



Fig. S2 ScPho4 and CgPho4 alignment and annotation. Protein sequence alignment was generated using ProbCons with 2 passes of consistency transformation and 100 iterative refinement, and was manually edited to align the known Pho85 recognition motifs (red boxes). The shading behind the amino acid symbols represent level of conservation based on BLOSUM62 scores. The functional annotation on the top were based on ScPho4 (Uniprot #P07270). The orange boxes and texts refer to the five breakpoints used for constructing chimeric Pho4 constructs (Fig. 5, 6).