Grouped plots

Group plots

The plots for the paper need to be grouped into larger figures. The roughly planned grouping so far can be seen in the file `figure_group_planning.md`.

Load dependencies

ggplotify function

The facet packages (patchwork and cowplot facet_grid etc) dont seem to work with non-ggplot plots. So this function is here to convert the plots to ggplot format

Figure 1 - Explanatory and introductory plots

```
# ADHD ancestor terms
namer = function(term){

  return (hpo$name[term])

}

terms = get_term_property(hpo,property="ancestors" ,term ="HP:0007018",

                          as_names=FALSE)

adhd_ancestors <- onto_plot(hpo, terms= terms[2:length(terms)],label = namer,

        shape="circle",fontsize = 80, edge_attributes = list(color="grey"))
```

```r
# APP Homepage screenshot
app_home = ggloadImage("figures/EWCE_home.png")


# Interactive app screenshot
app_interactive = ggloadImage("figures/interactive_cell_celect_acinar_demo.png")


# Print friendly network plot
cell = "Acinar cells"
printable_networkPlot <- one_cell_ontology_plot_heatmap(all_results_merged,cell=cell, heatmapped_value =
```

Here is an example of Figure 1

```r
adhd_ancestors <- ggplotify(adhd_ancestors)
printable_networkPlot <- ggplotify(printable_networkPlot)


(adhd_ancestors | app_home) /(printable_networkPlot | app_interactive)
```

Figure 2 - Overview results

These figrues are meant to give a general idea of how many results there are, and show that they make sense.

Here is Fig 2

```r
layout <- "
AA####BBBB##
AA####BBBB##
AA####BBBB##
AACCCCCCCCCC
AACCCCCCCCCC
AACCCCCCCCCC
AACCCCCCCCCC
AACCCCCCCCCC
```
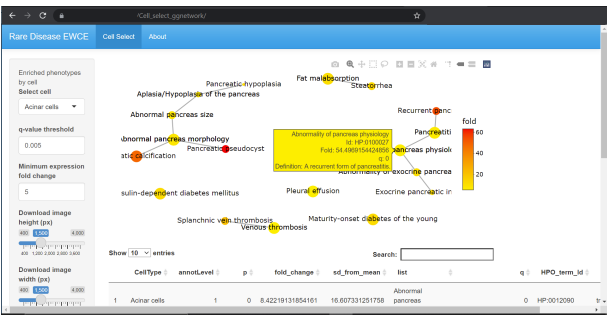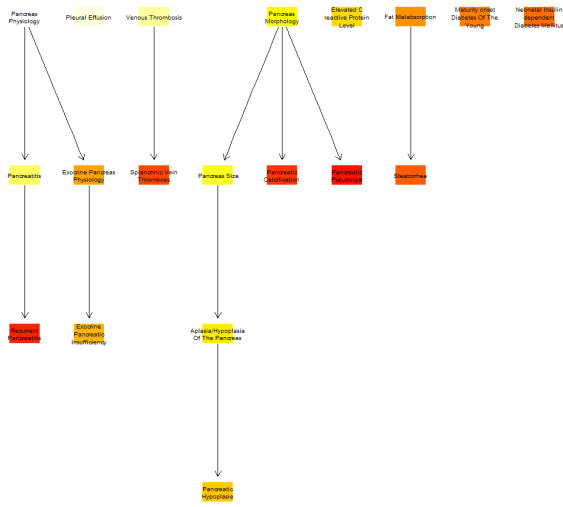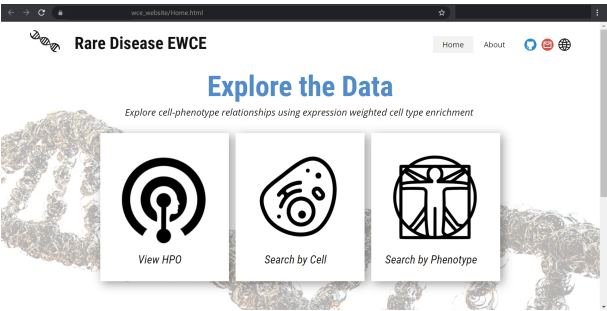
Figure 1: **Explanatory and Introductory plots.** These plots were mostly used in the introduction of my report.

```
AACCCCCCCCCC

##CCCCCCCCCC

"


print(

  (plot_npc + theme(legend.position = "top", legend.justification = "top", axis.text.y = element_text(s

  (main_branch_plt + theme(axis.text.y = element_text(size = 15))) +


      ( facet_branch_plt + theme(axis.title.y =element_text(margin = margin(l = -15, b = -10))) ) +

      plot_layout(design = layout) + plot_annotation(tag_levels = LETTERS) )
```

```
namer = function(term){

  return (hpo$name[term])

}

terms = ontologyIndex::get_term_property(hpo,property="children" ,term = hpo$id[which(hpo$name == "Phen

terms = append(terms,hpo$id[which(hpo$name == "Phenotypic abnormality")])



terms <- data.frame("terms" = terms, "colour" = "gray")




plot_branches = c("Abnormality of the nervous system","Abnormality of the cardiovascular system", "Abnor

named_colours <- c()

for (i in seq(length(plot_branches))) {

  named_colours[plot_branches[i]] <- palette_branch[i]

}


term_colours <- c()

term_names <- c()

term_labels <- c()

for (t in terms$terms) {

  cur_name <- hpo$name[t]

  term_names <- append(term_names, cur_name)
```

```r
  if( cur_name == "Phenotypic abnormality") {
    term_labels <- append(term_labels, cur_name)
    term_colours <- append(term_colours, "lightblue")
  } else if (cur_name %in% plot_branches) {
    term_labels <- append(term_labels, "")
    term_colours <- append(term_colours, named_colours[cur_name])
  } else {
    term_labels <- append(term_labels, " ")
    term_colours <- append(term_colours, "gray")
  }
}


terms$colour <- term_colours
terms$name <- term_names
terms$labels <- term_labels



phenotypic_abnormality_children <- ontologyPlot::onto_plot(hpo, terms= terms$terms,label = terms$labels
          shape="circle",fontsize = 80,fillcolor = terms$colour ,edge_attributes = list(color="grey"))




layout <- "
AA###BBBBB##
AA###BBBBB##
AACCCCCCCCCC
AACCCCCCCCCC
AADDDDDDDDDD
AADDDDDDDDDD
AADDDDDDDDDD
```

```
AADDDDDDDDDD

AADDDDDDDDDD

AADDDDDDDDDD

"




Fig2 = (

  (plot_npc + theme(legend.position =c(0.7,0.3), axis.text.y = element_text(size = 12)))  +

  (main_branch_plt + theme(axis.text.y = element_text(size = 13))) +

        ggplotify(phenotypic_abnormality_children, height_px = 300, width_px = 1200) + # try increase

       ( facet_branch_plt + theme(axis.title.y =element_text(margin = margin(l = -15, b = -10))) ) +

       plot_layout(design = layout) + plot_annotation(tag_levels = LETTERS) )


ggsave("fig2.png",Fig2, dpi = 400, width = 24, height = 20)
print(Fig2)
```

Testing ggnetwork plot

```
## adjacency_matrix
```

```
## ggnetwork_plot
```

```
## Saving 6.5 x 4.5 in image
```

Test with ggnetwork

```
layout <- "
AA#####BBBBB
AA#CCCCBBBBB
AA#CCCCBBBBB
AA#CCCCBBBBB
```
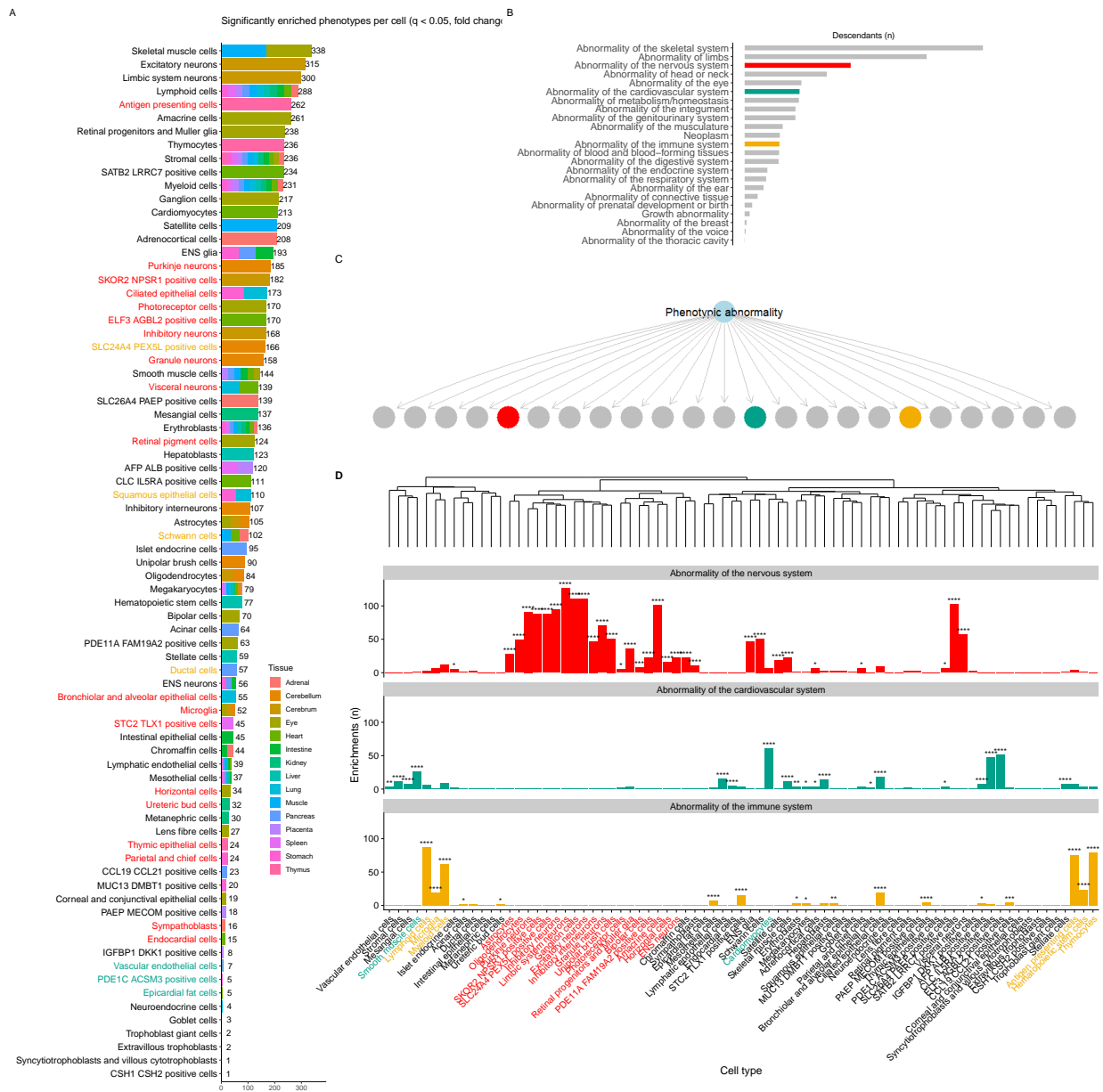
Figure 2: **Overview results** plots describing the number of significant results.

```
AADDDDDDDDDD

AADDDDDDDDDD

AADDDDDDDDDD

AADDDDDDDDDD

AADDDDDDDDDD

AADDDDDDDDDD

"


Fig2 = (
  (plot_npc + theme(legend.position =c(0.7,0.3), axis.text.y = element_text(size = 12)))  +
  (main_branch_plt + theme(axis.text.y = element_text(size = 13))) +
        ggnetPlt + # try increase height_px (orig 300,1200)
       ( facet_branch_plt + theme(axis.title.y =element_text(margin = margin(l = -15, b = -10))) ) +
       plot_layout(design = layout) + plot_annotation(tag_levels = LETTERS) )

ggsave("fig2.png",Fig2, dpi = 400, width = 24, height = 20)
print(Fig2)
```
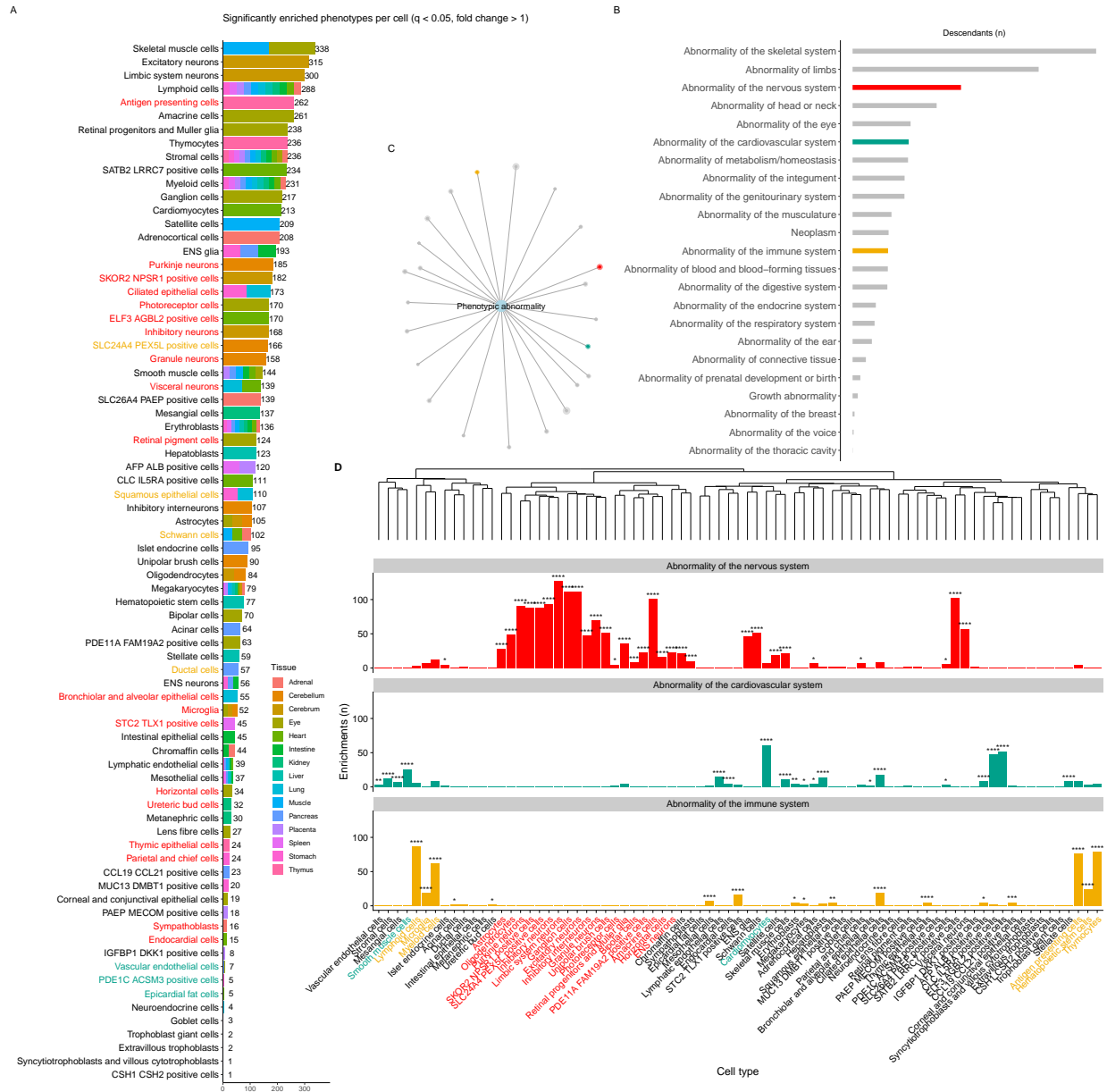
Not sure if this looks good here, but could be useful somewhere for showing the network structure and highlighting certain phenotypes by colour?

Figure 3 HPO Patterns and relationships

These show common patterns seen in HPO, related to ongology level, n genes etc.

Here is Fig 3

```
blank_x_axis <- theme(x.axis.title =  element_blank(), axis.text.x = element_blank())
print(
  ( ontlvl_ncells_plt /

    ontlvl_fold_plt /

    ontlvl_ngenes_plt)

  |

  ( proportion_plots[[1]]/

    proportion_plots[[2]]/

    proportion_plots[[3]])
)
```
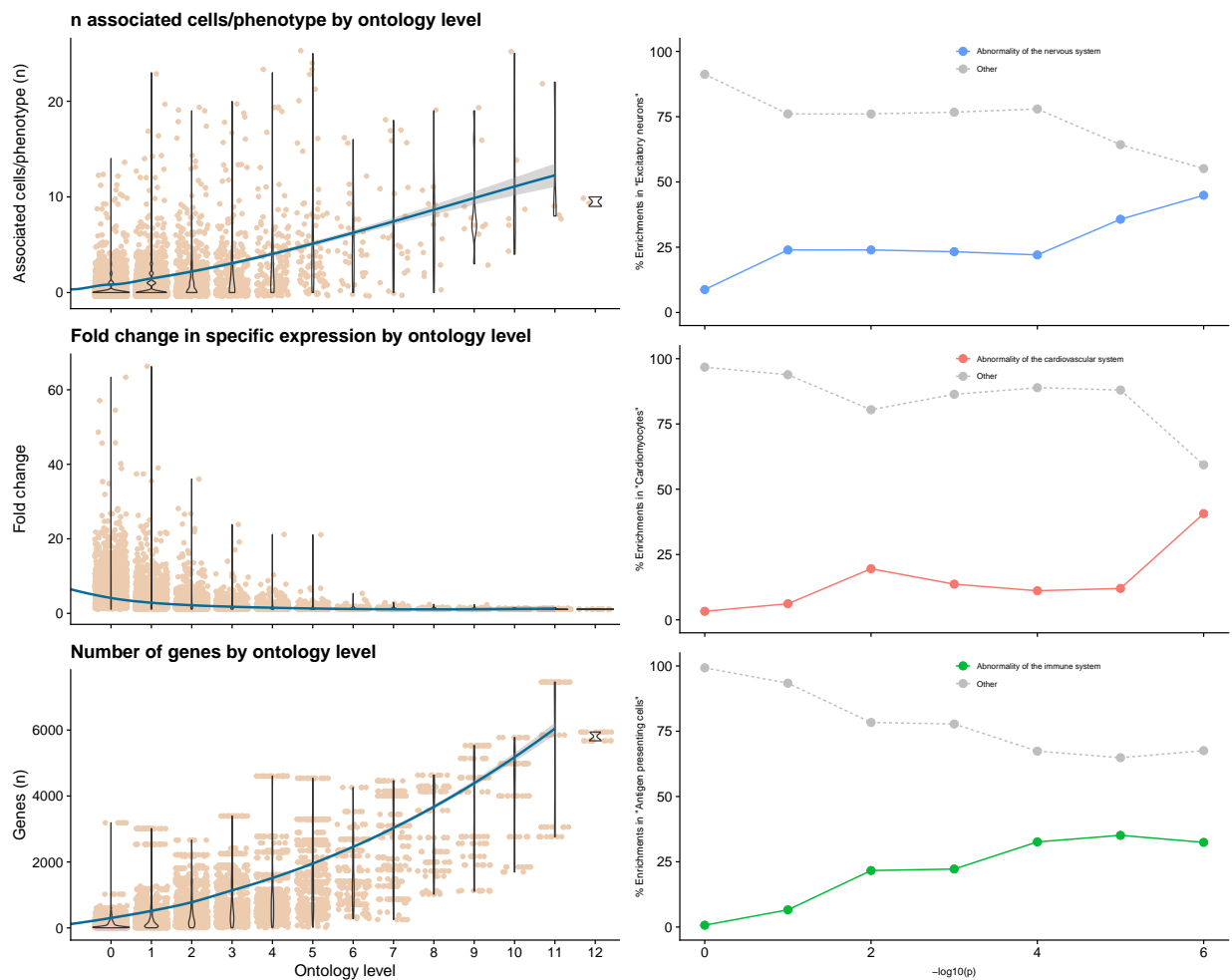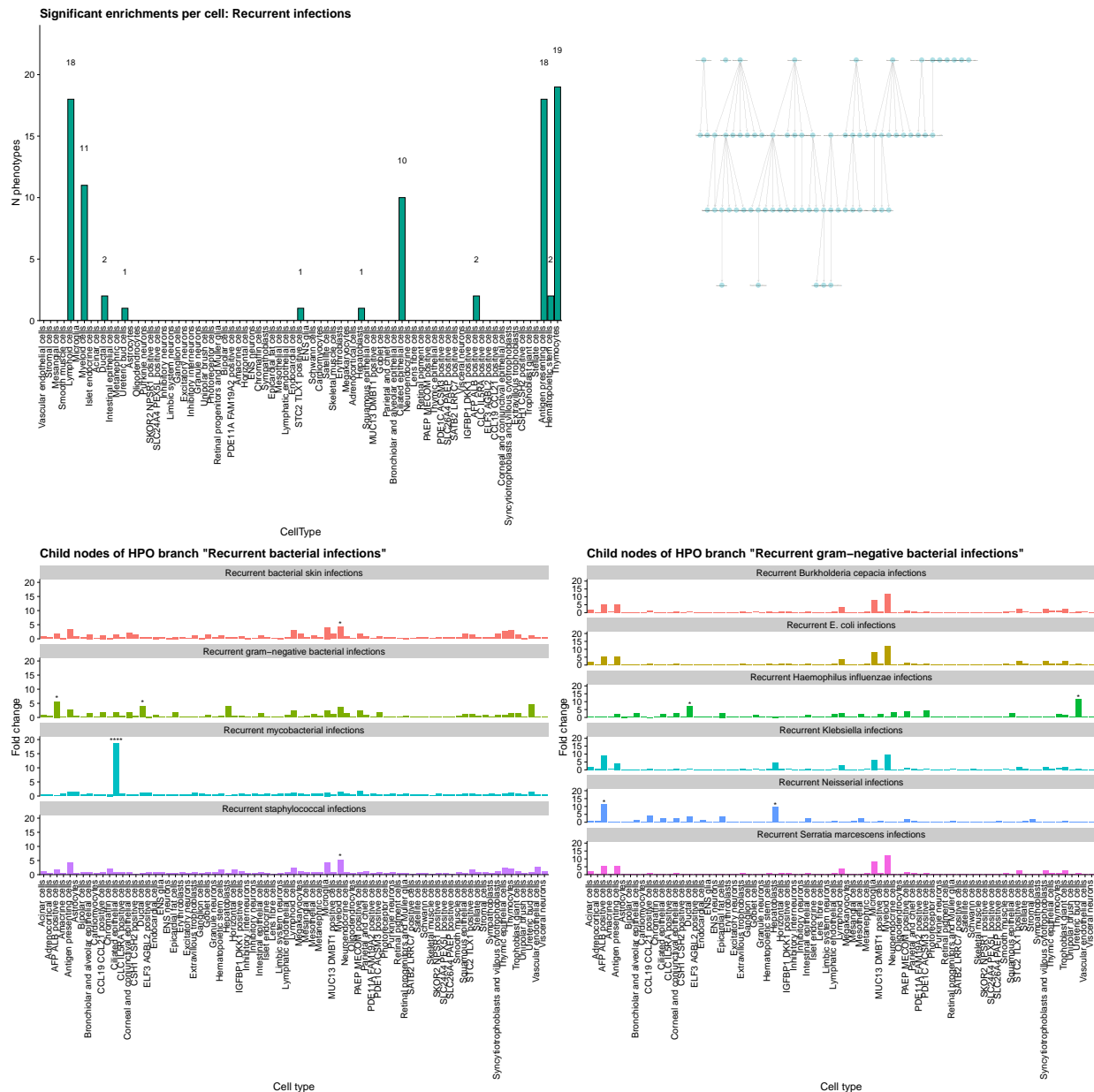

Figure 3: **ontology level plots** Plots describing relationships between expected cell types, significance, and ontology level.

Figure 4 infections

Significant enrichments per cell: Recurrent infections

Here is Fig **??**

Figure - social interactions

```
## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.
## Scale for 'x' is already present. Adding another scale for 'x', which will
```

replace the existing scale.

Here is Fig **??**

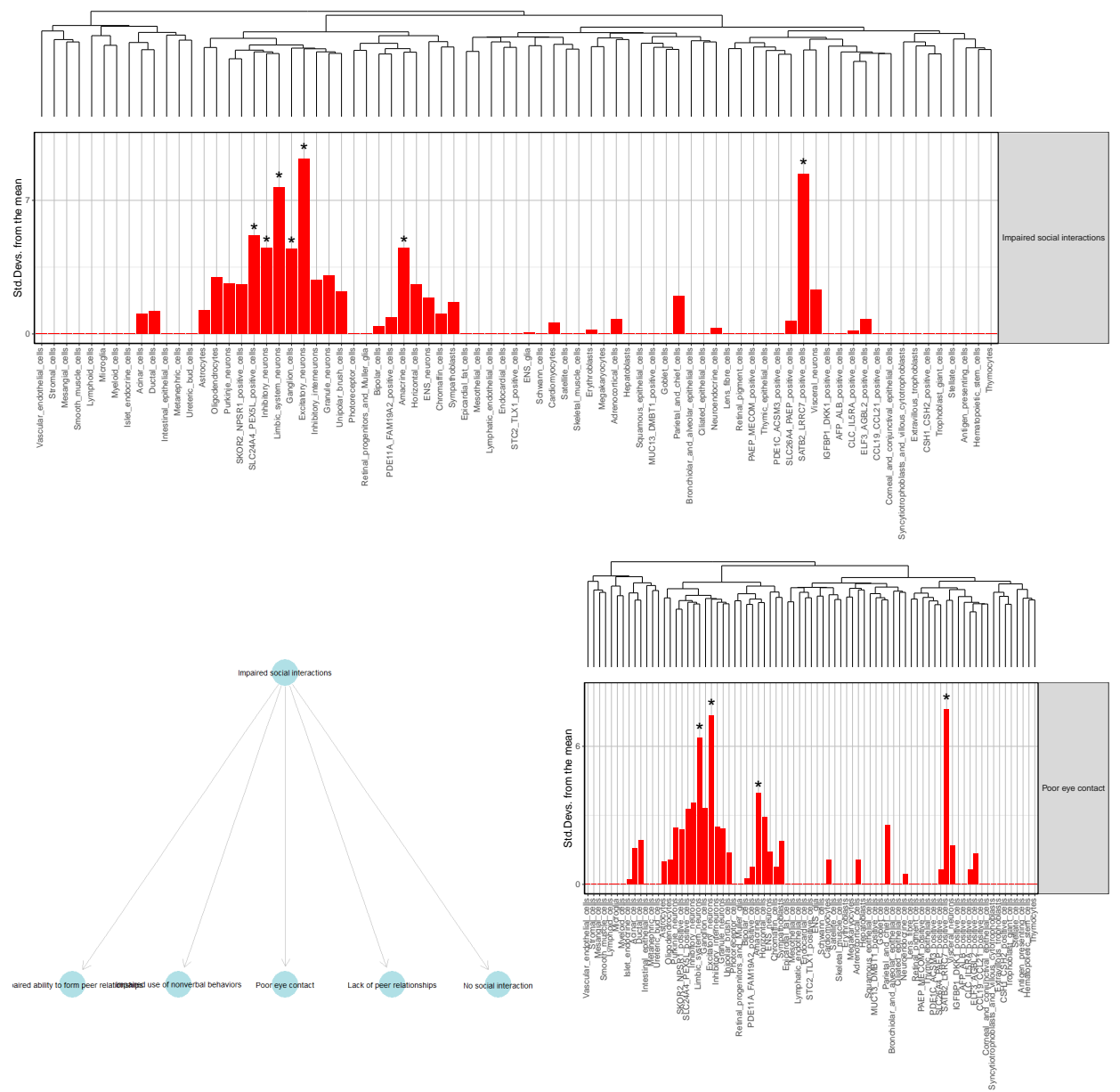```
print(plt1/ (social_ancestors | plt2))
```



Figure 4: **Social interactions** Enrichments in cell types for impaired social interactions.