

Supplemental Table 1: Statistical identification of differentially regulated pathways in *ceh1*, *ceh1/eds16*, and *eds16*. FDR-corrected p value of pathway enrichment from GAGE are shown for each pathway. Values shown in gray represent uncorrected p-values, shown to support related pathways or other analyses.

			<i>ceh1</i>		<i>ceh1/eds16</i>		<i>eds16</i>	
	KEGG identifier	Pathway name	RNA	protein	RNA	protein	RNA	protein
up	ath04141	Protein processing in endoplasmic reticulum	7.18E-09	0.010	0.001	0.035		
	ath04626	Plant-pathogen interaction	7.88E-07		4.82E-04			
	ath03050	Proteasome	7.73E-05		0.031			
	ath00480	Glutathione metabolism	0.012		0.002			
	ath03060	Protein export	0.038					
	ath04145	Phagosome	0.047					
	ath00592	alpha-Linolenic acid metabolism		0.078	0.039	0.015		
	ath00710	Carbon fixation in photosynthetic organisms				0.024	0.081	
	ath01200	Carbon metabolism				0.026		
	ath01230	Biosynthesis of amino acids				0.004		
	ath00630	Glyoxylate and dicarboxylate metabolism				0.008		
	ath00380	Tryptophan metabolism				0.016		
	ath00030	Pentose phosphate pathway				0.031		
	ath00195	Photosynthesis						2.51E-05
	KEGG identifier	Pathway name	RNA	protein	RNA	protein	RNA	protein
down	ath00195	Photosynthesis	1.24E-12	0.070	8.69E-09			
	ath01200	Carbon metabolism	1.41E-06					
	ath00710	Carbon fixation in photosynthetic organisms	5.15E-06	0.018	0.026			
	ath00630	Glyoxylate and dicarboxylate metabolism	9.76E-05	0.029				
	ath00860	Porphyrin and chlorophyll metabolism	8.72E-04		0.006			
	ath00260	Glycine, serine and threonine metabolism	0.003					
	ath01230	Biosynthesis of amino acids	0.015					
	ath00030	Pentose phosphate pathway	0.026					