

SUPPLEMENTARY MATERIALS

Analysis of Phylogeny and gene structure

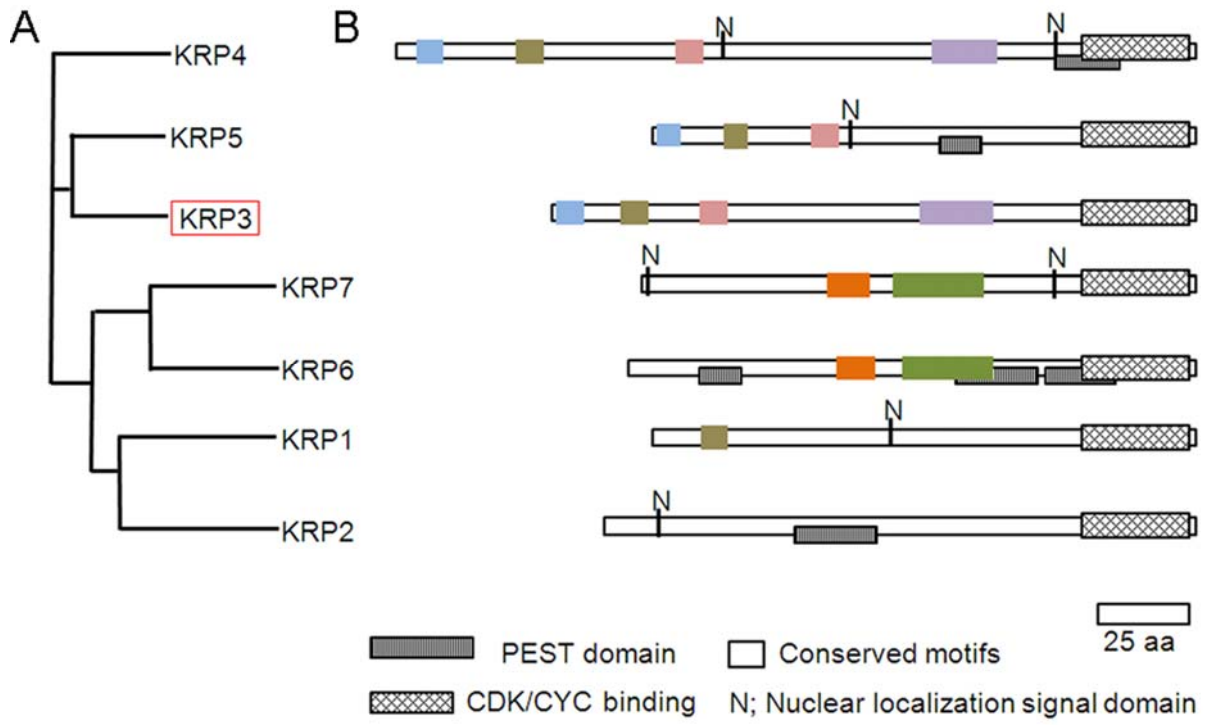
To analyze relationship of *Arabidopsis* seven KRPs, we carried out analysis of phylogeny and gene structure. We refer to nucleotide and amino acid sequences of seven KRPs from TAIR database (<http://www.arabidopsis.org>). Phylogenetic analysis was conducted using ClustalW2 from EMBL-EBI tools (<http://www.ebi.ac.uk>). Alignment and search of conserved sequence within KRP genes was performed with Uniprot (<http://www.uniprot.org/>) and MEME (http://meme.sdsc.edu/meme4_3_0/cgi-bin/meme.cgi). Putative nuclear localization signals (NLS) were identified through Psort (<http://psort.ims.u-tokyo.ac.jp/>).

Supplementary Table 1. Statistical analysis of growth inhibition by MG132 treatment of *Col-0* and *KRP3* OE transgenic plants.

	<i>Col-0</i>	<i>KRP3</i> OE-30	<i>KRP3</i> OE-45
Plant size (mm ²) after			
DMSO treatment	26.5 ± 3.1	15.6 ± 2.4	12.7 ± 3.0
MG132 treatment	16.7 ± 2.9	7.2 ± 2.0	5.3 ± 3.8
Reduction rate (%)	63.1	45.9	42.1

Wildtype (*Col-0*), *KRP3* OE-30, and *KRP3* OE-45 plants were germinated in MS media, then transferred and grown in MS media with DMSO or 100 μM MG132 dissolved in DMSO by 14 DAS. Plant size of 14 days old plants were measured by Image J. n=4

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4 **Supplementary Fig. 1.** Phylogeny and analysis of amino structures of KRP family in
5 *Arabidopsis thaliana*. (A) Phylogenetic tree of *Arabidopsis* KRPs. (B) Scheme of
6 motif in KRP protein.

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3 **Supplementary Fig. 2.** Schematic structure of *KRP3* T-DNA insertion mutants.

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