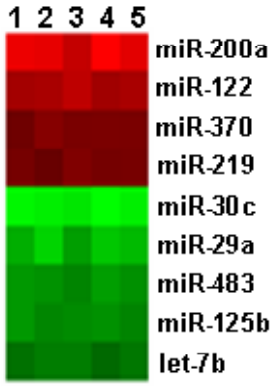
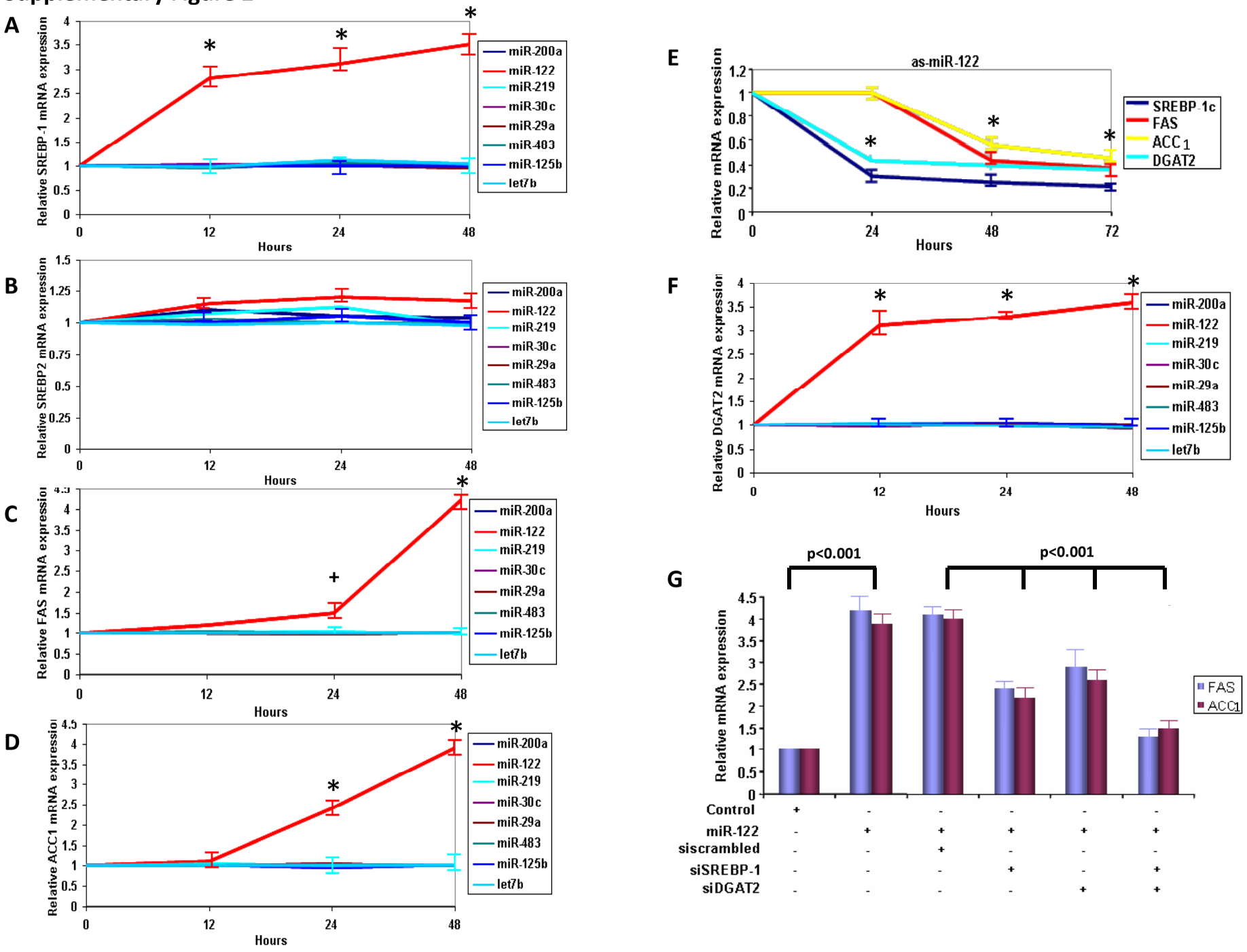
Supplementary Figure 1



Suppl. Figure 1. MicroRNA TaqMan array analysis of hepatic RNA obtained from five dn-cJun-treated mice *vs.* five control mice.

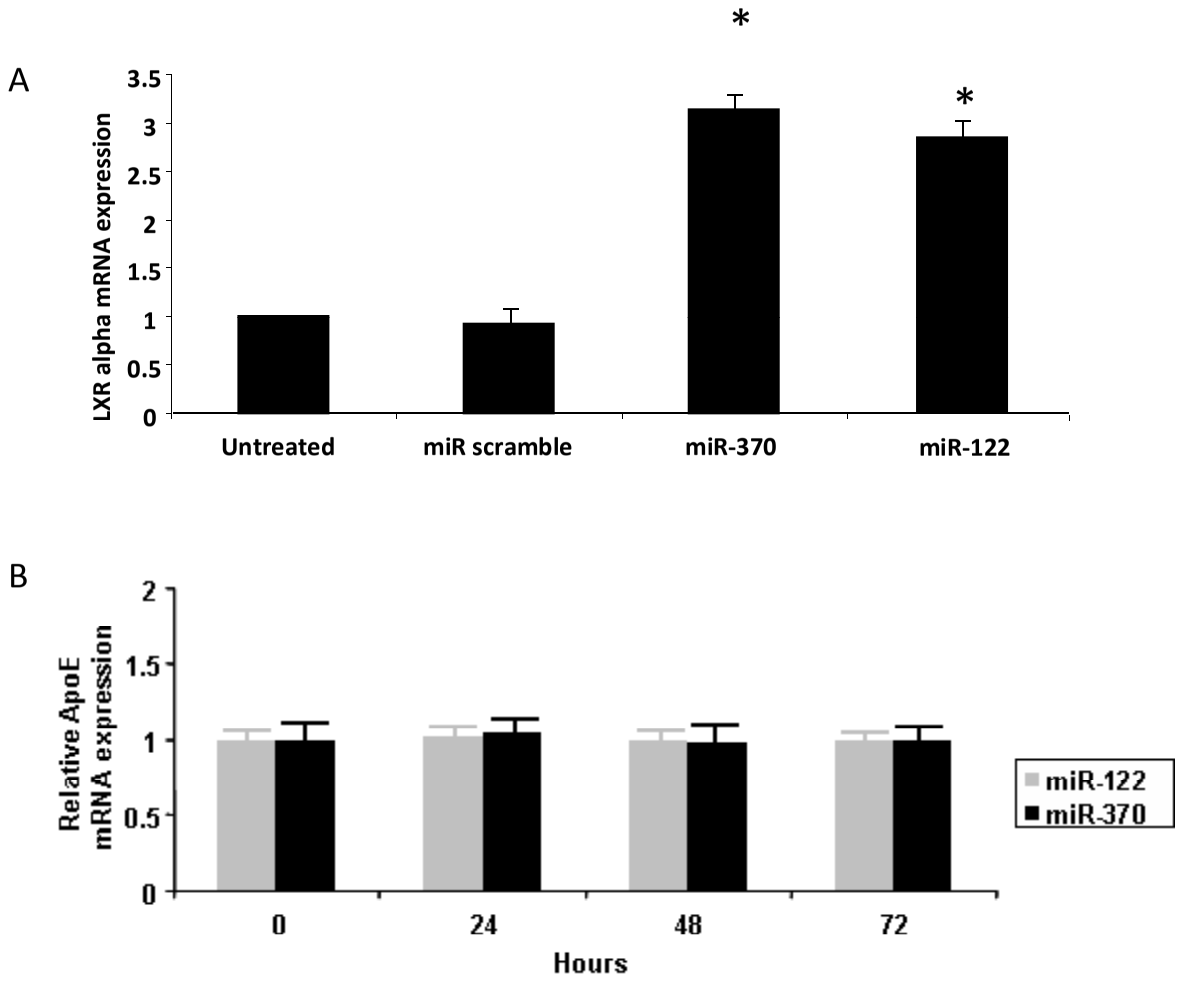
Supplementary Figure 2



Legend, Supplementary Figure 2

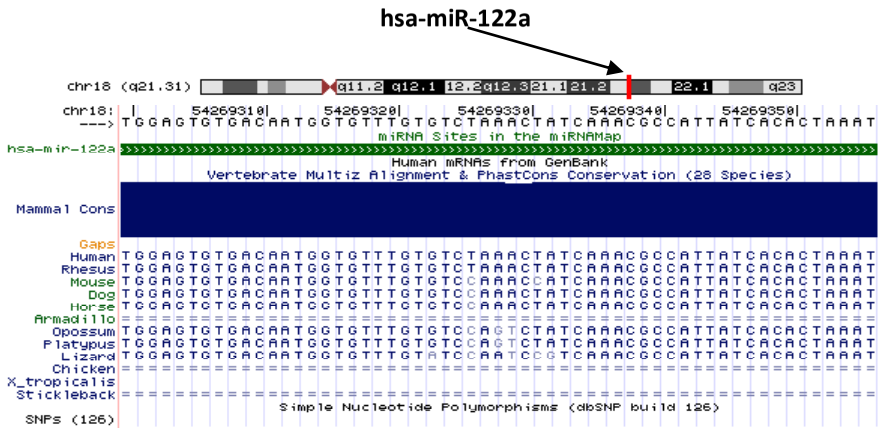
Suppl. Figure 2. Modulation of expression of specific microRNAs affects genes involved in hepatic lipogenesis in HepG2 cells. Real-time PCR analysis of **(A)**, SREBP-1c; **(B)**, SREBP2; **(C)**, FAS; **(D)**, ACC-1; **(E)**, DGAT2 mRNA after liposomal transfection of HepG2 cells with several microRNAs (miR-29a, miR-30c, miR-122, miR-125b, miR-200a, miR-219, miR-483, let7b). The figure shows that miR-122 affects SREBP-1, FAS, DGAT2 and ACC-1 but not SREBP-2 gene expression. SREBP-1 and DGAT2 respond early (starting 12h post-transfection), while FAS and ACC-1 respond later (starting 24h post-transfection) in miR-122 overexpression. **(F)**: Real-time PCR analysis of SREBP-1c, FAS, ACC1 and DGAT2 after antagomiR liposomal transfection (50nM) for inhibition of miR-122 in HepG2 cells. **(G)**: Real-time PCR analysis of FAS and ACC1 genes after treatment of HepG2 cells with miR-122 and downregulation of SREBP-1c or DGAT2, or both, by treatment with the corresponding siRNA (50 nM0 for 48 h. The figure indicates that regulation of SREBP-1c and DGAT2 by miR-122 precedes the regulation of FAS and ACC1 genes.

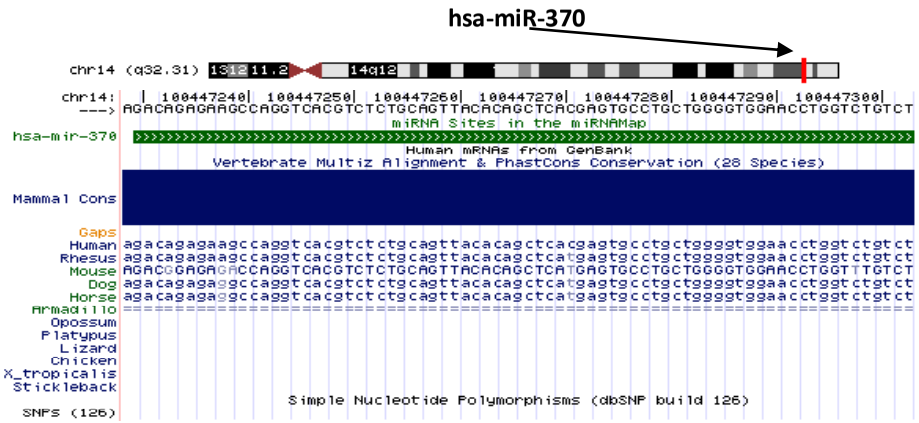
Supplementary Figure 3



Supplementary Figure 3A,B. ***Effect of miR-122 on the expression of LXRα and of miR-122 and miR-370 on the expression of apoE in HepG2 cells.*** (*A*) Real-time PCR analysis of LXRα mRNA levels 24 h after liposome transfection of HepG2 with miR-122 or miR-370. The experiment has been performed in triplicate and data represent mean ± SD. The analysis showed the miR-370 and miR-122 increased 3.2- and 3-fold respectively the expression of LXRα. (*B*) Real-time PCR analysis of apoE mRNA 72h after liposomal transfection (50nM) of HepG2 with miR-122 or miR-370. The analysis established that miR-122 and miR-370 have no effect on apoE gene expression.

Supplementary Figure 4





microRNA	hsa-miR-122a
Gene location	chr18:54269285-54269370
Exon/Intron/UTR	intergenic
Precursor	85 nt
Mature sequence	5'- UGGAGUGUGACAAUGGUGUUUGU -3'
Target genes related to lipid metabolism	None

microRNA	hsa-miR-370
Gene location	chr14:100447228-100447303
Exon/Intron/UTR	intronic
Precursor	75 nt
Mature sequence	5'- GCCUGCUGGGGUGGAACCUGG -3'
Target genes related to lipid metabolism	Cpt1

Suppl. Figure 4. miR-122a and miR-370 genomic location information and gene target prediction. Using Ensembl database (www.ensembl.org) we obtained genomic information on miR-122a and miR-370. The figure shows the gene location, the location of a microRNA on the gene structure, the length of the precursor molecule and the mature sequence of the microRNA. In order to predict specific and direct gene target of miR-122 and miR-370 we used the following criteria: **I)** The target gene must be predicted by 2/3 prediction algorithms (Sanger, PicTar, TargetScan);) **II)**Target genes should be related with lipid metabolism. Using these criteria, we did not detect any direct predicted gene target for miR-122. This result suggests the absence of miR-122 direct target related to fatty acid and triglyceride biosynthesis or the available algorithms are still insufficient to capture the breadth of microRNA gene networks. Using the same criteria, we found that miR-370 potentially targets (chr11:68281006-68281030 position), which corresponds to carnitine palmitoyl transferase (Cpt1α) (see Fig. 4A).