

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>	TCGGGGAGAAGGTTCGAGAGA	ATTCCAGGGCCAGTTCGCAT
<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	GATCACTAATACGACTCACTATAGGGGGGATGTCTCACATCTTGTTT
GFP-Olig-2	AAACAAGATGTGAGACATCCCCCTATAGTGAGTCGTATTAGTGATC
GFP-Olig-3	AAGGGATGTCTCACATCTTGTCCCTATAGTGAGTCGTATTAGTGATC
GFP-Olig-4	GATCACTAATACGACTCACTATAGGGACAAGATGTGAGACATCCCTT

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.