

## Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion

Babaei, Sepideh; Hulsman, Marc; Reinders, Marcel; de Ridder, Jeroen

### Publication date

2012

### Document Version

Final published version

### Citation (APA)

Babaei, S., Hulsman, M., Reinders, M., & de Ridder, J. (2012). *Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion*. 1.

### Important note

To cite this publication, please use the final published version (if applicable).  
Please check the document version above.

### Copyright

Other than for strictly personal use, it is not permitted to download, forward or distribute the text or part of it, without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license such as Creative Commons.

### Takedown policy

Please contact us and provide details if you believe this document breaches copyrights.  
We will remove access to the work immediately and investigate your claim.

# Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion

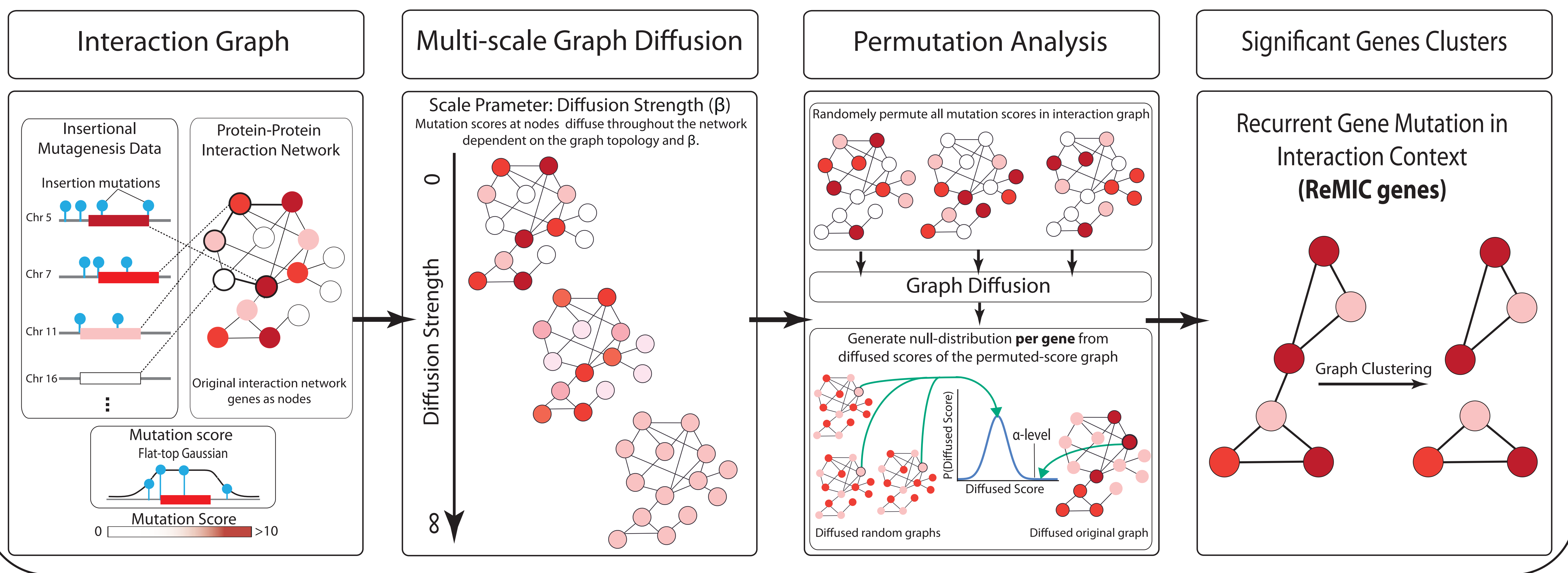
Sepideh Babaei<sup>1,2</sup>, Marc Hulsman<sup>1</sup>, Marcel Reinders<sup>1,2</sup>, Jeroen de Ridder<sup>1,2</sup>

<sup>1</sup>Delft Bioinformatics Lab, Delft University of Technology, <sup>2</sup>Netherlands Bioinformatics Center.

## Summary

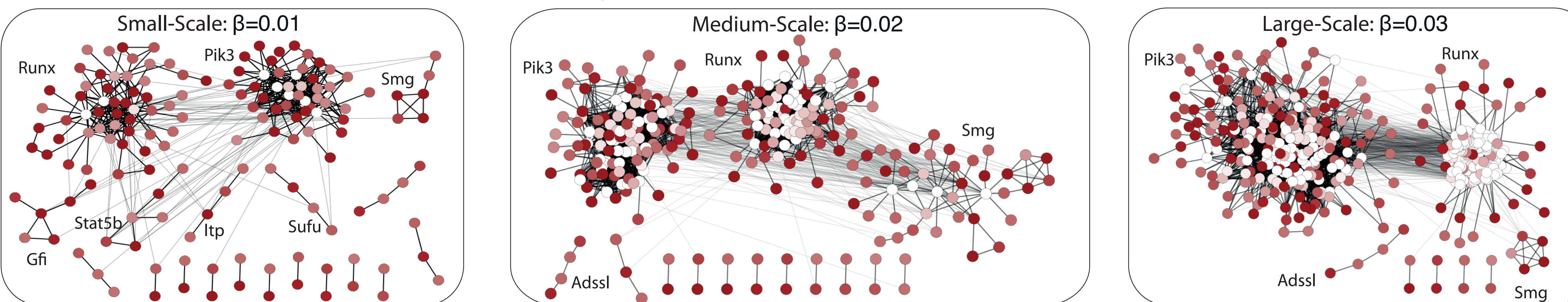
We introduce a multi-scale kernel diffusion framework and apply it to a large collection of murine retroviral insertional mutagenesis data. The diffusion strength plays the role of scale parameter. As a result, in addition to detecting genes with frequent mutations in their **genomic vicinity** (red nodes in the interaction graph) we can also find genes that harbor frequent mutations in their **interaction network context** (white and pink nodes).

## Methods

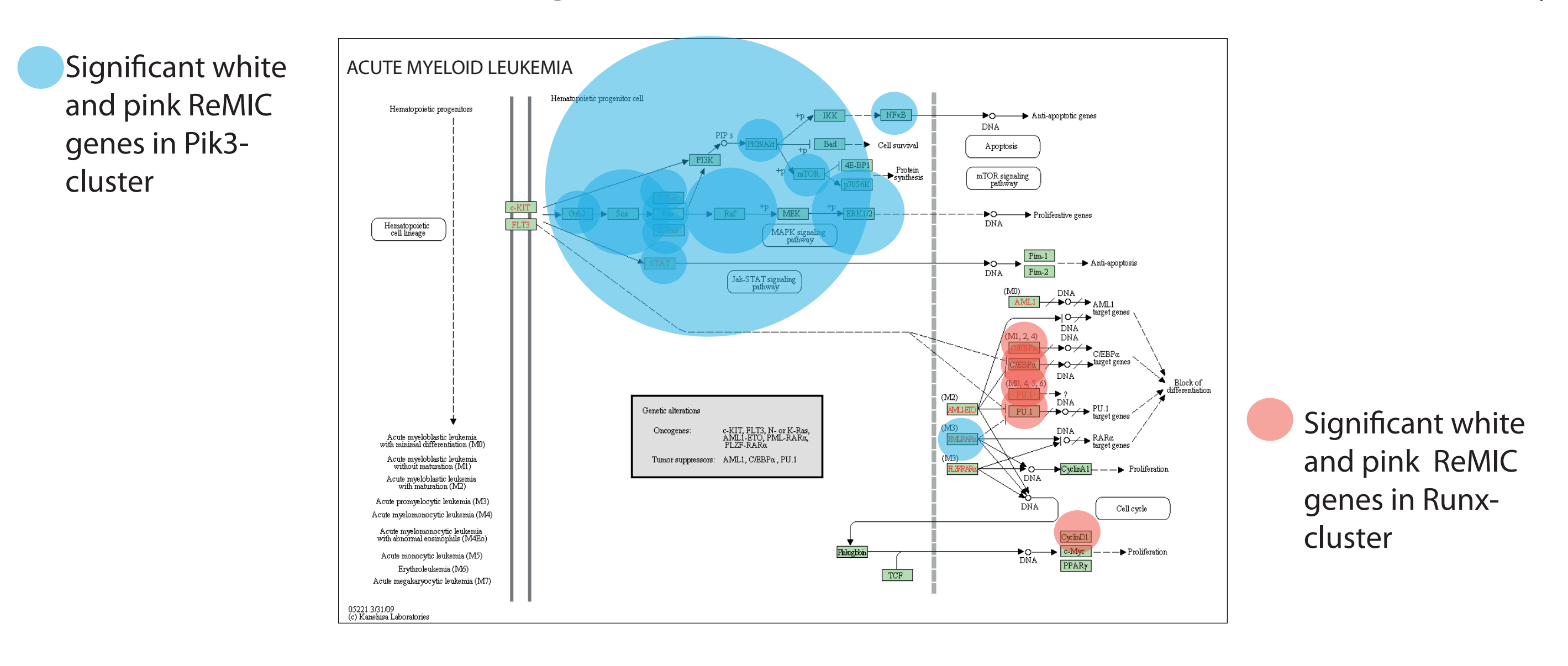


## Results

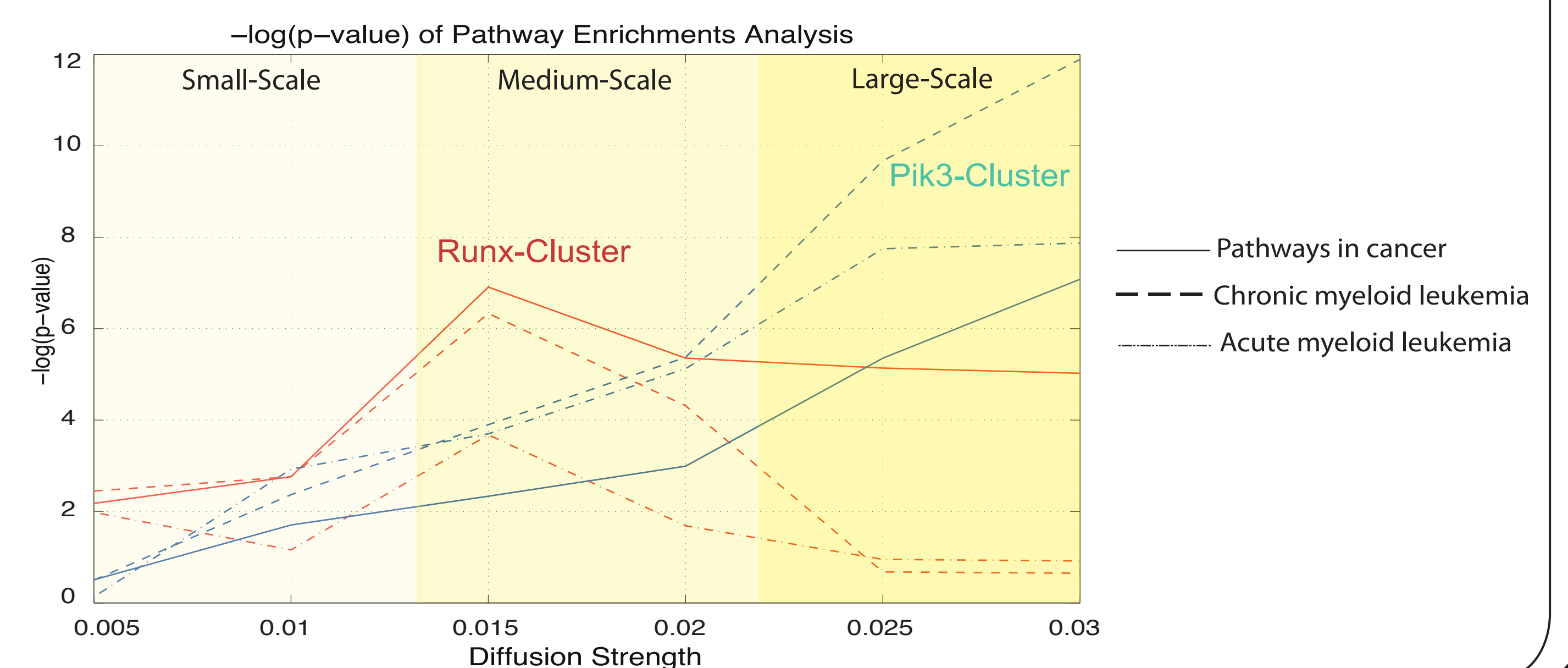
ReMIC genes clusters in 3 diffusion scale-levels



White and Pink ReMIC genes are co-localized in Leukemia Pathway



ReMIC clusters are enriched for cancer related pathways



## Conclusion

We identify densely connected components of known and novel cancer genes. They are strongly enriched for cancer related pathways across the diffusion scales. The mutations in the clusters exhibit a **significant pattern of mutual exclusion**. The results demonstrate the importance of defining recurrent mutations in the **interaction network context** at **multiple scales**.

Acknowledgments: The author is supported by the **Swiss Foundation for Excellence and Talent in Biomedical Research** fellowship to attend ECCB12.