

a)	GJQL01135962.1	AAACAGGGCAATATGGCACCTTACTACAAACAGGTATGTGAGGACTTGGAGCTGGGAGTTT	180
	GFTU01006765.1	AAACAGGGCAATATGGCTCCTTACTACAAAGAGGTATGTGCCACCTCGGGTGGGAGTTT	180

	GJQL01135962.1	GACAGCAAGCTGTATGATGAGATGTGTGTCGCCAACAAAGCGGCTTGAGGAGCTGGAG	240
	GFTU01006765.1	GATGGGAAGCTGTATGATGAAATGGCGGCCGCCAACGTCAAACGGCTGGAGGAGTTGGAG	240
		** * *****	
	GJQL01135962.1	AAGGAACATGAGAACAATGTGATGGACGAAGAGGACCAGAGTCAGCTATGTGGTGTGTGG	300
	GFTU01006765.1	AAGGAACATGAGAACAATGTGATGGACGAAGAGGACCAGAGTCAGCTATGTGGTGTGTGG	300

	GJQL01135962.1	CAGAGCAAACCTCGATTACCTGTGCTCCATCGGGGATAGTGAAAATGCAACGGTCTAGCC	360
	GFTU01006765.1	CAGAGCAAGCTGGACTACCTGTGCTCCATCGGTGACCGGACAAACGCCTCGACCTGGCC	360

	GJQL01135962.1	AACTCTAAGGTGGATGATAAGACAGTGCCCAAGAGTCACAGGATCGATGCGGTTTTTTCT	420
	GFTU01006765.1	AACTCCAAGTTGATGACAAGACGGTCCCAAGAGTCACAGGATCGATGCTGTATTTTCC	420

	GJQL01135962.1	CTCTTCAGAATCTCTTTTTTCCATGGATGTAACATTAAGGGAATGAGACAGCCATTGAC	480
	GFTU01006765.1	CTCTTCAGGATCTCTTTTTTCCATGGATGCAACATTAAGGGGATGAGTACAGCCATCGAG	480

	GJQL01135962.1	AAGGCGACTGAGCTGATTGAAGGTATCAGTGGAGTGACTGGAGTGCTCGCAACAAGCTG	540
	GFTU01006765.1	AAGGCCACTGAACATAATTGAAGGTATAAGCGGGGTGACTGGAGTGCTCGCAACAAGCTG	540

	GJQL01135962.1	AAAGCGTATGAGGGTGTGTGGAGCCTGGCTATCAGAGATTTACAAGAGCCGCTCATCTT	600
	GFTU01006765.1	AAGGCGTACGAAGTGTGTGGAGTTTGGCCATCAGGACTTCACCCGAGCTGCCACCTC	600
		** *****	

b)	dsRpn6	-----C	1	c)	dsRpn6	-----CTTGAGC	7
	XM_006568751.3	TAGAGAAAATCCCAATTGGAAATGGCCCAACAAAATTTTATTAACTGTGCCAGAAC	180		XM_026443943.1	CTTATCAAGATTCGATTAAATTAACCTCAGGAAATACCAAAATGATGACCACTTAAAA	120
		*				*	
	dsRpn6	TTGAGC-T---GGGAGTTTGACAGCAAGCTGTATGATG-----	35		dsRpn6	TGGGAGTTT---GA--CAGCAAGCTGTATGATGAGATGTGTGTCGCCAACACAAAGCGGC	62
	XM_006568751.3	ATAAGGATGATCCATTATTAAAGAACAACTGTAGATGCCATTAAAGCAGAAATATGG	240		XM_026443943.1	ACTGAATTTCTGATACATAA---AACCGGAAATATGACTCTTACTATGAAGATGT	176
		** *				** *	
	dsRpn6	-----AGATGTGTGTCGCCAACACAAACGGC---TTGAG	67		dsRpn6	TTGA-----GGAGCTG-----GAGAGCAACATGAGAA	98
	XM_006568751.3	CTCCATTTTATGAAGAAGTTGTAAAGATTGGCCGGTGCATGATCTCTTTAA	300		XM_026443943.1	TTGCAAGAATTCAATTGGAAATGTGAAGATCTTATCAACGCGATGAAGCATAAAAA	236
		*****				** *	
	dsRpn6	G-----AGCT--CGACAAGCAACATGAC--AACA-----ATCTGATGACAGAG	107		dsRpn6	CAATGTGATGGACGAAGAGGACAGAGTCAGCTAT-----GTGGT-----	131
	XM_006568751.3	CTTCTATGAAACTAAGAAATATGAAGAATTAGATGATGCAATTTGAAGATG	360		XM_026443943.1	CGAGTTA---CATGGAATGAATTAGAGTCTTCTGATATCTTACTCTTGAGGACACTGAA	294
		** *				** *	
	dsRpn6	AGGACCAAGTACGATGTGGTGTG---TGGCAGA--GC-----AAACTCGATT	152		dsRpn6	-----T-GTGGCAGAGCAAACTGATACCTGTGCTCATCGGGATAGTGAATGCA	184
	XM_006568751.3	CTGAAAGA---ATTAGGTGAATGGAGTGAGAGAGCTTAATCTTAAAAATCAGAAC	417		XM_026443943.1	AAAAAGATTGGAGAAAAAATTCGAATTTTTTTCGAGATTGGTGATCTCGATCGTCT	354
		** *				** *	
	dsRpn6	ACCCTGTCTCATCGGGATAGTGAAATGCAACGGTCTAGCCAACTCTAAGTGGATG	212		dsRpn6	ACGGTCTACGCCAACTCTAAGGTGGATGATGAAGACAGTCCCAAGAGTCACAGGATCGAT	244
	XM_006568751.3	ATTATGTGAATAGGTGATAAGGAAGTTCCATTT---GGCATTCAAAAATCTTACG	474		XM_026443943.1	ACAAATATCGCTACCTCAATTTTAAAGATGAATAATTCATAGCATTAGAAATTGAA	414
		** *				** *	
	dsRpn6	ATAAGACAGTGCACAGAGTCACAGGATCGATCGGTTTTTCTCTCTCAGAACTCTCT	272		dsRpn6	GCGGTTTTTCTCTCTCAGAACTCTTTTTTTCATGGATGAACATTAAGGAATGAGC	304
	XM_006568751.3	ATAAACTGTATCATAGGACATAGATATGATATTCATAACATAGAATGGAT	534		XM_026443943.1	GCTGCTTTTGGCTTATTTAGATACATACA---TAAGAAATATATCTGTCGATGGGA	471
		** *				** *	
	dsRpn6	TTTTCCATGGATGAACATTAAGGGAATGAGCAGCCATTGACAGGCGAGCTGAGCTGA	332		dsRpn6	ACAGCCATTGACAGGCGAGCTGAGCTGATTGAAGGTATCAGTGG-----AGGTGACTGG	358
	XM_006568751.3	TATTTTATTTAGATCATGATCATG---TTACAAGAATATAGAAAGCTAAAGTTTAA	591		XM_026443943.1	AAAATAATTGCCGAGATAACGATCTAATGGAAGATGCCATCGCATCGGTAGCAATTGG	531
		** *				** *	
	dsRpn6	TTGAAGGTATCAGTGGAGTGACTGGAGTCTCGCAACAGCTGAAAGCGTATGAGGGTG	392		dsRpn6	AGTGCTCGCAACAGCTGAAAGCGTATGAGGGTGTGTGGAGCTGGCTATCAGAGATTTT	418
	XM_006568751.3	TAGAAGA-----AGGTGGTATGGGATAGACGAATCGTTTAAAGGTATATCAAGGAA	645		XM_026443943.1	TGTGTCTGAATAAATTGAAAGTATACGAGCTGTTTATCTTGCACACGAAGCTTT	591
		** *				** *	
	dsRpn6	TGTGGAGCTGGCTATCAGAGATTTTCAAGAGCCGCTCAT-----	433		dsRpn6	ACAAGAGCCGCTC---AT-----	433
	XM_006568751.3	CATATTTGTATAGCTTCTGATTTTCAAGAGCTGCAATTTCTTTTGGATACAATTA	705		XM_026443943.1	TCCGCTGCTCAACACTTCTATGGATTGATACCTACTTTGAATCTTATGAATTATTA	651
		** *				** *	

Fig. S11: sequence alignment (supporting data summarised in **Table 1**)

a) *Scaphoideus titanus* (GJQL01135962.1) and *Euscelidius variegatus* (GFTU01006765.1) CDS aligned. Yellow highlighted region indicates the dsRNA sequence used in the study.

b, c) dsRpn6 sequence used in this study aligned with *Apis mellifera* XM_006568751.3 (**b**) and XM_026443943.1 (**c**). Stars indicate nucleotidic identity between aligned sequences. Alignments realised with ClustalOmega (EMBL-EBI).