



## **Supplementary Materials**



**Figure S1.** construct schematic of shRNA expression vectors in pJET1.2 cloning vector for all shRNAs used in this study.

sp P13717 NUCA_SERMA	PALNPADTLAPADYTGANAALKVDRG <mark>H</mark> QAPLASLAGVSDWESLNYL	129
AAEL004103-PA	TNYLYTVNKQRQTIAQILQSQDLADDIVRDVNSGIYMARG <mark>H</mark> IAARVDFIYGTQQNATFWF	259
AAEL004092-PA	INTLYTVNRQRQTLATVLGSQAIADDLVRDASTGIFMARG <mark>H</mark> IAARADFIYGTQQNATFWF	259
AAEL006348-PA	MTKLYNIESQRKTFEKILGSSARADALLN-SKQDMFLARG <mark>H</mark> LAAKADFVFGAHQRATFWF	271
AAEL006326-PA	$\tt MAEIYSFDVQHATLGLILGSTNRANNLLN-RRKDIFIAKGRLAAQADFVYGSQQAATFRY$	264
AAEL003123-PC	VSSAYNQESQLNRLVALFGADPNPWGSAEVYYNLSYLQRG <mark>H</mark> LVPDADQLFTTWQWSTYFY	346
AAEL025217-PA	LSTVYTQNSQRTRLANLLGSEELA KQYISSS - SFFAKG <mark>H</mark> LTPDGDAVLNSWAGATYFY	245
AAEL008857-PB	ADALYTQTTQFERFEALLGSKAQAEKYIEPGKTFLNRG <mark>H</mark> LTPRGDGIFQTWKHATFFY	290
AAEL008861-PA	PSTSYTQASQLERLTTLLGSAEQASRFVFTN-SFMARG <mark>H</mark> MSPDADGIYRSWQFTTYFF	246
AAEL008876-PA	PATSYTQQAQLTRLTELLGSEEQAKKFISGGSYYMARG <mark>H</mark> LAPDADGIYRSWQWATFFY	241
AAEL008858-PA	PASSYTTASQATRLAVLLGSQAQADRFITTS-SYMSRG <mark>H</mark> LSPDADGIFRSWQWATYFY	240
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**Figure S2.** Clustal Omega alignment of 10 *Ae. aegypti* putative dsRNase genes aligned to *Serratia marcescens nucA* (P13717). The predicted proton acceptor histidine residue is highlighted in yellow.

Accession #	GeneID	5'-3' forward primer sequence	5'-3' reverse primer sequence
AAEL009496	S7rp	AAATAAATTCGCTATGGTTTTC	CCTTCTTGCTGTTGAACTCG
AAEL004092		CGAGTGGAATAAACTAGCTTCAG	CAAGCTCCAAGTATTCGCCT
AAEL002042		ATGGTGACGCTGTGTTGAAC	GAGGGTCAGAACGTCGTAGA
AAEL004103	4103	AGATTCGCTCCATCCTGCTC	TGAACCCATTGCTGCAAACG
AAEL006348		AGAACCGCTGTAGAATCGCA	GCCCAAAGAAATTTTACAGCCGT
AAEL006326		GTACAACGGGGACTTCGACA	GCTCTACCTGTTCACCGCTT
AAEL003123		AGCATACGTGGAATAAATCTGGT	TTGGACTCGAGCTGCATCTG
AAEL008876		GGAGCTCACCTGGGAAGAAC	GACGCTGTATTGTTGTTTGCAT
AAEL008858	8858	CCGTTTTGTTGGGTTCGCAA	GCGTTGACAACCTGCCATTG
AAEL008857		GATTCGACTCCAAGCTGCTC	ACACCGATGCACTGGGATAC
AAEL008861		GGACGCGGATGGAATCTACC	GTTGACAACCTGCCACTTCG

Table S1 Primer sequences used in qRT-PCR assays in this study.

**Table S2.** Primer efficiency data for qRT-PCR assays used in this study. R<sup>2</sup> values and percent efficiency (E%) are shown for each primer set (Supplementary Table 2) and tissue type. PCR reactions with insufficient data are shown as not determined (ND).

Gene	Fema	le gut	Female	carcass	Larv	a gut	Larva	carcass
	<b>R</b> <sup>2</sup>	E%	R <sup>2</sup>	E%	R <sup>2</sup>	E%	R <sup>2</sup>	E%
AAEL009496	0.995	97.9	0.992	101.1	0.991	97.2	0.989	102.1
AAEL002042	0.977	101.6	0.986	99.2	0.982	97.8	0.972	96.1
AAEL003123	0.995	101.7	ND	ND	0.998	100.9	ND	ND
AAEL004092	0.989	98.5	ND	ND	0.991	99.1	ND	ND
AAEL004103	0.991	98.5	0.987	99.9	0.996	101.1	0.984	101.8
AAEL006326	0.988	96.2	ND	ND	0.984	97.8	ND	ND
AAEL006348	0.99	98.9	0.989	96.3	0.997	96.7	ND	ND
AAEL008857	0.986	95.9	0.982	96.4	0.986	96.9	0.982	95.8
AAEL008858	0.994	96.8	0.991	97.4	0.992	96.9	0.989	97.8
AAEL008861	0.949	97.6	ND	ND	0.988	99.2	ND	ND
AAEL008876	0.987	96.8	0.982	96.2	0.991	98.8	0.995	97.4

Table S3. shRNA	constructs used	in this	study.
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Strain Number	E. coli strain	Gene target and length	Target Sequence 5'-3'
1	HT115 (DE3)	pJET-8858 22mer	ACAAGTACCTCTTGCGGTGGCG
2	HT115 (DE3)	pJET-4103 22mer	ATTGCTCGGAGCTAGGAGTGAA
3	HT115 (DE3)	pJET-8858 26mer	CCTGTTCTGGAATTCTGGCGAGACTA
4	HT115 (DE3)	pJET-4103 26mer	ATATTGCTCGGAGCTAGGAGTGAATC
5	HT115 (DE3)	pJET-eCFP 21mer	CCATGATATAGACGTTGTGGCTG
6	HT115 (DE3)	pJET-scramble 23mer	GTATAGTATAGTATACCGTATAA
7	HT115 (DE3)	pJET-DsRed 23mer	ACCGTGAAGCTGAAGGTGACCAA

**Table S4.** Locations of ten *Ae. aegypti* dsRNase genes and current VectorBase (VB) community annotation status. Approximate locations of these genes on chromosome map are shown with arrows.

Gene	<b>Genome Location</b>	Description		
AAEL025217	Chromosome 2: 203659053	No description		
A A ET 008861	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community		
AAEL000001	236574296	Annotation]		
AAEL008857	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community		
	236610049	Annotation]		
A A ET 009976	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community		
AAELUU0070	236632143	Annotation]		
AAEL008858	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community		
	236643493	Annotation]		

AAEL003123	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community			
AAEL005125	277923934	Annotation]			
A A EL 006249	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community			
AAEL000340	396923473	Annotation]			
A A EL 006226	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community			
AAEL000520	396927710	Annotation]			
A A EL 004102	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community			
AAEL004105	401525211	Annotation]			
A A EL 004002	Chromosome 3:	deoxyribodsRNAse I, putative [Source:VB Community			
AAEL004092	401536506	Annotation]			
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**Table S5.** Mortality observed in ds8858 26mer shRNA feeding experiments compared to dsScramble controls. Survival was scored after five days of feeding on shRNA expressing bacteria in petri dishes with 20 larvae per dish. Abbott's adjusted mortality for all ds8858+dseCFP = 56.3% (n = 80).

Treatment	Replicates	Mean Survival	Standard Error
dsScramble	4 (n=80)	0.88	0.037
ds8858+dseCFP	4 (n=80)	0.38	0.062
ds4103+dseCFP	2 (n=40	0.83	0.053
2x dseCFP	2 (n=40)	0.90	0.071
ds4103+ds8858+dseCFP	2 (n=40)	0.70	0.035



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