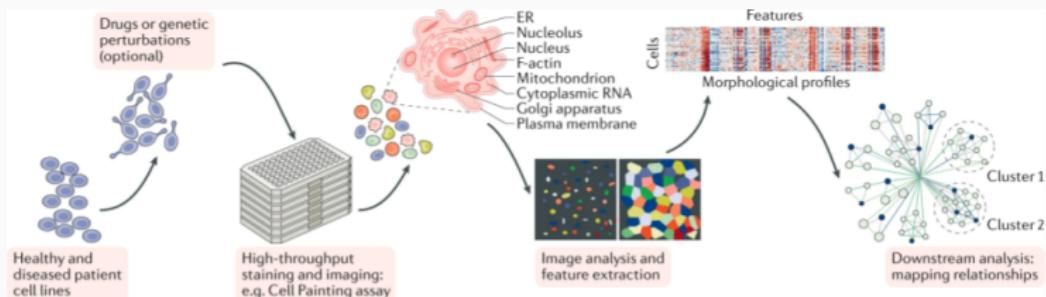


# Exploring the Joint-Undertaking for Morphological Profiling (JUMP) Dataset



Given gene X:

- How do the cells look?
- Which genes' KO/overexpression produce a similar phenotype?
- Which features are statistically better represented?

Alán F. Muñoz (amunozgo@broadinstitute.com)

# One example of our tools: How do the cells look?

JUMP documentation and examples

Home

How-To Guides

- Retrieve JUMP profiles
- Incorporate metadata into profiles
- Calculate phenotypic activity
- Plot all channels for one site
- Explore perturbation clusters
- Query information of genes

Explanations

- Frequently Asked Questions
- Glossary and Acronyms
- Available resources

Other Formats

Jupyter

JCP2022\_011844

plate:  
1053597806  
well: P13  
site: 2

### CRISPR Gallery

51,185 rows

- columns - + + +

Apply

View and edit SQL

This data can be viewed as CSV (Advanced)

Link	rowID	Y	Index	Gene/Compound	External resources	Metadata_JCP2022	Site 0	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8
1	1	0	0	non-targeting		JCP2022_800002									
2	2	1	1	MPP6	External	JCP2022_804257									
3	3	2	2	non-targeting		JCP2022_800022									
4	4	3	3	no-guide		JCP2022_800001									
5	5	4	4	no-guide		JCP2022_800001									
6	6	5	5	non-targeting		JCP2022_800002									
7	7	6	6	non-targeting		JCP2022_800002									

Our JUMP Hub concentrates resources and tutorials to use JUMP data.

We strive to make the JUMP data accessible and useful to both biologists and data scientists.

- Examples
- Tutorials
- FAQs
- Links and docs



Poster



JUMP Hub