**Table S7:** Number of indicator operational taxonomic units (OTUs) per dataset associated with the near-field or far-field station groups.

|  |  |  |  |
| --- | --- | --- | --- |
| **Datasets** | | | **Non-parametric t-test with 999 permutations** |
| Indicator OTUs1 |
| *Bacteria* | *Trimmed by singletons* | *eDNA* | 179 |
| *eRNA* | 96 |
| *Trimmed by shared OTUs* | *eDNA* | 127 (-29%) |
| *eRNA* | 70 (-27%) |
| *Eukaryote* | *Trimmed by singletons* | *eDNA* | 128 |
| *eRNA* | 112 |
| *Trimmed by shared OTUs* | *eDNA* | 29 (-77%) |
| *eRNA* | 26 (-77%) |

1 Differences in percentage of indicator OTUs when compared to the trimmed by singletons dataset are displayed inside brackets.