

mse-miR-9571b	2-deoxyglucose-6-phosphate phosphatase, ACBP, adrenodoxin, Bombyrin precursor, B. mori glutathione-S-transferase 4, B. mori glutathione-S-transferase 5, calcium-binding protein p22, carbonyl reductase, chitin binding domain 3 protein, copper transporter, fatty acid binding protein, glutathione S-transferase 13, His-triad nucleotide binding protein 3, hydroxybutyrate dehydrogenase (m.24658), isocitrate dehydrogenase (m.30761), kynureninase, MCT (m.94739), mitochondrial carrier like, MSBP, Pap-inositol-1,4-phosphatase, peripheral-type benzodiazepine receptor, α -1,3-fucosyltransferase, bhlhzip TF bigmax, lysosomal acid lipase, RAB6-interacting golgin like, vacuolar ATP synthase subunit S1, pyroglutamyl peptidase 1, Ras family protein, SCP related protein, serine protease (m.46246), short chain type dehydrogenase (m.81137), sugar transporter SWEET1, synaptic vesicle glycoprotein 2B, synaptobrevin, transporter (m.78218), v-type proton ATPase subunit F
mse-miR-9a*	chitin binding domain 3 protein, citrate synthase, cytochrome P450 4M1, ecdysoneless, glucose dehydrogenase, HoxX, lactoylglutathione lyase, LRR, metal transporter CNNM2 like, methylmalonyl-CoA carboxyltransferase 12S subunit, organic cation transporter (m.57266), peroxisomal biogenesis factor 19, harmonin, SCP related protein
mse-miR-10a*	glutathione S-transferase 13, HoxX22, methylcrotonoyl-CoA carboxylase 1 α , NADPH cytochrome P450 reductase, dipeptidyl peptidase, SSR β subunit
mse-miR-281*	cytochrome c-like, isochorismatase domain containing protein, phosphoenolpyruvate synthase, bhlhzip TF bigmax
mse-miR-283*	3-dehydroecdysone-3 α reductase, eIF2A, O-acyltransferase, peroxisomal biogenesis factor 19, prenyl-dependent CAAAX metalloprotease, bhlhzip TF bigmax, pyridoxal-phosphate dependent enzyme
mse-miR-316*	acetoacetyl-CoA thiolase, ARF, B. mori glutathione-S-transferase 4, cytochrome P450 6AE32, fatty acid binding protein, glutathione S-transferase 13, HoxX, innexin, isovaleryl CoA dehydrogenase, metal transporter CNNM2 like, ADK 3, regucalcin, retinol dehydrogenase, short chain type dehydrogenase (m.29729), v-type proton ATPase subunit C
mse-miR-750*	dimeric dihydrodiol dehydrogenase, lactoylglutathione lyase, methylcrotonoyl-CoA carboxylase 1 α , NADPH cytochrome P450 reductase

*If gene names are the same, the transcript IDs (m. number) were included in the parentheses.

Table 7. Potential regulatory pairs of miRNAs and mitochondrial genes

Gene	miRNA
mitochondrial ornithine transporter	mse-miR-100
mitochondrial carrier protein	mse-miR-8, t4742895*
mitochondrial solute carrier	mse-miR-279c
tricarboxylate transport protein	mse-miR-10a*
adrenodoxin	mse-miR-9571a, 9571b
mitochondrial cytochrome C oxidase subunit 6A	mse-miR-316
mitochondrial NADPH adrenodoxin oxidoreductase	mse-miR-9571a
mitochondrial succinate semialdehyde dehydrogenase	mse-miR-1, 277
mitochondrial short-chain specific acyl CoA dehydrogenase	mse-miR-137, 9571a
SCOT	mse-miR-277
mitochondrial carrier like	mse-miR-9571a, 9571b

Table S1. A list of 26 novel miRNA candidates*

name	candidate mature sequence	fat body	hemocytes	midgut	Predicted precursor				
					Scaffold	Strand	Start	End	MFE
t41312	AAAAUUCUUAACCAGGCGAG	5	113	2	35	minus	1397534	1397635	-37.2
t1349963	AUCAGAUUUGUGGCAACUCG	2	11	2	45	minus	1412730	1412832	-33.6
t1410244	AUCGUUCGUUCACACCUGAUG	56	18	54	945	plus	52822	52922	-20.77
t1578118	AUUACUAGUAAUUCUGAAGCUUC	14	0	2	389	plus	62033	62135	-39.69
t1743832	CAAUUGGGAAUUCUUGCAAGC	5	0	27	64	minus	103034	103132	-22.5
t1766011	CAACUUCGUUUUGGACAGAGC	8	0	10	755	minus	56820	56922	-29.1
t3046669	GACAAACAGUGACUAGUUAGAAAC	24	0	20	48	plus	517657	517760	-28.5
t3125494a	GACUUUUUGUAAUUGUAAUUUUUG	295	185	68	770	minus	68976	69079	-25.12
t3125494b	GACUUUUUGUAAUUGUAAUUUUUG	295	185	68	282	plus	446264	446367	-27.4
t3334552	GAUUUGUACGUUUUGCGCAGGC	4	0	14	741	minus	71483	71583	-31.9
t3857561	GUACGUGUUGUGACCUUGAUUA	5	0	6	18	minus	1109289	1109390	-28.3
t4065768	GUGGACUUUGCUUGAACUGGAG	30	0	5	22	plus	893289	893393	-30.8
t4085867	GUGGGGCAAAUUGCGAAAGCUG	3	1	10	62	plus	910038	910139	-53.3
t4142920	GUUUGUUGGAGAUGGACGCG	24	0	25	2	minus	2944506	2944608	-21
t4181099	GUUGAAGAUUCGCAUCGACGGC	12	0	9	132	minus	70953	71054	-36.01
t4247673	GUUUUGUUUGUUGUAAAGAAGGC	9	0	4	68	plus	42495	42596	-27.9
t4330184	UAGAAGUUUGGUAUGACAUCAC	0	0	12	268	plus	99888	99989	-45.2
t4639756	UAUAAUAAACAGCACUGUACU	8	6	6	216	plus	414243	414343	-36.62
t4780013	UAUUUGCGUUGUUUUUGCAG	73	492	38	6	minus	389208	389308	-18.12
t4973453	UCCGGAAGUUGAAGUCUACUAG	5	17	1	42	minus	57500	57600	-65.5
t5794030	UUAACGAUUGUAGAAAGGCAU	6	0	215	18	plus	1453068	1453169	-39.5
t5903013	UUUUGGCGUUGGUUUAUUAU	2	0	27	513	plus	25548	25650	-58.7
t5986234	UUCGAACCAACAUAGAUGUGCC	5	2	3	551	plus	138319	138420	-52.2
t6185971	UUUGCGGGAGGACAUUGGCG	38	1	0	102	plus	247629	247731	-28.4
t6322016a	UUUGAAUUAAGGAAAACAGC	7	17	6	352	plus	301079	301178	-54.2
t6322016b	UUUGAAUUAAGGAAAACAGC	7	17	6	352	minus	301078	301177	-51.3

* Read numbers are absolute values from each library. The unit of precursor MFE is kcal/mol.

Table S2. Abundances of conserved miRNAs with no precursors identified*

name	mature miRNA sequence	fat body	hemocytes	midgut
miR-1	UGGAAUGUAAAGAAGUAUGUAG	927	15	1468
miR-1	UGGAAUGUAAAGAAGUAUGUAGU	841	15	1451
miR-1	UGGAAUGUAAAGAAGUAUGUGA	833	15	1447
miR-1	UGGAAUGUAAAGAAGUAUGCGU	832	15	1445
miR-2	UAUCACAGCCAGCUUUGAUGAGU	15	21	6
miR-2	UAUCACAGCCAGCUUUGAUGUGC	1	1	
miR-7	UGGAAGACUAGUGAUUUUUAUGUU		1	
miR-8	UAAUACUGUCAGGUAAUGAUGUC	5		
miR-8	UAAUACUGUAGGUAAAGAUGCC	5	1	
miR-9	UCUUUGGUUUUCUAGCUGUAGA	25	4	24
miR-9	UCUUUGGUUUACCUAGCUGUAUGA	2		1
miR-13	UAUCACAGCCAUUUUUGACGAGU	6	19	2
miR-13	UAUCACAGCCACUUUGAUGUG	1	3	
miR-31	GGCAAGAAGUCGGCAUAGCUG	4	10	5
miR-33	GUGCAUUGUAGUUGCAUUGCAU	27	6	9
miR-33	GUGCAUUGUAGUUGCAUUGC	23	3	7
miR-33	GUGCAUUGUAGUUGCAUUG	2		
miR-34	UGGCAGUGUGGUUAGCUGGUAGU	8	9	7
miR-71	UGAAAGACAUGGGUAGUGAGAUU	34	28	15
miR-71	UGAAAGACAUGGGUAGUGAGACG	26	16	13
miR-79	UAAAGCUAGAUUACCAAAGCAU	18	5	6
miR-100	AACCCGUAGAUCCGAACUUGUGU	20619	14576	8001
miR-100	GACCCGUAGAUCCGAACUUGUG	176	406	117
miR-100	AACCCGUAAAUCGAACUUGUG	1	1	
miR-184	UGGACGGAGAACUGAUAAAGGGU	415146	2360658	243350
miR-184	UGGACGGAGAACUGAUAAAGGCU	205010	1273289	130574
miR-184	UGGACGGAGAACUGAUAAAGGA	840	1232	468
miR-184	UGGACGGAGAAUUGAUAAAGGGU	135	613	63
miR-184	UGGACGGAGAACUGAUAGGGC	40	231	18
miR-252	AUAAGUACUAGUGCCGCAGGAG	32	6	1
miR-252	CUAAGUACUAGUGCCGCAGGUGU	13	4	
miR-263	AAUGGCACUGAAAGAAUUCACGGG	9	1	9
miR-274	GUUUGUGACCGUCACUAACGGGCAGU	49320	7	7
miR-276	UAGGAACUUAUACCGUGCUCU	3	8	4
miR-278	UCGGUUGGAUUUUCGUCCGUUU	1		1
miR-281	ACUGUCAUGGAGUUGCUCUCUU	42		41
miR-305	AUUGUACUUAUCAGGUGCUCUGG	3292	2220	1426
miR-305	AUUGUACUUAUCAGGUGCUCU	75	49	23
miR-305	GGCGCUUGUUGGAGUACACUU	2	3	2
miR-317	UGAACACAGCUGGUGUAUAUCAGU	412	99	376
miR-750	AGUUGGACAGGGGAUCUUGACA	12	6	617
miR-927	UUUUAGAAUJCCUACGCUUUACC	2313	100	7
miR-932	UCAAUJCCGUAGUGCAUJGCAG	1	7	1
miR-970	UCAUAAGACACACGCGGCUAU	2	56	2
miR-981	UUCGUUGUCGACGAAACCUGCCU			1
miR-989	UGUGAUGUGACGUAGUGGAACA	2	1	1
miR-1175	UGAGAUUCAACUCCUCCAACUJGC	3		76
miR-1175	UGAGAUUCAACUCCUCCAACUJAA	19	8	1473
miR-1175	AAGUGGAGGUGUGAUCUUCUJCA	5	1	505
miR-1959	GGGGAUGUAGCUCAGUGGAG	391	32	174
miR-2478	GUAUCCACUUCUGACACCA	90	19	50
miR-2795	CAAGUUUGGUGAUACGCGGGCGC	60	146	23
mse-bantam-b	UGAGAUCAUUGUGAAAGCUJAU	162	111	147
mse-bantam-c	UGAGAUCAUUGUGAAAGCUJAUU	76	29	75
mse-let-7b	UGAGGUAGUAGGUUGUGUGGUU	49	7	23
mse-let-7c	UGAGGUAGUAGGUUGUJAUUGGUU	969	66	538
mse-let-7e	UGAGGUAGGAGGUUGUJAUJAGU	6	2	2
mse-let-7f	UGAGGUAGUUGGUUGUJAUJAGU	10	3	4
mse-let-7g	UGAGGUAGUAGUUUGUJAUJAGUU	17	9	6
mse-let-7h	UGAGGUAGGAGGUUGUJAUJAGUU	7	2	3
mse-let-7i	AGAGGUAGUAGGUUGCAUJAGUU	1		
mse-let-7j	UGAGGUAGUAGGUUGUJAUJAGUU	11	4	4

* Abundances are shown in normalized reads per million. Numbers are blank for those either non-detectable or with normalized values below 0.5.