

Table S1

Gene ID	Transcription factor type	<i>snc1</i>	Col-0
<i>At1g06160</i>	ERF/AP2	NC	NC
<i>At1g08930</i>	Zinc finger	-	NC
<i>At1g13260</i>	AP2/B3	-	NC
<i>At1g21910</i>	DREB	NC	NC
<i>At1g26800</i>	Zinc finger	NC	NC
<i>At1g28040</i>	Zinc finger	+	NC
<i>At1g62300</i>	WRKY6	NC	NC
<i>At1g67970</i>	HSFA8	NC	NC
<i>At1g68360</i>	Zinc finger	+	NC
<i>At1g68840</i>	ERF2	NC	NC
<i>At1g77570</i>	HSF	NC	NC
<i>At2g14760</i>	bHLH	+	+++
<i>At2g18670</i>	Zinc finger	NC	NC
<i>At2g31230</i>	ERF/AP2	+	+
<i>At2g32460</i>	MYB	NC	NC
<i>At2g47270</i>	bHLH	NC	NC
<i>At3g11020</i>	DREB2B	+	NC
<i>At3g24500</i>	ERF	NC	NC
<i>At3g28210</i>	Zinc finger	NC	NC
<i>At3g45260</i>	Zinc finger	-	NC
<i>At3g46640</i>	MYB	NC	+
<i>At3g50260</i>	DREB	NC	NC
<i>At3g55980</i>	Zinc finger	-	NC
<i>At3g61630</i>	AP2/ERF	NC	NC
<i>At4g01720</i>	WRKY	NC	NC
<i>At4g17500</i>	ERF	NC	NC
<i>At4g27410</i>	NAC	NC	NC
<i>At5g10380</i>	Zinc finger	NC	NC
<i>At5g47220</i>	ERF	NC	NC
<i>At5g49450</i>	bZIP	NC	NC
<i>At5g49700</i>	AT-hook DNA-binding	-	NC
<i>At5g52830</i>	WRKY	-	NC
<i>At5g58620</i>	Zinc finger	-	NC
<i>At5g61590</i>	ERF	+	++
<i>At5g67340</i>	Zinc finger	NC	NC
<i>At5g67450</i>	Zinc finger	NC	NC

Table S1. Summary of the transcription factors screened and their overexpression phenotypes in *snc1* and Col-0 background.

In *snc1* background, “-” indicates a suppressing phenotype, and “+” indicates an enhancing phenotype. In Col-0, “+” indicates dwarfism caused by the transgene. “NC” indicates no change. The number of “-” and “+” is correlated with the degrees of the phenotype. Note: A few genes, such as *At2g18670*, *At5g10380* and *At5g67340*, have been recently annotated as RING proteins or U-box proteins. They are more likely to be E3 ligases rather than TFs.