

Supplementary Material

**The clock gene *Gigantea 1* from *Petunia hybrida* coordinates vegetative growth and inflorescence architecture**

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Genotype:	W.T.	<i>iRNA::PhG</i> <i>l1</i>	<i>iRNA::PhG</i> <i>l1 (3.7)</i>	<i>iRNA::PhG</i> <i>l1 (4.7)</i>	<i>iRNA::PhG</i> <i>l1 (8.1)</i>	% GI1 versus W.T	P value	% GI1 (3.7) versus W.T.	P value	% GI1 (4.7) versus W.T	P value	% GI1 (8.1) versus W.T	P value
Plant Height (cm)	40.9 ± 0.8	44 ± 3.5	50	46	43	+7.6	2.89E-02	+22.2		+12.5		+5.1	
N° of leaves to the 1° flower	37 ± 1.4	36.5 ± 1.2	30	32	32	-1.4	7.62E-01	-18.9		-13.5		13.5	
Basal Internode (mm)	12.6 ± 0.9	16.9 ± 0.5	17.4 ± 0.5	16.7 ± 1.2	16.9 ± 0.7	+34.4	2.46E-20	+38.1 ***	7.64E-05	+40.5 *	2.55E-02	+34.1 **	2.31E-03
Median Internode (mm)	16.3 ± 0.6	10.2 ± 0.4	9.6 ± 0.5	9.9 ± 0.2	9.8 ± 0.6	-37.6	3.57E-30	-41.1 ***	2.22E-04	-39.3 ***	4.94E-18	-39.9 ***	7.31E-04
Apical Internode (mm)	20.5 ± 1.1	13.6 ± 0.3	13.8 ± 0.8	13.8 ± 0.8	13.4 ± 0.9	-33.7	2.51E-23	-32.7 ***	1.23E-03	-34.1 ***	9.79E-05	-34.6 **	1.96E-03
N° of axillary meristems	12.5 ± 1.3	27 ± 2.08	28	29	25	+116.0	4.08E-07	+124		+132		+100	
N° of branches	2 ± 0.0	2.4 ± 0.57	2	3	2	+20	2.73E-01	+0		+50		+0	
Basal Leaves length (mm)	64.57	91.75	88.2 ± 0.9	92.5 ± 1.5	88.3 ± 1.27	+42.1	4.42E-33	+36.6	1.02E-05	+43.3	2.17E-04	+36.8	1.17E-04
Basal leaves width (mm)	40.93	50.96	50.1 ± 0.7	53.8 ± 1.3	44.6 ± 0.5	+24.5	4.97E-30	+22.4	1.98E-05	+31.4	9.49E-04	+9.0	5.61E-07
Median Leaves length (mm)	72.7 ± 2.8	75.6 ± 1.6	70.3 ± 1.2	82 ± 1.6	73.4 ± 1.8	+4	8.23E-02	-3.3	5.71E-02	+12.8	2.95E-04	+0.9	6.55E-04
Median leaves width (mm)	43.8 ± 1.7	48.1 ± 1.4	45.4 ± 0.1	50.7 ± 1.7	49.4 ± 0.7	+9.7	1.13E-08	+3.6	1.40E-01	+5.5	8.70E-03	+2.1	4.94E-05

<b>Apical leaves length (mm)</b>	38.8 ± 1.3	48 ± 2.91	44.9 ± 1.3	49.5 ± 1.5	45.6 ± 1.8	+24	1.49E-22	+16	1.08E-02	+28	1.65E-03	+17.6	1.66E-02
<b>Apical leaves width (mm)</b>	22.5 ± 0.9	30.5 ± 2.5	30.1 ± 0.8	28.6 ± 1.6	31.1 ± 1.03	+35	2.02E-23	+34	3.60E-04	+27	1.60E-02	+38	1.65E-03
<b>Basal leaves Chlorophyll</b>	22.4 ± 1.1	14.9 ± 1.1	12.00 ± 1.1	13.97 ± 1.6	15.30 ± 0.8	-33.5	1.05E-23	-46.38	7.96E-04	-37.58	1.31E-02	-31.64	1.79E-04
<b>Median leaves Chlorophyll</b>	31.04 ± 2.3	37.26 ± 1.1	36.30 ± 0.6	35.97 ± 1.3	39.47 ± 1.4	+20	1.67E-25	+16.95	4.57E-04	+15.88	4.85E-03	+27.16	1.18E-02
<b>Apical leaves Chlorophyll</b>	21.27 ± 0.9	38.19 ± 1.7	35.33 ± 1.3	36.17 ± 1.5	38.97 ± 0.9	+79.5	2.76E-45	+66.1	1.26E-03	+70.05	1.29E-03	+83.22	1.58E-04

**Table S1. Comparison of vegetative parameters between wild type and the silenced lines 3.7, 4.7 and 8.1 of PhGI1 in the T1 generation.** Data are given as averages, based on at least three biological replicates. The height was calculated from the base to the first flowering meristem, when the first flowering event occurs. The number of total axillary meristems was calculated between the base and the first apical flowering meristem. **P** values ≤ 0.05 according to Students T-test were considered as significant.

Genotype:	W.T.	<i>iRNA::PhGI</i> 1	<i>iRNA::PhGI</i> 1 (3.7)	<i>iRNA::PhGI</i> 1 (4.7)	<i>iRNA::PhGI</i> 1 (8.1)	% GI1 versus W.T	P value	% GI1 (3.7) versus W.T.	P value	% GI1 (4.7) versus W.T	P value	% GI1 (8.1) versus W.T	P value
N° of flower buds	27.8 ± 2.8	11.3 ± 4.1	18	13	16	-42		-59.4		-35		-53	
N° of fully developed flowers	27.8 ± 2.8	6.8 ± 2.2	8	6	9	-68		-75.5		-71		-78	
% of fully developed flowers	100	60.2	44	46	56	-44		-39.8		-56		-54	
Corolla diameter (mm)	46.22 ± 3.4	34.21 ± 2.7	34.18 ± 2.7	34.38 ± 2.3	35.54 ± 0.7	-23.1	4.27E-21	-26.0	1.14E-04	-26.0	2.24E-05	-25.6	2.36E-15
Tube length (mm)	40.06 ± 2.1	35.57 ± 2.1	35.38 ± 2.4	35.86 ± 1.5	35.70 ± 1.9	-10.9	2.84E-15	-11.2	1.59E-03	-11.7	1.09E-03	-10.5	3.53E-03
Petiole length (mm)	35.96 ± 2.7	35.33 ± 3.2	36.99 ± 2.9	36.04 ± 2.7	33.83 ± 4.2	-5.9	2.67E-01	-1.8	6.67E-01	-2.9	8.03E-01	-0.2	3.04E-01

**Table S2. Comparison of floral parameters between wild type and silenced *PhGI1* in T1 generation.** Data are given as averages. based on at least three biological replicates. P values  $\leq 0.05$  according to Students T-test were considered as significant.

RT (min)	Hit Name	CAS Number
7.318	<i>Methyl Benzoate</i>	93-58-3
4.82	<i>Benzaldehyde</i>	100-52-7
13.311	<i>Isoeugenol (isomers)</i>	97-45-1; 5932-68-3
17.44	<i>Benzyl Benzoate</i>	120-51-4
6.711	<i>Phenylacetaldehyde</i>	122-78-1
6.511	<i>Benzyl Alcohol</i>	100-51-6
8.111	<i>2.phenylethanol</i>	60-12-8
9.615	<i>Methyl Salicylate</i>	119-36-8
12.211	<i>Eugenol</i>	97-53-0
9.077	<i>Benzyl Acetate</i>	140-11-4
7.063	<i>Acetophenone</i>	98-86-2
7.797	<i>Nonanal</i>	124-19-6
9.639	<i>Decanal</i>	112-31-2
9.063	<i>Ethyl Benzoate</i>	93-89-0

**Table S3. Main Volatile Organic Compounds analyzed.** Data are given as percentage based on at least three biological replicates. (RT) Retention time.

VOCs:	ZT 0			ZT 3			ZT 6			ZT 9			ZT 12			ZT 15			ZT 18			ZT 21		
	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value	W.T.	GI1	P value
Mehyl Benzoate	79.9	34.3	1.65E-04	85.8	66.3	3.02E-02	91.3	75.5	1.50E-01	85.7	75.2	1.82E-01	76.8	81.2	2.26E-01	77	77.5	3.01E-01	75.1	74.4	2.64E-01	76.4	67.0	4.13E-01
Benzaldehyde	2.6	0.00	1.18E-06	2.3	0.00	6.85E-04	0.3	0.8	8.77E-01	3.4	3.4	1.96E-01	6.5	8.5	2.66E-01	11.7	5.7	1.94E-01	11.3	4.9	1.97E-01	8.5	1.7	3.97E-02
Isoeugenol	5.0	54.3	7.03E-01	0.3	12.7	1.52E-03	1.7	15.7	1.35E-01	6.1	4.4	1.42E-01	8.7	9.4	2.29E-01	5.0	7.9	4.58E-01	5.7	8.3	3.69E-01	6.0	7.9	8.49E-01
Benzyl Benzoate	4.8	2.1	4.74E-02	4.7	3.7	1.12E-01	1.1	2.0	3.48E-02	2.5	2.3	1.68E-01	5.4	0.5	1.97E-01	3.4	5.6	4.61E-01	3.6	9.2	6.76E-01	3.5	5.2	7.01E-01
Phenylacetaldehyde	0.4	0.00	2.13E-08	0.3	0.00	8.18E-02	0.00	0.3	1.72E-02	0.3	0.3	2.22E-01	1.0	0.1	2.16E-01	1.6	0.9	2.10E-01	1.8	0.8	1.95E-01	1.3	0.4	4.15E-02
Benzyl Alcohol	2.7	0.6	1.41E-04	2.6	3.6	1.46E-01	0.9	0.3	8.95E-02	0.00	0.2	1.74E-02	0.1	0.01	2.29E-01	0.2	0.3	4.56E-01	1.1	1.0	2.47E-01	2.4	1.6	2.87E-01
2.phenylethanol	2.2	6.1	3.43E-05	1.8	3.2	1.83E-02	0.5	0.00	9.03E-02	0.1	0.3	8.32E-01	0.3	0.04	2.59E-01	0.5	0.6	3.63E-01	0.9	1.00	2.59E-01	1.5	1.3	3.90E-01
Methyl Salicylate	0.6	0.2	1.41E-02	0.9	1.6	2.54E-02	1.6	0.9	1.21E-01	1.09	1.05	1.93E-01	0.5	0.06	2.37E-01	0.3	0.3	3.19E-01	0.2	0.4	4.18E-01	0.2	0.8	1.07E-03
Eugenol	2.5	0.07	3.47E-06	0.6	1.3	1.05E-02	0.06	0.00	8.07E-02	0.05	0.12	6.10E-01	0.06	0.00	1.15E-01	0.04	0.1	9.81E-01	0.1	0.00	1.20E-01	0.1	0.4	1.55E-01
Benzyl Acetate	0.6	0.1	2.79E-04	0.6	0.5	9.94E-02	0.2	0.00	6.46E-02	0.00	0.00	1.00E+00	0.00	0.00	3.47E-01	0.03	0.02	2.37E-01	0.1	0.02	2.46E-01	0.00	0.3	9.52E-01
Acetophenone	0.03	0.4	5.00E-02	0.06	0.3	8.13E-01	0.1	0.00	1.39E-01	0.00	0.3	4.69E-02	0.1	0.01	1.85E-01	0.2	0.07	2.14E-01	0.06	0.00	1.39E-01	0.00	0.8	9.23E-02
Nonanal	0.04	0.10	4.34E-01	0.2	0.00	5.36E-03	0.7	2.3	7.75E-02	0.31	10.3	9.31E-01	0.07	0.02	6.94E-01	0.00	0.06	8.62E-02	0.00	0.00	1.00E+00	0.00	0.1	5.74E-02
Decanal	0.00	0.00	1.77E-01	0.08	0.00	8.47E-03	0.4	1.4	9.05E-02	0.00	0.3	3.67E-02	0.04	0.01	7.26E-01	0.00	0.00	1.00E+00	0.00	0.00	1.00E+00	0.00	0.01	3.47E-01
Ethyl Benzoate	0.05	0.6	3.58E-01	0.00	5.3	3.30E-04	0.00	0.6	2.73E-01	0.07	1.8	3.16E-02	0.04	0.2	3.55E-01	0.02	0.9	3.37E-01	0.00	0.00	1.00E+00	0.00	12.6	3.14E-01

**Table S4. Percentage of the main Volatile Organic Compounds analyzed during 24 hours between wild type and the silenced *PhGII* flowers of T1 generation. P values  $\leq 0.05$  according to Students T-test were considered as significant.**

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<b>PhGi1 For</b>	TGGAGAAAGGGCAGAGACAT
<b>PhGi1 Rev</b>	GTGGAGCCACCCTTACGTT
<b>PhGi1attb1 For</b>	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGGAGAAAGGGCAGAGACAT
<b>PhGi1attb2 Rev</b>	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTGGAGCCACCCTTACGTT
<b>SecpDON201 For</b>	TCGCGTTAACGCTAGCATGGATCTC
<b>SecpDON201 Rev</b>	GTAACATCAGAGATTTTGAGACAC
<b>nptII For</b>	CCTGCTTGCCGAATATCATGGTGG
<b>nptII Rev</b>	CGAAATCTCGTGATGGCAGGTTGG
<b>Agri 51</b>	CAACCACGTCTTCAAAGCAA
<b>Agri 56</b>	CTGGGGTACCGAATTCCTC
<b>Agri 64</b>	CTTGCGCTGCAGTTATCATC
<b>Agri 69</b>	AGGCGTCTCGCATATCTCAT
<b>PhAct For</b>	TGCACTCCCACATGCTATCCT
<b>PhAct Rev</b>	TCAGCCGAAGTGGTGAAAGAG
<b>PaxilGI1 For</b>	TTGTACGTGCACTCAGCACA
<b>PaxilGI1 Rev</b>	CCATTTTTGATTCGGCTGTT
<b>PhGi2 For</b>	TTTAGAGTCCTTCACTCATCCATC
<b>PhGi2 Rev</b>	AATACAGCATTTGTTACATGGAGGT
<b>PhZTL For</b>	TGCATCTGTTGGCTCTGTTT
<b>PhZTL Rev</b>	CCCCAACCCAATCTCTTAGC
<b>PhLHY For</b>	CGACGTGGTAGGAATTGCATC
<b>PhLHY Rev</b>	GACCGAAATGGTCATCAAAGGAC
<b>PhTOC1 For</b>	TGATGGTAAGGGGAGCAAAG
<b>PhTOC1 Rev</b>	CTGAAGCAGGATGCCCATTA
<b>PhELF4 For</b>	GCCACCACCAAACCTAAC
<b>PhELF4 Rev</b>	AGGCTTCAAAGGCAGTGCT

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**Table S5. List of primers used.**

PhGI1	GAAAGCAGAAAGGCAAAGGATCTAAGAAAGTAAAAAACAAGGACCTGTTTCAGCGTTTG	60
PhGI2	AAAAACCGAAACAGCTGGGAAGTAAAAAGGTGAAGAAACAAGGGCCCGTTGCAGCATTTG	60
FN036363	-----	0
PhGI1	ATTCTTATGTTCTTGCTGCTGTGTGCTCTTTTCATGTGAACCTCAACTCTTTCCTTTGA	120
PhGI2	ATTCTTACGTACTTGTGCTGTGTGCTCTTTCTTGTGAACCTCAGCTCTTCACTTTAA	120
FN036363	-----TTGCTGCTGTGTGCTCTTTCTTGTGAACCTCAGCTCTTCACTTTAA	48
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TTTCAAGAGGGACTAATTATTCAGATCCAAAACCATCCCCGATGCTGCAAAGCATGCAA	180
PhGI2	TTTCAAGAGGGACTAATCATCCAGATCCAAAATCATCATGGATGAAGCAAAGCCCGCAA	180
FN036363	TTTCAAGAGGGACTAATCATTAGATCCAAAATCATCATGGATGAAGCAAAGCCCGCAA	108
	***** * .***** * .***** * .***** * .***** *	
PhGI1	ATGATTCGTCTATTGAGTTAAAAAATGGGATGCATTCTGCTATCTATCATACTCGGAGGA	240
PhGI2	ATGATTCGTGATTGAGTTACGAAACGGGATTCATTCTGCAGTCTGTACATACTCGGAGAA	240
FN036363	ATGATTCGTGATTGAGTTACGAAACGGGATTCATTCTGCCGTCCTGATACTCGGAGAA	168
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TATTGGCAATTCTGGAGGCTCTTTTCTTTTGAACCATCATCTGTTGGAACCTCATGGA	300
PhGI2	TATTAGCAATTTAGAGGCTCTTTTTCTTTGAAACCATCATCTGTTGGAACCTCATGGA	300
FN036363	TATTAGCAATTTAGAGGCTCTTTTTCTTTGAAACCATCATCTGTTGGAACCTCATGGA	228
	*** * .***** * .***** * .***** * .***** *	
PhGI1	GCTACAGCTCAAATGAGATAGTTGCTGCAGTATGGTAGCTGCTCATATATCTGATTTGT	360
PhGI2	GCTACAGCTCAAATGAGATAGTTGCTGCAGTATGGTAGCTGCTCATATTTCTGATCTGT	360
FN036363	GCTACAGCTCAAATGAGATAGTTGCTGCAGTATGGTAGCTGCTCATATTTCTGATCTGT	288
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TTAGATGCTCCAAGGCTTGCATGCATTCTCTTCAATCTTAATAAGGTGTAAGTGGGATA	420
PhGI2	TTAGACGCTCCAAGGCTTGCATGCAGGGTCTTGCTATCTTGATACGGTGAAGTGGGATA	420
FN036363	TTAGACGCTCCAAGGCTTGCATGCAGGGTCTTGCTATCTTGATACGGTGAAGTGGGATA	348
	***** * .***** * .***** * .***** * .***** *	
PhGI1	ATGAAATTCACCTCCAGAGCATCTTCGCTGTATAACCTCATTGACATTCATAGCAAAGTTG	480
PhGI2	ATGAAATTCATTCAAGGGCATCTTCACTCTATAACCTAATTGATTCATAGTAAGACTG	480
FN036363	ATGAAATTCATTCAAGGGCATCTTCACTCTATAACCTAATTGATTCATAGTAAGACTG	408
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TTGCATCAATTGTTGACAAGGCCGAACATTGGAAGCACACCTAATACCTGCACCTGTTC	540
PhGI2	TTGCATCAATTGTCAACAAGGCTGAACATTGGAAGCTTATTTAATACATGCACCAATTC	540
FN036363	TTGCATCAATTGTCAACAAGGCTGAACATTGGAAGCTTATTTAATACATGCACCAATTC	468
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TTAATAAAGAAGCATGTGCGTGAATGGGAGAAACGTAATAAATATAGCACTTGTAGCT	600
PhGI2	TGAAGGAGCGGCCAGGTGCTTAAATGGGAGAAACATTATAAATATACCAATCGTAACT	600
FN036363	TGAAGGAGCGGCCAGGTGCTTAAATGGGAGAAACATTATAAATATACCAATCGTAACT	528
	* * . * . * . * * * * * . * . * * * * * . * * * * * . * * * * *	
PhGI1	GCTTAACAGCAGAACAATCATCGTTGCTCGAGTGAACCTCAACTGATTGTAAGTTTAA	660
PhGI2	GCTTAACAGCAGAAGGCCATCAGTGTACAGTGTAAAGATC-----CTCTA	648
FN036363	GCTTAACAGCAGAAGGCCATCAGTGTCTCAGTGTAAAGAT-----	569
	***** * .***** * .***** * .***** * .***** *	
PhGI1	TTATGAGTGAGAAAGTTTACACTCAAGTGAGGTTTACAGTGCGCCACTGGTAAAGGGA	720
PhGI2	ATTGGTGCACAAAGCTTACACCAAGTGAGGTTGCTGGAGGCCACCATCAGCAAAGTGT	708
FN036363	-----	569

**Figure S1.** DNA alignment of *PhGI1* (Peaxi132Scf1428Ctg026), *PhGI2* (Peaxi132Scf1428Ctg060) from *Petunia hybrida* and the *PhGI* sequence FN03636 reported by Fenske et al. (2015)<sup>24</sup>, using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).



(a)

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GI2_Amplicon ----- 0
PhGI1_3UTR ACATGCAATTCACAAGATTAGAAAAGTACTATCTATTGGCTTGAGGATGGAGAAAAGGGCA 120
GI1_Amplicon -----TGGAGAAAAGGGCA 13

GI2_Amplicon -----TTTAGAGTCCTTTCACTCAT 20
PhGI1_3UTR GAGACATAGAATGAGCTTTAGTTACAGTCAAGAAATGAGATTAGTGCTCTTTTACACAT 180
GI1_Amplicon GAGACATAGAATGAGCTTTAGTTACAGTCAAGAAATGAGATTAGTGCTCTTTTACACAT 73
* * * * *

GI2_Amplicon CCATCATTGGGTACGAGGGAATGT-AGATAGTCAGTCTCCTTTGGT----- 66
PhGI1_3UTR CCATGATTGGGTACAACGAAAATATAGATAACCCCTTCTCTGGTTGATTGTTATTTGGT 240
GI1_Amplicon CCATGATTGGGTACAACGAAAATATAGATAACCCCTTCTCTGGTTGATTGTTATTTGGT 133
* * * * *

GI2_Amplicon --TTTATATGCTCTGTTGATGTCCAAATACAACATGATTGTGCAAGAGTAGATATAGT 124
PhGI1_3UTR TCAGTTTATGTTGATGTACATCTGAATACGAACATGATTGTGAAAATAGGATGCTTAA- 299
GI1_Amplicon TCAGTTTATGTTGATGTACATCTGAATACGAACATGATTGTGAAAATAGGATGCTTAA- 192
* * * * *

GI2_Amplicon AGTTTAAATTCGAGTGACCTACAAAAGGCTGGCTCAATTTAGGATTTTTTCTGAGTCA 184
PhGI1_3UTR -----TATTCAGTGTGATCAACGTAAGGGTGGCTCCACTTTGGGACC-----AAAGTCA 348
GI1_Amplicon -----TATTCAGTGTGATCAACGTAAGGGTGGCTCCAC----- 225
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(b)

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GI1_Amplicon ----TGGAGAAAAGGGCAGAGACATAGAATGAGCTTTAGTTACAGTCAAGAAATGAGATTA 56
GI2_Amplicon -----TTT 3
lcl|Peaxi132Scf0042Ctg060 AGGATGAGAAAAGGGCAGTAATATAAATGCATATGATCTTGAGTTAGAAAATGATATTT 180
* *

GI1_Amplicon GTGTCTTTTACACATCCATGATTGGGTACAACGAAAATATAGATAACCCCTTCTCTGG 116
GI2_Amplicon AGAGTCCCTTTCACCTCATCCATCATTGGGTACAGGAAATGT-AGATAGTCAGTCTCCTT 62
lcl|Peaxi132Scf0042Ctg060 AGAGTCCCTTTCACCTCATCCATCATTGGGTACAGGAAATGT-AGATAGTCAGTCTCCTT 239
* * * * *

GI1_Amplicon TTGTATTGTTATTTGGTTCAGTTTATGTTGATGTACATCTGAATACGAACATGATTGTG 176
GI2_Amplicon TGGT-----TTTATATGCTCTGTTGATGTCCAATACAAACATGATTGTG 107
lcl|Peaxi132Scf0042Ctg060 TGGT-----TTTATATGCTCTGTTGATGTCCAATACAAACATGATTGTG 284
* * * * *

GI1_Amplicon AAAATAGGATGCTTAAT-----ATTCAAGTGTGATCAACGTAAGGGTGGCTCCAC---- 225
GI2_Amplicon CAAGAGTAGATATAGTAGTTAATATTCGAGTGACCTACAAAAGGCTGGCTCAATTTAG 167
lcl|Peaxi132Scf0042Ctg060 CAAGAGTAGATATAGTAGTTAATATTCGAGTGACCTACAAAAGGCTGGCTCAATTTAG 344
* * * * *

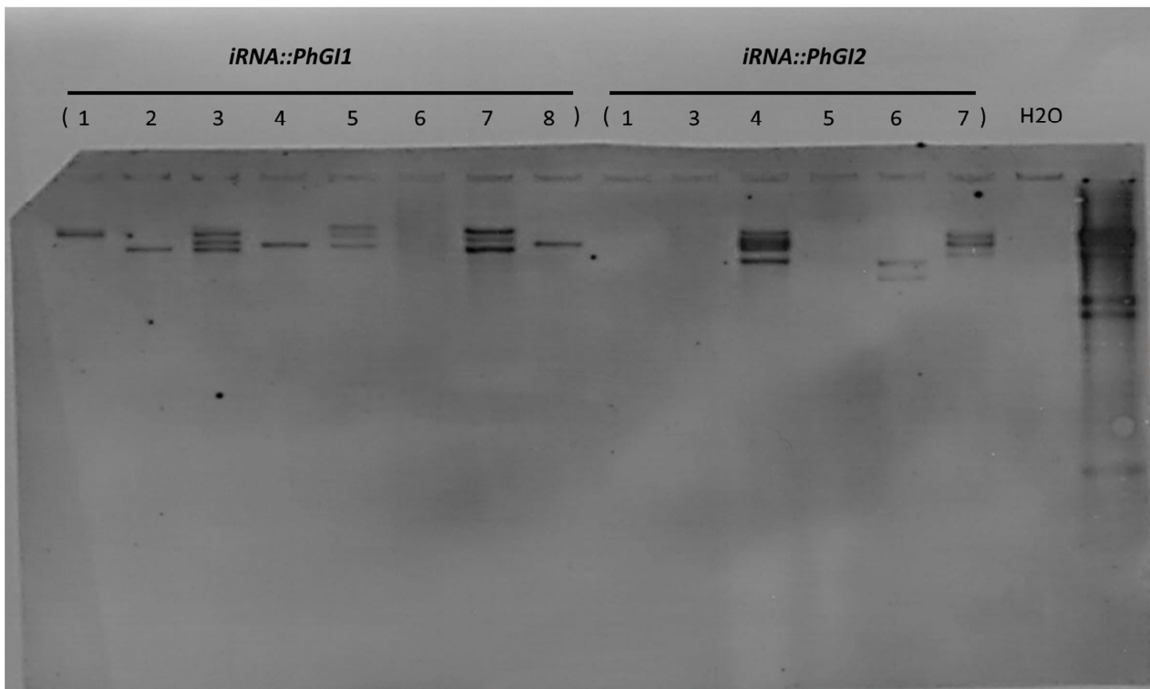
GI1_Amplicon ----- 225
GI2_Amplicon GATTTTTTCTGAGTCACCTCCATGTAACAATGCTGTATT----- 208
lcl|Peaxi132Scf0042Ctg060 GATTTTTTCTGAGTCACCTCCATGTAACAATGCTGTATTATTTTGTGTACATTCAGC 404
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**Figure S2. Figure S2.** Alignment between (a) amplified regions of *PhGI1* and *PhGI2* (*GI1\_Amplicon* and *GI2\_Amplicon*) and the 3'UTR region of *PhGI1* sequence from *Petunia hybrida* (*PhGI1\_3'UTR*) and (b) amplified regions of *PhGI1* and *PhGI2* (*GI1\_Amplicon* and *GI2\_Amplicon*) and *PhGI2* sequence from *Petunia axillaris* (Peaxi132Scf1428Ctg060) using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Regions marked in color emphasize on sequence similarity between amplicons and genomic clones.



**Figure S3.** Fully developed flower bud (left) of a wildtype line compared to aborted flower bud (right) of *iRNA::PhGI T1 line 3.7* as observed in all *iRNA::PhGI* lines.

(a)



(b)



**Figure S4.** Southern Blot analysis of the T0 generation. (a) Result of T0 lines of *iRNA::PhGI1* on the left and *iRNA::PhGI2* on the right. (b) Schematic representation of the localization of the marked digoxigenin probe used.