

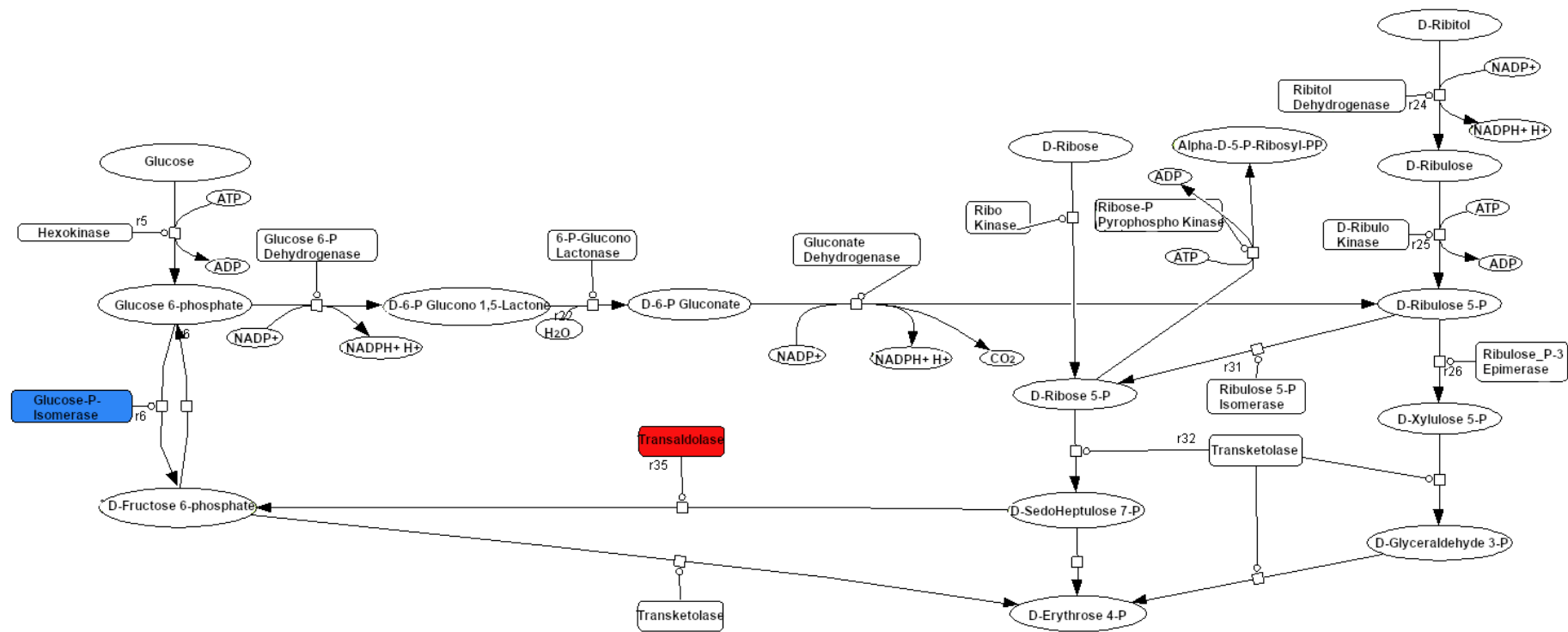
Supplementary Table S1. Pathways and their related differentially expressed genes identified in PHY.

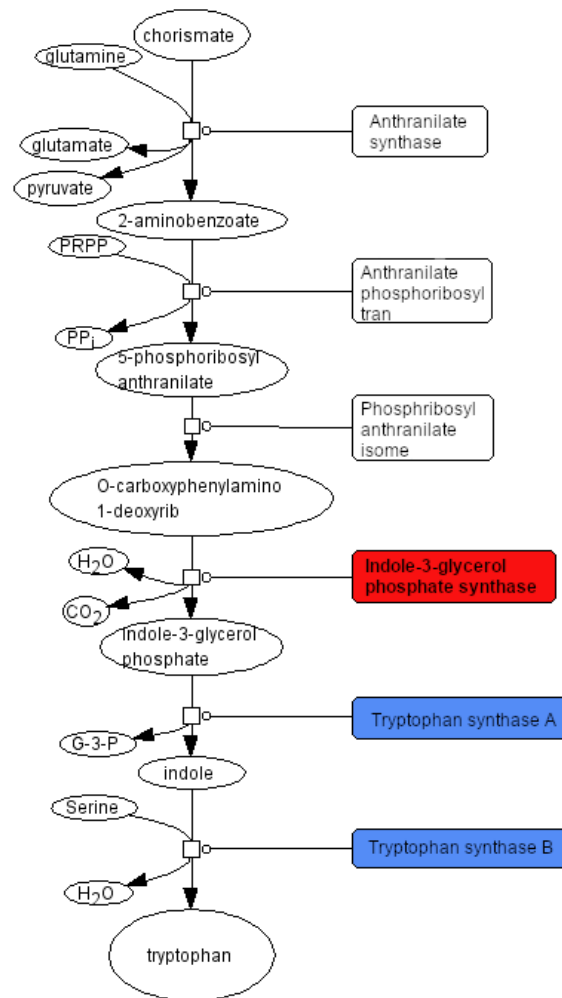
Pathway	Upregulated genes	Gene name (protein name)	Downregulated genes	Gene name (protein name)
5-Hydroxytryptamine biosynthesis	Os10g0400500	OsTDC1		
	Os07g0437500	TDC2		
	Os09g0539100	3-dehydroquinate synthase		
Chorismate biosynthesis	Os01g0102600	Shikimate kinase		
	Os10g0577700	Shikimate kinase		
	Os10g0510000	ACT2	Os03g0836000	ACT3
Cytoskeletal regulation by Rho GTPase	Os10g0323600	Profilin-A	Os12g0163700	-
	Os03g0718100	Actin-1		
	Os01g0282800	TUBB1		
	Os03g0661300	TUBB8		
	Os02g0778400	UMP-CMP kinase 4	Os08g0500900	Phosphoribosylglycinamide formyl transferase 1
De novo purine biosynthesis	Os03g0699300	PURA2	Os05g0270800	Phosphoribosylglycinamide formyl transferase 1
	Os03g0320900	V2		
	Os12g0236400	ADK-A		
	Os12g0548300	Nucleoside diphosphate kinase		
	Os03g0102100	Formyltetrahydrofolate deformylase family protein		
	Os08g19140	Adenylate monophosphate kinase 5		
	Os10g0503200	Folylpolyglutamate synthase		
Formyltetrahydrofolate biosynthesis	Os03g0102100	Formyltetrahydrofolate deformylase family protein		
	Os03g0337600	Uroporphyrinogen decarboxylase 2	Os01g0631200	Uroporphyrinogen-III C-methyltransferase
Heme biosynthesis	Os03g0340001	-		
	Os02g0168800	HEMC		
	Os02g0121000	Glutamate--tRNA ligase		
	Os01g0622300	Uroporphyrinogen decarboxylase 1		
	Os06g0704600	HEMB		
	Os08g0532200	GSA		
	Os05g0558400	Branched-chain-amino-acid aminotransferase		
Isoleucine biosynthesis	Os02g0510200	ALSI		
Leucine biosynthesis	Os05g0558400	Branched-chain-amino-acid aminotransferase		
	Os03g0655700	3-isopropylmalate dehydrogenase		
Lysine biosynthesis	Os03g0118600	Dihydrodipicolinate reductase, C-terminus family protein	Os07g0461900	-
	Os03g0850700	-	Os05g0129100	-
	Os02g0436400	DAPBI		
	Os03g0117000	-		
	Os07g0300900	Aspartate kinase		

Pyruvate metabolism	Os08g0562100	Malate dehydrogenase (NADP(+))	Os02g0232400	Citrate synthase
	Os02g0194100	Citrate synthase	Os12g0183100	2-oxoisovalerate dehydrogenase alpha subunit
	Os01g0300200	<i>ACLB-1</i>		
	Os02g0739600	Pyruvate dehydrogenase E1 component subunit alpha-1		
Salvage pyrimidine ribonucleotides	Os05g0455700	Uracil phosphoribosyl transferase		
	Os02g0778400	UMP-CMP kinase 4		
	Os05g0182201	Hypoxanthine phosphoribosyl transferase		
TCA cycle	Os08g0562100	Malate dehydrogenase (NADP(+))		
	Os02g0194100	Citrate synthase		
	Os02g0739600	Pyruvate dehydrogenase E1 component subunit alpha-1 (PDHE1-A)		
	Os07g0577700	Succinate--CoA ligase [ADP-forming] subunit alpha		

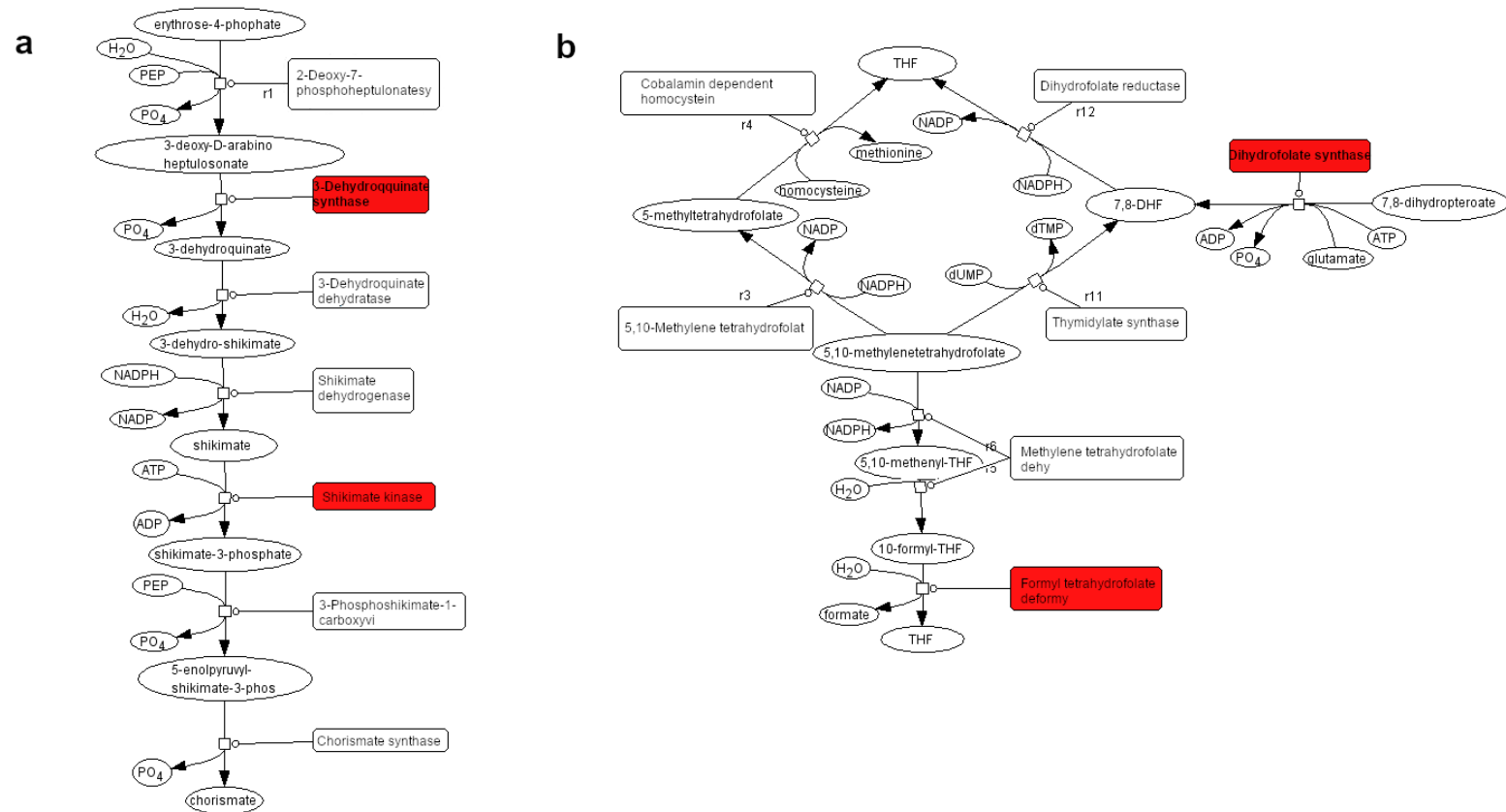
Supplementary Table S2. Pathways and their related differentially expressed genes identified in PHY.

Pathway	Upregulated genes	Gene name (protein name)	Downregulated genes	Gene name (protein name)
5-Hydroxytryptamine degradation	Os01g0591000	<i>ALDH1a</i>	Os02g0730000	<i>Aldh2a</i>
			Os06g0270900	<i>Aldh2b</i>
			Os09g0440300	Aldehyde dehydrogenase (NAD(+))
Apoptosis signalling pathway	Os01g0908100	<i>MPK3</i>	Os02g0148100	<i>MPK3</i>
	Os08g0157000	<i>MPK2</i>	Os03g0276500	70 kDa heat shock protein
	Os02g0797400	<i>MCM5</i>	Os11g0703900	Heat shock cognate 70 kDa protein
	Os01g0885000	CYTOCHROME C-2	Os06g0699400	<i>MPK4</i>
	Os05g0420600	<i>Cytochrome c</i>	Os03g0710500	<i>BIP2</i>
Cadherin signalling pathway	Os10g0510000	<i>Actin-2</i>	Os03g0836000	<i>ACT3</i>
	Os03g0718100	<i>Actin-1</i>	Os12g0163700	-
De novo pyrimidine ribonucleotides biosynthesis	Os02g0778400	UMP-CMP kinase 4	Os01g0616900	CTP synthase
	Os12g0548300	Nucleoside diphosphate kinase		
Folate biosynthesis	Os10g0503200	Folylpolyglutamate synthase	Os08g0500900	Phosphoribosylglycinamide formyl transferase 1
	Os03g0102100	Formyltetrahydrofolate deformylase family protein	Os05g0270800	Phosphoribosylglycinamide formyl transferase 1
Glycolysis	Os07g0181000	<i>OsPK2</i>	Os08g0478800	Glucose-6-phosphate isomerase
	Os09g0535000	Triosephosphate isomerase	Os09g0465600	Glucose-6-phosphate isomerase
Pentose phosphate pathway	Os08g0154300	Transaldolase	Os08g0478800	Glucose-6-phosphate isomerase
			Os06g0129100	-
			Os09g0465600	Glucose-6-phosphate isomerase
Threonine biosynthesis	Os03g0850700	-	Os01g0693800	Threonine synthase
	Os07g0300900	Aspartate kinase		
Tryptophan biosynthesis	Os04g0467700	Indole-3-glycerol-phosphate synthase	Os06g0632200	Tryptophan synthase
			Os08g0135900	Tryptophan synthase

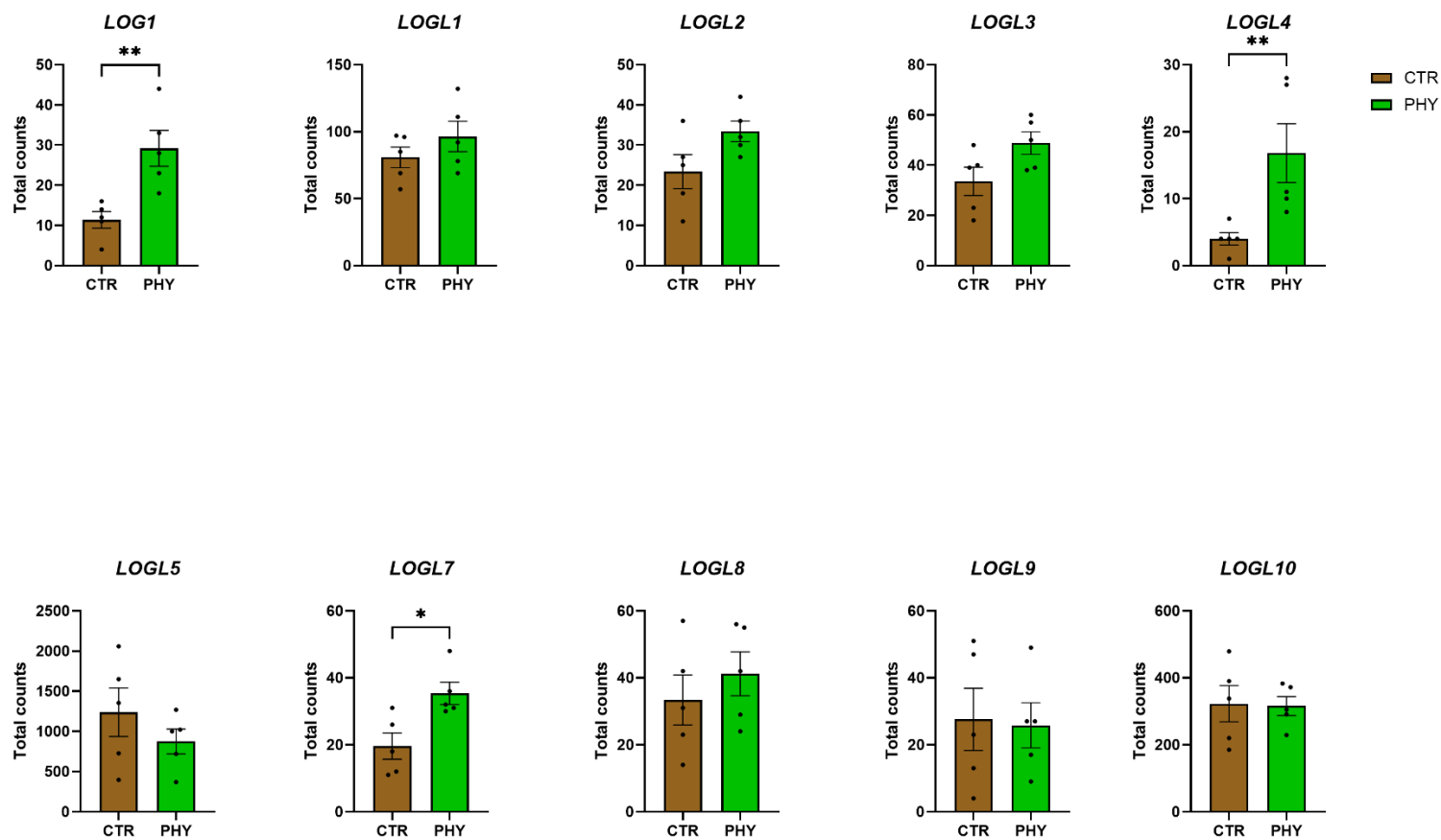




Supplementary Figure S2. Tryptophan biosynthesis with differential expressed genes in PHY. The inhibitory and activated enzymes are highlighted by blue and red, respectively.



Supplementary Figure S3. Pathways with differential expressed genes in PHY. Panel a) represents chorismate biosynthesis; panel b) represents formyltetrahydrofolate biosynthesis. Enzyme encoded by highly expressed gene is highlighted by red.



Supplementary Figure S4. *LOG* gene family RNA-seq count between control and PHY treatment. Data are mean \pm SEM ($n = 5$).

Asterisks indicate significant difference by Mann-Whitney t -test, * = $p < 0.05$, ** = $p < 0.01$.