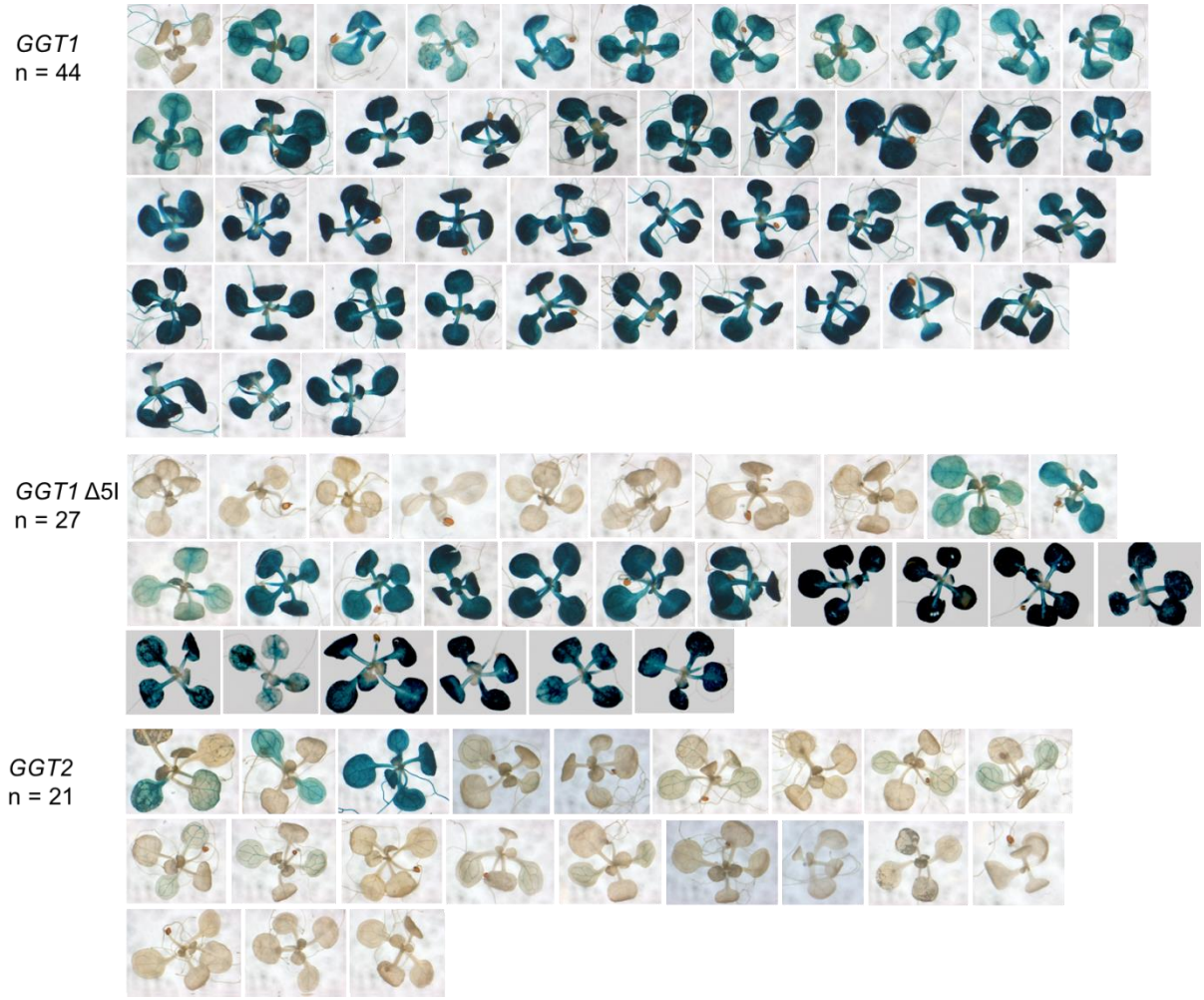
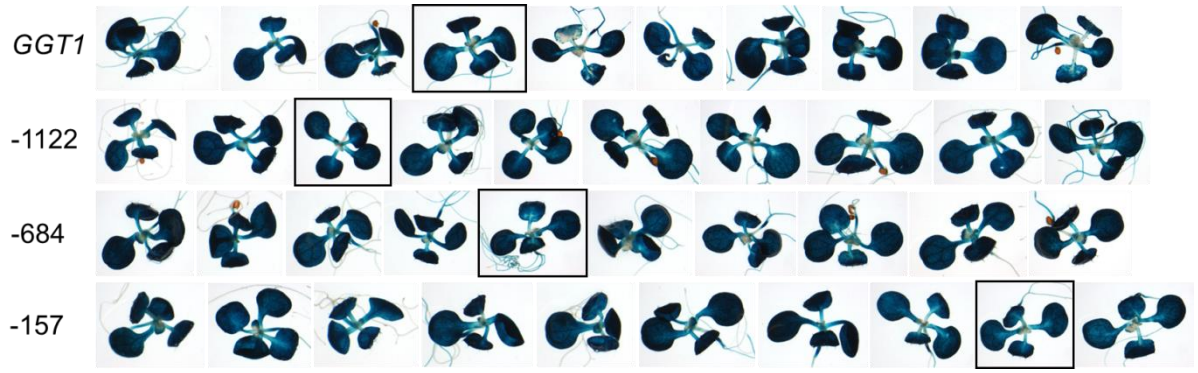
Supplemental figure S1 – Laxa et al.



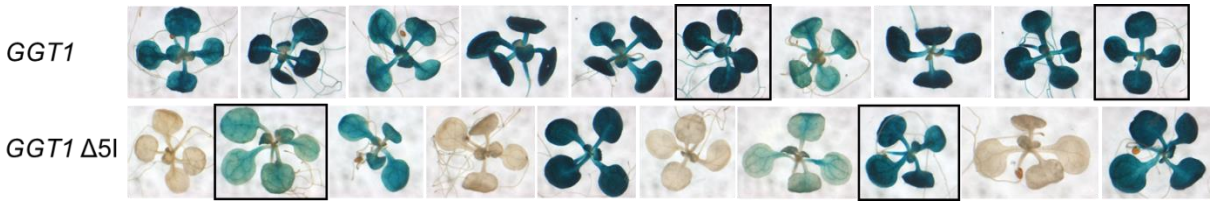
Supplemental figure S1: GUS staining of all available transformation events that have been generated for the constructs *GGT1*::*gusA*, *GGT1 Δ5I::gusA* and *GGT2*::*gusA*. Plants were grown under short day conditions for 16 days and stained for GUS.

Supplemental figure S2 – Laxa et al.



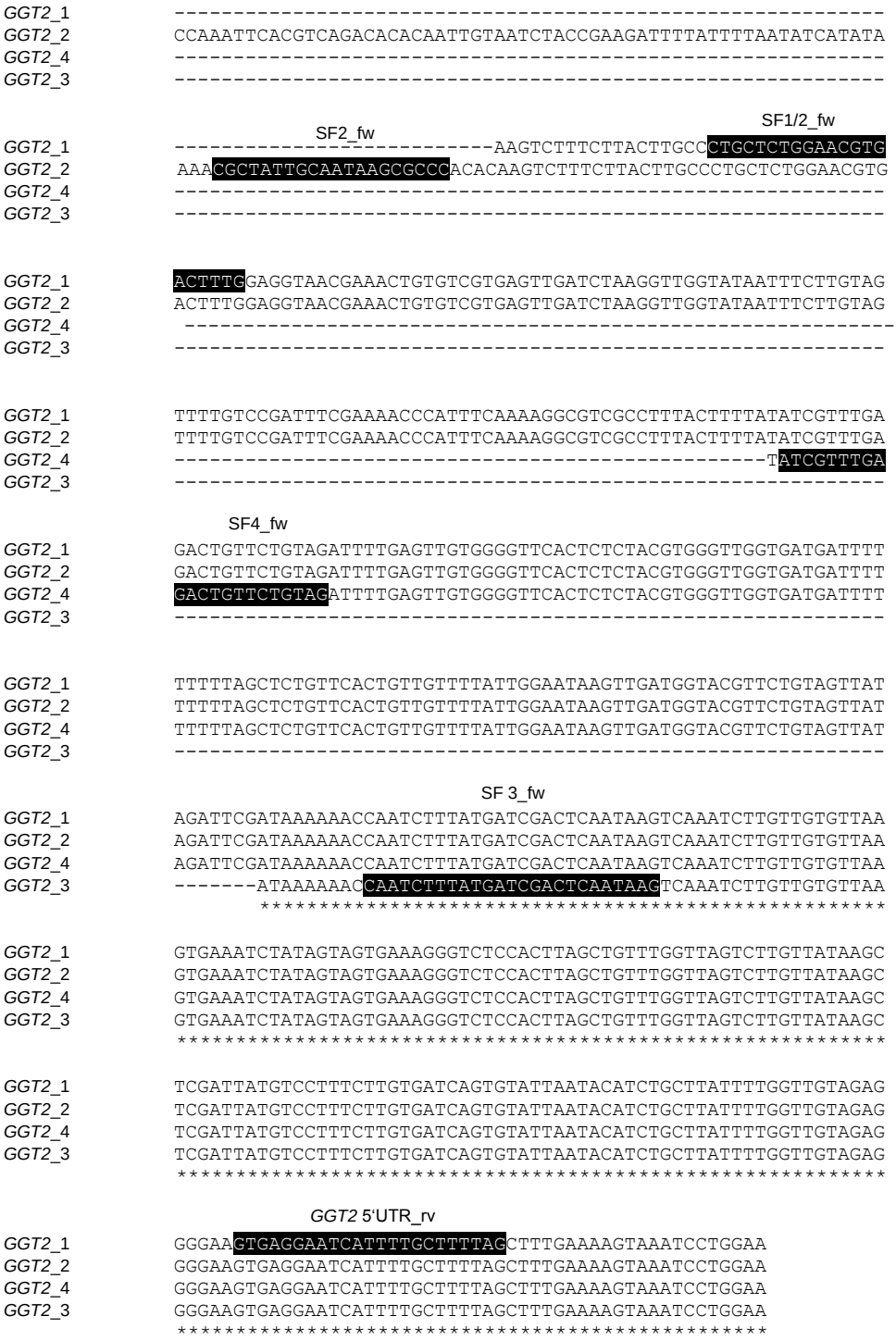
Supplemental figure S2: GUS staining of all transformation events that have been used to generate the quantitative qPCR data presented in Figure 2C and D. Plants were grown under short day conditions for 16 days and stained for GUS. Boxes indicate plants chosen for Figure 2B.

Supplemental figure S3 – Laxa et al.



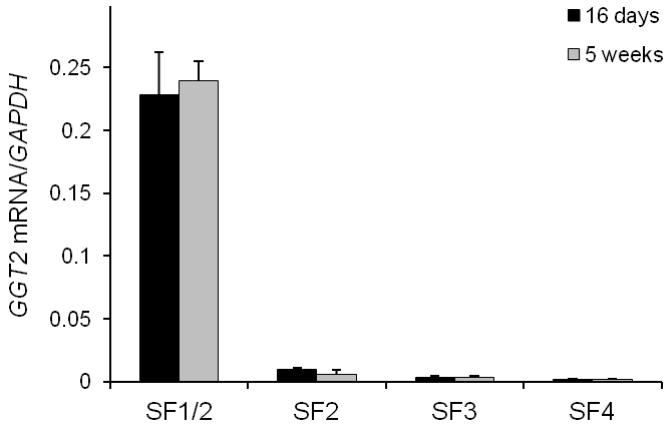
Supplemental figure S3: GUS staining of all transformation events that have been used to generate the quantitative qPCR data presented in Figure 3C and D. Plants were grown under short day conditions for 16 days and stained for GUS. Boxes indicate plants chosen for Figure 3B.

Supplemental figure S4 – Laxa et al.



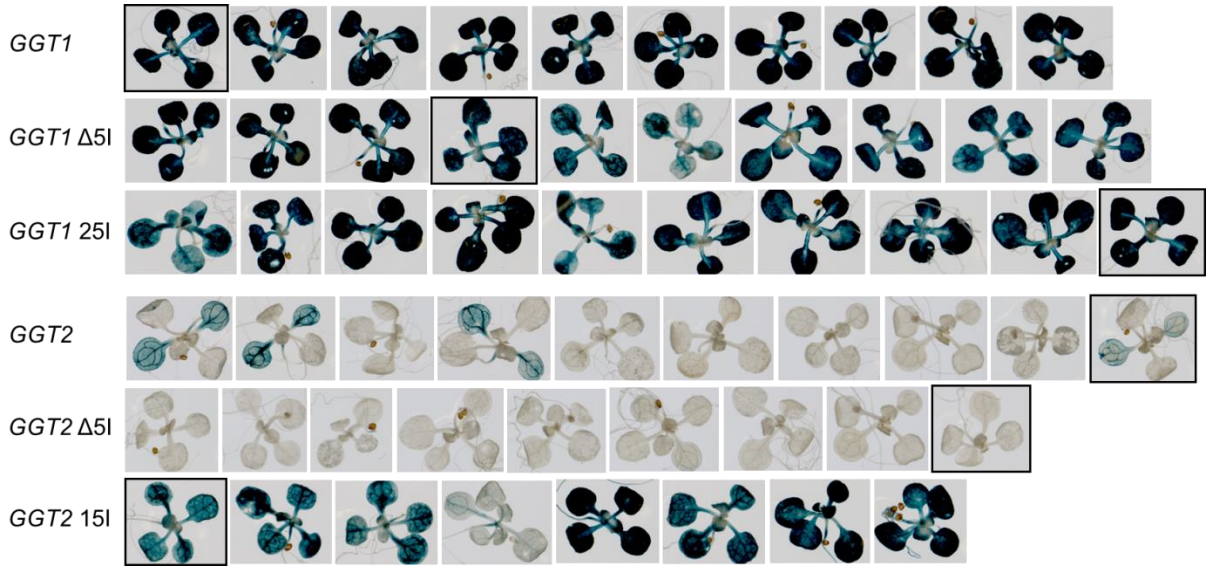
Supplemental figure S4: Alignment of the four predicted *GGT2* splice forms (SF). Black with white letters: primer positions chosen to differentiate between the different splice forms. Alignment was performed using the software program ClustalW (http://www.genome.jp/tools/clustalw/).

Supplemental figure S5 – Laxa et al.



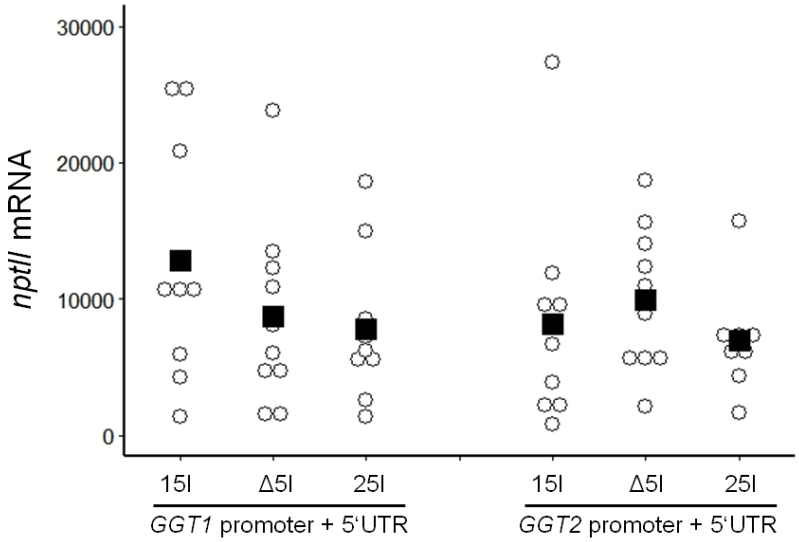
Supplemental figure S5: Splice form 1 is the most abundant splice form of *GGT2*. Plants were grown in short day conditions for either 16 days or five weeks before harvesting. Relative mRNA transcript levels of the individual *GGT2* splice forms were measured by quantitative PCR and standardized to *GAPDH*. Data represent the average of 3-5 biological replicates ± StDev. SF: splice form.

Supplemental figure S6 – Laxa et al.



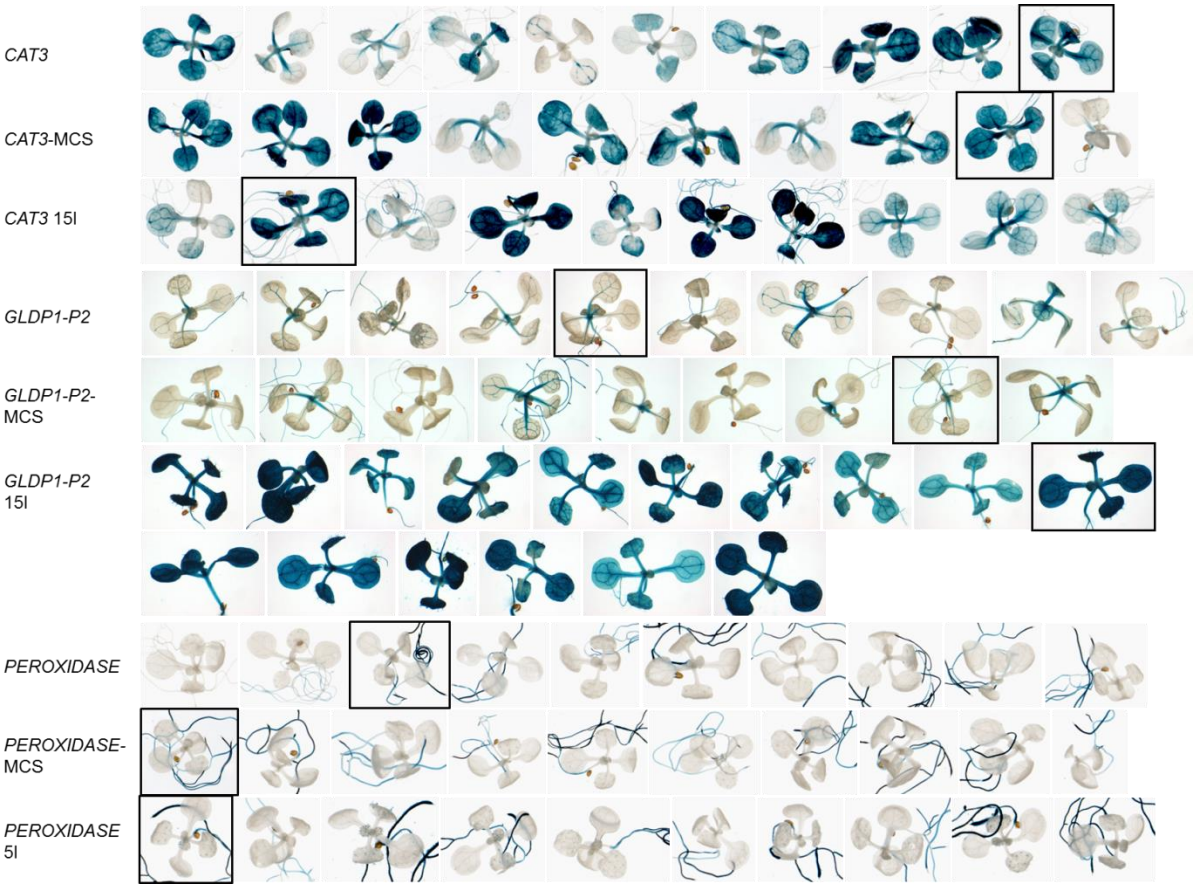
Supplemental figure S6: GUS staining of all transformation events that have been used to generate the quantitative qPCR data presented in Figure 5. Plants were grown under short day conditions for 16 days and stained for GUS. Boxes indicate plants chosen for Figure 4C.

Supplemental figure S7 – Laxa et al.



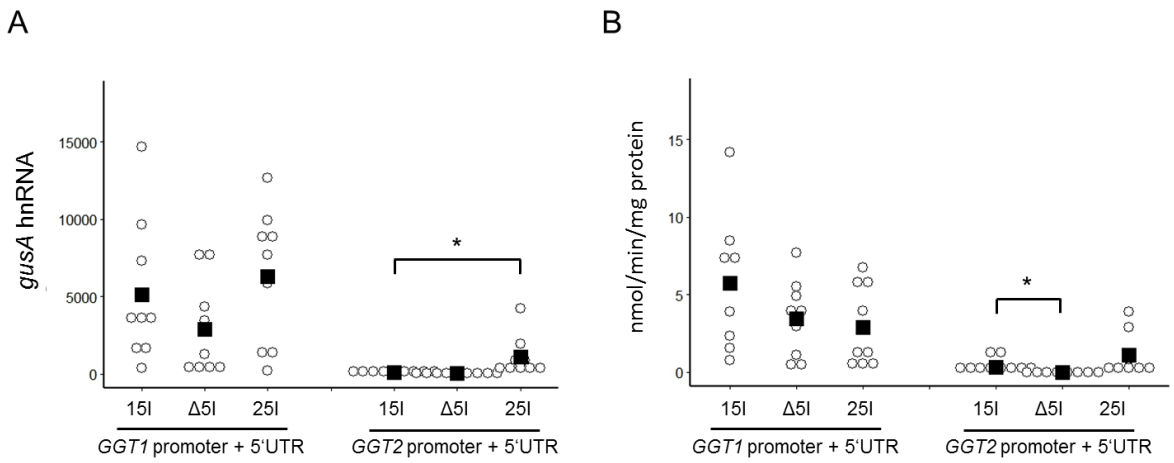
Supplemental figure S7: *NptII* expression indicates successful transformation of all transformation events chosen to generate the quantitative qPCR data presented in Figure 5. Relative *gusA* mRNA transcript levels of 16 days old transgenic plants were quantified by qPCR 1h after illumination in the diurnal rhythm (1hL). Individual transformation events of each construct are visualized by open circles while the mean of the data is indicated by a black square in the dot plot. Data represent the average of 8-10 individual transformation events. 15I: *GGT1* 5'UTR intron, 25I: *GGT2* 5'UTR intron, Δ5I: deletion of the 5'UTR intron, 1hL: 1h light.

Supplemental figure S8 – Laxa et al.



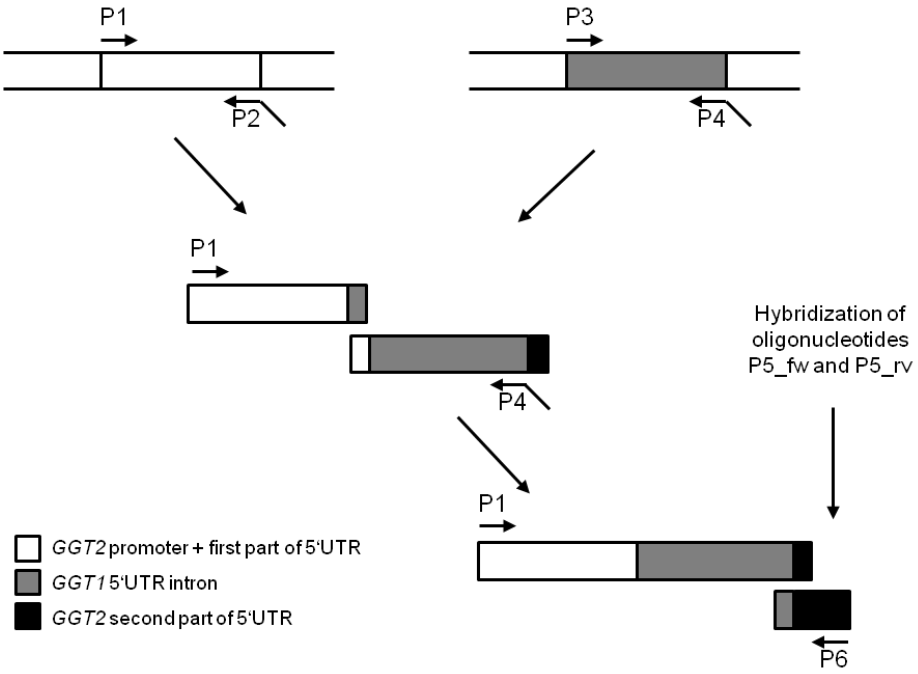
Supplemental figure S8: GUS staining of all transformation events that have been used to evaluate the effect of 5'UTR intron of *GGT1* on the tissue specificity of *CAT3, GLDP1*-P2 (Adwy et al., 2015) and a root-specific *PEROXIDASE*. Boxes indicate plants chosen for Figure 7B.

Supplemental figure S9 – Laxa et al.



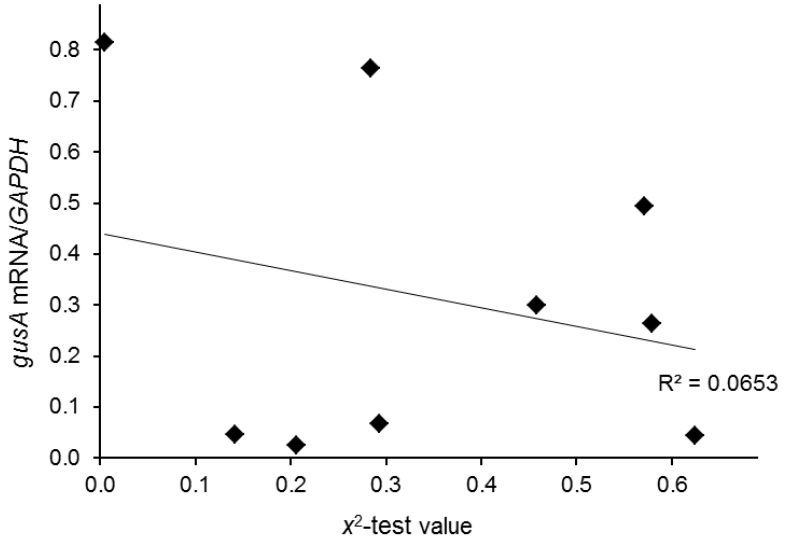
Supplemental figure S9: Relative *gusA* unspliced RNA transcript level and GUS activity in transgenic *GGT1* and *GGT2* lines. Plant material of 16 days old plant was harvest 1h after illumination (1hL) and analyzed either for relative transcript abundance by qPCR or for GUS activity by an assay according to Jefferson et al. (1987). Individual transformation events of each construct are visualized by open circles while the mean of the data is indicated by a black square in the dot plot. Data represent the average of 7-10 individual transformation events. 15I: *GGT1* 5'UTR intron, 25I: *GGT2* 5'UTR intron, Δ5I: deletion of 5'UTR intron, 1hL: 1h light. Student's t-test significance level is as followed: *, $p \leq 0.1$.

Supplemental figure S10 – Laxa et al.



Supplemental figure S10: Scheme of the different steps of the overlapping extension PCRs performed to generate the fragments *GGT1* 25I and *GGT2* 15I, respectively. Sequences of the different primers and oligonucleotides P1-P6 are given in Supplemental table II. The scheme exemplarily shows the amplification steps for the *GGT2* 15I fragment.

Supplemental figure S11– Laxa et al.



Supplemental figure S11: *GusA* mRNA levels standardized to *GAPDH* correlate to the corresponding x^2-test values of the individual transformation events of *GGT1 Δ5I*::*gusA* transgenic plants. Data are based on calculations shown in Supplemental table IV.