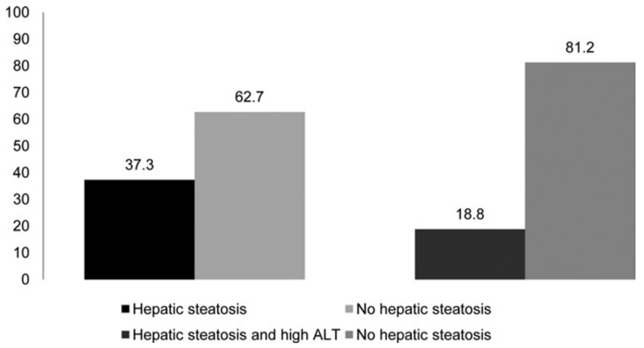
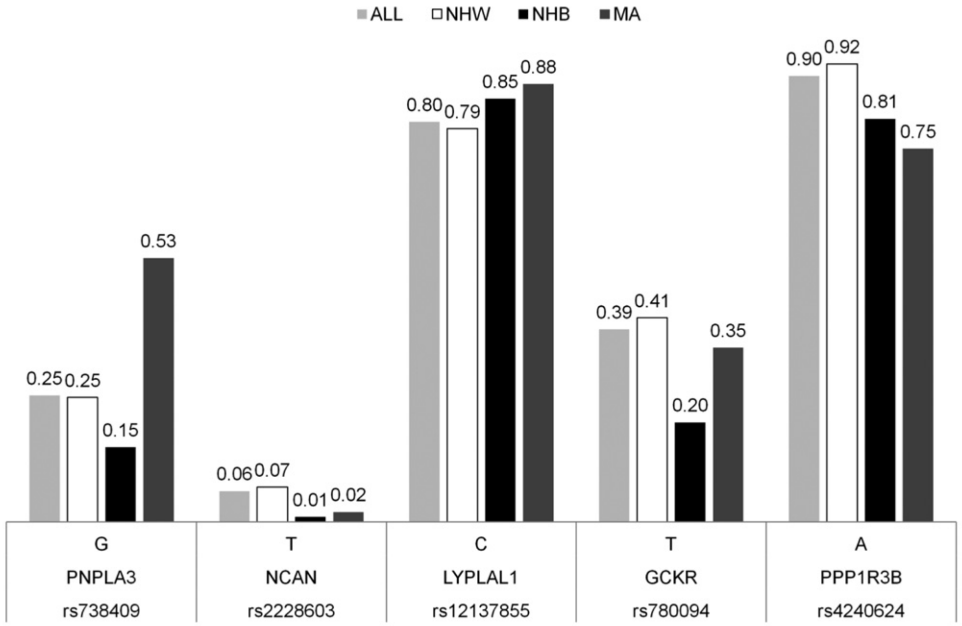
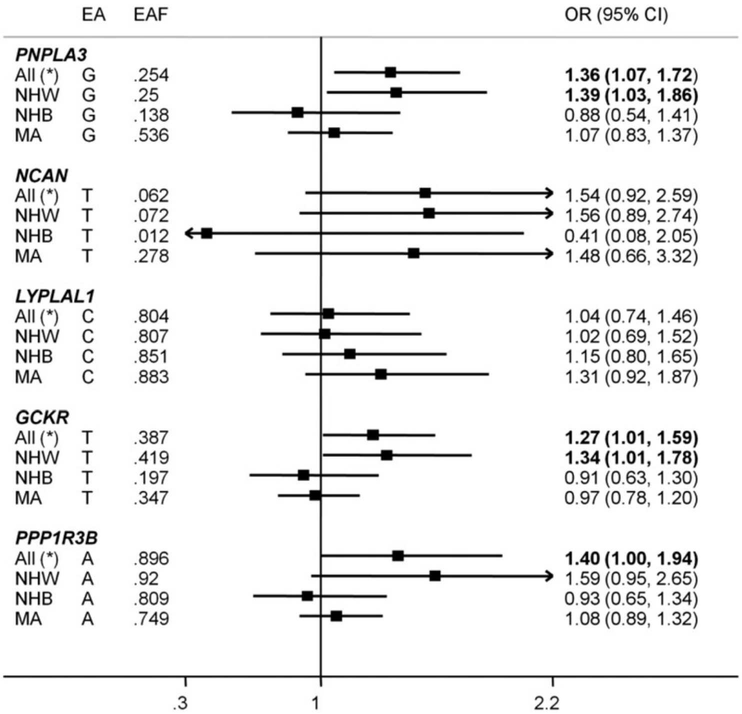


Supplementary Figure 1. Weighted liver phenotypes prevalence in the analytical sample of NHANES III (1991–1994).



PNPLA3: patatin-like phospholipase domain-containing protein 3 (HUGO Gene Nomenclature Committee, HGNC: 18590); *NCAN*: neurocan (HGNC: 2465); *LYPLAL1*: lysophospholipase-like 1 (HGNC: 20440); *GCKR*: glucokinase regulatory protein (HGNC: 4196); *PPP1R3B*: protein phosphatase 1, regulatory subunit 3b (HGNC: 14942). NHW: non -Hispanic White; NHB: non -Hispanic Black and MA: Mexican -American; ALL= NHW+NHB+MA

Supplementary Figure 2. Weighted allele prevalence in the analytical sample of NHANES III (1991–1994), by race/ethnicity.



EA: Effect allele; EAF: effect allele frequency; OR: Odds ratio; CI: confidence interval; *PNPLA3*: patatin-like phospholipase domain-containing protein 3 (HUGO Gene Nomenclature Committee, HGNC: 18590); *NCAN*: neurocan (HGNC: 2465); *LYPLAL1*: lysophospholipase-like 1 (HGNC: 20440); *GCKR*: glucokinase regulatory protein (HGNC: 4196); *PPP1R3B*: protein phosphatase 1, regulatory subunit 3b (HGNC: 14942). NHW: non -Hispanic White; NHB: non -Hispanic Black and MA: Mexican - American; (*) ALL= NHW+NHB+MA

Supplementary Figure 3. Association between high ALT level (>30 U/L in men or >19 U/L in women) and different SNPs, stratified by ethnicity in the NHANES III (1991–1994), population-weighted, additive model, adjusted for age, age squared, sex, and alcohol consumption.

Supplementary Table 1. Multivariate Analyses for Each Genetics of Obesity-related Liver Disease Consortium SNP in 4804 NHANES III Participants for Effects on AST/ALT Ratio, Weighted

			All[a]		NHW		NHB		MA	
SNP ID	Nearest	EA	Effect (SE)	*P* value	Effect (SE)	*P* value	Effect (SE)	*P* value	Effect (SE)	*P* value
rs738409	*PNPLA3*	G	−0.02 (0.05)	.69	0.01 (0.07)	.89	−0.03 (0.06)	.59	0.06 (0.04)	.14
rs2228603	*NCAN*	T	−0.08 (0.04)	.06	−0.09 (0.07)	.17	0.53 (0.14)	**<.01**	−0.14 (0.11)	.20
rs12137855	*LYPLAL1*	C	0.04 (0.04)	.32	0.04 (0.04)	.31	−0.05 (0.03)	.09	0.13 (0.06)	**.04**
rs780094	*GCKR*	T	0.01 (0.03)	.87	0.02 (0.04)	.60	−0.01 (0.03)	.86	0.06 (0.05)	.21
rs4240624	*PPP1R3B*	A	−0.09 (0.03)	**.01**	−0.12 (0.05)	**.03**	−0.01 (0.05)	.81	−0.07 (0.04)	.13

EA, effect allele; effect, increase in inverse normalized ALT/AST; SE, standard error; PNPLA3: HUGO Gene Nomenclature Committee (HGNC), 18590; NCAN: HGNC, 2465; LYPLAL1: HGNC, 20440; GCKR: HGNC, 4196; PPP1R3B: HGNC, 14942.

[a]All = NHW + NHB + MA.