

Table S1. Compositions of Experimental Diets

	CS	BR	WW
Component			
Casein, g	200	157.93	117.49
Corn starch, g	417.486	-	-
Brown rice flour, g	-	434.5	-
Whole wheat flour, g	-	-	547.9
Dextrin, g	132.0	132.0	132.0
Sucrose, g	80.0	80.0	80.0
Soy bean oil, g	70.0	60.9	58.3
Cellulose, g	50.0	38.7	22.4
AIN-93G-MX, g	35.0	35.0	35.0
AIN-93-VX, g	10.0	10.0	10.0
L-Cysteine, g	3.0	3.0	3.0
t-BHQ, g	0.014	0.014	0.014
Choline bitartrate, g	2.5	2.5	2.5
Total mass, g	1000	954.510	1008.612
Content			
Protein, g	182.8	182.8	182.8
Total fat, g	70.7	70.7	70.7
Carbohydrate, g	569.7	569.7	569.7
Dietary fiber, g	54.93	54.93	54.93
Soluble Fiber, g	0.13	3.87	6.74
Insoluble Fiber, g	54.80	51.06	48.19
Starch, g	347.2	347.2	347.2
Energy			
Protein, kcal, %	731, 20%	731, 20%	731, 20%
Total fat, kcal (%)	636, 17%	636, 17%	636, 17%
Carbohydrate, kcal, %	2279, 63%	2279, 63%	2279, 63%
Total energy, kcal	3646	3646	3646
Caloric density, kcal/g	3.646	3.820	3.615

Table S2. Primer Sequences for qRT-PCR

Gene	Sense Sequence (5' → 3')	Antisense Sequence (5' → 3')
miR-27a-3p-RT	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGGCGGAACT	
U6-RT	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAAAATATG	
miR-27a-3p	ACACTCCAGCTGGGTTACAGTGGCTA	CTCAAGTGTCGTGGAGTCGGCAA
U6	ACACTCCAGCTGGGCGCAAATTCGTGAAGC	CTCAAGTGTCGTGGAGTCGGCAA
HMGCR	AGCTTGCCCGAATTGTATGTG	TCTGTTGTGAACCATGTGACTTC
FASN	GGAGGTGGTGATAGCCGGTAT	TGGGTAATCCATAGAGCCCAG
GAPDH	ACATCATCCCTGCATCCACT	GTCCTCAGTGTAGCCCAAG

Table S3. The KEGG Pathway Analysis of Differentially Expressed MiRNAs

KEGG pathway	<i>p</i> -value	genes	miRNAs
Prion diseases	<1e-325	1	1
Mucin type O-Glycan biosynthesis	1.11E-16	11	4
Fatty acid biosynthesis	1.06E-06	1	1
Hippo signaling pathway	0.000113013	24	3
Proteoglycans in cancer	0.000178006	49	3
Lysine degradation	0.002269397	14	4
Axon guidance	0.002277791	26	3
Adrenergic signaling in cardiomyocytes	0.005772829	6	1
MAPK signaling pathway	0.00788276	76	4
Gap junction	0.009062834	5	3
Fatty acid metabolism	0.01199174	6	2
ErbB signaling pathway	0.01333858	26	3
Phosphatidylinositol signaling system	0.01470084	23	4
Amphetamine addiction	0.02234281	16	3
mTOR signaling pathway	0.03044699	17	2
Thyroid hormone synthesis	0.04628612	7	2

The KEGG pathway of screened 16 miRNAs was analyzed by DIANA-miRPath v3.0, using “pathways union”, microT-CDS (*P*-value threshold 0.05, microT threshold 0.7, Fisher’s exact test (Hypergeometric distribution)) and FDR correction.

Table S4. The GO Category Analysis of Differentially Expressed MiRNAs

GO category	<i>p</i>-value	genes	miRNAs
Nucleic acid binding transcription factor activity	0	280	8
Chromosome organization	0	202	8
Cell motility	0	218	9
Cellular protein modification process	0	782	10
Biosynthetic process	0	1073	10
Anatomical structure formation involved in morphogenesis	0	308	11
Cell morphogenesis	0	271	12
Cellular_component	0	5636	13
Cellular nitrogen compound metabolic process	0	1384	13
Embryo development	0	412	14
Ion binding	0	2085	14
Molecular_function	0	5938	15
Biological_process	0	6076	15
Organelle	0	3212	15
Intracellular	0	3840	16
Cell	0	4427	16
Cell differentiation	0	1080	16
Anatomical structure development	0	1472	16
Nuclear chromosome	3.46E-08	72	5
Developmental maturation	1.95E-07	58	6
Cell division	1.77E-05	132	4
Growth	2.20E-05	96	4
Homeostatic process	8.41E-05	116	2
Cell cycle	0.002369	196	4
Chromosome	0.007266	78	2
Cytoskeleton organization	0.007573	84	2
Cytoskeleton	0.077962	161	2
Protein complex	0.079994	273	1
Cellular component assembly	0.312578	77	1

Protein binding transcription factor activity	0.160368	37	1
Cytoplasmic membrane-bounded vesicle	0.530892	29	1
Positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.565781	7	2
Transcription, DNA-templated	0.715054	74	1
Positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	0.809769	2	1
Positive regulation of cytoplasmic mRNA processing body assembly	0.871556	4	1
Positive regulation of transcription, DNA-templated	0.893988	34	1
Nucleoplasm	0.917562	89	1
Micro-ribonucleoprotein complex	0.929023	4	1
Poly(A)-specific ribonuclease activity	0.96335	5	1
Golgi to lysosome transport	0.975785	3	1
Behavioral fear response	0.991812	11	1
Nuclear speck	0.993689	11	1
High voltage-gated calcium channel activity	0.997613	4	1
Positive regulation of neuron migration	0.998684	3	1
Positive regulation of NIK/NF-kappaB signaling	0.998739	3	1
Positive regulation of cellular senescence	0.999209	3	1
Positive regulation of natural killer cell degranulation	0.999394	2	1
Response to osmotic stress	0.99946	2	1
Regulation of aldosterone metabolic process	0.999986	1	1
Mitral valve morphogenesis	0.999602	3	1
Oncogene-induced cell senescence	0.999953	3	1

Eye blink reflex	0.999986	1	1
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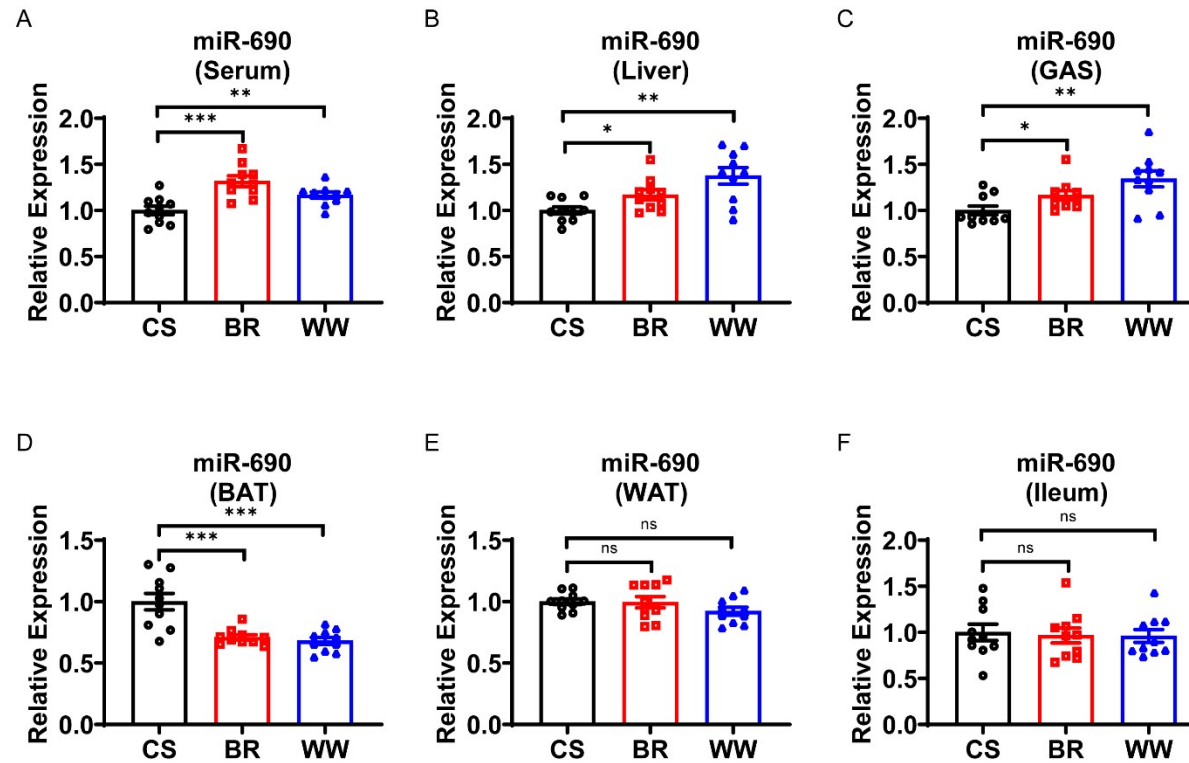
The GO enrichment of screened 16 miRNAs was analyzed by DIANA-miRPath v3.0, using “categories union”, microT-CDS (*P*-value threshold 0.05, microT threshold 0.7, Fisher’s exact test (Hypergeometric distribution)) and FDR correction.

Table S5 The GO Category Analysis of MiR-27a-3p

GO Category	<i>p</i> -value	Genes
Cell	1.79E-244	1088
Intracellular	2.49E-98	942
Anatomical structure development	2.82E-70	412
Cell differentiation	6.86E-39	307
BCiological_process	1.22E-33	1522
Ion binding	3.36E-26	575
Embryo development	1.21E-24	124
Molecular_function	7.80E-19	1499
Organelle	3.01E-14	792
Anatomical structure formation involved in morphogenesis	4.81E-14	98
Cell morphogenesis	6.27E-14	90
Chromosome organization	1.36E-11	73
Cellular protein modification process	1.90E-11	228
Growth	3.65E-07	58
Nucleic acid binding transcription factor activity	6.22E-07	105
Cellular nitrogen compound metabolic process	1.23E-06	372
biosynthetic process	1.46E-05	325
Cell motility	4.70E-05	67
Cellular_component	0.002310799	1445
Developmental maturation	0.013205738	19
Positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.021676564	7
Cell division	0.034732922	49
Nuclear chromosome	0.047887641	25

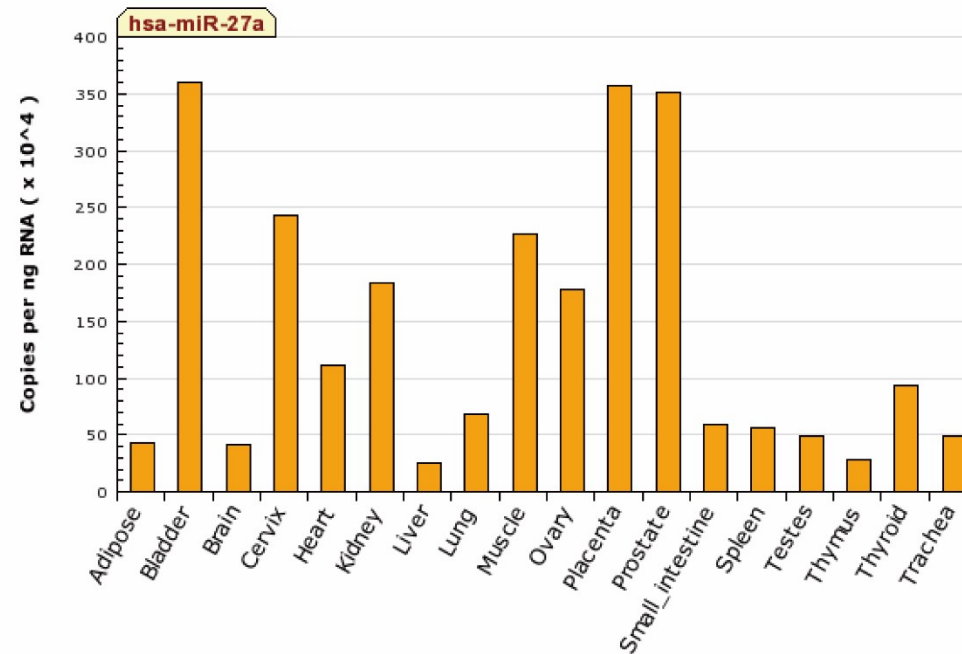
The GO enrichment of miR-27a-3p was analyzed by DIANA-miRPath v3.0, using “categories union”, microT-CDS (*P*-value threshold 0.05, microT threshold 0.7, Fisher’s exact test (Hypergeometric distribution)) and FDR correction.

Figure S1. The Different Expressions of MiR-690 in Different Tissues with the Treatment of Whole Grain Diets.



The different levels of miR-690 in serum (A), liver (B), GAS (C), BAT (D), WAT (E) and ileum (F) were analyzed by qRT-PCR in mice. Data are expressed as the mean \pm SD, $n=10$. * $p < 0.05$ versus CS, ** $p < 0.01$ versus CS; *** $p < 0.001$ versus CS; ns, no significant (Student's t-test). CS: corn starch group; BR: brown rice group; WW: whole wheat group.

Figure S2. The Relative Levels of Has-miR-27a-3p in Different Tissues



The relative levels of miR-27a-3p were calculated and distributed in different human tissues using online database-miRNAMap (<http://mirnamap.mbc.nctu.edu.tw/>), which integrated two data sets of miRNA expression profiles, which were obtained by different experimental methods including quantitative polymerase chain reaction and miRNA-bead array.

Figure S3. Uncropped Scans of the Western Blots Shown in Figures as Indicated.

Fig. 6D HMGCR



Fig. 6D FASN

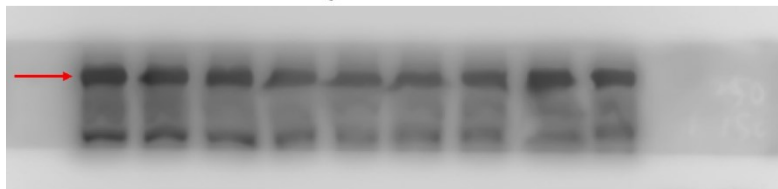


Fig. 6D GAPDH



Fig. 6G HMGCR

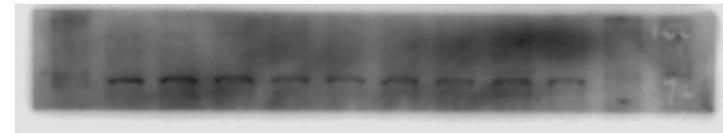


Fig. 6G FASN



Fig. 6G GAPDH

