Supplementary information guide

Table S1 | Data of translatome measurements by MS. Contains Uniprot Accession, Species annotation, Gene Symbol and normalized translation data for each replicate (Data was normalized using summed intensity normalisation for sample loading, followed by internal reference scaling and Trimmed mean of M normalisation). Log2 ratios and *P* values were computed for each group comparison (two-sided, unpaired t-test with equal variance assumed, *n* = 3 independent biological samples). See Fig. 2.

Table S2 | Data of proteome measurements by MS. Contains UniProt Accession, Gene Symbol and normalized protein abundances for each sample. (Data was normalized using summed intensity normalisation for sample loading, followed by internal reference scaling and Trimmed mean of M normalisation). Log2 ratios and *P* values were computed for each group comparison (two-sided, unpaired t-test with equal variance assumed, *n* = 3 independent biological samples). See Fig. 3, 4.

Table S3 | Results of Reactome pathway analysis of genes decreased in protein level during infection (Fig. 3a, S3). Pathway names, size of pathway, proteins found in dataset, *P* values and FDR are given (*P* values by binomial test and FDR by binomial test and Benjamini-Hochberg correction).

Table S4 | Results of Reactome pathway analysis of genes increased in protein level during infection (Fig. 3a, b). Pathway names, size of pathway, proteins found in dataset, *P* values and FDR are given (*P* values by binomial test and FDR by binomial test and Benjamini-Hochberg correction).

Table S5: |Results of gene ontology (biological process) analysis of genes following viral gene expression (Fig. 4). GO term, proteins found in dataset, GO size, *P* value and FDR are given (*P* values by binomial test and FDR by binomial test and Benjamini-Hochberg correction).