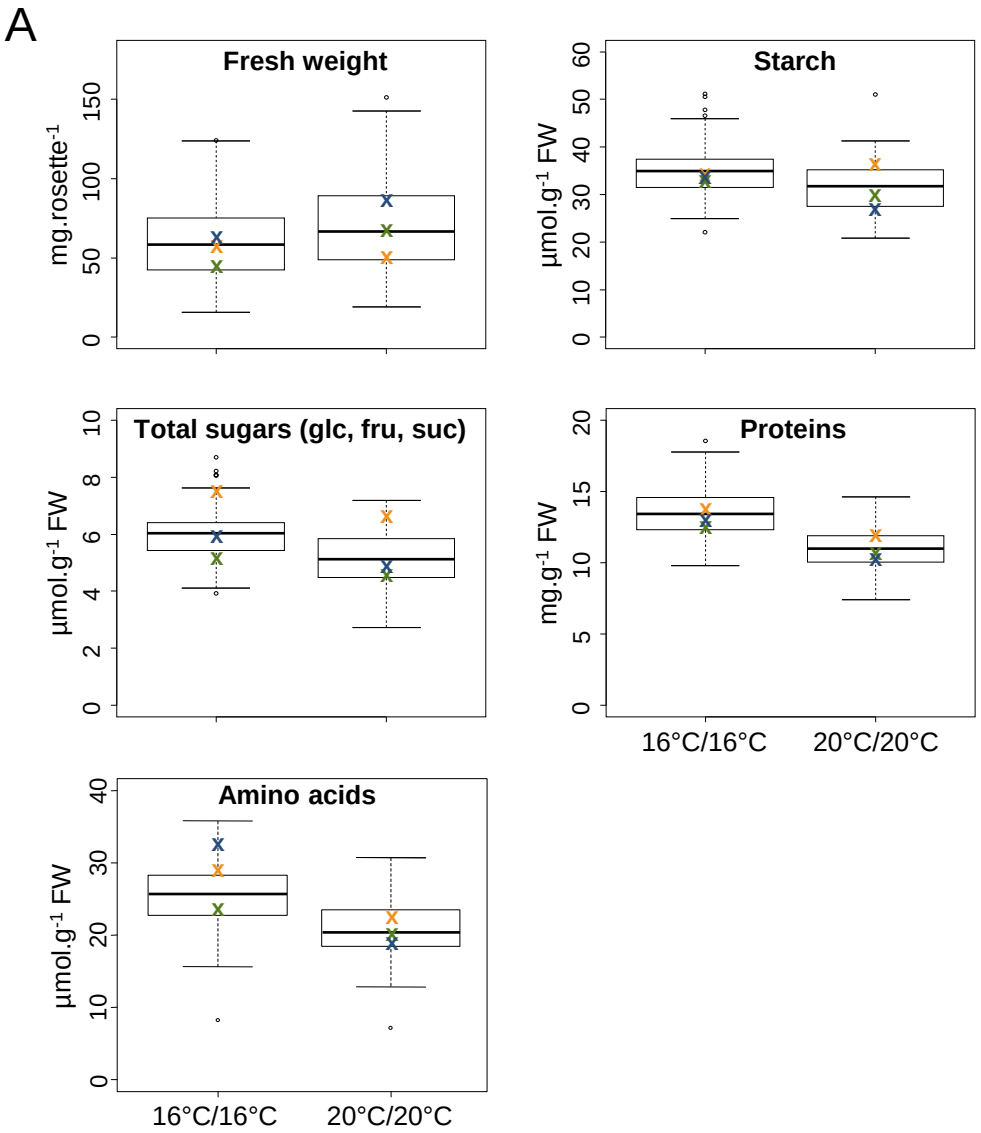
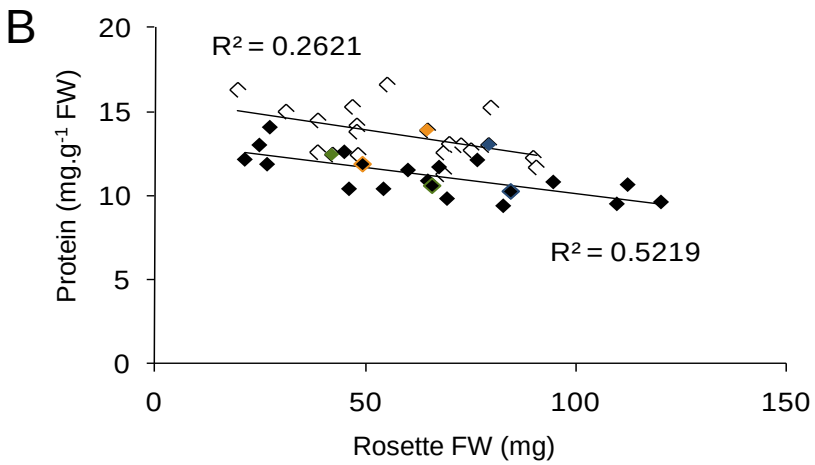
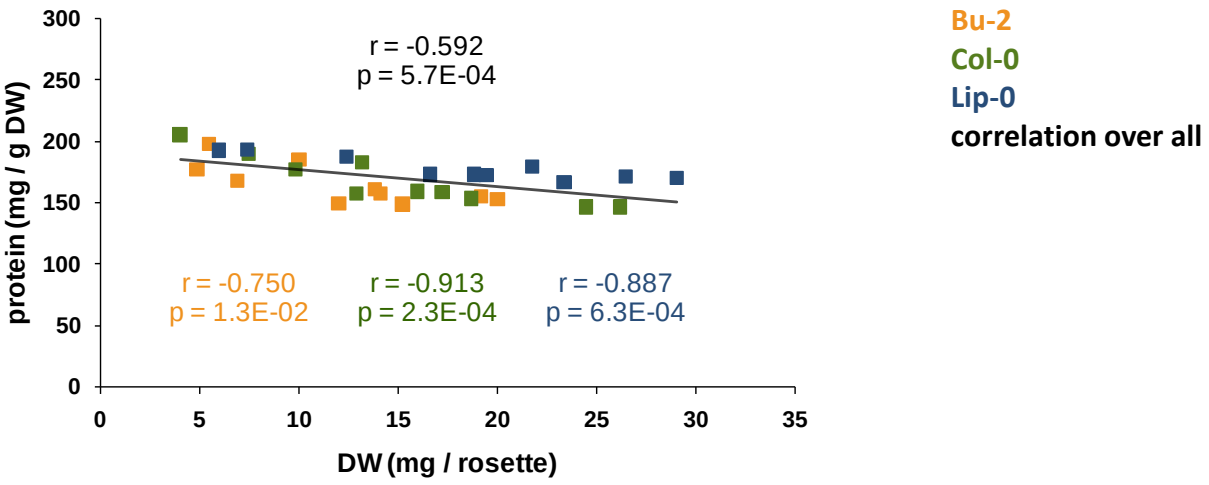


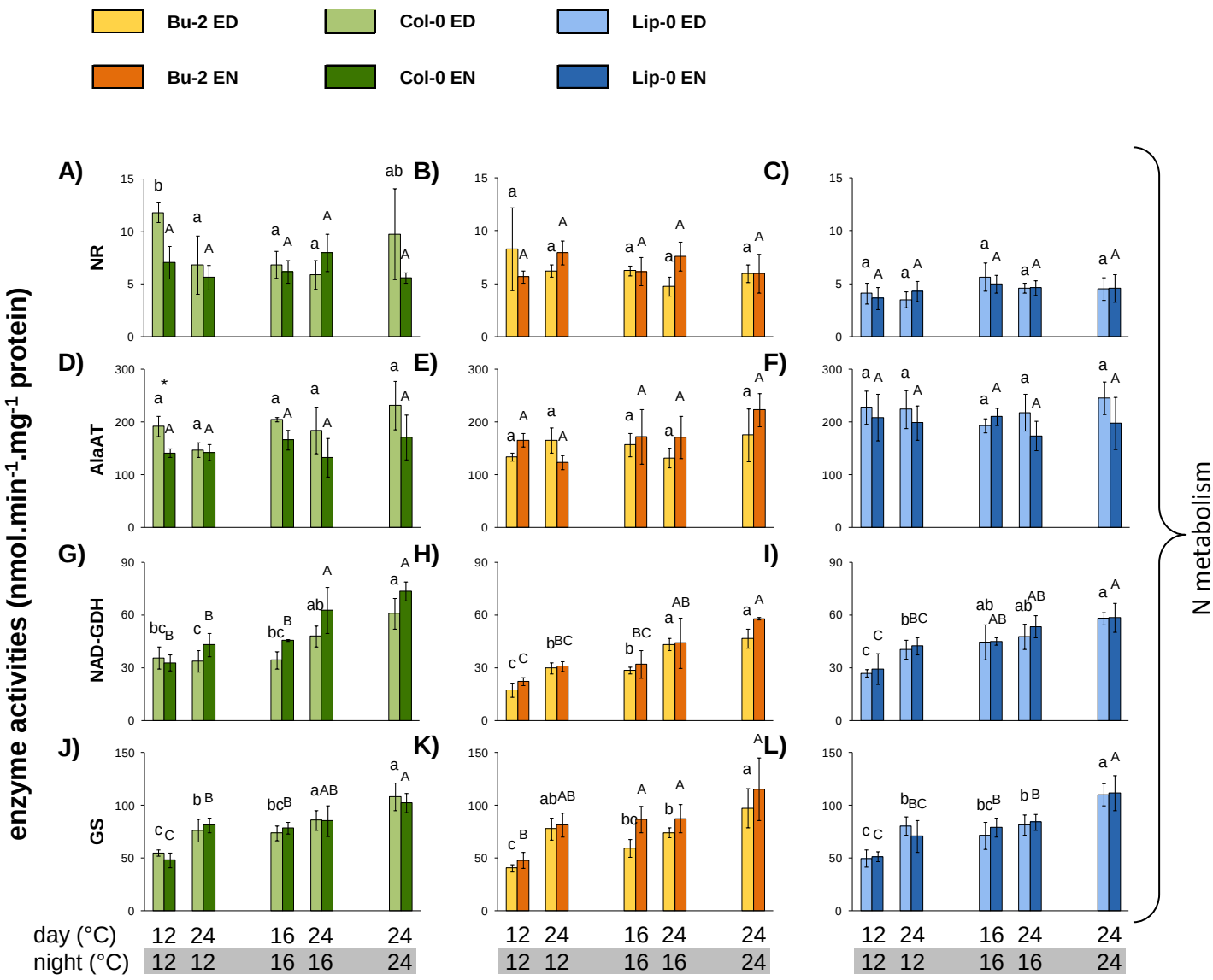


Supplemental Figure 1. (A) Box plots of the average fresh weight (FW), proteins amounts, starch, soluble sugars, and amino acids levels in 20 Arabidopsis accessions grown at constant daily temperatures of 16°C or 20°C. (B) Correlation between the protein amounts and rosette FW across the 20 accessions grown at constant daily temperatures of 16°C (open diamonds) or 20°C (closed diamonds). Values for Col-0 (green stars), Lip-0 (blue stars) and Bu-2 (orange stars) are indicated in the plots.

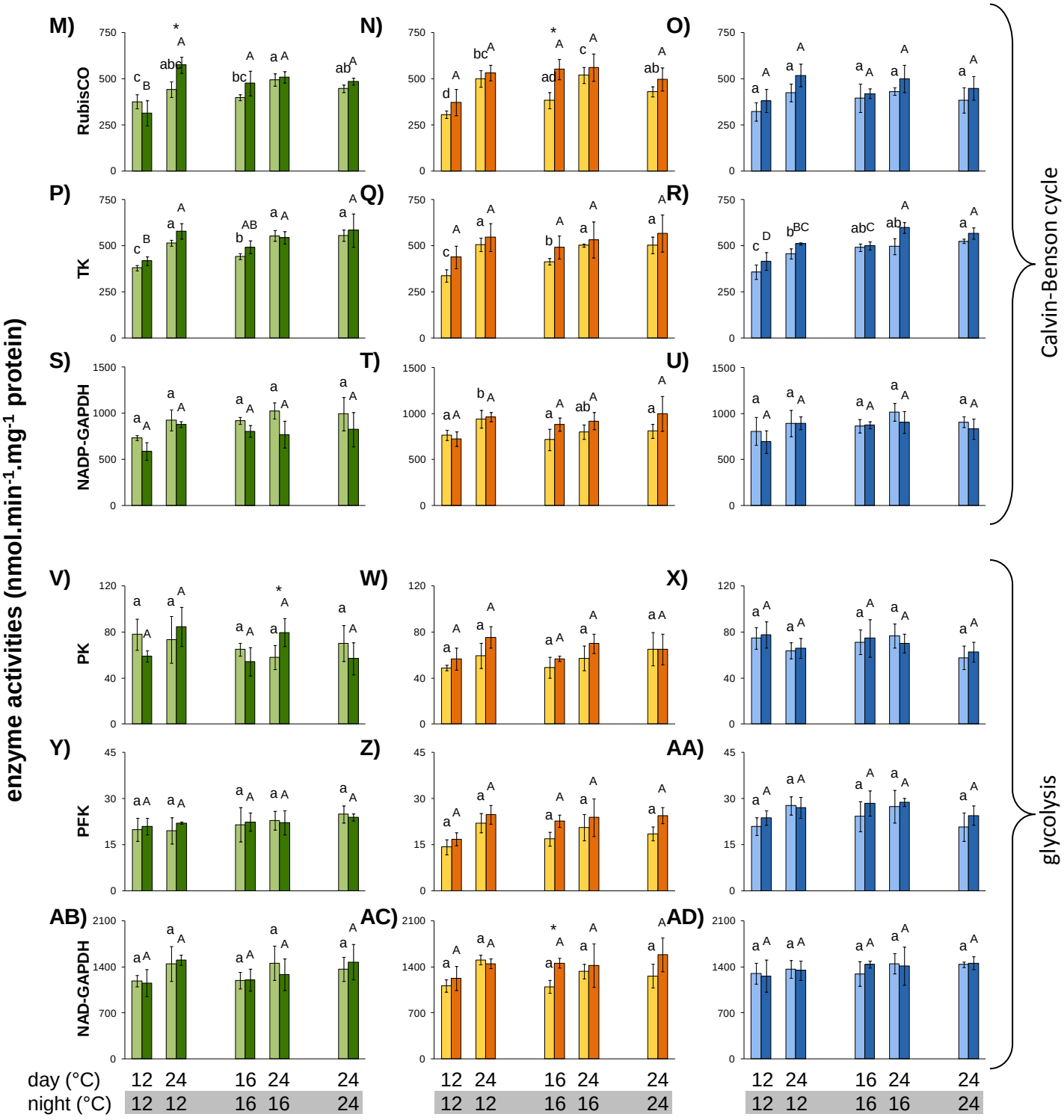


Supplemental Figure 2. Correlation plots between the protein amount and the DW for the three accessions grown in the five thermocycles (12°C/12°, 16°C/16°C, 24°C/12°C, 24°C/16°C and 24°C/24°C). Plants were grown for three weeks in standard conditions (see Material and Methods) and then transferred to the different thermocycles for the last two weeks of growth with short photoperiods (8h light/16h dark) and 160 µE of light. Bu-2, orange square; Col-0, green square; Lip-0, blue square. Each point represents the mean of four replicates, one replicate comprising five pooled rosette plants.

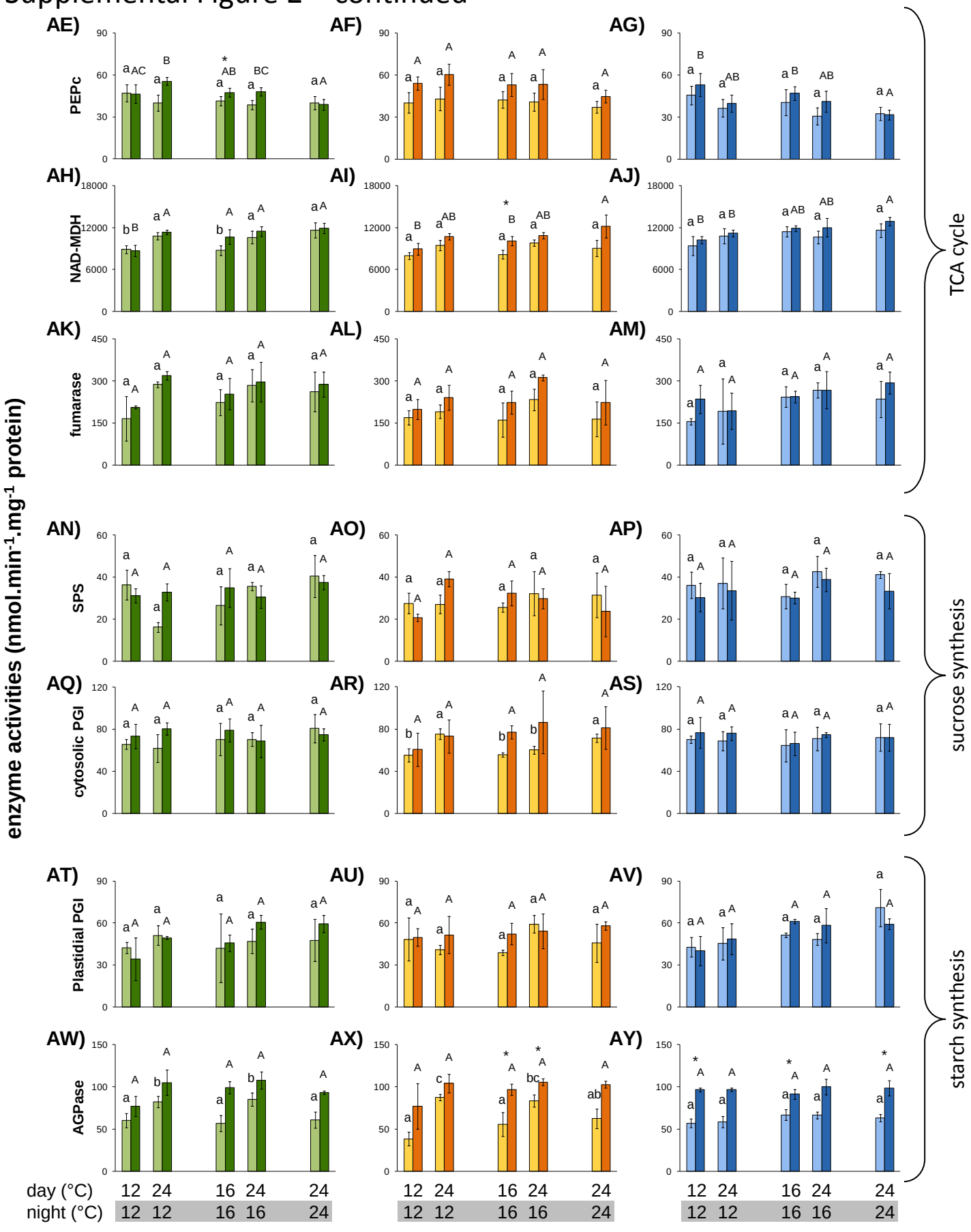
Supplemental Figure 3. Variation of 17 representative primary metabolism enzyme activities determined in rosettes of three accessions grown in 5 different thermocycles (12°C/12°C, 24°C/12°C, 16°C/16°C, 24°C/16°C, 24°C/24°C). Enzyme activities are expressed on a protein basis. For each thermocycle/accession pair, the activities were determined at the end of the day (ED) and the end of the night (EN). Data represents the mean ± SD (n=4), 1 replicate comprising 5 pooled rosette plants. One-way analysis of variance (ANOVA) was used to identify potential candidates for a statistically significant difference between treatments separately for each of the two time points. After ANOVA p-value correction using Holm's method ($p<0.05$), individual contrasts were then identified in a post-hoc Tukey HSD test ($p<0.05$). They are indicated by different letters within the same time point (ED, lower case; EN, upper case). All raw data are available in Supplemental Data Set 2 online.



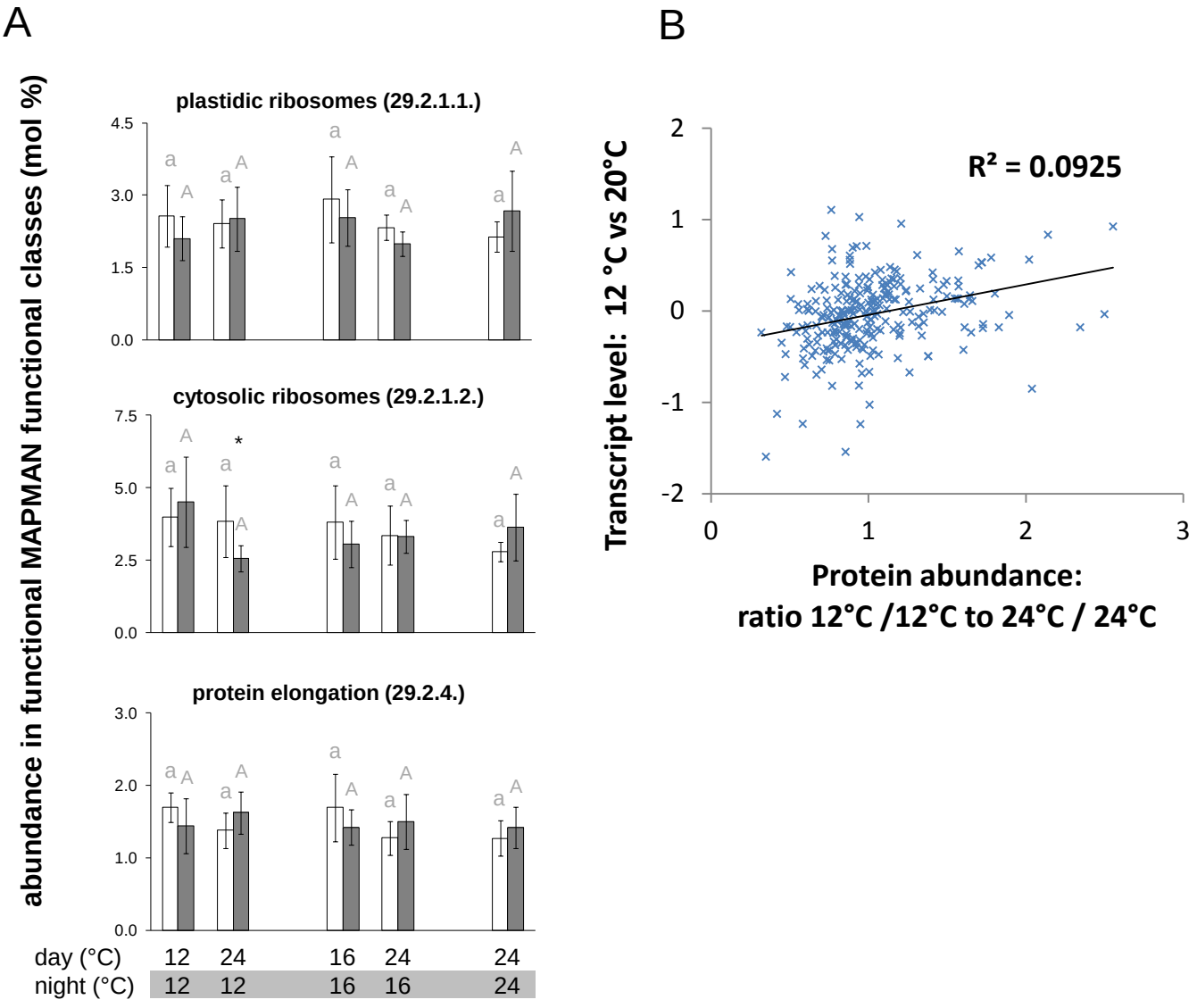
Supplemental Figure 2 – continued



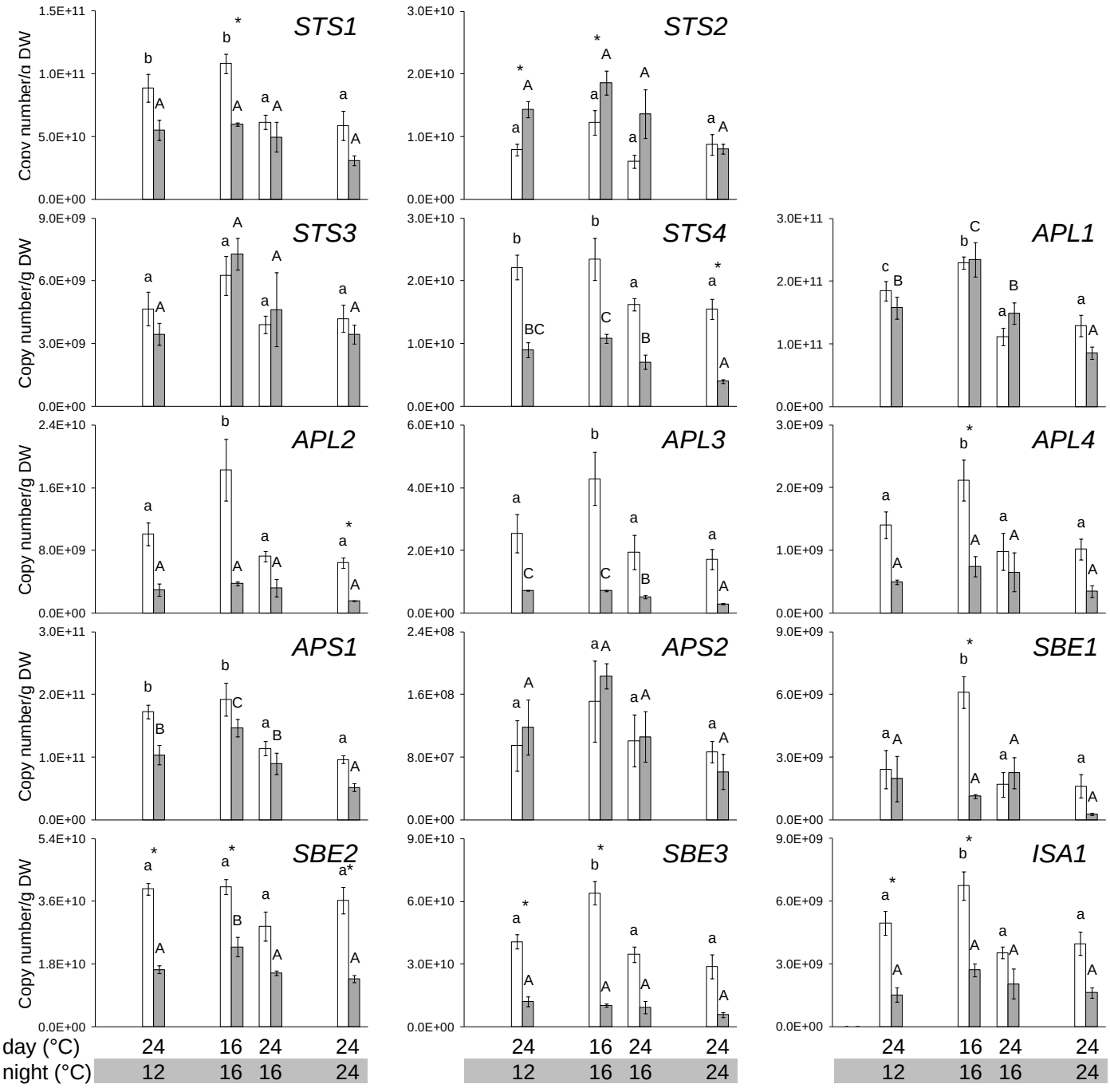
Supplemental Figure 2 – continued



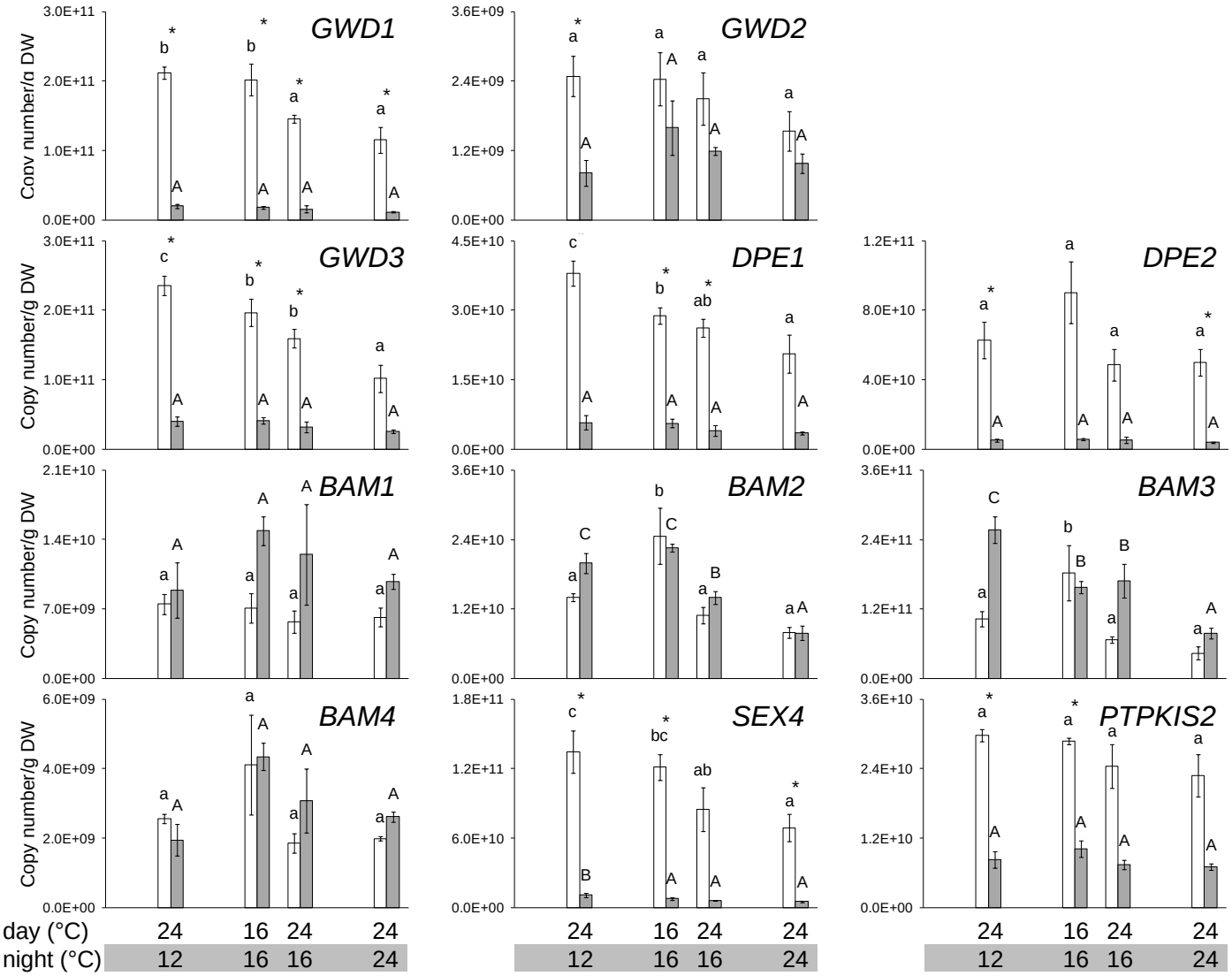
Supplemental Figure 4. Changes in protein levels (A) Qualitative variation in proteins comprised in protein related MAPMAN functional classes related to growth in rosettes of Col-0 plants grown in 5 different thermocycles. Data for each time point (ED, open bars; EN, closed bars) and thermocycle are expressed in mol% of proteins detected by LC-MS/MS. Values are the sum of proteins annotated to the respective functional class (± standard deviation). One-way analysis of variance (ANOVA) was used to identify potential candidates for a statistically significant difference between treatments separately for each of the two time points. After ANOVA p-value correction using Holm's method ($p<0.05$), individual contrasts were then identified in a post-hoc Tukey HSD test ($p<0.05$). They are indicated by different letters within the same time point (ED, lower case; EN, upper case). Comparisons between ED and EN using a paired t-test at a given thermocycle are indicated by an asterisk, if significant ($p<0.05$). All raw data and information about the proteins analysed are available in the Supplemental Data Set 4 online. (B) Relation between the change of protein and changes in transcripts in a published study in similar conditions. The y-axis shows for 252 proteins the abundance in a 12°C/12°C thermocycle, compared to a 24°C/24°C thermocycle (data from Supplemental Data Set 4 online). The ratio is estimated from the average value at ED and EN in a given thermocycle, unless one data point is missing, in which case the single data point is taken. The x-axis shows, for the corresponding transcript, the ratio between the transcript level at 20°C and 3 days after transfer to 12°C. Samples were taken at ED from Col-0 of a similar size growing in a 12 h light / 12 h dark cycle. The transcript data is from Usadel et al. (2008b), and is included in Supplemental Data Set 4 online.

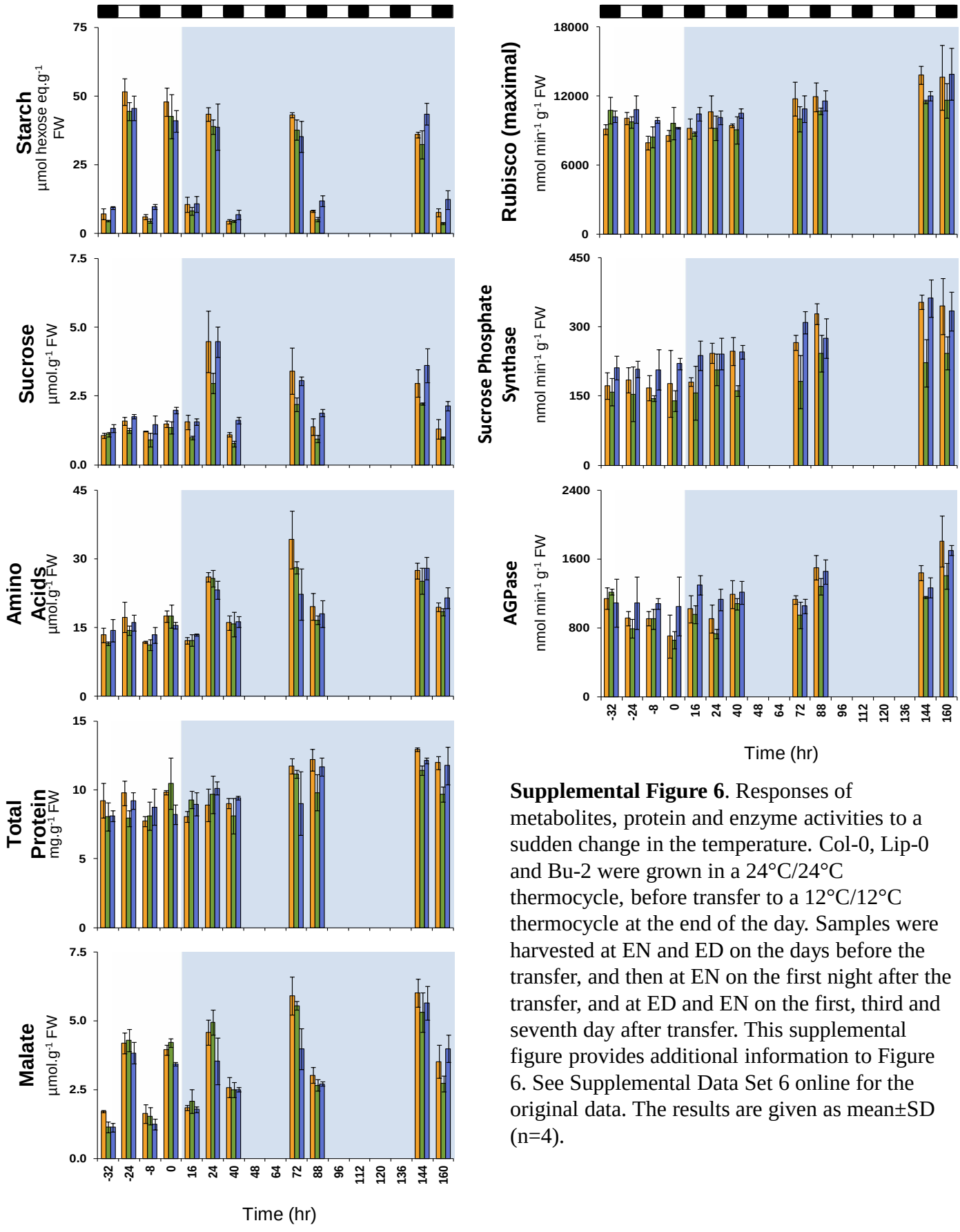


Supplemental Figure 5. Response of transcripts for proteins involved in starch synthesis and breakdown. Transcripts were measured by qRT-PCR in samples harvested at EN (solid bars) and ED (open bars) from plants growing in a 24°C/12°C, 16°C/16°C, 24°C/16°C and 24°C/24°C thermocycle as in Figure 7. Absolute quantification of transcripts was achieved by adding seven artificial RNA species at different concentrations to the extract before preparing the cDNA. The results are the mean±SD of three biological replicates. One-way analysis of variance (ANOVA) was used to identify potential candidates for a statistically significant difference between treatments separately for each of the two time points. After ANOVA p-value correction using Holm's method ($p<0.05$), individual contrasts were then identified in a post-hoc Tukey HSD test ($p<0.05$). They are indicated by different letters within the same time point (ED, lower case; EN, upper case). Significant differences in transcript levels between ED and EN were identified using a paired t-test at a given thermocycle and are indicated by an asterisk if significant ($p<0.05$).



Supplemental Figure 5 –Starch degradation - continued





Supplemental Figure 6. Responses of metabolites, protein and enzyme activities to a sudden change in the temperature. Col-0, Lip-0 and Bu-2 were grown in a 24°C/24°C thermocycle, before transfer to a 12°C/12°C thermocycle at the end of the day. Samples were harvested at EN and ED on the days before the transfer, and then at EN on the first night after the transfer, and at ED and EN on the first, third and seventh day after transfer. This supplemental figure provides additional information to Figure 6. See Supplemental Data Set 6 online for the original data. The results are given as mean±SD (n=4).