Introduction
Gene regulatory networks describe the causal relationships between multiple different genes and their expression levels. Recent methodological advances like dotears¹ allow inference of causal regulatory networks from interventional data. We apply dotears to a single cell genome-wide CRISPR screen to uncover regulatory relationships in lipid pathways.

Motivation
Perturb-seq screens use CRISPR interventions to interrogate network structure.

Approach
Filter Perturb-seq data² to control and target-gene subsets.

Results
We applied dotears to a subset of the Perturb-seq dataset focusing on 13 genes relevant to cholesterol levels, and found 17 relationships.

Discussion
We preprocessed single-cell RNA-seq data and ran dotears on a subset of genes. Two of the genes were shown to have a prominent influence within the network, TCP1 and CCT3. The relative importance of these genes within the network indicates that dotears correctly identified TCP1 and CCT3 as chaperonin molecules, which is consistent with prior research³.

References