

**OMTN, Volume 14**

## **Supplemental Information**

### **AntagomiR-103 and -107 Treatment Affects**

#### **Cardiac Function and Metabolism**

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## Supplemental information

### Supplemental figures

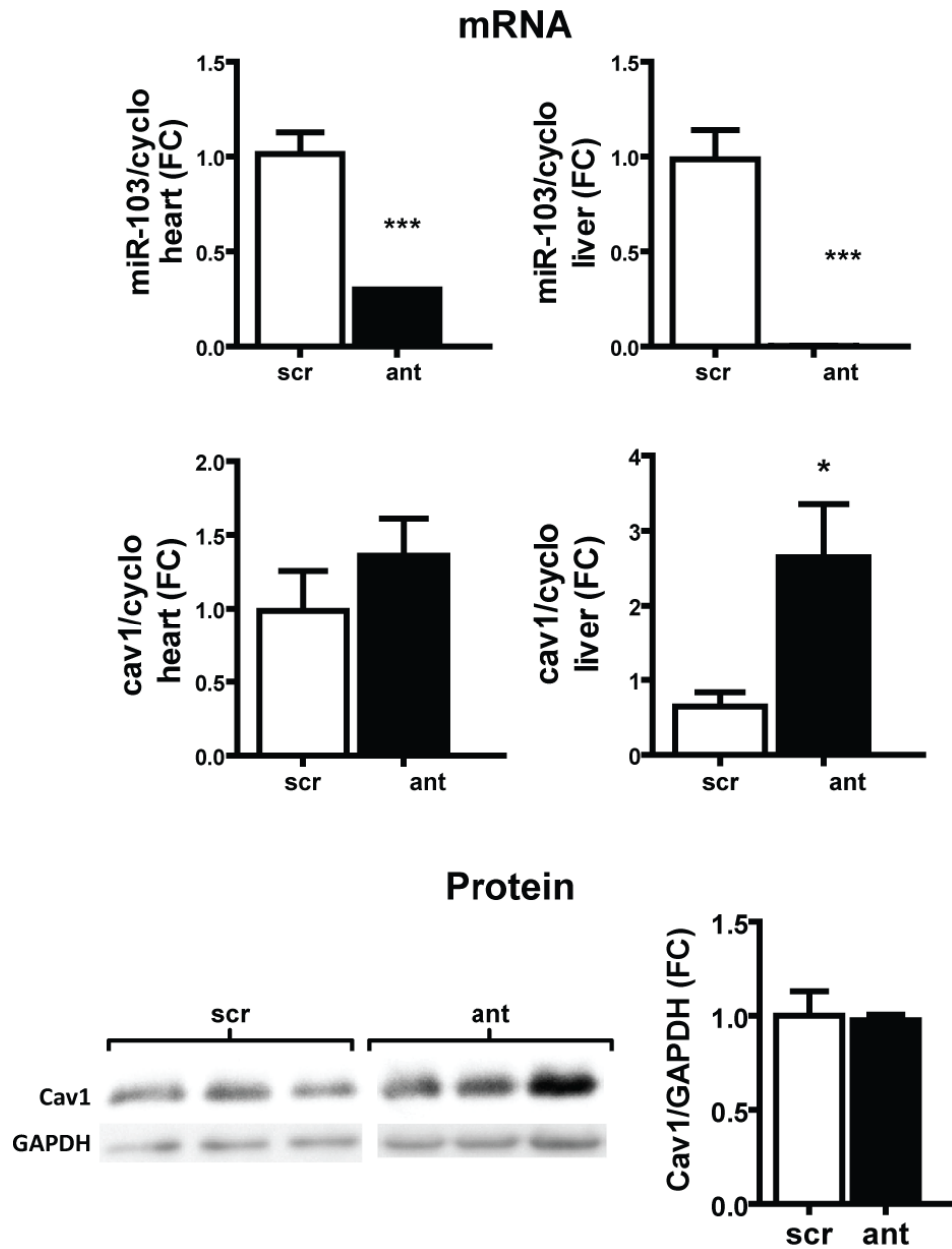
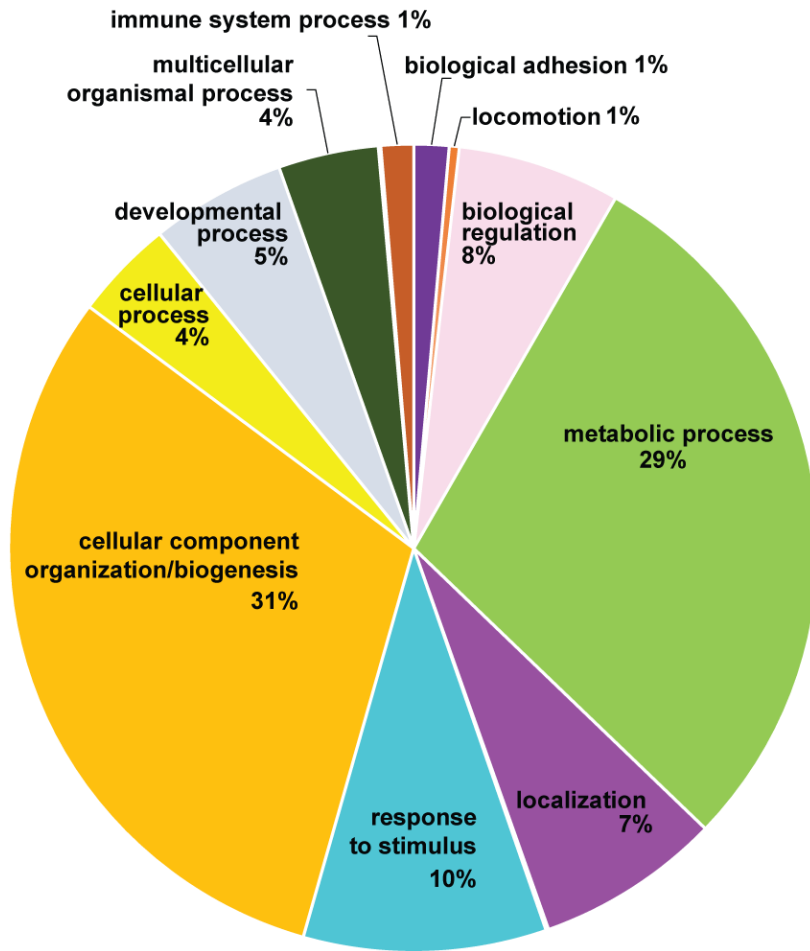


Figure S1. A) *MiR-103* and *Cav1* gene expression in heart and liver of animals treated with scrambled control or antagomiR-103/107, \*  $p < 0.05$  vs scrambled, \*\*\*  $p < 0.001$  vs scrambled,  $n = 7$  per group; B) representative western blot and quantification of Cav1 and GAPDH of the lysates of hearts treated with antagomiR-103/107 or scrambled,  $n = 3$  per group; data are shown as mean  $\pm$  SEM, scr, scrambled control, ant; antagomiR-103/107.



**Figure S2. Panther GO-slim biological processes annotation chart for predicted targets of miR-103/107. Total predicted genes: 838; total number of process hits: 1397**

## Supplemental tables

**Table S1. Hematological and immunological analysis in plasma of scrambled or antagomiR-103/107 treated mice at week 3.**

Immune formula	Scrambled		AntagomiR	
	Mean	± SEM	Mean	± SEM
<b>WBC (10<sup>3</sup>/μL)</b>	<b>5.17</b>	<b>0.24</b>	<b>3.94*</b>	<b>0.33</b>
Neutrophils (10 <sup>3</sup> /μL)	0.33	0.03	0.27	0.04
% Neutrophils	6.54	0.76	6.85	0.42
<b>Lymphocytes (10<sup>3</sup>/μL)</b>	<b>4.64</b>	<b>0.27</b>	<b>3.48*</b>	<b>0.28</b>
% Lymphocytes	89.54	1.61	88.30	0.91
Monocytes (10 <sup>3</sup> /μL)	0.04	0.01	0.04	0.01
% Monocytes	0.78	0.31	0.90	0.19
Eosinophils (10 <sup>3</sup> /μL)	0.01	0.00	0.03	0.03
% Eosinophils	0.22	0.04	0.87	0.64
Basophils (10 <sup>3</sup> /μL)	0.15	0.03	0.12	0.02
% Basophils	2.91	0.62	3.08	0.21
RBC (M/uL)	6.10	0.18	6.58	0.11
HGB (g/dL)	8.97	0.26	9.68	0.18
HCT (%)	48.29	1.48	52.23	0.85
MCV (fL)	79.11	0.47	79.38	0.35
MCH (pg)	14.71	0.10	14.70	0.07
MCHC (g/dL)	18.59	0.06	18.53	0.06
RDW (%)	15.77	0.51	17.07	0.59
PLT (K/dL)	853.29	20.48	823.17	32.20
MPV (fL)	5.84	0.16	5.82	0.07
PCT (%)	0.50	0.03	0.48	0.02
PDW (GSD)	16.94	0.23	16.93	0.21

n=7 per group; \* p<0.05 vs scrambled

**Table S2. Mass spectrometry analysis of heart apex of scrambled or antagomiR-103/107 treated mice.**

Protein	UniProt ID	Unique Peptides	Log2 Ratio	Q-value	Ant/ Scr	Ant [-]	Ser [-]	Data Points
26S proteasome non-ATPase regulatory subunit 7 [OS=Mus musculus]	P26516	4	0.52	1.81E-02	1.43	18129.9	12684.1	4
complement factor H [OS=Mus musculus]	P06909	2	0.42	1.22E-02	1.34	5832.5	4345.8	2
Hemopexin [OS=Mus musculus] <sup>a</sup>	Q91X72	18	0.38	6.04E-11	1.30	248566.8	191392.4	23
Peptidyl-prolyl cis-trans isomerase F, mitochondrial [OS=Mus musculus]	Q99KR7	8	0.35	1.96E-02	1.27	24018.7	18844.0	9
Complement C3 [OS=Mus musculus]	P01027-1	11	0.28	1.10E-02	1.21	50356.1	41446.4	12
Actin, alpha skeletal muscle [OS=Mus musculus]	P68134	3	0.28	1.84E-02	1.21	167488.3	138069.6	6
Cytochrome c, somatic [OS=Mus musculus]	P62897	24	0.27	9.73E-17	1.20	2779866.3	2307895.8	41
Acylphosphatase-2 [OS=Mus musculus]	P56375	7	0.27	9.64E-04	1.20	122844.4	102199.0	8
Aspartate aminotransferase, mitochondrial [OS=Mus musculus]	P05202	41	0.24	5.26E-14	1.18	1101538.9	933398.8	62
Fibrinogen gamma chain [OS=Mus musculus]	Q8VCM7	10	0.24	3.18E-03	1.18	68054.0	57702.7	10
Myosin-7 [OS=Mus musculus]	Q91Z83	65	0.20	6.88E-05	1.15	1948494.3	1701126.8	96
Fatty acid-binding protein, heart [OS=Mus musculus]	P11404	23	0.18	3.80E-05	1.13	5532021.5	4883083.0	50
Protein S100-A1 [OS=Mus musculus]	P56565	5	0.18	1.71E-02	1.13	183583.0	162465.1	8
Actin, alpha cardiac muscle 1 [OS=Mus musculus] <sup>a</sup>	P68033	60	0.15	2.20E-03	1.11	61439824.0	55271280.0	163
myosin regulatory light chain 2, ventricular/cardiac muscle isoform [OS=Mus musculus]	P51667	37	0.15	9.10E-03	1.11	7096360.5	6411138.5	83
Translationally-controlled tumor protein [OS=Mus musculus]	P63028	10	0.14	1.10E-02	1.11	297646.4	269287.2	13
Myosin-4 [OS=Mus musculus]	Q5SX39	14	0.14	3.85E-03	1.10	3429579.3	3111626.8	20
Pregnancy zone protein [OS=Mus musculus]	Q61838	13	0.12	9.46E-03	1.09	101444.3	93338.5	14
Myoglobin [OS=Mus musculus] <sup>a</sup>	P04247	36	0.12	3.72E-03	1.08	14948670.0	13778867.0	88
Acyl-coenzyme A thioesterase 13 [OS=Mus musculus]	Q9CQR4	13	0.10	1.04E-02	1.07	1336000.1	1245060.6	23
Telethonin [OS=Mus musculus]	O70548	4	0.10	2.50E-03	1.07	153428.2	143335.0	4
electron transfer flavoprotein subunit beta [OS=Mus musculus]	Q9DCW4	35	0.06	2.78E-06	1.04	3497220.5	3361798.3	57
Cytochrome b-c1 complex subunit 7 [OS=Mus musculus]	Q9D855	18	0.05	2.73E-05	1.04	1626810.6	1571087.5	30
ATP synthase subunit gamma, mitochondrial [OS=Mus musculus]	Q91VR2	28	0.04	7.14E-05	1.03	1369158.4	1327708.0	44
Laminin subunit alpha-2 [OS=Mus musculus]	Q60675	60	0.03	7.67E-04	1.02	167368.0	164485.1	69
glyceraldehyde-3-phosphate dehydrogenase [OS=Mus musculus]	P16858	38	0.02	4.55E-04	1.01	6986970.0	6887551.5	79
Beta-enolase [OS=Mus musculus]	P21550	52	-0.01	3.02E-04	0.99	2640891.5	2665133.0	92
Adenylate kinase isoenzyme 1 [OS=Mus musculus]	Q9R0Y5-1	25	-0.02	2.39E-04	0.99	2043768.6	2069378.4	40
Ornithine aminotransferase, mitochondrial [OS=Mus musculus]	P29758	17	-0.03	1.64E-02	0.98	193450.4	197165.2	26
Alpha-actinin-2 [OS=Mus musculus]	Q9JI91	120	-0.03	8.73E-04	0.98	2255220.0	2309955.8	209
Cysteine-rich protein 2 [OS=Mus musculus]	Q9DCT8	16	-0.04	1.76E-02	0.97	630263.5	648074.9	27
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 [OS=Mus musculus]	Q9CQ75	11	-0.05	1.33E-02	0.97	795473.6	821258.3	16
Myosin-3 [OS=Mus musculus]	P13541	9	-0.05	4.03E-03	0.97	1769777.5	1828452.1	11
Cytochrome c oxidase subunit 6B1 [OS=Mus musculus]	P56391	11	-0.05	5.96E-04	0.97	6591877.0	6821341.0	18
Malate dehydrogenase, cytoplasmic [OS=Mus musculus]	P14152	37	-0.05	8.40E-03	0.97	4713308.0	4881656.0	59
Alpha-crystallin B chain [OS=Mus musculus]	P23927	23	-0.06	1.23E-02	0.96	1099699.0	1147986.0	47

ATP synthase subunit d, mitochondrial [OS=Mus musculus]	Q9DCX2	21	-0.07	3.51E-03	0.95	2873328.3	3010304.5	37
Aspartate aminotransferase, cytoplasmic [OS=Mus musculus]	P05201	35	-0.07	1.52E-03	0.95	1689716.6	1777122.5	55
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial [OS=Mus musculus]	Q9D6R2	34	-0.08	6.38E-04	0.95	1214956.3	1279973.0	57
Malate dehydrogenase, mitochondrial [OS=Mus <sup>a</sup> musculus]	P08249	39	-0.08	3.74E-09	0.95	15937558.0	16827072.0	74
Cytochrome b-c1 complex subunit 2, mitochondrial [OS=Mus musculus]	Q9DB77	34	-0.08	7.17E-03	0.94	2317813.8	2453957.8	58
EH domain-containing protein 1 [OS=Mus musculus] <sup>a</sup>	Q9WVK4	15	-0.08	3.45E-03	0.94	72112.0	76449.4	20
Electron transfer flavoprotein subunit alpha, mitochondrial [OS=Mus musculus]	Q99LC5	32	-0.09	1.52E-04	0.94	4521429.5	4796793.5	58
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial [OS=Mus musculus]	Q91YT0	37	-0.09	3.95E-03	0.94	1150154.4	1222285.6	67
Troponin I, cardiac muscle [OS=Mus musculus]	P48787	31	-0.10	3.99E-04	0.93	5298699.0	5685937.0	49
Cytochrome c oxidase subunit 2 [OS=Mus musculus]	P00405	8	-0.10	1.64E-02	0.93	4445445.5	4772605.0	16
Heterogeneous nuclear ribonucleoproteins C1/C2 [OS=Mus musculus]	Q9Z204;-2;-3;-4;-5	5	-0.11	1.99E-02	0.93	39069.5	42063.2	5
Carnitine O-palmitoyltransferase 2, mitochondrial [OS=Mus musculus]	P52825	43	-0.11	1.84E-03	0.93	349260.2	376413.4	54
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Mus musculus]	P50544	48	-0.11	8.97E-03	0.93	1795736.5	1940154.9	69
Protein FAM136A [OS=Mus musculus] <sup>a</sup>	Q9CR98	5	-0.11	4.98E-03	0.92	46795.8	50645.9	7
O-acetyl-ADP-ribose deacetylase MACROD1 [OS=Mus musculus]	Q922B1	20	-0.12	9.49E-06	0.92	228717.3	247875.4	28
EH domain-containing protein 4 [OS=Mus musculus] <sup>a</sup>	Q9EQP2	14	-0.13	8.49E-06	0.92	179074.2	195609.8	15
Dystroglycan [OS=Mus musculus]	Q62165	5	-0.14	1.51E-03	0.91	17315.3	19054.6	6
Peroxisiredoxin-5, mitochondrial [OS=Mus musculus]	P99029;-2	15	-0.14	3.71E-03	0.91	2688488.0	2962060.0	26
Mitochondrial import inner membrane translocase subunit TIM44 [OS=Mus musculus]	O35857	10	-0.14	2.32E-03	0.91	36331.5	40140.4	11
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial [OS=Mus musculus]	Q3ULD5	25	-0.15	1.07E-03	0.90	228112.0	252481.9	30
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [OS=Mus musculus]	P62880	4	-0.15	1.83E-02	0.90	40107.8	44575.5	5
Heterogeneous nuclear ribonucleoprotein U [OS=Mus musculus]	Q8VEK3	7	-0.16	2.96E-03	0.90	24624.8	27453.8	11
medium-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Mus musculus]	P45952	38	-0.16	4.07E-03	0.90	3404054.5	3796175.8	65
haloacid dehalogenase-like hydrolase domain-containing protein 2 [OS=Mus musculus]	Q3UGR5-1	4	-0.16	1.18E-02	0.90	49349.2	55088.4	4
Long-chain-fatty-acid-CoA ligase 1 [OS=Mus musculus] <sup>a</sup>	P41216	55	-0.16	2.96E-08	0.89	849570.8	950392.8	73
Hemoglobin subunit beta-2 [OS=Mus musculus]	P02089	6	-0.16	1.58E-04	0.89	16437964.0	18395956.0	13
Long-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Mus musculus] <sup>a</sup>	P51174	36	-0.16	1.65E-02	0.89	4784476.5	5356746.5	58
Heterogeneous nuclear ribonucleoprotein M [OS=Mus musculus]	Q9D0E1;-2	8	-0.16	1.38E-03	0.89	41784.1	46842.8	8
Bifunctional glutamate/proline-tRNA ligase [OS=Mus musculus]	Q8CGC7	14	-0.17	5.65E-03	0.89	61504.2	69178.1	14
Branched-chain-amino-acid aminotransferase, mitochondrial [OS=Mus musculus] <sup>a</sup>	O35855	15	-0.19	4.74E-05	0.88	217851.4	248441.3	19
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial [OS=Mus musculus]	O35459	29	-0.19	5.16E-03	0.87	727510.5	831638.0	44
Dihydrolypoyllysine-residue succinyltransferase comp of 2-oxoglutarate dehydrogenase complex, [OS=Mus musculus]	Q9D2G2-1	28	-0.19	3.66E-03	0.87	2201266.3	2518189.5	38
T-complex protein 1 subunit delta [OS=Mus musculus]	P80315	4	-0.20	4.20E-03	0.87	13949.2	16061.8	4
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial [OS=Mus musculus]	Q9DC70	13	-0.22	6.39E-03	0.86	353860.3	411094.7	17
40S ribosomal protein S11 [OS=Mus musculus]	P62281	2	-0.22	7.82E-04	0.86	13002.6	15128.0	3
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 [OS=Mus musculus] <sup>a</sup>	Q9DCS9	21	-0.22	3.54E-03	0.86	734613.3	856187.3	32
sorting and assembly machinery component 50 homolog [OS=Mus musculus]	Q8BGH2	10	-0.22	1.68E-02	0.86	96777.8	112939.0	11
Acyl-coenzyme A thioesterase 2, mitochondrial [OS=Mus musculus] <sup>a</sup>	Q9QYR9	26	-0.23	1.49E-03	0.85	567183.2	663567.3	35

Laminin subunit beta-1 [OS=Mus musculus]	P02469	14	-0.23	2.37E-03	0.85	171563.8	200856.8	16
fructosamine-3-kinase [OS=Mus musculus]	Q9ER35	2	-0.23	4.66E-03	0.85	26484.9	31151.6	2
EH domain-containing protein 2 [OS=Mus musculus]	Q8BH64	18	-0.23	1.02E-03	0.85	133321.6	156871.3	25
60S ribosomal protein L10-like [OS=Mus musculus]	P86048;Q6ZWW3	5	-0.27	1.63E-05	0.83	65484.8	78754.8	5
adiponectin [OS=Mus musculus]	Q60994	3	-0.28	7.19E-03	0.82	22722.7	27560.4	3
Lon protease homolog, mitochondrial [OS=Mus musculus]	Q8CGK3	19	-0.28	2.78E-03	0.82	175859.7	213585.7	23
40S ribosomal protein S2 [OS=Mus musculus]	P25444	4	-0.29	3.19E-03	0.82	34421.7	41953.7	4
Selenium-binding protein 1 [OS=Mus musculus]	P17563	9	-0.29	5.88E-06	0.82	72690.8	88882.3	10
NAD kinase 2, mitochondrial [OS=Mus musculus];	Q8C5H8-1;-2;-3;-4	2	-0.30	7.84E-03	0.81	4520.9	5569.2	2
Transketolase [OS=Mus musculus]	P40142	9	-0.31	6.82E-03	0.81	20513.9	25462.9	9
C-1-tetrahydrofolate synthase, cytoplasmic [OS=Mus musculus]	Q922D8	3	-0.36	1.64E-02	0.78	5013.7	6419.4	3
Heat shock protein HSP 90-alpha [OS=Mus musculus]	P07901	8	-0.36	1.77E-02	0.78	180191.6	231620.6	11
histone H3.2 [OS=Mus musculus]	P84228	1	-0.36	8.62E-05	0.78	88267.4	113576.8	3
40S ribosomal protein S8 [OS=Mus musculus]	P62242	5	-0.38	1.73E-07	0.77	25016.8	32583.1	6
60S ribosomal protein L7a [OS=Mus musculus]	P12970	8	-0.41	1.73E-02	0.76	16516.1	21871.5	8
60S ribosomal protein L32 [OS=Mus musculus] <sup>a</sup>	P62911	4	-0.42	1.97E-02	0.75	8644.8	11577.0	5
Catenin beta-1 [OS=Mus musculus]	Q02248	5	-0.45	3.71E-03	0.73	9466.7	12930.9	5
Histone H1.0 [OS=Mus musculus]	P10922	5	-0.47	1.44E-05	0.72	23809.3	33064.0	5
60S ribosomal protein L27a [OS=Mus musculus]	P14115	5	-0.48	1.50E-02	0.72	37959.2	52889.9	5
Aspartyl aminopeptidase [OS=Mus musculus]	Q9Z2W0	3	-0.48	9.84E-04	0.72	28783.8	40217.2	3
Histone H1.3 [OS=Mus musculus]	P43277	11	-0.55	8.45E-05	0.68	74064.0	108330.6	16
60S ribosomal protein L7 [OS=Mus musculus]	P14148	6	-0.56	1.81E-02	0.68	9013.1	13247.8	6
histone H4 [OS=Mus musculus] <sup>a</sup>	P62806	11	-0.57	1.65E-09	0.67	1654453.1	2456581.3	16
Alpha-actinin-3 [OS=Mus musculus]	O88990	2	-0.61	1.82E-03	0.66	18781.9	28585.9	3
60S ribosomal protein L14 [OS=Mus musculus]	Q9CR57	3	-0.65	1.88E-03	0.64	10302.6	16135.4	4
40S ribosomal protein S25 [OS=Mus musculus]	P62852	3	-0.69	1.90E-03	0.62	37913.7	60990.8	3
Histone H3.1 [OS=Mus musculus]	P68433	14	-0.69	1.02E-19	0.62	1074207.0	1730754.3	18
Histone H3.3C [OS=Mus musculus];histone H3.3 [OS=Mus musculus]	P02301;P84244	2	-0.72	1.21E-03	0.61	39108.6	64587.5	3
Glutathione reductase, mitochondrial [OS=Mus musculus] <sup>a</sup>	P47791;P47791-2	2	-0.81	6.20E-03	0.57	8223.1	14383.9	2
Myosin-1 [OS=Mus musculus]	Q5SX40	1	-0.83	3.74E-06	0.56	262413.5	465269.9	2
Eukaryotic translation initiation factor 3 subunit I [OS=Mus musculus]	Q9QZD9	3	-0.94	1.96E-02	0.52	3608.7	6943.2	4

n=3 per group analyzed in technical triplicates. Ant [-], average of antagomiR-103/107; Scr [-], average of scrambled control; [-], no unit; Log2 ratio represents the average of the Log2 ratios of the 3 samples per group; <sup>a</sup>, target of miR-103/107 based on TargetScan prediction.