

Supplementary Figure S1: Protein alignment of novel PINA sequences from Elymus species with wild type from T. aestivum (bread wheat). Black boxes indicate main amino acid motif differences between the sequences. Those in the green boxes indicate same amino acid type (i.e. hydrophobic or hydrophilic) change.





Supplementary Figure S4: Nucleotide alignment of Pin a sequences for Agropyron cristatum, Agropyron mongolicum, and Agropyron repens. Number refers to clone number.


Supplementary Figure S5: Protein alignment of PINA sequences for Agropyron cristatum, Agropyron mongolicum, and Agropyron repens. Number refers to clone number.


Supplementary Figure S6: Nucleotide alignment of Pin a sequences for Pseudoroegneria spicata, Psathyrostachys juncea, Thinopyrum bessarabicum and Thinopyrum scripeum. Number refers to clone number
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Supplementary Figure S12: Nucleotide alignment of Pin b sequences for Elymus trachycaulus subsp. subsecundus and Elymus wawawaiensis. Number refers to clone number.




## 





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Supplementary Figure S17: Protein alignment of PINB-2 (variant) sequences for Agropyron repens, Elymus repens, Elymus angulutus, Elymus nutans, Elymus burchan-buddae and Elymus sibiricus. Number refers to clone number.


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Supplementary Figure S22: Nucleotide alignment of Gsp-1 sequences for Elymus trachycaulus subsp. subsecundus and Elymus wawawaiensis. Number refers to clone number.





