

Differential cell-cell communication between SCZ and NTC using cellchat V2

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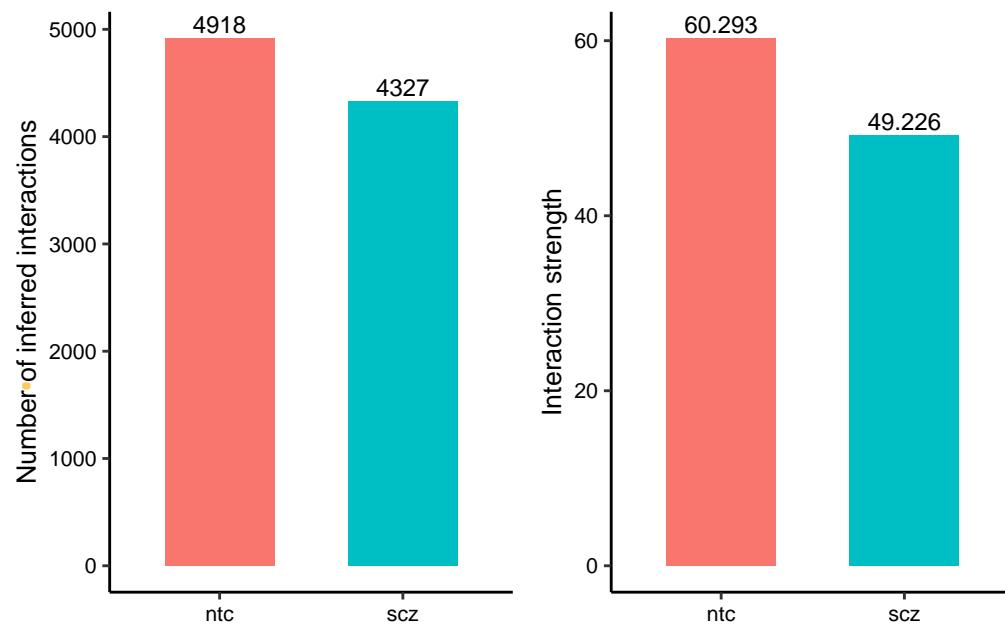
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Method

Results

Number of interaction and interaction strength

Overall level for SCZ and NTC respectively



Communication pattern between Neun+ and Claudin+ spots

Do heatmap based on a merged object

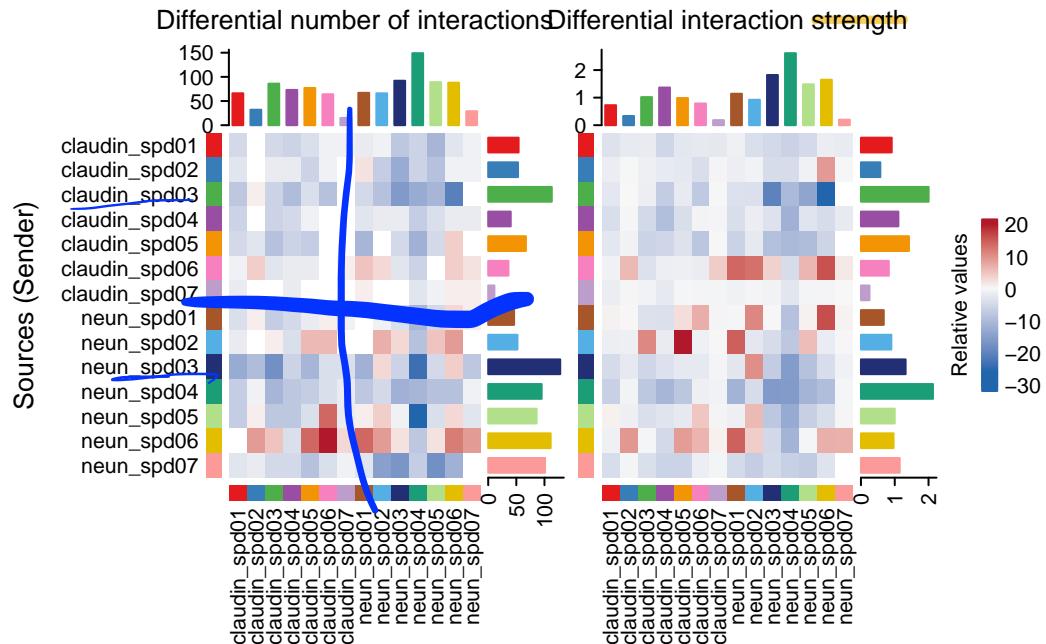
Do heatmap based on a merged object

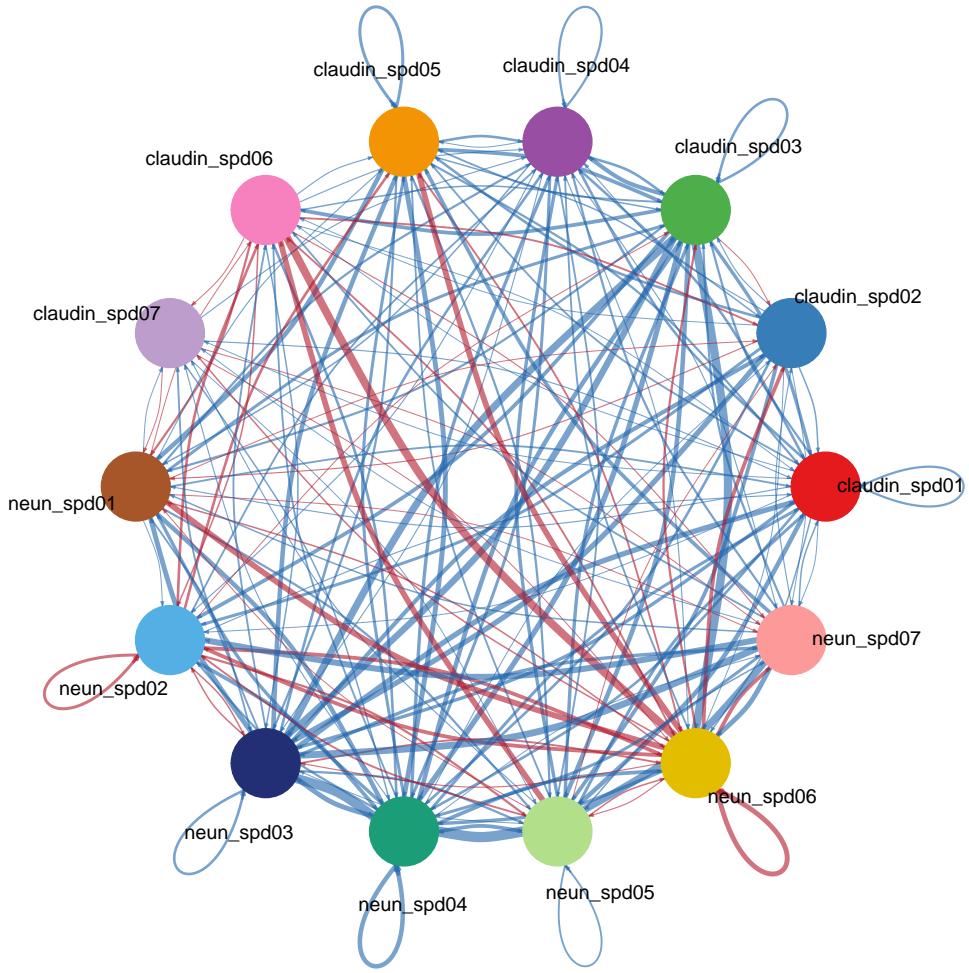
Warning: Heatmap/annotation names are duplicated: Relative values

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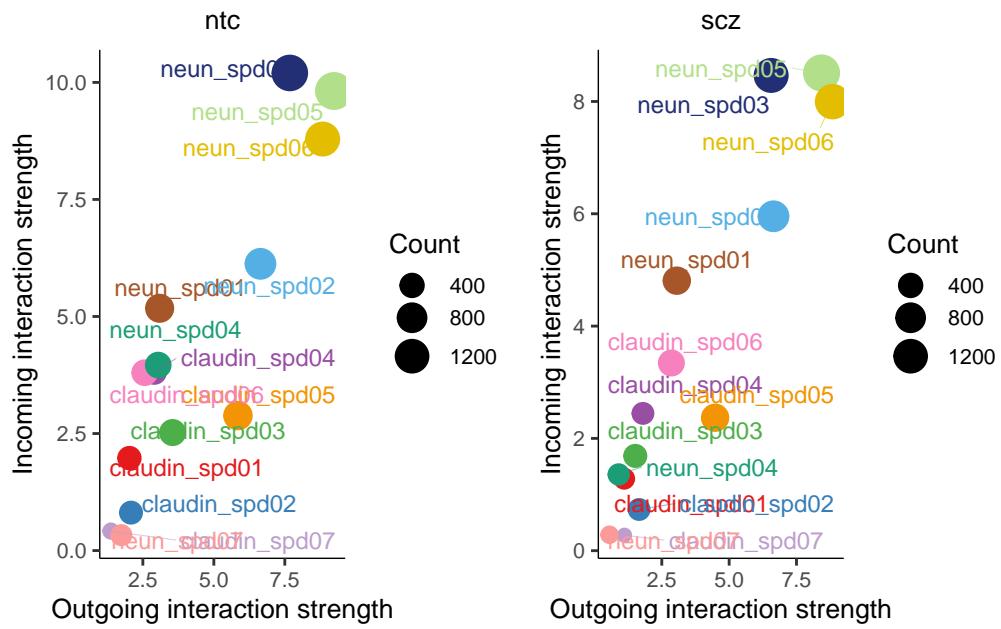
Warning: `legend_height` you specified is too small, use the default minimal height.



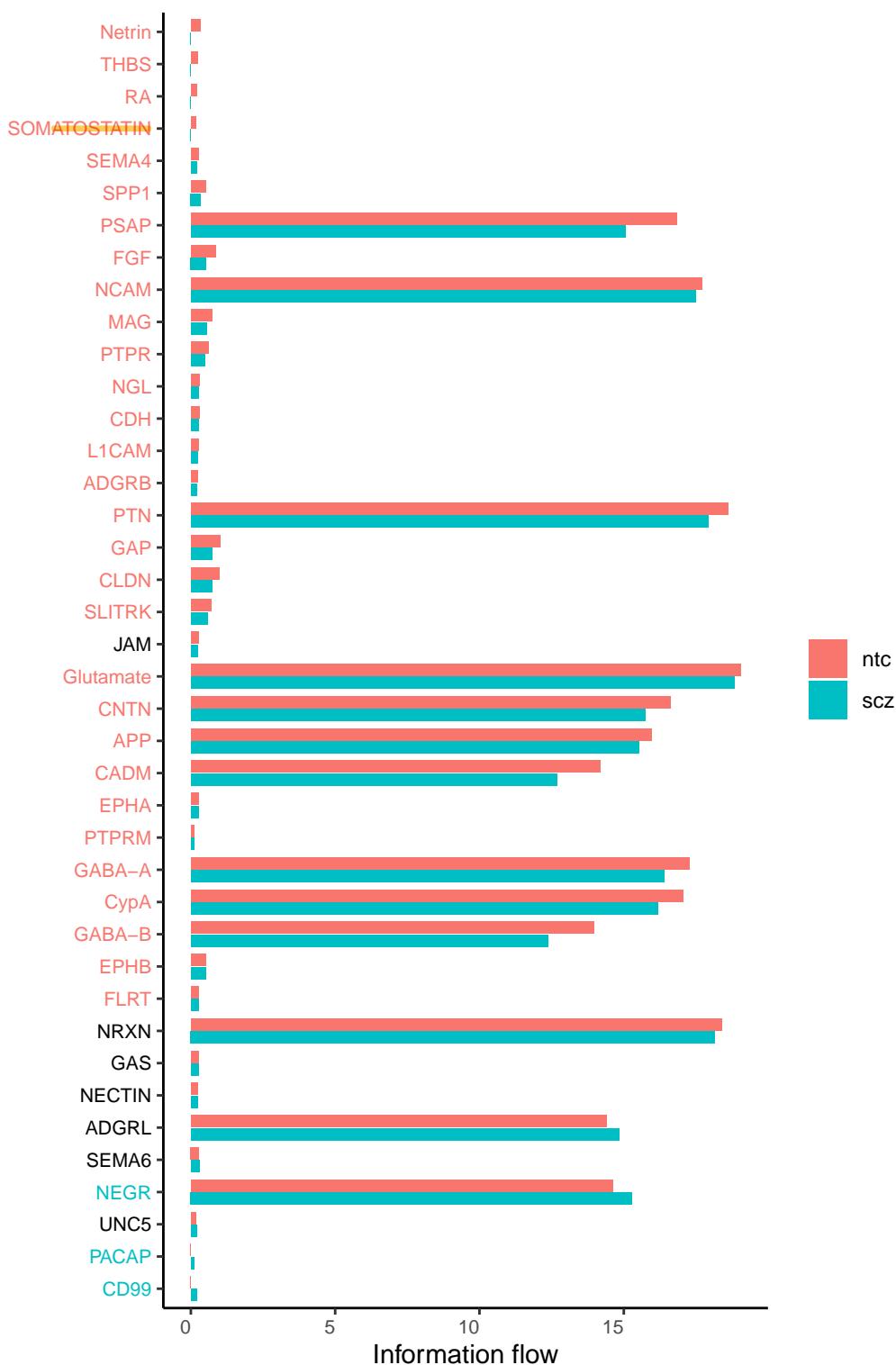


Compare major sources and targets - Not very informative

Signaling role analysis on the aggregated cell-cell communication network from all signaling
Signaling role analysis on the aggregated cell-cell communication network from all signaling



overall information flow of each signaling pathway or ligand-receptor pair



Overall

Loading required package: grid

```
=====
ComplexHeatmap version 2.20.0
Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
Github page: https://github.com/jokergoo/ComplexHeatmap
Documentation: http://jokergoo.github.io/ComplexHeatmap-reference
```

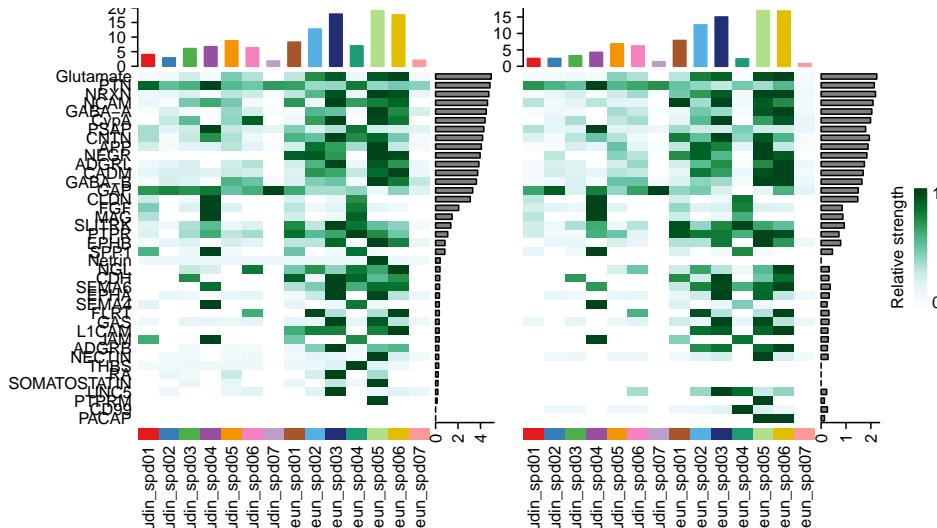
If you use it in published research, please cite either one:

- Gu, Z. Complex Heatmap Visualization. iMeta 2022.
- Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics 2016.

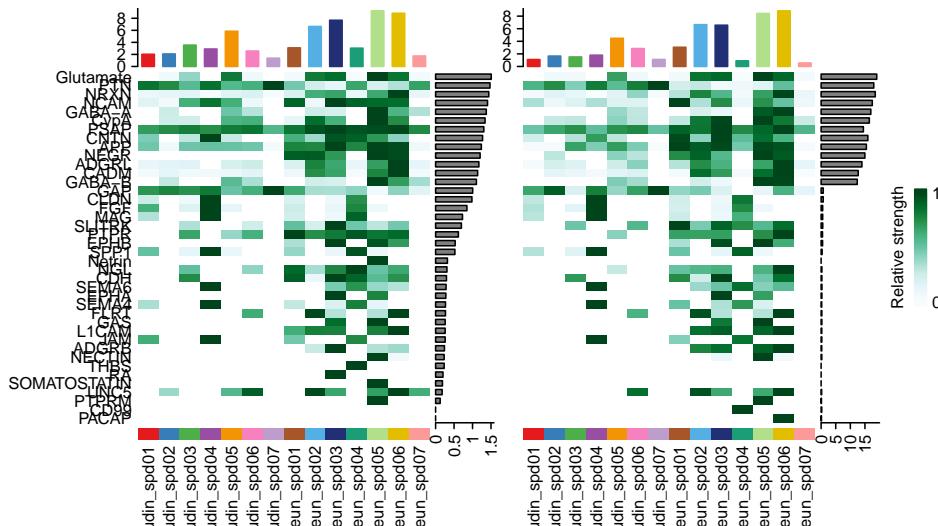
The new InteractiveComplexHeatmap package can directly export static complex heatmaps into an interactive Shiny app with zero effort. Have a try!

This message can be suppressed by:

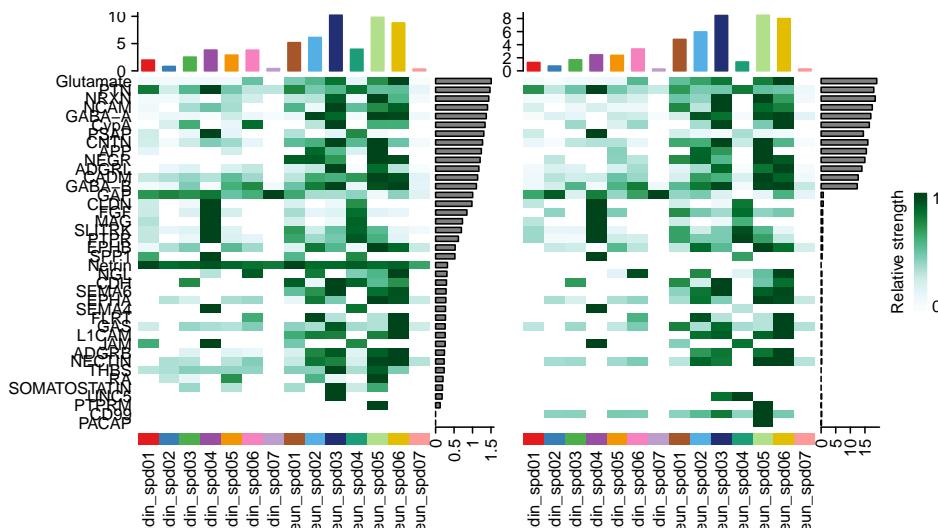
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suppressPackageStartupMessages(library(ComplexHeatmap))
```



Outgoing



Incoming

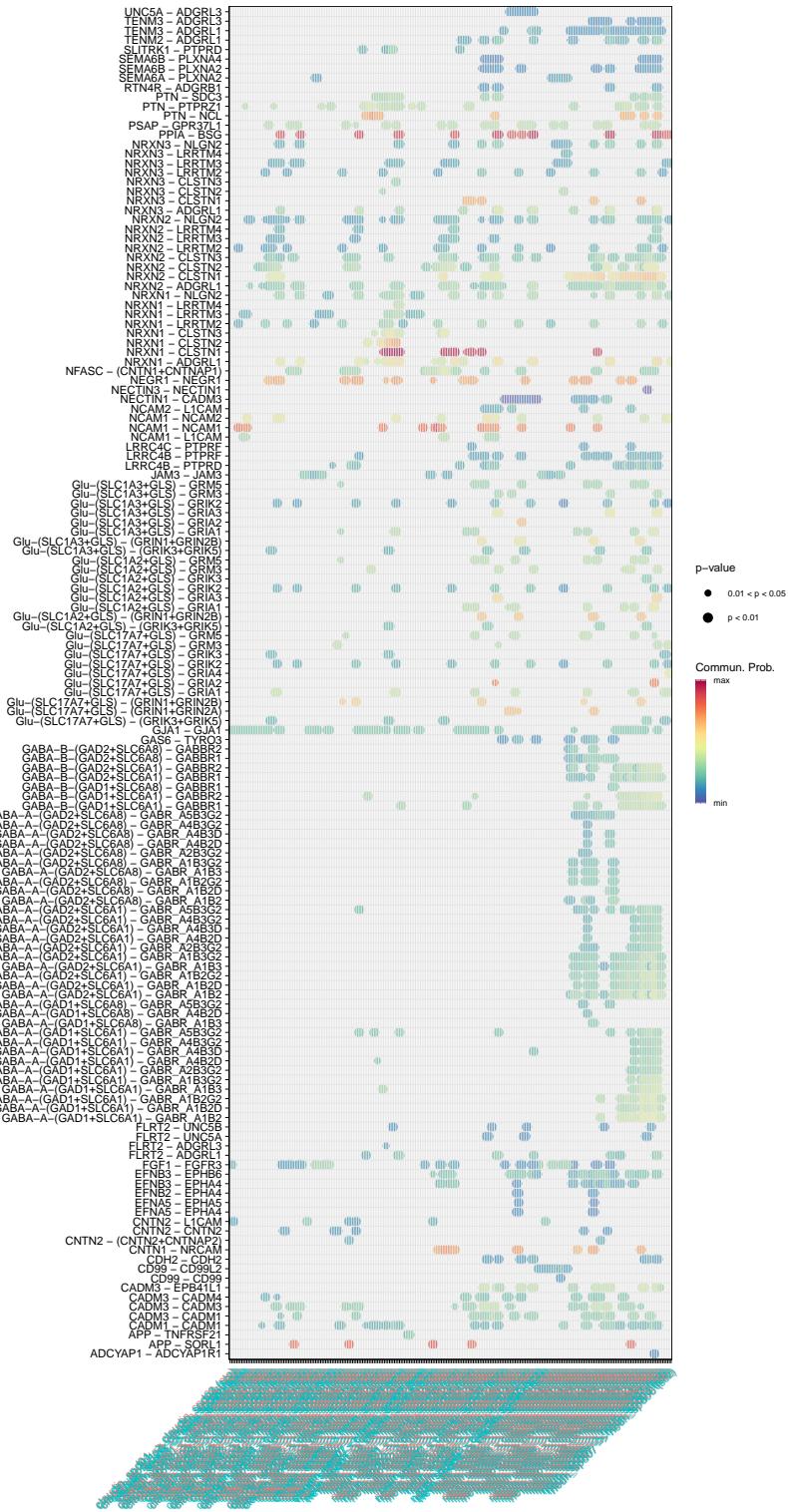


Upregulated and downregulated signaling LR pairs

Increased signaling in SCZ

Comparing communications on a merged object

Increased signaling in SCZ



Decreased signaling in SCZ

Comparing communications on a merged object

Decreased signaling in SCZ

