- Our first experiment attempted to answer whether genes in a disease-relevant LV could represent potential therapeutic targets.	+ We conducted a gene co-expression analysis to identify potential therapeutic targets for lipid regulation ([Methods](#sec:methods:coexp)).
- For this, the first step was to obtain a set of genes strongly associated with a phenotype of interest.	+ This analysis revealed two clusters of genes associated with lipid regulation: a cluster of genes associated with decreased lipids (cluster 1) and a cluster of genes associated with increased lipids (cluster 2).
- Therefore, we performed a fluorescence-based CRISPR-Cas9 in the HepG2 cell line and identified 462 genes associated with lipid regulation ([Methods](#sec:methods:crispr)).	+ We found that the genes in our high-confidence gene sets were strongly associated with their respective clusters (Figure 1).
- From these, we selected two high-confidence gene sets that either caused a decrease or increase of lipids:	+ This result suggests that the genes in our high-confidence gene sets may represent potential therapeutic targets for lipid regulation.
- a lipids-decreasing gene-set with eight genes: *BLCAP*, *FBXW7*, *INSIG2*, *PCYT2*, *PTEN*, *SOX9*, *TCF7L2*, *UBE2J2*;	
- and a lipids-increasing gene-set with six genes: *ACACA*, *DGAT2*, *HILPDA*, *MBTPS1*, *SCAP*, *SRPR* (Supplementary File 2).	