

GAND - Single Cell Analysis Report

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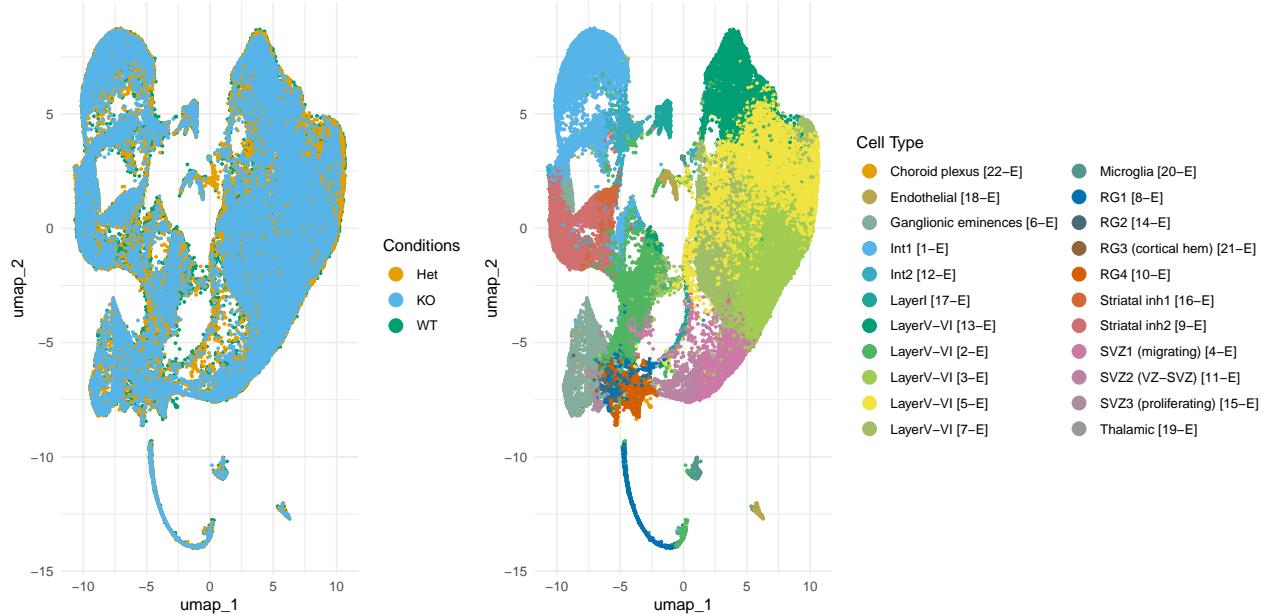
Auto-generated report The full analysis is available on GitHub

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
```

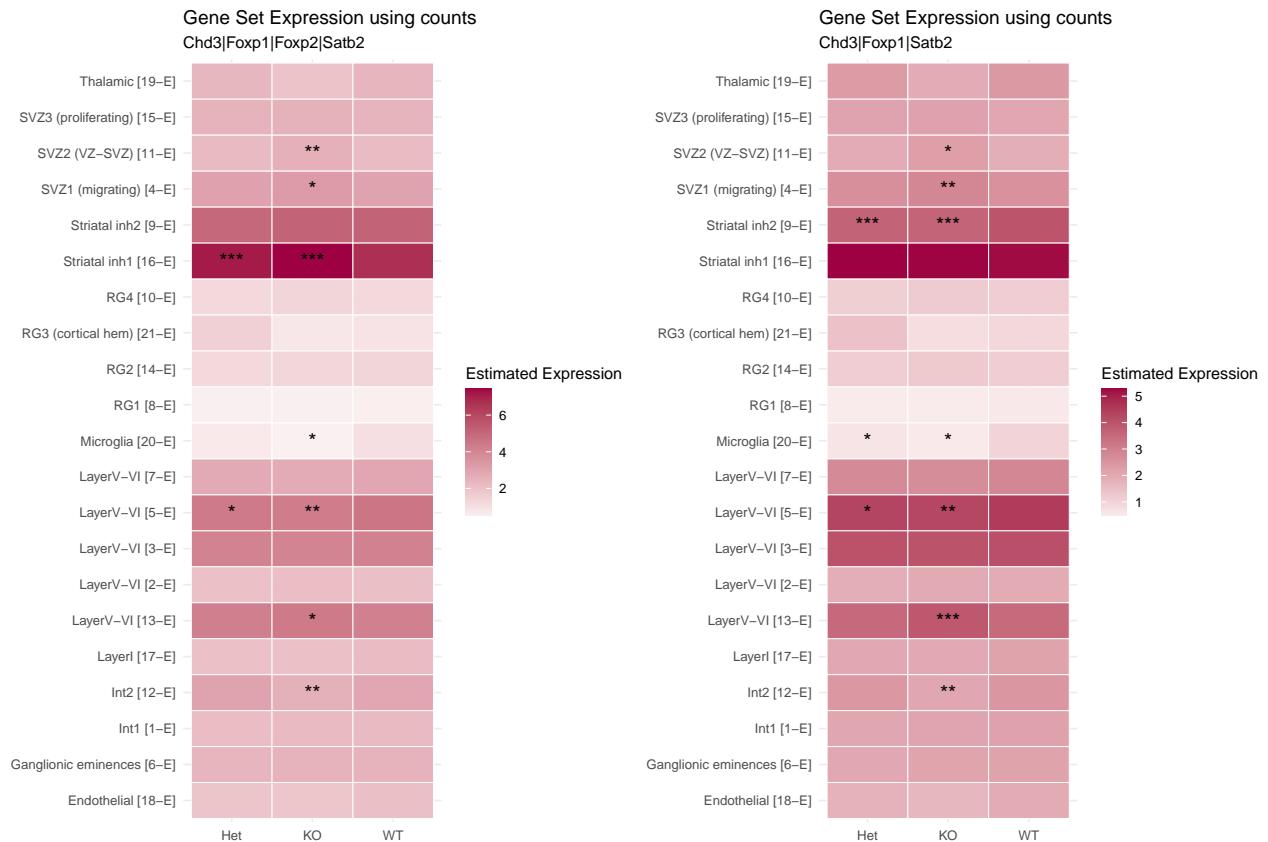
The LMM was run twice, once using a gene module score and a second time using count values directly. The gene module score (as implemented by Seurat's `AddModuleScore`) is a 0 centered score where positive value indicate a higher expression of a gene set compared to a random gene set. Negative scores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

Statistical significance threshold are represented as follows:

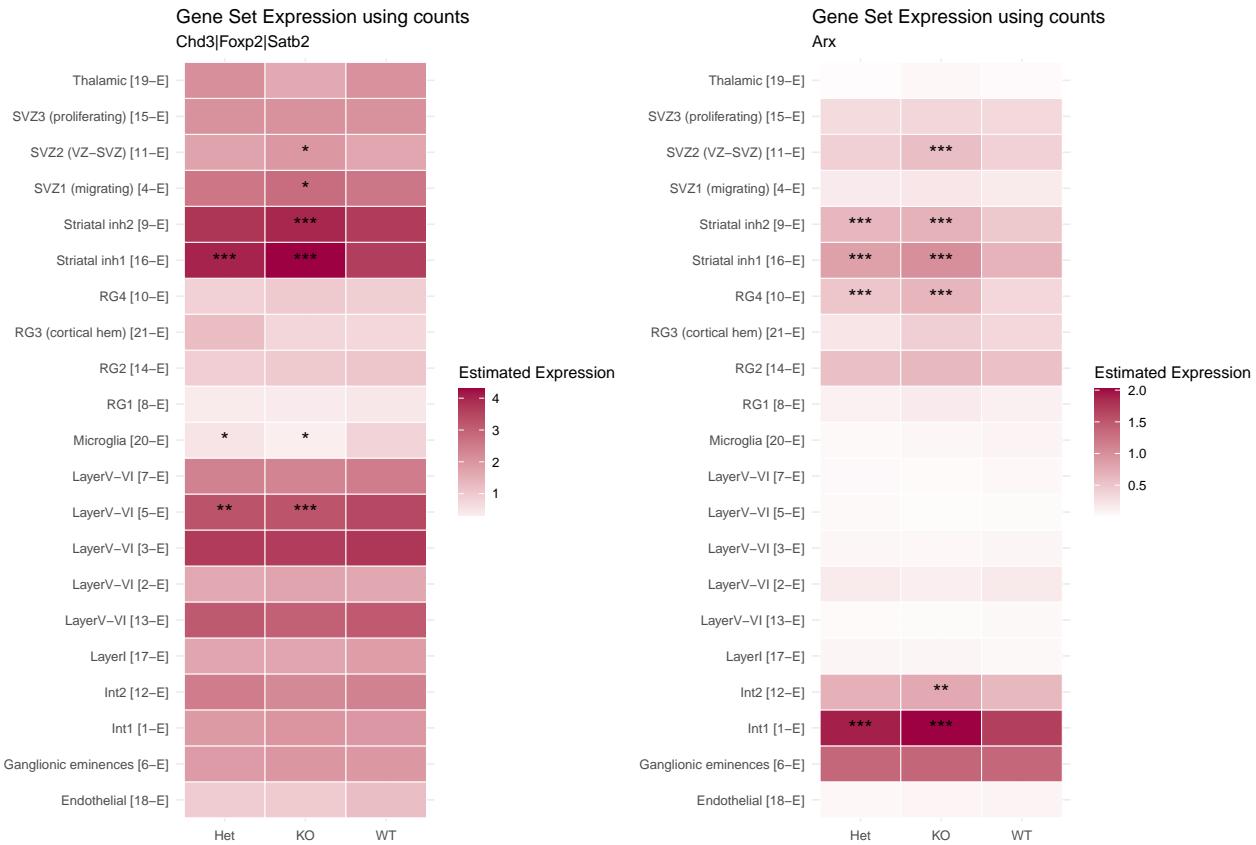
- * < 0.05
- ** < 0.01
- *** < 0.001

We show the gene module score plots.

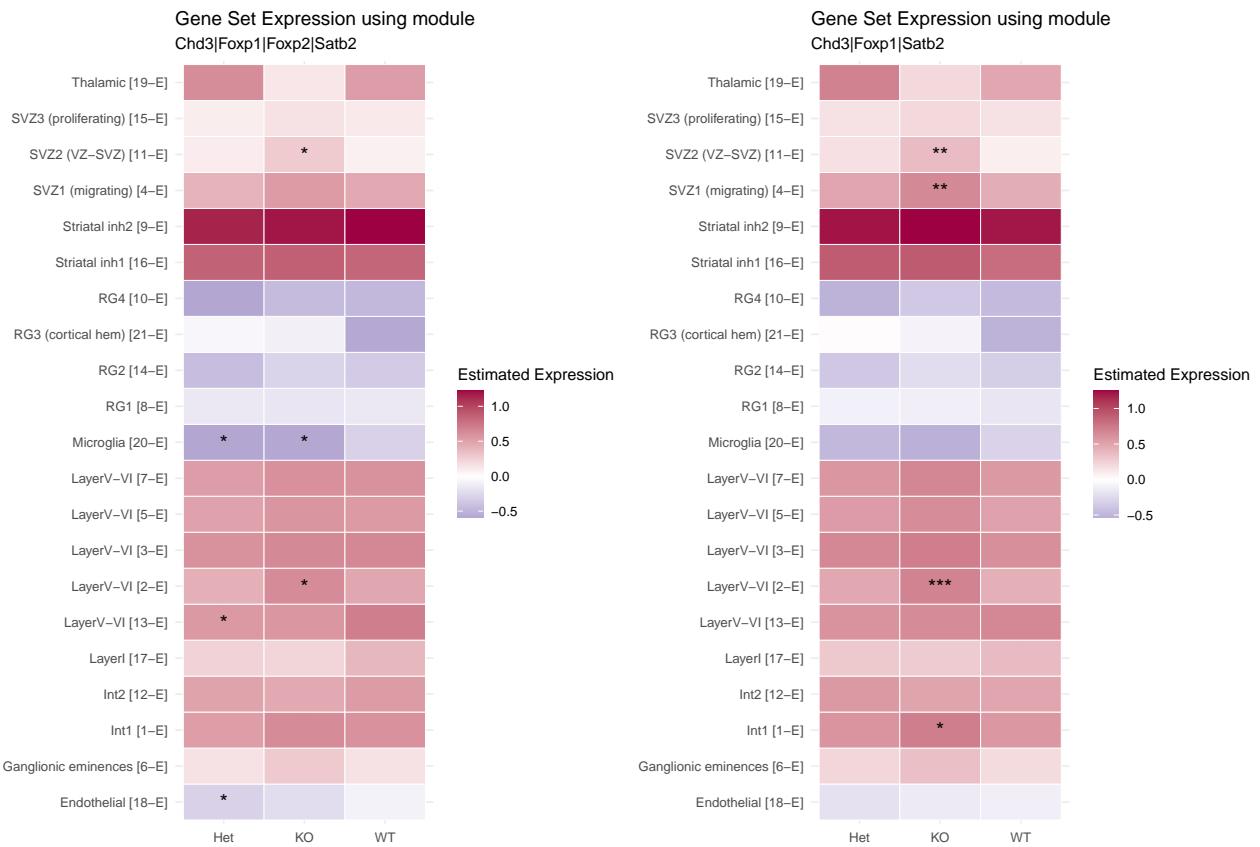
```
## $`1`
```



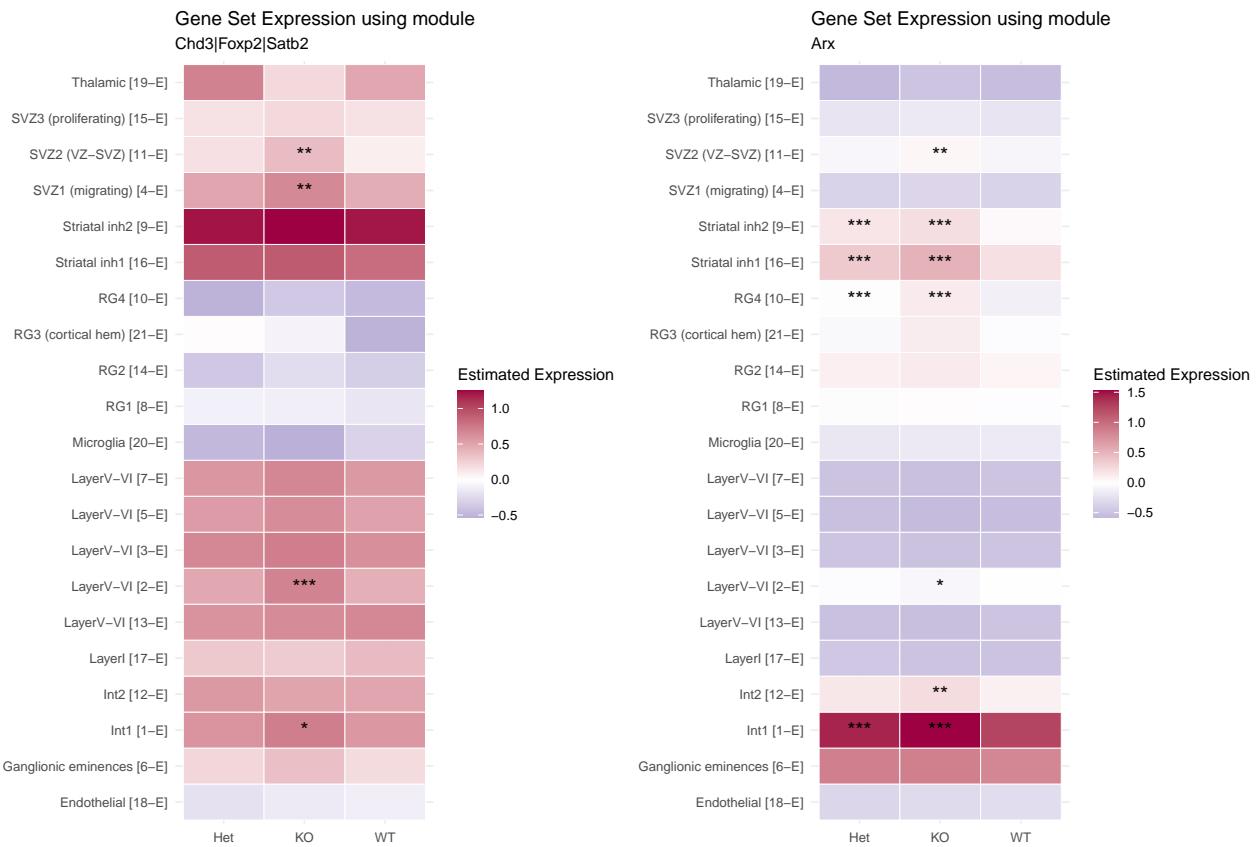
```
##  
## $ '2'
```



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



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



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