

Scer YFR034C/1-312	1	MGR T T S E G I H - - - - -	10
Cgla CAGL0D05170g/1-533	1	MGE Q V E D MDK - - - - -	10
Calb orf19.1253/1-659	1	- M D Q Q V W N P I F S P S G T T P G K S P S Y Y N E L A P Q S Q S H I S N Q D P Q L P L Q T Q H H Q L	51
Scer YFR034C/1-312	11	- - - - - G F V D D L E P K S S I L D K V G D F I	30
Cgla CAGL0D05170g/1-533	11	- - - - - L Y E T P I D M Q T T I F D Q V D N Y L	30
Calb orf19.1253/1-659	52	F H I D G G S N H S T P S G N I Q L P S S S Q Q N T P H I V S N T P T A F A D S D Q V F L Q H M E M Y D	103
Scer YFR034C/1-312	31	T V N T K - - - - -	35
Cgla CAGL0D05170g/1-533	31	H M V N S G L Q H D E K E D E H R - - - - -	47
Calb orf19.1253/1-659	104	N Q Q H T N Q S A G N T P G P I S F H N H N P N L Q Q A S Q Q P H Q H I S P H L N N L Q Q H S Q Q P Y Q	155
Scer YFR034C/1-312	36	- - - - - R H D G R - - - - -	40
Cgla CAGL0D05170g/1-533	48	- - - - - E H E D A I D - - - - -	54
Calb orf19.1253/1-659	156	H Q H S H S R S H I D S E A P S A N D T P T S S G A L G M A P Q P P L L S S T T N P Q S F D L G L D T I	207
Scer YFR034C/1-312	41	- - - - - E D F N E Q N D E L N S Q E N H N S S E N - - - - -	61
Cgla CAGL0D05170g/1-533	55	- - - - - G G A S L N M H L Y N I N D T L N G V S T D N G H F D M V D - - - - -	84
Calb orf19.1253/1-659	208	G F I I P E E L N F D - - T D P N H I S S A F P P Q L P A - - D Q T P S L L A V D K L K Q L Q Q Q Q Q Q	255
Scer YFR034C/1-312	62	- - - - - G N E N E N E Q D S L A L D D L D R - - - - - A F E L V E G M D	88
Cgla CAGL0D05170g/1-533	85	- - - - - L H F G P T L T T D D D P T K M A E - L Q H T T I H H - - - - - G H L D V N G N R	119
Calb orf19.1253/1-659	256	Q Q R Q Q D P L S E L S S P V L P G Q N D Q S Y N P H H Y Y H R Q S S S N S V F V A G K N T G S S V S A	307
Scer YFR034C/1-312	89	M D W M M P S H A H S P A T T A T I K P R - - - - - L L Y S P L I H T Q S - - - - -	121
Cgla CAGL0D05170g/1-533	120	S D S L F S P F D S F L V H D T P S L E A R N S I Q L T N E G S T S A L T T P F L S G K N H Y D D H G N	171
Calb orf19.1253/1-659	308	P S Q H V R P D A V F T P L V S P V V A P L D I N G K A D K E N G N N S G G H N N S H S S S F S P - - - - -	356
Scer YFR034C/1-312	122	- - - - - A V P V T I S P N L V A T - - - - -	134
Cgla CAGL0D05170g/1-533	172	S I N S Q S F N Y H N R N S S L S K V S G K F S P I S - S P A L T S T - - - - -	205
Calb orf19.1253/1-659	357	- - - Q P A V Q I S - - - - - F E P L T - S P A L N A E P S T I K S K G G K K N H K E T D	392
Scer YFR034C/1-312	135	- - - - - A T S T T S A N K V T K N K S N - - - - - S S P Y L N K R - - - - - R G K P G	163
Cgla CAGL0D05170g/1-533	206	N Q E Q Q H W N T S S R R A S N S S R S K R V L P S - G N S S V S S T S N K - - - - - V I K N S	248
Calb orf19.1253/1-659	393	D R R R S T S S A Y A P S K - D E N K Q Y K R R T P H - G T P I L Q G H T S N A T T V N G S G K P Y K S	442
Scer YFR034C/1-312	164	P D S A - - - - - T S L F E L P D S V I P T P - - - - -	181
Cgla CAGL0D05170g/1-533	249	P Y M N A S S R R L Q K T I S N G N S K R D E W D E - F M F S L P E S S L A N D L T T G N D E N M D I S	299
Calb orf19.1253/1-659	443	P I T K N G K N - - - S Q - - - - K Q D F S F T N - Q F E K L P E S T I I V K S E P M E T S V E P P L	485
Scer YFR034C/1-312	182	- - - - - K P K P K P K - Q Y P K V I L P S N S - - - - -	199
Cgla CAGL0D05170g/1-533	300	L P A G H S P T K E Y N S Y P K V I L P S H A A E N E S M E T D N Y E R A S L L E D S Q P D E T Q N N N	351
Calb orf19.1253/1-659	486	A P Q G Q Q Q D D S N P M L P P N G K P V - - E I T G A P L M G F T M G K L A E G G - - - - -	525
Scer YFR034C/1-312	200	T R R V S P V T A K T S S S A E G - - - - V V V A S E S P V I A P - - - - -	228
Cgla CAGL0D05170g/1-533	352	P Q N N N P H S N G S S I S P V G K N D S V M L A S G S P V I K P Q N S S S N I L Q T P Y S S K R V F K	403
Calb orf19.1253/1-659	526	A G T V A D K K S A K K A G A N N G K L - - - - S R K P S Y S K - - - - -	553
Scer YFR034C/1-312	229	- - - - - H G S S H S R S L S K R R S - - - - -	242

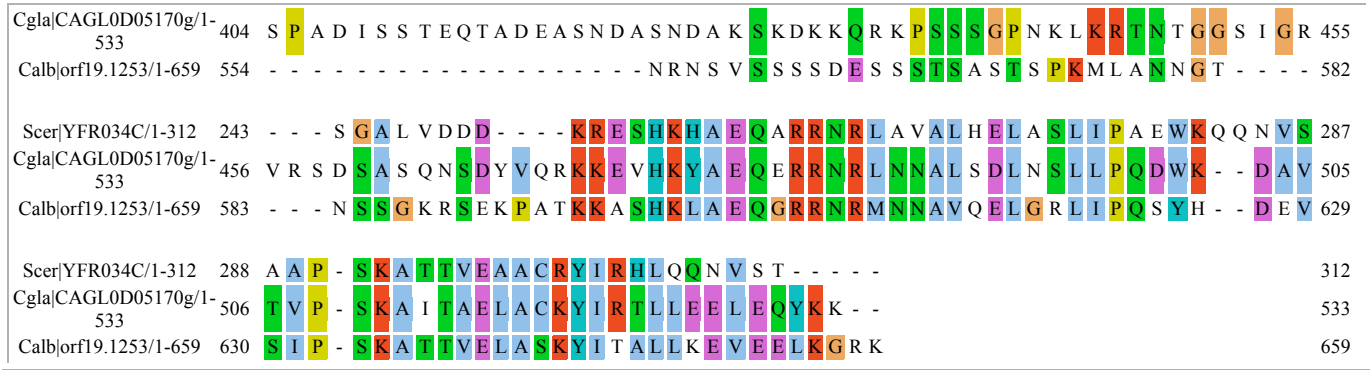


FIGURE S1.—Alignment of *ScPho4* with *CgPho4* and *CaPho4*. Utilizing a tree-assisted alignment of OG9983 which is the orthogroup of *Pho4*, we removed the other 16 species after CLUSTAL alignment, removed gaps common to all three proteins and colored residues according to the clustal option in Jalview. The most conserved portion of the proteins is in the C-terminal DNA binding domain. The known phosphorylation sites of *ScPho4* are surrounded by boxes.