

Supplementary Table 4. Unknown samples CT value prior to MinION™ library preparation and post preparation.  
Estimated copy number/ml based off of previously reported literature [13, 16, 29].

|            | PCR CT value Pre-MinION<br>Librabry Prep     | Estimated<br>number of<br>virus copies<br>(copies/ml) | PCR CT value Post-MinION<br>Librabry Prep      | Estimated<br>number of<br>virus copies<br>(copies/ml) | Unknown<br>Virus<br>Sequencing<br>Reads<br>Perecentage<br>s | Total<br>Number of<br>Reads per<br>virus | Percent of<br>Reads<br>belonging to<br>viruses out<br>of total<br>number of<br>reads |
|------------|--|---|--|---|---|--|--|
| UK1 Swine  | <i>Porcine Circovirus 2</i> CT=8             | 6.47E+11  | <i>Porcine Circovirus 2</i><br>CT=12.72        | 2.26E+10  | 19.67%  | 22,293                                   | 19.70%   |
|            | Porcine reproductive<br>syndrome virus CT=25 | 1.00E+05  | Porcine reproductive<br>syndrome virus CT = NA | NA  | NA  | NA                                       | NA   |
| UK2 Swine  | Porcine seneca valley virus A<br>CT=37       | 8.00E+01  | Porcine seneca valley<br>virus A CT=28.34      | 4.10E+02  | 0.01%   | 7  | 0.01%  |
| UK1 Bovine | Bovine viral diarrhea virus<br>CT=28.26      | 1.16E+08  | Bovine viral diarrhea virus<br>CT=35.23        | 1.13E+06  | 0.01%   | 1  | 0.01%  |

\* colors denotes if viruses were identified with conventional diagnostic methods (qPCR) and ONT sequencing pre or post library prep.

Green denotes samples identified in both qPCR assay and ONT sequencing pre and post library prep.

Red denotes samples that were identified in pre MinION prep but could not be identified in qpcr or sequencing post prep.