**Table S3. Identification and abundance of the major bacterial OTUs.** Basic information of the bacterial 14 most abundant OTUs and their relative abundance (percent) in unamended soil (C) and soil amended with untransformed DOR (DOR) or *C. floccosa*–transformed DOR (CORDOR) at 0 (T0), 30 (T1) and 60 (T2) days

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **OTU information** | | | | **Soil sample** | | | | | | | | |
| **OTU no.** | **Closest relative Eztaxon match**  **(GenBank accession no.), % similarity** | **Class** | **Nº seqs.1** | **CT0** | **DORT0** | **CORDORT0** | **CT1** | **DORT1** | **CORDORT1** | **CT2** | **DORT2** | **CORDORT2** |
| **1** | *Skermanella stibiiresistens* (HQ315828), 100 | *Alphaproteobacteria* | 619 | 12.4 | 14.4 | 17.4 | 13.7 | 10.5 | 6.8 | 10.8 | 7.1 | 6.8 |
| **2** | *Microvirga aerophila* (GQ421848), 100 | *Alphaproteobacteria* | 426 | 4.0 | 8.7 | 9.9 | 5.6 | 22.3 | 14.8 | 7.7 | 11.0 | 16.0 |
| **3** | Uncultured *Acidobacteria* (FJ152681), 100 | *Acidobacteria* | 348 | 10.3 | 9.2 | 8.3 | 12.1 | 13.8 | 17.8 | 10.3 | 8.6 | 9.5 |
| **4** | Uncultured *Dongia* sp. (FJ479524), 100 | *Alphaproteobacteria* | 312 | 10.3 | 11.2 | 11.5 | 11.2 | 13.5 | 7.1 | 12.8 | 14.7 | 7.7 |
| **5** | *Nocardioides mesophilus* (EF466117), 100 | *Actinobacteria* | 236 | 20.1 | 14.1 | 19.0 | 14.8 | 5.3 | 4.7 | 15.5 | 3.4 | 3.1 |
| **6** | Uncultured *Phenylobacterium* (AJ292592), 99 | *Alphaproteobacteria* | 186 | 0.0 | 3.8 | 4.3 | 2.2 | 21.0 | 22.0 | 2.7 | 21.5 | 22.6 |
| **7** | *Rhizobium rosettiformans* (EU781656), 100 | *Alphaproteobacteria* | 173 | 2.3 | 2.9 | 0.6 | 1.7 | 53.2 | 15.0 | 1.7 | 18.5 | 4.0 |
| **8** | Uncultured *Acidobacteria* (HM438150), 100 | *Acidobacteria* | 145 | 7.6 | 8.3 | 13.1 | 14.5 | 4.1 | 18.6 | 15.2 | 9.0 | 9.7 |
| **9** | *Skermanella aerolata* (DQ672568), 99 | *Alphaproteobacteria* | 145 | 12.4 | 16.6 | 18.6 | 14.5 | 12.4 | 7.6 | 8.3 | 4.1 | 5.5 |
| **10** | Uncultured *Acidobacteria* (FJ152840), 100 | *Acidobacteria* | 141 | 12.1 | 12.1 | 7.8 | 19.1 | 3.5 | 8.5 | 14.9 | 12.1 | 9.9 |
| **11** | Uncultured *Polyangiaceae* (EU134489), 86 | *Deltaproteobacteria* | 141 | 17.7 | 17.7 | 20.6 | 18.4 | 9.2 | 2.8 | 7.8 | 3.5 | 2.1 |
| **12** | Uncultured *Acidobacteria* (EF688341), 100 | *Acidobacteria* | 138 | 17.4 | 9.4 | 10.1 | 23.9 | 3.6 | 8.0 | 14.5 | 2.2 | 10.9 |
| **13** | Uncultured *Gemmatimonadaceae*(EU881161), 98 | *Gemmatimonadetes* | 138 | 14.5 | 6.5 | 8.0 | 14.5 | 3.6 | 7.2 | 20.3 | 9.4 | 15.9 |
| **14** | Uncultured *Alysiosphaera* (EU133443), 95 | *Alphaproteobacteria* | 134 | 9.7 | 9.0 | 20.9 | 9.7 | 6.7 | 5.2 | 11.9 | 16.4 | 10.4 |

1 total number of sequences in normalized samples