**Table 1.** Differences in gene presence/absence for each taxon based on strain origin, sequencing technology, and assembler method. PERMANOVA results for genome associations with each factor are reported.

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| --- | --- | --- | --- | --- |
| 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 |
| 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 |
| *S. aureus* | Strain Origin | BE-Earth (3), BE-ISS (21), Human (32), Human-pathogen (47), Soil (2) | 0.205 | 0.001 |
| Seq. Technology | Illumina (32), PacBio (15) | 0.023 | 0.006 |
| Assembler | A5 (13), CLC Genomics Workbench (51), PacBio HGAP3 (15), SeqMan NGen (16), SOAPdenovo (1), Spades (8), Velvet (1) | 0.385 | 0.001 |