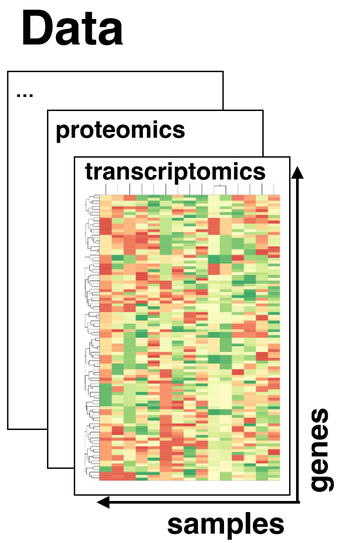
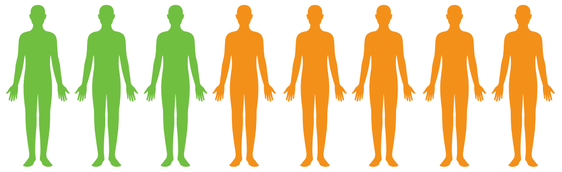
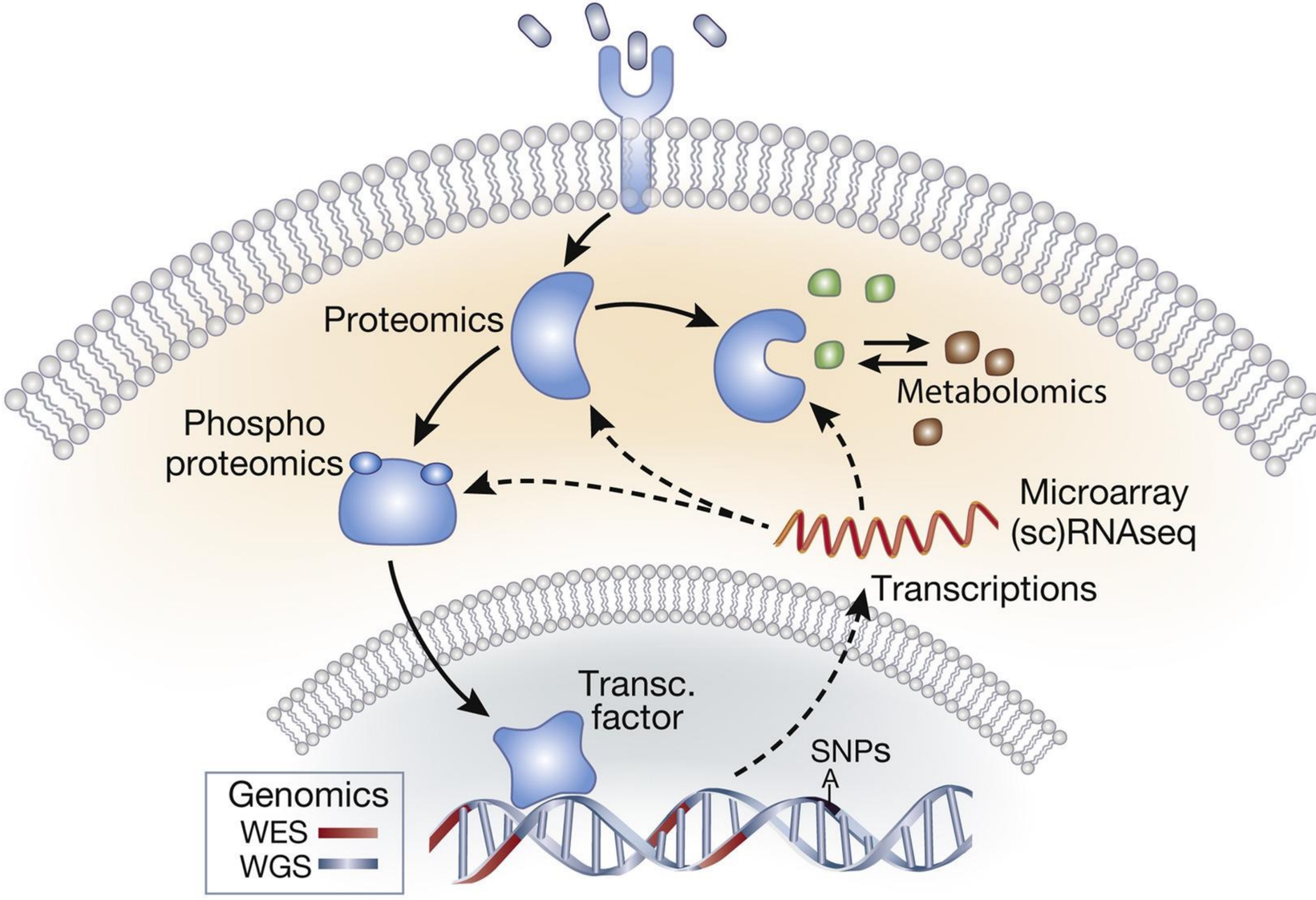
# Different omics technologies to measure molecular processes



Groups

Patient level




Saez-Rodriguez, Rinschen, Floege, Kramann. *Kidney International* 2019 95, 1326-1337. DOI: 10.1016/j.kint.2018.11.048
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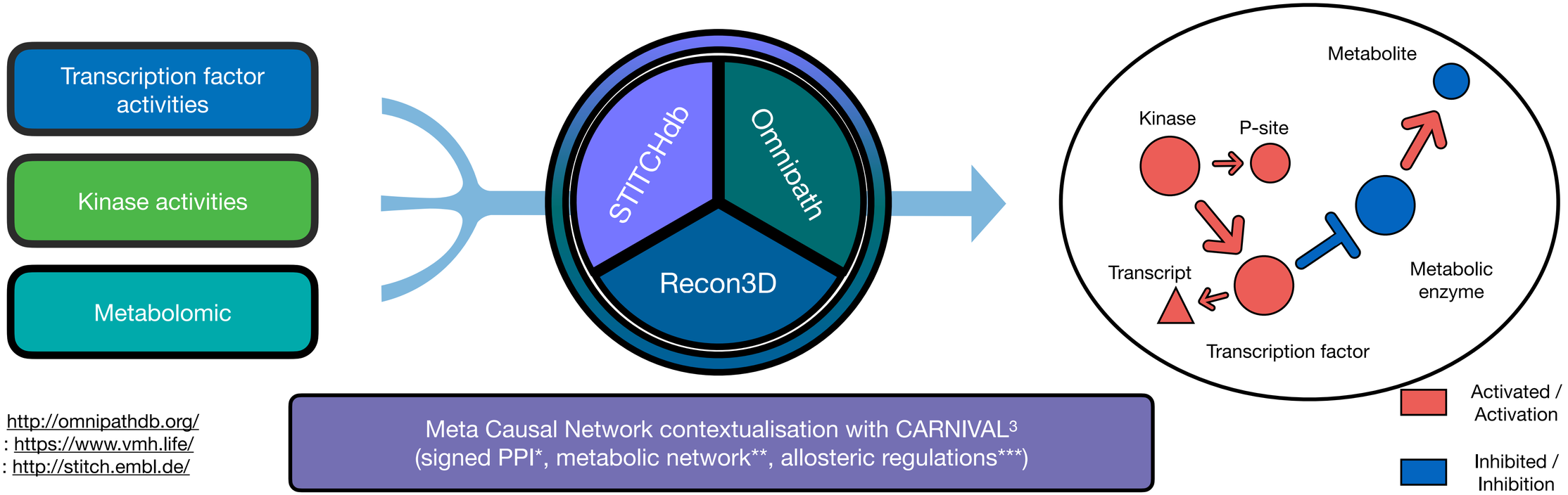
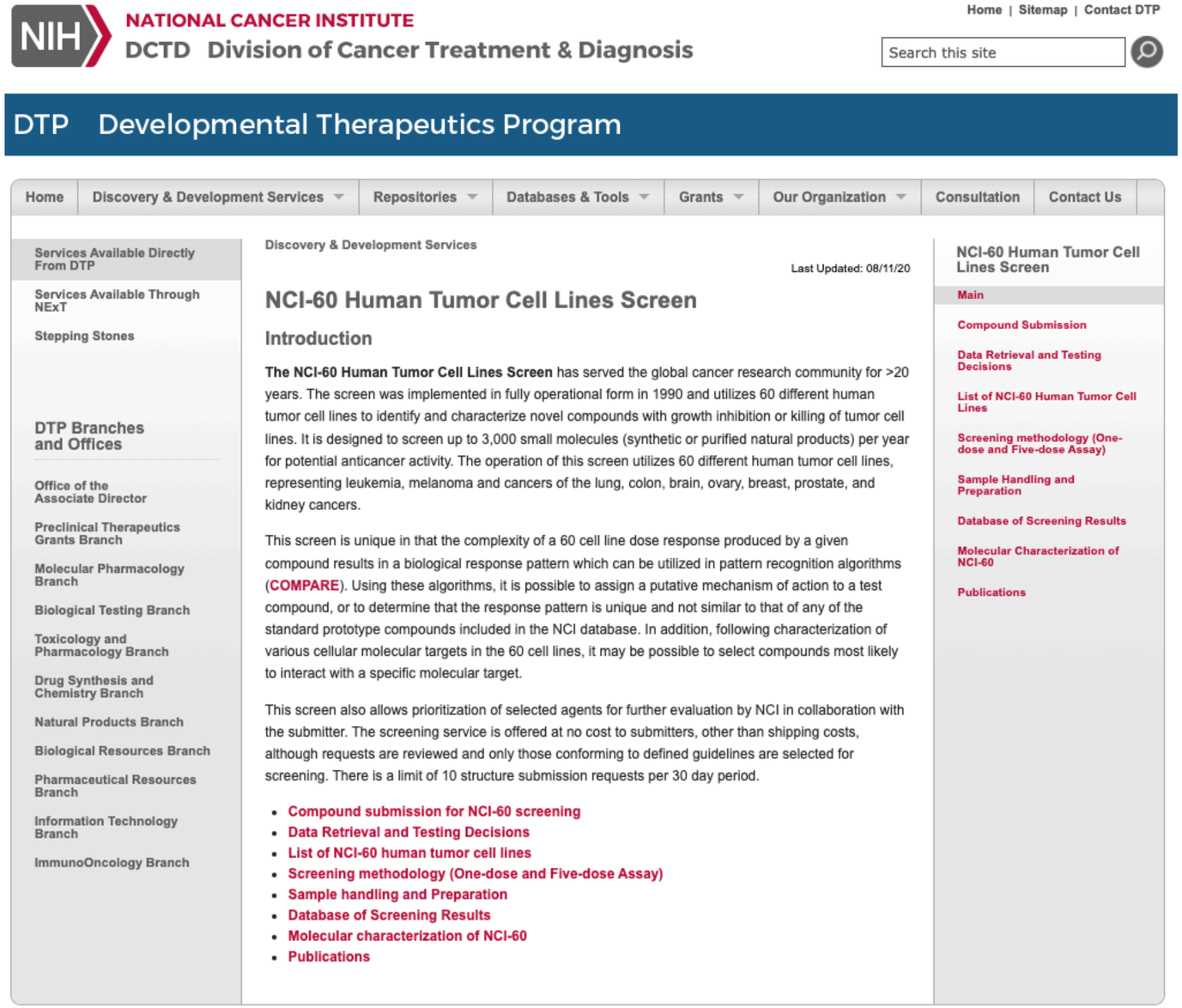
# COSMOS: Multi-omic integration pipeline



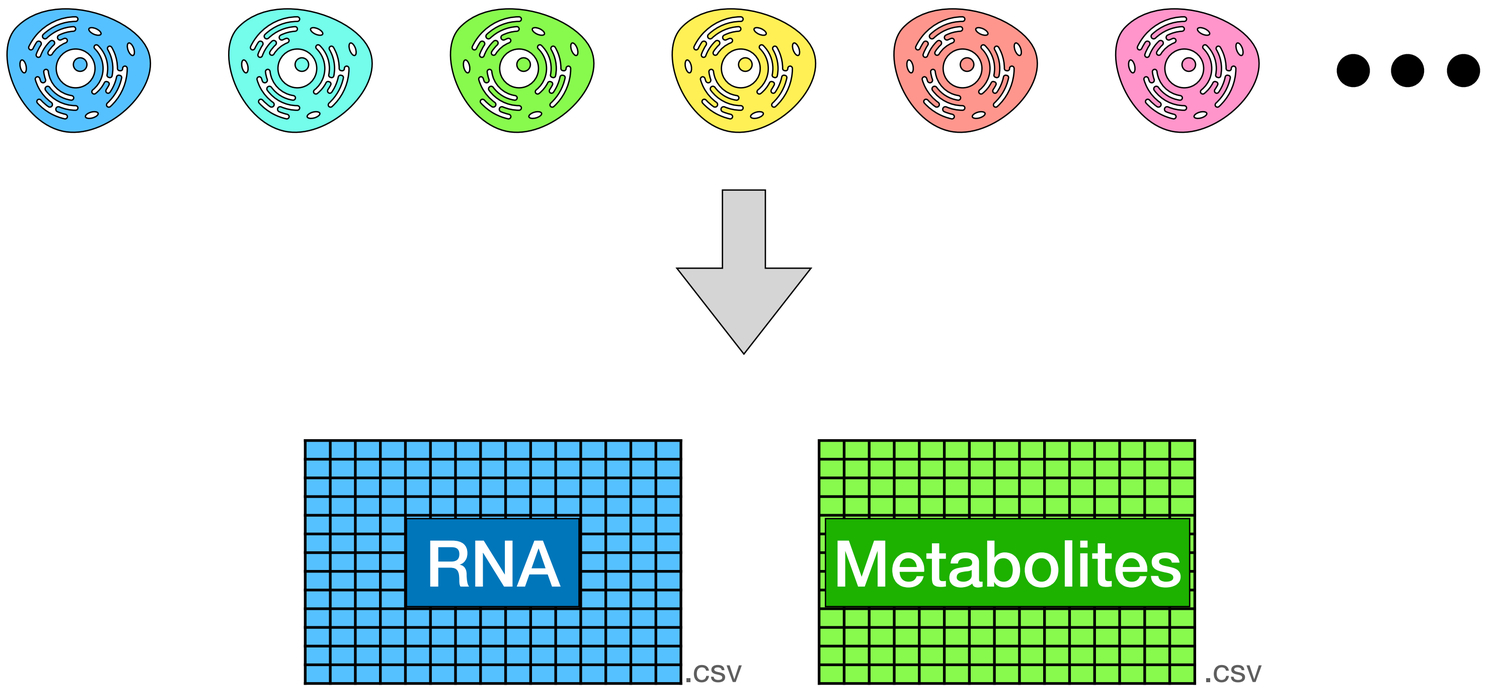

*Omnipath : http://omnipathdb.org/
**Recon3D : https://www.vmh.life/
***STITCH : http://stitch.embl.de/

Meta Causal Network contextualisation with CARNIVAL[3]
(signed PPI*, metabolic network**, allosteric regulations***)

# Systematic generation of testable hypothesis to connect signalling and metabolism with the NCI60 datasets



# NCI60 cancer cell lines



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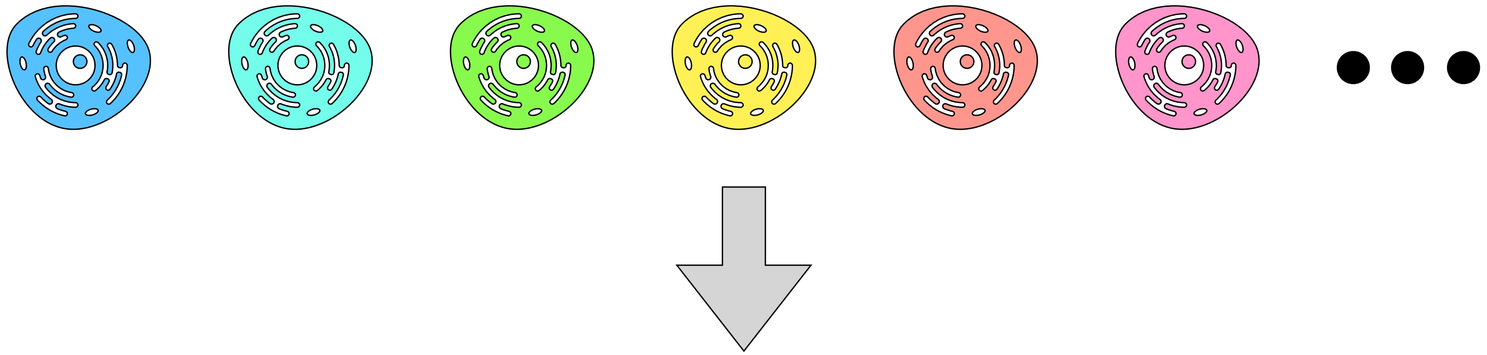

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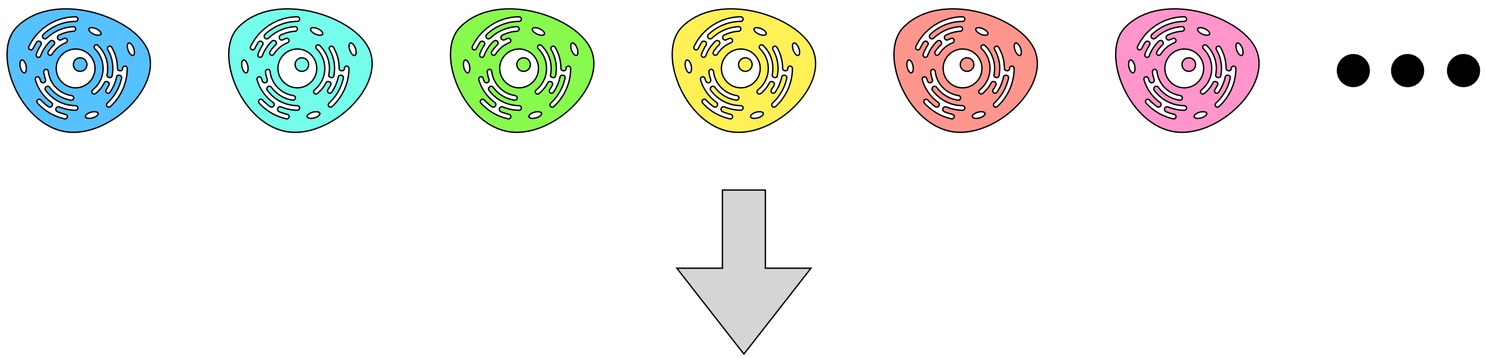

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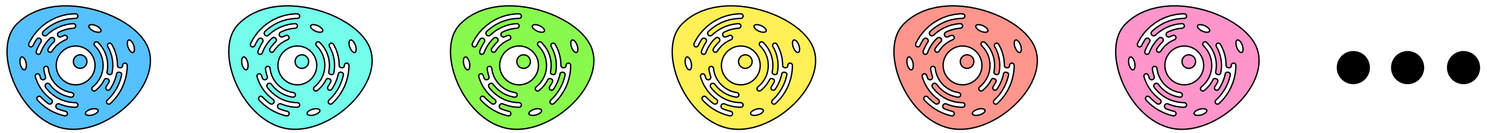
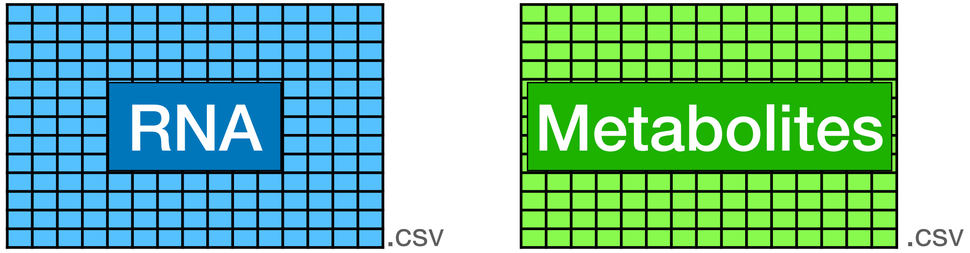
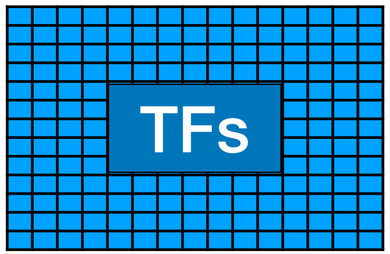
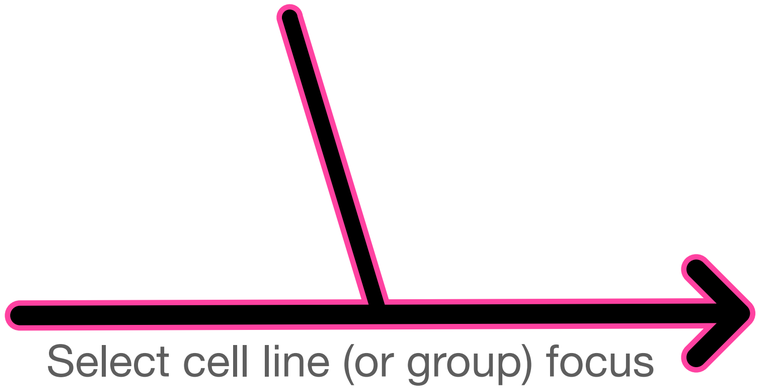
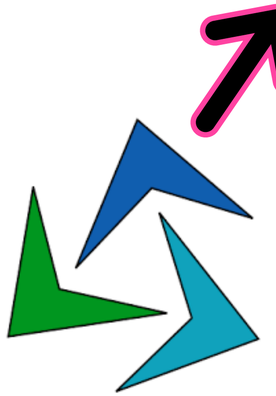
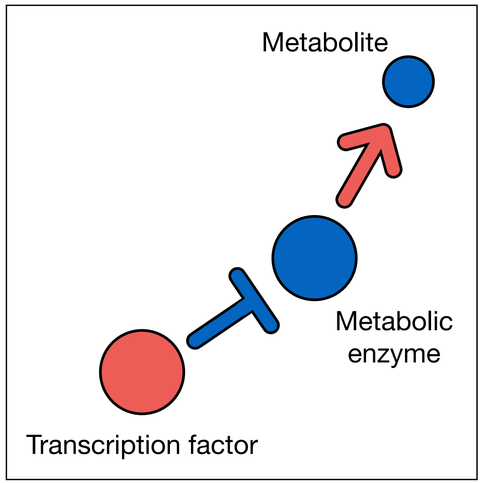




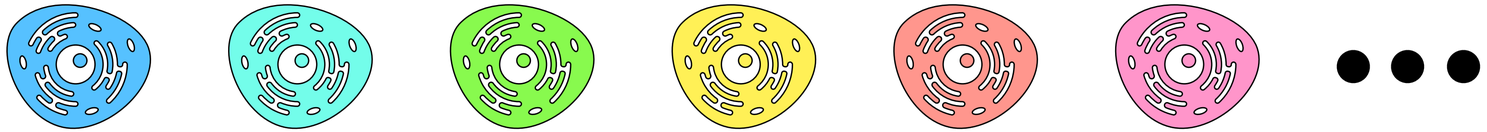




Testable hypotheses

Interpretation

# NCI60 cancer cell lines



```r
library(cosmosR)
library(readr)
library(dplyr)

data("meta_network")
load("data/cosmos/cosmos_inputs.RData")

names(cosmos_inputs)

cell_line <- "786-0"

sig_input <- cosmos_inputs[[cell_line]]$TF_scores
metab_input <- cosmos_inputs[[cell_line]]$metabolomic
RNA_input <- cosmos_inputs[[cell_line]]$RNA
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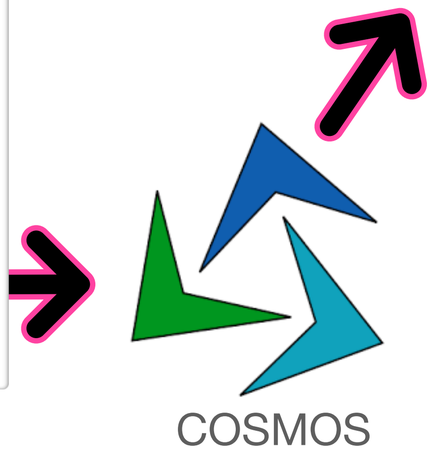


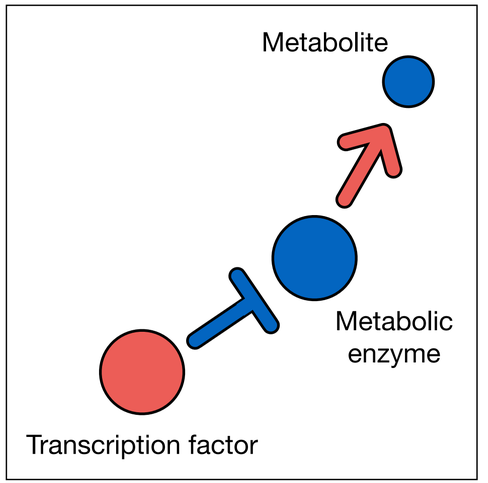


Testable hypotheses

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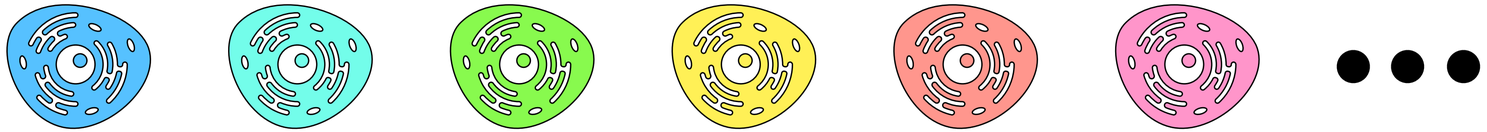

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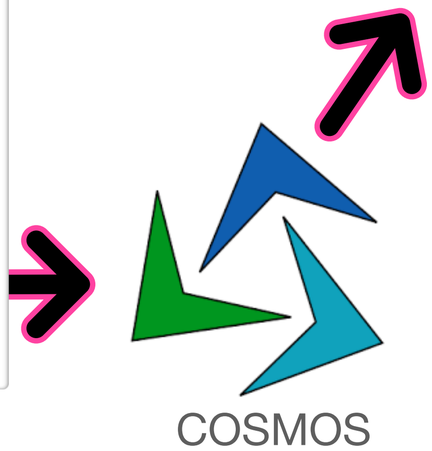
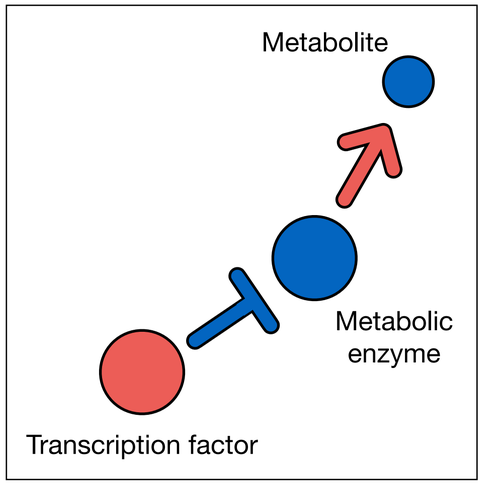
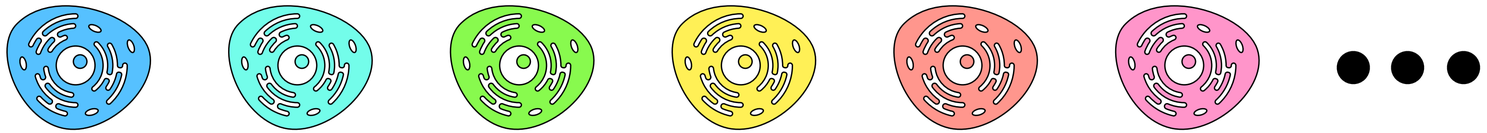


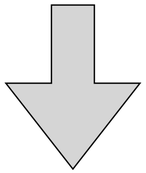



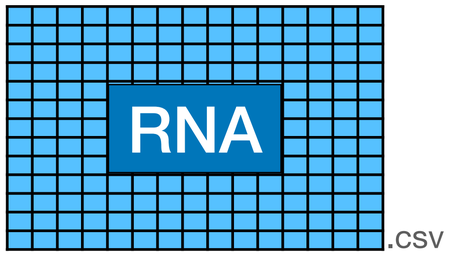

Testable hypotheses

Interpretation

# NCI60 cancer cell lines



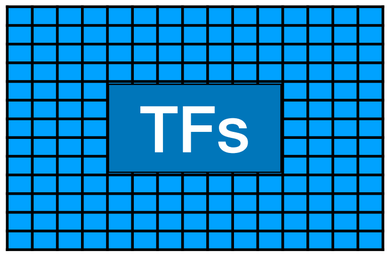


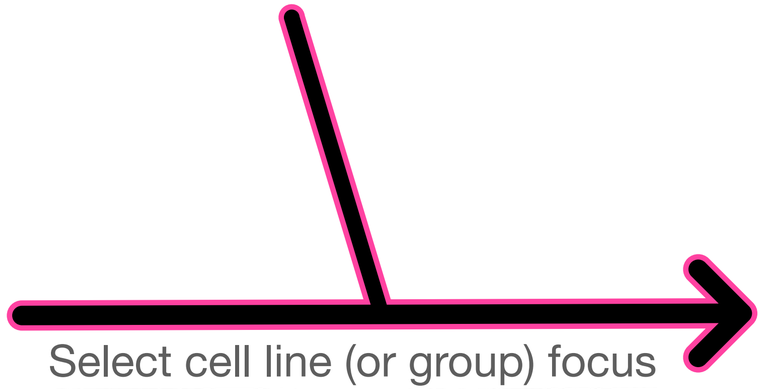



.csv

.csv

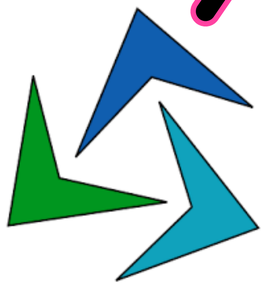




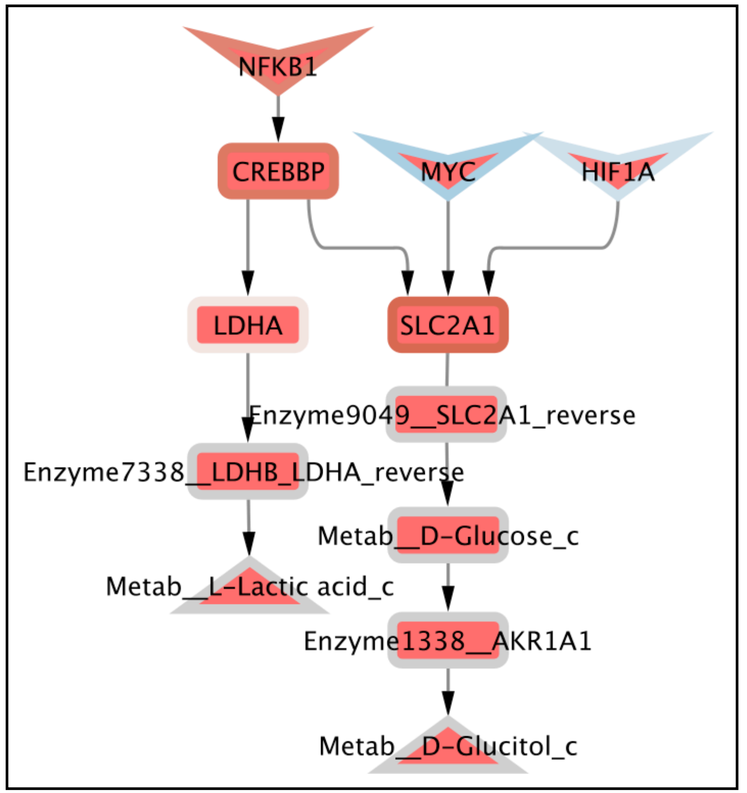



Select cell line (or group) focus

Example: 786-O



COSMOS

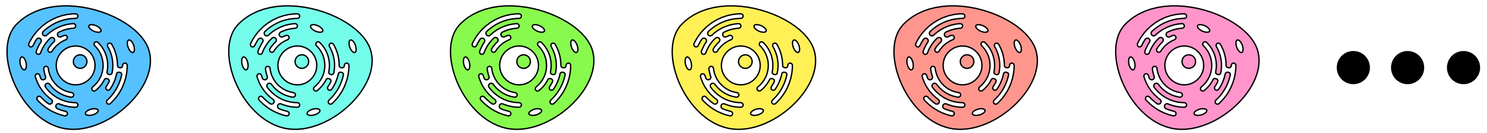


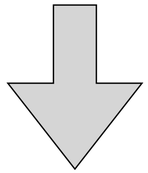

Testable hypotheses

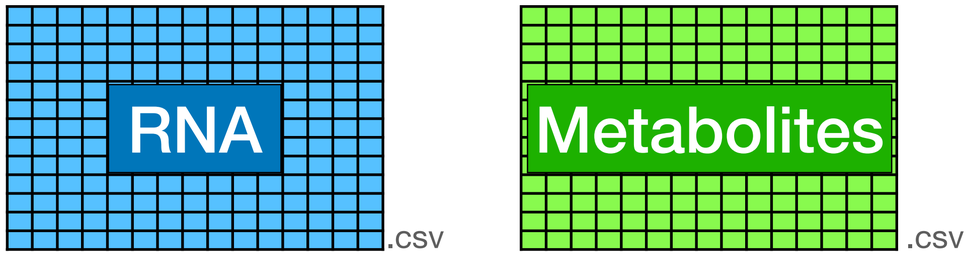
Interpretation

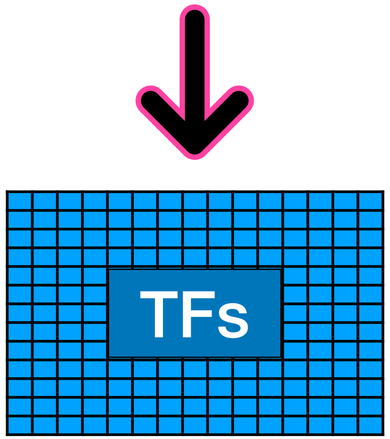
CREBBP key regulator of LDHA activity downstream of NFKB1 in 786-O?

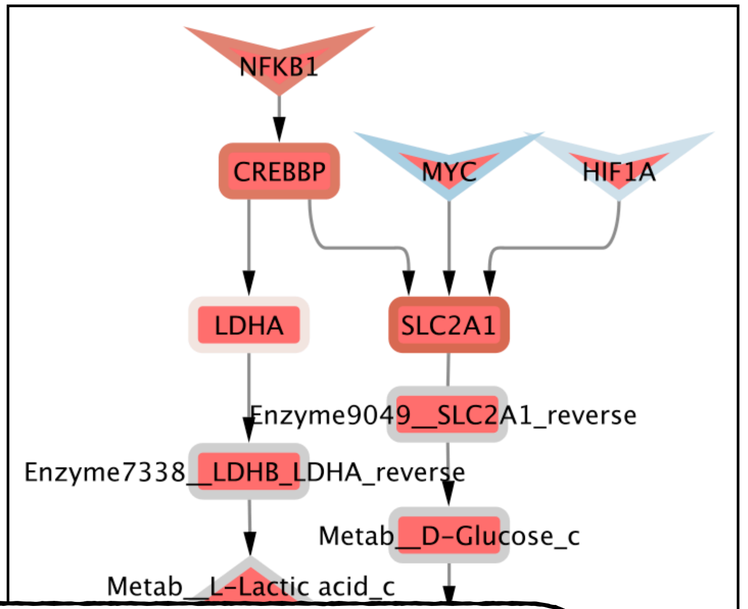
# NCI60 cancer cell lines








Test different cell lines, network depth, sig->metab / metab->sig

Testable hypotheses

Interpretation

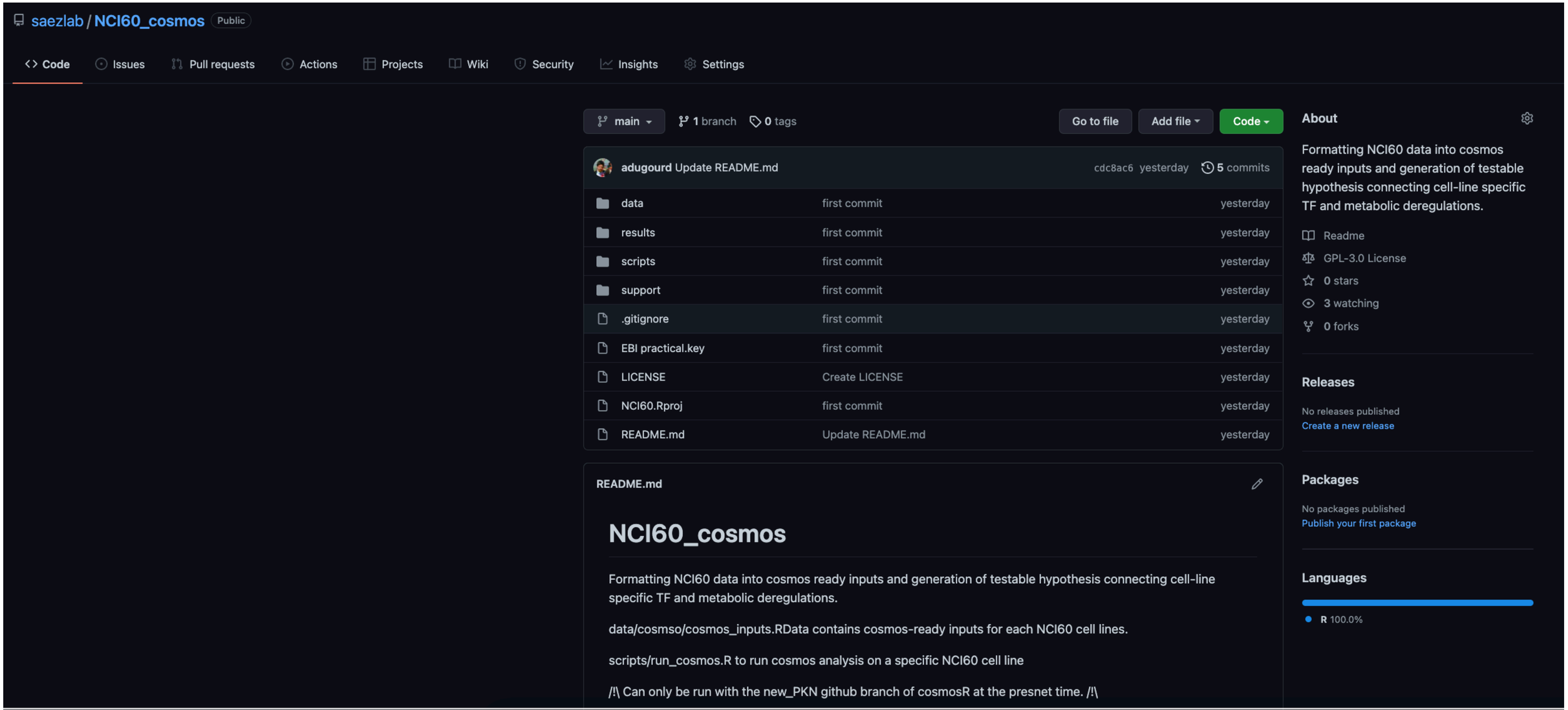
Select cell line (or group) focus

Example: 786-O

COSMOS

CREBBP key regulator of LDHA activity downstream of NFKB1 in 786-O?

# Formatted data and example script available in GitHub



Expected outcomes:

- Explore NCI60 cell line omic datasets

- Interpreting TF activities estimated from RNA seq data

- Learning to use cosmos to integrate signalling and metabolic data with prior knowledge

- Generate and interpret testable hypotheses

Softwares:

- CBC solver executable
- R 4.1>
- cosmosR R package
- (readr and dplyr R packages)