

Table S1. The detail information of homologous genes of *GpCHSA* and *GpCHSB* in different species in phylogenetic analysis

Gene name	GenBank No.	Species	Phylogenetic group
<i>OfCHSA</i>	ACF53745.1	<i>Ostrinia furnacalis</i>	Lepidoptera
<i>CmCHSA</i>	AJG44538.1	<i>Cnaphalocrocis medinalis</i>	Lepidoptera
<i>SeCHSA</i>	AAZ03545.1	<i>Spodoptera exigua</i>	Lepidoptera
<i>HaCHSA</i>	QEQ50332.1	<i>Helicoverpa armigera</i>	Lepidoptera
<i>CfCHSA</i>	ACD84882.1	<i>Choristoneura fumiferana</i>	Lepidoptera
<i>PxyCHSA</i>	API6 1827.1	<i>Plutella xylostella</i>	Lepidoptera
<i>HvCHSA</i>	AZQ19982.1	<i>Heortia vitessoides</i>	Lepidoptera
<i>BmCHSA</i>	AFB83705.1	<i>Bombyx mori</i>	Lepidoptera
<i>DmCHSA</i>	NP_524233.1	<i>Drosophila melanogaster</i>	Diptera
<i>MsCHSA</i>	AAL38051.2	<i>Manduca sexta</i>	Lepidoptera
<i>TcCHSA</i>	AAQ55060.1	<i>Tribolium castaneum</i>	Coleoptera
<i>LmCHSA</i>	ACY38589.1	<i>Locusta migratoria</i>	Acrididae
<i>AgCHSA</i>	XP_321336.5	<i>Anopheles gambiae</i>	Culicidae
<i>NICHSA</i>	XP_022187224.1	<i>Nilaparvata lugens</i>	Hemiptera
<i>MbCHSA</i>	ABX56676.2	<i>Mamestra brassicae</i>	Lepidoptera
<i>SlCHSA</i>	XP_022820393.1	<i>Spodoptera litura</i>	Lepidoptera
<i>AmCHSA</i>	XP_016770736.1	<i>Apis mellifera</i>	Hymenoptera
<i>CmCHSB</i>	AJG44539.1	<i>Cnaphalocrocis medinalis</i>	Lepidoptera
<i>OfCHSB</i>	ABB97082.1	<i>Ostrinia furnacalis</i>	Lepidoptera
<i>HvCHSB</i>	AZQ19981.1	<i>Heortia vitessoides</i>	Lepidoptera
<i>HaCHSB</i>	AKZ08595.1	<i>Helicoverpa armigera</i>	Lepidoptera
<i>MsCHSB</i>	AAX20091.1	<i>Manduca sexta</i>	Lepidoptera
<i>SeCHSB</i>	ABI96087.1	<i>Spodoptera exigua</i>	Lepidoptera
<i>DmCHSB</i>	NP_524209.3	<i>Drosophila melanogaster</i>	Diptera
<i>TcCHSB</i>	AAQ55061.1	<i>Tribolium castaneum</i>	Coleoptera
<i>LmCHSB</i>	AFK08615.1	<i>Locusta migratoria</i>	Acrididae
<i>SfCHSB</i>	AAS12599.1	<i>Spodoptera frugiperda</i>	Noctuidae
<i>AgCHSB</i>	XP_321951.2	<i>Anopheles gambiae</i>	Culicidae
<i>BmCHSB</i>	>AFC69002.1	<i>Bombyx mori</i>	Lepidoptera
<i>PtCHSB</i>	>XP_021004609.1	<i>Parasteatoda tepidariorum</i>	Araneae
<i>AmCHSB</i>	XP_001121152.2	<i>Apis mellifera</i>	Hymenoptera

Table S2 Primers used in RT-qPCR

Gene Names	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>GpCHSA</i>	TACGCTTCCACATCACCGC	ACGGGCCTTCTCTTCCTTGT
<i>GpCHSB</i>	ACTTGGCTTTGGGCAGCTTT	GGTCCCTCGTCAACGCATTT
<i>GpCDA1</i>	TTCAAGCCATTCGCTGTCCC	CCAGGAAGCCATCTTGGCAG
<i>GpCDA5</i>	GTGCTTCCCTCCTAACACGC	CCCTTTCGATGGCAGGGTTC
<i>GpCDA2</i>	TTGGTGTGCGTGCTCCTTAC	TATGGGCGTTACCGTTGCAC
<i>GpCHT-h</i>	GCGACCCTTACAGAGGCAAC	TTTTCGCTTCACCGCATCGT
<i>GpCHT3a</i>	TTCAACGACTACAGCCCCGA	GAGAAGTAGCCGTTTCAGGCG
<i>GpCHT3b</i>	TCGGGGAGAAGGTCGAGAGA	ATTCCAGGGCCAGTCGCAT
<i>GpRpl32</i>	CGATCACCTTCCGCTTCT	TGCTACCCAATGGCTTCC

Table S3 Primers used to synthesize dsRNA

Primer Names	Sequence(5'-3')
GpCHSA-1-Olig-1	GATCACTAATACGACTCACTATAGGGGCTTACTACGTCATGCTTATT
GpCHSA-1-Olig-2	AATAAGCATGACGTAGTAAGCCCCTATAGTGAGTCGTATTAGTGATC
GpCHSA-1-Olig-3	AAGCTTACTACGTCATGCTTACCCTATAGTGAGTCGTATTAGTGATC
GpCHSA-1-Olig-4	GATCACTAATACGACTCACTATAGGGTAAGCATGACGTAGTAAGCTT
GpCHSA-2-Olig-1	GATCACTAATACGACTCACTATAGGGCCATATATCGCTTACCAAATT
GpCHSA-2-Olig-2	AATTTGGTAAGCGATATATGGCCCTATAGTGAGTCGTATTAGTGATC
GpCHSA-2-Olig-3	AACCATATATCGCTTACCAAACCCTATAGTGAGTCGTATTAGTGATC
GpCHSA-2-Olig-4	GATCACTAATACGACTCACTATAGGGTTTGGTAAGCGATATATGGTT
GpCHSB-1-Olig-1	GATCACTAATACGACTCACTATAGGGGCACCAGAACTCGGCATTTTT
GpCHSB-1-Olig-2	AAAAATGCCGAGTTCTGGTGCCCCTATAGTGAGTCGTATTAGTGATC
GpCHSB-1-Olig-3	AAGCACCAGAACTCGGCATTTCCCTATAGTGAGTCGTATTAGTGATC
GpCHSB-1-Olig-4	GATCACTAATACGACTCACTATAGGGAAATGCCGAGTTCTGGTGCTT
GpCHSB-2-Olig-1	GATCACTAATACGACTCACTATAGGGGCGAGGCATTACGTGCAATTT
GpCHSB-2-Olig-2	AAATTGCACGTAATGCCTCGCCCCTATAGTGAGTCGTATTAGTGATC
GpCHSB-2-Olig-3	AAGCGAGGCATTACGTGCAATCCCTATAGTGAGTCGTATTAGTGATC
GpCHSB-2-Olig-4	GATCACTAATACGACTCACTATAGGGATTGCACGTAATGCCTCGCTT
GFP-Olig-1	GATCACTAATACGACTCACTATAGGGGGATGTCTCACATCTTGTTT
GFP-Olig-2	AAACAAGATGTGAGACATCCCCCTATAGTGAGTCGTATTAGTGATC
GFP-Olig-3	AAGGGATGTCTCACATCTTGCCCTATAGTGAGTCGTATTAGTGATC
GFP-Olig-4	GATCACTAATACGACTCACTATAGGGACAAGATGTGAGACATCCCTT

A

1 ATGCGCGCGTCGGGAGGGAAGCGCCGCGAGGAGGGCAGCGACAACCTCGGACGACGAGCTCACCCCGCTAGCCAACGG
1 M A A S G G K R R E E G S D N S D D E L T P L A N E
79 ATCTATGGCGGAGTCAAAGACAGTACACGAGACGAAAGGATGGGAGCTATTCGGGGAGTTCGCCCGGAGCAGGAC
I Y G G S Q R T V H E T K G W D V F R E F P P K Q D
157 AGTGTGCCATGGAGTGCAGAAGTGGCTGGAGTGCACGGTTCGGTCTCAAGTGTGGCGTACCTCGTCACTTC
S V S M E V Q K W L E C T V R F L K V L A Y L V T F
53 ATCGTGTGCTCCGCTCCGGCTTATGGCAAGGCCTGTGCTCTCATGCTCGCAGTTGAAGAGGACCGCGGA
I V V L G S G V I A K G T V L F M G T S Q L K K D R R
79 TTAGCGTATTGTAATGAAATTTAGGTAGAGATAAACAAATTTGTAGTGTCTACCGGACGAGGAGCGAGTGGCGTGG
313 L A Y C N R N L G R D K Q F V V S L P D E E R V A W
105 ATGTGGCCATCTTCGCGCATTTCGCGATCCCTGAGATAGGCACACTCATCCGATCAGTCAGGATATGCTTCTTCAA
391 M W A I F A A F A I P E I G T L I R S V R I C F F K
131 TCTTCTAAGAGGCACTTTTACACAGTCTGTGTGGTTTTATAGCGGAATCTTTACACACAATTTGGAATGGCTCTT
469 S S K R P S F T Q F E V V V F I A E S L H T I G M A L
157 TTGTTTTGCTCCTCGCTGAATGGATGTGGTCAAGGAGCCATGATAACAACCTTGTGTGGTTCCTCCGCT
547 L F F V I L P E L D V V K G A M I T N C L C V V P A
183 GTTCTTGGTTCCTGTCTGAAACTTAGAGACAACAAGATTTGTAAAAGTTATTTGGATATGGCGGCAATGTT
625 V L G L L S R N S R D N K R F V K V I V D M A A I V
209 GCCCAGTACGGGATTCATCGTTTGGCCTTGTCCGAAGACAACCTGTACTATCGCTAATTCGGTAVGACTCTTA
703 A Q V T G F I V W P L S E D K P V L W L I P V A S L
235 TGCATATCTCTGGATGGTGGAGAAGTACGTAACAGCAAAAGTCTTATGATATCAAAAAGTCTGGGAAGTCT
781 C I S L G W E N Y V T R Q S P I G I A K S I L G K L
261 AAAGAAGAACTGAATTCGCTCGTACTACACATATAGATTCATATCAGTGAAGATACTATTGTTTTATGTTG
859 K E E L N S S R Y Y T Y R F I S V W K I L L F L M C
287 ATTCATTTCCATATGGATGGATGGCGATGAGCCATCAATGTTCTTCCAAAGTGTACAATCCTGGGTTCCGACCA
937 I H F S I W M D G D E P S M F F Q M Y N P G F G P H
313 AACATTGTAGTCGAAGAGGTACAAGTACGCTTGGTGGCACATTAATTCGCGAATTCGCAACGTCGACCTTACCGGA
1015 N I V V E E V Q V T L G G T L I P D L A N V T L T G
339 GATTCGTAGAAGTAGCAGCTGTATATAAATCAGCTTACTACGTCATGCTTATCCAGATTTTGCAGGCTACCTTTC
1093 D S V E V A A V Y K S A Y Y V M L I Q I F A A Y L C
365 TATATTTTGGAAAGTTTGGCTGCAAGATCCTCATTCAAGTTTTCAGTACGCTTTCGCGATCAATCTAGTATTC
1171 Y I F G K F A C K I L I Q G F S Y A F P I N L V I P
391 TTGGTAGTCAATTTCTTGATAGCTGCGTGTGGATTAAGAAATGGAGATACGTTTCTTCCATGGAAGTGTGCCAG
1249 L V V N F L I A A C G L R N G D T C F F H G S V P D
417 TATCTCTTCTTGAAGCCCAAGCTTTTACCTTACTGATTTTACCGGACAATGGCATGGGTTTGGCTACTG
1327 Y L F F E S P P V F T L S D F I T R Q M A W V W L L
443 TGGTTACTATCTCAGACCTGGATAACGATACACATATGGACTCCCAAAGCTTGAAGCTTTAGCATCCCAAAAAGTTG
1405 W L L S Q T W I T I H I W T P K A E R L A S T E K L
469 TTTGTAATACCTATGTACAATGGGCTGTTAATAGATCAAAGTATGGCACTCAATCGCAAGAGGAGCATCATAAAGAT
1483 F V I P M Y N G L L I D Q S M A L N R K R D D H K D
495 GTAAGACTGAGGACCTCGCTGAAATAGAAAAGAGAAAGGTGACGAATACTATGAGACTATATCGGTTTCATACAGAT
1561 V K T E D L A E I E K E K G D E Y Y E T I S V H T D
521 AACACTGGTACTTCCAAAACAGTAAAGTCACTGTATCAATCACAAGGATATACCGTTCGGCTACTATGTGGCAC
1639 N T G T T P K T V K S S D Q I T R I Y A C A T M W H
547 GAAACGAAAGATGAAATGAGTCTTGAAGTCTATTTTACGTTTAGATGAGGATCAGTCGCTCGACGTGAGT
1717 E T K D E M E F L K S I L R L D E D Q C A R R V A
573 CAAAAGTATTACGAGTCTGATCCTGATATATGAAATCGAAACTCATATTTTGGATGACGCTTTTGAATA
1795 Q K Y L R V V D P D Y E F E T H I F L L D I P A F E I
599 GCAGACCAGTACGACGAGTTCGCAAGTGAATCGATTGTAACCTTCTAGTGGACACTATCGACGAAGCCGCTTCT
1873 A D H S D D D S Q V N R F V K L L V D T I D E A A S
625 GAAAGTTCATCAAAAGCAATTCGAATTCGACACCGAAGAAATATCCGGCGCCATCCGGGGACGACTTACGTTGGGT
1951 E V H Q T N I R I R P P K K Y P A P Y G G R L T W V
651 CTTCCAGAAAACATAAATGATCTGTCATTGAAAGATAAGCAAGATTCGACACAGGAAACGTTGGTCTCAGGTG
2029 L P G K T K M I C H L K D K A K I R H R K R W S Q V
677 ATGTACATGTACTACTTACTCGGTGATGGAGTCCCTATTTCTGTGGATCGCAAGAAAGTCAATGGCTGAG
2107 M Y M Y Y L L G H R L M E L P I S V D R K E V M A E
703 AATACGACTTGTGACCTTAGATGGAGCATTTGATTCBACCACCGCTGTGGGATGCTTATCGACTGTATGAG
2185 N T Y L T L D G D I D F Q P H A V R L L I D L M R
729 AAGAACAAGAACTCCGCGCTGCTTGGCGGATTCATCTGCTGTGGCTTCGAGCACTGCTGTGATATCAGATGTT
2263 K N K N L G A A C G A C G R I H P V G S G P M T W Y Q M F
755

2341 GAATATGCTATTGGTTCATTTGGCTGCAAAAAGCGGACTGAACACATGATTGGATGTGTACTCTGTAGTCCGGGATGTTTC
781 E Y A I G H W L Q K A T E H M I G C V L C S P G C F
2419 TCTCTTTTTCAGAGGGAAGCTCTGATGGACGACAACGCTCATGAAAAGTACACCTTGGCATCAGATGAAGTATGGCAT
807 S L F R G K A L M D D N V M K K Y T L R S D E A R H
2497 TACGTGCAGTACAGTCAAGGCAAGATTCGTTGGTGTGCACACTGTTGCTGCACGCTGCTATCGTGTAGAGTACTCG
833 Y V Q Y D O G E D R W L C T L L L O R G Y R V E Y S
2575 GCTGTTCCGATCGGTACACGATTCGCCAGAGGTTTACAGGAAATTTTACAACAACGCTGCGGTGGTGGCTCT
859 A A S D A Y T H C F E E G F S E F Y N Q R R R N V P S
2653 ACTATCGCCAATATTATGGACTTGCATATGGACTATAAGCACACGATAAAGATCAACGATAACATTTCTACGCCATAT
885 T I A N I M D L L M D Y K H T I K I N D N I S T P Y
2731 ATCGCTTACCAAAATGATGTTGATGGTGGTACAATTTTGGCCCTGGCAGCATTTTCTTATGTTGGTGGGAGCTTTC
911 I A Y Q M M L M G G T I L G P G T I F L M L V G A F
2809 GTGGCCGCTTCAAAATGACAATTCGACCTCCTTCGAATACAACCTGTACCCCATTTGCTGCTTCTCATGTTTGTTCG
937 V A A E R I D N W T S F E Y N L Y P I A V F M F V C
2887 TTCACAATGAAATCGAAATTCAGTACTGGTATGCCAGATATTGTCAACGGCAGATCGCTATGATAATGATGGCCGTC
963 F T M K S E I Q L L V A Q I L S T A Y A M I M M A V
2965 ATCGCTGCTGCTGCTGCGAGTATGGCGGAGGCGGATAGGTTTCTCCTCGGCTATTTTCTGTAGCTCTATCAAGT
989 I V G T A L Y Q L G E D G I G S P S A I F L I A L S S
3043 TCGTTCITTTAGTGTGTTCTCCATCGCAAGAGTCTGGTGTATTTGACCTGGTATCATTATCTGTTGTCTATA
1015 S F F I A A C L H P Q E F W C I V P G I I Y L L S I
3121 CCTCTATGCTGCTTGTATTTGATTTGATTCGATCATCAATCTGAATACGTTTACATGGGTCAGCGAGGATACAG
1041 P S M Y L L L L I L L Y S I I N L N V T W G T R E V T Q
3199 ACGAAAAGACTAAAAGGAAATAGACAAGAAAAGAAATGCGCGAAGAAAGCAAGGAAAAGGCAAGAAATCG
1067 T K K T K K E I E Q E K K D A E E A K K K A K Q K S
3277 TTGTAGTTCCTACAAGGTGTTAATGGCAATGAAGATGAAGGTCATAGAATTTTCTTCGCTGGACTTTCAA
1093 L L G F L Q G V N G N E D E G S I E F S F A G L F K
3355 TGATTTCTGCATCCTTAAAGGCGAAGAGAAAGTACAATTTGTCACATCGCTTCGACTTTGGAAAACG
1119 C M F S T H P K G S E E K V Q L L H I A S T L E K L
3433 GAAAAGAAATGGATGTCGTAAGAAGGACTGTTGACCCGATGTTTGAACAGAGGAGGAGGATTTATCGTTCGGTCC
1145 E K K M D V V E R T V D P H G L N R G R K L S V G H
3511 CGTGGTAGCCACCGGATCATGATGATGCTCTGCTGAAAGGACCTGAAGACGCAATGACTCAGACTCAGAA
1171 R G S T N G D H G L D A L A E G P E D D N S D S E
3589 ACAGATACCTTCCACATCCCGGGGAAAGTAGAGACGATTTAATAAATCTTACTGGATTGAAGCCCTGACTG
1197 T D T L S T S P R E S R D D L I N P Y W I E D P D L
3667 AAGAAGGAGAAGTCGATTTTGTACCCATCAGAGATTCAGTTTGGAAAGACCTTCTGGACAATACTTATTCCT
1223 K K G E A V D F L T P S E I Q F W K D L D K Y L F P
3745 ATTGATGAAAACAAGGAGGAGGCGGCTATCCAGGGATTTGAAAGCGTTAAGGGATACATCTGTCTTTAAATTT
1249 I D E N K E E K A R I S R D L K A L R D T S V F N F
3823 TTTATGTGCAATGCTCTTTTGTGCTGATTTATTTTGTGCAATGAAACAGGACAACTCCACTTAAATGGCCA
1275 F M C N A L F A V L I V F L L Q L N K D N L H F K P V
3915 CTCGGGATTAATAACATACATTTACAACGAGGTTACACAAGGATTAATCTCAAAGAGTATTTACAAGTGGAA
1301 L G V K T N I T Y N E V T Q E V L I S K E Y L Q L E
3979 CCGATTGGTTAGTATTCGATTTCTTCTTGTGATTTTGGTAAATCCAATTCAGTCTATGTTTCCATCGATTC
1327 P I G L V F V F F F A L I L V I Q F T A M L F H R F
4057 GAACTACTCGCATATTCAGCATACAGAACTGAATGGTCTGCGCAAAAGTCCGGAAGATCTTATCTCAAGT
1353 G T L S H I L A S T E L N W F C A K K S E D L S Q D
4135 GCTCTTATGATAAAAATAGCAATAGTGAAGATTTACAGAAATGAATGGTTAGATGATGATACGATAAC
1379 A L L D K N A I A I V K D L Q K L N G L D D Y D N
4213 GATTCCGGATCTGGGCTCATACGCTCGGCGAAGAAGACTATTACAATTTGGAGAAAGCCAGACAGAAAAGAGG
1405 D S G S G P H N V G R K T I H N L E K A R Q K R
4291 AATATCGAAATTTGGATGCTGCTTCAAGAAAGCTTTCTCAACATGAATGCTAATGATGGACAGGAAACCGGTA
1431 N I G T L D V A F K K R F F N M N A N D G P G T P V
4369 CTTAATAGGAAGTACGCTTAAAGAGAAACATTAAGAGCATTAGAAACAGAAAGGAAATTCGTAATGGCTGAGCCA
1457 L N R K M T L R R E T L K A L E T R R N S V M A E R
4447 AGAAAGTCCAAATGCAGCGTGGAGCTAATAATGAATGAGTACAGGATGTTGAAACAATATTTAGCGGTT
1483 R K S Q M Q T L G A N E Y G V T G M L N N N L G V
4525 CCACGACATCGAACCTCGCGGCAATTTTCAAGAGGATTTTGGGAACTAATGGAGGGCAAAATTAATCGA
1509 P R H R T S T A N I S V K D V F A E P N G G Q I N R
4603 GTTACGAACTACTCTTGGTGAAGAGAGCAACTCATTGAGACTCCAAACCAAGCAAAACCAAGTCTCATT
1535 G Y E T T L G D E D S N S L R L Q P R Q N Q V S F
4681 CAACGCTATCAATGA
1561 Q R Y Q *

Figure S1. Nucleotide and deduced amino acid sequences of GpCHSA (A) and GpCHSB (B) of *G. pyloalis*. The putative transmembrane segments predicted by TMHMM Server v. 2.0 are in shaded gray. The potential *N*-glycosylation sites predicted by PROSCAN are marked with bold lines. The amino acid sequence of the putative catalytic domain is in black background. The signature sequences (EDR and QRRRW) involved in catalytic function are in red boxes.