Supplemental Table S1 Number of bacterial network nodes at phyla level in bulk and rhizosphere soils under continuous cropping of soybean (CC) and soybean-corn crop rotation (CR) systems, respectively.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phyla/Class | CCB | CRB | CCR | CRR |
| Acidobacteria | 96 (15.9) | 106 (15.4) | 61 (4.10) | 92 (7.40) |
| Actinobacteria | 134 (11.6) | 146 (12.9) | 103 (5.18) | 132 (13.4) |
| Alphaproteobacteria | 111 (10.7) | 128 (10.8) | 95 (10.1) | 129 (15.8) |
| Armatimonadetes | 28 (1.00) | 41 (1.21) | 10 (0.16) | 19 (0.33) |
| Bacteroidetes | 32 (1.83) | 53 (2.05) | 35 (2.75) | 63 (6.16) |
| Betaproteobacteria | 40 (11.3) | 47 (8.62) | 38 (39.1) | 40 (25.7) |
| Chloroflexi | 118 (5.46) | 134 (6.04) | 35 (0.67) | 55 (1.59) |
| Cyanobacteira | 7 (0.30) | 14 (0.51) | 2 (0.06) | 7 (0.94) |
| Deltaproteobacteria | 59 (1.76) | 76 (2.29) | 13 (0.18) | 33 (0.67) |
| Firmicutes | 38 (1.96) | 35 (1.08) | 13 (0.65) | 20 (0.57) |
| Gammaproteobacteria | 26 (1.92) | 26 (1.77) | 21 (3.38) | 30 (4.70) |
| Gemmatimonadetes | 35 (5.51) | 42 (0.84) | 20 (1.25) | 30 (2.76) |
| Nitrospirae | 3 (0.23) | 7 (0.65) | 2 (0.05) | 6 (0.18) |
| Planctomycetes | 87 (2.71) | 89 (2.22) | 29 (0.49) | 43 (0.81) |

The relative abundance of each phylum/class in different treatment based on the proportional frequencies of 16S rRNA sequences were showed in parentheses.

Supplemental Table S2 Information of the nodes served as module hubs and connectors of bacterial networks in bulk and rhizosphere soils under continuous cropping of soybean (CC) and soybean-corn crop rotation (CR) systems, respectively.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatments  (No. of generalists) | OTU ID | Generalists | Zi | *Pi* | Node degree | Relative abundance | Phylum | Class | Order | Family | Genus |
| CCB (27) | OTU964\* | module hub | 4.28 | 0 | 16 | 0.04 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Rhodanobacter* |
| OTU2617\* | module hub | 3.805 | 0.142 | 13 | 0.03 | Actinobacteria | Actinobacteria | Solirubrobacterales | Patulibacteraceae | *Patulibacter* |
| OTU1787\* | module hub | 2.888 | 0.142 | 13 | 0.10 | Actinobacteria | Actinobacteria | Frankiales | Acidothermaceae | *Acidothermus* |
| OTU2485 | module hub | 3.805 | 0 | 12 | 0.05 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU1349 | module hub | 3.048 | 0 | 12 | 0.03 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Defluviicoccus* |
| OTU1816\* | module hub | 2.829 | 0 | 11 | 0.26 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Beijerinckiaceae | *Mehtylorosula* |
| OTU67\* | module hub | 2.54 | 0 | 11 | 0.03 | Proteobacteria | Deltaproteobacteria | Myxococcales | Haliangiaceae | *Haliangium* |
| OTU2224\* | module hub | 2.54 | 0 | 11 | 0.04 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Bradyrhizobiaceae | *Bradyrhizobium* |
| OTU2265 | module hub | 3.309 | 0 | 10 | 0.03 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Rhodanobacter* |
| OTU1069\* | connector | 0.732 | 0.691 | 9 | 0.09 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Hyphomicrobiaceae | *Unclassified* |
| OTU1632\* | module hub | 3.108 | 0.219 | 8 | 0.07 | Chloroflexi | Sphaerobacteridae | Sphaerobacterales | Sphaerobacterineae | *Sphaerobacter* |
| OTU1515\* | module hub | 2.857 | 0 | 8 | 1.14 | Gemmatimonadetes | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | *Gemmatimonas* |
| OTU1429\* | module hub | 3.41 | 0 | 6 | 0.05 | Actinobacteria | Actinobacteria | Streptosporangiales | Streptosporangiaceae | *Nonomuraea* |
| OTU438 | module hub | 2.728 | 0 | 6 | 0.03 | Planctomycetes | Planctomycetacia | Planctomycetales | Planctomycetaceae | *Unclassified* |
| OTU163\* | module hub | 2.558 | 0 | 6 | 0.05 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Sphingobacteriaceae | *Mucilaginibacter* |
| OTU626 | module hub | 3.05 | 0 | 5 | 0.32 | Acidobacteria | Acidobacteria | Subgroup 1 | Unclassified | *Unclassified* |
| OTU1656 | module hub | 2.966 | 0 | 5 | 0.09 | Actinobacteria | Actinobacteria | Pseudonocardiales | Pseudonocardiaceae | *Pseudonocardia* |
| OTU1464\* | module hub | 2.534 | 0 | 5 | 0.17 | Proteobacteria | Betaproteobacteria | Burkholderiales | Oxalobacteraceae | *Herbaspirillum* |
| OTU2874\* | module hub | 2.531 | 0 | 5 | 0.03 | Actinobacteria | Actinobacteria | Solirubrobacterales | Unclassified | *Unclassified* |
| OTU3094\* | module hub | 2.526 | 0 | 5 | 0.04 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Rhodanobacter* |
| OTU933\* | connector | -0.618 | 0.625 | 4 | 0.06 | Acidobacteria | Acidobacteria | Subgroup 4 | Unclassified | *Unclassified* |
| OTU1238\* | connector | -0.483 | 0.625 | 4 | 0.02 | Unclassified | Unclassified | Unclassified | Unclassified | *Unclassified* |
| OTU1663 | connector | -0.592 | 0.625 | 4 | 0.01 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Methylocystaceae | *Unclassified* |
| OTU2593\* | connector | -0.618 | 0.625 | 4 | 0.01 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU3018\* | connector | -0.618 | 0.625 | 4 | 0.04 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU3036 | connector | -0.289 | 0.625 | 4 | 0.01 | Actinobacteria | Actinobacteria | Acidimicrobiales | Acidimicrobiaceae | *Ferrimicrobium* |
| OTU3605 | connector | -0.979 | 0.667 | 3 | 0.14 | Planctomycetes | Phycisphaerae | WD2101 | Unclassified | *Unclassified* |
| CRB (31) | OTU94\* | module hub | 3.995 | 0 | 17 | 1.55 | Proteobacteria | Betaproteobacteria | Rhodocyclales | Rhodocyclaceae | *Unclassified* |
| OTU3395\* | module hub | 5.115 | 0 | 16 | 0.37 | Acidobacteria | Acidobacteria | Subgroup 3 | Unclassified | *Unclassified* |
| OTU2895\* | module hub | 5.493 | 0 | 15 | 0.04 | Chloroflexi | Chloroflexia | Kallotenuales | Unclassified | *Unclassified* |
| OTU138 | module hub | 3.376 | 0 | 15 | 0.11 | Actinobacteria | Actinobacteria | Solirubrobacterales | Patulibacteraceae | *Patulibacter* |
| OTU462 | module hub | 4.704 | 0 | 14 | 0.03 | Chloroflexi | Sphaerobacteridae | Sphaerobacterales | Sphaerobacterineae | *Sphaerobacter* |
| OTU2385 | module hub | 4.568 | 0.245 | 14 | 0.06 | Acidobacteria | Acidobacteria | Subgroup 6 | Unclassified | *Unclassified* |
| OTU1278\* | module hub | 3.851 | 0.142 | 13 | 0.04 | Actinobacteria | Actinobacteria | Kineosporiales | Kineosporiaceae | *Kineosporia* |
| OTU2026 | module hub | 2.757 | 0 | 13 | 0.37 | Chloroflexi | Sphaerobacteridae | Sphaerobacterales | Sphaerobacterineae | *Sphaerobacter* |
| OTU472\* | module hub | 4.332 | 153 | 12 | 0.02 | Chloroflexi | Chloroflexia | Kallotenuales | AKIW781 | *Unclassified* |
| OTU1911 | module hub | 3.459 | 0 | 11 | 0.03 | Chloroflexi | Chloroflexia | Chloroflexales | Chloroflexineae | *Chloroflexus* |
| OTU363\*\* | module hub | 3.131 | 0.18 | 10 | 0.06 | Proteobacteria | Alphaproteobacteria | Caulobacterales | Caulobacteraceae | *Caulobacter* |
| OTU1338 | module hub | 2.876 | 0 | 10 | 0.03 | Proteobacteria | Deltaproteobacteria | Myxococcales | Haliangiaceae | *Haliangium* |
| OTU949\* | module hub | 3.273 | 0.198 | 9 | 0.19 | Acidobacteria | Acidobacteria | Subgroup 6 | Unclassified | *Unclassified* |
| OTU768\* | module hub | 3.131 | 0 | 9 | 0.04 | Firmicutes | Bacilli | Bacillales | Bacillaceae | *Bcillus* |
| OTU3692 | module hub | 3.131 | 0 | 9 | 0.05 | Proteobacteria | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | *Pseudomonas* |
| OTU697 | module hub | 2.978 | 0 | 9 | 0.31 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | *Acidisphaera* |
| OTU3087\* | module hub | 2.651 | 0 | 9 | 0.03 | Proteobacteria | Deltaproteobacteria | Desulfuromonadales | Geobacteraceae | *Geobacter* |
| OTU2556\* | module hub | 2.591 | 0 | 8 | 0.03 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Dokdonella* |
| OTU143\* | connector | -0.257 | 0.719 | 8 | 0.08 | Proteobacteria | Deltaproteobacteria | Myxococcales | Haliangiaceae | *Haliangium* |
| OTU3162\* | module hub | 3.139 | 0 | 7 | 0.07 | Actinobacteria | Actinobacteria | Frankiales | Frankineae | *Unclassified* |
| OTU35 | module hub | 2.758 | 0.153 | 7 | 0.08 | Chloroflexi | TK10 | Unclassified | Unclassified | *Unclassified* |
| OTU933\* | module hub | 2.595 | 0.449 | 7 | 0.11 | Acidobacteria | Acidobacteria | Subgroup 4 | Unclassified | *Unclassified* |
| OTU2485 | module hub | 3.43 | 0 | 6 | 0.03 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU3399\* | module hub | 2.964 | 0 | 6 | 0.09 | Acidobacteria | Acidobacteria | Subgroup 10 | Unclassified | *Unclassified* |
| OTU780 | module hub | 2.529 | 0.278 | 6 | 0.03 | Firmicutes | Negativicutes | Selenomonadales | Veillonellaceae | *Pelosinus* |
| OTU3414 | connector | -0.257 | 0.667 | 6 | 0.23 | Nitrospirae | Nitrospira | Nitrospirales | Nitrospiraceae | *Nitrospira* |
| OTU1020\* | module hub | 3.048 | 0 | 5 | 0.02 | Proteobacteria | Betaproteobacteria | Nitrosomonadales | Nitrosomonadaceae | *Unclassified* |
| OTU38\* | connector | -0.647 | 0.625 | 4 | 0.56 | Actinobacteria | Actinobacteria | Frankiales | Geodermatophilaceae | *Blastococcus* |
| OTU172\* | connector | -0.796 | 0.625 | 4 | 0.20 | Gemmatimonadetes | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | *Gemmatimonas* |
| OTU813 | connector | -0.956 | 0.667 | 3 | 0.02 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU2921 | connector | -0.482 | 0.667 | 3 | 0.10 | Gemmatimonadetes | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | *Gemmatimonas* |
| CCR (12) | OTU2265\* | module hub | 2.822 | 0 | 14 | 0.68 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Rhodanobacter* |
| OTU2879 | module hub | 3.884 | 0.142 | 13 | 0.02 | Actinobacteria | Actinobacteria | Acidimicrobiales | Acidimicrobineae | *Unclassified* |
| OTU296\* | module hub | 3.439 | 0 | 13 | 0.03 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Unclassified* |
| OTU333\* | module hub | 3.439 | 0 | 13 | 0.03 | Actinobacteria | Rubrobacteria | Rubrobacterales | Rubrobacteraceae | *Unclassified* |
| OTU2769\* | module hub | 4.012 | 0 | 12 | 0.04 | Actinobacteria | Actinobacteria | Gaiellales | Gaiellaceae | *Gaiella* |
| OTU3362\* | module hub | 3.598 | 0 | 10 | 0.02 | Proteobacteria | Betaproteobacteria | Nitrosomonadales | Nitrosomonadaceae | *Unclassified* |
| OTU3219\* | module hub | 3.24 | 0 | 9 | 0.03 | Proteobacteria | Deltaproteobacteria | Myxococcales | Cystobacteraceae | *Anaeromyxobacter* |
| OTU3164\* | module hub | 2.855 | 0.219 | 8 | 0.06 | Acidobacteria | Acidobacteria | Subgroup 3 | Unclassified | *Unclassified* |
| OTU3464\* | module hub | 2.718 | 0.219 | 8 | 0.10 | Proteobacteria | Betaproteobacteria | Burkholderiales | Oxalobacteraceae | *Herbaspirillum* |
| OTU236 | module hub | 2.636 | 0 | 8 | 0.03 | Chloroflexi | Sphaerobacteridae | Sphaerobacterales | Sphaerobacterineae | *Sphaerobacter* |
| OTU983\* | module hub | 2.563 | 0 | 4 | 0.41 | Actinobacteria | Actinobacteria | Frankiales | Geodermatophilaceae | *Blastococcus* |
| OTU2216\* | connector | -0.151 | 0.625 | 4 | 0.06 | Planctomycetes | Planctomycetia | Planctomycetales | Unclassified | *Unclassified* |
| CRR (20) | OTU1947 | module hub | 2.572 | 0.142 | 13 | 0.33 | Acidobacteria | Acidobacteria | Subgroup 6 | Unclassified | *Unclassified* |
| OTU2603\* | module hub | 2.572 | 0.142 | 13 | 0.03 | Planctomycetes | Planctomycetia | Planctomycetales | Unclassified | *Unclassified* |
| OTU2056 | module hub | 2.572 | 0 | 12 | 0.01 | Planctomycetes | Planctomycetia | Planctomycetales | Unclassified | *Unclassified* |
| OTU1260 | module hub | 3.276 | 0.165 | 11 | 0.15 | Actinobacteria | Actinobacteria | Propionibacteriales | Nocardioidaceae | *Marmoricola* |
| OTU1039 | module hub | 4.304 | 0 | 9 | 0.04 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Sphingobacteriaceae | *Unclassified* |
| OTU2918\* | module hub | 4.039 | 0 | 9 | 0.06 | Actinobacteria | Actinobacteria | Micrococcales | Micrococcaceae | *Arthrobacter* |
| OTU128 | module hub | 2.663 | 0 | 9 | 0.02 | Planctomycetes | Planctomycetacia | Planctomycetales | Planctomycetaceae | *Singulisphaera* |
| OTU1521 | connector | 1.038 | 0.642 | 9 | 0.06 | Acidobacteria | Acidobacteria | Subgroup 3 | Unclassified | *Unclassified* |
| OTU2943\* | module hub | 3.189 | 0 | 8 | 0.06 | Proteobacteria | Alphaproteobacteria | Caulobacterales | Caulobacteraceae | *Phenylobacterium* |
| OTU2216\* | module hub | 3.231 | 0 | 6 | 0.02 | Planctomycetes | Planctomycetia | Planctomycetales | Unclassified | *Unclassified* |
| OTU2807 | module hub | 2.975 | 0 | 6 | 0.03 | Proteobacteria | Deltaproteobacteria | Myxococcales | Polyangiaceae | *Sorangium* |
| OTU1870\* | module hub | 2.961 | 0 | 6 | 0.07 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | *Sphingomonas* |
| OTU1931 | module hub | 2.954 | 0 | 6 | 0.13 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | *Lysobacter* |
| OTU2847 | module hub | 2.668 | 0.278 | 6 | 0.03 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadales | *Unclassified* |
| OTU3060 | module hub | 2.749 | 0 | 5 | 0.03 | Unclassified | Unclassified | Unclassified | Unclassified | *Unclassified* |
| OTU3061\* | module hub | 2.6 | 0 | 5 | 0.12 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Bradyrhizobiaceae | *Rhodopseudomonas* |
| OTU933 | module hub | 2.524 | 0 | 5 | 0.03 | Acidobacteria | Acidobacteria | Subgroup 4 | Unclassified | *Unclassified* |
| OTU3054 | connector | -0.776 | 0.64 | 5 | 0.01 | Armatimonadetes | Armatimonadia | Armatimonadales | Unclassified | *Unclassified* |
| OTU1331\* | connector | -1.213 | 0.75 | 4 | 0.01 | Actinobacteria | Actinobacteria | Pseudonocardiales | Pseudonocardiaceae | *Pseudonocardia* |
| OTU1345 | connector | -0.308 | 0.625 | 4 | 0.10 | Acidobacteria | Acidobacteria | Subgroup 7 | Unclassified | *Unclassified* |

\* indicated that OTUs identified as generalist OTUs in continuous cropping network but presented as specialist OTUs in rotation cropping network.