

# GAND - Single Cell Analysis Report

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February 16, 2026

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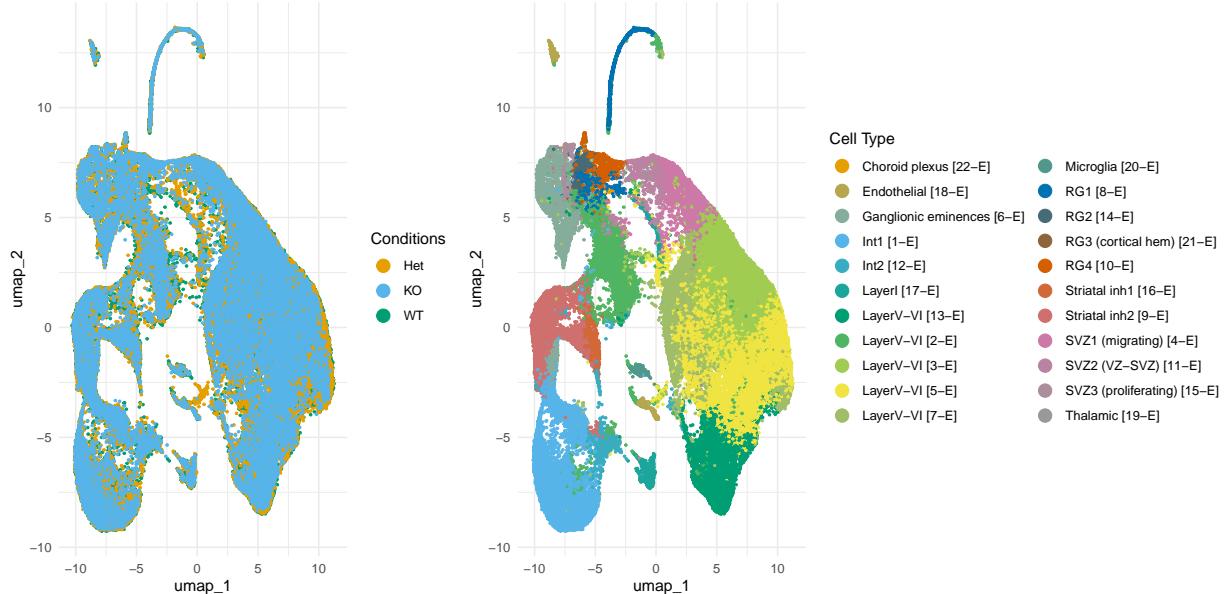
**Auto-generated report** The full analysis is available on [GitHub](#)

## 1 TLDR

### 1.1 Integration & Annotation

We performed single-cell RNA sequencing (scRNA-seq) on cortical samples obtained from *Gatad2bstop/+* and WT littermates at a single embryonic time point (E16.5) in order to explore underlying mechanisms of *Gatad2b* function. We also generated *Gatad2bstop/stop* scRNA-seq data to identify dosage sensitive targets of *Gatad2b*. The data is available under accession number GSE244477.

In total, there were 9 samples with 3 Wild Types, 3 Hets, and 3 KOs. All 9 samples were integrated using Seurat's Canonical Correlation Analysis (CCA). Next, we transferred labels to the integrated data set using an annotated reference available under accession number GSE123335.



## 1.2 Gene Set Expression

Using all 9 samples, we used a Linear Mixed Effects Model (LMM) to determine which cell types in which conditions were enriched with specific gene sets. We used the following gene sets:

```
## Chd3|Foxp1|Foxp2|Satb2
## Chd3|Foxp1|Satb2
## Chd3|Foxp2|Satb2
## Arx
```

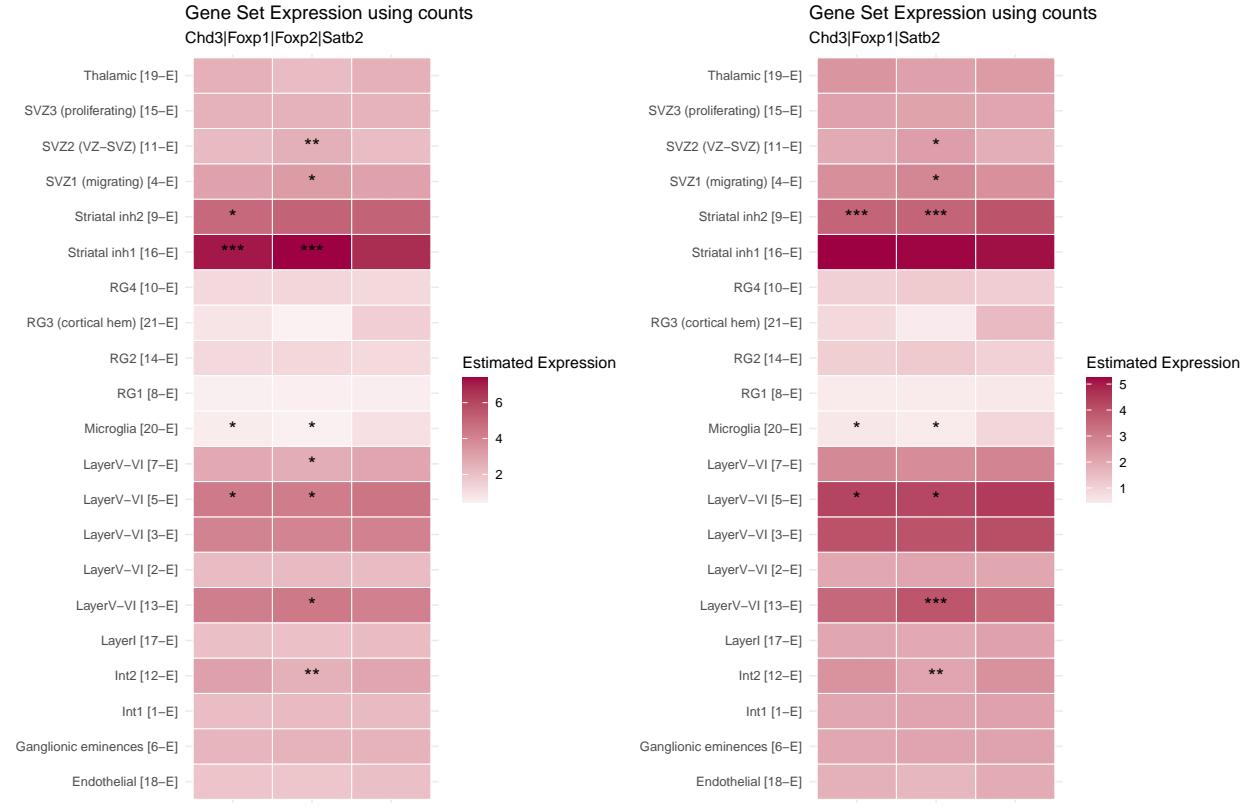
The LMM was run twice, once using a gene module score and a second time using count values directly. The gene module score (as implemented by Seurat's `AddModuleScore`) is a 0 centered score where positive values indicate a higher expression of a gene set compared to a random gene set. Negative scores represent a lower expression than the same random gene set.

Statistical significance threshold are represented as follows:

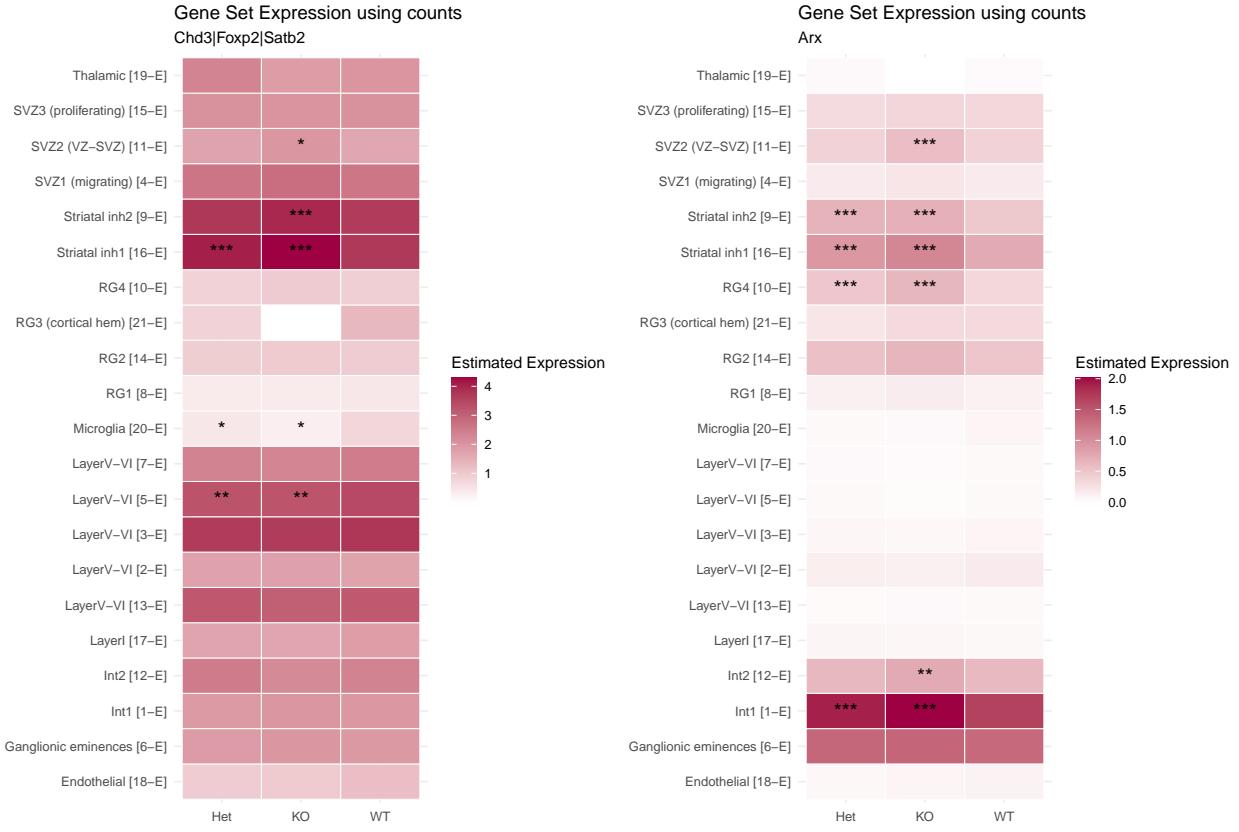
- \* < 0.05
- \*\* < 0.01
- \*\*\* < 0.001

We show the gene module score plots.

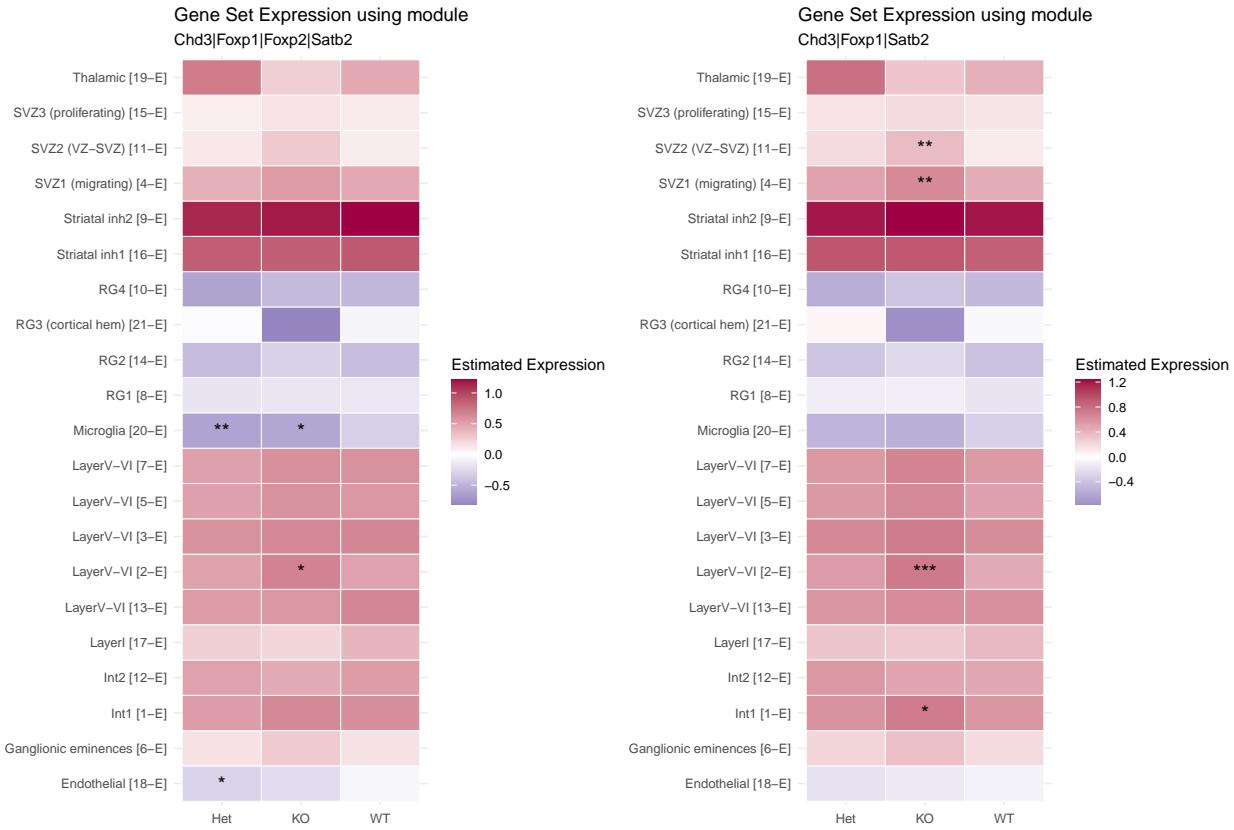
```
## $`1`
```



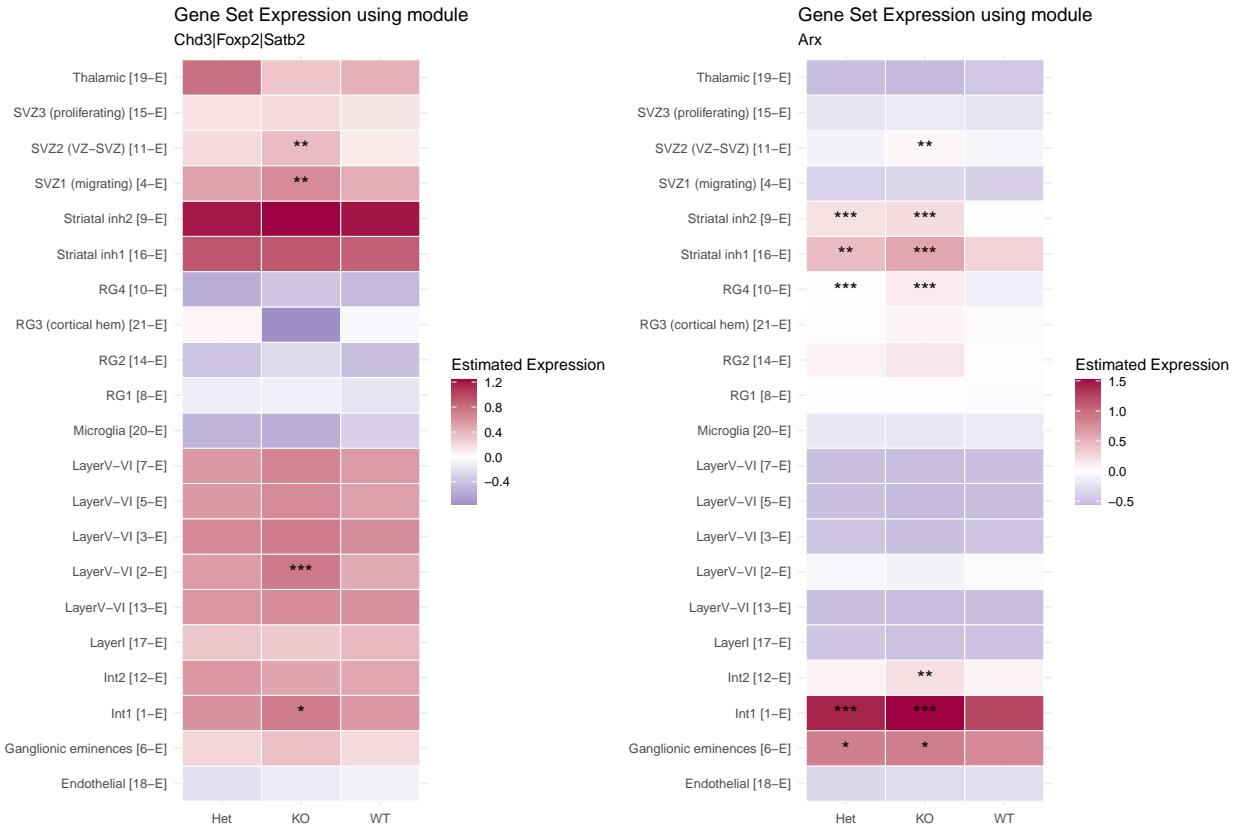
```
##
## $`2`
```



```
##  
## $`3`
```



```
##  
## $^4`
```



```
##  
## attr(,"class")  
## [1] "list"      "ggarrange"
```