

Table S1. The primers used in this experiment

Primer name	Primer sequences (5'-3')	Usage
Ae-GRD-1F	CTCTAAAGGCGGAATCACC	cDNA cloning
Ae-GRD-1R	CTTTCCCGACAACGATCC	
T7-dsGRD-F1	taatacgactcactatagggACATCTACAACACAGC CCCG	RNA interference
T7-dsGRD-R1	TGCATCAGACAGGACGCTTT	
T7-dsGRD-F2	ACATCTACAACACAGCCCCG	
T7-dsGRD-R2	taatacgactcactatagggTGCATCAGACAGGACG CTTT	
T7-dsGUS-F1	taatacgactcactatagggGCGGCCGCCCCTTACG CTGAAGAGATGC	
T7-dsGUS-R1	CTCGAGGGCACAGCACATCAAAGAGA	
T7-dsGUS-F2	GCGGCCGCCCCTTACGCTGAAGAGATGC	
T7-dsGUS-R2	taatacgactcactatagggCTCGAGGGCACAGCA CATCAAAGAGA	
miR-315-5p mimics-F	UUUUGAUUGUUGCUCAGAAAGC	Synthesis of microRNA mimics and NC
miR-315-5p mimics-R	UUUCUGAGCAACAAUCAAAAUU	
miR-10 mimics-F	ACCCUGUAGAUCCGAAUUUGUUTT	
miR-10 mimics-R	AACAAAUUCGGAUCUACAGGGUTT	
miR-71-5p mimics-F	AGAAAGACAUGGGUAGUGAGAUTT	
miR-71-5p mimics-R	AUCUCACUACCCAUGUCUUUCUTT	
mimics NC-F	UUCUCCGAACGUGUCACGUTT	
mimics NC-R	ACGUGACACGUUCGGAGAATT	
miR-71-5p inhibitor	AUCUCACUACCCAUGUCUUUCU	Synthesis of microRNA inhibitor and NC
inhibitor NC	CAGUACUUUUGUGUAGUACAA	

Table S1. The primers used in this experiment (continued)

Primer name	Primer sequences (5'-3')	Usage
miR-71-5p	GTCGTATCCAGTGCAGGGTCCGAGGTATT	RT stem-loop primer
	CGCACTGGATACGACATCTCA	
U6	GTCGTATCCAGTGCAGGGTCCGAGGTATT	
	CGCACTGGATACGACAAAAAT	
Ae-GRD-qF	AGGTGTACGTTCCGTGCATT	
Ae-GRD-qR	AGATCCGTCCTCGAGTCCAA	
RPS17-qF	AAGAAGTGGCCATCATTCCA	
RPS17-qR	GGTCTCCGGGTCGACTTC	qPCR
miR-71-5p-qF	CGCGAGAAAGACATGGGTAG	
miR-71-5p-qR	AGTGCAGGGTCCGAGGTATT	
U6-qF	CGCAAGGATGACACGCAAA	
U6-qR	GTCGTATCCAGTGCAGGG	

Table S2. Sequence information of GRD in different species of insect

Species	Protein sequence numbers	Length (aa)
<i>Aedes aegypti</i>	XP_021694939.1	683
<i>Aedes albopictus</i>	XP_062700266.1	688
<i>Armigeres subalbatus</i>	XP_062539564.1	674
<i>Culex pipiens pallens</i>	XP_039440121.1	702
<i>Culex quinquefasciatus</i>	XP_038105041.1	701
<i>Toxorhynchites rutilus septentrionalis</i>	XP_055618950.1	700
<i>Wyeomyia smithii</i>	XP_055522907.1	699
<i>Anopheles arabiensis</i>	XP_040174363.1	736
<i>Anopheles sinensis</i>	KFB34891.1	630
<i>Anopheles maculipalpis</i>	XP_050081393.1	732
<i>Anopheles gambiae</i>	XP_001237369.3	736
<i>Anopheles merus</i>	XP_041764767.1	734
<i>Anopheles nili</i>	XP_053678580.1	739
<i>Anopheles funestus</i>	XP_049286866.1	748
<i>Drosophila melanogaster</i>	NP_001162770.1	510
<i>Hermetia illucens</i>	XP_037920157.1	609
<i>Ceratitis capitata</i>	XP_012161002.1	739
<i>Bactrocera latifrons</i>	XP_018796579.1	735
<i>Anastrepha ludens</i>	XP_053949317.1	734
<i>Pseudolycoriella hygida</i>	KAJ6638698.1	582
<i>Glossina fuscipes</i>	XP_037894652.1	485
<i>Musca domestica</i>	XP_019893131.1	589
<i>Psylliodes chrysocephala</i>	CAH1106177.1	481
<i>Tribolium castaneum</i>	EFA02907.2	557
<i>Helicoverpa armigera</i>	PZC75662.1	576
<i>Spodoptera frugiperda</i>	XP_035431640.1	564
<i>Vespa mandarinia</i>	XP_035726979.1	536

Table S2. Sequence information of GRD in different species of insect (continued)

Gene Name	Gene ID	Length (aa)
<i>Apis mellifera caucasica</i>	KAG6804607.1	509
<i>Apis mellifera</i>	XP_026298420.1	520
<i>Nasonia vitripennis</i>	XP_008203400.1	569
<i>Bombyx mori</i>	NP_001182633.1	594
<i>Ixodes scapularis</i>	XP_040062219.1	525
<i>Tetranychus urticae</i>	AGC31413.1	

P.S: aa (amino acids).

Table S3. Prediction of miRNAs targeting *Ae-GRD*

Gain Way	Name	Sequences (5'-3')
miRanda	miR-71-5p	AGAAAGACAUGGGUAGUGAGAU
	miR-11923	ACAACGGCAGCCGGAACGAUCU
	miR-315-5p	UUUUGAUUGUUGCUCAGAAAGC
	miR-10	ACCCUGUAGAUCCGAAUUUGUU
	miR-11917	CUGAAAACUUAUUCGAUUGGUC
	miR-263a-5p	AAUGGCACUGGAAGAAUUCACGG
	miR-315-3p	CUUUCGAGCAGUAAUCAAGUC
	miR-375	UUUGUUCGUUUGGCUCGAGUUA
	miR-11925	CUGUCGAGCCGGUUGAACCAC
	miR-988-5p	GUGUGCUUUGUGACAAUGAGA
	miR-1890	UGAAAUCUUUGAUUAGGUCUGG
	miR-79-3p	UAAAGCUAGAUUACCAAAGCAU
	miR-71-5p	AGAAAGACAUGGGUAGUGAGAU
	miR-315-5p	UUUUGAUUGUUGCUCAGAAAGC
	miR-10	ACCCUGUAGAUCCGAAUUUGUU
TargetScan	bantam-5p	CCGGUUUUCAUUUUCGAUCUGAC
	miR-375	UUUGUUCGUUUGGCUCGAGUUA
	miR-988-5p	GUGUGCUUUGUGACAAUGAGA
	miR-1890	UGAAAUCUUUGAUUAGGUCUGG
	miR-79-3p	UAAAGCUAGAUUACCAAAGCAU
	miR-11-5p	AGAACUCCGGCUGUGACCUGUG
	miR-210	CUUGUGCGUGUGACAACGG

Table S3. Prediction of miRNAs targeting *Ae-GRD* (continued)

Gain Way	Name	Sequences (5'-3')
RNAhybrid	miR-315-5p	UUUUGAUUGUUGCUCAGAAAGC
	miR-10	ACCCUGUAGAUC CGAAUUUGUU
	miR-71-5p	AGAAAGACAUGGGUAGUGAGAU
	miR-988-5p	GUGUGCUUUGUGACAAUGAGA
	bantam-5p	CCGGUUUUCAUUUUCGAUCUGAC
	miR-1890	UGAAAUCUUUGAUUAGGUCUGG
	miR-11900	AUUUUUUUGACUGUAAUUUUAUAG

P.S: The results obtained by the three tools are highlighted in red font after they are crossed.