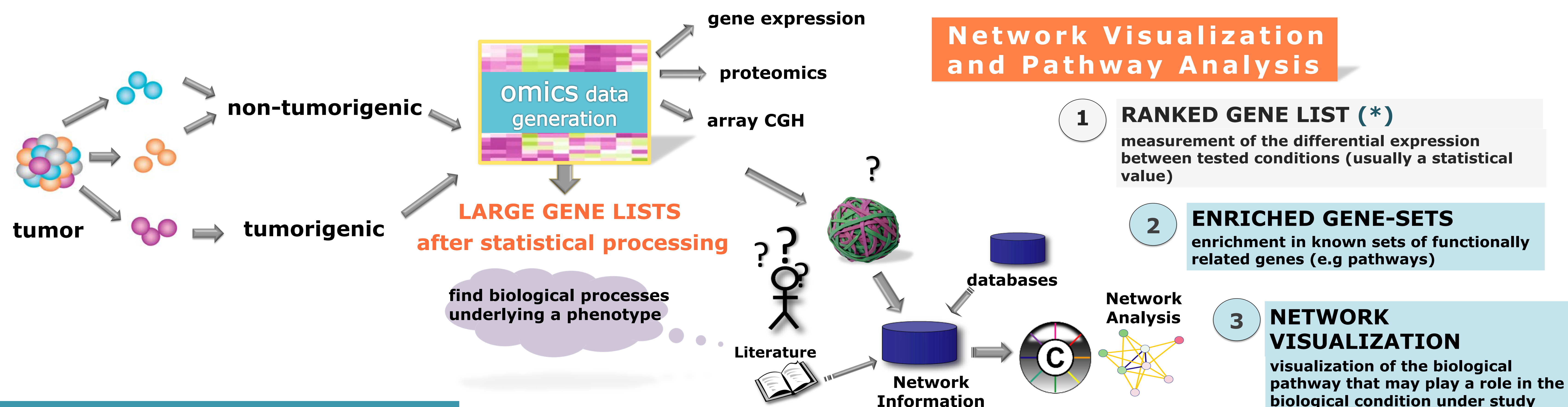


# PATHWAY AND NETWORK ANALYSIS OF CANCER STEM CELL DATA

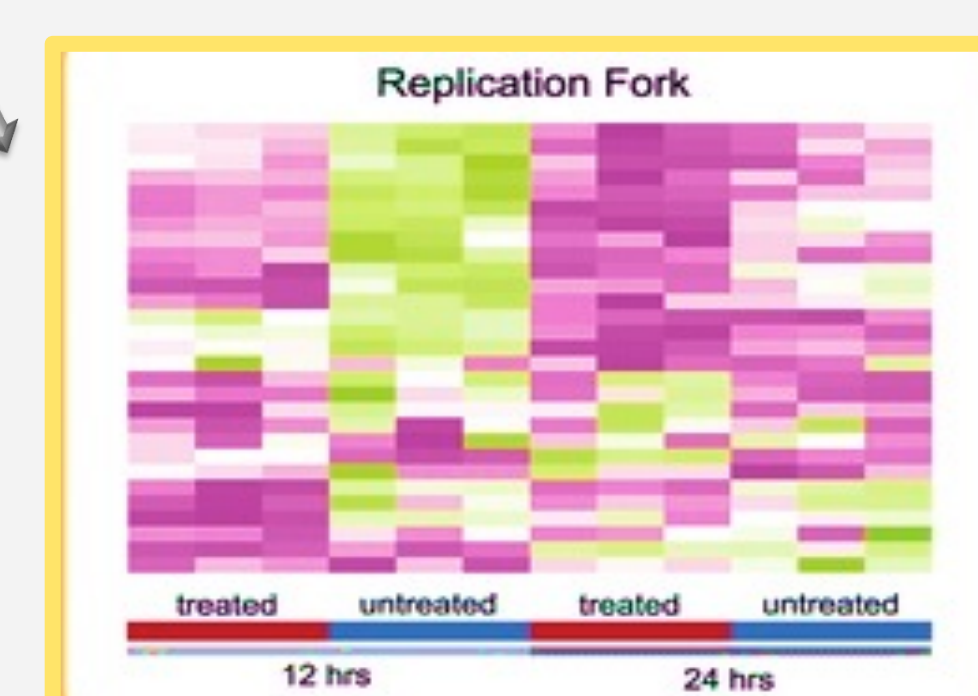
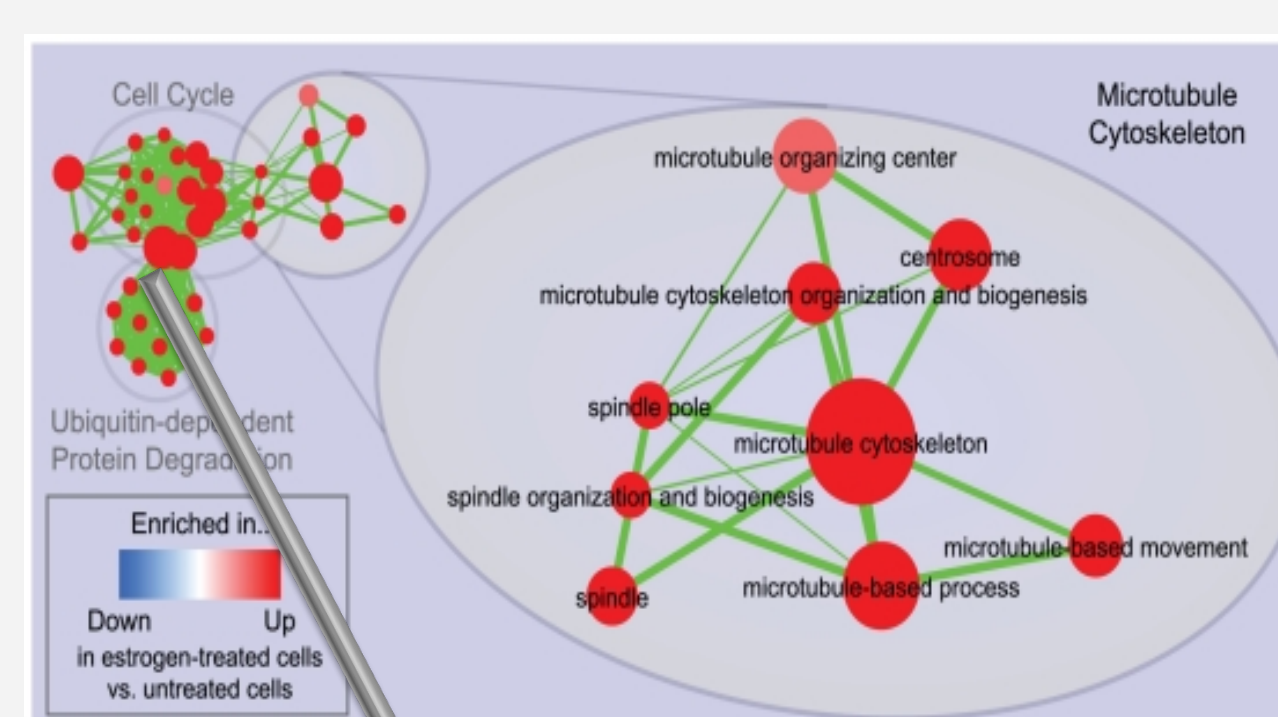
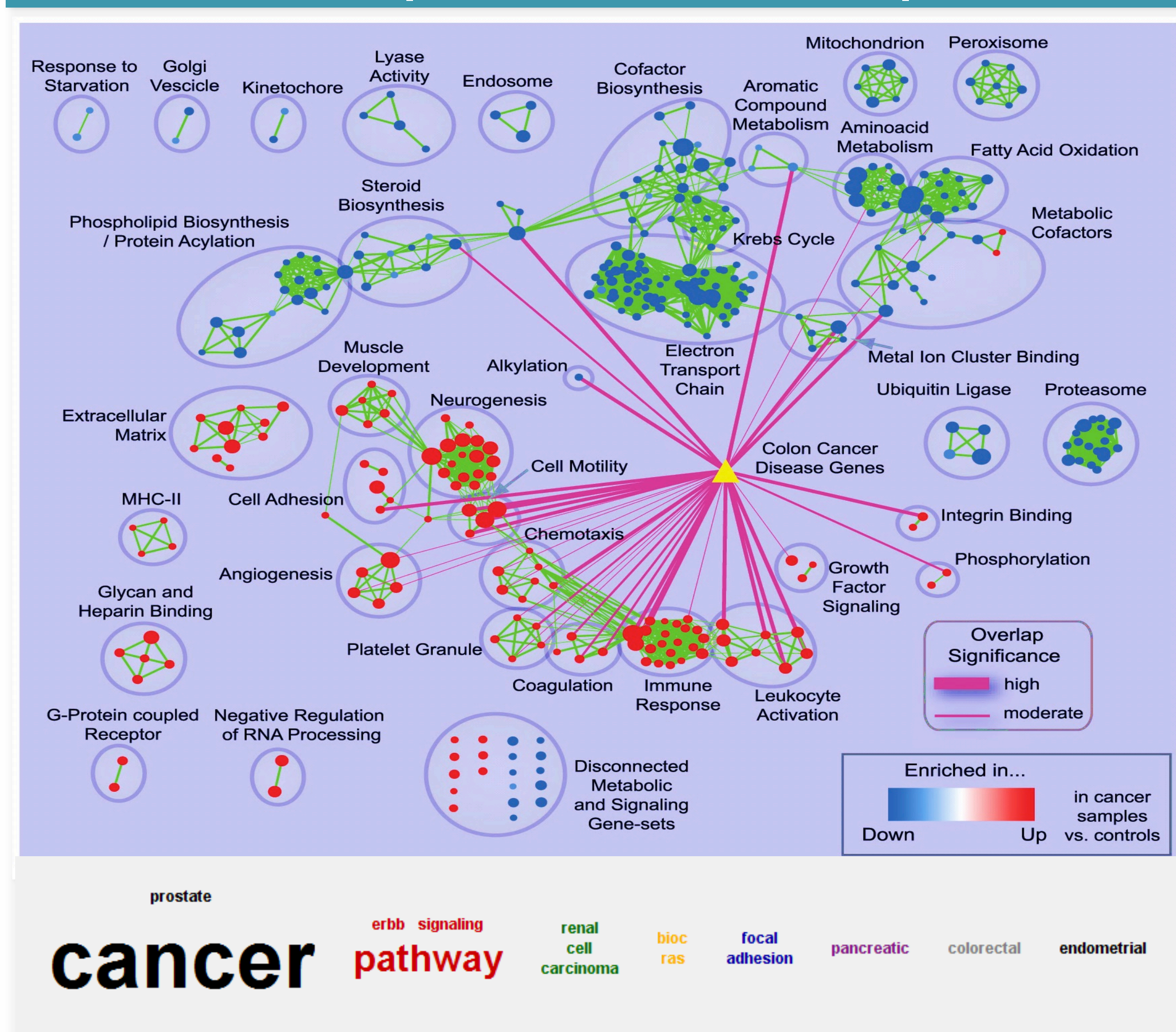
Veronique Voisin<sup>1</sup>, Daniele Merico<sup>1</sup>, Ruth Isserlin<sup>1</sup>, Jayne Danska<sup>2</sup>, John Dick<sup>3</sup>, Gary Bader<sup>1</sup>

<sup>1</sup>Donnelly Centre, <sup>2</sup>SickKids, <sup>3</sup>UHN

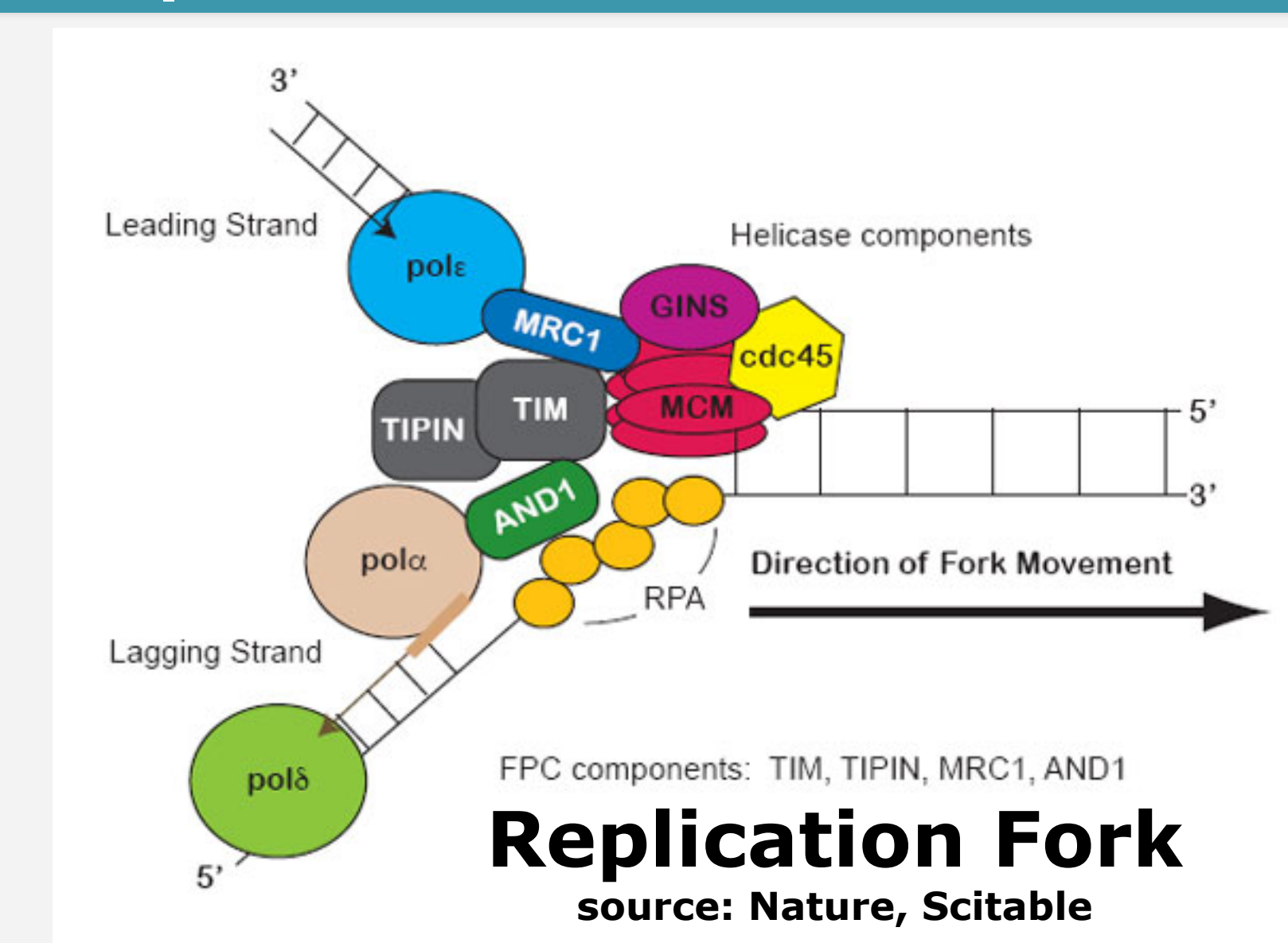
**LARGE GENE LISTS ? | WE CAN HELP.**



**SOFTWARE WE USE:** GSEA | CYTOSCAPE | ENRICHMENTMAP | WORDCLOUD | GENEMANIA



Shorter list of genes containing best targets

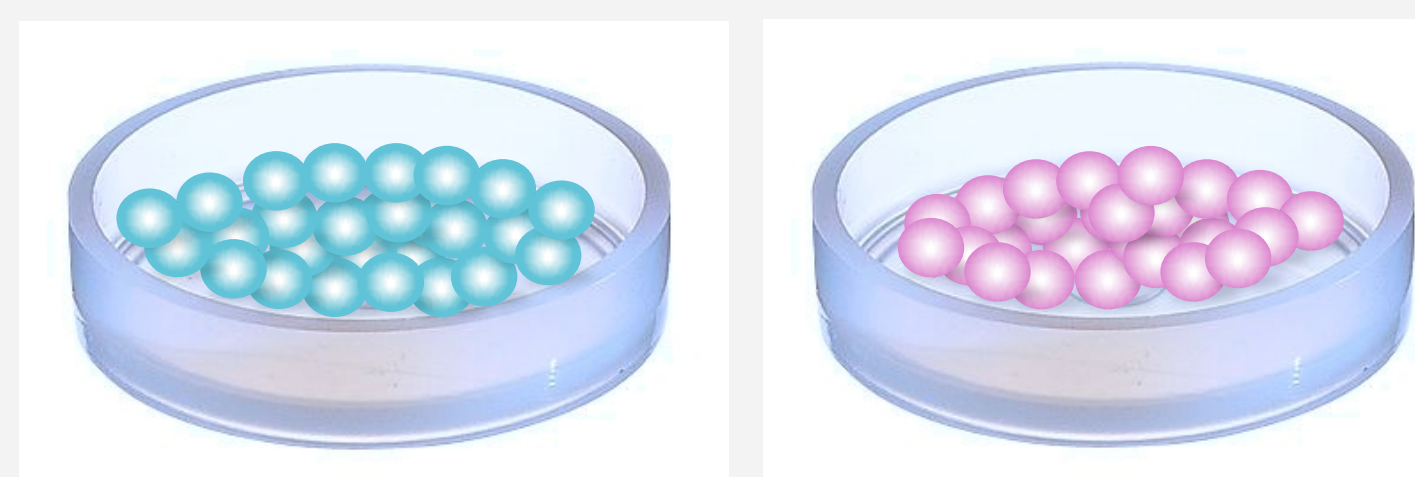


Identified candidate genes?



Back to the bench!

- shRNA
- over-expression
- specific inhibitors
- *in vivo* validation...



**OUTCOME AND IMPLICATIONS:**

- ✧ DECREASE ANALYSIS TIME.
- ✧ EASE GENERATION OF NEW HYPOTHESES AND DESIGN OF NEW EXPERIMENTS.
- ✧ ULTIMATE GOAL: IDENTIFICATION OF THERAPEUTIC OR BIOMARKER CANDIDATES.
- ✧ *Enrichment map: a network-based method for gene-set enrichment visualization and interpretation. MERICO ET AL. PLOS ONE. 2010 NOV 15;5(11).*

**Information about the service:**

- ✧ You can contact me at: [veronique.voisin@utoronto.ca](mailto:veronique.voisin@utoronto.ca)
- ✧ We have created a survey to assess your needs: please go to <http://www.surveymonkey.com/s/HZXD7VD>
- (\*) Standardized data input: only already statistically analyzed data in a correct format for GSEA analysis are accepted for pathway and network analysis