Supplemental table S1 – Laxa et al.

Supplemental table I. Diurnal expression of the individual transformation events used to generate the data in Figure 2D, 3D and 5. The table summarizes the relative mRNA *gusA* transcript levels 1h and 7h after illumination. Additionally, the ratio between 1h and 7h indicates the decrease of *gusA* transcript throughout the day reflecting the endogenous diurnal behavior of *GGT1*.

Figure 2D			
Line	1h	7h	Ratio 1h:7h
GGT1-1	7381.42	1432.13	5.15
GGT1-2	1885.53	308.21	6.12
GGT1-3	4322.97	2828.71	1.53
GGT1-4	13327.16	3198.18	4.17
GGT1-5	2891.19	1608.25	1.80
GGT1-6	4661.64	3003.14	1.55
GGT1-7	5270.45	1015.82	5.19
GGT1-8	8419.68	5360.64	1.57
-1122-1	4904.38	866.04	5.66
-1122-2	10805.33	3390.72	3.19
-1122-3	7990.88	2537.05	3.15
-1122-4	16325.01	2997.57	5.45
-1122-5	9813.33	5983.80	1.64
-1122-6	3892.76	406.68	9.57
-1122-7	1521.92	283.72	5.36
-1122-8	12755.77	3330.24	3.83
-684-1	6079.50	1654.54	3.67
-684-2	1454.54	469.40	3.10
-684-3	2020.74	248.72	8.12
-684-4	8405.23	1531.47	5.49
-684-5	10981.16	4191.67	2.62
-684-6	8802.29	740.97	11.88
-684-7	4055.72	1539.70	2.63
-684-8	5777.80	2243.63	2.58
-684-9	1526.53	959.30	1.59
-684-10	11437.66	4054.88	2.82
-157-1	1232.47	689.70	1.79
-157-2	4613.22	1299.17	3.55
-157-3	559.30	77.97	7.17
-157-4	13605.56	1218.32	11.17
-157-5	2348.68	2191.23	1.07
-157-6	9564.45	4138.74	2.31
-157-7	11642.15	1477.81	7.88
-157-8	7452.24	1660.24	4.49
-157-9	9548.04	1259.44	7.58
-157-10	3094.02	1434.99	2.16

Figure 3D			
Line	1h	7h	Ratio 1h:7h
GGT1-1	11250.99	2089.41	5.38
GGT1-2	6750.08	12545.02	0.54
GGT1-3	3071.11	799.25	3.84
GGT1-4	2019.54	181.70	11.11
GGT1-5	11887.34	2605.71	4.56
GGT1-6	1180.61	225.61	5.23
GGT1-7	15726.83	4111.26	3.83
GGT1-8	16228.31	2812.77	5.77
GGT1-9	4793.84	2962.11	1.62
GGT1-Δ5I-1	9808.88	2069.69	4.74
GGT1-Δ5I-2	2.70	16.07	0.17
GGT1-Δ5I-3	0.00	0.00	
GGT1-Δ5I-4	1.56	0.22	7.18
GGT1-Δ5I-5	2491.90	664.83	3.75
GGT1-Δ5I-6	2.85	0.00	
GGT1-Δ5I-7	3.48	1.18	2.95
GGT1-Δ5I-8	0.44	0.75	0.58
GGT1-Δ5I-9	1849.38	659.05	2.81
Figure 5A and B			
Line	1h	7h	Ratio 1h:7h
GGT1-1	21211.40	9939.05	2.13
GGT1-2	2281.58	3004.49	0.76
GGT1-3	10838.56	8599.98	1.26
GGT1-4	6176.47	1244.05	4.96
GGT1-5	11070.28	3023.53	3.66
GGT1-6	8140.45	998.59	8.15
GGT1-7	2507.03	1390.08	1.80
GGT1-8	5985.21	1182.72	5.06
GGT1-9	3437.55	479.01	7.18
GGT1-10	1001.86	1425.96	0.70
GGT1-Δ5I-1	6084.68	2363.96	2.57
GGT1-Δ5I-2	7983.21	4678.77	1.71
GGT1-Δ5I-3	7475.36	3760.27	1.99
GGT1-Δ5I-4	297.21	619.51	0.48
GGT1-Δ5I-5	951.95	512.43	1.86
GGT1-Δ5I-6	334.09	174.80	1.91
GGT1-Δ5I-7	3786.31	2521.27	1.50
GGT1-Δ5I-8	5001.94	307.91	16.24
GGT1-Δ5I-9	1061.36	169.21	6.27
GGT1-Δ5I-10	2302.04	459.51	5.01
GGT2-1	63.35	125.83	0.50
GGT2-2	171.72	170.85	1.01
GGT2-3	5.87	11.44	0.51
GGT2-4	84.71	160.76	0.53
GGT2-5	17.31	17.58	0.98

GGT2-7	7.69	7.44	1.03
GGT2-8	7.73	9.67	0.80
GGT2-9	18.63	15.79	1.18
GGT2-10	22.83	52.40	0.44
GGT2-Δ5I-1	3.16	1.35	2.35
GGT2-Δ5I-3	4.05	8.24	0.49
GGT2-Δ5I-4	13.27	7.80	1.70
GGT2-Δ5I-5	1.26	3.04	0.41
GGT2-Δ5I-6	23.13	14.40	1.61
GGT2-Δ5I-7	6.35	18.51	0.34
GGT2-Δ5I-8	1.62	8.44	0.19
GGT2-Δ5I-9	1.30	1.48	0.88
GGT1 25I-1	340.60	677.23	0.50
GGT1 25I-2	1571.02	1984.99	0.79
GGT1 25I-3	4955.78	1031.92	4.80
GGT1 25I-4	6462.45	9037.18	0.72
GGT1 25I-5	3549.35	329.69	10.77
GGT1 25I-6	6312.42	4856.22	1.30
GGT1 25I-7	21740.90	4332.06	5.02
GGT1 25I-8	10417.43	5810.84	1.79
GGT1 25I-9	15544.19	9515.55	1.63
GGT1 25I-10	14192.08	669.05	21.21
GGT2 15I-1	876.64	254.51	3.44
GGT2 15I-2	349.72	299.93	1.17
GGT2 15I-3	221.89	165.72	1.34
GGT2 15I-4	189.68	1004.09	0.19
GGT2 15I-5	245.85	312.92	0.79
GGT2 15I-6	635.40	42.85	14.83
GGT2 15I-7	482.73	1609.62	0.30
GGT2 15I-8	571.94	451.72	1.27

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Supplemental table II. List of primers used for quantitative real-time PCR analysis**.** For clarity the AGI code of *GAPDH* is given. P1 designates the position 146 bp downstream of ATG on the *gusA* coding sequence used for qPCR analysis after chromatin immunoprecipitation (ChIP). Fw: forward primer, rv: reverse primer, SF: splice form.

Primer	Sequence (5' to 3`)
*GAPDH*_mRNA_fw (At1g13440)	TTGGTGACAACAGGTCAAGCA
*GAPDH*_mRNA_rv	AAACTTGTCGCTCAATGCAATC
*GGT1*_unspliced RNA_fw	CGGTAATGGAGATGGGGTAA
*GGT1*_unspliced _rv	AGAATCTGCCAAACGGAAA
*GGT2*_SF1/2_fw	CTGCTCTGGAACGTGACTTTG
*GGT2*_SF2_fw	CGCTATTGCAATAAGCGCCC
*GGT2*_SF3_fw	CAATCTTTATGATCGACTCAATAAG
*GGT2*_SF4_fw	TATCGTTTGAGACTGTTCTGTAG
*GGT2*_5‘UTR_rv	CTAAAAGCAAAATGATTCCTCAC
*GusA*_ChIP_fw (P1)	CTGTGGAATTGGTCAGCGTTG
GusA _ChIP_rv (P1)	CAGACGTTGCCCGCATAATTAC
GusA _unspliced RNA_fw	GTTGATGTGCAGGTATCACCG
GusA _unspliced RNA_rv	TTGCCGTTTTCGTCGGTAATC
GusA _mRNA_fw	GAAGCCGATGTCACGCCG
GusA _mRNA_rv	TTGCCGTTTTCGTCGGTAATC
*NptII*_mRNA_fw	CTGTCCGGTGCCCTGAATG
*NptII*_mRNA_rv	CAACGTCGAGCACAGCTGC

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Supplemental table III. Primer used for the amplification of the *promoter::gusA* constructs used in this study. Besides the primer name and nucleotide sequences the table includes information on the relative position of the primer to the transcription initiation start (TIS), specific numbering for the overlap extension (OE) PCR (P1-P6; scheme available in Supplemental figure S10). Underlined nucleotide sequences (solid line) mark overlapping regions that were added for the OE PCR to generate of both *GGT1* 25I and *GGT2* 15I, respectively. Underlined nucleotide sequences (dashed line) mark the multiple cloning site introduced downstream of the 5'UTRs of *CAT3* (At1g26020), *GLDP1-P2* (At4g33010, Adwy et al., 2015) and a root-specific peroxidase (*PRX*, At3g01190). Underlined nucleotide sequences (dotted line) mark the restriction sites that have been introduced 5' and 3' of the *GGT1* 5'UTR intron, respectively. Fw: forward primer, rv: reverse primer.

Position relative to TIS	Primer	Sequence (5' to 3`)
	35S_fw	CACCGGTCCAAAGACCAGAGGGC
	35S_rv	TGTCCTCTCCAAATGAAATGAAC
-1458	*GGT1*_-1458_fw	CACCTAAAGCATTATTCAGTAGTATGTG
-1122	*GGT1*_-1122_fw	CACCCGGCTGAGAACTTGCATGAA
-684	*GGT1*_-684_fw	CACCCGGACAATAAATCGCTACAGAC
-157	*GGT1*_-157_fw	CACCCCTATTGGTCATGTTCCAAACG
	*GGT1*_5'UTR_rv	TTATGTTCACTCTGAACCAAT
	*GGT1*_Δ5I_rv	TTATGTTCACTCTGAACCAATCCCTAGCTCACTTCTTCCCTC CTCTTCAAACTCAATGTTGTGACTC
-347	*GGT2*_-347_fw	CACCATTTTGCACATTCATGTTACTTAAT
	*GGT2*_5'UTR_rv	TTCCAGGATTTACTTTTCAAAGC
	*GGT2*_Δ5I_rv	TTCCAGGATTTACTTTTCAAAGCTAAAAGCAAAATGATTCCTCA CTTCCCCCTTAGATCAACTCACGACAC
Overlap extension primer *Ggt*1 25I	Primer	Sequence (5' to 3`)
P1	*GGT1*_-1458_fw	CACCTAAAGCATTATTCAGTAGTATGTG
P6	*GGT1*_5'UTR_rv	TTATGTTCACTCTGAACCAAT
P2	*GGT1*_P2_rv	AGAAATTATACCAACCTTCAAACTCAATGTTGTGACTC
P3	*GGT2*_5I_fw	ACATTGAGTTTGAAGGTTGGTATAATTTCTTGTAGTTTTG
P4	*GGT2*_5I_rv	CACTTCTTCCCTCCTTCTACAACCAAAATAAGCAGATG
P5	*GGT1*_P5_fw	TATTTTGGTTGTAGAGGAGGGAAGAAGTGAGCTAGGGATTGGT TCAGAGTGAACATAACCTAAGGGTGGGCGC

P5	*GGT1*_P5_rv	GCGCCCACCCTTAGGTTATGTTCACTCTGAACCAATCCCTAGC TCACTTCTTCCCTCCTTCTACAACCAAAATA
Overlap extension primer *Ggt*2 15I	Primer	Sequence (5' to 3`)
P1	*GGT2*_-347_fw	CACCATTTTGCACATTCATGTTACTTAAT
P6	*GGT2*_5'UTR_rv	TTCCAGGATTTACTTTTCAAAGC
P2	*GGT2*_P2_rv	AACCAAATCACAAACCTTAGATCAACTCACGACACA
P3	*GGT1*_5I_fw	GTGAGTTGATCTAAGGTTTGTGATTTGGTTTTTCTTTCTC
P4	*GGT1*_5I_rv	ATTCCTCACTTCCCCCTACAATTGGAAGAAAACAATTCATC
P5	*GGT2*_P5_fw	TTCTTCCAATTGTAGAGGGGAAGTGAGGAATCATTTTGCTTTTA GCTTTGAAAAGTAAATCCTGGAACCTAAGGGTGGGCGC
P5	*GGT2*_P5_rv	GCGCCCACCCTTAGGTTCCAGGATTTACTTTTCAAAGCTAAAA GCAAAATGATTCCTCACTTCCCCCTACAATTGGAAGAA
Promoter 15I constructs	Primer	Sequence (5' to 3`)
	GGT1 5I Acc65I_fw	AAAAAGGTACCGTTTGTGATTTGGTTTTTCTTTC
	GGT1 5I BglII_rv	AAAAAAGATCTCTACAATTGGAAGAAAACAATTC
	GLDP1-P2_fw	CACCTATGTCCCATTAGAGGGGAA
	*GLDP1*_MCS_rv	AGGCCTGTCAGTAGATCTGTCAGTGGTACCTGGGAAAAAAGGT TGCAGTC
	*CAT3*_fw	CACCCGAGAATATTATCACACAAC
	*CAT3*_rv	GGTGATGATAGAAGGTTGATG
	*CAT3*_MCS_rv	GTCGACGTCAGTGGTACCGGTGATGATAGAAGGTTGATG
	*PRX*_fw	CACCTCTATTTTGACTCTTTCTATTCG
	*PRX*_rv	TTTCTTAAAAAATCTTTAGTTTGTTGC
	*PRX*_MCS_rv	GTCGACGTCAGTGGTACCTTTCTTAAAAAATCTTTAGTTTGTTG C

Supplemental table S4 – Laxa et al.

Supplemental table IV. Segregation analysis of *GGT1 Δ5I*::*gusA* transgenic lines (F2-generation) used to generate the data in Figure 4 and 5. The table summarizes the number of individuals analyzed per transgenic event, the number of kanamycin-sensitive and insensitive plants as well as the expected numbers according to mendelian segregation. Additionally, transcript levels of *gusA* mRNA (standardized to *GAPDH*) were added to correlate *gusA* expression to the probability of a single insertion indicated by the x^2-test.

Event	Individuals	insensitive	sensitive	expected insensitive	expected sensitive	*gusA* mRNA/ *GAPDH*	x^2-test
GGT1 Δ5I-1	49	39	10	36.75	12.25	0.299	0.46
GGT1 Δ5I-2	50	46	4	37.5	12.5	0.814	0.01
GGT1 Δ5I-3	49	40	9	36.75	12.25	0.764	0.28
GGT1 Δ5I-4	47	39	8	35.25	11.75	0.026	0.21
GGT1 Δ5I-5	51	35	16	38.25	12.75	0.067	0.29
GGT1 Δ5I-6	50	33	17	37.5	12.5	0.046	0.14
GGT1 Δ5I-7	51	40	11	38.25	12.75	0.493	0.57
GGT1 Δ5I-8	53	38	15	39.75	13.25	0.264	0.58
GGT1 Δ5I-9	50	36	14	37.5	12.5	0.044	0.62