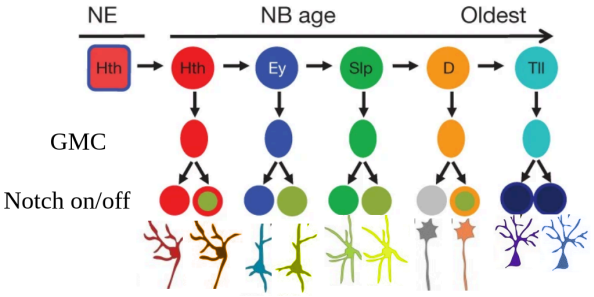

Figure A. ***Temporal transcription factors define early neuronal identity in a sequential cascade.***
Neuroblasts (NBs) express a cascade of temporal transcription factors, here Hth, Ey, Slp, D, and Tll, as they age, progressing from youngest to oldest (left to right).
Each NB division generates a GMC, which divides once to produce two post-mitotic neurons. Early neuronal fate is influenced by the NB's temporal identity and Notch signaling (on/off) in the daughter cells.

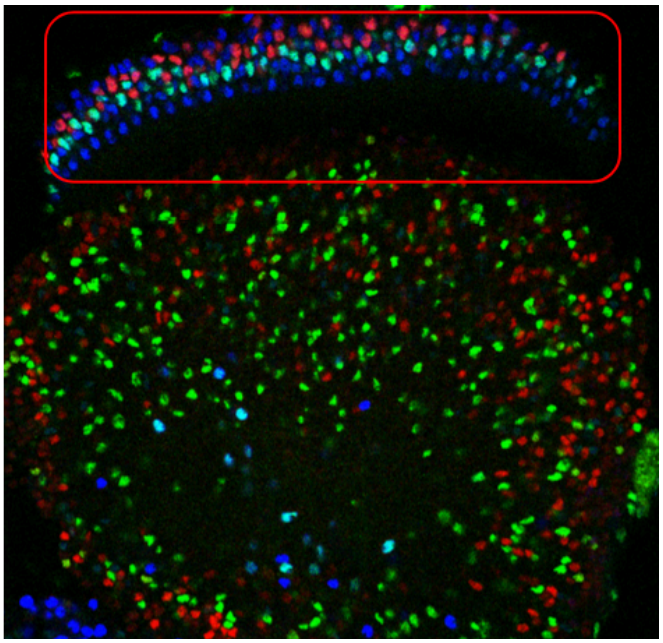

Figure 2. Presence of different transcription factors of the Lamina Cells, framed in red: Dan (blue), Svp (green), and Erm (red). Confirmation by immunofluorescence that while Dan is expressed in all other lamina neurons (L1, L2, L4, L5), it is not expressed in Erm-expressing L3 neurons.

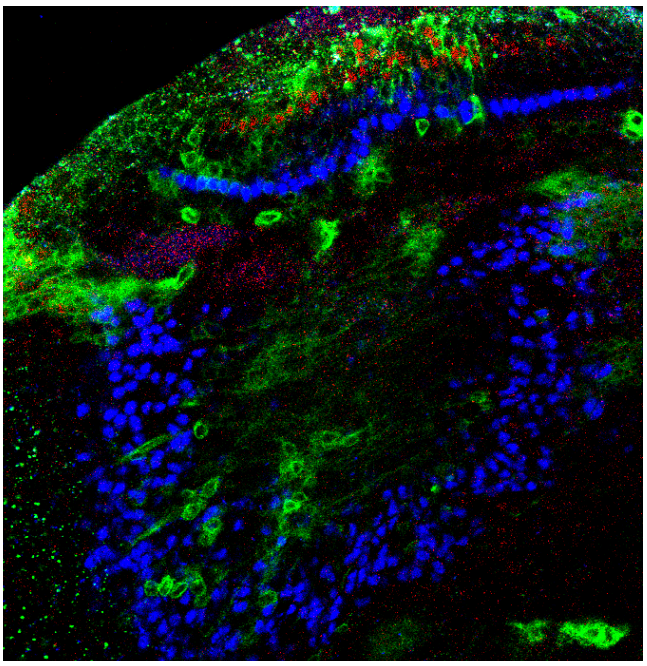

Figure 3. Double mutant of Dan and Danr in the Drosophila melanogaster using MARCM clones. Mutant cells are identified by the absence of GFP labeling, which marks wild-type cells in green (*Svp*). *Bsh* (blue) and *Erm* (red) label different neuronal populations. The MARCM clones lacking GFP appear as distinct patches (e.g., center and lower left), showing no apparent disruption in the expression of *Bsh* or *Erm*. This suggests that the composition of neuronal cell types remains unchanged despite the loss of both dan and danr.

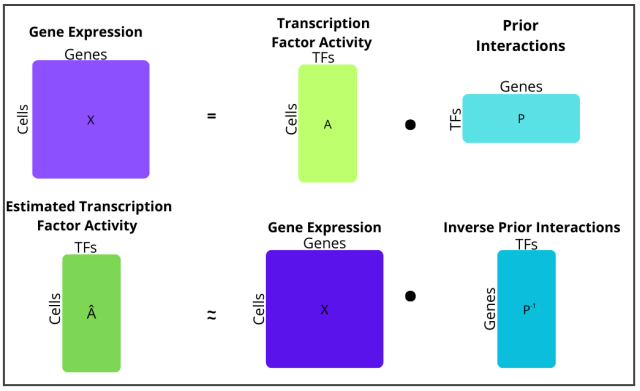

Figure 4. ***Schematic of TFA inference using gene expression and prior regulatory information.***

Top: Gene expression (**X**) is modeled as the linear product of latent transcription factor activity (**A**) and the prior connectivity matrix (**P**) describing TF-target relationships.

Bottom: TFA (**Â**) is estimated by the Inferelator as the dot product of the gene expression matrix (**X**) and the pseudoinverse of the prior matrix ($\mathbf{P}^{-1}$).

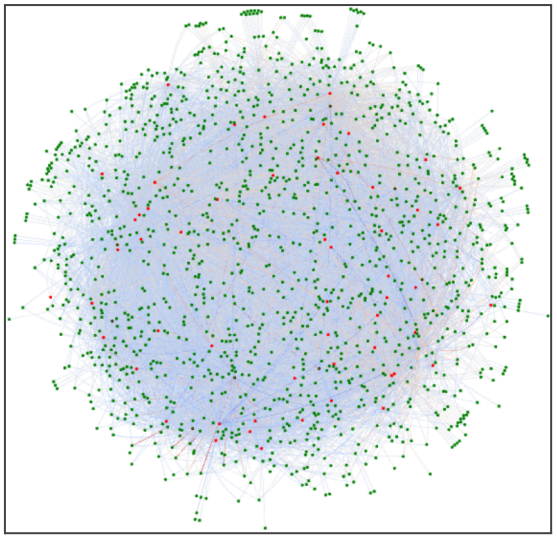

Figure 5. ***Result of the lamina gene regulatory network.*** Full inferred regulatory network showing predicted interactions

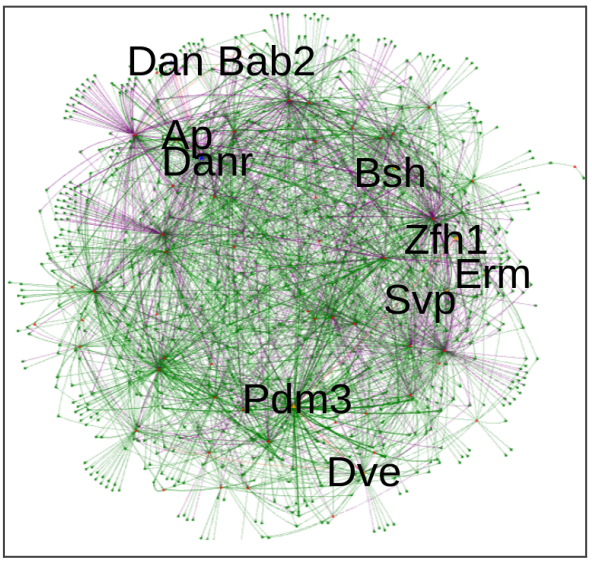

Figure 6. ***Result of the lamina GRN***

Subnetwork among lamina-associated Termina Selectors and all their targets with over 90% confidence.

Green edges represent activations, and purple represents repressions.

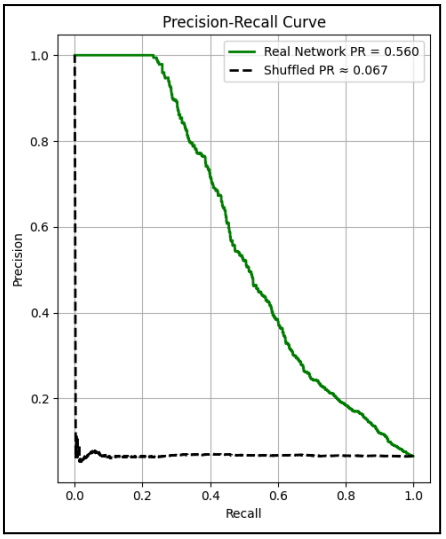

Figure 7. Validation of the Network.
Precision-recall curve showing performance of the inferred network (green) vs shuffled prior (black dashed), indicating high predictive value (PR = 0.560).

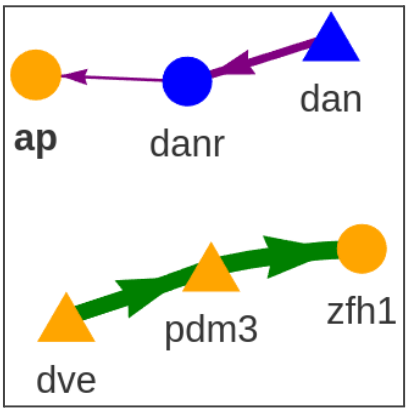

Figure 8. Subnetwork of only lamina-related TSs. Showing directional interactions inferred only with high confidence (90%). Green edges represent activations, and purple represents repressions.
Circles denote target genes, and triangles represent transcription factors.
The arrows indicate the direction of the regulation from the regulator to its target.

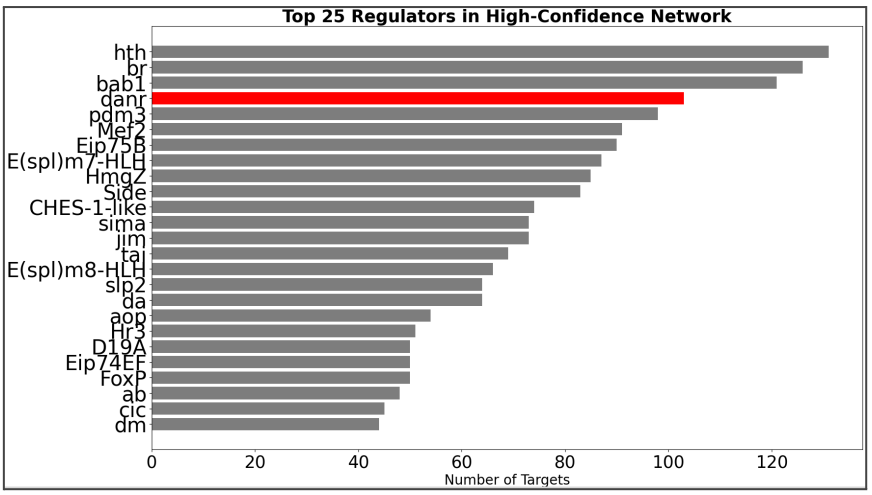

Figure 9. Transcription Factors and Their Predicted Impact

Distribution of top transcriptional regulators in lamina cells, showing Danr among the top regulators with over 90% confidence.

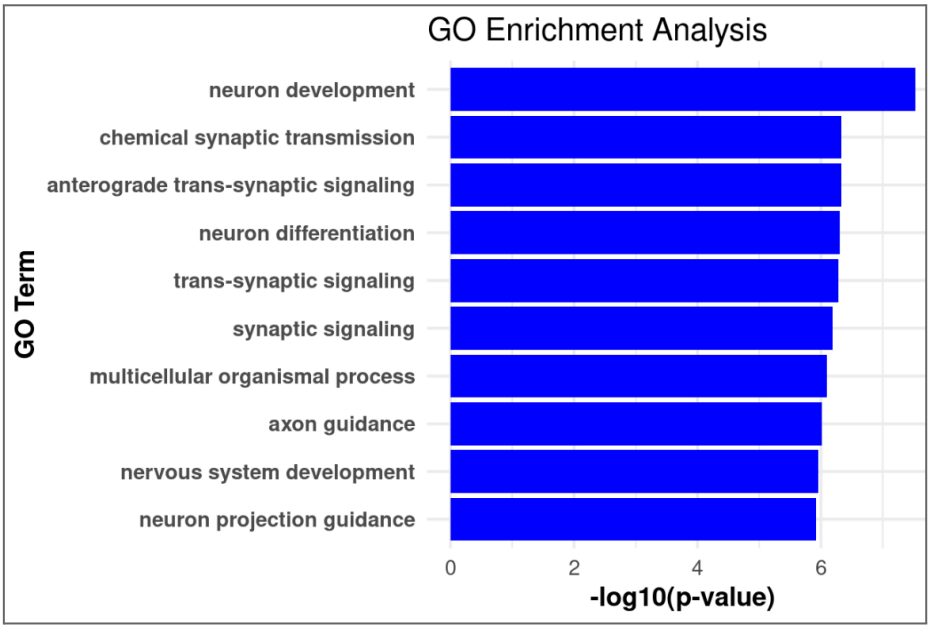

Figure 10. ***Gene Ontology (GO) enrichment analysis of the top 50 predicted Danr target genes (confidence ≥ 90%).***

Barplot displaying the top GO terms associated with neurodevelopmental processes, ranked by statistical significance ($-\log_{10}$(p-value)).