**Table 1.** Differences in gene presence/absence for each taxon based on metadata from Supp. Table 1. PERMANOVA results for genome associations with each factor are reported.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Taxon | Factor | Variables (n) | *R2* | *p*-value |
| *B. cereus* | Strain Origin | BE-Earth (1), BE-ISS (8), Culture-Earth (1), Culture-Shenzhou VIII (2), Human (33), Soil (11) | 0.203 | 0.001 |
| Culture Medium\* | *B. cereus* selective agar (8), Brain heart infusion media (2), Custom media (6), Fastidious broth to blood agar (3), HEPA filter to R2A agar (3), Luria-Bertani media (8), Tripticase soy agar (3) | 0.327 | 0.002 |
| Seq. Technology | Illumina (32), 454 (12), Combination (10) | 0.100 | 0.002 |
| Assembler | A5 (3), ABySS (10), CANU (1), Celera (4), CLC NGS Cell (2), IDBA-UD (5), Combination (5), Newbler (11), SOAPdenovo (3), Spades (8), Velvet (1) | 0.323 | 0.001 |
| Study | 19 different studies/NCBI references (Supp. Table 1) | 0.484 | 0.001 |
| *S. aureus* | Strain Origin | BE-Earth (3), BE-ISS (21), Human (24), Human-MRSA (55), Soil (2) | 0.233 | 0.001 |
| Culture Medium\* | Brain heart infusion agar (2), HCH-supplemented liquid media (1), Tripticase soy agar (28), Tripticase soy broth (37) | 0.218 | 0.001 |
| Seq. Technology | Illumina (32), PacBio (15) | 0.027 | 0.004 |
| Assembler | A5 (13), CLC Genomics Workbench (51), PacBio HGAP3 (15), SeqMan NGen (16), SOAPdenovo (1), Spades (8), Velvet (1) | 0.385 | 0.001 |
| Study | 9 different studies/NCBI references (Supp. Table 1) | 0.472 | 0.001 |

\*Reflects the media that was used in initial bacterial isolation or that which was used in isolate collection/processing, where available (i.e., not all studies provided culture method details, and some provided only information for how strains were processed rather than initial isolation)