

Supplemental Table 3. Biochemical pathways regulated by light in both rice and Arabidopsis.

Two sample enzymes for each pathway are given, with one rice gene and one Arabidopsis gene as examples. These two genes were from a best-matched homologous pair. Light-induced gene expression changes in fold are in parenthesis after each gene name. Pathways and Arabidopsis genes in each pathway were identified following the AraCyc pathway database (Mueller et al., 2003), while rice genes were identified based on homology to Arabidopsis genes.

	Pathway	Example Enzyme	Arabidopsis Gene	Rice Gene
Biosynthesis	Amino acids	O-acetylserine (thiol) lyase (cysteine biosynthesis)	At3g03630 (2.5)	OsJRFA065652 (2.3)
		Alanine aminotransferase (alanine biosynthesis)	At1g70580 (5.0)	OsIFCC030660 (1.9)
	Cell structures	4-coumarate coenzyme A ligase	At1g65060 (3.6)	OsJRFA105636 (2.3)
		UDP-galactose 4-epimerase	At4g23920 (2.0)	OsJRFA073610 (2.9)
	Cofactors, Prosthetic Groups, Electron Carriers	Chlorophyll synthetase	At3g51820 (5.1)	OsJRFA068855 (4.6)
		Tocopherol cyclase (vitamin E biosynthesis)	At4g32770 (2.5)	OsJRFA072052 (2.1)
	Secondary Metabolism	Chalcone synthase	At5g13930 (16.8)	OsIFCC022960 (3.4)
		Lycopene beta cyclase (carotenoid biosynthesis)	At3g10230 (2.0)	OsJRFA066182 (2.7)
	Sugars and Polysaccharides	Phosphoglucomutase	At1g23190 (2.2)	OsJRFA064893 (2.1)
		1,4-alpha-glucan branching enzyme	At5g03650 (2.2)	OsIFCC017437 (2.7)
Utilization/ Assimilation/ Degradation	Alcohols	Glyceraldehyde-3-phosphate dehydrogenase	At1g42970 (11.6)	OsIFCC017765 (5.7)
		Enolase (aerobic glycerol catabolism)	At1g74030 (1.9)	OsJRFA069316 (2.9)
	Amino Acids	Aminomethyltransferase (glycine degradation)	At1g11860 (4.3)	OsJRFA099234 (2.9)
		Aspartate aminotransferase (asparagine degradation)	At4g31990 (3.4)	OsJRFA072426 (2.1)
	C1 Compounds	Fructose biphosphate aldolase	At4g26520 (15.2)	OsJRFA105927 (2.6)
		Fructose cytosolic	At1g43670 (3.7)	OsIFCC004110 (5.3)
	Fatty Acids and Lipids	Lipase (triacylglycerol degradation)	At2g42690 (3.4)	OsJRFA059088 (2.0)
		Lipoxygenase	At1g55020 (2.1)	OsIFCC008021 (2.4)
	Inorganic nutrients	Nitrate reductase	At1g37130 (4.9)	OsJRFA102363 (2.1)
		ATP-sulfurylase	At4g14680 (3.9)	OsJRFA105831 (2.2)
Sugars and Polysaccharides	Galactose (galactoside and glucose catabolism)	At5g51820 (5.7)	OsJRFA068502 (2.4)	
	Fructokinase	At1g69200 (3.0)	OsIFCC004290 (2.1)	
Generation of precursor metabolites and energy	Glycolysis	Fructose biphosphate aldolase	At4g38970 (13.8)	OsJRFA099387 (1.9)
		Pyrophosphate-fructose-6-phosphate 1-phosphotransferase	At1g12000 (2.2)	OsJRFA065052 (2.7)
	Pentose phosphate pathways	Ribose 5-phosphate isomerase	At5g44520 (2.5)	OsJRFA060861 (3.4)
		Glucose-6-phosphate Dehydrogenase	At5g35790 (3.1)	OsJRFA064867 (2.4)
	Photosynthesis	Photosystem II oxygen-evolving complex 33	At5g66570 (3.3)	OsIFCC001915 (3.8)
		Light-harvesting chlorophyll A	At3g54890 (26.0)	OsIFCC026844 (16.0)