

Additional File 6

Analysis of 3'UTR miRNA cognate motifs

3'UTR motif	number of genes	ER	NC	p-value	miR [14]	miR (miRBase)
(A)						
o15.12	8	1.24	2.01	0.0005	miR-5	miR-18ab, miR-20ab
o15.22	10	1.17	1.47	0.0043	miR-94	miR-721
o28.5	14	0.86	-1.43	0.0030	miR-201	-
(B)						
o2.25	2	2.63	9.07	0.0011	miR-208(no.3) miR-99a,	-
o13.2	2	2.36	8.06	0.0035	miR-99b(no.3), miR-100	miR-99a,miR-100
o3.7	29	1.22	1.87	0.0033	miR-26	let-7d
(C)						
o2.25	2	1.99	4.08	0.0003	miR-208(no.3) miR-99a,	-
o13.2	2	1.75	3.34	0.0031	miR-99b(no.3), miR-100 miR-221(no.1),	miR-99a,miR-100
o46.1	17	1.20	1.07	0.0037	miR-222(no.1)	

The table shows a *t*-test analysis for a total of 111 3'UTR miRNA cognate sequence motifs, identified as in Xie et al. [14]. Additionally, the sequence code as found by searching for the reverse complement in miRBase are shown. (A) Basal differences between genotypes, (B) LPS induction in WT, and (C) differences between genotypes in LPS induction (genotype by treatment interaction). ER, approximate mean expression ratios, NC, mean normed coefficients, and p-values from *t*-tests.