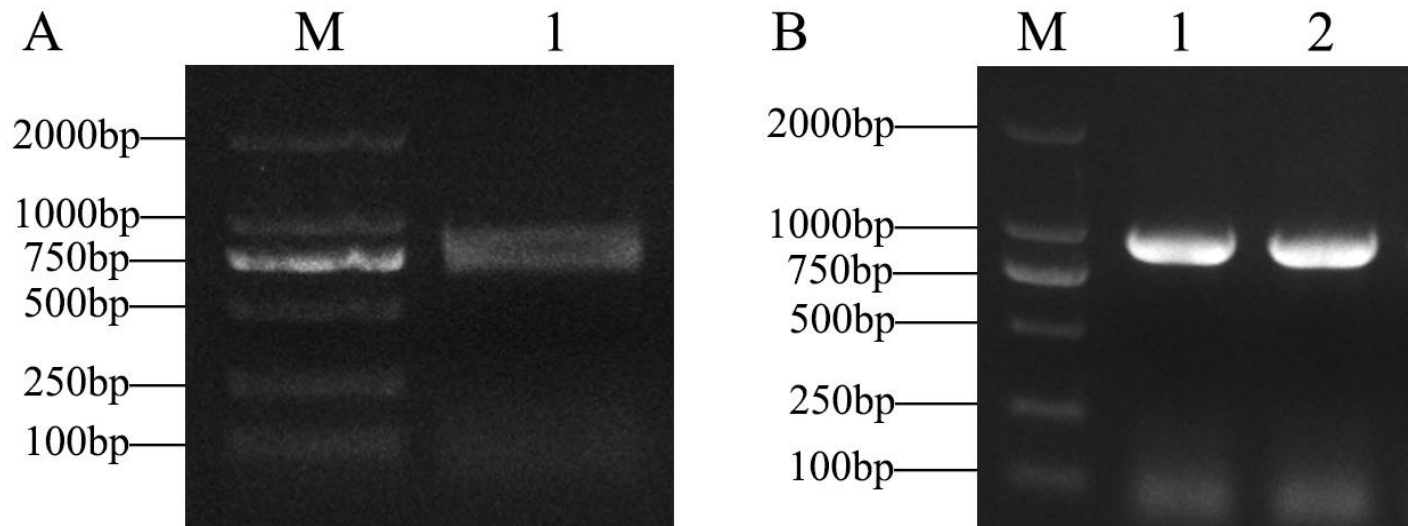


Supplemental Figures

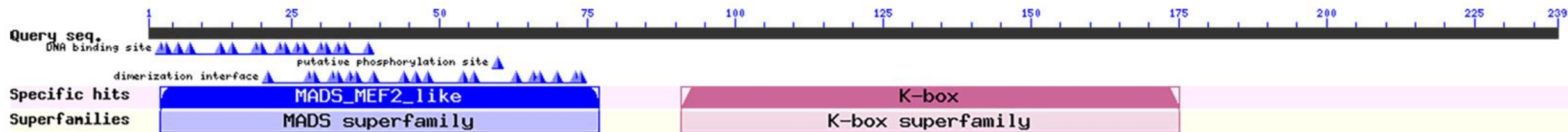
Supplemental Figure S1.



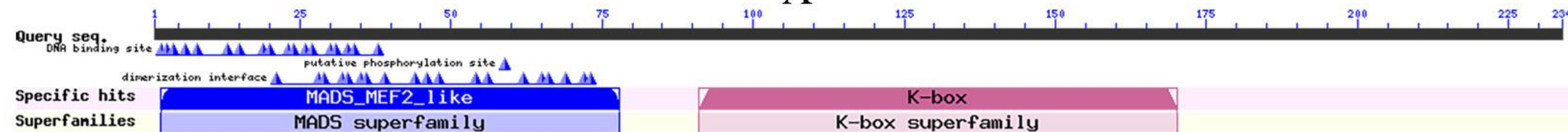
Supplemental Figure S2.

A	1	ATGGTGAGGGGAGAGTGGAGCTGAAGAGGATTGAGAACAGATCAACCGGCAGGTGACATTGCGCAAGAGGAGGAATGGGCTGCTCAAG
	1	M V R G R V E L K R I E N K I N R Q V T F A K R R N G L L K
	91	AAGGCCTACGAGCTGTCTGTGCTCTGCGACGCCGAGGTGCGTCTCATCATCTTCTCCAACCGAGGGAAGCTCTATGAGTTCTGCAGCAGC
	31	K A Y E L S V L C D A E V A L I I F S N R G K L Y E F C S S
	181	TCCAGCATGTTGAAAACTGGATAGGTATCAAAAAAGCAGTTATGGGCAACCTGATACCAGTGTACAAATAAGGGAGAATCAGTTGCTG
	61	S S M L K T L D R Y Q K S S Y G Q P D T S V Q I R E N Q L L
	271	CAGAGTAGTCATCAAGAATACTTGAAACTCAAAGCGCGTGTGGAAGCTTTACAACGATCACAAAGGAATCTTCTTGGTGAGGATCTTGGG
	91	Q S S H Q E Y L K L K A R V E A L Q R S Q R N L L G E D L G
	361	CCTCTAAGCAGCAAGGAGCTGGAGCAACTCGAAAGACAAGTAGACGCATCGTTAAAGCAAATAAGATCAACAAGGACACAGTATATGCTC
	121	P L S S K E L E Q L E R Q L D A S L K Q I R S T R T Q Y M L
	451	GACCAGCTTGCTGACCTTCAAAGAAAGGAACAGATGCTCTGTGAAGCTAACAGAAGTCTCAGGAAGAGGTGGAAGAAAGTAACCAGGCT
	151	D Q L A D L Q R K E Q M L C E A N R S L R K R L E E S N Q A
	541	GACCAGCAGGTCTGGGAGTCCAATGCTAATGCAATAGCATAAGTCGGCAAGCAAATCAACAAGGAGAAGAATTCTACCACTCTTA
	181	D Q Q V W E S N A N A I A Y S R Q A N Q Q Q G E E F Y H P L
	631	GATTGCCAGCCACTCTACAGATTGGGTTCCAACCTGATCAAAATGCCTGGTCCGAGTGTGACTGGTTATGTGCAGGGATGGCTTCCGTGA
	211	D C Q P T L Q I G F Q P D Q M P G P S V T G Y V Q G W L P *
B	1	ATGGCGAGGGAGAAGATACAGGTGCGGAAGATTGACAACGCGACGGCGAGGCAGGTGACCTTCTCGAAGAGGAGGAGGGGCTGTTCAAG
	1	M A R E K I Q V R K I D N A T A R Q V T F S K R R R G L F K
	91	AAGGCCGAGGAGCTCTCCGTCCTCTGCGACGCCGAGGTGCGGCTCATCATCTTCTCCGCCACCGGCAAGCTCTTCGAGTTCCGCGATTCC
	31	K A E E L S V L C D A E V G L I I F S A T G K L F E F A S S
	181	AGTATGAAAGATATCATTGAAAAGCGCAGCATGCATTCAAAGGACATATTGCAGGACAAACCATCACTGGACTTGAATTTAGAGAATTGT
	61	S M K D I I E K R S M H S K D I L Q D K P S L D L N L E N C
	271	AAITATTCAAGTCTGACAAAAACAGTCGCGAGGCAACTCAACAATAAGAAAGACGAAGGGTGAAGACCTTAAAGGCTTATCGATAGAG
	91	N Y S S L T K T V A E A T Q Q L R K T K G E D L K G L S I E
	361	GAGCTTCAACAGCTAGAGAAAACTCTTCAAAGTGGGTTAGATCGAGTTCTAGAGAAAAAGGTGAGCAGATTATGAAAAGGATCAGTGCT
	121	E L Q Q L E K T L Q T G L D R V L E K K G E Q I M K R I S A
	451	CTTGAAAAATAAGGACTCCAATTAATGGAAGAGAATACAGACTGAGACAACAAATGGAGCTCGATATGTCGACAGTGGGGAAGCAGGTT
	151	L E N K G L Q L M E E N T R L R Q Q M E L D M S T V G K Q V
	541	GTTACCGGCTCTGAAAATGGAATTATATGAAGATGGACAGTCCTCAGAATCAGTCACCAACGCTTACATTCTGGGGGGCCGCTCAAGAT
	181	V T G S E N G L Y E D G Q S S E S V T N A S H S G G P P Q D
	631	TATGATGACAGTTTTGACACCTCTCTCAAGTTAGGGCTTCCGTGGAAGGAATCGAAGGGCACGATGATGCAGTAG
	211	Y D D S F D T S L K L G L P W K E S K G T M M Q *

Supplemental Figure S3.

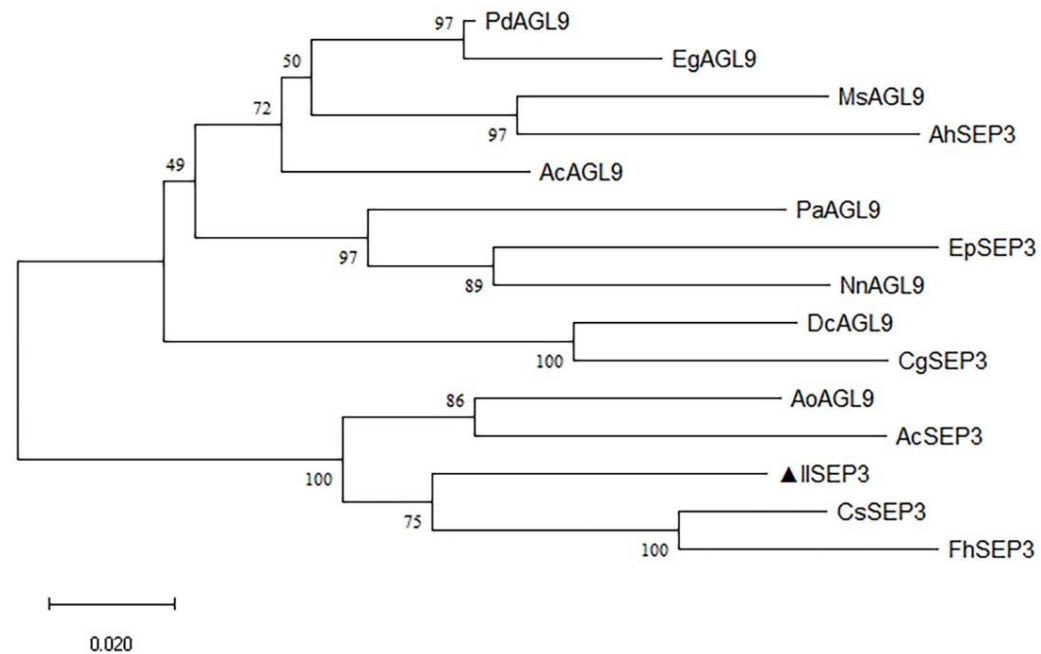


A

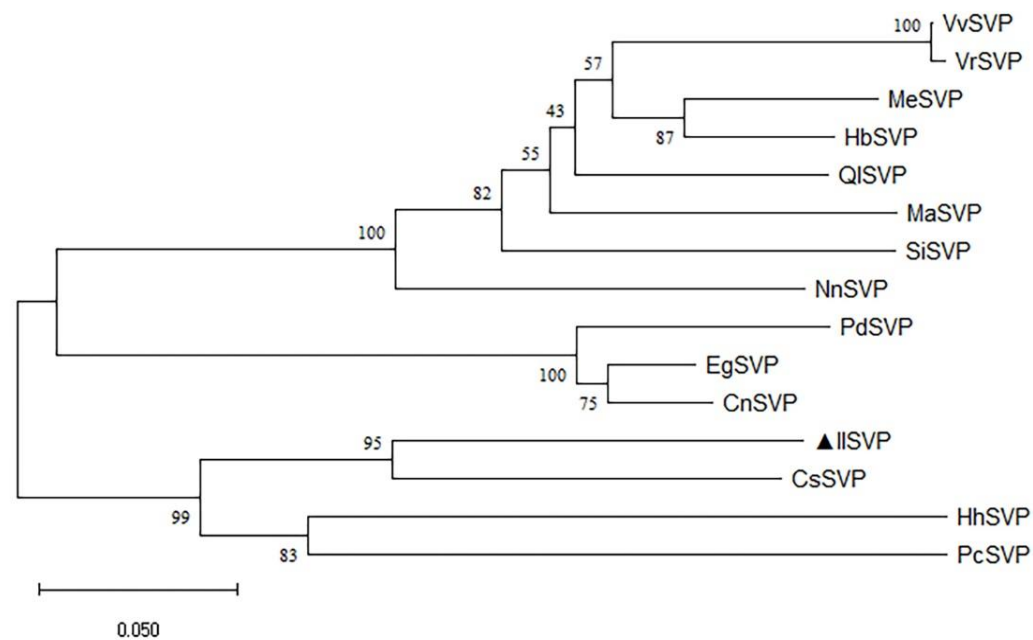


B

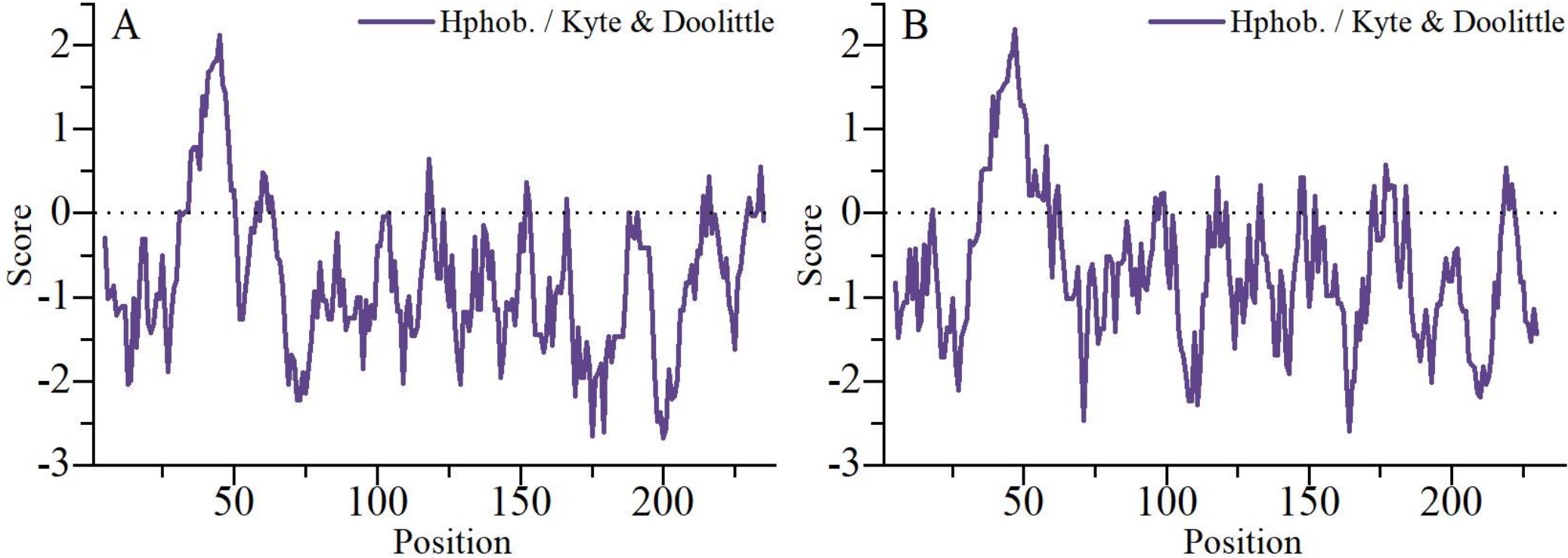
Supplemental Figure S4. A



B

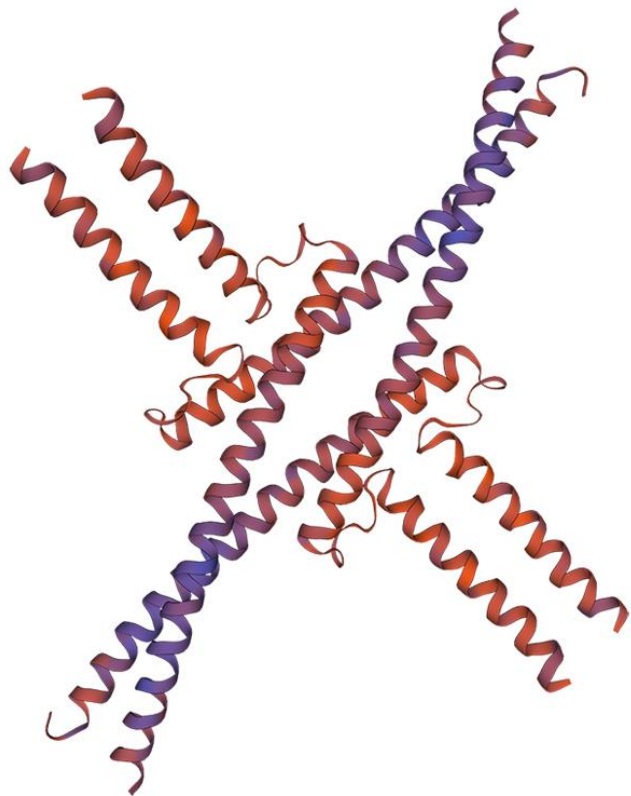


Supplemental Figure S5

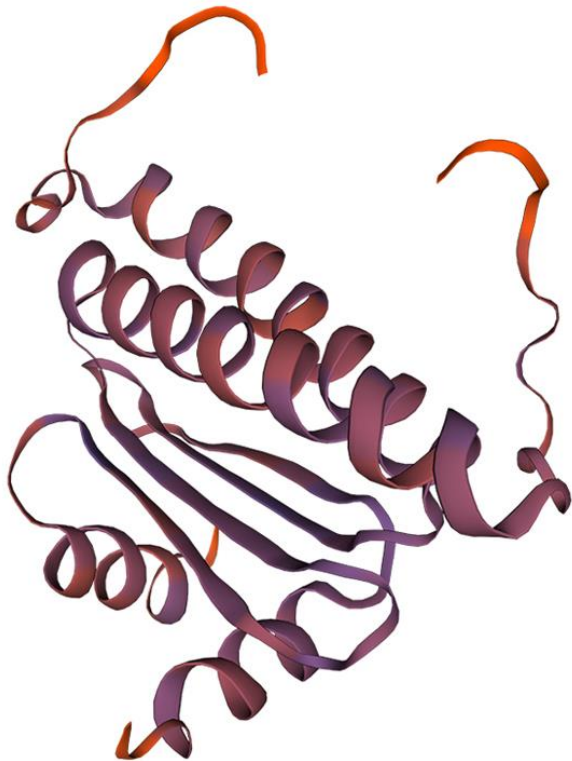


Supplemental Figure S6

A

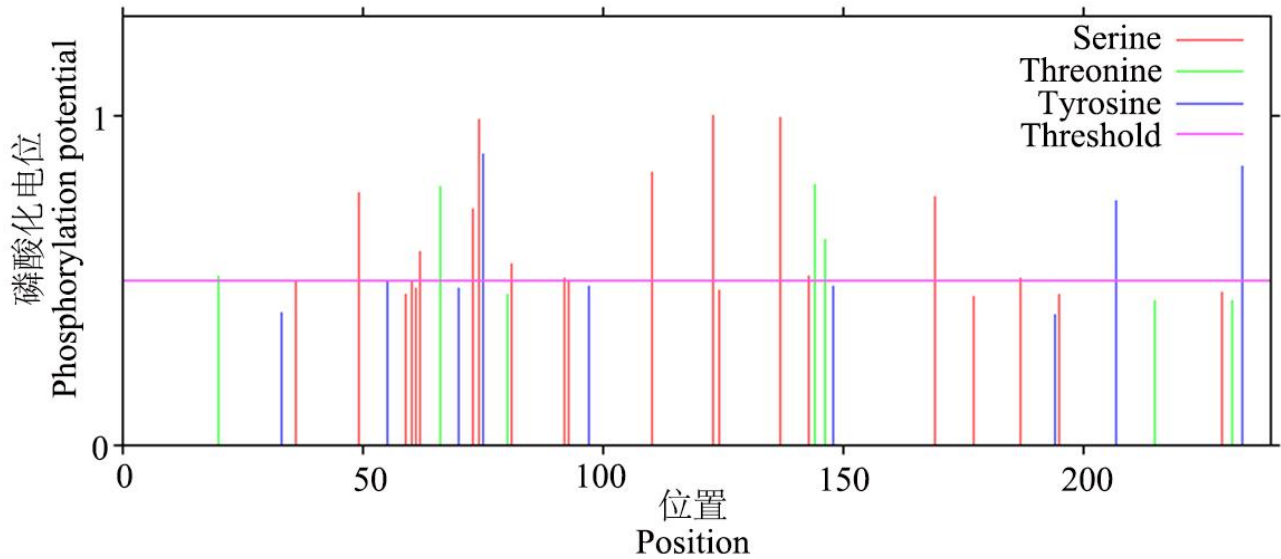


B

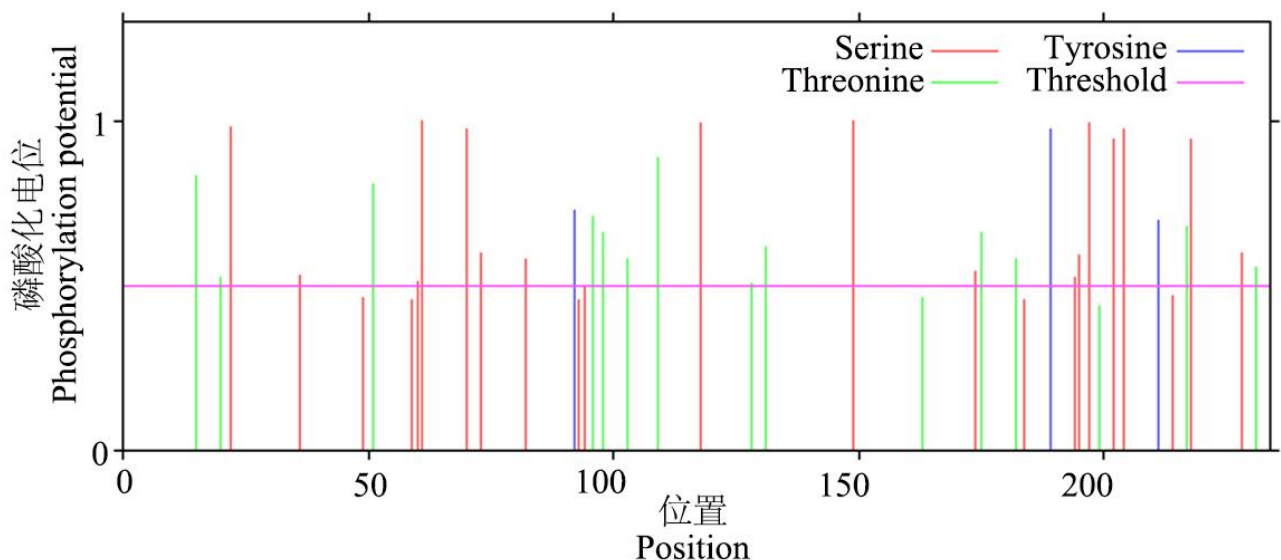


Supplemental Figure S7

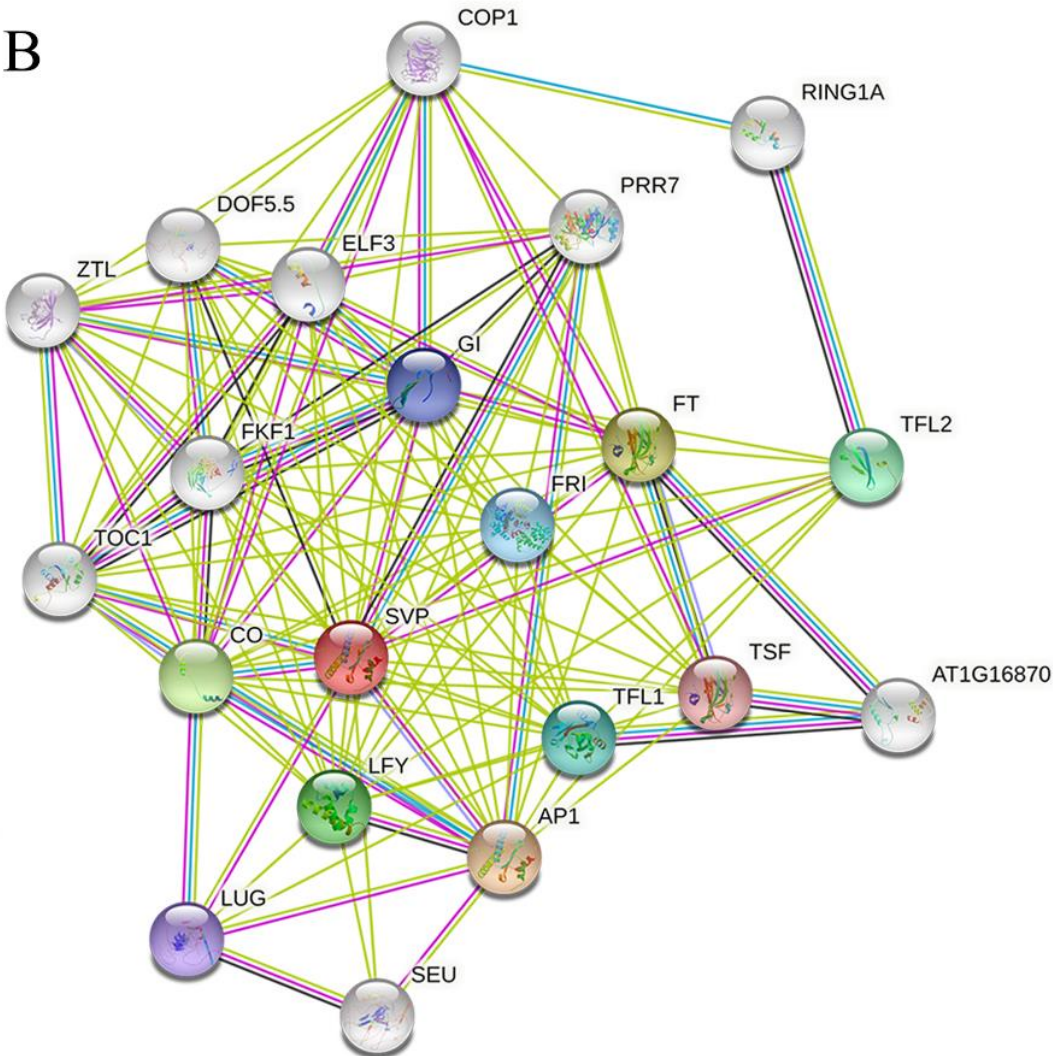
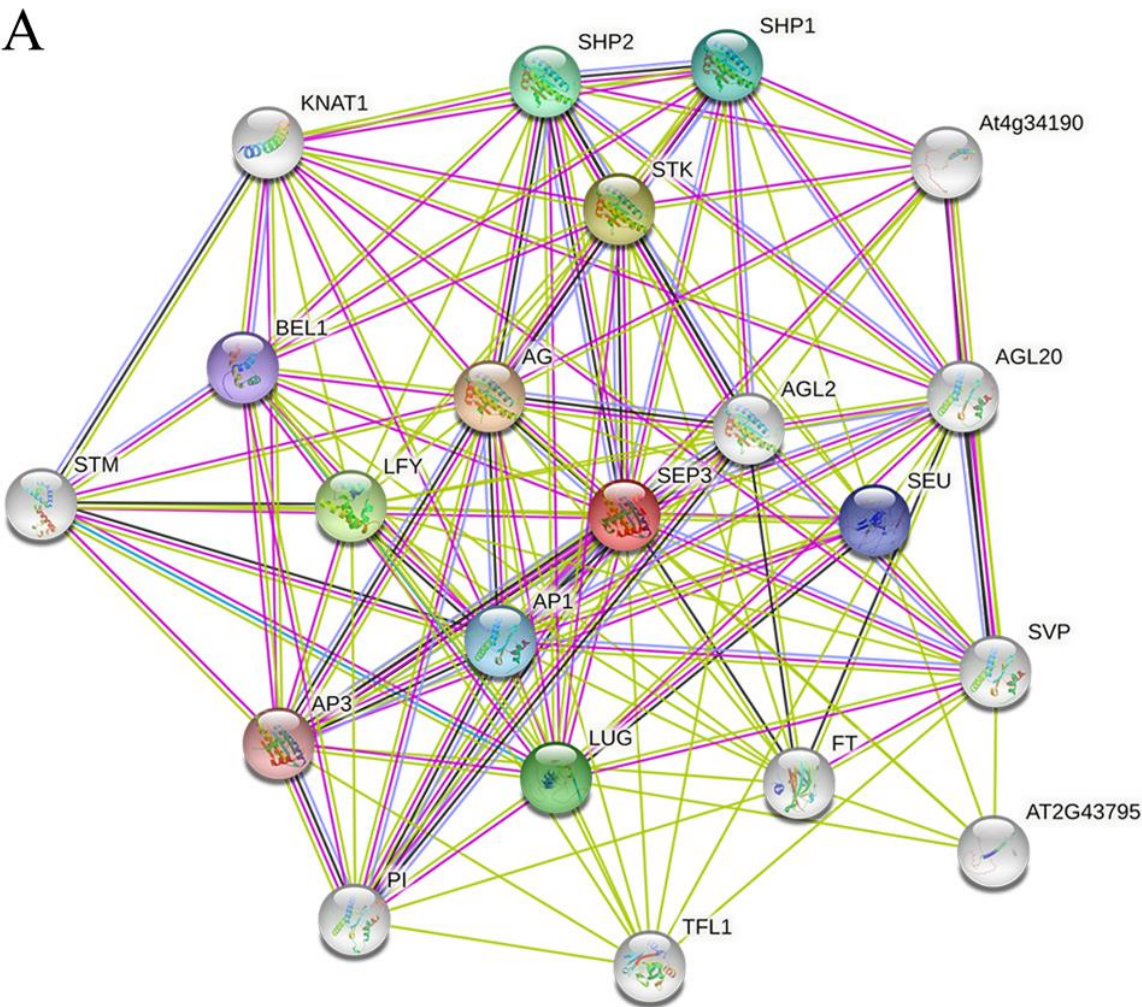
A NetPhos 3.1a: predicted phosphorylation sites in IlSEP3



B NetPhos 3.1a: predicted phosphorylation sites in IlSVP



Supplemental Figure S8



Supplemental Figure S9

