

Fig.S1 Scheme of the experimental set up used in the abiotic mineral weathering experiment. Reactors contained 3 g of calcite or apatite or obsidian particles. The reactors were placed on a rack revolving over 180° in 2 s. At both extremities of the reactors, 0.5 μm nylon filters were placed to avoid mineral particles loss. A flow rate of 2 ml.h⁻¹ was maintained by a peristaltic pump.

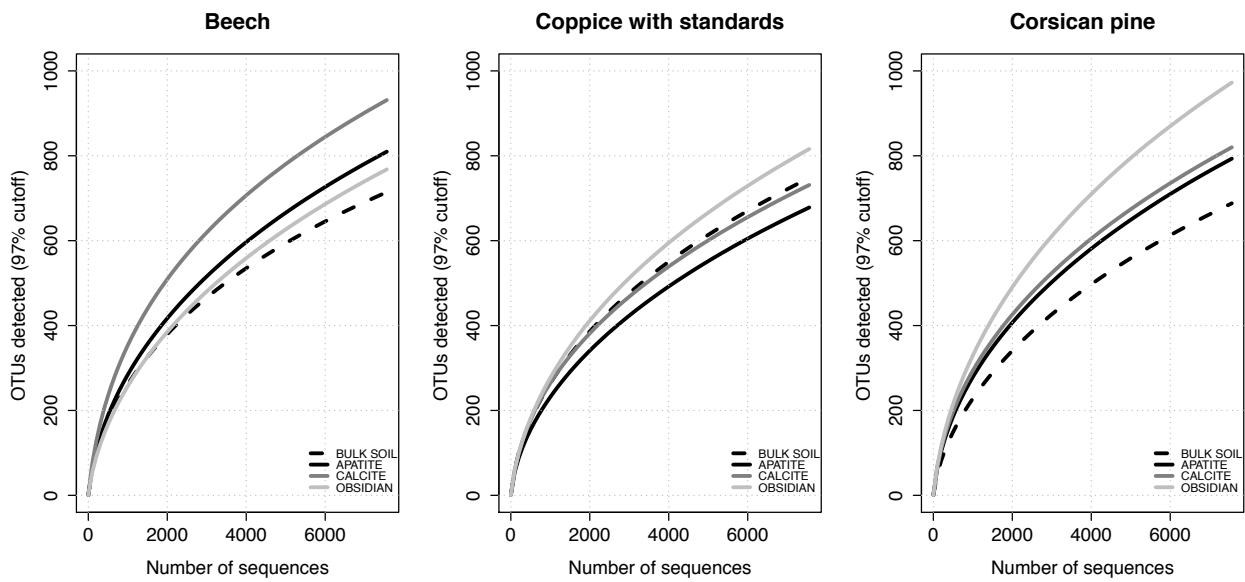


Fig.S2 Rarefaction curves indicating the number of operational taxonomic units (OTUs) at a genetic distance of 3% according to pyrosequencing data analyses, under beech, coppice with standards and corsican pine stands. Dotted lines refer to bulk soil samples and full lines to minerals samples.

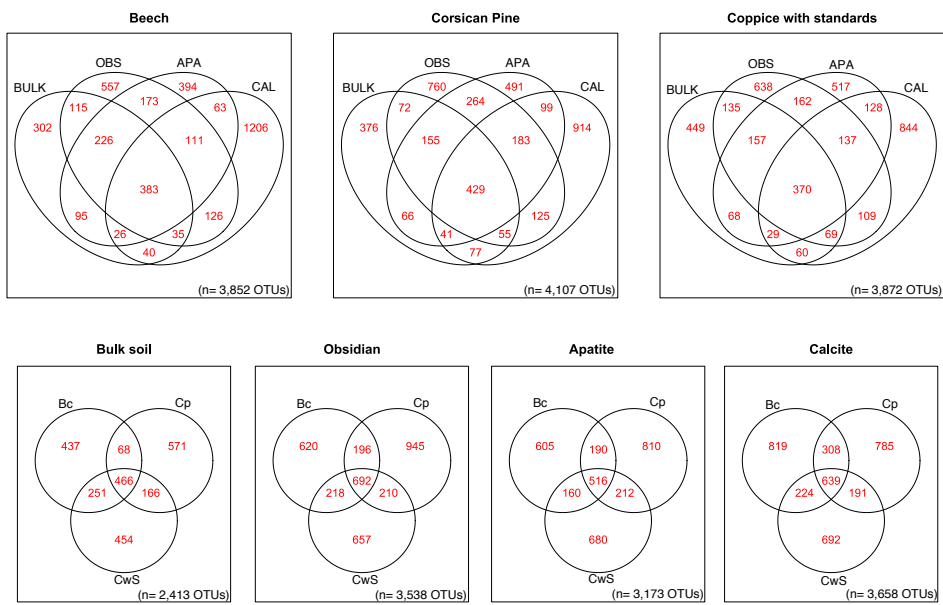


Fig.S3A Venn diagrams of the shared 16S rRNA gene based OTUs between the different sample types under a same tree stand and between the different tree stands for a same sample type. The number of OTUs (n) in each group is indicated. BULK: bulk soil, OBS: obsidian, APA: apatite, CAL: calcite; Bc: beech; Cp: corsican pine and CwS: coppice with standards.

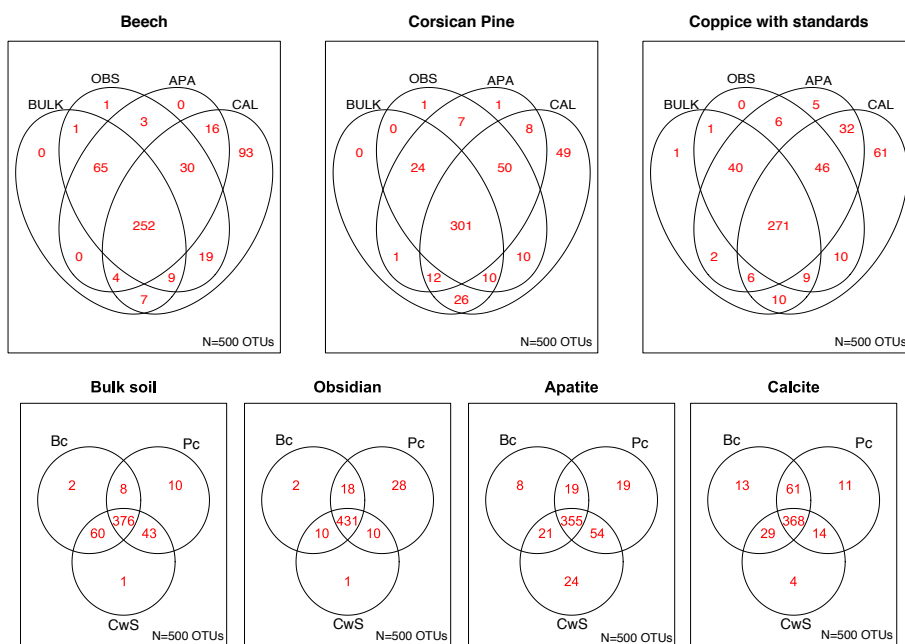


Fig.S3B Venn diagrams of the top 500 OTUs between the different sample types under a same tree stand and between the different tree stands for a same sample type. BULK: bulk soil, OBS: obsidian, APA: apatite, CAL: calcite; Bc: beech; Cp: corsican pine and CwS: coppice with standards.

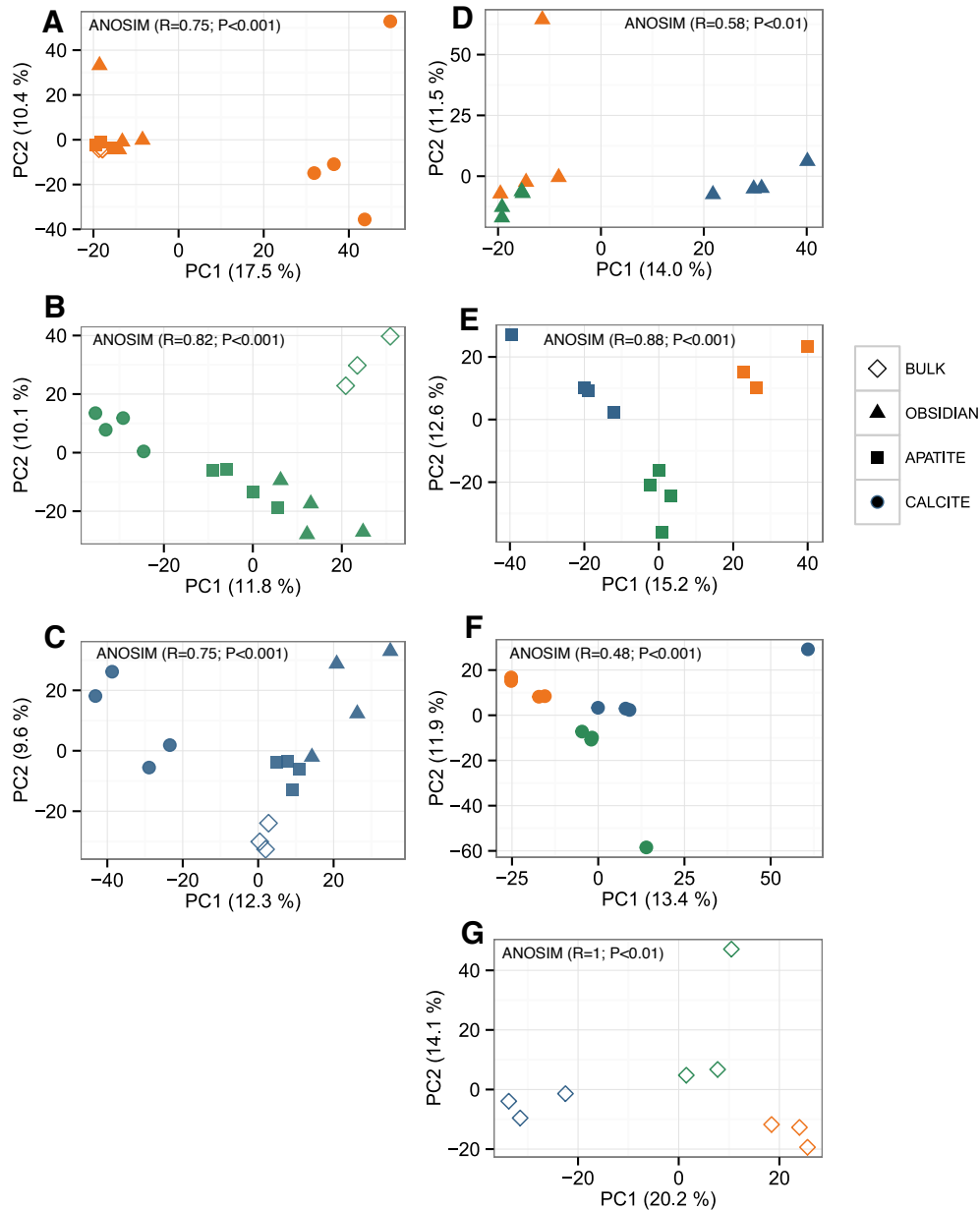


Fig.S4 Multivariate analysis of the bacterial communities based on the relative abundance of bacterial OTUs estimated by 16S rRNA gene pyrosequencing analysis. Multivariate analysis was conducted separately for each tree stand: A) beech, B) coppice with standards and C) corsican pine. The same analysis was conducted for each mineral type excluding the bulk soil samples: D) obsidian, E) apatite and F) calcite. At last, comparison of the bulk soil sample was done and is presented in panel G. For legibility the samples are presented as follow: beech (orange), coppice with standards (green) and corsican pine (blue) stands, calcite samples (round), apatite samples (square), obsidian samples (triangle) and bulk soil samples (open diamond). The percentages of the total variance explained by the first two axes PC1 and PC2 are presented on each graph. ANOSIM analyses have been done for each dataset presented in the different panels.

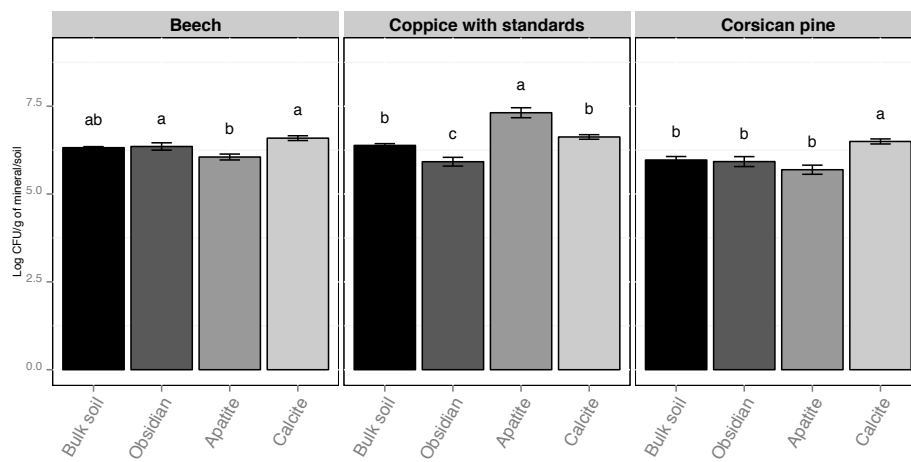


Fig.S5 Density of the culturable bacterial communities from bulk soil and mineral samples. Densities were expressed as log₁₀ CFU g⁻¹ dry weight of soil/mineral +/- sem, under beech, coppice with standards and corsican pine stands. Under a same tree stand, error bars with different letters are significantly different according to a one-factor ANOVA and a Tukey post hoc test (P < 0.05).

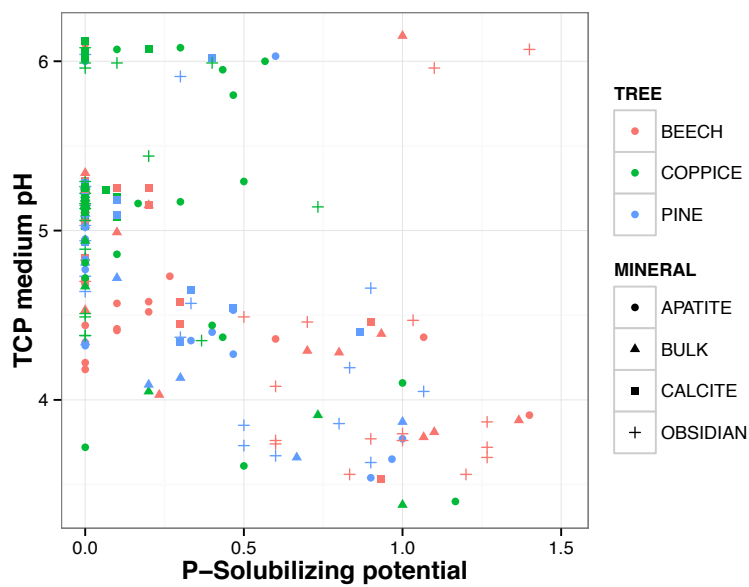


Fig.S6 Relationship between inorganic phosphorus solubilization and TCP medium acidification. Bacterial strains were grown 4 days at 25°C and medium acidification was estimated with Bromocresol green. The origin of the samples is presented as follow: beech (red), coppice with standards (green) and corsican pine (blue) stands, calcite samples (square), apatite samples (round), obsidian samples (cross) and bulk soil samples (triangle).

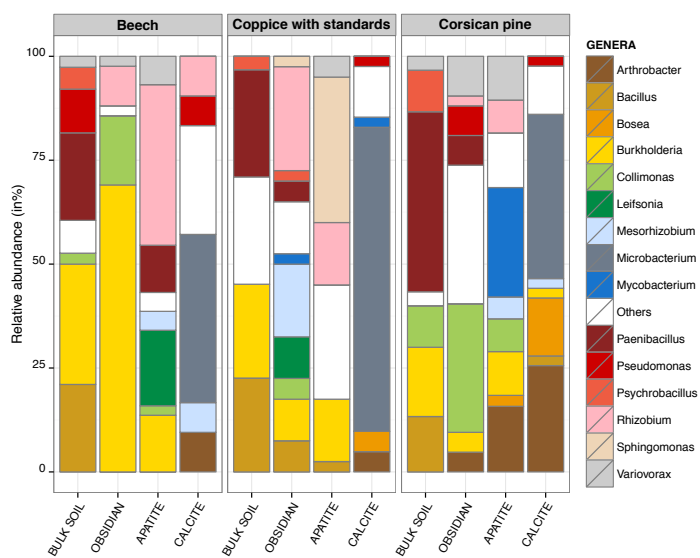


Fig.S7 Relative distribution of the partial 16S rRNA gene sequences of bacterial isolates at the genus level. For each treatment, the data presented are the mean of 3 independent replicates. Genera containing few representatives were grouped under the category "Others".

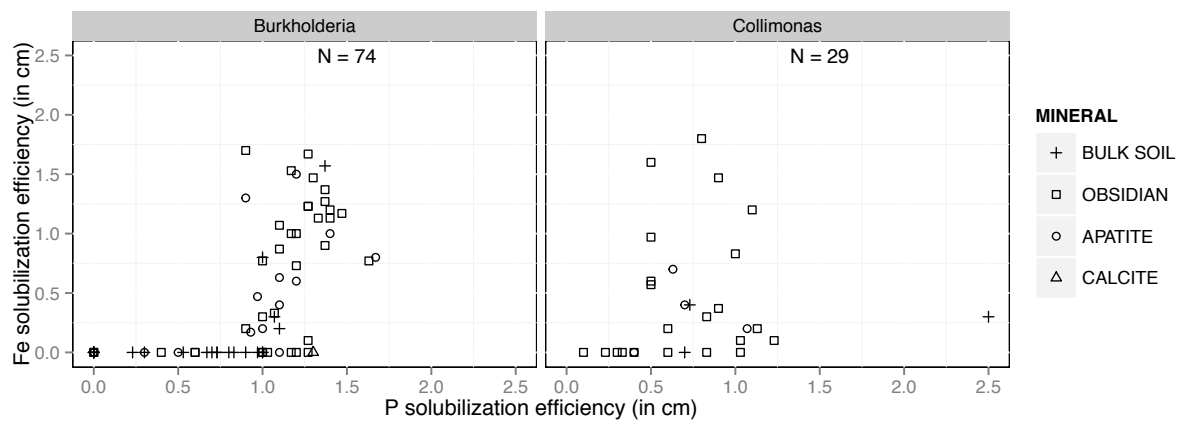


Fig.S8 Relationship between P- solubilization and Fe-mobilisation among bacterial strains that affiliated the *Burkholderia* and *Collimonas* genera.

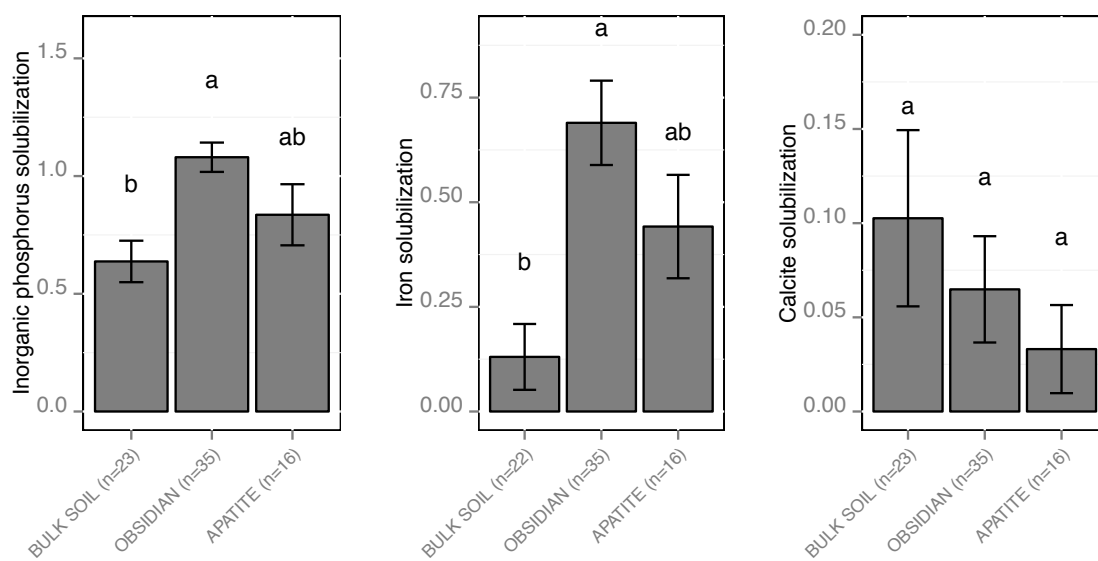


Fig.S9 Relative efficacy of *Burkholderia* isolates to solubilise phosphorus and calcite and to mobilise iron according to their sample origin. One-factor ANOVA analysis was carried out to compare efficacies within a same tree stand. Different letters indicate significant differences ($P < 0.05$).

Table.S1. Relative abundance (in %) of the major bacterial genera (>0.25%) that varied significantly between bulk soil and mineral samples for each tree stands. Each value is the mean of biological replicates (± Standard Error of the Mean).

| Phylum | Genus | BEECH | | | | | COPPICE | | | | | PINE | | | | |
|-----------------|-------------------|--------------------|------------------------|-----------------------|-----------------------|-------------|--------------------|------------------------|-----------------------|-----------------------|-------------|--------------------|------------------------|-----------------------|-----------------------|------|
| | | BULK mean ± sem | OBSIDIAN mean ± sem | APATITE mean ± sem | CALCITE mean ± sem | pval | BULK mean ± sem | OBSIDIAN mean ± sem | APATITE mean ± sem | CALCITE mean ± sem | pval | BULK mean ± sem | OBSIDIAN mean ± sem | APATITE mean ± sem | CALCITE mean ± sem | pval |
| Acidobacteria | Gp1 | 13.41 ± 0.97 | 5.48 ± 0.44 | 7.04 ± 1.66 | 0.58 ± 0.11 | *** | 8.99 ± 0.90 | 5.26 ± 0.98 | 2.22 ± 0.88 | 0.52 ± 0.18 | *** | 6.74 ± 1.29 | 5.35 ± 0.61 | 4.46 ± 1.49 | 1.19 ± 0.38 | *** |
| | Gp10 | 0.30 ± 0.21 | 0.10 ± 0.02 | 0.20 ± 0.05 | 0.16 ± 0.07 | | 0.49 ± 0.26 | 0.24 ± 0.13 | 0.10 ± 0.06 | 0.01 ± 0.01 | * | 0.74 ± 0.23 | 0.79 ± 0.12 | 1.04 ± 0.52 | 0.10 ± 0.04 | * |
| | Gp2 | 25.63 ± 1.63 | 3.55 ± 0.64 | 5.36 ± 0.76 | 0.52 ± 0.07 | *** | 13.35 ± 5.84 | 2.80 ± 0.59 | 1.12 ± 0.47 | 0.46 ± 0.17 | *** | 17.46 ± 6.70 | 6.59 ± 0.69 | 4.73 ± 1.13 | 2.32 ± 0.85 | *** |
| | Gp3 | 0.95 ± 0.10 | 0.17 ± 0.08 | 0.29 ± 0.09 | 0.02 ± 0.01 | *** | 0.69 ± 0.29 | 0.18 ± 0.02 | 0.06 ± 0.02 | 0.03 ± 0.00 | *** | 0.63 ± 0.28 | 0.42 ± 0.04 | 0.32 ± 0.12 | 0.15 ± 0.08 | *** |
| | Bryobacter | 0.88 ± 0.07 | 0.58 ± 0.15 | 0.69 ± 0.14 | 1.11 ± 0.17 | | 0.55 ± 0.19 | 0.40 ± 0.04 | 0.37 ± 0.20 | 0.74 ± 0.12 | *** | 0.51 ± 0.09 | 0.80 ± 0.03 | 0.61 ± 0.07 | 0.71 ± 0.15 | * |
| | Gp5 | 0.19 ± 0.06 | 0.08 ± 0.03 | 0.08 ± 0.04 | 0.29 ± 0.03 | * | 0.04 ± 0.04 | 0.03 ± 0.01 | 0.03 ± 0.03 | 0.04 ± 0.04 | | 0.13 ± 0.02 | 0.12 ± 0.03 | 0.03 ± 0.01 | 0.05 ± 0.03 | * |
| | Gp7 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.02 ± 0.02 | 1.50 ± 1.34 | | 0.02 ± 0.01 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | | 0.00 ± 0.00 | 0.01 ± 0.00 | 0.08 ± 0.08 | 0.19 ± 0.08 | *** |
| Actinobacteria | Geothrix | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.00 ± 0.00 | | 0.07 ± 0.05 | 0.36 ± 0.09 | 0.22 ± 0.11 | 0.05 ± 0.05 | * |
| | Ilumatobacter | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.06 ± 0.06 | 0.25 ± 0.04 | ** | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.22 ± 0.13 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.18 ± 0.05 | *** |
| | Phycococcus | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.44 ± 0.15 | ** | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.10 ± 0.10 | 4.61 ± 4.27 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.02 ± 0.02 | 0.07 ± 0.03 | *** |
| | Arthrobacter | 0.00 ± 0.00 | 0.04 ± 0.01 | 0.07 ± 0.02 | 4.85 ± 1.23 | *** | 0.20 ± 0.19 | 0.22 ± 0.17 | 0.32 ± 0.28 | 3.16 ± 0.51 | *** | 0.15 ± 0.12 | 0.26 ± 0.12 | 3.02 ± 1.62 | 1.37 ± 0.53 | * |
| | Mycobacterium | 0.71 ± 0.20 | 1.68 ± 0.76 | 3.44 ± 0.95 | 0.90 ± 0.16 | | 1.10 ± 0.17 | 1.44 ± 0.42 | 1.00 ± 0.19 | 1.30 ± 0.34 | | 0.78 ± 0.54 | 1.31 ± 0.50 | 2.15 ± 0.44 | 1.05 ± 0.58 | * |
| | Marmoricola | 0.02 ± 0.02 | 0.10 ± 0.04 | 0.09 ± 0.02 | 0.31 ± 0.02 | *** | 0.11 ± 0.11 | 0.25 ± 0.09 | 0.35 ± 0.24 | 0.34 ± 0.07 | * | 0.09 ± 0.07 | 0.17 ± 0.05 | 2.16 ± 1.74 | 0.71 ± 0.41 | * |
| | Nocardiodides | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.20 ± 0.20 | 1.25 ± 0.34 | ** | 0.00 ± 0.00 | 0.01 ± 0.00 | 0.07 ± 0.07 | 0.67 ± 0.45 | | 0.01 ± 0.00 | 0.00 ± 0.00 | 0.61 ± 0.61 | 0.44 ± 0.17 | |
| Armatimonadetes | Streptomyces | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.25 ± 0.23 | 0.10 ± 0.03 | | 0.02 ± 0.01 | 0.68 ± 0.61 | 7.24 ± 3.76 | 0.05 ± 0.02 | * | 0.18 ± 0.18 | 0.26 ± 0.16 | 1.19 ± 0.65 | 0.10 ± 0.05 | |
| | Conexibacter | 0.07 ± 0.01 | 0.17 ± 0.04 | 0.42 ± 0.13 | 0.01 ± 0.01 | * | 0.15 ± 0.04 | 0.13 ± 0.05 | 0.06 ± 0.04 | 0.01 ± 0.00 | | 0.01 ± 0.01 | 0.05 ± 0.02 | 0.02 ± 0.02 | 0.02 ± 0.00 | |
| | gp5 | 0.19 ± 0.06 | 0.39 ± 0.08 | 0.40 ± 0.13 | 0.60 ± 0.18 | | 0.26 ± 0.02 | 0.47 ± 0.13 | 0.31 ± 0.13 | 0.78 ± 0.24 | | 0.23 ± 0.11 | 0.58 ± 0.11 | 0.43 ± 0.20 | 0.56 ± 0.05 | * |
| | Ohtaekwangia | 0.03 ± 0.02 | 0.05 ± 0.01 | 0.20 ± 0.11 | 1.50 ± 0.56 | * | 0.09 ± 0.03 | 0.17 ± 0.10 | 0.62 ± 0.52 | 0.42 ± 0.19 | | 0.12 ± 0.05 | 0.37 ± 0.11 | 0.22 ± 0.12 | 0.46 ± 0.09 | ** |
| | Fluviicola | 0.00 ± 0.00 | 0.02 ± 0.02 | 0.00 ± 0.00 | 0.12 ± 0.04 | * | 0.00 ± 0.00 | 0.15 ± 0.15 | 0.21 ± 0.21 | 0.72 ± 0.71 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.02 ± 0.02 | ** |
| | Chitinophaga | 0.05 ± 0.02 | 0.01 ± 0.01 | 0.02 ± 0.02 | 0.61 ± 0.17 | ** | 0.13 ± 0.05 | 0.73 ± 0.68 | 6.76 ± 2.33 | 0.63 ± 0.61 | *** | 0.05 ± 0.03 | 0.03 ± 0.01 | 0.08 ± 0.03 | 0.02 ± 0.00 | |
| | Ferruginibacter | 0.04 ± 0.02 | 0.12 ± 0.04 | 0.13 ± 0.04 | 2.94 ± 0.62 | *** | 0.07 ± 0.05 | 0.18 ± 0.04 | 1.09 ± 0.89 | 6.68 ± 2.94 | ** | 0.07 ± 0.05 | 0.08 ± 0.04 | 0.48 ± 0.46 | 2.59 ± 0.57 | *** |
| Bacteroidetes | Terrimonas | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.02 ± 0.02 | 0.23 ± 0.07 | ** | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.07 ± 0.07 | 0.25 ± 0.14 | * | 0.02 ± 0.02 | 0.00 ± 0.00 | 0.08 ± 0.08 | 1.79 ± 0.08 | *** |
| | Mucilagibacter | 0.82 ± 0.11 | 4.37 ± 1.19 | 2.47 ± 0.72 | 0.14 ± 0.01 | ** | 4.23 ± 3.72 | 8.30 ± 1.50 | 3.86 ± 0.98 | 0.21 ± 0.12 | ** | 0.94 ± 0.77 | 4.09 ± 1.20 | 2.45 ± 0.64 | 0.15 ± 0.04 | ** |
| | Penobacter | 0.00 ± 0.00 | 0.06 ± 0.02 | 0.02 ± 0.01 | 0.24 ± 0.10 | * | 0.00 ± 0.00 | 0.57 ± 0.56 | 1.92 ± 0.96 | 0.07 ± 0.01 | * | 0.02 ± 0.02 | 0.12 ± 0.05 | 0.16 ± 0.14 | 0.07 ± 0.05 | |
| | Nitrospira | 0.02 ± 0.02 | 0.03 ± 0.03 | 0.12 ± 0.12 | 1.04 ± 0.07 | *** | 0.12 ± 0.05 | 0.01 ± 0.01 | 0.26 ± 0.26 | 0.20 ± 0.13 | | 0.40 ± 0.20 | 0.13 ± 0.05 | 0.36 ± 0.23 | 1.37 ± 0.40 | ** |
| | Brevundimonas | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.14 ± 0.10 | | 0.00 ± 0.00 | 0.04 ± 0.03 | 0.11 ± 0.09 | 0.37 ± 0.04 | *** | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.07 ± 0.07 | 0.19 ± 0.05 | *** |
| | Phenyllobacterium | 1.15 ± 0.09 | 2.29 ± 0.47 | 1.95 ± 0.57 | 0.39 ± 0.10 | * | 0.93 ± 0.32 | 2.15 ± 0.67 | 1.16 ± 0.50 | 0.35 ± 0.17 | * | 0.90 ± 0.57 | 3.01 ± 0.06 | 1.44 ± 0.43 | 0.64 ± 0.12 | *** |
| | Afipia | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.02 ± 0.01 | 0.49 ± 0.18 | ** | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.24 ± 0.24 | 0.56 ± 0.17 | *** | 0.01 ± 0.01 | 0.03 ± 0.03 | 0.15 ± 0.11 | 0.22 ± 0.03 | *** |
| Proteobacteria | Bosea | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.50 ± 0.23 | * | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.33 ± 0.14 | 0.49 ± 0.15 | ** | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.20 ± 0.20 | 0.59 ± 0.22 | *** |
| | Bradyrhizobium | 0.68 ± 0.27 | 0.71 ± 0.20 | 1.03 ± 0.34 | 0.16 ± 0.07 | | 0.68 ± 0.23 | 0.82 ± 0.25 | 0.99 ± 0.37 | 0.51 ± 0.05 | | 0.49 ± 0.10 | 0.60 ± 0.11 | 0.87 ± 0.39 | 0.19 ± 0.09 | ** |
| | Devosia | 0.00 ± 0.00 | 0.01 ± 0.00 | 0.00 ± 0.00 | 0.60 ± 0.10 | *** | 0.00 ± 0.00 | 0.01 ± 0.00 | 0.91 ± 0.52 | 0.75 ± 0.42 | | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.19 ± 0.18 | 0.86 ± 0.12 | *** |
| | Hypomicrobium | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.73 ± 0.31 | * | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.14 ± 0.08 | 0.43 ± 0.18 | ** | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.01 ± 0.01 | 0.10 ± 0.05 | * |
| | Rhizobium | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.04 ± 0.03 | 0.03 ± 0.01 | | 0.00 ± 0.00 | 0.20 ± 0.18 | 1.09 ± 0.81 | 0.04 ± 0.02 | | 0.01 ± 0.01 | 0.05 ± 0.01 | 0.04 ± 0.01 | 0.03 ± 0.02 | * |
| | Novosphingobium | 0.00 ± 0.00 | 0.03 ± 0.02 | 0.03 ± 0.02 | 0.54 ± 0.09 | *** | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.07 ± 0.04 | 0.92 ± 0.43 | * | 0.02 ± 0.02 | 0.09 ± 0.02 | 0.11 ± 0.05 | 3.67 ± 3.44 | * |
| | Sphingomonas | 0.01 ± 0.01 | 0.05 ± 0.02 | 0.07 ± 0.01 | 2.64 ± 0.78 | ** | 0.00 ± 0.00 | 0.33 ± 0.30 | 0.80 ± 0.32 | 0.64 ± 0.33 | * | 0.06 ± 0.06 | 0.08 ± 0.03 | 0.55 ± 0.53 | 1.08 ± 0.42 | ** |
| | Burkholderia | 0.66 ± 0.03 | 3.50 ± 0.54 | 2.60 ± 0.73 | 0.15 ± 0.03 | ** | 1.11 ± 0.70 | 2.62 ± 0.73 | 2.49 ± 0.71 | 1.10 ± 0.03 | *** | 0.89 ± 0.50 | 1.20 ± 0.13 | 1.28 ± 0.38 | 0.15 ± 0.06 | ** |
| | Aquabacterium | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.04 ± 0.04 | 0.34 ± 0.04 | *** | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.02 ± 0.00 | 0.18 ± 0.09 | | 0.03 ± 0.03 | 0.03 ± 0.01 | 0.02 ± 0.02 | 0.27 ± 0.04 | ** |
| | Collimonas | 0.03 ± 0.01 | 0.21 ± 0.16 | 0.21 ± 0.05 | 0.01 ± 0.01 | | 0.07 ± 0.06 | 0.07 ± 0.01 | 0.24 ± 0.12 | 0.00 ± 0.00 | | 0.30 ± 0.29 | 0.50 ± 0.16 | 0.44 ± 0.26 | 0.03 ± 0.02 | * |
| | Massilia | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.01 ± 0.00 | 0.29 ± 0.15 | | 0.00 ± 0.00 | 0.01 ± 0.00 | 0.01 ± 0.01 | 0.15 ± 0.06 | * | 0.00 ± 0.00 | 0.02 ± 0.01 | 0.08 ± 0.06 | 0.21 ± 0.08 | ** |
| | Nitrospiro | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.12 ± 0.08 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.50 ± 0.50 | 0.52 ± 0.14 | * | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.07 ± 0.05 | |
| | Rhizobactera | 0.01 ± 0.01 | 0.03 ± 0.01 | 0.07 ± 0.06 | 0.47 ± 0.02 | *** | 0.01 ± 0.01 | 0.03 ± 0.01 | 0.02 ± 0.02 | 0.24 ± 0.01 | * | 0.02 ± 0.02 | 0.05 ± 0.02 | 0.24 ± 0.19 | 0.51 ± 0.14 | *** |
| | Nevskia | 0.04 ± 0.00 | 1.05 ± 0.55 | 0.86 ± 0.30 | 0.16 ± 0.03 | | 2.06 ± 1.99 | 1.83 ± 0.72 | 1.24 ± 0.50 | 0.02 ± 0.02 | * | 0.85 ± 0.83 | 2.78 ± 0.73 | 2.98 ± 1.19 | 4.44 ± 2.10 | * |
| | Singularimonas | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | 0.25 ± 0.06 | ** | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.01 ± 0.01 | | 0.00 ± 0.00 | 0.00 ± 0.00 | 0.02 ± 0.02 | 0.33 ± 0.27 | |
| | Steroidobacter | 0.04 ± 0.01 | 0.28 ± 0.12 | 0.45 ± 0.13 | 0.08 ± 0.03 | ** | 0.04 ± 0.02 | 0.18 ± 0.08 | 0.04 ± 0.01 | 0.00 ± 0.00 | * | 0.10 ± 0.02 | 0.27 ± 0.11 | 0.21 ± 0.08 | 0.13 ± 0.06 | * |
| | Arenimonas | 0.01 ± 0.01 | 0.00 ± 0.00 | 0.04 ± 0.04 | 0.52 ± 0.10 | *** | 0.01 ± 0.00 | 0.01 ± 0.00 | 0.51 ± 0.51 | 0.76 ± 0.37 | * | 0.03 ± 0.01 | 0.01 ± 0.01 | 1.03 ± 1.02 | 0.93 ± 0.38 | * |
| Dakdonella | 0.00 ± 0.00 | 0.08 ± 0.04 | 0.13 ± 0.04 | 0.01 ± 0.01 | * | 0.19 ± 0.17 | 0.52 ± 0.29 | 0.74 ± 0.33 | 0.01 ± 0.00 | *** | 0.01 ± 0.01 | 0.05 ± 0.01 | 0.26 ± 0.10 | 0.03 ± 0.02 | * | |
| Dyella | 0.32 ± 0.01 | 0.76 ± 0.18 | 1.46 ± 0.61 | 0.07 ± 0.01 | | 1.49 ± 0.85 | 1.44 ± 0.08 | 0.97 ± 0.16 | 0.18 ± 0.02 | ** | 0.34 ± 0.23 | 0.39 ± 0.10 | 0.49 ± 0.14 | 0.03 ± 0.03 | ** | |

Table.S2. Relative abundance (in %) of the major bacterial genera (>0.25%) that varied significantly between the three soil types (beech, coppice with standards and corsican pine) in bulk soil, obsidian, apatite and calcite samples. Each value is the mean of biological replicates (\pm Standard Error of the Mean).

| phylum | genus | BULK | | | | | | OBSIDIAN | | | | | | APATITE | | | | | | CALCITE | | | | | | | | | |
|----------------|------------------|------------|------------|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------|------------|------------|------------|------------|------------|------------|------|------------|------------|------------|------------|------------|------------|------|
| | | BEECH | | COPPICE | | PINE | | pval | BEECH | | COPPICE | | PINE | | pval | BEECH | | COPPICE | | PINE | | pval | BEECH | | COPPICE | | PINE | | Pval |
| | | mean | sem | mean | sem | mean | sem | | mean | sem | mean | sem | mean | sem | | mean | sem | mean | sem | mean | sem | | mean | sem | mean | sem | mean | sem | |
| Acidobacteria | Gp1 | 13.41 | \pm 0.97 | 9.86 | \pm 0.47 | 6.95 | \pm 1.13 | ** | 5.48 | \pm 0.44 | 5.85 | \pm 1.11 | 5.61 | \pm 0.38 | * | 7.04 | \pm 1.66 | 3.11 | \pm 1.08 | 5.23 | \pm 0.89 | * | 0.58 | \pm 0.11 | 0.77 | \pm 0.28 | 1.03 | \pm 0.32 | |
| | Gp10 | 0.30 | \pm 0.21 | 0.59 | \pm 0.18 | 0.95 | \pm 0.08 | | 0.10 | \pm 0.02 | 0.25 | \pm 0.12 | 0.61 | \pm 0.13 | * | 0.20 | \pm 0.05 | 0.09 | \pm 0.06 | 1.29 | \pm 0.41 | * | 0.16 | \pm 0.07 | 0.02 | \pm 0.01 | 0.09 | \pm 0.03 | |
| | Gp13 | 0.10 | \pm 0.06 | 0.15 | \pm 0.05 | 0.32 | \pm 0.00 | | 0.01 | \pm 0.01 | 0.01 | \pm 0.01 | 0.06 | \pm 0.01 | * | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.07 | \pm 0.01 | *** | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.01 | \pm 0.01 | |
| | Gp2 | 25.61 | \pm 1.63 | 17.95 | \pm 1.58 | 24.09 | \pm 0.56 | * | 3.55 | \pm 0.64 | 2.83 | \pm 0.57 | 6.32 | \pm 0.89 | * | 5.36 | \pm 0.76 | 1.23 | \pm 0.50 | 5.61 | \pm 0.50 | *** | 0.52 | \pm 0.07 | 0.67 | \pm 0.24 | 2.15 | \pm 0.63 | |
| | Gp3 | 0.95 | \pm 0.10 | 0.95 | \pm 0.03 | 0.99 | \pm 0.24 | | 0.17 | \pm 0.08 | 0.15 | \pm 0.02 | 0.38 | \pm 0.07 | * | 0.29 | \pm 0.09 | 0.09 | \pm 0.05 | 0.39 | \pm 0.08 | * | 0.02 | \pm 0.01 | 0.05 | \pm 0.02 | 0.13 | \pm 0.06 | |
| | Gp5 | 0.88 | \pm 0.07 | 0.77 | \pm 0.06 | 0.65 | \pm 0.11 | | 0.58 | \pm 0.15 | 0.33 | \pm 0.06 | 0.69 | \pm 0.10 | * | 0.69 | \pm 0.14 | 0.24 | \pm 0.07 | 0.67 | \pm 0.10 | * | 1.11 | \pm 0.17 | 0.79 | \pm 0.10 | 0.68 | \pm 0.11 | |
| Actinobacteria | Geothrix | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.01 | \pm 0.01 | | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.33 | \pm 0.10 | ** | 0.00 | \pm 0.00 | 0.01 | \pm 0.01 | 0.30 | \pm 0.08 | ** | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.04 | \pm 0.04 | |
| | Actinospica | 0.10 | \pm 0.03 | 0.25 | \pm 0.05 | 0.04 | \pm 0.02 | * | 0.51 | \pm 0.37 | 0.66 | \pm 0.23 | 0.22 | \pm 0.13 | | 1.10 | \pm 0.69 | 0.50 | \pm 0.22 | 0.09 | \pm 0.05 | | 0.02 | \pm 0.01 | 0.52 | \pm 0.40 | 0.03 | \pm 0.01 | |
| | Mycobacterium | 0.71 | \pm 0.20 | 0.85 | \pm 0.10 | 0.21 | \pm 0.04 | ** | 1.68 | \pm 0.76 | 1.62 | \pm 0.35 | 1.08 | \pm 0.29 | | 3.44 | \pm 0.95 | 0.78 | \pm 0.04 | 2.43 | \pm 0.42 | * | 0.90 | \pm 0.16 | 1.37 | \pm 0.25 | 1.19 | \pm 0.43 | |
| | Marmoricola | 0.02 | \pm 0.02 | 0.00 | \pm 0.00 | 0.02 | \pm 0.01 | | 0.10 | \pm 0.04 | 0.31 | \pm 0.07 | 0.15 | \pm 0.04 | * | 0.09 | \pm 0.02 | 0.11 | \pm 0.02 | 0.40 | \pm 0.16 | | 0.31 | \pm 0.02 | 0.52 | \pm 0.18 | 2.37 | \pm 1.68 | |
| | Sporichthya | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.01 | \pm 0.01 | | 0.08 | \pm 0.05 | 0.13 | \pm 0.05 | 0.06 | \pm 0.01 | | 0.06 | \pm 0.01 | 0.03 | \pm 0.02 | 0.49 | \pm 0.21 | * | 0.33 | \pm 0.15 | 0.04 | \pm 0.03 | 0.77 | \pm 0.31 | |
| Bacteroidetes | Conexibacter | 0.07 | \pm 0.01 | 0.12 | \pm 0.04 | 0.00 | \pm 0.00 | * | 0.17 | \pm 0.04 | 0.16 | \pm 0.04 | 0.04 | \pm 0.02 | | 0.42 | \pm 0.13 | 0.03 | \pm 0.01 | 0.03 | \pm 0.02 | ** | 0.01 | \pm 0.01 | 0.05 | \pm 0.04 | 0.01 | \pm 0.01 | |
| | Ohtaekwangia | 0.03 | \pm 0.02 | 0.06 | \pm 0.02 | 0.06 | \pm 0.04 | | 0.05 | \pm 0.01 | 0.09 | \pm 0.04 | 0.38 | \pm 0.10 | ** | 0.20 | \pm 0.11 | 0.18 | \pm 0.09 | 0.13 | \pm 0.05 | | 1.50 | \pm 0.56 | 0.86 | \pm 0.46 | 0.48 | \pm 0.07 | |
| | Chitinophaga | 0.05 | \pm 0.02 | 0.15 | \pm 0.03 | 0.01 | \pm 0.01 | ** | 0.01 | \pm 0.01 | 0.05 | \pm 0.02 | 0.05 | \pm 0.02 | | 0.02 | \pm 0.02 | 7.35 | \pm 1.80 | 0.04 | \pm 0.01 | *** | 0.61 | \pm 0.17 | 0.57 | \pm 0.44 | 0.06 | \pm 0.04 | |
| | Ferruginibacter | 0.04 | \pm 0.02 | 0.01 | \pm 0.01 | 0.08 | \pm 0.04 | | 0.12 | \pm 0.04 | 0.17 | \pm 0.03 | 0.08 | \pm 0.04 | | 0.13 | \pm 0.04 | 0.21 | \pm 0.04 | 0.02 | \pm 0.01 | ** | 2.94 | \pm 0.62 | 5.95 | \pm 2.20 | 2.41 | \pm 0.44 | |
| | Terrimonas | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.03 | \pm 0.02 | | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.02 | \pm 0.02 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.23 | \pm 0.07 | 0.25 | \pm 0.10 | 1.42 | \pm 0.38 | |
| Nitrospirae | Mucilaginibacter | 0.82 | \pm 0.11 | 0.48 | \pm 0.03 | 0.14 | \pm 0.05 | ** | 4.37 | \pm 1.19 | 8.44 | \pm 1.59 | 4.36 | \pm 1.02 | | 2.47 | \pm 0.72 | 6.39 | \pm 1.58 | 2.65 | \pm 0.46 | * | 0.14 | \pm 0.01 | 0.40 | \pm 0.21 | 0.27 | \pm 0.12 | |
| | Pedobacter | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.06 | \pm 0.02 | 0.01 | \pm 0.01 | 0.13 | \pm 0.04 | * | 0.02 | \pm 0.01 | 2.26 | \pm 0.90 | 0.02 | \pm 0.00 | * | 0.24 | \pm 0.10 | 0.27 | \pm 0.21 | 0.20 | \pm 0.14 | |
| | Nitrospira | 0.02 | \pm 0.02 | 0.13 | \pm 0.04 | 0.57 | \pm 0.12 | ** | 0.03 | \pm 0.03 | 0.01 | \pm 0.01 | 0.13 | \pm 0.05 | | 0.12 | \pm 0.12 | 0.01 | \pm 0.01 | 0.13 | \pm 0.05 | | 1.04 | \pm 0.07 | 0.41 | \pm 0.23 | 1.29 | \pm 0.30 | |
| | Phenylobacterium | 1.15 | \pm 0.09 | 0.75 | \pm 0.15 | 0.29 | \pm 0.05 | ** | 2.29 | \pm 0.47 | 2.24 | \pm 0.63 | 2.73 | \pm 0.23 | | 1.95 | \pm 0.57 | 0.84 | \pm 0.26 | 2.18 | \pm 0.36 | | 0.39 | \pm 0.10 | 0.89 | \pm 0.55 | 0.54 | \pm 0.13 | |
| | Bradyrhizobium | 0.68 | \pm 0.27 | 0.43 | \pm 0.02 | 0.44 | \pm 0.12 | | 0.71 | \pm 0.20 | 0.73 | \pm 0.18 | 0.48 | \pm 0.05 | | 1.03 | \pm 0.34 | 1.07 | \pm 0.39 | 1.09 | \pm 0.27 | | 0.16 | \pm 0.07 | 0.68 | \pm 0.17 | 0.14 | \pm 0.08 | |
| Proteobacteria | Rhizobium | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.01 | \pm 0.01 | 0.01 | \pm 0.01 | 0.05 | \pm 0.01 | * | 0.04 | \pm 0.03 | 1.28 | \pm 0.75 | 0.05 | \pm 0.01 | | 0.03 | \pm 0.01 | 0.03 | \pm 0.02 | 0.02 | \pm 0.01 | |
| | Acidocella | 0.03 | \pm 0.01 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | * | 0.03 | \pm 0.02 | 0.02 | \pm 0.01 | 0.16 | \pm 0.15 | | 0.01 | \pm 0.01 | 0.04 | \pm 0.03 | 0.38 | \pm 0.30 | | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | |
| | Dongia | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.01 | \pm 0.01 | | 0.01 | \pm 0.01 | 0.02 | \pm 0.00 | 0.00 | \pm 0.00 | * | 0.13 | \pm 0.13 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.08 | \pm 0.02 | 0.10 | \pm 0.05 | 0.29 | \pm 0.25 | |
| | Novosphingobium | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.03 | \pm 0.02 | 0.02 | \pm 0.01 | 0.10 | \pm 0.01 | * | 0.03 | \pm 0.02 | 0.02 | \pm 0.02 | 0.07 | \pm 0.05 | | 0.54 | \pm 0.09 | 0.73 | \pm 0.35 | 2.79 | \pm 2.59 | |
| | Sphingomonas | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.05 | \pm 0.02 | 0.03 | \pm 0.01 | 0.12 | \pm 0.03 | * | 0.07 | \pm 0.01 | 1.01 | \pm 0.29 | 0.01 | \pm 0.01 | ** | 2.64 | \pm 0.78 | 0.58 | \pm 0.24 | 1.35 | \pm 0.40 | |
| | Burkholderia | 0.66 | \pm 0.03 | 0.42 | \pm 0.03 | 0.33 | \pm 0.20 | | 3.50 | \pm 0.54 | 2.09 | \pm 0.34 | 1.34 | \pm 0.20 | * | 2.60 | \pm 0.73 | 3.55 | \pm 0.37 | 1.53 | \pm 0.17 | * | 0.15 | \pm 0.03 | 0.17 | \pm 0.07 | 0.17 | \pm 0.04 | |
| | Aquabacterium | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | 0.00 | \pm 0.00 | | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.05 | \pm 0.01 | * | 0.04 | \pm 0.04 | 0.03 | \pm 0.01 | 0.00 | \pm 0.00 | | 0.34 | \pm 0.04 | 0.14 | \pm 0.08 | 0.22 | \pm 0.06 | |
| | Rhizobacter | 0.01 | \pm 0.01 | 0.00 | \pm 0.00 | 0.02 | \pm 0.02 | | 0.03 | \pm 0.01 | 0.04 | \pm 0.01 | 0.03 | \pm 0.01 | | 0.07 | \pm 0.06 | 0.03 | \pm 0.01 | 0.07 | \pm 0.02 | | 0.47 | \pm 0.02 | 0.18 | \pm 0.06 | 0.58 | \pm 0.13 | |
| | Nevskia | 0.04 | \pm 0.00 | 0.07 | \pm 0.03 | 0.02 | \pm 0.01 | | 1.05 | \pm 0.55 | 3.01 | \pm 1.22 | 2.27 | \pm 0.44 | | 0.86 | \pm 0.30 | 1.42 | \pm 0.46 | 4.11 | \pm 0.70 | ** | 0.16 | \pm 0.03 | 0.17 | \pm 0.15 | 3.34 | \pm 1.85 | |
| | Steroidobacter | 0.04 | \pm 0.01 | 0.02 | \pm 0.01 | 0.07 | \pm 0.02 | | 0.28 | \pm 0.12 | 0.19 | \pm 0.08 | 0.29 | \pm 0.10 | | 0.45 | \pm 0.13 | 0.05 | \pm 0.01 | 0.21 | \pm 0.08 | * | 0.08 | \pm 0.03 | 0.01 | \pm 0.00 | 0.11 | \pm 0.05 | |
| Dokdonella | 0.00 | \pm 0.00 | 0.03 | \pm 0.02 | 0.01 | \pm 0.00 | | 0.08 | \pm 0.04 | 0.30 | \pm 0.09 | 0.05 | \pm 0.02 | * | 0.13 | \pm 0.04 | 1.07 | \pm 0.25 | 0.26 | \pm 0.09 | ** | 0.01 | \pm 0.01 | 0.01 | \pm 0.01 | 0.03 | \pm 0.01 | | |
| Dyella | 0.32 | \pm 0.01 | 0.74 | \pm 0.15 | 0.09 | \pm 0.05 | ** | 0.76 | \pm 0.18 | 1.89 | \pm 0.43 | 0.43 | \pm 0.14 | * | 1.46 | \pm 0.61 | 1.12 | \pm 0.16 | 0.62 | \pm 0.07 | | 0.07 | \pm 0.01 | | | | | | |

Table.S3 (Part A). Pearson correlation between mineral chemistry and the relative abundance of the mineral-associated bacterial genera. The r-value is provided for significant correlations (P<0.01 and ***P<0.001).**

| Phylum | Genus | SiO ₂ | Al ₂ O ₃ | Fe ₂ O ₃ | MnO | MgO | CaO | Na ₂ O | K ₂ O | TiO ₂ | P ₂ O ₅ |
|------------------|-----------------------|------------------|--------------------------------|--------------------------------|-----------|-----------|-----------|-------------------|------------------|------------------|-------------------------------|
| Acidobacteria | Gp1 | 0.459** | 0.457** | 0.501** | -0.693*** | 0.593*** | -0.483** | 0.486** | 0.454** | 0.454** | |
| | Gp2 | | | | -0.563*** | 0.45** | | | | | |
| | Gp3 | | | | -0.496** | | | | | | |
| | Bryobacter | | | | 0.462** | | | | | | |
| Actinobacteria | Ilumatobacter | | | -0.457** | 0.647*** | -0.544*** | 0.44** | -0.443** | | | |
| | lamia | | | | 0.496** | | | | | | |
| | Catenulispora | | | | -0.531*** | | | | | | |
| | Terrabacter | | | -0.426** | 0.701*** | -0.523** | | | | | |
| | Arthrobacter | | | -0.443** | 0.591*** | -0.521** | 0.428** | -0.431** | | | |
| | Allocatelliglobospora | | | | | | | | | | |
| | Aeromicrobium | | | | 0.474** | | | | | | |
| | Nocardioides | | | | 0.614*** | -0.498** | | | | | |
| | Pseudonocardia | | | | 0.479** | | | | | | |
| Streptomyces | | | | | | | | | | 0.441** | |
| Bacteroidetes | Ohtaekwangia | | | | 0.547*** | | | | | | |
| | Ferruginibacter | | | | 0.676*** | -0.504** | | | | | |
| | Lacibacter | | | | 0.55*** | | | | | | |
| | Terrimonas | | | | 0.559*** | | | | | | |
| | Hymenobacter | 0.43** | 0.429** | 0.441** | | 0.46** | -0.437** | 0.438** | 0.429** | 0.429** | |
| | Mucilagibacter | 0.546*** | 0.544*** | 0.575*** | -0.528*** | 0.635*** | -0.562*** | 0.565*** | 0.542*** | 0.542*** | |
| Solitalea | | | 0.429** | | 0.456** | | 0.424** | | | | |
| Elusimicrobia | Elusimicrobium | | | 0.429** | | 0.438** | -0.426** | 0.427** | | | |
| Firmicutes | Paenibacillus | | | | | -0.442** | | | | | |
| Gemmatimonadetes | Gemmatimonas | | | | 0.632*** | -0.478** | | | | | |

Table.S3 (Part B). Pearson correlation between mineral chemistry and the relative abundance of the mineral-associated bacterial genera. The r-value is provided for significant correlations (**P<0.01 and ***P<0.001).

| Phylum | Genus | SiO ₂ | Al ₂ O ₃ | Fe ₂ O ₃ | MnO | MgO | CaO | Na ₂ O | K ₂ O | TiO ₂ | P ₂ O ₅ |
|-----------------------|----------------------|------------------|--------------------------------|--------------------------------|-----------|-----------|----------|-------------------|------------------|------------------|-------------------------------|
| Nitrospira | Nitrospira | | | -0.459** | 0.712*** | -0.557*** | 0.44** | -0.444** | | | |
| | Rhizomicrobium | 0.432** | 0.431** | 0.439** | | 0.449** | -0.436** | 0.437** | 0.431** | 0.431** | |
| | Brevundimonas | -0.427** | -0.425** | -0.47** | 0.703*** | -0.565*** | 0.451** | -0.455** | | | |
| | Phenylobacterium | 0.556*** | 0.554*** | 0.581*** | -0.466** | 0.63*** | -0.57*** | 0.572*** | 0.553*** | 0.553*** | |
| | Afipia | -0.428** | -0.425** | -0.472** | 0.719*** | -0.57*** | 0.453** | -0.457** | | | |
| | Bosea | -0.464** | -0.461** | -0.506** | 0.707*** | -0.601*** | 0.488** | -0.492** | -0.459** | -0.459** | |
| | Bradyrhizobium | | | | -0.572*** | | | | | | 0.531*** |
| | Devosia | -0.433** | -0.431** | -0.457** | 0.435** | -0.508** | 0.447** | -0.449** | -0.43** | -0.43** | |
| | Hyphomicrobium | | | | 0.554*** | -0.44** | | | | | |
| | Labrys | | | | | | | | | | |
| | Rhodobacter | | | | 0.46** | | | | | | |
| | Sphingobium | | | | | | | | | | |
| | Sphingomonas | | | -0.445** | 0.524** | -0.512** | 0.432** | -0.435** | | | |
| | Sphingopyxis | | | | 0.487** | | | | | | |
| | Burkholderia | | | | -0.724*** | 0.469** | | | | | 0.436** |
| Proteobacteria | Aquabacterium | | | -0.447** | 0.712*** | -0.546*** | 0.428** | -0.432** | | | |
| | Polaromonas | | | | 0.494** | | | | | | |
| | Collimonas | | | | -0.487** | | | | | | |
| | Massilia | | | | 0.635*** | -0.452** | | | | | |
| | Nitrospira | | | | 0.443** | | | | | | |
| | Sulfuritalea | | | | 0.593*** | -0.443** | | | | | |
| | Peredibacter | | | | 0.479** | | | | | | |
| | Acinetobacter | | | | 0.484** | | | | | | |
| | Rhizobacter | -0.438** | -0.435** | -0.482** | 0.721*** | -0.58*** | 0.463** | -0.466** | -0.432** | -0.432** | |
| | Singularimonas | | | | 0.439** | | | | | | |
| | Steroidobacter | | | | | | | | | | |
| | Arenimonas | | | | 0.598*** | -0.45** | | | | | |
| | Dokdonella | | | | -0.511** | | | | | | 0.537*** |
| | Dyella | | | | -0.529*** | | | | | | |
| Spirochaetes | Turneriella | | | | 0.555*** | | | | | | |

Table.S4. Relative abundance (in %) of the most abundant bacterial genera detected by cultivation-independent approach. Each value is the mean of biological replicates. Bacterial genera in bold were also recovered in our cultivation -dependent approach.

| Rank | Genus | mean (in %) |
|------|-------------------------|-------------|
| 1 | Acidobacteria Gp2 | 7.02 |
| 2 | Acidobacteria Gp1 | 5.10 |
| 3 | Mucilaginibacter | 2.72 |
| 4 | Nevskia | 1.47 |
| 5 | Burkholderia | 1.44 |
| 6 | Mycobacterium | 1.41 |
| 7 | Serratia | 1.40 |
| 8 | Phenylbacterium | 1.39 |
| 9 | Arthrobacter | 1.11 |
| 10 | Ferruginibacter | 1.08 |
| 11 | Streptomyces | 0.89 |
| 12 | Chitinophaga | 0.79 |
| 13 | Dyella | 0.67 |
| 14 | Bryobacter | 0.67 |
| 15 | Bradyrhizobium | 0.65 |
| 16 | Sphingomonas | 0.52 |
| 17 | TM7 | 0.50 |
| 18 | Chryseobacterium | 0.49 |
| 19 | Armatimonadetes Gp5 | 0.43 |
| 20 | Marmoricola | 0.39 |
| 21 | Novosphingobium | 0.39 |
| 22 | Acidobacteria Gp10 | 0.37 |
| 23 | Phycoccus | 0.36 |
| 24 | Ohtaekwangia | 0.35 |
| 25 | Actinospica | 0.35 |
| 26 | Acidobacteria Gp3 | 0.34 |
| 27 | Nitrospira | 0.33 |
| 28 | Arenimonas | 0.30 |
| 29 | Pedobacter | 0.29 |
| 30 | Nocardioides | 0.27 |