|  |  |  |  |
| --- | --- | --- | --- |
| Band | Organism | %Identity | Best match in GenBank  (Accession Number) |
| 1 | *Desulfotomaculum* sp. | 100 | NR\_044832.2 |
| 2 | *Blautia* sp. | 84 | NR\_112789.1 |
| 3 | *Clostridium* sp. | 78 | NR\_115345.1 |
| 4 | *Anaerostipes* sp. | 83 | NR\_117139.2 |
| 5 | *Lactobacillus* sp. | 98 | JQ805621.2 |
| 6 | *Lysinibacillus* sp. | 91 | NR\_146821.1 |
| 7 | *Staphylococcus* sp. | 100 | NR\_113351.1 |
| 8 | *Kurthia gibsonii* | 99 | NR\_119002.1 |
| 9 | *Exiguobacterium* sp. | 95 | NR\_075006.1 |
| 10 | *Bacillus* sp. | 83 | NR\_144712.1 |
| 11 | *Bacteroides* sp. | 96 | NR\_113069.1 |
| 12 | *Selenomonas* sp. | 86 | NR\_117597.1 |

**Table S1.** Molecular identification of band of bacteria during recovery by self-recovery, dilution with BE 8:2, 0.14% w/v NaOH, 0.50% w/v Ca(OH)2, and 8.0% w/v palm oil ash from DGGE analysis.