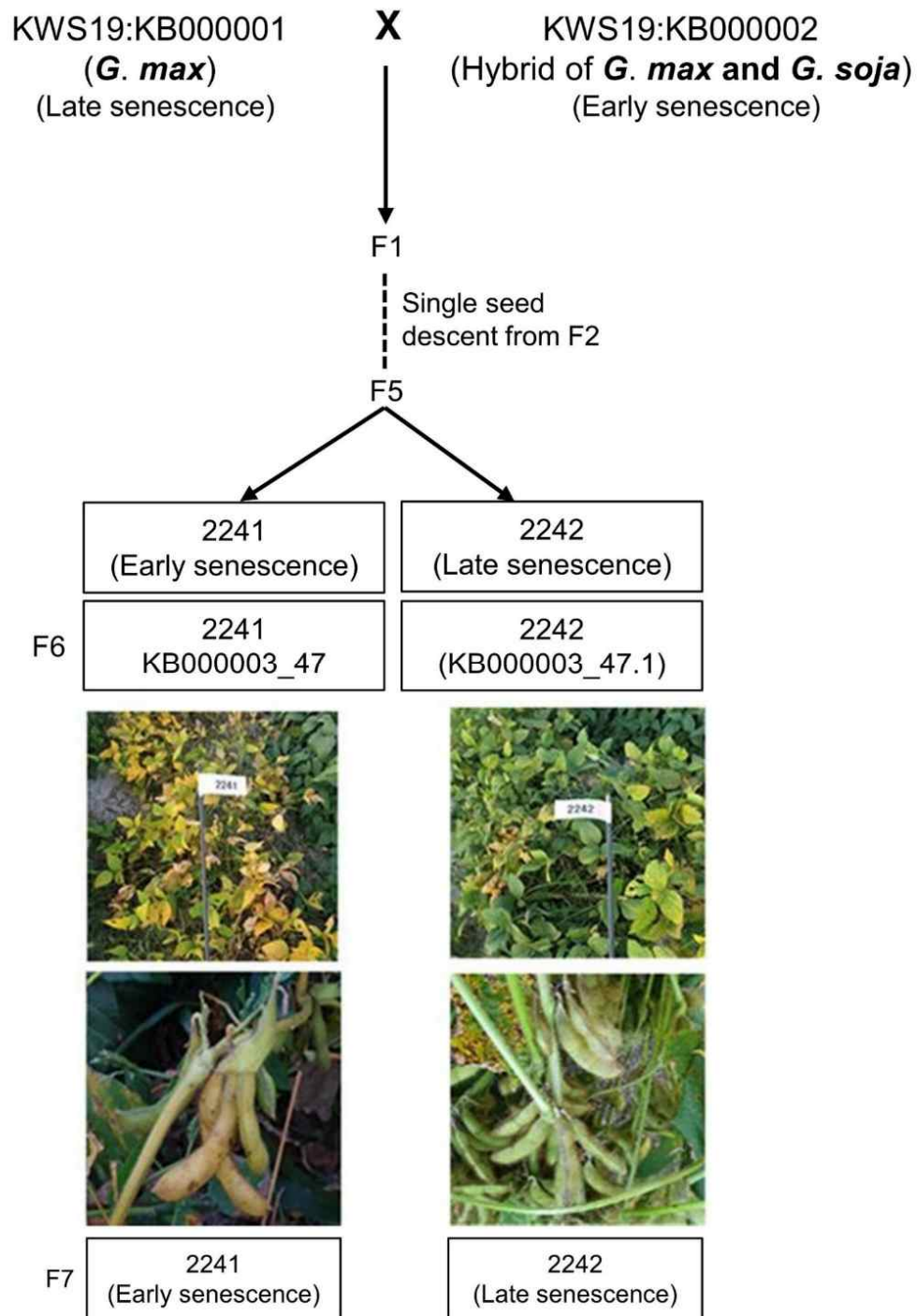




Additional file 1: Crossing scheme for the development of recombinant inbred lines (RILs).

Standard parents, a hybrid of *G. max* and *G. soja* (KWS: KB000002) and *G. max* (KWS19: KB000001), were used for the crossing and generation of RILs via the single-seed descent (SSD) method. Individual lines (2241 and 2242) selected from F5 were grown in the field under normal conditions and presented early- and late-senescence phenotypes. F6 and F7 presented similar senescence patterns (leaves and pods). 2241 represents the early senescence (ES) type, and 2242 represents the late senescence (LS) type.



Additional file 2: Flowers 35 and 50 days after sowing (DAS) of early senescence (ES)- and late senescence (LS)-type plants. Representative images of ES-LS plants at 35 (top) and 50 (bottom) days after sowing (DAS) demonstrate differences in flowering time.

Additional file 3: Summary of the sequencing data from a high-throughput DNA sequencing platform 50 and 95 days after sowing (DAS) of early-senescence (ES)- and late-senescence (LS)-type plants

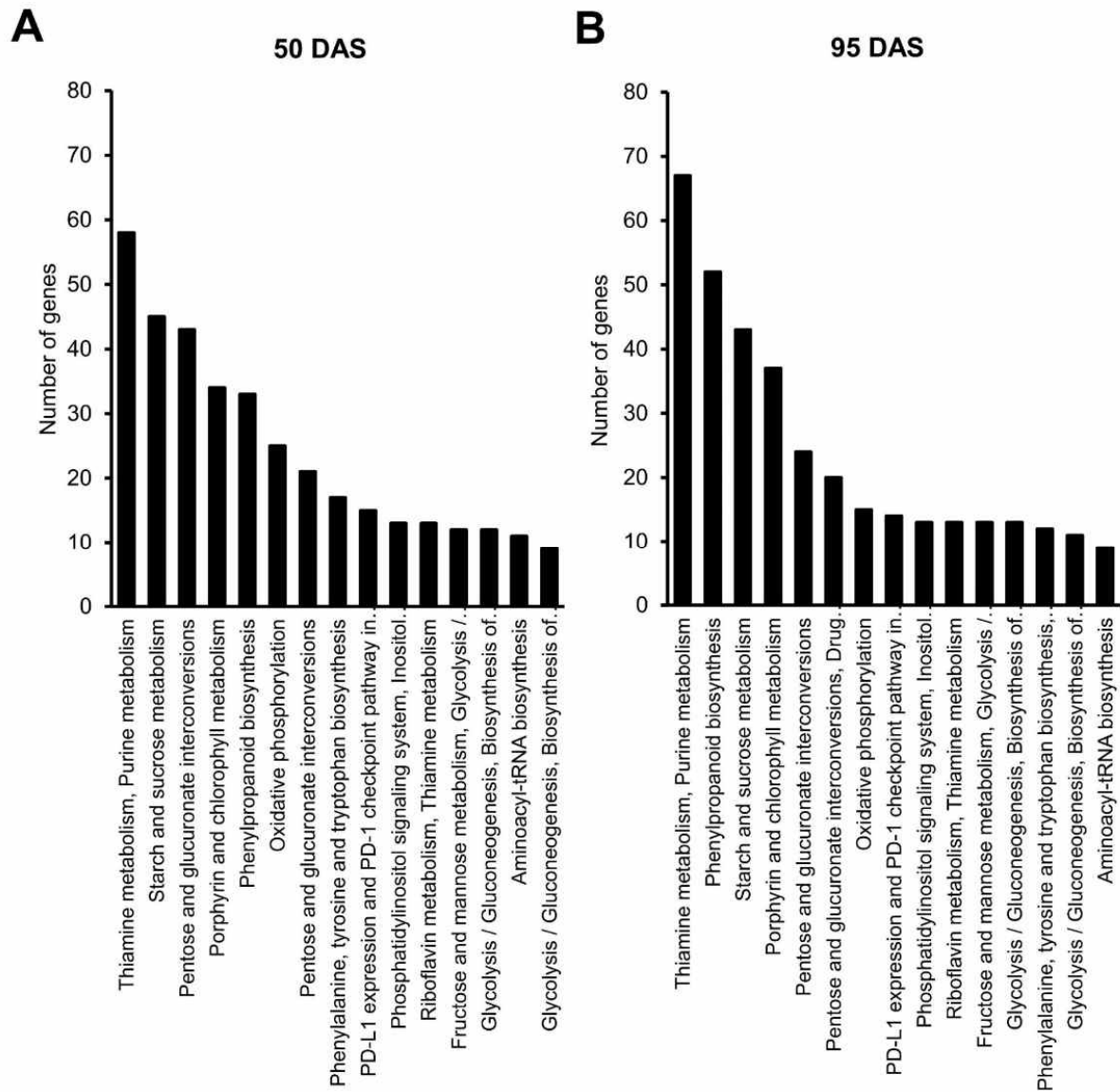
Sample ID	Raw Data		Trimmed Data		
	Total Reads	Total read bases (bp)	Total Reads	Total read bases (bp)	%
ES_50days	37,790,488	5,706,363,688	35,109,512	5,157,984,647	90.40%
LS_50 days	31,287,366	4,724,392,266	28,734,034	4,201,497,733	88.90%
ES_95 days	24,941,238	3,766,126,938	23,448,088	3,428,270,974	91.00%
LS_95 days	35,469,210	5,355,850,710	32,087,748	4,700,283,338	87.80%

Additional file 4 : Mapping reads at 50 and 95 days after sowing (DAS) of early senescence (ES)- and late senescence (LS)-type plants with reference *Glycine max* (Wm82.a2.v1)

Sample ID	Processed reads	Mapped reads	Mapping rate
ES-50 days	35,109,512	33,530,934	95.5 %
LS-50 days	28,734,034	27,542,656	95.9 %
ES-95 days	23,448,088	22,183,844	94.6 %
LS-95 days	28,734,034	30,583,054	95.3 %

Additional file 5: : Status of DEGs at 50 and 95 days after sowing (DAS) in early-senescence (ES)-type and late-senescence (LS)-type plants.

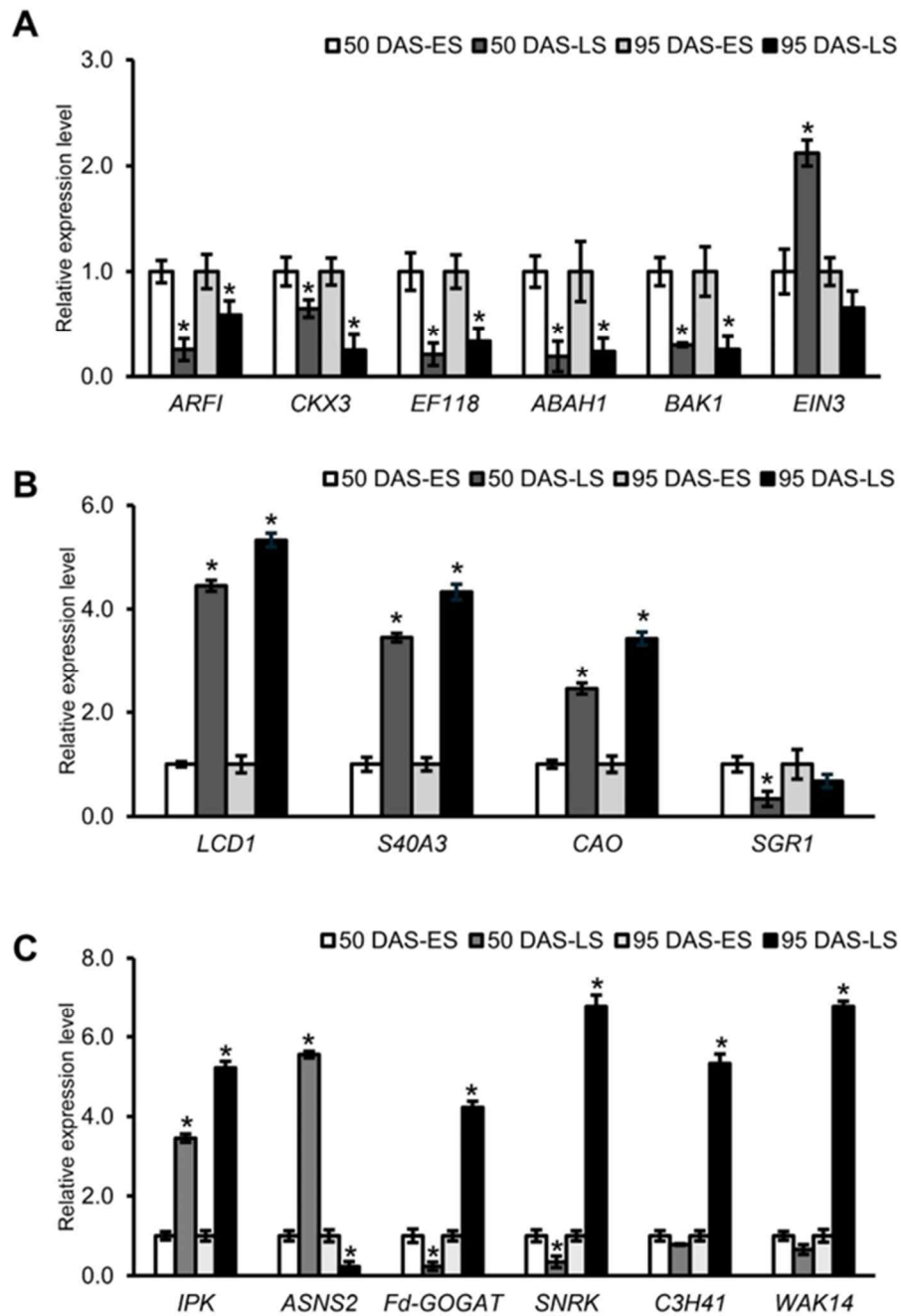
Groups	LogFoldchange $\geq$ 2, p-value <0.05		
	Up-regulated	Down-regulated	Total
ES Vs LS (50 days)	946	1,468	2,414
ES Vs LS (95 days)	1,317	1,154	2,471



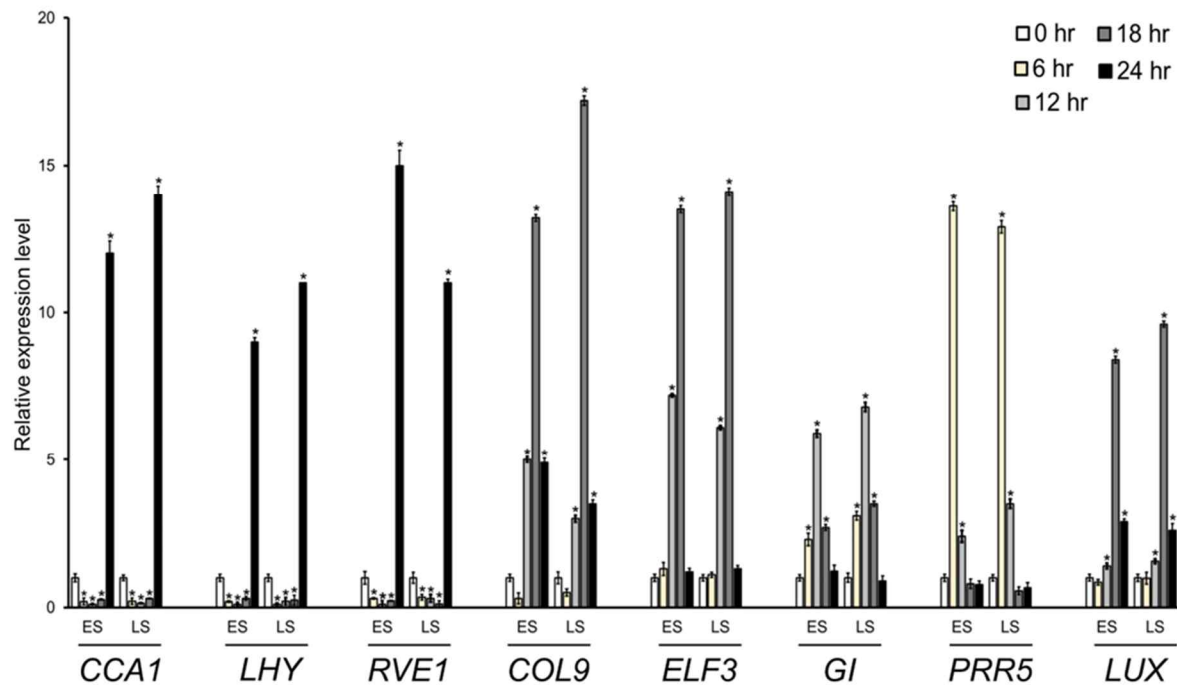
Additional file 6: Kyoto Encyclopedia of Genes and Genomes (KEGG) functional classifications of the DEGs at 50 and 95 days after sowing (DAS) of early-senescence (ES)- and late-senescence (LS)-type plants. KEGG describes the most enriched at 50 (A) and 95 DAS (B) DEGs. The x-axis represents KEGG terms, and the y-axis represents the number of DEGs.

Additional file 7: Significantly regulated senescence associated genes in 50 and 95 days after sowing (DAS) of early senescence (ES) and late senescence (LS) type plants with respect to ES plants.

Category	Unigene	Symbol	Gene Description	50 days		95 days	
				Log2FoldChange	pvalue	Log2FoldChange	pvalue
Phytohormone responsive gene	Glyma.01G103500	<i>ARF1</i>	auxin response factor 1	-8.0364	0.005288	-7.6443	0.013
	Glyma.09G063900	<i>CKX3</i>	cytokinin dehydrogenase 3	-4.9019	0.043969	-5.3524	0.0357
	Glyma.01G081100	<i>ERF118</i>	ethylene-responsive transcription factor ERF118	-7.4724	0.02496	-8.258	0.0265
	Glyma.09G218600	<i>ABAHI</i>	abscisic acid 8'-hydroxylase 1	-8.8117	0.000885	-8.6948	0.0019
	Glyma.05G119500	<i>BAK1</i>	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase	-7.6801	0.0026	-8.524	0.0002
	Glyma.20G051500	<i>EIN3</i>	protein ETHYLENE INSENSITIVE 3	6.5101	0.041655	-7.1969	0.0366
chlorophyll biosynthesis-related genes	Glyma.15G127400	<i>LCD1</i>	cysteine desulphydrase 1, chloroplastic	11.8028	0.000005	6.525	0.0023
	Glyma.10G146600	<i>S40A3</i>	solute carrier family 40, chloroplastic	9.5557	0.000806	7.5557	0.0042
	Glyma.14G150600	<i>CAO</i>	chlorophyllide a oxygenase, chloroplastic	6.275	0.002441	5.978	0.0042
	Glyma.17G132900	<i>SGR1</i>	protein STAY-GREEN, chloroplastic	-9.306	0.019442	-5.8577	0.0432
senescence-associated protein kinase	Glyma.08G138200	<i>IPK</i>	inositol polyphosphate kinase	6.78036	0.006206	5.0875	0.0034
	Glyma.18G061100	<i>ASNS2</i>	asparagine synthetase 2	9.344	0.001752	-8.7463	0.0038
	Glyma.19G130800	<i>Fd-GOGAT</i>	ferredoxin-dependent glutamate synthase	-12.0615	0.000022	5.042	0.0208
	Glyma.13G060400	<i>SNRK</i>	SNF-1-like serine/threonine protein kinase	-10.5262	0.000345	11.0037	0.0003
	Glyma.19G004000	<i>C3H41</i>	zinc finger CCCH domain-containing protein 41	-8.9337	0.005005	7.7943	0.0138
	Glyma.02G061700	<i>WAK14</i>	wall-associated receptor kinase-like 14	-8.6084	0.00096	8.3819	0.0017



Additional file 8: Analysis of the expression of senescence-related candidate genes at 50 and 95 days after sowing (DAS) in early senescence (ES)- and late senescence (LS)-type plants. RT-qPCR analysis of the expression levels of phytohormone-responsive genes (A), chlorophyll biosynthesis-related genes (B) and senescence-associated protein kinases (C) in LS-type plants at 50 and 95 DAS. Total RNA was prepared from the leaves of the indicated samples. The ES-type plants in the control group were 50 and 95 DAS, respectively. The data are the mean values of three biological replicates, and the error bars indicate the SDs. Asterisks indicate statistically significant differences between the corresponding samples and their controls ($p < 0.01$, student t-test). *Act11* was used as the internal control, and the relative expression levels are shown as fold values.



Additional file 9: Comparison of the expression patterns of circadian clock-related genes in early senescence (ES)- and late senescence (LS)-type plants under light and dark conditions. RT-qPCR analysis of the expression levels of *CCA1*, *LHY*, *RVE1*, *COL-9*, *ELF3*, *GI*, *PRR5* and *LUX* at 35 DAS in ES and LS plants under light and dark conditions. Total RNA was prepared from the leaves of the indicated time samples. The controls were 0 hrs. for both the ES-type and LS-type plants. The data are the mean values of three biological replicates, and the error bars indicate the SDs. Asterisks indicate statistically significant differences between the corresponding samples and their controls ($p < 0.01$, student t-test). *Act11* was used as the internal control, and the relative expression levels are shown as fold values.

Additional file 10: List of primers used in this study

Gene ID	Gene symbol	Forward	Reverse
Glyma.16G017400	<i>CCA1</i>	TCGATCTGAGGTTTTGGCGCT	TGATGATGATGATGCTACGAGGG
Glyma.19G260900	<i>LHY</i>	GCTCCCCCTCATTCTTCCTTTT	CTCCACAGCGCCAAAACCTTG
Glyma.14G190400	<i>COL-9</i>	GAAGCTGCTGAGTGGGCATA	GGACACACAATCTGCTCCTGA
Glyma.02G162600	<i>LUX</i>	ACAACATCGACGAGGAACCC	GGCGTTCTTGATCCCCAAGT
Glyma.04G050200	<i>ELF3</i>	GGCTTCCCCTTCCGTAAGTC	ACACTTCCTAATCCTAATCTTCTGG
Glyma.13G135900	<i>PRR5</i>	AGCGGAAGTGTAAGTGCCAA	TCTGCTCTGATATCGAACCTTTT
Glyma.10G221500	<i>GI</i>	ACACACAAGGATTGAGAGGCA	GGGAGGCCAGAACAATGAGG
Glyma.01G103500	<i>ARFI</i>	GCGAATGGTTTTGTTGTCGTGA	CAGAACCAACCACTTCGCCA
Glyma.09G063900	<i>CKX3</i>	TGGACGTCATCACTGGAAAGG	AGAGCGATTCTTGCCCTTGT
Glyma.01G081100	<i>EF118</i>	CAGGGAAAGCGACAGGCA	ACACCCCACTCTCCCTCTTATG
Glyma.09G218600	<i>ABAHI</i>	ACCACAAAGTACAGGTGGTCT	GCTACTATGAAGCCATTGTTGAGT
Glyma.05G119500	<i>BAK1</i>	GGGTGCTGCACTGTTGTTTG	GATCCTCCTCAGCTGCAACA
Glyma.20G051500	<i>EIN3</i>	CCACCACTGTGACCCATTTCT	AACAAATTAGCTTTTCACCCATGA
Glyma.15G127400	<i>LCD1</i>	GCCAGCGCCTTCAGAAAAAG	TGCCACTCCATGCTGTTGAT
Glyma.10G146600	<i>S40A3</i>	AGGGAAGAGGGGTGGTTGAG	CCTCGGACAAAACAAATGTGG
Glyma.14G150600	<i>CAO</i>	GGAGTGTTCCCAGCTTGGTG	CTCCAGTCTCCCAGGCTTTG
Glyma.17G132900	<i>SGR1</i>	TTAAGCCATCGCATTCGGG	GAACAACCTAGCAACAGGCACT
Glyma.03G236900	<i>SNF4/IPK</i>	CCAGGCATTGCTTTTGGGAC	ACAAGTCTCCTAACCCCAGGA
Glyma.18G061100	<i>ASNS2</i>	GAAGCTGCTGAGTGGGCATA	GAAGCTGCTGAGTGGGCATA
Glyma.19G130800	<i>Fd-GOGAT</i>	AGCTTTAAGACCTCAGGTTGC	CCACGATGTTCCATACACCC
Glyma.19G004000	<i>C3H41</i>	CCATTCCACGTCTCAGAAAATCA	GTCCGCAACTGTGATTGGG
Glyma.02G061700	<i>WAK14</i>	TGAGTAACTCCTGCCACTGC	AGTGTTGTAATCATCACCTTCTGA
Glyma.02G091900	<i>Act11</i>	ATTTTGACTGAGCGTGGTTATTCCTT	GAGCTGGTCCTGGCTGTCTCC