

Transcriptional interferences ensure one olfactory receptor per ant neuron

Qiu shihang 20260123

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<https://doi.org/10.1038/s41586-025-09664-x>

Received: 8 December 2024

Accepted: 22 September 2025

Published online: 22 October 2025

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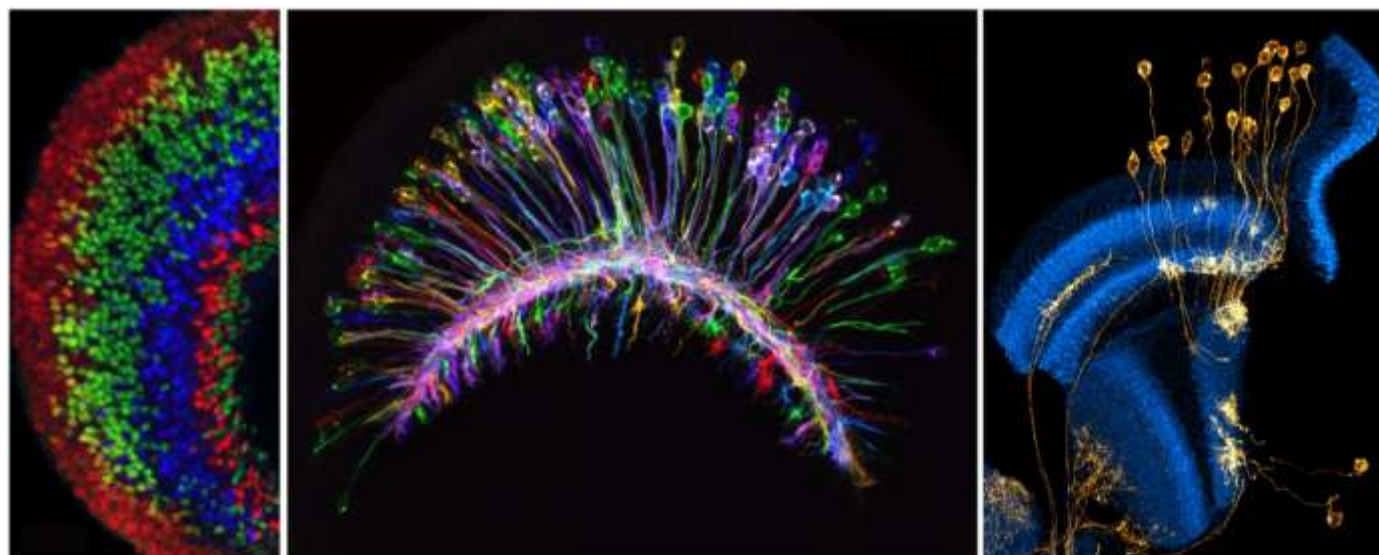
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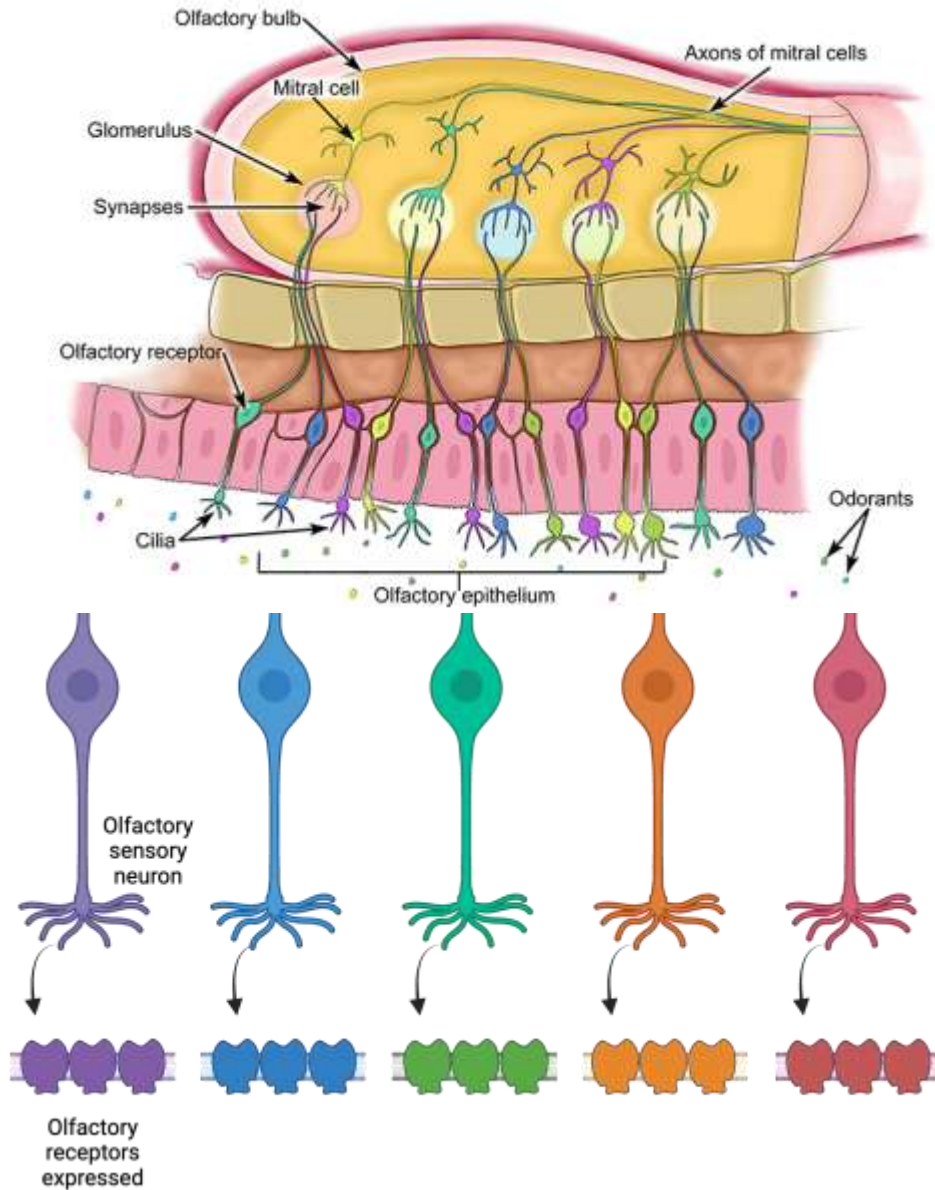


Lu Lu
New York University

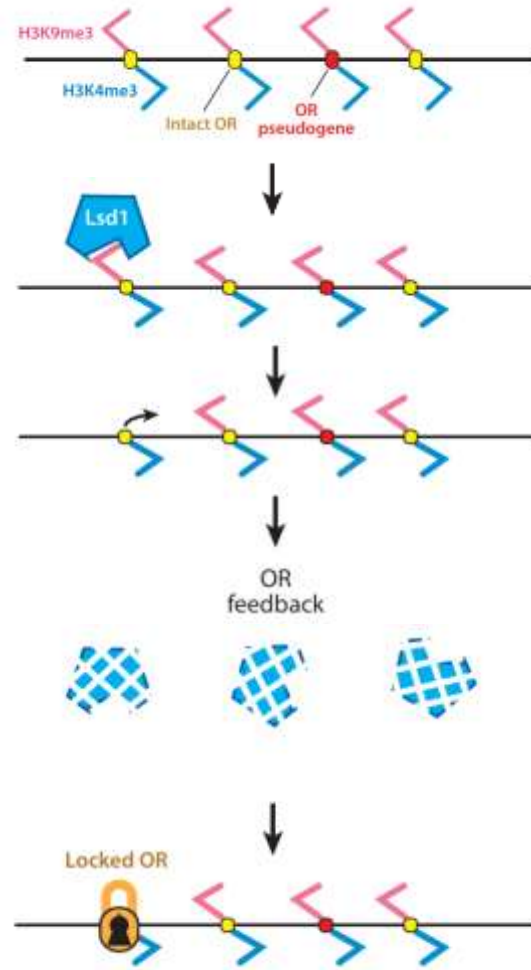


Welcome to the **Desplan Lab**! Our lab focuses on issues of neural development and aging in *Drosophila* and in ants:

One-Neuron-One-Receptor

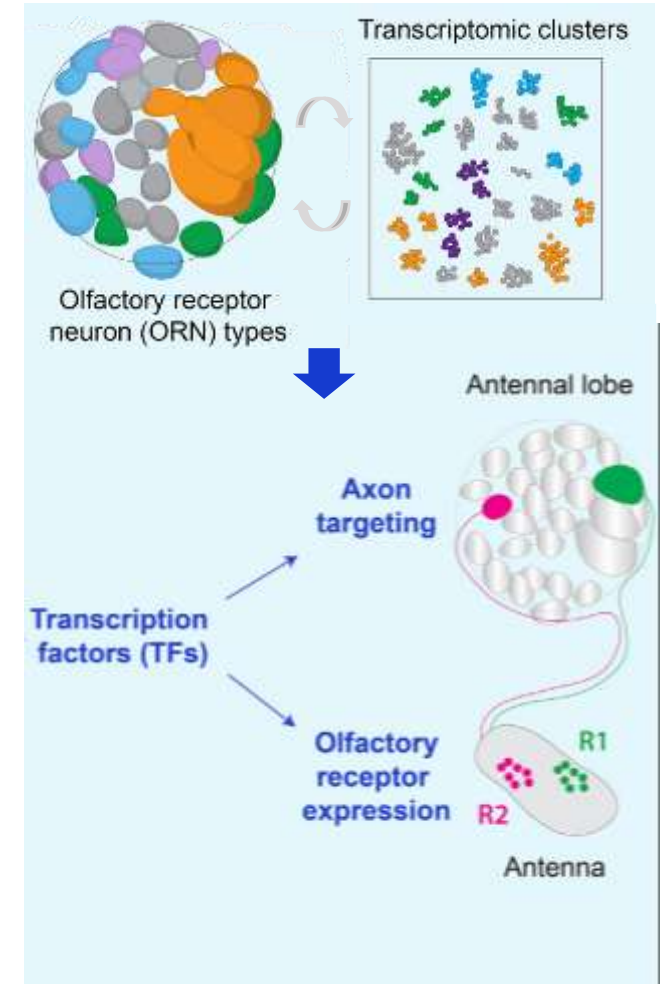


Mouse – over 1,400 Or genes



Dalton, R. P. & Lomvardas, S. Chemosensory receptor specificity and regulation. *Annu. Rev. Neurosci.* 38, 331–349 (2015).

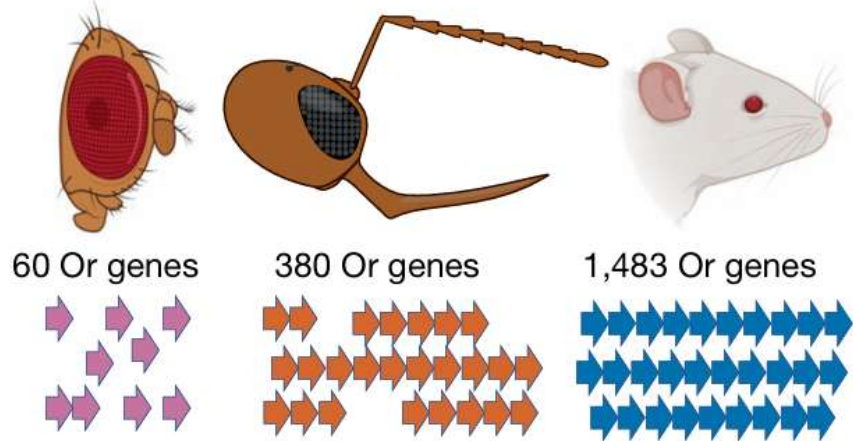
Fly – 60 Or genes



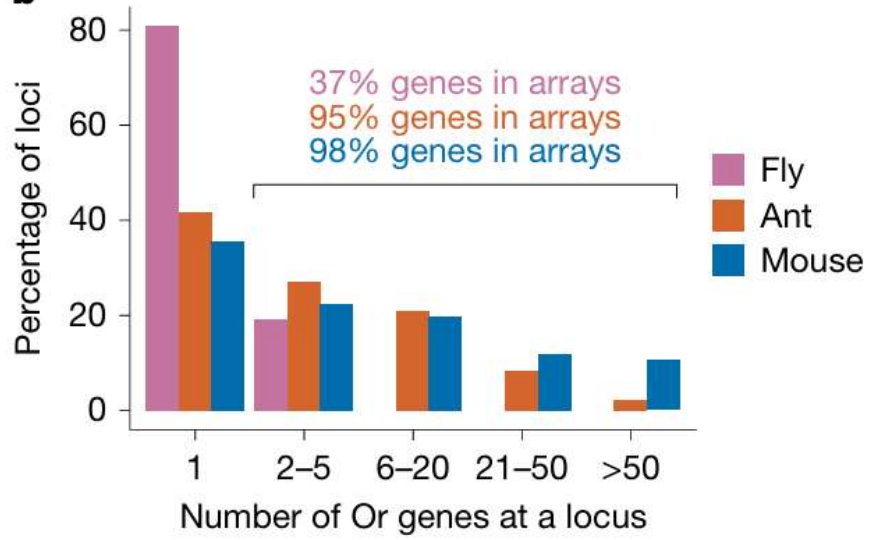
McLaughlin, C. N. et al. Single-cell transcriptomes of developing and adult olfactory receptor neurons in *Drosophila*. *eLife* 10, e63856 (2021).

Case in *Harpegnathos saltator*.

a



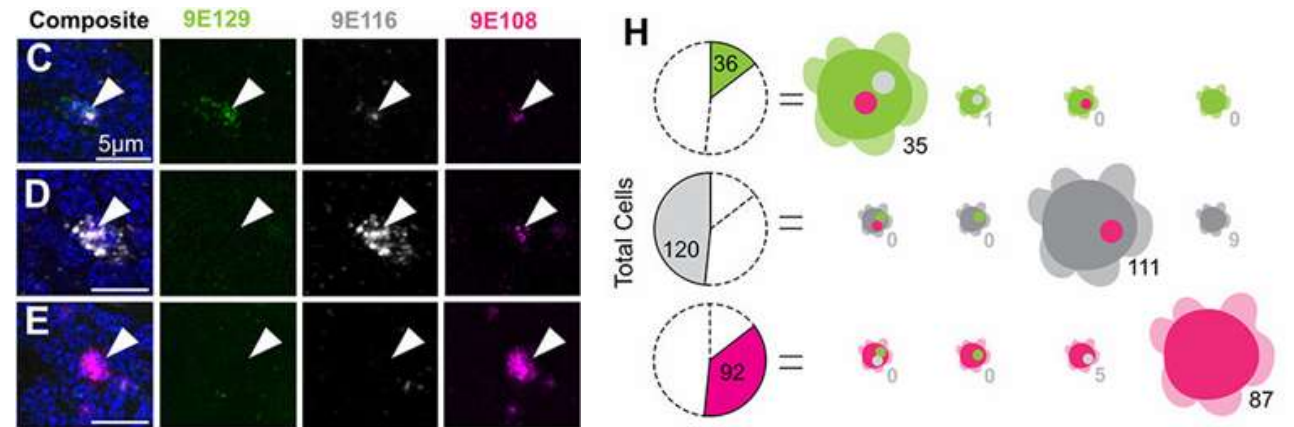
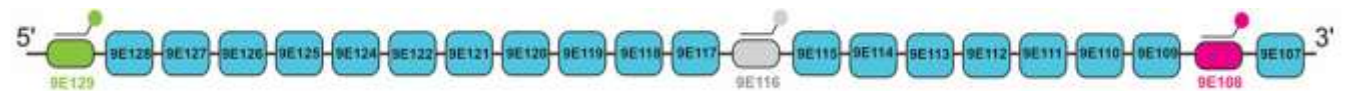
b



Tandem duplications

Only RNA from a single odorant receptor is exported into the cytoplasm

Transcriptional and post-transcriptional control of odorant receptor choice in ants

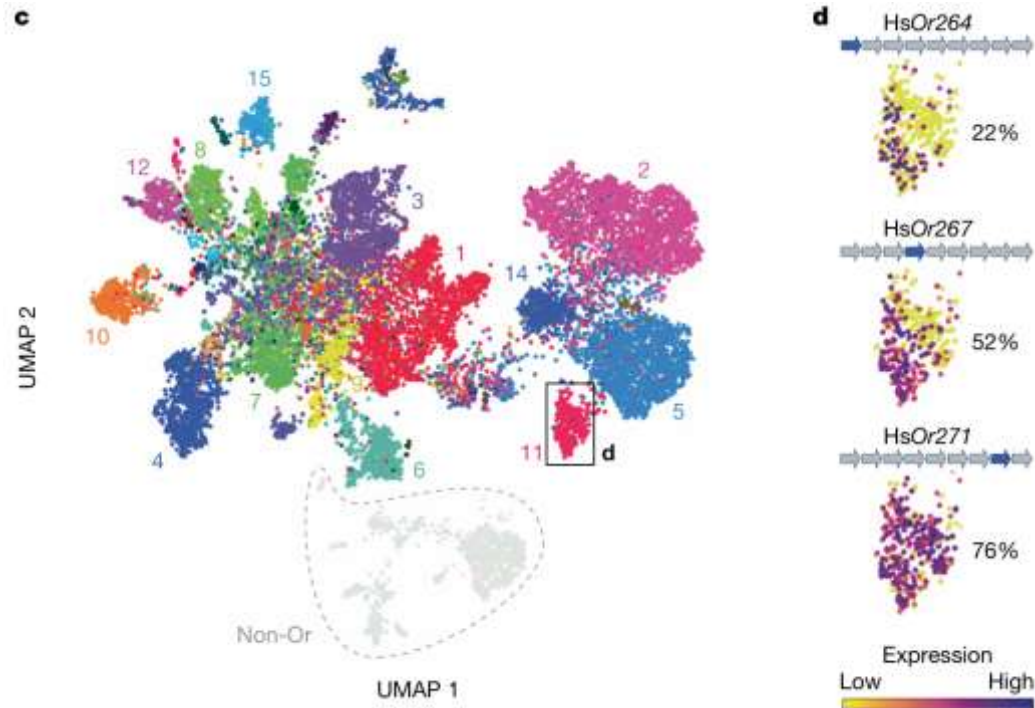


Brahma, A. et al. Transcriptional and post-transcriptional control of odorant receptor choice in ants. Curr. Biol. 33, 5456–5466 (2023).

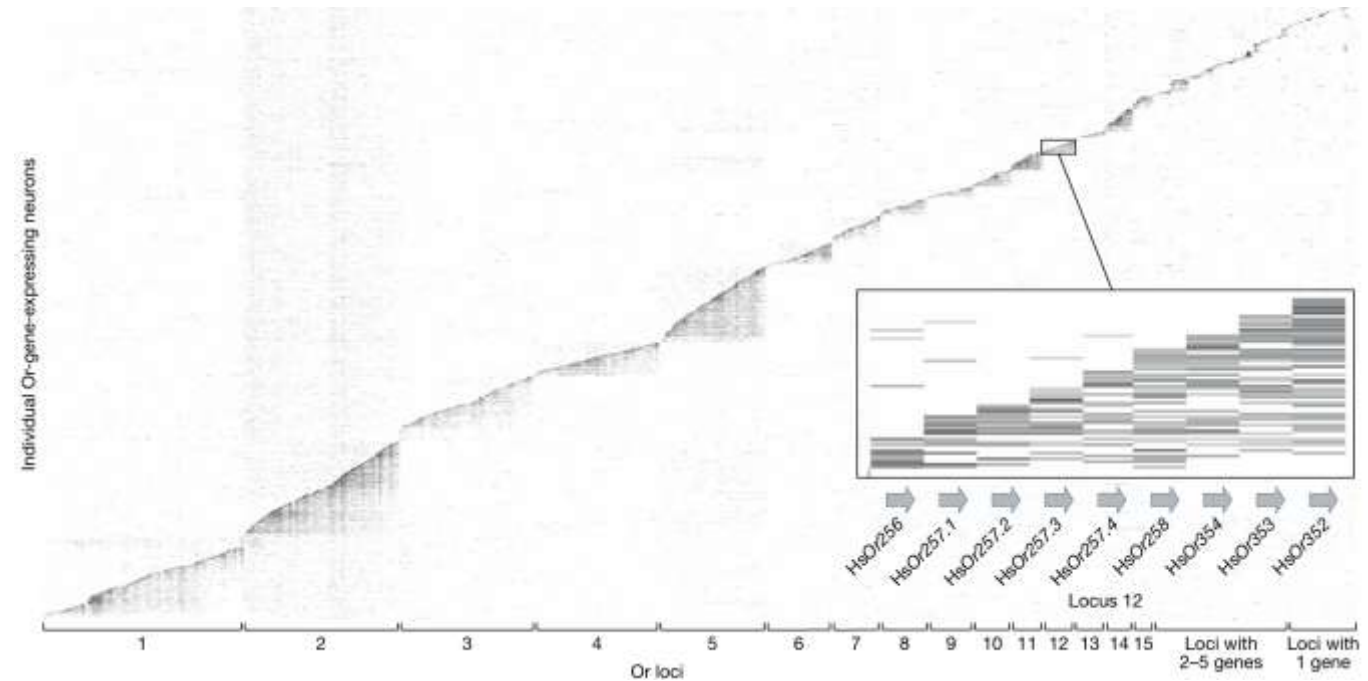
Or – gene expression pattern



Neurons expressing Or genes from the same genomic array clustered together



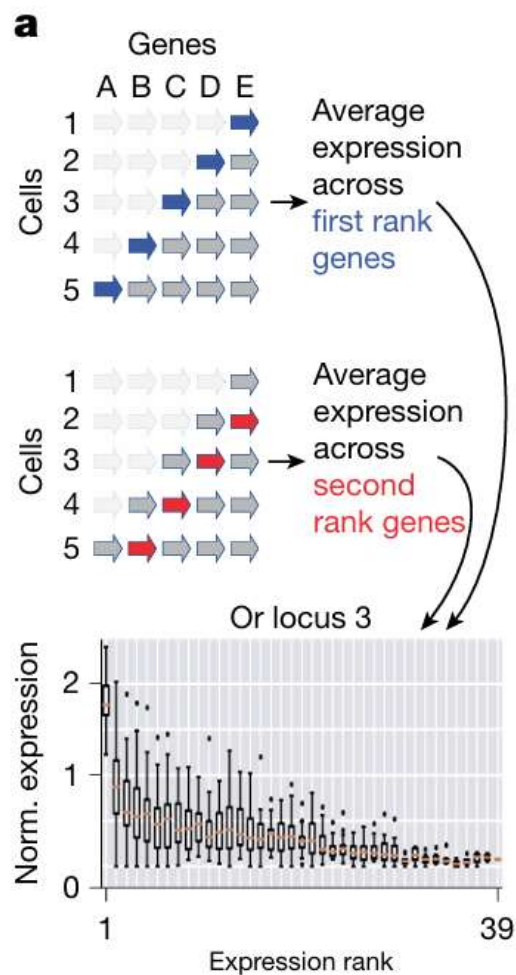
Stair-step co-expression pattern



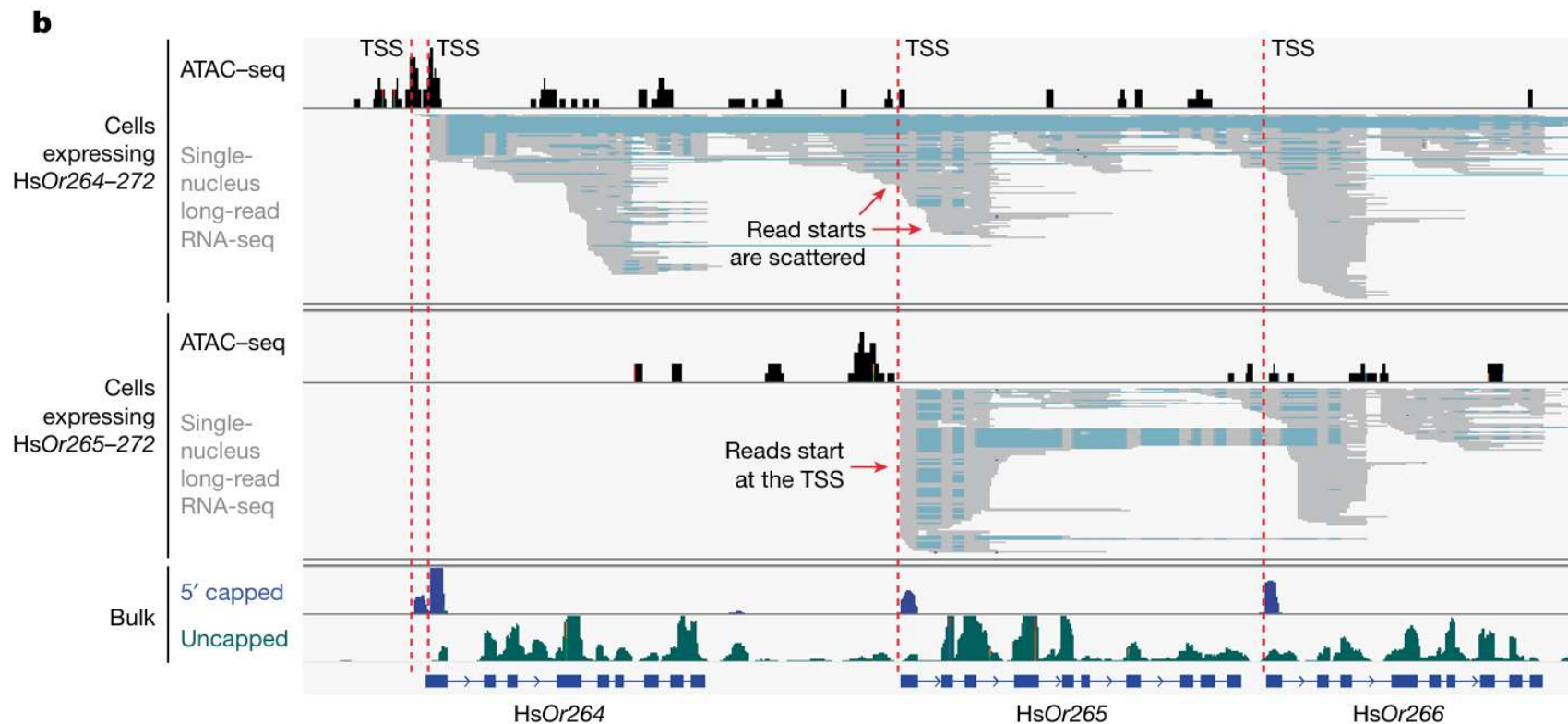
multimodal snRNA-seq and snATAC-seq

Co-transcription through Pol II readthrough

Only the promoter of the first transcribed OR gene in an array exhibited a peak of open chromatin



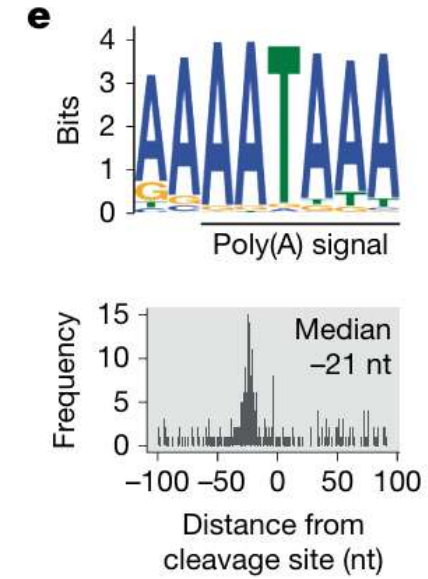
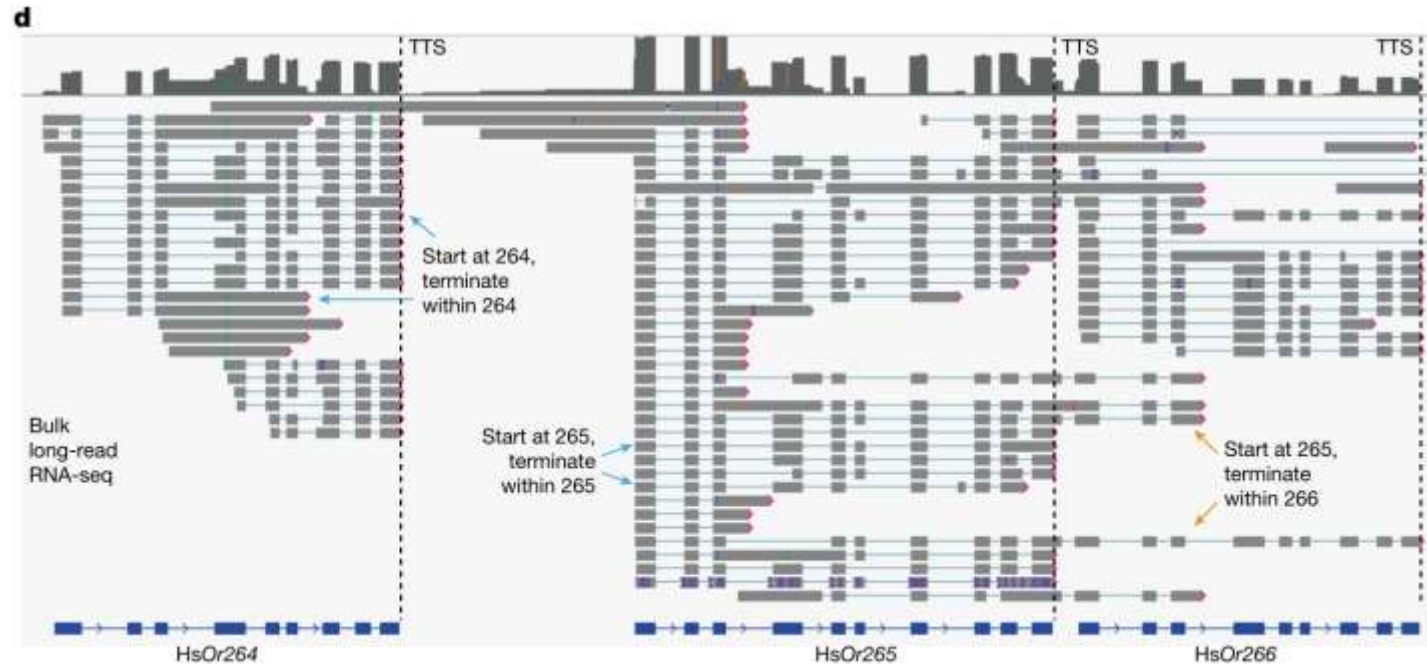
snRNA-seq



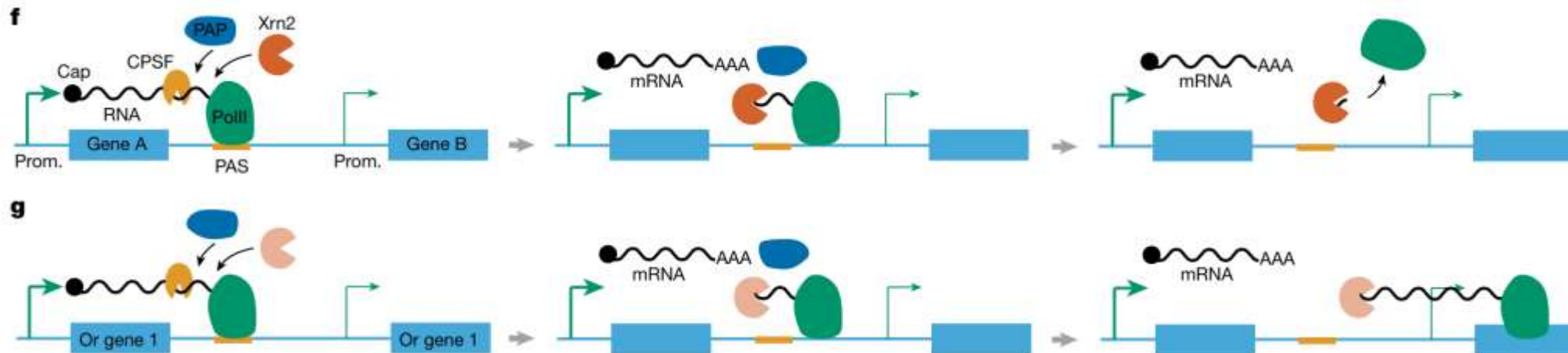
What caused Pol II readthrough ?



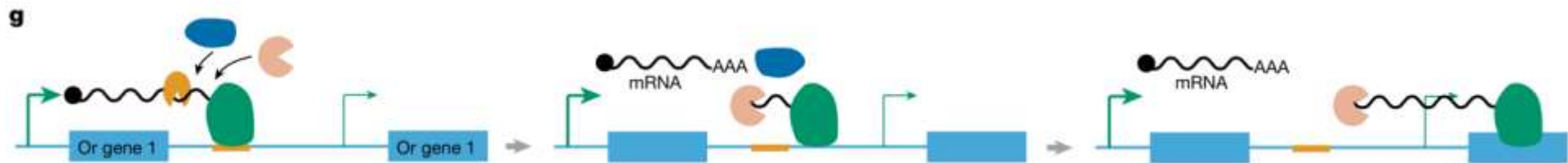
Lack functional polyA signals? --Normal 3' cleavage and polyadenylation



Defective transcription termination



浙江大学
生命演化研究中心

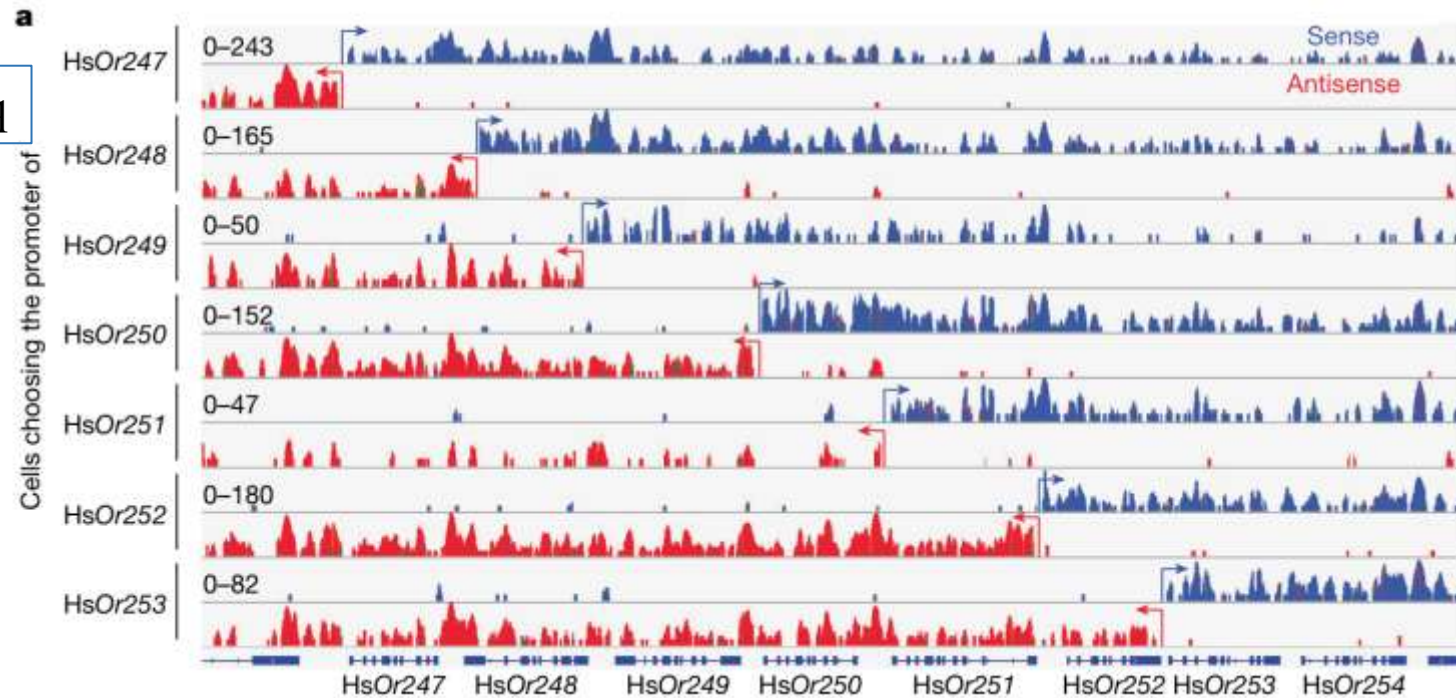


Or promoters produce antisense RNAs

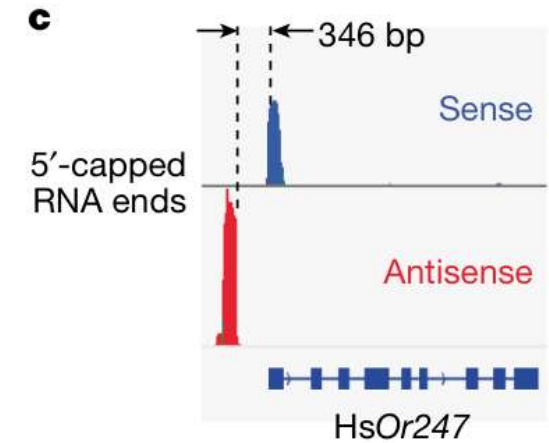


The entire locus was covered by either sense or antisense transcripts that were mutually exclusive

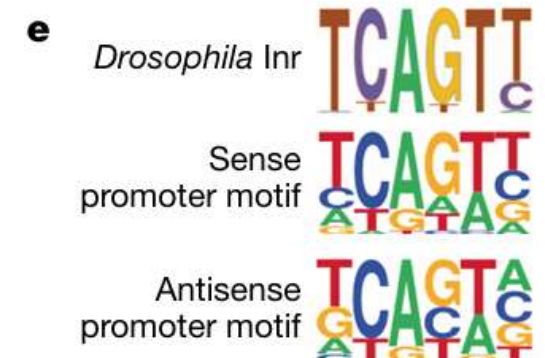
snRNA-seq



bulk RNA-seq of 5'-capped transcripts



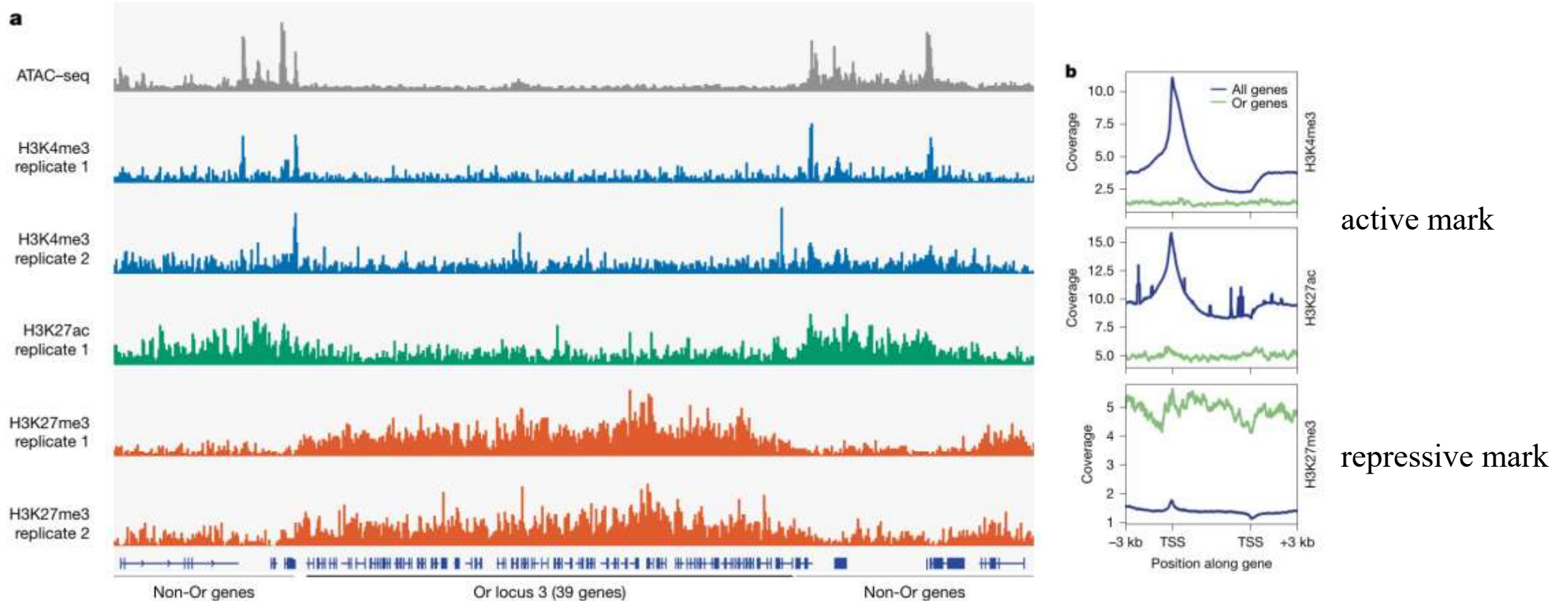
bulk Iso-seq



No obvious shared enhancers in Or gene arrays



Or genes are transcriptionally silent in most cells



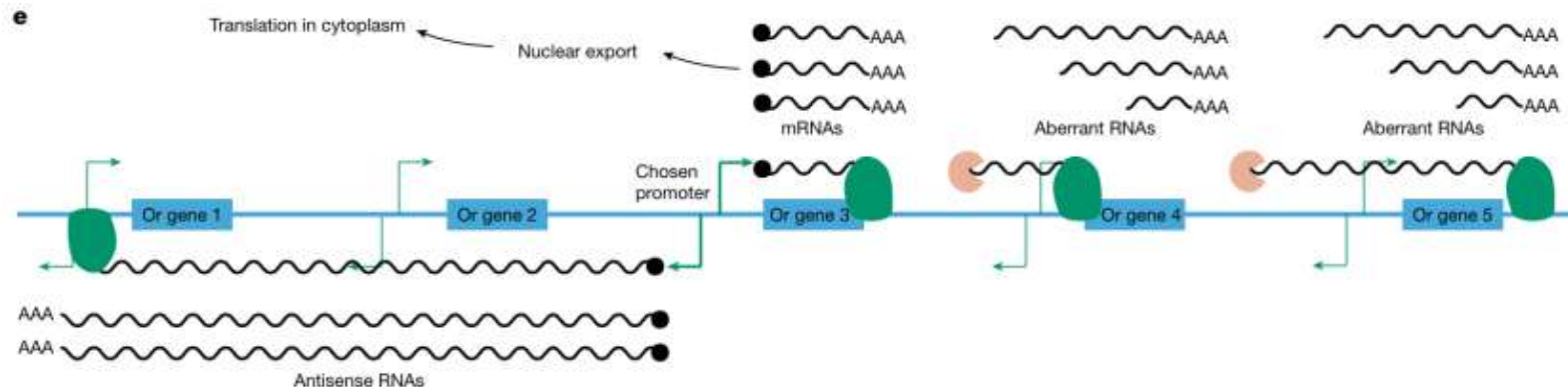
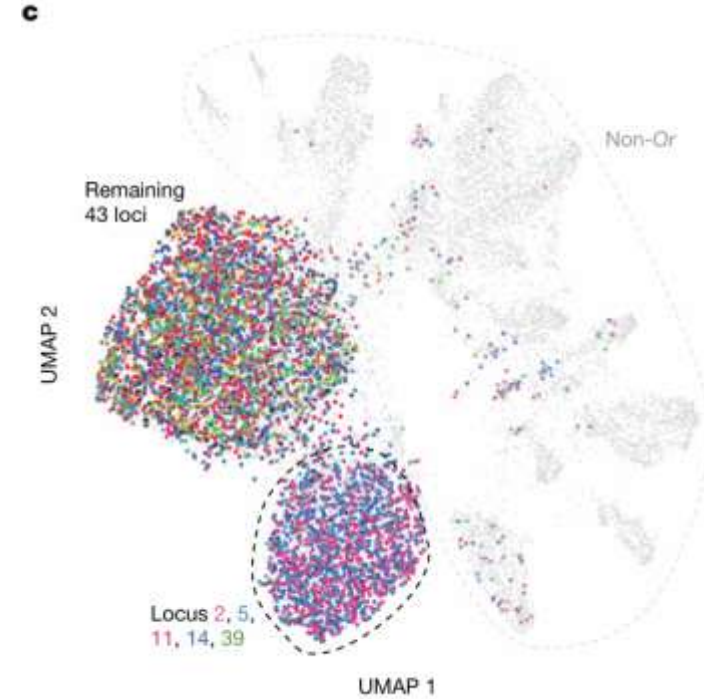
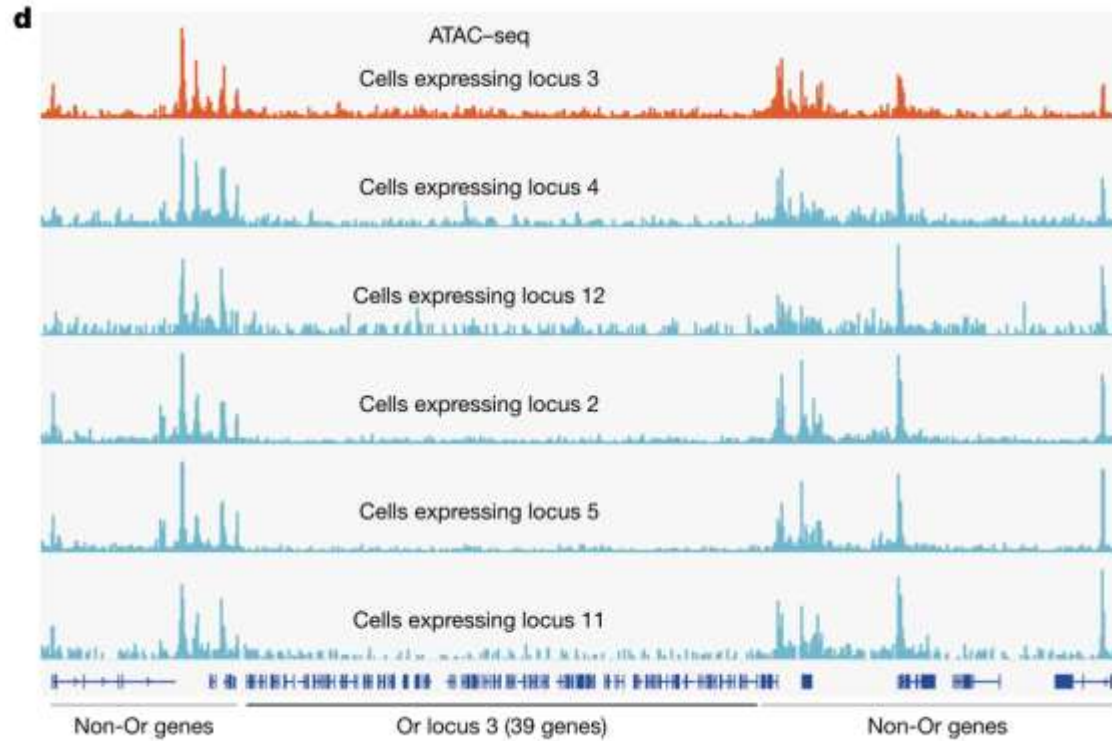
Pseudobulk snATAC-seq and bulk CUT&RUN

No obvious shared enhancers in Or gene arrays

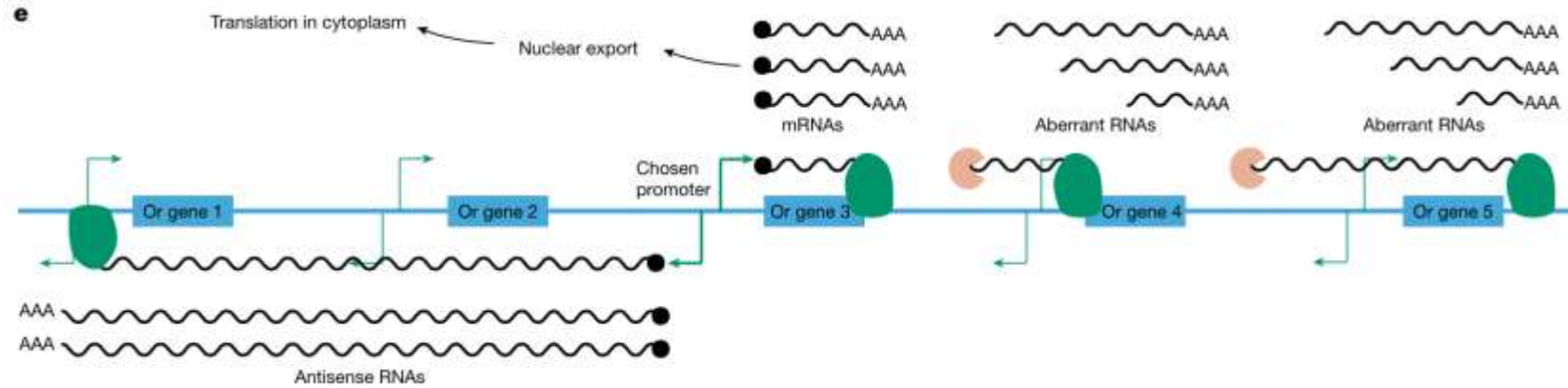


no specific, shared regions of open chromatin

large-scale epigenetic state defines general neuronal function, not the choice of a specific receptor gene.

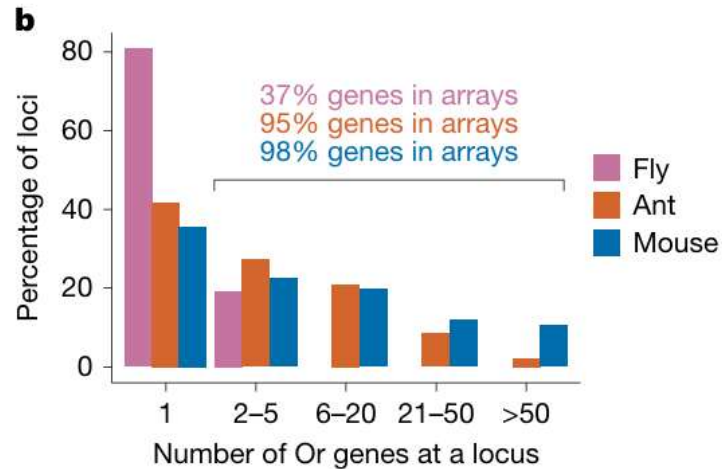


Transcription-interference-based mechanism



Why transcription termination is defective specifically at these loci ?

How the initial promoter is chosen ?



Thanks!

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