Supplemental materials

Figure S1

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H.sapiens       : -----------------------MAGRSMQAARCPTDELSLTNCAVVNEKDFQSGQHVIV---RTSPNHRYTFTLKTH-- :  52
B.mori          : -----------------------MSSMRMKAAKCPSDELAITNCALIHQDDFPSDIKHIEVST--GPSQHFVFSIRFY-- :  53
S.frugiperda    : -----------------------MSAMRMKAAKCPSDELAITNCALINPDDFNSDVKHIEVST--GPSQHFVFSIRFY-- :  53
A.mellifera     : -----------------------MSAMRMKAVRCPTDELSITNCAIINPDDFPDDIRHIEVTT--APNHHFVFTVRQH-- :  53
D.melanogaster1 : ------------------------MAYILKATKCPTDELSLTNRAIVNVGDFPEEIKYADISP--APGQHFIFALEKT-- :  52
D.melanogaster2 : ------------------MS--IEKAHRMRAIKCPTDELSLTNKAIVNVSDFTEEVKYVDISP--GPGLHYIFALEKISG :  58
T.castaneum     : --------------------------MLFKVVKCPSDELSLTNCAVVNDADFSQSTEHIEVIT--GGVKKFIFSIKKD-- :  50
A.pisum         : -------------------------MVVFKAIKCMADDWALTNCAVVNDEDFRSDTKYIEVQHQTKPDLKFWFTTLFV-K :  54
P.corporis      : ----------------------------MKATKCPTDELSLTNRAICNPADFSADVKHIEVNT---GSGHFIFTIKLD-- :  47
S.cerevisiae    : MFKIPGFGKAAANHTPPDMTNMDTRTRHLKVSNCPNNSYALANVAAVSPNDFPNNIYIII-------DNLFVFTTRHS-- :  71

H.sapiens       : PSVVPGSIAFSLPQRKWAGLSIGQEIEVSLYTFDK-A--KQCIGTMTIEIDFLQKKSI--DSNPYDTDKMAAEFIQQFNN : 127
B.mori          : NGVDRGTVGFSAPQRKWATLSIGQTIDVKPFK----PSSAECLCSVTLEADFMMKKTT--STDPYDSEQMARDFLIQFAN : 127
S.frugiperda    : SGVDRGTVGFSAPQRKWATLSIGQPIDVKPFK----AQNAECLCSMTLEADFMLKKTT--SMEPYDSEQMARDFLIQFSN : 127
A.mellifera     : HEVPRGSVGFSLPQRKWATLSLNQEIEVRPYHFNP-TSSTECLCVIVLEADFLQKKST--TLEPYNTDEMAKDFLFQFSG : 130
D.melanogaster1 : VEVPSGYVGFSLVQRKWAMVSINQELEVRPYRFDA-S--SDVITCVSFETDFLQKKTV--SQEPYDSDQMAKEFIMQFAG : 127
D.melanogaster2 : PELPLGHVGFSLVQRKWATLSINQEIDVRPYRFDA-S--ADIITLVSFETDFLQKKTT--TQEPYDSDEMAKEFLMQFAG : 133
T.castaneum     : PRVHRNEVAFSVPQRKWATLSINDDIEVNPYKE------EDYITSIVLEADYMQKKTT--SQEQYDTDEMAKEFIYSFPN : 122
A.pisum         : DPPPRGCIAFSVNQREWAQLSINQPISITSYPGNT-A--IDFLCSVEAEIDYFQKNKTKSANEQFDTDMMAREFLVNFTN : 131
P.corporis      : ANVPSGYVGFSMPQRKWASLSLNQDIAVKPYYFDP-KSDSELLSNVVLEADFLQKKSA--TTEPYDTDLMAKEFIAQFCG : 124
S.cerevisiae    : NDIPPGTIGFNGNQRTWGGWSLNQDVQAKAFDLFKYSGKQSYLGSIDIDISFRARGKA--VSTVFDQDELAKQFVRCYES : 149
                                                   NSF-N
H.sapiens       : QAFSVGQQLVFSFNE-KLFGLLVKDIEAMDPSILKGEPAT--------GKRQKIEVGLVVGNSQVAFEKAENSSLNLIGK : 198
B.mori          : QVFTVGQQLAFLFQEKKVLSLIVKNLEAVDVVALAAGA---------NAVPRRVRMGRLLPDASVQFDKAENSSLNLIGK : 198
S.frugiperda    : QIFTVGQQLAFSFQEKKVLSLIVKNLEAVDVQALAAGA---------NAVPRRVRMGRLLPDGAIQFDKAENSSLNLVGK : 198
A.mellifera     : QAFTVGQQLVFQFKDKKMLGLLVKSLEAADLSAINSGQ---------NTVPKKTQMGRCLGNTVIQFEKAENSSLNLVGK : 201
D.melanogaster1 : MALTVGQSLVFNFKDKKLLGLAVKSLEAIDPKSLGEGK---------DTAMRNVRFGRILGNTVVQFEKAENSSLNLQGK : 198
D.melanogaster2 : MPLTVGQTLVFQFKDKKFLGLAVKTLEAVDPRTVGDSL---------P-KTRNVRFGRILGNTVVQFEKAENSVLNLQGR : 203
T.castaneum     : QMFTVGQQLAFLFKDKKILSLLVKDIEVVNINTLKQGG---------EAKPKKGKLGKLTPNTVIQFEKAETSALNLVGK : 193
A.pisum         : HVLSVSQTLLFQLPEKPLMAIKIKSIEGVNSQEINSGA-----------KPRSIQYGKCLSNTAVRFVVGSNTTLLLVGK : 200
P.corporis      : LAFTVGQQLVFSFKDKKLLGLVVKELLSVDLTALNAGK---------EAKTRKTNFGKLLGNTVVQFEKVESSSLNLTGK : 195
S.cerevisiae    : QIFSPTQYLIMEFQG-HFFDLKIRNVQAIDLGDIEPTSAVATGI---------ETKGILTKQTQINFFKGRDGLVNLKSS : 219

H.sapiens       : AKTKE--NRQSIINPDWNFEKMGIGGLDKEFSDIFRRAFASRVFPPEIVEQMGCKHVKGILLYGPPGCGKTLLARQIGKM : 276
B.mori          : AKGKQ--PRQSIINPDWDFGKMGIGGLDNEFNAIFRRAFASRVFPPEVVEQLGCKHVKGILLYGPPGTGKTLMARQIGKM : 276
S.frugiperda    : AKGKQ--PRQSIINPDWDFGKMGIGGLDREFNAIFRRAFASRVFPPEVVEQLGCKHVKGILLYGPPGTGKTLMARQIGKM : 276
A.mellifera     : AKGKV--VRQSIINPDWDFQKMGIGGLDKEFTAIFRRAFASRVFPPEIVTQLGCKHVKGILLYGPPGTGKTLMARQIGTM : 279
D.melanogaster1 : SKGKV--VRQSIINPDWDFGKMGIGGLDKEFNSIFRRAFASRVFPPELVEQLGCKHVKGILLYGPPGTGKTLMARQIGTM : 276
D.melanogaster2 : SKGKI--VRQSIINPDWDFGKMGIGGLDKEFNAIFRRAFASRVFPPELVEQLGIKHVKGILLYGPPGTGKTLMARQIGTM : 281
T.castaneum     : AKGKI--VRQSIINPDWDFQKMGIGGLGKEFNAIFRRAFASRVFPPEIVEQLGCKHVKGILLYGPPGTGKTLMARQIGKM : 271
A.pisum         : SKCQQ--ARVSIINPDFDFNKMGIGGLDTEFNAIFRRAFASRVFPQEIIEQLGCKHVKGILLFGPPGTGKTLMARQIGQM : 278
P.corporis      : ARGQA--PRQSIINPDWDFQKMGIGGLDTEFNAIFRRAFASRVYPPETIEKLGCKHVKGILLYGPPGTGKTLLARQIGKM : 273
S.cerevisiae    : NSLRP--RSNAVIRPDFKFEDLGVGGLDKEFTKIFRRAFASRIFPPSVIEKLGISHVKGLLLYGPPGTGKTLIARKIGTM : 297

H.sapiens       : LNAREPKVVNGPEILNKYVGESEANIRKLFADAEEEQRRLGANSGLHIIIFDEIDAICKQRGSMAGSTGVHDTVVNQLLS : 356
B.mori          : LNAREPKIVNGPQILDKYVGESEANIRRLFADAEEEEKRCGANSGLHIIIFDEIDAICKARGSVGGNTGVHDTVVNQLLS : 356
S.frugiperda    : LNAREPKIVNGPQILDKYVGESEANIRRLFADAEEEEKRCGPNSGLHIIIFDEIDAICKARGSVGGNTGVHDTVVNQLLS : 356
A.mellifera     : LNAREPKIVNGPQILDKYVGESEANIRRLFADAEEEEKRLGPNSGLHIIIFDEIDAICKSRGSVAGNTGVHDTVVNQLLA : 359
D.melanogaster1 : LNAREPKIVNGPQILDKYVGESEANVRRLFAEAEEEEKRLGPNSGLHIIIFDEIDAICKQRGSVAGNSGVHDTVVNQLLT : 356
D.melanogaster2 : LNAREPKIVNGPQILDKYVGESEANIRRLFAEAEEEEKRLGPNSGLHIIIFDEIDAICKARGSVAGNSGVHDTVVNQLLA : 361
T.castaneum     : LNAREPKIVNGPQILDKYVGESEANIRRLFAEAEEEEKRAGPNSGLHIIIFDEIDAICKQRGSVAGNTGVHDTVVNQLLS : 351
A.pisum         : LNAREPKIVNGPQILDKYVGESEANIRRLFADAEEEEKKSGSSSGLHIIIFDEIDAICKARGSVGGNTGVHDTVVNQLLA : 358
P.corporis      : LNAREPKIVNGPQILDKYVGESEANIRRLFAEAEEEEKRLGPNSGLHIIIFDEIDAICKARGSVAGAAGVHDTVVNQLLT : 353
S.cerevisiae    : LNAKEPKIVNGPEILSKYVGSSEENIRNLFKDAEAEYRAKGEESSLHIIIFDELDSVFKQRGSRGDGTGVGDNVVNQLLA : 377
                                      D1                          ▲
                                                                 E329
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H.sapiens        : KIDGVEQLNNILVIGMTNRPDLIDEALLRPGRLEVKMEIGLPDEKGRLQILHIHTARMRGHQLLSADVDIKELAVETKNF : 436
B.mori           : KIDGVDQLNNILVIGMTNRRDMIDEALLRPGRLEVQMEIGLPDEKGRVQILNIHTKRMREYKKIADDVDSMELATLTKNF : 436
S.frugiperda     : KIDGVDQLNNILVIGMTNRRDMIDEALMRPGRLEVQMEIGLPDENGRVQILNIHTKRMKEYKKIADDVDSKELAALTKNF : 436
A.mellifera      : KIDGVEQLNNILVIGMTNRRDMIDEALLRPGRLEVQMEISLPDEHGRFQILNIHTSRMRDYKKISTDVDLKELAALTKNF : 439
D.melanogaster1  : KIDGVDQLNNILVIGMTNRRDMIDEALLRPGRLEVQMEISLPNEQGRVQILNIHTKRMREFNKINDDVDNKEIAALTKNF : 436
D.melanogaster2  : KIDGVEQLNNILVIGMTNRRDMIDEALLRPGRLEVQMEISLPNEQGRVQILNIHTKRMRDFNKIASDVDNNEIAAKTKNF : 441
T.castaneum      : KIDGVEQLNNILVIGMTNRRDMIDEALLRPGRLEVQVEISLPNEDGRFEILNIHTSRMRQYKKISSDVDTRELATLTKNF : 431
A.pisum          : KIDGVEQLNNILVIGMTNRRDMIDEALLRPGRLEVQMEISLPDEHGRHQILNIHTTRMKEFKKIADDVDMKELSVRTKNF : 438
P.corporis       : KIDGVDQLNNILVIGMTNRKDMIDEALLRPGRLEVQMEIGLPDEKGRLQILNIHTSRMREHKKLNEDVDLKELAAITKNF : 433
S.cerevisiae     : KMDGVDQLNNILVIGMTNRKDLIDSALLRPGRFEVQVEIHLPDEKGRLQIFDIQTKKMRENNMMSDDVNLAELAALTKNF : 457
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R385

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H.sapiens        : SGAELEGLVRAAQSTAMNRHIKAST-KVEVDMEKAESLQVTRGDFLASLENDIKPAFGTNQEDYASYIMNGIIKWGDPVT : 515
B.mori           : SGAELEGLVRAAQSTAMNRLIKASS-KVEVDPEAMEKLMVERTDFLHALENDIKPAFGTSAEALEHFLARGIVNWGSPVS : 515
S.frugiperda     : SGAELEGLVRAAQSTAMNRLIKASS-KVEVDPEAMEKLMVERGDFLHALENDIKPAFGTAAEALEHFLSRGIINWGSPVS : 515
A.mellifera      : SGAELEGLVRAAQSTAMNRLIKASS-KVEVDPAAMEKLMVSRADFLHALENDVKPAFGTSAEALDYLLIRGIINWGKPVA : 518
D.melanogaster1  : SGAELEGLVRAAQSSAMNRLIKADA-KVTVDPEAMEKLKVNRDDFLHSLEHDIKPAFGTAQEILDNMLARGVINWGAPVS : 515
D.melanogaster2  : SGAELEGLVRAAQSTAMNRLIKADS-KVHVDPEAMEKLRVTRADFLHALDNDIKPAFGAAQEMLENLLARGIINWGPPVT : 520
T.castaneum      : SGAELEGLVRAAQSTAMNRLIKASN-KVEVDPEAISKLLVTRGDFLNALENDIKPAFGTALEILEQFLARGITVWGSPVS : 510
A.pisum          : SGAELEGLVRAAQSTAMNRLIKANN-KVEVDPDASEKLQVCKDDFLHALEYDIKPAFGASAEALEHFLARGIINWGSSVS : 517
P.corporis       : SGAELEGLVRAAQSTALNRFIKATS-KVEVDPNAIENLSVNRADFLHALENDIKPAFGLSAEILDQLLLHGIINWGKPVE : 512
S.cerevisiae     : SGAEIEGLVKSASSFAINKTVNIGKGATKLNTKDIAKLKVTREDFLNAL-NDVTPAFGISEEDLKTCVEGGMMLYSERVN : 536
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H.sapiens        : RVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIAEESNFPFIKICSPDKMIGFSETAKCQAMKKIFDDAYKS : 595
B.mori           : SIFEDGQLYIQQARATEASGLVSVLLEGPPNSGKTALAAQLAKLSDFPFVKVCSPEDMVGFTETAKCLQIRKVREKY--- : 592
S.frugiperda     : SLLEDGQLYIQQARATEASGLVSVLLEGPPNSGKTALAAELAKLSDFPFVKVCSPEDMVGFTESSKCLQIRKYFDDAYRS : 595
A.mellifera      : EILSDGNLYIQEARSTEGSGLVSVLLEGPPNSGKTALAAQIAKNSDFPFVKVCTPEDMVGFTESAKCLSIRKIFDDAYRS : 598
D.melanogaster1  : NLLEDGMLYVQQAKAPESSGLVSVLVAGAPNSGKTALAAQLAKMSDFPFVKVCSPEDMVGYTESAKCLHIRKIFDDAYRS : 595
D.melanogaster2  : ELLEDGMLSVQQAKATESSGLVSVLIEGAPNSGKSALAANLAQLSDFPFVKVCSPEDMVGFTESAKCLHIRKIFDDAYRS : 600
T.castaneum      : SILEDGRLFIQQAKATDTSGLVSVLIEGPPNAGKTALAAQLAKESDFPFVKVCSPEEMVGYTETAKCLHIRKVFDDAYRS : 590
A.pisum          : GILEDGTLLTQQARVADTFGLVSVLIEGPPNSGKTALAAKLAKDSDFPFVKVCSPEDMVGFTETAKCLQIRKIFDDAYRS : 597
P.corporis       : HIYEVGKILIDQAKSP--DSVVSVLLEGPPNSGKTALAGQLAKMSNFPFIKVCTPEDMVGFTESAKCLLIRKIFDDAHRS : 590
S.cerevisiae     : SILKNGARYVRQVRESDKSRLVSLLIHGPAGSGKTALAAEIALKSGFPFIRLISPNELSGMSESAKIAYIDNTFRDAYKS : 616
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H.sapiens        : QLSCVVVDDIERLLDYVPIGPRFSNLVLQALLVLLKKAPPQGRKLLIIGTTSRKDVLQEMEMLNAFSTTIHVPNIATGEQ : 675
B.mori           : --KCDIYVSI------------------------------------------------------------------- : 600
S.frugiperda     : SLSCILVDNIERLLDYGPIGPRYSNLTLQALLVLLKKQPPKGRKLLILCTSSRRQVLEDMEMLSAFTGVLHVPNLSQPEH : 675
A.mellifera      : QLSCILVDNIERLLDYGPIGPRYSNLTLQALLVLLKKQPPRGRKLLILCTTSRRQVLDDMEMLSAFSKILHVPNLSTPDH : 678
D.melanogaster1  : MLSCIVVDNVERLLDYGSIGPRYSNMTLQALLVLLKKQPPKGRKLLILCTSSRREVLEEMEMLTAFTSVLHVPNLSKPDH : 675
D.melanogaster2  : TLSCIVVDNVERLLDYGPIGPRYSNLTLQALLVLLKKQPPKGRKLLILCTSSRRDVLEEMEMLSAFTSVLHVSNLSTPEN : 680
T.castaneum      : TLSCILVDNIERLLDYGPIGPRYSNLTLQALLVLLKKQPPPGKKLLILCTTSRRQVLEDMEMLSAFTAVLHLPNLSKADQ : 670
A.pisum          : QLSCILVDNIERLLDYGSIGPRYSNLTLQALLVLLKKQPPKGKKLLVLCTSSRKQVLEEMEMLSAFTAVLHVPNLSQPEE : 677
P.corporis       : TLSCILVDNIERLLDYGAVGPRYSNLTLQALLVLLKKEPPKGRRLMVLCTSSRRQVLEDLELLSAFTSILHVPNISDPKD : 670
S.cerevisiae     : PLNILVIDSLETLVDWVPIGPRFSNNILQMLKVALKRKPPQDRRLLIMTTTSAYSVLQQMDILSCFDNEIAVPNMTNLDE : 696
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D2

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H.sapiens        : LLEALEL-LGNFKDKERTTIAQQV--KGKKVWIGIKKLLMLIEVSLQMDPEYR-VRKFLALLREECASPLDFD--- : 744
B.mori           : ------------------ILLTTV--FFYRIFIGIKKLLALIDMVKQTDEEYR-VFKFLTKLQEECCVDLGTTIQ- : 654
S.frugiperda     : VMSVLEE-SDAFSKKDLLKIQQDI--RGARIFIGIKKLLALIDMVKQTDEEYR-VFKFLTKMQEECGLDLGTNVQ- : 746
A.mellifera      : LLSVLEE-VDLFNKNEIASLHAKL--QGKRVFIGIKKLLCLIDMVRQVEPSYR-IVKFLLELEGECALE------- : 743
D.melanogaster1  : VLAVLEN-TDIFSKGEIQAIGKKM--AGKRVFIGIKKLLGLIDMARQTEQSQR-AIKFLSKMEEECGLDMVARQ-- : 745
D.melanogaster2  : VLAVLDD-SDLFSPEELQSIARKM--AGKRLCIGIKKLLALIDMIRQSEPHQR-VIKFLSKMEEECGLEMDRVQGH : 752
T.castaneum      : LLTVLEN-SEVFSQQELKKISQQV--HGKRIFIGIKKLLALIDMARQTDEKFR-VMKLITKLEEDCALEDPGMA-- : 740
A.pisum          : LITVLEQ-FDLFTKQDIHKIYNQI--SGHNVFIGIKKLLALIDMARQTDPKVR-VIKFLTKMEEECCLDLGTMIH- : 748
P.corporis       : FLNVLEE-TNVFTKKDIQSIAKQI--HCQKIFVGIKKLLALVDMARQTNPQIR-VSHFLSTLEEECCLSDTGNR-- : 740
S.cerevisiae     : LNNVMIE-SNFLDDAGRVKVINELSRSCPNFNVGIKKTLTNIETARHDEDPVNELVELMTQSA-------------- : 758
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Figure S1 legend

Multiple sequence alignment of *S. frugiperda* NSF with the homologs from yeast, human, and other insects. Identical residues are shaded in black, while the lesser conserved positions (identity>= 60%) are shaded in gray. The N-terminal domain (NSF-N) and two ATP-binding domains (D1, D2) of NSF are underlined. The two conserved residues E329 and R385 are indicated with black triangles. NSF sequences are from *Acyrthosiphon pisum* (XP001948990), *Apis mellifera* (XP006572124), *Bombyx mori* (XP012550741), *Drosophila melanogaster* 1 (NP524877), *Drosophila melanogaster* 2 (NP788676), *Homo sapiens* (NP006169), *Pediculus humanus corporis* (XP002423289), *Tribolium castaneum* (XP008197594), *Saccharomyces cerevisiae* (NP009636), and *Spodoptera frugiperda* (KY548397).

Table S1. mRNA expressing levels of the components of *T.ni* SNARE complex (≥ 5 RPKM are shown)

Function sites	Gene	T.ni Ortholog	RPKM								STDEV							
			Control	1h	6h	12h	18h	24h	36h	48h	Control	1h	6h	12h	18h	24h	36h	48h
Endosome /Lysosome	Syx6	UN065189	4.52	4.30	5.58	4.58	2.91	2.57	1.47	1.20	0.28	0.51	0.15	0.32	0.21	0.11	0.19	0.08
	Syx7	UN043481	14.06	12.35	14.17	11.60	5.50	4.03	1.79	1.03	0.12	0.80	0.68	0.27	0.32	0.15	0.37	0.06
	Syx17	UN068650	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	Syx20	UN051686	8.22	7.20	10.36	9.93	5.66	4.05	2.26	1.38	0.24	0.34	0.99	0.25	0.22	0.08	0.30	0.14
	VAMP7	UN045870	11.46	7.93	11.26	6.66	4.66	4.02	2.27	1.35	0.73	0.49	0.58	0.29	0.26	0.17	0.24	0.14
	Vti1	UN053818	6.06	9.45	8.61	7.53	5.18	3.62	1.81	0.81	0.39	1.03	0.60	0.45	0.28	0.18	0.13	0.25
Endoplasmic reticulum	Sec20	UN006929	38.23	40.61	82.24	33.60	23.87	18.29	9.24	3.52	2.16	2.71	2.35	1.47	2.17	1.11	0.52	0.74
	Sec22	UN012616	22.11	33.60	46.89	34.26	20.93	17.80	7.06	2.67	0.11	2.66	4.87	1.90	0.72	1.87	0.28	0.13
	Syx18	UN033038	38.14	13.34	27.50	9.34	6.76	5.82	2.80	1.89	1.59	0.18	1.11	0.37	0.65	0.13	0.30	0.46
	Use1	UN042407	10.97	15.01	22.95	9.60	6.71	5.42	1.72	0.70	0.81	0.52	0.98	0.71	0.66	0.38	0.17	0.30
Golgi apparatus	Bet1	UN027084	7.50	10.03	21.05	8.02	6.42	4.80	2.06	0.92	0.52	0.75	1.86	0.59	0.31	0.57	0.16	0.19
	Gos28	UN019930	43.77	37.84	34.90	16.69	10.23	6.21	3.75	1.81	2.68	2.31	2.46	0.91	0.55	0.83	0.90	0.16
	Memb	UN063443	5.83	5.43	8.41	4.32	3.04	1.70	0.96	0.48	0.61	0.52	0.24	0.34	0.53	0.21	0.19	0.07
	Syx5	UN034994	15.55	8.55	16.87	6.92	4.77	4.21	1.32	0.80	0.33	0.14	1.01	0.45	0.70	0.36	0.13	0.06
	Syx16	UN068698	3.85	5.08	5.56	3.41	2.12	1.52	0.95	0.51	0.08	0.22	0.26	0.55	0.07	0.07	0.13	0.14
	Ykt6	UN018597	22.17	22.28	34.29	20.63	13.56	11.42	4.89	3.28	1.09	1.98	1.55	0.59	0.33	0.62	0.17	0.42
Polarization	Lgl	UN037152	20.10	22.95	18.63	13.31	6.08	3.64	2.21	1.41	0.69	0.61	0.44	0.51	0.28	0.13	0.23	0.18
	Tom	UN002466	7.84	2.50	2.05	1.53	0.89	0.41	0.54	0.18	0.82	0.06	0.29	0.11	0.25	0.16	0.08	0.05
Regulatory complex	α-SNAP	UN006562	58.80	64.80	73.18	40.42	21.71	14.55	4.50	1.96	3.36	0.79	1.70	1.04	1.16	0.44	0.32	0.22
	γ-SNAP	UN007066	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	NSF	UN023897	28.98	27.95	21.76	12.78	7.95	5.95	2.87	1.71	0.35	0.92	1.04	0.52	0.17	0.88	0.23	0.28
Secretion pathway	SNAP-25	UN030792	9.75	14.63	19.24	17.37	9.61	6.74	3.54	2.18	0.80	0.65	0.63	0.50	0.25	0.20	0.22	0.09
	SNAP-29	UN011395	20.24	43.64	52.71	36.14	23.24	16.92	7.95	3.96	1.22	1.75	5.15	1.07	1.56	0.18	0.92	0.40
	Syb	UN022470	149.30	343.81	368.95	218.12	120.32	93.27	38.54	12.34	2.70	5.15	6.00	9.00	0.57	1.01	2.96	0.93
	Syx1	UN000635	48.66	47.91	43.74	26.01	12.38	8.65	4.44	2.50	0.71	1.78	2.65	0.67	0.67	0.20	0.46	0.51
	Syx4	?	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Note: The numbers represent RPKM values. The RPKM values (total RPKM<5) for γ-SNAP and Syx17 were cutoff in the transcriptome analysis (Chen et al. 2014).

?, The ortholog of Syx4 was not found in the trancriptome database. h, hours post infeciton, RPKM, reads per kilobases per million reads, STDEV, standard deviation,

T.ni, *Trichoplusia ni*