

Table S1. Relative abundance of the microbial community of site FAV2 in Pantelleria Island based on 16S rRNA gene sequences retrieved from the metagenome. Values are expressed in % and results of both DNA extraction method (CTAB and Power Soil kit) are shown separately.

| | 1-10 cm | | 10-15 cm | | 15-20 cm | |
|-------------------------|---------|--------|----------|--------|----------|--------|
| | CTAB | PS kit | CTAB | PS kit | CTAB | PS kit |
| Archaea | 45 | 18 | 47 | 55 | 73 | 60 |
| Bacteria | 55 | 82 | 53 | 45 | 27 | 40 |
| Archaea | | | | | | |
| Crenarchaeota | 0 | 0 | 0 | 4 | 0 | 0 |
| Euryarchaeota | 65 | 48 | 68 | 59 | 92 | 90 |
| Thaumarchaeota | 35 | 52 | 32 | 37 | 8 | 10 |
| Bacteria | | | | | | |
| Acidobacteria | 4.8 | 7.7 | 0.0 | 0.0 | 2.4 | 15.6 |
| Actinobacteria | 14.3 | 20.7 | 6.7 | 26.6 | 1.5 | 22.2 |
| Chloroflexi | 31.4 | 40.9 | 36.6 | 31.5 | 11.2 | 24.3 |
| Firmicutes | 33.0 | 13.6 | 33.3 | 18.2 | 62.9 | 17.6 |
| Proteobacteria | 5.8 | 4.2 | 6.2 | 7.0 | 11.9 | 4.6 |
| Verrucomicrobia | 8.4 | 6.0 | 14.5 | 9.1 | 8.6 | 6.6 |
| Other | 2.3 | 6.8 | 2.7 | 7.6 | 1.6 | 9.2 |
| Chloroflexi | | | | | | |
| AKIW781 | 5.4 | 0.0 | 0.0 | 3.9 | 0.0 | 3.8 |
| Ktedonobacteraceae | 61.9 | 88.2 | 72.9 | 46.4 | 69.6 | 58.4 |
| Thermobaculaceae | 0.0 | 2.1 | 0.0 | 0.0 | 0.0 | 0.0 |
| Uncultured | 32.7 | 9.7 | 27.1 | 49.7 | 30.4 | 37.8 |
| Firmicutes | | | | | | |
| Bacillaceae | 79.7 | 100.0 | 60.8 | 22.9 | 30.4 | 84.3 |
| Family XVII | 0.0 | 0.0 | 3.2 | 28.1 | 0.0 | 0.0 |
| Paenibacillaceae | 0.0 | 0.0 | 6.6 | 24.5 | 0.0 | 0.0 |
| Thermoanaerobacteraceae | 20.3 | 0.0 | 23.6 | 0.0 | 61.8 | 5.2 |
| TSAC18 | 0.0 | 0.0 | 0.0 | 0.0 | 1.2 | 0.0 |
| TTA-B61 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 |
| Uncultured | 0.0 | 0.0 | 5.8 | 24.5 | 5.6 | 10.5 |
| Proteobacteria | | | | | | |
| Burkholderiaceae | 0.0 | 12.9 | 13.9 | 38.5 | 6.5 | 0.0 |
| Methylococcaceae | 0.0 | 36.6 | 38.7 | 0.0 | 0.0 | 100.0 |
| Methylomonaceae | 42.9 | 0.0 | 0.0 | 0.0 | 21.5 | 0.0 |
| Rhizobiaceae | 8.3 | 12.9 | 20.2 | 23.0 | 18.7 | 0.0 |
| Sphingomonadaceae | 48.8 | 37.6 | 0.0 | 38.5 | 16.1 | 0.0 |
| Xanthomonadaceae | 0.0 | 0.0 | 27.2 | 0.0 | 37.1 | 0.0 |
| Verrucomicrobia | | | | | | |
| Chthoniobacteraceae | 14.7 | 19.2 | 8.4 | 18.8 | 0.0 | 58.2 |
| Methylacidiphilaceae | 85.3 | 80.8 | 91.6 | 81.2 | 100.0 | 41.8 |