

Supplementary Material

Title

Comparative proteomic analysis of wild-type *Physcomitrella patens* and an OPDA-deficient *Physcomitrella patens* mutant with disrupted *PpAOS1* and *PpAOS2* genes after wounding

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Supplementary Fig. S1.

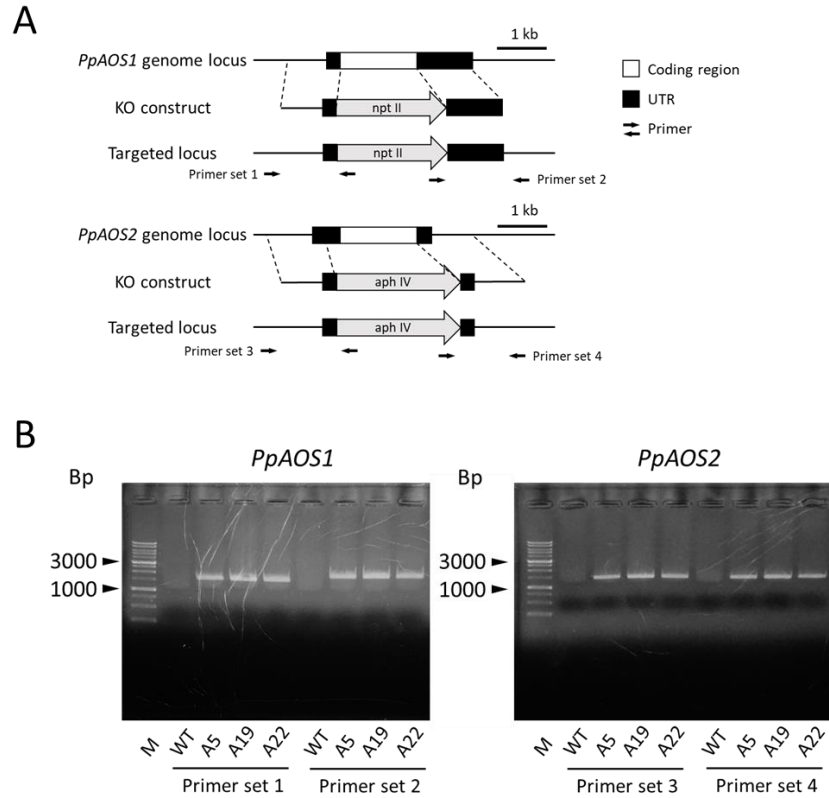


Fig. S1. Disruption of *PpAOS1* and *PpAOS2* genes in *P. patens*.

A, Genomic structures of *PpAOS1* and *PpAOS2* in the wild-type and targeted *PpAOS1* and *PpAOS2* knock-out mutants (A5, A19, and A22). The *npt II* and *aph IV* expression cassettes were inserted in A5, A19, and A22 strains. B, Genomic PCR data of wild-type, and A5, A19 and A22 strains. *P. patens* genomic DNA was isolated from protonemata by the CTAB method (Nishiyama et al., Ref. 32). PCR was performed in 50 μ L of a reaction mixture containing 1 μ L of genomic DNA solution, 1.5 μ L of each primer (5 μ M), 25 μ L of KOD One PCR Master Mix (Toyobo, Japan), and 21 μ L of Milli-Q water. PCR was conducted with the following conditions: 30 cycles of 98°C for 10 s, 58°C for 5 s, and 68°C for 15 s. The PCR products were analyzed by gel electrophoresis and visualized by ethidium bromide. The primers used are listed in Supplemental Table

S5.
Supplementary Fig. S2.

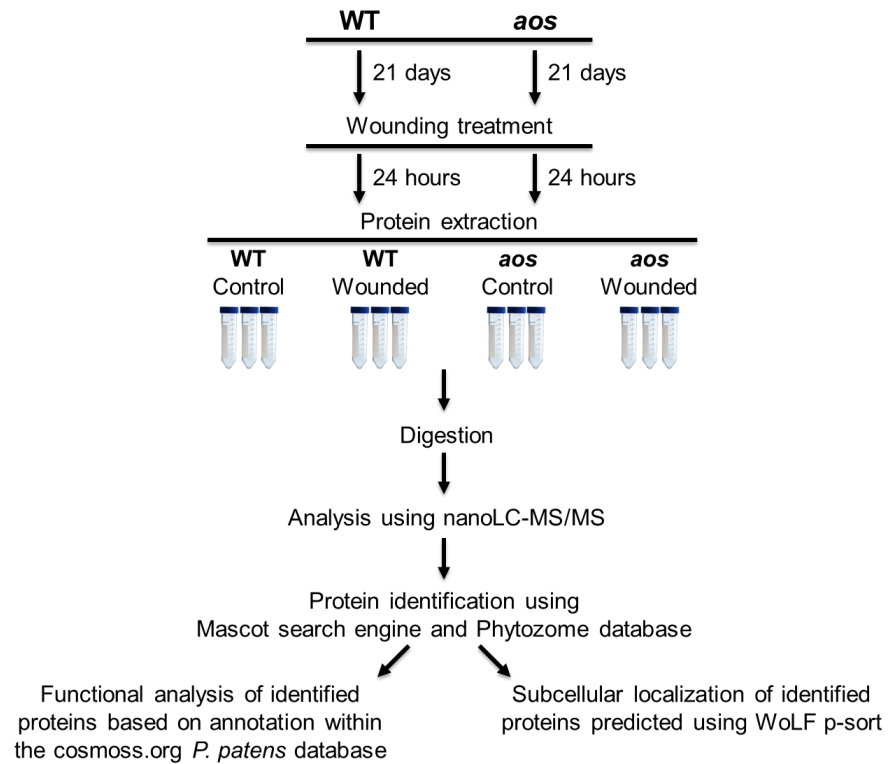


Fig. S2. Experimental design for the proteomic analysis of *P. patens* proteins.

Three-week-old *P. patens* (wild-type and the *aos* mutant) were treated with wounding treatment. *P. patens* (wild-type and the *aos* mutant) without wounding treatment were used as the controls. Extracted proteins were digested, and the obtained peptides were analyzed using nano LC-MS/MS. Three independent experiments were conducted as biological replicates for the proteome experiments.

Supplementary Table S1. Proteins identified as responsive to wounding in wild-type *P. patens*.

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s141_125V6.1	Chaperonin (Cpn60/TCP-1)	Protein folding	Chloroplast	2	3.13
Pp1s201_109V6.1	Chaperonin (Cpn60/TCP-1)	Protein folding	Chloroplast	2	3.13
Pp1s56_219V6.1	Chaperonin (Cpn60/TCP-1)	Protein folding	Chloroplast	6	3.13
Pp1s434_27V6.1	Lipase/lipoxygenase, PLAT/LH2	Lipid metabolism	Chloroplast	3	2.90
Pp1s207_94V6.1	Protein synthesis factor, GTP-binding	Protein synthesis	Endoplasmic reticulum	3	2.78
Pp1s73_232V6.2	Ribosomal Protein L14b/L23e	Protein synthesis	Endoplasmic reticulum	4	2.73
Pp1s114_79V6.1	Ribosomal Protein L14b/L23e	Protein synthesis	Endoplasmic reticulum	4	2.66
Pp1s16_112V6.1	Ribosomal Protein L14b/L23e	Protein synthesis	Endoplasmic reticulum	4	2.66
Pp1s62_136V6.1	Ribosomal Protein L14b/L23e	Protein synthesis	Endoplasmic reticulum	2	2.66
Pp1s60_179V6.1	Ketol-acid reductoisomerase	Amino acid metabolism	Chloroplast	3	2.37
Pp1s290_40V6.1	Dehydrogenase, multi-helical	Amino acid metabolism	Cytoplasm	2	2.37
Pp1s103_66V6.1	ATPase	Energy synthesis	Chloroplast	3	2.32
Pp1s131_71V6.3	Superoxide dismutase	Redox	Chloroplast	2	2.31
Pp1s359_40V6.1	Pyridoxal phosphate-dependent enzyme	Photosystem	Chloroplast	7	2.29
Pp1s78_56V6.2	Dihydrolipoamide acetyltransferase, long form	Photosystem	Chloroplast	7	2.26
Pp1s97_112V6.1	Cytochrome P450 (allene oxide synthase 2)	Lipid metabolism	Chloroplast	4	2.22
Pp1s345_25V6.1	Photosystem I reaction center Protein Psf, subunit III	Photosystem I	Chloroplast	5	2.20
Pp1s80_23V6.1	Photosystem I reaction center Protein Psf, subunit III	Photosystem I	Chloroplast	5	2.19
Pp1s251_44V6.1	Ribulose biphosphate carboxylase, small subunit (RuBisCO)	Carbon fixation	Chloroplast	4	2.19
Pp1s38_300V6.1	Malate dehydrogenase	TCA cycle	Cytoplasm	7	2.19
Pp1s98_132V6.1	Dihydrolipoamide dehydrogenase	TCA cycle	Mitochondrial	3	2.16
Pp1s39_428V6.1	Malate dehydrogenase	TCA cycle	Cytoplasm	8	2.15
Pp1s25_66V6.1	Photosystem II manganese-stabilizing Protein PsbO	Photosystem II	Chloroplast	8	2.13
Pp1s121_54V6.1	Photosystem I reaction center Protein Psf, subunit III	Photosystem I	Chloroplast	5	2.13
Pp1s19_276V6.1	Photosystem I reaction center Protein Psf, subunit III	Photosystem I	Chloroplast	5	2.13
Pp1s228_3V6.1	Acetohydroxy acid isomeroreductase	Amino acid metabolism	Chloroplast	6	2.12

Supplementary Table S1. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s172_22V6.1	Translation elongation factor EF1B	Protein synthesis	Cytoplasm	3	2.12
Pp1s206_126V6.1	Germin-like protein GLP2	Photosystem	Chloroplast	2	2.05
Pp1s311_58V6.1	Eukaryotic translation initiation factor	Protein synthesis	Cytoplasm	3	2.02
Pp1s215_81V6.1	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	4	2.02
Pp1s98_250V6.1	GDP-mannose 3-epimerase	Carbohydrate metabolism	Cytoplasm	2	2.01
Pp1s330_36V6.1	Ribosomal protein L3	Protein synthesis	Endoplasmic reticulum	2	2.01
Pp1s77_207V6.1	Ribosomal protein L3	Protein synthesis	Endoplasmic reticulum	3	2.01
Pp1s112_169V6.1	Cytochrome b6-f complex iron-sulfur subunit	Photosystem	Chloroplast	3	2.01
Pp1s215_71V6.1	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	3	2.00
Pp1s72_222V6.1	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	7	2.00
Pp1s39_223V6.2	Protein disulfide isomerase	Protein synthesis	Endoplasmic reticulum	3	2.00
Pp1s133_103V6.1	Histone H4	Gene expression	Nuclear	3	1.99
Pp1s269_48V6.1	Histone H5	Gene expression	Nuclear	3	1.99
Pp1s342_32V6.1	Histone H6	Gene expression	Nuclear	5	1.99
Pp1s8_168V6.1	Acetyl-biotin carboxylase	Lipid metabolism	Chloroplast	14	1.96
Pp1s283_22V6.1	UDP-glucose pyrophosphorylase	Carbohydrate metabolism	Cytoplasm	3	1.92
Pp1s154_131V6.1	Ribosomal protein L3	Protein synthesis	Endoplasmic reticulum	4	1.91
Pp1s40_48V6.3	Multicopper oxidase type 2	Redox	Cytoplasm	6	1.91
Pp1s18_23V6.1	Acetyl-biotin carboxylase	Lipid metabolism	Chloroplast	12	1.90
Pp1s308_11V6.1	L-ascorbate oxidase	Redox	Cytoplasm	3	1.89
Pp1s106_16V6.2	Formate dehydrogenase	Redox	Cytoplasm	4	1.87
Pp1s182_26V6.1	Photosystem II oxygen evolving complex protein PsbQ	Photosystem II	Chloroplast	3	1.86
Pp1s131_153V6.1	Superoxide dismutase (SOD)	Redox	Chloroplast	11	1.85
Pp1s306_84V6.1	Photosystem II manganese-stabilizing protein PsbO	Photosystem II	Chloroplast	6	1.84
Pp1s127_74V6.1	Ribosomal protein S3	Protein synthesis	Endoplasmic reticulum	6	1.79

Supplementary Table S1. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s136_175V6.1	Ribosomal protein S3	Protein synthesis	Endoplasmic reticulum	4	1.79
Pp1s91_109V6.1	Heat shock protein, HSP70	Stress	Cytoplasm	3	1.76
Pp1s21_165V6.1	Ribosomal protein 60S	Protein synthesis	Endoplasmic reticulum	2	1.76
Pp1s14_438V6.1	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	2	1.75
Pp1s185_81V6.1	Non-green plastid inner envelope membrane Protein	Transport	Plasma Membrane	10	1.75
Pp1s258_52V6.1	Heat shock protein, HSP90	Stress	Cytoplasm	4	1.73
Pp1s26_173V6.2	Quinohemoprotein ethanol dehydrogenase type I (QH-EDH1)	Glycolysis	Plasma Membrane	15	1.72
Pp1s39_82V6.1	UDP-glucose pyrophosphorylase	Carbohydrate metabolism	Cytoplasm	10	1.71
Pp1s79_110V6.1	Malate dehydrogenase	TCA cycle	Cytoplasm	9	1.70
Pp1s21_36V6.1	DJ-1/PfpI family	Protein synthesis	Cytoplasm	10	1.70
Pp1s201_6V6.1	Mitochondrial NAD-dependent malate dehydrogenase	Glycolysis	Cytoplasm	2	1.69
Pp1s85_94V6.1	Non-green plastid inner envelope membrane protein	Transport	Plasma Membrane	9	1.68
Pp1s133_10V6.1	Phosphoenolpyruvate carboxykinase	Gluconeogenesis	Cytoplasm	2	1.67
Pp1s144_37V6.1	Ribosomal protein L19	Protein synthesis	Endoplasmic reticulum	11	1.65
Pp1s60_65V6.1	Photosystem II manganese-stabilizing protein PsbO	Photosystem II	Chloroplast	2	1.65
Pp1s294_50V6.1	Dihydroorotate dehydrogenase family protein	Energy synthesis	Mitochondrial	2	1.64
Pp1s40_57V6.2	Dihydropyrimidine dehydrogenase	Amino acid metabolism	Chloroplast	9	1.64
Pp1s145_172V6.1	Elongation factor 1-delta 1	Protein synthesis	Cytoplasm	16	1.63
Pp1s154_66V6.1	ATP synthase beta chain	Energy synthesis	Mitochondrial	5	1.63
Pp1s12_289V6.1	Pyruvate kinase	Glycolysis	Cytoplasm	5	1.63
Pp1s12_307V6.1	Pyruvate kinase	Glycolysis	Cytoplasm	6	1.63
Pp1s425_20V6.1	Geranylgeranyl reductase	Photosystem	Chloroplast	5	1.62
Pp1s106_68V6.2	Thioredoxin m	Redox	Mitochondrial	5	1.62
Pp1s23_109V6.1	Thioredoxin m	Redox	Mitochondrial	5	1.62
Pp1s317_49V6.1	Thioredoxin m	Redox	Mitochondrial	5	1.62

Supplementary Table S1. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s326_66V6.1	Thioredoxin m	Redox	Mitochondrial	9	1.62
Pp1s17_59V6.1	Pyridoxal phosphate-dependent enzyme (oas-tl4 cysteine) synthase	Amino acid metabolism	Mitochondrial	11	1.62
Pp1s27_81V6.1	Vitamin-B12 independent methionine 5-methyltetrahydropteroyltriglutamate-homocysteine	Amino acid metabolism	Chloroplast	9	1.62
Pp1s291_62V6.1	Heat shock protein, HSP90	Stress	Cytoplasm	11	1.61
Pp1s628_7V6.1	Light-harvesting complex II protein Lhcb5	Photosystem II	Chloroplast	3	1.61
Pp1s156_57V6.1	Pyruvate dehydrogenase E1 component subunit beta	Glycolysis	Cytoplasm	12	1.61
Pp1s6_313V6.1	Light-harvesting complex II protein Lhcb5	Photosystem II	Chloroplast	11	1.60
Pp1s131_154V6.1	Ferredoxin--NADP+ reductase-like protein	Photosystem	Chloroplast	2	1.59
Pp1s233_94V6.1	RNase I inhibitor-like protein	Protein synthesis	Cytoplasm	2	1.59
Pp1s402_8V6.1	RNase I inhibitor-like protein	Protein synthesis	Cytoplasm	2	1.59
Pp1s425_20V6.2	Geranylgeranyl reductase	Photosystem	Chloroplast	7	1.58
Pp1s348_15V6.1	14-3-3 protein Lil 1433-3	Signaling	Nuclear	7	1.58
Pp1s67_176V6.1	14-3-3 protein Lil 1433-3	Signaling	Nuclear	7	1.58
Pp1s154_69V6.1	ATPase alpha subunit protein ATPB	Energy synthesis	Mitochondrial	17	1.58
Pp1s310_30V6.1	ATP synthase beta chain	Energy synthesis	Mitochondrial	17	1.58
Pp1s147_10V6.1	Clathrin heavy chain	Transport	Cytoplasm	6	1.57
Pp1s7_102V6.1	Clathrin heavy chain	Transport	Cytoplasm	6	1.57
Pp1s62_236V6.4	Glutamate dehydrogenase	Amino acid metabolism	Mitochondrial	6	1.57
Pp1s20_284V6.1	Geranylgeranyl reductase	Photosystem	Chloroplast	5	1.57
Pp1s62_236V6.7	Glutamate dehydrogenase	Amino acid metabolism	Mitochondrial	4	1.56
Pp1s309_84V6.1	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	Glycolysis	Cytoplasm	9	1.55
Pp1s33_110V6.2	Vitamin-B12 independent methionine 5-methyltetrahydropteroyltriglutamate-homocysteine	Amino acid metabolism	Chloroplast	16	1.55
Pp1s419_7V6.1	Lipoxygenase	Lipid metabolism	Chloroplast	26	1.53
NC_005087.1_cd sid_NP_904171.1	Cytochrome b6	Photosystem	Chloroplast	3	1.53

Supplementary Table S1. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s100_117V6.1	ATP synthase subunit beta	Energy synthesis	Mitochondrial	6	1.52
Pp1s425_12V6.1	Vacuolar ATPase beta subunit	Energy synthesis	Mitochondrial	6	1.52
Pp1s85_75V6.2	ATP synthase subunit beta	Energy synthesis	Mitochondrial	6	1.52
Pp1s254_25V6.1	Chloroplast precursor (Plastocyanin)	Photosystem II	Chloroplast	5	1.52
Pp1s309_73V6.2	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	Glycolysis	Cytoplasm	9	1.52
Pp1s10_102V6.1	Ribosomal protein L4/L1e	Protein synthesis	Endoplasmic reticulum	9	1.51
Pp1s99_201V6.1	Amino acid binding	Amino acid metabolism	Cytoplasm	4	1.51
Pp1s214_86V6.1	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	3	1.50
Pp1s214_87V6.1	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	3	1.50
Pp1s429_33V6.1	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	3	1.50
Pp1s100_107V6.1	Geranylgeranyl reductase	Photosystem	Chloroplast	5	1.50
Pp1s399_19V6.1	Vitamin-B12 independent methionine 5-methyltetrahydropteroyltriglutamate-homocysteine	Amino acid metabolism	Chloroplast	14	1.50
Pp1s220_79V6.1	Heat shock protein, HSP90	Stress	Cytoplasm	10	1.50
Pp1s220_83V6.1	Heat shock protein, HSP90	Stress	Cytoplasm	10	1.50
Pp1s125_81V6.5	Unknown	Unknown	Cytoplasm	5	0.67
Pp1s334_17V6.1	Photosystem I reaction center subunit IV/PsaE	Photosystem I	Chloroplast	4	0.66
Pp1s351_24V6.1	Heat shock protein, HSP70	Stress	Cytoplasm	5	0.65
Pp1s24_254V6.1	Unknown	Transport	Mitochondrial	4	0.59
Pp1s114_95V6.1	Rubisco subunit-binding protein alpha subunit	Carbon fixation	Chloroplast	6	0.56
Pp1s125_81V6.2	Unknown	Unknown	Cytoplasm	6	0.54
Pp1s165_12V6.2	Nucleoside diphosphate kinase	Gene expression	Cytoplasm	3	0.54
Pp1s61_17V6.4	S-formylglutathione hydrolase (esterase d)	Stress	Chloroplast	2	0.51
Pp1s259_76V6.1	Photosystem II 5 kDa protein, chloroplast precursor (PSII-T)	Photosystem II	Chloroplast	2	0.51
Pp1s54_166V6.1	Photosystem II protein PsbR (Photosystem II 10-kDa polypeptide)	Photosystem II	Chloroplast	3	0.50

Supplementary Table S1. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
NC_005087.1_cd sid_NP_904203.1	Photosystem I P700 chlorophyll a apoprotein A2	Photosystem I	Chloroplast	7	0.50
Pp1s131_72V6.1	Serine carboxypeptidase	Amino acid metabolism	Chloroplast	2	0.49
Pp1s170_46V6.1	Rubisco subunit-binding protein alpha subunit	Carbon fixation	Chloroplast	2	0.48
Pp1s200_89V6.1	Uncharacterized protein family UPF0133	Unknown	Chloroplast	2	0.44
Pp1s475_2V6.1	Sucrase/ferredoxin-like protein	Hydrolysis	Cytoplasm	2	0.41
Pp1s309_77V6.1	Glycoside hydrolase (chitinase)	Hydrolysis	Extracellular	3	0.40
Pp1s153_153V6.2	Heat shock protein, HSP70	Stress	Cytoplasm	2	0.39
Pp1s87_57V6.1	Clathrin light chain (expressed protein)	Transport	Nuclear	2	0.37
Pp1s15_183V6.1	AMP-activated protein kinase	Energy synthesis	Chloroplast	2	0.35
Pp1s240_68V6.1	Signal-peptide (unknown)	Signaling	Extracellular	5	0.32
Pp1s77_158V6.2	GY-Box (GY)	Gene expression	Nuclear	4	0.27
Pp1s52_261V6.1	Late embryogenesis abundant (plants) LEA-related	Stress	Nuclear	2	0.25

¹Protein IDs are from Phytozome ver. 11.0.9 (<http://www.phytozome.net/>).

²MP indicates the number of matched peptides.

³The ratio indicates the fold change between the control and wounding treatment group

Supplementary Table S2. Proteins identified as responsive to wounding in the *aos* mutant of *P. patens*.

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s306_59V6.1	Signal-peptide (Expressed protein)	Unknown	Vacuolar	2	4.68
Pp1s52_261V6.1	Late embryogenesis abundant (plants) lea-related	Stress	Nuclear	2	4.10
Pp1s75_107V6.2	Glutathione S-transferase (glutathione s-transferase)	Detoxification	Chloroplast	2	3.06
Pp1s109_234V6.1	26S proteasome subunit P45 (26s proteasome subunit 4)	Degradation	Cytoplasm	2	2.59
Pp1s12_207V6.1	26S proteasome subunit P45 (26s proteasome subunit 4)	Degradation	Cytoplasm	2	2.59
Pp1s4_277V6.1	26S proteasome subunit P45 (26s proteasome subunit 4)	Degradation	Cytoplasm	2	2.59
Pp1s106_16V6.1	NAD(P)-binding domain (formate dehydrogenase)	Redox	Cytoplasm	2	2.57
Pp1s31_343V6.1	Eukaryotic translation initiation factor 3F, EIF3F	Gene expression	Cytoplasm	2	2.54
Pp1s170_67V6.1	NADH:ubiquinone oxidoreductase, subunit G	Photosystem II	Chloroplast	2	2.31
Pp1s315_40V6.1	Pre-pro-cysteine proteinase	Protein synthesis	Extracellular	2	2.25
Pp1s33_172V6.1	Leucyl aminopeptidase-like protein	Protein synthesis	Cytoplasm	2	2.23
Pp1s215_81V6.1	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	3	2.22
Pp1s6_50V6.1	Glycoside hydrolase, family 31	Hydrolysis	Vacuolar	2	2.18
Pp1s156_53V6.1	Germin-like protein GLP4	Stress	Cytoplasm	4	2.15
Pp1s121_144V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	2	2.08
Pp1s235_118V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	2	2.08
Pp1s302_25V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	2	2.08
Pp1s3_375V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	2	2.08
Pp1s83_173V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	2	2.08
Pp1s14_318V6.1	26S proteasome non-ATPase regulatory subunit 4	Degradation	Cytoplasm	2	2.07
Pp1s350_23V6.2	Asparagine synthetase	Amino acid metabolism	Cytoplasm	2	2.05
Pp1s58_224V6.1	GY-box (GY)	Gene expression	Nuclear	7	2.05
Pp1s73_232V6.2	Ribosomal protein L14b/L23e	Protein synthesis	Endoplasmic reticulum	3	2.05
Pp1s50_102V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	3	2.05
Pp1s28_321V6.1	Formate dehydrogenase/DMSO reductase, domains 1-3	Redox	Cytoplasm	3	2.04

Continued

Supplementary Table S2. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s75_99V6.1	LATE embryogenesis ABUNDANT (LEA)	Stress	Nuclear	5	2.03
Pp1s9_107V6.2	12-oxophytodienoate reductase OPR	Stress	Chloroplast	2	2.02
Pp1s335_17V6.1	MRO11.7; expressed protein	Unknown	Chloroplast	2	1.98
Pp1s206_126V6.1	Germin-like protein GLP2	Photosystem	Chloroplast	2	1.98
Pp1s293_81V6.1	Unknown	Unknown	Nuclear	9	1.97
Pp1s13_231V6.1	Unknown	Unknown	Nuclear	3	1.95
Pp1s252_67V6.2	Gene abcb16 multidrug resistance protein	Transport	Plasma Membrane	7	1.95
Pp1s86_31V6.1	Germin-like protein (GLP4) (GLP5)	Stress	Cytoplasm	5	1.92
Pp1s95_65V6.1	Methionine sulfoxide reductase type	Redox	Chloroplast	2	1.89
Pp1s326_44V6.1	12-Oxophytodienoate reductase 2	Stress	Chloroplast	2	1.88
Pp1s17_304V6.2	Ribosomal protein S27e	Protein synthesis	Chloroplast	2	1.88
Pp1s92_45V6.1	Ribosomal protein S27e	Protein synthesis	Chloroplast	2	1.88
Pp1s144_37V6.1	Ribosomal protein L19/L19e	Protein synthesis	Nuclear	3	1.85
Pp1s218_59V6.1	Serine threonine-protein kinase	Protein synthesis	Cytoskeleton	2	1.84
Pp1s240_91V6.1	Serine threonine-protein kinase	Protein synthesis	Cytoskeleton	2	1.84
Pp1s75_99V6.2	Unknown	Unknown	Nuclear	4	1.82
NC_007945.1_cd sid_YP_539003.1	ATPase subunit 8	Energy synthesis	Mitochondrial	2	1.82
Pp1s159_85V6.2	SOUL heme-binding protein (soul-like protein)	Signaling	Nuclear	2	1.81
Pp1s285_10V6.1	Cysteine protease	Degradation	Vacuolar	3	1.80
Pp1s348_22V6.1	Plastid-lipid-associated protein	Transport	Chloroplast	4	1.77
Pp1s69_133V6.1	Putative protein	Transport	Chloroplast	4	1.76
Pp1s180_8V6.1	Neuromodulin (Growth-associated protein 43)	Degradation	Cytoplasm	3	1.75
Pp1s44_58V6.1	GTP-binding protein	Signaling	Cytoplasm	3	1.73
Pp1s214_86V6.1	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	4	1.72
Pp1s214_87V6.2	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	4	1.72
Pp1s429_33V6.1	Type III chlorophyll a/b-binding protein	Photosystem II	Chloroplast	4	1.72

Continued

Supplementary Table S2. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s131_107V6.1	Sucrose-phosphate synthase	Glycolysis	Cytoplasm	2	1.70
Pp1s181_57V6.4	Unknown	Lipid metabolism	Vacuolar	4	1.70
Pp1s84_187V6.1	Pirin-like protein	Signaling	Chloroplast	2	1.69
Pp1s157_11V6.1	Glucan endo- -beta-glucosidase	Signaling	Plasma Membrane	2	1.68
Pp1s121_168V6.1	Glycoside hydrolase family	Hydrolysis	Chloroplast	4	1.67
Pp1s72_222V6.2	Ribosomal protein S13	Protein synthesis	Endoplasmic reticulum	3	1.64
Pp1s215_71V6.1	Ribosomal protein S14	Protein synthesis	Endoplasmic reticulum	4	1.63
Pp1s72_222V6.1	Ribosomal protein S15	Protein synthesis	Endoplasmic reticulum	4	1.63
Pp1s55_66V6.2	Late embryogenesis abundant (plants) LEA-related	Stress	Chloroplast	3	1.63
Pp1s152_13V6.1	26S protease regulatory subunit 7	Degradation	Cytoplasm	4	1.62
Pp1s49_256V6.1	26S protease regulatory subunit 7	Degradation	Cytoplasm	4	1.62
Pp1s235_138V6.1	Lactate dehydrogenase (LDH)	Glycolysis	Cytoplasm	2	1.62
Pp1s140_60V6.1	Eukaryotic translation initiation factor 3	Gene expression	Cytoplasm	2	1.61
Pp1s26_26V6.1	Malate dehydrogenase	TCA cycle	Mitochondrial	7	1.60
Pp1s97_166V6.1	Methionine sulfoxide reductase type	Redox	Chloroplast	2	1.60
Pp1s40_48V6.3	Multicopper type 2(Multicopper oxidase, type 2&3)	Redox	Cytoplasm	4	1.60
Pp1s379_40V6.1	Signal transduction protein with CBS domains	Protein synthesis	Chloroplast	3	1.59
Pp1s82_6V6.1	Germin-like protein (GLP4) (GLP5)	Stress	Extracellular	8	1.59
Pp1s2_600V6.1	Mitochondrial phosphate carrier protein	Transport	Mitochondrial	3	1.58
Pp1s2_605V6.1	Mitochondrial phosphate carrier protein	Transport	Mitochondrial	3	1.58
Pp1s86_72V6.2	Outer membrane lipoprotein BLC	Transport	Chloroplast	4	1.58
Pp1s55_65V6.1	Late embryogenesis abundant (plants) LEA-related	Stress	Chloroplast	2	1.57
Pp1s55_66V6.1	Late embryogenesis abundant (plants) LEA-related	Stress	Chloroplast	2	1.57
Pp1s59_239V6.1	Heat shock protein, HSP70	Stress	Mitochondrial	9	1.54
Pp1s8_209V6.1	Heat shock protein, HSP20	Stress	Chloroplast	2	1.53
Pp1s94_106V6.1	Pyrophosphate-fructose-6-phosphate 1-phosphotransferase (PFP)	Carbohydrate metabolism	Cytoplasm	3	1.52

Continued

Supplementary Table S2. Continued

Protein ID ¹	Description	Function	Subcellular location	MP ²	Ratio ³
Pp1s9_103V6.1	Succinate-CoA ligase	TCA cycle	Mitochondrial	2	1.52
Pp1s12_415V6.1	GRAM domain-containing protein	Signaling	Nuclear	7	1.51
Pp1s333_15V6.1	Pyruvate kinase	Glycolysis	Cytoplasm	2	1.51
Pp1s70_15V6.1	Pyruvate kinase	Glycolysis	Cytoplasm	2	1.51
Pp1s37_247V6.2	60s ribosomal protein l2	Protein synthesis	Cytoplasm	4	1.50
Pp1s582_3V6.1	60s ribosomal protein l2	Protein synthesis	Cytoplasm	4	1.50

¹Protein IDs are from Phytozome ver. 11.0.9 (<http://www.phytozome.net/>).

²MP indicates the number of matched peptides.

³The ratio indicates the fold change between the control and wounding treatment group

Supplementary Table S3. List of primers used to construct the double-knockout mutant.

Primer name	Sequence
PpAOS1KO5'-F	5'-ATCTCGAGGGATCCCCATAGGAATAGG-3'
PpAOS1KO5'-R	5'-ATGAATTCGCTTGCCCAACACTACCA-3'
PpAOS1KO3'-F	5'-ATGCATGCGGAGTTCGTCTCCGAGAAC-3'
PpAOS1KO3'-R	5'-ATCATATGCACAACCTCACAGCCTCGTT-3'
PpAOS2KO5'-F	5'-ATAGGTACCAAGCCAGTAGATTGC-3'
PpAOS2KO5'-R.	5'-TATAAGCTTGCAACAACACATTTGGC-3'
PpAOS2KO3'-F	5'-TAGCATGCAGGATTGGAGCAAGTG-3'
PpAOS2KO3'-R	5'-TGAGCTCGGTACCTCAAATCGAATCATG-3'
PpAOS1KO5'-F2	5'-TCAACGAATCCACAGAACGTGAAGTG-3'
PpAOS1KO3'-R2	5'-GCAACACCATATGCCATCACATC-3'
PpAOS2KO5'-F2	5'-AGAGCCAAGTTCGAAACAAGACTGCG-3'
PpAOS2KO3'-R2	5'-TGTTTGTAACACCATCCTTGCAGCG-3'
Pcmv-R	5'-GAGGAAGGGTCTTGCGAAGGATAGTG-3'
35SPA-F	5'-AGGAGGAAGACAAGGAAGGATAAGG-3'

Supplementary Table S4. List of primers used for qRT-PCR analyses.

Protein name	Protein ID	Primer name	Sequence
Chaperonin	Pp1s141_125V6.1	Pp_chap_1S	GCCGGAGTTTGAAGCCCTAT
		Pp_chap_1A	CATCTGCCACCGCCTTAGAG
Histone H4	Pp1s342_32V6.1	20190830-1-F	TATCACCAAGCCTGCCATCC
		20190830-1-R	TTAGCCTCCGAAACCATACAAAG
Ketol-acid reductoisomerase	Pp1s60_179V6.1	20190830-3-F	GAGGTGAGCACCCCAGGTAT
		20190830-3-R	CTTTTGAGCCGATTTTGAGC
PsbQ	Pp1s182_26V6.1	20190830-5-F	GAAGCTATTAAGGCTGTTAAGGATGT
		20190830-5-R	GCTGCGTAGTCCAAATTGTTTCAG
PsbO	Pp1s306_84V6.1	20190830-6-F	AAGAGTTGGTGGCAGAAGGTAAA
		20190830-6-R	CTTGGCAATGCTGAAGGTGA
Pyruvate dehydrogenase e1 component subunit β	Pp1s156_57V6.1	20190830-7-F	ATGGTACGGCCAAGTTCCTG
		20190830-7-R	TCACTCCCTCCCTCATTATCT
Malate dehydrogenase	Pp1s79_110V6.1	20190830-9-F	GGATGGCGACTCTGATGTTTAT
		20190830-9-R	AGACAGTGGCAGCTTGCTTG
ATP synthase β chain	Pp1s310_30V6.1	20190830-10-F	TTGAACACCGGGTCTCCTATC
		20190830-10-R	CGCCGAACAGTCCAATCTTAC
Actin	Ppactin-3U1*	Actin F	CGGAGAGGAAGTACAGTGTGTGGA
		Actin R	ACCAGCCGTTAGAATTGAGCCCAG

*The primers for actin are referenced in the following paper: Aoki S, Kato S, Ichikawa K, and Shimizu M. Circadian expression of the PpLhcb2 gene encoding a major light-harvesting chlorophyll a/b-binding protein in the moss *Physcomitrella patens*. *Plant Cell Physiol.*, 45, 68–76 (2004).