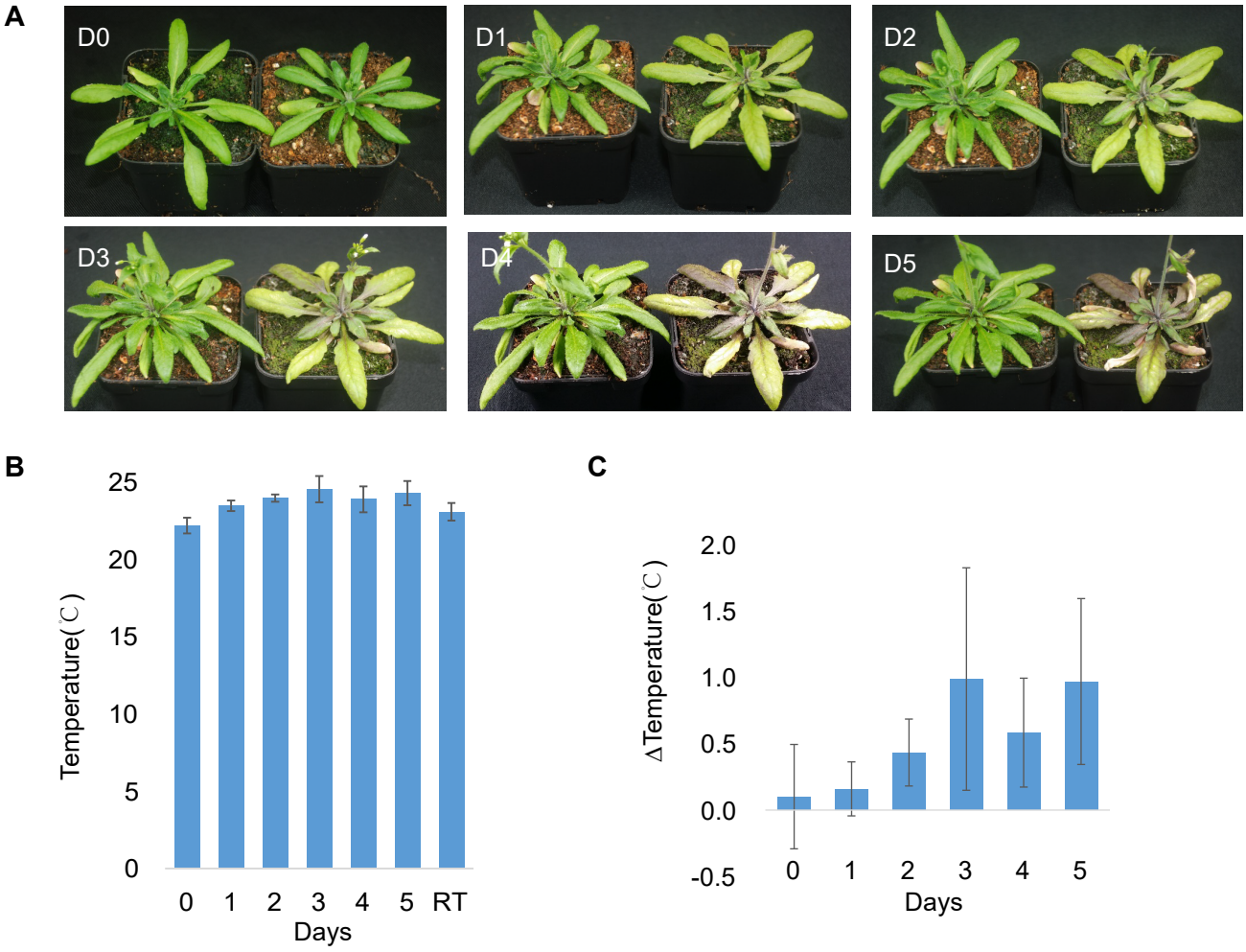

Fig S1 LED high light treatment effect on Arabidopsis growth, appearance and leaf surface temperature.

Arabidopsis grown under the same conditions were transferred to standard (100 µmol protons $m^{-2}{\cdot}S^{-1}$) and high (500 µmol protons $m^{-2}{\cdot}S^{-1}$) LED illumination for up to five days (D0-D5). Two representative Arabidopsis plants under low light (left) and high (right) light were shown (A). Leaf adaxial surface temperature and room temperature (RT) was measured by a far-red thermometer at noon everyday (B). ΔTemperature showed the temperature differences between leaf surface and room temperature. Error bars show standard deviations from four biological replicates.

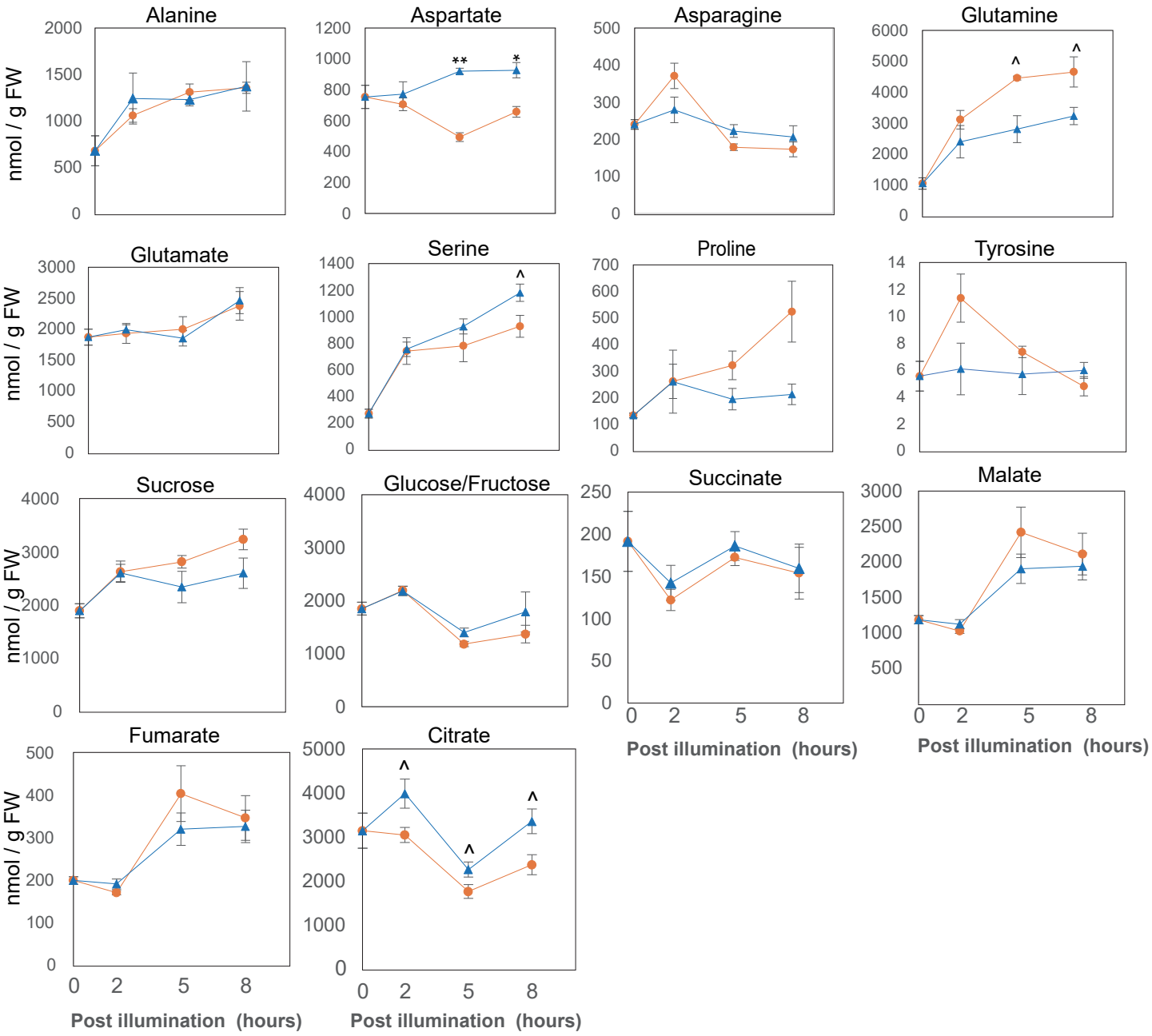

Fig S2 High light induced changes in abundance of specific amino acids and organic acids.
Specific amino acids (measured by LC-QQQ MS) and organic acids (measured by LC-Q-TOF MS) that increase in abundance in response to high light treatment. Error bars show standard errors (biological replicates n=3). Statistical significance tests were performed with a student's t test (**P<0.01, * P<0.05, ^ P<0.1).

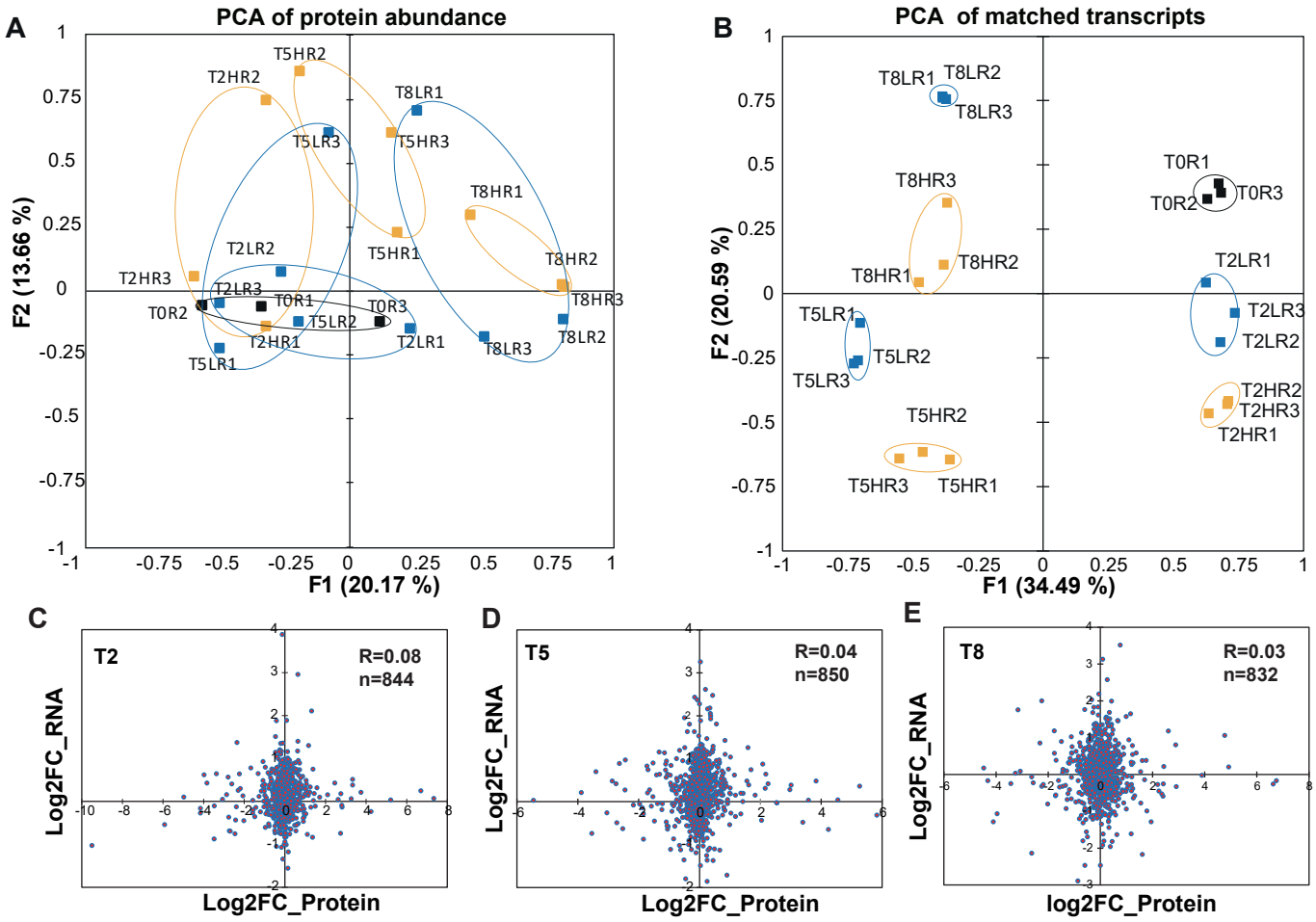

Fig S3 Principal components analysis and correlations of protein and mRNA abundance showing the relationship between transcriptional responses and protein abundance in standard light and high light conditions.

PCA analysis for 370 proteins with measured transcript abundance (DataS1) and protein abundance (DataS2) in the dark (black), standard (blue), and high light (yellow) conditions (A-B). Scatterplots display the relationship between log2 fold-change in protein abundance (x-axis) and mRNA abundance (y-axis), in response to high light. Pearson's r was calculated to quantify their correlation at 2h (T2), 5h (T5) and 8h (T8) (C-E).

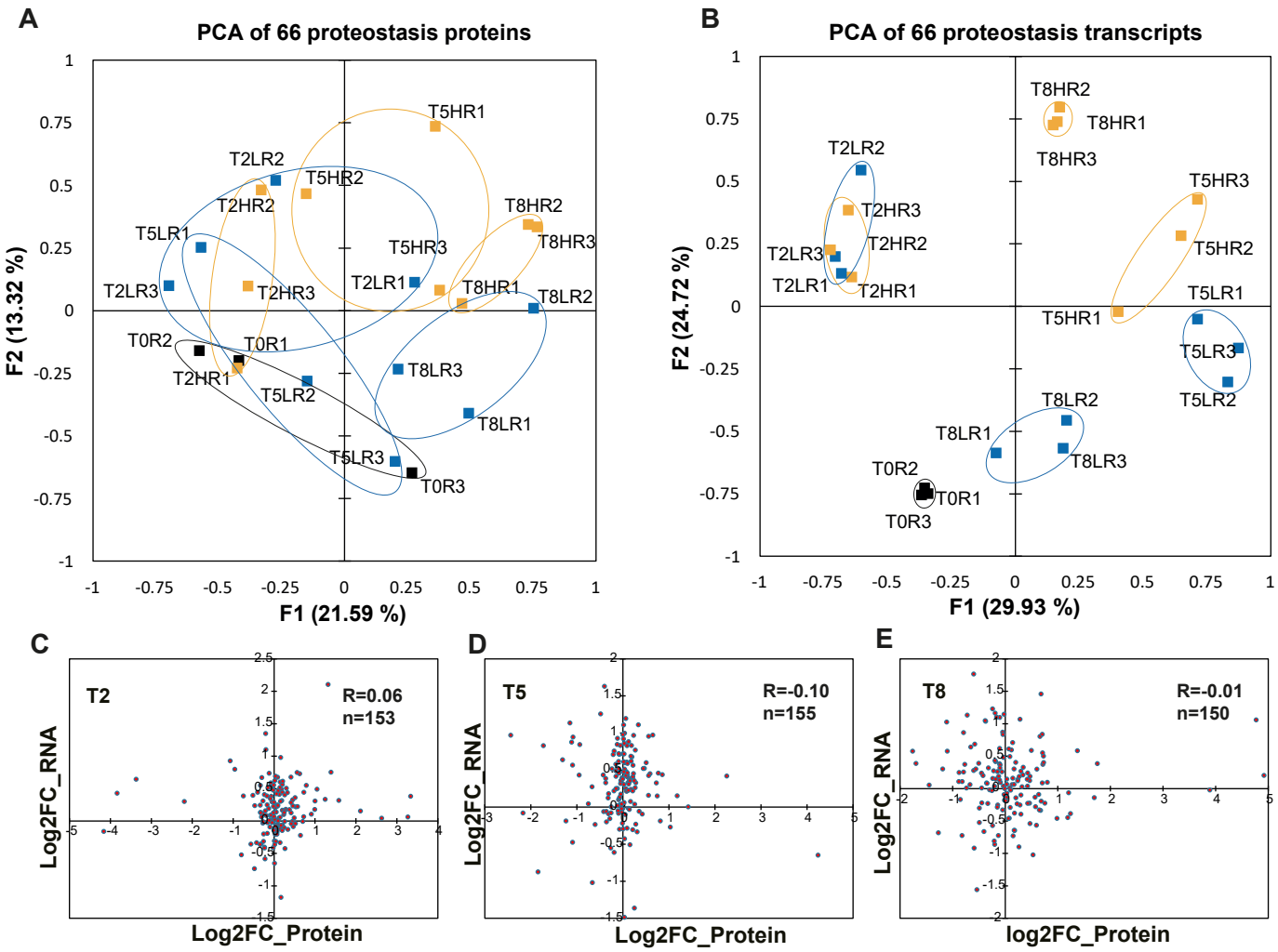

Fig S4 Principal components analysis and correlations of protein and mRNA abundance for protein components of protein homeostasis machinery in standard light and high light conditions.

PCA analysis for 66 proteins involved in protein homeostasis (protein synthesis, degradation, folding and targeting) for which both transcript abundance (DataS1) and protein abundance (DataS2) in the dark (black), standard (blue), and high light (yellow) conditions was available (A-B). Scatterplots display the relationship between log2 fold-change in protein abundance (x-axis) and mRNA abundance (y-axis), in response to high light. Pearson's r was calculated to quantify their correlation at 2h (T2), 5h (T5) and 8h (T8) (C-E).

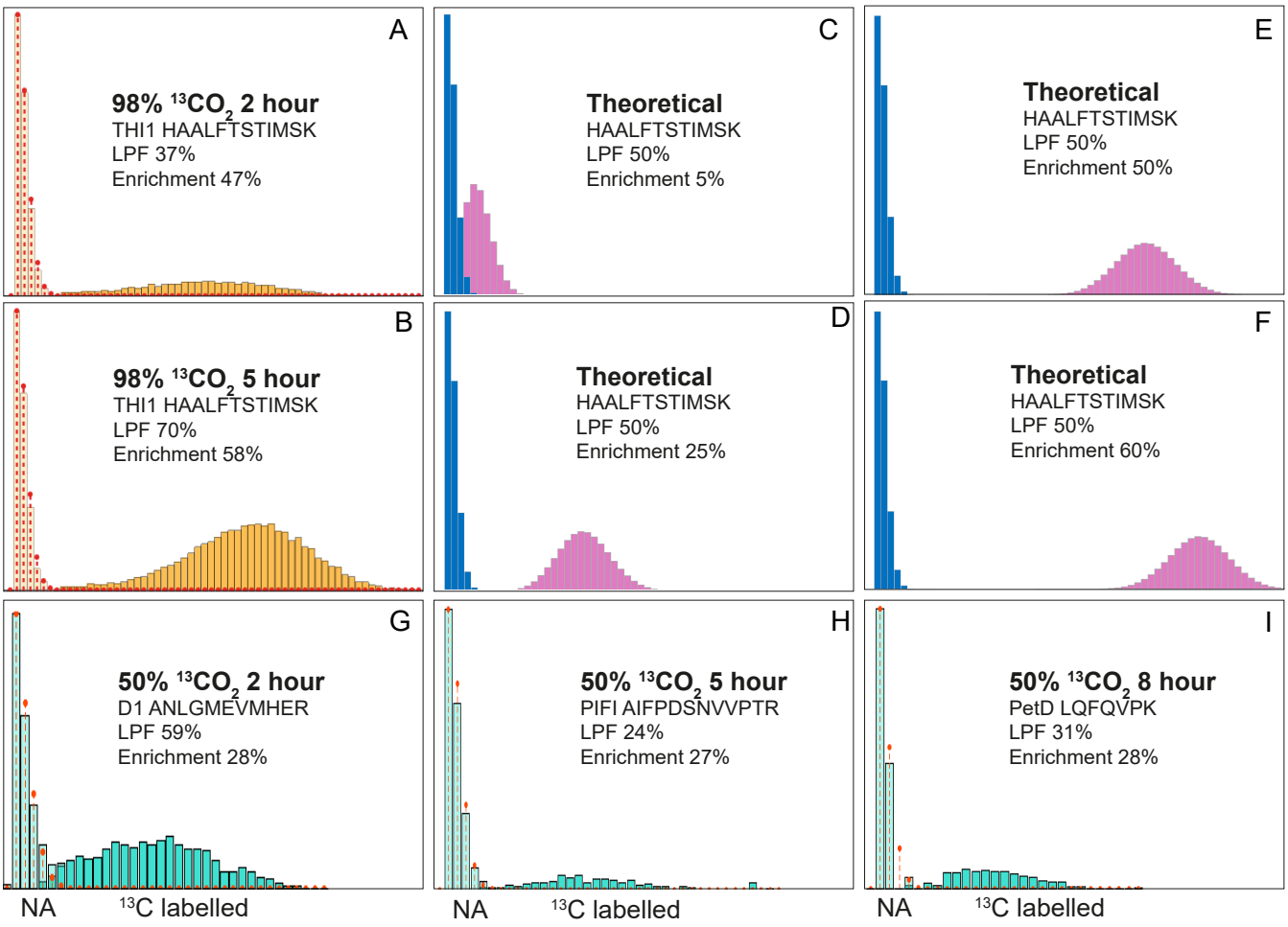

Fig S5 ^{13}C labelling optimisation based on 98%, 50% $^{13}CO_2$ air labelling and theoretical modelling.

Mass spectra of a THI1 peptide HAALFTSTIMSK (NA-light yellow, ^{13}C labelled-yellow) from 98% $^{13}CO_2$ air labelled Arabidopsis shoot after 2 and 5 hours (A-B). Theoretical modelling of HAALFTSTIMSK mass spectra (NA-blue, ^{13}C labelled-purple) with 5, 25, 50 and 60% levels of $^{13}CO_2$ enrichment (C-F). Mass spectra of three peptides with 7-12 amino acids (D1-ANLGMEVMHER, PIFI-AIFPDSNVVPTR and PetD-LQFQVPK; NA-light green, ^{13}C labelled-green) from 50% $^{13}CO_2$ air labelled Arabidopsis shoots after 2, 5 and 8 hours (G-I).

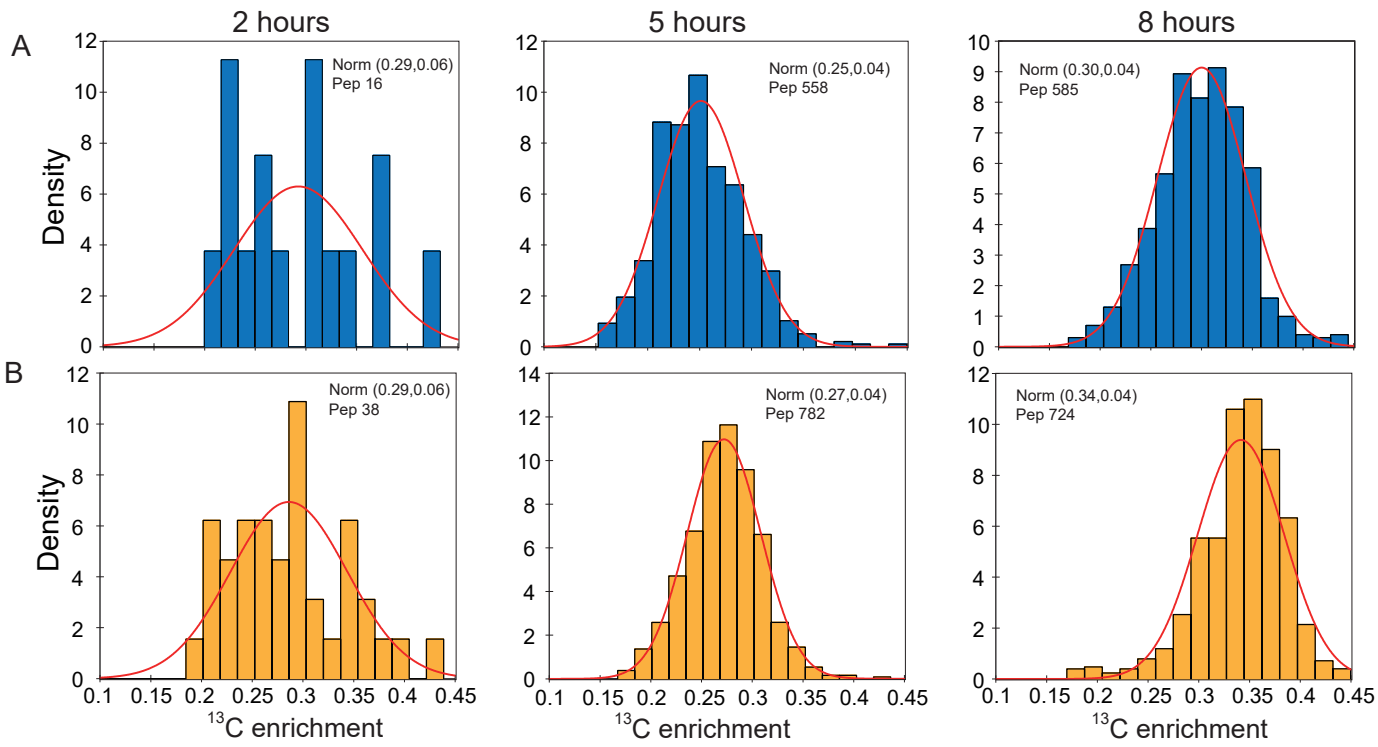

Fig S6 ^{13}C enrichment level of the heavy labelled ^{13}C peptide population under standard (blue) and high light (yellow) conditions.
The calculated ^{13}C enrichment level for all peptides identified under each condition from the progressive labelling experiments combined. In each histogram, the bars are the actual peptide number, the median and standard deviation are shown as a plotted red line normal distribution (norm). The number of unique peptides (pep) included in each analysis is shown.