

Between-SPD Differential cell-cell communication between SCZ and NTC for Neun+

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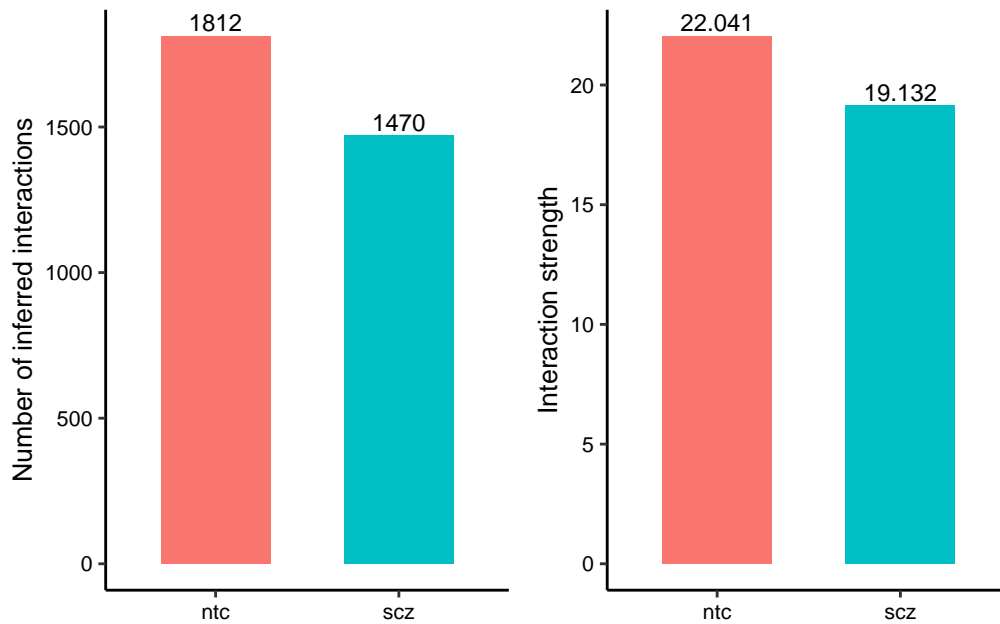
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Method

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

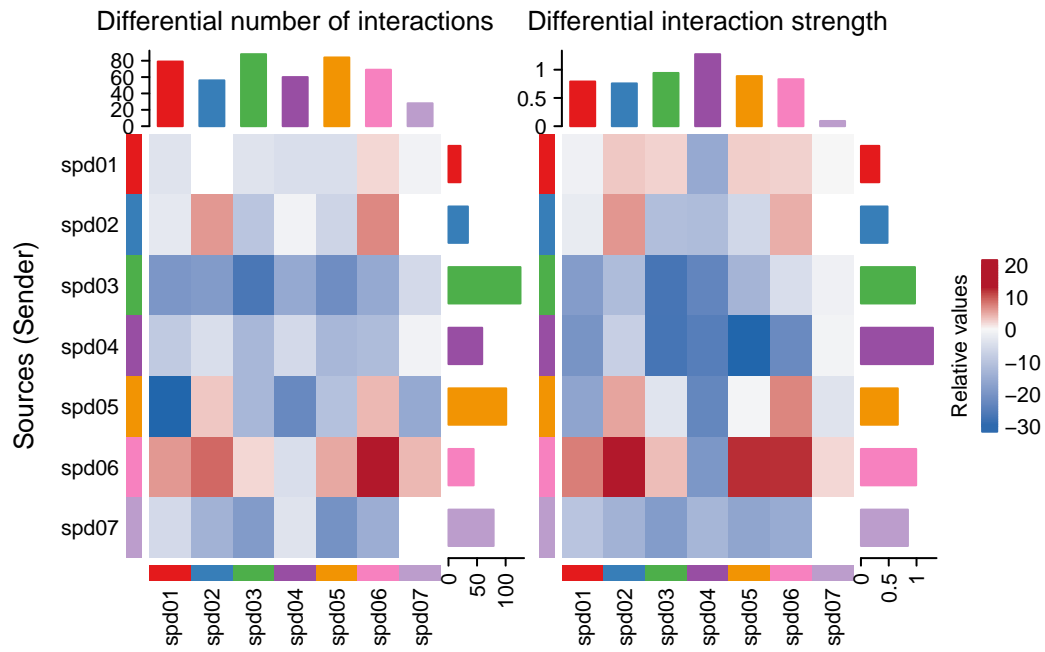
Do heatmap based on a merged object

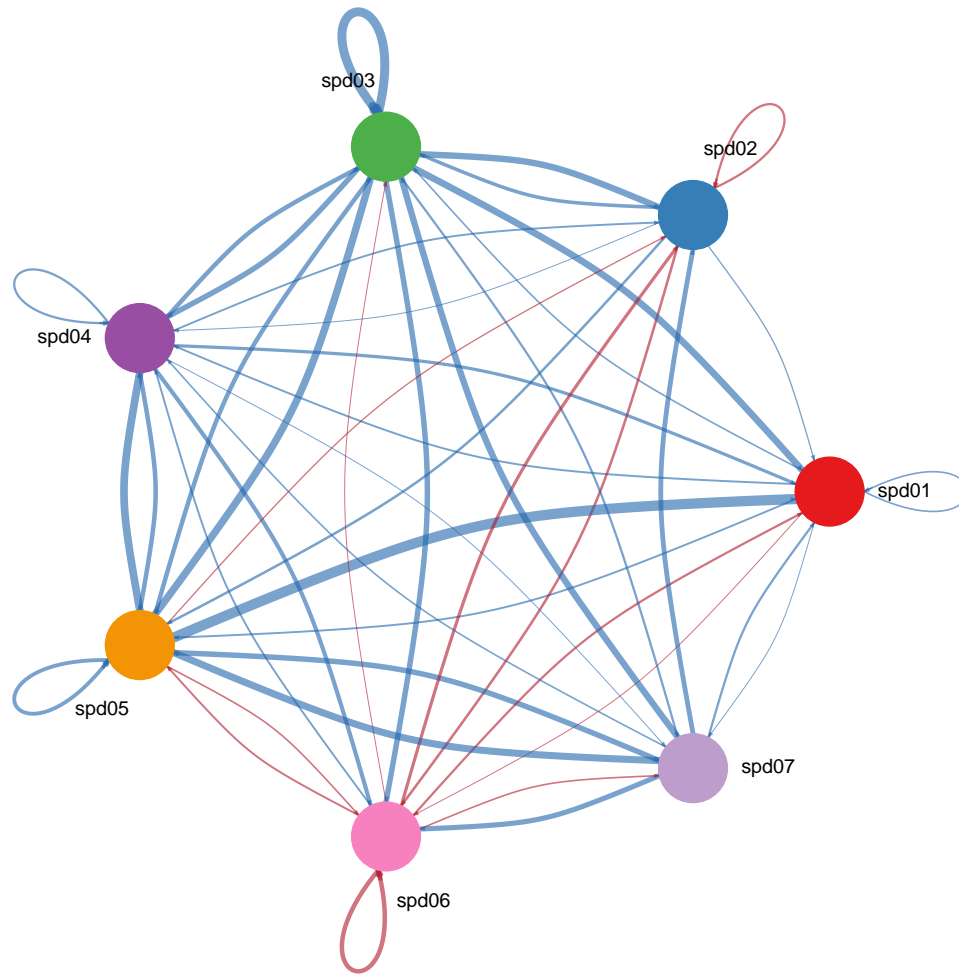
Warning: Heatmap/annotation names are duplicated: Relative values

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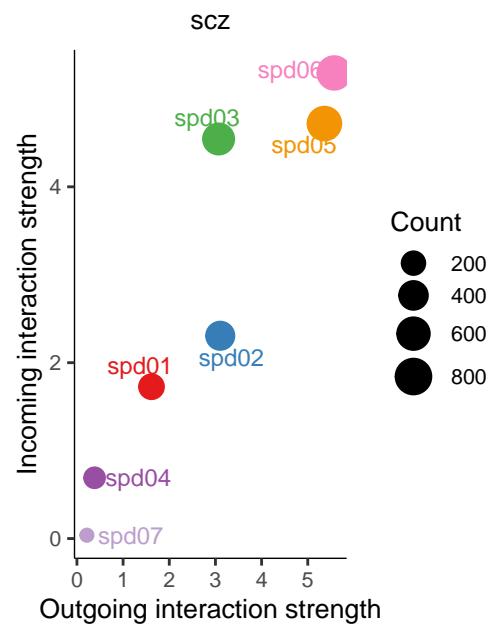
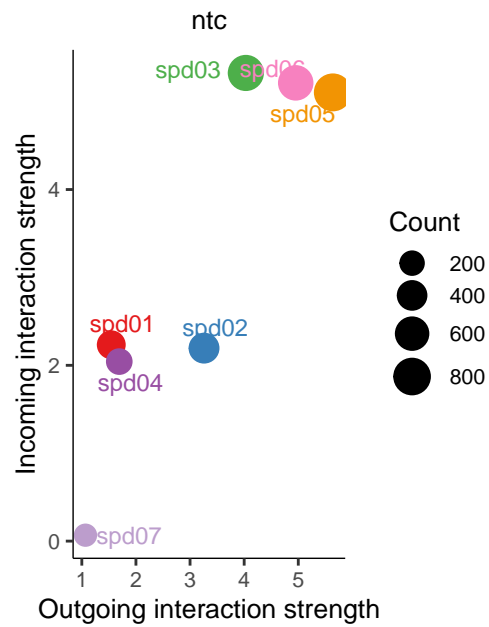
Warning: `legend_height` you specified is too small, use the default minimal height.



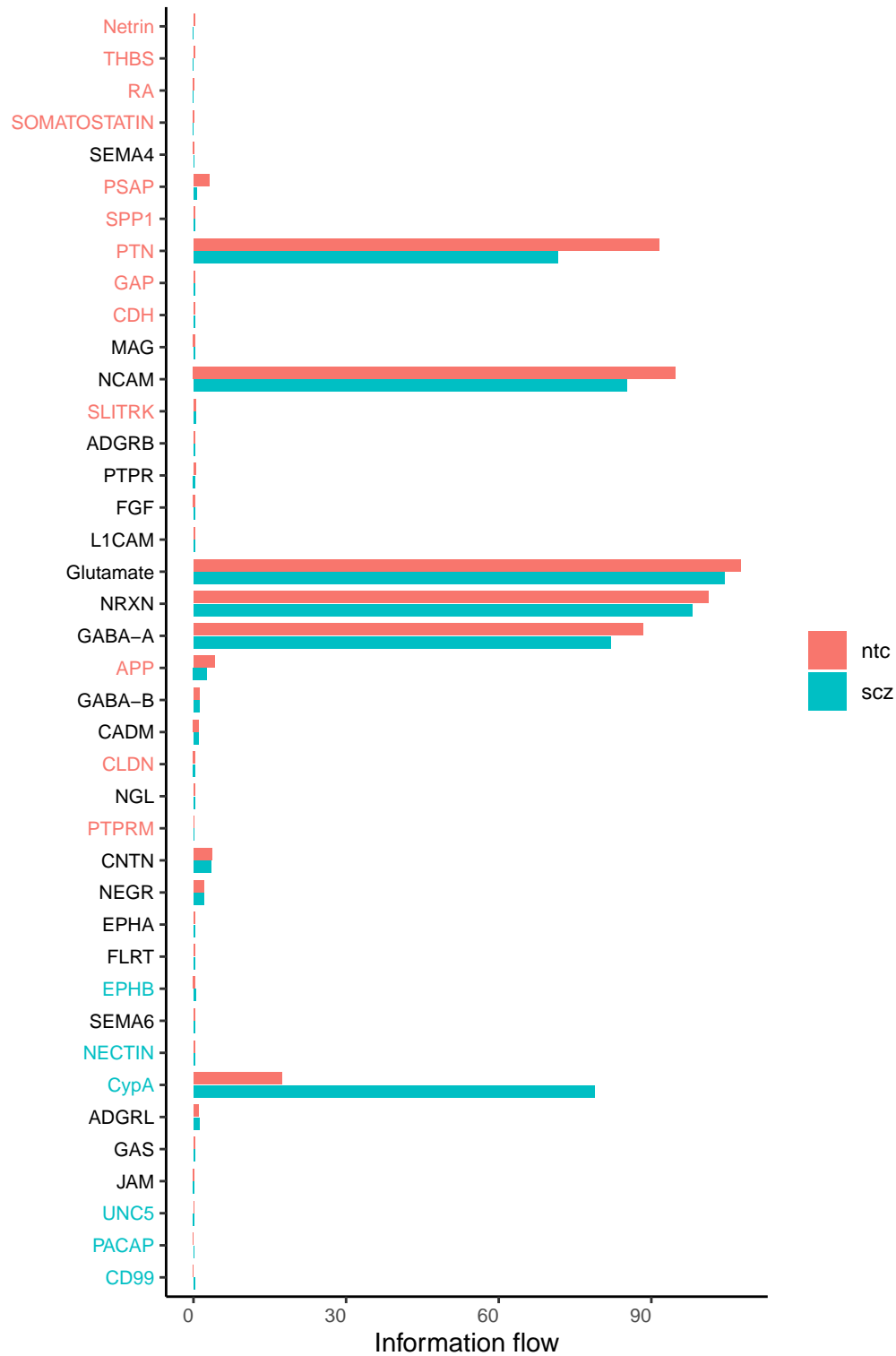


Compare major sources and targets - Not very informative

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

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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:

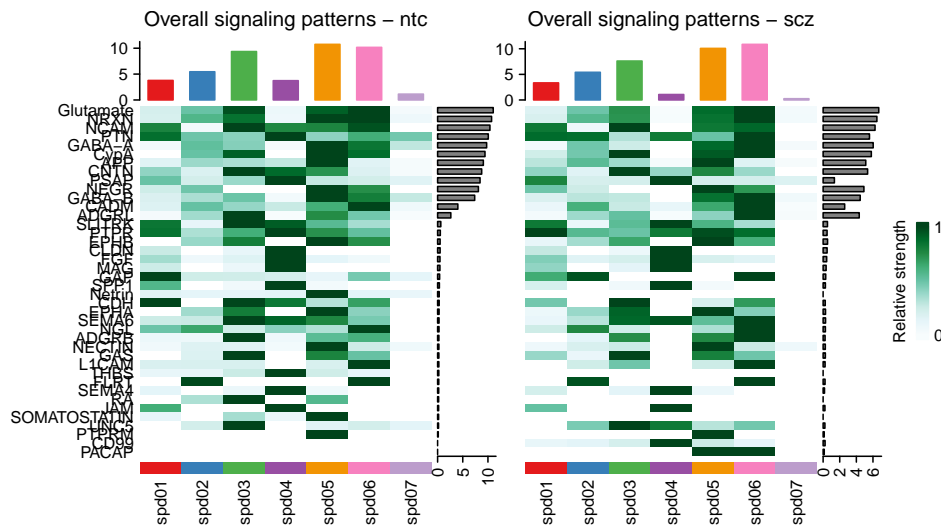
- Gu, Z. Complex Heatmap Visualization. iMeta 2022.
- Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics 2016.

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

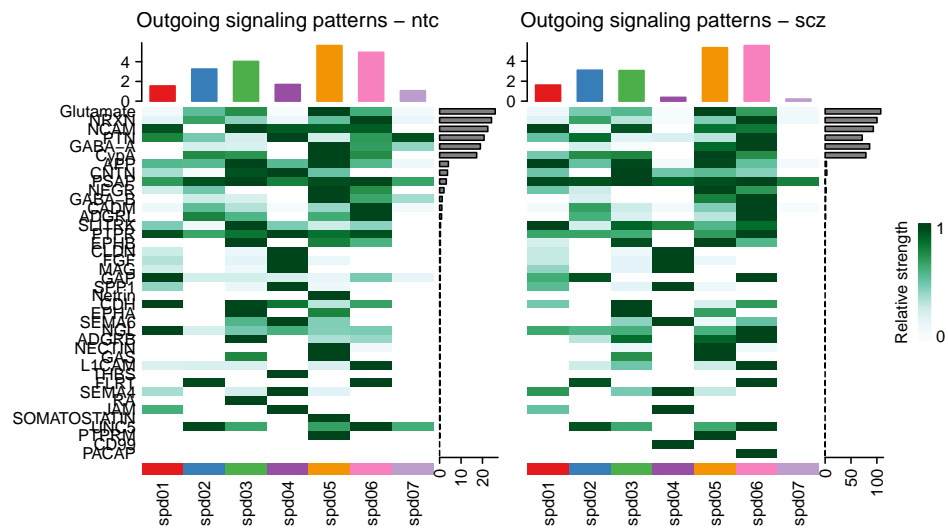
This message can be suppressed by:

```
suppressPackageStartupMessages(library(ComplexHeatmap))
```

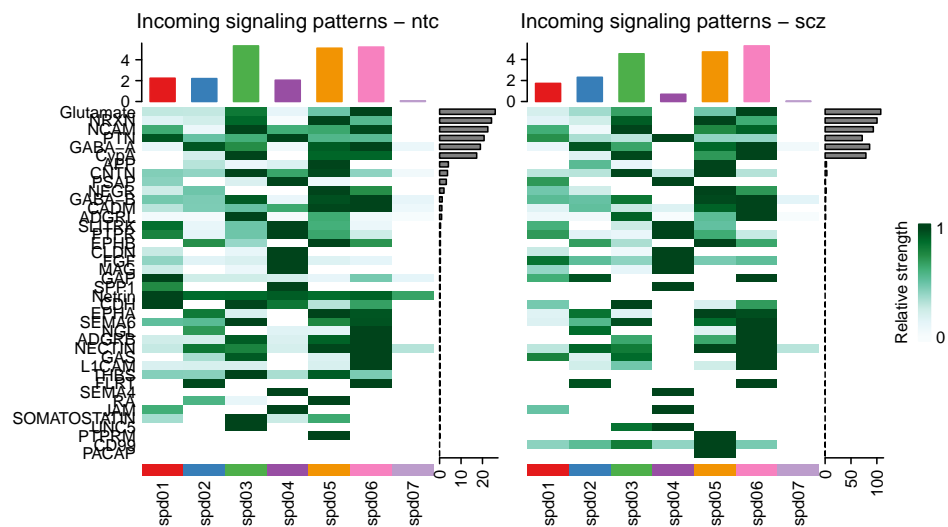
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Outgoing



Incoming



Upregulated and downregulated signaling LR pairs

Increased signaling in SCZ

Comparing communications on a merged object

Decreased signaling in SCZ

Comparing communications on a merged object

