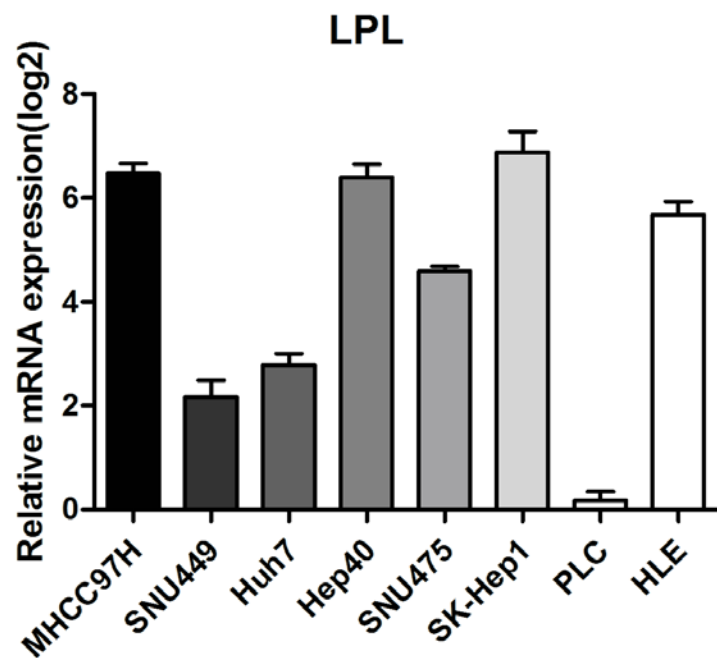
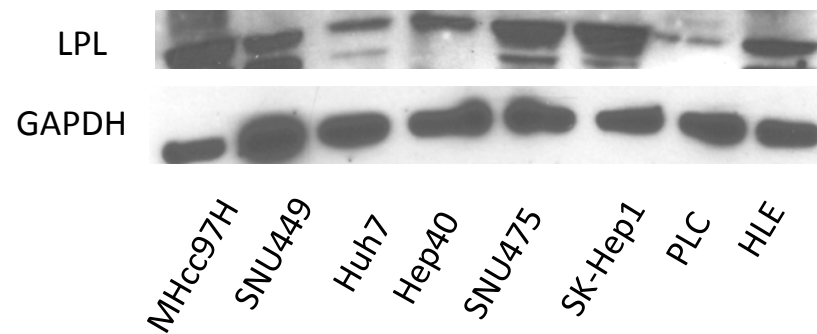
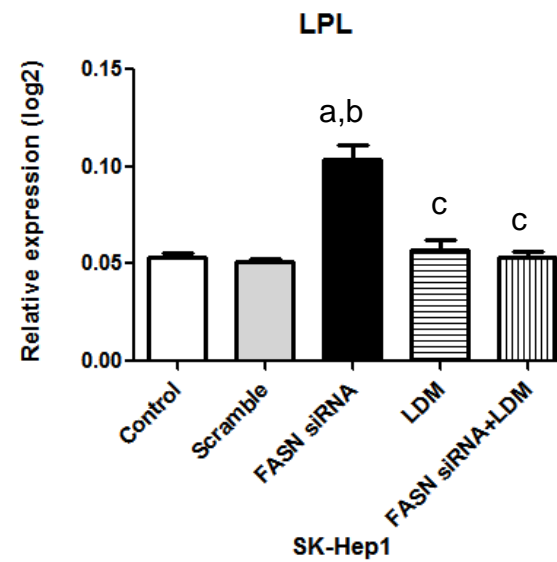
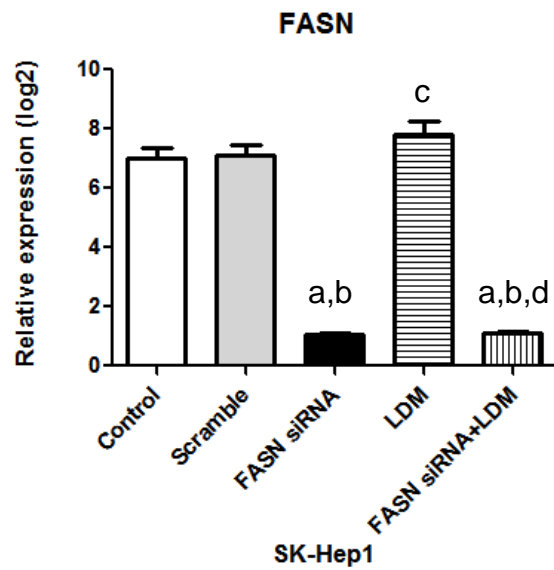


Supplementary Figure 1. Expression of LPL in surrounding non-tumor tissues (S) and HCC samples from a HCC collection, as detected by microarray. Data were retrieved from TCGA (S, n=59; HCC, n=374) and Fudan (S, n=239; HCC, n=247) databases. *** p<0.001.

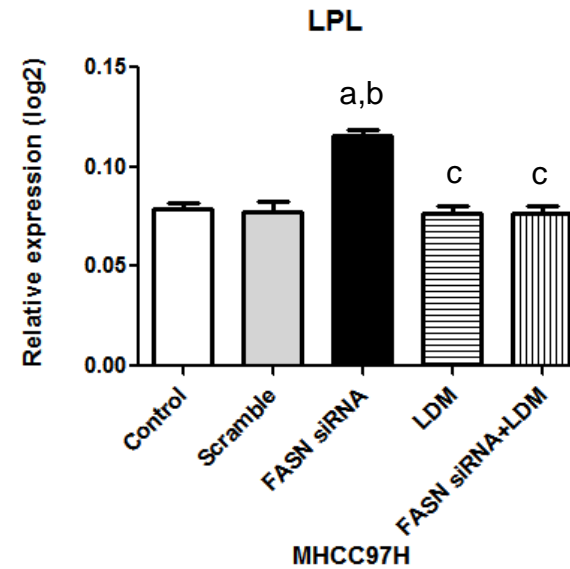
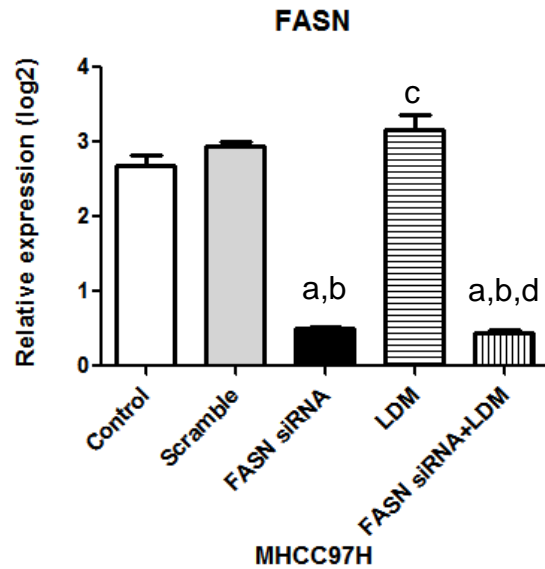
A**B**

Supplementary Figure 2. Levels of *LPL* mRNA (A) and protein (B) expression in human HCC cell lines, as determined by qRT-PCR analysis or Western blotting.

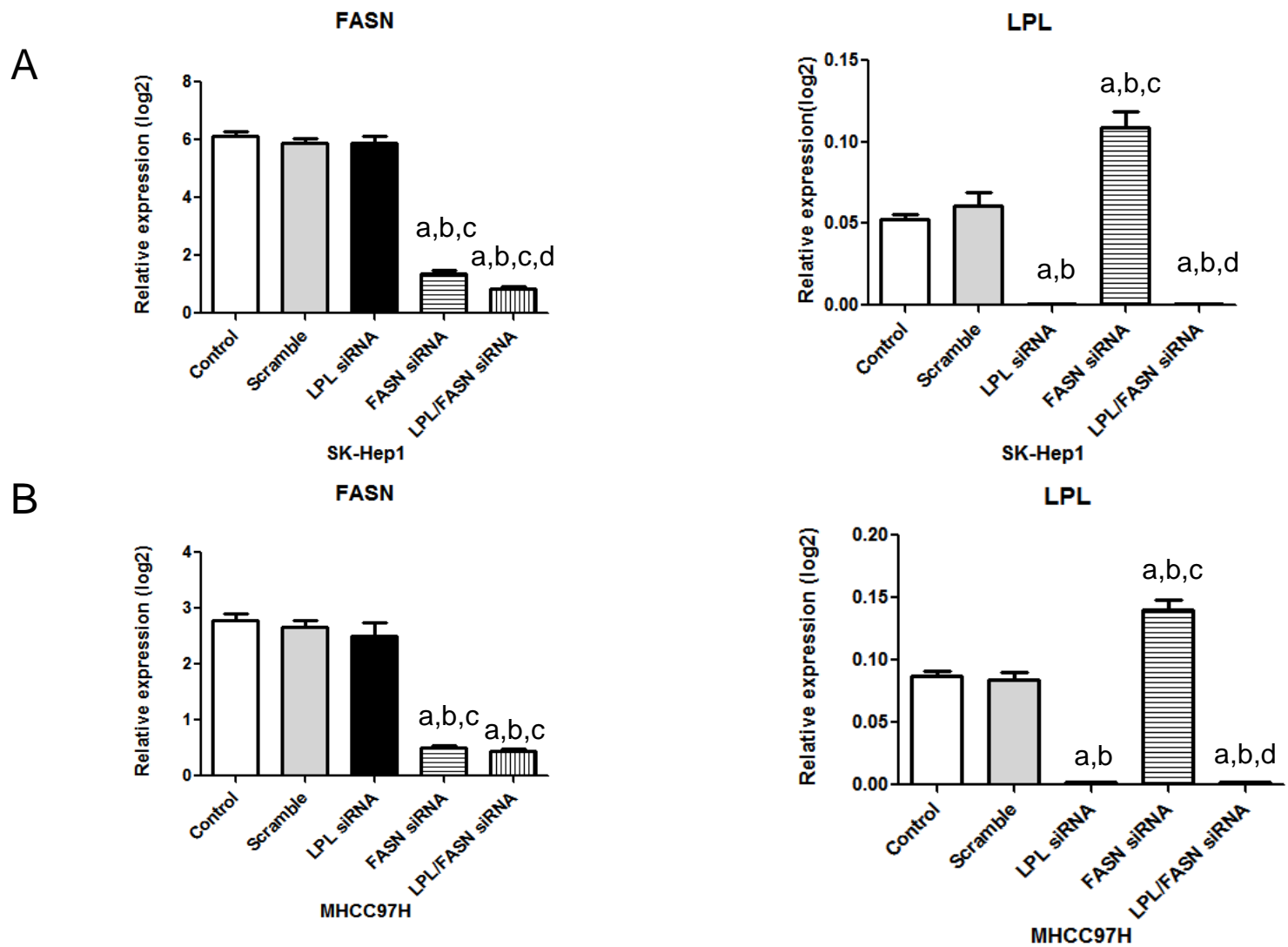
A



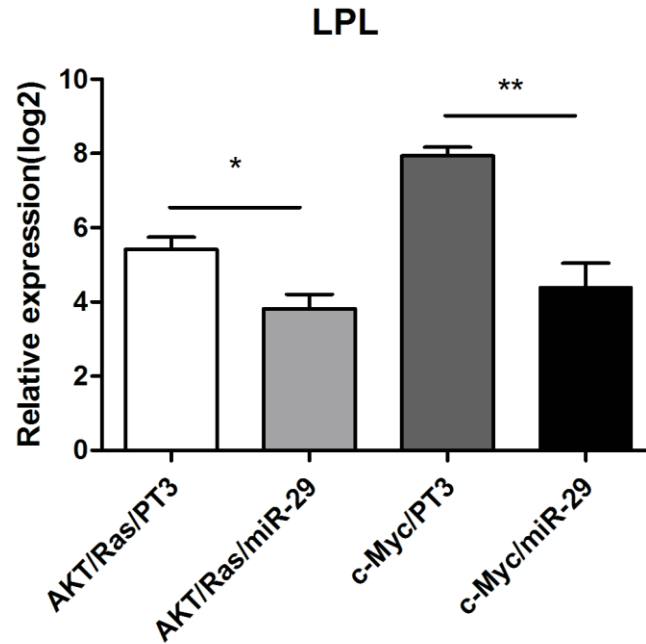
B



Supplementary Figure 3. qRT-PCR analysis of FASN (left) and LPL (right) expression in control, scramble siRNA, FASN siRNA, LDM or FASN siRNA+LDM treated SK-Hep1 (A) or MHCC97H (B) human HCC cell lines. $P < 0.05$, a: vs control; b: vs scramble siRNA; c: vs FASN siRNA; d: vs FASN LDM.



Supplementary Figure 4. qRT-PCR analysis of FASN (left) and LPL (right) expression in control, scramble siRNA, LPL siRNA, FASN siRNA, or LPL/FASN siRNA treated SK-Hep1 (A) or MHCC97H (B) human HCC cell lines. $P < 0.05$, a: vs control; b: vs scramble siRNA; c: vs LPL siRNA; d: vs FASN siRNA.



Supplementary Figure 5. *LPL* mRNA expression is significantly downregulated in cMyc/miR29 and AKT/Ras/miR29 liver tumor samples when compared to c-Myc/pT3 and AKT/Ras/pT3 liver tumors; n=5 in each group. Δ Ct value of each sample was calculated by subtracting the average Ct value of *LPL* gene from the average Ct value of the *18S rRNA* gene. Tukey Kramer's test: *P < 0.05 and **P < 0.01