

Figure S1. Specificity of anti-*NIPCE3* antibody analysed by western blot. Anti-*NIPCE3* antibody was purified from New Zealand rabbit. Anti-beta actin rabbit polyclonal antibody (Abbkine, USA) was taken as the positive control. The whole body of females was used to evaluate the specificity of the anti-*NIPCE3* antibody.

Neodiprion lecontei Athalia rosae Cephus cinctus Linepithema humile Camponotus floridanus Pseudomyrmex gracilis Culex guinguefasciatus Aethina tumida Anoplophora glabriponnis Vanessa tameamea Papilio xuthus Drosophila guanche Nilaparvata lugens

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Neodiprion lecontei Neodiprion lecontei Athalia rosae Cephus cinctus Linepithema humile Camponotus floridanus Pseudomyrmex gracilis Culex quinquel'asciatus Aethina tumida Aethina tumida Anoplophora glabripennis Vanessa tameamea Papilio xuthus Drosophíla guanche Nilaparvata lugens

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Neodiprion lecontei Athalia rosae Cenhus cinctus Linepithema humile Camponotus floridanus Pseudomyrmex gracilis Culex quinquefasciatus Aethina tumida Anoplophora glabripennis Vanessa tameamea Papilio xuthus Drosophíla guanche Nilaparvata lugens

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Neodiprion lecontei Athalia rosac Cephus cinctus Linepithema humile Camponotus floridanus Pseudomyrmex gracilis Culex quinquefasciatus Aethina tumida Aethina tumida Anoplophora glabripennis Vanessa tameamea Papilio xuthus Drosophila guanche Nilaparvata lugens

Neodiprion lecontei Neodiprion lecontei Athalia rosae Cephus cinctus Linepithema humile Camponotus floridanus Pseudomyrmex gracilis Culex quinquefasciatus Aethina tumida Anoplophora glabripennis Anopiophora giaorip Vanessa tameamea Papilio xuthus Drosophila guanche Nilaparvata lugens

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SKSYQADAA GDKNCHORH LAGVLEEFRTDIVRFMD	FOV LEQTYVGVCCPDR	AETLRINFSNREDTVAGPLPATATDESEKESKNST	5	175
-NKAYQAGLTI DEKKEITORII SKOVLEDERSNFARFMDY	WCITERTYVCVCCPDQ	TEVLEVNSLG-AESLAGVLPAVASNDDGKPIWGTAEDETSSTGVN	:	136
-QKTYQADTALGNQSCHCKH COVLEEFRSNFARFVDV	WCIIEQTYVGWCCPDS		:	176
QKTHQADIA GNQPCHCKHF GOVLEQFRLNFERFMD)	ACT LEQTY IGVCCPDS	IVTTRSDKTF_DDDLASVLPATANLDDDKEEWD ENENEP	:	148
-QKKYQAOTAFGNQSCHOVHF=GCVLEEFRSNFERFANY		VATARSNKAF-NDDLASMLPMTASLDNNTERWERMSENDEASEPS	:	164
TKKTFQNCTT SGVKHCKRYQHCQQLDPKEHIWKILGO		LTEGTG PEFSARLPALG DDGYDPVDGLDGTN	:	180
NGGDTRYTTT EGLPSYOND SDOPQLLLN LGNLRQS		STDV IQTTTKPP IVPAPS ITYTTTS IPPPTVQSYTTKQP	1	256
SRIETT EGQDEYEND SDCPQLLLNLCNLRQS	S GFKSLFVPGYCCPN	TNDVANPSFTTTTSTTTSTTTTTTRPVTFAATYYNTE	:	263
P-NDSKOTT EGEOWED NUPQLLLNLVSLRES	SECFKDLFVPCVCCPKDAVVPSTQAIE	KPWVSTTSKPTYLVPVTTQRPTQKPTTTKKPSAILVLTTKKPRPQTTSTA	1	327
QENDAKYOTTEEGEAGWOED SNOPQLLLN LINLRES	S CFKDLEVPGYCCPRDAVIPS ITAVE	KPVVATTSKPTYLLPVSSQKPVTKPTTTKRPSAVLVLTTKKPKPQTTRPP	:	328
GKDAENYCKT SGRACROED SCPALLLNLSSLRES	S <mark>CFKSLFVPGVCCP</mark> LSSVSTSE	SSAPQSTTQRPLKLTAKPTPSSTTKRTTARPVTARPSTRPTSGLVLIPQK	:	441
PIRYGYNGQKERGLR EIGFLQPLKENYIKYRA	TYCIIG-SEVENCEPNAIAIPEKYNEN	QFLPAARRNSTGRRRSSRSVTYEMTPAYSESKVLGRPSDVYEDQQSKSKF	:	158

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	DPNKNVTQGSGATRTSLQ-	PRGPR	G	- CCVSTRSRT	IVGG	RP D	QEWPWIAAI	LR-KEA	ASH CCC	VI. I IDRI	VLTAAHOVFQ	:	256
	SEATRSAGE	PRGPR	G	CGVSTKSRV:	I V G G	RP-D	CENPWIAA	J.R EHS	STH CGG	MINTORE	VLTAAHOVYQ	:	246
	DTR DTGAELNRK	PRSPR	G	-CGVSTKSRT	VGG	RP D	KE@PW V I	LR KDA	ASH CCC	VI. I TDRI	VLTAAHOVYR	: 1	210
	SSDNNNT ILRKNATLSDTKE	EMRNPRRPR	G	-CGTSARTKI	VVGG-	RP D	KE <mark>@PW</mark> WAAI	LR—QG/	AIQ CGG	VI. I IDRE	VLTAAHOVYR	: :	262
	STDDKDA ISRNNATLSD1KE	AMRKSRRPR	G	CG TTTKTKI]	AGG	QP-D	KE@PWRAAI	LR QGA	ALQ CCC	M. TIDRE	VLTAAHOVYR	: :	234
	ADDKDDTTLRKDGTSTQTKK	EETRKSQKR	G	CONTARMENT	NAGG	QP D	KENPW V I		STQ CCC		VLTAAIIOVYR		250
	NIESRDGID-	RPEER	C	-CCIATKQLF	ISCC	-RP D	CENTRALI	IAN-LCC	QQS CCC	V LIDR	VLTAAHCVLN	: :	252
	VTIPSSTTTLNPFVPSLADLF	TGGNTVDPE	E	COQPESAKY]	V V G G	EEAL	GROPWRAA	FLHGSRR1	TEF / CGG	SI. ISAHY	VLTAAHOTRDSRQ	:	349
is :	KTSAESSIISSEVSKP-LNKPA	VENNEVDPQ	E	-COQPENSKP1	vIGG-	EQL		FLIIGSRR1	TEP CGG	n li at)	ILTAAIICTRDSRQ	:	355
	RPITTFSTATTRAPSTTSYYSVTSPIIA	NYSNIVDIN	D	-COQREDECC	TVGG-	TE K	CANT AND	YLHCNKRI	REFICEC	T LVCPNI	VLTAAHCTRDSKQ	: -	427
	-TTTVAAVTTPRPVSTTSFYTELPPS1A	NYSNIVDAS	E	COREDEGE	VGG	TEAKS	(GA <mark>@PW</mark> RAA)	YLHGNKRE	REF ¹ CGG	I LY DKRI	VLTAAHOTRDSKQ	: -	427
	KPPTTTTTTTTEVPLEPEGLDE	LGNNIVDPD	E	-CCQQEYSTC	IVGG	VE PN	CQNPWHAAI	FLIICPKRI	TEF CCCS	SLICT N	ILTAAIICTRDSRQ	:	535
	PKKYSSDNHDKKKIPKKYSINKKKSMKE	MNAVEVEGK	SRHRRS I GDQDQQ	ICCRNGRLLSQ	N NNK?	QNVEN	KANPWAVT	IN-ANTI	(EHH <mark>CCC</mark>	T IN RY	VISAAHC FIIDGG	:	271

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			TLRY AN ALEQUSRY							LPWKNE :
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	KOV T T RUPD KOV S V RUPE KOA T T RUPE ROV S T RUPE	AMCAAAFECGRD SMCAAAYDGGRD AMCACAYECGRD TMCACAYEGGRD	SOGEDSGEPLEH LENGEN SOGEDSGEPLEH LENGEN SOGEDSGEPLEH LENGEN VOGEDSGEPLEH LENGEN	N NGIYSWGI C N NGIYSWGI C N NIGIYSWGI C N NIGIYSWGI C	EPOHPGVYTRV EPOHPGTYTRV EPOHPGVYTRV EPOHPGVYTRV	VRVLENTFA A NSVLENTFA A NINLENTFA A SSVLENTFA A	IF : 434 IF : 398 VF : 450			
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	KIN T T RIPD KIN S N RIPE KIN S T RIPE RIV S T RIPN RIV S T RIPN GOI S T RIPN DIGOY INRIYE	ANCAAAFBOORD SICAAAYDOORD AMCACAYBOORD TICACAYBOORD TICACAYBOORD TICACAYBOORD SICACDYQOORD SICACDYQOORD	COCDSOGPLLHULGNOF COCDSOGPLLHULGNOF COCDSOGPLLHULGNOF COCDSOGPLLHULSNOF COCDSOGPLLHULSNOF COCDSOGPLLHULSNOF COCDSOGPLLHULSNOF	A WGIYSWGI C A WGIYSWGI C A WIGIYSWGI C A WIGIYSWGI C WIGIYSWGI C W WIGIYSWGI C A WGIYSWGI C	HPGVYT M IPGIYT M IPGVYT V FPGIYT V FPGIYT V FPGIYT W ANHPGIYT W	NRYLLWIFA A NSYLLWIFA A NIKLWIFA A SSYLLWIFA A SSYLLWIFA A SSYLLWIFA A SSYNGWIFA A	IF : 434 IF : 398 VF : 450 VF : 422 VF : 438 VF : 440			
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s	KIV T T RIPP KV S V RIPE KA T T RIPE RV S T RIPN KV S T RIPN Q I S T RIPN D QDV ISROFF ONQA F PITS D NEA F PITS	AMCAAAFEGORD SMCAAATDOORD AMCACATEGORD TMCACAYEGORD TLCACAYEGORD SICACDYGGORD SICACDYGGORD FICACYSEGOTD	COODSOGPILLE LENGT COODSOGPILLE LENGT COODSOGPILLE LENGT VICEDSOGPILLE LENGT VICEDSOGPILLE LENGT VICEDSOGPILLE LENGT VICEDSOGPILLE LENGT VICEDSOGPILLE VICE VICEDSOGPILNIELS	I VGTYSWETE A NGTYSWETE A NIGTYSWETE A NIGTYSWETE A NIGTYSWETE A NIGTYSWETE A NIGTYSWETE A OVGYYSTAN A OVGYYSTAN C	PGYYT V PGTPCTYT V PGTPCYT V PGTYT V PGTYT V PGTYT V YPGYYT V CYPGYYT V	RUU WIFA A SSU WIFA A	IF : 434 IF : 398 VF : 450 VF : 422 VF : 438 VF : 440 RN : 542 RT : 548			
s	KIV T T RIPD KIV S V RIPD KAX S V RIPD KAX T T RIPS RIV S T RIPN OG S T RIPN DGDV INRIFE DONGA F PITS DONA F PITS DONA F PITD	ANC A A A FEGGRE SNC A A A YDOGRE ANC A C A YEGGRE THC A C A YEGGRE THC A C A YEGGRE SI C A C A YEGGRE SI C A C A YEGGRE FI C A C YER GC E FI C A C YER GC E FI C A C YER GC E	COCDSOGPILIE LENGT SOCDSOGPILIE LENGT COCDSOGPILIE LENGT COCDSOGPILIE LENGT COCDSOGPILIE LENGT COCDSOGPILIE LANCT SOCDSOGPI MY LENGT COCDSOGPI MY LENGT COCDSOGPI MY LENGT	I VGTYSWETHO ANVETYSWETHO ANVETYSWETHO ANVETYSWETHO ANVETYSWETHO ANTOTYSWETHO ANTVETYSWETHO AVETYSTEAN C TOVETYSTEAN C TOVETYSTEAN C	HPGVYT N TPGTYT V FPGTYT V FPGTYT V FPGTYT V FPGTYT V ANHPGTYT V YPGVYT V YPGVYT V	RYL WIFA A SSYL ATFA A STULATFA A SSYL ATFA A FEYL ATFA A FEYL ANT 90 JU	IF : 434 IF : 398 VF : 450 VF : 422 VF : 428 VF : 438 VF : 440 RN : 542 RT : 548 T : 619			
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Figure S2. Amino acid sequence comparison of clip-SPs. The locations of the clip domain and serine proteinase domain are in the dot-lined box and full-lined box, respectively. *Neodiprion lecontei* (XP_015524395.1), *Athalia rosae* (XP_012252741.1), *Cephus cinctus* (XP_015592174.1), *Linepithema humile* (XP_012222599.1), *Camponotus floridanus* (XP_011264758.1), *Pseudomyrmex gracilis* (XP_020295935.1), *Culex quinquefasciatus* (XP_001851428.1), *Aethina tumida* (XP_019880431.1), *Anoplophora glabripennis* (XP_018570111.1), *Vanessa tameamea* (XP_026500245.1), *Papilio xuthus* (XP_013173234.1), *Drosophila guanche* (SPP83732.1).

NIPCE2 : NIPCE5 :		20	*	10	*	60	*	80	*	100	*	12
NIPCE1 :	MDRLRNLLESPLSW	MDELNTYKFN	QIADFEKCTFQ	FHMFFIRDWI	SYSSASRLG	SNEPFQNVSRS	YRQGGASGA	APGYTMMSGPF	FPSRITPAGD	RSRSSLMFDGO	GYDLRRPQW	: - NQAPSS : 119 : -
N/PCE2 : N/PCE5 : N/PCE1 : N/PCE4 : N/PCE3 :		140	* NSKIAPEFLAPI	160 NQRPGADDES	*	180 ATISETLGAIN	*	TRASTAPGDRV	(KAWERYFI) SIII YQMIAI 'DAVHTPPVV		MAEDDEFD CHEQSLLD TISKNVLG	Œ : 34 ₹ : 32
NIPCE2 : NIPCE5 : NIPCE1 : NIPCE4 :	40 * :N -FRRQAAN :E ILPHMAV- :I RSKRQV : IAPLV GLPPLVGS :VDELSHRLR-	SEDLVEF1 HYLDTDANVN TGKTQAAAVGI	DANAASGGPRP	KTPDNEE H	RCTPLSSCHP 20TSILDCES /CDDLSNCPQ		IINK RE TPEEYMF TQ RQ	<u>320</u> SFCGYENEK F LTCGYKAHE FI SHCGFEGDL F STCFKSLFV FC	* VCCP VCCP VCCP ^{KRGDT}	340 R0 QCSRI LESS FNVGDYSTESS	* QQ I SA EL SP I GEGGI SEPT I L T S I PV I HTT7/	-PRPPS : 101 -PRPPS : 117 STIA : 117 AVTTTR : 347 RRNSTG : 120
N/PCE2 : N/PCE5 : N/PCE1 : N/PCE4 : N/PCE3 :	HP KP RPPIISATSVPLHI		NSRQC EFRPP PFPAFSKEEI	-GHPQLYNWG -SFPS (SHPKQIVF)	GTTLIKAQV	QPWAVRVGFKN DCGRAG-RI RPPTTSDESKS	KSSEESEEE	FDDDDDDDESA/	DDFSPEIQF		IKKMPRGRP	: 131 : 166 : 155 FYAVPV : 464 GRLLS- : 218
NJPCE2 : NJPCE5 : NJPCE1 : NJPCE4 : NJPCE3 :	VEEETMECGQPEVA	RTVGGRPA KFRVVGGEEA	ILRAWP®MAL C	GYNSMTRPAV FLHGPRRTEI	VN A A SS WCG S GP	R <mark>y</mark> vvtaalic <mark>ij</mark> Khiltaahoti	DKRLTIVRL RDTRQ	GDLDWN	TTADNANHI	DIPVERAIMH	QQ PQYNRARRT:	IDLPV1 : 174 SDIGLV : 253 : 533
NIPCE5 :		CVRV I CLPSSDLLR	NKNLENISPYI	GGAGSLG N	SNLSYPSQLY G	—SVP_SMNEI EAQVDVRSNEG	CAAAYARLG CVGG CAKDFAKL-	-TRVTIDHS	/LCAGGEATD EEGKD IVCAASPGVD	ACSOFGOAPLV ACLODSOGPLA	VLMDKISKG MLPHEN-I	H TQIC : 228 RYHLYC : 364 : 535
N/PCE2 : N/PCE5 : N/PCE1 : N/PCE4 : N/PCE3 :	: IVSFC <mark>SEKCGVEG</mark> : VVSYG IGCANPIN	GANTRATE ISV VRADQA GLARATE	VDWTQSNT VDWTKLNSPNE VDWTESNVSS	3 : 264 : 397 :								

Figure S3. Amino acid sequence comparison of *NIPCE1-5*. The locations of the clip domain and serine proteinase domain in the dot-lined box and full-lined box, respectively. *NIPCE1* (AGK40913.1), *NIPCE2* (AGK40914.1), *NIPCE4* (AGK40916.1), *NIPCE5* (AGK40917.1).