**Supplemental Data**

**Supplemental Table 3**. Kruskal-Wallis results for the alpha diversity metrics for the different types of methods used in the current study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | | **Pielou's Evenness1**  P = 0.00 H=19.93 | | | **Shannon's Diversity1**  P = 0.00 H=18.7 | | |
| Group 1 | Group 2 | H2 | p-value | q-value | H2 | p-value | q-value |
| Direct (n=22) | PEG (n=23) | 0.116 | 0.733 | 0.733 | 0.404 | 0.525 | 0.525 |
| Direct (n=22) | Qiagen (n=7) | **12.727** | **0.000** | **0.004** | **12.010** | **0.001** | **0.005** |
| Direct (n=22) | MQC (n=21) | 3.591 | 0.058 | 0.075 | 1.658 | 0.198 | 0.220 |
| Direct (n=22) | MQ  (n=20) | **5.252** | **0.022** | **0.044** | **7.398** | **0.007** | **0.016** |
| PEG (n=23) | Qiagen (n=7) | **11.282** | **0.001** | **0.004** | **9.392** | **0.002** | **0.011** |
| PEG (n=23) | MQC (n=21) | **4.522** | **0.033** | **0.056** | 2.369 | 0.124 | 0.171 |
| PEG (n=23) | MQ  (n=20) | **5.239** | **0.022** | **0.044** | **5.578** | **0.018** | **0.036** |
| Qiagen (n=7) | MQC (n=21) | **7.466** | **0.006** | **0.021** | **7.466** | **0.006** | **0.016** |
| Qiagen (n=7) | MQ  (n=20) | 3.539 | 0.060 | 0.075 | 2.232 | 0.135 | 0.171 |
| MQC (n=21) | MQ  (n=20) | 0.425 | 0.514 | 0.572 | 2.210 | 0.137 | 0.171 |

1Bolded values are those with significant p and q values

2H value is the test statistic for the Kruskal-Wallis test. A sufficiently high test statist indicates that at least one difference between the medians is statistically significant.

**Supplemental Table 4**. ANOSIM pairwise results for the beta diversity metrics for the different types of methods used in the current study.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | |  |  | Bray-Curtis1  P = 0.01 R=0.13 | | | Weighted Unifrac1  P = 0.001 R=0.11 | | |
| Group 1 | Group 2 | Sample size | Permutations | R2 | p-value | q-value | R2 | p-value | q-value |
| Direct | PEG | 45 | 999 | -0.020 | 0.903 | 0.903 | -0.017 | 0.778 | 0.864 |
| Direct | Qiagen | 29 | 999 | 0.557 | **0.001** | **0.005** | 0.467 | **0.001** | **0.005** |
| Direct | MQC | 43 | 999 | 0.047 | **0.036** | **0.045** | -0.001 | 0.382 | 0.478 |
| Direct | MQ | 42 | 999 | 0.122 | **0.004** | **0.010** | 0.167 | **0.002** | **0.005** |
| PEG | Qiagen | 30 | 999 | 0.451 | **0.003** | **0.010** | 0.401 | **0.002** | **0.005** |
| PEG | MQC | 44 | 999 | 0.062 | **0.012** | **0.017** | 0.016 | 0.196 | 0.280 |
| PEG | MQ | 43 | 999 | 0.107 | **0.005** | **0.010** | 0.138 | **0.008** | **0.013** |
| Qiagen | MQC | 28 | 999 | 0.344 | **0.007** | **0.012** | 0.325 | **0.001** | **0.005** |
| Qiagen | MQ | 27 | 999 | 0.059 | 0.207 | 0.230 | -0.137 | 0.932 | 0.932 |
| MQC | MQ | 41 | 999 | 0.137 | **0.001** | **0.005** | 0.113 | **0.007** | **0.013** |

1Bolded values are those with significant p and q values.

2R is the ANOSIM statistic, compares the mean of ranked dissimilarities between groups to the mean of ranked dissimilarities within groups.

**Supplemental Table 7**. Kruskal-Wallis results for the alpha diversity metrics for the different DNA extraction protocols used in the current study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | | Pielou's Evenness1 | | | Shannon's Diversity1 | | |
| Group 1 | Group 2 | H2 | p-value | q-value | H2 | p-value | q-value |
| 1 Day Direct (n=22) | PEG  (n=23) | 0.116 | 0.733 | 0.733 | 0.404 | 0.525 | 0.525 |
| 1 Day Direct (n=22) | Qiagen Stool\_Kit (n=48) | 9.142 | **0.002** | **0.004** | 8.393 | **0.004** | **0.009** |
| PEG  (n=23) | Qiagen Stool\_Kit (n=48) | 9.663 | **0.002** | **0.004** | 7.643 | **0.006** | **0.009** |

1Bolded values are those with significant p and q values

2H value is the test statistic for the Kruskal-Wallis test. A sufficiently high test statist indicates that at least one difference between the medians is statistically significant.

**Supplemental Table 8**. ANOSIM pairwise results for the beta diversity metrics for the different DNA extraction protocols used in the current study.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Treatment | |  | Bray-Curtis1 | | | |
| Group 1 | Group 2 | Sample size | Permutations | R | p-value | q-value |
| 1 Day Direct | PEG | 45 | 999 | -0.020 | 0.906 | 0.989 |
| 1 Day Direct | Qiagen Stool Kit | 70 | 999 | -0.096 | 0.989 | 0.989 |
| PEG | Qiagen Stool Kit | 71 | 999 | -0.056 | 0.865 | 0.989 |

1Bolded values are those with significant p and q values.

2R is the ANOSIM statistic, compares the mean of ranked dissimilarities between groups to the mean of ranked dissimilarities within groups.

**Supplemental Table 11**. Kruskal-Wallis results for the alpha diversity metrics for the different types of modification to protocols used in the current study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | | Pielou's Evenness1  P = 0.038 H = 4.30 | | | Shannon's Diversity1  P = 0.057 H = 4.30 | | |
| Group 1 | Group 2 | H2 | p-value | q-value | H2 | p-value | q-value |
| Bead Beating (n=41) | None (n=52) | 4.300 | **0.038** | **0.038** | 3.594 | 0.058 | 0.058 |

1Bolded values are those with significant p and q values

2H value is the test statistic for the Kruskal-Wallis test. A sufficiently high test statist indicates that at least one difference between the medians is statistically significant.

**Supplemental Table 12**. ANOSIM pairwise results for the beta diversity metrics for the different types of modification to protocols used in the current study.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | |  |  | Bray-Curtis1  P = 0.025 R=0.04 | | | Weighted Unifrac1  P = 0.034 R=0.039 | | |
| Group 1 | Group 2 | Sample size | Permutations | R2 | p-value | q-value | R2 | p-value | q-value |
| Bead Beating | None | 93 | 999 | 0.044 | **0.038** | **0.038** | 0.040 | **0.040** | **0.040** |

1Bolded values are those with significant p and q values.

2R is the ANOSIM statistic, compares the mean of ranked dissimilarities between groups to the mean of ranked dissimilarities within groups.

**Supplemental Table 15.** Kruskal-Wallis results for the alpha diversity metrics for the different types of DNA purification used in the current study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment |  | Pielou's Evenness1 | |  | Shannon's Diversity1 | |  |
| Group 1 | Group 2 | H2 | p-value | q-value | H2 | p-value | q-value |
| Cellite (n=21) | Ethanol  (n=45) | 5.381 | **0.020** | **0.031** | 2.661 | 0.103 | 0.103 |
| Cellite (n=21) | Silica Membrane (n=27) | 2.528 | 0.112 | 0.112 | 5.085 | **0.024** | **0.036** |
| Ethanol (n=45) | Silica Membrane (n=27) | 14.159 | **0.000** | **0.001** | 15.229 | **0.000** | **0.000** |

1Bolded values are those with significant p and q values

2H value is the test statistic for the Kruskal-Wallis test. A sufficiently high test statist indicates that at least one difference between the medians is statistically significant.

**Supplemental Table 16**. ANOSIM pairwise results for the beta diversity metrics for the different types of DNA purification used in the current study.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Treatment | |  | Bray-Curtis1  P = 0.001 R=0.18 | | | |
| Group 1 | Group 2 | Sample size | Permutations | R2 | p-value | q-value |
| Cellite | Ethanol | 66 | 999 | 0.085 | 0.109 | 0.109 |
| Cellite | Silica Membrane | 48 | 999 | 0.049 | 0.077 | 0.109 |
| Ethanol | Silica Membrane | 72 | 999 | 0.273 | **0.001** | **0.003** |

1Bolded values are those with significant p and q values.

2R is the ANOSIM statistic, compares the mean of ranked dissimilarities between groups to the mean of ranked dissimilarities within groups.