**Table 2.** Summary (mean values) of different alpha-diversity metrics and number of reads for habitats and soil types according to each dataset (16S rRNA: archaea/bacteria; 18S rRNA: eukaryotes; 16S rRNA: nematode-associated microbiome). Kruskal-Wallis (KW) analysis was used to test for significant differences (p<0.05) among habitats and between soil types.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **Metrics** | **Habitats1** | | | | | | **Kruskal-Wallis** | | | **Soil Type2** | | **Kruskal-Wallis** | | |
| **CHA** | **CSS** | **NGR** | **HLC** | **OWL** | **RIP** | **X2** | **df** | ***P*3** | **COMP** | **UNCOMP** | **X2** | **df** | ***P*** |
| **16S rRNA:**  **Archaea/**  **Bacteria**  **(Soil)** | **Number of**  **Reads** | 18,233 | 20,637 | 17,343 | 16,980 | 14,533 | 18,195 | 6.21 | 5 | 0.286 | 18,737 | 16,339 | 2.97 | 1 | 0.085 |
| **Number of**  **ASVs** | 608.4 | 668.4 | 590.1 | 569.4 | 460.7 | 663.83 | 11.56 | 5 | 0.041 | 622.3 | 551.5 | 4.42 | 1 | **0.036** |
| **Shannon**  **(H')** | 5.9 | 6.0 | 5.8 | 5.8 | 5.4 | 5.93 | 20.59 | 5 | **0.001** | 5.89 | 5.65 | 7.69 | 1 | **0.006** |
| **Simpson**  **(D)** | 232.2 | 254.0 | 214.6 | 184.9 | 90.1 | 238.94 | 28.29 | 5 | **<0.0001** | 233.62 | 161.89 | 12.34 | 1 | **0.0004** |
| **Evenness**  **(J')** | 0.920 | 0.924 | 0.920 | 0.912 | 0.881 | 0.921 | 25.83 | 5 | **0.0001** | 0.921 | 0.902 | 11.80 | 1 | **0.0006** |
| **18S rRNA:**  **Eukaryotes**  **(Soil)** | **Number of**  **Reads** | 29,637 | 22,080 | 24,923 | 19,057 | 19,577 | 17,753 | 9.50 | 5 | 0.091 | 25,547 | 18,998 | 6.98 | 1 | **0.008** |
| **Number of**  **ASVs** | 326.0 | 230.6 | 322.8 | 286.7 | 301.8 | 222.8 | 4.89 | 5 | 0.429 | 293.1 | 279.2 | 0.11 | 1 | 0.737 |
| **Shannon**  **(H')** | 4.6 | 4.1 | 4.6 | 4.5 | 4.1 | 3.8 | 12.20 | 5 | 0.032 | 4.4 | 4.2 | 2.56 | 1 | 0.110 |
| **Simpson**  **(D)** | 44.3 | 30.4 | 52.3 | 43.5 | 19.6 | 15.4 | 19.26 | 5 | **0.002** | 42.3 | 26.7 | 5.81 | 1 | **0.016** |
| **Evenness**  **(J')** | 0.798 | 0.795 | 0.820 | 0.795 | 0.733 | 0.741 | 12.87 | 5 | **0.025** | 0.8 | 0.755 | 7.47 | 1 | **0.006** |
| **16S rRNA**  **(Nematode-associated microbiome)** | **Number of**  **Reads** | 5,643 | 3,784 | 8,989 | 8,832 | 8,035 | 7,276 | 35.85 | 5 | **<0.0001** | 6,170 | 8,044 | 5.81 | 1 | **0.020** |
| **Number of**  **ASVs** | 10.81 | 9.93 | 11.36 | 17.79 | 15.22 | 13.51 | 41.11 | 5 | **<0.0001** | 10.7 | 15.5 | 22 | 1 | **<0.0001** |
| **Shannon**  **(H')** | 1.63 | 1.49 | 1.49 | 2.03 | 1.73 | 1.81 | 37.13 | 5 | **<0.0001** | 1.5 | 1.9 | 22.8 | 1 | **<0.0001** |
| **Simpson**  **(D)** | 4.94 | 4.36 | 4.41 | 6.82 | 5.83 | 5.40 | 28.88 | 5 | **<0.0001** | 4.6 | 6.0 | 17.6 | 1 | **<0.0001** |
| **Evenness**  **(J')** | 0.75 | 0.75 | 0.65 | 0.78 | 0.74 | 0.76 | 11.67 | 5 | **0.04** | 0.71 | 0.76 | 4.73 | 1 | **0.030** |

1 Habitats: Chaparral (CHA), Coastal Scrub Sage (CSS), Native Grass (NGR), Holly-leaf Cherry (HLC), Oak Woodland (OWL), and Riparian (RIP).

2 Soil types: compacted (COMP) and uncompacted (UNCOMP).

3 Pairwise comparisons among habitats with adjusted p-values (BH method) are given in Table VV.