

Table S1. List of genes misregulated in the *php-2* mutant

AGI Gene	Fold change (Log2; php-2/wild-type)	P value for fold change	Gene description
At4g16590	3.87	3.9E-03	"ATCSLA01 (Cellulose synthase-like A1); glucosyltransferase/ transferase, transferring glycosyl groups"
At1g54020	3.68	9.6E-03	"myrosinase-associated protein, putative"
At2g45660	3.08	5.3E-05	AGL20 (AGAMOUS-LIKE 20); transcription factor
At4g14130	2.80	7.1E-03	"XTR7 (XYLOGLUCAN ENDOTRANGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds"
At1g20390	2.65	5.5E-04	transposable element gene
At4g35770	2.16	6.2E-03	SEN1 (DARK INDUCIBLE 1)
At5g26270	2.05	9.5E-04	unknown protein
At3g53250	1.96	9.7E-03	auxin-responsive family protein
At1g09350	1.84	2.8E-03	"ATGOLS3 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups"
At3g28500	1.77	1.6E-04	60S acidic ribosomal protein P2 (RPP2C)
At1g62540	1.73	6.8E-03	flavin-containing monooxygenase family protein / FMO family protein
At5g52310	1.70	1.1E-03	COR78 (COLD REGULATED 78)
At5g09440	1.65	5.5E-03	"phosphate-responsive protein, putative"
At1g51090	1.53	1.9E-03	heavy-metal-associated domain-containing protein
At3g26460	1.49	1.4E-04	major latex protein-related / MLP-related
At4g23680	1.44	1.4E-03	major latex protein-related / MLP-related
At1g65310	1.43	8.2E-03	"ATXTH17 (XYLOGLUCAN ENDOTRANGLUCOSYLASE/HYDROLASE 17); hydrolase, acting on glycosyl bonds"
At3g14395	1.40	1.5E-03	unknown protein
At2g47880	1.35	5.8E-03	glutaredoxin family protein
At2g42760	1.32	7.8E-03	
At1g70270	1.31	3.9E-04	unknown protein
At4g10390	1.28	8.4E-03	protein kinase family protein
At1g09530	1.20	7.9E-03	PAP3/PIF3/POC1 (PHYTOCHROME INTERACTING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription regulator
At1g29395	1.18	5.3E-04	COR414-TM1 (cold regulated 414 thylakoid membrane 1)
At5g57550	1.18	5.8E-03	"XTR3 (XYLOGLUCAN ENDOTRANGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds"
At2g33830	1.17	7.6E-04	dormancy/auxin associated family protein
At4g10380	1.17	4.2E-03	NIP5;1/NLM6/NLM8 (NOD26-like intrinsic protein 5;1); boron transporter/ water channel
At5g10650	1.16	2.4E-03	zinc finger (C3HC4-type RING finger) family protein
At1g12080	1.12	5.8E-03	
At5g62360	1.11	8.9E-05	invertase/pectin methylesterase inhibitor family protein
At1g11080	1.11	6.1E-03	SCPL31 (serine carboxypeptidase-like 31); serine carboxypeptidase
At4g33150	1.11	1.5E-04	LKR (SACCHAROPINE DEHYDROGENASE)
At4g15440	1.08	9.7E-03	HPL1 (HYDROPEROXIDE LYASE 1); heme binding / iron ion binding / monooxygenase
At4g30270	1.07	4.0E-03	"MERI5B (MERISTEM-5); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase"
At1g22690	1.05	3.4E-03	"gibberellin-responsive protein, putative"
At1g68600	1.04	2.2E-03	
At1g52190	1.03	7.6E-03	proton-dependent oligopeptide transport (POT) family protein
At1g27590	1.02	2.7E-03	
At4g12430	-1.02	1.9E-03	"trehalose-6-phosphate phosphatase, putative"

At5g59330	-1.03	1.4E-04	
At2g43590	-1.04	2.2E-04	"chitinase, putative"
At4g24050	-1.04	5.9E-03	short-chain dehydrogenase/reductase (SDR) family protein
At1g69526	-1.07	6.4E-04	UbiE/COQ5 methyltransferase family protein
At4g01870	-1.08	6.4E-03	tolB protein-related
At4g21610	-1.08	1.5E-03	LOL2 (LSD ONE LIKE 2); transcription factor
At1g17050	-1.08	1.8E-04	SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyltranstransferase/ trans-octaprenyltranstransferase
At3g25740	-1.10	9.8E-03	MAP1B (METHIONINE AMINOPEPTIDASE 1C); metalloexopeptidase
At2g40300	-1.12	2.1E-04	ATFER4 (FERRITIN 4); ferric iron binding
At1g13650	-1.16	6.9E-04	
At3g16670	-1.17	2.2E-03	
At1g78000	-1.24	2.0E-04	SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter
At3g46370	-1.28	3.2E-03	"leucine-rich repeat protein kinase, putative"
At3g60070	-1.29	1.4E-04	lactose permease-related
At5g04950	-1.33	2.1E-03	"nicotianamine synthase, putative"
At5g03350	-1.33	1.1E-04	legume lectin family protein
At5g07870	-1.38	2.9E-03	transferase family protein
At3g05730	-1.39	1.0E-03	
At5g16970	-1.44	2.0E-04	AT-AER (ALKENAL REDUCTASE); 2-alkenal reductase
At1g17190	-1.56	5.4E-04	ATGSTU26 (Arabidopsis thaliana Glutathione S-transferase (class tau) 26); glutathione transferase
At1g76930	-1.58	7.2E-03	ATEXT4 (EXTENSIN 4)
At1g01060	-1.68	4.6E-03	LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription factor
At2g38940	-1.72	6.4E-03	ATPT2 (PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen ion symporter
At1g65330	-1.73	5.8E-04	PHE1 (PHERES1); DNA binding / transcription factor
At5g45380	-1.85	1.4E-04	sodium:solute symporter family protein
At2g43570	-1.86	4.4E-03	"chitinase, putative"
At1g73260	-1.98	9.6E-04	trypsin and protease inhibitor family protein / Kunitz family protein
At5g10140	-2.01	2.3E-04	FLC (FLOWERING LOCUS C); transcription factor
At4g12480	-2.04	1.6E-05	pEARLI 1; lipid binding
At4g11650	-2.06	2.7E-03	ATOSM34 (OSMOTIN 34)
At3g18250	-2.14	6.2E-04	
At5g08030	-2.19	1.7E-06	glycerophosphoryl diester phosphodiesterase family protein
At5g17890	-2.28	1.6E-03	LIM domain-containing protein / disease resistance protein-related
At4g12500	-2.34	3.7E-05	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At4g12490	-2.89	5.7E-05	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At3g22590	-3.03	6.1E-04	RNA pol II accessory factor Cdc73 family protein

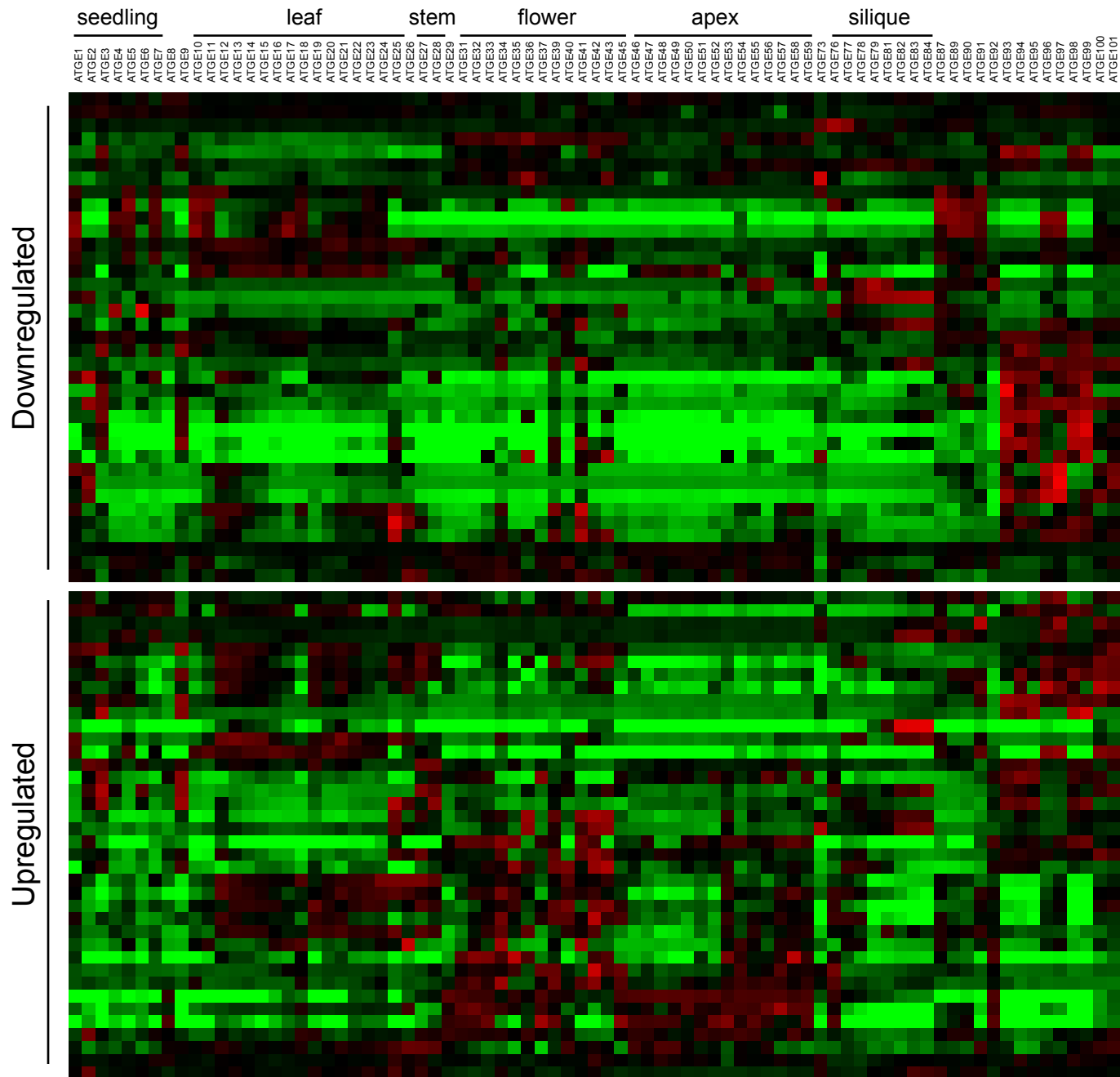


FIG. S2. Developmental regulation of PHP-targeted genes.