**Figure 3. Seasonal and photoperiodic effects over gene expression profiles.** **(A)** Boxplot representing rhythmic genes amplitude or maximum expression level reached under long day conditions (LD, alternating 16h light / 8h dark, blue) and under short day conditions (SD, alternating 8h light / 16h dark, red). Medians are represented by central horizontal lines, upper and lower quartiles by boxes, minimum and maximum values by whisker ends. Gene expression levels are measured as FPKM (Fragments Per Kilobase of transcript per Million fragments mapped). SD amplitudes are significantly reduced with respect to LD according to a p-value of 1.16 × 10-111 computed using Mann-Whitney-Wilcoxon test possibly due to a decline in culture synchrony under SD. **(B)** Histograms showing the distribution of the number of genes with phase or maximum expression level at specific time points during the day under LD conditions (blue, top) and SD conditions (red, bottom). ZTN, Zeitgeber time N, marks the time point N hours after dawn (lights on). Backward phase shifts are apparent under SD when gene phases are mostly reached around SD midnight ZT12 to ZT16 whereas, under LD, phases are uniformly distributed from dusk (ZT12) to the end of the night. **(C)** Gene expression profiles under LD (blue line) and SD (red line) of *Cyclin B* (*ostta01g06150*, *CYCB*, top) and *Delta-9 acyl-lipid desaturase 1* (*ostta01g00790*, *ADS1*, bottom). White rectangles represent photoperiods (light periods or days), blue and red filled rectangles correspond to skotoperiods under LD and SD respectively (dark periods or nights). Gene expression levels are measured as FPKM (Fragments Per Kilobase of transcript per Million fragments mapped). Blue and red vertical dotted arrows mark LD and SD phases. Horizontal black arrow represents backward phase shifts under SD when compared to LD. Blue and red horizontal dashed lines mark LD and SD amplitudes. Vertical black arrows represent the reductions in amplitude under SD with respect to LD. **(D)** Barplot representing in different green colours the number of non rhythmic, single peak rhythmic and two peaks rhythmic genes under LD, ND (neutral day, alternating 12h light / 12h dark) and SD conditions. An increase in the number of two peaks rhythmic genes is observed as the photoperiod or day shortens from LD to ND and SD conditions. **(E)** Gene expression profiles under LD (blue line) and SD (red line) of *Ferredoxin-NADP+ reductase* (*ostta18g01250*, *FNR*). This gene illustrates how specific single peak rhythmic expression patterns under LD conditions become two peaks rhythmic expression profiles under SD conditions. **(F)** Gene expression profiles under SD and free running conditions consisting of constant light (LL) or constant dark (DD) of *Ferredoxin-NADP+ reductase* (*ostta18g01250*, *FNR*). This gene exemplifies how two peaks expression patterns under SD conditions could emerge as the combination of two distinct rhythmic profiles. One depending on the photoperiod (dotted line) with phase marked with a grey vertical arrow maintaining its rhythmicity only under LL (top). Another expression profile is apparent depending on the skotoperiod (dashed line) with phase marked with a black vertical arrow maintaining its rhythmicity only under DD (bottom). **(G)** Circular heatmap representing the temporal organization of gene expression profiles under LD conditions. Dark blue stands for low expression whereas yellow represents high expression. Genes are clustered depending on their phase or time of maximum expression being genes with phase at ZT0 located in the outer circle and being genes with phase at subsequent ZTs placed sequentially into inner circles. Biological enriched processes in the gene set with phase at each specific time point are depicting capturing the diurnal transcriptional program over diurnal cycles under LD conditions. **(H)** Similarly, circular heatmap representing the temporal organization of the diurnal transcriptional program under SD conditions. A shift as well as a rearrangement is observed in the SD diurnal transcriptional program when compared to the one inferred for LD.