

## Supplementary Materials—Table and Figures

**Table S1.** Primers for this manuscript.

Primer Names	Sequence	Tm	PCR Product	
MEF2-YG-F	GGATCAAATCAGAACCCATCA	57°C	176bp	qRT-PCR
MEF2-YG-R	TAGATGGCCTGAGAGTGTATT			
18S-F	TATACGCTAGTGGAGCTGGAA	56°C	136bp	
18S-R	GGGGAGGTAGTGACGAAAAAT			
dsMEF2-F	TAATACGACTCACTATAAGGG AATGGCTTACAGTCTCCGA	60°C	592bp	primers for dsRNA synthesis template amplification
dsMEF2-R	TAATACGACTCACTATAAGGG TGAGAGGGTTAACCGAAATG			
dsEGFP-F	TAATACGACTCACTATAAGGG CAGTGCTTCAGCCGCTACCC	60°C	289bp	
dsEGFP-R	TAATACGACTCACTATAAGGG AGTTCACCTTGATGCCGTTCTT			
LVAN23936-F	TGTTTATCACCCCTGGCACCTG	58°C	121bp	transcriptome validation
LVAN23936-R	CTCGGGAGCAGAACGATGAAGGAT			
LVAN06526-F	AGTGGTTGCCGGACTAATGG	58°C	138bp	
LVAN06526-R	CCTTGCCTGCCGTACTTCTT			
LVAN17308-F	GACGGGCAAGGAGAACAAAGA	58°C	233bp	
LVAN17308-R	TAATGATGGTCTCGCGTCG			
novel-2124-F	TAGGTGCGGTAAGACAAAGGTAT	58°C	181bp	
novel-2124-R	CCGCTGCAGAACTACAAGGGATA			
LVAN06763-F	AGAGAAGGTGCCAACACACA	58°C	148bp	
LVAN06763-R	GCCGTACAGCTCTCGAACAA			
LVAN2347-F	ACGGACAACGCTGAATCACT	58°C	143bp	
LVAN2347-R	AGGCAGTACCAGCAGAACAC			
LVAN23843-F	CTGCGGTGACGAGATGACTT	58°C	155bp	
LVAN23843-R	CAGCCTTCACGCTGATCTCT			
LVAN14378-F	GGATAGCATAACCGGAAGGAAAC	58°C	115bp	
LVAN14378-R	GAGAAGAGGCCAACACACGAAGG			
LVAN15846-F	CATGGAGGCCAAGGACTACGAC	60°C	242bp	
LVAN15846-R	TTGAATCTTCTGTTACAGGGGG			
novel-2155-F	TCCTCGATATTGCCGGCTTC	60°C	172bp	
novel-2155-R	TCCATGCCGAAGTCAACGAA			

MEF2-1 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-2 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-3 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-4 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-5 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-6 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-7 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-8 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-9 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-10 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-11 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-12 .....  
 MEF2-13 .....  
 MEF2-14 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-15 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-16 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP  
 MEF2-17 MGRKKIQCISRITDERNRQVITEIKRKFGILMKKAYELSVLCDCEIALIIFNSNKIIFQYASTMDKVLKYTEYNEPHESRTNNIDIVCALNKKKEHKNGLQSP

Consensus

MADS-MEF

HJURP-C

MEF2-1 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-2 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-3 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-4 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-5 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-6 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-7 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-8 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-9 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-10 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 194  
 MEF2-11 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 194  
 MEF2-12 .....  
 MEF2-13 .....  
 MEF2-14 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 72  
 MEF2-15 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-16 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200  
 MEF2-17 DSDPGEQDYTLTPRTEAKYNKIDEETFLMMQRNCINGGTIPYLAAQCPVGLNNYIMAVTVFVNNTAYDPAIMQSPQMASHASLSPRGSSGMILDNGSN 200

Consensus

HJURP-C

MEF2-1 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-2 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-3 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-4 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-5 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-6 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-7 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-8 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-9 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 299  
 MEF2-10 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 294  
 MEF2-11 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 294  
 MEF2-12 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 171  
 MEF2-13 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 144  
 MEF2-14 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 299  
 MEF2-15 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-16 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300  
 MEF2-17 GYEGSTSPLPQGGAPSEGLLSRHSSKTHSPTRNLRVHIPNPQGCQICNPRPGSPSLNTFVVSHCTAGNPFSTTYSPLNTFPHQDCFICNSDISLNPLNSL 300

Consensus gyegstsplpqggapsgpellsrhsskthsptrnrvhpqgqgq - nprpgspslntpvvshqgttagnptstysplntfpqhdqfqlnsdinspnsl

MEF2-1 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-2 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-3 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-4 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-5 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-6 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-7 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-8 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-9 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 399  
 MEF2-10 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 394  
 MEF2-11 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 394  
 MEF2-12 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 271  
 MEF2-13 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 244  
 MEF2-14 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 399  
 MEF2-15 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-16 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400  
 MEF2-17 NSLHQWNPGSILGMHSGLPHLSVSSSTTPPAPSSFFVRIKSEFISPPRDNANCVPASHLQRFASTDPGHLSPAPPSHLGPSSNHVFVHTHYNTLSGHLTPTSH 400

Consensus nslhqwnpgsilmgschlphlsvssstpppapssppvriksefispprdnancvpashlqrpastdpghlspappshlgpssnhvhqgttagnptstysplntfpqhdqfqlnsdinspnsl

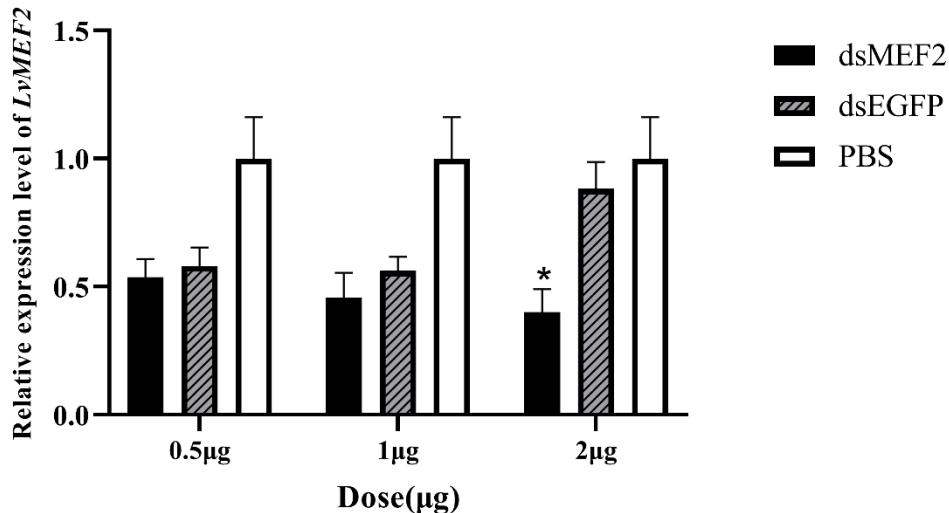
MEF2-1 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-2 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-3 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-4 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-5 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-6 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
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 MEF2-8 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-9 ASPDGTSHHTEYDTPLSKRPRLITEGWT 426  
 MEF2-10 ASPDGTSHHTEYDTPLSKRPRLITEGWT 421  
 MEF2-11 ASPDGTSHHTEYDTPLSKRPRLITEGWT 421  
 MEF2-12 ASPDGTSHHTEYDTPLSKRPRLITEGWT 298  
 MEF2-13 ASPDGTSHHTEYDTPLSKRPRLITEGWT 271  
 MEF2-14 ASPDGTSHHTEYDTPLSKRPRLITEGWT 426  
 MEF2-15 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-16 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427  
 MEF2-17 ASPDGTSHHTEYDTPLSKRPRLITEGWT 427

Consensus aspdgtshhteydtplsksrprlitechwt

**Figure S1. Multiple sequence alignment for the 17 protein sequences of LvMEF2.** The yellow box corresponds to mutually exclusive exon 2. The green box corresponds to alternative 5' splice site of exon 4. The red box corresponds to alternative 5' splice site of exon 5. The red background corresponds to the functional domains. The black background corresponds to the C-terminal.

ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	100
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	100
NP_995789_1.DROSOPHILA_MELANOGASTER	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	96
NP_001124398_1.HOMO_SAPIENS_A	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	96
NP_002388_2.HOMO_SAPIENS_C	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	96
NP_005911_1.HOMO_SAPIENS_D	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	96
NP_001139257_1.HOMO_SAPIENS_B	MGRKVICIDRIRMDERNRCVTEPKRKFQGKMKAYVELSVLCDCIEIALIINPNSN...QYASTDMDEVLLKYTYEPHESTDNVNEPA...A...NNKKHHKGICSP	95
Consensus	mgkkkiqi ri d rnrgvtf krkfqg mkkayelsvlvdceialif n l qyastdmde vllkytye ephes tn i e	
	MADS-MEF2	
ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	197
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	197
NP_995789_1.DROSOPHILA_MELANOGASTER	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	189
NP_001124398_1.HOMO_SAPIENS_A	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	189
NP_002388_2.HOMO_SAPIENS_C	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	192
NP_005911_1.HOMO_SAPIENS_D	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	192
NP_001139257_1.HOMO_SAPIENS_B	DSFD...GECDYILIPRPIAKYWKIDPEFTLMCGNCINGGYTR...VLAQACQFVGNNNNMAMV...VNNNTAYDPAIMCPSPCMHSASLSPRGSSGMIDMN	190
Consensus		
	HTURP-C	
ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	297
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	297
NP_995789_1.DROSOPHILA_MELANOGASTER	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	275
NP_001124398_1.HOMO_SAPIENS_A	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	275
NP_002388_2.HOMO_SAPIENS_C	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	283
NP_005911_1.HOMO_SAPIENS_D	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	283
NP_001139257_1.HOMO_SAPIENS_B	GSGNYGGSSTSPLPGCGGAPFSPLGSRPSKSKTHPTPNLHVIFNPQGTQNPGRPSPLSNTPVSHQTTAGNPM...TSPVSHLTPNQTCRQFCFLNSDLSISNLN	286
Consensus	g	
	HTURP-G	
ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	394
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	394
NP_995789_1.DROSOPHILA_MELANOGASTER	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	368
NP_001124398_1.HOMO_SAPIENS_A	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	375
NP_002388_2.HOMO_SAPIENS_C	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	373
NP_005911_1.HOMO_SAPIENS_D	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	382
NP_001139257_1.HOMO_SAPIENS_B	NSLNSLHQWNP...GSLGMHSGLPHLSVSSSTPPFAPASSPP.VRIKSEFISPRIDANCVPASHLQRPASTDDEGHLSPAPFSHLGPSSNNHVHTHYNTLSGH	368
Consensus		
	HTUTS-H	
ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
NP_995789_1.DROSOPHILA_MELANOGASTER	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
NP_001124398_1.HOMO_SAPIENS_A	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
NP_002388_2.HOMO_SAPIENS_C	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
NP_005911_1.HOMO_SAPIENS_D	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
NP_001139257_1.HOMO_SAPIENS_B	LTPTSHASPDGTSIHSHTEVDTLSKRKRPLTEGWTT.....	428
Consensus		
	HTUTS-G	
ANFO6985_1.[_LITOPENAEUS_VANNNAMEI]2A	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	468
ANFO6987_1.[_LITOPENAEUS_VANNNAMEI]2B	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	468
NP_995789_1.DROSOPHILA_MELANOGASTER	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	475
NP_001124398_1.HOMO_SAPIENS_A	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	473
NP_002388_2.HOMO_SAPIENS_C	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	482
NP_005911_1.HOMO_SAPIENS_D	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	368
NP_001139257_1.HOMO_SAPIENS_B	NNVSLAUGGGCGGGGGGNGSNVQEQTALHSLVSLQAHQQHHLGMNFSRSPSTGHITFTFGHDKRYEGYFYRALMGCHNRWLNIFAGAFSDQVPLVLA...	368
Consensus		

**Figure S2. Multiple alignment of the MEF2 genes.** The black, blue and red background correspond to the conserved sequences. The degrees of conservation are black>red>blue.



**Figure S3. The optimal interference efficiency of *LvMEF2* after 48 hours of RNA interference.** Significant differences of the gene expression levels between three treatments are shown as \*  $p < 0.05$ .

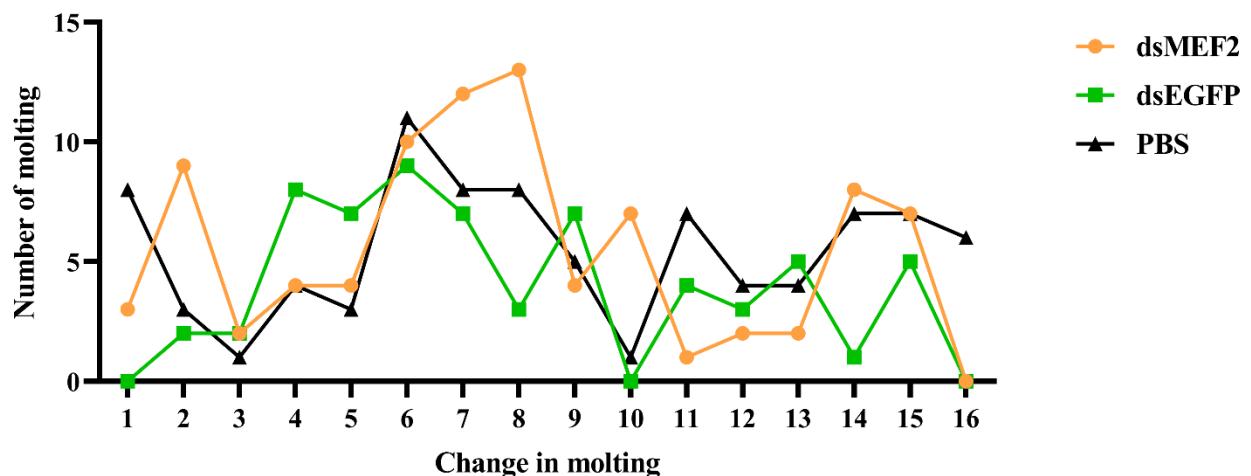


Figure S4. The molting situation during two weeks of RNA interference.

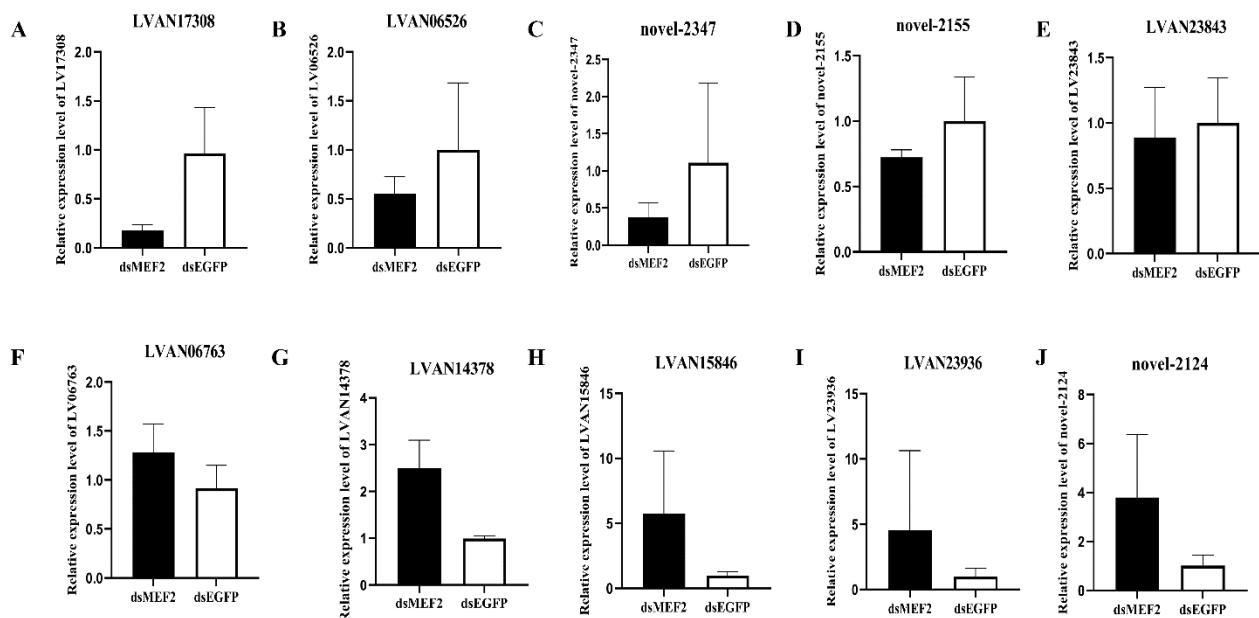


Figure S5. Expressions of related differential expression genes were verified after *LvMEF2* RNA interference.

The gene annotations corresponding to the transcript numbers are as follows: A, LVAN17308 (Heat shock 70 kDa protein); B, LVAN06526 (Mitochondrial glycine transporter); C, novel2347 (E3 ubiquitin-protein ligase); D, novel-2155 (Myosin heavy chain, muscle); E, LVAN23843 (Heat shock protein 20); F, LVAN06763 (MAP kinase-interacting serine/threonine-protein kinase); G, LVAN14378 (Immunoglobulin I-set domain); H, LVAN15846 (Glutaminase kidney isoform, mitochondrial); I, LVAN23936 (Myosin-4); J, novel-2124 (Myosin heavy chain, muscle).