**Table S1:** 16S rRNA, *nifH*, and *amoA* gene clones amplified from DNA extracts of tailings plus 15% compost at t0 and Buffalo grass (BG) at t3. 16S rRNA clones were assigned to phyla with ≥90% confidence using the RDP II classifier with 16S rRNA training set 9. *nifH* and *amoA* clones were grouped in OTUs with ≥ 98% identity.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Sample Time** | **Putative Group** | **Clone Abundance** |
| **16S rRNA** | **t0** | *Actinobacteria* | 6 |
|  |  | *Bacteroidetes* | 8 |
|  |  | *Chloroflexi* | 1 |
|  |  | *Alpha-proteobacteria* | 1 |
|  |  | *Gamma-proteobacteria* | 2 |
|  |  | Unclassified | 3 |
|  |  | **TOTAL** | **21** |
| **16S rRNA** | **t3** | *Actinobacteria* | 2 |
|  |  | *Bacteroidetes* | 4 |
|  |  | *Chlamydiae* | 1 |
|  |  | *Alpha-proteobacteria* | 5 |
|  |  | *Beta-proteobacteria* | 1 |
|  |  | *Gamma-proteobacteria* | 4 |
|  |  | Unclassified | 2 |
|  |  | **TOTAL** | **19** |
| ***nifH*** | **t0** | OTU 1 | 7 |
|  |  | OTU 2 | 4 |
|  |  | OTU 3 | 2 |
|  |  | OTU 4 | 1 |
|  |  | **TOTAL** | **14** |
| ***nifH*** | **t3** | OTU 1 | 15 |
|  |  | **TOTAL** | **15** |
| ***amoA*** | **t0** | OTU 1 | 21 |
|  |  | OTU 2 | 1 |
|  |  | OTU 3 | 1 |
|  |  | OTU 4 | 1 |
|  |  | **TOTAL** | **24** |
| ***amoA*** | **t3** | OTU 1 | 19 |
|  |  | OTU 2 | 2 |
|  |  | **TOTAL** | **21** |