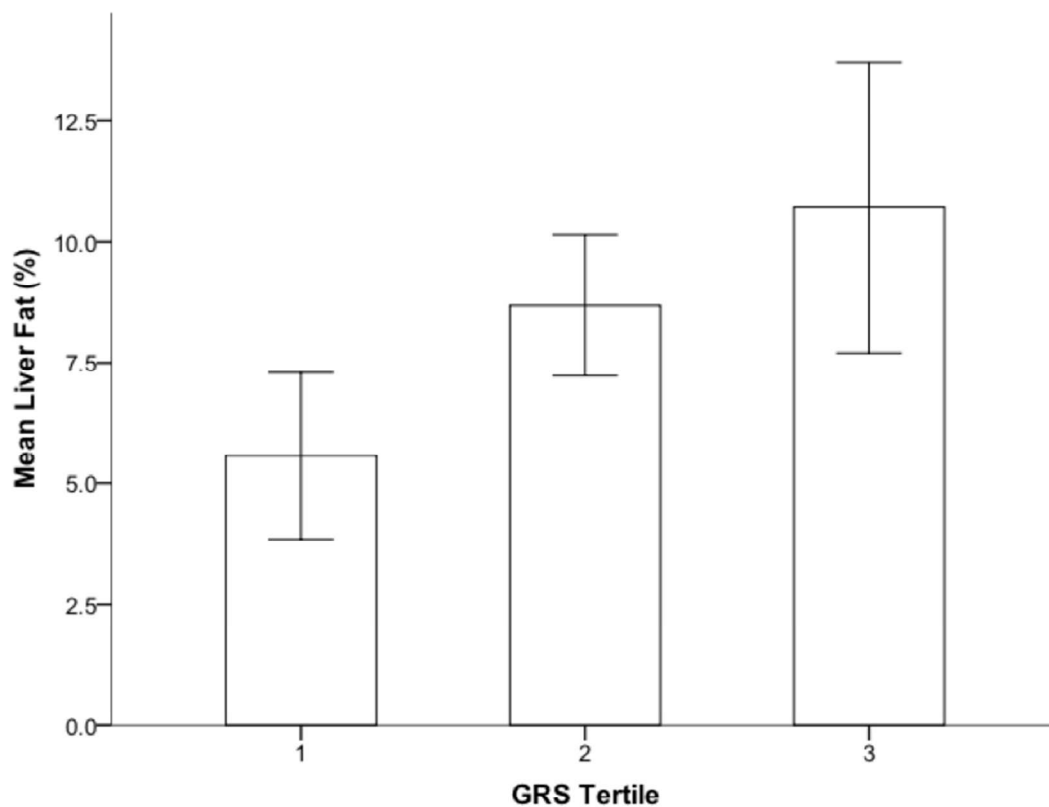


Supplemental Material:**Supplemental Figure 1. Combined genetic effects six SNPs on liver fat content.**

Comprehensive 6-SNP GRS tertile category (1-3) is shown along the x-axis and mean liver fat is plotted on the y-axis. The comprehensive GRS was based on tertiles of risk alleles (T1=0-3, n=22; T2= 4-6, n=143; and T3=7-9, n=44) and tested for an association with liver fat. Mean liver fat was not significantly increased as a function of comprehensive GRS ($p_{\text{trend}}=0.08$).



Supplemental Table 1. Power calculation for six SNPs previously associated with liver fat content.

Gene	SNP ID	Effect _{Palmer}	EAF _{Walker}	n _{Required}
<i>PNPLA3</i>	rs738409	0.28†	0.52	94
<i>PPP1R3B</i>	rs4240624	0.15†	0.67	392
<i>NCAN</i>	rs2228603	0.27†	0.03	891
<i>GCKR</i>	rs780094	0.10†	0.32	901
<i>LYPLAL1</i>	rs12137855	0.07†	0.92	5328

Assuming 80% power, an α -error of 0.05, and the observed allele frequencies in our Hispanic study population (EAF_{Walker}), our sample size was sufficient to detect a significant association with *PNPLA3* utilizing regression coefficients from Palmer et al.¹ (†=Effect_{Palmer}). However, there was insufficient power to detect association of liver fat content with the *GCKR*, *LYPLAL1*, *NCAN*, and *PPP1R3B* variants in our study population. EAF=effect allele frequency. Calculations performed in Quanto Ver 1.2.4.

References:

1. Palmer ND, Musani SK, Yerges-Armstrong LM, Feitosa MF, Bielak LF, Hernaez R et al. Characterization of European-ancestry NAFLD-associated Variants in individuals of African and Hispanic descent. *Hepatology*. 2013 Apr 8. doi: 10.1002/hep.26440. [Epub ahead of print]