**Figure 4. Proteome rhythmicity under alternating light/dark cycles and integration with the transcriptome. (A)** Barplots representing the number of identified rhythmic proteins under long day condition (top, in blue, LD, 16h light / 8h dark) and under short day condition (bottom, in red, SD, 16h light / 8h dark).. Non rhythmic proteins are represented in white. **(B)** Example of protein abundance profiles under LD (top, blue) and SD (bottom, red) conditions represented together with gene expression profiles under LD (top, light blue) and SD (bottom, light red) conditions for *Minichromose Maintenance 2* (*ostta11g00910*, *MCM2*). White rectangles represent photoperiods (light periods), blue and red filled rectangles correspond to skotoperiods under LD and SD respectively (dark periods). ZTN, Zeitgeber time N, marks the time point N hours after dawn (lights on, ZT0). *MCM2* illustrates that commonly protein rhythmic profiles exhibit an offset with respect to gene expression profiles. **(C)** Histograms showing the distribution of the number of proteins with maximum abundance at specific time points under LD condition (top, blue) and SD condition (bottom, red). Offsets are apparent in protein abundance phases with respect to gene expression phases (time points of maximum protein abundance or gene expression). Under both LD and SD conditions, protein abundance phases accumulate at the end of the skotoperiods (dark periods) and during photoperiods (light periods). **(D)** Boxplot representing the offset in hours between protein abundance and gene expression maximum under LD (blue) and SD (red) conditions. Central horizontal lines represent medians, boxes represent upper and lower quartiles and whisker ends indicate , minimum and maximum values. Protein/gene offsets are significantly longer under SD conditions with respect to LD conditions according to a p-value of 1.2 × 10-9 computed using Mann-Whitney-Wilcoxon test. **(E)** Boxplots representing protein/gene offsets under LD (left, blue) and SD (right, red) conditions for different gene sets with specific maximum expression time points. Under LD condition, no significant difference is observed whereas under SD condition, genes with maximum expression during the skotoperiod (dark period ZT8, ZT12, ZT16 and ZT20) present significantly longer offsets when compared to those genes with maximum expression during the photoperiod (light period ZT0 and ZT4) according to Mann-Whitney-Wilcoxon test. **(F)** Boxplot illustrating how genes involved in different biological processes according to their gene ontology (GO) annotation present distinct protein/gene offsets, that are longer under SD (red) than LD (blue) conditions. DNA replication (GO:0006260), photosynthesis (GO:0009521) and translation (GO:0006412) are chosen as examples. **(G)** Protein abundance and gene expression profiles under LD and SD conditions for *Sister Chromatid Cohesion 1* (left, *ostta03g03780*, *SMC1*), *Photosystem I Light Harvesting Complex 2* (center, *ostta03g04920*, *LHCA2*) and *Ribosomal Protein S1* (right, *ostta02g04680*, *RPS1*). This illustrates how genes involved in DNA replication or photosynthesis present short gene/protein offsets whereas genes involved in translation present long offsets.