Table 2

Table 2: GSEA of significantly changing phosphoproteins at the D-L and L-D transition. GSEA was performed using SetRank (corr P value ≤ 0.01; FDR ≤ 0.05, minProt = 2).

D-L Transition					
Name	**Description**	**Database**	**Size**	**SetRank**	**Corr P value**
GO:0016020	membrane	GOCC	273	0.125972	0.000913639
GO:0005524	ATP binding	GOMF	104	0.110291	0.006818059
GO:0009416	response to light stimulus	GOBP	32	0.059617	0.000197647
M00428	eIF4F complex	KEGG	4	0.032225	0.000207554
GO:0005618	cell wall	GOCC	20	0.059617	0.000666835
GO:0009941	chloroplast envelope	GOCC	33	0.032225	0.000828511
GO:0009785	blue light signaling pathway	GOBP	2	0.032225	0.001166915
GO:0016310	phosphorylation	GOBP	60	0.032225	0.001933236
GO:0046527	glucosyltransferase activity	GOMF	5	0.032225	0.007552696
GO:0015291	transmembrane transporter activity	GOMF	9	0.032225	0.008195815
GO:0048528	post-embryonic root development	GOBP	10	0.032225	0.004122321
META_PWY-101	photosynthesis light reactions	BIOCYC	3	0.032225	0.004299686
GO:0009523	photosystem II	GOCC	2	0.032225	0.004363247
GO:0009555	pollen development	GOBP	6	0.032225	0.005631461
GO:1902580	single-organism cellular localization	GOBP	12	0.032225	0.005682244
ath04141	Protein processing in endoplasmic reticulum	KEGG	5	0.032225	0.007587253
GO:0050832	defense response to fungus	GOBP	11	0.032225	0.007657975
GO:0042126	nitrate metabolic process	GOBP	5	0.032225	0.009137088
GO:0003924	GTPase activity	GOMF	6	0.032225	0.009196556
L-D Transition					
Name	**Description**	**Database**	**Size**	**SetRank**	**Corr P value**
GO:0009507	chloroplast	GOCC	116	0.130435	0.000316305
GO:0009108	coenzyme biosynthetic process	GOBP	3	0.048309	0.002527376
GO:0016903	oxidoreductase activity	GOMF	4	0.048309	0.005222496
GO:0005829	cytosol	GOCC	213	0.048309	0.007059263
GO:0016310	phosphorylation	GOBP	52	0.048309	0.009610197
GO:0006997	nucleus organization	GOBP	3	0.048309	0.000925019
GO:0009637	response to blue light	GOBP	9	0.048309	0.001227825
GO:0009573	RuBisCO complex	GOCC	2	0.048309	0.00637449
GO:0009785	blue light signaling pathway	GOBP	2	0.048309	0.006496782
GO:0010359	regulation of anion channel activity	GOBP	2	0.048309	0.006496782
GO:0009416	response to light stimulus	GOBP	31	0.048309	0.008163336
GO:0016192	vesicle-mediated transport	GOBP	31	0.048309	0.002856364
GO:0090407	organophosphate biosynthetic process	GOBP	11	0.048309	0.003001091
GO:0097306	cellular response to alcohol	GOBP	11	0.048309	0.004964197
GO:0003924	GTPase activity	GOMF	6	0.048309	0.006375452
GO:0071365	cellular response to auxin stimulus	GOBP	8	0.048309	0.008146711