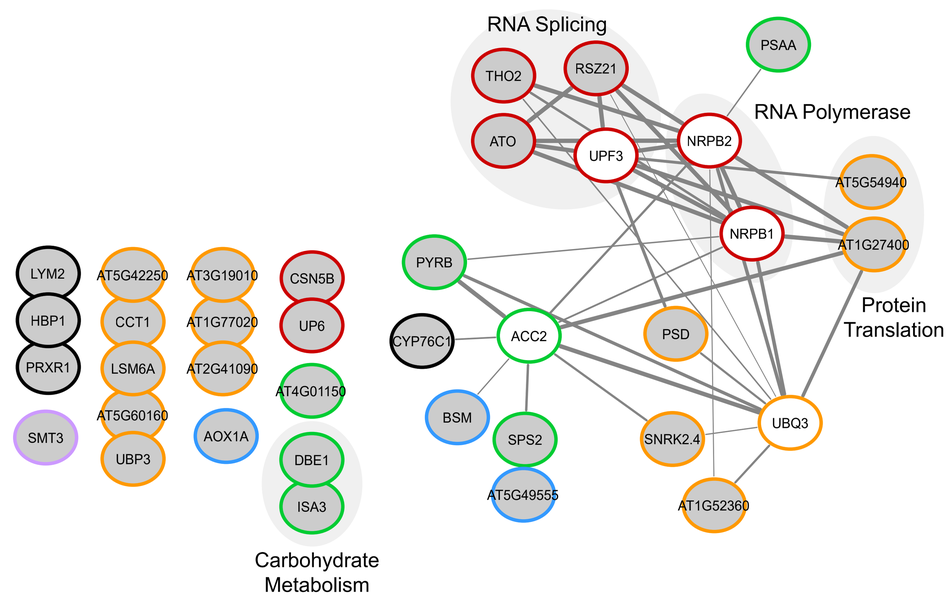
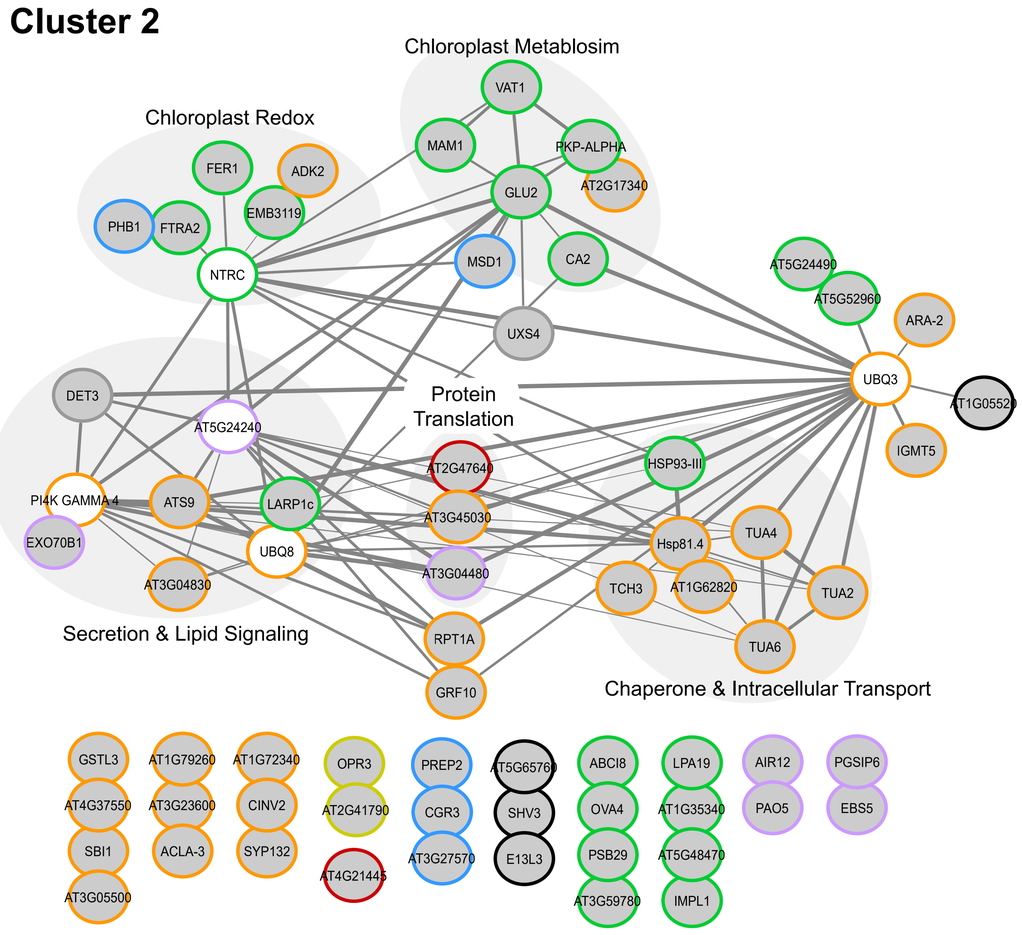
Figure 2

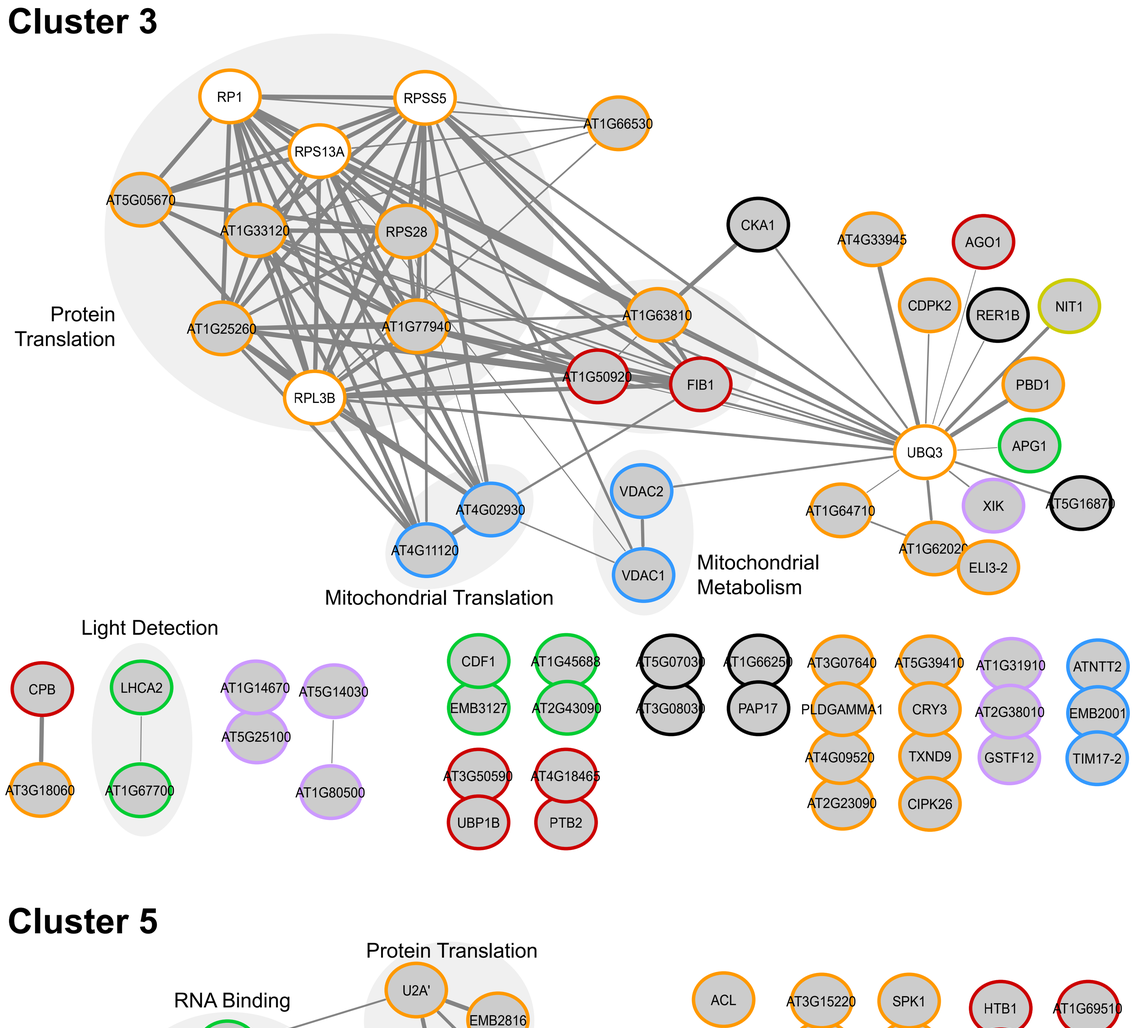
Cluster 1



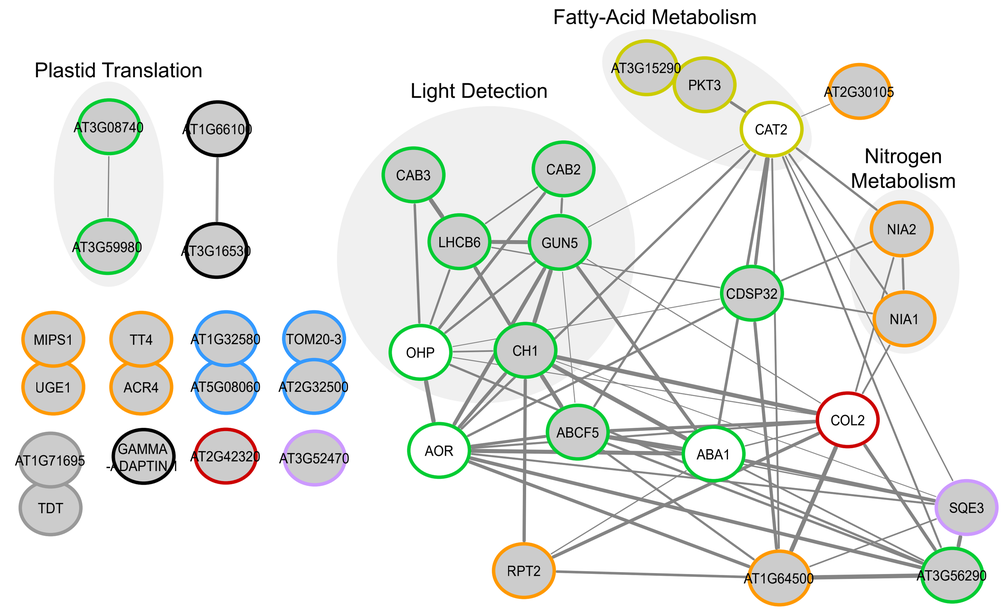
Cluster 2



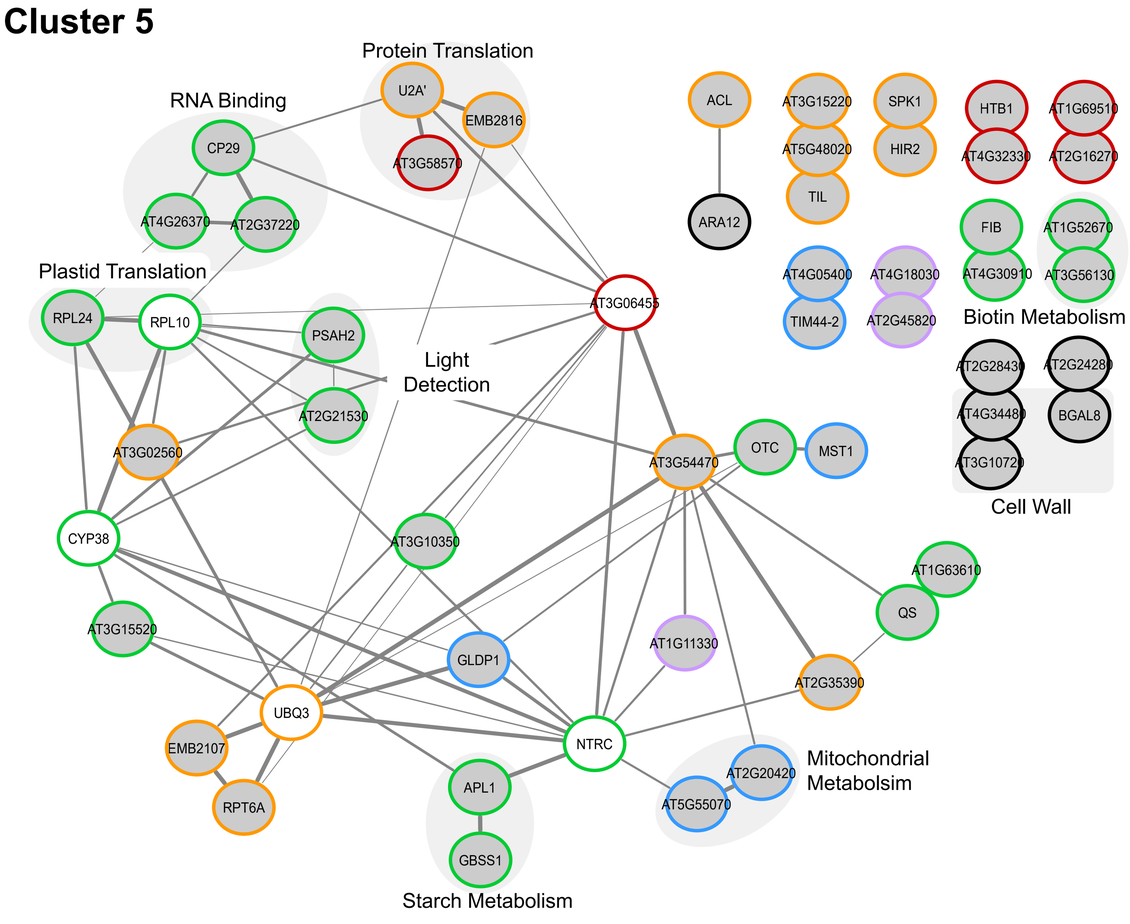
Cluster 3



Cluster 4



Cluster 5



Cluster 6

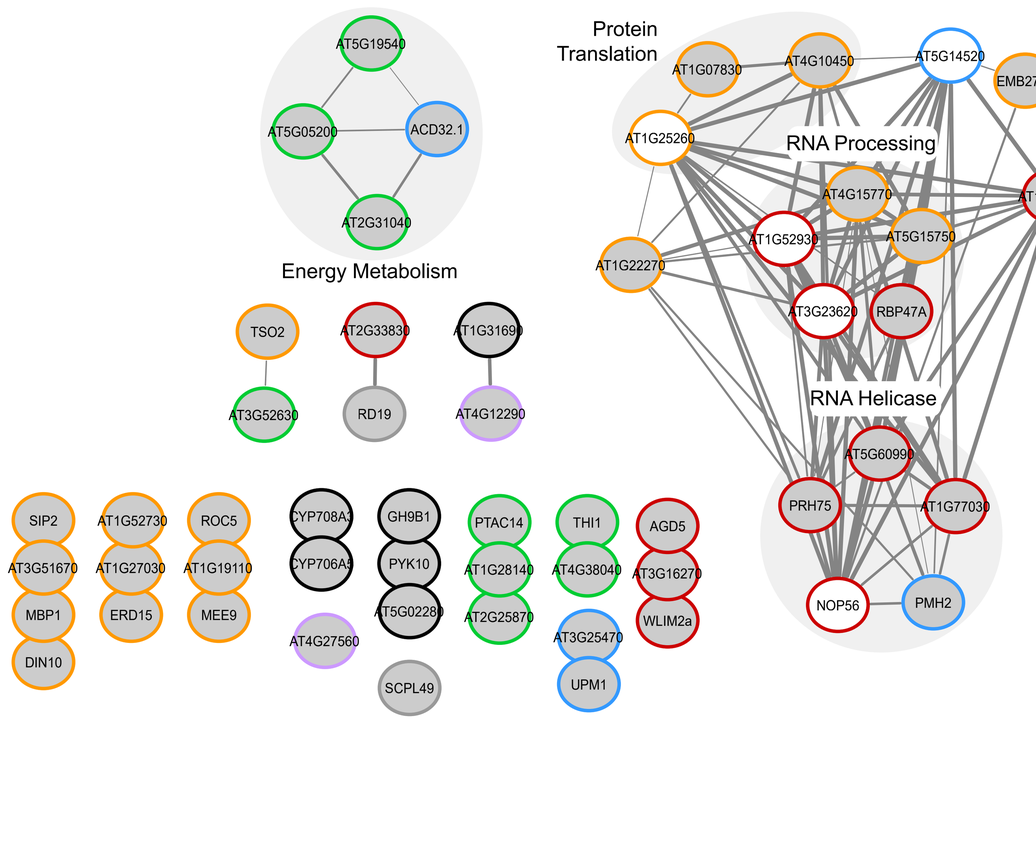


Figure 2: Interaction networks of the diurnal proteome. Using STRING-DB (https://string-db.org/), association network analysis of statistically significant diurnally changing proteins was performed using the generated unsupervised clusters (Figure 1). Edge thickness indicates confidence of the connection between two nodes (0.5 - 1.0). Changing proteins (grey circles) are labeled by either their primary gene annotation or Arabidopsis gene identifier (AGI). The colored outline of each node represents that proteins in silico predicted subcellular localization (SUBAcon; suba3.plantenergy.uwa.edu.au). Nucleus (red), cytosol (orange), plastid (green), mitochondria (blue), plasma membrane (purple), peroxisome (dark yellow), endoplasmic reticulum/golgi/secreted (black) are depicted. A second layer of STRING-DB identified proteins (white nodes) not found in each respective significantly changing protein cluster was used to highlight the interconnectedness of proteins in the cluster. Multiple nodes encompassed by a labelled grey circle represent proteins involved in the same cellular process.