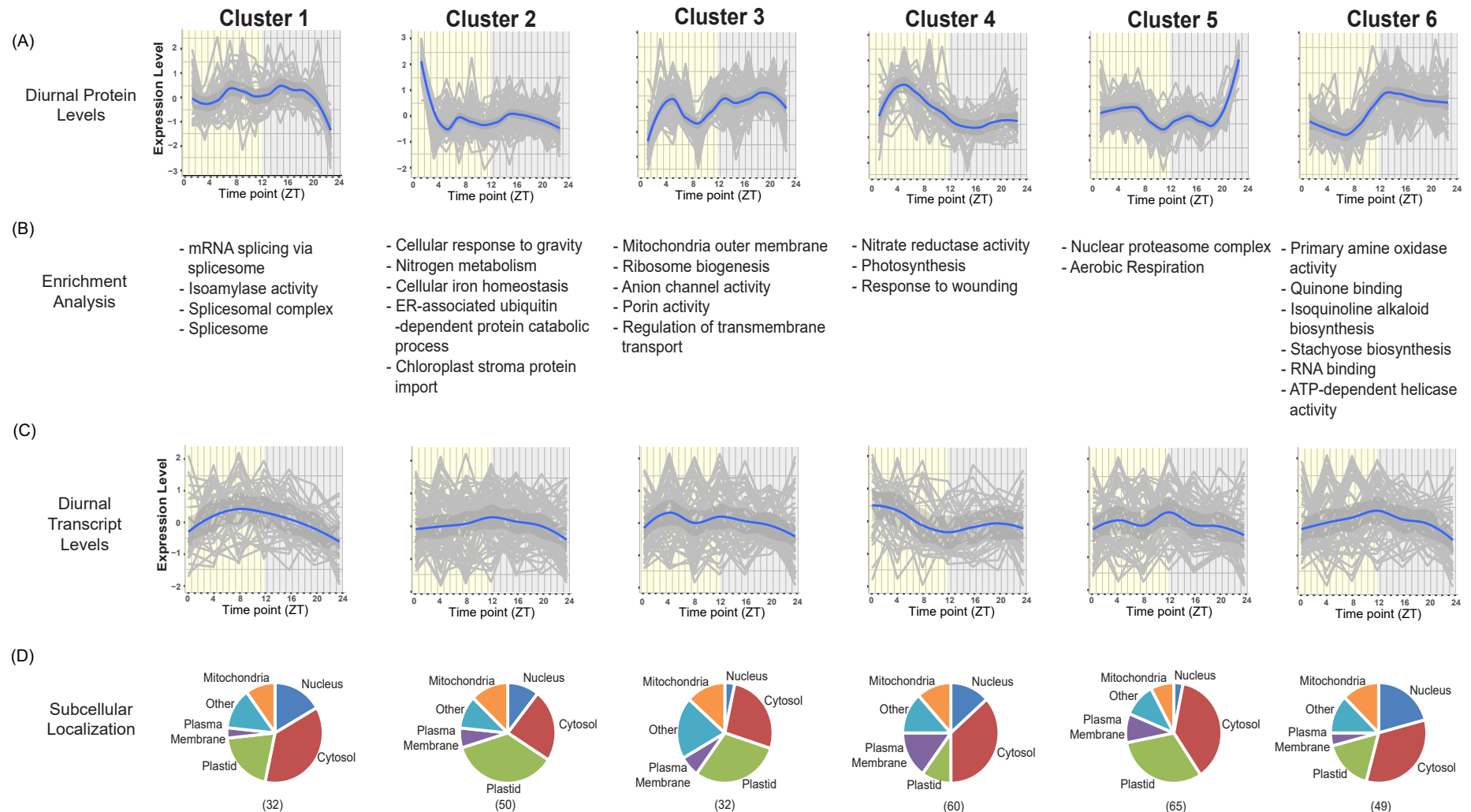**Figure 1**

Figure 1: Analysis of the diurnal proteome: clustering, enrichment analysis and subcellular localization. (A) Significantly changing proteins (Fold-change (FC) ≥ 1.5, ANOVA P value ≤ 0.05, ≥ 2 peptides) were subjected to an unsupervised clustering analysis (GProX; http://gprox.sourceforge.net) resolving 6 protein clusters. Y- and X-axis depict standardized expression level and harvest time (Zeitgeber time; ZT), respectively. Median expression is depicted in blue. (B) Term enrichment analysis of significantly changing proteins using SetRank (P value ≤ 0.01, size ≥ 2). (C) Standardized diurnal transcript expression level of each corresponding clustered protein (Log10). Median expression is depicted in blue. Transcript expression level was obtained from Diurnal DB (http://diurnal.mocklerlab.org/). (D) *In silico* subcellular localization analysis of significantly changing proteins using SUBAcon (SUBA3; http://suba3.plant-energy.uwa.edu.au). Bracketed numbers represent the number of proteins per cluster.