**Supplementary Figure 10. Proteomic data normalization and reliability. (A)** Boxplots representing global distributions of protein abundances over the three technical replicates of the six time points corresponding to three consecutive days under long day conditions (LD, 16h light / 8h dark) on the left and under short day conditions (SD, 8h light / 16h dark) on the right. Top graphs correspond to raw data and bottom graphs correspond to log2 quantile normalized data. Medians are represented by central horizontal lines, upper and lower quartiles by boxes, minimum and maximum values by whisker ends. ZTN, Zeitgeber time N, marks the time point N hours after dawn (lights on). **(B)** Enrichment map representing the cellular components or organelle significantly covered by the proteins detected in our data. Dots or nodes sizes represent the number of proteins identified located in the corresponding organelle. A blue to red gradient is used to represent the level of significance. Lines or edges link dots or nodes representing related organelle. **(C)** Principal Component Analysis of the time point global rhythmic proteomes under LD conditions. Small dots correspond to the 2D projection of each time point global rhythmic proteome. Big dots correspond to the average of the three replicates 2D projections for each time point. Ellipses mark the 95% confidence regions corresponding to each time point global rhythmic proteome. A clear circular distribution emerges capturing the cycling structure in diurnal rhythmic LD proteomes. (D) Principal Component Analysis of the time point global rhythmic proteomes under SD conditions. Points and ellipses are used as described before. A circular arrangement similar to LD conditions is observed.