling; *aprA* (dissimilatory adenosine-5'-phospo-sulfate reductase), *dsrA* (Dissimilatory sulfite reductase) and *sox* (sulfite oxidase) for S cycling.