

668 variants in HDL genes that passed quality filtering

Known variants



Novel or rare variants (MAF<1% in 1000 Genomes and <4% in study samples) in gene known to cause high or low HDL-C

“Disease-causing” (DM) for high or low HDL-C in HGMD

Nonsense, indel, splice site

Missense

PATHOGENIC  
(n=18)

Predicted deleterious by all of:  
SIFT, Polyphen 2 [HumDiv], Polyphen 2 [HumVar], PROVEAN and Condel

PROBABLY PATHOGENIC  
(n=17)

**Supplemental Figure 1.** Prioritization approach to variants identified in this study.