

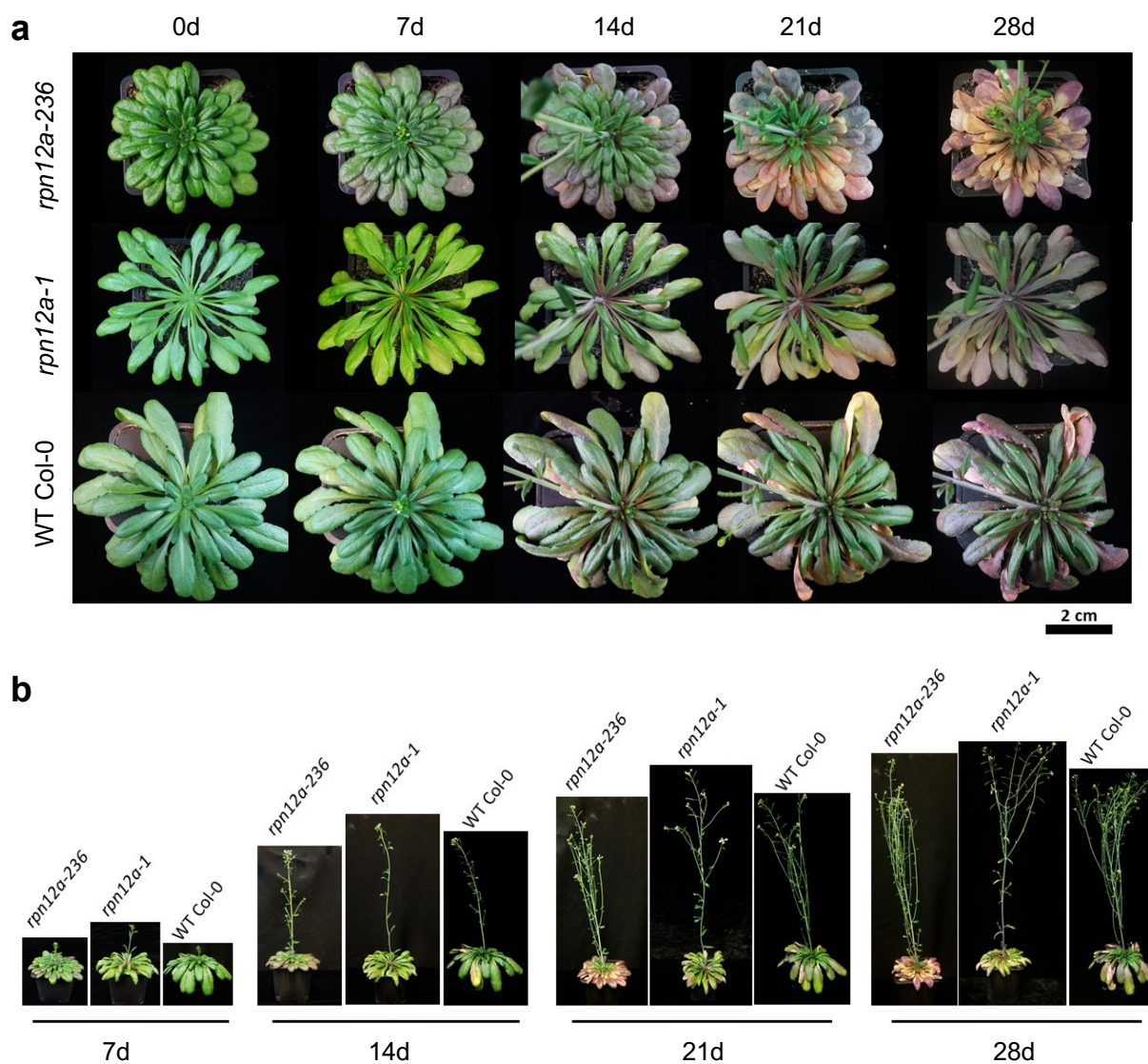


Figure S1. Comparison between WT and *rpn12a* mutants plants undergoing developmental senescence. Pictures were taken once a week after the first flower bud was visible (stage 5.10; Boyes et al., 2001). **(a)** Top view. **(b)** Front view.

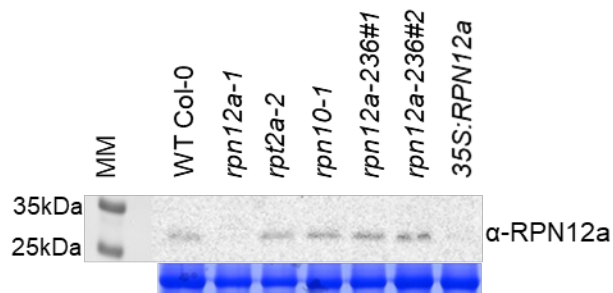


Figure S2. RPN12a immunoblot. Immunoblot analysis of total protein extracts from WT Col-0, *rpn12a-1*, *rpt2a-2*, *rpn10-1*, *rpn12a-236* and 35S:*RPN12a* with antibodies raised against RPN12a. Loading control (Coomassie blue staining, focus on Rubisco large subunit) shows that equal amounts of proteins (10 µg) were loaded. MM = molecular mass marker. kDa = kilo Dalton.

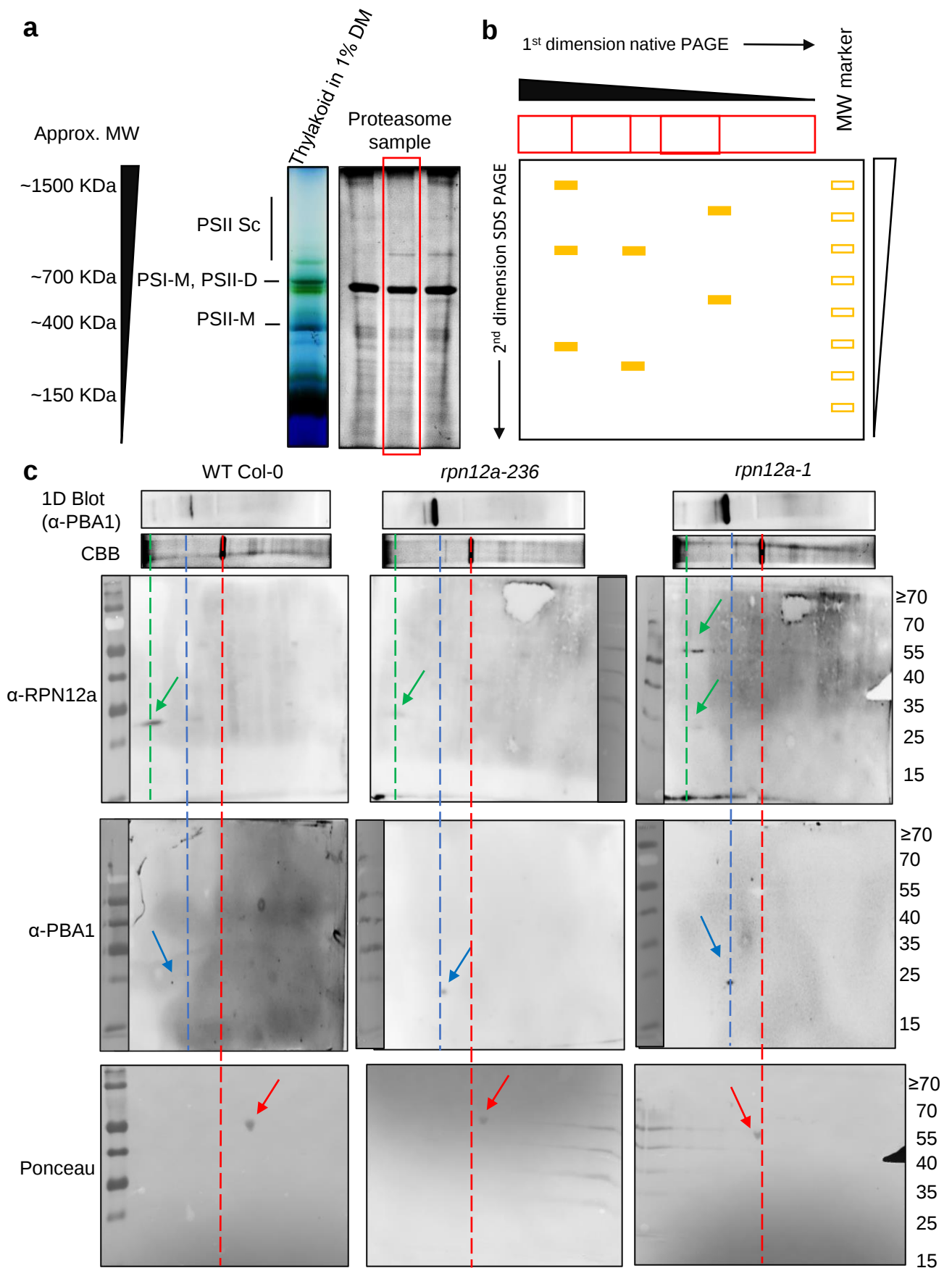


Figure S3. Second-dimension Native PAGE immunoblots. (a) The photosystem (PS) complexes and the proteasome samples were loaded on a 1D-gel. Molecular weight of the complexes were estimated by comparing with known molecular weights of *Arabidopsis thaliana* Col-0 photosynthetic pigment protein complexes separated under the same native conditions. (b) Schematic representation of a second-dimension run. (c) Native PAGE followed by a run on a second dimension SDS-PAGE on Col-0, *rpn12a-236* and *rpn12a-1*. Immunoblot analyses of the RPN12a subunit (top) PBA1 subunit (middle) were done on total protein extracts from 10-day-old seedlings. Ponceau staining are shown on the bottom. Green: 26S proteasome; Blue: 20S proteasome; red: proteasome-independent.

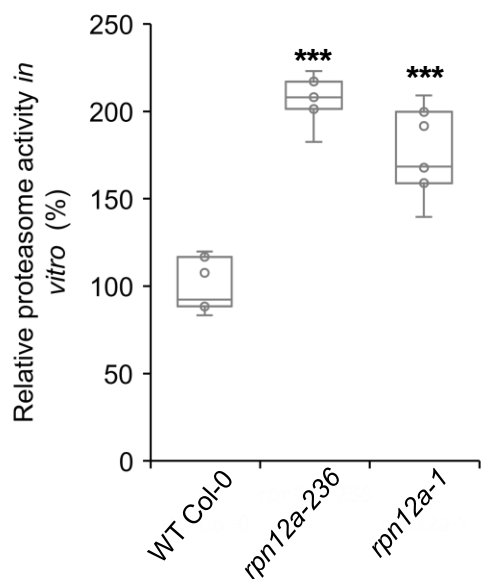


Figure S4. 20S Proteasome *in vitro* activity. *In vitro* activity test was performed in a UV microplate (n=7). Data are presented as corrected relative fluorescence normalized to the WT Col-0 level. The interquartile range of the box is from the 25th to 75th percentiles, and the middle line is the median; whiskers represent min and max values; a Student's t-test showed statistically significant differences at *** $p < 0.0001$.

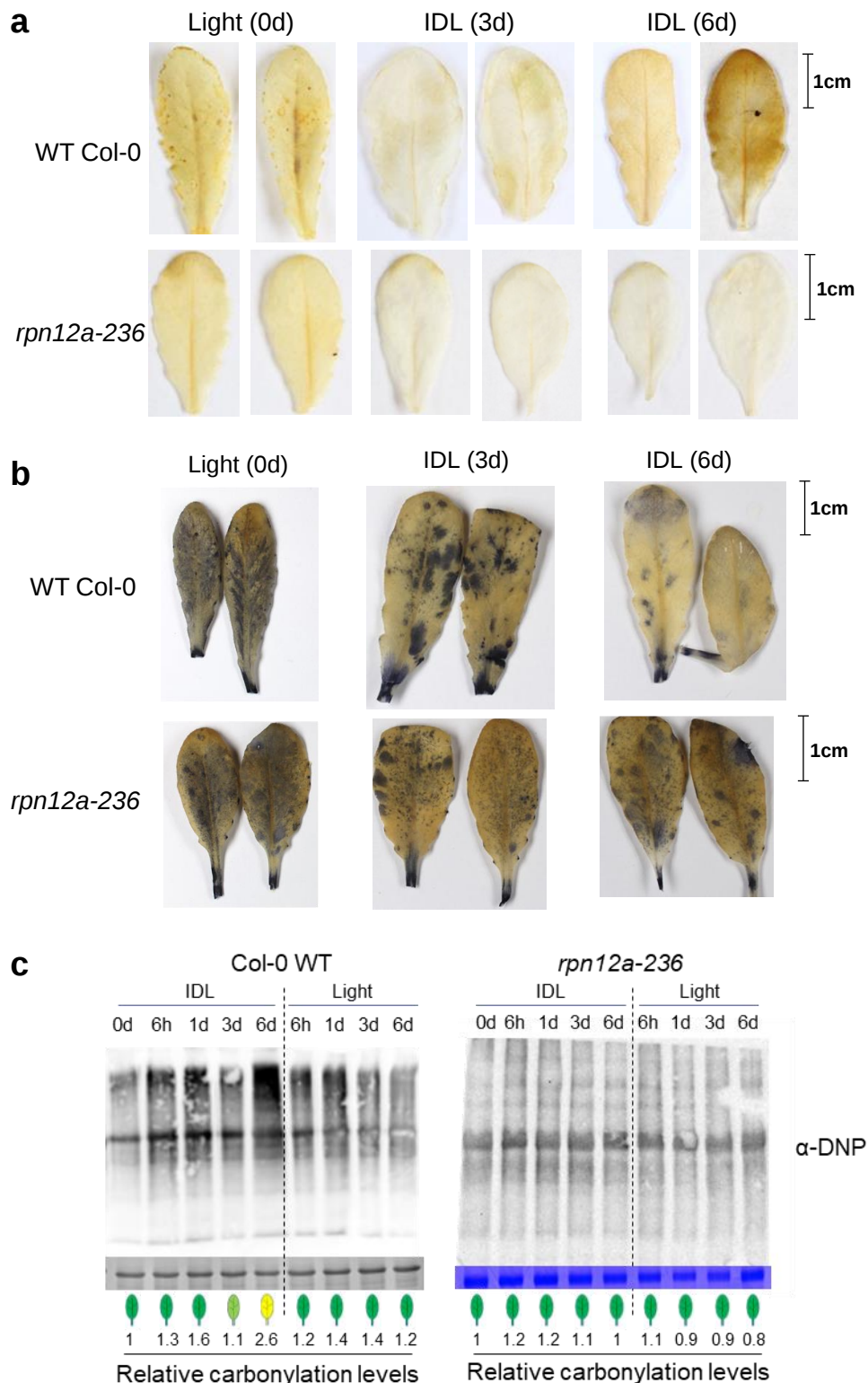


Figure S5. Levels of oxidation in a 19S proteasome mutant during DIS. (a) DAB coloration assay of H_2O_2 accumulation, and (b) NBT coloration assay of O_2^- accumulation in WT Col-0 and *rpn12a-236* mutant. IDL treatment was used to induce senescence on 6-week-old plants grown in SD for 0 day, 3 days, and 6 days. (c) Oxidized protein levels in Col-0 and *rpn12a-236* mutant. Equal amounts of total protein (20 μg) (Coomassie blue staining, focus on Rubisco large subunit) were subjected to SDS-PAGE and immunoblot analysis with anti-ubiquitin antibodies. Carbonylation levels were estimated, and fold-change compared to levels at the 0d time point (set to 1) was reported below the immunoblot. Proteins were extracted from 6- to 7-week-old SD grown plants treated with IDL or light for 0, 6h, 1 day, 3 days and 6 days. DNPH was derivatized by carbonyls and DNP levels were assessed by immunoblot anti-DNP

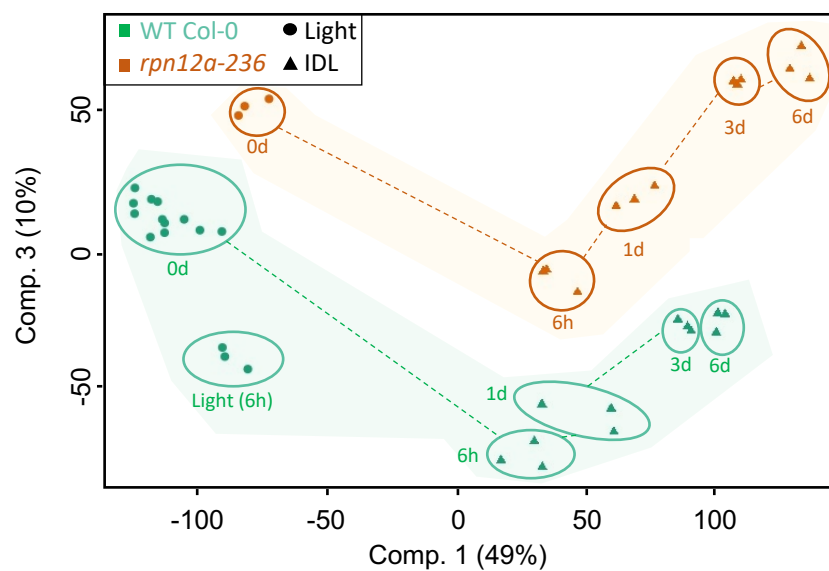


Figure S6. Principal Component Analysis from RNAseq data. Here, the first component (49%) versus third component (10%) are represented.

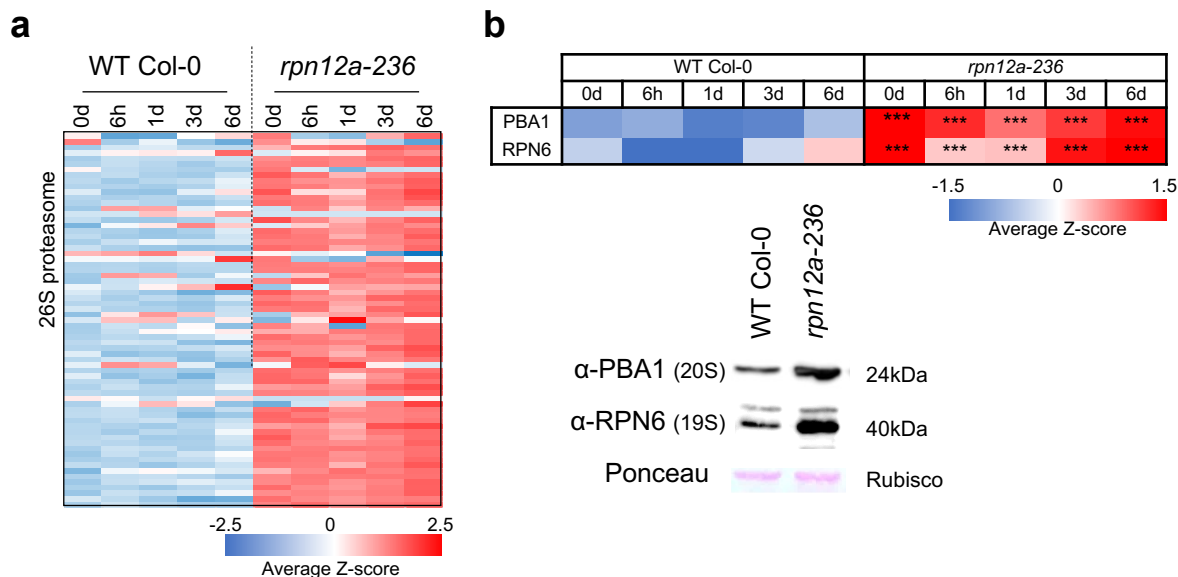


Figure S7. Regulation of the proteasome subunits. (a) Heatmap of proteasome subunits and interactants transcripts during DIS (n=66). (b) Focus on PBA1 (20S) and RPN6 (19S). Top: *PBA1* and *RPN6* expression was obtained from RNAseq experiment on Col-0 and *rpn12a-236*. The average Z-score is shown. A Student's t-test showed statistically significant differences from WT Col-0 at *** $p < 0.0001$. Bottom: Immunoblots using PBA1 and RPN6 antibodies targeting the 20S and the 19S particles, respectively. 10 μ g of total proteins, extracted from 6 week-old leaves of Col-0 and *rpn12a-236* grown in short day condition, were used. A ponceau staining was added as a loading control.

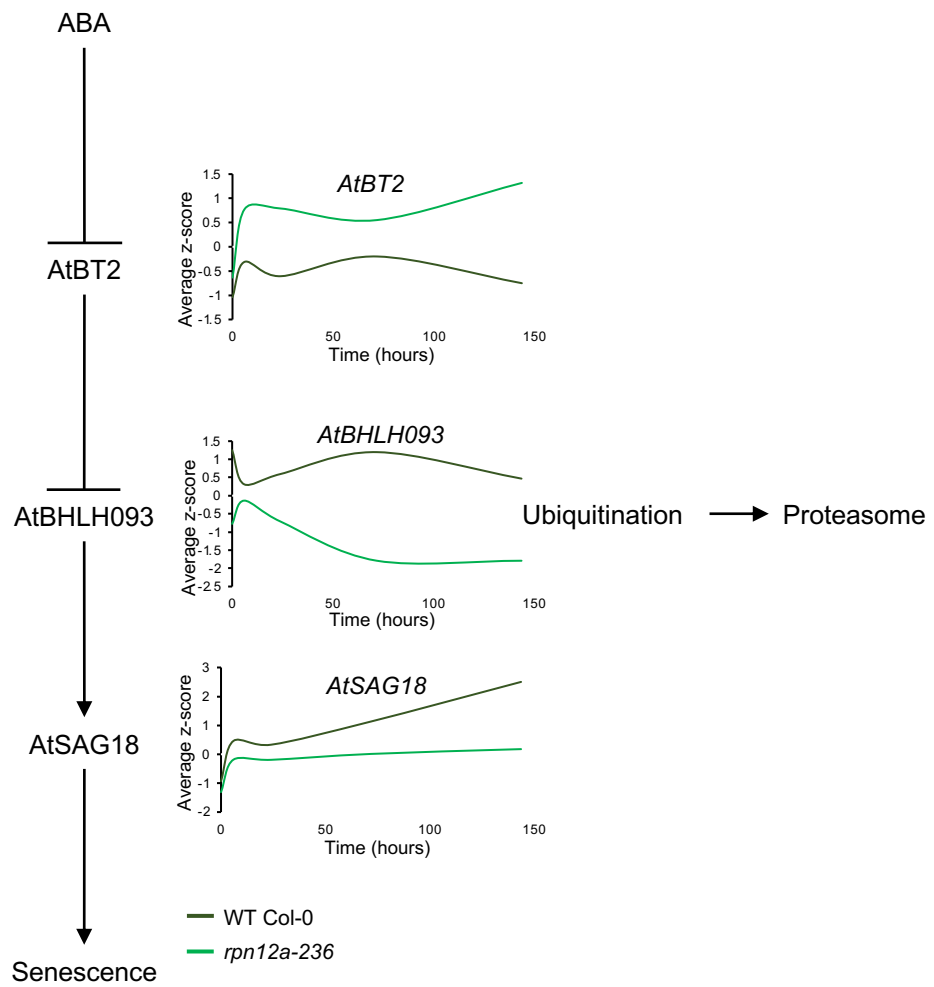


Figure S8. Current model for the regulation of senescence through the action of AtBT2. In this model, AtBHLH093 activates the transcription of *AtSAG18*. AtBT2 induces the ubiquitination and subsequent degradation of AtBHLH093 by the proteasome delaying leaf senescence (model adapted from An et al. (2018) in *Malus domestica*).

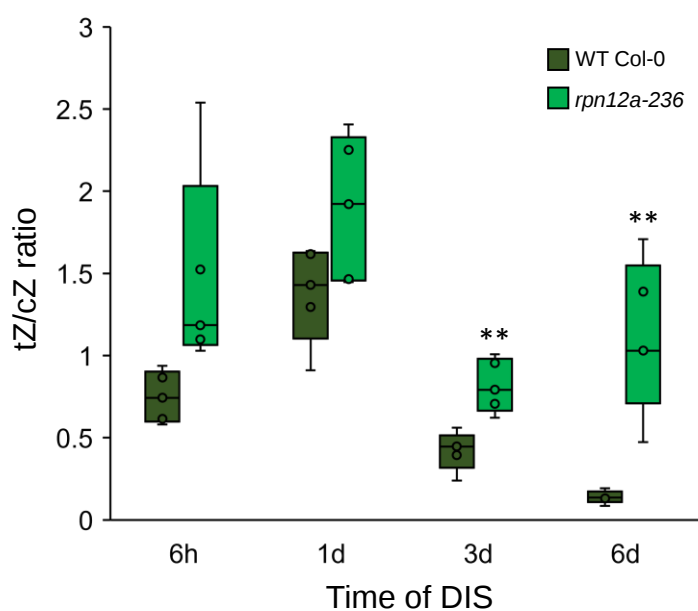


Figure S10. tZ/cZ ratio. Values obtained from the LC/MS were used to visualize the variation in the tZ/cZ ratio during DIS. The interquartile range of the box is from the 25th to 75th percentiles, and the middle line is the median; whiskers represent min and max values. A Student's t-test showed statistically significant differences at ** $p < 0.01$.

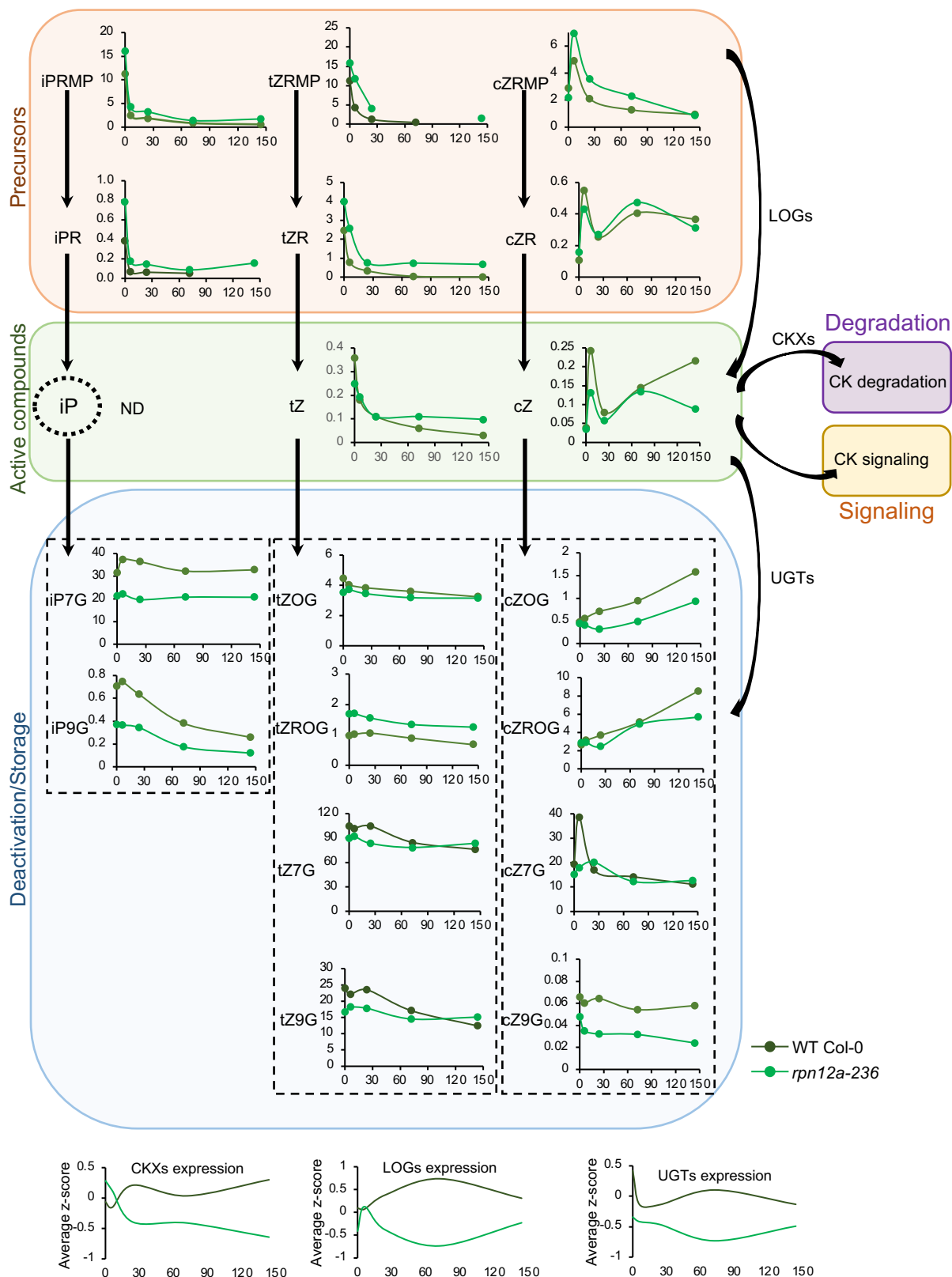


Figure S11. Cytokinin-related metabolites in response to DIS. For each metabolite, total pools (in pmol/g FW) were plotted over time. Normalized average abundance of transcripts obtained from the RNAseq dataset are shown on the bottom heatmap. ND=not detected.

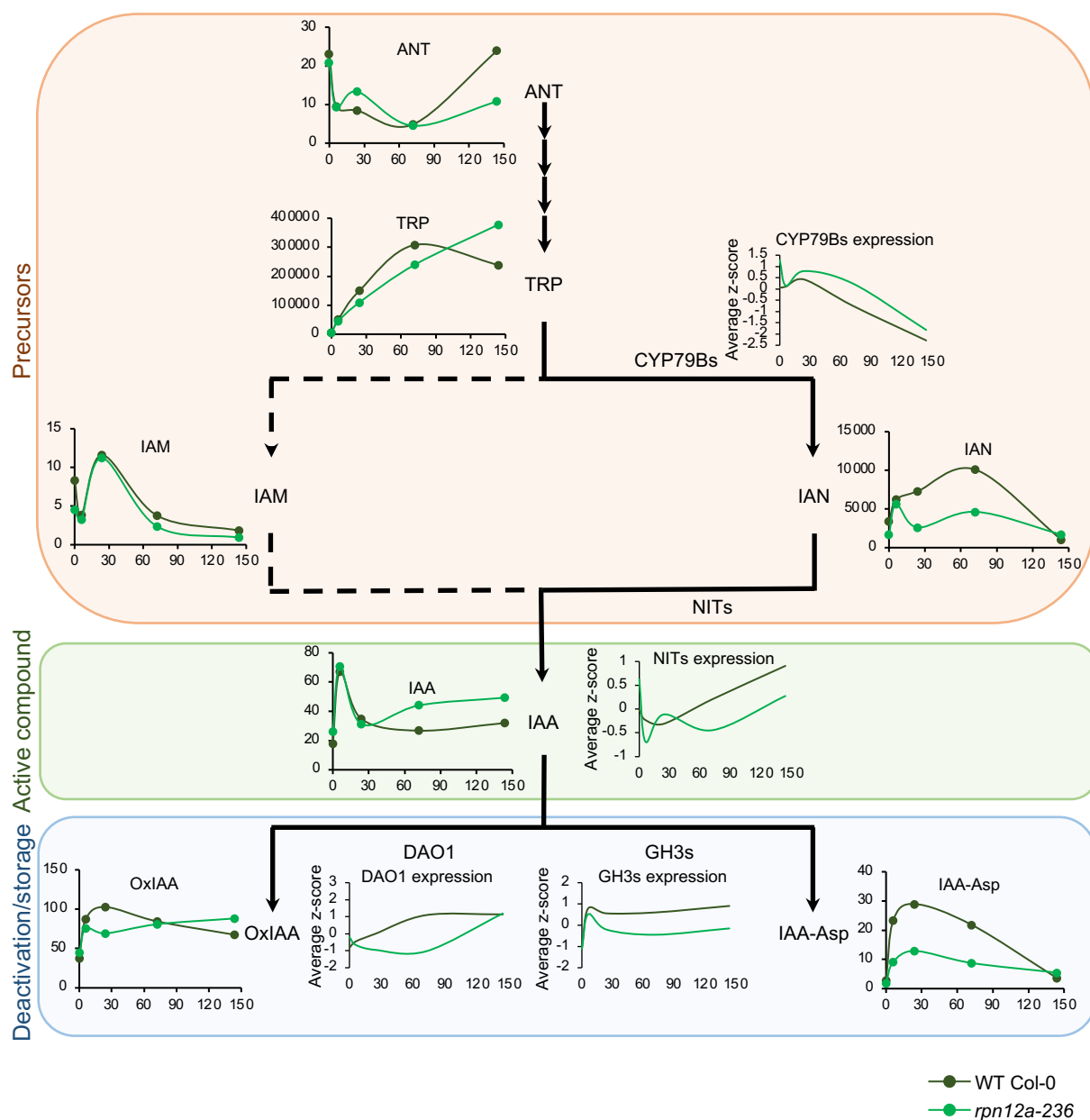


Figure S12. Auxin-related metabolites in response to DIS. For each metabolite, total pools (in pmol/g FW) were plotted over time. Normalized average abundance of transcripts obtained from the RNAseq dataset is shown on the bottom heatmap. Dashed lines indicate unclear metabolic paths.