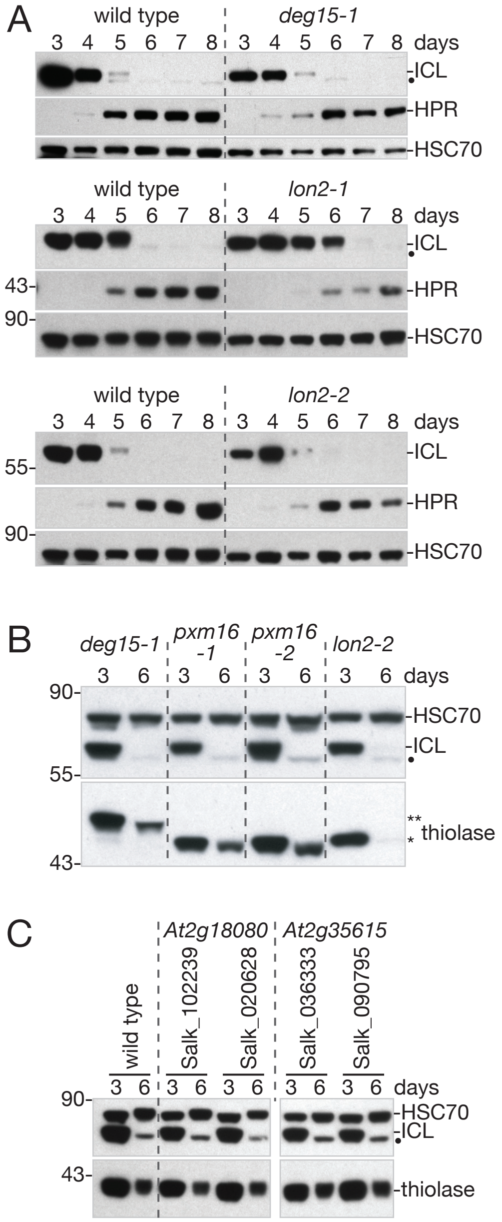

Supplemental Figure 1. The glyoxylate enzyme isocitrate lyase is degraded with near wild-type kinetics in identified putative peroxisomal protease mutants.

(A) Immunoblots of protein extracts from wild-type (Col-0), *deg15-1, lon2-1,* and *lon2-2* cotyledons (12 per lane) cut from 3- to 8-day-old light-grown seedlings.
(B) Immunoblot of protein extracts from *deg15-1, pxm16-1, pxm16-2,* and *lon2-2* cotyledons (12 per lane) from 3- and 6-day-old light-grown seedlings.
(C) Immunoblot of protein extracts from cotyledons of mutants disrupted in putative peroxisomal proteases At2g18080 and At2g35615 from 3- and 6-day-old light-grown seedlings. Blots were probed with antibodies raised against isocitrate lyase (ICL), hydroxypyruvate reductase (HPR), PED1 (thiolase), and HSC70. Positions of molecular weight markers (in kDa) are indicated on the left. Processed and unprocessed thiolase are marked by one or two asterisks, respectively, and a filled circle marks the position of a protein that cross-reacts with the ICL antibody but is not found in the *icl* null mutant (Zolman et al., 2005).

Supplemental Table I. *Primers used to determine mutant genotypes.*

Genotype	Primers[1]	Amplicon size (bp)
deg15-1	R005: CCTCCCTGTGGTGATGATTTATGAAGCC LB1-SALK: CAAACCAGCGTGGACCGCTTGCTGCAACTC	246
DEG15	R005: CCTCCCTGTGGTGATGATTTATGAAGCC R006: TGGCCATGAAGTTAGCGTTGTGTG	487
lon2-1	R008: TTACCATATGGGCCAACACAGTCC LB1-SALK	278
lon2-2	R008: TTACCATATGGGCCAACACAGTCC LB1-SALK	248
LON2	R007: ATTGGCTGCACACCGGTATGGTAT R008: TTACCATATGGGCCAACACAGTCC	466
pxm16-1	R002: ACTTTACGAATCAGTAAGCGATAATCCA LB1-SALK	378
PXM16-1	R001: GGGATATATTCATTATACAAATGACGTGGC R002: ACTTTACGAATCAGTAAGCGATAATCCA	403
pxm16-2	R004: GGGTTAGAGCCATCTTGGTGGTAGAA LB1-SALK	273
PXM16-2	R003: GGCAGCCATATCACCAAGCAATGT R004: GGGTTAGAGCCATCTTGGTGGTAGAA	458
ped1-96	PED1-16: ATCTGGGCTTCAGGCTGTTGCTGAT PED1-17: TGCCTTTCTGTGCGAGTCAACCTA	[2]502
PED1	PED1-16: ATCTGGGCTTCAGGCTGTTGCTGAT PED1-17: TGCCTTTCTGTGCGAGTCAACCTA	[3]305, 197

[1] Primers are given in the 5′ to 3′ orientation.

[2] The *ped1-96* mutation destroys a *Hin*P1I site.

[3] The 502-bp *PED1* amplicon is cleaved once by *Hin*P1I.

Supplemental Table II. *Accession numbers for LON homologs used in phylogenetic analysis.*

Organism	Protein name	Protein accession number
Anaeromyxobacter sp. Fw109-5	La / Anae109_2098	YP_001379285
Arabidopsis thaliana	LON1 / At5g26860	NP_568490
Arabidopsis thaliana	LON2 / At5g47040	NP_568675
Arabidopsis thaliana	LON3 / At3g05780	NP_566258
Arabidopsis thaliana	LON4 / At3g05790	NP_566259
Caenorhabditis elegans	C34B2.6	NP_492796
Danio rerio	LONP1	XP_691712
Danio rerio	LONP2	NP_001008573
Debaryomyces hansenii	DEHA0G02310g	XP_461623
Drosophila melanogaster	CG8798	NP_649133
Escherichia coli	La	YP_003053061
Gallus gallus	LONP2	XP_414106
Homo sapiens	LONP1	NP_004784
Homo sapiens	LONP2	NP_113678
Kluyveromyces lactis	KLLA0B01892g	XP_451615
Micromonas sp. RCC299	MICPUN_113675	ACO63129
Myxococcus xanthus	La	YP_632173
Oryza sativa	Os09g0533400	NP_001063769
Physcomitrella patens	PHYPADRAFT_161045	XP_001757793
Pichia angusta	PLN	ABB88892
Pichia pastoris	PAS_chr1-1_0174	XP_002489820
Populus trichocarpa	POPTRDRAFT_827676	XP_002329591
Saccharomyces cerevisiae	Pim1p	NP_009531
Schizosaccharomyces pombe	LON1	NP_593035
Yarrowia lipolytica	YALI0F23595g	XP_505795