

## SUPPLEMENTARY DATA

FIG. S1. Alignment of the deduced amino acid sequences of *Brachypodium distachyon* VRN1 related proteins. The alignment was generated by comparing the *Brachypodium* VRN1 sequence with the *Triticum monococcum* VRN1 (ACI24357.2) and *Triticum aestivum* VRT-1 (AAP33790.1) sequences. Identical and similar amino acids are shaded in black and grey, respectively. MADS-box domain, DNA-binding domain; I domain, intervening region; K domain, keratin-like domain; C domain, C terminal region; serine stretch, region rich in phosphorylation sites. Residues identified as being part of a nuclear targeting signal are indicated by \*.

			MADS-box	
Bradilg08340.1	1	MGRGK <b>V</b> Q <b>L</b> K <b>R</b> IENKINRQ <b>V</b> T <b>F</b> SKRR <b>S</b> G <b>L</b> L <b>K</b> KAHEISV <b>L</b> CD <b>A</b> EV <b>L</b> I <b>I</b> F <b>S</b> T <b>K</b> G <b>K</b> L <b>Y</b> E <b>F</b> A <b>T</b> D		
TmVRN1	1	MGRGK <b>V</b> Q <b>L</b> K <b>R</b> IENKINRQ <b>V</b> T <b>F</b> SKRR <b>S</b> G <b>L</b> L <b>K</b> KAHEISV <b>L</b> CD <b>A</b> EV <b>L</b> I <b>I</b> F <b>S</b> T <b>K</b> G <b>K</b> L <b>Y</b> E <b>F</b> S <b>T</b> E		
TaVRT-1	1	MGRGK <b>V</b> Q <b>L</b> K <b>R</b> IENKINRQ <b>V</b> T <b>F</b> SKRR <b>S</b> G <b>L</b> L <b>K</b> KAHEISV <b>L</b> CD <b>A</b> EV <b>L</b> I <b>I</b> F <b>S</b> T <b>K</b> G <b>K</b> L <b>Y</b> E <b>F</b> S <b>T</b> E		
		**	***	
		I domain	K domain	
Bradilg08340.1	61	SC <b>M</b> D <b>K</b> IL <b>E</b> RY <b>E</b> RY <b>S</b> Y <b>A</b> E <b>K</b> V <b>L</b> V <b>S</b> <b>T</b> E <b>S</b> E <b>I</b> Q <b>G</b> N <b>W</b> C <b>H</b> E <b>Y</b> R <b>K</b> L <b>K</b> A <b>K</b> V <b>E</b> T <b>I</b> Q <b>K</b> C <b>Q</b> K <b>H</b> L <b>M</b> G <b>E</b> D <b>L</b> E <b>S</b> L		
TmVRN1	61	SC <b>M</b> D <b>K</b> IL <b>E</b> RY <b>E</b> RY <b>S</b> Y <b>A</b> E <b>K</b> V <b>L</b> V <b>S</b> <b>S</b> E <b>S</b> E <b>I</b> Q <b>G</b> N <b>W</b> C <b>H</b> E <b>Y</b> R <b>K</b> L <b>K</b> A <b>K</b> V <b>E</b> T <b>I</b> Q <b>K</b> C <b>Q</b> K <b>H</b> L <b>M</b> G <b>E</b> D <b>L</b> E <b>S</b> L		
TaVRT-1	61	SC <b>M</b> D <b>K</b> IL <b>E</b> RY <b>E</b> RY <b>S</b> Y <b>A</b> E <b>K</b> V <b>L</b> V <b>S</b> <b>S</b> E <b>S</b> E <b>I</b> Q <b>G</b> N <b>W</b> C <b>H</b> E <b>Y</b> R <b>K</b> L <b>K</b> A <b>K</b> V <b>E</b> T <b>I</b> Q <b>K</b> C <b>Q</b> K <b>H</b> L <b>M</b> G <b>E</b> D <b>L</b> E <b>S</b> L		
Bradilg08340.1	121	N <b>L</b> K <b>E</b> L <b>Q</b> Q <b>L</b> E <b>Q</b> Q <b>L</b> E <b>S</b> S <b>L</b> K <b>H</b> I <b>R</b> S <b>R</b> K <b>N</b> Q <b>L</b> M <b>H</b> E <b>S</b> I <b>S</b> E <b>L</b> Q <b>K</b> K <b>E</b> R <b>S</b> L <b>Q</b> E <b>N</b> K <b>A</b> L <b>Q</b> K <b>E</b> L <b>V</b> E <b>K</b> Q <b>K</b> A <b>H</b> T		
TmVRN1	121	N <b>L</b> K <b>E</b> L <b>Q</b> Q <b>L</b> E <b>Q</b> Q <b>L</b> E <b>S</b> S <b>L</b> K <b>H</b> I <b>R</b> S <b>R</b> - <b>N</b> Q <b>L</b> M <b>H</b> E <b>S</b> I <b>S</b> E <b>L</b> Q <b>K</b> K <b>E</b> R <b>S</b> L <b>Q</b> E <b>N</b> K <b>V</b> L <b>Q</b> K <b>E</b> L <b>V</b> E <b>K</b> Q <b>K</b> A <b>H</b> A		
TaVRT-1	121	N <b>L</b> K <b>E</b> L <b>Q</b> Q <b>L</b> E <b>Q</b> Q <b>L</b> E <b>S</b> S <b>L</b> K <b>H</b> I <b>R</b> S <b>R</b> K <b>N</b> Q <b>L</b> M <b>H</b> E <b>S</b> I <b>S</b> E <b>L</b> Q <b>K</b> K <b>E</b> R <b>S</b> L <b>Q</b> E <b>N</b> K <b>V</b> L <b>Q</b> K <b>E</b> L <b>V</b> E <b>K</b> Q <b>K</b> A <b>Q</b> A		
Bradilg08340.1	181	Q <b>Q</b> A <b>Q</b> W <b>E</b> <b>Q</b> T <b>H</b> P <b>O</b> T <b>S</b> S <b>S</b> S <b>S</b> S <b>S</b> - <b>M</b> Q <b>R</b> E <b>A</b> P <b>P</b> T <b>T</b> N <b>I</b> S <b>N</b> R <b>P</b> A <b>A</b> A <b>G</b> E <b>R</b> T <b>E</b> <b>A</b> A <b>G</b> Q <b>-</b> - <b>N</b> Q <b>A</b> R <b>V</b> G <b>L</b> P <b>P</b> W <b>M</b>	C domain	
TmVRN1	180	<b>A</b> Q <b>Q</b> - <b>-</b> D <b>Q</b> T <b>O</b> P <b>O</b> T <b>S</b> S <b>S</b> S <b>S</b> S <b>S</b> S <b>S</b> F <b>M</b> R <b>D</b> A <b>P</b> P <b>A</b> A <b>N</b> T <b>S</b> I <b>H</b> P <b>A</b> A <b>A</b> G <b>E</b> R <b>A</b> E <b>D</b> A <b>A</b> V <b>O</b> P <b>Q</b> A <b>P</b> P <b>R</b> T <b>G</b> L <b>P</b> P <b>W</b> M		
TaVRT-1	181	<b>A</b> Q <b>Q</b> - <b>-</b> D <b>Q</b> T <b>O</b> P <b>O</b> T <b>S</b> S <b>S</b> S <b>S</b> S <b>S</b> S <b>S</b> F <b>M</b> R <b>D</b> A <b>P</b> P <b>A</b> A <b>N</b> T <b>S</b> I <b>H</b> P <b>A</b> A <b>S</b> G <b>E</b> R <b>A</b> E <b>D</b> A <b>A</b> V <b>O</b> P <b>Q</b> A <b>P</b> P <b>R</b> T <b>G</b> L <b>P</b> L <b>W</b> M	Serine stretch	
Bradilg08340.1	238	<b>V</b> S <b>H</b> I <b>S</b> G		
TmVRN1	238	<b>V</b> S <b>H</b> I <b>N</b> G		
TaVRT-1	239	<b>V</b> S <b>H</b> I <b>N</b> G		

FIG S2. Alignment of the deduced amino acid sequences of *Brachypodium distachyon* COR413 with related proteins. The following protein sequences were used to generate the alignment: *Zea mays* COR413 (NM\_001155133), *Oryza sativa* COR413 (AF283006.1), *Triticum aestivum* COR413 (U73216.1), *Arabidopsis thaliana* COR413 (NM\_127156.3) and *hordeum vulgare* COR413 (AK356898.1). Identical and similar amino acids are shaded in black and grey, respectively.

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BRADICOR413  1  MG-KMPSFLEPMKTGAASGASE-PAQXLIESDLRELGVAARKLANHAAVVLGGGLGFGSSLI
ZmCOR413     1  MGKGFASYLAMKTGPEGGDAAAACQALITADLRELGVAARKLANHAFVLGGGLGFGTSFL
OsCOR413    1  MGKGFMSYLAMKTDAAAGGER--AQALITADLQELGVAARKLANHAAVVLGGGLGFGTTF
TaCOR413    1  ---MAKSEFLAMKTGPAAGASE-ASQALIESDLREITMAARKLANHAAVVLGGGLGFIGTFL
AtCOR413    1  --MGRMDYLAMKTDDV-----DTVALVNSDVEIKVAAKKIFSDVSK-IGGLGFGVSFL
HvCOR413    1  ---MAPSEFLAMKTGAASGASE-PAQALIESDLRELGVAARKLANHAAVVLGGGLGFGRHFL

BRADICOR413  59  KWLAFIAAVYLLILDRTNWKTNMLTGLLVPIFFTLPGVLFSLIRGEVGCWIAFIWVILR
ZmCOR413    61  KWLAFIAAVYLLILDRTNWKTNMLTGLLVPIFFTLPEVLFSLIRGEVGCWIAFIWVILR
OsCOR413    59  KWLAFIAAVYLLILDRTNWKTNMLTGLLVPIFFTLPGGLFSLIRGEIGKWIAFIWVILR
TaCOR413    57  QWLAFIAAVYLLVLDKTNWKTNMLTGLLVPIFFTPGGLFSGFIRGEIGWIAFVWVILR
AtCOR413    52  KELASFAAIYLLILDRTNWKTKMLTSLLPYIFLSLPSVIFNFLSGDVGWIAFVWVILR
HvCOR413    57  KWLAFIAAVYLLVLDRTNWKTNMLTGLLVPIFFTLPGVLFSLIRGEVGCWIAFIWVILR

BRADICOR413  119 LFFPRHFDPDWLELPGSLILLTVVAPSLFADTFRGDF--VGVGICLAIGCYLLOEHIRASG
ZmCOR413    121 LFFPRHFDPDWLELPGSIILLTVVAPSLFADTFRGDL--VGVFICLVIGCYLLOEHIRASG
OsCOR413    119 LFFPRHFDPDWLELPGAVILLIAVAENLFASTFRGDL--VGFICLIIGCYLLOEHIRASG
TaCOR413    117 LFFPRHFDPDWLELPGSLILLTVVAEAFADTFRGSWLIIGVGVCLVIGCYLLEHIRASG
AtCOR413    112 LFFPQHFPDWLEMPGSLILLTVVSEHFLAHHIRGTW--IGTVISLIFIGCYLLOEHIRASG
HvCOR413    117 LFFPRHFDPDWLELPGSLILLTVVAPSLFAHFRNDL--VGVFICLAIGCYLLOEHIRVSG

BRADICOR413  177  GFREAFRKANGVSNTIGIVLLFIYPVWALVLMFL
ZmCOR413    179  GFRNAPFRKNGVSNSIGILLFIYPVWAGVLQVL
OsCOR413    177  GFRNAPFRKNGVSNSIGILLFIYPVWALVNFPL
TaCOR413    177  GLKEAFCKPNGVSNTIGILLFIYPVWAVVMWFL
AtCOR413    170  GFRNSFTQPRGVSNTLGIILLFIYPVWALIVRM
HvCOR413    175  GFREAFRKANGVSNTIGIVLLFIYPVWVLVWFL

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