**SUPPLEMENTAL INFORMATION**

Uranium contamination mediating soil and ore microbial community assembly at four mining sites, South China

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|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | U (mg/kg) | SiO2 (wt%) | TiO2 (wt%) | Al2O3 (wt%) | Fe2O3 (wt%) | MnO (wt%) | MgO (wt%) | CaO (wt%) | Na2O (wt%) | K2O (wt%) | P2O5 (wt%) |
| XC-015 | 3399 | 69.43 | 0.93 | 12.41 | 5.03 | 0.06 | 1.16 | 2.22 | 0.97 | 3.00 | 0.16 |
| XC-030 | 3643 | 64.29 | 1.02 | 12.68 | 6.64 | 0.09 | 1.51 | 3.17 | 0.90 | 3.21 | 0.23 |
| XC-050 | 3950 | 63.59 | 0.89 | 12.56 | 6.26 | 0.09 | 1.27 | 4.28 | 1.47 | 3.33 | 0.17 |
| XC-070 | 4126 | 63.42 | 0.91 | 13.35 | 6.47 | 0.08 | 1.50 | 3.61 | 1.64 | 3.36 | 0.21 |
| XC-090 | 4204 | 42.80 | 0.49 | 12.36 | 8.43 | 0.80 | 0.00 | 21.90 | 0.50 | 2.29 | 0.36 |
| XC-110 | 4041 | 2.66 | 0.04 | 9.56 | 10.23 | 1.56 | 0.00 | 61.71 | 0.00 | 0.09 | 0.41 |
| XC-130 | 4113 | 1.37 | 0.02 | 8.59 | 9.94 | 1.64 | 0.00 | 61.93 | 0.54 | 0.03 | 0.37 |
| XC-150 | 4454 | 1.14 | 0.01 | 8.53 | 9.49 | 1.81 | 0.00 | 63.56 | 0.00 | 0.01 | 0.38 |
| XC-170 | 5099 | 54.24 | 0.41 | 16.28 | 6.26 | 0.14 | 0.56 | 8.84 | 0.58 | 3.79 | 0.28 |
| XC-190 | 5288 | 61.44 | 0.32 | 19.39 | 3.24 | 0.07 | 0.54 | 3.13 | 0.54 | 4.33 | 0.12 |
| XC-210 | 5510 | 52.92 | 0.53 | 16.73 | 6.74 | 0.11 | 0.74 | 7.82 | 0.45 | 3.51 | 0.28 |
| ZSX-1-1 | 6785 | 65.85 | 0.14 | 20.74 | 1.35 | 0.07 | 0.68 | 0.79 | 0.54 | 4.35 | 0.03 |
| ZSX-1-2 | 170 | 66.67 | 0.11 | 20.69 | 1.06 | 0.07 | 0.61 | 0.17 | 0.65 | 4.72 | 0.02 |
| GX2 | 900 | 66.80 | 0.58 | 15.75 | 5.22 | 0.04 | 0.90 | 0.41 | 1.95 | 3.76 | 0.22 |
| GX3 | 1100 | 64.03 | 0.45 | 16.02 | 5.84 | 0.05 | 0.60 | 1.20 | 2.30 | 3.98 | 0.39 |
| GX4 | 16000 | 66.15 | 0.46 | 12.49 | 3.25 | 0.07 | 0.94 | 4.76 | 0.73 | 2.87 | 0.13 |
| GX5 | 6800 | 71.36 | 0.63 | 13.60 | 3.12 | 0.08 | 0.72 | 1.96 | 0.94 | 2.43 | 0.14 |
| GX7 | 1175 | 74.29 | 0.48 | 13.37 | 2.25 | 0.04 | 0.55 | 0.57 | 1.58 | 3.37 | 0.14 |
| XS2 | 2700 | 62.32 | 0.45 | 13.35 | 4.25 | 0.86 | 0.64 | 7.78 | 1.35 | 3.16 | 0.35 |
| XS3 | 700 | 62.81 | 0.90 | 19.34 | 7.04 | 0.07 | 0.34 | 0.16 | 0.28 | 2.15 | 0.14 |
| XS4 | 18000 | 44.47 | 0.54 | 19.39 | 3.40 | 0.14 | 0.52 | 17.27 | 0.49 | 4.81 | 0.95 |
| XS5 | 9000 | 51.63 | 0.53 | 24.91 | 3.05 | 0.16 | 0.59 | 3.60 | 1.76 | 5.55 | 1.46 |
| XS6 | 10000 | 76.25 | 0.21 | 12.07 | 1.77 | 0.07 | 0.17 | 1.51 | 1.58 | 2.03 | 0.68 |
| XS7 | 2201 | 52.70 | 0.59 | 28.19 | 3.93 | 0.08 | 0.75 | 0.59 | 1.64 | 5.96 | 0.28 |
| XS8 | 11750 | 49.12 | 0.50 | 28.77 | 3.83 | 0.14 | 0.56 | 1.38 | 0.25 | 6.70 | 0.49 |

**Table S1** Geochemical parameters of samples in this work

**Table S1. continued** Geochemical parameters of samples in this work

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | LOI | TOC (ppm) | TN (%) | TC (%) | H (%) | S (%) | Moisture (%) | pH |
| XC-015 | 4.09 | 1674.15 | 0.02 | 0.13 | 0.499 | 1.059 | 9.49 | 5.43 |
| XC-030 | 5.55 | 33.37 | 0.01 | 0.07 | 0.313 | 0.263 | 8.88 | 4.98 |
| XC-050 | 5.20 | 98.62 | 0.01 | 0.04 | 0.25 | 0.377 | 9.25 | 4.66 |
| XC-070 | 5.26 | 188.27 | 0.01 | 0.03 | 0.249 | 0.332 | 9.42 | 5.19 |
| XC-090 | 9.36 | 1016.83 | 0.01 | 0.11 | 0.671 | 2.432 | 21.64 | 6.3 |
| XC-110 | 14.21 | 12535.18 | 0.03 | 2.13 | 1.928 | 6.131 | 30.62 | 7.29 |
| XC-130 | 15.83 | 27928.38 | 0.03 | 2.03 | 2.229 | 5.285 | 44.03 | 7.56 |
| XC-150 | 15.35 | 22475.84 | 0.03 | 2.74 | 2.095 | 4.897 | 54.14 | 7.61 |
| XC-170 | 8.10 | 825.43 | 0.01 | 0.07 | 0.355 | 1.213 | 12.03 | 7.6 |
| XC-190 | 6.32 | 1148.58 | 0.02 | 0.16 | 0.364 | 0.872 | 11.05 | 7.53 |
| XC-210 | 9.37 | 188.40 | 0.01 | 0.07 | 0.332 | 0.615 | 12.94 | 7.34 |
| ZSX-1-1 | 4.90 | 1007.41 | 0.01 | 0.06 | 0.248 | 0.029 | 10.25 | 3.98 |
| ZSX-1-2 | 4.74 | 175.90 | 0.01 | 0.03 | 0.097 | 0.074 | 11.32 | 4.63 |
| GX2 | 4.72 | 262.41 | 0.01 | 0.05 | 0.173 | 0.134 | 3.00 | 3.93 |
| GX3 | 5.05 | 381.36 | 0.01 | 0.05 | 0.139 | 0.146 | 5.90 | 4.49 |
| GX4 | 7.59 | 2095.86 | 0.04 | 0.89 | 0.225 | 0.064 | 11.85 | 7.67 |
| GX5 | 4.27 | 361.73 | 0.02 | 0.41 | 0.126 | 0.041 | 8.94 | 7.91 |
| GX7 | 3.44 | 1354.38 | 0.03 | 0.31 | 0.148 | 0.044 | 6.53 | 6.86 |
| XS2 | 4.93 | 86.60 | 0.03 | 0.29 | 0.236 | 0.697 | 11.83 | 8.26 |
| XS3 | 7.19 | 12801.08 | 0.06 | 1.1 | 0.7 | 0.227 | 7.14 | 4.25 |
| XS4 | 7.22 | 206.40 | 0.01 | 0.07 | 0.493 | 0.732 | 1.04 | 4.99 |
| XS5 | 6.45 | 77.18 | 0.02 | 0.22 | 0.673 | 0.413 | 11.13 | 5.57 |
| XS6 | 2.67 | 613.30 | 0.01 | 0.07 | 0.198 | 0.126 | 2.32 | 4.33 |
| XS7 | 4.91 | 104.90 | 0.02 | 0.06 | 0.54 | 0.16 | 8.04 | 3.55 |
| XS8 | 7.34 | 1975.47 | 0.03 | 0.26 | 0.721 | 0.227 | 5.45 | 4.08 |

**Table S2.** Read counts at each step of 16S QIIME2 quality control

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | Input | Filtered | Percentage of input passing filter | Denoised | Merged | Percentage of input merged | Non-chimeric | Percentage of input non-chimeric |
| XC-015 | 122303 | 101567 | 83.05 | 96918 | 90919 | 74.34 | 89257 | 72.98 |
| XC-030 | 139194 | 115847 | 83.23 | 111981 | 106768 | 76.7 | 105199 | 75.58 |
| XC-050 | 78528 | 65352 | 83.22 | 62844 | 60505 | 77.05 | 57285 | 72.95 |
| XC-070 | 94556 | 77924 | 82.41 | 76071 | 73414 | 77.64 | 72937 | 77.14 |
| XC-090 | 73870 | 61030 | 82.62 | 60214 | 59136 | 80.05 | 58709 | 79.48 |
| XC-110 | 97420 | 79984 | 82.1 | 79104 | 78319 | 80.39 | 78171 | 80.24 |
| XC-130 | 78008 | 64000 | 82.04 | 63282 | 62534 | 80.16 | 62510 | 80.13 |
| XC-150 | 86606 | 71435 | 82.48 | 70496 | 69674 | 80.45 | 69665 | 80.44 |
| XC-170 | 125643 | 102003 | 81.18 | 99766 | 96961 | 77.17 | 96131 | 76.51 |
| XC-190 | 151954 | 121521 | 79.97 | 116586 | 110936 | 73.01 | 108089 | 71.13 |
| XC-210 | 110367 | 90136 | 81.67 | 86366 | 82015 | 74.31 | 81657 | 73.99 |
| ZSX-1-1 | 157752 | 130834 | 82.94 | 124269 | 113084 | 71.68 | 109209 | 69.23 |
| ZSX-1-2 | 163984 | 136736 | 83.38 | 128608 | 114314 | 69.71 | 110763 | 67.55 |
| GX2 | 131855 | 108000 | 81.91 | 103893 | 97623 | 74.04 | 95119 | 72.14 |
| GX3 | 137176 | 113440 | 82.7 | 110692 | 107742 | 78.54 | 104766 | 76.37 |
| GX4 | 189302 | 157832 | 83.38 | 145506 | 125631 | 66.37 | 123929 | 65.47 |
| GX5 | 151122 | 125305 | 82.92 | 113961 | 96930 | 64.14 | 95292 | 63.06 |
| GX7 | 100250 | 83563 | 83.35 | 80690 | 77542 | 77.35 | 75279 | 75.09 |
| XS2 | 145543 | 121143 | 83.24 | 116975 | 111401 | 76.54 | 108016 | 74.22 |
| XS3 | 163970 | 136476 | 83.23 | 131111 | 123669 | 75.42 | 119233 | 72.72 |
| XS4 | 130635 | 108529 | 83.08 | 104906 | 100696 | 77.08 | 97658 | 74.76 |
| XS5 | 156872 | 130825 | 83.4 | 126191 | 119486 | 76.17 | 118117 | 75.3 |
| XS6 | 153422 | 125467 | 81.78 | 122378 | 117241 | 76.42 | 111569 | 72.72 |
| XS7 | 139247 | 110048 | 79.03 | 108343 | 101115 | 72.62 | 99107 | 71.17 |
| XS8 | 170192 | 140780 | 82.72 | 134979 | 125080 | 73.49 | 119615 | 70.28 |

**Table S3.** Alpha diversity of samples

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Observed | Chao1 | se.chao1\* | ACE | se.ACE\* | Shannon | Simpson | InvSimpson | Fisher |
| XC-015 | 1299 | 1419.41 | 21.79 | 1415.86 | 17.16 | 5.66 | 0.98 | 62.82 | 310.78 |
| XC-030 | 1266 | 1420.07 | 25.79 | 1420.07 | 17.42 | 5.52 | 0.98 | 60.48 | 300.50 |
| XC-050 | 675 | 734.90 | 15.59 | 730.87 | 12.69 | 4.13 | 0.91 | 10.60 | 134.83 |
| XC-070 | 925 | 992.50 | 15.40 | 994.66 | 14.37 | 4.69 | 0.94 | 16.96 | 200.55 |
| XC-090 | 664 | 690.56 | 9.87 | 681.25 | 12.59 | 5.12 | 0.98 | 65.71 | 132.10 |
| XC-110 | 428 | 475.12 | 17.62 | 454.73 | 10.51 | 3.75 | 0.89 | 9.40 | 76.91 |
| XC-130 | 552 | 566.17 | 6.76 | 561.15 | 11.37 | 4.27 | 0.93 | 15.00 | 105.06 |
| XC-150 | 445 | 462.45 | 7.36 | 462.28 | 10.34 | 3.89 | 0.93 | 13.63 | 80.65 |
| XC-170 | 984 | 1050.02 | 15.09 | 1055.68 | 15.40 | 5.46 | 0.99 | 72.72 | 217.01 |
| XC-190 | 978 | 1116.62 | 25.58 | 1121.91 | 16.05 | 5.04 | 0.97 | 33.06 | 215.32 |
| XC-210 | 1215 | 1306.02 | 17.96 | 1317.67 | 17.28 | 5.92 | 0.99 | 124.26 | 284.83 |
| ZSX-1-1 | 1279 | 1432.14 | 25.73 | 1429.48 | 17.33 | 5.30 | 0.97 | 32.65 | 304.54 |
| ZSX-1-2 | 1511 | 1731.43 | 32.18 | 1717.07 | 18.72 | 5.56 | 0.98 | 48.71 | 379.26 |
| GX2 | 685 | 729.51 | 12.58 | 731.61 | 13.06 | 5.12 | 0.99 | 69.37 | 137.33 |
| GX3 | 500 | 552.92 | 14.75 | 564.08 | 11.66 | 4.38 | 0.96 | 27.28 | 93.02 |
| GX4 | 3053 | 3449.47 | 41.67 | 3420.84 | 24.97 | 7.40 | 1.00 | 789.39 | 1004.06 |
| GX5 | 2685 | 2936.91 | 31.07 | 2928.44 | 22.96 | 7.19 | 1.00 | 412.81 | 834.49 |
| GX7 | 550 | 578.11 | 9.38 | 586.91 | 11.90 | 4.44 | 0.94 | 16.23 | 104.59 |
| XS2 | 902 | 1021.35 | 25.11 | 997.97 | 15.19 | 5.26 | 0.97 | 37.79 | 194.22 |
| XS3 | 1086 | 1200.61 | 22.44 | 1191.24 | 16.33 | 5.60 | 0.99 | 95.45 | 246.31 |
| XS4 | 991 | 1091.56 | 19.68 | 1101.95 | 15.17 | 4.70 | 0.95 | 20.85 | 218.99 |
| XS5 | 1560 | 1755.00 | 28.83 | 1759.69 | 19.04 | 5.81 | 0.98 | 55.45 | 395.69 |
| XS6 | 530 | 587.59 | 16.01 | 583.39 | 11.53 | 3.98 | 0.93 | 14.69 | 99.92 |
| XS7 | 314 | 314.22 | 0.52 | 315.78 | 8.83 | 3.83 | 0.94 | 16.76 | 52.88 |
| XS8 | 1009 | 1187.14 | 31.55 | 1154.27 | 15.66 | 5.07 | 0.97 | 39.65 | 224.09 |

\*se: standard error

**Table S4.** Uranium sensitive taxon which had significant correlations with uranium concentrations

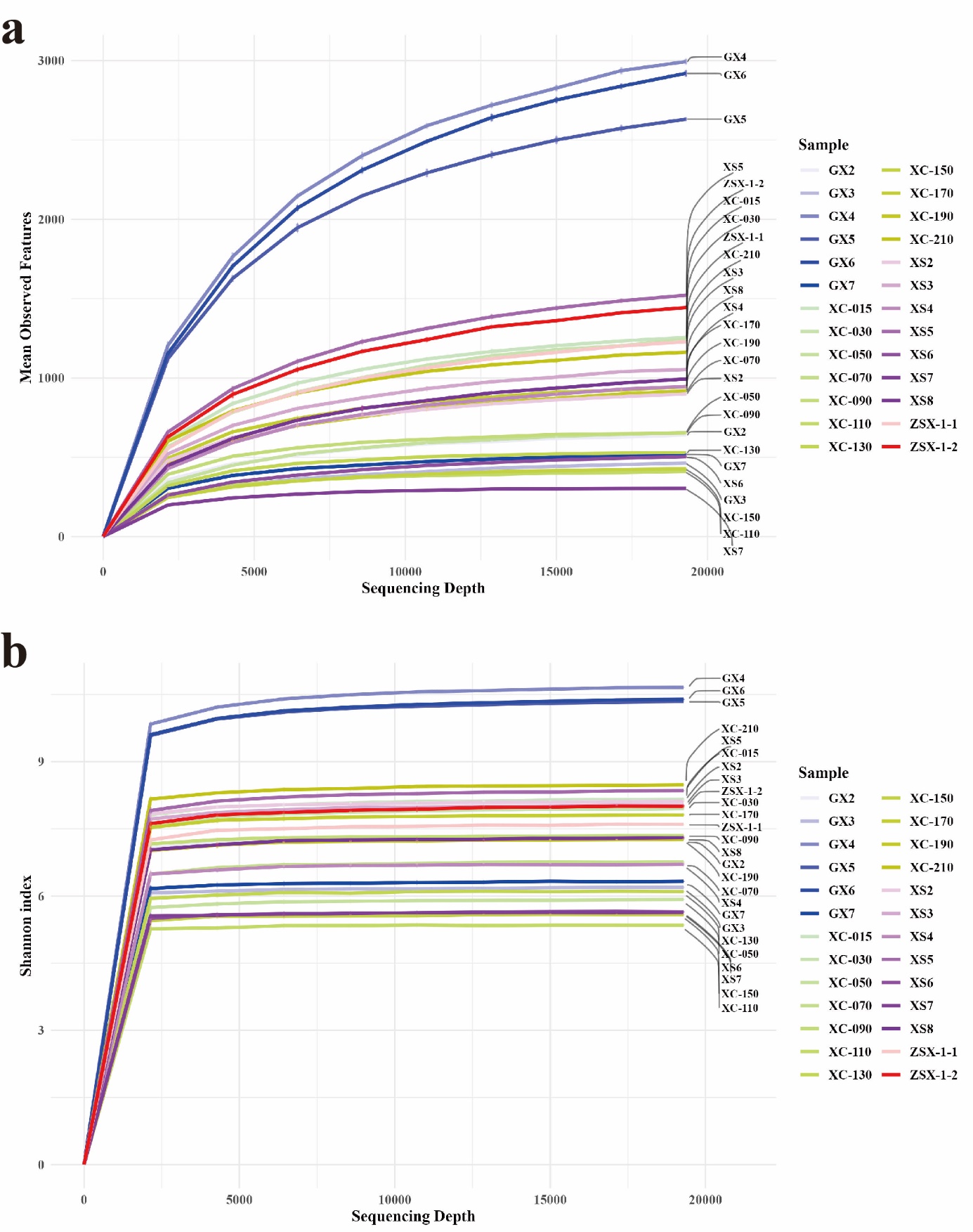
|  |  |  |  |
| --- | --- | --- | --- |
| **Taxon** | **p-value** | **r** | **z-score** |
| Bacteria;Verrucomicrobiota;Chlamydiae | 0.03 | 0.14 | 2.23 |
| Bacteria;Verrucomicrobiota;Verrucomicrobiae;Methylacidiphilales | 0.04 | 0.23 | 1.98 |
| Bacteria;Verrucomicrobiota;Verrucomicrobiae;UA11 | 0.01 | 0.23 | 2.21 |
| Bacteria;Verrucomicrobiota;Verrucomicrobiae;Opitutales;Puniceicoccaceae | 0.03 | 0.19 | 1.82 |
| Bacteria;Verrucomicrobiota;Verrucomicrobiae;Opitutales;Opitutaceae; | 0.03 | 0.21 | 1.91 |
| Bacteria;Verrucomicrobiota;Verrucomicrobiae;Opitutales;Puniceicoccaceae; | 0.01 | 0.20 | 2.03 |
| Bacteria;Bacteroidota; | 0.05 | -0.18 | -1.94 |
| Bacteria;Bacteroidota;Kryptonia | 0.00 | 0.35 | 3.16 |
| Bacteria;Bacteroidota;Bacteroidia;Cytophagales | 0.03 | 0.18 | 2.05 |
| Bacteria;Bacteroidota;Bacteroidia;Chitinophagales;Chitinophagaceae;Heliimonas | 0.04 | -0.21 | -2.03 |
| Bacteria;Bacteroidota;Bacteroidia;Chitinophagales;Chitinophagaceae;Lacibacter | 0.03 | 0.22 | 1.94 |
| Bacteria;Bacteroidota;Bacteroidia;Cytophagales;Cytophagaceae;Sporocytophaga | 0.02 | 0.20 | 1.93 |
| Bacteria;Bacteroidota;Bacteroidia;Cytophagales;Microscillaceae;OLB12 | 0.01 | 0.22 | 2.03 |
| Bacteria;Bacteroidota;Bacteroidia;Cytophagales;Spirosomaceae;Huanghella | 0.01 | 0.31 | 2.79 |
| Bacteria;Acidobacteriota;Acidobacteriae;Acidobacteriales | 0.02 | 0.28 | 2.32 |
| Bacteria;Acidobacteriota;Acidobacteriae;Subgroup 2 | 0.02 | 0.23 | 2.08 |
| Bacteria;Acidobacteriota;Blastocatellia;Pyrinomonadales | 0.04 | 0.26 | 2.06 |
| Bacteria;Acidobacteriota;Holophagae;Holophagales | 0.04 | 0.18 | 1.88 |
| Bacteria;Acidobacteriota;Acidobacteriae;Acidobacteriales;Acidobacteriaceae (Subgroup 1) | 0.04 | 0.22 | 1.93 |
| Bacteria;Acidobacteriota;Acidobacteriae;Acidobacteriales;Acidobacteriaceae (Subgroup 1);Edaphobacter | 0.01 | 0.24 | 2.21 |
| Bacteria;Acidobacteriota;Acidobacteriae;Acidobacteriales;Acidobacteriaceae (Subgroup 1);Occallatibacter | 0.01 | 0.25 | 2.36 |
| Bacteria;Acidobacteriota;Acidobacteriae;Acidobacteriales;Acidobacteriaceae (Subgroup 1);Terracidiphilus | 0.04 | 0.23 | 2.04 |
| Bacteria;Planctomycetota;Planctomycetes;Planctomycetales | 0.01 | 0.38 | 2.80 |
| Bacteria;Planctomycetota;Planctomycetes;Planctomycetales; | 0.01 | -0.24 | -2.28 |
| Bacteria;Planctomycetota;Planctomycetes;Planctomycetales;uncultured | 0.03 | 0.32 | 2.34 |
| Bacteria;Cyanobacteria;Cyanobacteriia | 0.00 | 0.35 | 4.31 |
| Bacteria;Cyanobacteria;Cyanobacteriia;Cyanobacteriales | 0.00 | 0.35 | 3.37 |
| Bacteria;Cyanobacteria;Cyanobacteriia;Cyanobacteriales; | 0.02 | 0.28 | 2.27 |
| Bacteria;Cyanobacteria;Cyanobacteriia;Cyanobacteriales;Chamaesiphonaceae | 0.01 | 0.33 | 2.92 |
| Bacteria;Cyanobacteria;Cyanobacteriia;Cyanobacteriales;Chroococcidiopsaceae | 0.05 | 0.20 | 1.90 |
| Bacteria;Cyanobacteria;Cyanobacteriia;Cyanobacteriales;Coleofasciculaceae; | 0.01 | -0.23 | -2.34 |
| Bacteria;Chloroflexi;Anaerolineae | 0.03 | 0.18 | 2.15 |
| Bacteria;Chloroflexi;Chloroflexia | 0.00 | 0.35 | 3.57 |
| Bacteria;Chloroflexi;P2-11E | 0.00 | 0.52 | 4.39 |
| Bacteria;Chloroflexi;Chloroflexia;Chloroflexales | 0.00 | 0.46 | 4.23 |
| Bacteria;Chloroflexi;Chloroflexia;Kallotenuales | 0.03 | 0.26 | 2.12 |
| Bacteria;Chloroflexi;Dehalococcoidia; | 0.04 | -0.17 | -1.82 |
| Bacteria;Chloroflexi;Dehalococcoidia;SAR202 clade | 0.05 | 0.22 | 1.91 |
| Bacteria;Chloroflexi;Ktedonobacteria;B10-SB3A | 0.04 | 0.17 | 1.82 |
| Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae | 0.02 | 0.27 | 2.54 |
| Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;AKIW781 | 0.03 | 0.27 | 2.20 |
| Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;uncultured | 0.02 | 0.27 | 2.48 |
| Bacteria;Chloroflexi;Ktedonobacteria;Ktedonobacterales;Ktedonobacteraceae;FCPS473 | 0.01 | -0.22 | -2.38 |
| Bacteria;Actinobacteriota;Acidimicrobiia | 0.03 | 0.26 | 2.26 |
| Bacteria;Actinobacteriota;Coriobacteriia | 0.01 | 0.20 | 2.06 |
| Bacteria;Actinobacteriota;Thermoleophilia | 0.00 | 0.35 | 3.41 |
| Bacteria;Actinobacteriota;Acidimicrobiia;Acidimicrobiales | 0.03 | 0.20 | 1.94 |
| Bacteria;Actinobacteriota;Acidimicrobiia;IMCC26256 | 0.03 | 0.26 | 2.12 |
| Bacteria;Actinobacteriota;Actinobacteria;Catenulisporales | 0.01 | 0.21 | 2.26 |
| Bacteria;Actinobacteriota;Coriobacteriia;CG2-30-50-142 | 0.01 | 0.20 | 1.97 |
| Bacteria;Actinobacteriota;Thermoleophilia;Gaiellales | 0.02 | 0.26 | 2.43 |
| Bacteria;Actinobacteriota;Acidimicrobiia;Actinomarinales; | 0.05 | 0.18 | 1.66 |
| Bacteria;Actinobacteriota;Actinobacteria;Catenulisporales;Actinospicaceae | 0.00 | 0.24 | 2.43 |
| Bacteria;Actinobacteriota;Actinobacteria;Corynebacteriales; | 0.03 | 0.22 | 1.92 |
| Bacteria;Actinobacteriota;Actinobacteria;Corynebacteriales;Corynebacteriaceae | 0.03 | 0.15 | 1.94 |
| Bacteria;Actinobacteriota;Actinobacteria;Corynebacteriales;Nocardiaceae | 0.01 | 0.31 | 2.66 |
| Bacteria;Actinobacteriota;Actinobacteria;Frankiales;Acidothermaceae | 0.04 | 0.21 | 1.88 |
| Bacteria;Actinobacteriota;Actinobacteria;Frankiales;Geodermatophilaceae | 0.01 | -0.24 | -2.37 |
| Bacteria;Actinobacteriota;Actinobacteria;Micrococcales;Intrasporangiaceae | 0.04 | -0.22 | -2.04 |
| Bacteria;Actinobacteriota;Thermoleophilia;Gaiellales;uncultured | 0.02 | 0.26 | 2.58 |
| Bacteria;Actinobacteriota;Actinobacteria;Corynebacteriales;Nocardiaceae;Nocardia | 0.01 | 0.29 | 2.76 |
| Bacteria;Actinobacteriota;Actinobacteria;Frankiales;Geodermatophilaceae;Modestobacter | 0.03 | -0.22 | -2.12 |
| Bacteria;Actinobacteriota;Actinobacteria;Micrococcales;Intrasporangiaceae; | 0.04 | -0.21 | -2.10 |
| Bacteria;Actinobacteriota;Actinobacteria;Micrococcales;Microbacteriaceae;Microbacterium | 0.01 | 0.31 | 2.78 |
| Bacteria;Actinobacteriota;Actinobacteria;Micrococcales;Microbacteriaceae;Parafrigoribacterium | 0.03 | 0.22 | 1.91 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Elsterales | 0.01 | 0.30 | 2.89 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Beggiatoales | 0.03 | 0.23 | 2.06 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Coxiellales | 0.04 | 0.22 | 2.06 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Diplorickettsiales | 0.02 | 0.15 | 2.37 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis | 0.04 | 0.18 | 2.12 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Defluviicoccales;uncultured | 0.02 | 0.22 | 2.05 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Elsterales;uncultured | 0.01 | 0.30 | 2.91 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylopilaceae | 0.01 | -0.22 | -2.16 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis | 0.03 | 0.24 | 2.16 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Nitrosomonadaceae | 0.01 | 0.32 | 2.96 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Rhodocyclaceae | 0.03 | 0.18 | 1.77 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Sulfuricellaceae | 0.02 | -0.18 | -2.21 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae | 0.02 | 0.24 | 2.16 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Steroidobacterales;Woeseiaceae | 0.00 | 0.26 | 2.35 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;Acidicaldus | 0.05 | 0.22 | 1.94 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;Craurococcus-Caldovatus | 0.04 | 0.18 | 1.83 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;Rhodovastum | 0.04 | 0.19 | 1.71 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Azospirillaceae; | 0.01 | 0.21 | 2.12 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Methylocella | 0.02 | 0.19 | 1.90 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Devosiaceae;Arsenicitalea | 0.03 | 0.19 | 1.86 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methyloligellaceae;uncultured | 0.02 | 0.23 | 2.11 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis;Bauldia | 0.04 | 0.22 | 2.07 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Nitrobacter | 0.04 | 0.18 | 1.66 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas | 0.05 | -0.21 | -2.04 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Hydrogenophilaceae;Hydrogenophilus | 0.00 | 0.25 | 2.52 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Hydrogenophilaceae;uncultured | 0.03 | -0.21 | -2.17 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Nitrosomonadaceae;Ellin6067 | 0.00 | 0.43 | 3.53 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Rhodocyclaceae; | 0.02 | 0.20 | 1.87 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Sulfuricellaceae;Sulfuriferula | 0.04 | -0.20 | -1.94 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter | 0.04 | 0.22 | 1.94 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Dokdonella | 0.02 | 0.21 | 1.88 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Luteimonas | 0.04 | 0.17 | 1.74 |

**Table S5.** Correlation between physicochemical parameters and relative abundance of Acidobacteria

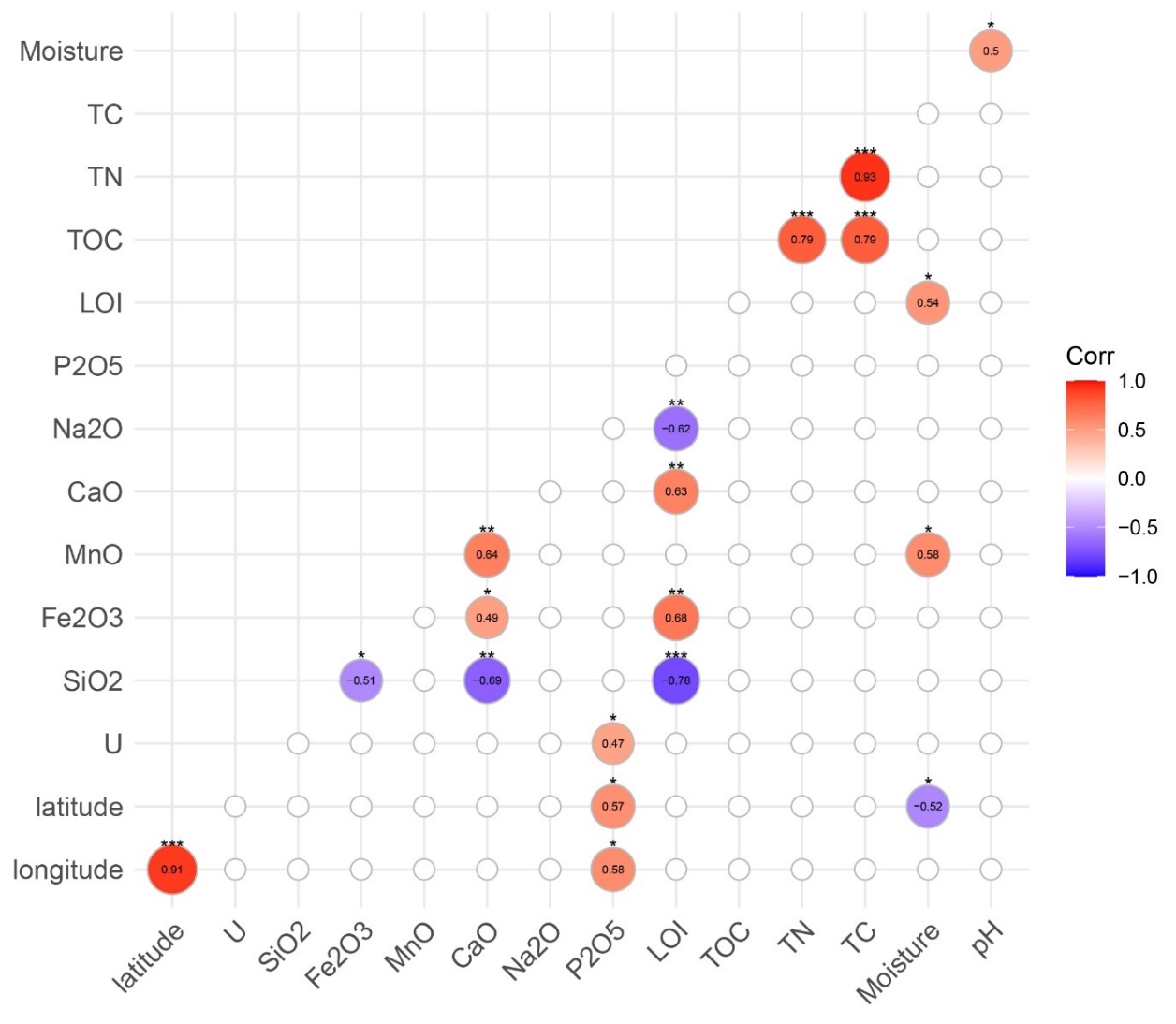
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Al2O3 | K2O | pH | P2O5 | Moisture (%) | MgO | Fe2O3 | Na2O | C [%] | TiO2 | S [%] | CaO |
| Correlation | -0.58 | -0.49 | 0.42 | -0.41 | 0.29 | 0.28 | 0.26 | -0.24 | 0.24 | 0.18 | 0.17 | 0.16 |
| p-value | 0.00 | 0.01 | 0.04 | 0.04 | 0.16 | 0.17 | 0.21 | 0.24 | 0.25 | 0.40 | 0.41 | 0.46 |

**Table S5.** Continued

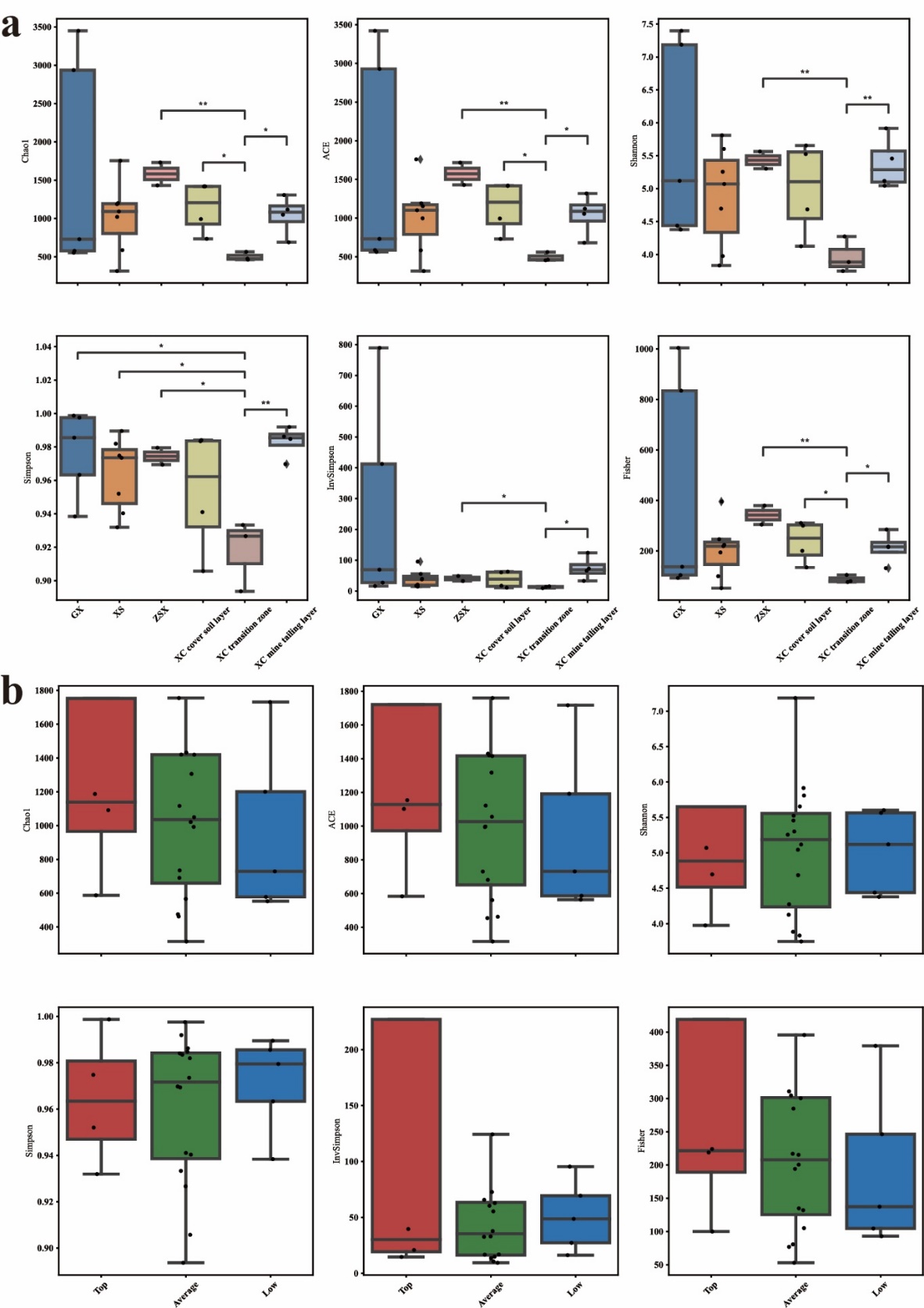
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | TOC(ppm) | LOI | MnO | U | H [%] | SiO2 | N [%] |
| Correlation | 0.15 | 0.14 | 0.12 | -0.08 | 0.06 | -0.01 | 0.00 |
| p-value | 0.49 | 0.51 | 0.58 | 0.72 | 0.76 | 0.96 | 0.99 |

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**Figure S1.** Rarefaction curves of samples. The x-axis represents sequencing depth with a maximum depth of 19285, which is the minimum reads count after filtering. The y-axis indicates the alpha diversity metrics, a) mean observed features, b) Shannon index for each sample. The curve demonstrated that most samples approached saturation at a sequencing depth of 19285, supporting its suitability as the rarefaction depth for downstream analyses.



**Figure S2.** Correlation matrix of environmental variables. Red circles denote positive correlations, while blue circles denote negative correlations, with both the color intensity and circle size reflecting the positive or negative correlation and the magnitude of the correlation coefficient (Corr), respectively. Significant correlations were marked with asterisks (\*P ≤ 0.05, \*\*P ≤ 0.01, \*\*\*P ≤ 0.001). p-values greater than 0.05 are not shown. Abbreviations: TC, Total Carbon; TN, Total Nitrogen; TOC, Total Organic Carbon; LOI, Loss on Ignition.



**Figure S3.** Alpha-diversity of microbial communities across different categories. (a) Boxplots of alpha diversity indices (Chao1, ACE, Shannon, Simpson, InvSimpson, and Fisher) for samples from various sites (GX, XS, ZSX) and layers within site XC, including the cover soil layer, transition zone, and mine tailing layer. Statistically significant differences between groups are indicated by asterisks (\*P ≤ 0.05, \*\*P ≤ 0.01, \*\*\*P ≤ 0.001). (b) Boxplots of the same alpha diversity indices categorized by uranium contamination levels (high, average, and low), with no significant differences observed.