

1 **Supplementary Data Table descriptions**

2 **Table S1.** Interactive spreadsheet of all mass spectrometry data. The “DATA” worksheet shows
3 minimally annotated protein data, with only formatting and normalisation modifying the raw data.
4 The “Plotter” worksheet enables generation of individual protein abundance changes for both viral
5 and human proteins over time from experiments 1 and 2. The total number of quantified peptides
6 and proteins from experiments 1 and 2 are shown in separate workbook sheets.

7 **Table S2.** A list of all quantified proteins from experiments 1 and 2 that match the UniProt keywords
8 terms ‘Innate Immunity’ and ‘Antiviral Defense’ and their corresponding fold changes post-BKPyV
9 infection.

10 **Table S3.** Proteins modulated during BK infection. All proteins downregulated or upregulated >2-
11 fold at any time point during the course of infection (compared to the average of the mock samples).
12 Results from experiments 1 and 2 are presented.

13 **Table S4.** DAVID functional enrichment analysis from proteins upregulated or downregulated >2-
14 fold against a background of all proteins quantified. Only significant (Benjamini-Hochberg
15 corrected) clusters from experiments 1 and 2 are shown. There were no significant clusters amongst
16 proteins downregulated >2-fold in experiment 2.

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