

Supplemental Data. Kaiserli *et al.* (2009) Domain swapping to assess the mechanistic basis of *Arabidopsis* phototropin 1 receptor kinase activation and endocytosis by blue light.

Supplemental Datasets. MASCOT search results of proteins identified in GFP immunoprecipitations by LC-MS/MS.

GFP fusions were immunoprecipitated from 3-day-old dark grown seedlings expressing either phot1-GFP or GFP-Lti6b, after irradiation with blue-light at $100 \mu\text{mol m}^{-2} \text{s}^{-1}$ for 5 min. The gi number (prot_acc) and protein description (prot_desc) identify protein matches from the NCBI database. The protein score (prot_score) is derived from the combined scores of all observed mass spectra that can be matched to amino acid sequences within that protein. Protein matches (prot_matches) gives the number of mass spectra assigned to this protein. Peptide rank (pep_rank) is the rank of the ions match (1 to 10, where 1 is the best match). The pep_isbold statement (0 = false, 1 = true) denotes whether it is the first time the peptide is matched to a protein in the MASCOT report. Pep_miss is the number of missed trypsin cleavage sites within the peptide sequence (limited to a maximum of 1). The peptide score (pep_score) is a probability based MASCOT score: $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Peptide match expectation value (pep_expect) is the number of matches with equal or better scores that are expected to occur by chance alone. The sequence of the peptide is shown in pep_seq, together with the residues that bracket the peptide sequence in the protein (pep_res_before and pep_res_after). If the peptide forms the protein terminus, then a dash is shown instead. The presence of variable modifications (limited to methionine oxidation and phosphorylation of serine, threonine and tyrosine) is shown (pep_var_mod) and their position within the peptide sequence is indicated (pep_var_mod_pos).