# S5 Table. Pair-wise comparison of microbiome distance matrices across utilities (ANOSIM, permutation=999).

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| **Utility Pair** | **Unweighted UniFrac** | **Weighted UniFrac** |
| **Global R** | **P** | **Global R** | **P** |
| **A, E** | 0.886 | 0.001 | 0.394 | 0.001 |
| **A, B** | 0.948 | 0.001 | 0.249 | 0.001 |
| **A, C** | 0.997 | 0.001 | 0.883 | 0.001 |
| **A, D** | 0.955 | 0.001 | 0.451 | 0.001 |
| **E, B** | 0.93 | 0.001 | 0.399 | 0.001 |
| **E, C** | 0.997 | 0.001 | 0.757 | 0.001 |
| **E, D** | 0.85 | 0.001 | 0.398 | 0.001 |
| **B, C** | 1 | 0.001 | 0.869 | 0.001 |
| **B, D** | 0.696 | 0.001 | 0.497 | 0.001 |
| **C, D** | 0.999 | 0.001 | 0.822 | 0.001 |