**Supplementary Table 3: Student t-test results to identify significant differences between the number of circular 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 depth.** Significant differences are highlighted in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sequencing depth (Gbp)** | ***p*-value** | **Mean count of circular viral contigs (short-read only)** | **Mean count of circular viral contigs (hybrid)** | **Fold-difference** |
| 3.08 | 0.26 | 8.00 | 13.7 | 1.71 |
| 6.17 | 0.08 | 11.7 | 22.7 | 1.94 |
| 9.25 | 0.05 | 18.3 | 31.00 | 1.70 |
| **12.34** | **0.00** | **20.7** | **33.3** | **1.61** |
| **15.42** | **0.04** | **18.7** | **36.7** | **1.96** |
| **18.50** | **0.01** | **23.3** | **36.0** | **1.54** |
| **21.59** | **0.01** | **25.3** | **39.7** | **1.56** |