TimiRGeN : Multi-omic network generation R package

ISGSB meeting - 10th September

Krutik Patel [1] Sharmilla Chandrasegaran [1] David Young [2]
Daryl Shanley 1

[1]Newcastle University Institute of Ageing

[2]Newcastle University Institute of Genetic Medicine

10th September 2020

Objectives

Objective 1

- Introduce a novel tool, TimiRGeN, which can be used for generation of Gene Regulatory Networks (GRNs) from big multi-omic expression datasets.

Objective 2

- Display how microRNAs may be effecting mechanistic systems. This will be shown in the GRNs created from using TimiRGeN on multiple datasets.

Objective 3

- Highlight current modelling efforts on a chondrogenesis based model which was found using TimiRGeN.

Transcriptomic expression profiles provide an excellent resource for generation of dynamic model

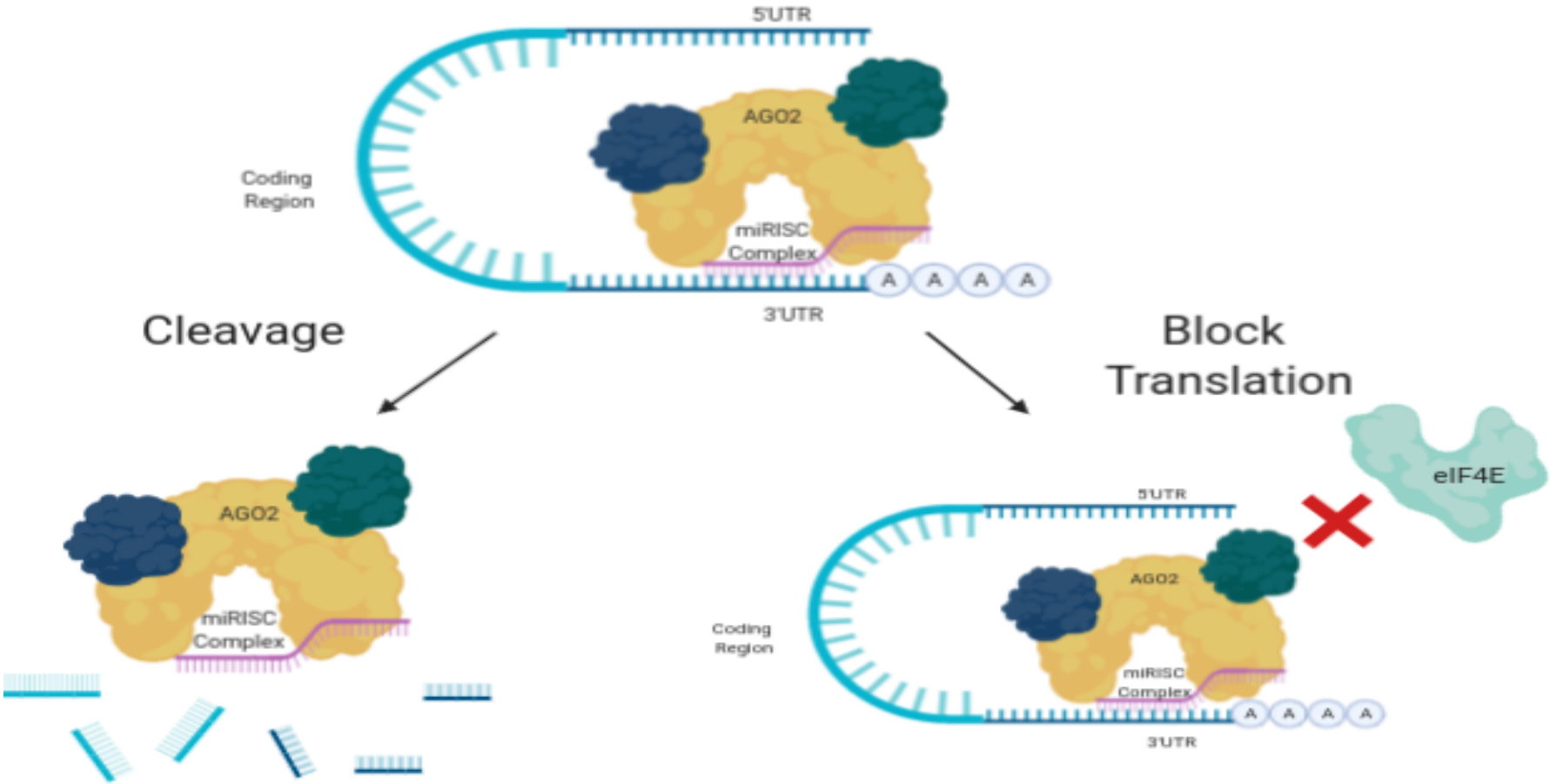
Large expression profiling experiments are becoming more common

- Researcher groups are creating more sophisticated datasets, due to reducing costs of high through-put technologies.
- Longitudinal and multi-omic (mRNA and microRNA) datasets are being created.

Overall

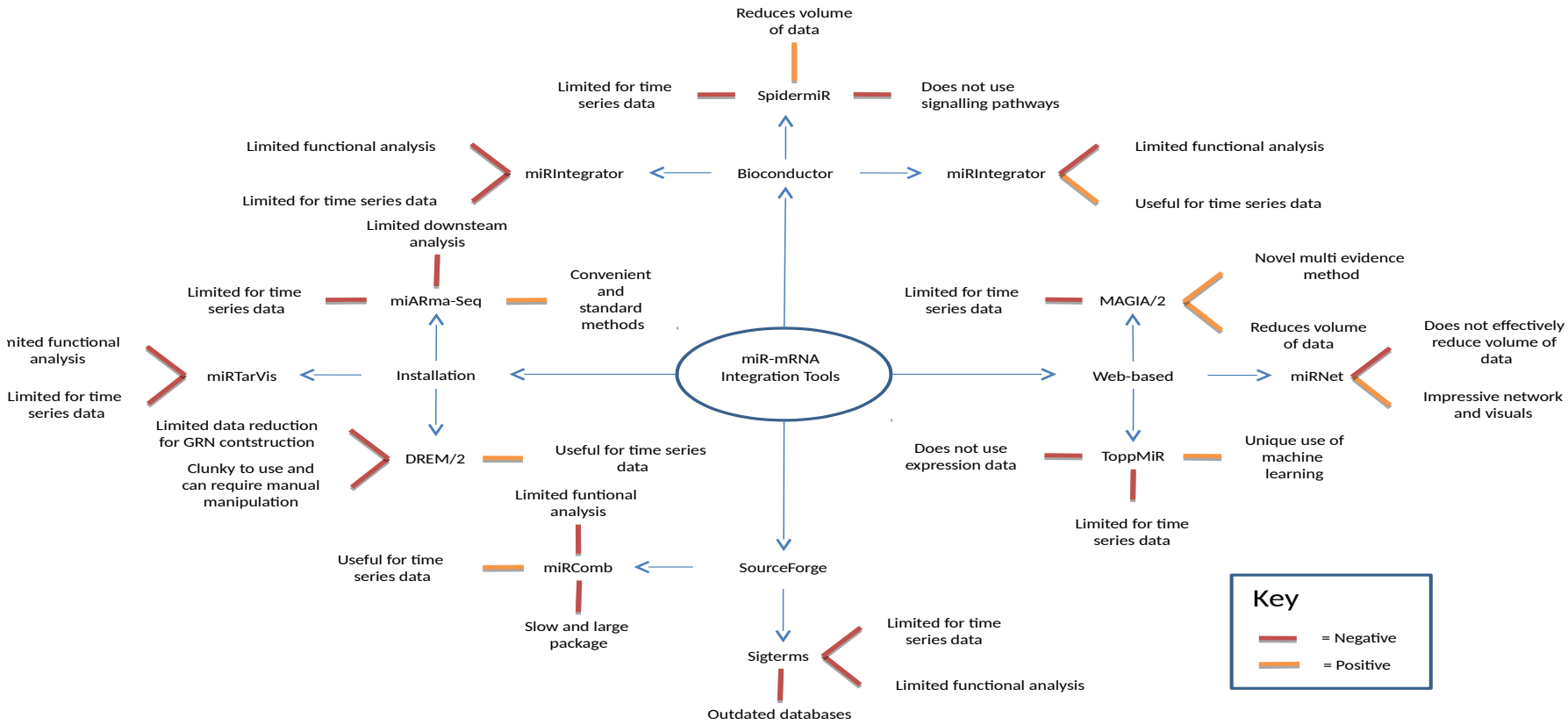
This is a good resource for modelling!

miRNAs negatively regulate mRNAs



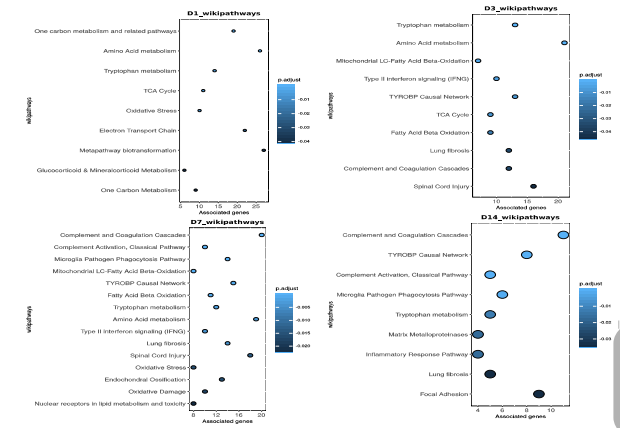
Are there bioinformatic tools to integrate and investigate miRNA-mRNA interactions?

Current miRNA-mRNA analysis tools are insufficient for GRN generation

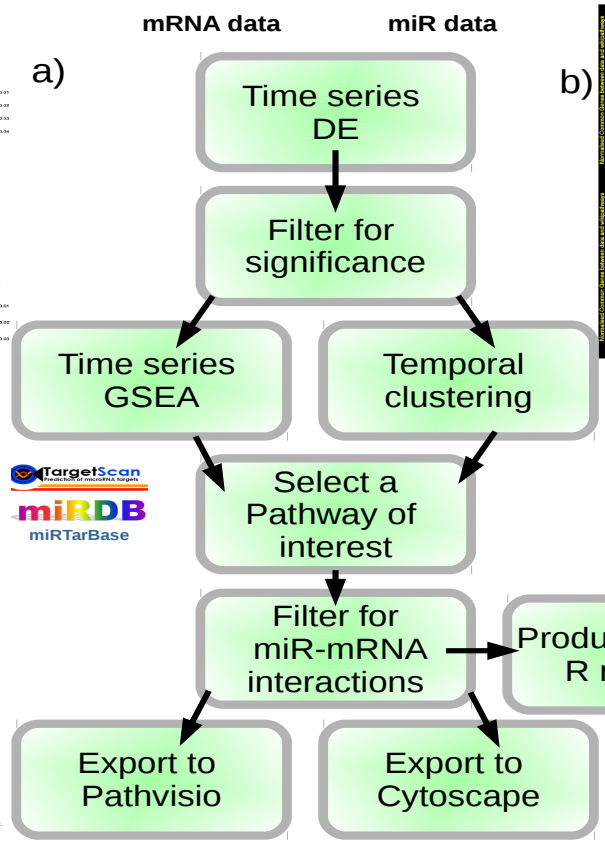


Unfortunately none were sufficient to reduce the big data enough to start generating GRNs.

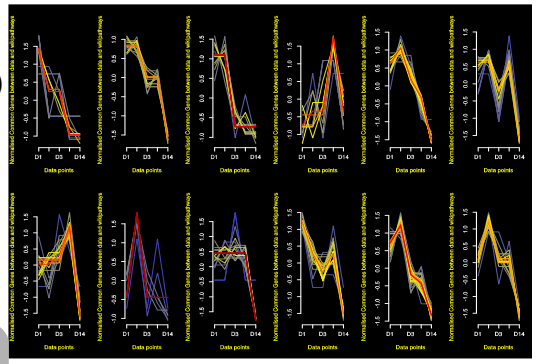
TimiRGeN R package



a)



b)



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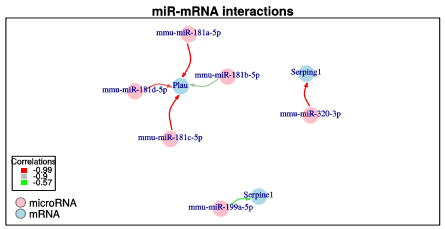

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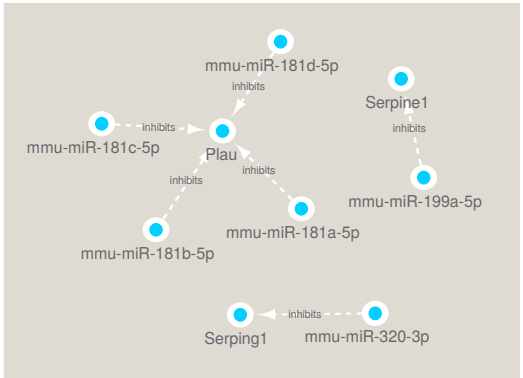
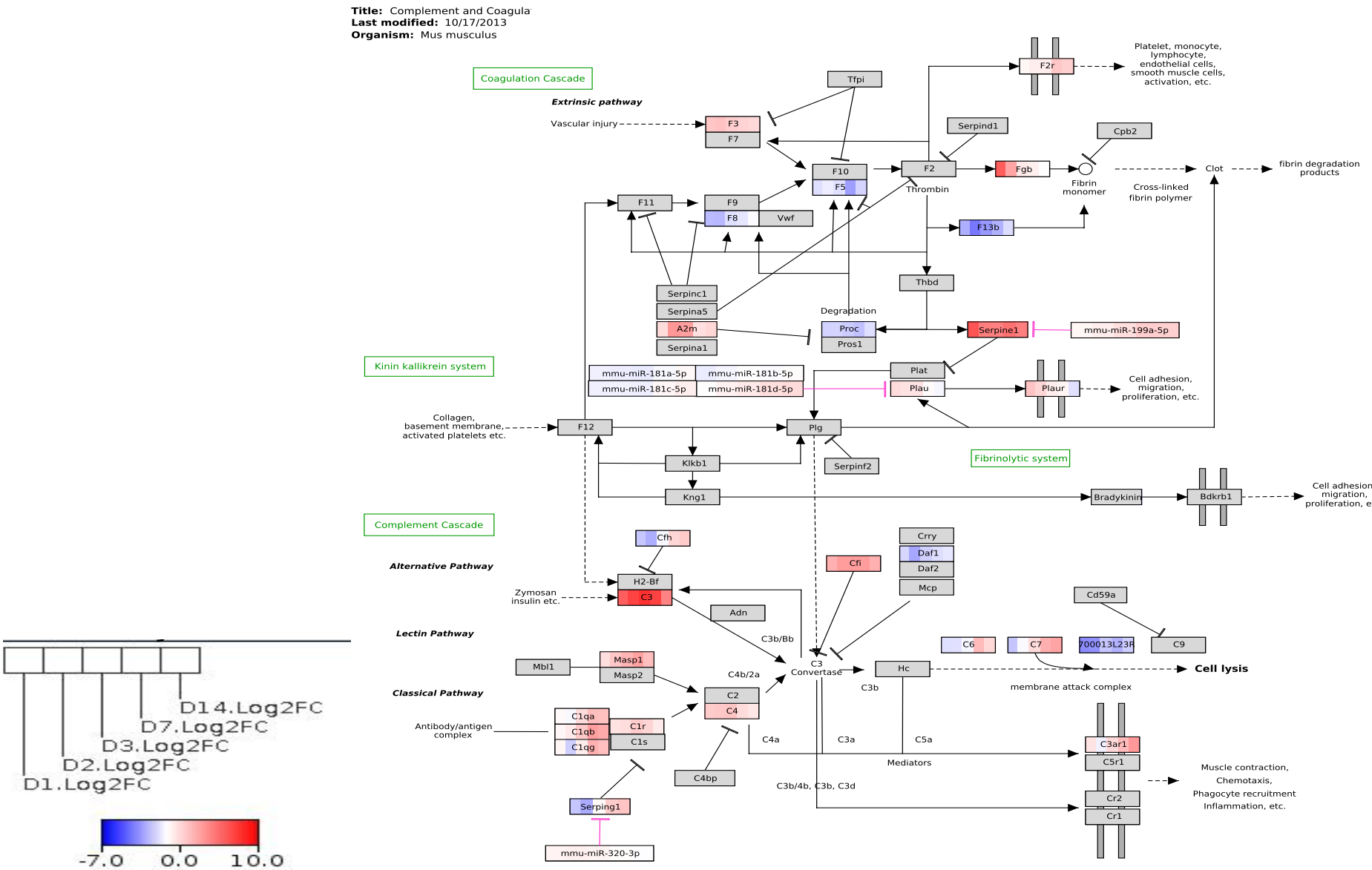
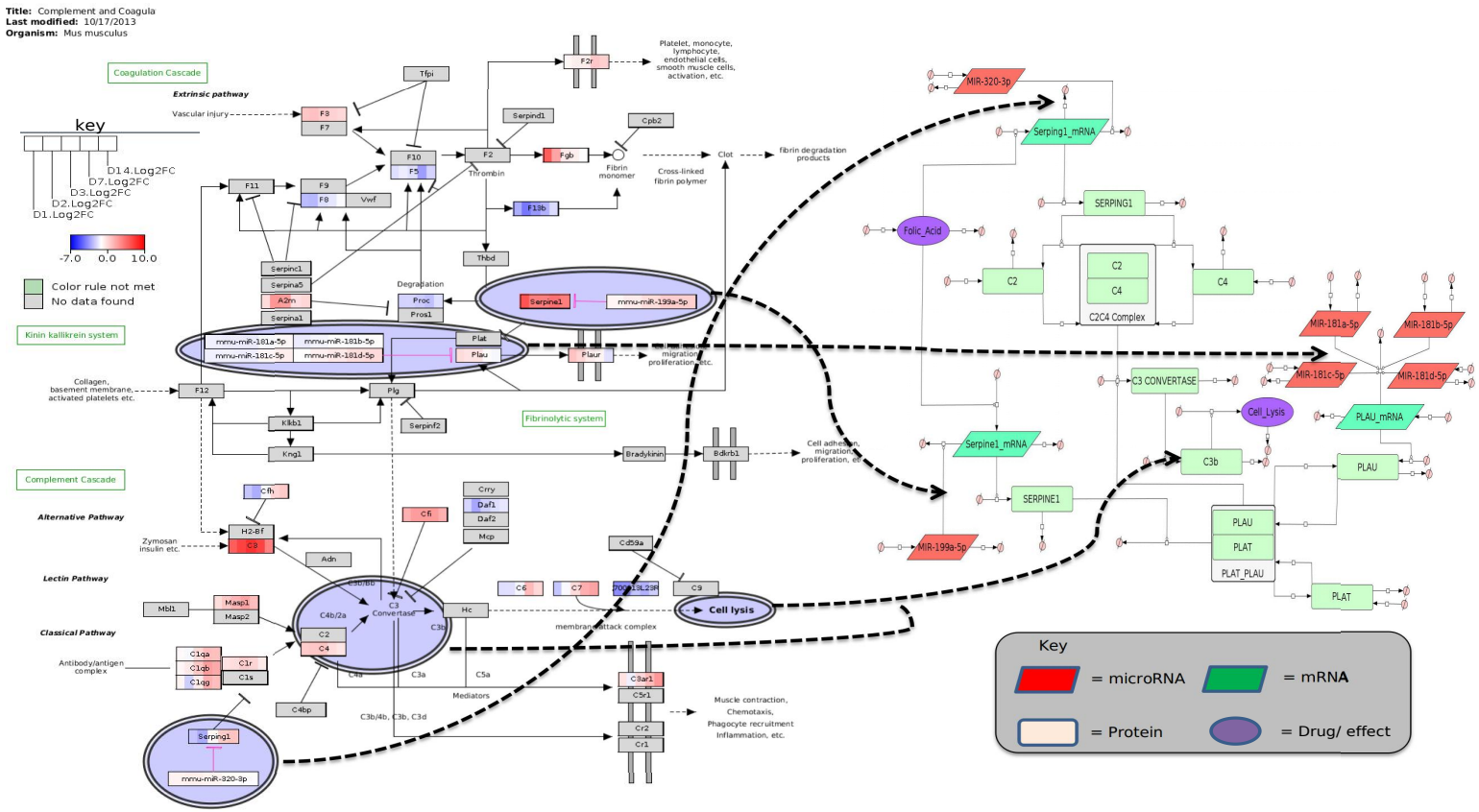


Final stages of review as a Bioconductor packgage.

TimiRGeN - Export to pathvisio



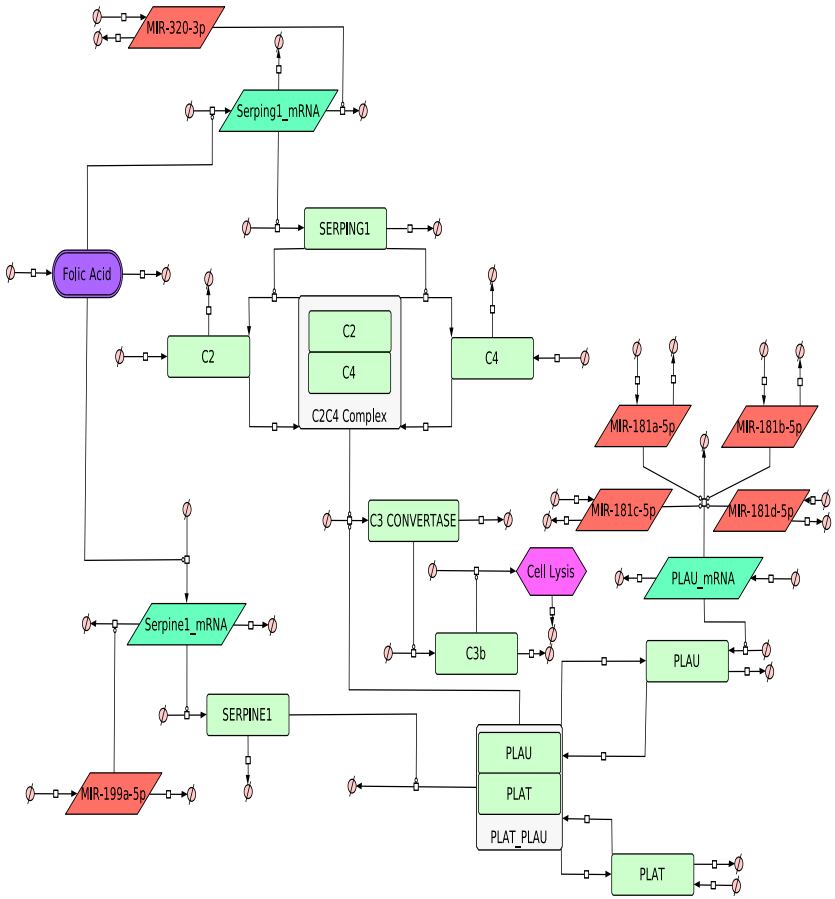
Generation of Gene Regulatory Networks from TimiRGeN

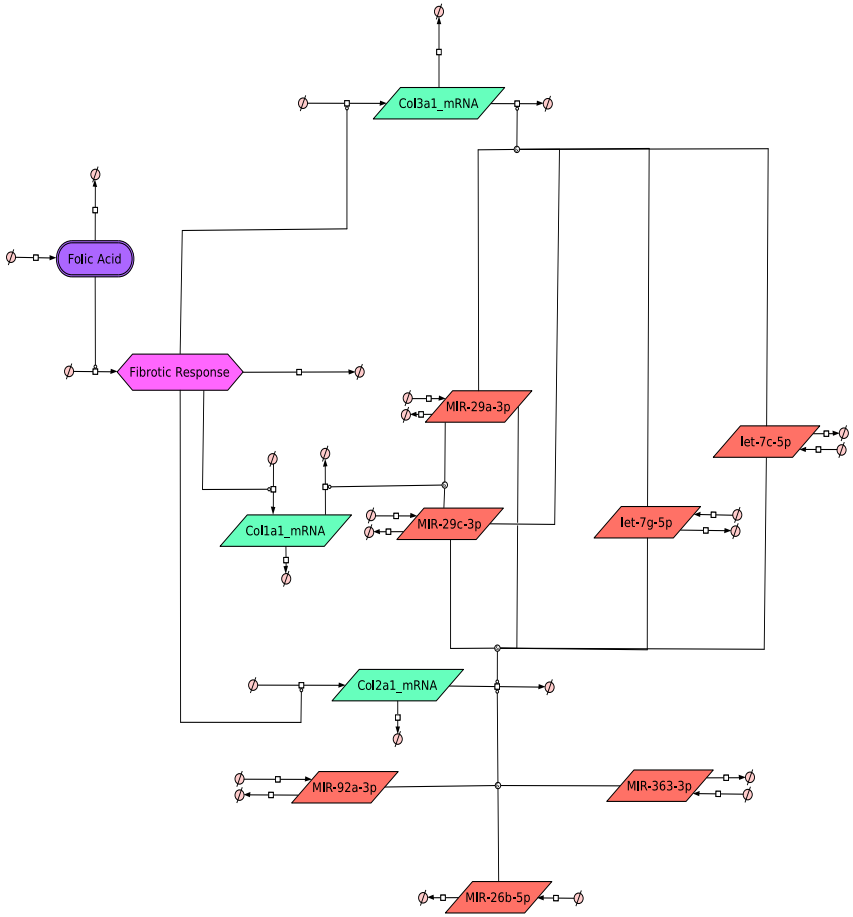


This is a hypthesis generation tool!

GRN construction should be supplemented with a literature search.

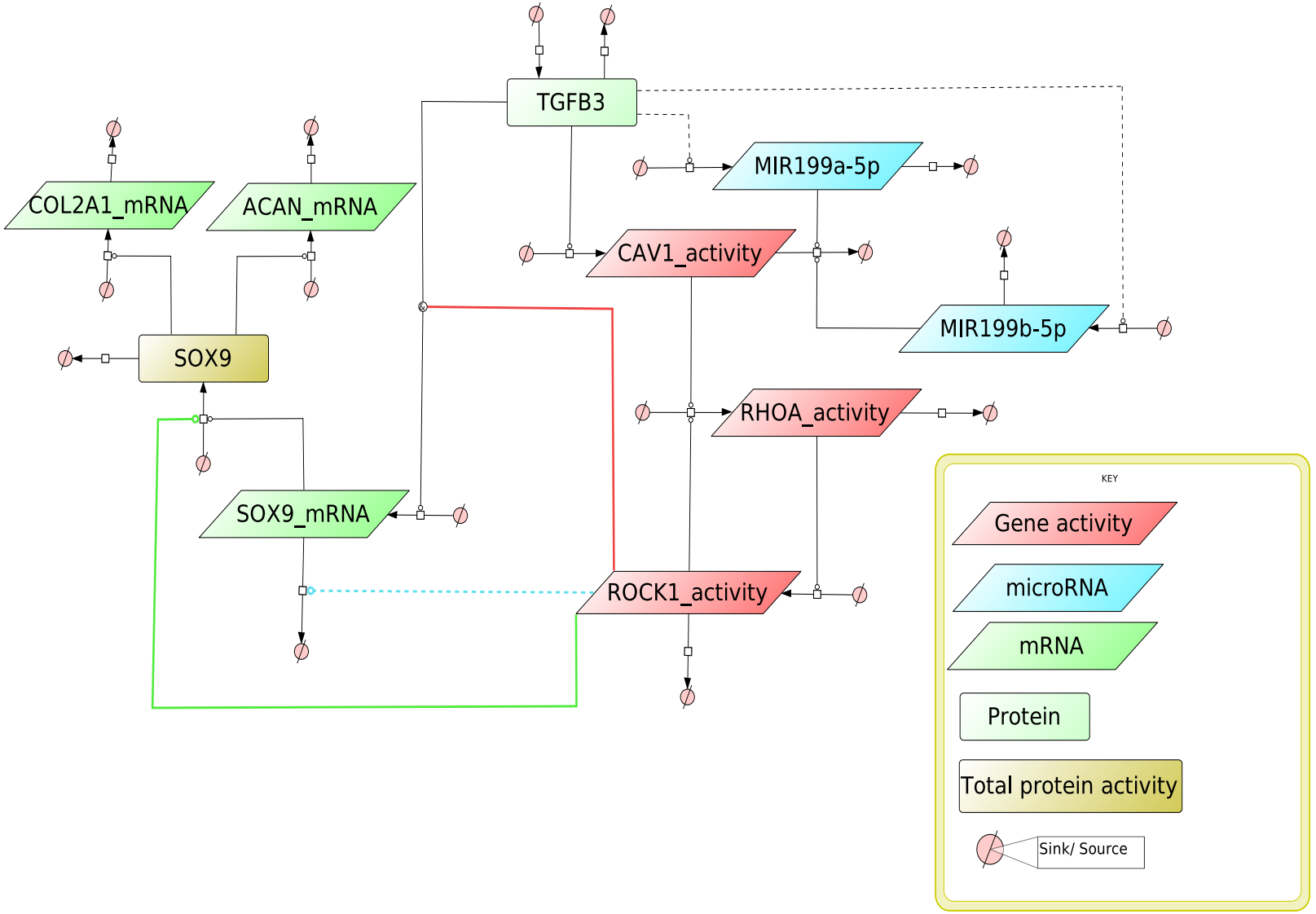
Mouse Kidney Fibrosis GRNs



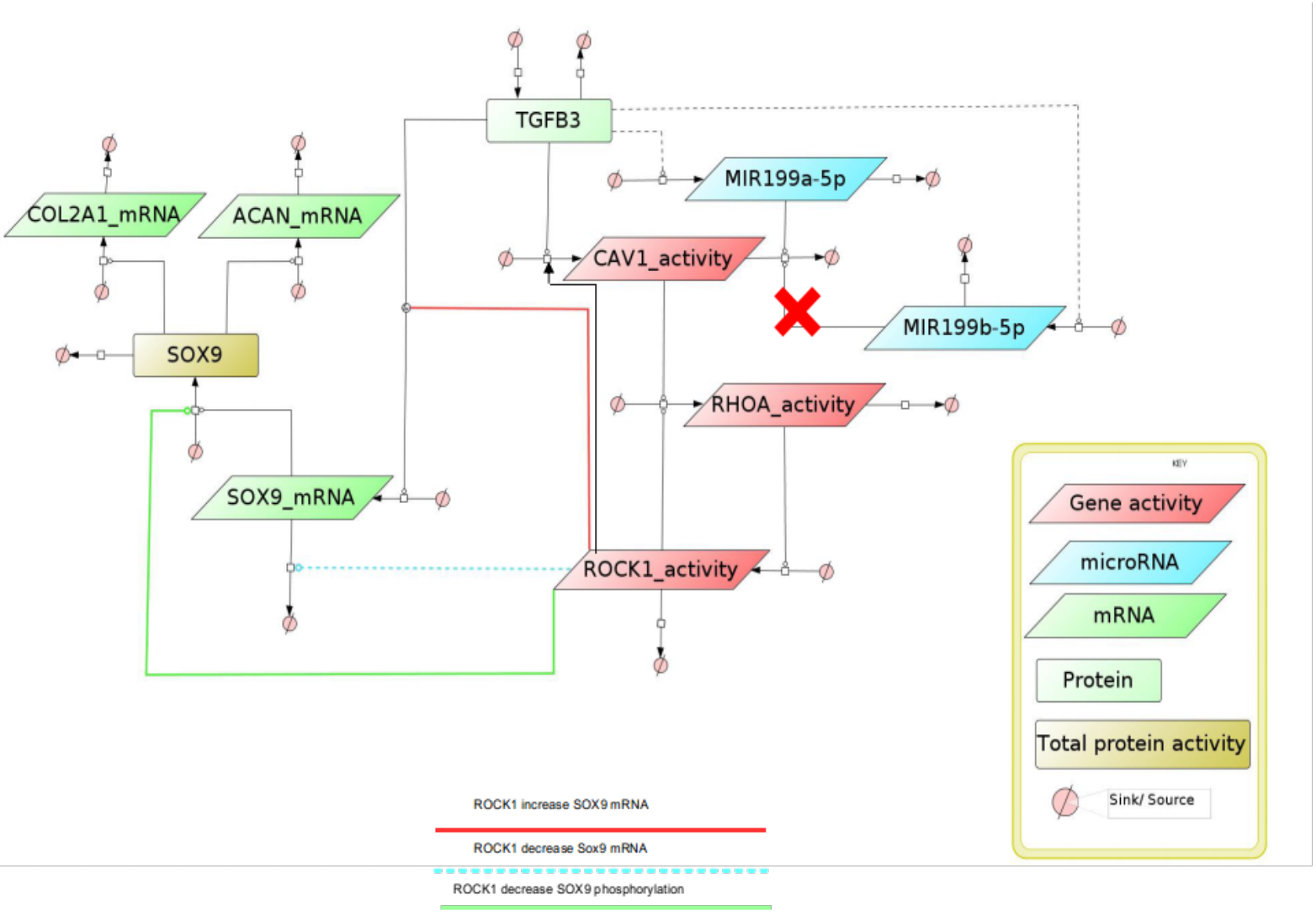


GRNs created respectively from Complement and Coagulation pathway and the Inflammatory Response pathway.

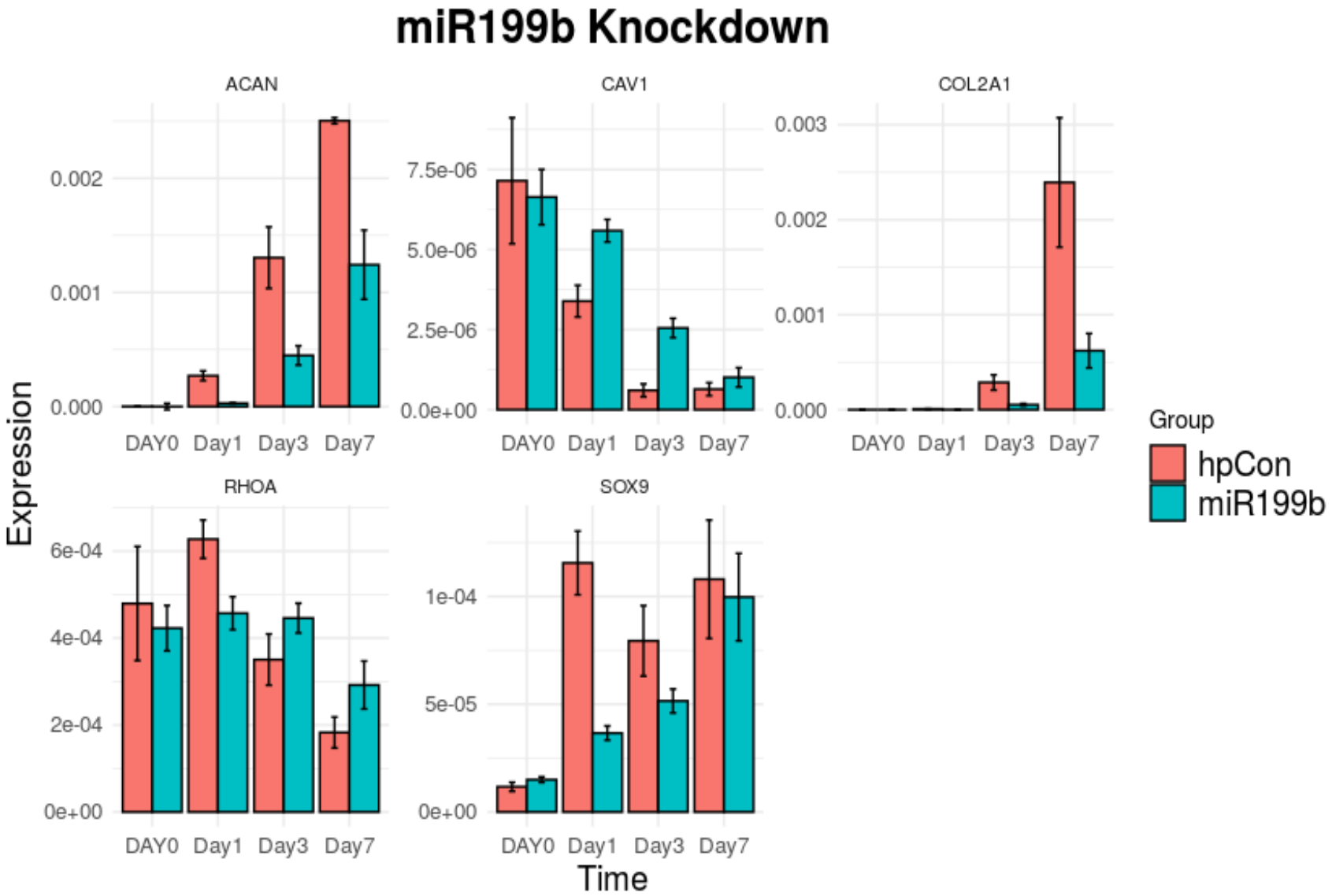
Human Chondrogenesis GRN



Human Chondrogenesis GRN



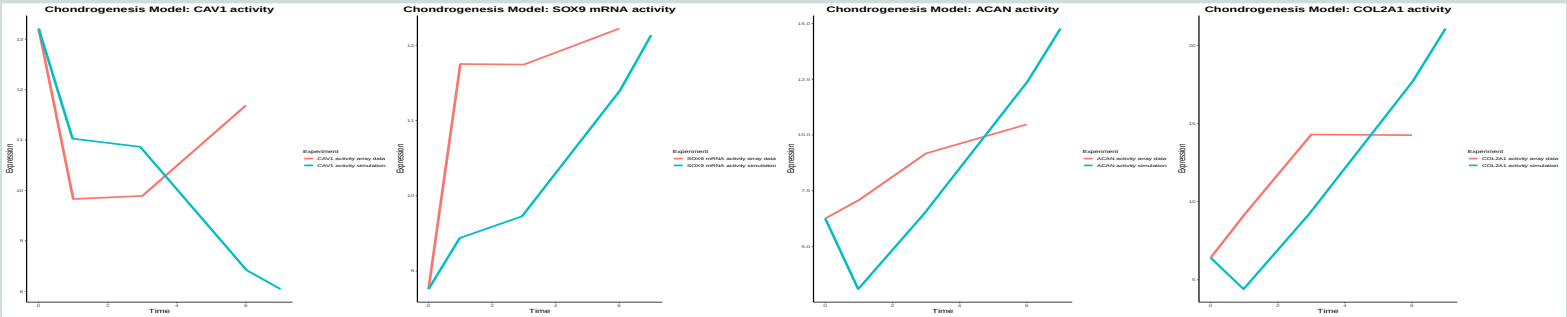
Human Chondrogenesis Data for Model Calibration and Validation



Human Chondrogenesis Modelling

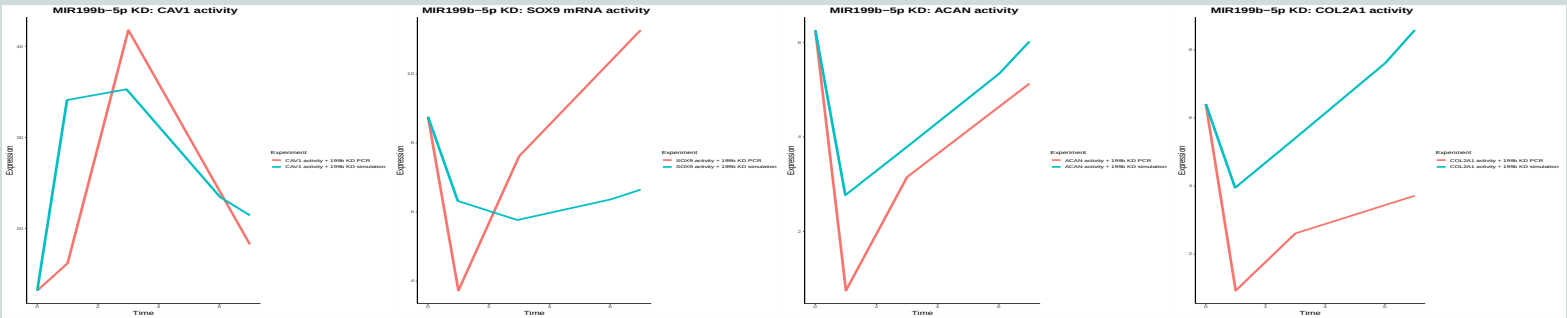
Model Calibration

CAV1 mRNA.....SOX9 mRNA.....ACAN mRNA...COL2A1 mRNA



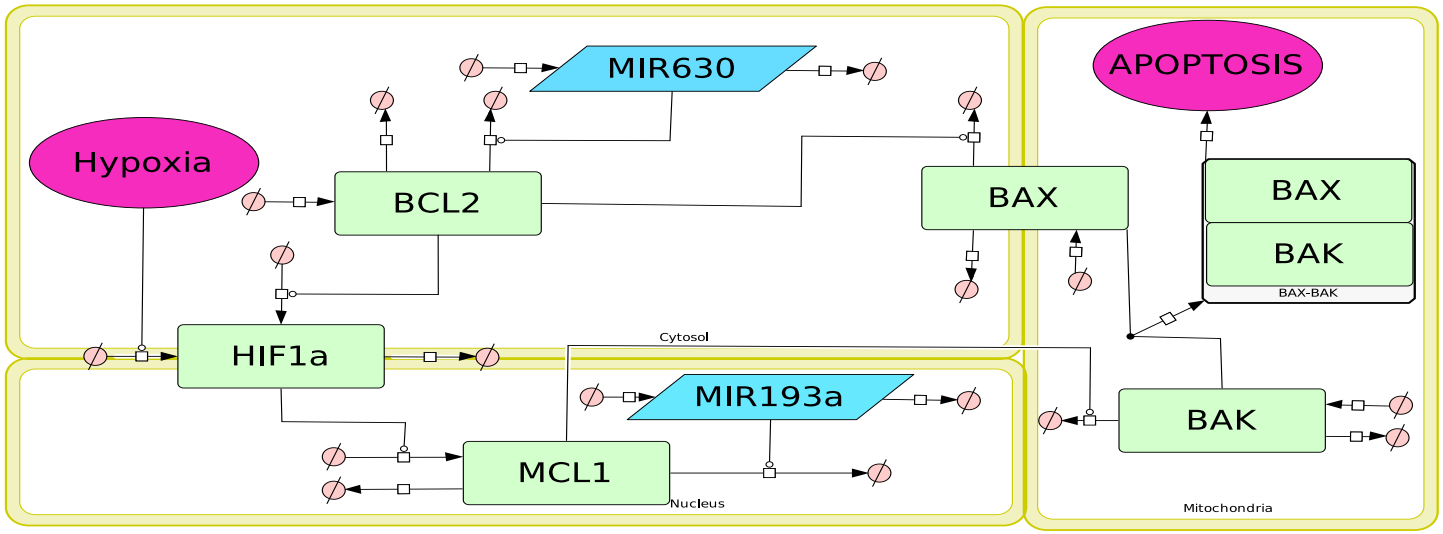
Model Validation - MIR199b KD

CAV1 mRNA.....SOX9 mRNA.....ACAN mRNA...COL2A1 mRNA



Hypoxia-Apoptosis GRN

MIR630-MIR193a Apoptosis model



miR-mRNA interactions reported in cancers

Oncotarget. 2018 Mar 2; 9(17): 13758–13767. PMCID: PMC5862613
Published online 2018 Feb 9. doi: 10.18632/oncotarget.24474 PMID: 29568392

MicroRNA-630 may confer favorable cisplatin-based chemotherapy and clinical outcomes in non-small cell lung cancer by targeting Bcl-2

Ming-Jenn Chen,[1,2,*] De-Wei Wu,[3,*] Gao-Chang Wang,[3] Yao-Chen Wang,[4,6] Chi-Yi Chen,[5,6] and Huei Lee[3]

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Original Paper | Published: 02 April 2013

Ionizing radiation-inducible microRNA miR-193a-3p induces apoptosis by directly targeting Mcl-1

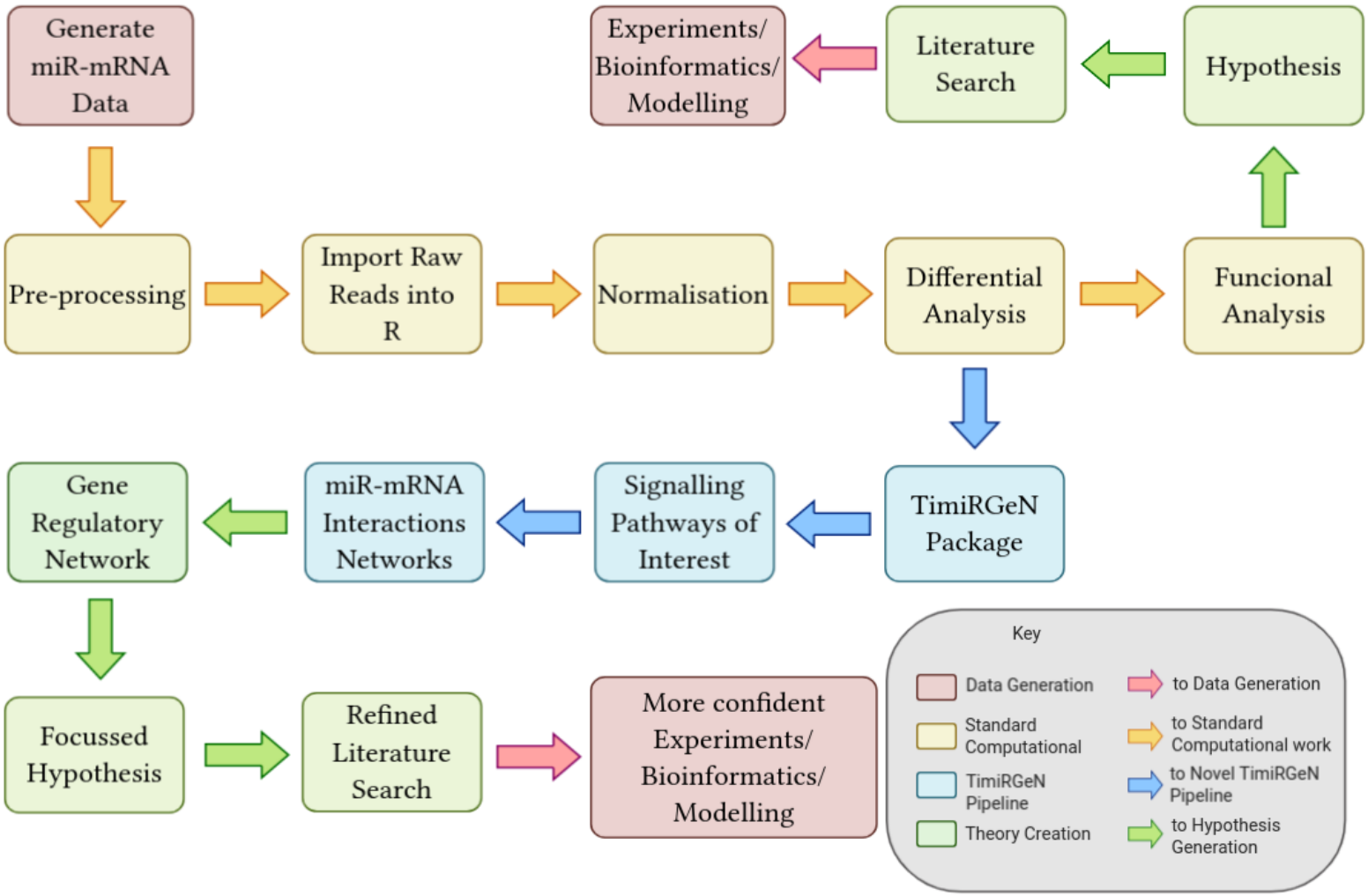
Jeong-Eun Kwon, Bu-Yeon Kim, Seo-Young Kwak, In-Hwa Bae & Young-Hoon Han

Apoptosis **18**, 896–909(2013) | Cite this article

1201 Accesses | **63** Citations | Metrics

Abstract

TimiRGeN as part of general miR expression analysis



Thanks

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