Supplementary Materials:







Figure S2. Biological process of GO function classifications on the phosphorylated proteins in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons, respectively.



Figure S3. Cellular component of GO function classifications on the phosphorylated proteins in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons, respectively.



Figure S4. Molecular function of GO function classifications on the phosphorylated proteins in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons, respectively.



Figure S5. Subcellular localization prediction of GO function classifications on the phosphorylated proteins in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons, respectively.

			-	log1	0(Fi	sher'	exa	et test p value)				
			0	0.5	1	1.5	2	2.5	3	3.5	4	
Y1 vs Y2	Up-regulated	photosynthetic membrane		1	1	1		2	.5	1		
		photosystem						2	.5			
		thylakoid						2	.5			
		thylakoid part						2	.5			
		photosystem I reaction center					1.8	34				
		photosystem I					1.8	34				
		extrinsic component of membrane				1.3	9					
		thylakoid membrane				1.3	9					
1 vs G1	Up-regulated	photosynthetic membrane								3.11		
		photosystem								3.11		
		thylakoid								3.11		
		thylakoid part								3.11		
		extrinsic component of membrane					2	2.05				
		thylakoid membrane					2	2.05				
Y		photosystem II oxygen evolving complex					2	2.05				
		photosystem II					1.7	9				
	Dow n- regul ated	non-membrane-bounded organelle				1.3	3					
		intracellular non-membrane-bounded organelle				1.3	3				4 100	
Y2 vs G2	Up-regulated	photosynthetic membrane	_							3	.5	
		photosystem	_							3	.5	
		thylakoid	_							3	.5	
		thylakoid part	_					_		3	.5	
		photosystem I reaction center	_						2.8	;		
		photosystem I	_				50		2.8	,		
		extrinsic component of membrane	_			1	.53					
		photosystem II oxygen evolving complex				1	.53	0.11				
	. p	intracentular	-					2.11				
	vn- late	cell	-					.90				
	voC	cell part	-					.96				
	I e	ribonucieoprotein complex				1	1.0/					
		intracellular part				1.4	40					

Figure S6. GO enrichment analysis on cellular component in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons.



Figure S7. GO enrichment analysis on molecular function in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons.

	0	-log10(Fisher' exact test p valu
	Argonaute, linker 1 domain	
	Protein argonaute, N-terminal	
	Argonaute linker 2 domain	
	PAZ domain	
	Piwi domain	
	Protein argonaute, Mid domain	2.59
	Aquaporin-like	2.5
Up-regulated	Ribonuclease H-like domain	2.5
	Outer membrane protein/outer membrane enzyme PagP, beta	2.1
	Pyridoxal phosphate-dependent transferase	1.73
	Pyridoxal phosphate-dependent transferase, major region	1.73
	Dynamin central domain	1.65
	Dynamin, GTPase domain	1.65
	Dynamin GTPase effector	1.65
	GTPase effector domain	1.65
	NAD(P)-binding domain	1.4
	ABC-transporter extracellular N-terminal domain	1.38
	Dynamin-type guanine nucleotide-binding (G) domain	1 38
	CTLH. C-terminal LisH motif	1.38
	START-like domain	1 38
dage - so D	Chlorophyll a/b binding protein domain	1.55
H • > L H and O	Pyridoxal phosphate-dependent transferase	1.55
	Pyridoxal phosphate-dependent transferase major region	3
	Pyridoxal phosphate-dependent transferase, major region	2.61
Up-regulated	Protein argonaute, Mid domain	2.01
	ClnP/crotonase-like domain	2.21
	NAD(P)-binding domain	2.21
	Small GTP-binding protein domain	2.00
	Aguanorin-like	2.03
	Glyceraldehyde 3-phosphate dehydrogenase NAD(P) binding	1.85
	Argonaute linker 1 domain	1.85
	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain	1.85
	Protein argonaute N-terminal	1.85
	Argonaute linker 2 domain	1.85
	Alpha crystallin/Hsp20 domain	1.85
	PAZ domain	1.85
	Piwi domain	1.85
	Tryptophan synthese beta subunit-like PLP-dependent enzyme	1.85
	Outer membrane protein/outer membrane enzyme PagP beta-	1.85
	VTH domain	1.85
	Pentidase M41	1.85
	ATPase A A A-type core	1.64
	HSP20-like chaperone	1.04
	P-loon containing nucleoside trinhosnhate hydrolose	1.37
	Dynamin central domain	1.42
	Dynamin GTPase domain	1.41
>	Chlorophyll a/b hinding protein domain	1.41
Dov sgu	Tetrotricopentide repeat containing domain	1./0
	Nucleotide diphospha sugar transformers	1.00
Up- sgu	ATDase AAA time core	1./4
a <u>e -</u>	A I rase, AAA-type, core	1.05
wn lat		1.89
o ng	Aldolase-type TIM barrel	1./2

Figure S8. Domain enrichment analyses in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons, respectively.



Figure S9. Protein-protein interaction networks of phosphorylated proteins in the Y1 vs G1, Y1 vs Y2 and Y2 vs G2 comparisons.