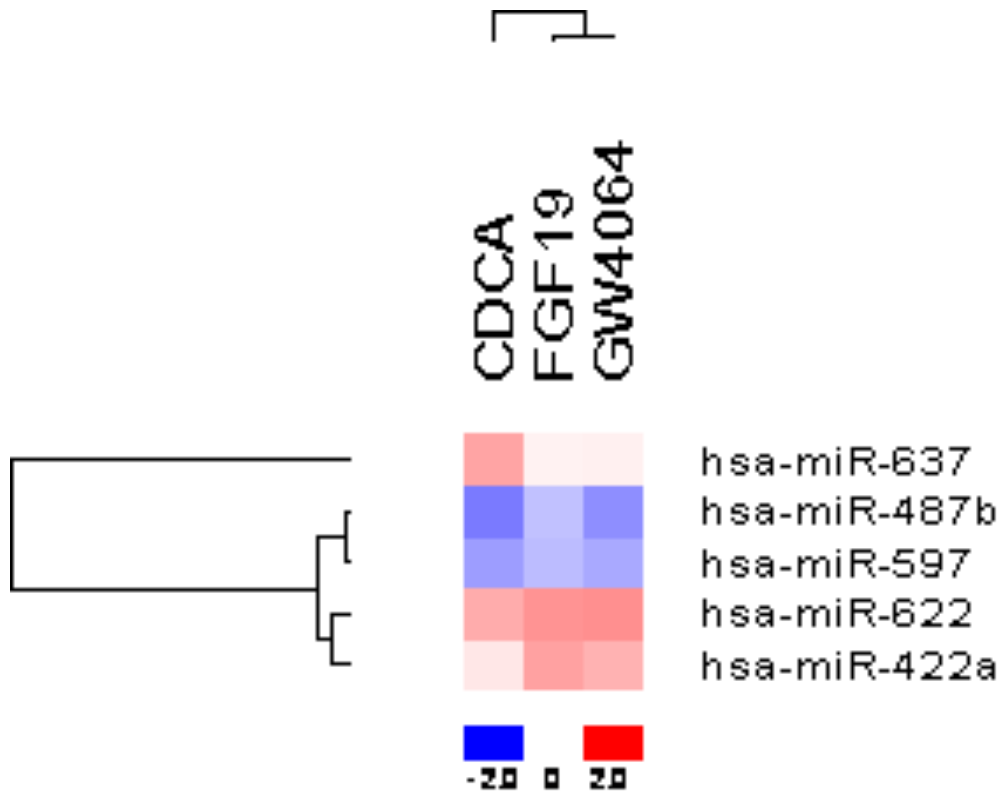


Supplemental Figure 1



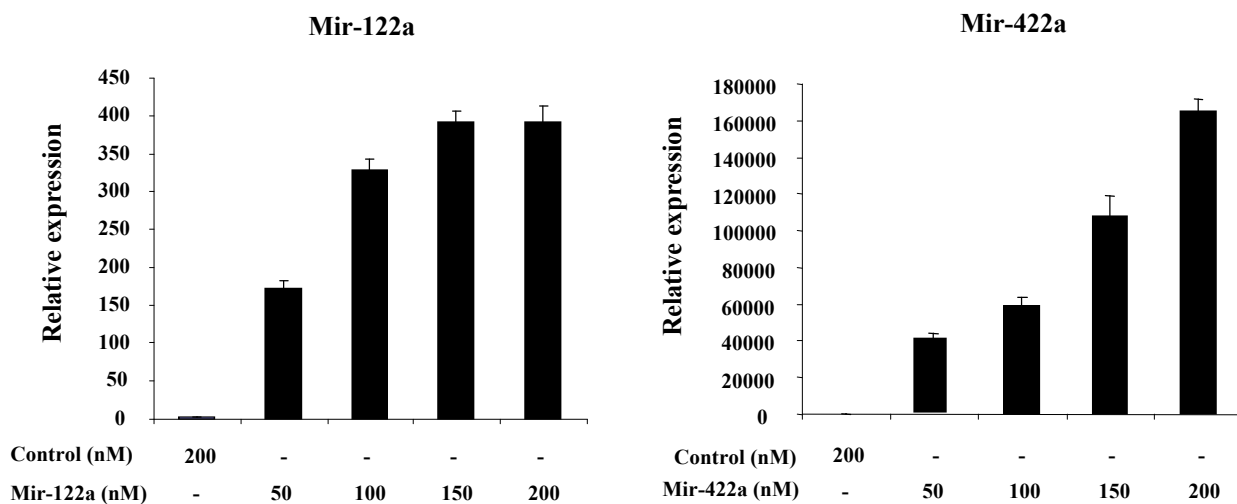
Supplemental Fig. 1. Heat Map and Unsupervised Hierarchical Clustering. The heat map diagram shows the result of the two-way hierarchical clustering of miRNAs and samples. Each row represents a miRNA and each column represents a sample. The miRNA clustering tree is shown on the left, and the sample clustering tree appears at the top. The color scale shown at the bottom illustrates the relative expression level of a miRNA across all samples: red color represents an expression level above mean, blue color represents expression lower than the mean. Gray color means that the specific miRNA on a given slide has been flagged (i.e. the signal is below background).

Supplementary Figure 2

	PHHs	HepG2	Huh7
Mir-122a	21.45±0.49	34.98±0.62	28.12±0.12
Mir-422a	29.31±0.24	32.83±0.28	30.43±0.17
RNU48	20.60±0.16	20.84±0.14	19.73±0.16
CYP7A1	32.52±2.60	30.07±0.05	39.25±0.95
CYP8B1	25.86±0.52	28.71±0.25	33.19±0.17
SHP	24.29±0.52	21.40±0.05	24.31±0.26
HNF4	24.53±0.41	23.50±0.05	24.85±0.16
FXR	24.21±1.48	27.00±0.11	21.93±0.27
FGF19	30.67±2.25	32.60±0.35	22.18±0.26
FGFR4	24.98±0.95	19.10±0.26	20.07±0.11
βklotho	28.23±2.01	25.38±0.07	25.27±0.05
UBC	20.18±0.15	20.01±0.02	19.91±0.24

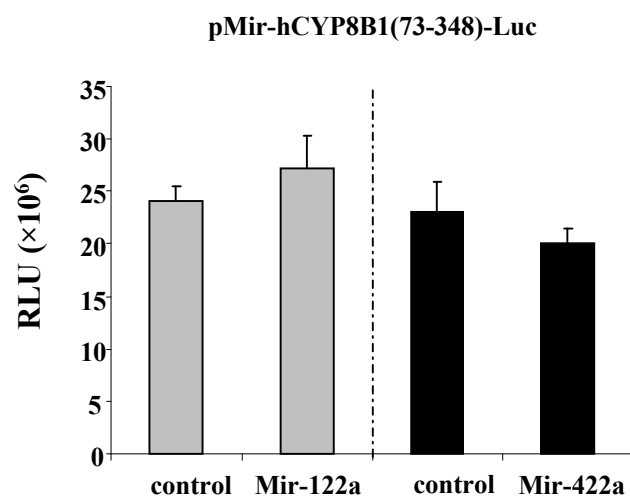
Supplementary Figure 2. Quantitative real time PCR analysis of microRNAs and mRNA expression levels of CYP7A1, CYP8B1, nuclear receptors, FGF19, FGFR4 and β klotho in human primary hepatocytes, HepG2 and Huh7 cells. The Ct value means the number of PCR cycles where the reporter dye signal is sufficiently high to cross an automatically or manually determined threshold value. The earlier the signal passes the threshold value, the higher is the expression of that gene in that sample. In a standard setup 40 cycles are run.

Supplemental Figure 3



Supplementary Figure 3. Quantitative real time PCR analysis of microRNAs mir-122a and mir-422a in transfected HepG2 cells. HepG2 cells were transfected with control miRNA or increasing dose of mir-122a-mimic or mir-422a-mimic as indicated for 48 hr. total RNA was isolated for real time PCR detection of mir-122a and mir-422a levels. Results of triplicate assays are expressed as mean \pm SD.

Supplemental Fig 4



Supplemental Fig 4: Effect of miR-122a-mimic and miR-422a-mimic on CYP8B1 3'-UTR reporter activity. A Luciferase reporter plasmid pMir-hCYP8B1 (73-348)-Luc containing the putative miR-422a target sequence inserted downstream of the luciferase gene was used for reporter assays. Reporter activities were assayed in HepG2 cells transfected with 50 nM miR-122a-mimic (Mir-122a) or miR-422a-mimic (Mir-422a) or their respective negative control (Control). All experiments were done in triplicates and data represent the mean \pm SD of three individual experiments.