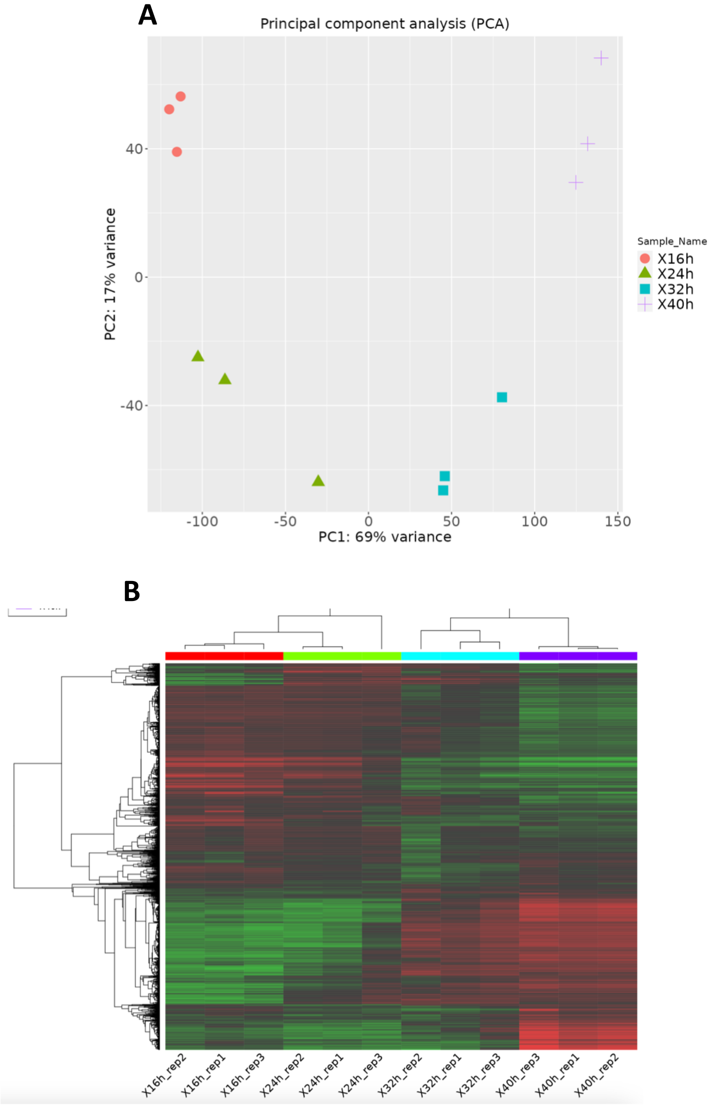
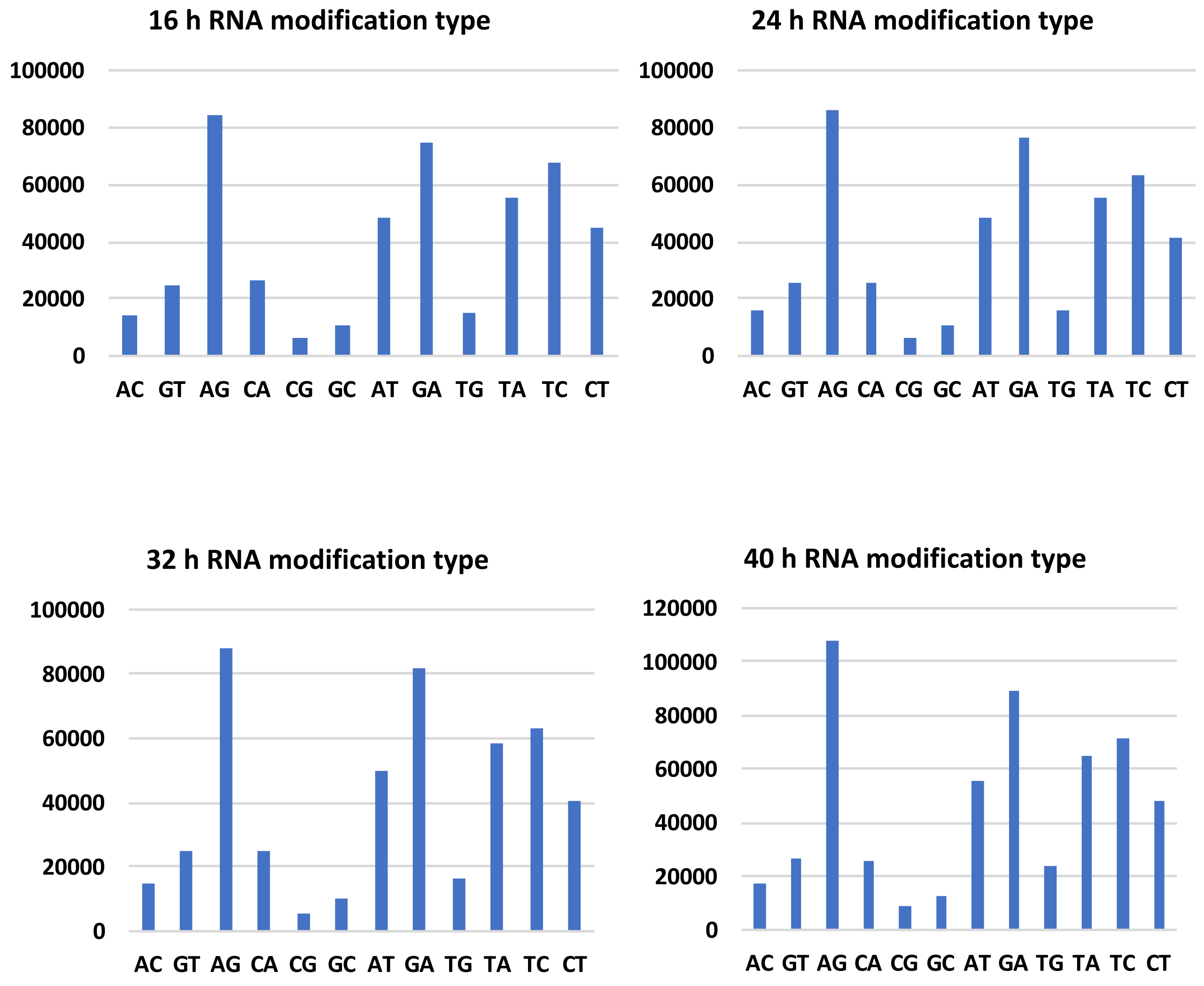
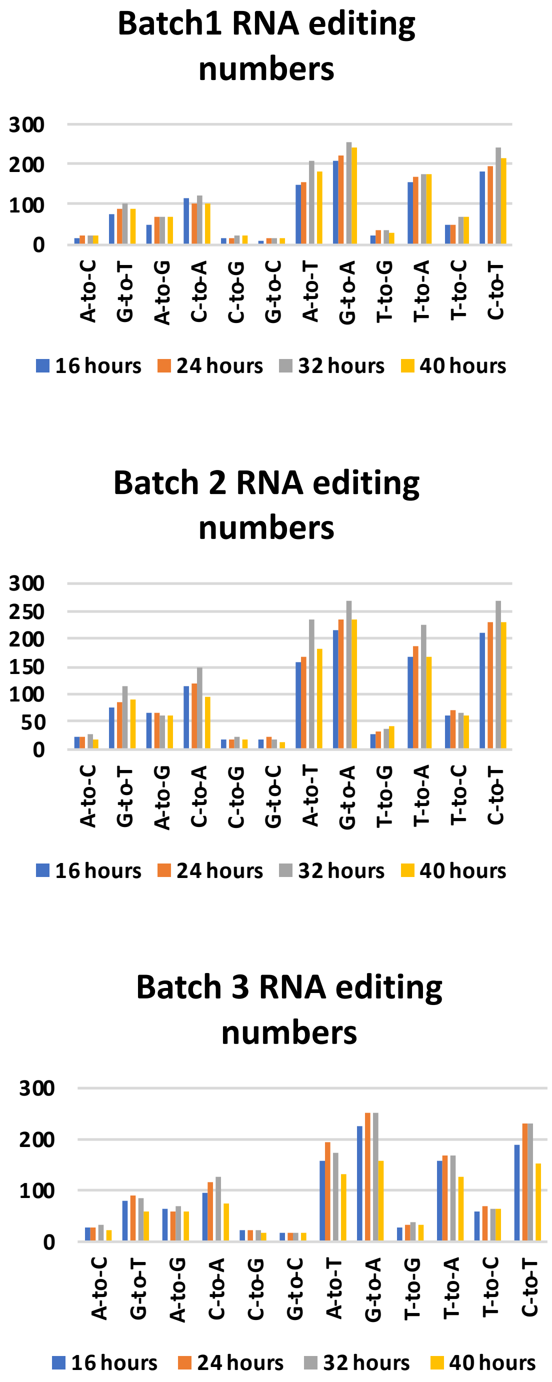


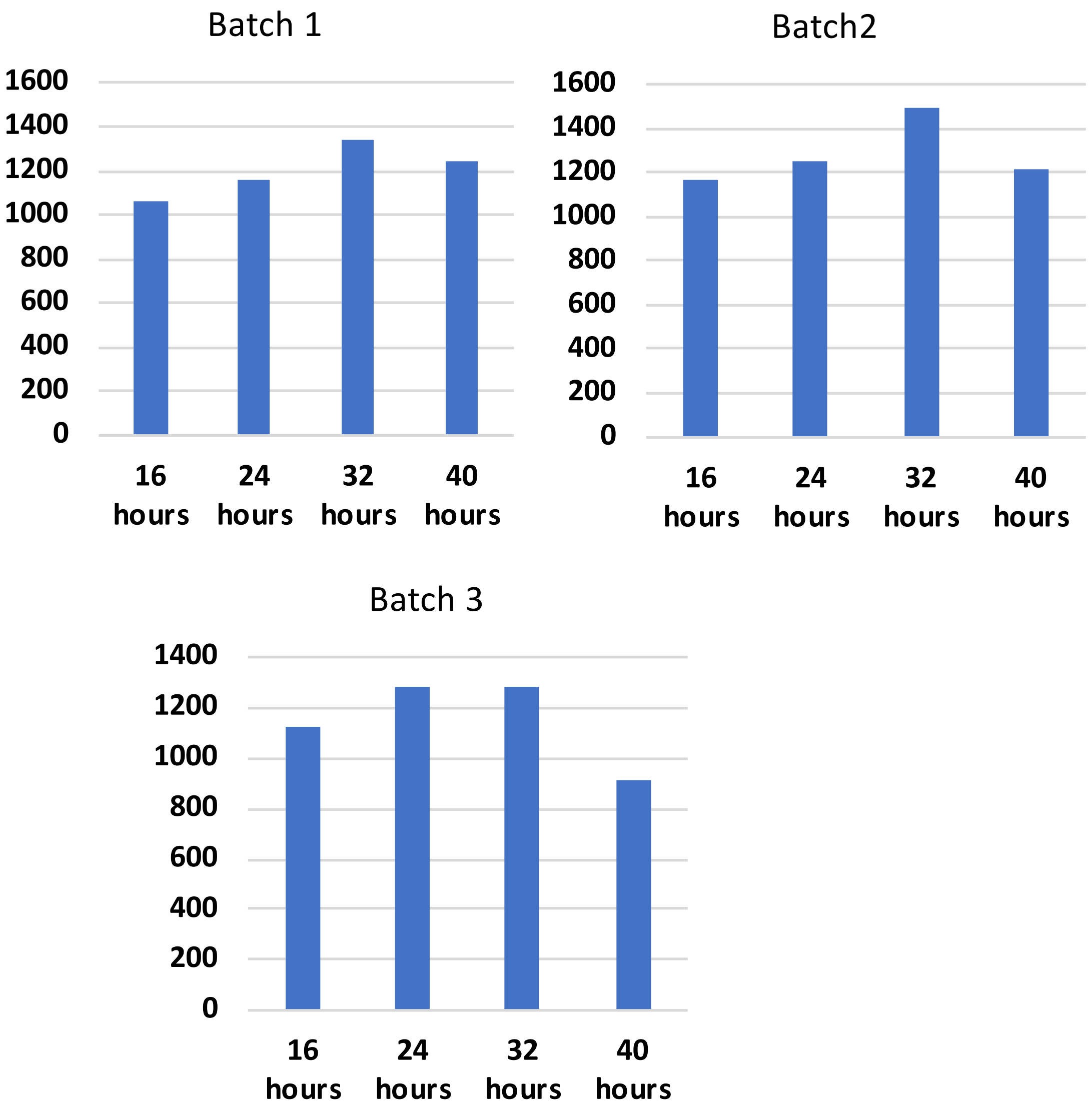
Supplementary Figure 1. A. PCA analyses indicate that the samples can be analyzed further. B. About 2100 genes are included; replicates of samples are clustered together.



Supplementary Figure 2. RNA variation detection by REDItools1, Denovo.

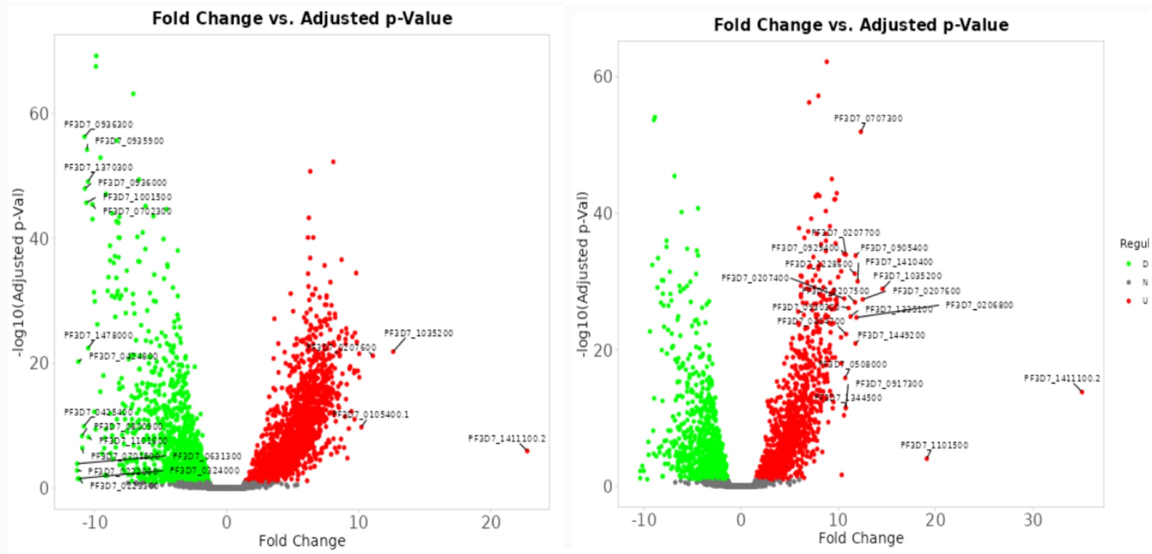


Supplementary figure 3. Distribution of the diiferent types of RNA editing as determined by using the REDitools2 approach.



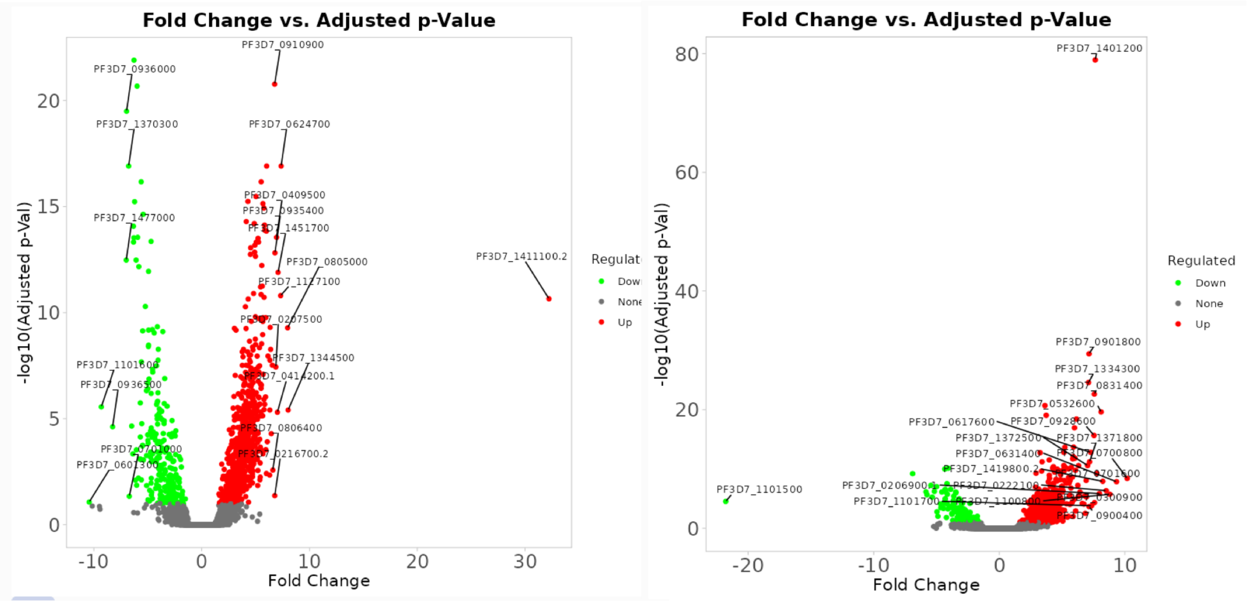
Supplementary Figure 4. Number of RNA editing events as determined by REDitools2 in three different replicates.

Stage-specific volcano plot



40 h-16 h

40 h -24 h

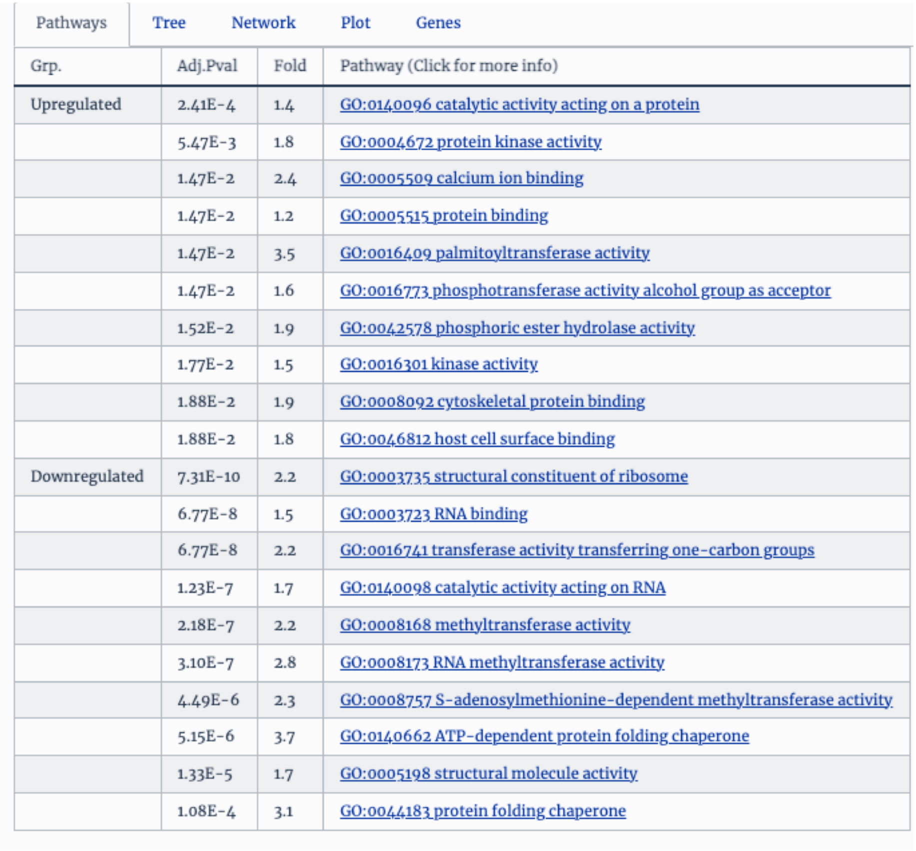


32 h-24 h

24 h-16 h

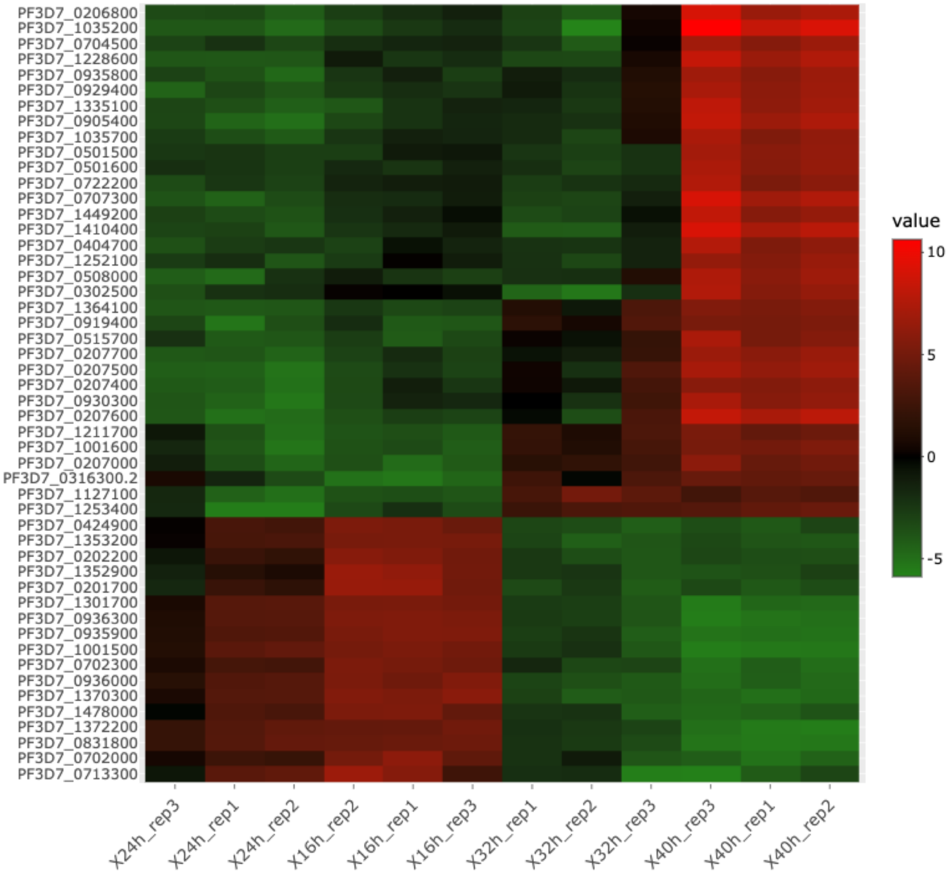
Supplementary Figure 5. Stage-specific volcano plots of 40 h -16 h, 40 h -24 h, 32 h -24 h, and 24 h -16 h. Of the 20 most affected genes, the number of downregulated genes is higher.

A



Grp.	Adj.Pval	Fold	Pathway (Click for more info)
Upregulated	2.41E-4	1.4	GO:0140096 catalytic activity acting on a protein
	5.47E-3	1.8	GO:0004672 protein kinase activity
	1.47E-2	2.4	GO:0005509 calcium ion binding
	1.47E-2	1.2	GO:0005515 protein binding
	1.47E-2	3.5	GO:0016409 palmitoyltransferase activity
	1.47E-2	1.6	GO:0016773 phosphotransferase activity alcohol group as acceptor
	1.52E-2	1.9	GO:0042578 phosphoric ester hydrolase activity
	1.77E-2	1.5	GO:0016301 kinase activity
	1.88E-2	1.9	GO:0008092 cytoskeletal protein binding
	1.88E-2	1.8	GO:0046812 host cell surface binding
Downregulated	7.31E-10	2.2	GO:0003735 structural constituent of ribosome
	6.77E-8	1.5	GO:0003723 RNA binding
	6.77E-8	2.2	GO:0016741 transferase activity transferring one-carbon groups
	1.23E-7	1.7	GO:0140098 catalytic activity acting on RNA
	2.18E-7	2.2	GO:0008168 methyltransferase activity
	3.10E-7	2.8	GO:0008173 RNA methyltransferase activity
	4.49E-6	2.3	GO:0008757 S-adenosylmethionine-dependent methyltransferase activity
	5.15E-6	3.7	GO:0140662 ATP-dependent protein folding chaperone
	1.33E-5	1.7	GO:0005198 structural molecule activity
	1.08E-4	3.1	GO:0044183 protein folding chaperone

B



Supplementary Figure 6. A. Affected pathways at 40 h-32 h. B. Expression of the 50 most affected genes in different stages of the samples. Gene IDs are included to the left of the figure.