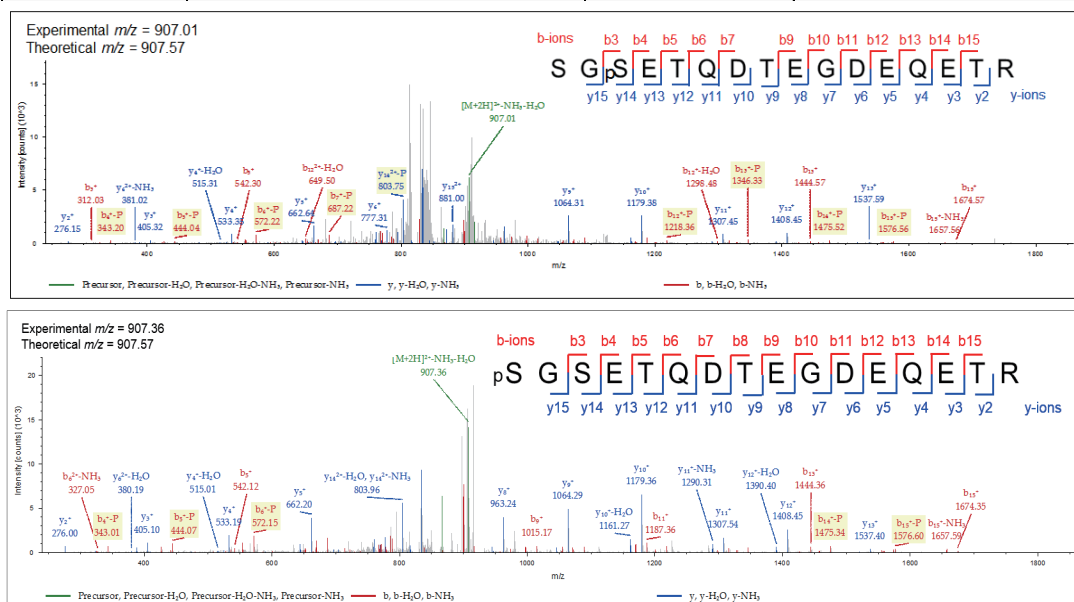


a

R/K - x x S x P Mode I
 R/K x x x S x P Mode II
 R K S S L S PHOT1
 RDYF R S G S ETQD PIF7(S139,S141)
 RDYF R A G A ETQD PIF7(2A)
 RDYF R D G D ETQD PIF7(2D)
 RDYF - - - - ETQD PIF7△
 KTVSLC CDC25C
 KDGS SCS PIF7(S78,S80)
 PIF7(5A): S78A,S80A,S125A,S139A,S141A
 PIF7(5D): S78D,S80D,S125D,S139D,S141D

b

Light condition	Sequence	Modifications	Phospho site Probabilities
White light	SGSETQDTEGDEQETR	S3(Phospho)	S(1):50.0;S(3):50.0
White light	SGSETQDTEGDEQETR	S1(Phospho)	S(1):50.0;S(3):50.0
White light	SGSETQDTEGDEQETR	S3(Phospho)	S(1):6.1;S(3):93.4; T(5):0.4
5 min Shade	SGSETQDTEGDEQETRGEAGR	S3(Phospho)	S(1):8.1;S(3):91.8;T(5):0.1
5 min Shade	SGSETQDTEGDEQETR		
1hr Shade	SGSETQDTEGDEQETR		
1hr Shade	SGSETQDTEGDEQETR		



c

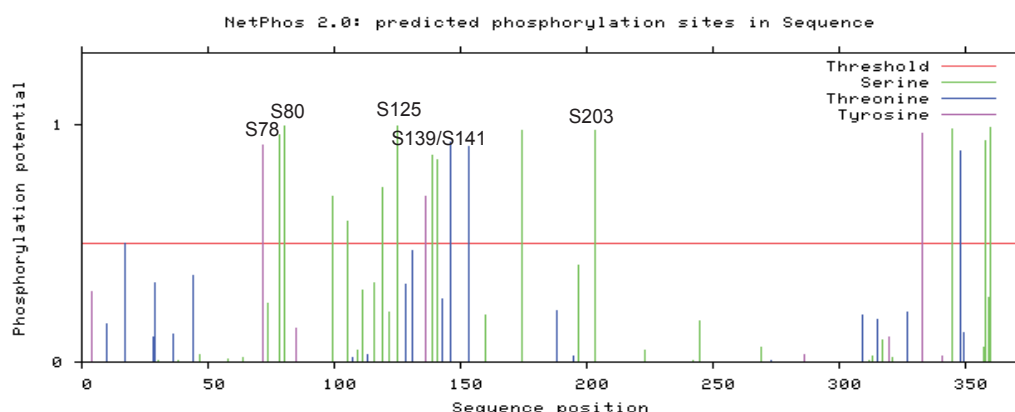


Figure 3-figure supplement 1. Potential phosphorylation sites on PIF7. (a) Two known 14-3-3 binding sequences (mode I and mode II) and putative 14-3-3 binding sequences in PIF7, PHOT1 and CDC25C are listed. The consensus phosphorylation sites are labeled in red. S139 and S141 of PIF7 were identified by LC-MS/MS from PIF7 immunoprecipitated proteins isolated from transgenic plants overexpressing PIF7-Flash. S78 and S80 of PIF7 were predicted as phosphorylation sites by NetPhos 2.0. (b) Identification of PIF7 phosphorylation sites from an LC-MS/MS experiment using immunoprecipitated PIF7 proteins isolated from 35S::PIF7-Flash transgenic plants. The light treatment of the samples, the sequence of the mapped peptide, the modifications of the peptide and the probability for each site are presented in the table. The peptide with phosphorylated modifications was identified by mass spectrometry. (c) Phosphorylation sites of PIF7 as predicted by NetPhos 2.0 (<http://www.cbs.dtu.dk/services/NetPhos/>).