Quantitative multi-omic data analysis and integration in kidney cancer and metastasis

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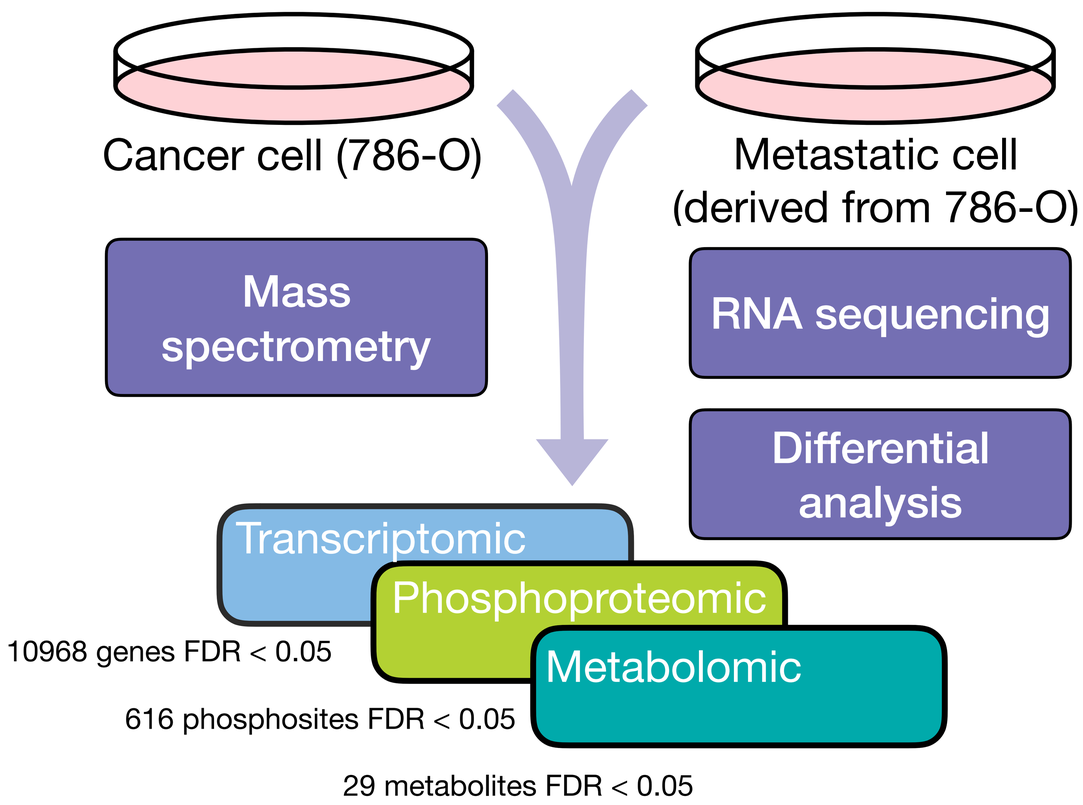
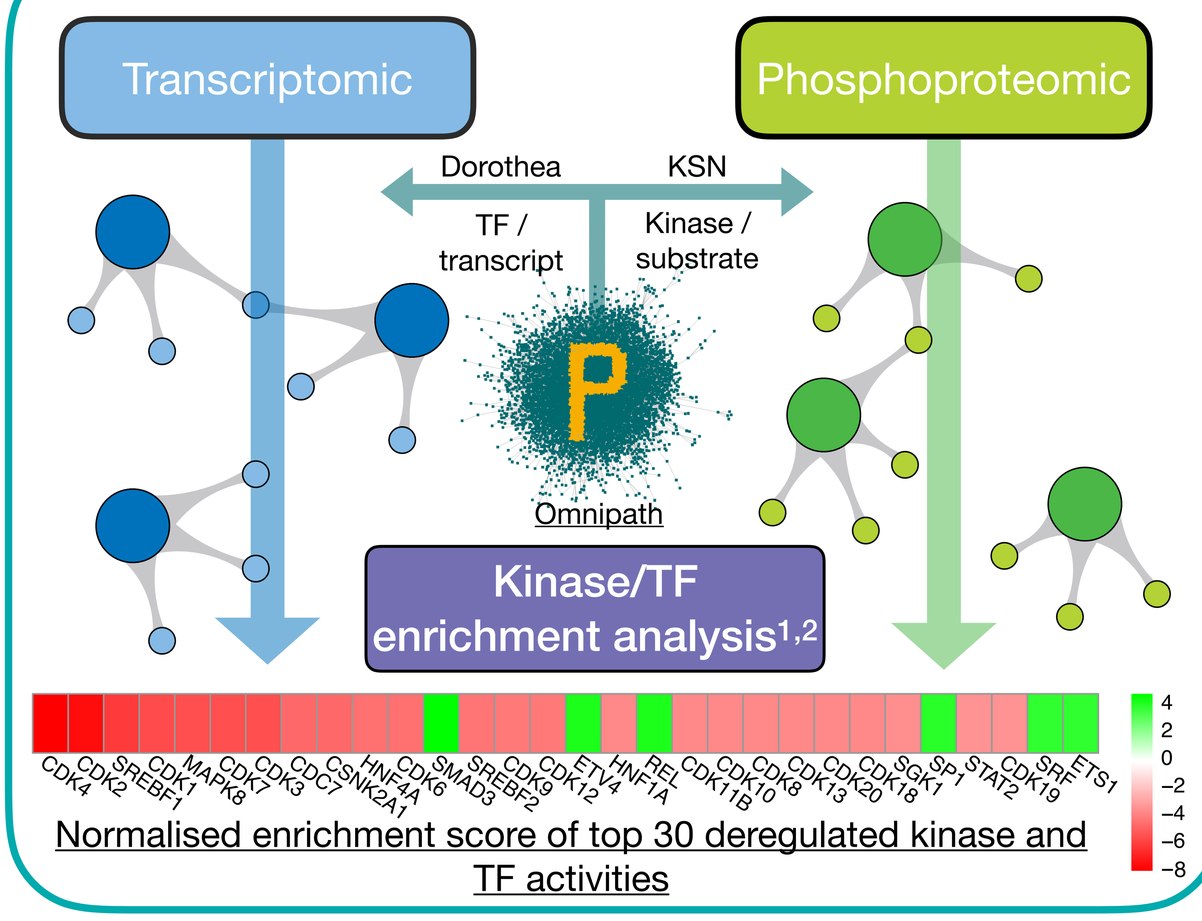
Motivation and project outline

Understanding the interplay of signalling and metabolism in disease is critical for the identification of new therapeutic targets. To do so, we developed an analysis pipeline consisting of two main steps. First, we systematically characterised the activity of signalling enzymes from transcriptomic and phosphoproteomic datasets. Then, these inferred enzymatic activities were connected with metabolic deregulation, with the support of a causal network combining signalling, metabolic and allosteric reactions.

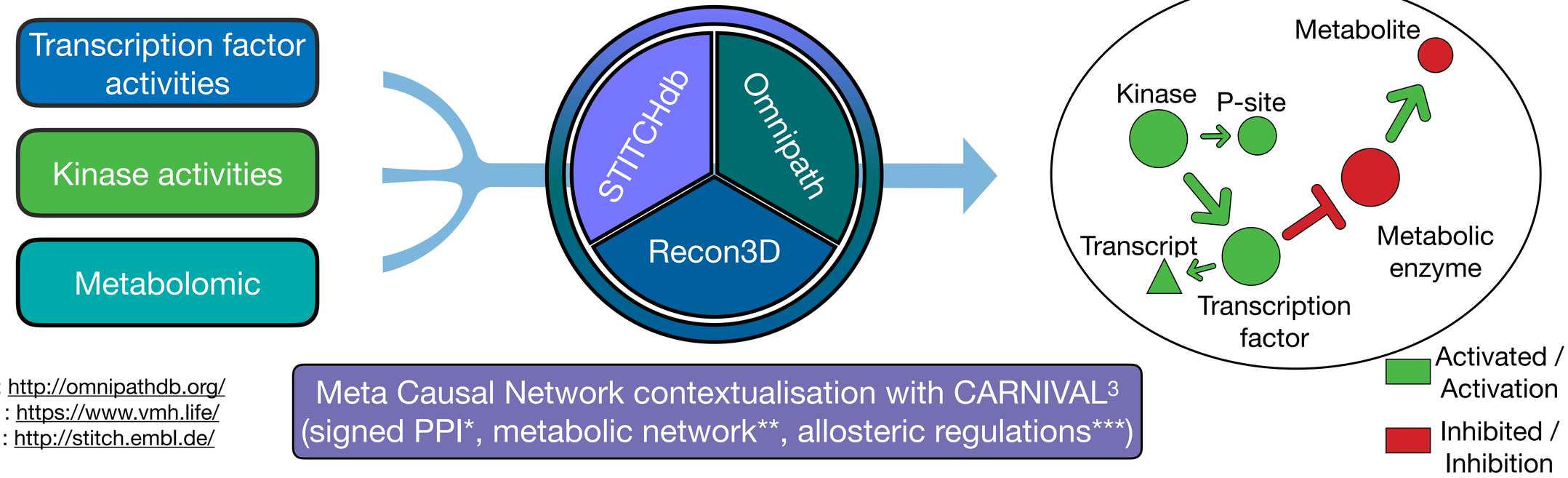
Experimental context



Footprint analysis



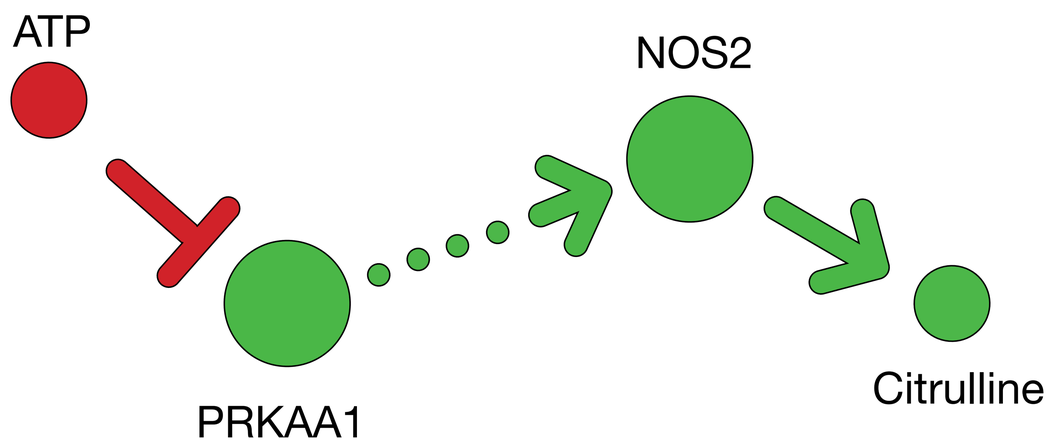
Causal network integration

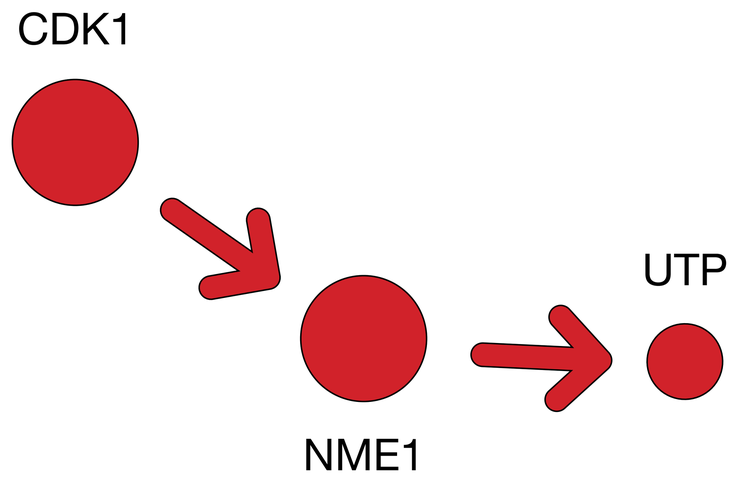


*Omnipath : http://omnipathdb.org/
**Recon3D : https://www.vmh.life/
***STITCH : http://stitch.embl.de/

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

Two examples of connections between signalling and metabolism deregulations found in kidney metastasis





The predicted activities of NOS2 and NME1 will be experimentally validated. Such mechanism may help to find specific therapeutic targets to impair cancer progression.

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3)Liu, Anika, Panuwat Trairatphisan, Enio Gjerga, Athanasios Didangelos, Jonathan Barratt, and Julio Saez-Rodriguez. 2019. "From Expression Footprints to Causal Pathways: Contextualizing Large Signaling Networks with CARNIVAL." *bioRxiv*. https://doi.org/10.1101/541888.