Cloning and characterization of *TaSnRK2.*3, a novel SnRK2 gene in common wheat

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Table S1 Plant materials used for identification of genomic origins

[1] Accession numbers are for the Chinese National Gene Bank, CAAS.

[2] Refers to the country of origin.

Species	Accession No.[1]	Genome	Origin[2]	Species	Accession No.	Genome	Origin
T. urartu	UR201	AA	Lebanon	*Ae. tauschii*	Y92	DD	China
T. urartu	UR204	AA	Lebanon	*Ae. tauschii*	Y215	DD	Mexico
T. urartu	UR206	AA	Lebanon	*T. dicoccoide*	DS1	AABB	France
T. urartu	UR209	AA	Syria	*T. dicoccoide*	DS6	AABB	German
Ae. speltoides	Y2003	SS	Syria	*T. dicoccoide*	DS10	AABB	Canada
Ae. speltoides	Y2009	SS	Syria	*T. dicoccum*	DM 51	AABB	Canada
Ae. speltoides	Y2017	SS	Syria	*T. aestivum*	Hanxuan 10	AABBDD	China
Ae. speltoides	Y2021	SS	Iran	*T. aestivum*	Lumai 14	AABBDD	China
Ae. tauschii	AE38	DD	Iran	*T. aestivum*	Opata 85	AABBDD	Mexico
Ae. tauschii	AE46	DD	China	*T. aestivum*	W7984	AABBDD	Mexico

Table S2 oligonucleotides for genetic assays

Name	Sequence	Experimental purpose
GTF	5′ -CCGTGGAATGTTTGTTCAGTAA-3′	Genomic sequence amplification
GTR	5′ -GTAGGTCTCCCCCTCGGCT-3′	
GBF	5′ -TTCACAGTCGGTTTCGTTCG-3′	
GBR	5′ -CCGTGGAATGTTTGTTCAGTAA-3′	
AGSF	5′ -GTTGGTACTCCAGCATACATAGCGC-3′	Chromosome localization
BGSF	5′ -TAAGTACCGCTTATGACAATCTGTGGTT-3′	
DGSF	5′ -ACTGATGGTTACTGCTATGTTTCAAGTC-3′	
GSR1	5′ -TCAAGTGTCACAAGACGTGCATTC-3′	
GSR2	5′ -GGAATGGAGTATTGCACGCCA-3′	
CAPSF	5′ -TGTGTGTCCTCCAGAAAGC-3′	Gene (*TaSnRK2.3-B*) mapping
CAPSR	5′ -CAGAAAGACCATATTATAGCAAGC-3′	
PF	5'-GAATCATGGTCATTAATACTGCCATA-3'	Promoter amplification
PR	5'- CGTGGTGATCCTTGATGATGTTG-3'	
DF	5'-AGGCCCCCGGCGAAAT-3'	qRT-PCR analysis
QR	5'-CAGACAGACCGTATGAACTGCGAT-3'	

Table S3 Comparison of *cis*-acting elements identified in the promoter regions of *TaSnRK2.3s*

Name	ProA	ProB	ProD	Sequence function
	Number			
5´ UTR Py-rich stretch	1	1	1	*cis*-acting element conferring high transcription levels
CAAT-box	25	29	23	common *cis*-acting element in promoter and enhancer regions
TATA-box	26	27	31	core promoter element around -30 of transcription start
ABRE	9	8	11	*cis*-acting element involved in the abscisic acid responsiveness
Motif lib	1	1	1	abscisic acid responsive element
CE3	1	0	1	*cis*-acting element involved in ABA and VP1 responsiveness
C-repeat/DRE	1	1	1	regulatory element involved in cold- and dehydration-responsiveness
CCAAT-box	1	1	0	MYBHv1 binding site
HSE	0	1	1	*cis*-acting element involved in heat stress responsiveness
MBS	0	2	1	MYB binding site involved in drought-inducibility
TC-rich repeats	0	0	1	*cis*-acting element involved in defense and stress responsiveness
GARE-motif	2	1	0	gibberellin-responsive element
TCA-element	2	2	3	*cis*-acting element involved in salicylic acid responsiveness
CGTCA-motif	3	0	4	*cis*-acting regulatory element involved in the MeJA-responsiveness
TGACG-motif	3	4	4	*cis*-acting regulatory element involved in the MeJA-responsiveness
Circadian	0	2	2	*cis*-acting regulatory element involved in circadian control

The *cis*-elements were identified in the upstream of promoters (1500bp)

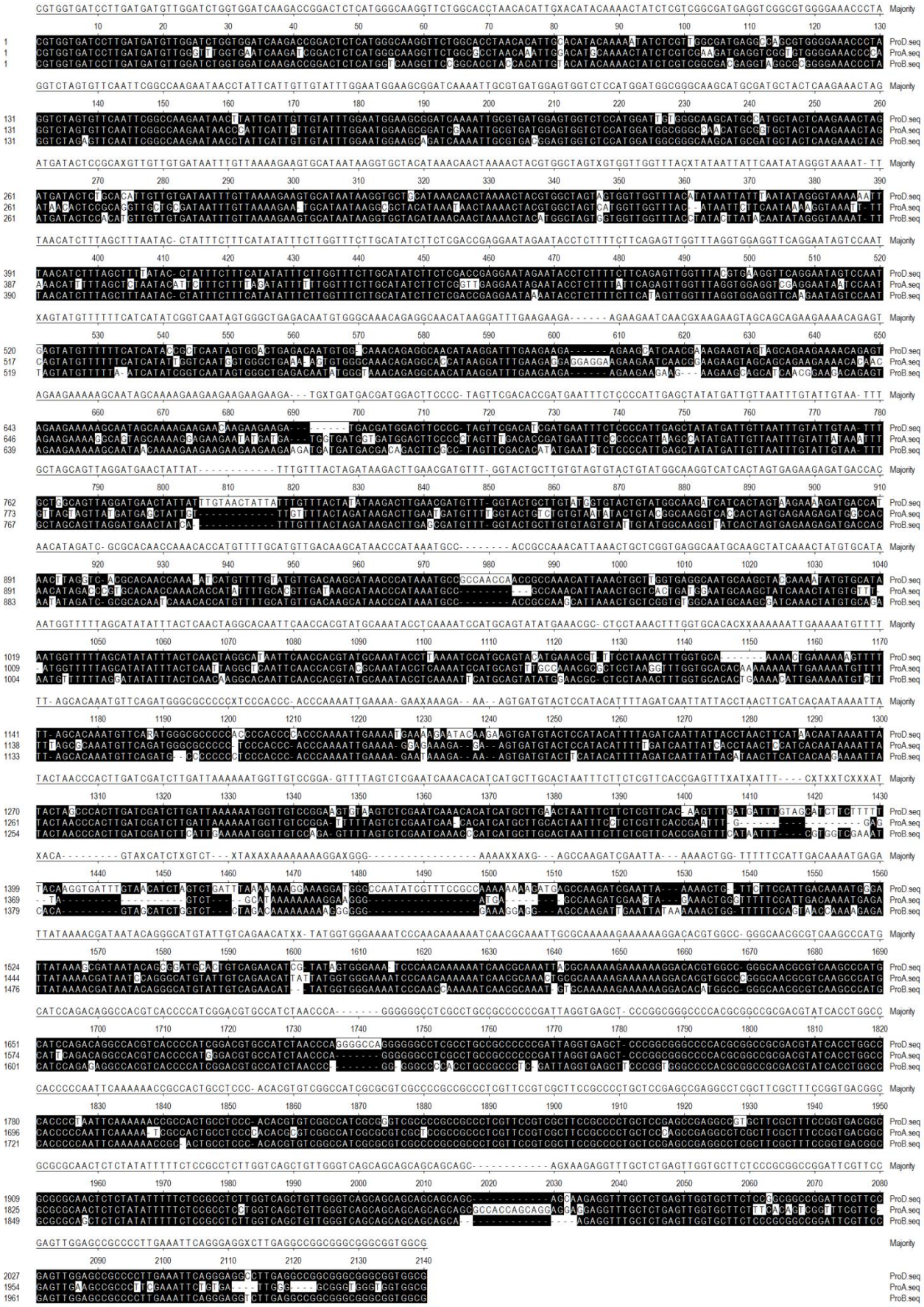

Fig. S1 Sequence alignment of the promoter regions for *TaSnRK2.3s*

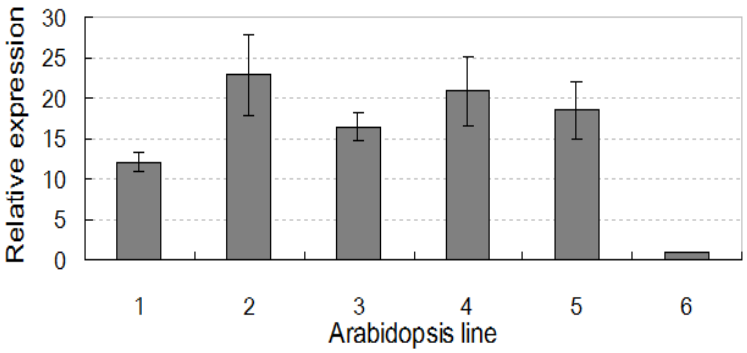

Fig. S2 Gene expression levels of *TaSnRK2.3* in different transgenic lines

1-6: six individual *TaSnRK2.3* transgenic lines, values are the means ± SE.

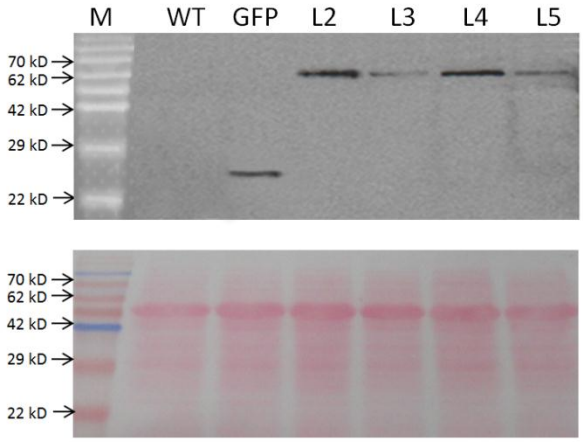

Fig. S3 Protein levels for TaSnRK2.3 in transgenic lines

M, visible protein marker; WT, wild type; GFP, GFP transgenics; L2-5, transgenic lines.