

Characterizing clinically relevant lncRNAs in cancer



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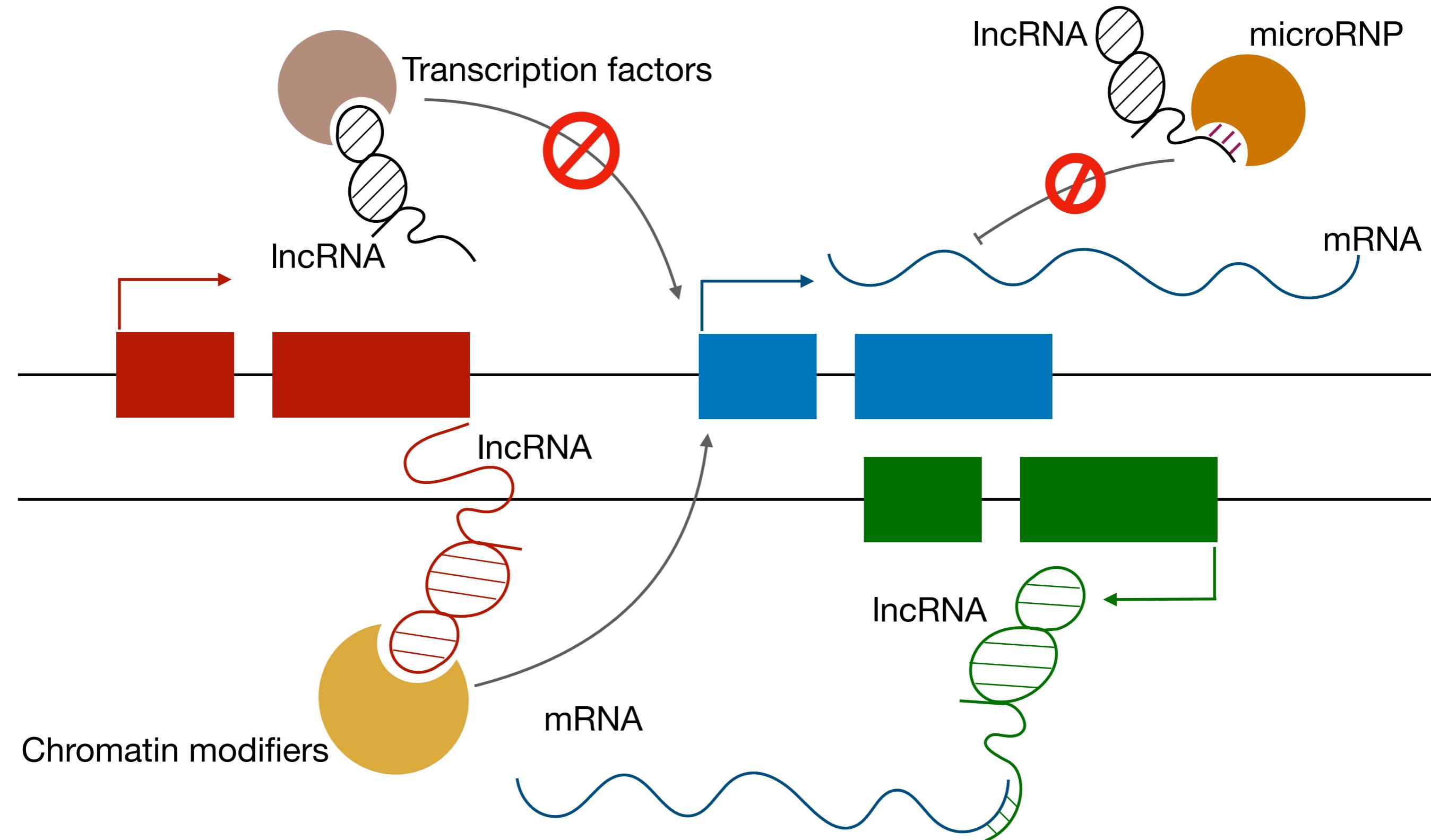
integrative
network
biology

ontario institute for cancer research | university of toronto | canada

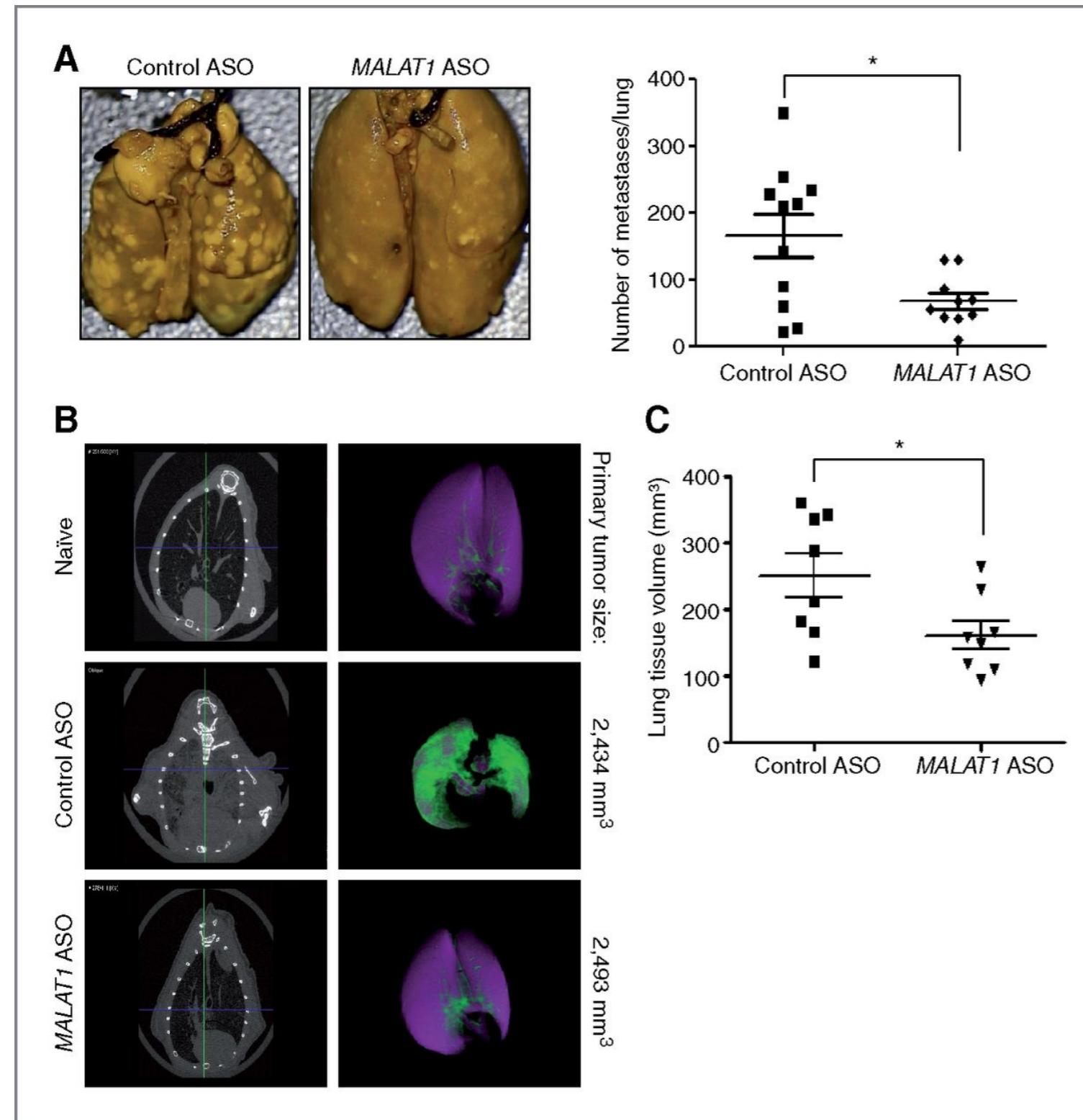


Karina Isaev
MSc. Candidate

Functions of Long non-coding RNAs (lncRNAs)



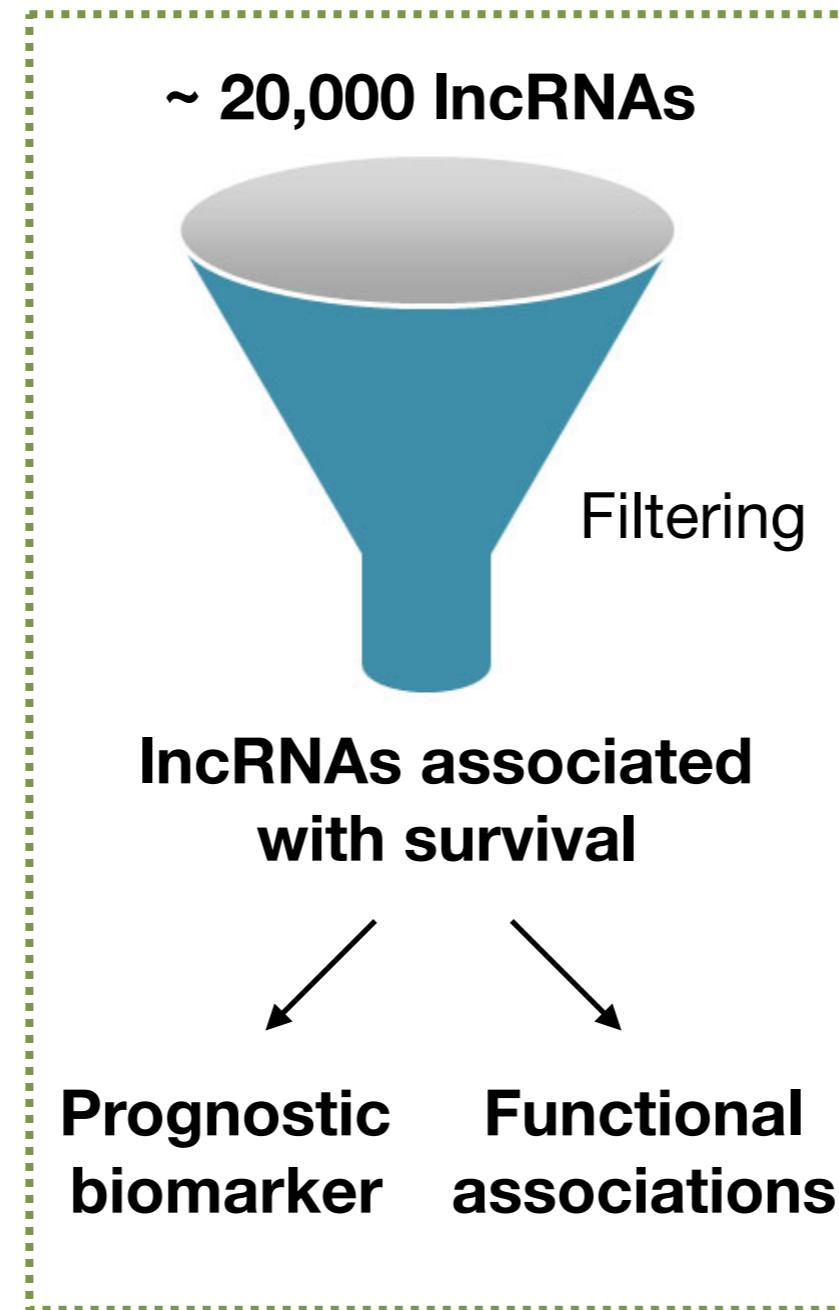
Long non-coding RNAs (lncRNAs) in cancer



MALAT1

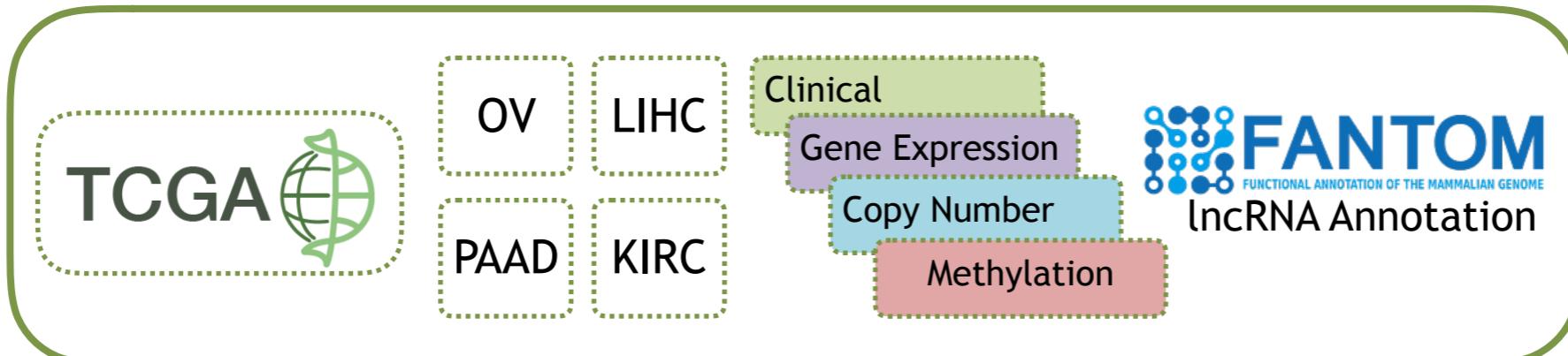
- Highly conserved
- Nuclear lncRNA
- Predictive marker of metastasis in lung cancer

Long non-coding RNAs (lncRNAs) in cancer



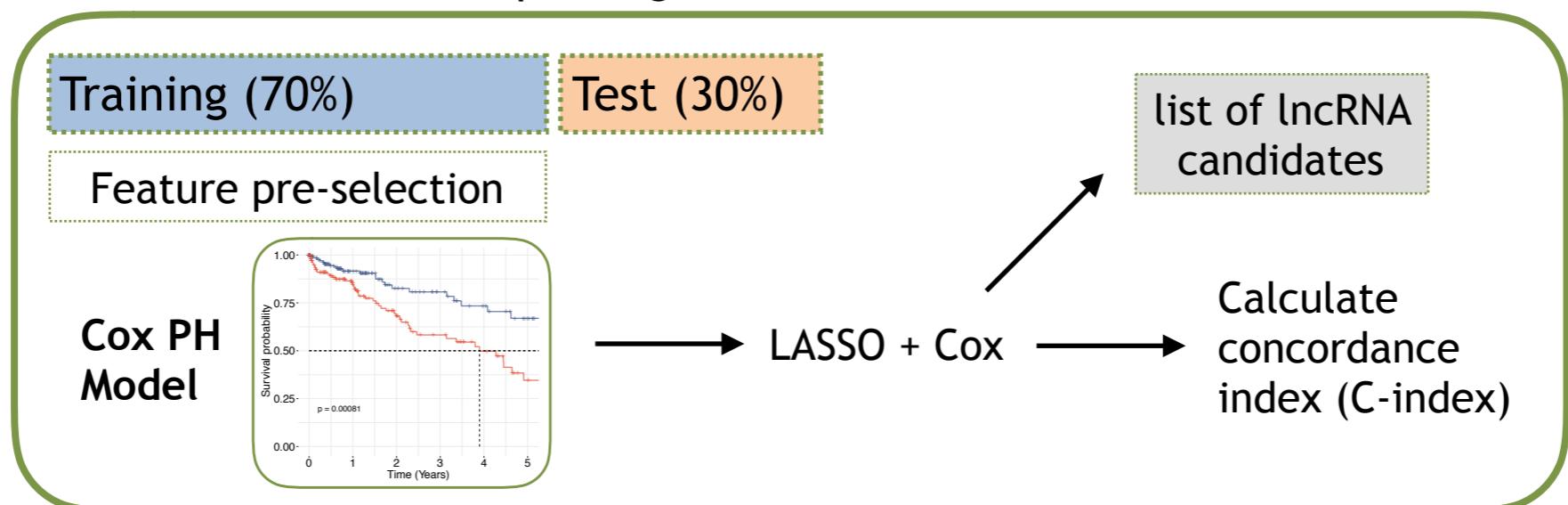
Methods and Workflow

Data

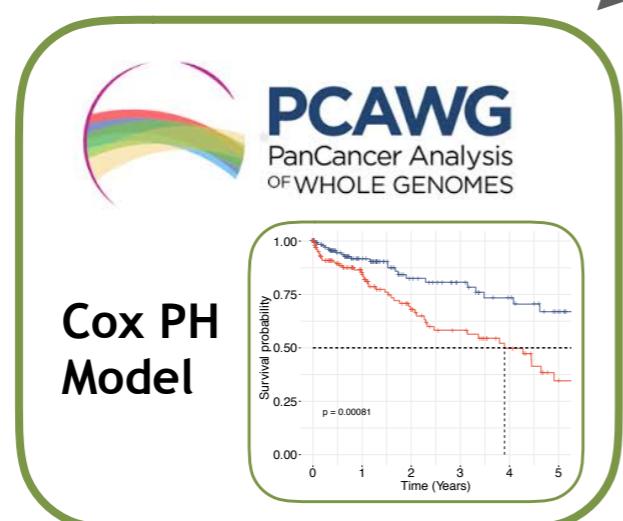


1000 times of random splitting

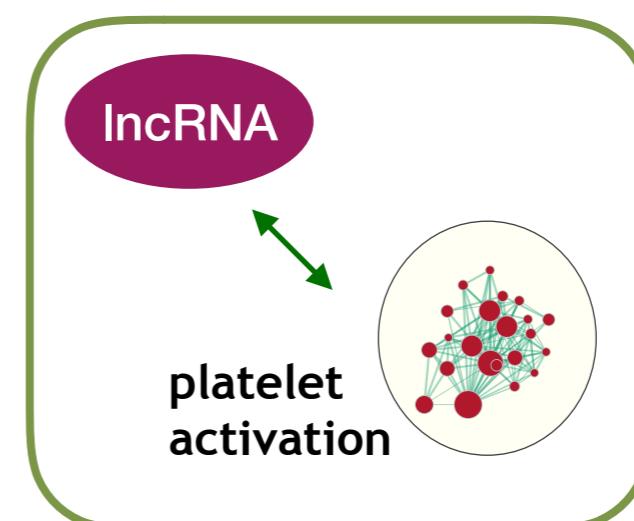
Identifying lncRNA Candidates



External Validation

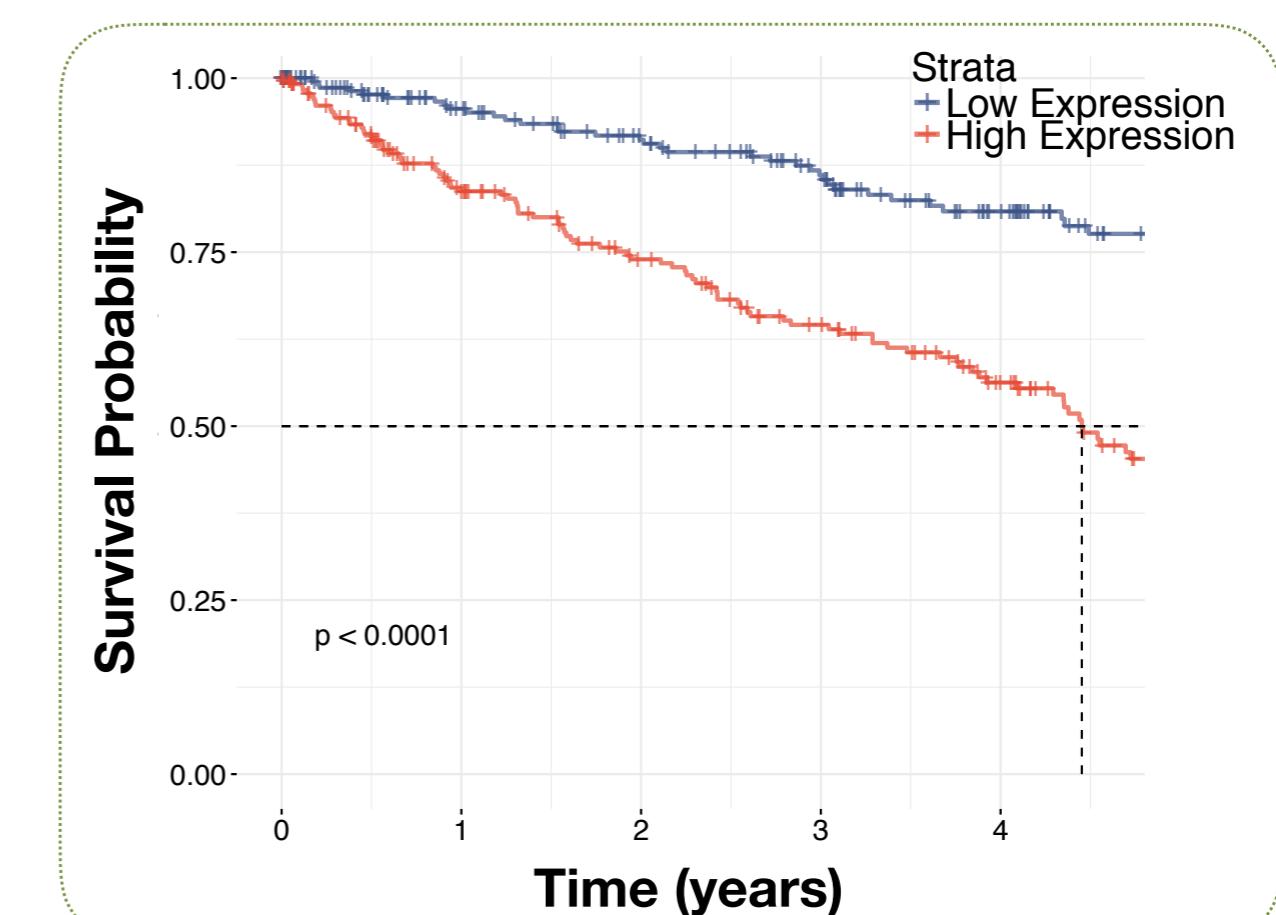
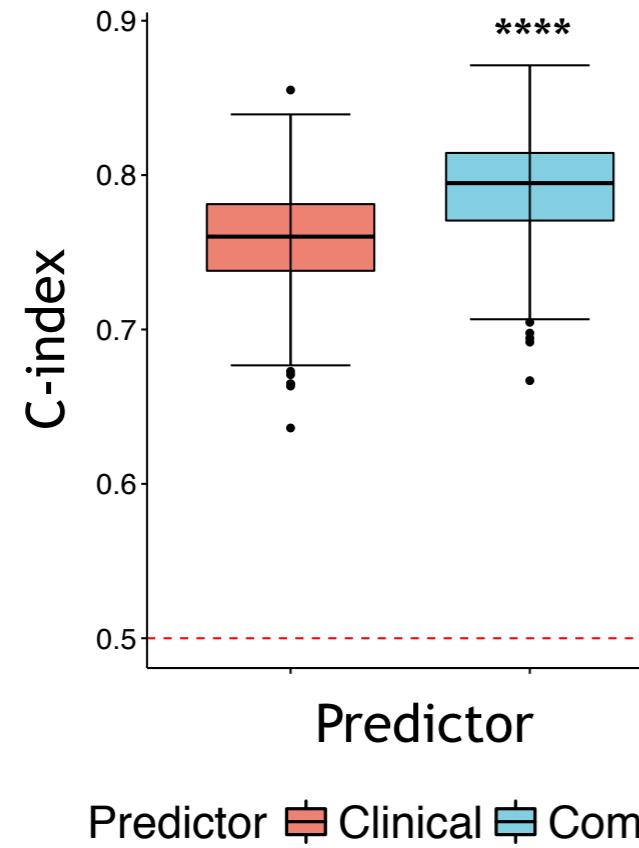


Functional Associations

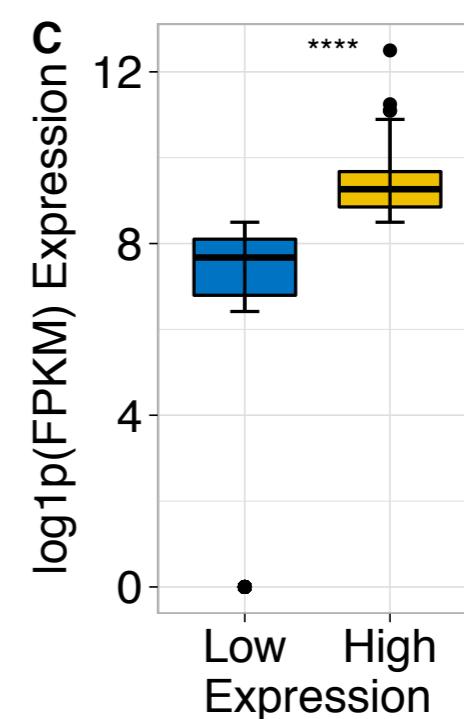
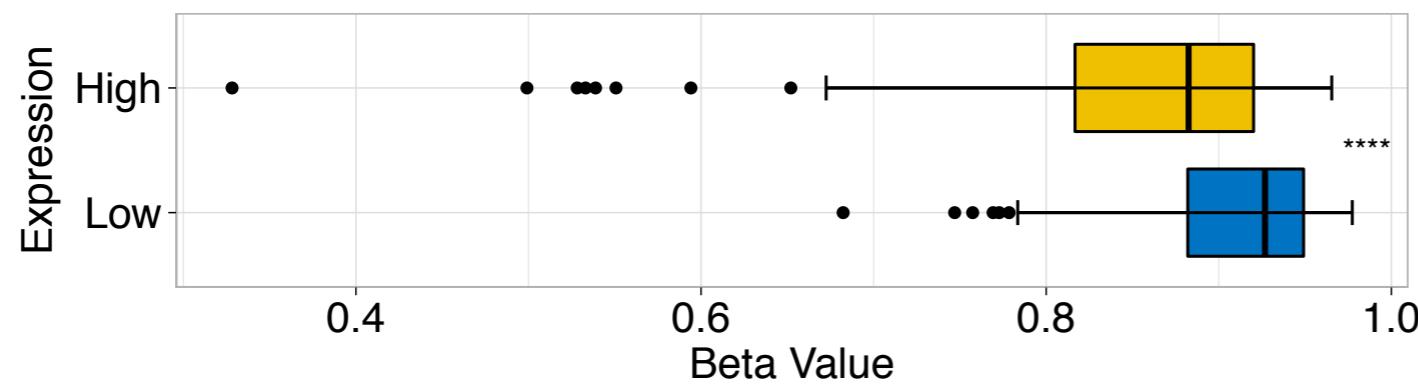


CTA-384D8.34 is the top candidate in KIRC

Comparison of Cox Models in KIRC

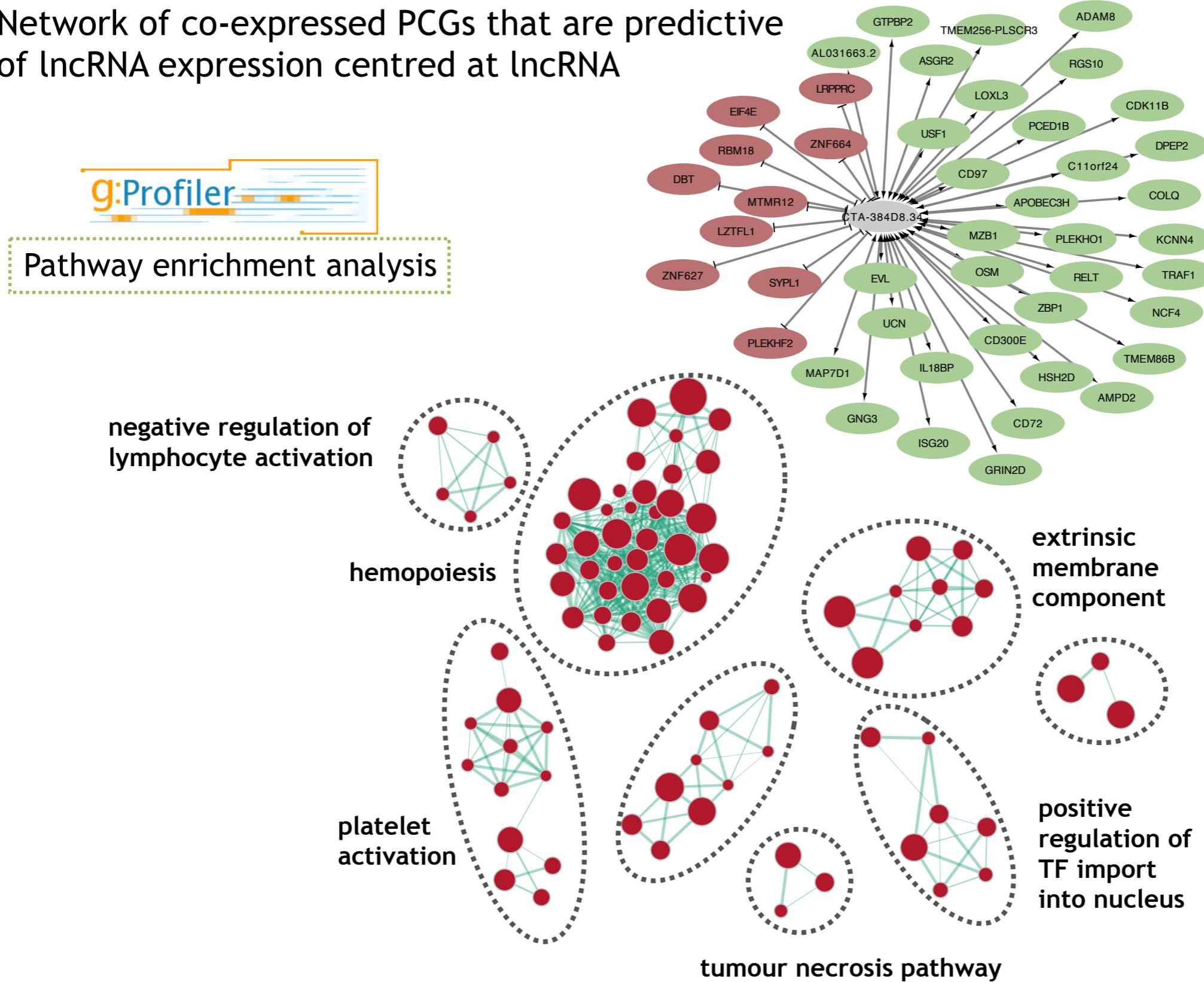


CTA-384D8.34 promoter methylation is inversely correlated with gene expression and is clinically favourable in KIRC



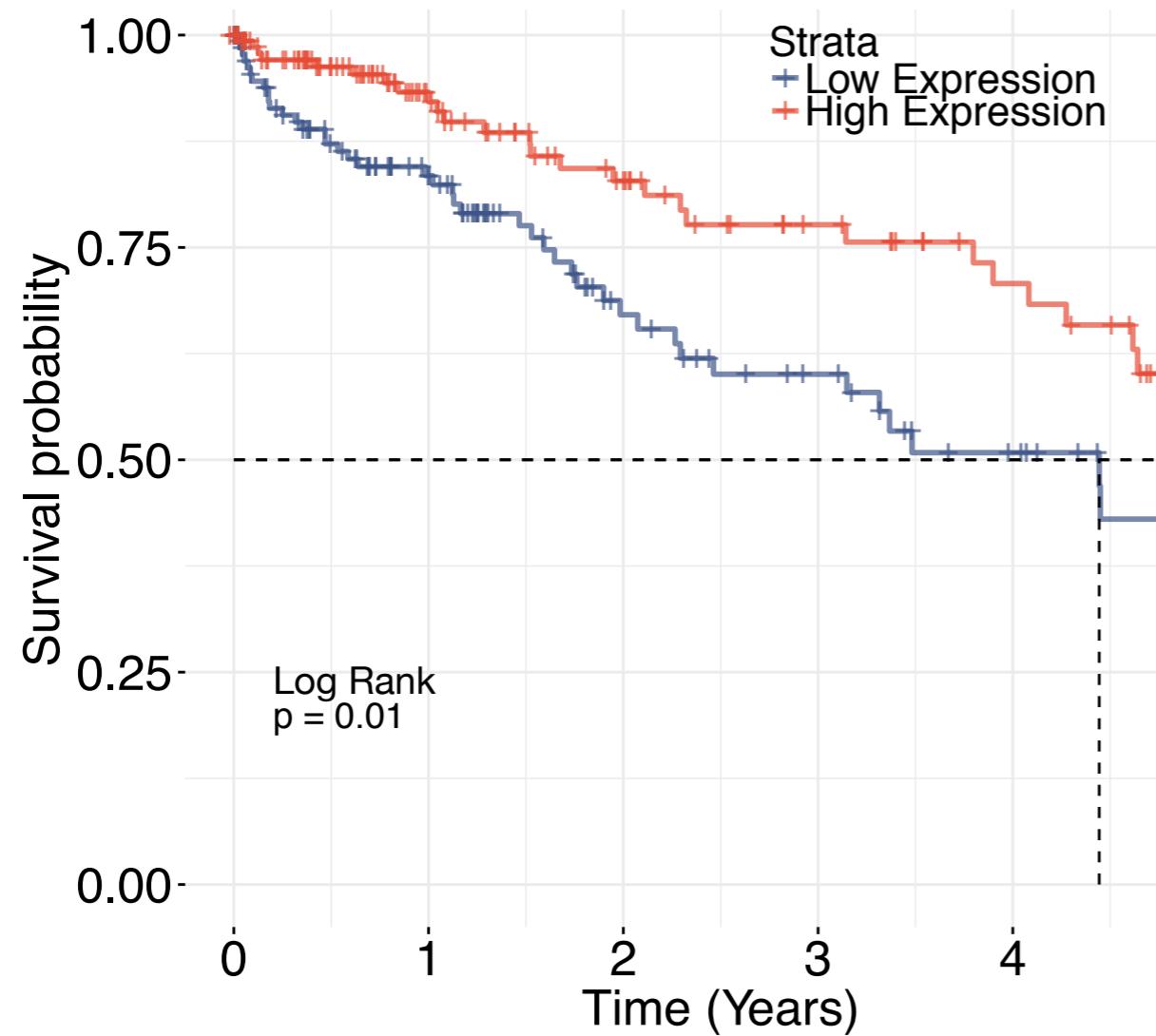
Genes co-expressed with *CTA-384D8.34* are associated with immune response

Network of co-expressed PCGs that are predictive of lncRNA expression centred at lncRNA

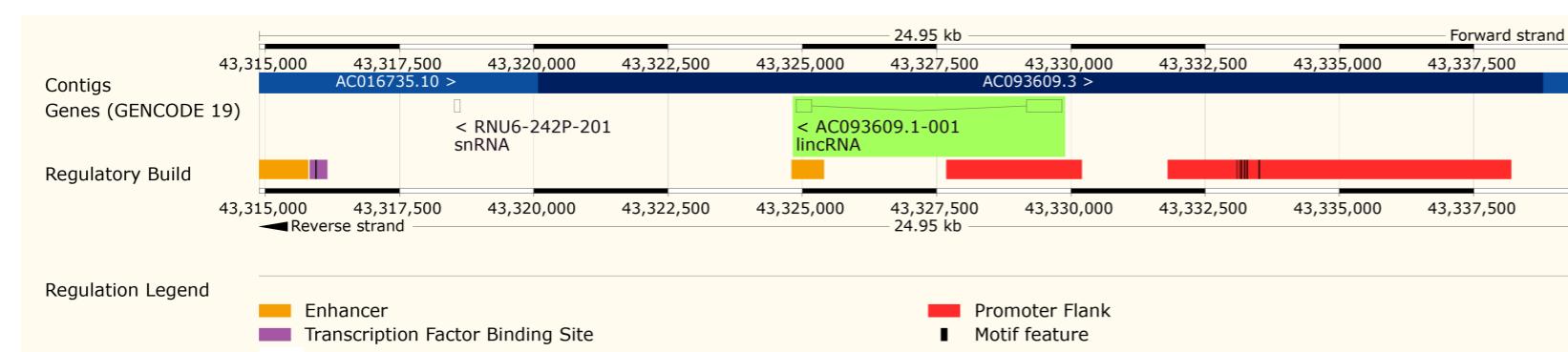
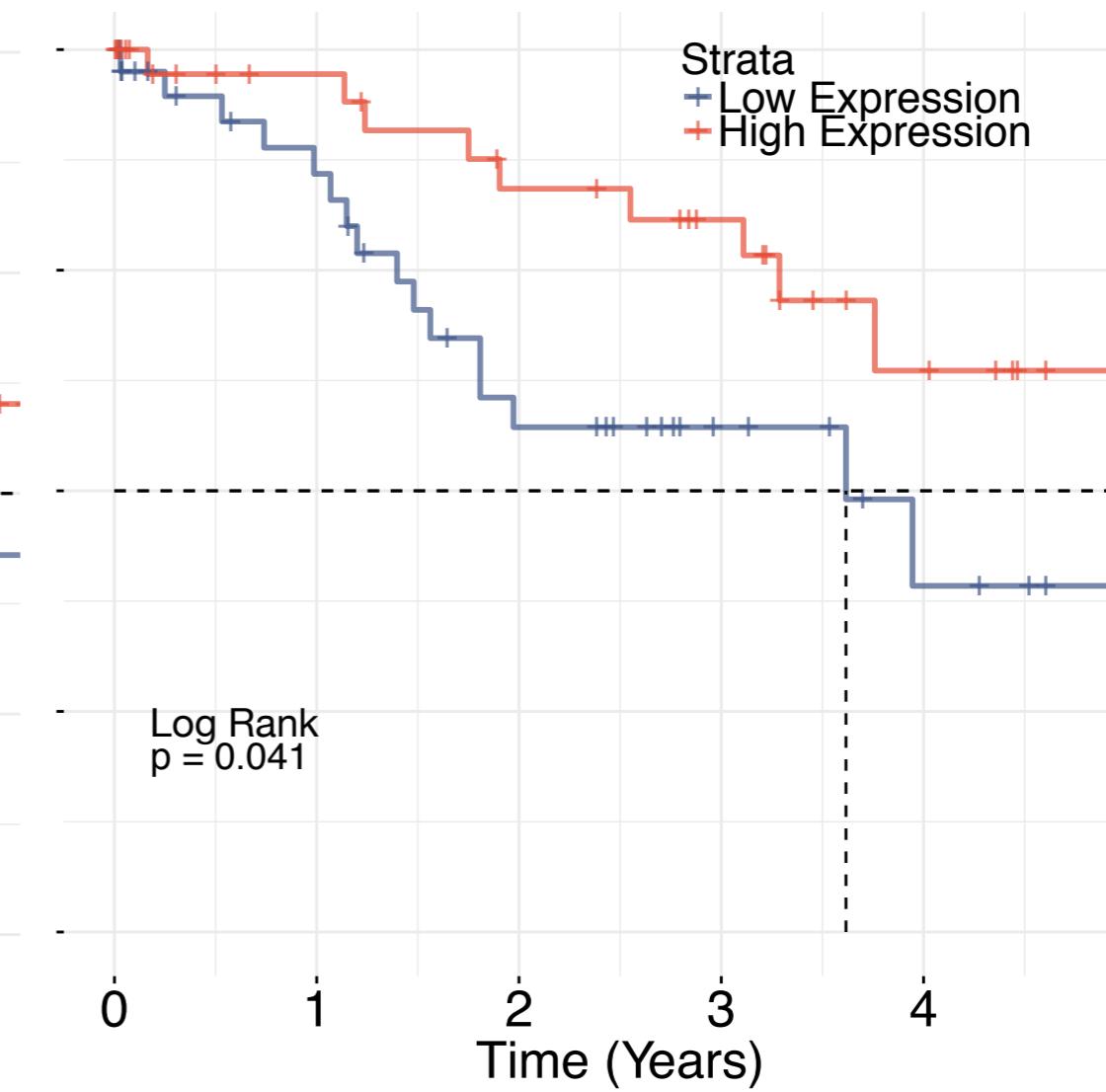


Preliminary external validation of lncRNA prognostic expression

AC093609.1 expression in TCGA LIHC is favourable, HR = 0.47



AC093609.1 expression in PCAWG LIHC is favourable, HR = 0.44



Thank you!

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