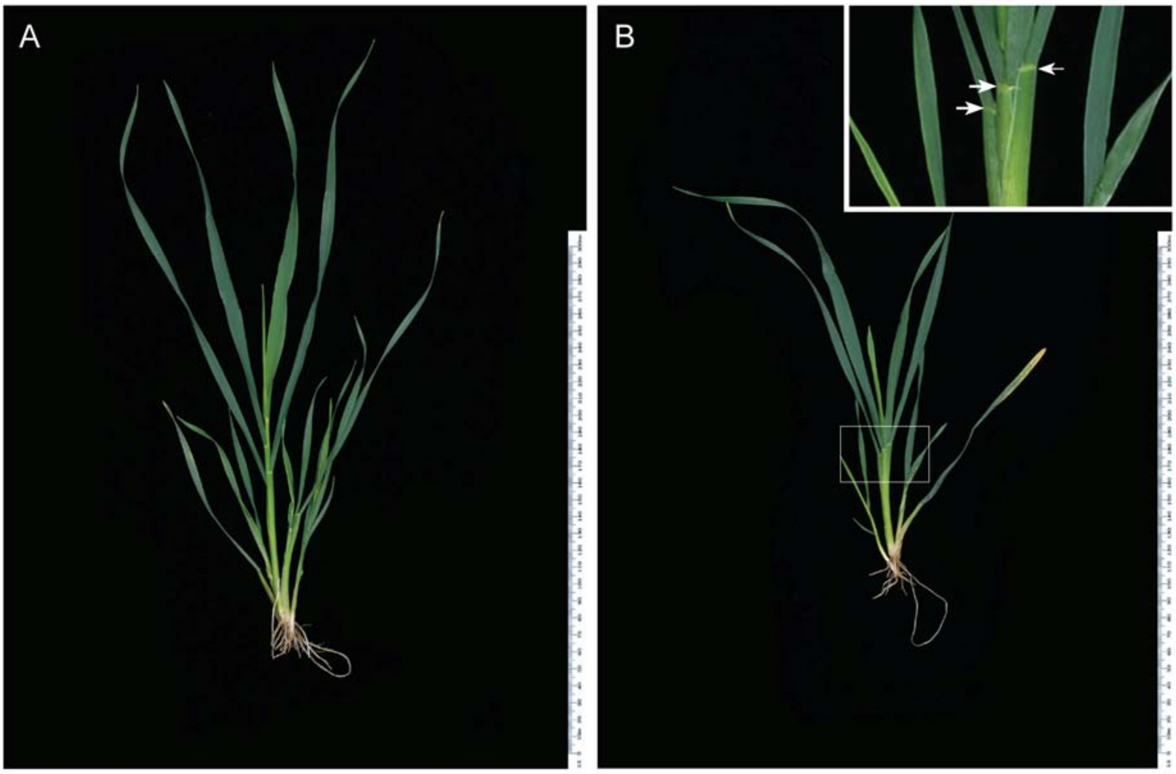

Figure S1. Normal (A) and stunted (B) *tin* plants of wheat. The stunted plant displays a rosette-like growth habit (indicated by arrow) with no distance between ligules of successively formed leaves. The stunted plant may recover and mature or die depending on the severity of the stunting. Arrows in (B) indicate the close position of ligules in the stunted plant.

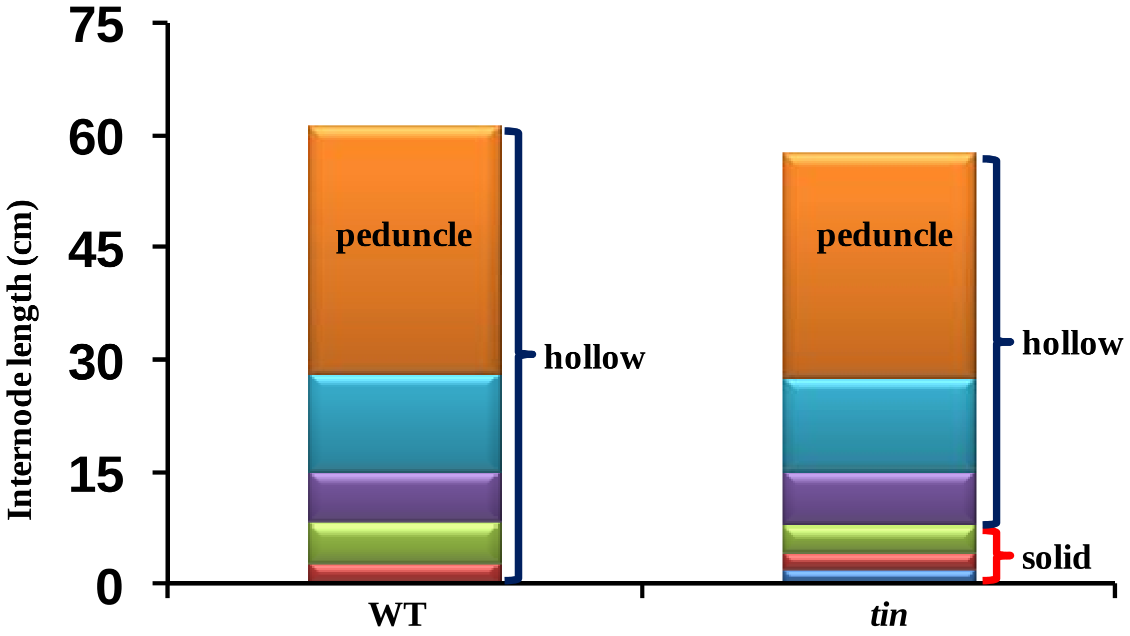

Figure S2. Mature stem internode length of WT and *tin*. The peduncle is the upper-most internode. In WT, all the internodes are hollow, while in *tin* the basal three internodes are solid.

Supplemental Table 1. Wheat ESTs, the accession number and primer sequences used for expression analysis

Amino acid sequence used in tBlastn (accession #, species)	Predicted function	Wheat cDNA/EST accession #	Length (nt)	% identity (predicted amino acid sequences)	Remark	Forward / reverse primers for qPCR
AAB84193 pea	Dormancy associated (*DRM1*)	DN828863	684	54%	EST includes the whole ORF	CAACCTGGCCACCAAGAG/ CTCCTTGTCCTCGTCTCGTC
AAK60235 maize	Inhibits bud outgrowth (*Teosinte branched1, TB1*)	BJ314006	623	68%	EST contains the TCP domain	GCTGCTCGATCGCTAGTACC/ ATGGCGATTACGACGAAGAC
AAP37733 Arabidopsis	Sugar-inducible (putative pyrophosphate-fructose-6-phosphate-1-phosphotransferase; glucose metabolism)	AK332443	2286	76%	Full length cDNA	TTTTGTCGGCCATAGAAACC/ CTGCCATAAAAGTGGGCAAT
AAL31889 Arabidopsis	Sugar starvation-inducible or dark-inducible (asparagine synthase 1 *ASN1*; Nitrogen metabolism)	AK334107	2006	81%	Full length cDNA	TTCGTCTTGCTCGATACACG/ CATACCGACCCATCAATTCC
AAL83926 maize	cell cycle (*CycD2*)	AF512432	1645	75%	EST	CTCCAGCAACATGCTACCAA/ ACACACCTGAAGCACAGCAC
ACG31293 maize	Cell cycle (*His4*)	CJ966253	368	100%	EST	ATCAACGACCACGAACCCTA/ CTTCCTCGAGAACGTCATCC
NP_001105461 maize	Cell cycle (*PCNA*)	CF182087	706	93%	EST	CGACATCATCACCATCAAGG/ TGTCCATGAGCTTCATCTCG
BAE93883 rice	Cell cycle (*CDKB*)	CD897467	753	86%	EST	CGGGATTTAAAGCCACAAAA/ CTCTGCTTAGCCCAAGATCG