

Table S1. Primers used for dsRNA synthesis and RT-qPCR.

Experiment	Primer names and sequence (5' to 3')	Amplification efficiency
dsRNA synthesis	ds <i>Hunchback</i> -F: taatacgactcactatagggGCATCACCGTACTCGATGCAA	
	ds <i>Hunchback</i> -R: taatacgactcactatagggGGGAGCCACTGAGTCTCTGCT	
	ds <i>GFP</i> -F: taatacgactcactatagggGGTGAGCAAGGGCGAGGAGCTG	
	ds <i>GFP</i> -R: taatacgactcactatagggGGCTCGATGCGGTTCAACCAG	
qPCR analysis	<i>EF1α</i> -F: CTGTGCTTATTGTCGCTGCT	98.0%
	<i>EF1α</i> -R: TCGCTGTATGGTGGTTCAGT	
	<i>RPS20</i> -F: AAGTGTGTGCTCCGAGATGA	104.0%
	<i>RPS20</i> -R: CAGCAATGACACCGGGTTC	
	q <i>Ago1a</i> -F: CCTGTATTTGATGGTCGCAACA	96.5%
	q <i>Ago1a</i> -R: GCGGCCTTCTAATGCTTCTT	
	q <i>Ago1b</i> -F: CGGCATCACACCAGATTGTT	103.4%
	q <i>Ago1b</i> -R: GGCCGACTAGTTCCCTGAAT	
	q <i>Dicer1a</i> -F: GGAAGAGCCTAGACCTGGAA	93.1%
	q <i>Dicer1a</i> -R: TCCCAAACCCATGAACGGAT	
	q <i>Dicer1b</i> -F: TGACAGATCTTCGTTTCAGCAC	105.0%
	q <i>Dicer1b</i> -R: CGGTGCCTCAACATCTTCAG	
	q <i>Pasha1</i> -F: CACGTGGAGTTGCGGGAATA	98.7%
	q <i>Pasha1</i> -R: TCTCGACGACGATTACACCG	
	q <i>Pasha2</i> -F: GCAGAGAAACTTTGGTGAGTGT	103.3%
	q <i>Pasha2</i> -R: ACCGTAAAGCCGTAACAACG	
	q <i>Pasha3</i> -F: TGGTAAAAGCTGATCGAAGGC	104.4%
	q <i>Pasha3</i> -R: TGGCTGAGTTTTGAGTACACG	

qPasha4-F: TCGCTGCACTATGACTGTAGA	107.7%
qPasha4-R: GATGAGTTCTACATTGTTTCGGC	
qDrosha-F: CGATCAGTAGACGGTGGTGA	101.3%
qDrosha-R: AACGCACTATTGGCAGCATT	
qExportin5-F: CCACTGTGCGTTCAATGTCA	106.0%
qExportin5-R: AGCAGAATTGACCAGGCTCA	
qLoquacious1-F: TCCACCGTTAACCACAGTCT	103.1%
qLoquacious1-R: GGAGATTTCAAGCTGTCCTGT	
qLoquacious2-F: CGATTGGCATGCTTCAGGAA	98.1%
qLoquacious2-R: TCTACATTCTCAGCCGCTCC	
qAgo2-F: CAGGCACCACAGAAACAAA	94.3%
qAgo2-R: AATTTGTTGACCGCCTTGAG	
qDicer2-F: TGGTCTCAACAGCAATGGAA	97.5%
qDicer2-R: AATACGGGGACGTTTCATCAG	
qR2D2-F: AGAAGGACAAGCCCATGCTA	109.7%
qR2D2-R: TGGATTCCCTTCCATTACCA	
qAgo3a-F: TATGCCCTTGTGAGACGGAG	108.2%
qAgo3a-R: CTTCTTCCGCGAGCAACTTG	
qAgo3b-F: AATGATGCGTCCAATCCCAG	101.0%
qAgo3b-R: GCCGTTTCCTTCATCTCTTGG	
qPiwi1-F: CAACGGCGGACAAGACATTC	106.9%
qPiwi1-R: AGTTCTTTGTGTGCGCTCAA	
qPiwi2-F: AGAGCAGTACCGTCACAAGT	102.9%
qPiwi2-R: TCCGCTGGCTATCATGACAA	

q <i>Piwi</i> 3-F: CTTTGGCCCGGGTATGAAAC	104.9%
q <i>Piwi</i> 3-R: TCATCACCGTGGTACCAACA	
q <i>Piwi</i> 4-F: AGCAGGTCCCAGTGAAAGAA	102.8%
q <i>Piwi</i> 4-R: CACAAGTGAACATGGGTGCA	
q <i>Piwi</i> 5-F: GCAGTACCGTCCCAAGTAGT	106.7%
q <i>Piwi</i> 5-R: TCCGCTGGCTATCATGACAA	
q <i>Piwi</i> 6-F: GGAGCAAAGGGAAAACAGGG	107.5%
q <i>Piwi</i> 6-R: GGTGGATCAAATCGGCTTCC	
q <i>Piwi</i> 7-F: CATGACTGATTGGCGGTGT	100.2%
q <i>Piwi</i> 7-R: GCTAGATGTCCAATCTGCTGC	
q <i>Piwi</i> 8-F: AAACAATGCAGCTACGCCAA	99.7%
q <i>Piwi</i> 8-R: CCCGAGTGACTCTGCTGTAA	
<i>miR</i> -3024-F: CTTCTTTGGGATTTAATAGAGCCGG	95.57%
<i>U6</i> : CGATACAGAAGATTAGCATGG	92.61%

Table 2. Accession number of genes used in this study.

Gene	Accession number
<i>Dicer2</i>	XM_008189326
<i>R2D2</i>	NM_00162172.2
<i>Ago2</i>	XM_001944817.3
<i>Drosha</i>	XM_003247865
<i>Pasha1</i>	XM_016808185.3
<i>Pasha2</i>	XM_001947368.8
<i>Pasha3</i>	XM_001948642.4
<i>Pasha4</i>	XM_001951974.4
<i>Exp-5</i>	XM_003241026.1
<i>Dicer1a</i>	XM_001944314.1
<i>Dicer1b</i>	XM_016807644.1
<i>Loquacious1</i>	XM_016804908
<i>Loquacious2</i>	XM_016802268
<i>Ago1a</i>	XM_003240572.3
<i>Ago1b</i>	XM_001944279.4
<i>Piwi1</i>	XM_003243306
<i>Piwi2</i>	XM_016805294
<i>Piwi3</i>	XM_008184469
<i>Piwi4</i>	XM_01680282833
<i>Piwi5</i>	XM_016804870
<i>Piwi6</i>	XM_008188500
<i>Piwi7</i>	XM_001948406
<i>Piwi8</i>	XM_001947555.4
<i>Ago3a</i>	XM_016800535
<i>Ago3b</i>	XM_003245551
<i>EF1α</i>	XM_001948705.4
<i>RPS2</i>	NM_001162819.2
<i>U6</i>	KX638479
<i>Hunchback</i>	NM_001162510.1

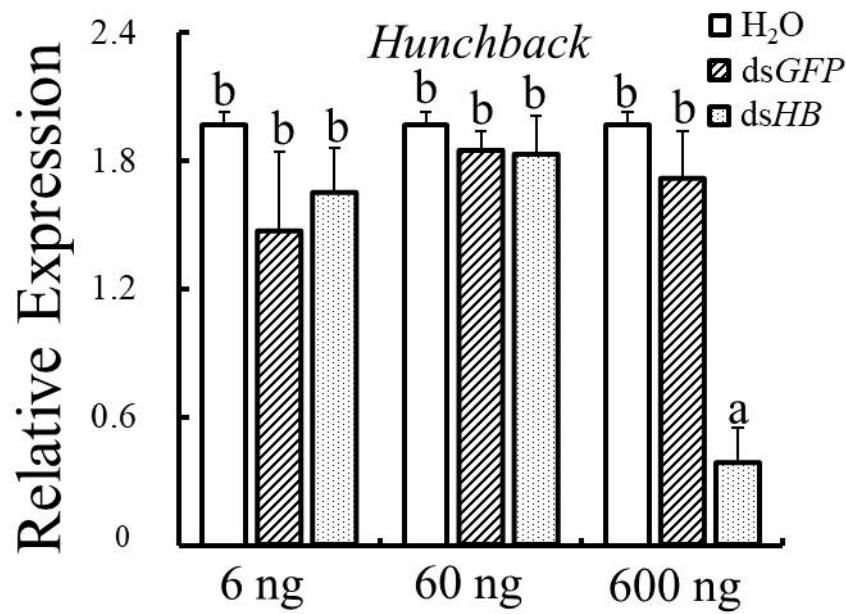


Figure S1. The relative mRNA expression profiles of *Hunchback* upon dsHB administration. The mean ($\pm$ SE) expression level is based on four biological replicates. The relative expression was calculated based on the value of the reference genes. Lowercase letters above each bar indicate significant differences (one-way ANOVA followed by Tukey's honestly significant difference multiple comparison test; $P < 0.01$).

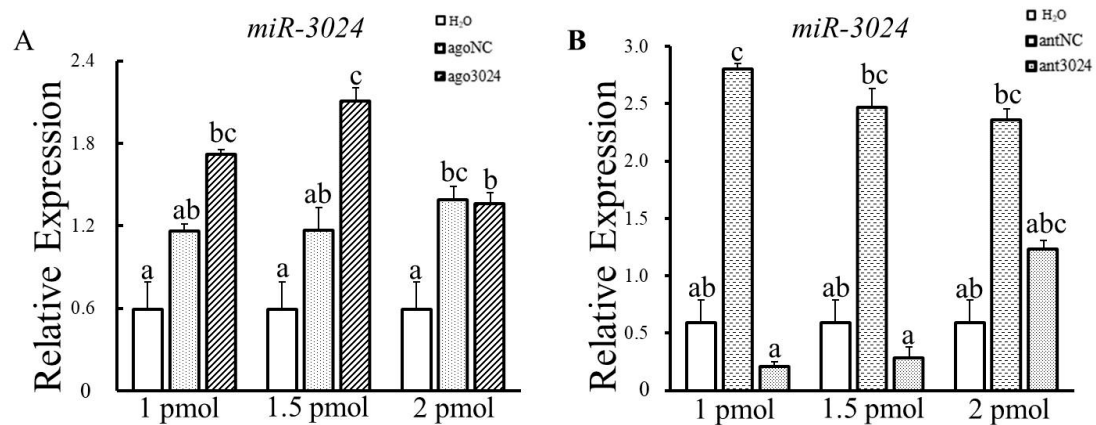


Figure S2. Relative expression profiles of *miR-3024* upon *miR-3024* agomir (A) and antagomir (B) administration. The mean ($\pm$ SE) expression level is based on four biological replicates. The relative expression was calculated based on the value of the reference genes. Lowercase letters above each bar indicate significant differences (one-way ANOVA followed by Tukey's honestly significant difference multiple comparison test; $P < 0.01$).