**Table S2.** Characterization of 16S rDNA clones in composite samples collected from tailings + compost treatment at time 0 (t0) and buffalo grass treatment at 3 months (t3).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Time** | **Putative Groupa** | **Clone ID**  **(Accession no.)** | **Closest GenBank relative (Accession no.)** | **Identity %**b | **Source** |
| **t0** |  |  |  |  |  |
|  | *Actinobacteria* | s2  (KF573465) | *Nocardiopsis* sp. CNP-957\_SD01 (EU214944.1) | 98 | marine sediment |
|  | *Actinobacteria* | s4  (KF573470) | *Nitriliruptor alkaliphilus* DSM 45188 strain ANL-iso2 (EF422408.1) | 97 | soda lake sediment |
|  | *Actinobacteria* | s7  (KF573472) | Uncultured bacterium clone AB-Mi79 (DQ347886.1) | 97 | soil-feeding termite mound |
|  | *Actinobacteria* | s16  (KF573467) | Uncultured *Actinobacterium*, clone: CGC65 (FJ486148.1) | 99 | root of copper-tolerant plant |
|  | *Actinobacteria* | s23  (KF573466) | Uncultured *Actinobacterium*, clone: Alchichica\_AQ2\_2\_1B\_75 (JN825539.1) | 97 | microbialites from alkaline lake |
|  | *Actinobacteria* | s24  (KF573474) | *Streptomyces hainanensis* type strain YIM 47672T (AM398645.1) | 97 | soil |
|  | *Bacteroidetes* | s9  (KF573475) | Uncultured bacterium, clone: TX4CB\_18 (FJ152887.1) | 97 | alkaline saline soils |
|  | *Bacteroidetes* | s10, s11  (KF573464) | Uncultured bacterium, clone: SN9 (EU735650.1) | 99 | pristine soil in oilfield |
|  | *Bacteroidetes* | s12  (KF573459) | Uncultured bacterium, clone: F2\_04X (GQ262972.1) | 98 | simulated radioactive waste site |
|  | *Bacteroidetes* | s15  (KF573463) | Uncultured bacterium, clone: DGS1-13 (GU056052.1) | 95 | soil above gas/oil field |
|  | *Bacteroidetes* | s17  (KF573469) | Uncultured *Bacteroidetes* , clone: BC\_COM484 (HQ727599.1) | 98 | petroleum-contaminated soil |
|  | *Bacteroidetes* | s19  (KF573471) | Uncultured *Bacteroidetes*, clone: EK\_CK642 (JN038257.1) | 99 | petroleum-contaminated soil |
|  | *Bacteroidetes* | s25  (KF573477) | Uncultured bacterium, clone: DGS1-13 (GU056052.1) | 97 | soil above gas/oil field |
|  | *Chloroflexi* | s14  (KF573460) | Uncultured *Chloroflexus* sp., clone: RC8C38 (EU921207.1) | 100 | compost bioreactor |
|  | *Alpha-proteobacteria* | s13  (KF573458) | Soil *Phyllobacteriaceae* BG.Sph.052 (DQ099469.1) | 99 | garden soil |
|  | *Gamma-proteobacteria* | s1  (KF573461) | Uncultured *Gamma-proteobacterium*, clone: Ppss\_Ma283 (JF421137.1) | 99 | phytoremediated saline-alkali soil |
|  | *Gamma-proteobacteria* | s8  (KF573476) | *Halomonas rifensis* strain HK31 (HM026177.1) | 99 | solar saltern |
|  | Unclassified | s3  (KF573468) | Uncultured bacterium, clone: SS1\_B\_03\_59 (EU050889.1) | 93 | sediment from Arctic |
|  | Unclassified | s5  (KF573473) | *Frankia* sp. strain FMr16 (AY502033.1) | 92 | root nodules |
|  | Unclassified | s18  (KF573462) | Uncultured bacterium, clone: TX4CB\_76 (FJ152945.1) | 94 | alkaline soil |
| **t3** |  |  |  |  |  |
|  | *Actinobacteria* | 16s6  (KF573490) | Uncultured bacterium, clone: SN46 16S (EU735662.1) | 100 | pristine soil in oil field |
|  | *Actinobacteria* | 16s24  (KF573487) | *Nocardiopsaceae* bacterium CXB832 (GU253338.1) | 97 | salt pond sediment |
|  | *Bacteroidetes* | 16s4  (KF573485) | *Flavobacterium* sp. MH51 (EU182879.1) | 100 | soil |
|  | *Bacteroidetes* | 16s15  (KF573484) | Uncultured *Bacteroidetes* bacterium, clone: 0-1\_6 (FJ517666.1) | 99 | epithelium of *Hydra magnipapillata* |
|  | *Bacteroidetes* | 16s2, 16s7c  (KF573463) | Uncultured bacterium, clone: DGS1-13 (GU056052.1) | 95 | soil above gas/oil field |
|  | *Chlamydiae* | 16s11  (KF573481) | *Chlamydia* sp. CH301104 (DQ011662.1) | 97 | Atlantic salmon in freshwater |
|  | *Alpha-proteobacteria* | 16s1  (KF573478) | *Brevundimonas nasdae* strain 14D (JF792080.1) | 100 | coral |
|  | *Alpha-proteobacteria* | 16s5  (KF573488) | Uncultured *Pseudolabrys* sp. clone BacBotLow045 (JF731561.1) | 100 | plant microbial fuel cell |
|  | *Alpha-proteobacteria* | 16s8  (KF573495) | *Sphingopyxis chilensis* strain T3AR9 (JF459975.1) | 100 | tap water |
|  | *Alpha-proteobacteria* | 16s16  (KF573486) | *Prosthecomicrobium consociatum* strain 11 (FJ560750.1) | 96 | soil |
|  | *Alpha-proteobacteria* | 16s25  (KF573489) | *Sphingopyxis* sp. AX-A (JQ418293.1) | 100 | activated sludge |
|  | *Beta-proteobacteria* | 16s10  (KF573479) | Uncultured *Achromobacter* sp., clone: F5oct.43 (GQ416247.1) | 100 | biological degreasing system |
|  | *Gamma-proteobacteria* | 16s3  (KF573483) | *Thermithiobacillus* sp. ParkerM (HM173631.1) | 99 | culture collection |
|  | *Gamma-proteobacteria* | 16s19  (KF573493) | *Pseudomonas* sp. UYSO21 (JF262576.1) | 100 | sugarcane stem |
|  | *Gamma-proteobacteria* | 16s13, 16s22  (KF573482) | Uncultured *Dyella* sp. clone sen190 (JN590679.1) | 100 | cluster roots |
|  | Unclassified | 16s9  (KF573494) | Uncultured bacterium, clone: B4 (JN882054.1) | 99 | crude oil sample |
|  | Unclassified | 16s18  (KF573491) | Uncultured bacterium clone (DQ888119.1) | 98 | yard waste compost |

a: Taxonomic assignment based on RDP II classifier with ≥90% confidence

bPercent identity of clone sequences with closest GenBank relative

c 16s2 and 16s7 are the same as s15