



*Supplementary materials*

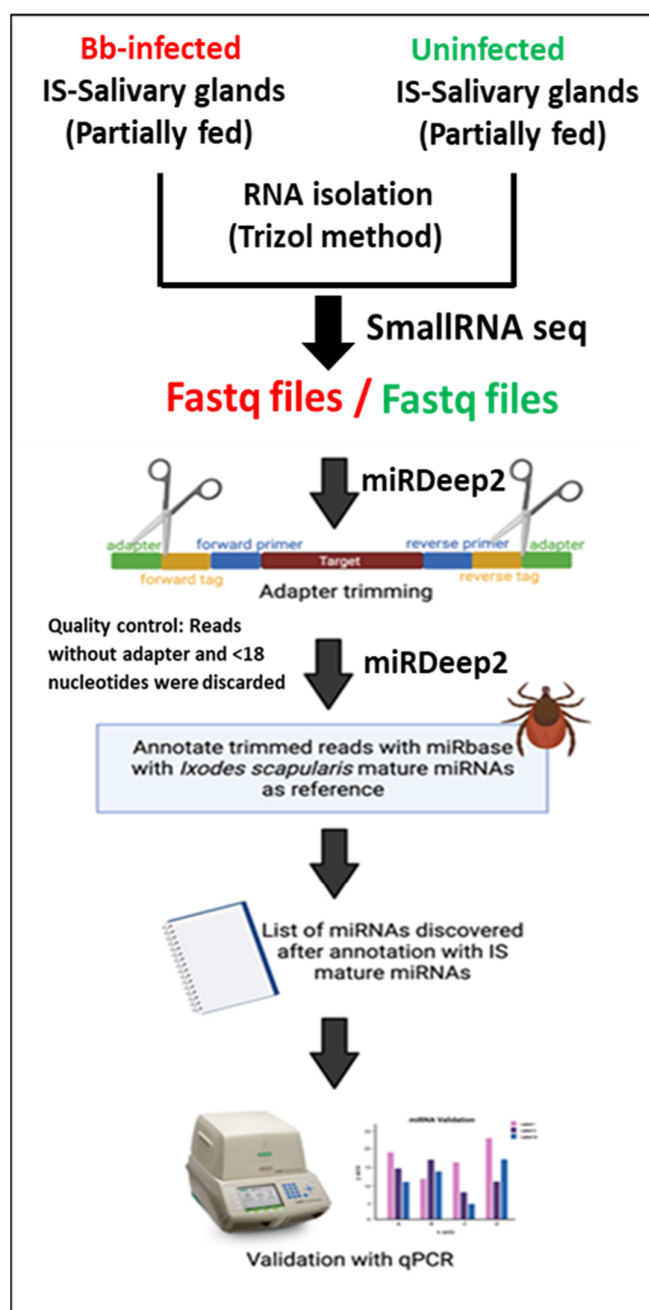
# Identification of microRNAs in the Lyme Disease Vector *Ixodes scapularis*

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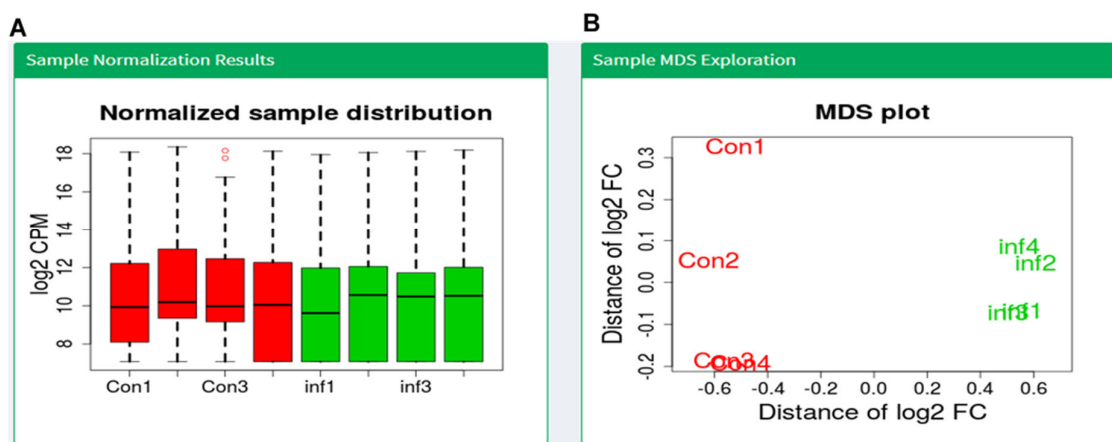
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**Figure S1.** Schematic of the experimental plan and data analysis.



**Figure S2.** A. Normalized sample distribution for *B. burgdorferi*-infected (inf1, inf2, inf3, and inf4) and uninfected (Con1, Con2, Con3, and Con4) salivary glands. B. Multidimensional scaling (MDS) plot shows variation in differential expression among uninfected samples (Con1, Con2, Con3, and Con4), where the distance between sample labels indicates dissimilarity in log2-fold change (FC).

**Table S1.** A. MicroRNA profiling of *Ixodes scapularis* salivary glands (novel miRNAs predicted by miRDeep2).

Provisional id	miRDeep2 Score	mature read count	miRbase miRNA with same seed	consensus mature sequence
isc-miR-4968-5p	1.80E+04	36306	dme-miR-4968-5p	aagcugcccaaugaagggcug
NW_002532706.1_43464 isc-miR-92a-3p	1.50E+04	29572	dme-miR-92a-3p	uauugcacucguccggccuuu
NW_002871802.1_367 isc-miR-125-5p	1.20E+04	12052	dme-miR-125-5p	ucccugagaccuaacuuguga
NW_002692816.1_23152 isc-miR-6-3p	7.60E+03	10940	dme-miR-6-3p	uauacagccauuuugaugacc
nDs_002867181.1_816	2.40E+03	4514		gccacccacuaacugacggga
nDs_002653147.1_27921	2.30E+03	4514		gccacccacuaacugacggga
nDs_002794895.1_10282	2.30E+03	4514		gccacccacuaacugacggga
nDs_002645436.1_28906	1.80E+03	3392		gcuguuaguuuguggguuggu
nDs_002860940.1_1699	1.80E+03	3392		gcuguuaguuuguggguuggu
nDs_002508325.1_46074	1.80E+03	3279		gcuguuaguuuguggguuggu
nDs_002699119.1_22404	1.70E+03	3392		gcuguuaguuuguggguuggu
NW_002767753.1_13364 isc-miR-958-3p	1.70E+03	3446	dme-miR-958-3p	ugagauuacuccuccaacuucu
nDs_002667887.1_26137	1.70E+03	3392		gcuguuaguuuguggguuggu
nDs_002810888.1_8213	1.70E+03	3392		gcuguuaguuuguggguuggu
nDs_002642603.1_29251	1.70E+03	3392		gcuguuaguuuguggguuggu
nDs_002815928.1_7504	1.00E+03	2109		caagaagauagaaucaaugaga
nDs_002861213.1_1662	9.50E+02	1855		cuugggcuggaguucgcuuguu
isc-miR-190-5p	6.60E+02	621	dme-miR-190-5p	agauauguuugauuuuugguu
nDs_002614457.1_32408	6.30E+02	1205		cacgucgagguucagguuguu
nDs_002614457.1_32404	5.20E+02	844		uacgucgagaccucagguuga
nDs_002867165.1_832	5.00E+02	994		ucguuuucgagauucgugaaccu
nDs_002728031.1_18707	4.90E+02	952		aguggucaugucucgcacugga
nDs_002621331.1_31664	4.50E+02	812		gugugagaaaugguuggcaca
nDs_002614457.1_32406	4.50E+02	857		cacgucgagauuucagcuauug

nDs_002735932.1_17756	4.10E+02	752		ugaggucaugcucggugccuug
nDs_002873519.1_126	3.70E+02	733		auauuuuuuuuuaacaucggcu
nDs_002784743.1_11607	2.10E+02	361		cauucuugcagcgaaggguguu
nDs_002620414.1_31747	1.50E+02	213		cagugcuucugcagugcaggc
nDs_002871485.1_401	1.40E+02	280		acagaaucgagcgcuaggcgca
nDs_002668420.1_26105	1.10E+02	200		ggcacaaggcugcggauugcga
nDs_002680650.1_24606	1.00E+02	146		cucagaaaugcuaggcuauagg
NW_002527183.1_43988 isc-miR-263b-5p	1.00E+02	184	dme-miR-263b-5p	cuuggcacugaaagaauucaca
nDs_002685244.1_24008	9.90E+01	185		cuuguuuggggcaauugggugac
nDs_002814339.1_7692	9.60E+01	185		cacgggccccagcugaacgcu
nDs_002737590.1_17488	9.00E+01	170		cagucaguggcuuugguucauc
nDs_002737673.1_17464	8.60E+01	173		guacacguucgggcuuccaccc
nDs_002564688.1_39220	7.40E+01	96		gguuuuuuucagcgugucgcu
nDs_002871133.1_436	7.00E+01	146		agccauuuuuugaagucgaca
nDs_002737711.1_17449	4.80E+01	84		agagugacgcagagaacaaauuc
nDs_002675644.1_25181	4.50E+01	84		aaaaggacagaacauguagaca
nDs_002763926.1_13886	3.90E+01	69		uguagccggauugugggacugg
nDs_002531612.1_43580	3.70E+01	53		cacugugcggaugguucaaac
nDs_002722741.1_19330	3.30E+01	75		auugaacgagaggacauaguc
nDs_002567548.1_38945	3.10E+01	52		ucaguguccgucgggaagg
NW_002787101.1_11264 isc-miR-31b-5p	3.10E+01	26	dme-miR-31b-5p	aggcaagaagucuuuagggaug
nDs_002754008.1_15271	3.00E+01	70		ucacuuuacgucguaguacaag
nDs_002538194.1_42559	3.00E+01	53		uuaguacgaucgucgaaagac
nDs_002801682.1_9417	3.00E+01	54		uguagcaugcuccaagcggagg
nDs_002508917.1_46002	3.00E+01	54		uguagcaugcuccaagcggagg
nDs_002568676.1_38752	2.70E+01	48		aaggagacaaggaaacaaacacc
nDs_002642725.1_29244	2.60E+01	58		acaacccggaaucgucauggcc
nDs_002670695.1_25779	2.60E+01	40		gcuggaucguaaaacuggugcca
nDs_002721909.1_19420	2.40E+01	44		gagaggucggauagaguugcgc
nDs_002548557.1_41255	2.40E+01	40		cuagugugacugucacagugg
nDs_002856865.1_2668	2.40E+01	40		cccggcgagaaaucggcgcccg
nDs_002588255.1_36295	2.10E+01	24		agacacgcuacugacuauugcug
nDs_002591771.1_35729	1.80E+01	12		cccgguaaggacugcgcauguc
NW_002637235.1_29734 isc-miR-4987-5p	1.80E+01	20	dme-miR-4987-5p	augcaacagaggcgagauagagacg
nDs_002730915.1_18372	1.80E+01	21		gagggaagaaaacgcgaaaggac
nDs_002527216.1_43980	1.70E+01	26		aggugaauagaauacccagucgaug
nDs_002829027.1_5932	1.60E+01	15		acgaaaucccgcggaucgcauug
nDs_002741178.1_17075	1.60E+01	27		uugggcuuuuaacaucaugagc
nDs_002718594.1_19992	1.50E+01	25		ucacaggacgugcaacggugcu
nDs_002718594.1_19994	1.50E+01	25		ucacaggacgugcaacggugcu
NW_002681830.1_24464 isc-bantam-3p	1.40E+01	17	dme-bantam-3p	cgagaucauacgucgguggugg
nDs_002515969.1_45216	1.40E+01	17		acaauugaaguggaucccgaau
nDs_002770056.1_13170	1.40E+01	24		aacgaaucgaagguaaagugc
nDs_002635366.1_29915	1.30E+01	36		cuugugaugcucucguuugacc
nDs_002745696.1_16495	1.20E+01	16		uccgagggaaguguccugacaga
nDs_002633080.1_30207	1.10E+01	17		uauuccuuccuuuuguccgguc
nDs_002862093.1_1546	1.00E+01	18		cuauuggacgaaaaggauagcu
nDs_002770523.1_13144	8.5	11		ugaagaucccaacuuggccucg
nDs_002637837.1_29679	8	10		aaagaaauacggacgacaggag
NW_002716687.1_20192 isc-miR-5-5p	5.7	209	dme-miR-5-5p	caaggaaccgacgaucgagugu

NW_002522525.1_44526 isc-miR-1007-5p	5.6	30	dme-miR-1007-5p	ucaguguuuggcuggaacccg
NW_002784743.1_11604 isc-miR-277-3p	5.4	1487	dme-miR-277-3p	uaaaugcauuauucuggaug
NW_002788893.1_11074 isc-miR-4957-3p	5.3	52	dme-miR-4957-3p	ucagcugcgugaacgcggcgcc
NW_002799140.1_9764 isc-miR-2a-1-5p	4.5	101	dme-miR-2a-1-5p	uucucaaauguccgccacucg
nDs_002745459.1_16501	2.7	25		accccgggguggucacgugac
nDs_002813294.1_7883	2.5	19		acggagcgacugaacaagaca
nDs_002829114.1_5911	2.4	19		agagaaaaagacagguagaacg
nDs_002759900.1_14325	2.4	95		uugccgcccugcuucauggaugg
nDs_002815075.1_7597	2.4	98		uugccgcccugcuucauggaugg
nDs_002513235.1_45498	2.3	26		ccucgguuuucggcuggcacucg
nDs_002676299.1_25117	2.3	22		ccaccgguuacgcucugcgcc
nDs_002700913.1_22252	2.3	123		gggacgaaacagacgacacagc
nDs_002684507.1_24073	2.3	258		caggcgggagaacaauuccu
nDs_002756339.1_14956	2.3	13		caagucgcggcugcacggcgcc
nDs_002774760.1_12785	2.3	12		cuucucucugcugccguggcc
nDs_002696292.1_22736	2.3	39		cugccucgcgugcugcuccgu
nDs_002550131.1_40913	2.2	19		cgccucagcuguuucugucc
nDs_002542368.1_42013	2.2	18		cacgucacagcugccgcucaag
nDs_002586787.1_36439	2.2	37		uuggacgaaaaaagagccgacu
nDs_002607638.1_33547	2.2	17		cuagccaaucgugggcgugggc
nDs_002836532.1_4888	2.2	22		ccaccgguuacgcucugcgcc
nDs_002597262.1_35126	2.1	11		cgggaucucggaggccaugaa
nDs_002662116.1_26803	2.1	21		caggauccugacgucgugggcaca
nDs_002636820.1_29767	2.1	7545		caaggcaugaacaugaucuca
nDs_002799981.1_9646	2.1	24		uccguccguuccguccucuc
nDs_002612646.1_32606	2.1	7545		caaggcaugaacaugaucuca
nDs_002629651.1_30593	2.1	819		cuucguagucggauuauagacu
nDs_002601819.1_34393	2.1	32		ucgaccgcucgccacggcugg
nDs_002540798.1_42197	2.1	20		caugucacugcugcccgcaag
nDs_002654127.1_27778	2	200		uuuccgcugcugcuuguaug
nDs_002860687.1_1738	2	15		gcagauucagguuagugauc
nDs_002665175.1_26443	2	217		aacuucgugcugcaggagcccu
nDs_002751908.1_15689	2	49		uaauuggucuuugugagucuu
nDs_002543222.1_41886	2	149		gccggugucgaucuugaaguuc
nDs_002569324.1_38643	2	22		ccaccgguuacgcucugcgcc
nDs_002590536.1_35849	2	22		uucgguuuguccgcuugccu
nDs_002601819.1_34394	2	32		ucgaccgcucgccacggcugg
nDs_002792777.1_10524	2	15		ugagaucucggagucgugcgcc
nDs_002714141.1_20473	2	83		ggcuucguagucggauuauaga
nDs_002744939.1_16574	1.9	829		cuucgaaucggauuauagacu
nDs_002533105.1_43443	1.9	7545		caaggcaugaacaugaucuca
nDs_002753934.1_15280	1.9	1842		cauccgguccuaagaagucgaa
nDs_002692659.1_23173	1.9	11		cugccgaaguagcgucugcucu
nDs_002733141.1_18085	1.9	7545		caaggcaugaacaugaucuca
nDs_002816672.1_7394	1.9	200		uuuccgcugcugcuuguaug
nDs_002738551.1_17311	1.9	77		cgcgcggacgcugugacgcagc
nDs_002523780.1_44319	1.9	7545		caaggcaugaacaugaucuca
nDs_002828015.1_6065	1.9	2093		ccaggauuugaacucuggccu
nDs_002829464.1_5811	1.9	7545		caaggcaugaacaugaucuca
nDs_002545827.1_41513	1.9	44		aagggaaccgugcgagagcugcu

nDs_002692659.1_23171	1.8	11		cugccgaaguagcgucugcucu
nDs_002661855.1_26902	1.8	70		gacauaguaaggauugacg
nDs_002765967.1_13675	1.8	17		uauuccuuccuuuuguccgguc
nDs_002574390.1_37989	1.8	259		uuccgccgucgaucguagaug
nDs_002550131.1_40914	1.8	19		cgccucagcuguuucugcucc
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nDs_002673151.1_25529	1.8	29		gcgacacagagacgaagacug
nDs_002809300.1_8415	1.8	1873		cauccgguccuaagaagucgaa
nDs_002738154.1_17397	1.8	35		cggaggauaguggguggaccug
nDs_002532161.1_43535	1.8	1943		cauccgguccuaagaagucgaa
nDs_002798374.1_9856	1.8	271		uucgagcgcuaaggacagagccg
nDs_002724962.1_19022	1.8	339		agaaagugcgucugcgcgcg
nDs_002692659.1_23176	1.8	108		acuaaaaaaacaggacaagu
nDs_002744911.1_16578	1.8	11		auucggacaucccgaggacguc
nDs_002545470.1_41626	1.8	11		auucggacaucccgaggacguc
nDs_002785931.1_11413	1.8	7545		caaggcaaugaacaugaucuca
nDs_002685244.1_24007	1.8	185		cuuguuugggcaauugggugac
nDs_002784743.1_11583	1.7	12		aggacgauugagcucgac
nDs_002587969.1_36333	1.7	53		cacgauugccaacuguaugcu
nDs_002661304.1_26957	1.7	39		aguccgucgucgaucugccu
nDs_002707270.1_21452	1.7	26		uucgcguucggacgugucgaa
nDs_002549652.1_41058	1.7	1892		caugccguggcuuagacca
nDs_002737099.1_17587	1.7	379		uuuggcaggcuuagaauacacuc
nDs_002511156.1_45736	1.7	95		uuugcaccgucgucguagaug
nDs_002608667.1_33381	1.7	30		auaggacuugauguuuuaggcucagu
nDs_002699570.1_22364	1.7	108		acuaaaaaaacaggacaagu
nDs_002537755.1_42809	1.6	53		acaccgguaauuuaaggguuauucug
nDs_002553320.1_40621	1.6	11		auucggacaucccgaggacguc
nDs_002581904.1_37014	1.6	12		gccauagcguaacagagugacg
nDs_002541749.1_42092	1.6	1943		cauccgguccuaagaagucgaa
nDs_002509761.1_45913	1.6	74		gacuucagguccaucuggacg
nDs_002542368.1_42015	1.6	18		cacgucacagcguccgucaag
nDs_002650258.1_28240	1.6	56		gcuguuaguuuugugggauggu
nDs_002745745.1_16473	1.6	259		uuccgccgucgaucguagaug
nDs_002692816.1_23143	1.6	105		uuucacaguccuuugacgg
nDs_002664372.1_26487	1.6	18		acuaccgaccgugugugaccg
nDs_002677543.1_24907	1.6	1862		cauccgguccuaagaagucgaa
nDs_002505804.1_46391	1.6	74		gacuucagguccaucuggacg
nDs_002855841.1_2713	1.6	137		acugugauugaacugaacgaca
nDs_002592079.1_35704	1.6	14		gaguagaaugccugaauuguugcu
nDs_002653831.1_27809	1.6	114		aaggcgaacgcugaccugggcc
nDs_002630829.1_30421	1.5	17		cgacgaauuucuggagaucgca
nDs_002535729.1_43080	1.5	331		cuucgcucugcuuaaguggacc
nDs_002590762.1_35829	1.5	95		uugccgccgucguucauggaugg
nDs_002617786.1_32035	1.5	18		ucugucccugguuuugcgcu
nDs_002834843.1_5113	1.5	21		cgagggcuguccagaguucuuug
nDs_002844434.1_4087	1.5	258		uuccgccgucgaucguagaug
nDs_002838169.1_4671	1.5	47		accuuuugggucucuguccucu
nDs_002567550.1_38944	1.5	97		uuugcaccgucgucguagaug
nDs_002639690.1_29492	1.5	2928		guuguaccagucgucgauguc
nDs_002530398.1_43703	1.4	31		cagggccuaaaugacauuuacacu
nDs_002829616.1_5794	1.4	15		acggcuggcgucucgucgacc
NW_002626049.1_30948 isc-miR-981-3p	1.4	4936	dme-miR-981-3p	uucguugucguagaaaccugau

nDs_002790353.1_10903	1.4	20		cacgucacagcguccgcucaag
nDs_002721909.1_19415	1.4	312		caugacugucaucuuugcaucu
nDs_002592028.1_35707	1.4	26		cucgaggucuaacccgucuccu
nDs_002697784.1_22512	1.4	121		uuggacuuugagcauggcgagg
nDs_002515625.1_45241	1.3	24		augccacugucccaguuucugc
nDs_002815935.1_7502	1.3	15		ucugcgagacgcucaacgacag
nDs_002650258.1_28243	1.2	23		cucaagauucuccgagucgc
nDs_002663292.1_26641	1.2	137		acugugauugaacugaacgaca
nDs_002744911.1_16577	1.2	11		auucggacaucgcaggagcug
nDs_002827450.1_6124	1.2	20		cacgucacagcguccgcucaag
nDs_002545470.1_41625	1.2	11		auucggacaucgcaggagcug
nDs_002553320.1_40622	1.2	11		auucggacaucgcaggagcug
nDs_002598280.1_35014	1.1	28		ucaacuccuacgucggugcug
nDs_002756375.1_14945	1.1	52		uucacgaaucugaacgggaca
nDs_002613137.1_32572	1.1	19		ugugaaggccuccugucucu
nDs_002563762.1_39378	1	18		aagaauaaacaagguacggau
nDs_002768943.1_13309	0.9	121		ugacgucaucguagugcugcu
nDs_002546088.1_41480	0.8	18		aucuuuugacacguuggaucu
nDs_002856883.1_2662	0.8	38		ugugagauuguuugcauagcg
nDs_002615653.1_32278	0.8	257		uuccgccgucgucguagaug
nDs_002655152.1_27700	0.8	321		ugaaagcagauaccaugacugu
nDs_002808312.1_8698	0.6	59		uuguggacgccugacaagccu
nDs_002784518.1_11647	0.5	26		aucuuuugacacguuggaucu
nDs_002860612.1_1764	0.4	11		aacaugagcgacgucguaccg
NW_002847019.1_3755 isc-miR-1000-3p	0.3	49	dme-miR-1000-3p	augcuggggacacugaaaucc
nDs_002585048.1_36632	0.3	9		cuucguagucggauuauga
nDs_002569020.1_38698	0.2	353		gccggaacagucaucguugcug
nDs_002820844.1_6987	0.2	39		auucggcgccacuuugaacgaa
NW_002573167.1_38165 isc-miR-2494-3p	0	79	dme-miR-2494-3p	uucccaguaguccaggaccug

**Table S1.** B. mature miRNAs of *Ixodes scapularis* (already available in miRBase) detected in miRDeep2 analysis.

tag id	miRDeep2 score	mature read count	mature miRBase miRNA	consensus mature sequence
NW_002860020.1_1824	6.60E+05	1296028	isc-miR-375	uuuguucguucggcucgaguuu
NW_002784743.1_11596	3.90E+05	773543	isc-miR-10	uaccugugagauccgaauuugu
NW_002651209.1_28145	3.60E+05	706969	isc-miR-2001	uugugaccguuacaauugggcaug
NW_002835324.1_5031	1.80E+05	356093	isc-miR-12	ugagauuuacauaggguacuggu
NW_002509761.1_45916	1.60E+05	327576	isc-bantam	ugagaucauuuguaaagcugauu
NW_002505804.1_46394	1.60E+05	327576	isc-bantam	ugagaucauuuguaaagcugauu
NW_002871802.1_369	4.90E+04	96352	isc-miR-100	aaccgugagauccgaacuugug
NW_002656291.1_27550	4.10E+04	81041	isc-miR-3931	uacuuugagucgguaacgaauccu
NW_002648701.1_28526	3.60E+04	70402	isc-miR-8	uaauacugucagguaaagauugc
NW_002835324.1_5033	3.40E+04	66800	isc-miR-5307	uaauucuuuuugguaucucuggg
NW_002778756.1_12266	2.80E+04	54755	isc-miR-79	ucuuugguuauucuaugcugaua
NW_002527183.1_43986	2.20E+04	43978	isc-miR-263a	aauggcacuggaagaauucacgg
NW_002527216.1_43977	2.20E+04	42981	isc-miR-279	ugacuagauccacacucaucca
NW_002741283.1_17066	1.50E+04	29423	isc-miR-276	uaggaacuucuaaccaugcucg
NW_002822737.1_6809	1.40E+04	25686	isc-miR-87	gugcccggaacuugucucagccu
NW_002697059.1_22632	1.30E+04	25752	isc-miR-184	uggacggagaacugauaagggc
NW_002784743.1_11606	9.80E+03	19228	isc-miR-317	ugaacacagcuggugguauaucagu
NW_002838206.1_4665	8.70E+03	16890	isc-miR-305	auuguacuucacaggugcucugga

NW_002692816.1_23154	6.90E+03	13241	isc-miR-2b	uaucaacagccaccuuugaugagcu
NW_002692816.1_23150	5.60E+03	10571	isc-miR-2a	uaucaacagccagcuuugaugagc
NW_002692816.1_23156	5.50E+03	7193	isc-miR-71	ucucacuaaccuugucuuuguug
NW_002804504.1_9143	4.60E+03	5941	isc-miR-307	ccucacucaguuuggcugugug
NW_002535453.1_43180	3.00E+03	5915	isc-miR-153	uugcauagucacaaaagugaug
NW_002764570.1_13794	2.80E+03	5474	isc-miR-252b	uuuaguuagugccgcagguaa
NW_002604667.1_33926	2.80E+03	5463	isc-miR-315	uuuaguuagugcucagaaggcg
NW_002704625.1_21791	1.80E+03	3647	isc-miR-1	uggaauuuuaagaaguaggag
NW_002734393.1_17986	1.00E+03	1901	isc-miR-278	ccggaugaaauucuccuggcc
NW_002848014.1_3640	6.90E+02	1368	isc-miR-5314	uauagaugaugucuucaugaug
NW_002627241.1_30834	6.60E+02	1302	isc-miR-5315	aacacaaacuccggacaagcac
NW_002527183.1_43990	3.70E+02	575	isc-miR-96	uuuggcacuaagcacuuuuugu
NW_002522955.1_44449	3.10E+02	434	isc-miR-7	uggaagacuaguuuuuguuguu
NW_002784743.1_11634	2.10E+02	330	isc-miR-993	gaagcucguuuuacagguaucu
NW_002805128.1_9069	1.00E+02	90	isc-miR-5308	ucugugcugaggaguuauau
NW_002589297.1_36170	9.40E+01	76	isc-miR-5305	uaaguuauucuccaagcccau
NW_002733905.1_18011	5.3	272	isc-miR-124	uaaggcacgcggugaaugcc
NW_002506863.1_46298	5.3	1270	isc-miR-133	uuggucccuuacaccagugu
NW_002542293.1_42026	2.1	147	isc-miR-5310	uguagucuggcagaaacguc
NW_002610401.1_33095	2	69	isc-miR-5306	agaguaucacgugacgucucu
NW_002755260.1_15039	2	28	isc-miR-1993	cauuuagcuaguuucgcgggg
NW_002796881.1_10053	1.9	28	isc-miR-1993	cauuuagcuaguuucgcgggg
NW_002638804.1_29568	1.8	693	isc-miR-5309	caaucccauggaaccgccgaa
NW_002793850.1_10420	1.7	743	isc-miR-5312	uggcugaacguuuuauucgu
NW_002838206.1_4667	1.2	17097	isc-miR-275	ucagguaccugaaguagcgcg
NW_002784743.1_11605	1.1	19228	isc-miR-317	ugaacacagcuggguauuacagu
NW_002822737.1_6807	-0.8	3011	isc-miR-87	gugagcaaguuucaggugugu
NW_002796881.1_10054	-2.2	28	isc-miR-1993	cauuuagcuaguuucgcgggg
NW_002741199.1_17073	-5.1	12	isc-miR-137	uuauugcuugagaauacacgu

Table S2. KEGG pathways targeted by differentially expressed miRNAs.

Target proteins	KEGG ID	KEGG pathways
EEC07251.1	KEGG:R02541	RAS-related protein, putative, Sphingolipid metabolism pathway
EEC06395.1	KEGG:R04030	Ubiquinone and other terpenoid-quinone biosynthesis,
		Metabolic pathways
		Biosynthesis of secondary metabolites
		Biosynthesis of cofactors
EEC17038.1	KEGG:R02541	
EEC08267.1	KEGG:R00253	Arginine biosynthesis
		Alanine, aspartate and glutamate metabolism
		Glyoxylate and dicarboxylate metabolism
		Nitrogen metabolism
		Metabolic pathways
		Microbial metabolism in diverse environments
		Biosynthesis of amino acids
EEC06395.1	KEGG:R04030	Fatty-acyl-CoA Synthase (Fatty acid biosynthesis pathway)
EEC17038.1	KEGG:R02541	RAB-33, putative [Ixodes scapularis], exosome biogenesis and secretion between arthropods and mammals.
EEC08267.1	KEGG:R00253	
EEC10220.1	KEGG:R04188	4-aminobutyrate aminotransferase, Valine, leucine and isoleucine degradation
EEC02614.1	KEGG:R01178	medium-chain acyl-CoA dehydrogenase, putative, Lipid transport and metabolism
EEC07988.1	KEGG:R05982	alpha-mannosidase putative, Protein processing in endoplasmic reticulum, Various
	KEGG:R06722	types of N-glycan biosynthesis

EEC02307.1	KEGG:R01178	medium-chain acyl-CoA dehydrogenase, putative,
EEC07756.1	KEGG:R03876	ubiquitin protein ligase, putative,
EEC20239.1	KEGG:R03532	thioredoxin-dependent peroxide reductase, which confer a protective role in cells through its peroxidase activity by reducing hydrogen peroxide
EEC04717.1	KEGG:R03876	RNA polymerase II transcription elongation factor, putative,
EEC17038.1	KEGG:R02541	RAB-33, putative [Ixodes scapularis], exosome biogenesis and secretion between arthropods and mammals.
EEC09178.1	KEGG:R07364	acireductone dioxygenase, putative, Cysteine and methionine metabolism
EEC17038.1	KEGG:R02541	RAB-33, putative [Ixodes scapularis], exosome biogenesis and secretion between arthropods and mammals.
EEC08267.1	KEGG:R00253	glutamine synthetase, putative,
EEC09478.1	KEGG:R02324	nicotinamide riboside kinase, putative, Nicotinate and nicotinamide metabolism
EEC06118.1	KEGG:R02530	4-hydroxyphenylpyruvate dioxygenase, putative, Pyruvate metabolism
EEC07756.1	KEGG:R03876	ubiquitin protein ligase, putative,
EEC07147.1	KEGG:R05330	short-chain dehydrogenase, putative, Primary bile acid biosynthesis, Biosynthesis of unsaturated fatty acids
EEC11438.1	KEGG:R02541	RAS-related protein, putative, exosome biogenesis and secretion between arthropods and mammals
EEC08160.1	KEGG:R02541	GTP-binding protein Rhes, putative, exosome biogenesis and secretion between arthropods and mammals.
EEC10220.1	KEGG:R04188	4-aminobutyrate aminotransferase, Valine, leucine and isoleucine degradation
EEC07981.1	KEGG:R01049	ribose-phosphate pyrophosphokinase 1 putative,
		rn00030 Pentose phosphate pathway
		rn00230 Purine metabolism
		rn01100 Metabolic pathways
		rn01110 Biosynthesis of secondary metabolites
		rn01120 Microbial metabolism in diverse environments
		rn01200 Carbon metabolism
		rn01230 Biosynthesis of amino acids
EEC08267.1	KEGG:R00253	glutamine synthetase putative, Arginine biosynthesis, Alanine, aspartate and glutamate metabolism, Glyoxylate and dicarboxylate, nitrogen metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids
EEC05869.1	KEGG:R02268	cytochrome P450 putative, Arachidonic acid metabolism
EEC04717.1	KEGG:R03876	RNA polymerase II transcription elongation factor, putative
EEC08267.1	KEGG:R00253	glutamine synthetase putative, Arginine biosynthesis, Alanine, aspartate and glutamate metabolism, Glyoxylate and dicarboxylate, nitrogen metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids
EEC07251.1	KEGG:R02541	RAS-related protein putative, exosome biogenesis and secretion between arthropods and mammals
EEC17749.1	KEGG:R02541	RAB-9 and, exosome biogenesis and secretion between arthropods and mammals
EEC09478.1	KEGG:R02324	nicotinamide riboside kinase (putative), Nicotinate and nicotinamide metabolism
EEC05808.1	KEGG:R03876	
EEC02290.1	KEGG:R00004	secreted inorganic pyrophosphatase, putative,
EEC15523.1	KEGG:R02265	Microsomal prostaglandin E synthase 2, Arachidonic acid metabolism
EEC08267.1	KEGG:R00253	glutamine synthetase putative, Arginine biosynthesis, Alanine, aspartate and glutamate metabolism, Glyoxylate and dicarboxylate, nitrogen metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids
EEC10220.1	KEGG:R04188	(S)-3-amino-2-methylpropionate transaminase, Valine, leucine and isoleucine degradation
EEC01042.1	KEGG:R00310	Ferrochelatase, Porphyrin and chlorophyll metabolism, Biosynthesis of secondary metabolites, Heme biosynthesis

**Table S3.** Gene-specific PCR and qRT-PCR primers used in this study.

Gene	GenBank ID	Forward Primer (5'-3')	Reverse Primer (5'-3')	Size (bp)
<i>RPS4 (qPCR)</i>	DQ066214.1	GGTGAAGAAGATTGTCAAGCAGAG	TGAAGCCAGCAGGGTAGTTTG	80
<i>flaB (qPCR)</i>	Stone et al., 2015	GGG TCT CAA GCG TCT TGG	GAA CCG GTG CAG CCT GAG	139