Supplemental Figure S1

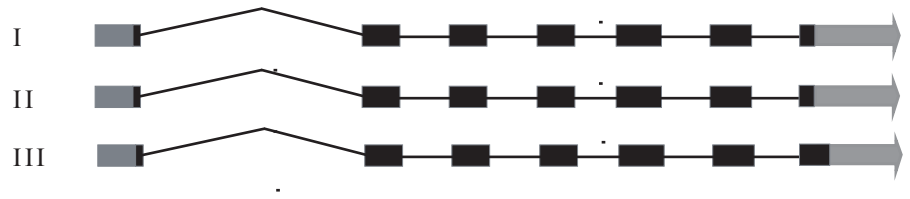
A

```
AtPDCD5 (I)          MADPELEAIRQRRMQELMARQGM-GKQGNQQNPEQEKQQEDAKREADERRQMMLSQVLSS 59
AtPDCD5 (II)         MADPELEAIRQRRMQELMARQGMQGKQGNQQNPEQEKQQEDAKREADERRQMMLSQVLSS 60
AtPDCD5 (III)        MADPELEAIRQRRMQELMARQGM-GKQGNQQNPEQEKQQEDAKREADERRQMMLSQVLSS 59
OsPDCD5              MADPELEAIRQRRMQELMAQHGA----ANPQNAGQQKAQEDAKQEAEERRQMMLAQILSS 56
HsPDCD5              MADEELEALRRQRLAELQAKHGD---------PGDAAQQEAKHREAEMR-NSILAQVLDQ 50
                     *** ****:*::*: ** *::*          . :   **  ::**: * : :*:*:*..

AtPDCD5 (I)          QARERIARIALVKPEKARGVEDVILRAAQMGQIVEKVSEERLITLLEQINSQTTKQTKVT 119
AtPDCD5 (II)         QARERIARIALVKPEKARGVEDVILRAAQMGQIVEKVSEERLITLLEQINSQTTKQTKVT 120
AtPDCD5 (III)        QARERIARIALVKPEKARGVEDVILRAAQMGQIVEKVSEERLITLLEQINSQTTKQTKVT 119
OsPDCD5              EARERLSRIALVKPDKARGVEDVLLRAAQSGGISEKVSEERLISLLEQINTHTSKQTKVT 116
HsPDCD5              SARARLSNLALVKPEKTKAVENYLIQMARYGQLSEKVSEQGLIEILKKVSQQTEKTTTVK 110
                     .** *::.:*****:*::.**: ::: *: * : *****: ** :*::::. :* * *.*.

AtPDCD5 (I)          YQRRRGV-------DDD--------------- 129
AtPDCD5 (II)         YQRRRGV-------DDD--------------- 130
AtPDCD5 (III)        VSTNGAVGWTTIRKEEEYYDVLCISMEISLLC 151
OsPDCD5              IQRRRSVLD-----DDD--------------- 128
HsPDCD5              FNRRKVMDSD---EDDDY-------------- 125
                      . .  :       :::
```

B

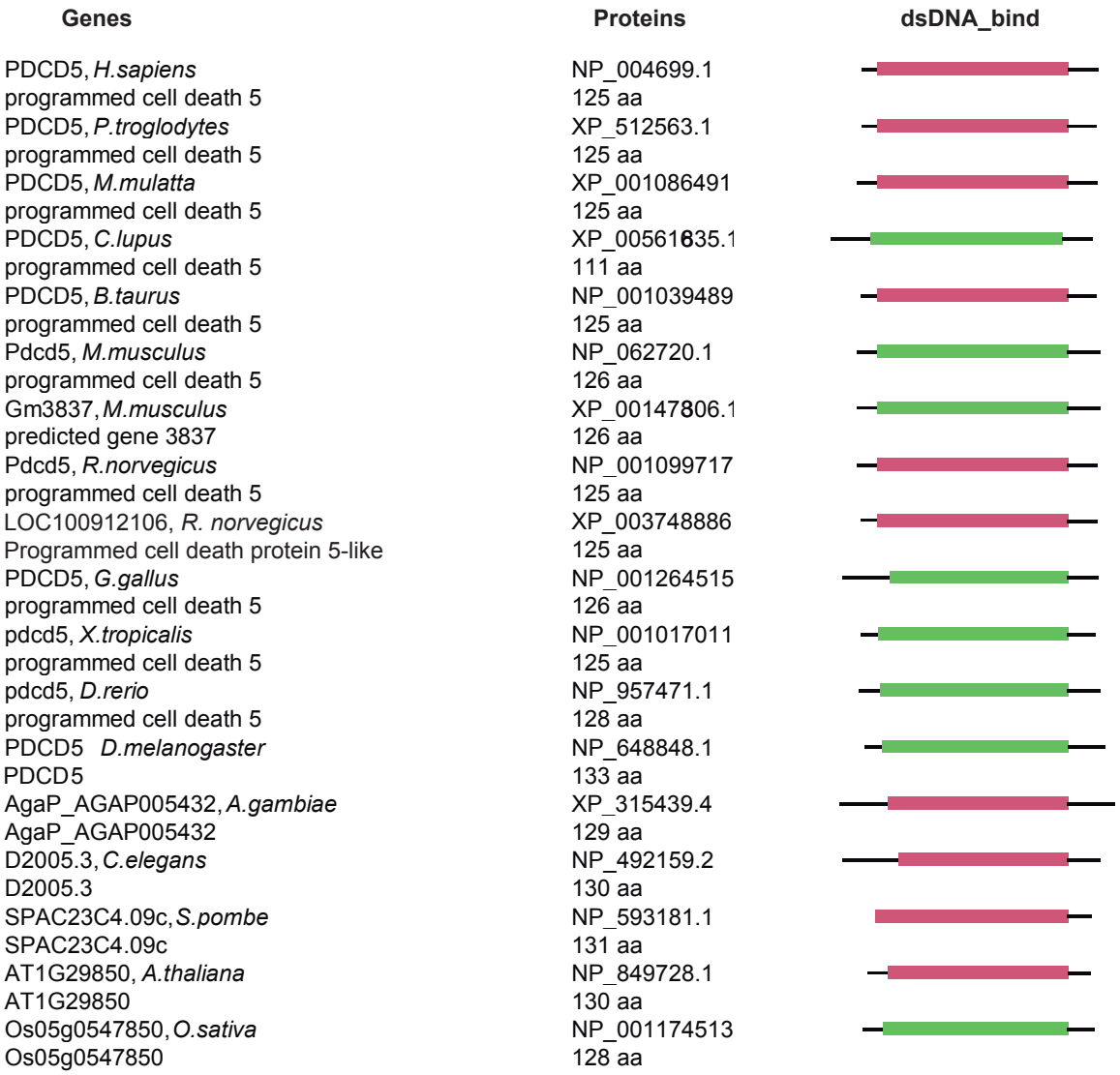
	*Os*PDCD5	*Hs*PDCD5	*At*PDCD5 (III)	*At*PDCD5 (II)
***At*PDCD5 (I)**	76.6	43.2	93.0	100
***At*PDCD5 (II)**	76.6	44.0	92.3	
***At*PDCD5 (III)**	71.9	40.0		
***Hs*PDCD5**	45.9			

C



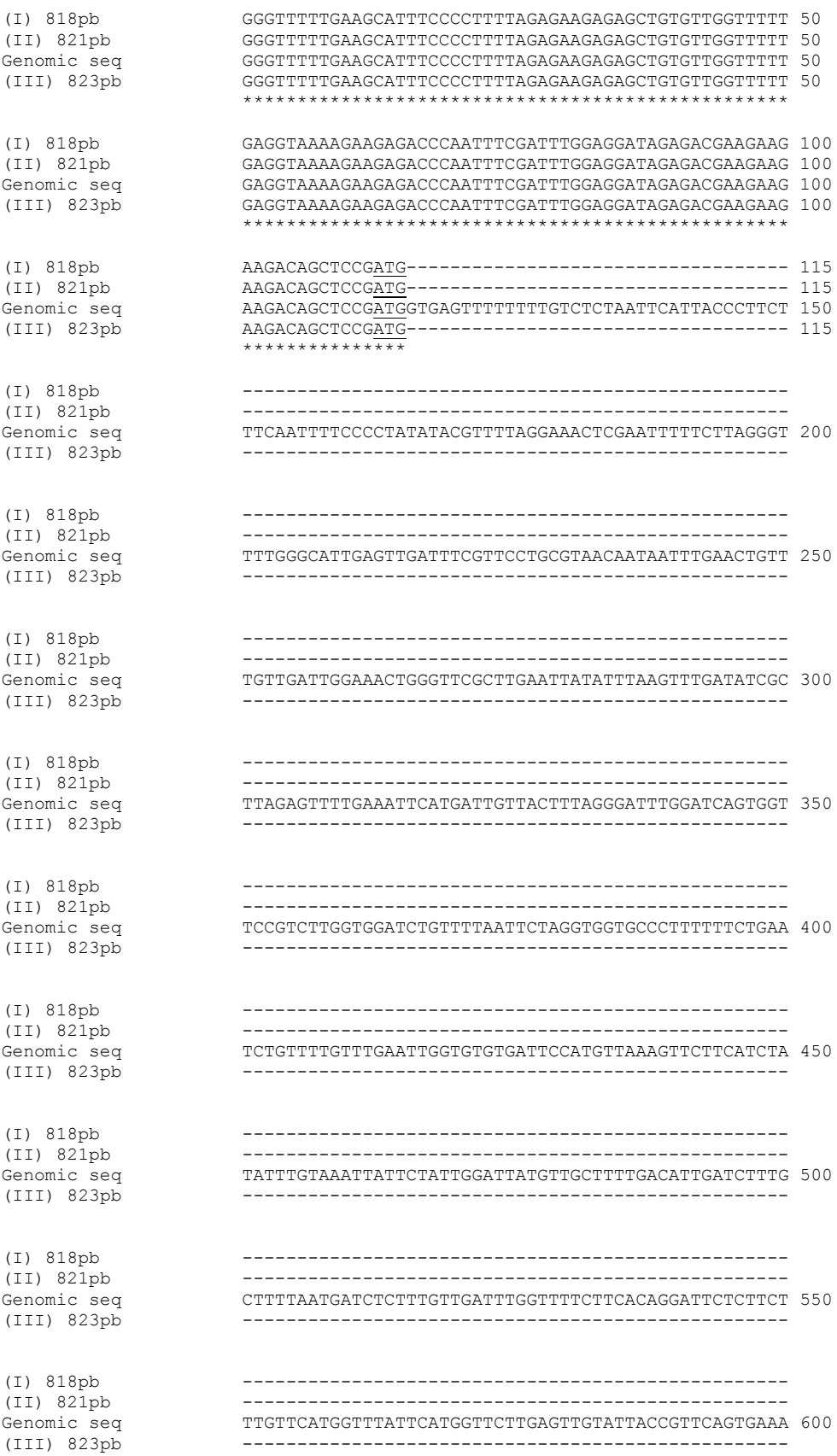
PDCD5 proteins and different *PDCD5* mRNA spliced forms from *A. thaliana*. (A) Amino acid sequences alignment of the predicted different *At*PDCD5 spliced forms with PDCD5 proteins from *O. sativa* and humans. The sequences were aligned using the Clustal W2 program. Dashes (-) indicate spaces introduced to promote optimal alignment, perfect matches are indicated by an asterisk (*), high amino-acid similarities by double dots (:), and weak similarities by a single dot (·).The proposed double-stranded DNA-binding domain is highlighted in grey. (B) Percentage of amino acid sequence similarity between different *At*PDCD5 spliced forms and PDCD5 proteins from *O. sativa* and humans. (c) Scheme of different *At*PDCD5 mRNA spliced forms. Exons are represented by boxes, grey and black boxes indicate UTR and coding regions, respectively, and black lines represent non-coding regions.

Supplemental Figure S2



Representative scheme of the double strand DNA binding domain conserved in PDCD5 proteins from eukaryotic species. The scheme was obtained using the HomoloGene tool (NCBI) that identifies homologs among the annotated genes of several sequenced eukaryotic genomes. Double-stranded DNA-binding domain is represented by green (pfam01984) and pink (cl00928) boxes.

Supplemental Figure S3



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(III) 823pb         ----------------------------------------------------


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(III) 823pb         ----------------------------------------------------


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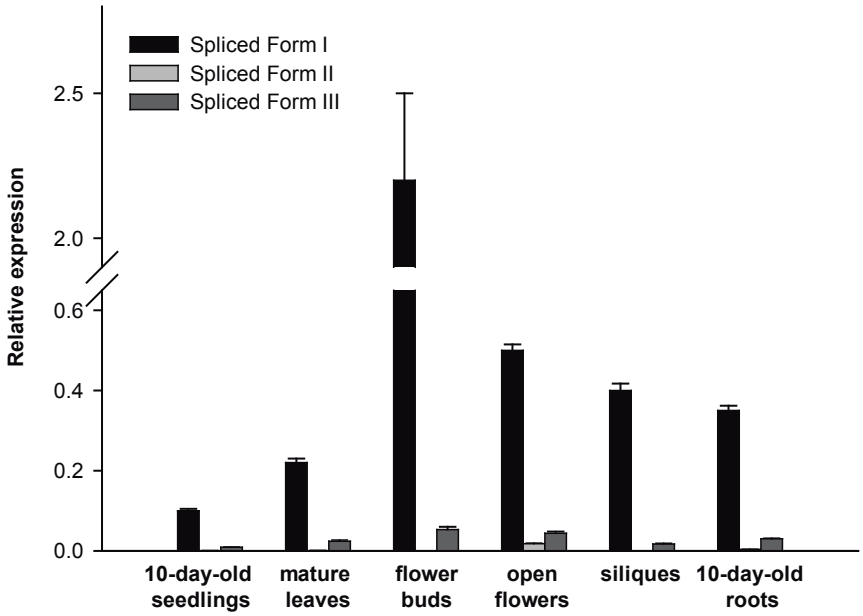
Alignment of the *AtPDCD5* genomic sequence with the three *AtPDCD5* mRNA spliced forms. Matches are indicated by an asterisk (*), sequence differences between the mRNA spliced forms are marked in gray.

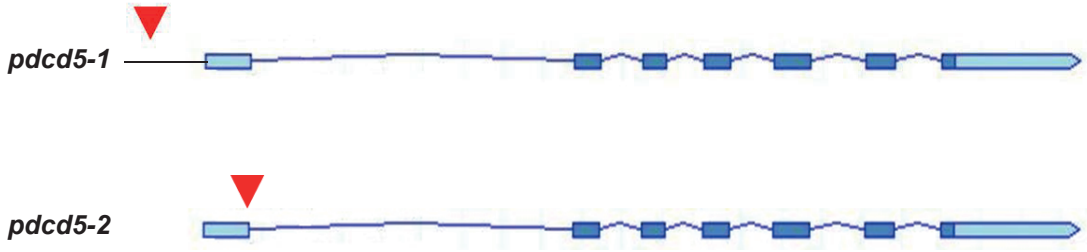
Supplemental Figure S4



AtPDCD5 spliced forms I, II and III expression analysis in Arabidopsis. *AtPDCD5* spliced forms expression levels in different Arabidopsis tissues determined by qRT-PCR. The relative *AtPDCD5* spliced forms I, II and III transcript abundance was analyzed in seedlings (10-day-old), mature leaves (28-day-old), flower buds, open flowers, siliques and roots (10-day-old). The means of the results obtained using three independent RNAs as a template are shown, the error bars indicate the S.D. of the samples. Each reaction was normalized using the Ct values corresponding to the *UBQ10* mRNA.

Supplemental Figure S5

A



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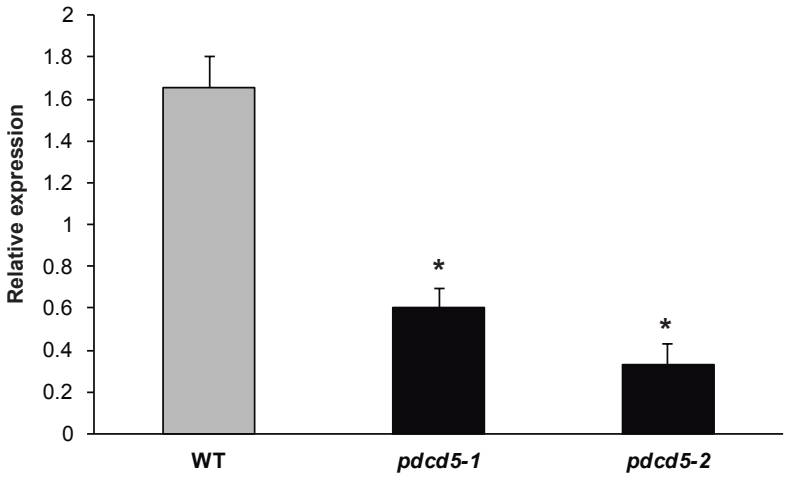
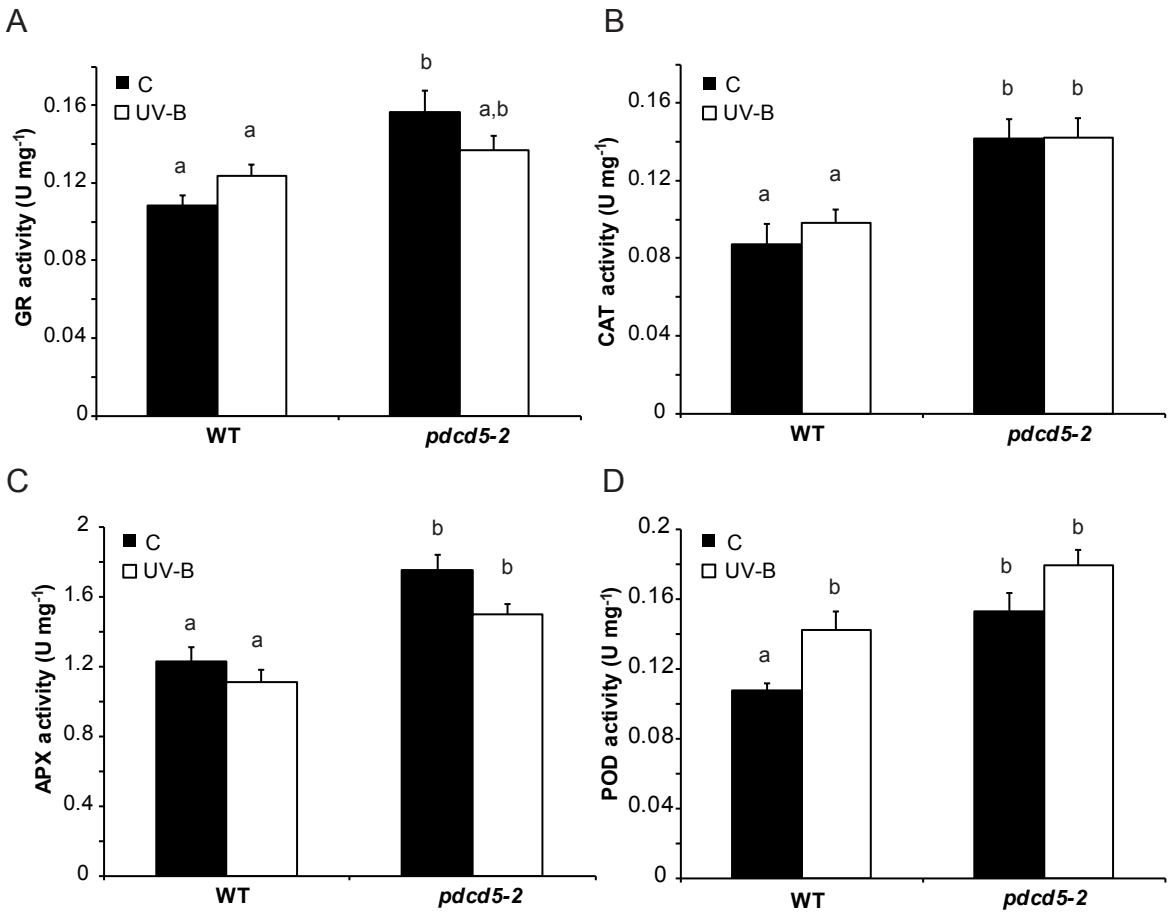


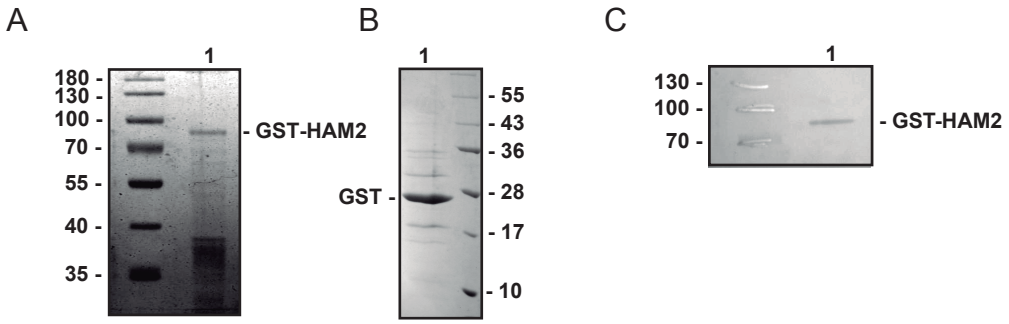
Characterization of *pdcd5* mutant lines. (A) Structure of *A. thaliana PDCD5* gene. Boxes indicate exons (coding regions are in blue, while 5´and 3´UTRs are in light blue), and blue and black lines represent introns and promoter regions, respectively. The open triangles show the T-DNA positions. (B) *PDCD5* transcript abundance in T-DNA lines and wild-type (WT) plants analyzed by qRT-PCR. The means of the results obtained using three independent RNAs as a template are shown, the error bars indicate the S.D. of the samples. Each reaction was normalized using the C_t values corresponding to the *UBQ10* mRNA. For each *pdcd5* mutant line analyzed, asterisks over the bars indicate statistically significant differences between wild type and *pdcd5* mutant plants applying Student's *t*-test ($P < 0.05$).

Supplemental Figure S6



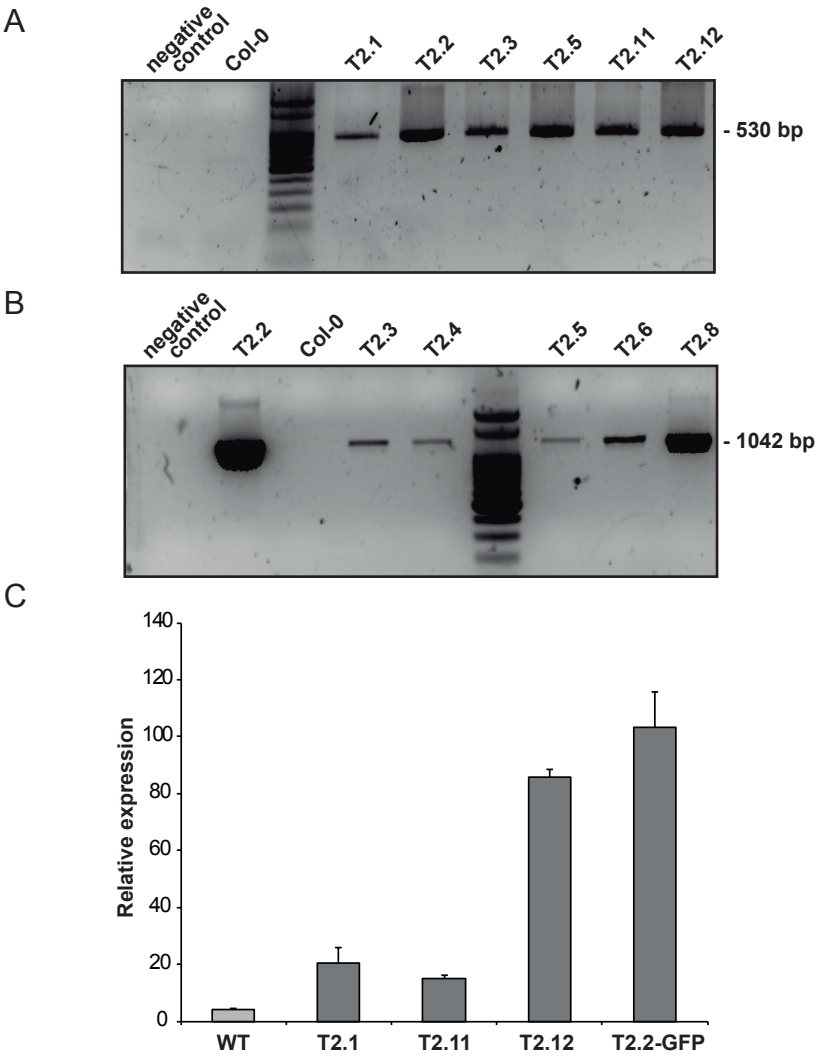
Analysis of antioxidant enzyme activities in wild type (WT, Col-0) and *pdcd5* mutant plants under control conditions and after UV-B treatment**.** Glutathione reductase (GR) (A), catalase (CAT) (B), ascorbate peroxidase (APX) (C) and peroxidase (POD) (D) activities were determined under control conditions (C) and after a 4h-UV-B treatment at an intensity of 0.2 W m^{-2}. Results represent the average ± S.E.M. of three independent biological replicates. Statistical significance was analyzed using ANOVA, for each sample analyzed, different letters indicate significant difference with $P < 0.01$.

Supplemental Figure S7



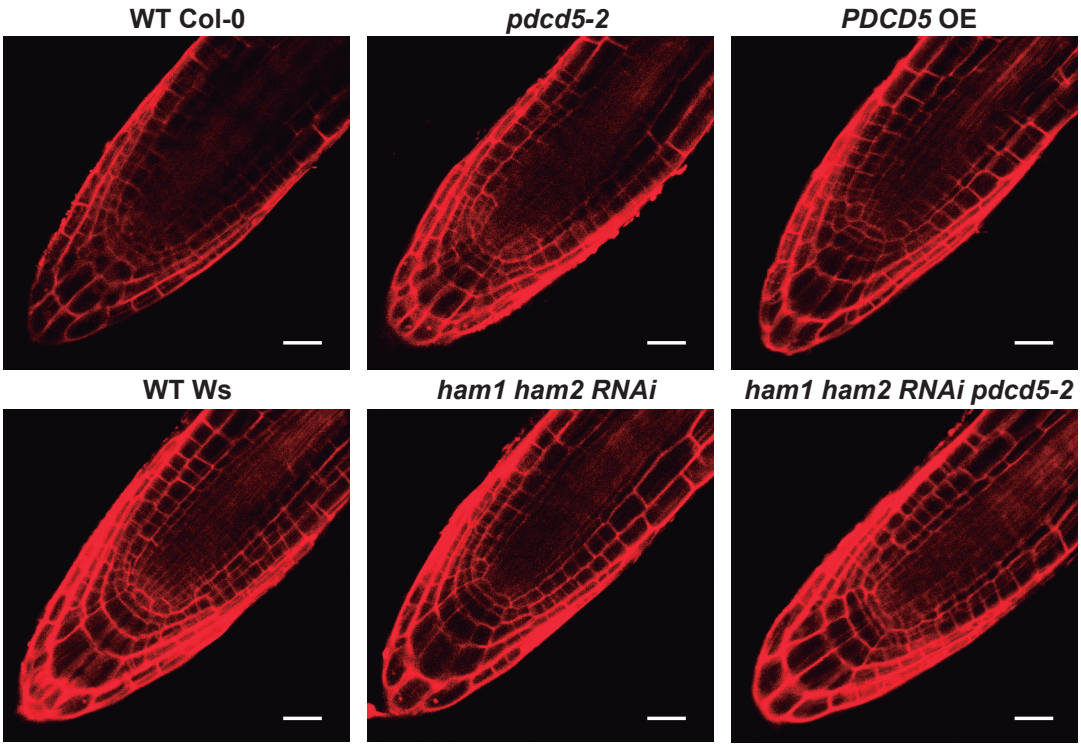
Recombinant expression of GST-*At*HAM2 and GST proteins. (A) SDS-PAGE analysis (10%) of the recombinant purified GST-*At*HAM2 fusion protein (lane 1, 3 µg). (B) SDS-PAGE analysis (15%) of the recombinant purified GST protein (lane 1, 6 µg). (C) Immunoblot analysis of the recombinant purified GST-*At*HAM2 fusion protein (lane 1) using anti-GST antibodies. One µg of the purified protein was loaded. The numbers on the sides of gels indicate the molecular mass in kDa.

Supplemental Figure S8



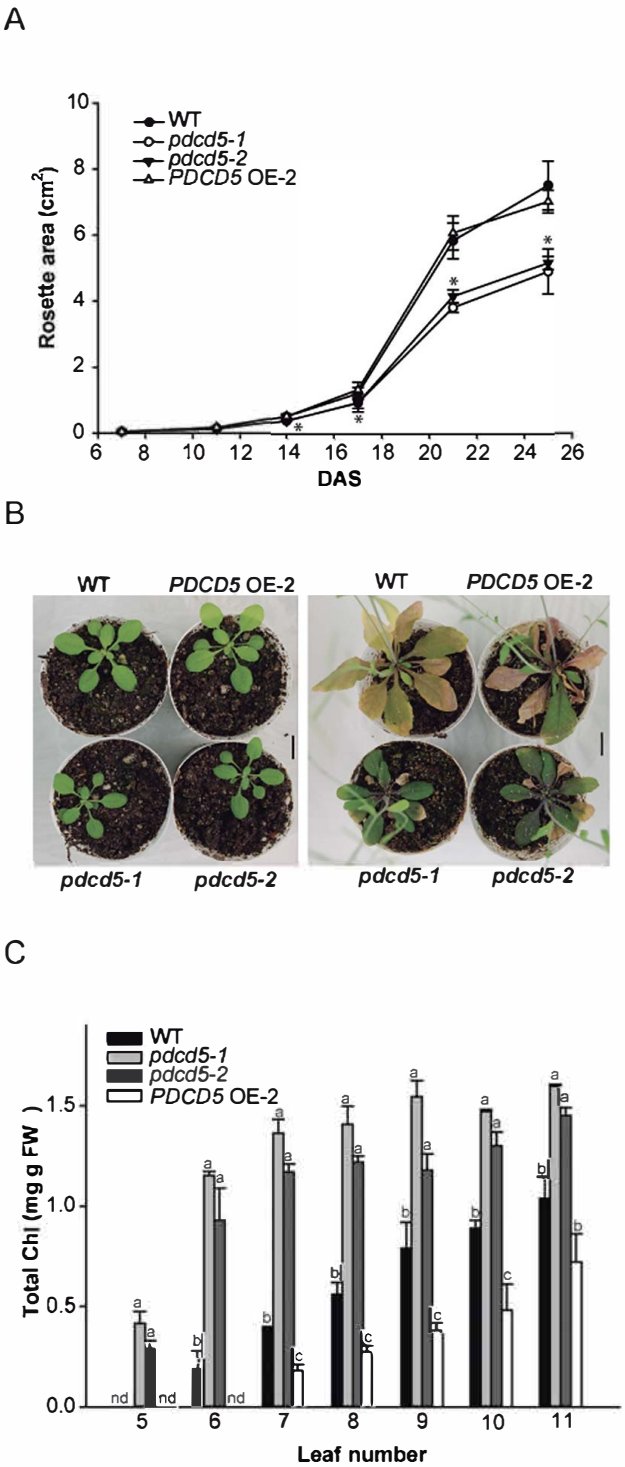
Analysis of Arabidopsis transgenic plants expressing *AtPDCD5-GFP* and *AtPDCD5.* The presence of the *Pro$_{35S}$:AtPDCD5* (A) and *Pro$_{35S}$:AtPDCD5-GFP* (B) transgenes was analyzed by PCR on genomic DNA from non-transformed plants (WT, Col-0) and six independent lines (indicated by numbers) for each *Pro$_{35S}$:AtPDCD5* and *Pro$_{35S}$:AtPDCD5-GFP* transgenic plants. The negative control was done without genomic DNA. Positive PCR reactions amplified 530 and 1042 bp products for *Pro$_{35S}$:AtPDCD5* (A) and *Pro$_{35S}$:AtPDCD5-GFP* (B) transgenic plants, respectively. (C) Transcript levels of *AtPDCD5* in transgenic plants analyzed by qRT-PCR, the expression level of *AtPDCD5* in wild type plants (WT, Col-0) is shown. Each reaction was normalized using the C_t values corresponding to the *UBQ10* mRNA.

Supplemental Figure S9



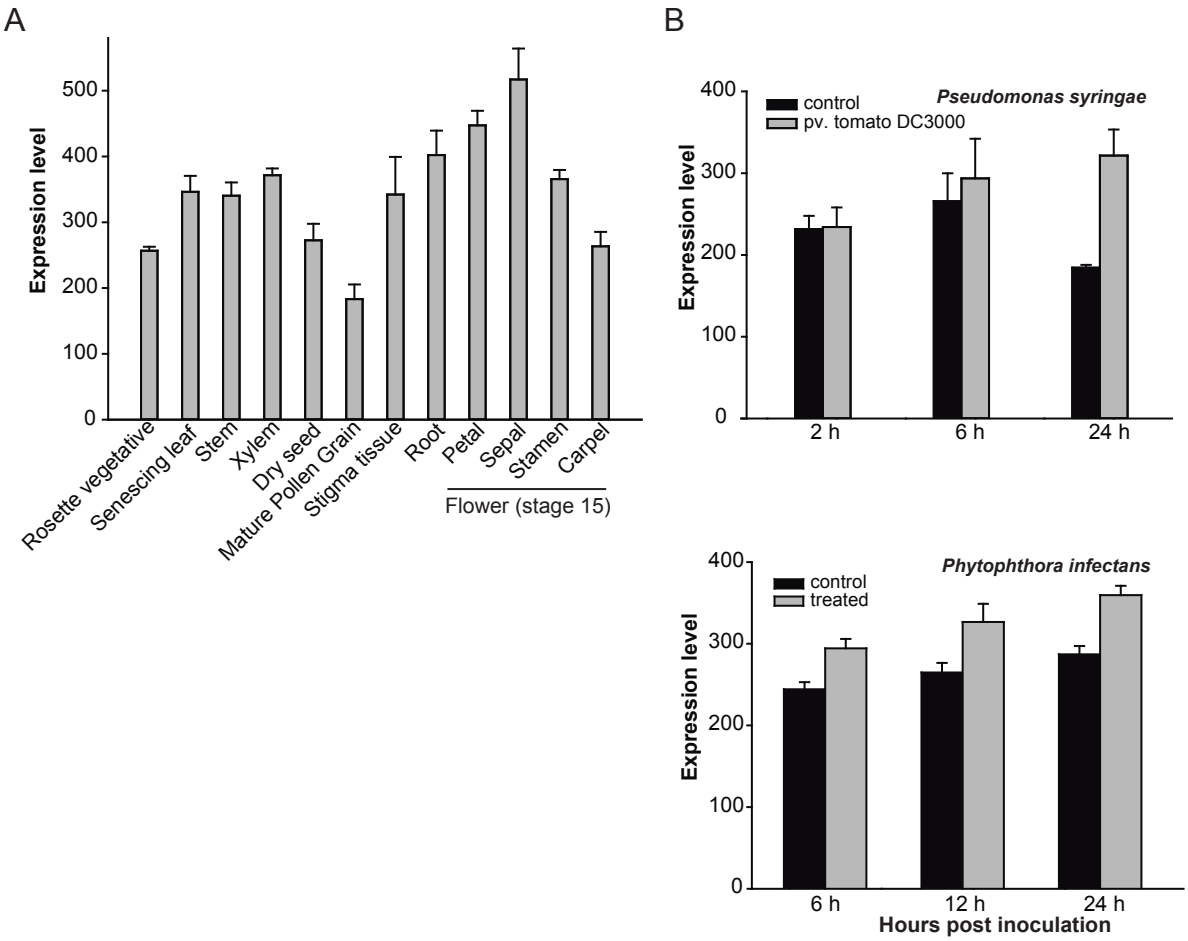
Images of root tips from WT (Col-0, Ws), *pdcd5-2*, *ham1ham2* RNAi, and *ham1ham2* RNAi/*pdcd5* mutants and *PDCD5* overexpressing plants (*PDCD5* OE) under control conditions (C) without UV-B. Bar corresponds to 50 µm.

Supplemental Figure S10



Phenotypic analysis of *pdcd5* mutants and transgenic *PDCD5* OE plants. (A) Rosette area of *pdcd5* mutants and transgenic *PDCD5* OE plants measured every 3-4 days from day 7-25 after stratification (DAS). Asterisks indicate statically significant differences ($P < 0.01$, one-way Anova test). (B) Col-0 (WT), *pdcd-1*, *pdcd5-2* mutants and *PDCD5* OE plants at 21 (left) and 40 (right) DAS. Scale bar: 1 cm. (C) Total chlorophyll content in leaves of Col-0 (WT), *pdcd-1*, *pdcd5-2* mutants and *PDCD5* OE plants at 40 DAS. For each leaf, statically significant differences between plants are marked with different letters ($P < 0.05$, one-way ANOVA test).

Supplemental Figure S11



Relative expression level of *AtPDCD5* in different tissues (A) and in leaves from plants exposed infected with *Pseudomonas syringae* and *Phytophthora infestans*, B). Microarrays data were retrieved from the Arabidopsis electronic Fluorescent Pictograph (eFP) Browser (Winter et al., 2007).

Supplemental Table S1. Primers used for cloning, RT-qPCR and screening.

Name	Sequence
F-*BamH*I-*PDCD5-OE*	5'GAGTACGGATCCATGGCTGATCCTGAACTA3'
R-*Sal*I-*PDCD5-OE*	5'CGCGGCGTCGACTTAAGTGAACTCACTAAC3'
F-*Kpn-PDCD5-GFP*	5'GAGTACGGTACCATGGCTGATCCTGAACTA3'
R-*BamH*I-*PDCD5-GFP*	5'TATGGATCCATCGTCGTCCACCCCACGGCG3'
F-*AtPDCD5*-1	5'GGCTCGACAAGGCATGGG3'
R-*AtPDCD5*-1	5'ACGGCGCCGTTGGTACGT3'
F-*AtPDCD5*-2	5'GGCTCGACAAGGCATGCA3'
R-*AtPDCD5*-2	5'CGGCGCCGTTGGTACTTAC3'
F-*AtPDCD5*-sc	5'TTCCCTGAGACGAATCCA3'
R-*AtPDCD5*-sc	5' CGCAGGAACGAAATCAAC3'
$35S_{prom}$	5'GAGGAGCATCGTGGAAAAAGA3'
R-*GFP*	5'CTGCAGTCAAGCTTTGTATAGTTCATC3'
F-*Hind*III-*AtPDCD5*$_{prom}$	5'GCGAAGCTTCCCCTTGAAGTCTTAC3'
R-*BamH*I-*AtPDCD5*$_{prom}$	5'CGGGGATCCAAAAAAACTCACCATC3'
F-*AtHAM2-Eco*RI	5'CACCAGAATTCATGGGATCGTCAGCGAATACAGAAACCAA3'
R-*AtHAM2-Xho*I	5 TGTCACTCGAGTTAACTCTGGTCCTTGTAAGGTGTCCAA3'
F-*AtUBQ10*	5'AAGCAGCTTGAGGATGGAC3'
R-*AtUBQ10*	5'AGATAACAGGAACGGAAACATAGT3'
F-AtCDPK3	5'-CGCTGAGAACCTTTCTGAAG-3'
R-AtCDPK3	5'-CCATCTCCATCCATATCAGC-3'
LB-SALK	5'-GTCCGCAATGTGTTATTAAGTTGTC-3'
F-AtUVR2	5'-GACCCGAGTGGATATGTTGG-3'
R-AtUVR2	5'-GAGCTGTTCTTCAGCTTTCC-3'
F-AtUVR7	5'-TACATTCGGGTCTCTTGCTC-3'
R-AtUVR7	5'-TCCTCGTCTTCTTCAACAGG-3'
F-AtUVH6	5'-CAAAGGCTGATTATGGGATG-3'
R-AtUVH6	5'-CACCAGTCTCAGCCATCTTC-3'