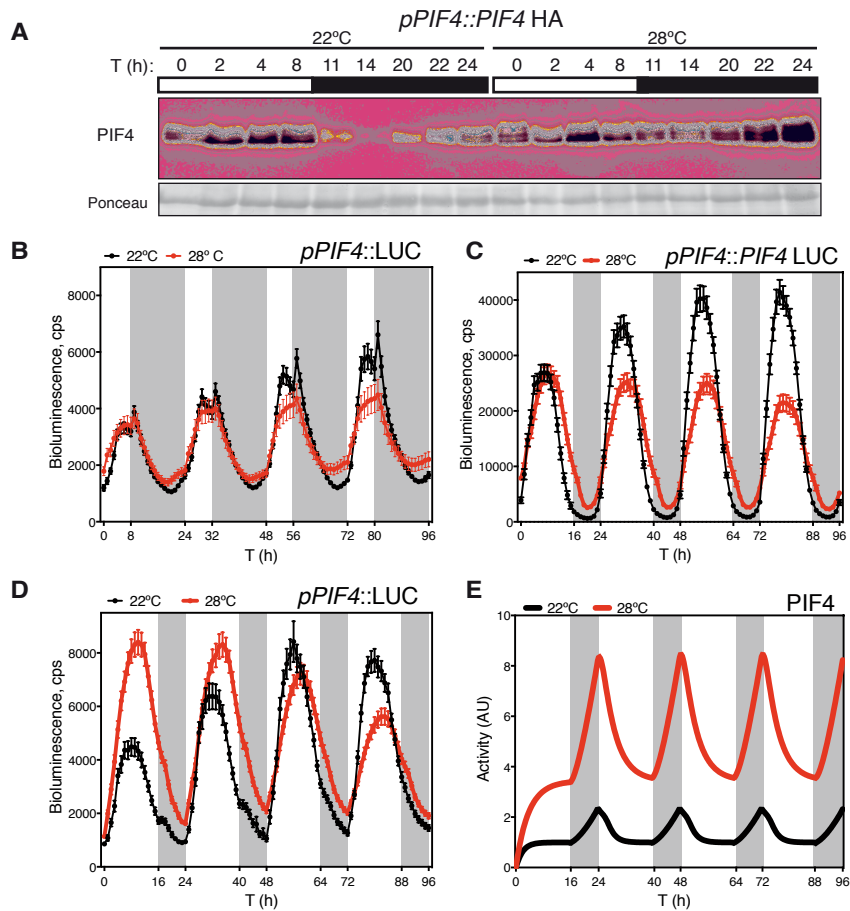


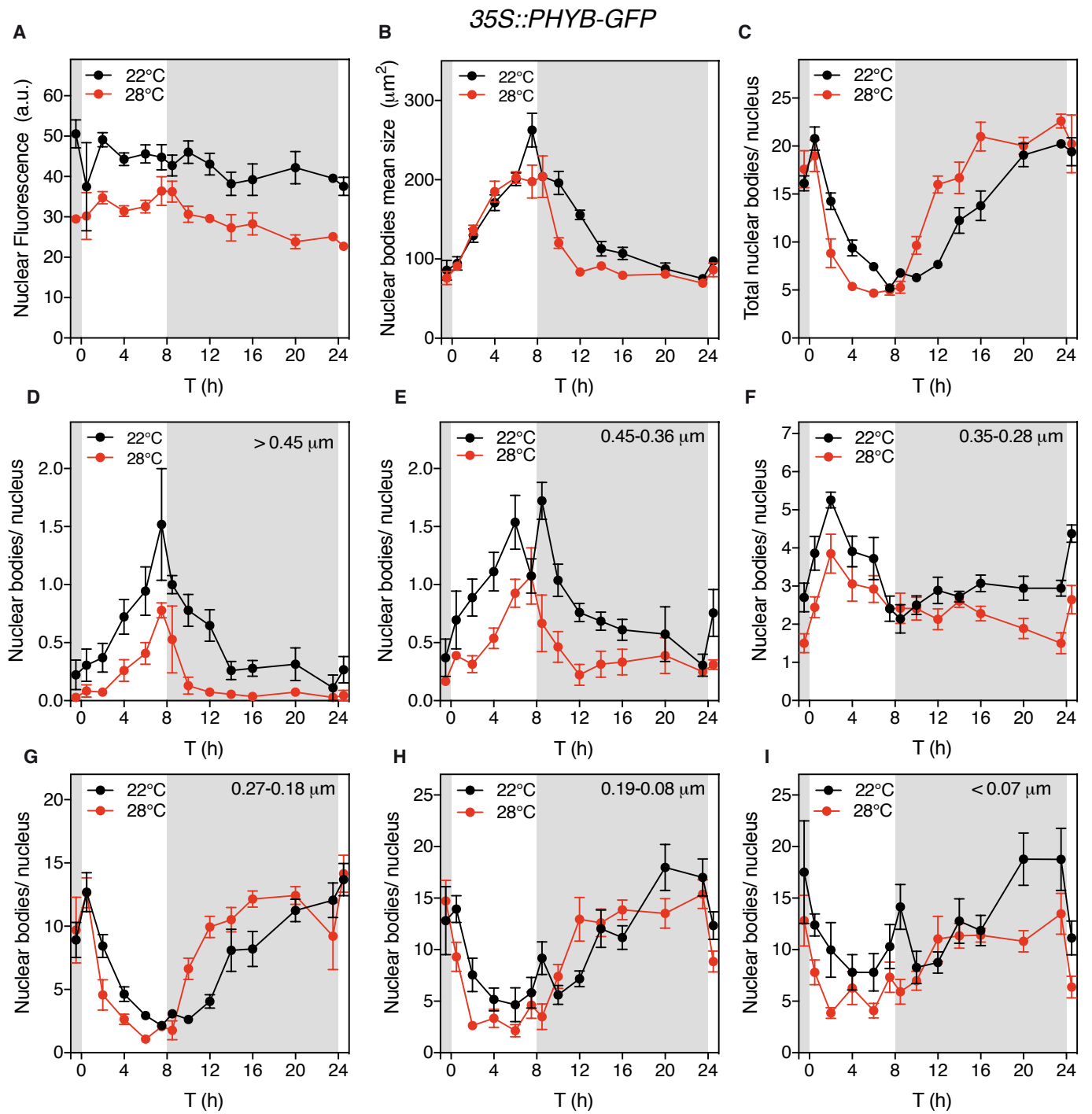
**Fig. S1. Effect of warm temperature on ELF3 expression and protein abundance.**

**(A)** Total protein extracts from *pELF3::ELF3-myc* transgenic lines were analyzed by Western blot using an anti-myc antibody. RPT5 was used for loading control and detected using an anti-RPT5 antibody. Seedlings were grown for 5 days at 22°C or 28°C under short day conditions. Samples were collected at the indicated time points. **(B)** Bioluminescence detection of Col-0 lines expressing the *pELF3::LUC* construct, grown in short days. **(C and D)** Bioluminescence recorded from transgenic seedlings expressing the *pELF3::ELF3-LUC* and *pELF3::LUC* constructs, grown in long days and 22°C/28°C. Values represent mean  $\pm$  SE of the 2 sec absolute bioluminescence of at least 24 seedlings. **(E)** ELF3 activity predicted by the model in long days.



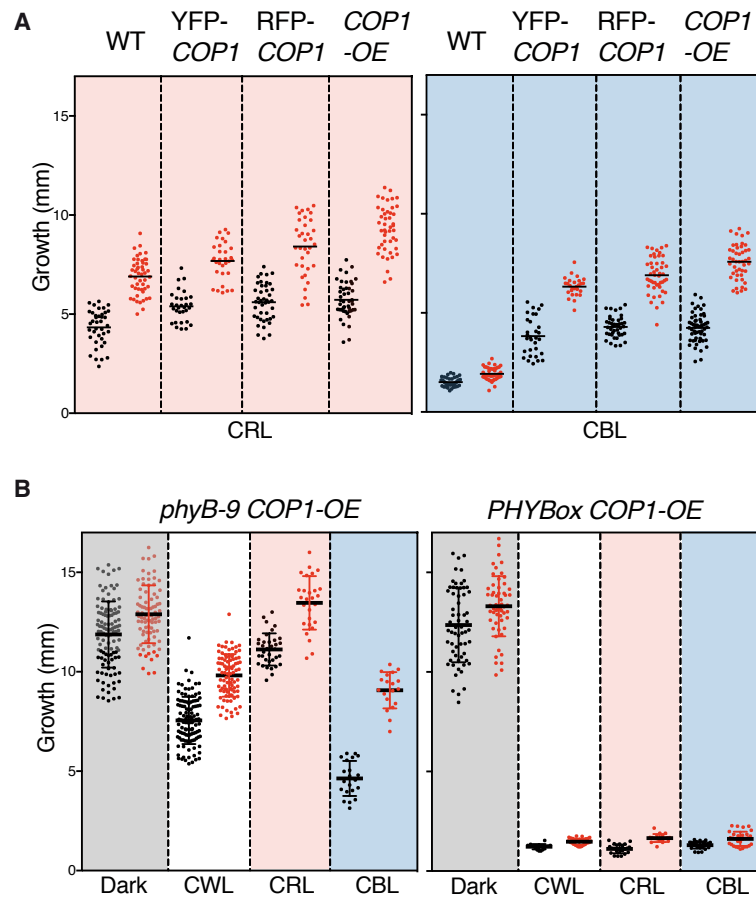
**Fig S2. Effect of warm temperature on PIF4 expression and protein abundance.**

**(A)** Western blot of *pPIF4::PIF4-HA* transgenic lines. The PIF4-HA protein was detected using an anti-HA anti-body. Ponceau staining was used as loading control. Rectangles indicate light conditions: white, lights on, and grey, lights off. Samples were collected at the indicated time points. **(B)** Bioluminescence detection of Col-0 lines expressing *pPIF4::LUC* construct, grown in short days. **(C and D)** Bioluminescence recorded from transgenic seedlings expressing the *pPIF4::PIF4-LUC* and *pPIF4::LUC* constructs, grown in long days and 22°C/28°C. Values represent mean  $\pm$  SE of 2 sec absolute bioluminescence of at least 24 seedlings. **(E)** PIF4 activity predicted by the model in long days.



**Fig. S3. phyB nuclear bodies formation is affected by temperature.**

*35S::PHYB-GFP* transgenic seedlings were grown under  $50 \mu\text{mol.m}^{-2}.\text{s}^{-1}$  white light in short day cycles at  $22^\circ\text{C}$  or  $28^\circ\text{C}$ . **(A)** Total nuclear fluorescence expressed in arbitrary units (a.u.). **(B)** Nuclear photobodies mean size ( $\mu\text{m}^2$ ). **(C)** Number of total bodies per nucleus. **(D-I)** Number of phyB nuclear bodies, sorted by size categories, as measured with Matlab Software. The rectangles indicate the light conditions: white, lights on, and grey, lights off. Values represent mean  $\pm$  SE of two independent experiments. Each replicate is the average of 3 seedlings and 3 nuclei/plant were analyzed. T(h) indicates time in hours.



**Fig. S4. Thermal response of *COP1* lines in red and blue light.**

**(A)** Hypocotyl length phenotypes of the different *COP1* overexpressor lines in continuous red (CRL) and continuous blue (CBL) light. n=27-57 seedlings (table S6). **(B)** Phenotypes of *phyB-9 COP1-OE* and *PHYBox COP1-OE* seedlings grown for 5 days either in darkness, CWL, CRL and CBL, at 22°C or 28°C. Bars indicate standard deviation of n=13-112 seedlings (table S5).

# COP1 dynamics integrate conflicting seasonal light and thermal cues in the control of Arabidopsis elongation

## Supplementary Text

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## Code availability

All code and data to fit and simulate the mathematical model can be found at:

<https://github.com/pablocatalan/hypocotyl>

## Mathematical model

### Final model

The mathematical model used to obtain the results in the main text is as follows:

$$\begin{aligned}
 \frac{dB(t)}{dt} &= p_B(T)L(t)(mut_B - B(t)) - k_r(T)B(t) \\
 \frac{dE(t)}{dt} &= p_E(t, T, D, mut_E) - d_E E(t) \\
 \frac{dC(t)}{dt} &= mut_C [p_{CL}(T)L(t) + p_{CD}(1 - L(t))] - d_C C(t) \\
 \frac{dP(t)}{dt} &= mut_P \frac{p_P}{1 + p_{PE}(T)E(t)} - \frac{d_P}{1 + k_{PC}C(t)} P(t) - d_{PB} B(t) P(t) \\
 \frac{dG(t)}{dt} &= p_G + k_G \frac{p_{GP}P(t)}{1 + p_{GP}P(t) + p_{GE}E(t) + p_{GB}B(t) + \frac{p_{GH}}{1 + p_{HC}C(t)}},
 \end{aligned} \tag{1}$$

where  $t$  is time,  $B(t)$  represents the concentration of the active form of phyB, Pfr, in the nucleus;  $E(t)$  represents the concentration of ELF3 protein in the nucleus;  $P(t)$  represents the nuclear concentration of PIF1, PIF3, PIF4 and PIF5;  $C(t)$  represents COP1 in the nucleus, and  $G(t)$  measures hypocotyl growth in mm.  $G(t)$  is an effective variable used as proxy for the expression of PIF-targeted, growth related genes. Parameters that are a function of  $T$  (temperature) can have different values at 22°C and 28°C.  $L(t)$  represents light, and it is either 0 at night, or 1 during daytime.

Parameters have the following meaning: for a given species  $K$ ,  $d_K$  is the decay rate of molecule  $K$ ,  $p_B$  is phyB's rate of activation and traslocation to the nucleus under light;  $k_r$  is the rate of dark reversion, which following earlier reports (4,5) we assume happens during the day and night;  $p_P$  is PIFs' production rate;  $p_{PE}$  is the intensity of ELF3's inhibition of *PIFs* expression;  $k_{PC}$  is the intensity of COP1's inhibition of PIFs degradation;  $d_{PB}$  is the intensity of phyB's promotion of PIFs degradation and inactivation;  $p_{CL}$  and  $p_{CD}$  are, respectively, COP1's production rates during the day and the night;  $p_G$  is the basal rate of hypocotyl growth;  $k_G$  is the conversion between PIFs targets gene expression and growth;  $p_{GK}$  is molecule  $K$ 's intensity of its effect on growth,  $p_{GH}$  is related to the levels of HY5 (see below), and  $p_{HC}$  is the intensity of COP1's inhibition (through degradation) of HY5. Finally,  $mut_K$  is a multiplier that alters molecule  $K$ 's production to accomodate knock-out and over-expressor lines; i.e.  $mut_K = 1$  for the wild-type,  $mut_K < 1$  for weak mutants and  $mut_K > 1$  for over-expressor lines. In phyB and ELF3's case, knock-out mutants *phyB* and *elf3.8* have  $B = 0$  and  $E = 0$  at all times, respectively; the  $mut_E$  parameter in Eq. (2) below is only used with values greater than 1 to model over-expression.

ELF3's expression follows a quasi-square wave:

$$p_E(t, T) = \begin{cases} mut_E p_{E1}(T) + p_{E2}(T) & \text{if } D = 0 \text{ hours.} \\ mut_E p_{E1}(T) - p_{E2}(T) \left( -1 + \frac{2}{1+\exp(-k_0 t_0)} - \frac{2}{1+\exp(-k_0 t_1)} + \frac{2}{1+\exp(-k_0 t_2)} \right) & \text{if } 0 < D < 24 \text{ hours.} \\ mut_E p_{E1}(T) - p_{E2}(T) & \text{if } D = 24 \text{ hours.} \end{cases} \quad (2)$$

where  $D$  is the number of hours of light in the day;  $p_{E1} + p_{E2}$  and  $p_{E1} - p_{E2}$  are ELF3's average production in darkness and light, respectively;  $t_0 = t \bmod 24$ ,  $t_1 = t_0 - D$  and  $t_2 = t_0 - 24$ , and  $k_0 = 5 \text{ h}^{-1}$ . With this function, ELF3 oscillates between  $p_{E1} + p_{E2}$  and  $p_{E1} - p_{E2}$  rapidly. The advantage over using a simpler square wave is that this function is smooth, which prevents numerical anomalies. The value  $k_0 = 5 \text{ h}^{-1}$  defines the timescale of the rise and fall of the function when changing light conditions. It has been assigned arbitrarily to produce a smooth function but maintaining a sharp distinction between expression during light and darkness. Our results do not depend on the exact value, within reason, of this parameter.

We also assume that the over-expressor line *ELF3ox* increases ELF3's production level  $p_{E1}$ , but that day-night oscillations, represented by  $p_{E2}$ , are maintained.

## Development of the model

We have used the following experimental observations in order to develop the initial model:

1. phyB is activated by light and tends to spontaneously revert back to its inactive form. This 'dark reversion' is faster with higher temperatures. We follow the modeling in Jung et al. (4) of phyB's activation and dark reversion with small modifications.
2. phyB is marked for degradation by COP1, and this degradation constant is enhanced by PIFs (27).
3. phyB mediates the degradation of PIF4 and PIFs enhance the degradation of phyB (29,30).
4. ELF3 is transcribed less during the day, and more during the night, in a sinusoidal pattern (15).
5. phyB physically interacts with ELF3, and this could potentially stabilize ELF3 (28).
6. COP1 also marks ELF3 for degradation (26).
7. PIF4 expression is suppressed by ELF3 as part of the evening complex (15). This regulation is weaker at warmer temperatures, as the EC is impaired by temperature (6).

8. COP1 stabilizes PIF4 and PIF5 (32,33).
9. COP1 is inactivated by phyB (19).
10. Hypocotyl growth is enhanced by the PIFs (10).
11. phyB prevents PIFs from binding to their targets (12,13).
12. ELF3 (independently from the evening complex) also prevents PIFs from binding to their targets (7,28).
13. HY5 represses hypocotyl growth, while COP1 mediates degradation of HY5 (16).

From these interactions, we developed the following model:

$$\begin{aligned}
\frac{dB(t)}{dt} &= p_B(T)L(t)(mut_B - B(t)) - k_r(T)B(t) - d_{BC}C(t)B(t) - d_{BP}P(t)B(t) \\
\frac{dE(t)}{dt} &= p_E(t, T, D, mut_E) - d_{EC}C(t)E(t) - \frac{d_E}{1 + k_{EB}B(t)}E(t) \\
\frac{dC(t)}{dt} &= mut_C [p_{CL}(T)L(t) + p_{CD}(T)(1 - L(t))] - d_C C(t) - d_{CB}B(t)C(t) \\
\frac{dP(t)}{dt} &= mut_P \frac{p_P}{1 + p_{PE}(T)E(t)} - \frac{d_P}{1 + k_{PC}C(t)}P(t) - d_{PB}B(t)P(t) \\
\frac{dG(t)}{dt} &= p_G + k_G \frac{p_{GP}P(t)}{1 + p_{GP}P(t) + p_{GE}E(t) + p_{GB}B(t) + p_{GH}H(t)}.
\end{aligned} \tag{3}$$

Here  $H(t)$  is HY5 concentration. As we do not have an equation for HY5, we assume it is in equilibrium and that its average levels are determined only by COP1:  $H(t) = p_H / (1 + p_{HC}C(t))$ . The parameter  $p_H$  is therefore no longer necessary and the effect of varying it is equivalent to variation of  $p_{GH}$ . Due to lack of additional information, we set the initial conditions for all variables to zero for our numerical simulations. That is,  $B(0) = P(0) = E(0) = C(0) = G(0) = 0$ .



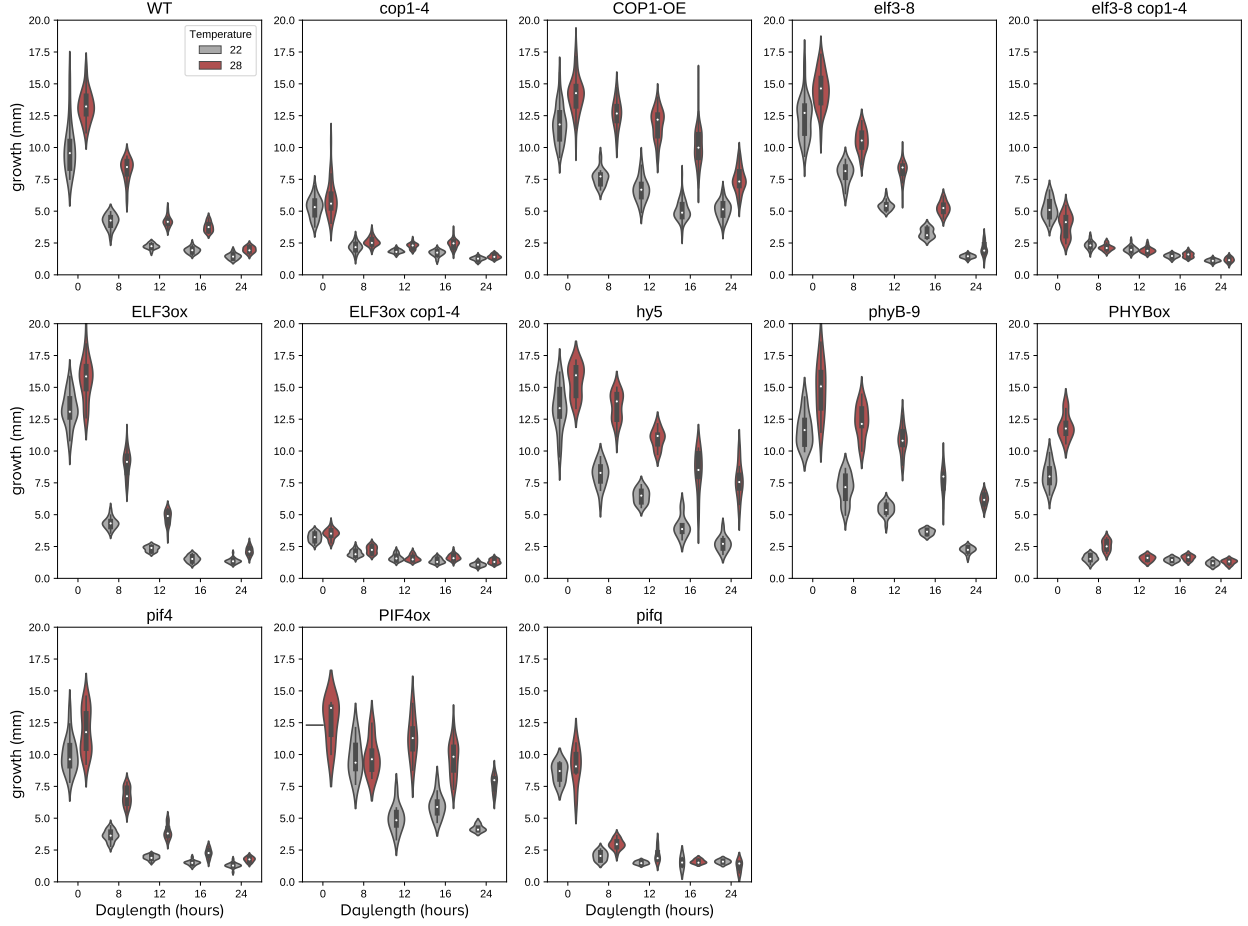


Figure S5: **Experimental data used to fit the model (I)**. We grew several mutant and over-expressor lines under different temperature and photoperiod conditions for five days (Methods), and used final hypocotyl length to fit our mathematical model. This figure is a replot of Fig. 1A, using a violin plot that shows the distribution of all the individual values resulting in each data point.

## Simulated annealing

We wrote a custom simulated annealing algorithm (74) to fit Eqs. (3) to our experimental data (Fig. 1A, main text). We simulated the model for 5 days under all experimental conditions and for all genotypes and tried to minimize an energy function that was the sum of all the squared errors between our experimental data, fig. S5, and the model predictions. Together with growth data, we also used differences between model predictions and ELF3 levels in Col-0 and *phyB-9* backgrounds, fig. S6. The energy function was

$$E = \sum_{k \in \mathcal{G}} (o_k - e_k)^2 + w \sum_{k \in \mathcal{E}} (o_k - e_k)^2 \quad (4)$$

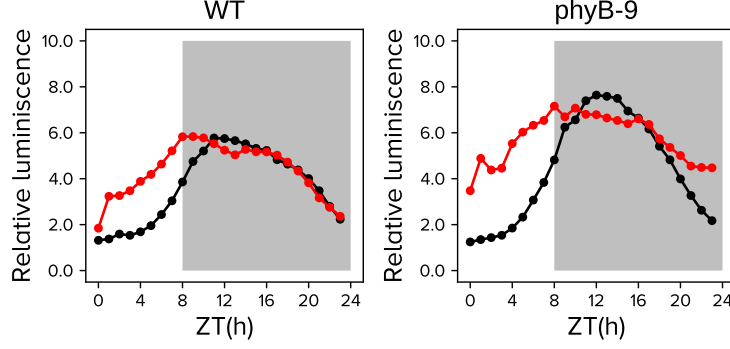


Figure S6: **Experimental data used to fit the model (II)**. We measured ELF3 levels using *pELF3::ELF3* LUC transgenic lines under two different backgrounds: Col-0 and *phyB-9*, and used that information to fit our model. Data from a similar experiment in the Col-0 background is also plotted in Fig. 4A.

where  $\mathcal{G}$  and  $\mathcal{E}$  are the sets of growth and expression datapoints, respectively, and  $w$  is the weight we give to expression data. We used  $w = 1$ , that is, each datum contributed equally to the function.

We used 3,544 growth datapoints and 96 expression datapoints (see the Github repository for more details). We fixed  $k_r(22) = 0.232 \text{ h}^{-1}$  and  $k_r(28) = 0.411 \text{ h}^{-1}$ , based on experimental measurements from Jorge Casal's lab, see Ref. (5);  $p_B(22) = 10$  in order to follow Ref. (4); furthermore,  $p_P$  and  $p_{CL}(22)$  were set to 1 in order to reduce the dimensionality of the search space. All other parameters were set to 1 at the beginning of the search, allowing them to change ( $p_{E2}(22)$  and  $p_{E2}(28)$  were set to 0.9 at the beginning of the search so as to allow variation in ELF3's production).

We started the process with all parameters set to 1. At each step  $i$ , we perturbed a randomly chosen parameter by adding to it a Gaussian random number with mean 0 and variance 0.1, always checking that no parameter became negative. For this perturbed set of parameters, we computed the energy function  $E_{\text{new}}$ , compared it with the energy of the old parameter set  $E_{\text{old}}$ , and accepted the set with probability

$$p_{\text{acc}} = \begin{cases} 1 & \text{if } E_{\text{old}}/E_{\text{new}} \geq 1, \\ \frac{E_{\text{old}}}{E_{\text{new}}} T_A & \text{if } E_{\text{old}}/E_{\text{new}} < 1. \end{cases}$$

where  $T_A = \frac{0.8}{\sqrt{1+i}}$ ; this particular form for  $T_A$  was chosen after an initial trial-and-error stage. This means that the probability of accepting changes that increase the error decreased with each annealing step. A typical run for our model ran this process for 10,000 steps, after which the variable  $i$  was reset to zero and the process was started again, using as initial condition the final parameters of the previous run. This process was repeated 10 times, to ensure the process did not get trapped in suboptimal

minima. We then used the parameter configuration that minimized the energy function from among all visited configurations.

After obtaining a stable set of parameters for Eqs. (3), a few parameters in the model were close to 0. New fits were made forcing these parameters to be zero, and the values obtained for the energy function were as good or even lower than those obtained considering the parameters free. The improvement in the fit when excluding these parameters can be explained by the increase in the efficiency of sampling the parameter space when its dimension is reduced. Finding these parameters consistent with zero in our fit does not mean that the interactions they represent do not exist, but rather that they are not important in our experimental conditions, or that their effect is already captured in an effective way by other parameters of the model. After exclusion of the parameters deemed negligible by our fitting procedure, the model given by Eqs. (3) is simplified to Eqs. (1). This final model was then fitted to the data using the simulated annealing procedure. Independent runs of this process (with the same initial conditions described above) converge to the same (or a very similar) set of parameters, shown in table S1.

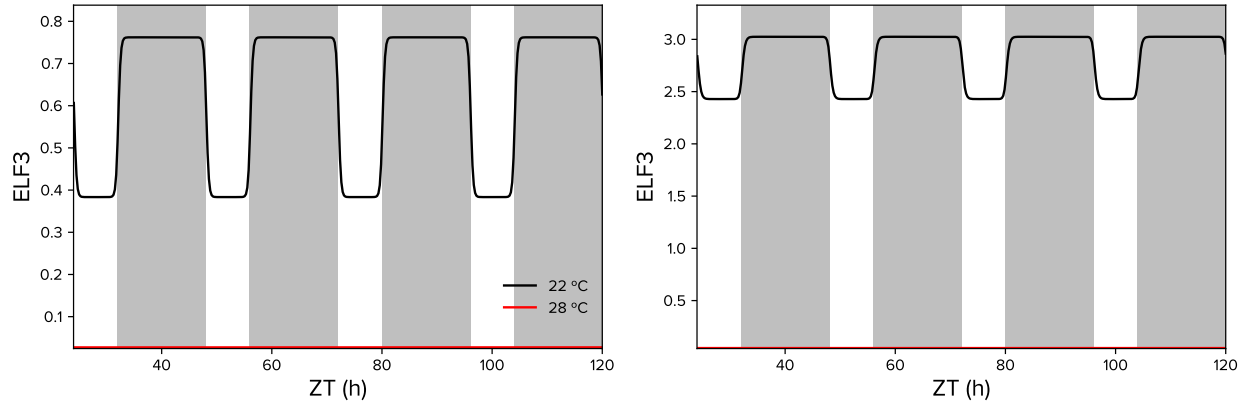


Figure S7: **ELF3 dynamics are not captured by the model if expression data is not included in the training dataset.** The two plots represent ELF3 dynamics from two parameter sets obtained in two simulated annealing runs where the expression data had no weight on the energy function ( $w = 0$  in Eq. (4)). These two parameter sets can fit the growth data as well as the parameter set we have used in the main text (figures not shown). The result is that these ELF3 dynamics are not similar to the ones we observe experimentally.

### The need for ELF3 expression

Ideally, we would like to use the least amount of data to fit our model, in order to increase its predictive capabilities. If a model trained only with growth data is able to predict with some precision expression timeseries, then it means that the model is somewhat accurate and we can use it for further predictions that we can test later. When we tried to do this, however, the model was not able to accurately reproduce ELF3 expression timeseries. We ran two simulated annealing runs with an energy function that did not give any weight to the expression data. In other words, we set  $w = 0$  in Eq. (4). The resulting sets of parameters were able to fit the growth data as well as the final parameters used in the main text. However, they did not reproduce ELF3 expression accurately. In both cases, levels of ELF3 at 22°C were much higher than those at 28°C, which are almost null, fig. S7.

As a result, we decided to set  $w = 1$  in Eq. (4), so as to force the model to reproduce the expression dynamics of ELF3.

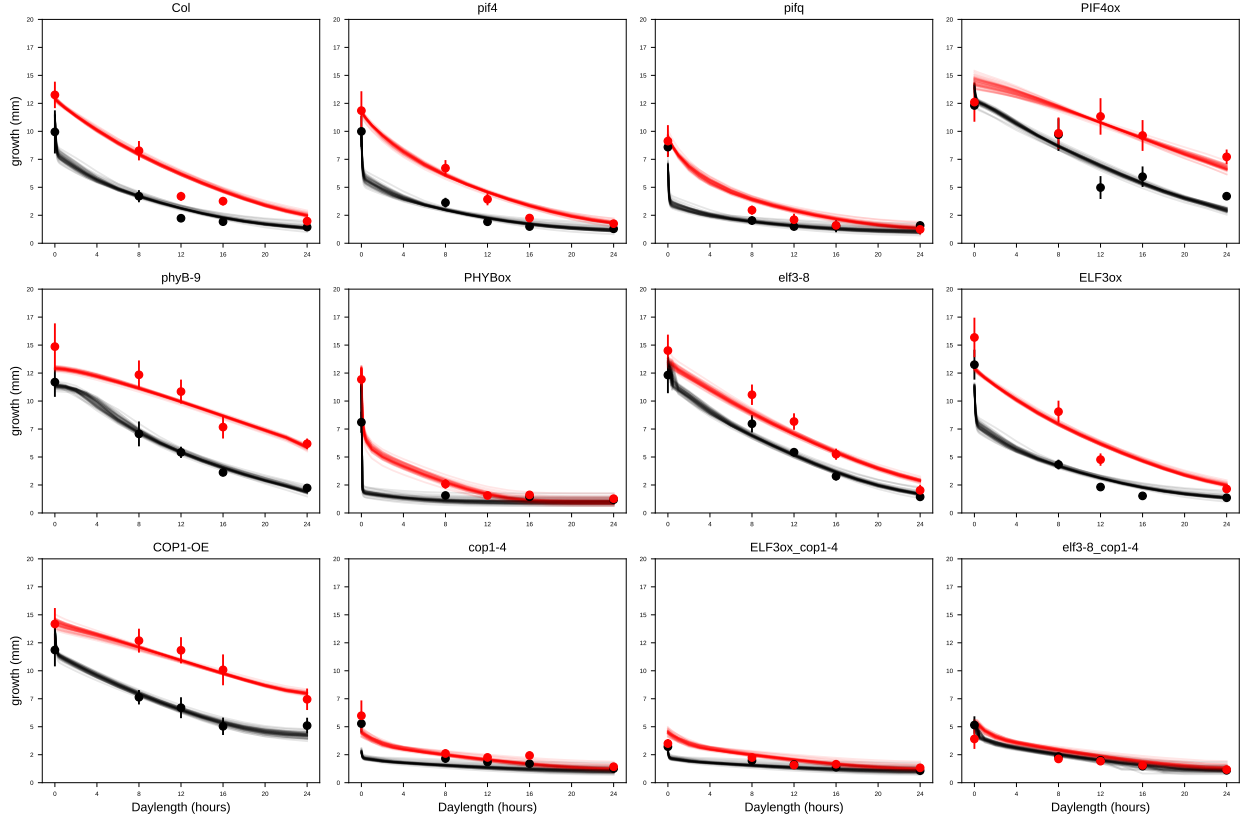


Figure S8: **Several parameter sets reproduce the growth data accurately.** The plot shows the growth predictions of 48 different parameter sets obtained from independent simulated annealing runs (solid lines). Most lines overlap and their discrepancies are small in comparison with the experimental variance of the dataset (filled circles are averages, lines represent one standard deviation).

## Robustness of the fit

We ran several independent runs of the simulated annealing algorithm, where the initial values for the parameters were chosen at random from a normal distribution of mean 1 and standard deviation 0.1 (except those that were fixed at the beginning, as explained above). We obtained 48 parameter sets (including the one we used in the main text) that accurately reproduced our growth data, fig. S8. Parameter values, however, varied widely between fits fig. S9.

The explanation for this is that the optimal set of parameters lies on a high-dimensional manifold. This is especially clear in the case of the ELF3 parameters, which lie on a one-dimensional manifold in  $\mathbb{R}^5$ , fig. S10. In fact, the line given by the equation

$$p_{E1}(22) = 1.806p_{E1}(28) - 0.759p_{E2}(22) - 0.611p_{E2}(28) - 3.213d_E - 0.616$$

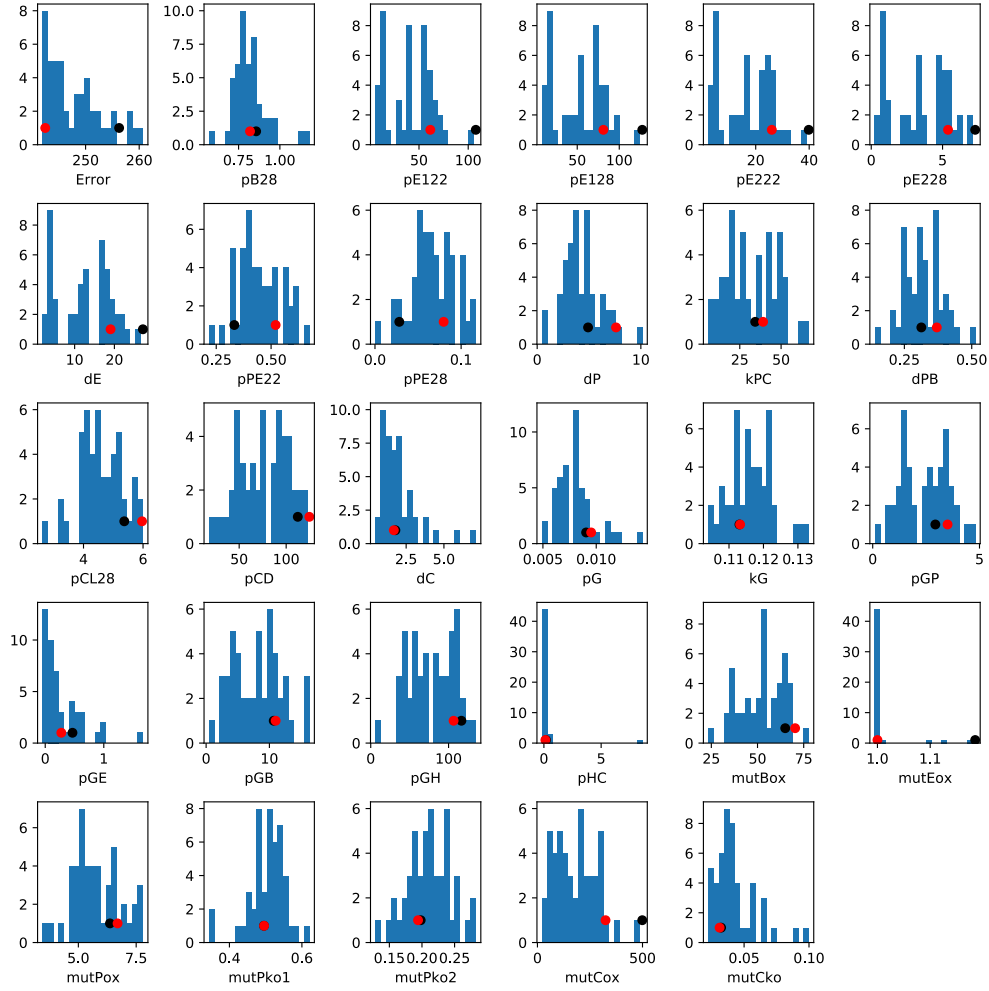


Figure S9: **Parameter values vary widely among parameter sets.** Histograms of all parameters in the model (including the energy function, first subplot)) made from 48 independent parameter sets that accurately fit our growth data.  $y$  axes represent histogram counts, while  $x$  axes represent parameter values. While some parameters are more restricted in their values, most of them have a wide range of variation. Red dots mark the value of the parameter corresponding to the set that has a minimal energy function, while black dots represent the value of the parameter corresponding to the set used in the main text, table S1. Parameter labels: *mutBox* represents the multiplier associated with *phyB*'s overexpressor line (and similarly with *mutCox*, *mutEox* and *mutPox*), *mutPko1* and *mutPko2* represent the multiplier associated with *pif4* and *pifq*, respectively, while *mutCko* represents the multiplier associated with *cop1-4*.

fits the five-dimensional data extremely well ( $R^2 = 0.9997$ ). If we had experimental information to fix one of these ELF3 parameters, the others would be automatically determined. In the case of parameters

related to other variables, the relationships are harder to infer, due to their nonlinear nature and the high dimensionality of the problem.

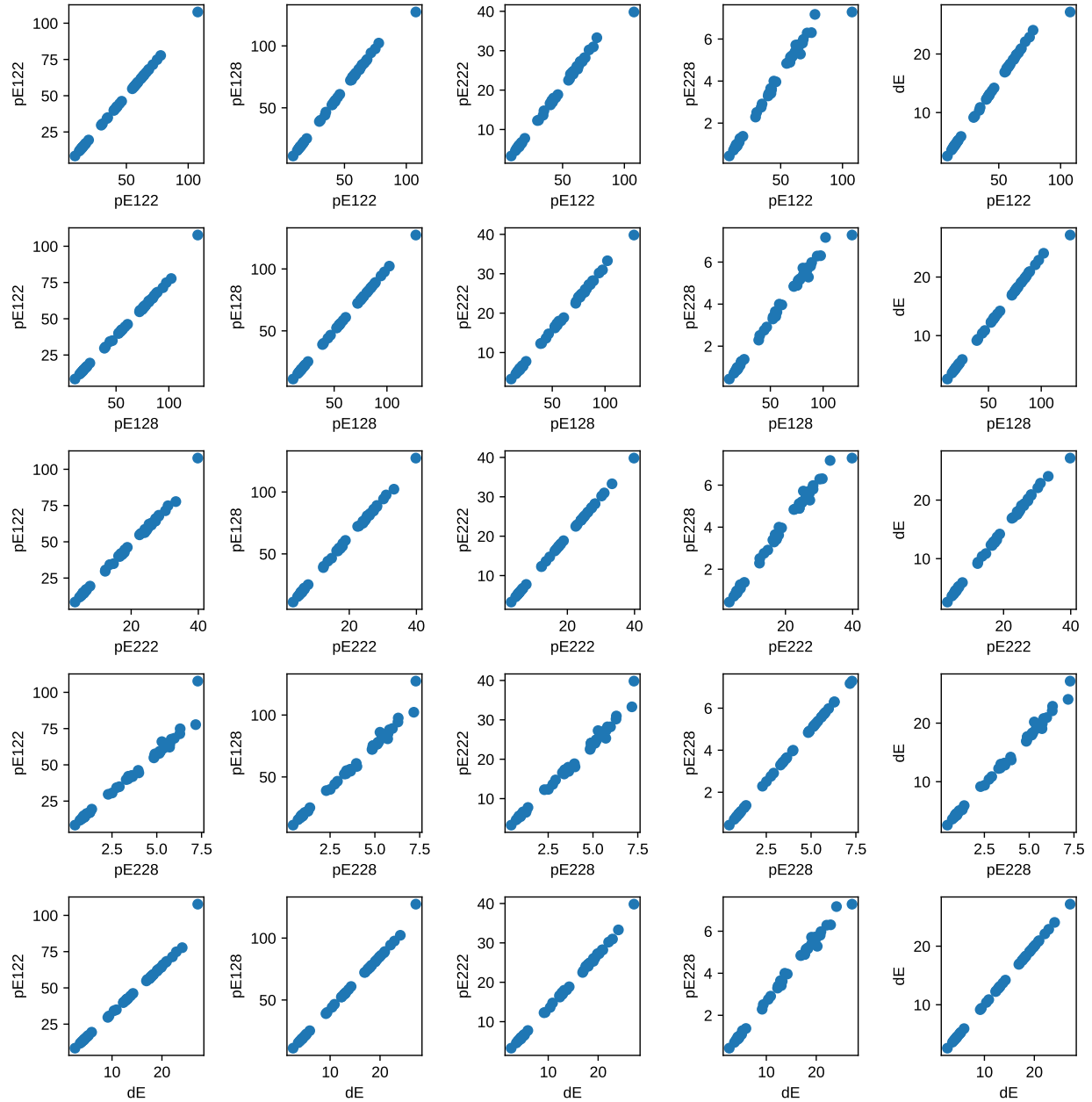


Figure S10: **ELF3 parameters lie on a five dimensional line in  $\mathbb{R}^5$ .** Parameters  $pE1(22)$ ,  $pE1(28)$ ,  $pE2(22)$ ,  $pE2(28)$  and  $d_E$  vary widely among parameter sets that reproduce the growth data, fig. S9. However, their values are highly correlated: representing the values of one parameter in all sets against the values of another parameter, we see that the points lie on lines for all parameter combinations. This means that they are actually lying on a five dimensional line, which we can find numerically (see text).

It is not the case that, given a parameter set, we can change one of the parameter values within the observed range of variation in fig. S9 with complete freedom. This can be checked with a sensitivity analysis, where we study the change in the energy function due to a small perturbation in each of the parameters, fig. S11. More precisely, we estimate the partial derivative of the energy function  $E(\theta_1, \dots, \theta_n)$  in Eq. (4) with respect to each of the parameters  $\theta_i$  using the central finite difference, that is

$$\frac{\partial E}{\partial \theta_i} \approx \frac{E(\dots, \theta_i + h, \dots) - E(\dots, \theta_i - h, \dots)}{2h}, \quad (5)$$

where we have used  $h = 5 \cdot 10^{-5} * \theta_i$  (i.e. a 0.005% change in  $\theta_i$ ), although the results are not dependent on the exact value of  $h$ . We then normalize this approximate derivative by the value of  $E$  at the original parameter set, in order to represent a relative change in  $E$ .

While some parameters can be changed for some parameter sets, thus informing us that the fit could be improved, every parameter has a non-zero effect on  $E$  for at least one parameter set. In some cases this change is quite large, even greater than 100%. This informs us that all remaining parameters in the model are necessary and cannot be removed without incurring a cost in our ability to reproduce the growth data.

## Different model topologies

In minimizing our energy function, we found that some parameters in the original model (3) were close to zero, and so we removed them from the model for computational purposes. But is this final topology of interactions between molecular species the only one that can fit the data? The number of combinations of possible topologies is astronomically high, but we can try to answer this question by performing some tests. We can set to zero one of the nonzero parameters in the final model (1), and substitute it for one of the parameters that was discarded from the original model (3). We have done this three times:

1. We set  $k_r$  to zero in the  $dB/dt$  equation of Eqs. (1), and include the terms  $d_{BC}$  and  $d_{BP}$  discarded from Eqs. (3). The modified equation for phyB is then

$$\frac{dB(t)}{dt} = p_B(T)L(t)(mut_B - B(t)) - d_{BC}B(t)C(t) - d_{BP}B(t)P(t).$$

That is, we neglect the thermal reversion rate in phyB and instead model the decay of phyB in dependence with PIF4 and COP1.

2. We set  $d_E$  to zero in the  $dE/dt$  equation of Eqs. (1), and include the term  $d_{EC}$  that was discarded



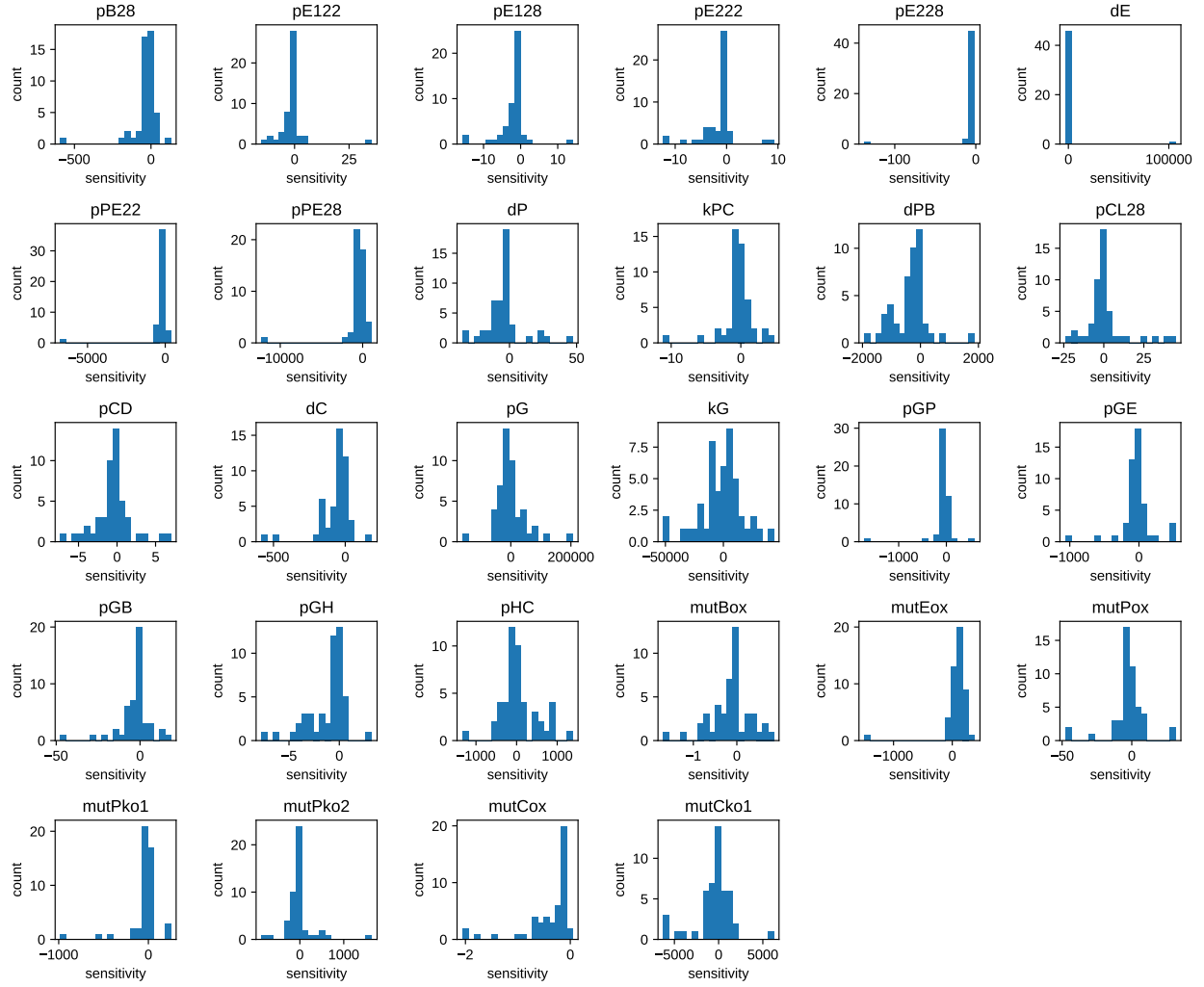


Figure S11: **Sensitivity of the energy function to small changes in the parameters.** Histograms showing sensitivity in the energy function  $E$  due to small changes in each of the parameters, Eq. (5). Each subplot represents small changes in one parameter, listed in the subtitle. Histograms made from 48 independent parameter sets that accurately fit our growth data.  $y$  axes represent histogram counts, while  $x$  axes represent percent changes in the energy function  $E$ . Small changes in some parameters can cause very large changes in the energy function.

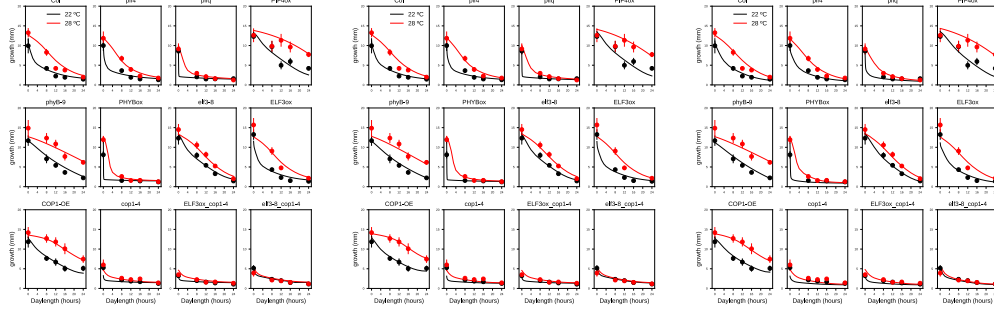
from Eqs. (3). The modified equation for ELF3 is then

$$\frac{dE(t)}{dt} = p_E(t, T, D, \text{mut}_E) - d_{EC}E(t)C(t).$$

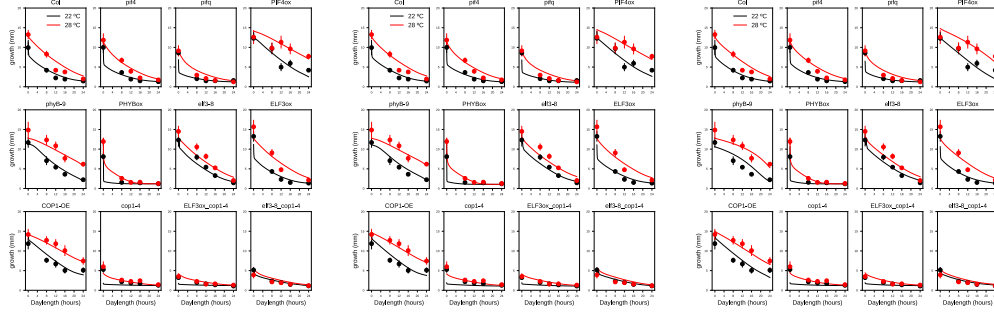
That is, we neglect the decay of ELF3 due to any reason except its interaction with COP1.

3. We set  $d_C$  to zero in the  $dC/dt$  equation in Eqs. (3), and include the term  $d_{CB}$  that was discarded

a)  $k_r=0$ ,  $d_{BC}$  and  $d_{BP}$  not zero



b)  $d_E=0$ ,  $d_{EC}$  not zero



c)  $d_C=0$ ,  $d_{CB}$  not zero

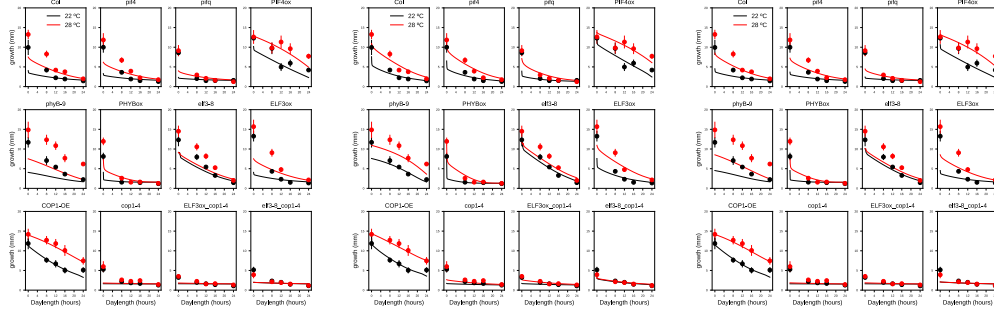


Figure S12: **Alternative network topologies can reproduce the growth data.** We performed nine simulated annealing runs with three alternative models (see text for an extended explanation), obtaining nine parameter sets that were able (in some cases) to reproduce the growth data as well as the final model (1). **(Upper row)** Setting  $k_r = 0$  and including in the model the terms  $d_{BC}$  and  $d_{BP}$  results in fits that reproduce the data very well. **(Middle row)** Similarly, setting  $d_E = 0$  and including in the model the term  $d_{EC}$  results in a very good fit of the data, visually indistinguishable from the fits obtained in fig. S8. **(Lower row)** Setting  $d_C = 0$  and including in the model the term  $d_{CB}$  from Eqs. (3) results in fits that do not reproduce the data accurately (notice in particular the bad fits of *Col*, *pif4*, *phyB-9*, *elf3-8* and *ELF3ox*).

from Eqs. (3). The modified equation for COP1 is then

$$\frac{dC(t)}{dt} = \text{mut}_C [p_{CL}(T)L(t) + p_{CD}(1 - L(t))] - d_{CB}C(t)B(t).$$

That is, we neglect the decay of COP1 due to any reason except its interaction with phyB.

We performed three simulated annealing runs with each of the modified models, thus obtained nine parameter sets. This is not an exhaustive computational experiment by any means, but it serves to test the hypothesis that these alternative models could fit the data as well as our final model (1). The results are very instructive:

1. Setting  $k_r = 0$  and allowing the model to change both  $d_{BC}$  and  $d_{BP}$  results in fits that are visually indistinguishable from Eqs. (1) at predicting the growth data (predictions shown in fig. S12, upper row). Whereas the minimum value of the energy function  $E$  is 242 in fig. S8, here we obtain  $E < 237$  for all three parameter sets. However, we cannot conclude from this that the dark reversion of phyB does not occur. Indeed, this molecular process has been extensively documented and is essential in understanding phyB's dynamics. These results simply show that, mathematically, a model including phyB's degradation by both PIFs and COP1 is enough to reproduce our growth data. The reason for this is that all three terms are correlated: the role of phyB's dark reversion is more relevant during the night. The same happens with PIF and COP1-mediated degradation: as the activity of these proteins is higher during the night, so too is their inhibitory effect on phyB. The three terms therefore send a coherent signal downstream: phyB levels go down during the night. This coherence makes sense from the biological point of view, as systems benefit from being robust and typically have many redundant components (56). However, from the mathematical point of view, this means that the model has some flexibility in the sense of accepting different terms that act in the same direction.
2. Setting  $d_E = 0$  and allowing the model to change  $d_{EC}$  results in fits that are slightly worse than the original model at capturing the growth data (predictions shown in fig. S12, middle row). However, visually there is no big difference with the fits we found for the simple model (compare with fig. S8). Since the energy function is slightly higher ( $E = 256$  and  $E = 259$  for the two left subplots in the middle row of fig. S12), it makes sense that the simulated annealing algorithm "chooses" to discard  $d_{EC}$  and focuses on a fit using  $d_E$  alone. Note that values of the energy function for the simple model (1) are on average lower than 250 (fig. S9, first subplot). However, from a biological standpoint, the difference is not high enough for us to claim that COP1-mediated

degradation of ELF3 is not relevant in our system. We would need additional studies to separate the effect of COP1 and other elements that can contribute to the decay of ELF3 protein levels. As in the previous example, the model shows some flexibility when incorporating terms that act in the same direction.

3. Finally, setting  $d_C = 0$  and allowing the model to change  $d_{CB}$  results in fits that do not capture the growth data accurately enough, with values of the energy function higher than 280 in all three cases (fig. S12, lower row). Notice for instance the bad fits of *Col*, *pif4*, *phyB-9* or *elf3-8* mutants. This suggests that the removal of COP1 from the nucleus is dependent not only on phyB but also on other photoreceptors, in line with our experimental data, fig. S4.

In summary, a closer inspection of alternative topologies allows us to conclude that COP1 dynamics are not mediated by phyB alone, and needs additional elements. However, we cannot conclude that COP1 and PIF-mediated inhibition of phyB is biologically irrelevant, or that COP1-mediated degradation of ELF3 does not have a role in the regulation of hypocotyl growth. In its current version, the model accepts some flexibility regarding these terms, as they all act in a correlated manner. In further works we will develop and improve the model in order to discern these contributions.

## Heatmaps

As a final robustness test, we recreated the thermoelongation heatmaps in Fig. 6 (main text) for several parameter sets, in order to check whether model predictions were consistent. Results are shown in figs. S13, S14, and S15. The heatmaps change quantitatively (as expected), but not qualitatively. The “blue” and “red” regions remain invariant, and only some minor quantitative features change. The consistency of predictions among parameter sets proves that our results are not dependent on specific parameter values, thus supporting our main conclusions.

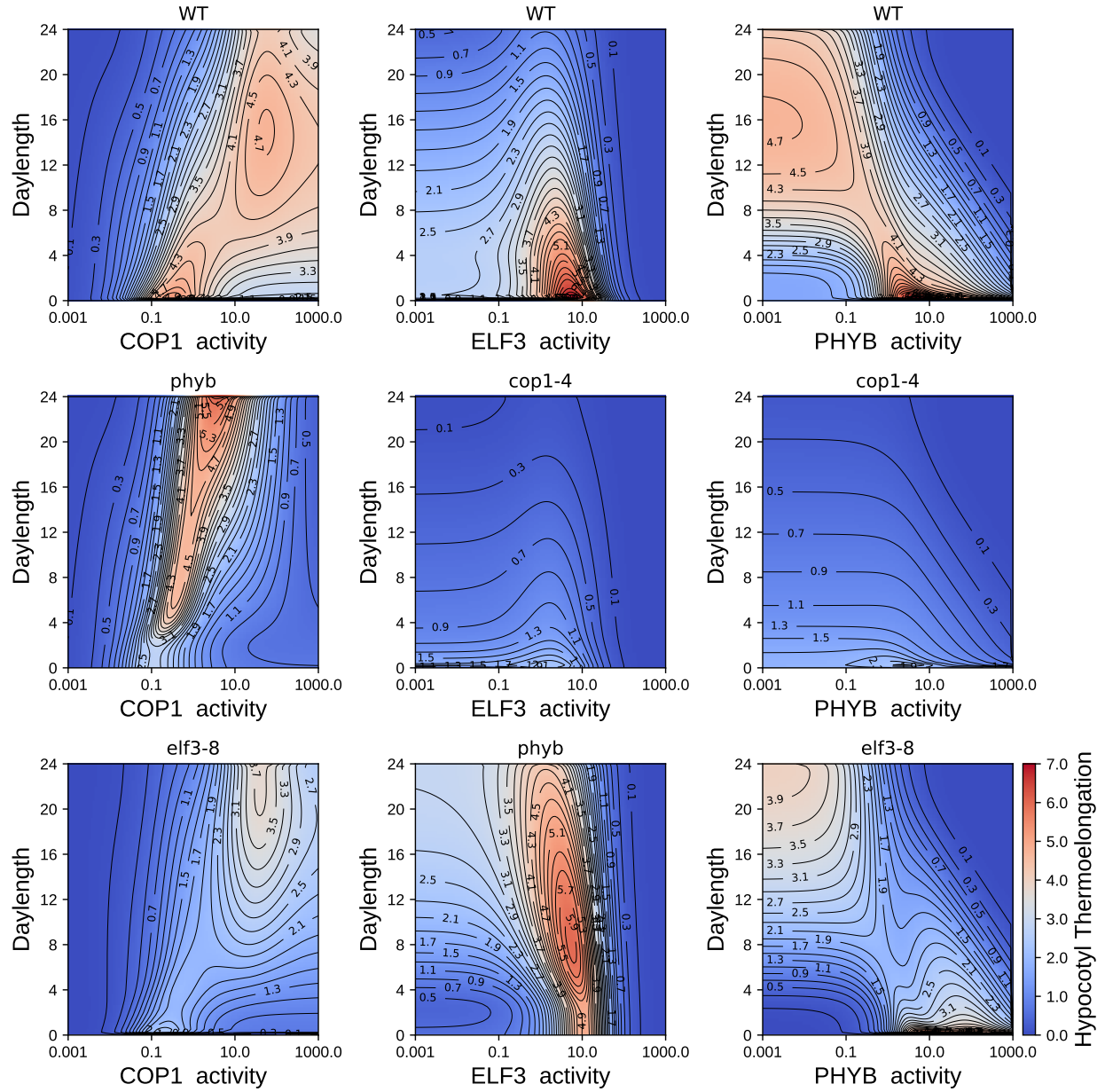


Figure S13: **Heatmap plots representing hypocotyl thermoelongation for several genotypes under different experimental conditions (I).** As in Fig. 6 (main text), but re-created using a different parameter set.

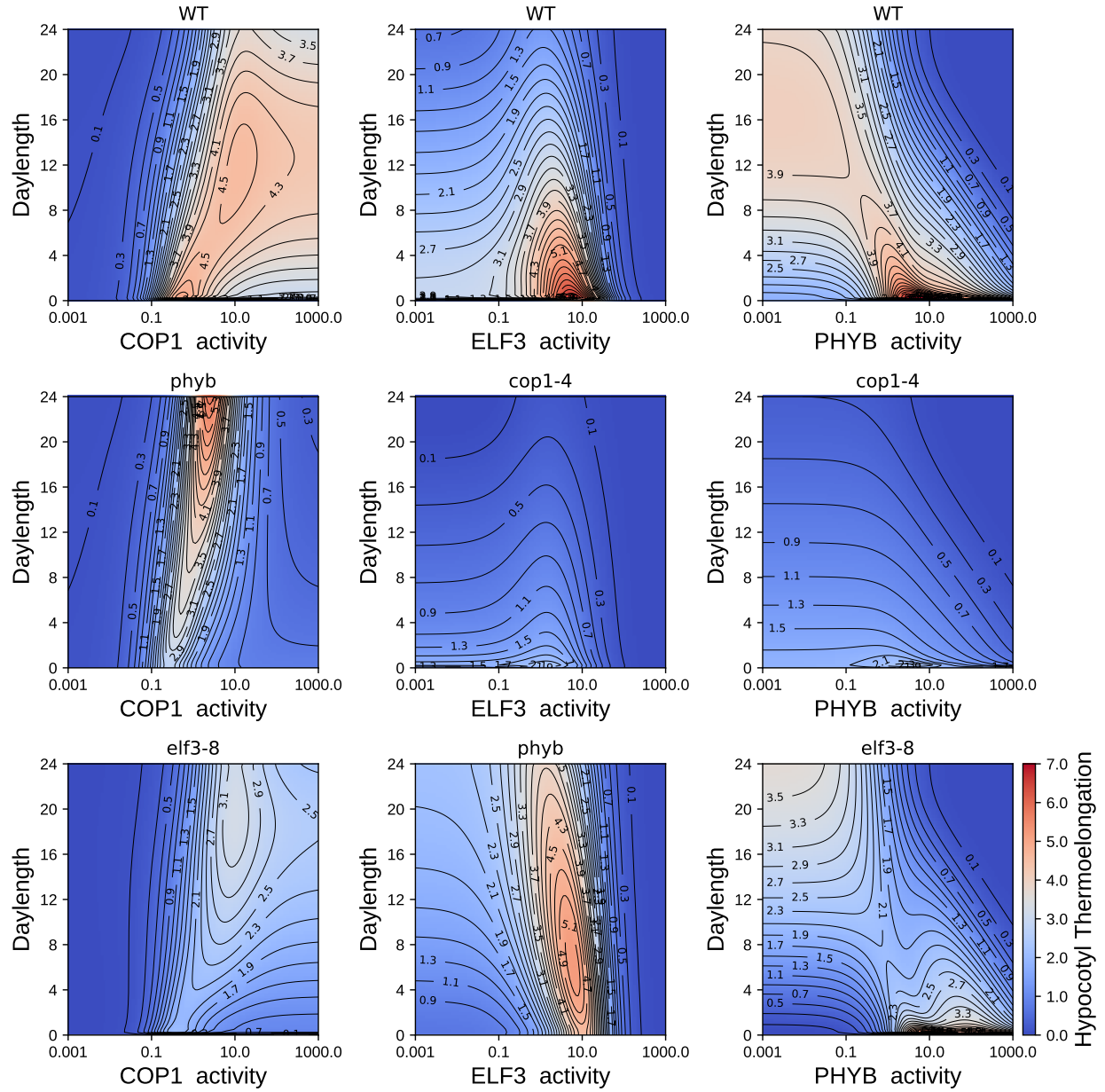


Figure S14: **Heatmap plots representing hypocotyl thermoelongation for several genotypes under different experimental conditions (II).** As in Fig. 6 (main text), but re-created using a different parameter set.

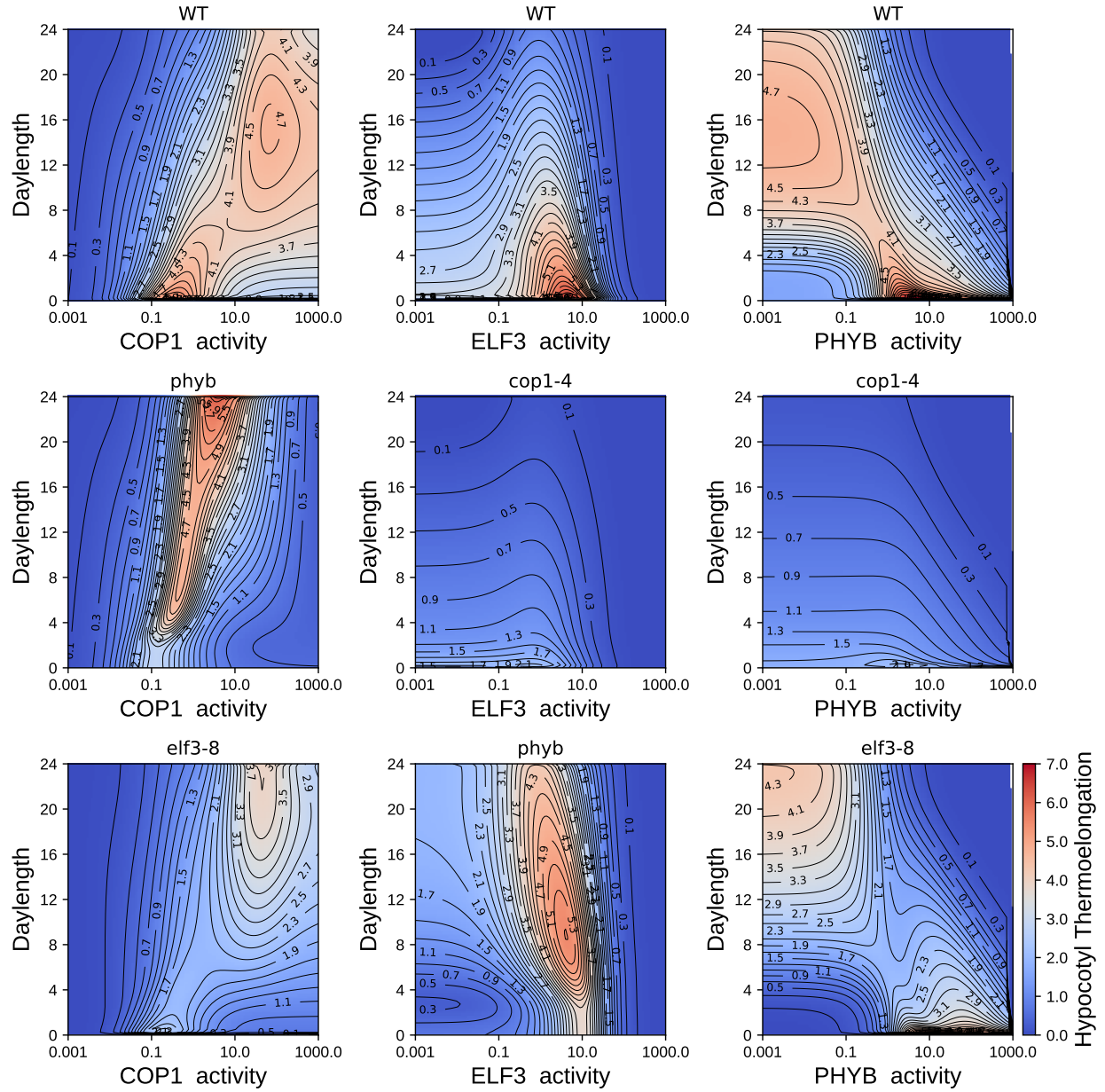


Figure S15: **Heatmap plots representing hypocotyl thermoelongation for several genotypes under different experimental conditions (III).** As in Fig. 6 (main text), but re-created using a different parameter set.

## Supplementary Tables

Table S1 shows the parameters used for the simulation results shown in the main text. Tables S2 to S6 show the number of seedlings used to quantify each experimental condition.

Table S1: **Parameters used in Eq. (1). The unit used for time is hours, concentrations are taken as non-dimensional.**

$p_B(22)$	10.000	$p_B(28)$	0.860
$k_r(22)$	0.232	$k_r(28)$	0.411
$p_{E1}(22)$	107.721	$p_{E1}(28)$	127.371
$p_{E2}(22)$	39.828	$p_{E2}(28)$	7.286
$d_E$	27.172		
$p_{CL}(22)$	1.000	$p_{CL}(28)$	5.370
$p_{CD}$	112.374	$d_C$	1.789
$p_P$	1	$d_{PB}$	0.313
$p_{PE}(22)$	0.332	$p_{PE}(28)$	0.028
$d_P$	4.908	$k_{PC}$	34.324
$p_G$	0.009	$k_G$	0.113
$p_{GP}$	2.933	$p_{GE}$	0.465
$p_{GB}$	10.683	$p_{GH}$	116.486
$p_{HC}$	0.180		
$mut_B(phyB-9)$	0	$mut_B(PHYBox)$	64.996
$mut_B(elf3-8)$	0	$mut_E(ELF3ox)$	1.185
$mut_C(cop1-4)$	0.032	$mut_C(COP1-OE)$	498.851
$mut_P(pif4)$	0.495	$mut_P(PIF4ox)$	6.367
$mut_P(pifq)$	0.198		



Table S2: Datapoints used to generate Fig. 1, for every experimental treatment measured. Seedlings of ELF3ox at 28°C and 16 hours of light, and PHYBox at 22°C and 12 hours of light, failed to germinate. Experiments of these conditions on different sets produced results as expected with the behavior in Fig. 1, but were not included for consistency of the dataset.

Genotype	Daylength	Temperature	Datapoints	Genotype	Daylength	Temperature	Datapoints
COP1-OE	0	22	74	elf3-8	0	22	35
COP1-OE	0	28	71	elf3-8	0	28	31
COP1-OE	8	22	14	elf3-8	8	22	11
COP1-OE	8	28	15	elf3-8	8	28	31
COP1-OE	12	22	43	elf3-8	12	22	22
COP1-OE	12	28	52	elf3-8	12	28	25
COP1-OE	16	22	74	elf3-8	16	22	9
COP1-OE	16	28	74	elf3-8	16	28	16
COP1-OE	24	22	56	elf3-8	24	22	28
COP1-OE	24	28	60	elf3-8	24	28	25
Col	0	22	20	elf3-8 cop1-4	0	22	34
Col	0	28	20	elf3-8 cop1-4	0	28	35
Col	8	22	19	elf3-8 cop1-4	8	22	32
Col	8	28	18	elf3-8 cop1-4	8	28	35
Col	12	22	15	elf3-8 cop1-4	12	22	23
Col	12	28	19	elf3-8 cop1-4	12	28	27
Col	16	22	30	elf3-8 cop1-4	16	22	10
Col	16	28	25	elf3-8 cop1-4	16	28	11
Col	24	22	13	elf3-8 cop1-4	24	22	25
Col	24	28	11	elf3-8 cop1-4	24	28	19
ELF3ox	0	22	34	hy5	0	22	24
ELF3ox	0	28	35	hy5	0	28	15
ELF3ox	8	22	33	hy5	8	22	21
ELF3ox	8	28	35	hy5	8	28	19
ELF3ox	12	22	17	hy5	12	22	14
ELF3ox	12	28	22	hy5	12	28	11
ELF3ox	16	22	22	hy5	16	22	13
ELF3ox	16	28	0	hy5	16	28	16
ELF3ox	24	22	27	hy5	24	22	14
ELF3ox	24	28	31	hy5	24	28	14
ELF3ox cop1-4	0	22	31	phyB-9	0	22	15
ELF3ox cop1-4	0	28	31	phyB-9	0	28	17
ELF3ox cop1-4	8	22	35	phyB-9	8	22	23
ELF3ox cop1-4	8	28	29	phyB-9	8	28	22
ELF3ox cop1-4	12	22	36	phyB-9	12	22	17
ELF3ox cop1-4	12	28	25	phyB-9	12	28	16
ELF3ox cop1-4	16	22	19	phyB-9	16	22	4
ELF3ox cop1-4	16	28	24	phyB-9	16	28	11
ELF3ox cop1-4	24	22	25	phyB-9	24	22	19
ELF3ox cop1-4	24	28	20	phyB-9	24	28	17
PHYBox	0	22	16	pi4	0	22	21
PHYBox	0	28	15	pi4	0	28	27
PHYBox	8	22	12	pi4	8	22	27
PHYBox	8	28	11	pi4	8	28	29
PHYBox	12	22	0	pi4	12	22	29
PHYBox	12	28	3	pi4	12	28	26
PHYBox	16	22	2	pi4	16	22	15
PHYBox	16	28	6	pi4	16	28	15
PHYBox	24	22	2	pi4	24	22	18
PHYBox	24	28	4	pi4	24	28	19
PIF4ox	0	22	1	pi4q	0	22	6
PIF4ox	0	28	5	pi4q	0	28	7
PIF4ox	8	22	8	pi4q	8	22	10
PIF4ox	8	28	10	pi4q	8	28	16
PIF4ox	12	22	12	pi4q	12	22	5
PIF4ox	12	28	8	pi4q	12	28	8
PIF4ox	16	22	14	pi4q	16	22	2
PIF4ox	16	28	20	pi4q	16	28	3
PIF4ox	24	22	4	pi4q	24	22	2
PIF4ox	24	28	15	pi4q	24	28	3
cop1-4	0	22	31				
cop1-4	0	28	30				
cop1-4	8	22	29				
cop1-4	8	28	33				
cop1-4	12	22	21				
cop1-4	12	28	20				
cop1-4	16	22	25				
cop1-4	16	28	29				
cop1-4	24	22	26				
cop1-4	24	28	26				

Table S3: **Datapoints used to generate Fig. 3, for every experimental treatment measured.**

Genotype	Daylength	Light	Temperature	Datapoints
WT	4	White	22	33
WT	4	White	28	31
phyB-9	4	White	22	28
phyB-9	4	White	28	24
PHYBox	4	White	22	58
PHYBox	4	White	28	56
COP1-OE	4	White	22	29
COP1-OE	4	White	28	26
cop1-4	4	White	22	19
cop1-4	4	White	28	19
elf3-8	4	White	22	31
elf3-8	4	White	28	37

Table S4: **Datapoints used to generate Fig. 5C, for every experimental treatment measured.**

Genotype	Daylength	Light	Temperature	Datapoints
WT	24	White	22	23
WT	24	White	28	21
YFP-COP1	24	White	22	15
YFP-COP1	24	White	28	14
RFP-COP1	24	White	22	24
RFP-COP1	24	White	28	24
COP1-OE	24	White	22	24
COP1-OE	24	White	28	22
cop1-4	24	White	22	19
cop1-4	24	White	28	19
WT	0	White	22	14
WT	0	White	28	21
YFP-COP1	0	White	22	18
YFP-COP1	0	White	28	18
RFP-COP1	0	White	22	24
RFP-COP1	0	White	28	22
COP1-OE	0	White	22	23
COP1-OE	0	White	28	22
cop1-4	0	White	22	18
cop1-4	0	White	28	19

Table S5: Datapoints used to generate Fig. 5G and fig. S4B, for every experimental treatment measured.

Genotype	Daylength	Light	Temperature	Datapoints
PHYBox COP1OE	0		22	63
PHYBox COP1OE	0		28	57
PHYBox COP1OE	24	White	22	17
PHYBox COP1OE	24	White	28	34
PHYBox COP1OE	24	RED	22	26
PHYBox COP1OE	24	RED	28	20
PHYBox COP1OE	24	BLUE	22	30
PHYBox COP1OE	24	BLUE	28	31
phyB COP1 OE	0		22	111
phyB COP1 OE	0		28	87
phyB COP1 OE	24	White	22	112
phyB COP1 OE	24	White	28	91
phyB COP1 OE	24	RED	22	37
phyB COP1 OE	24	RED	28	28
phyB COP1 OE	24	BLUE	22	22
phyB COP1 OE	24	BLUE	28	20
PHYBox COP1OE	4	White	22	33
PHYBox COP1OE	4	White	28	30
PHYBox COP1OE	8	White	22	21
PHYBox COP1OE	8	White	28	16
PHYBox COP1OE	16	White	22	17
PHYBox COP1OE	16	White	28	18
phyB COP1 OE	4	White	22	52
phyB COP1 OE	4	White	28	44
phyB COP1 OE	8	White	22	13
phyB COP1 OE	8	White	28	26
phyB COP1 OE	16	White	22	39
phyB COP1 OE	16	White	28	42

Table S6: **Datapoints used to generate fig. S4A, for every experimental treatment measured.**

<b>Genotype</b>	<b>Daylength</b>	<b>Light</b>	<b>Temperature</b>	<b>Datapoints</b>
WT	24	BLUE	22	39
WT	24	BLUE	28	46
YFP-COP1	24	BLUE	22	31
YFP-COP1	24	BLUE	28	27
RFP-COP1	24	BLUE	22	46
RFP-COP1	24	BLUE	28	48
COP1-OE	24	BLUE	22	43
COP1-OE	24	BLUE	28	46
WT	24	RED	22	44
WT	24	RED	28	49
YFP-COP1	24	RED	22	31
YFP-COP1	24	RED	28	31
RFP-COP1	24	RED	22	42
RFP-COP1	24	RED	28	35
COP1-OE	24	RED	22	57
COP1-OE	24	RED	28	46