

Supplementary Information

1	acatgggagctcttctccttggtatcgaaacgattctatcgagagagaaaaaanaataatcgacacatgaagatgcgt	2699	ATCGATGAATCTTCAGACGTTGTGATACACGACGGAGCTGAAGAGACGATTAAGTCTAAATCTTCTTCAAA
	M K I A	880	I D E I F K T L G I T E R A E E A E A K V K L F F
74	CTTTTGTCTCGAGCTCTCGTAGTCTCAGCTTTGCGTGGTGAATTCACCTCAACCAATCGATTAAAGTT	2774	TTGTTCGAACAACTTCCTCTTCACTTTGGACAACACCACTCGAGCTGCTTACAAACAATCAACCATGTT
	L F V L G L F V V S A F A G E I Q P Q P I R F K V	905	L F E Q T S L F T L D K H T I E A A Y K Q F N H V
149	GATCAAAATTCAAAATGATGATACAGTGCCACGTTTAAACGCGATCTCGATCAGGCTCAAGCTTTACTCT	2849	GTTCGAAGTCTCGTGCAAGTATACGCCGAGCATGATACATGGTTCGATCAGTCGATCAGGATCAGTAC
30	D Q I Y K Y D Y S G H V L T G L P E S G S S L Y S	930	V R N F V G Q V N A R T E Y N N W V R F T M P S G Y
224	GGTCATCAATGAAGTCAAGTGTGAATGTCCATCAATCTCCAGTACAGGTGATCAATGAAAGACATC	2924	GTTCGATTTGCCAAGTGCCTGGTTTACCGATTCTCTCAAAACACGACCAAACTGTTGCTCTCGA
	G H Q L N S T V S I I K S S R S G D N G K F T I	954	V H V P F S D G L C T L F I V S K Q R F N I V A L R
299	ATCAAGATGGAATGACCAACATGCTTTGGGTCAATCTCAGAGAGTAACAGCTGTCAGAGAGCAAGCTTTC	2999	CTCGAAGGACCAACATCAACCGGATATCCAGCTTGAAGTCACTCAGTGAAGTCTCAGTGAAGTCTTGTGCCAA
80	I K M E L T N I V L G H L L E V N A V E K A T F	980	L E A E A T T C A A K P D T T L K S V S E A C T A T L P V Q
374	ATCAAGACGATCTTAAACAAAGATGCTGATGTTTACGCTTCCCGTCAATTACTTCTGATGAGATACAC	3074	CTTTACATCACTTCAATCAATGCTGCTCTGCTTTCCACAGGAATACAGAAAACTTGTGCTACTCACTC
105	I K D D L K Q K V R D V L A L L P V Q T T F N E D T	1005	L Y T T S S M S V S G F Q Q G I K N N F G A Y S L
449	GATCCTTTGAATGATGATGATCAAAAATCTGATGCCCTTGTGCGATTAACTCAAGAACTCAATCTGAT	3149	AAGAAGTCAATGTCACGTTCCCGTTAAGGTTTATTCACTTCAGGCGCGCTACCGAGTTTGGACCTAC
130	E S F E W I E V Q K S D A P W S V N I K K S I I	3234	K K F N V H V P V K V S F N F E A A T R V L T A C
524	TTGCTCCAATTGACATTTGTGTAAAGAGCTGACAGAGTGCAATGATGTCATCAATCTGGTCTTCAG	1020	GTTCGACCAACCTTTCAGATTAAGTCTGACGATCTTCCAGCTTCCAGCTGCTTCTGTGTACTGATCAT
155	L L Q L N I V G K N A R S A N D V D Q S G L L K	1055	V E P T L D T K V L T S T N T N R A F L A G N Y I
589	GATATGCACTTTCTAAAGTTTAAACGTTTGGTGTCCATGAATCAACATCAGGCTGAATGTGAACCAAC	3299	GGTCTCCCGCCACGAAGTTCATACAGGAAGTGTCTCATGATACATGTCGCCAGCTTCAGAGCAAC
	D M Q L S N G L T S F G V H E S T I K G E C E T	1080	G L P A N S E S P I T K K V L I E S H V P A F K T N
674	TACCAAAATGCTCAGCGCGTATCAGCAAAAGTTCGATGATGCTTCTCGTGCTGATTAATCTCAATCTTAC	3374	CCAGCATCCCATCAGAGAAATGGCATGACATGAACTTCTTCCGAATCAAGCAAGCTGCTTCTTAC
205	Y Q I V T A A D P T K V R D A L G D A D K F H F T	3740	P R L P S R E L G M D I E L S F R T E H P W F L N
749	GTCTCAACGACCCCAAGTTGACACTGTGCTACGAGCAACTATTCCTACCAATTTGGATGCGAAGTGT	3449	GTTCGAAGATCCCAACGAAGGCTTCCCAACTGTGATCTCGGAATACGCTGAGATGACGAATCAACTCT
230	V I K T R N F D N C V Y E P S F A S H N W D R G T	1130	V E K I P T K G P T T W I L E K E A N E N F E A T
824	TGCGTTGAATCTGCAAAAGTTTGTCTGCTTCAACCCATTAAGATGACGATTGAACAACATCTTCCAAT	3524	GATCGCGTTTAACTCTCGACGCAACAAACAAACCCATCAGCTGAGTTCGCGGTTTATTGACTCAACTC
255	C V E Y E C K R F A A S T H I K M D D L N K H L P	1155	D A A L T L R A N K Q N P S A G V A G S F D Y N F
899	CCGATGAAGCTGAACCTTATGTCATGTCAAGAGAACTCAACGATGTGACCAATCAACATCTCGA	3599	GCTTTCGCGGTGTATACAGAACTTAAACATGTGTAAGACACACCATGTCGACGACATCATCTCAAG
280	P D E T E T S C S C D P K E T Q P V D Q Y S T I R	1180	A F A G D Y K E L K H S E N H M V H E R S M L K
974	TACAAGTTCACCTTAGCTGTGAAGCCCAATCTTCTGAAAGCGTTAGTAGGGTGAAGATGCTGTGACAC	3674	AAMCTCGCGCCACGAAGATCTCCAGTCCGAAATCACCAGGAGGAGTCCGGAAGATCGCCGAAGAAATGGTC
55	Y N V L T D S E A P T I T T E A L G K G K I V D N	1205	K L G Q E Q T E S L N I T K E E I R K I A E M V
1049	CATGTCACAAAGTGTGTCTACATCAACATCAATCTGTTGTCTGAGCAAACTCAAGCAAAATCTCC	3749	TACAACTCAACCTGGTGTGTCTGACGAAGAGCTCAACTCTTCCAGGAGCATTAACGTGGTCACTCGAAGT
330	H G T K F V V Y T H S I V F V S E Q I Q R N I P	1230	Y N Y P G V L L N R K T P T L T R A I N W S F R T
1124	CTCATCCGAGAGAGCGTATCCGAGTTAGAGTGTACCTTCACTCTTCTCCATCAACGATGTATGATGT	3824	CTTCCAAAGAGAGCGTACCACTACAGCGTACTCTTATCTCATCAATCCCTGACTACCAACTACTG
355	L I P E E S V I R V N E L T F L F Y K G M D A	1255	L S K E D D G T H Y N A T L I T G S L D Y Q T Y W
1199	CAAGTTACCCAGCCGATTTCCGAGTTTACAACATTTTGTGCCAAATCATCTGAAGCTTGTGTGCGA	3899	GTCAAAATAGTCTCAACCTTGAGCAGCTGAAGTGTCTTCTATGTTTACAGAGTTTTCAAATCGAAGCT
380	Q V Y P S H V I P V Y N I L V P K S S E N L V G P	1280	V K Y V S T L T E R P E G S F Y G L L P R V F Q I E A
1274	ACTGTGCATCTCTTAAACAGTTCGCCAAGCATTTAGGAAGTGCTTCAAGCAAGCTCAATCCAGAGCCGCG	3974	ACATCGCTGACGCTGCTTCCCACTGAATCAATGGGAAGTTCGCCAATGGAACAAATTCATCGAAGAA
405	T V D L L N Q V A K T V M E G A S N E A Q S K A A	1305	N I A R P A L P T E L K W E V P Q L N K F I G K Y
1349	TGTCATCGTTCAAGTTGTCCAAAGTTGGCTCACCTTTCAGCCGAGACATCAACAAATTTACGATGACGA	4049	ATGCTCACTTACCTGGGTGAATCTTGCAGATCTTCCGACGAAGACCAACCTTCTCATCAATGGTTTC
430	W Y M V Y Q N L A R L S A D I K Q I Y D D E	1330	I A N L T W G E S F E T L A H E D R T I F I N G
1424	GCCGAAATGAGACAGGAGCAATGATCCACACGGAACATCAGTTGTGCGACAGCTTTACTGACGGCTTG	4124	TTACACGATGTTGAGACAGAGTTGTGCGTGAACAAATGAAGGCCAAATCATGTCAGAGCAACATGTTCA
455	A R I E D K E R F T T N E H S V R Q L L D L A L	1355	L H R T V D D Q V V G E Q M K A K S W Y H E Q C S
1499	GTCCAGTGTGTACAGCACTCCGCTGAATGTTCCAAATGTTCTGCGTGAAGAACTCACTTCAGCATGAA	4199	AMGATATCAAGCAAAAGCTTTCATGAGTACGCTTCCCACTTGTGCTGACGAGCAATCATATCTCAAC
480	A H V G T K A T A E W F M L V A E K S L S A Y E	1380	K D I K I O K T F T M S Y A C Q L V A H E Q S Y F N K
1574	GAGCAGAGATCTGTTGAACCATCCACGAACACATACGCTTCATCAGCAACTTCTTGTCCATCATGAAGAG	4274	GTCACTGGTACCGTGAATCTCAAGTCAAACTTAAGCAAAAATGTCGAATCAACCACTCTTCTTACCAAGTA
505	E R R F V T E I P R N T Y A P S R T L L A I M K E	1405	V T G T V E F K S N L N E K L V N S T N L F Y Q V
1649	CAAAATCAAGAGCCGTCGAAACAAAGATGATGACAGCACTTTCAGCTTCTGCTGTACTGACGTAACATCATC	4349	GTCAGTCCCACTTAACTCATCTGGCAGCCTGTGCAACATCTGCTCATACGCT

Figure S1. Nucleotide and amino acid sequences of vitellogenin 1 (Vg1) from *Panonychus citri* (*PcVg1*). The ATG start codon and TAA stop codon are in bold, and the signal peptide is underlined with a dashed line. The cleavage signal K/RXXR is indicated by an open box. The GLCG conserved motif is bold and italicized. The polyadenylation signal is underlined with a wavy line.

