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online data

SUPPLEMENTARY ONLINE DATA

A new principle of oligomerization of plant DEG7 protease based on interactions of degenerated protease domains

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Table S1 DEG7 orthologues and their accession numbers (SwissProt Protein Database)

*JGI protein ID, no entry in SwissProt Database; **GenBank® accession number, no entry in SwissProt Database.

Organism	Accession number
Arabidopsis thaliana	Q8RY22
Aspergillus nidulans	Q5B1Z4
Aspergillus niger	A5AB13
Aspergillus oryzae	Q2TYB1
Aureococcus anophagefferens	322*
Candida albicans	Q5A946
Chlamydomonas reinhardtii	A8JH35
Chlorella sp. NC64A	37665*
Emiliania huxleyi (1)	452178*
Emiliania huxleyi (2)	245118*
Gibberella zeae (1)	UPI000023D1E1
Gibberella zeae (2)	UPI000023F481
Glycine max	AK287315**
Magnaporthe grisea	A4RJH4
Micromonas pusilla	35996*
Neosartorya fischeri	A1DP85
Neurospora crassa	Q7S9D2
Oryza sativa	B9F2C1
Penicillium marneffei	B6QAL6
Phaeosphaeria nodorum	Q0UY70
Physcomitrella patens (1)	A9TIB2
Physcomitrella patens (2)	A9RQ61
Phytophtora capsici	27218*
Phytophtora soja (1)	133655*
Phytophtora soja (2)	199402*
Podospora anserina	B2ASP9
Populus trichocarpa (1)	B9GV35
Populus trichocarpa (2)	B9H390
Populus trichocarpa (3)	B9H391
Pyrenophora tritici-repentis	B2WNT3
Saccharomyces cerevisiae	P53920
Schizosaccharomyces japonicus (1)	B6K3R7
Schizosaccharomyces japonicus (2)	B6JWG1
Schizosaccharomyces pombe (1)	Q9P7S1
Schizosaccharomyces pombe (2)	O74325
Sclerotinia sclerotiorum	A7E9G4
Selaginella moellendorffii	165477*
Solanum lycopersicum	AK321684**
Sorghum bicolor	5004613*
Vanderwaltozyma polyspora	A7TGI3
Volvox carteri	79278*

Table S2 List of oligonucleotides used as PCR primers

Name	Sequence (5′→3′)
0724	GGTACTAAAGGTGGTTCAGCTGGTTCTCCCGTCATTG
0725	CAATGACGGGAGAACCAGCTGAACCACCTTTAGTACC
0734	TATGTCGACTTACTGCAAGGCTTTC
0740	CACCATGGGAGATCCGTTGGA
0747	GCGCCGCGGTTACTGCAAGGCTTTC
0765	GCGTTACTTATCCGTCCGCGAGTC
0767	GCGTTATGAGTGTAAATCTTGTACTGATA
0771	GCGTTATTGTTTCTTTGCTTCTGAGCC
0774	CACCTCCGTTGCCACCGCTGAAGATTG
0775	CACCGATAAGCCAAAAGCAGTTCATATTC
0776	CACCTCAAAAGCCCGGAGTTTTGGTC
0777	CACCGAACCCATGCATGAAGTGAATG
0793	CACCGGCAGTGAATTTAAATCTGATG
0797	CGCTTATCCATTTCCACCGGTTATGATT
0799	CGCTTAATCTTGTTTCAGAGTCAATACTC

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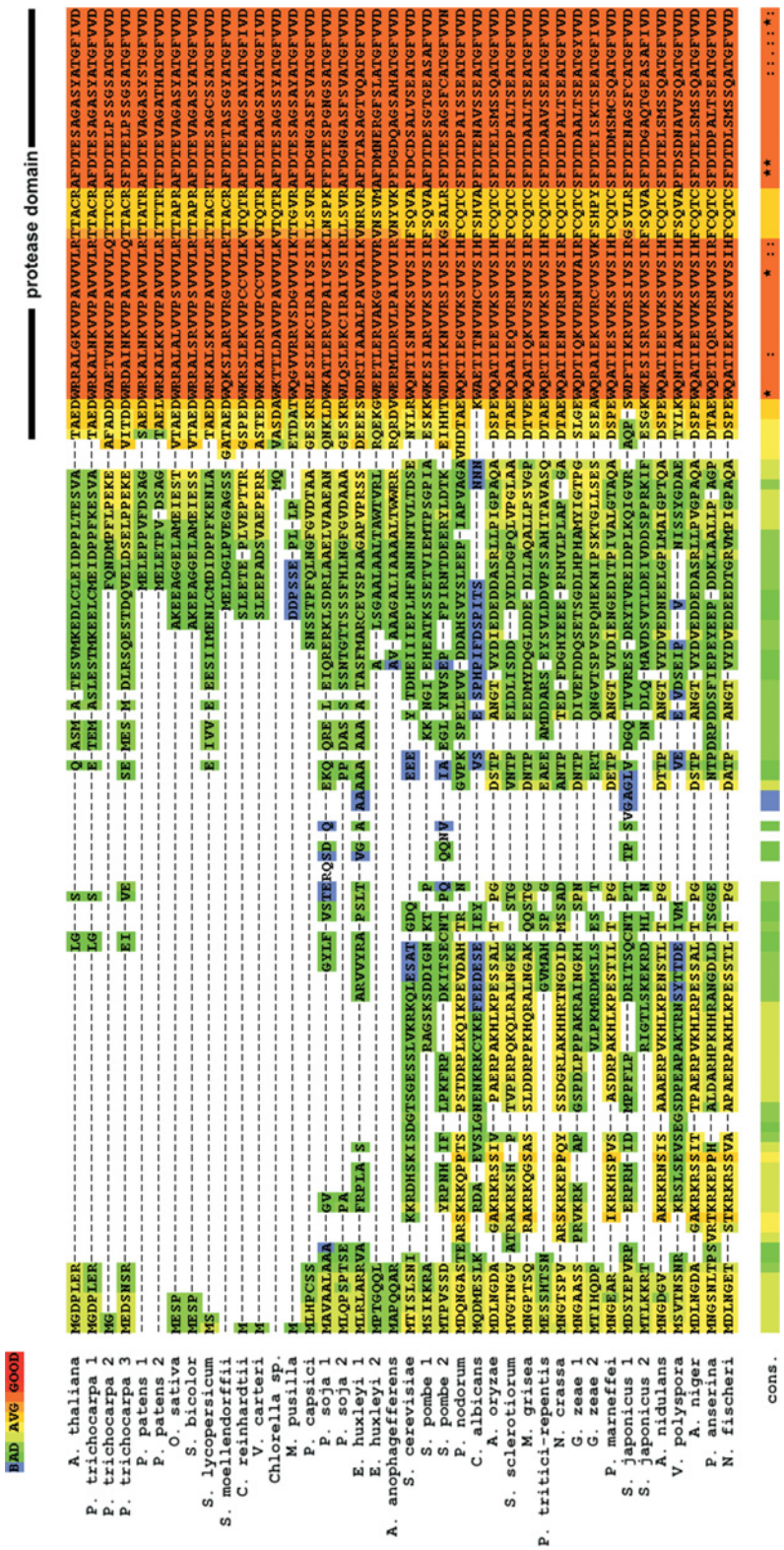

Figure S1 M-Coffee multiple sequence alignment of the amino acid sequences of the DEG7 orthologues used in the present study

The approximate position of the domains (as determined by using the InterProScan and HHpred prediction servers) are indicated by black bars on top of the alignment. Conserved residues of catalytic triad are shown as blue letters above the alignment. For full names of organisms, see Supplementary Table S1. cons., consensus; *, identity; :, conserved replacement; ., non-conserved replacement.

Continues...

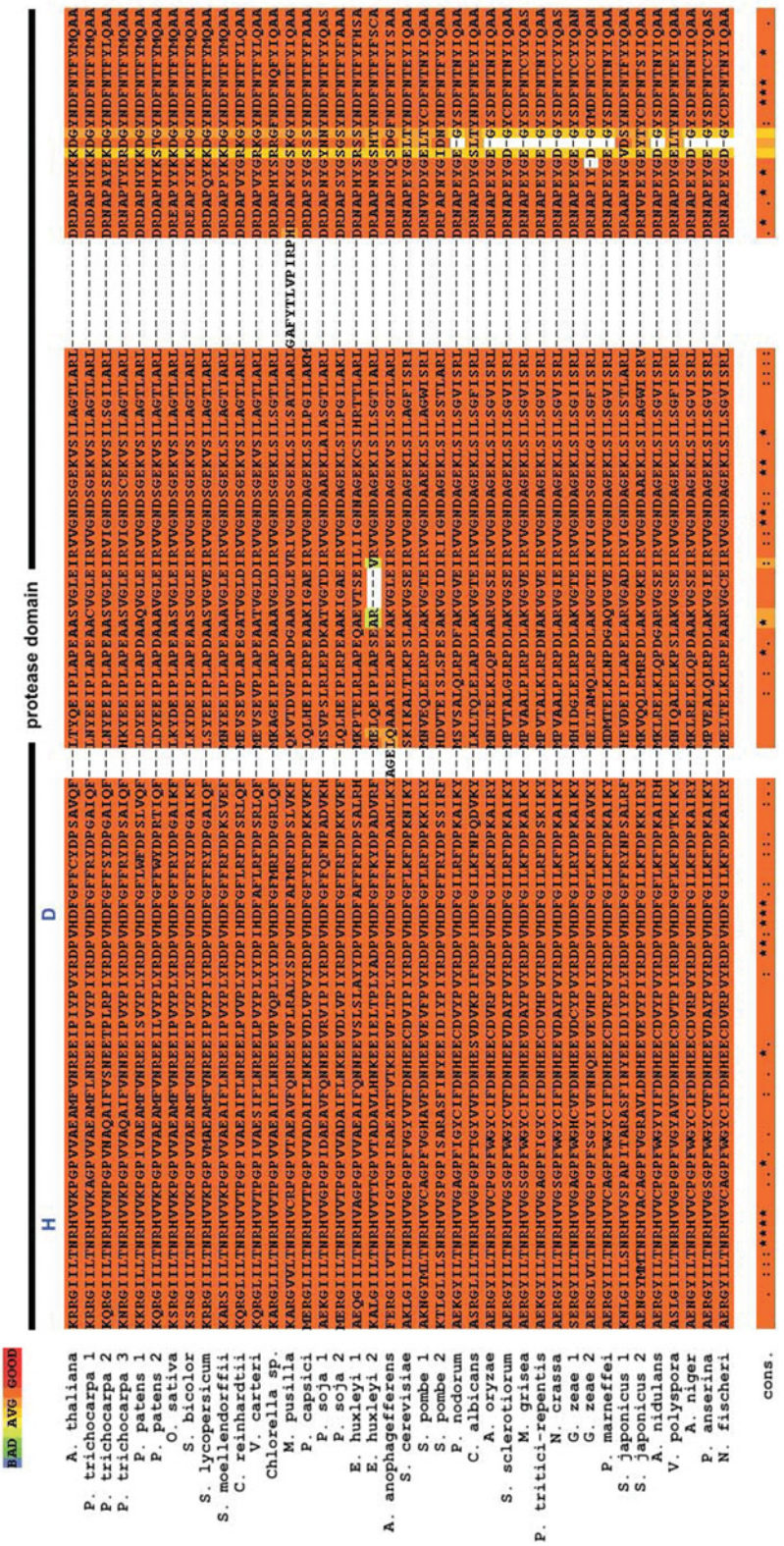

Figure S1 Continued

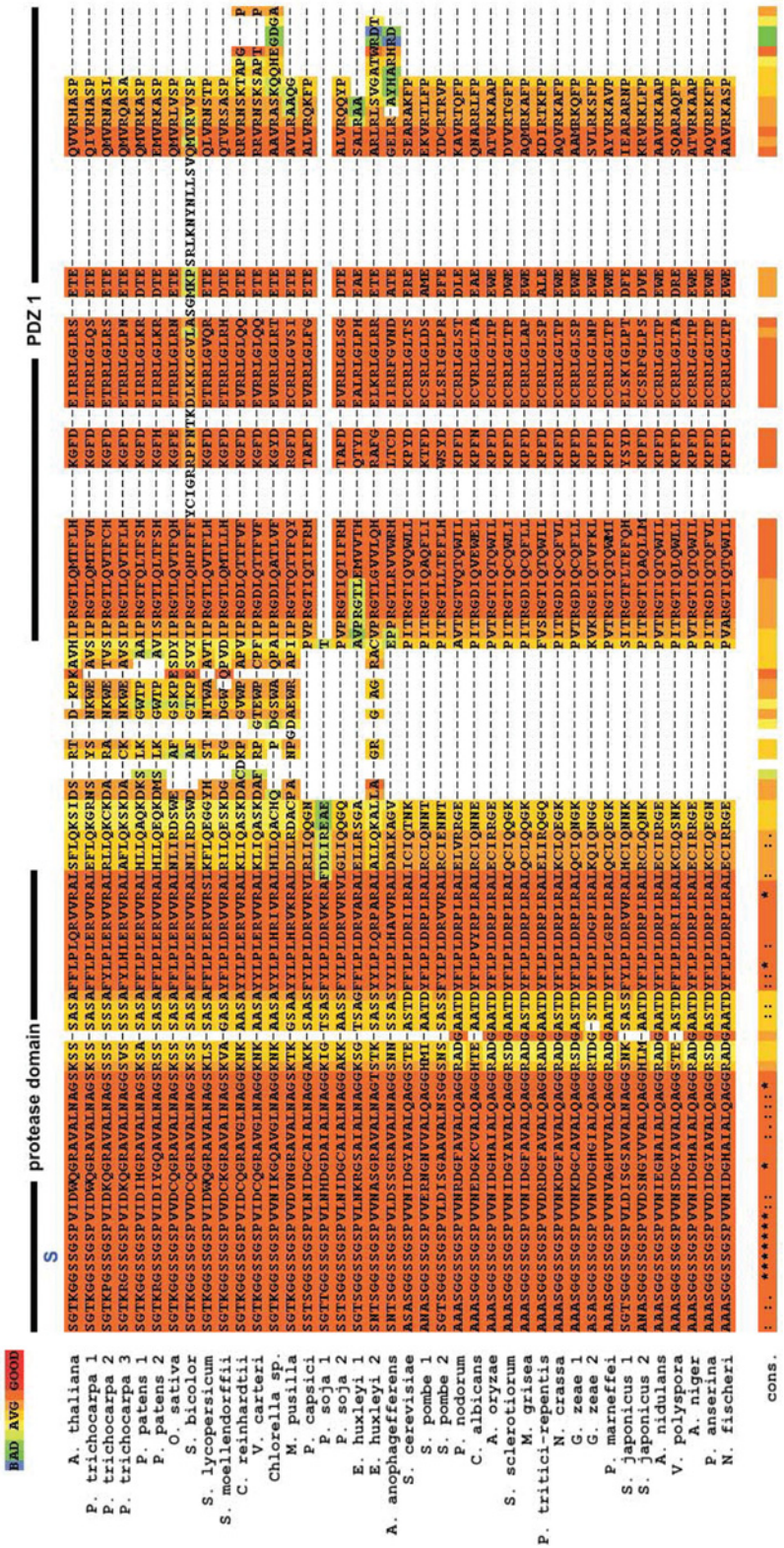

Figure S1 Continued

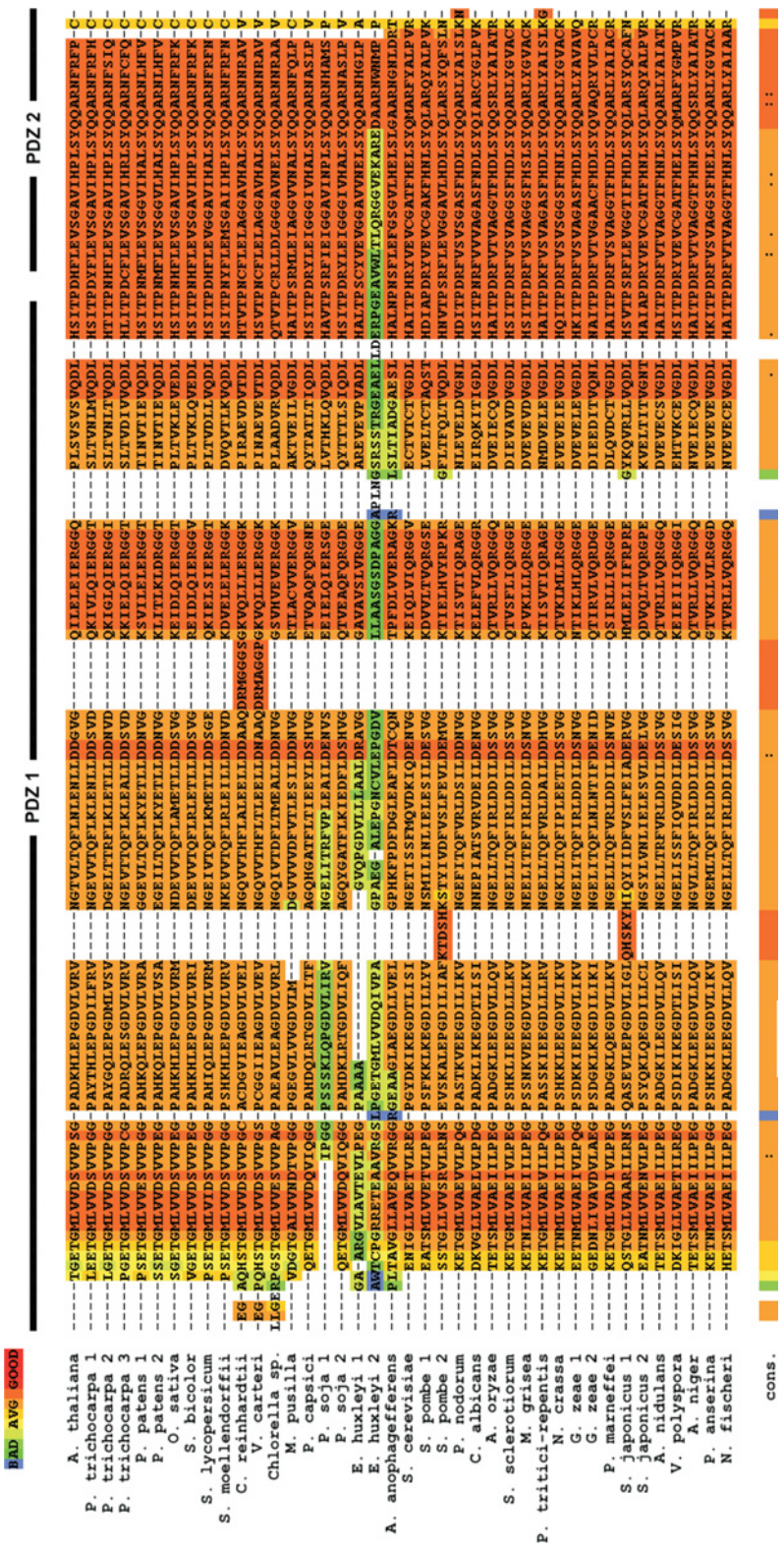

Figure S1 Continued

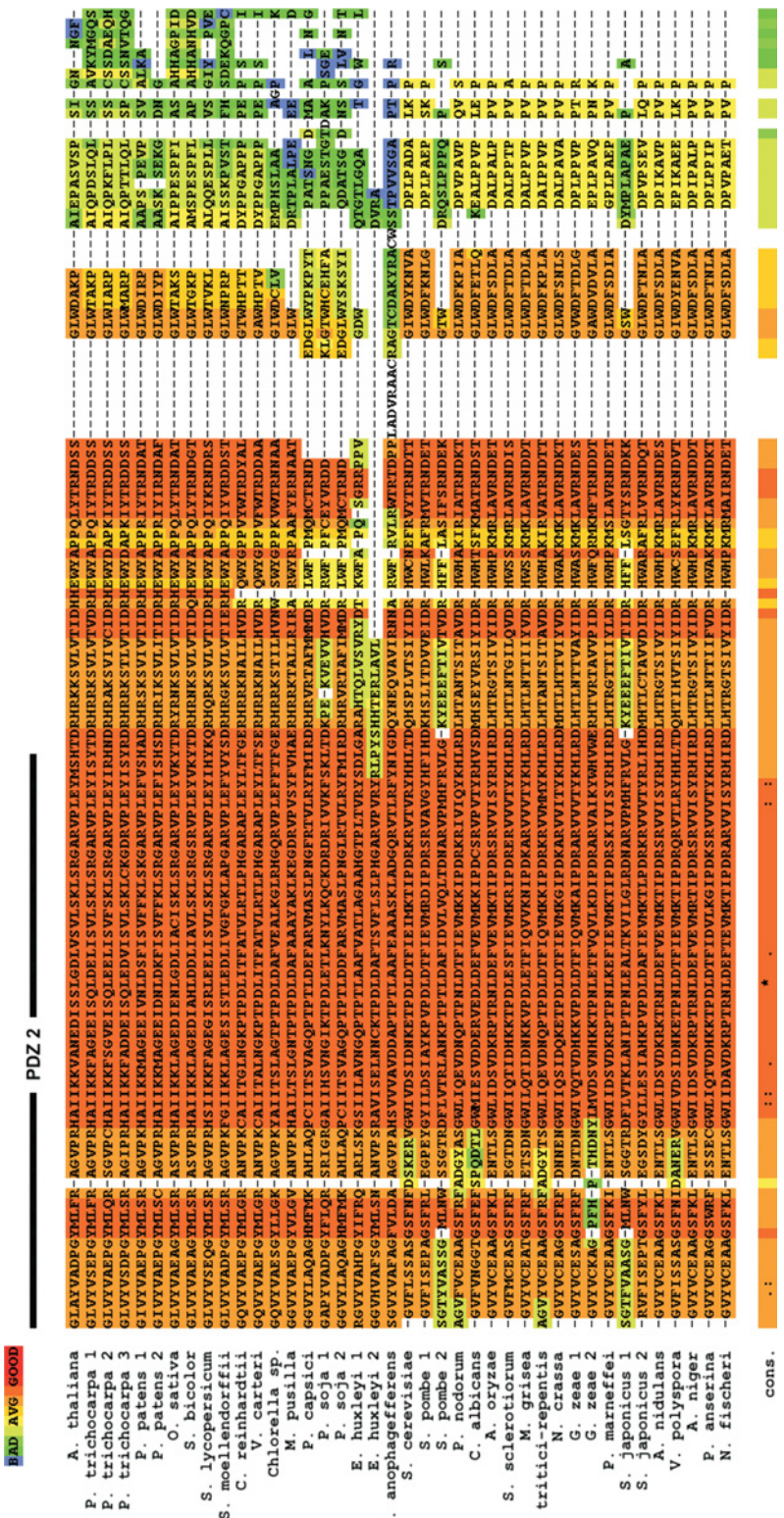

Figure S1 Continued

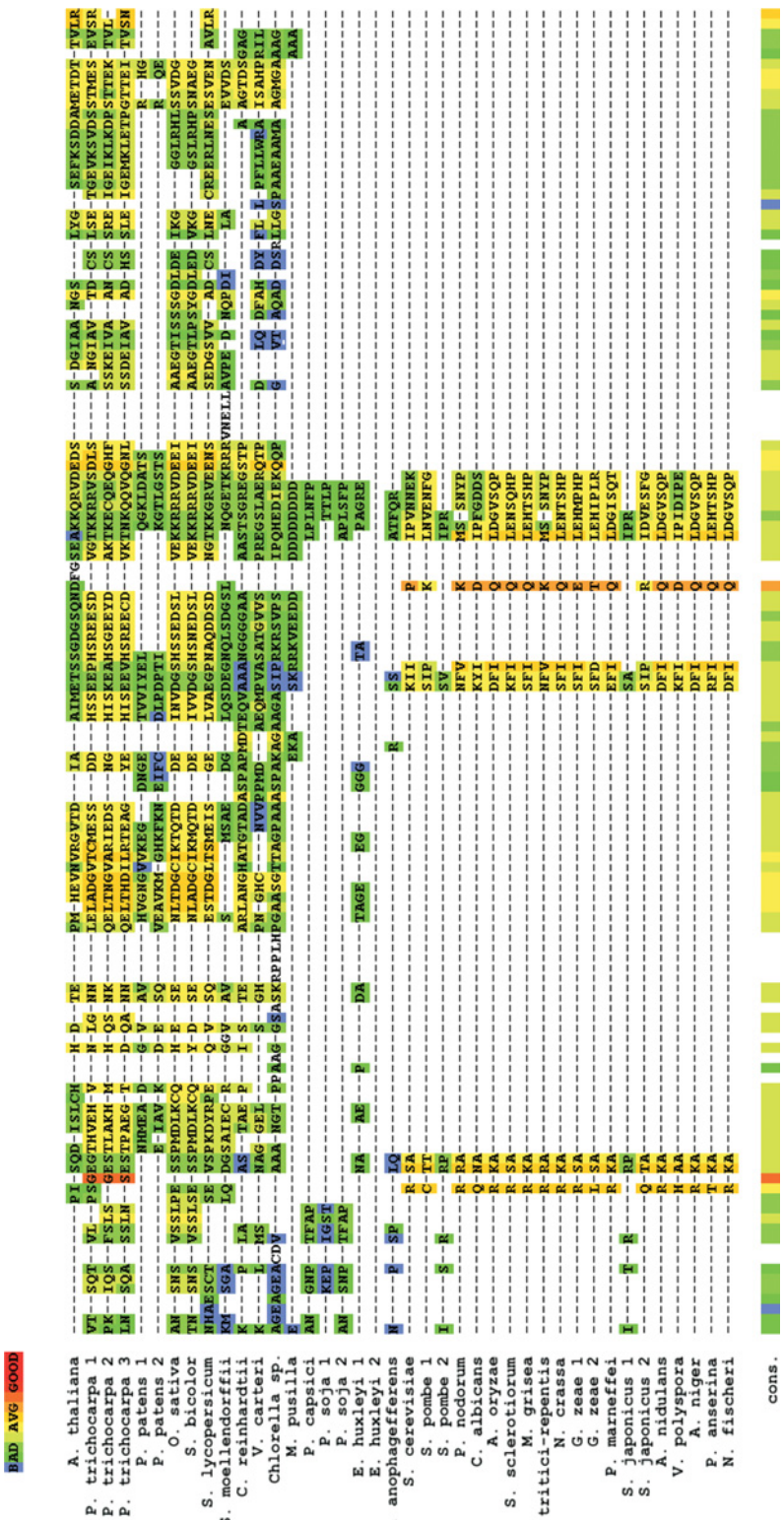

Figure S1 Continued

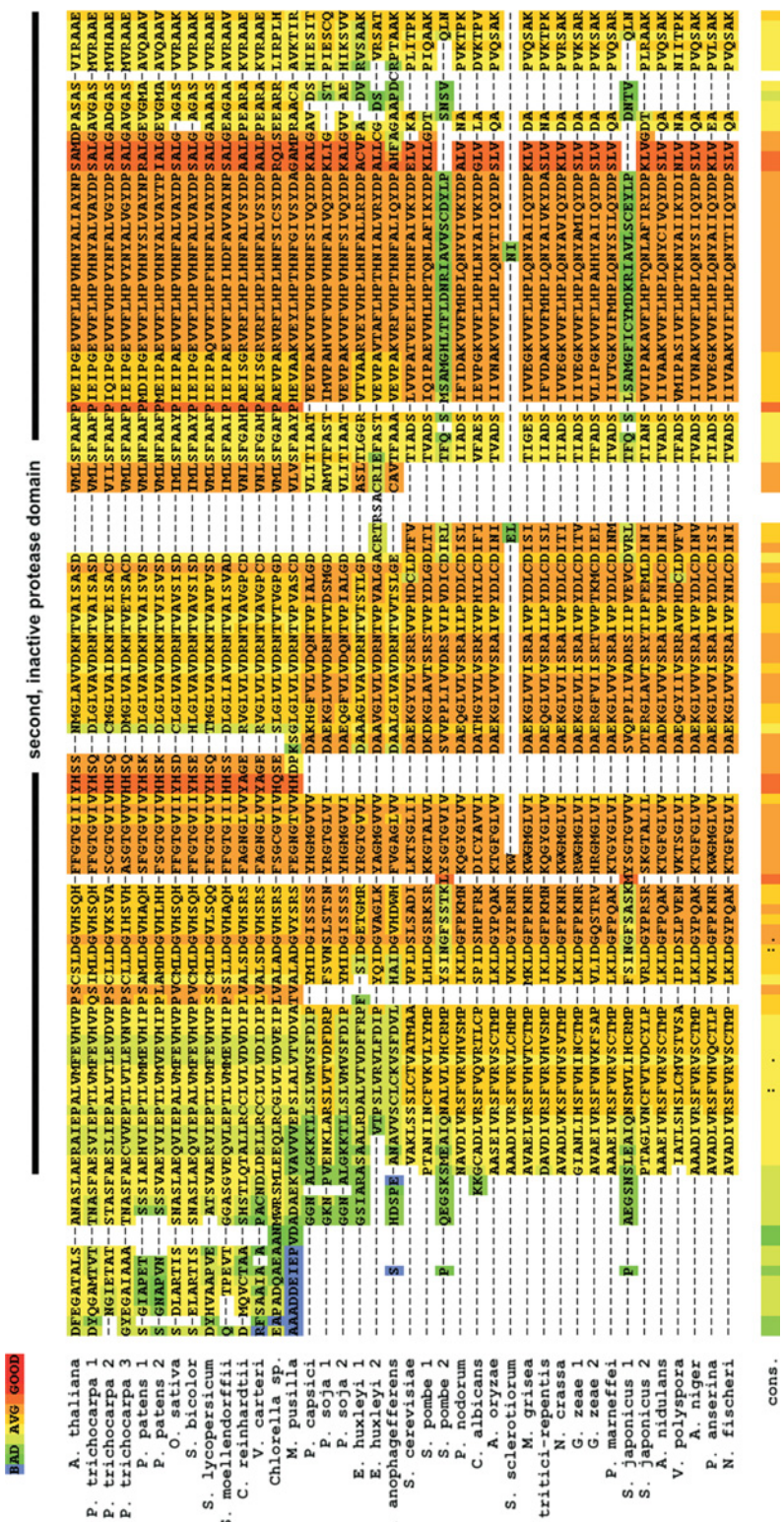

Figure S1 Continued

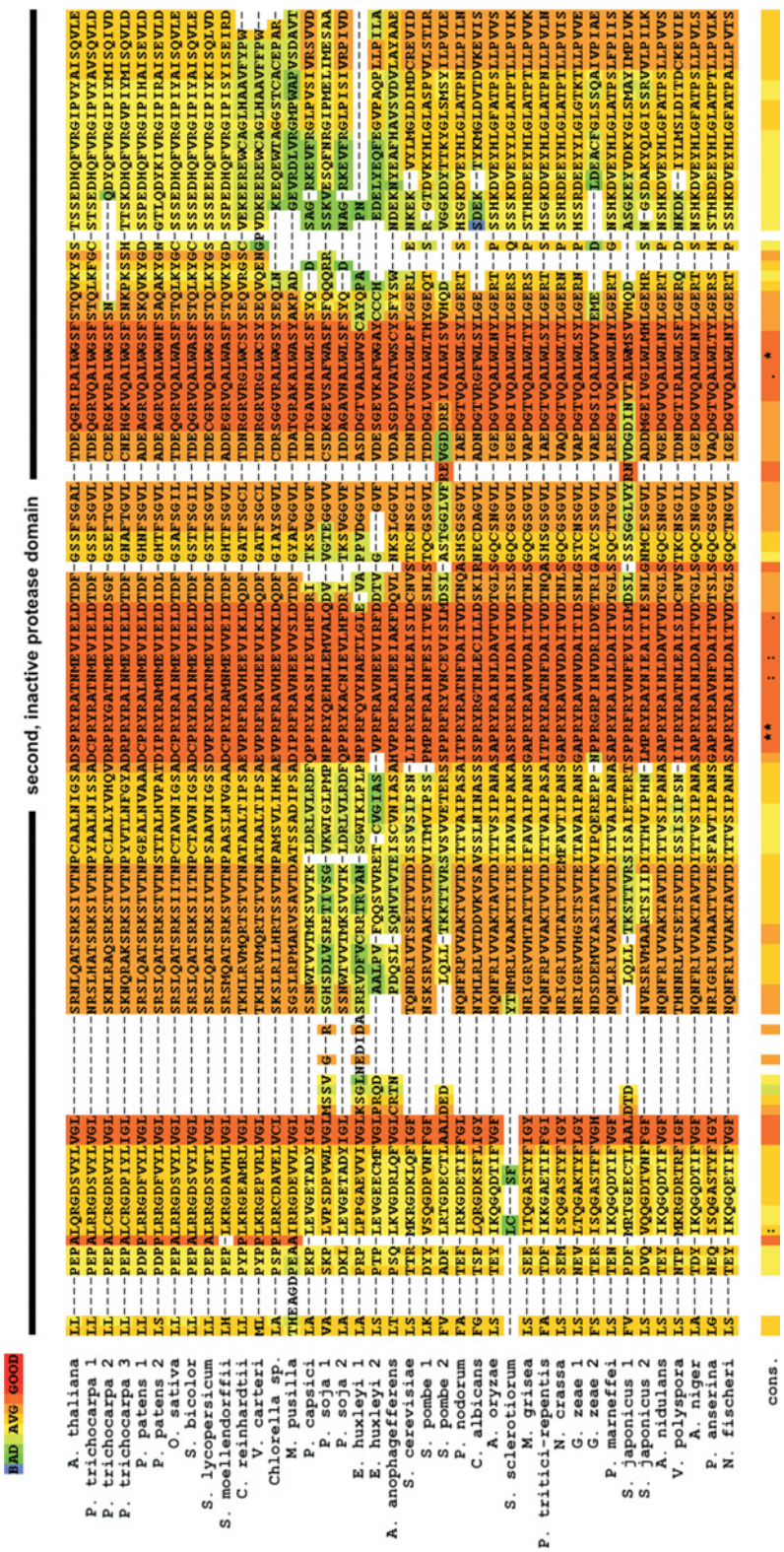

Figure S1 Continued

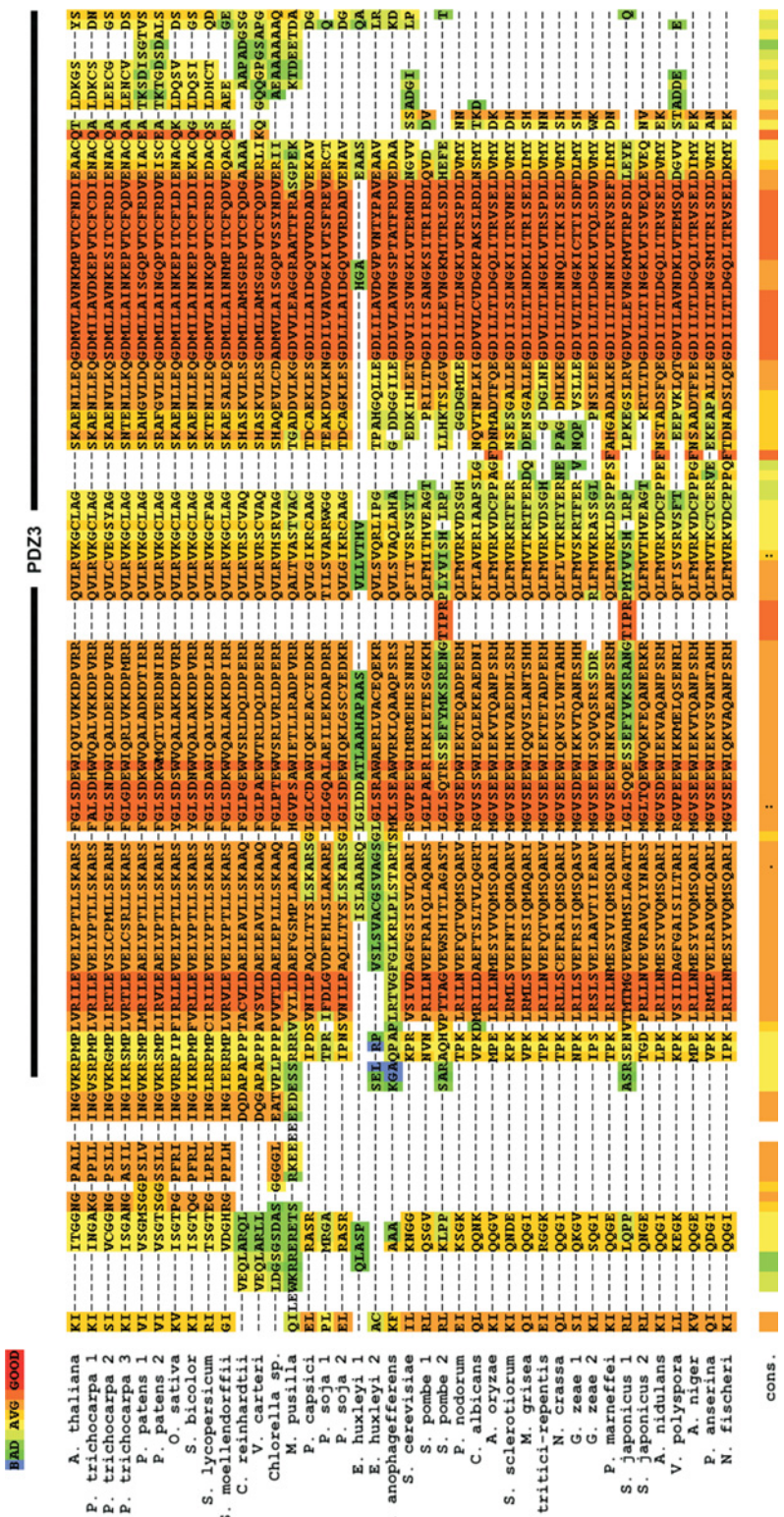

Figure S1 Continued

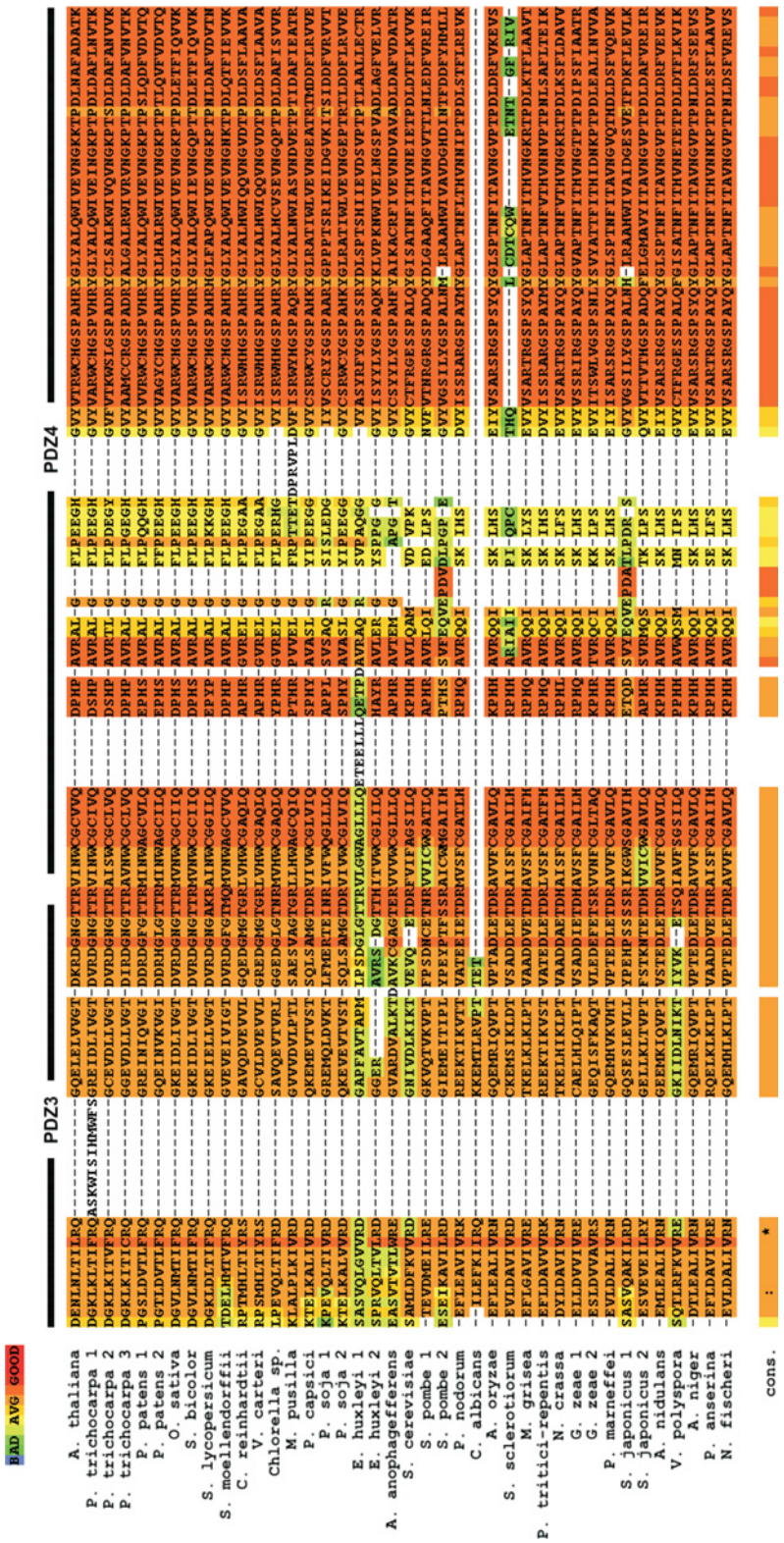

Figure S1 Continued

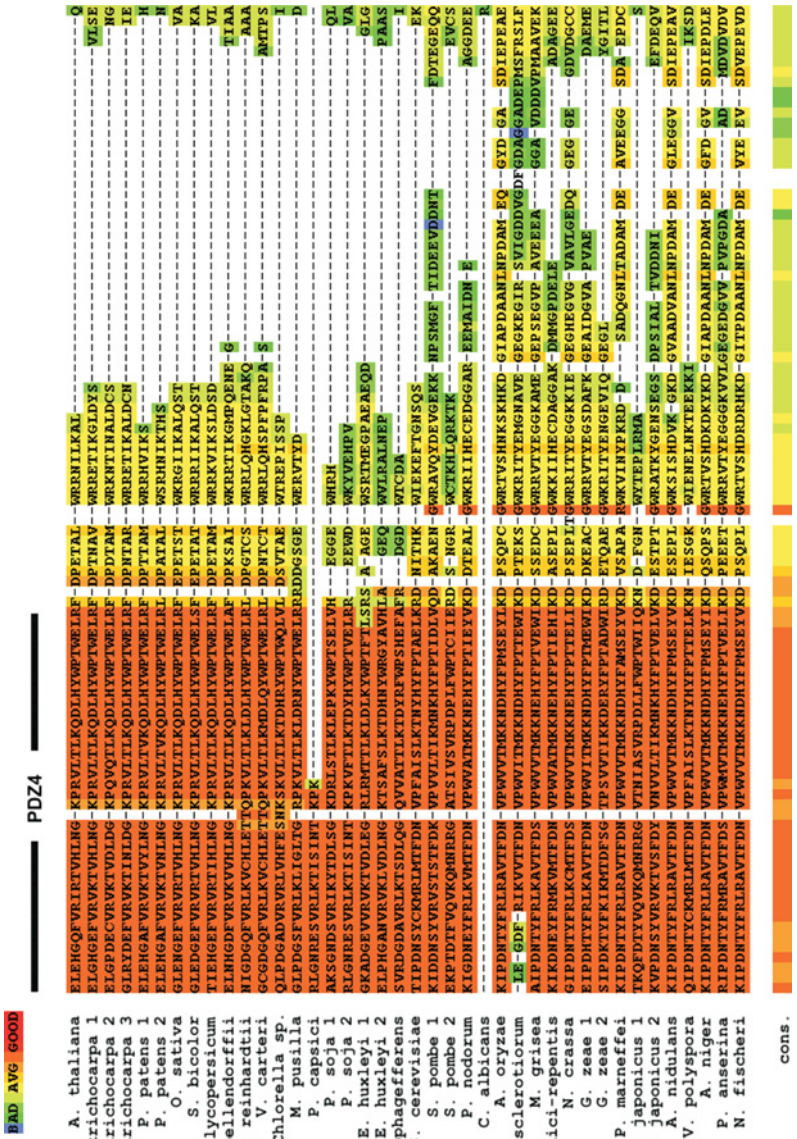

Figure S1 Continued

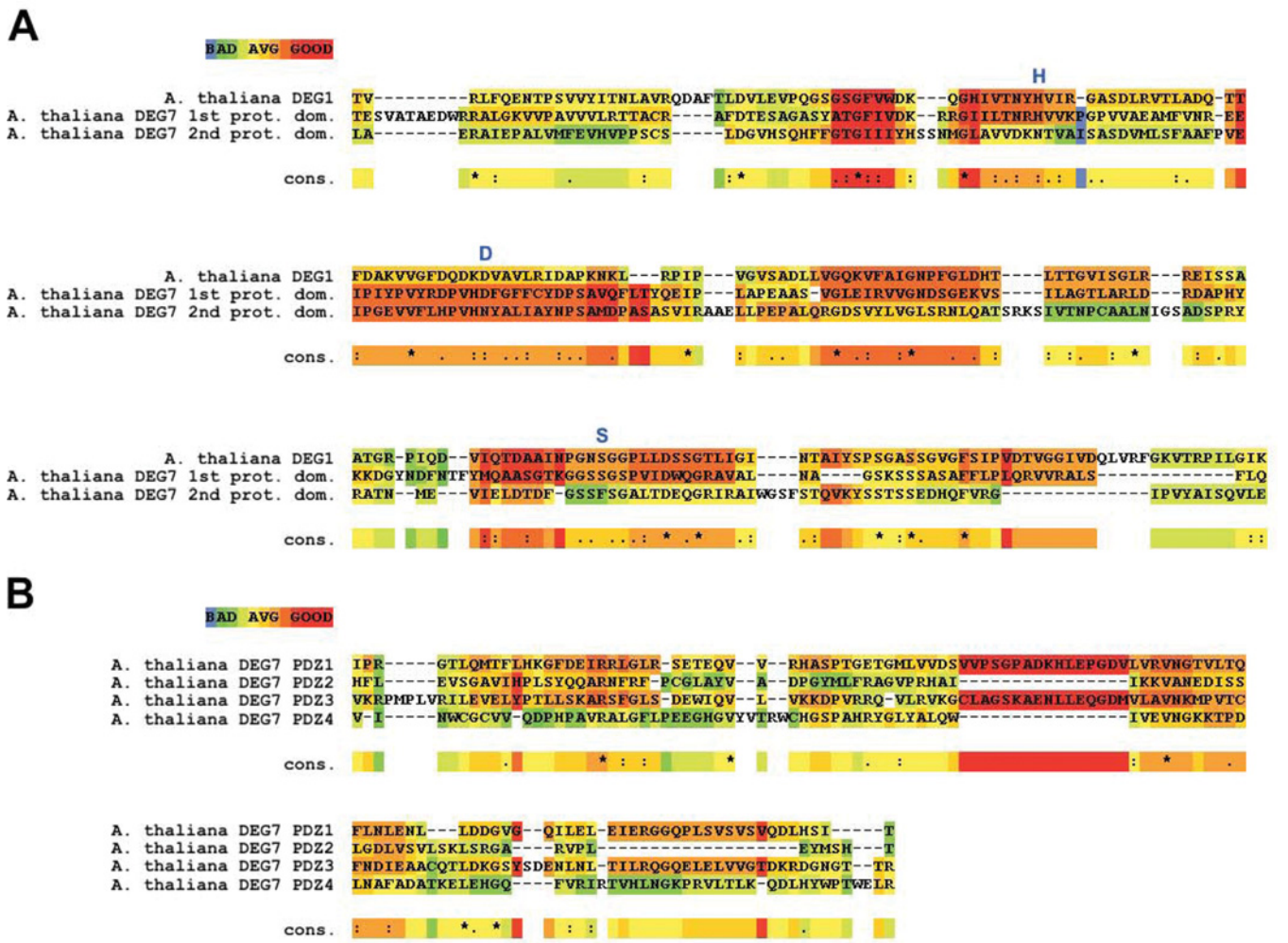

Figure S2 M-Coffee multiple sequence alignment of the amino acid sequences of protease domains and PDZ domains of *A. thaliana* DEG7

(**A**) Alignment of the first (active) protease domain (*A. thaliana* DEG7 1st prot. dom.) and the second (degenerate) protease domain (*A. thaliana* 2nd prot. dom.). The sequence of the protease domain of *A. thaliana* DEG1 is included to facilitate identification of catalytic side chains (shown in blue above the alignment). (**B**) Alignment of the PDZ domains. PDZ1 and PDZ3 both contain a stretch of additional amino acids not present in PDZ2 and PDZ4, indicating a whole-gene-duplication event as presented in Figure 1 of the main text. cons., consensus: *, identity; :, conservative replacement; ., non-conservative replacement.

```
A. thaliana           AEDWR-RALGKVVPAVVVLRTTACRAFDTESAGASYATGFIVDKRRGIILTN
G. max                AEDWR-KALNRVVPAVVVLRTTATRSFDTESAAASYATGFIVDKRRGIILTN
P. trichocarpa 1      AEDWR-KALNKVVPAVVVLRTTACRAFDTESAGASYATGFVVDKRRGIILTN
P. trichocarpa 2      ADDWA-ETVNKVVPAVVVLQTTTCRAFDTELPSSGSATGFVVDKQRGIILTN
P. trichocarpa 3      TDDWR-DAINKVVPAVVVLQTTACRSFDTELPSSGSATGFVVDKNRGIILTN
S. lycopersicum       AEDWR-KALSKVVPAVVVLRTTACRTFDTESAGCSSATGFVVDKRRGIILTN
P. patens 1           AEDWR-KALNKVVPAVVVLRTTATRAFDTEVAGASYSTGFVVDKKRGILLTN
P. patens 2           AELWR-KALKKVVPAVVVLRITTTRTFDTEVAGATHATGFVVDKQRGIILTN
O. sativa             AEDWR-RALALVVPSVVVLRTTAPRAFDTEVAGASYATGFVVDKSRGIILTN
S. bicolor            AEDWR-RALSRVVPSVVVLRTTAPRAFDTEVAGASYATGFVVDKSRGIILTN
S. moellendorffii     AEDWQ-KSLARVVRGVVVLRTTACRAFDTETASSGYATGFVVDKARSIILTN
C. reinhardtii        PEDWK-RSLEKVVPCCVVLKVTQTRAFDTEAAGSAYATGFIVDKQRGLILTN
V. carteri            TEDWK-KALDRVVPCCVVLKVTQTRAFDTEAAGSAYATGFIVDKQRGLILTN
M. pusilla            DATWQ-GVVRRVSDGVVVIKTTGVRAFDTESAGSAYATGFVVDKARGVVLTN
Chlorella sp. NC64A   SDAWK-TTLDAVVPAVVVLKVTQTRAFDTESAGSSYATGFVVDKARGLILTN
P. capsici            SKRWL-ESLEKCIRAIVSIRILSVRAFDGNGASFSVATGFVVDMERGLILTN
P. soja 1             KLDWK-ATLERVVPAIVSLKLNSPKFFDTESPGNGSATGFVVDAEKGIILTN
P. soja 2             SKRWL-QSLEKCIRAIVSIRLLSVRAFDGNGASFSVATGFVVDMERGIILTN
E. huxleyi 1          EESWD-RTIAAALPAVVAIKVNRVRAFDTASAGTVQATGFVVDAEQGIILTN
E. huxleyi 2          EKGWE-ETLERVAKGVVVVRVNSVMAFDMNERGFSLATGFVVDKALGIILTN
A. anophagefferens    RDVWE-RMLDRVLPAIVVIRVNYVKPFDGDQAGSAHATGFVVDFERGIIVTN
S. cerevisiae         YLRWQ-NTISNVVKSVVSIHFSQVAPFDCDSALVSEATGFVVDAKLGIILTN
S. pombe 1            SKKWK-ESIARVVKSVVSIRFSQVAAFDTDESGTGEASAFVVDAKNGYMLSN
S. pombe 2            HHTWD-NTIKNVVRSIVSIKGSALRSFDTESAGSFCATGFVVNKTLGLILSN
S. japonicus 1        QPSWD-FTIKRVVRSIVSIRGSVLRSFDTENAGSFCATGFVVDKNLGIILTN
S. japonicus 2        SGKWK-ESISRVVKSVVSIRFSQVASFDTDGAQTGEASAFIVDAENGYMMTN
P. nodorum            TAEWQ-KTIEGVVKSVVSIHFCQTCSFDTDPAISSEATGFVVDAEKGYILTN
C. albicans           NNKWA-ETITNVVNCVVSIHFSHVAPFDTENAVSSEATGFVVDASRGLILTN
A. oryzae             SPEWQ-ATIEEVVKSVVSIHFCQTCSFDTELSMSSQATGFVVDAERGYILTN
A. nidulans           SPEWQ-ATIEEVVKSVVSIHFCQTCSFDTELSMSSQATGFVVDAERGYILTN
A. niger              SPEWQ-ATIEEVVKSVVSIHFCQTCSFDTELSMSSQATGFVVDAENGYILTN
S. sclerotiorum       TAEWQ-AAIEQVVRNVVSIRFCQTCSFDTDPALTSEATGFVVDAERGYILTN
M. grisea             TVEWQ-ATIQKVVSNVVSIRFCQTCSFDTDAALTSEATGFVVDAERGYILTN
P. tritici-repentis   TAEWQ-RTIENVVKSVVSIHFCQTCSFDTDAAVSSEATGFVVDAEKGYILTN
N. crassa             TAEWQ-ATIENVVRNVVSIRFCQTCSFDTDPALTSEATGFVVDAERGYILTN
G. zeae 1             LGEWQ-DTIQKVVRNVVAIRFCQTCSFDTDAALTSEATGYVVDSERGYILTN
G. zeae 2             SEAWQ-RAIEKVVRCVVSVKFSHPYSFDTEISKTSEATGFIVDAERGLVLTN
P. anserina           TAEWQ-ETIQRVVRNVVSIRFCQTCSFDTDPALTSEATGFVVDAERGYILTN
N. fischeri           SPEWQ-ATIEKVVKSVVSIHFCQTCSFDTDLSMSSQATGFVVDAERGYILTN
P. marneffei          SPEWQ-ATIESVVKSVVSIHFCQTCSFDTDMSMCSQATGFVVDAERGYILTN
V. polyspora          YLKWQ-NTIAKVVKSVVSIHFSQVAPFDSDNAVVSQATGFVVDASLGIILTN
EcDegP                DSPFCQEG-SPFQSSPFCQGGQGGNGGGQQQKFMALGSGVIIDADKGYVVTN
HsHtrA2               QYNFIADVVEKTAPAVVYIEILDRHPFLGREVPISNGSGFVVAAD-GLIVTN
AtDEG1                TVRLFQENTPSVVYITNLAVRQDAFTLDVLEVPQGSGSGFVWDKQ-GHIVTN
                                                      .:. :     . :::*
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Figure S3 Alignment of the amino acid sequences of the active protease domains of DEG7 proteins from higher plants, mosses, algae and fungi

Amino acid sequences of DEG7 active protease domains were aligned with those of the protease domains of DegP from *Escherichia coli* (EcDegP), human HtrA2 (HsHtrA2) and Deg1 from *Arabidopsis thaliana* (AtDEG1) as described in the Experimental section of the main text. For full names of organisms, see Supplementary Table S1. Identical residues are indicated by asterisks. Active-site residues of the catalytic triad are in bold. Conservative replacements are indicated by : symbols; non-conservative replacements are indicated by . symbols.

Continues...

```
A. thaliana          RHVVKPGPVVAEAMFVNREEIPIYPVYRDPVHDFGFFCYDPSAVQF---LTY
G. max               RHVVKPGPVVAEAMFLNREEVPVHPIYRDPVHDFGFFRYDPGAIQF---LNY
P. trichocarpa 1     RHVVKAGPVVAEAMFLNREEIPVYPIYRDPVHDFGFFRYDPGAIQF---LNY
P. trichocarpa 2     RHVVNPGPVNAQAIFVSNEETPLRPIYRDPVHDFGFFSYDPGAIQF---LNY
P. trichocarpa 3     RHVVKPGPVVAQAIFVNNEEIPVYPIYRDPVHDFGFFRYDPSAIQF---HKY
S. lycopersicum      RHVVKPGPVMAEAMFVNREEIPVYPIYRDPVHDFGFFRYDPGAIQF---LSY
P. patens 1          RHVVKPGPIVAEAMFVNREEISVYPLYRDPVHDFGFLWFDPSLVQF---LDY
P. patens 2          RHVVKPGPVVAEAMFVNREEILVYPLYRDPVHDFGFFWYDPRTIQF---LDY
O. sativa            RHVVKPGPVVAEAMFVNREEIPVYPLYRDPVHDFGFFRYDPGAIKF---LKY
S. bicolor           RHVVKPGPVVAEAMFVNREEIPVYPLYRDPVHDFGFFRYDPGAIKF---LKY
S. moellendorffii    RHVVKPGPVVAEAIFLNREEIPVYPLYRDPVHDFGFFRFDPKSVEF---MNY
C. reinhardtii       RHVVTPGPIVAEAIFLNREELPVVPLYYDPIHDFGFLRFDPSRLQF---MEV
V. carteri           RHVVTPGPIVAESIFLNREELPVYPLYYDPIHDFAFLRFDPSRLQF---MEV
M. pusilla           RHVCRPGPVTAEAVFQNREEVPLRALYSDPVHDFAFMRFDPSLVKF---QKV
Chlorella sp NC64A   RHVVTPGPVVAEAIFLNREEVPVQPLYYDPVHDFGFMRFDPGRLQF---MKA
P. capsici           RHVVTPGPVVADAIFLNKEEVDLVPVYRDPVHDFGFYRFDPKKVKF---LQL
P. soja 1            RHVVGPGPIDAEAVFQNNEEVRVIPIYRDPVHDFGFFQFNPADVKH---MSV
P. soja 2            RHVVTPGPVVADAIFLNKEEVDLVPIYRDPVHDFGFFRFDPKKVKF---LQL
E. huxleyi 1         RHVAGPGPVVAEAIFQNNEEVSLSLAYYDPVHDFAFFRFDPSALRH---MKP
E. huxleyi 2         RHVVTTGPVTADAVLHNKEEIELTPLYADPVHDFGFFKYDPADVRF---MEL
A. anophagefferens   RHVIGTGPIRAEATFVTKEEVPLTPLYRDPVHDFGFFHFDAAHLKYAGELQA
S. cerevisiae        RHVVGPGPFVGYVVFDNHEECDVIPIYRDPVHDFGFLKFDPKNIKY---SKI
S. pombe 1           RHVVCAGPFVGHAVFDNHEEVEVFPVYRDPVHDFGFLRFDPKKIRY---MNV
S. pombe 2           RHVVSPGPISARASFINYEEIDIYPIYRDPVHDFGFFRYDPSSIRF---HDV
S. japonicus 1       RHVVSPAPITARASFINYEEIDIYPLYRDPVHDFGFFRYNPSALRF---HEV
S. japonicus 2       RHVACAGPFVGRAVLDNHEEVEVYPIYRDPVHDFGILKFDPKKIRY---MKV
P. nodorum           RHVVGAGPFIGYCIFDNHEECDVYPVYRDPVHDFGILRFDPKAIKY---MSV
C. albicans          RHVVGPGPFTGYVVFDNHESVDVKPIFRDPIHDFGILKFNPQDVKY---LKL
A. oryzae            RHVVCPGPFWGYCIFDNHEECDVRPVYRDPVHDFGILKFDPKAIRY---MNL
A. nidulans          RHVVCPGPFWGYVIFDNHEECDVYPVYRDPVHDFGFLKFDPKAIRH---MKL
A. niger             RHVVCPGPFWGYCIFDNHEECDVRPVYRDPVHDFGILKFDPKAIRY---MKL
S. sclerotiorum      RHVVGSGPFWGYCVFDNHEEVDAYPVYRDPVHDFGILRFDPKAIKY---MPV
M. grisea            RHVVGSGPFWGYCIFDNHEEVDAYPVYRDPVHDFGILKFDPKAIKY---MPV
P. tritici-repentis  RHVVGAGPFIGYCIFDNHEECDVHPVYRDPVHDFGILRFDPSKIKY---MPV
N. crassa            RHVVGSGPFWGYCIFDNHEEVDAYPVYRDPVHDFGILKFDPKAIKY---MPV
G. zeae 1            RHVVGAGPFWGHCVFDNHEEVDCYPVYRDPVHDFGILRYDPKAIKY---MHI
G. zeae 2            RHVVGPGPFSGYIVFNNQEEVEVHPIYRDPVHDFGFLKFDPKAVKY---MEL
P. anserina          RHVVGSGPFWGYCVFDNHEEVDAYPVYRDPVHDFGILKFDPKAIKY---MPV
N. fischeri          RHVVCAGPFWGYCIFDNHEECDVRPVYRDPVHDFGILKFDPKAIRY---MEL
P. marneffei         RHVVCAGPFWGYCIFDNHEECDVRPVYRDPVHDFGILKFDPKAIKY---MDM
V. polyspora         RHVVGPGPFVGYAVFDNHEECDVTPIYRDPVHDFGFLKFDPTKIKY---MNI
EcDegP               NHVV-DNATVIKVQLSDGRKFDAKMVGKDPRSDIALIQIQ--NPKN-----L
HsHtrA2              AHVV-ADRRRVRVRLLSGDTYEAVVTAVDPVADIATLRIQ--TKEP-----L
AtDEG1               YHVI-RGASDLRVTLADQTTFDAKVVGFDQDKDVAVLRID--APKN----KL
                      **          :             *   *..    :    .
```

Figure S3 Continued

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A. thaliana          QEIPLAPEAA-SVGLEIRVVGNDSGEKVSILAGTLARL----------DRD
G. max               EEIPLAPEAA-CVGLEIRVVGNDSGEKVSILAGTLARL----------DRD
P. trichocarpa 1     EEIPLAPEAA-CVGLEIRVVGNDSGEKVSILAGTLARL----------DRD
P. trichocarpa 2     EEIPLAPEAA-SVGLEIRVIGNDSSEKVSILSGILARL----------DRN
P. trichocarpa 3     EEIPLAPEAA-SVGLEIRVIGNDSCEKVSILAGTLARL----------DRN
S. lycopersicum      EEIPLAPDAA-SVGVEIRVVGNDSGEKVSILAGTLARL----------DRD
P. patens 1          EEIPLAPDAA-QVGLEIRVVGNDSGEKVSILAGTLARL----------DRD
P. patens 2          EEIPLAPDAA-AVGLEIRVVGNDSGEKVSILAGTLARL----------DRD
O. sativa            DEIPLAPEAA-SVGLEIRVVGNDSGEKVSILAGTLARL----------DRE
S. bicolor           DEIPLAPEAA-SVGLEIRVVGNDSGEKVSILAGTLARL----------DRE
S. moellendorffii    EEIPLAPEAA-AVGLEIRVVGNDSGEKLSILAGTIARL----------DRD
C. reinhardtii       SEVPLAPEGA-TVGLDIRVVGNDSGEKVSILAGTLARL----------DRD
V. carteri           SEVPLAPEAA-TVGLDIRVVGNDSGEKVSILAGTLARL----------DRD
M. pusilla           TDVPLAPDGA-AVGLEVRIVGNDSGEKLSILSATLARLGAFYTLVPIRPHRD
Chlorella sp. NC64A  GEIPLAPDAA-AVGLDIRVVGNDSGEKLSILSGTLARL----------DRD
P. capsici           HEIPLRPEAA-KIGAEIRVVGNDAGEKLSILPGILAKM----------DRD
P. soja 1            PSLRLEPDKA-TVGTDIRVVGNDAAEKLAIASGTLARL----------DRD
P. soja 2            HEIPLRPEAA-KIGAEIRVVGNDAGEKLSILPGILAKL----------DRD
E. huxleyi 1         TELRLAPEQA-EVTSEILIIGNNAGEKCSIHRTTLARL----------DRN
E. huxleyi 2         QEIPLAPSEA-RV----RVVGNDAGEKISILSGTIARL----------DRA
A. anophagefferens   AAIELAPEKA-KVGLEIRVVGNDAGEKVSILSGTLARL----------DRN
S. cerevisiae        KALTLKPSLA-KVGSEIRVVGNDAGEKLSILAGFISRI----------DRN
S. pombe 1           EQLELRPDLA-KVGTEIRVVGNDAAEKLSILAGWISRI----------DRN
S. pombe 2           TEISLSPESA-KVGIDIRIIGNDAGEKLSILSSTLARL----------DRP
S. japonicus 1       DEIPLAPELA-RVGADIRVIGNDAGEKLSILSSTLARL----------DRA
S. japonicus 2       QQLEMRPDLA-KVGKEIRVVGNDAAEKLSILAGWISRV----------DRN
P. nodorum           SALQLRPDFA-KVGVEIRVVGNDAGEKLSILSGVISRL----------DRN
C. albicans          TQLELAPDLA-KVGTEIRVVGNDAGEKLSILSGFISRL----------DRN
A. oryzae            TELKLQPDAA-RVGSEIRVVGNDAGEKLSILSGVISRL----------DRN
A. nidulans          RELKLQPDGA-RVGSEIRVVGNDAGEKLSILSGVISRL----------DRN
A. niger             RELKLQPDAA-KVGSEIRVVGNDAGEKLSILSGVISRL----------DRN
S. sclerotiorum      TALGLRPDLA-KVGSEIRVVGNDAGEKLSILSGVISRL----------DRN
M. grisea            AALPLRPDLA-KVGVEIRVVGNDAGEKLSILSGVISRL----------DRN
P. tritici-repentis  TALKLRPDNA-KVGVEIRVVGNDAGEKLSILSGVISRL----------DRN
N. crassa            AALPLRPDLA-RVGIEIRVVGNDAGEKLSILSGVISRL----------DRN
G. zeae 1            DGLELRPDLA-KVGTEIRVVGNDAGEKLSILSGIISRL----------DRN
G. zeae 2            TAMQLRPDLA-KVGTEIKVIGNDSGEKLGILSGFISRL----------DRN
P. anserina          EALQLRPDLA-KVGIEIRVVGNDAGEKLSILSGVISRL----------DRN
N. fischeri          TELKLRPEAA-RVGCEIRVVGNDAGEKLSILSGVISRL----------DRN
P. marneffei         TELKLNPDGA-QVGVEIRVVGNDAGEKLSILSGVISRL----------DRN
V. polyspora         QALELKPSLA-KVGSEIRVVGNDAGEKLSILSGFISRL----------DRN
EcDegP               TAIKMADSDALRVGDYTVAIGNPFGLGETVTSGIVSAL----------GRS
HsHtrA2              PTLPLGRSADVRQGEFVVAMGSPFALQNTITSGIVSSA----------QRP
AtDEG1               RPIPVGVSADLLVGQKVFAIGNPFGLDHTLTTGVISGL----------RRE
                       : :  .           :*.       :    ::             *
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Figure S3 Continued

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A. thaliana           APHYKKDGYNDFNTFYMQAASGTKGGSSGSPVIDWQGRAVALNAGSKSS-SA
G. max                APHYKKDGYNDFNTFYMQAASGTKGGSSGSPVIDWQGRAVALNAGSKSS-SA
P. trichocarpa 1      APHYKKDGYNDFNTFYMQAASGTKGGSSGSPVIDWQGRAVALNAGSKSS-SA
P. trichocarpa 2      APAYEKDGYNDFNTFYLQAASGTKPGSSGSPVIDKQGRAVALNAGSSSS-SS
P. trichocarpa 3      APTYRRDGYNDFNTFYMQAASGTKRGSSGSPVIDKQGRAVALNAGGSVS-SS
S. lycopersicum       APQYKKDGYNDFNTFYMQAASGTKGGSSGSPVIDWQGRAVALNAGSKLS-SA
P. patens 1           APHYKKDGYNDFNTFYMQAASGTKGGSSGSPVIDIHGRAVALNAGSKSA-SA
P. patens 2           APHYKSTGYNDFNTFYMQAASGTKRGSSGSPVIDIYGQAVALNAGSRSS-SA
O. sativa             APYYKKDGYNDFNTFYMQAASGTKGGSSGSPVVDCQGRAVALNAGSKSS-SA
S. bicolor            APYYKKDGYNDFNTFYMQAASGTKGGSSGSPVVDCQGRAVALNAGSKSS-SA
S. moellendorffii     APPYKKDGYNDFNTFYMQAASGTKGGSSGSPVVDCKGRAVAINAGSKVA-GA
C. reinhardtii        APVYGRKGYNDFNTFYLQAASGTKGGSSGSPVIDCQGRAVGLNAGGKNK-AA
V. carteri            APVYGRKGYNDFNTFYLQAASGTKGGSSGSPVIDCQGRAVGLNAGGKNK-AA
M. pusilla            APKYGSKGYNDFNTFYIQAASGTKGGSSGSPVVDVNGRAVALNAGSKTK-GS
Chlorella sp. NC64A   APHYSRRGFNDFNQFYIQAASGTKGGSSGSPVVNIKGQAVGLNAGGKNK-AA
P. capsici            APSYGSSSYNDFNTFYFAAASSTSGGSSGSPVLNIDGCAIALNAGGAKK-SA
P. soja 1             APNYGYNNYNDFNTFYYQASSGTTGGSSGSPVLNHDGDAIALNAGGKIG-TS
P. soja 2             APSYGSGSYNDFNTFYFAAASSTSGGSSGSPVLNIDGCAIALNAGGAKK-AA
E. huxleyi 1          APHYSRSSYNDFNTFYFHSASGTSGGSSGSPVLNKRGSAIALNAGGKSG-TS
E. huxleyi 2          APNYGSHTYNDFNTFYFSCASNTSGGSSGSPVVNASGRAVALNAGTSTK-SA
A. anophagefferens    APHYQSDGFNDFNTFYISAASNTSGGSSGSPVLDSSGRAVALNAGGSNN-SS
S. cerevisiae         APEYGELTYNDFNTEYIQAAASASGGSSGSPVVNIDGYAVALQAGGSTE-AS
S. pombe 1            VPDYGELTYCDFNTNYIQAAANASGGSSGSPVVERNGNVVALQAGGHMI-AA
S. pombe 2            APNYGIDNYNDFNTFYYQAASGTSGGSSGSPVLDISGAAVALNSGGSNS-SA
S. japonicus 1        APNYGVDSYNDFNTFYYQAASGTSGGSSGSPVLDISGSAVALNAGGSNK-SA
S. japonicus 2        VPEYGEYTYCDFNTSYIQAAANASGGSSGSPVVDSNGYVVALQAGGHLM-AA
P. nodorum            APEYGE-GYSDFNTNYIQAAAAASGGSSGSPVVNRDGFAVALQAGGRADGAA
C. albicans           APDYGSLTYNDFNTEYIQAAAAASGGSSGSPVVNEDGKCVALQAGGHTE-AA
A. oryzae             APEYGE-GYSDFNTNYIQAAAAASGGSSGSPVVNIDGHAIALQAGGRADGAA
A. nidulans           APEYGD-GYSDFNTNYIQAAAAASGGSSGSPVVNIEGNAIALQAGGRADGAA
A. niger              APEYGD-GYSDFNTNYIQAAAAASGGSSGSPVVNIDGHAIALQAGGRADGAA
S. sclerotiorum       APEYGD-GYCDFNTNYIQAAAAASGGSSGSPVVNIDGYAVALQAGGRSDGAA
M. grisea             APEYGE-GYSDFNTCYYQASAAASGGSSGSPVVNIDGFAVALQAGGRADGAS
P. tritici-repentis   APEYGE-GYSDFNTNYIQAAAAASGGSSGSPVVDRDGFAVALQAGGRADGAA
N. crassa             APEYGD-GYSDFNTCYYQASAAASGGSSGSPVVNKDGFAVALQAGGRADGAS
G. zeae 1             APEYGE-GYSDFNTCYYQANAAASGGSSGSPVVNKDGCAVALQAGGRSDGAS
G. zeae 2             APIY-D-GYMDFNTCYYQANASASGGSSGSPVVNVDGHGIALQAGGRTD-GS
P. anserina           APEYGE-GYSDFNTCYYQASAAASGGSSGSPVVDIDGYAVALQAGGRSDGAS
N. fischeri           APEYGD-GYCDFNTNYIQAAAAASGGSSGSPVVNIDGHAIALQAGGRADGAA
P. marneffei          APEYGE-GYSDFNTNYIQAAAAASGGSSGSPVVNVAGHVVALQAGGRADGAA
V. polyspora          APDYGELTYNDFNTEYIQAAAAASGGSSGSPVVNSDGYAVALQAGGSTE-AS
EcDegP                GLN-AEN-Y----ENFIQTDAAINRGNSGGALVNLNGELIGINTAILAPDGG
HsHtrA2               ARDLGLPQT---NVEYIQTDAAIDFGNSGGPLVNLDGEVIGVNTMKVT----
AtDEG1                ISSAATGRP---IQDVIQTDAAINPGNSGGPLLDSSGTLIGINTAIYSPSGA
                                          :    *.**..:::  *  :.:::
```

Figure S3 Continued

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A. thaliana           S---AFFLPLQRVVRALSFLQKS---------------------I
G. max                S---AFFLPLERVVRALRFLQKGS--------------------E
P. trichocarpa 1      S---AFFLPLERVVRALEFLQK----------------------
P. trichocarpa 2      S---AFYLPLERVVRALRLLQKC---------------------K
P. trichocarpa 3      S---AFYLHLERVVRALAFLQKS---------------------K
S. lycopersicum       S---AFFLPLERVVRSLKFLQE----------------------
P. patens 1           S---AFFLPLERVVRALHLLQAQ---------------------K
P. patens 2           S---AFFLPLERVVRALHLLQEQ---------------------K
O. sativa             S---AFFLPLERVVRALNLIRD----------------------
S. bicolor            S---AFFLPLERVVRALNLIRDS---------------------W
S. moellendorffii     S---AYFLPLDRVVRALRILQES---------------------K
C. reinhardtii        S---AYYLPLERVVRALKLIQAS---------------------K
V. carteri            S---AYYLPLERVVRALKLIQASKDAFRPGTEWP-C----PF--IP
M. pusilla            A---AYYLPLHRVKRALDLLRDACP---------------A--NP
Chlorella sp. NC64A   S---AYYLPLHRIVRALHLLQACHQ---PDGSWA-Q----PA--IP
P. capsici            A---SFYLPLDRVVRVLRLIQQGNP-------------------VP
P. soja 1             A---SFYLPLDRVKRAFDLIREAET-------------------IP
P. soja 2             S---SFYLPLDRVVRVLGLIQQGQP-------------------VP
E. huxleyi 1          A---GFFLPLDRVARALELLRSGAA-------------------VP
E. huxleyi 2          S---SYYLPLQRPARALALLQKALLAGRGAG----R----AC--VP
A. anophagefferens    A---SYYLPLHAVVRALDALKAG----------------------V
S. cerevisiae         T---DFFLPLDRILRALICIQTNKP-------------------IT
S. pombe 1            T---DYFLPLDRPLRALRCLQNNTP-------------------IT
S. pombe 2            S---SFYLPLDRVVRALRCIENNTP-------------------IT
S. japonicus 1        S---SFYLPLDRVVRALHCIQNNKS-------------------IT
S. japonicus 2        T---DYFLPLDRPLRALRCLQQNKP-------------------IT
P. nodorum            T---DYFLPLDRPLRALELVRRGEA-------------------VT
C. albicans           T---DYFLPVYRPLRALRCIQNNEP-------------------IT
A. oryzae             T---DYFLPLDRPLRALECIRRGEP-------------------VT
A. nidulans           T---DYFLPLDRPLRALECIRRGEP-------------------VT
A. niger              T---DYFLPLDRPLRALECIRRGEP-------------------VT
S. sclerotiorum       T---DYFLPLDRPLRALQCIQQGKP-------------------IT
M. grisea             T---DYFLPLDRPLRALQCLQQGKP-------------------IT
P. tritici-repentis   T---DYFLPLDRPLRALELIRQGQF-------------------VS
N. crassa             T---DYFLPLDRPLRALKCLQEGKP-------------------IT
G. zeae 1             T---DYFLPLDRPLRALQCIQNGKP-------------------VT
G. zeae 2             T---DYFLPLDGPLRALKQIQNGGK-------------------VK
P. anserina           T---DYFLPLDRPLRALKCLQEGNP-------------------IT
N. fischeri           T---DYFLPLDRPLRALECIRRGEP-------------------VA
P. marneffei          T---DYFLPLGRPLRALQCLQEGKP-------------------VT
V. polyspora          T---DFFLPLDRILRALKCLQSNKP-------------------IT
EcDegP                NIGIGFAIPSNMVKNLTSQMVEYGQVK-----RG-E----LGIMGT
HsHtrA2               -AGISFAIPSDRLREFLHRGEKKNSSG-----ISGSQRRYIG--VM
AtDEG1                SSGVGFSIPVDTVGGIVDQLVRFGKVT-----RP-I----LG--IK
                           : :
```

Figure S3 Continued

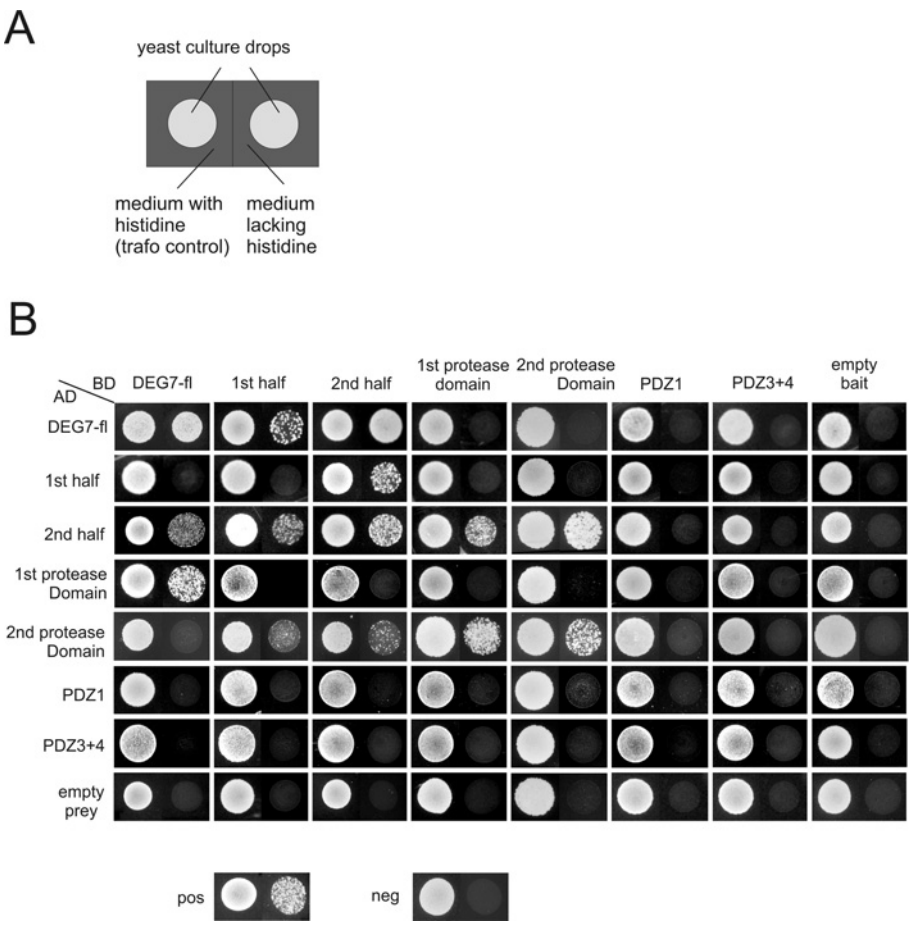

Figure S4 Y2H assay shows that oligomerization of DEG7 is mediated by the second (degenerated) protease domain (extended version)

(**A**) Schematic outline of the experiment. Yeast drop cultures on medium containing histidine, but lacking tryptophan and leucine were used as transformation controls, indicating that the strain contains both the AD and the BD vector. (**B**) Y2H assay as summarized in Table 1 and Figure 4 of the main text. Empty AD and BD vectors were used as autoactivation controls. Every yeast strain growing on histidine-free medium contains the second protease domain in at least one construct. The AD–first half, BD–first half, AD–active protease domain, and BD–active protease domain constructs respectively mediated growth on histidine-free medium in at least some combinations, indicating that lack of gene expression in the combinations first half/first half and active protease domain/active protease domain is not due to a lack of protein expression. pos, positive control; neg, negative control.

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