|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Recruitment to whole genome** | | | | | | | | | | | **Fuess et al., 2015** | | | | | | | **Gudenkauf & Hewson, 2015** | | | | |
|  | **ONP2** | **ONP3** | **ONP4** | **SCD6** | **SCD7** | **SCD8** | **V30** | **V31** | **V32** | **V33** | **Treated L** | | **Control PH** | **Control DB** | **Ccontrol FHL** | **Phel Treated FHL** | **Treated FHL** | **T1** | | **T2** | **T3** | **T4** |
|  | **A** | **A** | **S** | **S** | **S** | **S** | **A** | **A** | **S** | **S** | **T** | | **C** | **C** | **C** | **T** | **T** | **A** | | **A** | **S** | **S** |
|  | **Reads Recruited** | | | | | | | | | | | | | | | | | | | | | | |
| **ARV1** | 10,064 | 65 | 5,739 | 34 | 709 | 257,147 | 2 | 0 | 0 | 142 | 72 | | 4 | 11 | 1 | 0 | 0 | 2 | | 7 | 99 | 0 |
| **ARV2** | 129 | 113 | 79 | 0 | 0 | 0 | 4 | 86 | 9 | 3,321 | 2 | | 47 | 0 | 23 | 12 | 12 | 3 | | 0 | 98 | 0 |
| **ARV3** | 197,059 | 227,216 | 216,363 | 124,714 | 233,551 | 144,142 | 0 | 2 | 12 | 48 | 69 | | 2 | 0 | 4 | 0 | 0 | 0 | | 2 | 102 | 0 |
| **ARV4** | 442,646 | 472,142 | 496,850 | 328,520 | 449,255 | 297,129 | 0 | 1 | 0 | 23 | 69 | | 2 | 0 | 4 | 0 | 0 | 0 | | 0 | 108 | 0 |

**Supplemental Table 8:** Recruitment of RNA viral metagenomes and transcriptomes (Fuess et al., 2015; Gudenkauf & Hewson, 2015) to asteroid RNA viruses assembled from RNA viral metagenomes. Recruitment was performed using BLASTn using an e-value cut-off of 1e-10. A= asymptomatic, S = SSWD-affected, C= control, T = treated with filtered viruses.