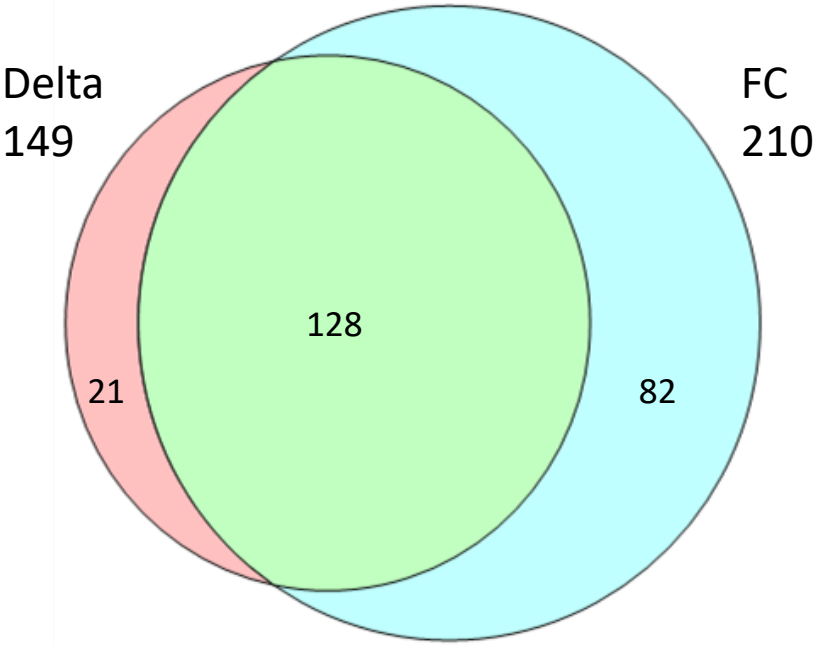
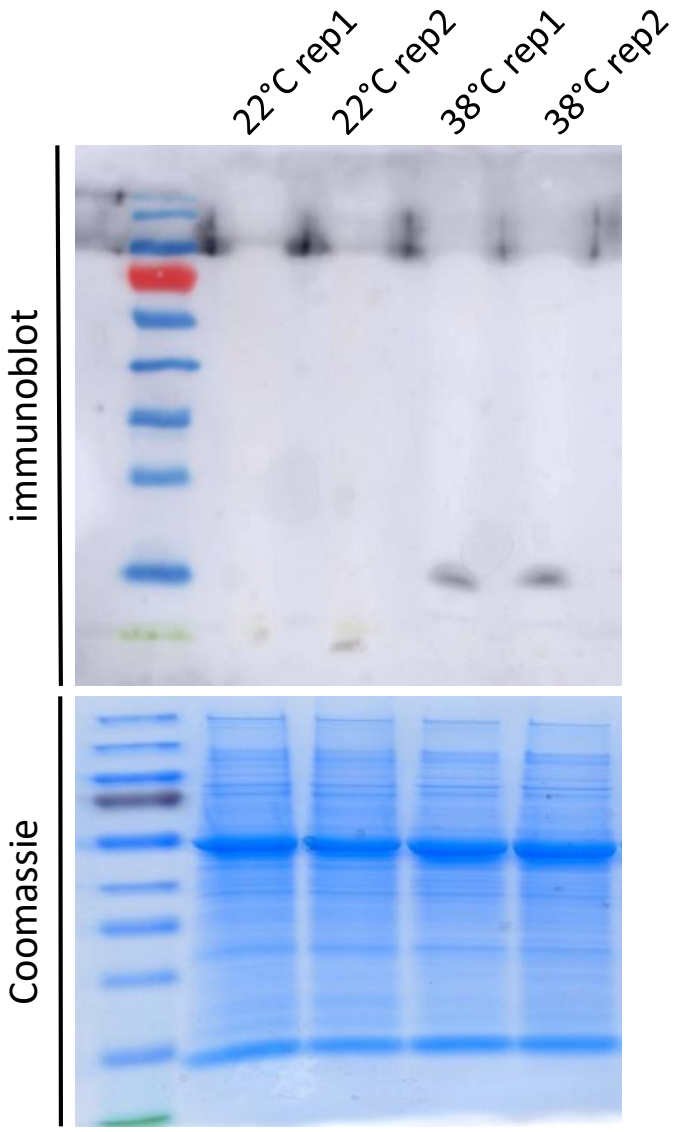
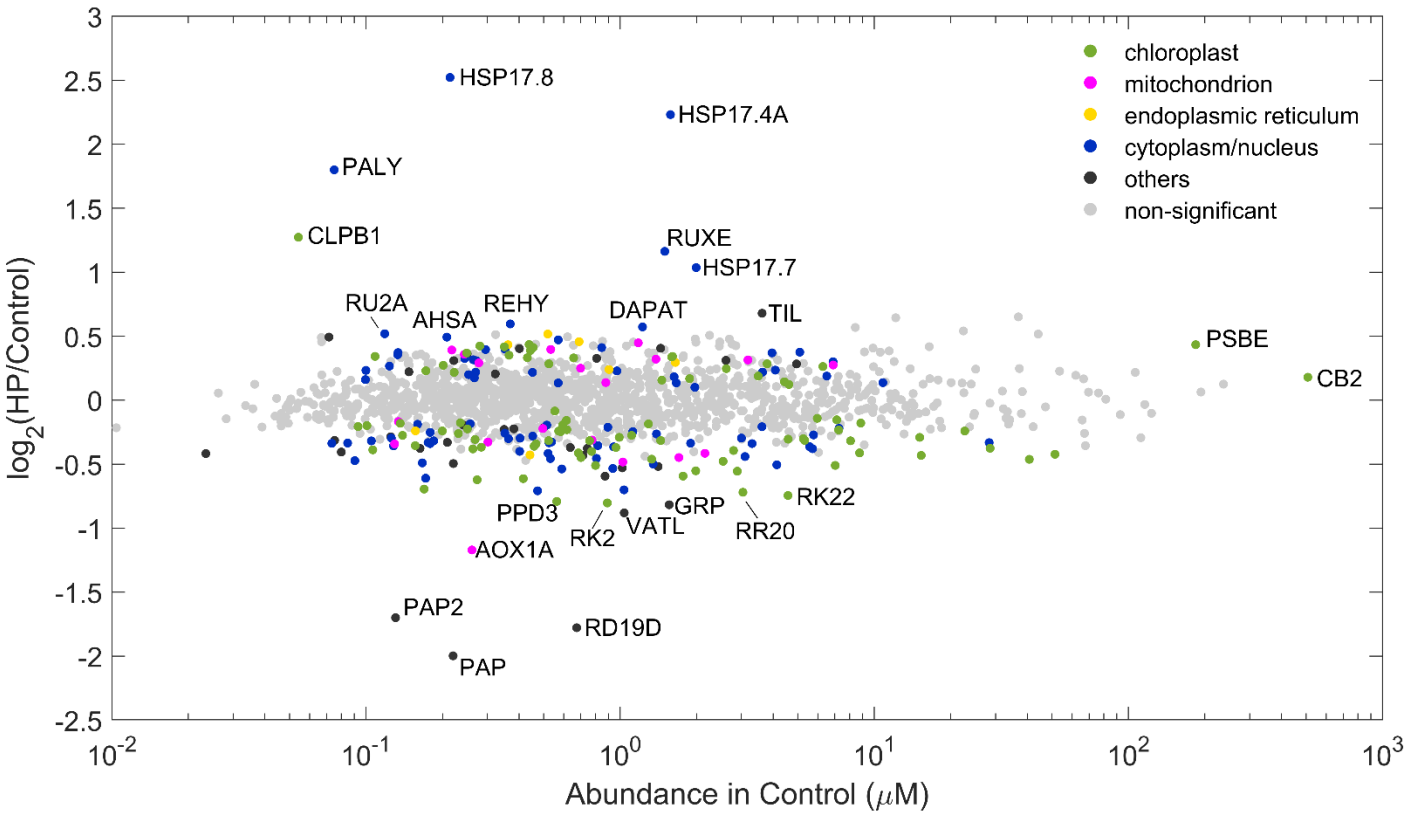


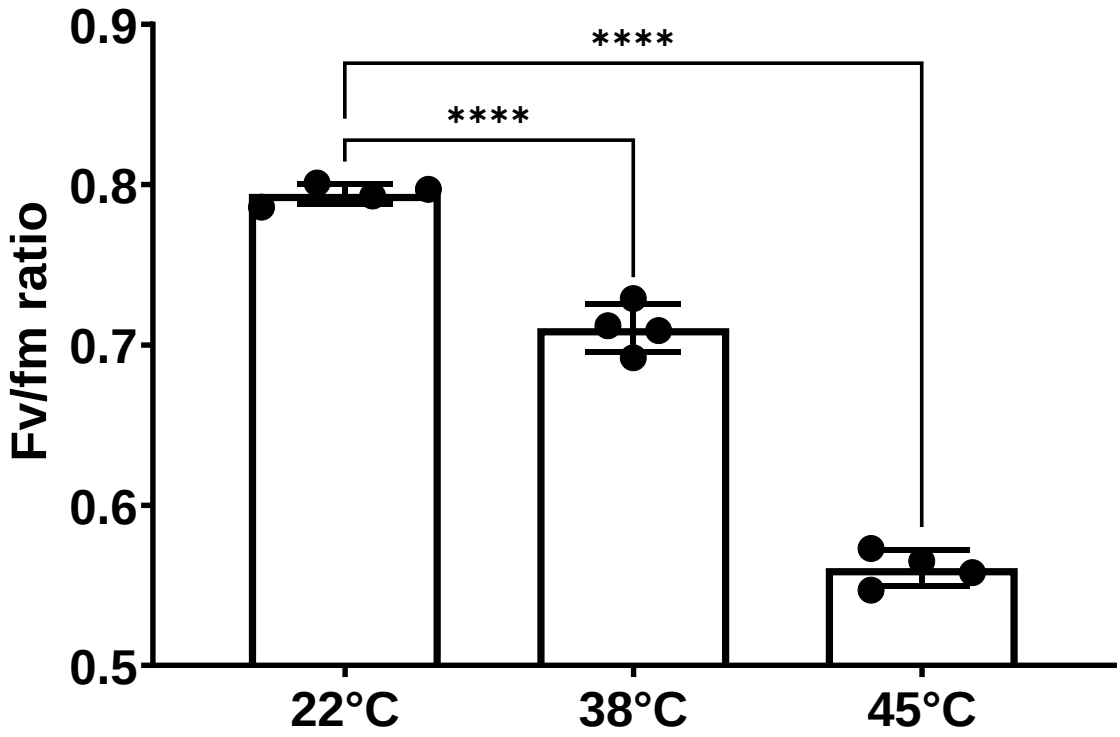
Supplementary Figure S1. Venn diagram diagram showing the number of overlapping and not overlapping proteins identified, significantly quantified and significantly differentially accumulated proteins in *Physcomitrium patens* under heat priming in fold-change and in delta (differences of mass).



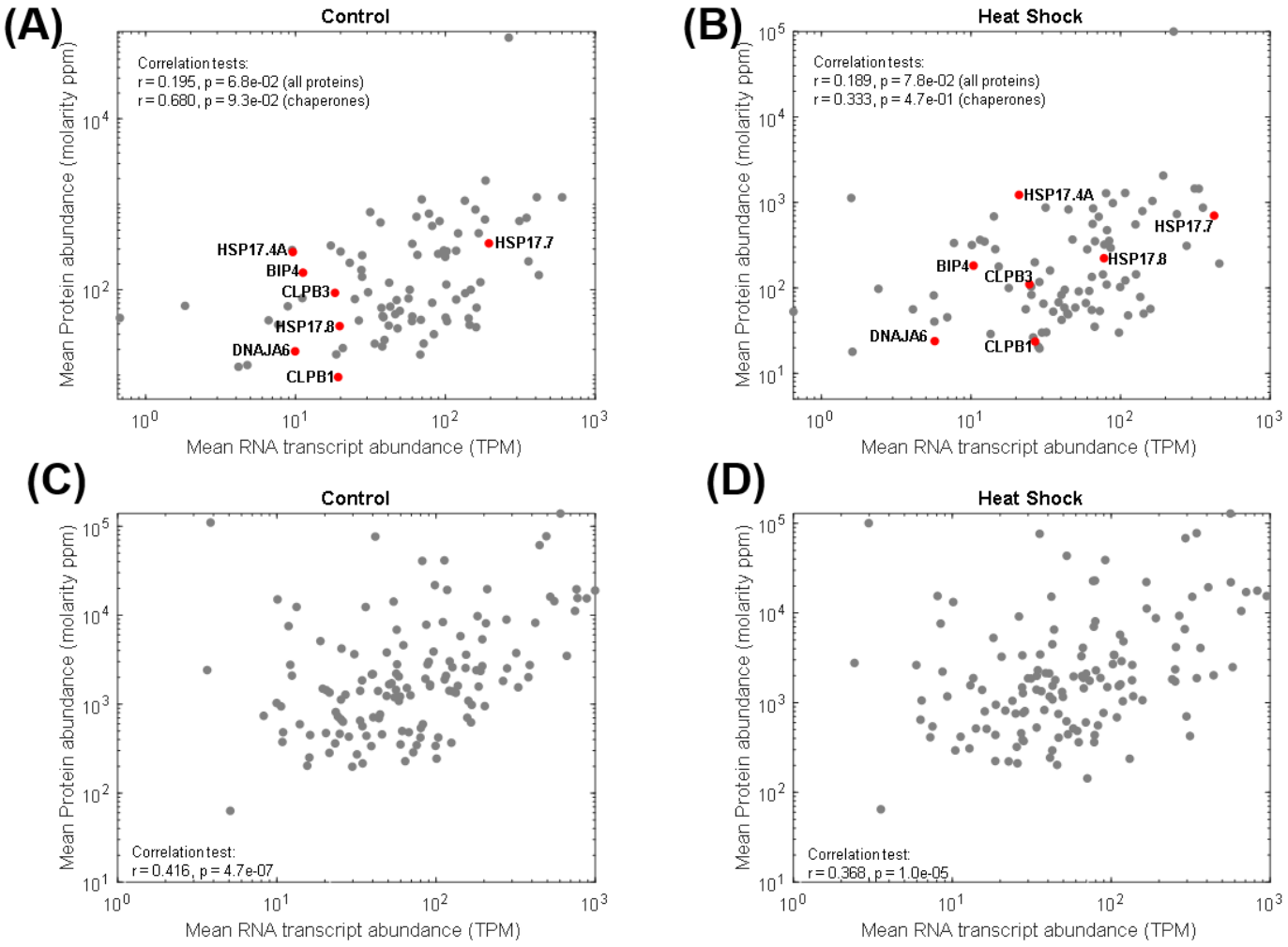
Supplementary Figure S2. Immunoblot showing the relative expression levels of HSP17.7 in *Physcomitrella patens* HSP-GUS line following 4 hours priming at 38°C and at 22°C. The coomassie gel showing the large Rubisco subunit (~ 53kDa) was used as a loading control.



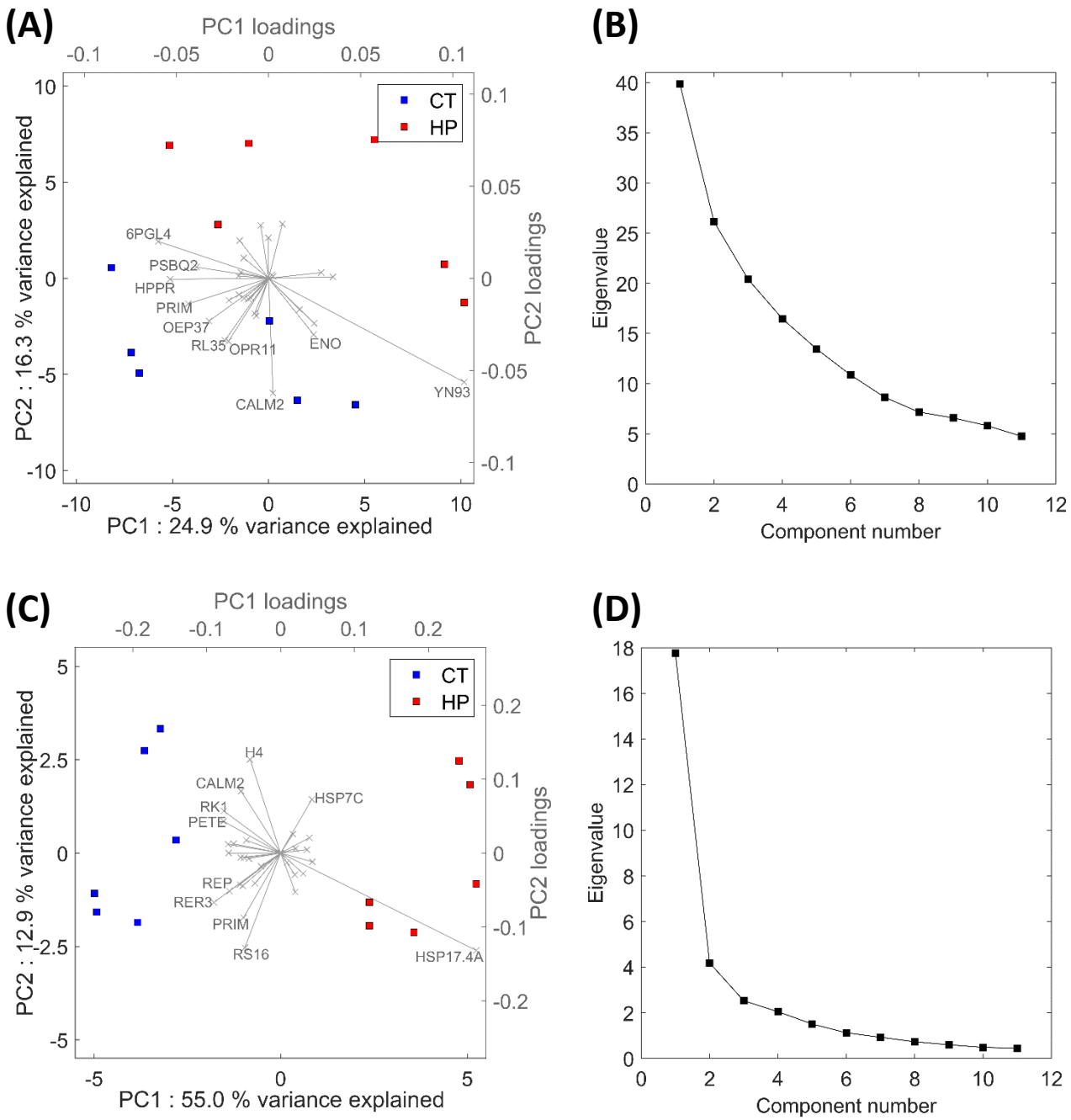
Supplementary Figure S3. Distribution of differentially expressed proteins by subcellular localization. MA-plot showing log ratio versus abundance plots in molarity for heat treated moss protonemata compared to control. Each protein is represented as a dot and is mapped according to its mass fraction in fold change on the abscissa axis (x) and its fold change on the ordinate axis (y). Proteins considered as significantly regulated (p-value < 0.05) are plotted in full dot; or grey dot if they are not significant. Subcellular localization is represented in green for chloroplast, pink for mitochondrion, yellow for endoplasmic reticulum, blue for cytoplasm and nucleus and in dark for others.



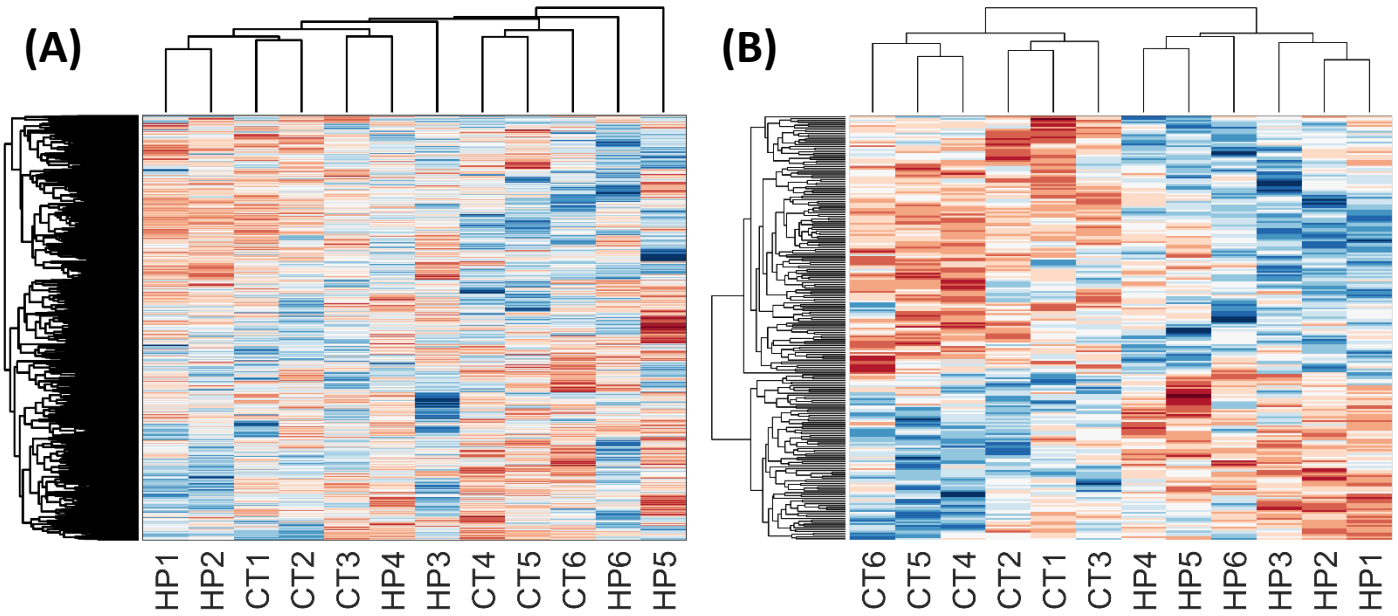
Supplementary Figure S4. Bar diagram showing the effect of 4 hours at various temperature on photosynthesis activity by calculating Fv/fm ratio. Each black dot represents biological replicate and the asterisks designate the significance of changes from their resultant control (**** $p < 0.001$).



Supplementary Figure S5. ScatterPlot showing a correlation between upregulated proteins in Parts Per Million (ppm) mapped against RNAseq data in Transcripts Per Million (tpm) at 22°C (A) and under heat priming (B), and between downregulated proteins in ppm mapped against RNAseq data in tpm at 22°C (C) and under heat priming (D). Chaperones are shown as red dots.



Supplementary Figure S6. Principal Component Analysis. **(A)** PCA biplot obtained from the abundances of the 1514 significantly quantified proteins, with the corresponding scree plot in **(B)**. **(C)** PCA biplot obtained from the abundances of the 231 significantly varying proteins between CT and HP, with the corresponding scree plot in **(D)**. Note that the GUS transgene was excluded from the data before performing PCAs.



Supplementary Figure S7. Clustered heatmaps from the standardized, log-transformed protein mass fractions obtained either from **(A)** the 1514 significantly quantified proteins, or **(B)** from the 231 significantly varying proteins between CT and HP. Hierarchical clustering was computed using Euclidean distances and average linkages. Red and blue colors indicate standardized abundances above and below the per-protein average, respectively.