
**Deciphering the role of pipsqueak family genes Dan/Danr in the
identity of Lamina Neurons in the *Drosophila* Visual System**

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Supplementary Materials

This document presents additional figures that support the main findings of our analysis on
the regulatory roles of Dan and Danr in lamina neuron identity.

The PDF file includes: Figures from S1 to S5

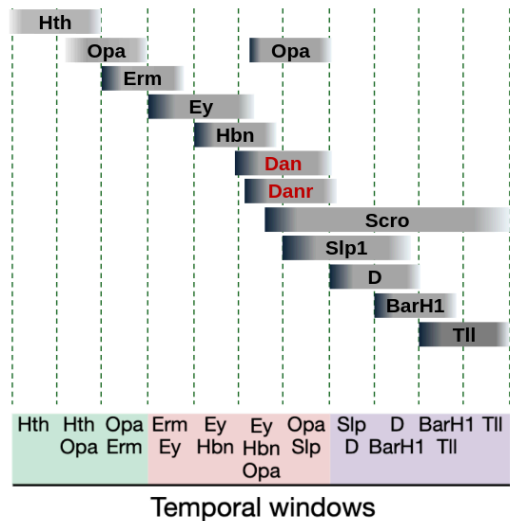


Figure S1. Bakshi et. al, unpublished. Temporal expression windows of transcription factors during Drosophila neuroblast lineage progression.

Sequential temporal transcription factor (tTF) expression in type II neuroblasts during *Drosophila* development. Each bar shows the expression window of individual TFs. Dan and Danr appear in midlineage phases alongside Ey and Hbn, suggesting a potential role in neurogenesis. These expression windows define temporal competence intervals critical for fate determination.

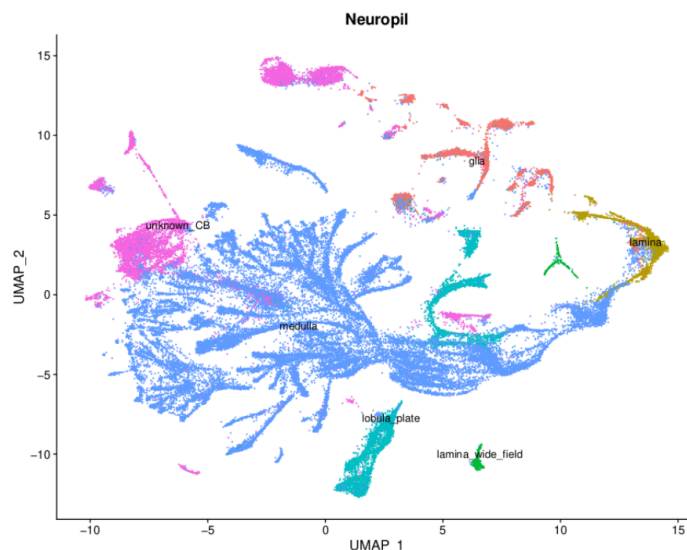


Figure S2. UMAP embedding of single-cell RNA-seq data from the *Drosophila* optic lobe.

Cells are clustered by transcriptional similarity and annotated by region, with distinct separation of lamina, medulla, glia, lobula plate, and other neuronal subtypes. The lamina cluster (highlighted in gold) was the main focus of this study. This visualization supports the regional specificity used to extract lamina-related gene expression profiles for network inference. Dataset: [GSE167266](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE167266), scRNA-seq of the *Drosophila* optic lobe.

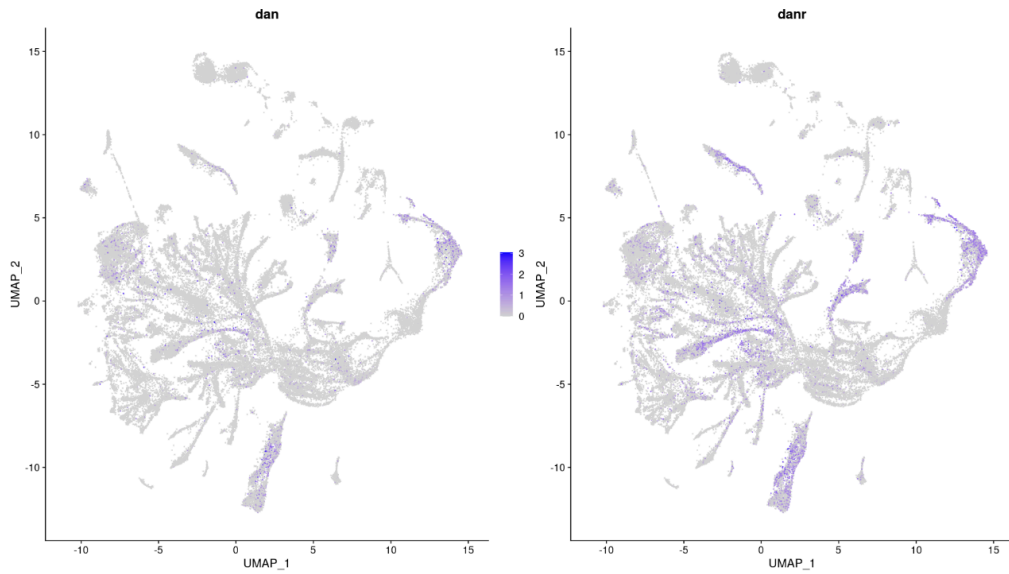


Figure S3. UMAP visualization of single-cell RNA-seq data with *Dan* and *Danr* expression.

Each panel shows the same UMAP embedding of optic lobe cells, colored by expression of *Dan* (left) and *Danr* (right), respectively.

Expression is indicated by intensity in a blue color scale (log-normalized counts). *Danr* appears more broadly and strongly expressed across clusters, including within the lamina region, supporting its prominence in regulatory network predictions.

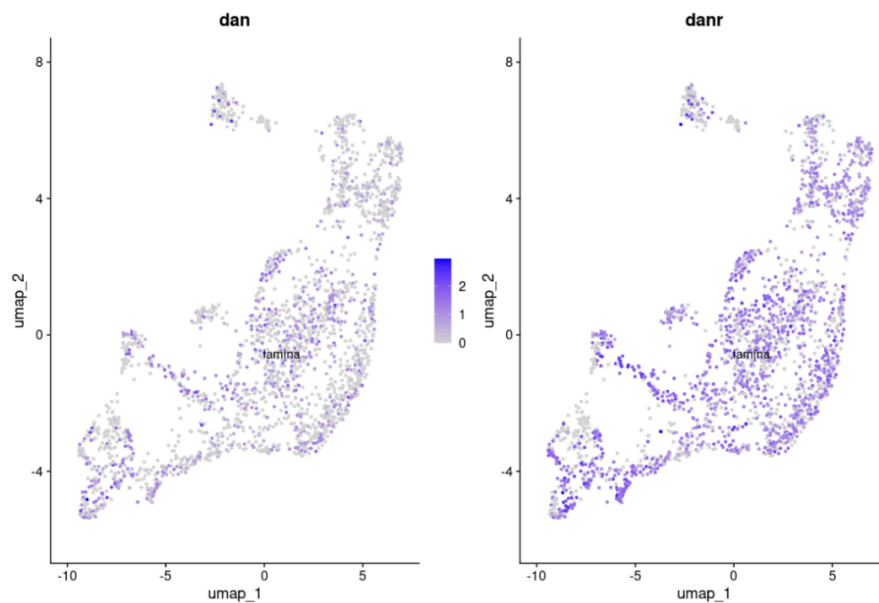
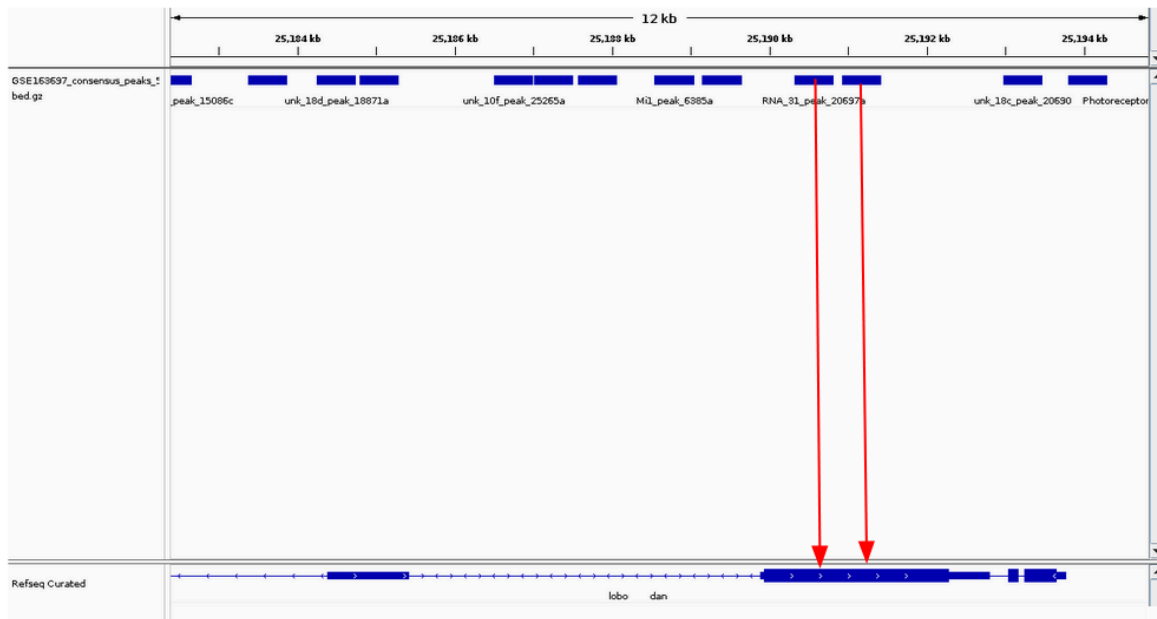
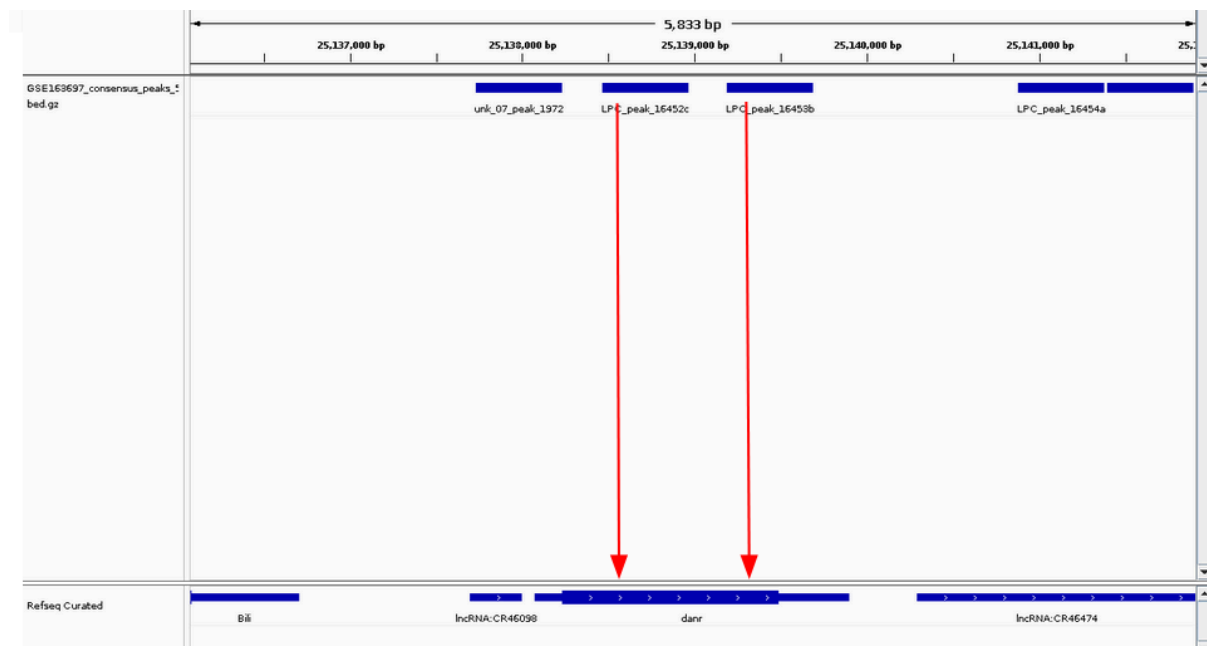


Figure S4. UMAP visualization of the lamina cluster from scRNA-seq, showing expression of *Dan* (left) and *Danr* (right).

Cells are colored by log-normalized expression levels (blue scale). *Danr* shows broader and stronger expression across the lamina cluster, while *Dan* expression is more limited.



A



B

Figure S5. Chromatin accessibility at the *Dan* (A) and *Danr* (B) loci visualized using IGV. ATAC-seq peaks (blue bars) from the consensus peak set ([GSE163697](#)) are shown aligned to the *Drosophila melanogaster* genome (BDGP6), highlighted with the red arrows. Multiple accessible regions overlap or flank both *Dan* and *Danr*, indicating regulatory potential.