**Supplementary Figure 1. Experimental design and transcriptomic RNA-seq data reliability.** **(A)** Photochemostats used for the culture of *Ostreococcus tauri* in continuous regime under diurnal and seasonal cycles. (1) Jacketed sterilized bubble column containing 1.8 L of cell suspension. Water flowing through the external jacket maintains a constant 20ºC temperatur in the cultures. (2) Light panels simulating the different light/dark cycles with gradual increase and decrease in light intensity during photoperiods. (3) Continuous air is sparged to ensure culture homogenization from the bottom of the column. CO2 is injected into the air stream on demand to maintain pH 8. (4) Temperature and pH probe for temperature and pH monitorization. (5) Peristaltic pump continuously supplying fresh medium during photoperiods at a flow rate of 45 mL h-1 (dilution rate 0.3 d-1). (6) Overflow tube collecting excess culture. **(B)** The experimental settings to study transcriptome, proteome and physiological rhythmicity: three days under summer long day conditions (LD, 16h light : 8h dark) followed by three days under free running conditions consisting of constant light or constant dark; three days under winter short day conditions (SD, 8h light : 16h dark) followed by three days under free running conditions consisting of constant light or constant dark. ZTN, Zeitgeber time N, marks the time point N hours after dawn (lights on, ZT0). Samples were collected every four hours during the three days of alternating light/dark cycles. No samples were collected during the first day of free running condition to allow culture acclimation. Samples were collected every four hours starting at subjective dawn during two days. Long day conditions are represented in blue and short day conditions in red. Photoperiods (light periods) correspond to white rectangles and skotoperiods (dark periods) to blue/red filled rectangles. Light blue and red filled rectangles are used to represent subjective photoperiods and skotoperiods under free running conditions. **(C)** Hierarchical clustering of the RNA-seq data corresponding to the 36 time points collected under alternating dark/light cycles simulating long and short day conditions. The three global transcriptomes corresponding to the same time points from different days cluster together showing robust rhythmicity in our cultures. Three distinct clusters are observed corresponding to midday (blue rectangle: LD ZT4, SD ZT4 and LD ZT8), dusk (yellow rectangle: SD ZT8, LD ZT16 and LD ZT12) and night/dawn (grey rectangle with two clear subclusters distinguishing between LD and SD: LD ZT0 and LD ZT20 on one hand and SD ZT12, SD ZT16, SD ZT20 and ZT0 on the other hand). **(D)** Principal Component Analysis of the time point global transcriptomes under long day conditions. Small dots correspond to the 2D projection of each time point global transcriptome. 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 transcriptome. A clear circular distribution emerges supporting the rhythmic and cycling structure in diurnal LD transcriptomes. **(E)** Principal Component Analysis of the time point global transcriptomes under short day conditions. Points and ellipses are used as described before. Under SD conditions an elliptic rather than circular distribution emerges suggesting more complex rhythmic and cycling patterns than under LD conditions and a reduced synchrony in the cultures.