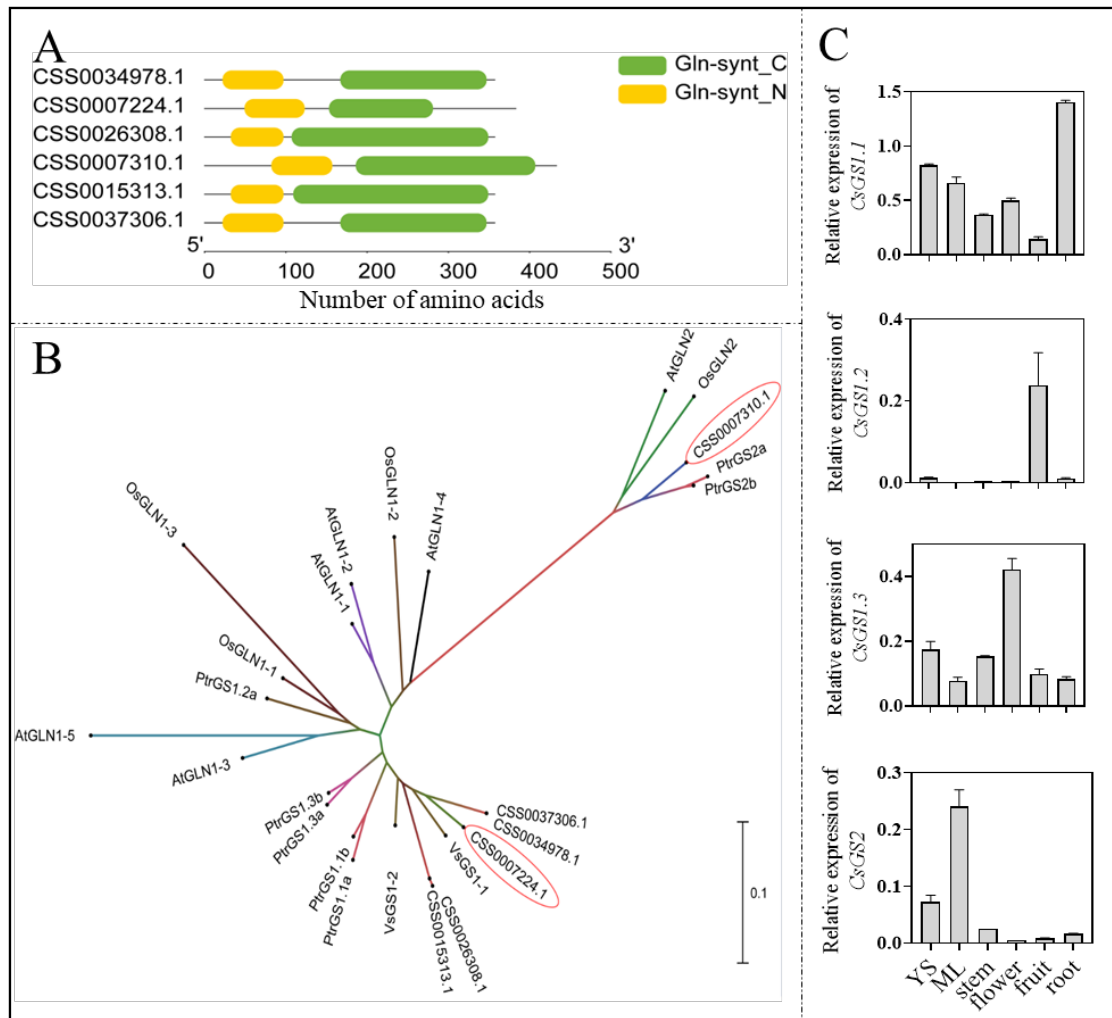
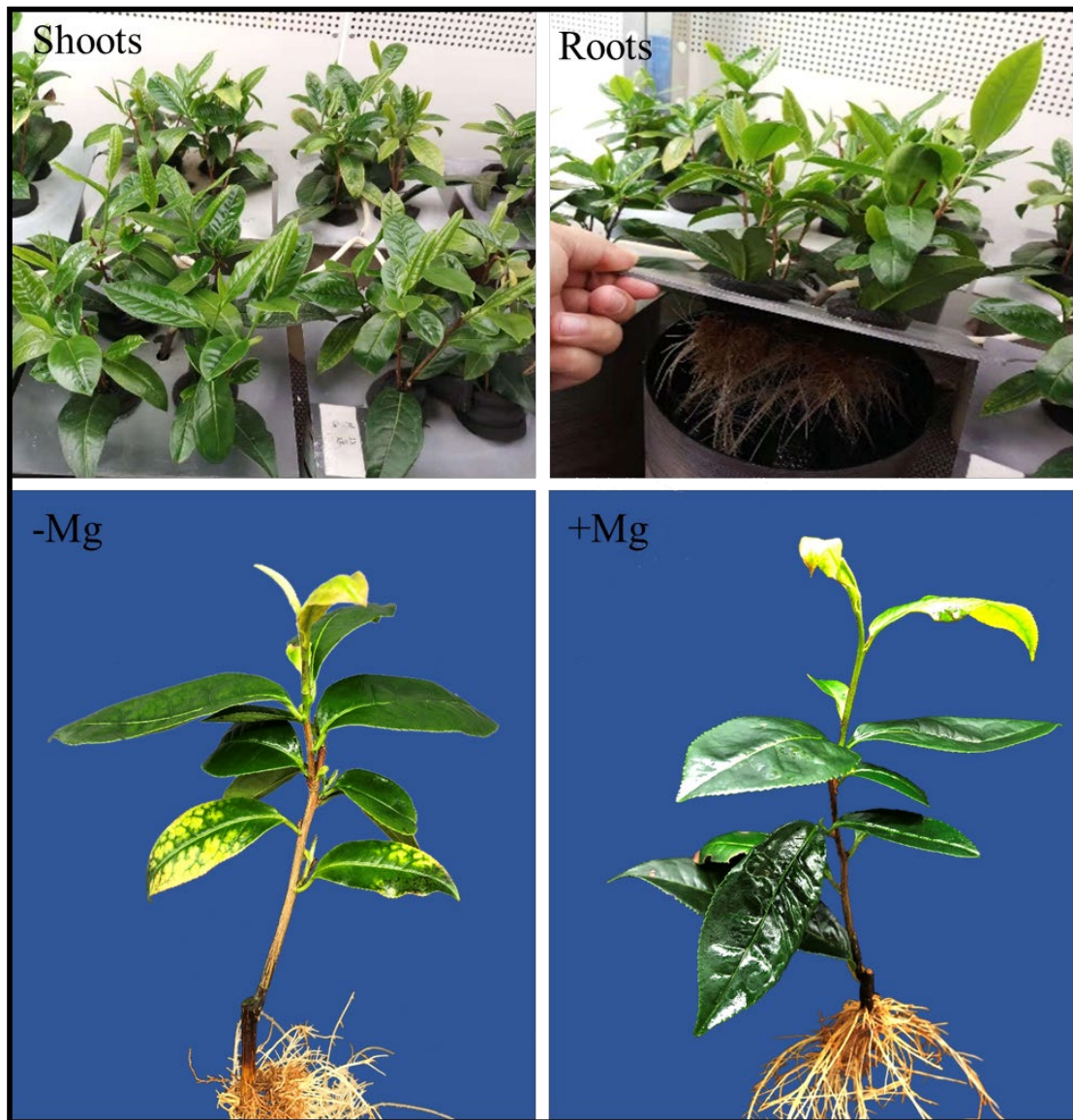


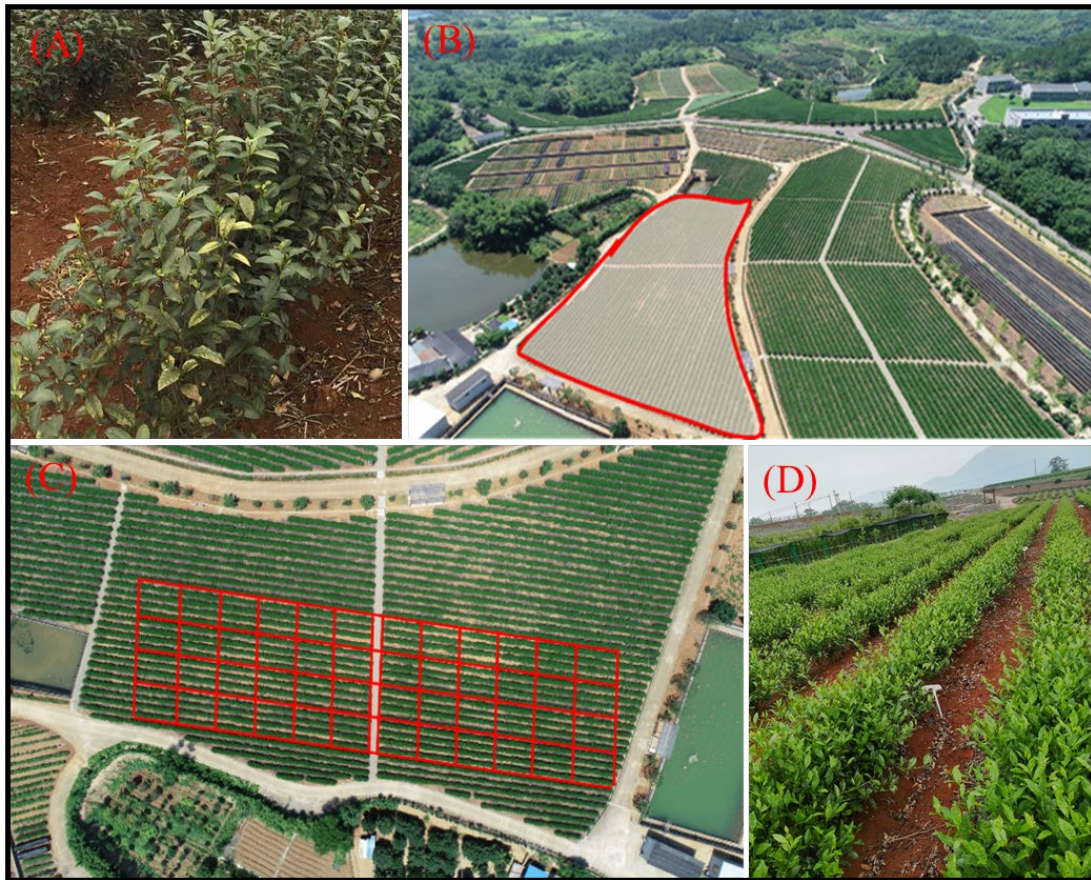
Supplemental Figure S1. Relative expression levels of genes associated with N metabolism and enzyme activities of glutamine synthetase (GS) in mature leaf (ML), root, and young/new shoot (YS) of tea plants under different treatments. -Mg, Mg deficiency; Mg1, Mg concentration in the full-strength nutrient solution (0.4 mmol/L); Mg2, two times the Mg concentration in the full-strength nutrient solution. Error bars show the mean values \pm SD (n=3). Statistical analysis was carried out with Duncan's multiple range test. Different letters indicate significant differences (p < 0.05). FW, fresh weight; ns, not significant.



Supplemental Figure S2. Identification of potential CsGS members. (A) CsGS homologues in the tea plant genome. (B) Phylogenetic analysis of CsGS1s and GS1s from other plant species. Ptr, *Populus trichocarpa*; At, *Arabidopsis thaliana*; Vs, *Vitis vinifera*; Os, *Oryza sativa*. Protein ID used here were PtrGS1.1a (genome ID, Potri.004G085400.1), PtrGS1.2a (Potri.005G093200.1), PtrGS1.2b (Potri.007G069600.1), PtrGS2a (Potri.008G200100.14), PtrGS2b (Potri.010G029100.5), PtrGS1.3a (Potri.012G043900.1), PtrGS1.3b (Potri.015G034700.1), PtrGS1.1b (Potri.017G131100.1), AtGLN1-1 (uniprot ID, Q56WN1), AtGLN1-2 (Q43127), AtGLN1-3 (Q9LVI8), AtGLN1-4 (Q9FMD9), AtGLN1-5 (Q8GXW5), AtGLN2 (Q43127), VsGS1-1 (uniprot ID, P51118), VsGS1-2 (P51119), OsGLN1-1 (uniprot ID, P14656), OsGLN1-2 (P14654), OsGLN1-3 (Q4W8D0), and OsGLN2 (P14655). The scale bar indicates number of amino acid substitutions per site. (C) Relative expression levels of CsGSs in young shoot (YS), mature leaf (ML), stem, flower, fruit, and root of tea plant. Error bars show the mean values \pm SD (n =3).



Supplemental Figure S3. Phenotype of hydroponic tea plants under different Mg supply conditions. The images in the bottom row were digitally extracted for comparison.



Supplemental Figure S4. Field experiment investigating the interaction effect of Mg and N in tea production. (A) Phenotype of tea plants under Mg deficiency treatment. (B) Tea plantation for experimental design. (C)-(D) Split-plot design in tea plantation located in Shengzhou, Zhejiang, China.

1 Supplemental Table S1. Putatively identified primary metabolites that showed significant changes in relative abundance in tea plants treated with Mg
 2 deficiency (-Mg), Mg concentration in the full-strength nutrient solution (Mg1), and two times the Mg concentration in the full-strength nutrient solution
 3 (Mg2).

	Root		Stem		Shoot		Leaf	
	Mg1/-Mg	Mg2/Mg1	Mg1/-Mg	Mg2/Mg1	Mg1/-Mg	Mg2/Mg1	Mg1/-Mg	Mg2/Mg1
Asparagine	0.52 ^{a*}	1.30	1.16	1.30	0.77	1.56 *	0.72	1.59 *
Arginine	1.14	1.08	1.01	1.26	0.62	2.84	0.86	0.82
Glutamine	0.64 *	0.78 *	0.78	0.67 *	0.63 *	1.28 *	0.62 *	0.79
Citrulline	1.10	0.91	0.57	1.15	0.94	1.31	0.52 *	1.12 *
Glutamic acid	0.82	0.74	1.30	0.64	0.92	0.80	0.79	0.99
Glutathione (reduced)	0.99	0.47 *	0.81	0.44	0.82	1.13	0.78	1.14 *
Phenylalanine	0.47 *	1.77 *	1.05	1.13	1.00	1.14 *	1.33	0.84
Theanine	0.79*	1.36*	1.17	0.65*	0.53*	1.28*	0.45*	0.79*
Threonine	1.31	1.48	0.91	1.21	0.33	3.61 *	0.99	0.85
Tryptophan	0.88	0.07 *	0.73	0.89	-	-	1.30	0.77
γ-Glu-Leu	0.76 *	0.92	0.69 *	2.08 *	1.08	1.54 *	14.52	0.50
Citric acid	2.46 *	0.37 *	0.78	1.57	0.58	1.23	0.33	0.49
Salicylic acid O-glucoside	0.82	0.84	0.54 *	1.30	7.86 *	0.96	0.79	1.33
Vitamin C	0.83 *	1.02	1.00	1.19	1.10	0.68	0.94	0.76 *
Fructose	1.01	0.79 *	1.35	0.78	0.91	1.25 *	0.80	0.83
Fucose	0.89	1.07	1.03	1.09	1.76 *	1.17	1.45	0.50 *
Glucose	1.59 *	1.11	-	-	0.88	1.20	-	-
Apigenin C-pentoside	2.12 *	1.37	0.61	1.02	1.30	1.34	0.11 *	3.90 *
Kaempferol-glucoside	1.45	0.48	-	-	0.71	2.10	0.14 *	3.59 *
Procyanidin A2	0.86	0.67 *	1.27	0.64 *	0.52 *	0.54	0.51	0.94
Rutin	5.52	0.10	0.59	1.24	1.25	1.27	0.13 *	3.90 *

4 ^a Fold change between different treatments, based on the peak intensity of the metabolite.

5 * Significant difference ($p < 0.01$), and VIP value > 1 in partial least squares discriminant analysis (PLS-DA).

Supplemental Table S2. Identified candidate genes associated with N and amino acid metabolism that is affected by Mg nutrition with weighted gene co-expression network analysis.

Number	Gene ID	Annotation	Class_annotation
i	CSS0050330	Conserved region in glutamate synthase	Amino acid transport and metabolism
ii	CSS0033052	Transmembrane amino acid transporter protein	Amino acid transport and metabolism
iii	CSS0014110	Dof domain, zinc finger	--
iv	CSS0006318	Glycosyl hydrolase family 14	--
v	CSS0001107	Glycosyl transferase family 8	Carbohydrate transport and metabolism
vi	CSS0029616	Myb-like DNA-binding domain	Transcription
vii	CSS0007224	Glutamine synthetase, catalytic domain	Amino acid transport and metabolism
viii	CSS0007310	Glutamine synthetase, catalytic domain	Amino acid transport and metabolism
ix	CSS0010308	UDP-glucuronosyl and UDP-glucosyl transferase	--
x	CSS0019985	UDP-glucuronosyl and UDP-glucosyl transferase	--