

Table 1 Suppl. Primers used in this study

Primer name	Forward sequence (5'-3')	Reverse sequence (5'-3')
<i>Actin 1</i>	ATCCTGACGGAGCGTGGTTAC	CCTAATATCCACGTCGCACTTC
<i>Actin 2</i>	ACCTTCAACACCCCTGCTAT	CACCATCACCAGAGTCCAAC
<i>Bd 1</i>	CGGATCCGATGGGCATCTCCA	CGAGCTCGCTAGTAGTAGTFAATC
<i>Bd 2</i>	ATCTCCAGCATGCCGGCGCC	ATCGCGAAGATGTGCTCGTC
<i>Bd 3</i>	CGACGAGCACATCTTCGCGA	TGGCCAGGCACACGCGGCG
<i>HPT</i>	TAGGAGGGCGTGGATATGTC	TACACAGCCATCGGTCCAGA

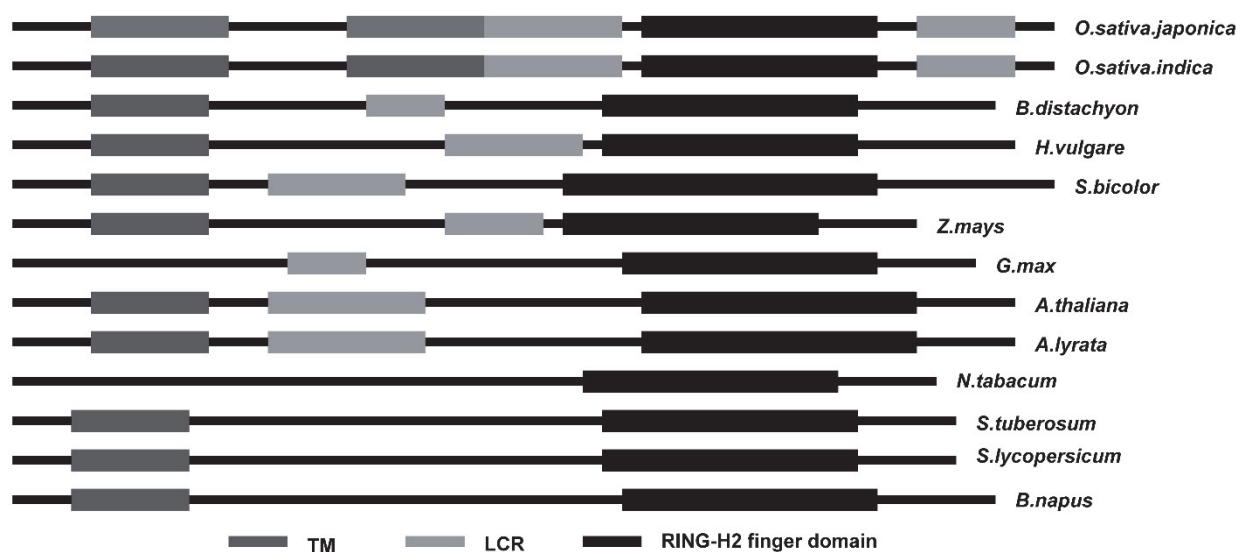


Fig. 1 Suppl. Protein motif prediction of *Brachypodium distachyon* RING-H2 (BdRHP1) and homologs. TM indicates Transmembrane motif, LCR indicate low complexity region

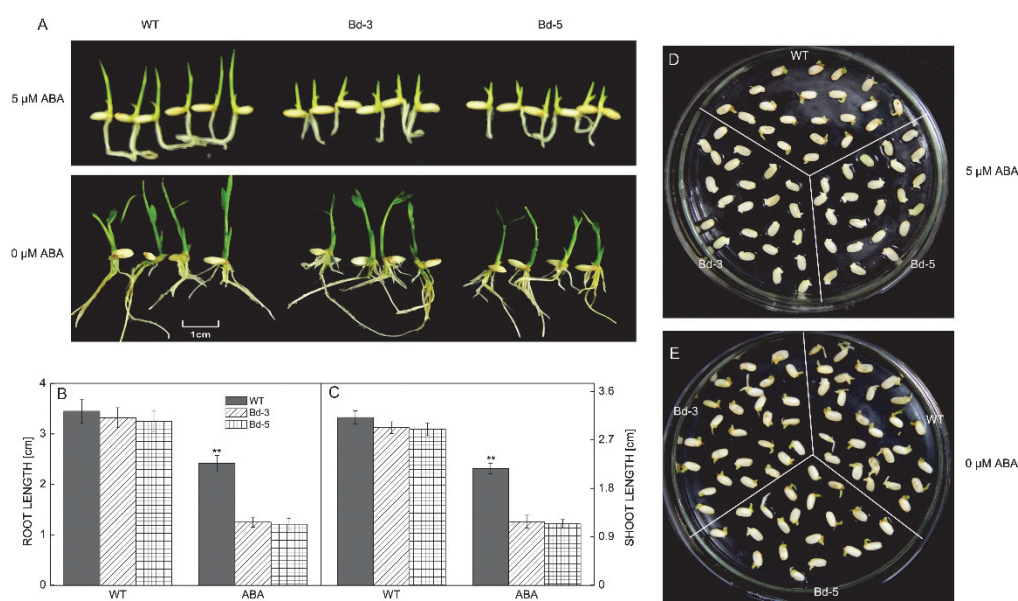


Fig. 2 Suppl. *A* - Seedling development of transgenic plants Bd-3 and Bd-5 and WT under 0 and 5 μ M abscisic acid (ABA) treatment. *B* - Root length of transgenic lines and WT at 0 and 5 μ M ABA. *C* - Shoot length of transgenic plants and WT at 0 and 5 μ M ABA. Means $\pm$ SEs from three independent experiments, *asterisks* indicate significant differences at $P < 0.05$ (*t*-test). *D,E* - Germination of transgenic plants and WT under 0 (*E*) or 5 μ M (*D*) ABA treatments.

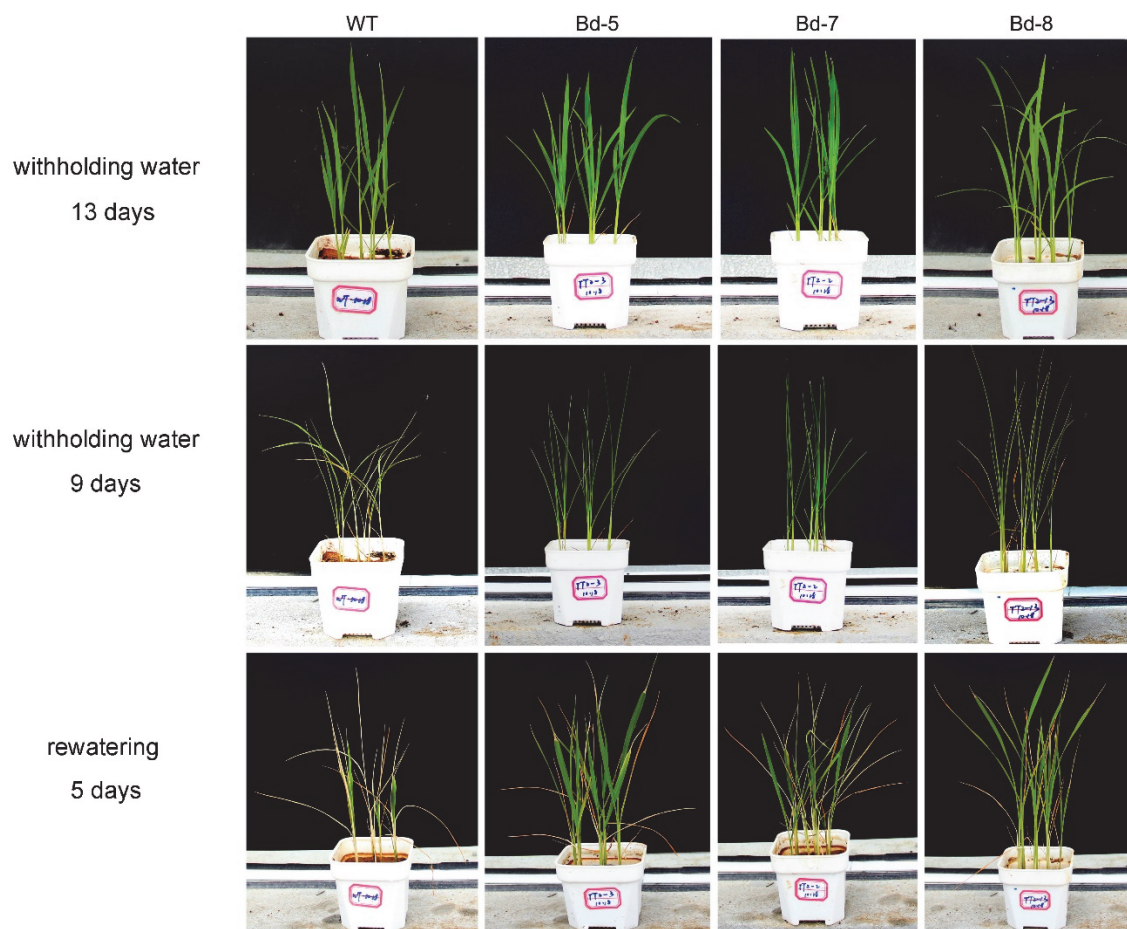


Fig. 3 Suppl. Overexpression of *BdRHP1* in rice enhances tolerance to drought stress.

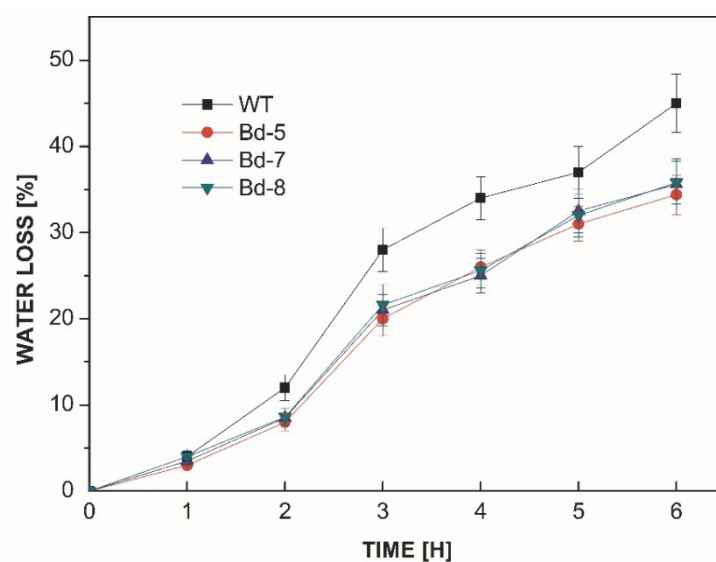


Fig. 4 Suppl. Differences in water loss curves between WT and transgenic plants. Means $\pm$ SEs from three independent experiments



Bd-5



WT

Fig. 5 Suppl. Morphology of transgenic line Bd-5 and WT in a reproductive stage.