SUPPLEMENTARY FIGURE LEGENDS

Fig. S1: Reproducibility between biological replicates of Spike in-SILAC samples. Scatter plot analysis of biological replicates at indicated time points p.i. Displayed are log2(L/H) values of Pan (upper panel) and Mal (lower panel) infected cells, replicate 1 at y axis and replicate 2 at x axis. Numbers indicate number of quantified protein groups (black) and the corresponding Pearson correlation (blue); dots represent protein groups.

Fig. S2: Biological processes executed by 16 differentially regulated proteins (Pan vs. Mal infected cells). Classification of 16 proteins with significant log2(fold change) >1 or <-1 upon infection with Pan in comparison to Mal virus infected cells at indicated time points according to their gene ontology terms “biological process” (GOBP) using PANTHER (Protein analysis through evolutionary relationships) Classification System Version 10.0.

Fig. S3: siRNA transfection does not affect cell viability. WST-1 assay was performed 48 h post transfection by adding WST-1 reagent to the cells, followed by incubation at 37 °C for 1.5 h. Absorbance was measured at 460 nm and at the reference wavelength 590 nm. Non-targeting siRNA (AllStars) and siPLK1 were used as positive and negative controls, respectively.

Fig. S4: SAMHD1 expression levels are down-regulated in Pan infected cells. A549 cells were infected with Pan or Mal virus at an MOI of 0.5. At 4 h and 16 h p.i. cells were fixed, permeabilized, stained with specific primary antibody against NP, SAMHD1 and with DAPI. Images were representative for three independent experiments. White arrows indicate NP positive cells with low SAMHD1 expression

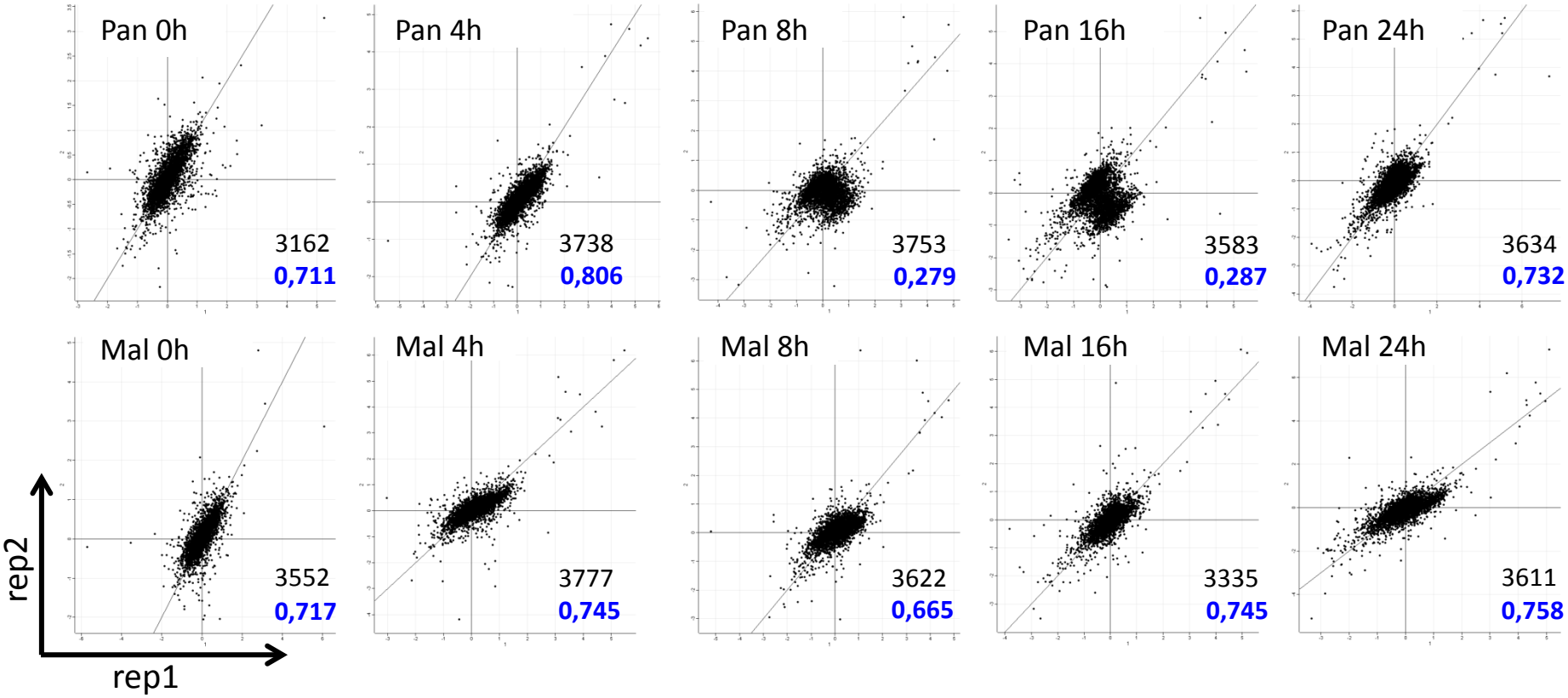
levels, yellow arrows mark infected cells with high levels of SAMHD1. Scale bar: 10 µm. SAMHD1: green, NP: red, DAPI: blue.

Supplementary Table 1: All identified proteins summarized as protein groups. Sequence coverage (%) and number of unique peptides were stated for all samples (total) and separately for each individual sample. Displayed are also gene names as well as L/H ratios, variability and count.

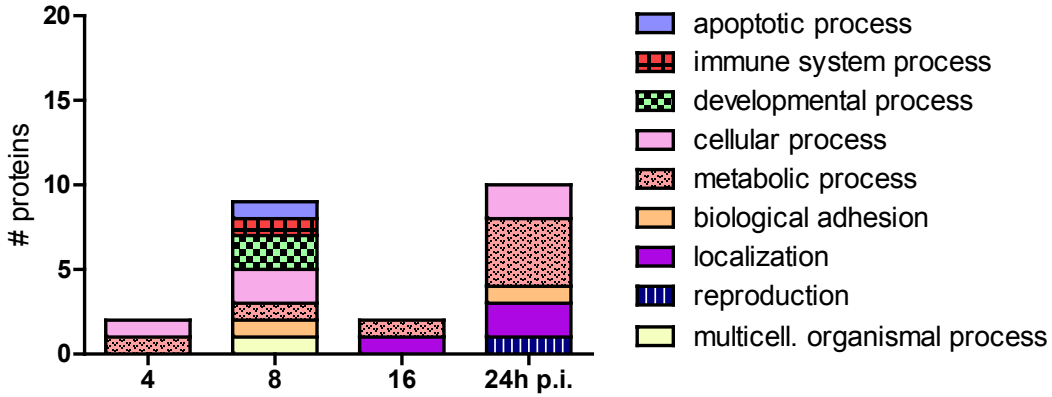
Supplementary Table 2: All peptides used for protein identification including their sequence, charge, m/z, modifications, score, PEP, mass error (Da), retention time and mass. Potential contaminants are also indicated as well as gene names, proteins and protein group IDs.

Supplementary Table 3: Classification of peptide sequences as unique peptide for a specific protein or protein group. Potential contaminants are also indicated as well as gene names, proteins and protein group IDs.

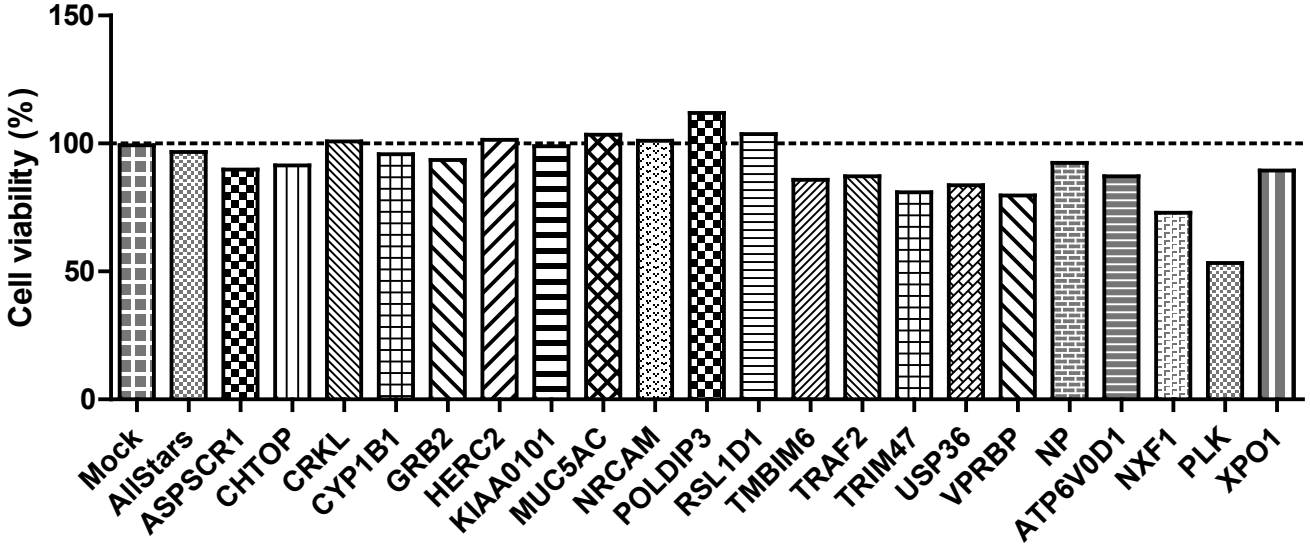
Supplementary Table 4: Significantly regulated proteins in each individual sample compared to 0 h time point. Listed are gene names, -Log(P-value), difference (of two time points), Protein IDs, Protein names, Symbol color (see volcano plots – Fig. 4), GOBP name, GOMF name, GOCC name as well as [log2(L/H)] ratios of the respective samples.


Pan 0h
3162
0,711
Pan 4h
3738
0,806
Pan 8h
3753
0,279
Pan 16h
3583
0,287
Pan 24h
3634
0,732
Mal 0h
3552
0,717
Mal 4h
3777
0,745
Mal 8h
3622
0,665
Mal 16h
3335
0,745
Mal 24h
3611
0,758
rep2
rep1

Supplementary Fig. 2



Supplementary Fig. 3



Supplementary Fig. 4