

Using *de novo* transcriptome assembly and analysis to study RNAi in *Phenacoccus solenopsis* Tinsley (Hemiptera: Pseudococcidae)

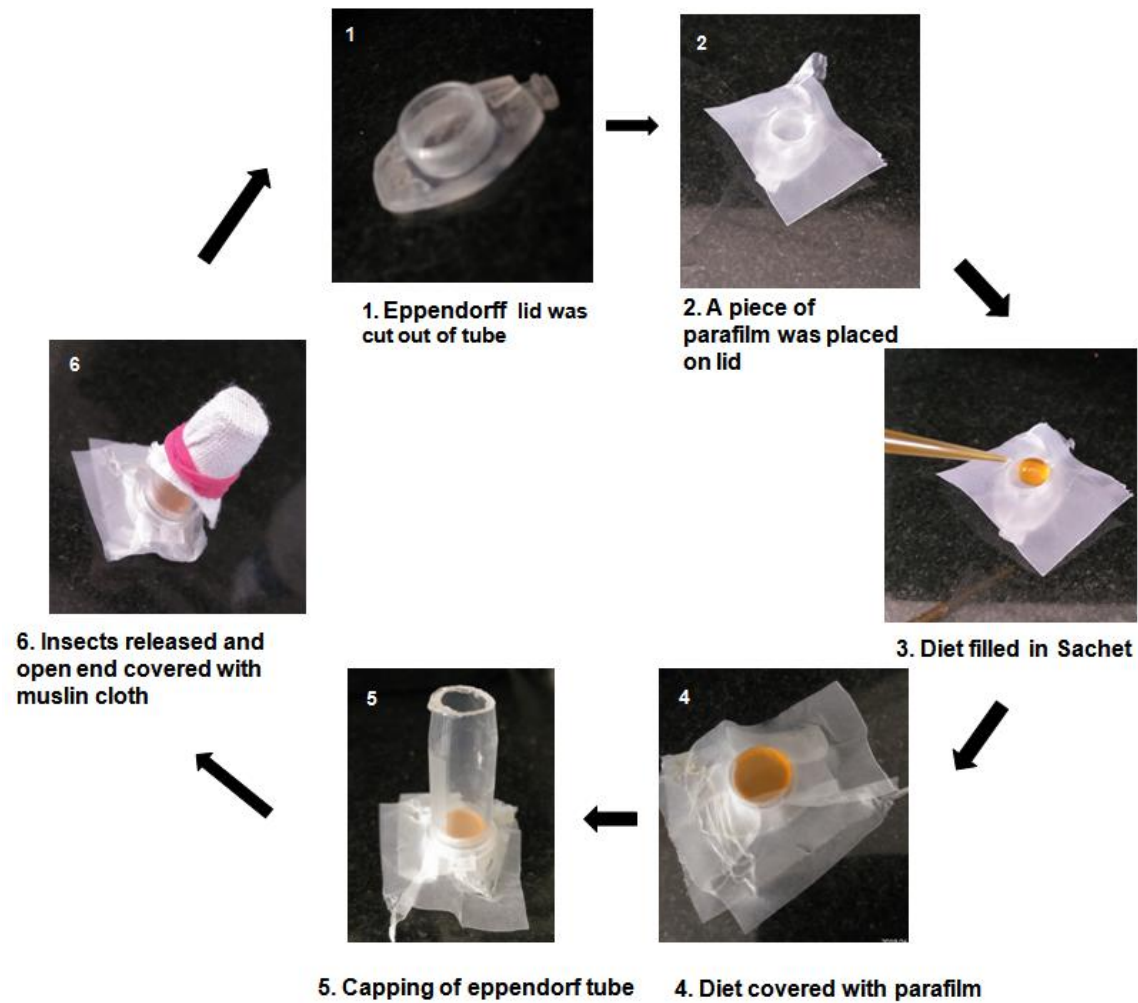
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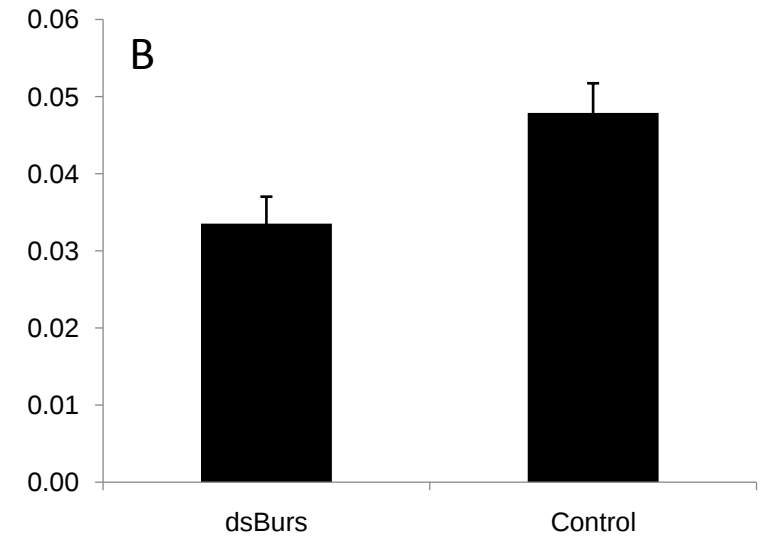
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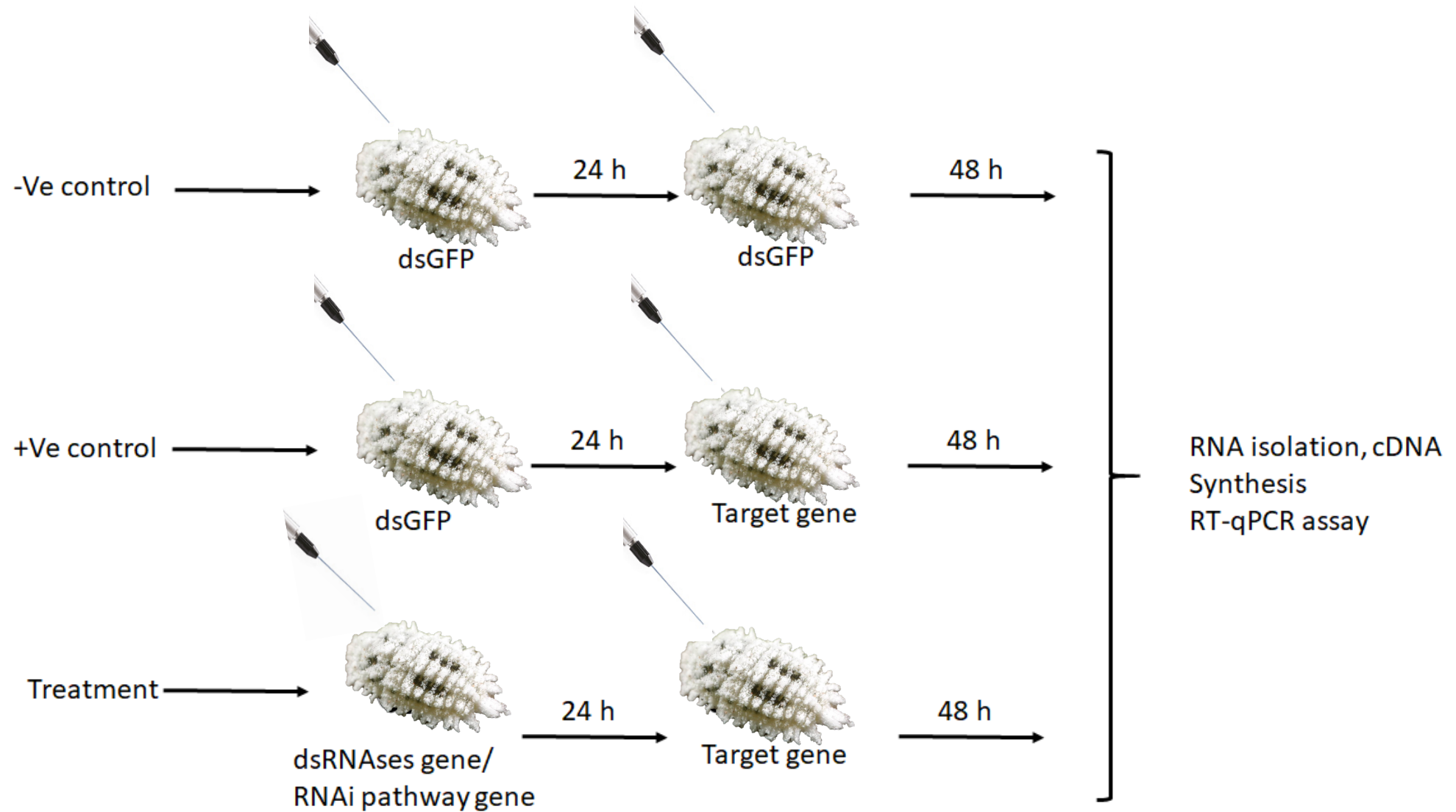
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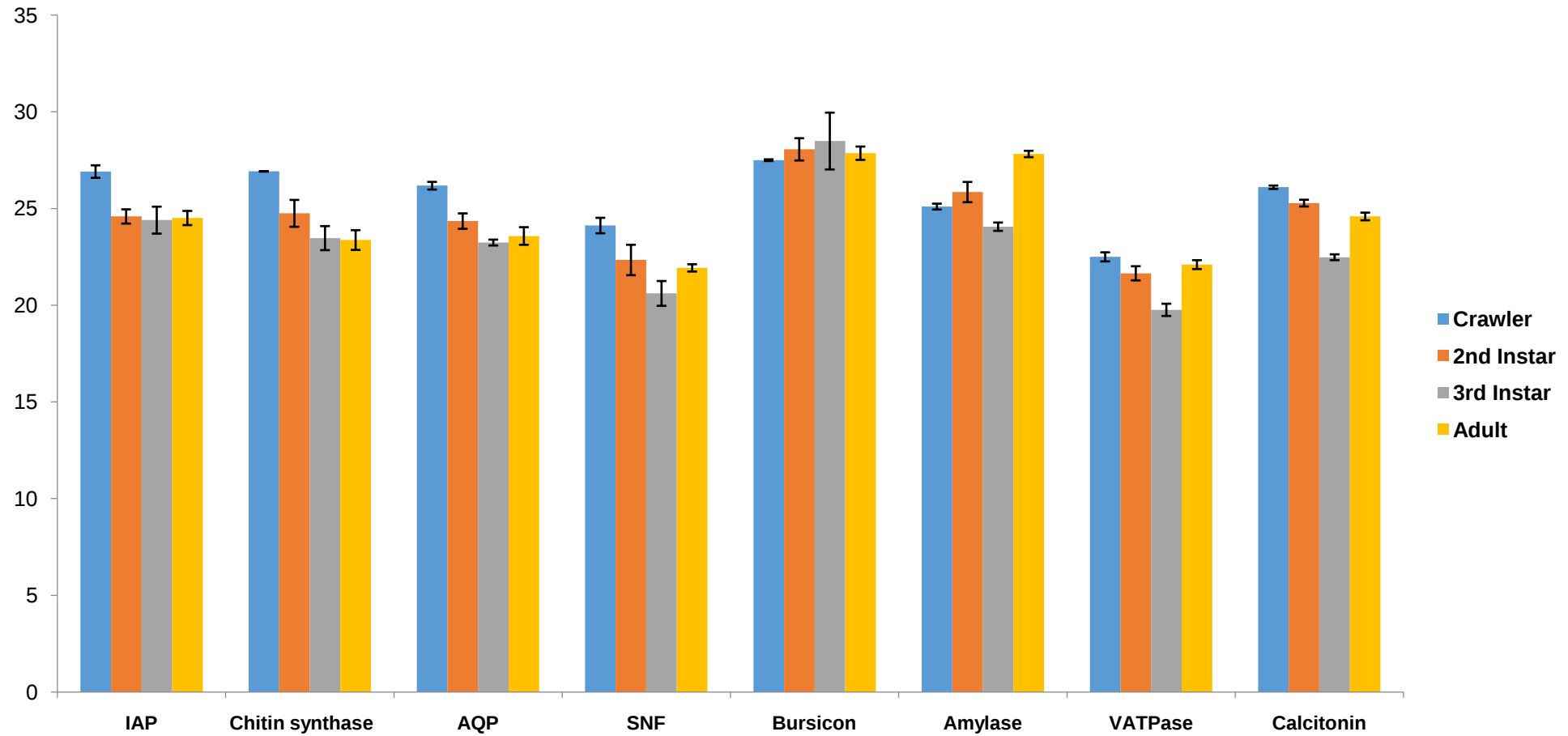
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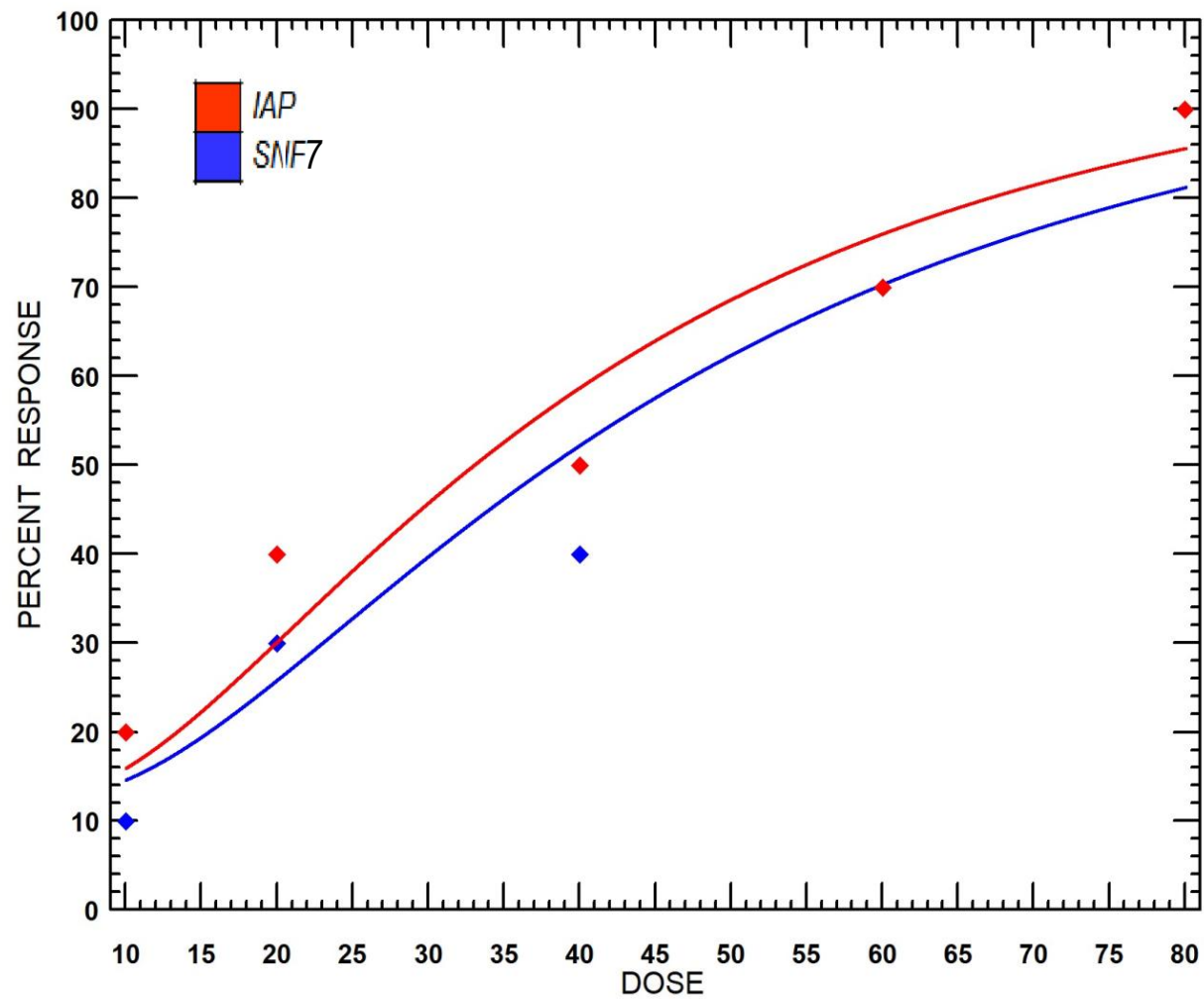
Supplementary Information 4 : SI_Fig. 1: A. Schematic diagram for membrane feeding of 2nd instar mealybug. B. Feeding dsBurs (dsRNA of Bursicon) in artificial diet to 2nd instar nymphs caused knockdown 30.01 % reduction in mRNA levels of *Bursicon* compared to control. The error bars represent the standard deviation (n=3) and the knockdown efficiency was non significant ($P \leq 0.05$, Student's t-test). Thus Petiole dip assay was preferred for feeding RNAi over membrane feeding assay.



Supplementary Information 4 : SI_Fig.2 Schematic diagram for the methodology followed for assay of dsRNases and RNAi pathway genes for studying their effect on knockdown efficiency of targeted gens



Supplementary information 4 SI_Fig. 3 Cq values $\pm$ S.D. obtained for eight RNAi target genes in *P. solenopsis* across developmental stages. Each data point signifies the Mean $\pm$ S. D. of Cq values for three biological replications in each developmental stage.



Supplementary information 4 SI_Fig. 4: Probit analysis to calculate mortality for dsSNF7 and dsIAP at different doses in insect

Supplementary Information SI_Table 1: Primer sequences of target genes of *Phenacoccus solenopsis*

Genes	Primers	Accession No.
Calcitonin_F	CCTATGGTTGGTATGGTACA	MK956911
Calcitonin_R	GTATATGTGGCTGCGTGCTATG	
IAP_F	GGTAGAGCATCGTCGTTATTC	MK956912
IAP_R	CGACCGAGTTGGCAGAATTA	
AQP_F	GGAATGATCTCGCCGATTAC	MK956913
AQP_R	TAGACGCTTCGCCCATATCT	
SNF7_F	GGGCCTTCCTTACCGAATAG	MK956916
SNF7_R	CATACGCCTGGTGTCTCTATCT	
Bursicon_F	GGGCCAATACCATCCTTTGC	MK956917
Bursicon_R	GCATTCTAGAGGTGCCTTTG	
Amylase_F	GCCTTGCCAGATGATTAC	MK956914
Amylase_R	GGTGTCTAGCTTTGTCCCT	
VATPase_F	GCTCCTTATCCGTTTCGGTATC	MH712873.1
VATPase_R	TCCGAGACCACTGTAGAATTTG	
ChitinSyntahse_F	GGGGTGGAGAGTGAAGATAC	MK956915
ChitinSyntahse_R	ACGACGTTTCGGTTTGTAGAG3	

Supplementary information SI_Table 2: Transcripts involved in RNAi Machinery in *Phenacoccus solenopsis*

Sequence name	Sequence description	Sequence length	Hit description	Hit Acession #	E-Value	Similarity	Alignment length
Gene9128_Transcript_11147	argonaute partial	1350	gi 516306731 gb AGO85968.1 ar gonaute 1, partial [Locusta migratoria]	AGO85968	0	99	411
Gene3146_Transcript_3574	protein argonaute-2 isoform x2	1089	gi 939687392 ref XP_014287703.1 PREDICTED: protein argonaute-2 isoform X2 [Halyomorpha halys] >gi 939687396 ref XP_014287704.1 PREDICTED: protein argonaute-2 isoform X2 [Halyomorpha halys]	XP_014287703	0	99	363
Gene3801_Transcript_4261	protein argonaute-2-like isoform x3	2670	gi 939641506 ref XP_014271332.1 PREDICTED: protein argonaute-2-like isoform X3 [Halyomorpha halys]	XP_014271332	0	64	862
Gene42_Transcript_45	protein argonaute-2-like	534	gi 239791844 dbj BAH72335.1 A CYP1008293 [Acyrtosiphon pisum]	BAH72335	1.1E-70	77	161
Gene8190_Transcript_9845	protein argonaute-2-like	639	gi 939240900 ref XP_014239688.1 PREDICTED: protein argonaute-2-like [Cimex lectularius]	XP_014239688	1.2E-40	59	212
Gene9285_Transcript_11346	protein argonaute-2-like isoform x1	348	gi 939277460 ref XP_014259236.1 PREDICTED: protein argonaute-2-like isoform X1 [Cimex lectularius] >gi 939277462 ref XP_014259237.1 PREDICTED: protein argonaute-2-like isoform X1 [Cimex lectularius]	XP_014259236	6.3E-23	68	102
Gene10017_Transcript_12350	argonaute- partial	336	gi 426204656 gb AFY13246.1 ar gonaute-2, partial [Schistocerca gregaria]	AFY13246	2.2E-10	52	118

Gene12903_Transcript_16707	protein argonaute-2	636	gi 645033016 ref XP_008214880.1 PREDICTED: protein argonaute-2 [Nasonia vitripennis]	XP_008214880	2E-39	57	219
Gene15251_Transcript_21173	argonaute- partial	336	gi 426204656 gb AFY13246.1 argonaute-2, partial [Schistocerca gregaria]	AFY13246	4E-10	52	118
Gene4726_Transcript_5389	endoribonuclease dicer	4296	gi 817086281 ref XP_012265864.1 PREDICTED: endoribonuclease Dicer [Athalia rosae] >gi 817086283 ref XP_012265865.1 PREDICTED: endoribonuclease Dicer [Athalia rosae]	XP_012265864	0	53	1489
Gene5260_Transcript_6138	dicer 2	4653	gi 406034947 emb CCF23094.1 Dicer 2 [Blattella germanica]	CCF23094	0	51	1635
Gene6974_Transcript_8197	endoribonuclease dicer isoform x2	600	gi 939652846 ref XP_014275311.1 PREDICTED: endoribonuclease Dicer isoform X2 [Halyomorpha halys]	XP_014275311	4.1E-40	64	183
Gene4616_Transcript_5250	dicer-1	1926	gi 240247227 emb CAX68236.1 dicer-1 [Blattella germanica]	CAX68236	5E-164	58	715
Gene672_Transcript_675	dicer-1	1170	gi 411170363 gb AFW16070.1 dicer-1 [Nilaparvata lugens]	AFW16070	3E-177	87	363

Gene1438_Transcript_1421	ribonuclease 3 isoform x2	2181	gi 936561859 ref XP_014213267.1 PREDICTED: ribonuclease 3 isoform X2 [Copidosoma floridanum] >gi 936561859 ref XP_014213272.1 PREDICTED: ribonuclease 3 isoform X2 [Copidosoma floridanum] >gi 936561862 ref XP_014213280.1 PREDICTED: ribonuclease 3 isoform X2 [Copidosoma floridanum] >gi 936561865 ref XP_014213290.1 PREDICTED: ribonuclease 3 isoform X2 [Copidosoma floridanum]	XP_014213264	0	85	707
Gene14701_Transcript_20015	ribonuclease 3	1419	gi 952511297 gb KRT78218.1 hypothetical protein AMK59_8687, partial [Oryctes borbonicus]	KRT78218	3.1E-86	74	230
Gene4609_Transcript_5243	protein aubergine-like	2262	gi 516306739 gb AGO85970.1 PIWI 2, partial [Locusta migratoria]	AGO85970	0	68	697
Gene5857_Transcript_6894	piwi-like protein 1	2760	gi 646703429 gb KDR12118.1 Piwi-like protein 1 [Zootermopsis nevadensis]	KDR12118	0	65	832
Gene7823_Transcript_9404	clathrin heavy chain	5064	gi 566601502 gb AHC70342.1 clathrin, partial [Locusta migratoria]	AHC70342	0	95	1654
Gene5995_Transcript_7047	epsin-2 isoform x1	552	gi 820848555 ref XP_012342069.1 PREDICTED: epsin-2 [Apis florea]	XP_012342069	3.7E-11	52	122
Gene12975_Transcript_16803	epsin-2 isoform x3	519	gi 939638764 ref XP_014270393.1 PREDICTED: epsin-1 isoform X6 [Halyomorpha halys]	XP_014270393	2E-100	91	173

Gene1868_Transcript_1861	transferrin-like isoform x1	1248	gi 328714357 ref XP_001946481.2 PREDICTED: transferrin-like isoform X1 [Acyrtosiphon pisum] >gi 641667912 ref XP_008184264.1 PREDICTED: transferrin-like isoform X1 [Acyrtosiphon pisum]	XP_001946481	6E-105	62	407
Gene12514_Transcript_16084	PREDICTED: transferrin-like	1794	gi 817186381 ref XP_012287691.1 PREDICTED: transferrin-like [Orussus abietinus]	XP_012287691	7E-127	56	608
Gene1610_Transcript_1586	scavenger receptor class b member 1 isoform x1	1605	gi 939679484 ref XP_014285135.1 PREDICTED: scavenger receptor class B member 1 isoform X1 [Halyomorpha halys]	XP_014285135	0	85	530
Gene5224_Transcript_6092	scavenger receptor class b member 1	774	gi 662201869 ref XP_008474202.1 PREDICTED: scavenger receptor class B member 1-like [Diaphorina citri]	XP_008474202	9E-105	79	249
Gene7805_Transcript_9386	scavenger receptor class b member 1-like isoform x2	1398	gi 985389068 ref XP_015379122.1 PREDICTED: scavenger receptor class B member 1-like isoform X2 [Diuraphis noxia]	XP_015379122	4E-160	74	390
Gene14106_Transcript_18831	low-density lipoprotein receptor-related protein 2	2016	gi 328709384 ref XP_001944217.2 PREDICTED: low-density lipoprotein receptor-related protein 2 [Acyrtosiphon pisum]	XP_001944217	0	83	677
Gene14150_Transcript_18913	low-density lipoprotein receptor-related protein 1	708	gi 985385516 ref XP_015364616.1 PREDICTED: low-density lipoprotein receptor-related protein 1 [Diuraphis noxia]	XP_015364616	2.9E-69	68	239
Gene14175_Transcript_18984	low-density lipoprotein receptor-related protein 2- partial	615	gi 926640456 ref XP_013786325.1 PREDICTED: low-density lipoprotein receptor-related protein 2-like, partial [Limulus polyphemus]	XP_013786325	1.3E-38	58	205

Gene14222_Transcript_19058	low-density lipoprotein receptor-related protein 1	4425	gi 985385516 ref XP_015364616.1 PREDICTED: low-density lipoprotein receptor-related protein 1 [Diuraphis noxia]	XP_015364616	0	58	1586
Gene3773_Transcript_4232	low-density lipoprotein receptor-related protein 2-like	2646	gi 926616750 ref XP_013773508.1 PREDICTED: low-density lipoprotein receptor-related protein 2-like [Limulus polyphemus]	XP_013773508	4.2E-78	47	759
Gene4579_Transcript_5209	low-density lipoprotein receptor-related protein 5	1296	gi 915664608 gb KOC66743.1 Low-density lipoprotein receptor-related protein 5 [Habropoda laboriosa]	KOC66743	5.8E-56	51	381
Gene4685_Transcript_5343	oxidized low-density lipoprotein receptor 1	792	gi 328713134 ref XP_003245001.1 PREDICTED: oxidized low-density lipoprotein receptor 1 [Acyrtosiphon pisum]	XP_003245001	4.2E-95	76	260
Gene5181_Transcript_6033	low-density lipoprotein receptor-related protein 6	3540	gi 646695912 gb KDR08547.1 Low-density lipoprotein receptor-related protein 6 [Zootermopsis nevadensis]	KDR08547	0	69	1109
Gene6387_Transcript_7509	low-density lipoprotein receptor-related protein 3-like	315	gi 926632472 ref XP_013782004.1 PREDICTED: low-density lipoprotein receptor-related protein 3-like [Limulus polyphemus]	XP_013782004	4E-13	63	71
Gene9066_Transcript_11071	low-density lipoprotein receptor-related protein 2	2991	gi 646704521 gb KDR12649.1 Low-density lipoprotein receptor-related protein 2 [Zootermopsis nevadensis]	KDR12649	0	79	1015
Gene1279_Transcript_1256	low-density lipoprotein receptor-related protein 2	6453	gi 328709384 ref XP_001944217.2 PREDICTED: low-density lipoprotein receptor-related protein 2 [Acyrtosiphon pisum]	XP_001944217	0	88	2160

Gene1280_Transcript_1256	low-density lipoprotein receptor-related protein 2	1548	gi 985386327 ref XP_015369125.1 PREDICTED: low-density lipoprotein receptor-related protein 2, partial [Diuraphis noxia]	XP_015369125	0	89	508
Gene3285_Transcript_3724	v-type proton atpase catalytic subunit a	852	gi 646720897 gb KDR22470.1 V-type proton ATPase catalytic subunit A [Zootermopsis nevadensis]	KDR22470	0	95	284
Gene3445_Transcript_3894	v-type proton atpase subunit e	681	gi 121543569 gb ABM55510.1 putative vacuolar ATP synthase subunit E [Maconellicoccus hirsutus]	ABM55510	2E-118	95	226
Gene3704_Transcript_4171	v-type proton atpase 116 kda subunit a isoform 1	492	gi 641675444 ref XP_008187043.1 PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1 [Acyrtosiphon pisum]	XP_008187043	2.3E-51	80	161
Gene4446_Transcript_5046	v-type proton atpase 116 kda subunit a isoform 1- partial	528	gi 662205529 ref XP_008476181.1 PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1-like, partial [Diaphorina citri]	XP_008476181	1.1E-93	91	176
Gene537_Transcript_549	v-type proton atpase 116 kda subunit a isoform 1 isoform x6	2025	gi 939679002 ref XP_014284998.1 PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1 isoform X6 [Halyomorpha halys]	XP_014284998	0	87	675
Gene5614_Transcript_6639	v-type proton atpase catalytic subunit a	627	gi 239791896 dbj BAH72354.1 ACYPI002584 [Acyrtosiphon pisum]	BAH72354	3E-142	97	208
Gene5619_Transcript_6645	v-type proton atpase subunit b	1506	gi 328716950 ref XP_003246082.1 PREDICTED: V-type proton ATPase subunit B [Acyrtosiphon pisum]	XP_003246082	0	97	490

Gene6016_Transcript_7073	v-type proton atpase 116 kda subunit a isoform 1 isoform x3	1149	gi 985388666 ref XP_015378903.1 PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1 isoform X3 [Diuraphis noxia]	XP_015378903	0	91	350
Gene6218_Transcript_7307	v-type proton atpase subunit c	1164	gi 193702420 ref XP_001946227.1 PREDICTED: V-type proton ATPase subunit C [Acyrtosiphon pisum] >gi 641660018 ref XP_008181338.1 PREDICTED: V-type proton ATPase subunit C [Acyrtosiphon pisum]	XP_001946227	0	94	387
Gene888_Transcript_894	v-type proton atpase 16 kda proteolipid subunit	456	gi 817207734 ref XP_012279848.1 PREDICTED: V-type proton ATPase 16 kDa proteolipid subunit [Orussus abietinus]	XP_012279848	9.2E-60	92	151
Gene12393_Transcript_15904	v-type proton atpase 16 kda proteolipid subunit	474	gi 156550753 ref XP_001600237.1 PREDICTED: V-type proton ATPase 16 kDa proteolipid subunit [Nasonia vitripennis]	XP_001600237	4.6E-93	99	154
Gene12512_Transcript_16082	v-type proton atpase 116 kda subunit a isoform 1-like	468	gi 808124622 ref XP_012165459.1 PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1-like [Bombus terrestris]	XP_012165459	4.6E-62	86	127
Gene13948_Transcript_18554	v-type proton atpase subunit s1	789	gi 380024605 ref XP_003696084.1 PREDICTED: uncharacterized protein LOC100865627 [Apis florea]	XP_003696084	2.4E-23	57	200
Gene4497_Transcript_5111	vacuolar atp synthase subunit	372	gi 665790581 ref XP_008560982.1 PREDICTED: V-type proton ATPase subunit F 1 [Microplitis demolitor]	XP_008560982	8.8E-76	95	123
Gene8823_Transcript_10656	vacuolar atp synthase subunit d	630	gi 46561758 gb AAT01084.1 putative vacuolar ATP synthase subunit D [Homalodisca vitripennis]	AAT01084	1E-140	99	207

Gene10316 _Transcript _12796	vacuolar atp synthase 21 kda proteolipid subunit	423	gi 121543963 gb ABM55646.1 p utative vacuolar ATP synthase proteolipid subunit [Maconellicoccus hirsutus]	ABM55646	1.4E-60	87	143
Gene12919 _Transcript _16729	vacuolar atpase g subunit-like protein	309	gi 121543630 gb ABM55524.1 v acuolar ATPase G subunit-like protein [Maconellicoccus hirsutus]	ABM55524	3.9E-29	93	81
Gene13684 _Transcript _18047	guanine nucleotide exchange factor for rab-3a-like isoform x3	798	gi 985410349 ref XP_015370616 .1 PREDICTED: guanine nucleotide exchange factor for Rab-3A-like isoform X3 [Diuraphis noxia]	XP_015370616	3.2E-65	81	166
Gene1587_ Transcript_ 1559	rab gtpase- activating protein 1 isoform x1	2313	gi 646722305 gb KDR23318.1 R ab GTPase-activating protein 1, partial [Zootermopsis nevadensis]	KDR23318	0	74	771
Gene15489 _Transcript _21726	rab gtpase- activating protein 1 isoform x1	423	gi 646722305 gb KDR23318.1 R ab GTPase-activating protein 1, partial [Zootermopsis nevadensis]	KDR23318	3.3E-54	82	130
Gene4452_ Transcript_ 5049	rab6 gtpase activating	312	gi 242017802 ref XP_002429375 .1 rab6 GTPase activating protein, gapcena, putative [Pediculus humanus corporis] >gi 212514288 gb EEB16637.1 rab6 GTPase activating protein, gapcena, putative [Pediculus humanus corporis]	XP_002429375	5.7E-07	65	64
Gene6169_ Transcript_ 7260	rab gtpase-binding effector protein 1 isoform x3	1227	gi 646688535 gb KDR06357.1 hy pothetical protein L798_04283, partial [Zootermopsis nevadensis]	KDR06357	2E-112	73	349
Gene7787_ Transcript_ 9363	rab3 gtpase- activating protein catalytic subunit	2076	gi 642923339 ref XP_008193708 .1 PREDICTED: rab3 GTPase- activating protein catalytic subunit [Tribolium castaneum]	XP_008193708	5E-147	58	707

Gene781_Transcript_789	rab3 gtpase-activating protein catalytic subunit	633	gi 662201644 ref XP_008474082.1 PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC103511145 [Diaphorina citri]	XP_008474082	9.6E-27	56	205
Gene9672_Transcript_11823	rab3 gtpase-activating protein non-catalytic subunit	4017	gi 936572042 ref XP_014218422.1 PREDICTED: rab3 GTPase-activating protein regulatory subunit isoform X1 [Copidosoma floridanum]	XP_014218422	0	55	1399
Gene1083_Transcript_1078	adp-ribosylation arf	420	gi 158300992 ref XP_320779.3 AGAP011730-PA [Anopheles gambiae str. PEST] >gi 157013426 gb EAA00052.3 AGAP011730-PA [Anopheles gambiae str. PEST]	XP_320779	8E-76	94	139
Gene10965_Transcript_13743	adp-ribosylation factor-like protein 13b	1245	gi 646707352 gb KDR14158.1 ADP-ribosylation factor-like protein 13B [Zootermopsis nevadensis]	KDR14158	1.2E-66	66	277
Gene1105_Transcript_1097	adp ribosylation factor 102f	570	gi 568255707 gb ETN64433.1 ADP ribosylation factor 102F [Anopheles darlingi] >gi 668457326 gb KFB45367.1 hypothetical protein ZHAS_00013319 [Anopheles sinensis]	ETN64433	2E-116	96	179

Gene14263 _Transcript _19125	adp-ribosylation factor-related protein 1	606	gi 76655655 ref XP_011687533.1 PREDICTED: ADP-ribosylation factor-related protein 1 [Wasmannia auropunctata] >gi 815795692 ref XP_012218502.1 PREDICTED: ADP-ribosylation factor-related protein 1 isoform X1 [Linepithema humile] >gi 826412849 ref XP_012543513.1 PREDICTED: ADP-ribosylation factor-related protein 1 [Monomorium pharaonis]	XP_011687533	1E-120	92	199
Gene14501 _Transcript _19600	adp-ribosylation factor-like protein 3 isoform x2	543	gi 193580240 ref XP_001949993.1 PREDICTED: ADP-ribosylation factor-like protein 3 isoform X2 [Acyrtosiphon pisum] >gi 985384640 ref XP_015365815.1 PREDICTED: ADP-ribosylation factor-like protein 3 isoform X2 [Diuraphis noxia]	XP_001949993	1E-104	91	180
Gene3480 _Transcript _3927	adp-ribosylation factor-like protein 2	579	gi 91087357 ref XP_975625.1 PREDICTED: ADP-ribosylation factor-like protein 2 [Tribolium castaneum] >gi 270010616 gb EFA07064.1 hypothetical protein TcasGA2_TC010041 [Tribolium castaneum]	XP_975625	4.6E-83	91	160

Gene5740_ Transcript_ 6776	adp-ribosylation factor-like protein 6-interacting protein 4	339	gi 662188172 ref XP_008487746.1 PREDICTED: ADP-ribosylation factor-like protein 6-interacting protein 4 [Diaphorina citri] >gi 662188174 ref XP_008487747.1 PREDICTED: ADP-ribosylation factor-like protein 6-interacting protein 4 [Diaphorina citri]	XP_008487746	1E-06	77	40
Gene6130_ Transcript_ 7219	adp-ribosylation factor-like protein 5b isoform x1	540	gi 817071423 ref XP_012257776.1 PREDICTED: ADP-ribosylation factor-like protein 5B isoform X1 [Athalia rosae]	XP_012257776	3E-113	93	179
Gene6914_ Transcript_ 8124	adp-ribosylation factor-binding protein gga3	1923	gi 972211465 ref XP_015188148.1 PREDICTED: ADP-ribosylation factor-binding protein GGA3 [Polistes dominula]	XP_015188148	1E-102	55	687
Gene8021_ Transcript_ 9639	adp-ribosylation factor gtpase- activating	1623	gi 985397038 ref XP_015366044.1 PREDICTED: ADP-ribosylation factor GTPase-activating protein 2 [Diuraphis noxia]	XP_015366044	5E-156	67	549

Gene8201_ Transcript_ 9860	adp-ribosylation factor 6	528	.1 PREDICTED: ADP- ribosylation factor 6 [Bombus terrestris] >gi 345498024 ref XP_00342812 6.1 PREDICTED: ADP- ribosylation factor 6 [Nasonia vitripennis] >gi 345498026 ref XP_00160380 4.2 PREDICTED: ADP- ribosylation factor 6 [Nasonia vitripennis] >gi 350406774 ref XP_00348787 8.1 PREDICTED: ADP- ribosylation factor 6 isoform X1 [Bombus impatiens] >gi 380019019 ref XP_00369341 5.1 PREDICTED: ADP- ribosylation factor 6 [Apis floreana] >gi 383847271 ref XP_00369927 8.1 PREDICTED: ADP- ribosylation factor 6 isoform X2 [Megachile rotundata] >gi 512922083 ref XP_00493003 2.1 PREDICTED: ADP- ribosylation factor 6 [Bombyx mori] >gi 572307215 ref XP_00661947 9.1 PREDICTED: ADP- ribosylation factor 6-like [Apis dorsata]	XP_003399058	4E-125	100	175
Gene8451_ Transcript_ 10169	adp-ribosylation factor-like protein 4c	621	gi 914562894 gb KOB68938.1 A DP-ribosylation factor-like protein 4A [Operophtera brumata]	KOB68938	5E-117	91	195

Gene9039_ Transcript_ 11027	adp-ribosylation factor 1	429	gi 939648957 ref XP_014273936.1 PREDICTED: ADP-ribosylation factor 1 [Halyomorpha halys] >gi 939648959 ref XP_014273937.1 PREDICTED: ADP-ribosylation factor 1 [Halyomorpha halys]	XP_014273936	3.9E-98	100	143
Gene9063_ Transcript_ 11064	adp-ribosylation factor gtpase- activating protein 1 isoform x1	1086	gi 939233759 ref XP_014241811.1 PREDICTED: ADP-ribosylation factor GTPase-activating protein 1 isoform X1 [Cimex lectularius]	XP_014241811	1.3E-71	64	282
Gene10371_ Transcript_ _12869	adp-ribosylation factor-like protein 8b-a	336	gi 328712016 ref XP_003244709.1 PREDICTED: ADP-ribosylation factor-like protein 8B-A [Acyrtosiphon pisum] >gi 985403789 ref XP_015369611.1 PREDICTED: ADP-ribosylation factor-like protein 8B-A [Diuraphis noxia]	XP_003244709	3.6E-67	96	108
Gene7779_ Transcript_ 9354	small rna degrading nuclease 5 isoform x1	1917	gi 817073780 ref XP_012259049.1 PREDICTED: small RNA degrading nuclease 5 isoform X2 [Athalia rosae]	XP_012259049	2E-145	63	587
Gene1727_ Transcript_ 1715	hermansky-pudlak syndrome 3 protein homolog isoform x1	2661	gi 939676728 ref XP_014284227.1 PREDICTED: Hermansky-Pudlak syndrome 3 protein homolog isoform X2 [Halyomorpha halys]	XP_014284227	3.6E-41	42	951

Gene4502_Transcript_5120	hermansky-pudlak syndrome 1 protein homolog	1350	gi 328707951 ref XP_001947892.2 PREDICTED: Hermansky-Pudlak syndrome 1 protein homolog [Acyrtosiphon pisum] >gi 641660668 ref XP_008181570.1 PREDICTED: Hermansky-Pudlak syndrome 1 protein homolog [Acyrtosiphon pisum]	XP_001947892	1.9E-71	57	434
Gene6833_Transcript_8046	hermansky-pudlak syndrome 4 protein homolog isoform x2	2298	gi 939238527 ref XP_014261955.1 PREDICTED: uncharacterized protein LOC106674035 isoform X1 [Cimex lectularius]	XP_014261955	4E-142	53	780
Gene9133_Transcript_11156	hermansky-pudlak syndrome 1 protein	549	gi 646701961 gb KDR11428.1 Hermansky-Pudlak syndrome 1 protein-like protein [Zootermopsis nevadensis]	KDR11428	2.6E-76	79	179
Gene3307_Transcript_3754	dead box atp-dependent rna helicase-like partial	606	gi 506968895 gb AGM32791.1 DEAD box ATP-dependent RNA helicase-like protein, partial [Coptotermes formosanus]	AGM32791	3E-110	91	201
Gene5469_Transcript_6476	dead box atp-dependent rna helicase	378	gi 170071047 ref XP_001869798.1 DEAD box ATP-dependent RNA helicase [Culex quinquefasciatus] >gi 167866996 gb EDS30379.1 DEAD box ATP-dependent RNA helicase [Culex quinquefasciatus]	XP_001869798	3.4E-84	99	125
Gene10557_Transcript_13106	dead box atp-dependent rna	2403	gi 328723280 ref XP_001943847.2 PREDICTED: probable ATP-dependent RNA helicase DDX20 [Acyrtosiphon pisum]	XP_001943847	5.9E-89	62	406

Gene11894_Transcript_15117	dead-box helicase dbp80	1002	gi 646714912 gb KDR18709.1 D EAD-box helicase Dbp80 [Zootermopsis nevadensis]	KDR18709	8E-135	86	258
Gene1351_Transcript_1319	dead box atp-dependent rna helicase	2088	gi 501295923 dbj BAN20948.1 D EAD box ATP-dependent RNA helicase [Riptortus pedestris]	BAN20948	0	85	423
Gene13970	dead box atp-	645	EAD box ATP-dependent RNA	AGM32791	2E-109	91	201
Gene2362_Transcript_2432	protein abnormal spindle	1107	gi 646720534 gb KDR22214.1 Pr otein abnormal spindle [Zootermopsis nevadensis]	KDR22214	1.6E-24	46	365
Gene2900_Transcript_3160	protein abnormal spindle-like isoform x2	1677	gi 985409495 ref XP_015370146.1 PREDICTED: protein abnormal spindle-like isoform X2 [Diuraphis noxia]	XP_015370146	1.2E-21	42	635
Gene8995_Transcript_10955	protein abnormal spindle	573	gi 91080169 ref XP_970176.1 PREDICTED: protein abnormal spindle [Tribolium castaneum]	XP_970176	6.9E-24	61	192
Gene9359_Transcript_11438	spindle assembly abnormal protein 6 homolog	1212	gi 817212012 ref XP_012282172.1 PREDICTED: spindle assembly abnormal protein 6 homolog [Orussus abietinus]	XP_012282172	2.4E-20	51	337
Gene15684_Transcript_22192	spindle assembly abnormal protein 6-like protein	462	gi 646715514 gb KDR19091.1 S pindle assembly abnormal protein 6-like protein [Zootermopsis nevadensis]	KDR19091	4.6E-15	52	149
Gene9648_Transcript_11795	rna binding protein fox-1 homolog 2-like isoform x7	1059	gi 951517270 ref XP_014489079.1 PREDICTED: RNA binding protein fox-1 homolog 2-like isoform X7 [Dinoponera quadriceps]	XP_014489079	2.6E-42	71	126
Gene11782_Transcript_14945	rna binding protein	339	gi 952530824 gb KRT83885.1 R NA binding protein [Oryctes borbonicus]	KRT83885	2.2E-25	96	57
Gene15039_Transcript_20698	rna binding protein	366	gi 478251698 gb ENN72152.1 hy pothetical protein YQE_11209, partial [Dendroctonus ponderosae]	ENN72152	3.5E-53	94	108

Gene3139_Transcript_3564	rna binding partial	594	gi 952512384 gb KRT79126.1 RNA binding protein, partial [Oryctes borbonicus]	KRT79126	9E-110	94	176
Gene6274_Transcript_7368	rna binding motif protein x-linked 2	420	gi 357611289 gb EHJ67406.1 RNA binding motif protein X-linked 2 [Danaus plexippus]	EHJ67406	8.4E-58	88	107
Gene15449_Transcript_21644	protein arginine n-methyltransferase 1	342	gi 972206976 ref XP_015185745.1 PREDICTED: protein arginine N-methyltransferase 1 [Polistes dominula]	XP_015185745	1.8E-34	73	109
Gene3626_Transcript_4082	protein arginine n-methyltransferase 8	1107	gi 646689677 gb KDR06666.1 Protein arginine N-methyltransferase 8 [Zootermopsis nevadensis]	KDR06666	0	87	358
Gene4217_Transcript_4763	protein arginine n-methyltransferase 5	1869	gi 646718675 gb KDR21061.1 Protein arginine N-methyltransferase 5 [Zootermopsis nevadensis]	KDR21061	0	69	623
Gene5341_Transcript_6273	protein arginine n-methyltransferase 9	2142	gi 939684922 ref XP_014286911.1 PREDICTED: putative protein arginine N-methyltransferase 9 [Halyomorpha halys]	XP_014286911	4E-90	52	709
Gene6224_Transcript_7315	protein arginine n-methyltransferase 1	600	gi 26353886 dbj BAC40573.1 unnamed protein product [Mus musculus]	BAC40573	1E-33	58	162
Gene8949_Transcript_10875	protein arginine n-methyltransferase 7	1953	gi 646710226 gb KDR15803.1 Protein arginine N-methyltransferase 7 [Zootermopsis nevadensis]	KDR15803	0	67	653
Gene9751_Transcript_11925	protein arginine n-methyltransferase 6	1089	gi 642927466 ref XP_008195284.1 PREDICTED: protein arginine N-methyltransferase 6 [Tribolium castaneum]	XP_008195284	8E-101	67	337

Gene10397 _Transcript _12911	protein arginine n- methyltransferase 1	1023	gi 939279237 ref XP_014260190.1 PREDICTED: protein arginine N-methyltransferase 1 [Cimex lectularius] >gi 939279239 ref XP_014260191.1 PREDICTED: protein arginine N-methyltransferase 1 [Cimex lectularius]	XP_014260190	4E-106	69	323
Gene10512 _Transcript _13063	protein arginine n-	687	gi 242014396 ref XP_002427877.1 protein arginine N-methyltransferase, putative [Pediculus humanus corporis] >gi 212512346 gb EEB15139.1 protein arginine N-methyltransferase, putative [Pediculus humanus corporis]	XP_002427877	2.3E-15	51	224
Gene12394 _Transcript _15906	maternal protein tudor-like isoform x2	906	gi 826478596 ref XP_012537619.1 PREDICTED: maternal protein tudor-like isoform X2 [Monomorium pharaonis]	XP_012537619	1.1E-25	54	235
Gene1274 _Transcript _1249	tudor domain- containing protein 7	2298	gi 409194603 gb AFV31612.1 tdrd7 [Gryllus bimaculatus]	AFV31612	1.3E-65	50	580
Gene14706 _Transcript _20031	tudor domain- containing protein 12	723	gi 646710823 gb KDR16241.1 Tudor domain-containing protein 12 [Zootermopsis nevadensis]	KDR16241	5.7E-17	55	141

Gene14745_Transcript_20105	tudor domain-containing protein 7b-like isoform x1	615	gi 817217549 ref XP_012284701.1 PREDICTED: tudor domain-containing protein 7A [Orussus abietinus] >gi 817217549 ref XP_012284703.1 PREDICTED: tudor domain-containing protein 7A [Orussus abietinus] >gi 817217551 ref XP_012284704.1 PREDICTED: tudor domain-containing protein 7A [Orussus abietinus] >gi 817217554 ref XP_012284705.1 PREDICTED: tudor domain-containing protein 7A [Orussus abietinus]	XP_012284701	1.9E-13	49	202
Gene15609_Transcript_22006	tudor domain-containing protein 1	576	gi 646715533 gb KDR19110.1 Tudor domain-containing protein 1 [Zootermopsis nevadensis]	KDR19110	6.8E-15	48	189
Gene1960_Transcript_1963	tudor domain-containing protein 1 isoform x1	1632	gi 939649280 ref XP_014274051.1 PREDICTED: uncharacterized protein LOC106679416 [Halyomorpha halys]	XP_014274051	1.3E-08	65	73
Gene3006_Transcript_3347	tudor domain-containing protein 7-like isoform x1	372	gi 157125859 ref XP_001654423.1 AAEL010311-PA [Aedes aegypti] >gi 108873488 gb EAT37713.1 AAEL010311-PA [Aedes aegypti]	XP_001654423	1.4E-10	52	128
Gene3369_Transcript_3817	tudor domain-containing protein 1 isoform x1	1242	gi 939649280 ref XP_014274051.1 PREDICTED: uncharacterized protein LOC106679416 [Halyomorpha halys]	XP_014274051	3.9E-21	44	376

Gene3816_Transcript_4277	tudor domain-containing protein 1-like	333	gi 926641110 ref XP_013786678.1 PREDICTED: uncharacterized protein LOC106470659, partial [Limulus polyphemus]	XP_013786678	2.1E-11	50	112
Gene4769_Transcript_5450	tudor domain-containing protein 5	3156	gi 646703152 gb KDR11968.1 Tudor domain-containing protein 5 [Zootermopsis nevadensis]	KDR11968	1.2E-32	44	522
Gene774_Transcript_782	maternal protein tudor isoform x1	627	gi 815921522 ref XP_012245640.1 PREDICTED: maternal protein tudor isoform X3 [Bombus impatiens]	XP_012245640	2.5E-11	51	172
Gene7853_Transcript_9434	tudor domain-containing protein 7a-like	723	gi 817073456 ref XP_012258869.1 PREDICTED: tudor domain-containing protein 7A-like isoform X2 [Athalía rosae]	XP_012258869	7.6E-15	66	90
Gene9746_Transcript_11912	tudor domain-containing protein 7-like isoform x2	615	gi 157125859 ref XP_001654423.1 AAEL010311-PA [Aedes aegypti] >gi 108873488 gb EAT37713.1 AAEL010311-PA [Aedes aegypti]	XP_001654423	3.2E-31	56	205
Gene986_Transcript_989	tudor and kh domain-containing	1200	gi 662213226 ref XP_008480390.1 PREDICTED: tudor and KH domain-containing protein-like [Diaphorina citri]	XP_008480390	1.4E-41	49	364
Gene10660_Transcript_13254	tudor domain-containing protein 1	2271	gi 646715533 gb KDR19110.1 Tudor domain-containing protein 1 [Zootermopsis nevadensis]	KDR19110	1.1E-16	42	349
Gene13540_Transcript_17773	atp-dependent clp protease atp-binding subunit clpx-mitochondrial isoform x1	1836	gi 646712236 gb KDR17084.1 ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial [Zootermopsis nevadensis]	KDR17084	0	87	505

Gene12427 _Transcript _15966	atp-dependent clp protease proteolytic mitochondrial	717	gi 646720905 gb KDR22478.1 P utative ATP-dependent Clp protease proteolytic subunit, mitochondrial [Zootermopsis nevadensis]	KDR22478	1E-127	91	212
Gene2042 _Transcript _2064	reverse rna- dependent dna polymerase domain-containing protein	507	gi 528890629 gb EPZ31199.1 Re verse transcriptase, RNA- dependent DNA polymerase domain-containing protein [Rozella allomyces CSF55]	EPZ31199	3.4E-07	58	75
Gene4609 _Transcript _5243	protein aubergine-like	2262	gi 516306739 gb AGO85970. 1 PIWI 2, partial [Locusta migratoria]	AGO85970	0	68	697
Gene1983 _Transcript _1997	risc-loading complex subunit tarbp2-like isoform x1	978	gi 951535376 ref XP_014471 217.1 PREDICTED: RISC- loading complex subunit TARBP2-like isoform X1 [Dinoponera quadricaps]	XP_01447121 7	1.8E-20	45	341

Supplementary information SI_Table 3: Transcripts involved in RNAi Machinery in *Phenacoccus solenopsis*

Sequence name	Sequence description	Sequence length	Hit description	Hit Acession #	E-Value	Similarity	Alignment length
Gene10997_Transcript_13810	vacuolar h	1380	gi 501293539 dbj BAN20615.1 vacuolar H[+] ATPase subunit [Riptortus pedestris]	BAN20615	0	89	461
Gene12538_Transcript_16116	tubulin-folding cofactor b	762	gi 913324565 ref XP_013193607.1 PREDICTED: tubulin-folding cofactor B [Amyeloidis transitella]	XP_013193607	6.62605E-60	64	252
Gene12514_Transcript_16084	PREDICTED: transferrin-like	1794	gi 817186381 ref XP_012287691.1 PREDICTED: transferrin-like [Orussus abietinus]	XP_012287691	6.5393E-127	56	608
Gene6001_Transcript_7054	glutamyl-trna amidotransferase subunit mitochondrial	1488	gi 646699587 gb KDR10141.1 Glutamyl-tRNA(Gln) amidotransferase subunit A-like protein [Zootermopsis nevadensis]	KDR10141	6.3114E-172	70	503
Gene617_Transcript_627	28s ribosomal protein mitochondrial-like	501	gi 913302294 ref XP_013200341.1 PREDICTED: 28S ribosomal protein S2, mitochondrial-like [Amyeloidis transitella]	XP_013200341	2.26408E-45	70	148
Gene8506_Transcript_10241	elongation of very long chain fatty acids protein aael008004-like isoform x2	822	gi 985399759 ref XP_015367517.1 PREDICTED: elongation of very long chain fatty acids protein AAEL008004-like [Diuraphis noxia]	XP_015367517	2.4072E-157	92	264
Gene9672_Transcript_11823	rab3 gtpase-activating protein non-catalytic subunit	4017	gi 936572042 ref XP_014218422.1 PREDICTED: rab3 GTPase-activating protein regulatory subunit isoform X1 [Copidosoma floridanum]	XP_014218422	0	55	1399

Gene10258_Transcript_12711	aquaporin	744	gi 208609314 dbj BAG72254.1 aquaporin [Coptotermes formosanus]	BAG72254	2.82858E-93	72	243
Gene11098_Transcript_13966	cathepsin b-like cysteine proteinase 4	672	gi 985396557 ref XP_015365780.1 PREDICTED: cathepsin B-like cysteine proteinase 4 [Diuraphis noxia]	XP_015365780	7.00674E-66	61	239
Gene15042_Transcript_20711	golgi snap receptor complex member 1	708	gi 646717139 gb KDR20120.1 Golgi SNAP receptor complex member 1 [Zootermopsis nevadensis]	KDR20120	3.6821E-109	83	234
Gene12640_Transcript_16263	actin-related protein	1080	gi 501297067 dbj BAN21097.1 actin-related protein [Riptortus pedestris]	BAN21097	0	94	358
Gene13947_Transcript_18552	adp atp translocase	930	gi 478346160 gb AGI96985.1 ADP/ATP translocase [Nilaparvata lugens] >gi 787071538 dbj BAR13242.1 adenine nucleotide translocase insect1 [Nilaparvata lugens]	AGI96985	0	95	300
Gene7807_Transcript_9388	protein toll	891	gi 646706355 gb KDR13629.1 Protein toll [Zootermopsis nevadensis]	KDR13629	2.07135E-25	55	232
Gene3468_Transcript_3918	vitellogenin isoform x1	1332	gi 985397648 ref XP_015366382.1 PREDICTED: vitellogenin isoform X1 [Diuraphis noxia]	XP_015366382	5.82E-110	63	437
Gene12751_Transcript_16434	protein white-like	1023	gi 662190368 ref XP_008467946.1 PREDICTED: uncharacterized protein LOC103505393 [Diaphorina citri]	XP_008467946	7.4934E-121	83	280

Gene2226_Transcript_2284	carboxylesterase	1641	gi 586831179 gb AHJ81323.1 carboxylesterase [Locusta migratoria]	AHJ81323	1.90702E-71	51	556
Gene2609_Transcript_2758	cytochrome p450 6bq11	1566	gi 646716643 gb KDR19800.1 putative cytochrome P450 6a13 [Zootermopsis nevadensis]	KDR19800	6.5181E-115	55	511
Gene5961_Transcript_7013	acetylcholinesterase 1	2625	gi 985414258 ref XP_015372572.1 PREDICTED: acetylcholinesterase 1 [Diuraphis noxia]	XP_015372572	0	74	744
Gene12172_Transcript_15491	glutathione s-transferase c-terminal domain-containing protein	1365	gi 646716168 gb KDR19528.1 Glutathione S-transferase C-terminal domain-containing protein-like protein [Zootermopsis nevadensis]	KDR19528	8.5231E-138	63	475
Gene170_Transcript_184	inter-alpha-trypsin inhibitor heavy chain h3 isoform x2	783	gi 328712314 ref XP_001943110.2 PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X2 [Acyrtosiphon pisum]	XP_001943110	1.23378E-80	75	245
Gene13116_Transcript_17002	coagulation factor x	960	gi 939279779 ref XP_014260482.1 PREDICTED: chymotrypsinogen A-like [Cimex lectularius]	XP_014260482	2.36912E-24	50	254
Gene10279_Transcript_12750	juvenile hormone acid methyltransferase	819	gi 631793773 gb AHZ20738.1 juvenile hormone acid methyltransferase [Diptera punctata]	AHZ20738	3.5274E-58	55	273
Gene11975_Transcript_15219	homeodomain transcription factor	876	gi 646708434 gb KDR14746.1 Putative homeodomain transcription factor [Zootermopsis nevadensis]	KDR14746	1.56701E-27	68	141

Gene3355_Transcript_3808	chitin deacetylase 2	816	gi 762060959 gb AJQ20733.1 chitin deacetylase 2 [Nilaparvata lugens]	AJQ20733	2.0716E-161	86	277
Gene5817_Transcript_6847	probable chitinase 3	615	gi 939264426 ref XP_014252214.1 PREDICTED: probable chitinase 3 [Cimex lectularius]	XP_014252214	6.7854E-128	91	204
Gene6609_Transcript_7763	carboxypeptidase d	2937	gi 985400959 ref XP_015368174.1 PREDICTED: carboxypeptidase D [Diuraphis noxia]	XP_015368174	0	58	919
Gene6594_Transcript_7745	atpase n2b	1416	gi 646713527 gb KDR17842.1 Putative ATPase N2B [Zootermopsis nevadensis]	KDR17842	0	79	410
Gene3458_Transcript_3908	cullin-1 isoform x2	2310	gi 646702041 gb KDR11477.1 Cullin-1 [Zootermopsis nevadensis]	KDR11477	0	91	768
Gene3569_Transcript_4021	homeobox protein homothorax isoform x3	1227	gi 939663689 ref XP_014279414.1 PREDICTED: homeobox protein homothorax isoform X3 [Halyomorpha halys]	XP_014279414	0	85	410
Gene12025_Transcript_15291	pumilio homolog 2 isoform x7	2214	gi 939249020 ref XP_014244019.1 PREDICTED: pumilio homolog 2 isoform X7 [Cimex lectularius]	XP_014244019	1.28737E-50	72	202
Gene11059_Transcript_13913	ubiquinol-cytochrome c rieske iron-sulfur polypeptide 1	831	gi 121543951 gb ABM55640.1 putative ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Maconellicoccus hirsutus]	ABM55640	1.9229E-123	84	276

Gene7226_Transcript_8548	protein wingless	600	gi 970905347 ref XP_015118605.1 PREDICTED: protein wingless [Diachasma alloeum]	XP_015118605	1.133E-106	86	203
Gene9154_Transcript_11178	swi snf complex subunit smarcc2 isoform x2	2169	gi 939257713 ref XP_014248678.1 PREDICTED: SWI/SNF complex subunit SMARCC2 isoform X2 [Cimex lectularius]	XP_014248678	0	81	647
Gene9382_Transcript_11467	apoptosis inhibitor 5	1605	gi 815816842 ref XP_012229529.1 PREDICTED: apoptosis inhibitor 5 [Linepithema humile]	XP_012229529	8.0973E-143	66	499
Gene11474_Transcript_14436	ecdysone-induced protein 74ef isoform b	1467	gi 662184902 ref XP_008474349.1 PREDICTED: ecdysone-induced protein 74EF isoform A [Diaphorina citri]	XP_008474349	4.14442E-87	81	216
Gene9169_Transcript_11192	peptidyl-prolyl cis-trans isomerase-like 3	486	gi 357619503 gb EHJ72048.1 putative cyclophilin-10 [Danaus plexippus]	EHJ72048	1.62716E-96	89	161
Gene12357_Transcript_15846	serine protease p54	681	gi 546674814 gb ERL86100.1 hypothetical protein D910_03514, partial [Dendroctonus ponderosae]	ERL86100	5.9079E-108	82	228
Gene10998_Transcript_13818	coatomer subunit delta	840	gi 939669103 ref XP_014281485.1 PREDICTED: coatomer subunit delta [Halyomorpha halys]	XP_014281485	9.8051E-116	77	277
Gene14516_Transcript_19656	tetraspanin-17 isoform x2	762	gi 939688420 ref XP_014288110.1 PREDICTED: tetraspanin-17 isoform X2 [Halyomorpha halys]	XP_014288110	2.79916E-56	67	197

Gene11103_Transcript_13971	insulin-like growth factor 2 mrna-binding protein partial	687	gi 646724118 gb KDR24489.1 Insulin-like growth factor 2 mRNA-binding protein 1, partial [Zootermopsis nevadensis]	KDR24489	2.29156E-89	79	224
Gene14323_Transcript_19239	homeobox protein prospero isoform x1	2076	gi 939237231 ref XP_014259951.1 PREDICTED: homeobox protein prospero isoform X2 [Cimex lectularius]	XP_014259951	0	69	689
Gene10292_Transcript_12769	protein crumbs-like	519	gi 501295329 dbj BAN20858.1 crumbs [Riptortus pedestris]	BAN20858	3.13687E-59	71	174
Gene1084_Transcript_1079	armadillo segment polarity protein isoform x2	2112	gi 749735954 ref XP_011154161.1 PREDICTED: armadillo segment polarity protein isoform X2 [Harpegnathos saltator]	XP_011154161	0	92	694
Gene7271_Transcript_8602	creb-binding protein	774	gi 972203828 ref XP_015184076.1 PREDICTED: CREB-binding protein [Polistes dominula]	XP_015184076	3.41864E-24	53	223
Gene741_Transcript_752	heat shock protein	1338	gi 699979698 gb AIU47025.1 heat shock protein [Phenacoccus solenopsis]	AIU47025	0	100	446
Gene147_Transcript_161	heat shock protein 70	420	gi 675275127 gb AIL52739.1 heat shock protein 70 [Phenacoccus solenopsis]	AIL52739	6.01972E-94	100	140
Gene9220_Transcript_11266	histone deacetylase 6	501	gi 646723938 gb KDR24372.1 Histone deacetylase 6 [Zootermopsis nevadensis]	KDR24372	1.90153E-40	64	162

Gene2523_Transcript_2639	calcitonin gene-related peptide type 1 receptor-like isoform x1	1473	gi 939279519 ref XP_014260343.1 PREDICTED: calcitonin gene-related peptide type 1 receptor-like isoform X1 [Cimex lectularius] >gi 939279521 ref XP_014260344.1 PREDICTED: calcitonin gene-related peptide type 1 receptor-like isoform X1 [Cimex lectularius]	XP_014260343	1.4351E-177	76	410
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Supplementary information 4 SI_Table 4: Probit analysis: LD values for dsSNF7 and dsIAP at different doses in *Phenacoccus solenopsis*. The dose-mortality relationship could not be established for dsVATPase and dsAmylase due to negligible mortality at 20 to 80 µg dsRNA of respective gene.

Target gene dsRNA	LD	Effective doses	Slope	Chi-square
SNF7	LD10	17.52	0.040	0.712
	LD50	49.74		
	LD90	81.95		
IAP	LD10	2.38	0.031	0.485
	LD50	43.83		
	LD90	85.27		