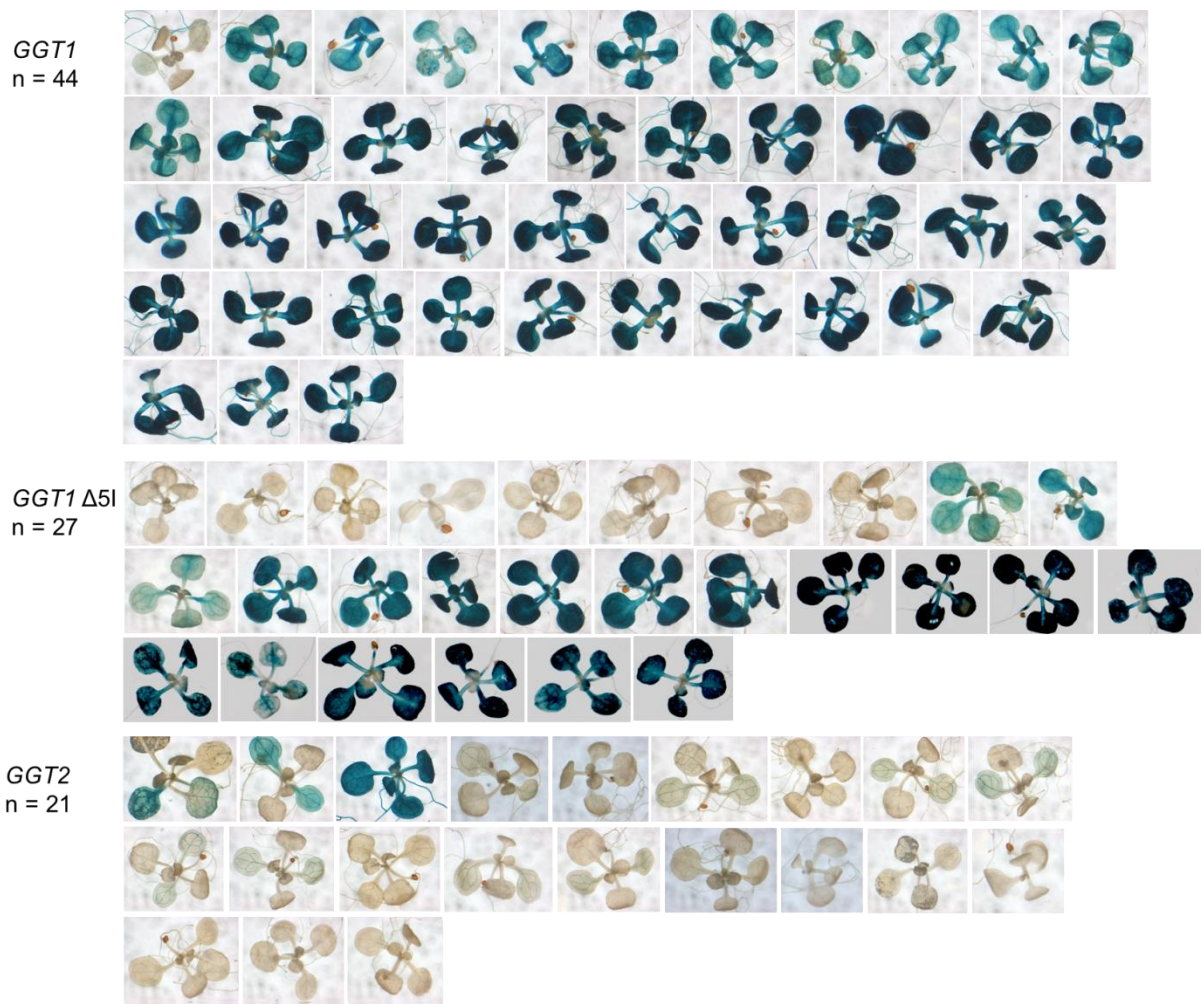
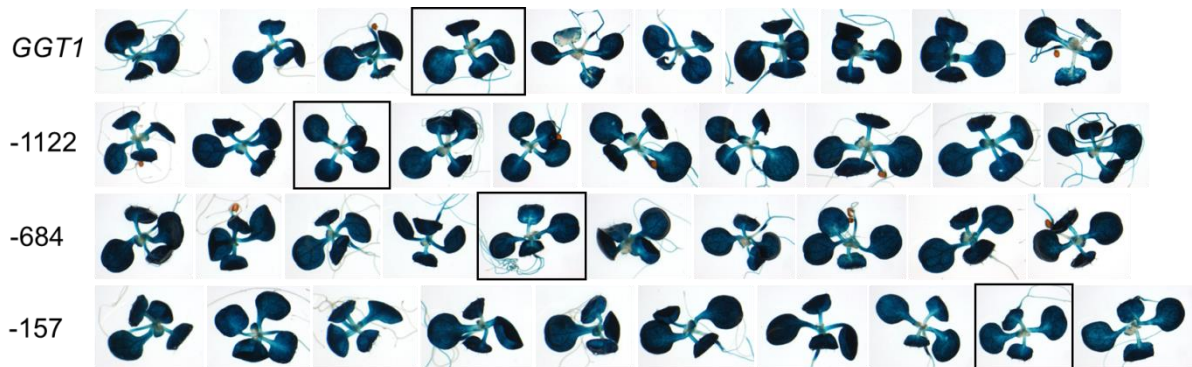


Supplemental figure S1 – Laxa et al.



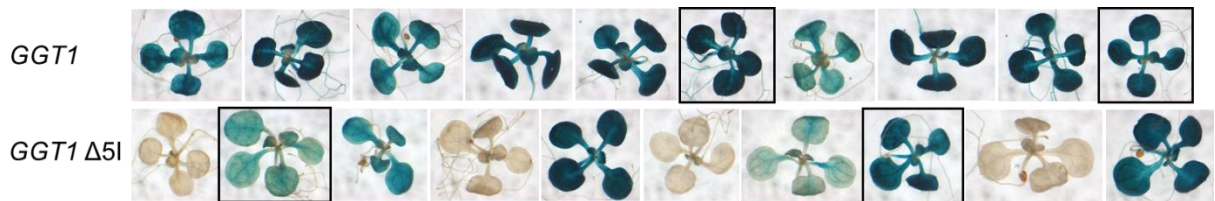
Supplemental figure S1: GUS staining of all available transformation events that have been generated for the constructs *GGT1::gusA*, *GGT1 Δ5l::gusA* and *GGT2::gusA*. Plants were grown under short day conditions for 16 days and stained for GUS.

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.

```

GGT2_1 -----
GGT2_2 CCAAATTCACGTCAGACACACAATTGTAATCTACCGAAGATTTTATTTAATATCATATA
GGT2_4 -----
GGT2_3 -----

                SF2_fw                                SF1/2_fw
GGT2_1 -----AAGCTTTTCTTACTTGCCCTGCTCTGGAACGTG
GGT2_2 AAACGCTATTGCAATAAGCGCCCACACAAGTCTTTCTTACTTGCCCTGCTCTGGAACGTG
GGT2_4 -----
GGT2_3 -----

GGT2_1 ACTTTGGAGGTAACGAAACTGTGTCGTGAGTTGATCTAAGGTTGGTATAAATTTCTTGTAG
GGT2_2 ACTTTGGAGGTAACGAAACTGTGTCGTGAGTTGATCTAAGGTTGGTATAAATTTCTTGTAG
GGT2_4 -----
GGT2_3 -----

GGT2_1 TTTTGTCCGATTTTCGAAAACCCATTTCAAAGGCGTCGCCTTACTTTTATATCGTTTGA
GGT2_2 TTTTGTCCGATTTTCGAAAACCCATTTCAAAGGCGTCGCCTTACTTTTATATCGTTTGA
GGT2_4 -----TATCGTTTGA
GGT2_3 -----

                SF4_fw
GGT2_1 GACTGTTCTGTAGATTTTGAGTTGTGGGGTTCACTCTCTACGTGGGTTGGTGATGATTTT
GGT2_2 GACTGTTCTGTAGATTTTGAGTTGTGGGGTTCACTCTCTACGTGGGTTGGTGATGATTTT
GGT2_4 GACTGTTCTGTAGATTTTGAGTTGTGGGGTTCACTCTCTACGTGGGTTGGTGATGATTTT
GGT2_3 -----

GGT2_1 TTTTGTAGCTCTGTTCACTGTTGTTTTATTGGAATAAGTTGATGGTACGTTCTGTAGTTAT
GGT2_2 TTTTGTAGCTCTGTTCACTGTTGTTTTATTGGAATAAGTTGATGGTACGTTCTGTAGTTAT
GGT2_4 TTTTGTAGCTCTGTTCACTGTTGTTTTATTGGAATAAGTTGATGGTACGTTCTGTAGTTAT
GGT2_3 -----

                SF 3_fw
GGT2_1 AGATTCGATAAAAAACCAATCTTTATGATCGACTCAATAAGTCAAATCTTGTGTGTAA
GGT2_2 AGATTCGATAAAAAACCAATCTTTATGATCGACTCAATAAGTCAAATCTTGTGTGTAA
GGT2_4 AGATTCGATAAAAAACCAATCTTTATGATCGACTCAATAAGTCAAATCTTGTGTGTAA
GGT2_3 -----ATAAAAAACCAATCTTTATGATCGACTCAATAAGTCAAATCTTGTGTGTAA
                *****

GGT2_1 GTGAAATCTATAGTAGTGAAAGGGTCTCCACTTAGCTGTTTGGTTAGTCTTGTGTATAAGC
GGT2_2 GTGAAATCTATAGTAGTGAAAGGGTCTCCACTTAGCTGTTTGGTTAGTCTTGTGTATAAGC
GGT2_4 GTGAAATCTATAGTAGTGAAAGGGTCTCCACTTAGCTGTTTGGTTAGTCTTGTGTATAAGC
GGT2_3 GTGAAATCTATAGTAGTGAAAGGGTCTCCACTTAGCTGTTTGGTTAGTCTTGTGTATAAGC
                *****

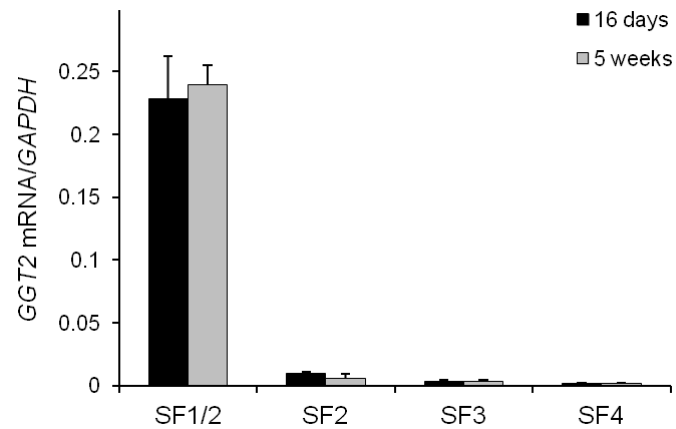
GGT2_1 TCGATTATGTCCTTTCTTGTGATCAGTGTATTAATACATCTGCTTATTTGGTTGTAGAG
GGT2_2 TCGATTATGTCCTTTCTTGTGATCAGTGTATTAATACATCTGCTTATTTGGTTGTAGAG
GGT2_4 TCGATTATGTCCTTTCTTGTGATCAGTGTATTAATACATCTGCTTATTTGGTTGTAGAG
GGT2_3 TCGATTATGTCCTTTCTTGTGATCAGTGTATTAATACATCTGCTTATTTGGTTGTAGAG
                *****

                GGT2 5'UTR_rv
GGT2_1 GGGAAGTGAGGAATCATTTTGCTTTTAGCCTTGAAAAGTAAATCCTGGAA
GGT2_2 GGGAAAGTGAGGAATCATTTTGCTTTTAGCTTTGAAAAGTAAATCCTGGAA
GGT2_4 GGGAAAGTGAGGAATCATTTTGCTTTTAGCTTTGAAAAGTAAATCCTGGAA
GGT2_3 GGGAAAGTGAGGAATCATTTTGCTTTTAGCTTTGAAAAGTAAATCCTGGAA
                *****

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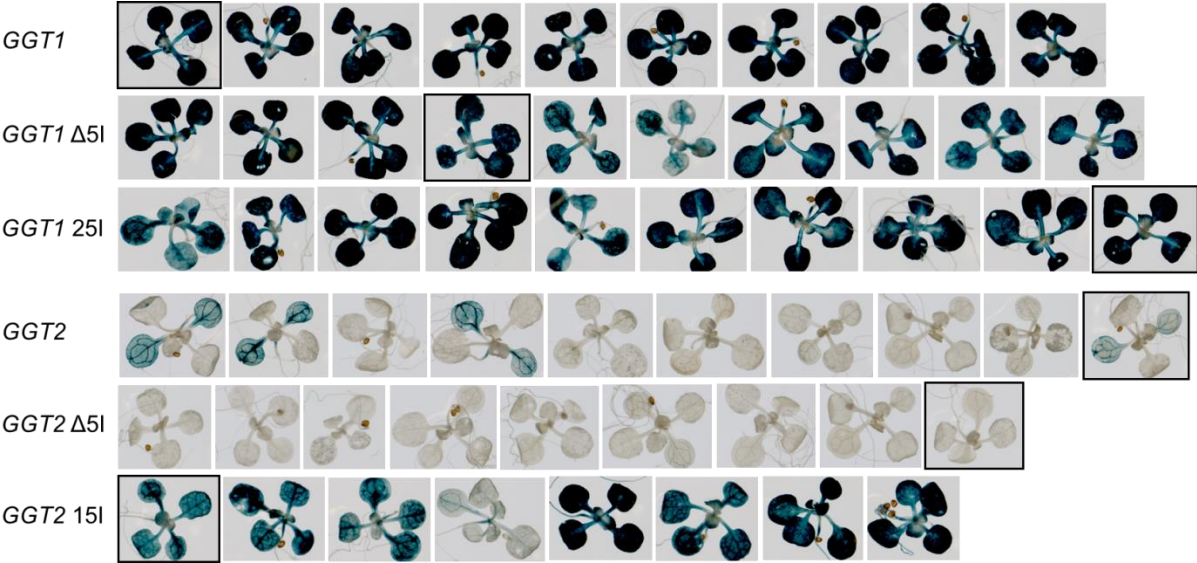
Supplemental figure S4: Alignment of the four predicted *GGT2* splice forms (SF). Black with white letters: primer positions chosen to differentiate between the different splice forms. Alignment was performed using the software program ClustalW (<http://www.genome.jp/tools/clustalw/>).

Supplemental figure S5 – Laxa et al.



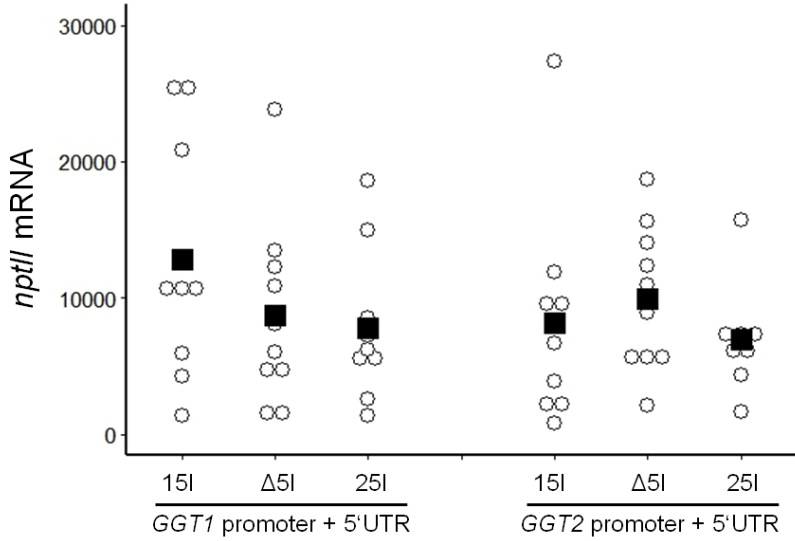
Supplemental figure S5: Splice form 1 is the most abundant splice form of *GGT2*. Plants were grown in short day conditions for either 16 days or five weeks before harvesting. Relative mRNA transcript levels of the individual *GGT2* splice forms were measured by quantitative PCR and standardized to *GAPDH*.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

Supplemental figure S6 – Laxa et al.



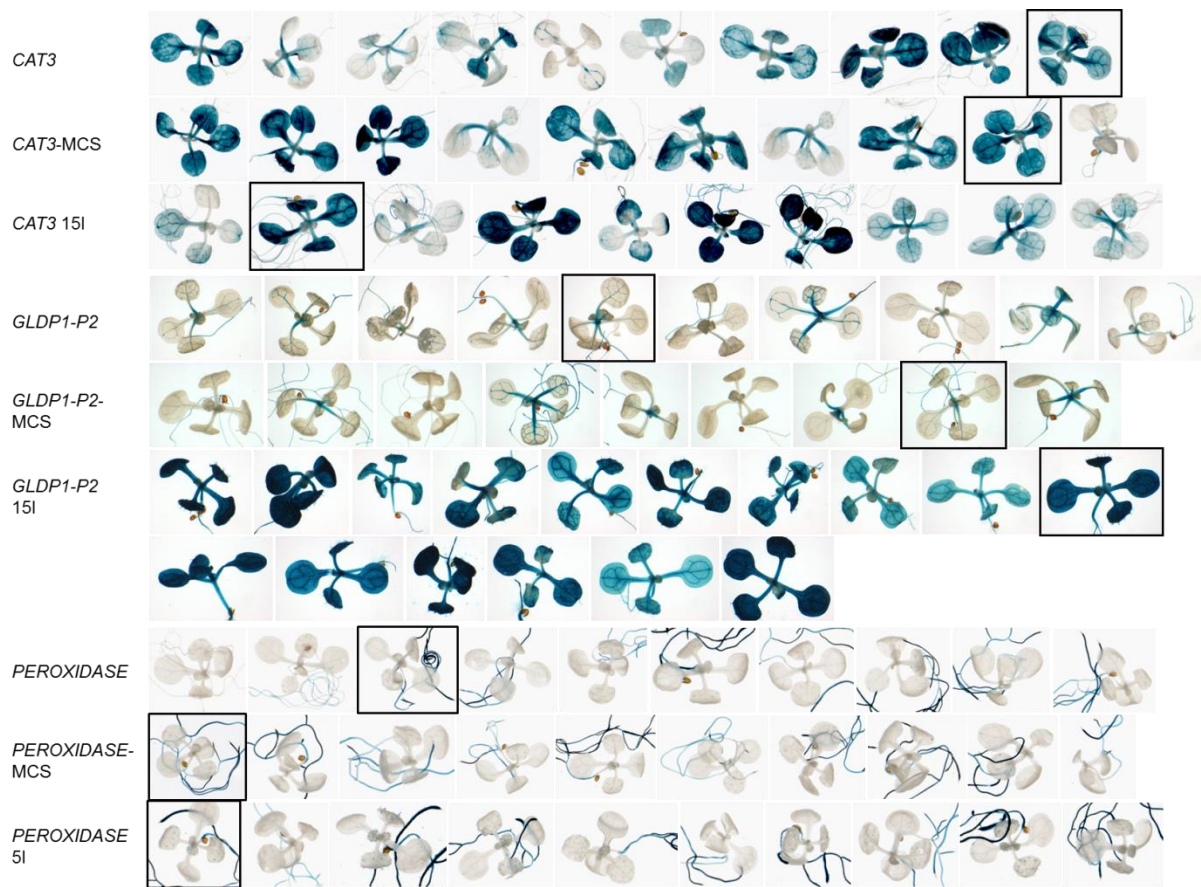
Supplemental figure S6: GUS staining of all transformation events that have been used to generate the quantitative qPCR data presented in Figure 5. Plants were grown under short day conditions for 16 days and stained for GUS. Boxes indicate plants chosen for Figure 4C.

Supplemental figure S7 – Laxa et al.



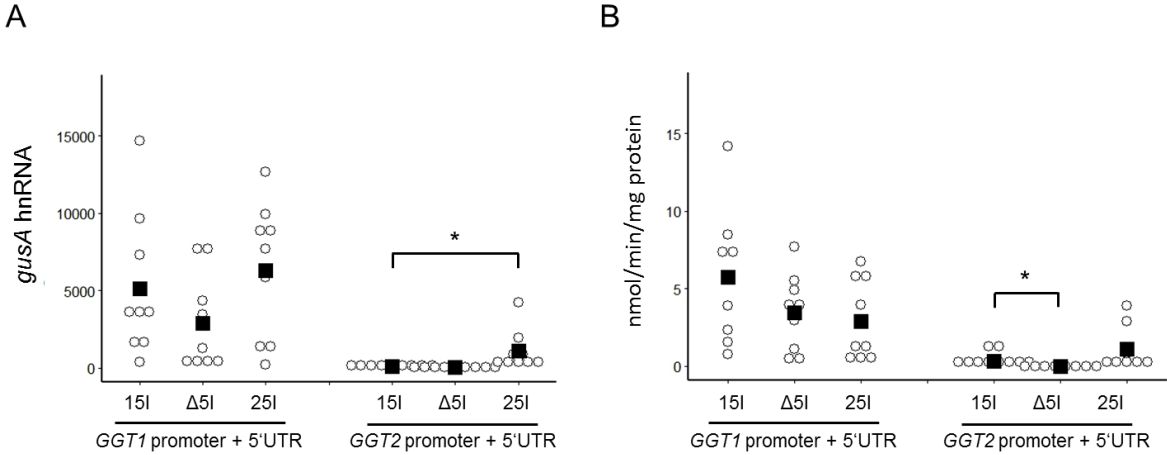
Supplemental figure S7: *NptII* expression indicates successful transformation of all transformation events chosen to generate the quantitative qPCR data presented in Figure 5. Relative *gusA* mRNA transcript levels of 16 days old transgenic plants were quantified by qPCR 1h after illumination in the 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.



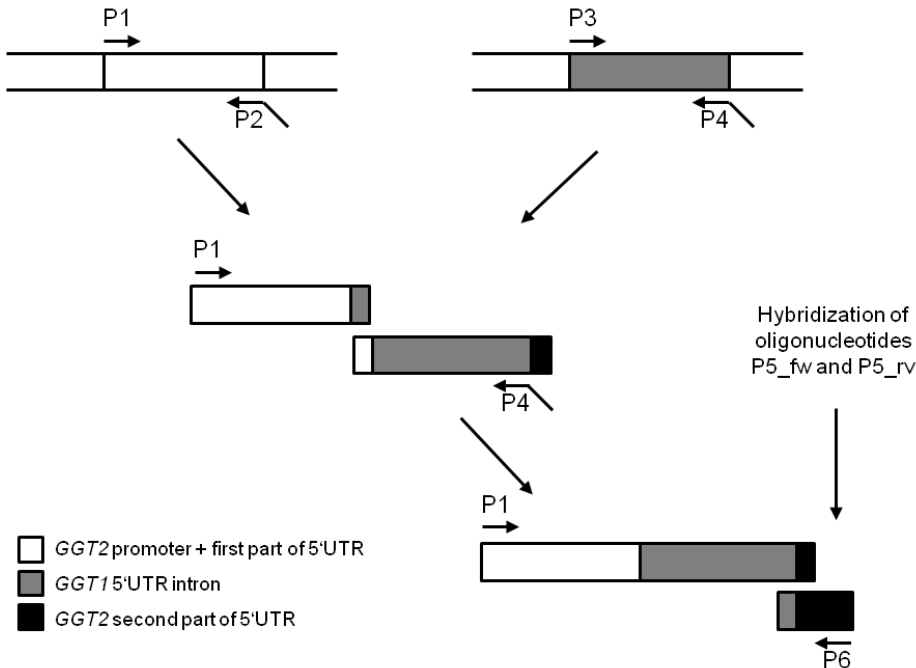
Supplemental figure S8: GUS staining of all transformation events that have been used to evaluate the effect of 5'UTR intron of *GGT1* on the tissue specificity of *CAT3*, *GLDP1-P2* (Adwy et al., 2015) and a root-specific *PEROXIDASE*. Boxes indicate plants chosen for Figure 7B.

Supplemental figure S9 – Laxa et al.



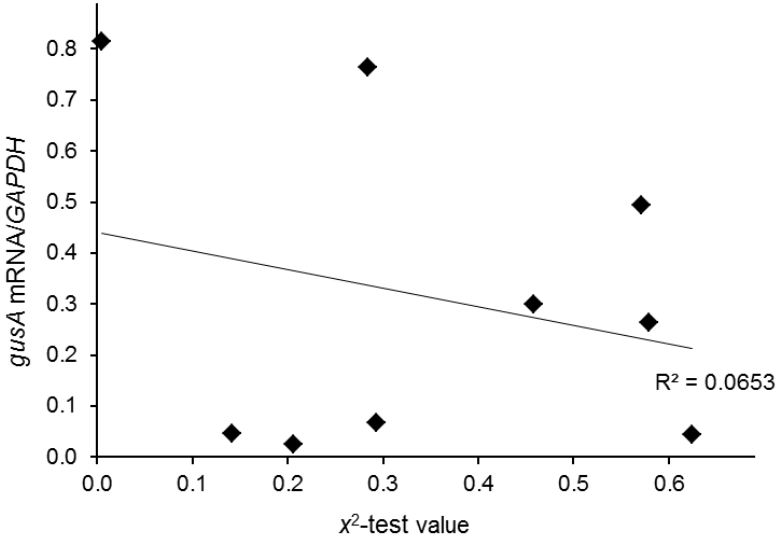
Supplemental figure S9: Relative *gusA* unspliced RNA transcript level and GUS activity in transgenic *GGT1* and *GGT2* lines. Plant material of 16 days old plant was harvest 1h after illumination (1hL) and analyzed either for relative transcript abundance by qPCR or for GUS activity by an assay according 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 χ^2 -test values of the individual transformation events of *GGT1 Δ5l::gusA* transgenic plants. Data are based on calculations shown in Supplemental table IV.