Figure 2 The optimal flux distribution for the objective function (A) The $\log_{10}$ representation is more informative as the distribution of flux values covers several orders of magnitude (B)
Fig. 3 Using FVA, minimum and maximum allowable flux values were estimated for the model.
Fig. 4 Robustness analysis. The predicted optimal starch production rate as a function of the flux through each of 69 reactions.
Figure 5 Some results of sampling flux distribution. Flux distribution histograms (diagonal) and pairwise scatterplots (off diagonal) for 4 initial and 4 final reactions of the model pathway (reaction names are the same as in Fig G.1) X axis corresponds to the magnitude of the flux through the particular reaction. The off-diagonal scatterplots show the relationships between fluxes through two reactions.
Figure 6 Transcripts encoding the enzymes of starch metabolism in O. tauri.
Figure 7. Investigation of effect of single gene rhythmic expression on the overall diurnal starch pattern. Time 0 corresponds to the light onset, time 12 - to the dark onset.

A. 3D representation of each gene impact to the shape of the diurnal starch flux. Shown is the null hypothesis: all genes except one are at most expressed. Note time points 1 to 8 shown from right to left for the purposes of visualization. B. The effect of expression pattern of Ot03g03190 (beta-amylase), Ot03g01510 (glucan water dikinase) and Ot12g00310 (isoamylase) on the overall starch shape. Ot13g01250 corresponds to the unperturbed shape of the step-function. C. The effect of Ot07g02930 (AGPase), Ot14g02550 (isoamylase). Ot7g02010 and Ot16g01560 correspond to the unperturbed step-function.
Figure 8 Simulation of effect of flux upper bounds constraining on the resulting starch flux pattern.
Control (red) represents unconstrained case: all the flux upper bound values set to their maximum value (unit); Gng (light blue): the flux upper bounds for reactions for gluconeogenesis are constrained, the rest set to the maximum value. Starch (green): the flux upper bounds for the starch pathway reactions are constrained, reactions for gluconeogenesis set to the maximum value; all genes (dark blue): all reactions flux upper bounds are constrained. Constraining of flux upper bounds four reactions for gluconeogenesis influences the starch flux value from 6 to 12h.
Figure 9 The log flux distribution at ZT0, ZT3, ZT6 and ZT9 (only non-zero fluxes represented)
Figure 10 The log fluxes distribution at ZT12, ZT15 and ZT18 (only non-zero fluxes are presented)
Figure 11. The weekly pattern of the starch content dynamics.
Figure 12 The effect of the in silico single gene deletion on the pattern of diurnal maltose production. A. The 3D representation of the effect of single gene deletion on the shape of the maltose diurnal pattern. B. The effect of the deletion of the Ot03g03190 (beta-amylase) on the maltose diurnal pattern. Ot12g00310 corresponds to the unperturbed shape. C. The effect of the deletion of the Ot06g03200 (GBSSI) and Ot13g01510 (glucan, water dikinase) on the shape of the maltose diurnal pattern. Ot13g01250 correspond to the unperturbed shape. D. The effect of the deletion of the Ot07g02930 (AGPase), Ot0402110 (starch phosphorylase), Ot09g03160 (MEX1) on the shape of the maltose diurnal pattern. Ot07g03280 correspond to the unperturbed shape.
Figure 13. GWD1 (alpha glucan, water dikinase) from *A. thaliana*, *S. tuberosum*, *C. reinhardtii*, *O. tauri*, *O. lucimarinus*, *M. pusilla* and *M. CCCP490*. The sequence CFATC responsible for disulfide bond formation could not be found in unicellular green algae.