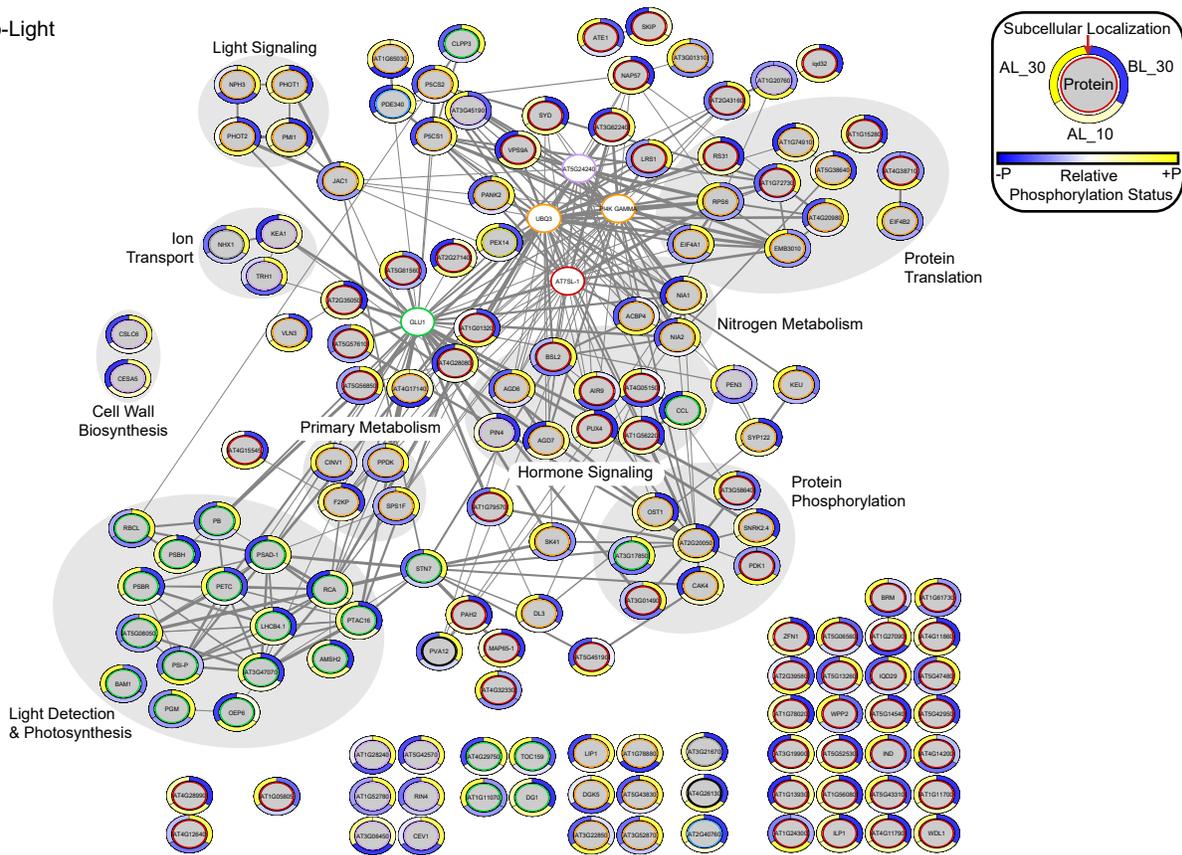
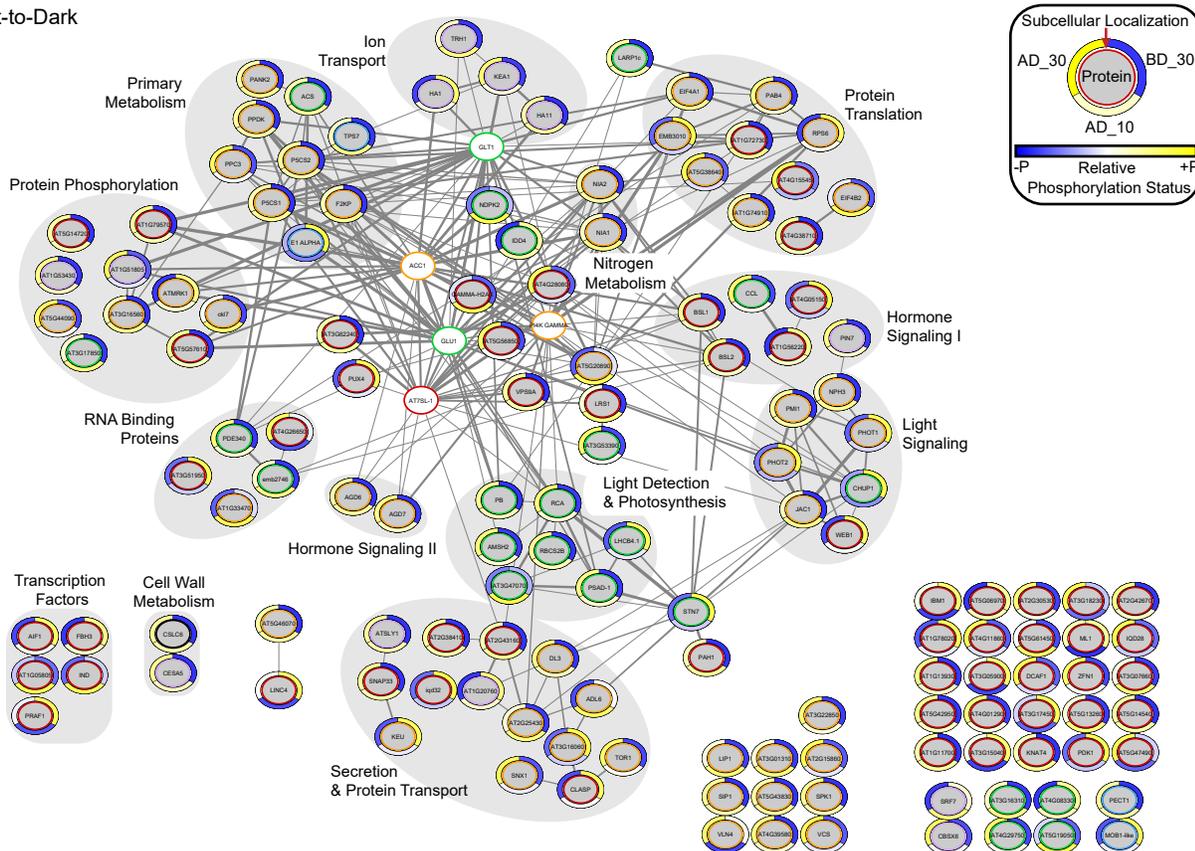


**Figure 4**

(A) Dark-to-Light  
(D-L)



(B) Light-to-Dark  
(L-D)



**Figure 4: Interaction networks of the diurnal phosphoproteome at the D-L and L-D transitions.** Using the STRING-DB, association network analysis of statistically significant diurnally changing phosphorylated proteins was performed (ANOVA P value  $\leq 0.05$ ). Edge thickness indicates strength of the connection between two nodes (0.5 - 1.0). Phosphorylated proteins (grey circles) are labeled by either their primary gene annotation or Arabidopsis gene identifier (AGI). Outer circle around each node depicts the standardized relative log<sub>2</sub> FC in that proteins phosphorylation status between time-points. The sliding scale of yellow to blue represents a relative increase and decrease in phosphorylation, respectively. The inner colored circles represent *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 shell of STING-DB proteins (white circles) not found in our dataset was used to highlight the interconnectedness of the network. Multiple nodes encompassed by a labelled grey circle represent proteins involved in the same cellular process.