DATA COLLECTION

|	Sample 1	Sample 2
Gene 1	6	3
Gene 2	1438	739
Gene 3	2361	1852
Gene 4	400	951
Gene 5	299	142

Obtain RNA-seq data from TCGA in the form of raw counts. (Genes are features, samples are data points/variables)
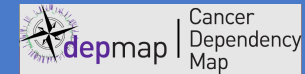
DATA PROCESSING
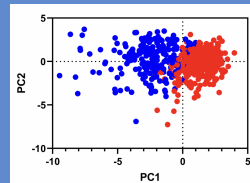
Normalize and transform raw RNA-seq data, identify sources of variation, batch effects. Do samples cluster according to biological conditions?

DIFFERENTIAL EXPRESSION
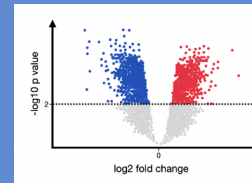
Perform differential gene expression analysis to identify genes that are differentially expressed in tumor tissue.

SYNTHETIC LETHALITY

Find potential candidate SL pairs for differentially expressed genes using CRISPr gene essentiality data from DepMap.