**Supplementary Table 4: Student t-test results to identify significant differences between the number of viral contigs (as identified by VirSorter** [(Roux et al., 2015)](https://paperpile.com/c/ssJt3i/qxHI)**) from short read only vs. hybrid assemblies with VirION reads using metaSPAdes assemblies from triplicate random subsamples of short reads across different levels of sequencing coverage.** Significant differences are highlighted in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sequencing depth (Gbp)** | ***p*-value** | **Mean count of viral contigs (short-read only)** | **Mean count of viral contigs (hybrid)** | **Fold-difference** |
| **3.08** | **0.00** | **373.0** | **552.3** | **1.48** |
| **6.17** | **0.00** | **752.0** | **889.7** | **1.18** |
| **9.25** | **0.02** | **1038.3** | **1100.0** | **1.06** |
| 12.34 | 0.17 | 1300.0 | 1330.3 | 1.02 |
| 15.42 | 0.32 | 1497.0 | 1507.3 | 1.01 |
| 18.50 | 0.33 | 1651.0 | 1672.7 | 1.01 |
| 21.59 | 0.96 | 1810.67 | 1811.67 | 1 |