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Supplementary Material

Regulation of the chloroplastic copper chaperone (CCS) and cuprozinc superoxide dismutase (CSD2) by alternative splicing and copper excess in *Glycine max*

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Table S1. Primers used for RT-PCR

Gene name	Primer name	Primer sequence (5′- 3′)
GmCCS	F-CCS	gagctcATGGACCACAAACTCT
	R-CCS	ggtaccCTATCAGACCTTGCTA
GmCSD2	F-CSD2	GTGGCTCTGTGAGTGAGTGAG
	R-CSD2	GCTTCACAGAAGACATAACATCAG
NSP1-GmCCS	F-NSP1CCS	GTTAGTTCCTTGTTGTCTG
NSP2-GmCCS	F-NSP2CCS	GCATGCCATGGATTTCCGTC
NSP3-GmCCS	R-NSP3CCS	GTCAGCCATCATGATGCATC
NSP-GmCSD2	R-NSPCSD2	CATAAGCAGGTCCAGGATCCAG
Actin	F-ACT	ATTGTAGGTCGTCCTCGTC
	R-ACT	TTGCATAAAGTGAAAGAACAG

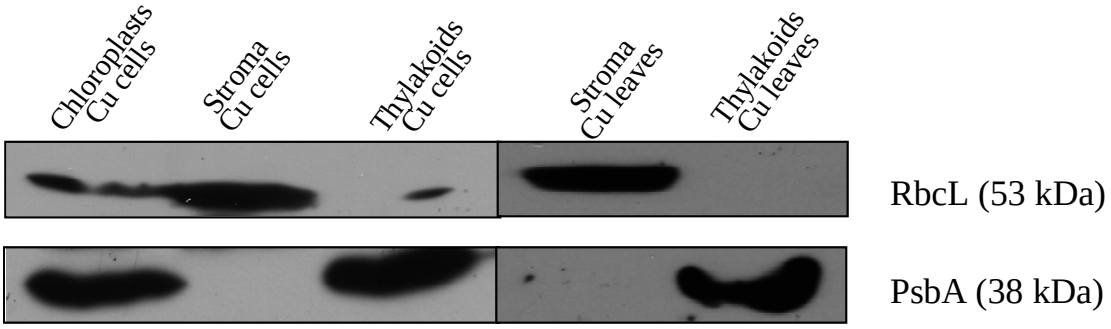

Fig. S1. Western blots of soybean cell suspensions and plant leaves. Anti-RbcL and anti-PsbA were used as specific markers for stroma and thilakoid fractions, respectively. The amount of protein loaded was 18 µg of chloroplasts from Cu-treated cells, 30 µg of stroma from Cu-treated cells, 13 µg of thylakoids from Cu-treated cells, 9 µg of stroma from CuL leaves and 20 µg of thylakoids from CuL leaves.