Supplementary Information

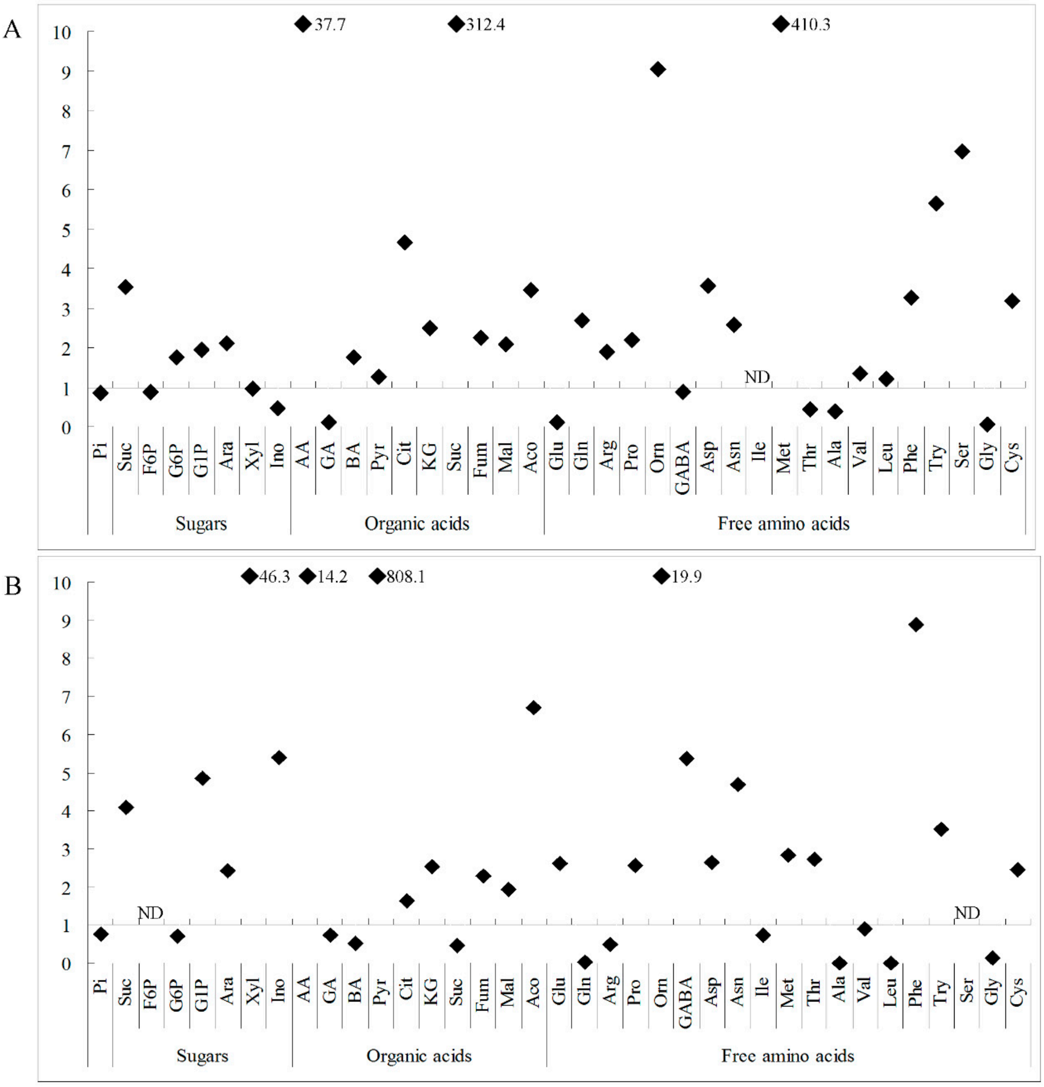

Figure S1. The fold change corresponds to the ratio of the concentration of individual metabolites involved in carbon and nitrogen metabolism in the *GS2*-cosuppressed plants relative to the wild-type plants for the leaves (**A**) and roots (**B**) at the tillering stage. Pi, phosphate; Suc (in the group of sugars), sucrose; Fru, fructose; F6P, frutose-6-P; G6P, glucose-6-P; G1P, glucose-1-P; Ara, arabinose; Xyl, xylitol; Ino, inositol; AA, ascorbic acid; GA, glutaric acid; BA, benzoic acid; Pyr, pyruvate; Cit, citrate; KG, ketoglutarate; Suc (in the group of organic acids), succinate; Fum, fumarate; Mal, malate; Aco, aconitase; Glu, glutamate; Gln, glutamine; Arg, arginine; Pro, proline; Orn, ornithine; GABA, aminobutyric; Asp, aspartate; Asn, asparagine; Ile, isoleucine; Met, methionine; Thr, threonine; Ala, alanine; Val, valine; Leu, leucine; Phe, phenylalanine; Try, tryptophan; Ser, serine; Gly, glycine; Cys, cysteine.

Table S1. The fold change corresponding to the ratio of the gene expression level in the *GS2*-cosuppressed plants relative to the wild-type plants for the roots and leaves at the seedling stage and the tillering stage under N (NH_4NO_3), G (Gln) and N + G (NH_4NO_3 + Gln) conditions.

Genes	**Seedling Stage**						**Tillering Stage**					
	NH_4NO_3		**Gln**		**NH_4NO_3 + Gln**		**NH_4NO_3**		**Gln**		**NH_4NO_3 + Gln**	
	Root	**Leaf**	**Root**	**Leaf**	**Root**	**Leaf**	**Root**	**Leaf**	**Root**	**Leaf**	**Root**	**Leaf**
NRT1;1	0.54 **	1.42 **	1.29	0.48 **	0.49 **	0.42 **	5.36 **	0.60 **	4.00 **	0.69 **	1.50 **	0.46 **
NRT1;2	1.23	0.17 **	0.45 **	1.60 **	0.39 **	0.06 **	2.09 **	1.55 **	4.83 **	1.17	1.94	1.02
NRT2	0.60 *	0.23 **	1.82 **	0.93	0.13 **	0.21 **	2.87 **	0.68 *	1.66 **	5.40 **	2.17 **	3.82 **
NR1	1.73 **	1.99 **	0.33 **	3.10 **	1.25	1.78 **	1.46	0.31 **	0.67	0.85	3.26 **	0.12 **
NR2	0.70 **	1.72 **	0.33 **	0.98	0.31 **	1.46 *	1.56 **	0.53 **	1.99 *	0.73 **	26.83 **	0.11 **
GS1;1	0.77	1.57 **	0.51 *	0.79 **	0.84 *	0.75 **	9.05 **	0.72 *	1.48 **	1.17	2.06 **	0.66 **
GS1;2	0.82 **	1.97 **	0.68 **	0.68 *	0.60 **	0.68 **	1.22 *	0.99	3.24 **	1.39 **	3.15 **	0.86
GS1;3	1.97 **	0.48 **	0.49 **	4.47 **	1.73 **	0.21 **	2.16 **	0.59 *	1.95 **	1.01	1.41 *	7.19 **
GS2	35.06 **	2.35 **	65.44 **	0.79 *	40.77 **	0.76 **	475.34 **	0.43 **	91.91 **	0.61 **	537.49 **	0.48 **
Fd-GOGAT1	0.75 **	1.35 **	0.72	0.63 **	1.13	0.48 **	10.97 **	0.64 **	4.68 **	1.29	2.33 **	0.62 **
Fd-GOGAT2	0.80 *	1.45 **	0.86	0.67 *	0.56 **	0.73 *	6.74 **	0.42 **	1.94 **	1.03	9.95 **	0.33 **
NADH-GOGAT1	1.00	1.03	0.66 **	0.97	1.32 **	0.83 *	5.77 **	1.63 **	6.23 **	0.64 **	5.24 **	0.99
NADH-GOGAT2	0.73 **	0.36 **	0.37 **	0.21 **	0.53 **	0.21 **	19.78 **	0.35 **	9.43 **	0.93	13.2 **	0.59 **
RUBISCO	0.43 **	1.89 **	1.67 **	0.80	1.30 *	0.64 **	21.95 **	0.56 **	2.71 **	1.70 **	25.76 **	0.79 *
PEPC1	2.16 **	1.38 **	2.10 *	0.93	0.37 **	1.71 **	8.17 **	0.49 **	1.83 **	0.59 *	46.93 **	0.35 **
PEPC2	0.71 *	0.98	0.54 **	0.50 **	0.52 **	1.11	6.70 **	0.32 **	3.60 **	1.25 **	7.65 **	0.30 **
PEPC3	0.41 **	2.99 **	0.38 **	0.55 **	3.04 **	0.34 **	2.30 *	1.41 **	1.86 **	0.99	1.53 *	0.70 **
PEPC4	0.60 **	1.23	0.89	0.48 **	2.67 **	0.36 **	6.70 **	1.27	3.84 **	0.71 *	1.60 **	0.75 **
PEPC6	0.72 *	1.60 *	2.29 **	0.71 **	1.62 **	0.48 **	7.88 **	0.96	1.23 **	1.03	19.86 **	0.92
PEPC7	0.53 **	1.24 *	0.88 *	0.53 **	3.01 **	0.62 **	7.21 **	0.85	1.80 **	1.25 *	3.03 **	0.85

Values are mean from three independent experiments using three randomly mixed plant materials. *, ** Significant differences at the level of p = 0.05 and p = 0.01, respectively. NRT: nitrate transporter; NR: nitrate reductase; GS: glutamine synthetase; GOGAT: glutamate synthase; RUBISCO: Ribulose-1,5-bisphosphate carboxylase/oxygenase; PEPC: phosphoenolpyruvate carboxylase.

Table S2. Primer sequences of the key genes involved in the carbon and nitrogen metabolism used in qRT-PCR.

Gene Name	cDNA Accession No.	Primer Sequence (5′–3′)
NRT1;1	AK066920	F: CCTCGCAAGTGACCCTTGAAT
		R: CGATGGCTAATGAGGAACCCTT
NRT1;2	AK101480	F: GAACATGCGGATCATGTCGTT
		R: CGATCACGGAGCTGTACATGAG
NRT2	AK109733	F: TTCGCGAACCCGCATATGA
		R: GTTGAGGTTGTCGCGGATGAT
NR1	AK102178	F: ACTACCATTACCGCGACAACC
		R: CTCGTTTATCATGTACTCCGGC
NR2	AK121810	F: AGCTGAACGTGAACTCGGTGA
		R: AGGCGTATCCCTTCATGGTGT
GS1;1	AK109397	F: GAGTCGTCGTCTCATTTGACCC
		R: GTAGCCACCATCGTTCCTCATC
GS1;2	AK243037	F: TTTTCAAGGACCCGTTCAGGA
		R: CGGCACTGTGCCTCTTGTTAGT
GS1;3	AK099290	F: TCAAGCCATCTTCAGAGACCCA
		R: TACCGGTTGTTCGTCGGAATC
GS2	AK063706	F: AGGATCGGACAAATCGTTTGG
		R: GCATGACCTCTCCATTTGTTCC
Fd-GOGAT1	AK102025	F: AAATGCCTCTTTGCAAGGCC
		R: GACTGTGAG CCCCATCCAAATA
Fd-GOGAT2	AK068130	F: CCGATGCGATTGAGAATGAGA
		R: CTTCTTGGCAATGACACCTGC
NADH-GOGAT1	AK105755	F: TGCTTGAGAGAATGGCGCA
		R: AACCCAGCATCCTTTGTCACC
NADH-GOGAT2	AK070485	F: GGTTGTCATTGGTGGTGGAGA
		R: TGGTGGCTCTGGCAAAAGTT
RUBISCO	AK243615	F: AGGCTTCAAATTGCCGTTGA
		R: TCTAGGCCATCCAGTTCCTCCT
PEPC1	AK100688	F: ACATTCCGTGTTGCTGCAGAG
		R: TGCAACAGTTCAACCGCTAGG
PEPC2	AK066635	F: CAGAAGCACGCAAGCATTAGG
		R: CGCGAGAATCTCTCTCTGAAGG
PEPC3	AK101274	F: ACCGGTCCATTGTCTTCCAAG
		R: CGTTTTGATGGCCTACTTCCAA
PEPC4	AK065425	F: TGGATGAGATGGCTGTTGTGG
		R: TTCTGTCTCAGGTGTTGCCGA
PEPC6	AK073703	F: ATGTCTGCCAGGCTTACACGAT
		R: CGGCTTAGACCAGTCCATGATC
PEPC7	AK242583	F: GAGTATTTCCGCCTTGCAACAC
		R: ACGGAGTGATTCAATGCCTCC
ACTIN	AK070531	F: GACAATGGAACCGGAATGGTC
		R: CCCAACCATAACGCCTGTATGT