

## Supplementary Material

### Overexpression of *NtSnRK2.2* enhances salt tolerance in *Nicotiana tabacum* by regulating carbohydrate metabolism and lateral root development

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**Figure S1.** Identification of the *NtSnRK2.2* transformed tobacco plants.

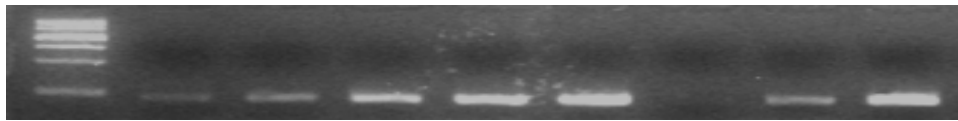
**Figure S2.** Comparison of plant biomass between Control and *NtSnRK2.2* over-expression lines in the solution culture experiment.

**Figure S3.** Comparison of plant biomass between Control and *NtSnRK2.2* over-expression lines on MS medium.

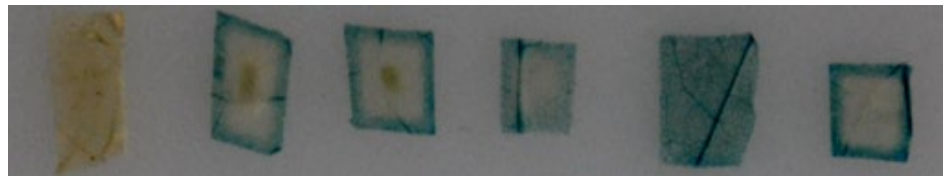
**Figure S4.** Phenotypes and sugar contents of 35S:*NtSnRK2.2* lines under a normal condition.

A

M L1 L2 L3 L4 L5 L6 L7 L8

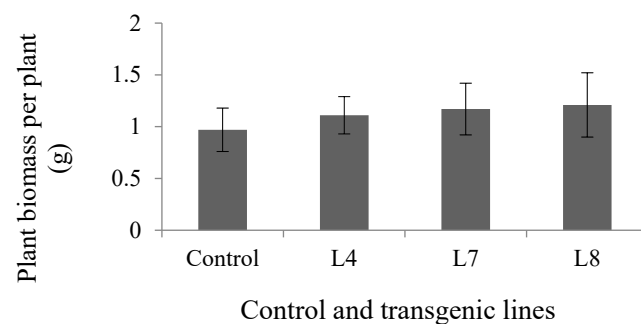


B

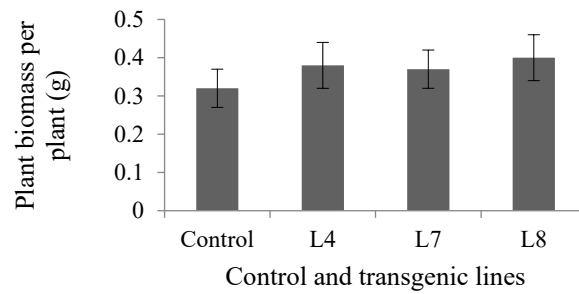


Control L3 L4 L5 L7 L8

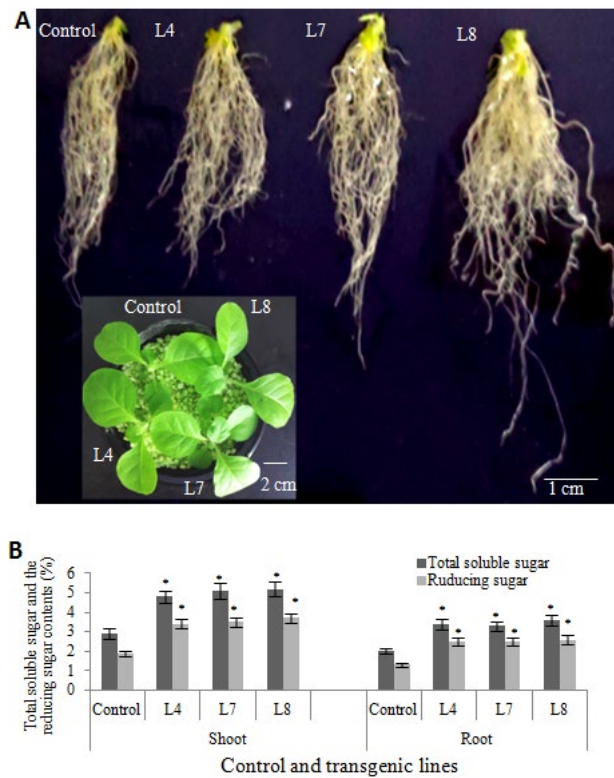
**Figure S1.** Identification of the *NtSnRK2.2* transformed tobacco plants. (A) Identification of transgenic *NtSnRK2.2* plants by RT-PCR. M: 200-bp ladder; L1-8, transgenic p35S-*NtSnRK2.2-GUS* lines. (B) Identification of positive transgenic plants by GUS histochemical staining.



**Figure S2.** Comparison of plant biomass between Control and *NtSnRK2.2* over-expression lines in the solution culture experiment.



**Figure S3.** Comparison of plant biomass between Control and *NtSnRK2.2* over-expression lines on MS medium.



**Figure S4.** Phenotypes and sugar contents of 35S:*NtSnRK2.2* lines under a normal condition. (A) The morphology of *NtSnRK2.2* over-expression lines. (B) Total soluble sugars and reducing sugars in tobacco shoots and roots. Two-week-old seedlings were cultured in Hoagland solution for two weeks. Control: untransformed plants; L4, 7, 8: three individual *NtSnRK2.2* transgenic lines. Values are mean  $\pm$  SD (n=9). \* Significantly different from control at  $P < 0.05$ .