

## Supplemental Material

### **Proteomic and transcriptomic analysis of *Microviridae* $\phi$ X174 infection reveals broad up-regulation of host membrane damage and heat shock responses.**

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Table S1: TMT Labelling scheme

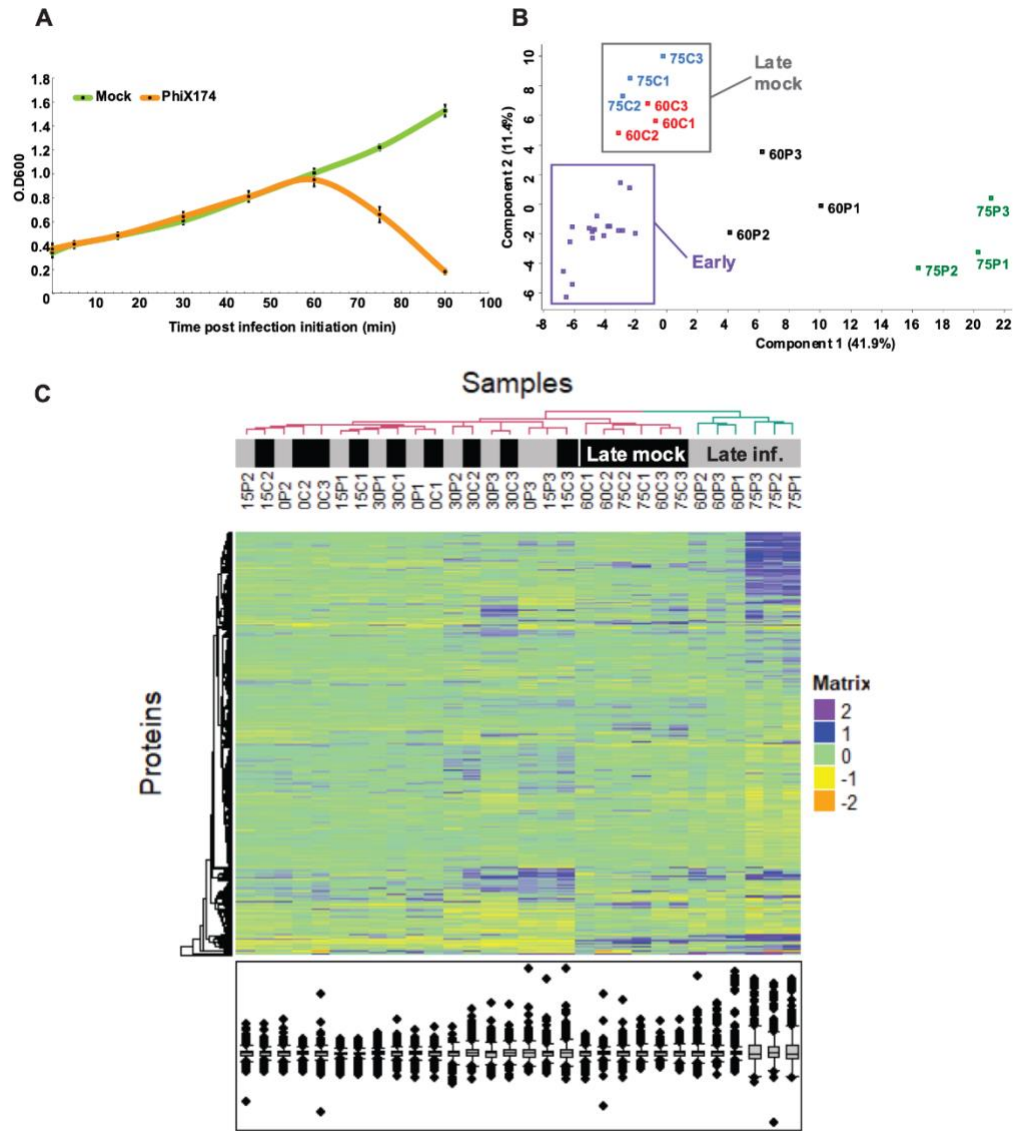
### FILES

Supplementary File S1: TMT proteomics data

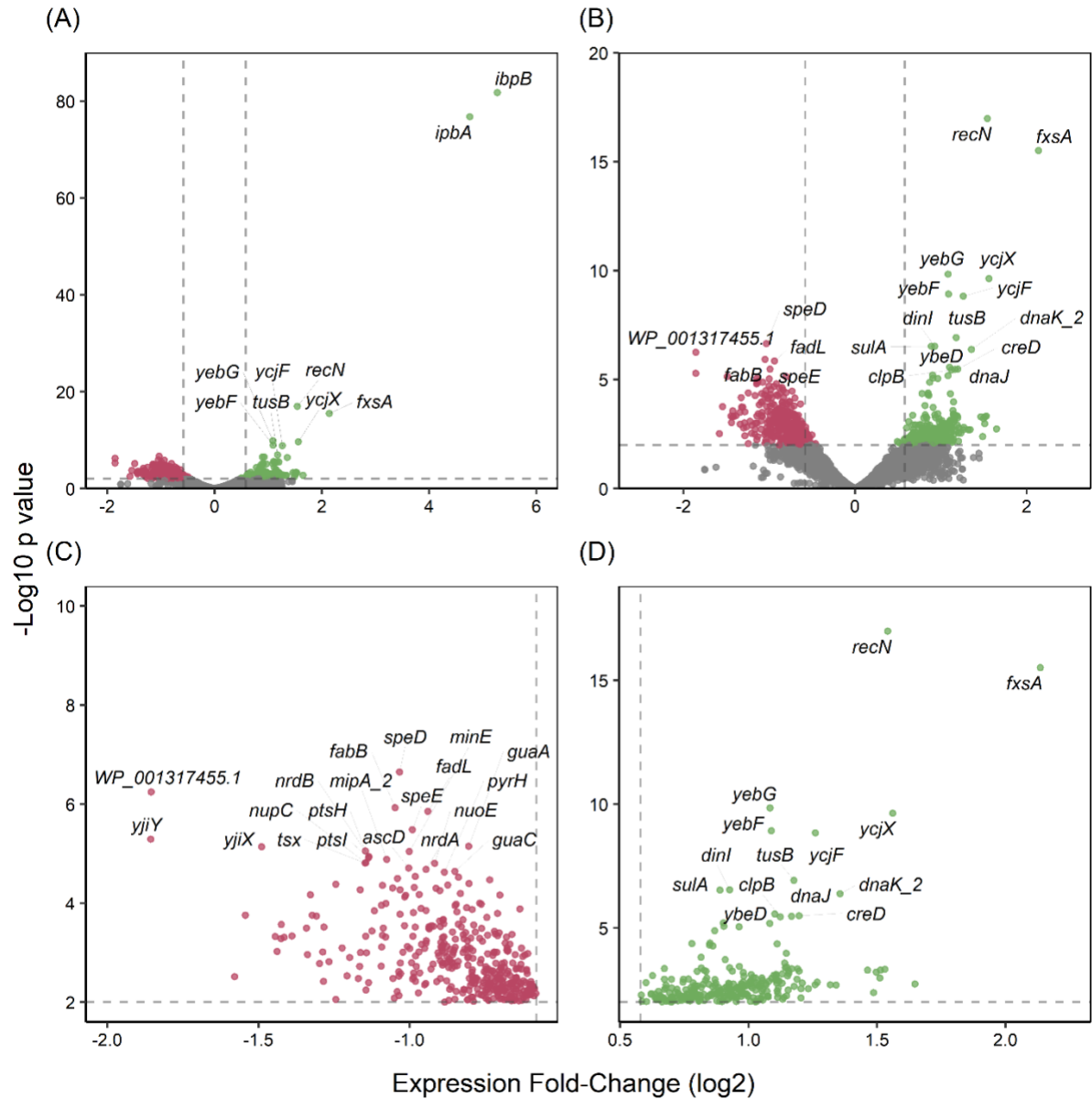
Supplementary file S2: Transcriptional dataset of all C122 genes

Supplementary File S3: Sigma32 and Sigma38 analysis

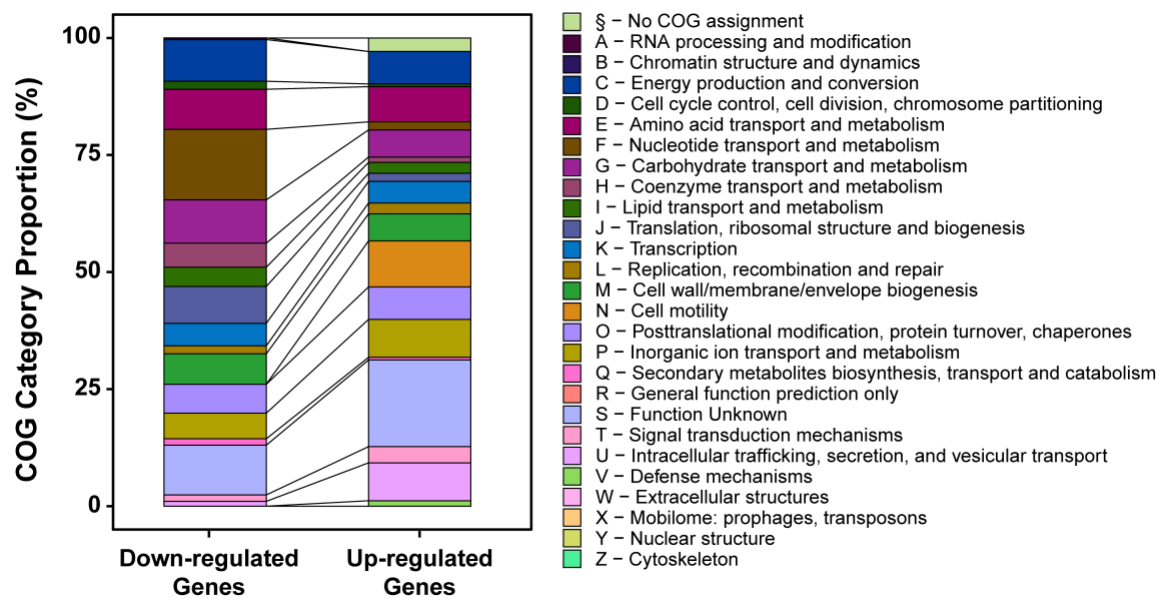
Supplementary File S4: MS protein database



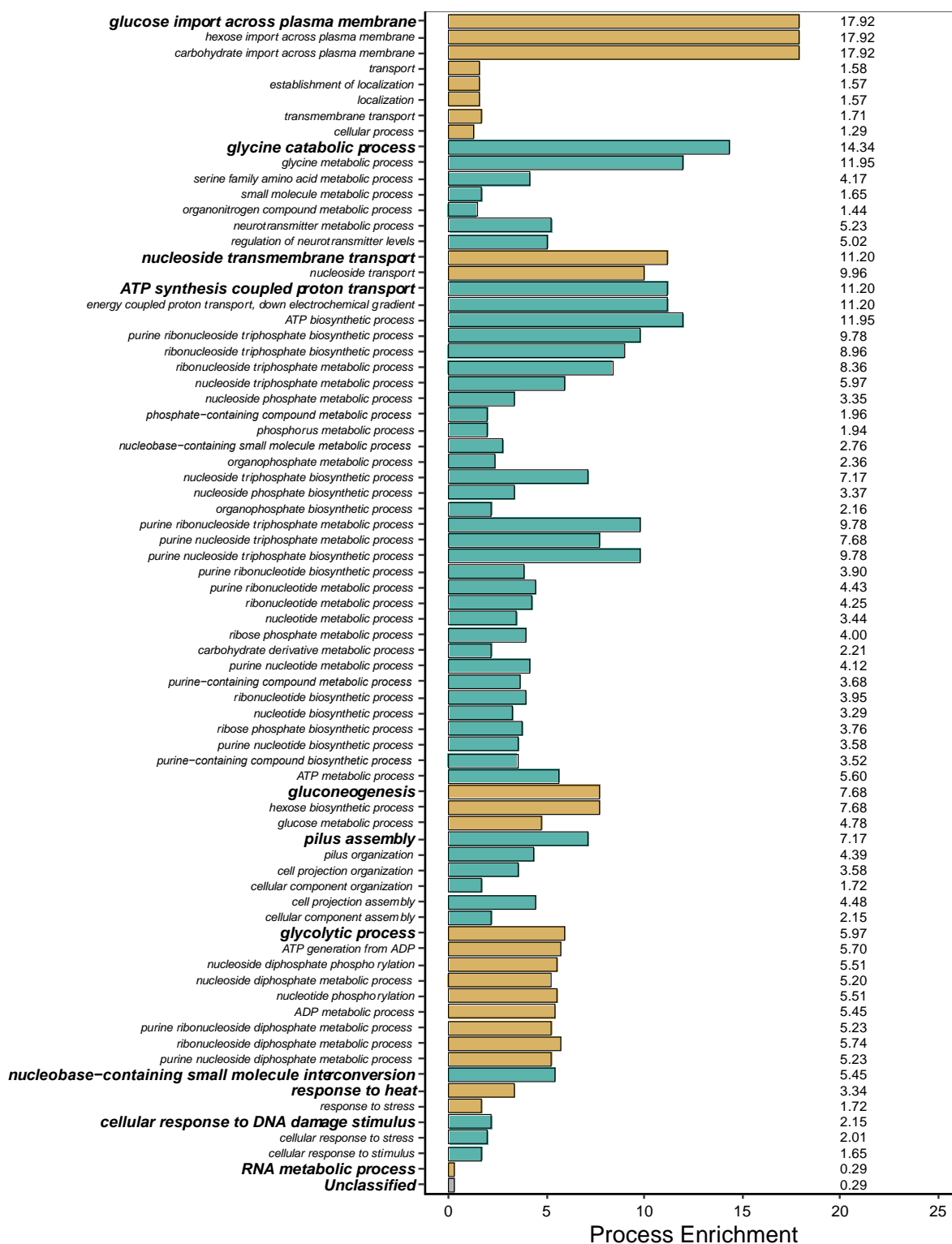
**Figure S1 Mock and  $\phi$ X174 infected *E. coli* C122 Analysis.** **(A)** Lysis curve of  $\phi$ X174 and *E. coli* C122. Lysis was observed at 60-minutes post-infection initiation. **(B)** 2-Dimensional principle component analysis (PCA) of mock-infected (C) and  $\phi$ X174-infected (P) samples. Separate clustering of the later time-point control samples (Late mock) to that of the early time-points of both mock-infected and  $\phi$ X174-infected (Early) can be observed. Similarly, separate clustering of later time points of the 60-minute and 75-minute  $\phi$ X174-infected samples (60P and 75P) to each other and of the late mock and early groupings is observed. **(C)** Hierarchical clustering with Euclidean distance of quantified proteins. Clustering of later time-points (late), and their associated condition (mock = mock-infected, inf. =  $\phi$ X174-infected) highlights the change in the proteome over time and by  $\phi$ X174 infection.



**Figure S2. Differential expression *E. coli* C122 genes during  $\phi$ X174 infection.** (A) Differential expression of all genes within infected *E. coli* C122 with significantly up-regulated genes shown in green and significantly down-regulated genes shown in red. Dashed lines represent significance criteria ( $\log_2$  fold change =  $\pm 0.585$  and p values < 0.05). (B) Differentially expressed genes excluding highly up-regulated genes *ibpA* and *ibpB*. (C) Down-regulated genes (close up). (D) Up-regulated genes (close up). Comparison were made between RNA-sequencing outputs from cultures harvested at lysis in the infected and mock infected samples, samples were analyzed using Rsubread and DESeq2 in biological triplicates.


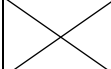


**Figure S3 Biological function COG distributions for differentially expressed *E. coli* C122 genes in the RNA-seq dataset.** The enrichment of COG terms in the down- and up-regulated RNA-seq datasets from C122 at lysis. UniProt IDs mapped to COG terms using EggNOG-Mapper (1). Gene ID with multiple COG terms were converted to multiple single term entries for analysis.



**Figure S4 Major biological function GO terms differentially expressed in RNA-seq dataset.** Differentially expressed genes from *E. coli* C122 were analyzed using the PANTHER over-representation test using the GO terms for Biological Function (2). All presented data displayed a p value of < 0.01.

**Table S1: TMT Labelling scheme.** There were four TMT 10-plex experiments with each channel comprising a different sample, except for the 128C and 131 channels. Channel 128C contained the pooled mock-infected samples (designated N.C), and channel 131 contained the pooled  $\phi$ X174-infected samples (designated N.P)

	Mock-infected					$\phi$ X174-infected				
TMT	126	127N	127C	128N	128C	129N	129C	130N	130C	131
1	0 <sub>1</sub>	15 <sub>1</sub>	30 <sub>1</sub>	60 <sub>1</sub>	N.C	0 <sub>1</sub>	15 <sub>1</sub>	30 <sub>1</sub>	60 <sub>1</sub>	N.P
2	75 <sub>1</sub>	0 <sub>2</sub>	15 <sub>2</sub>	30 <sub>2</sub>	N.C	75 <sub>1</sub>	0 <sub>2</sub>	15 <sub>2</sub>	30 <sub>2</sub>	N.P
3	60 <sub>2</sub>	75 <sub>2</sub>	0 <sub>3</sub>	15 <sub>3</sub>	N.C	60 <sub>2</sub>	75 <sub>2</sub>	0 <sub>3</sub>	15 <sub>3</sub>	N.P
4	30 <sub>3</sub>	60 <sub>3</sub>	75 <sub>3</sub>		N.C	30 <sub>3</sub>	60 <sub>3</sub>	75 <sub>3</sub>		N.P

Subscript = replicate number

## References

1. Huerta-Cepas, J., Forslund, K., Coelho, L.P., Szklarczyk, D., Jensen, L.J., von Mering, C. and Bork, P. (2017) Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. *Molecular Biology and Evolution*, **34**, 2115-2122.
2. Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X. and Thomas, P.D. (2019) Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v.14.0). *Nature protocols*, **14**, 703-721.