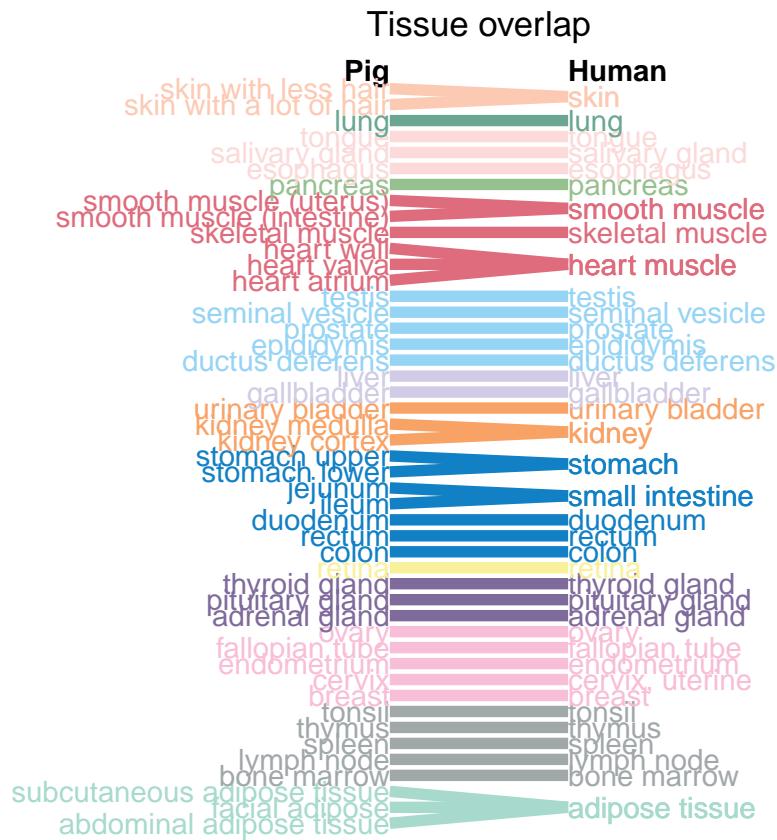
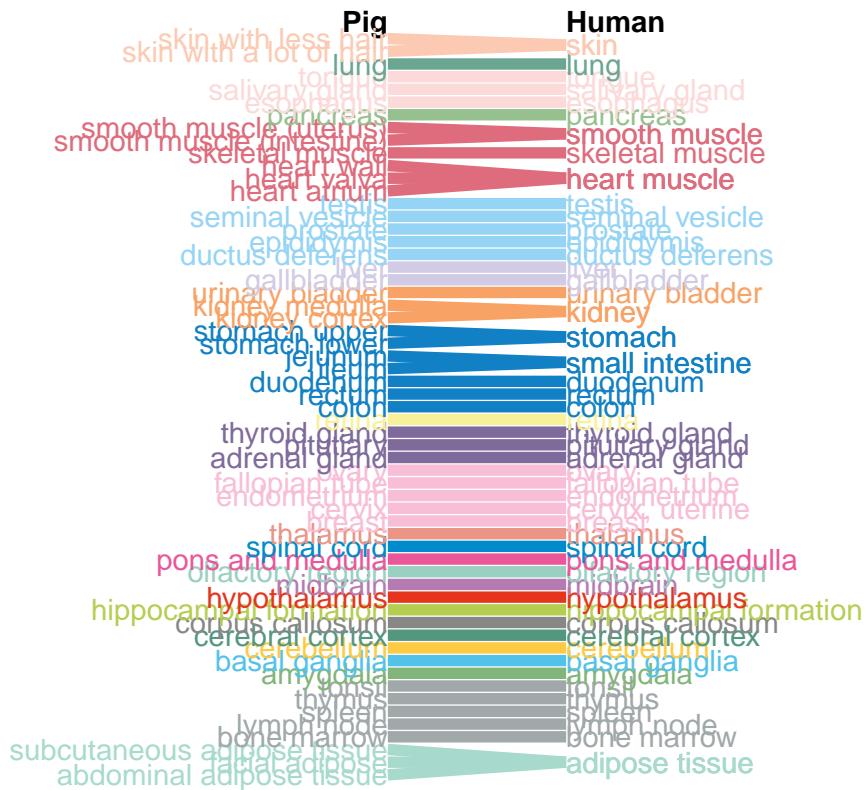


The Pig protein Atlas

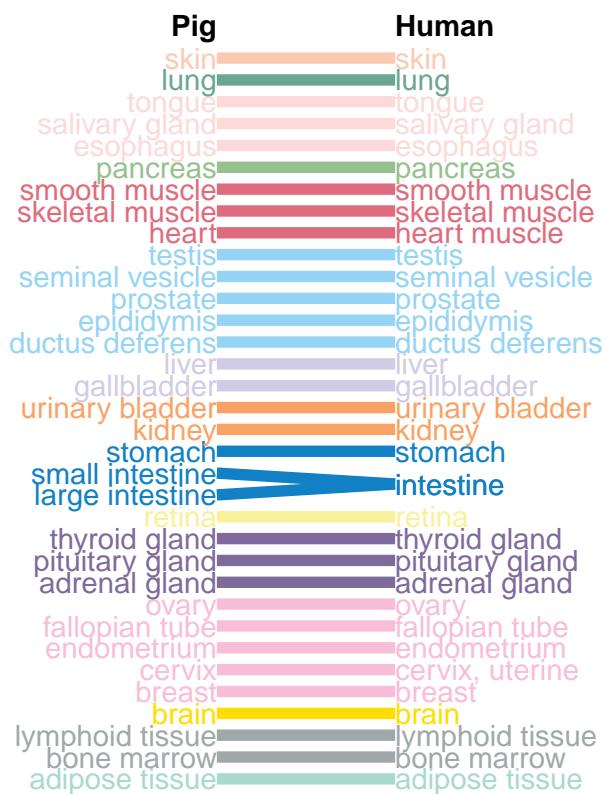
Max Jonatan Karlsson



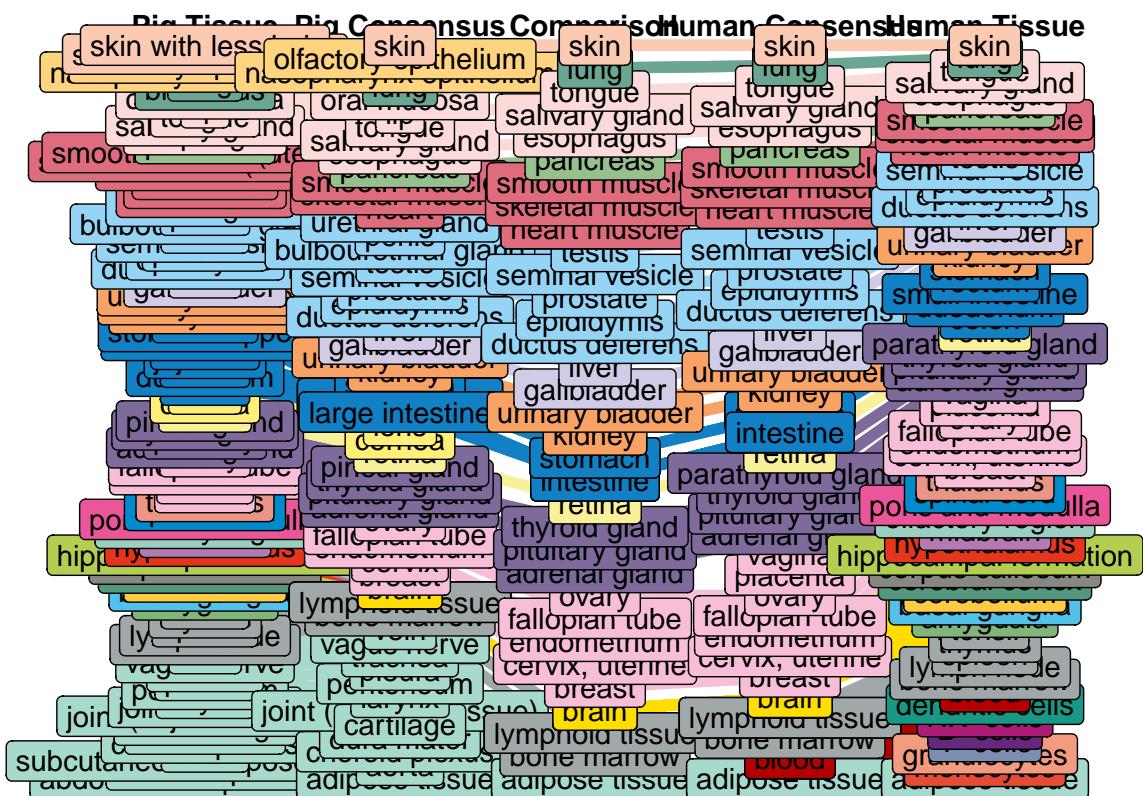
Region overlap



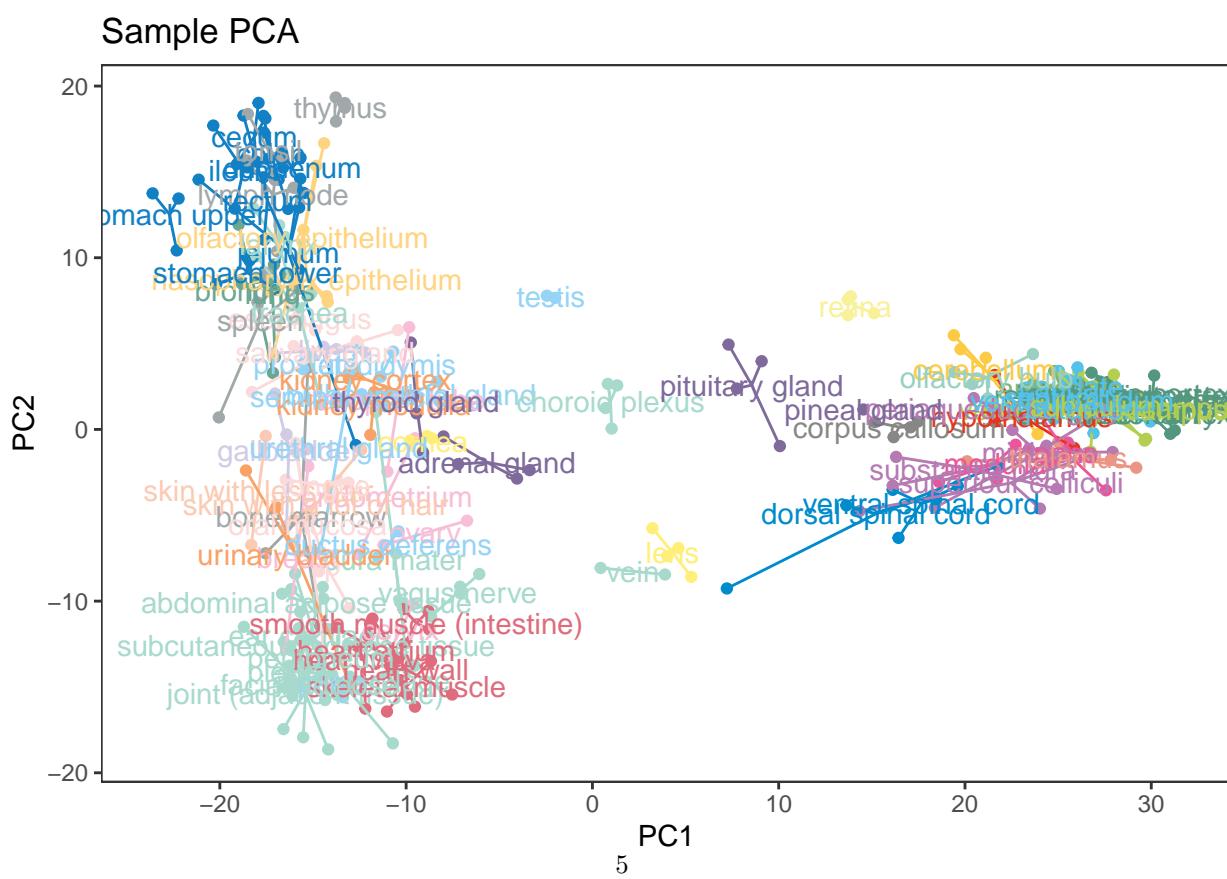
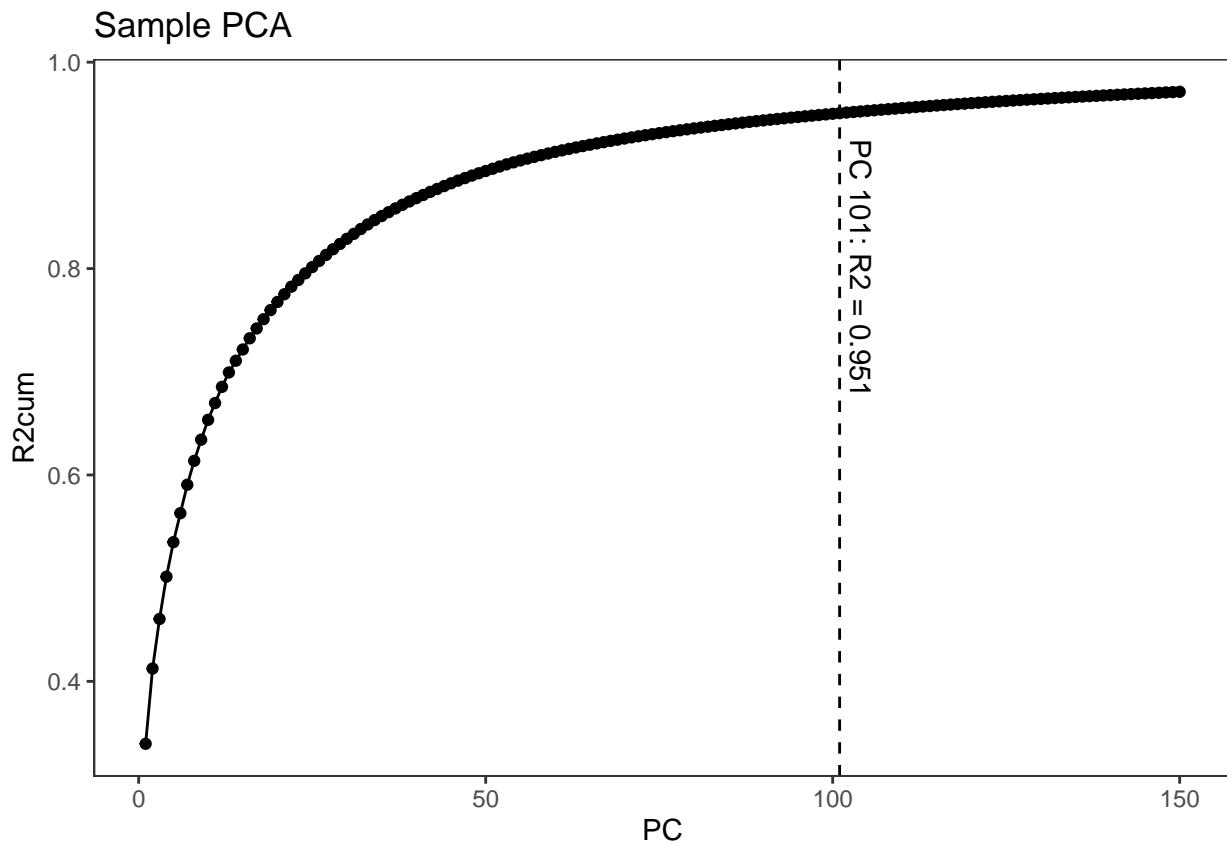
Consensus overlap



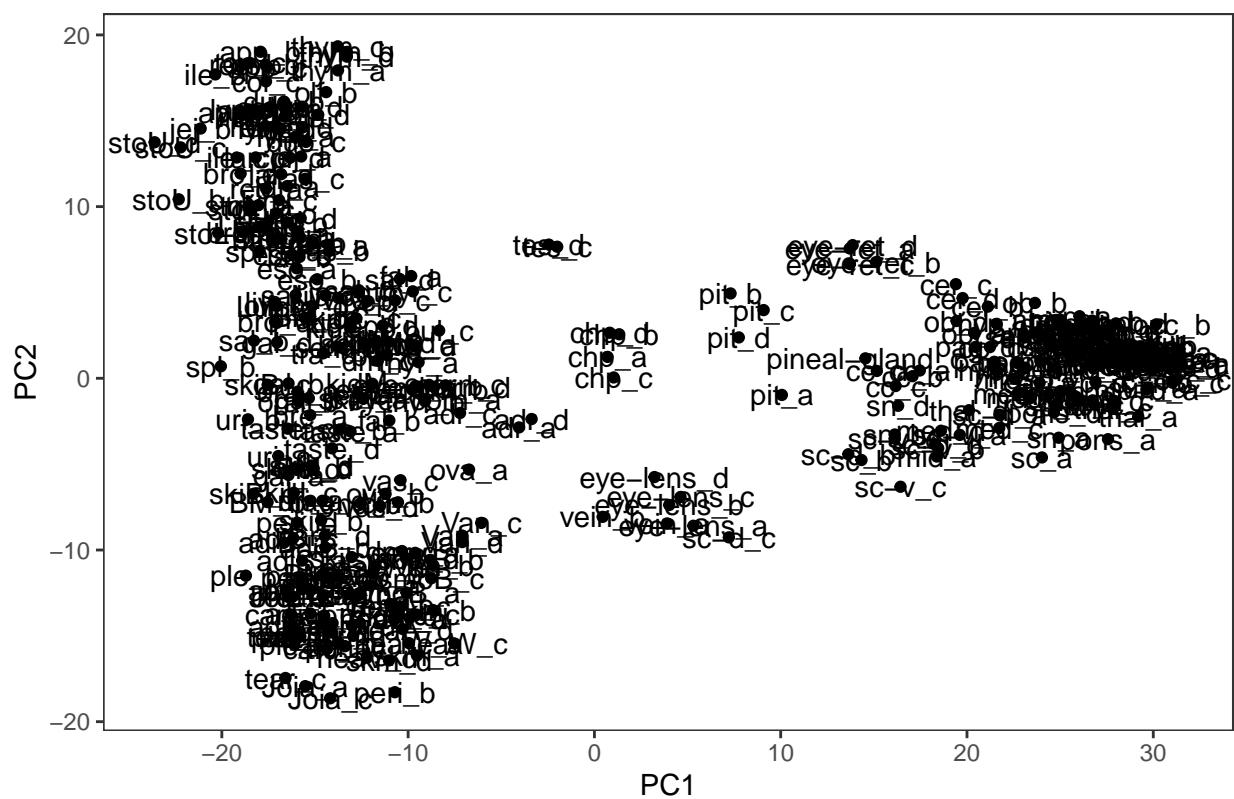
Comparison overlap



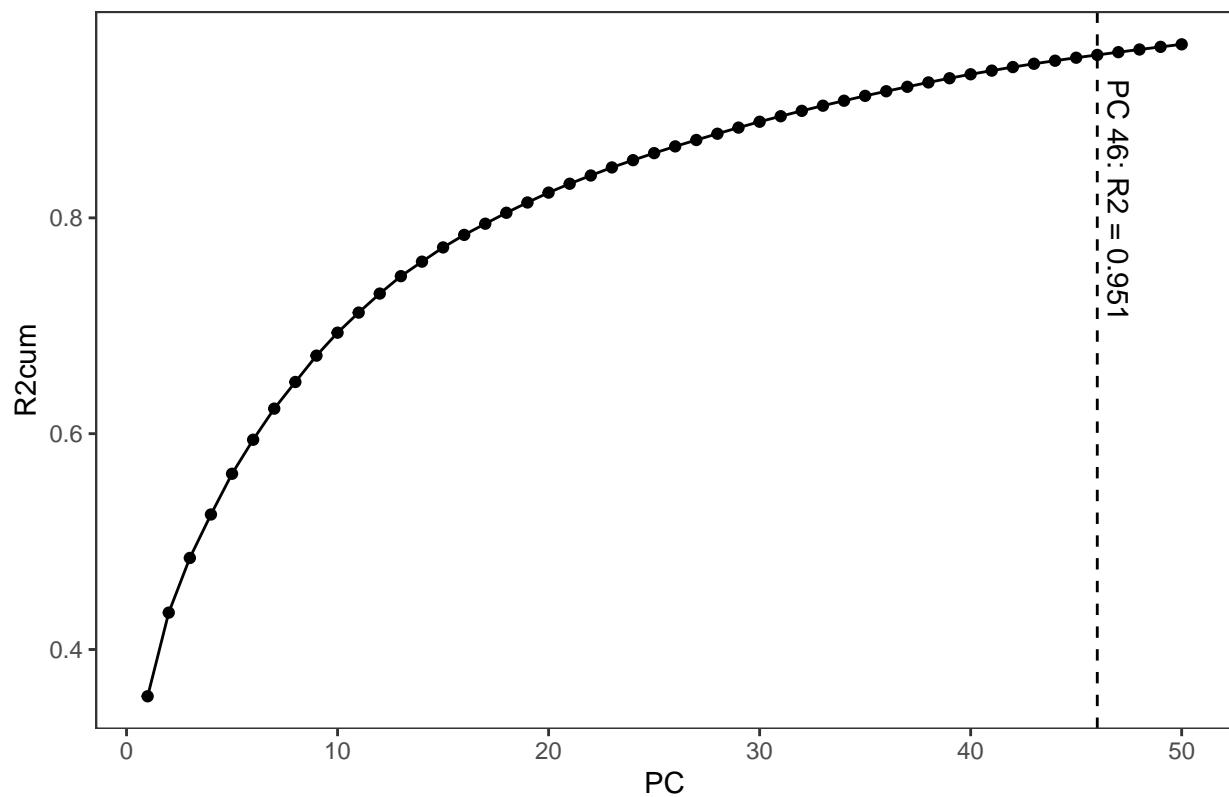
Normalization



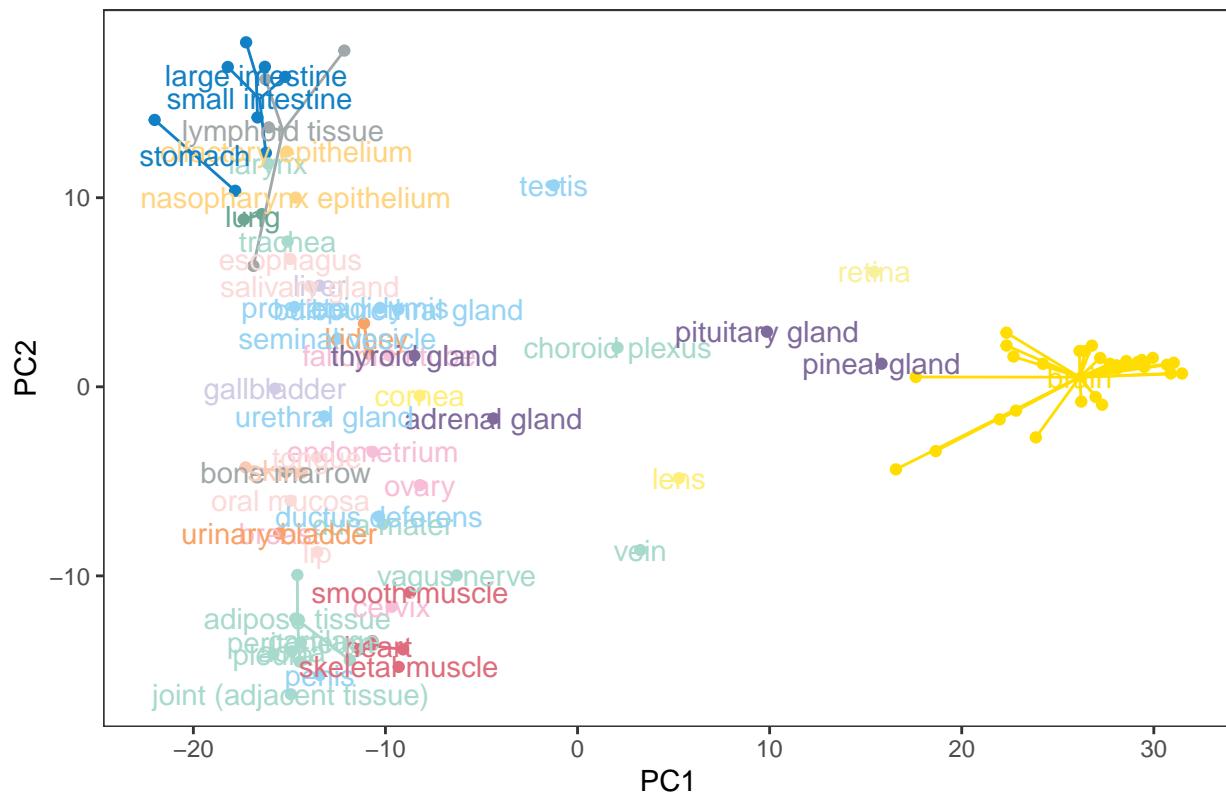
Sample PCA



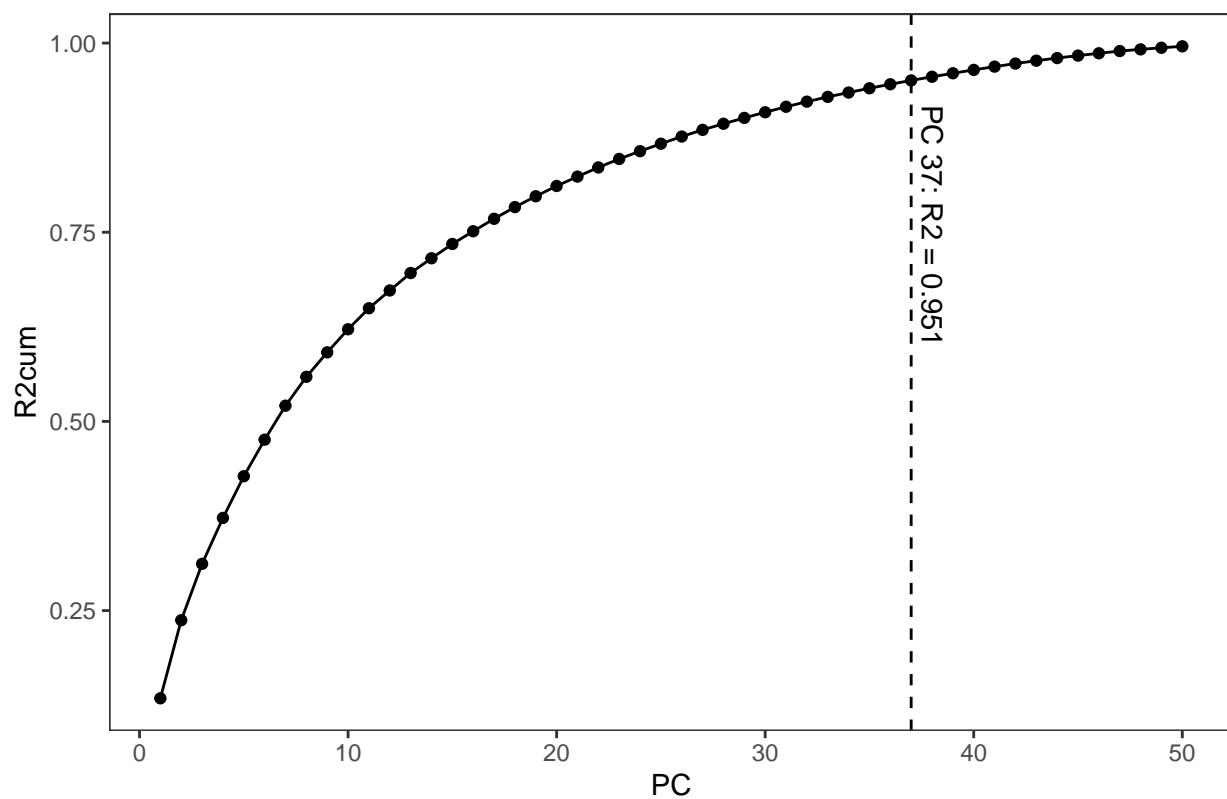
Tissue PCA



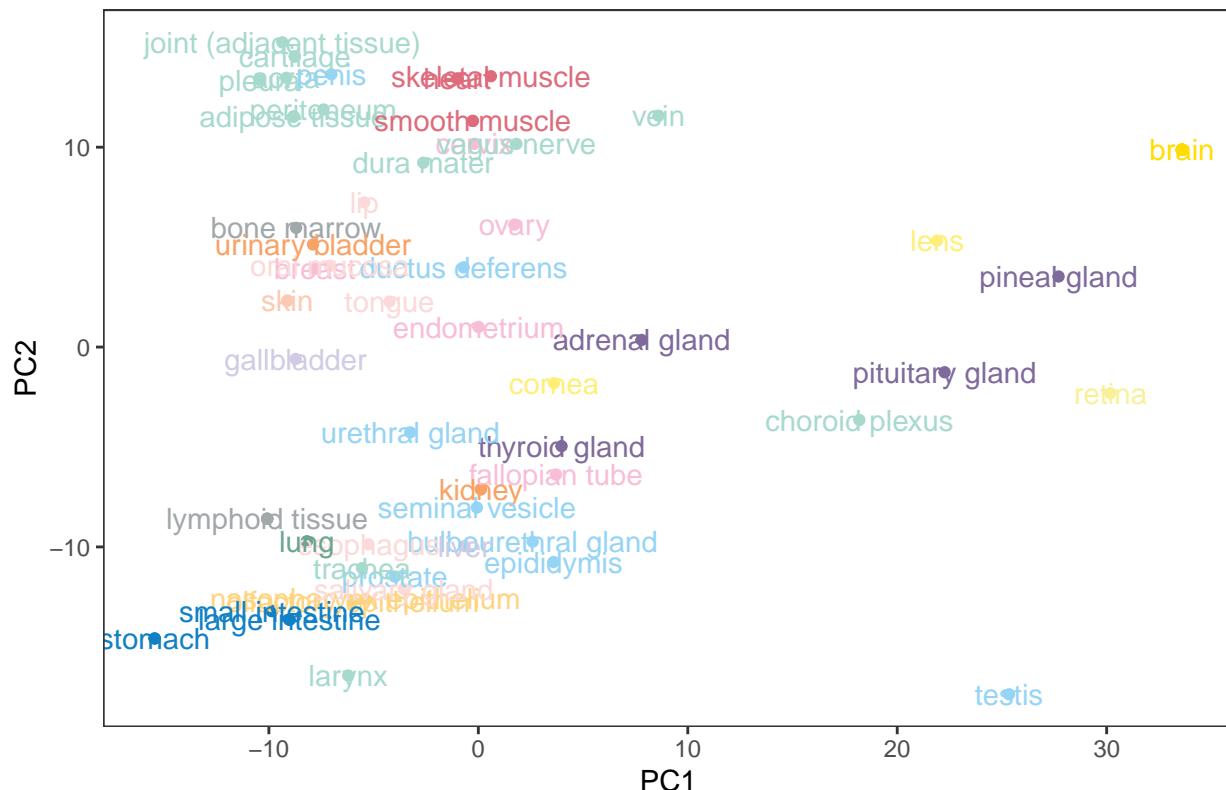
Tissue PCA



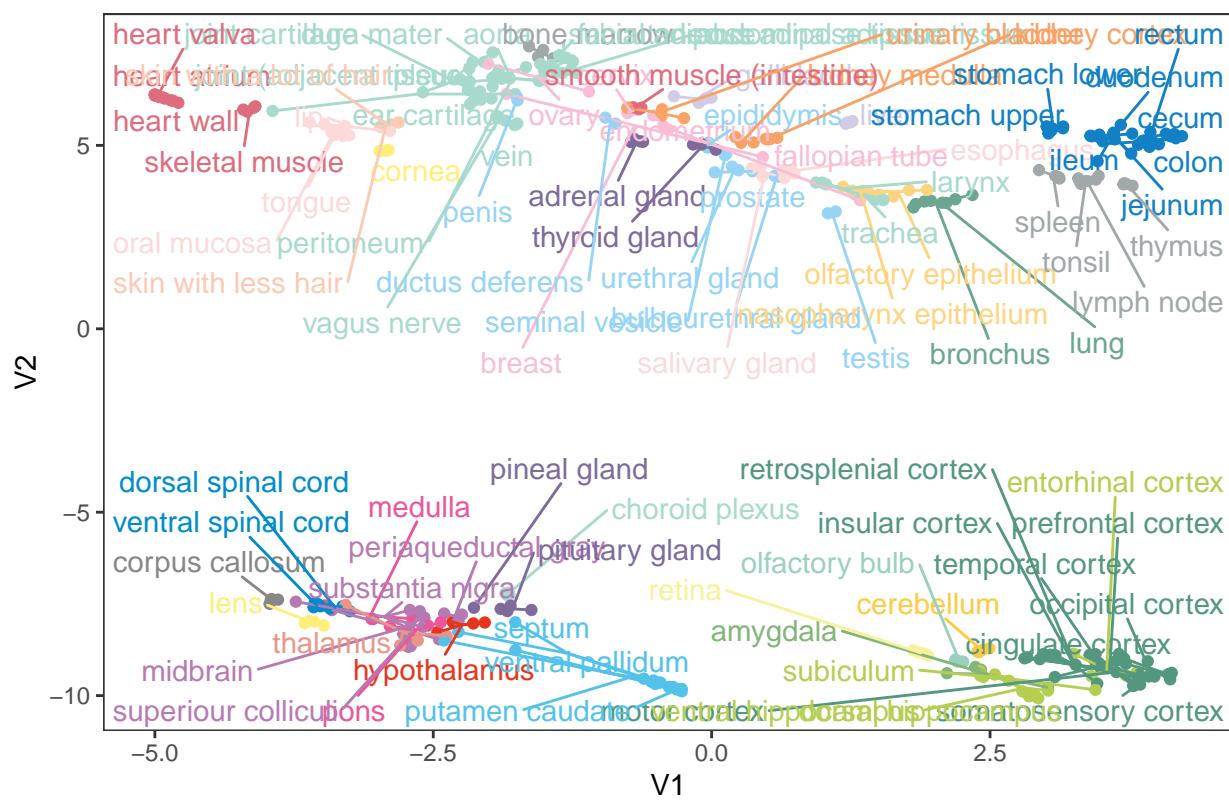
Consensus PCA



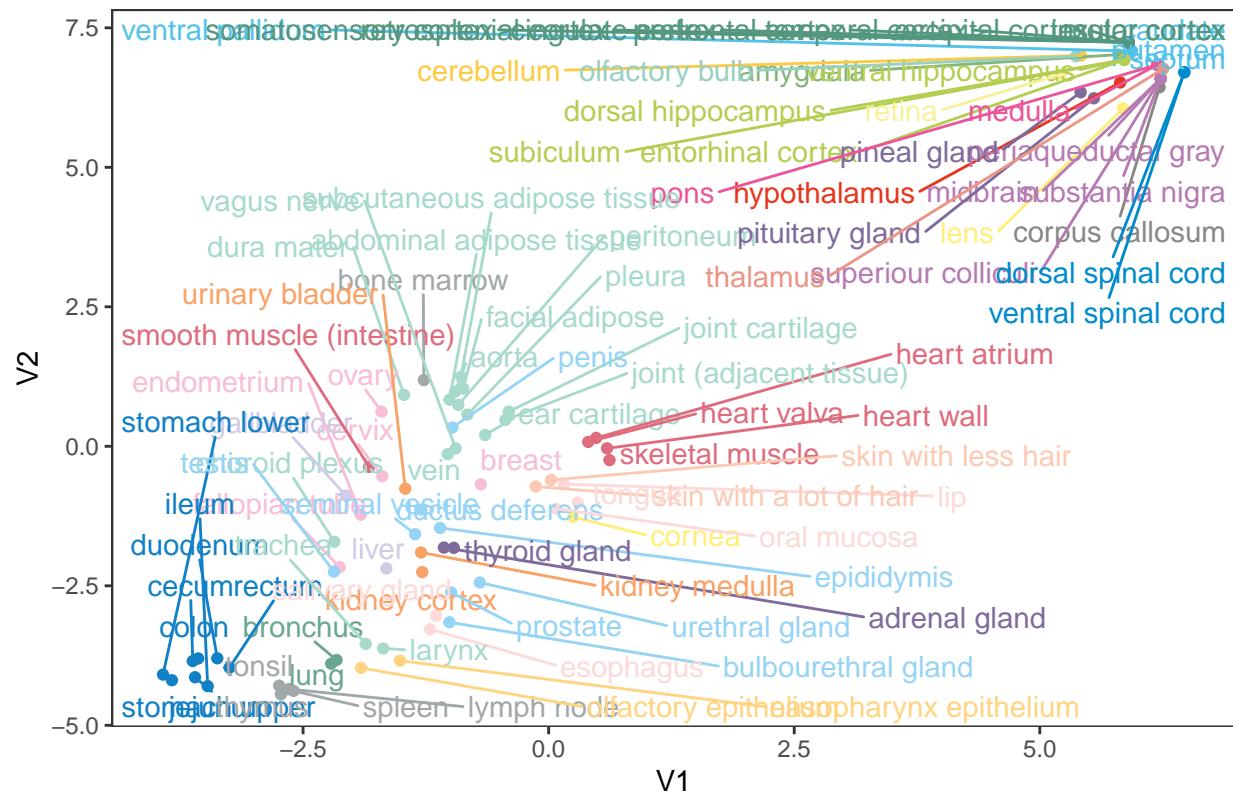
Consensus PCA

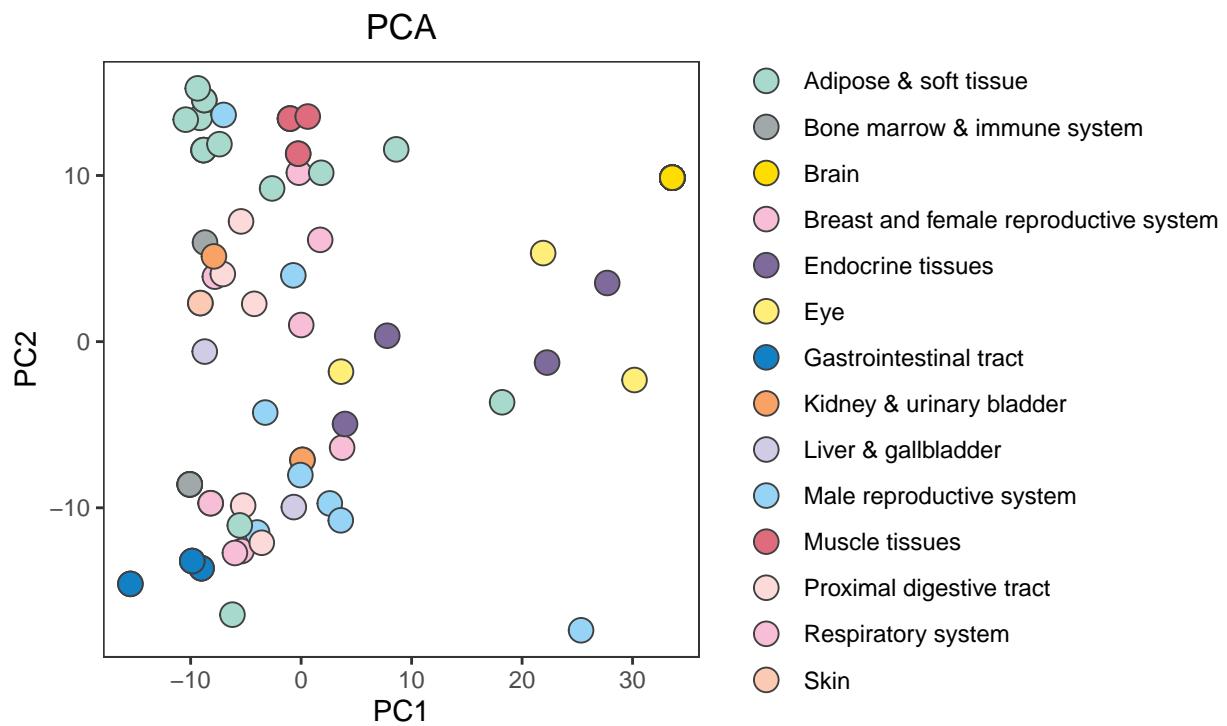


Sample UMAP

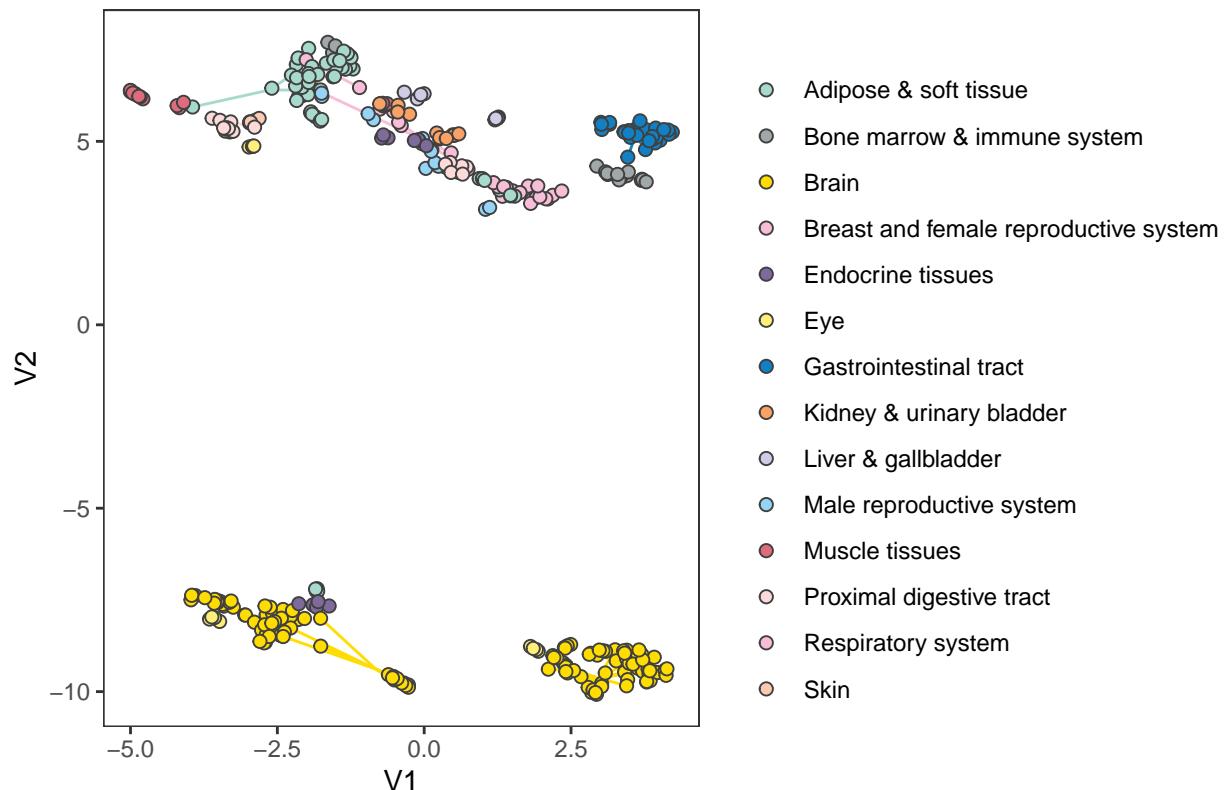


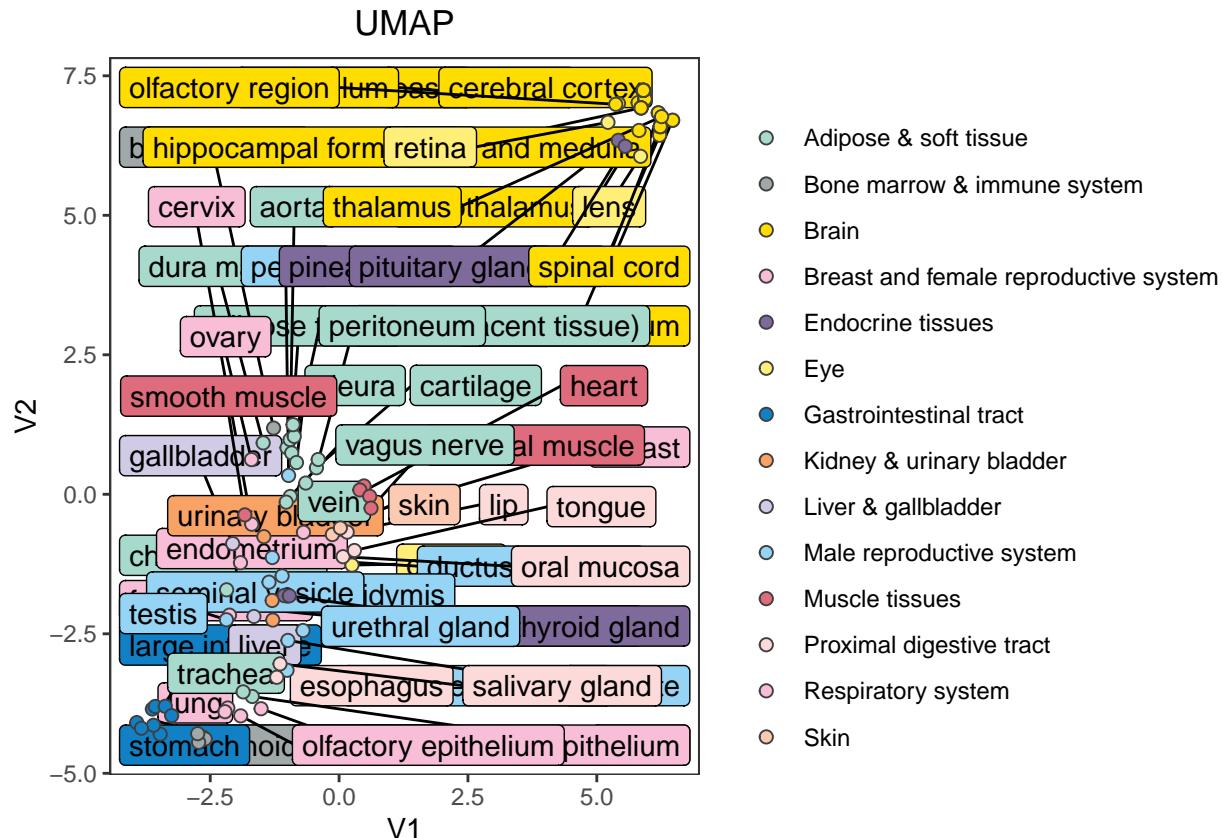
Sample UMAP



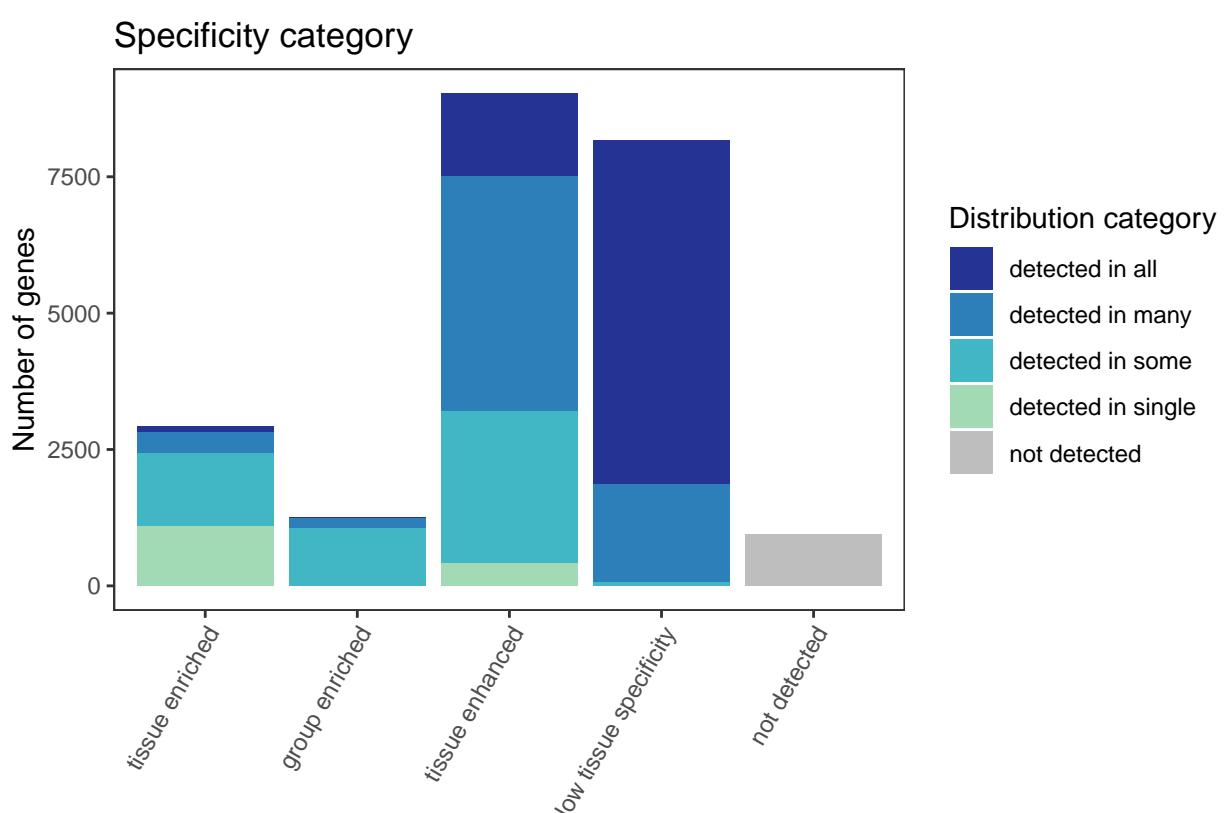
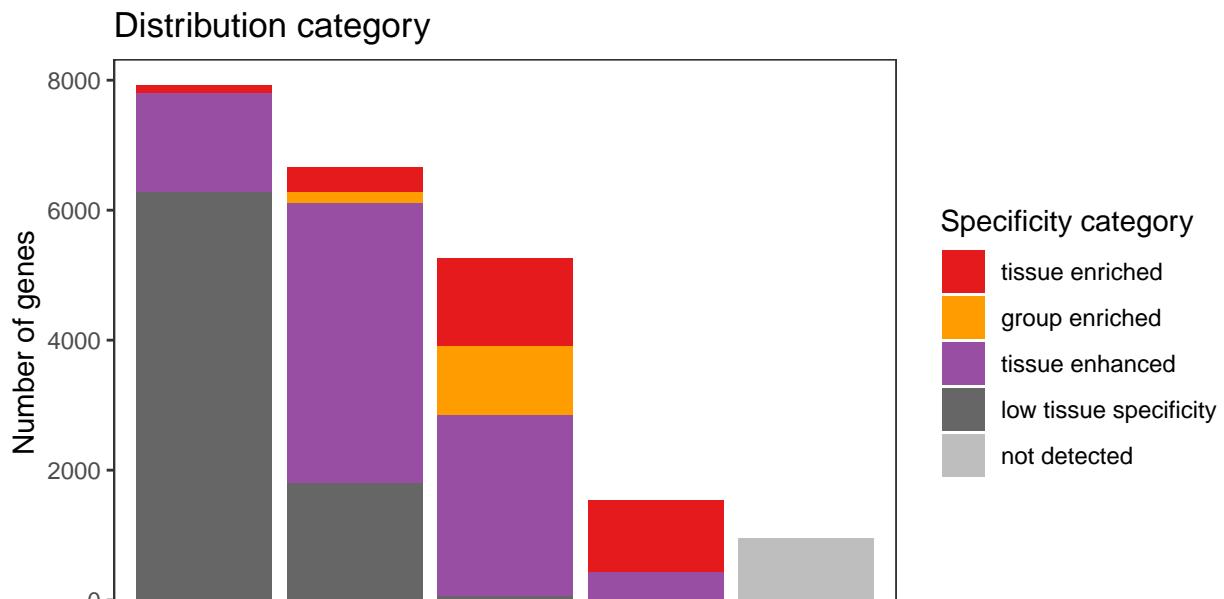


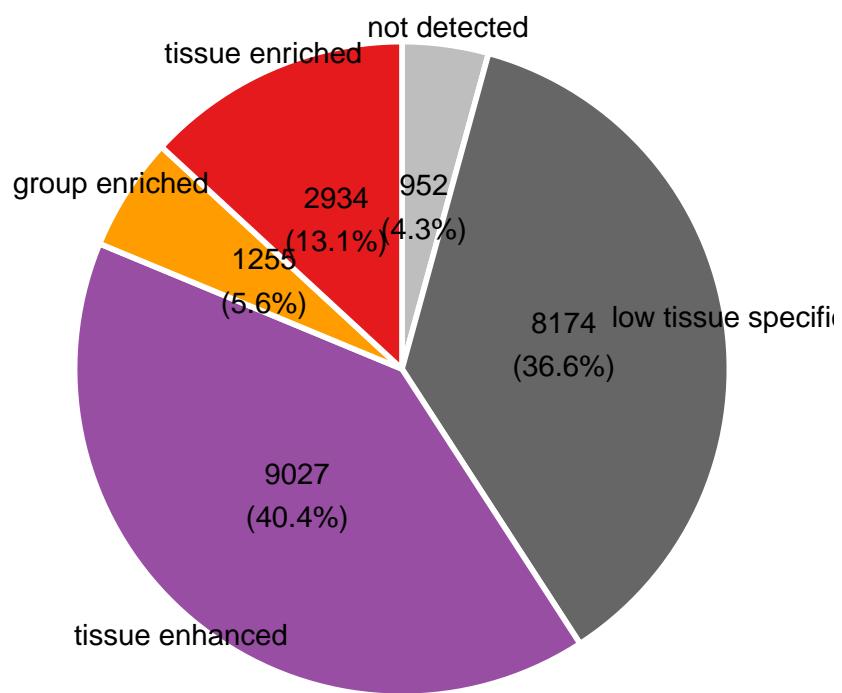
UMAP

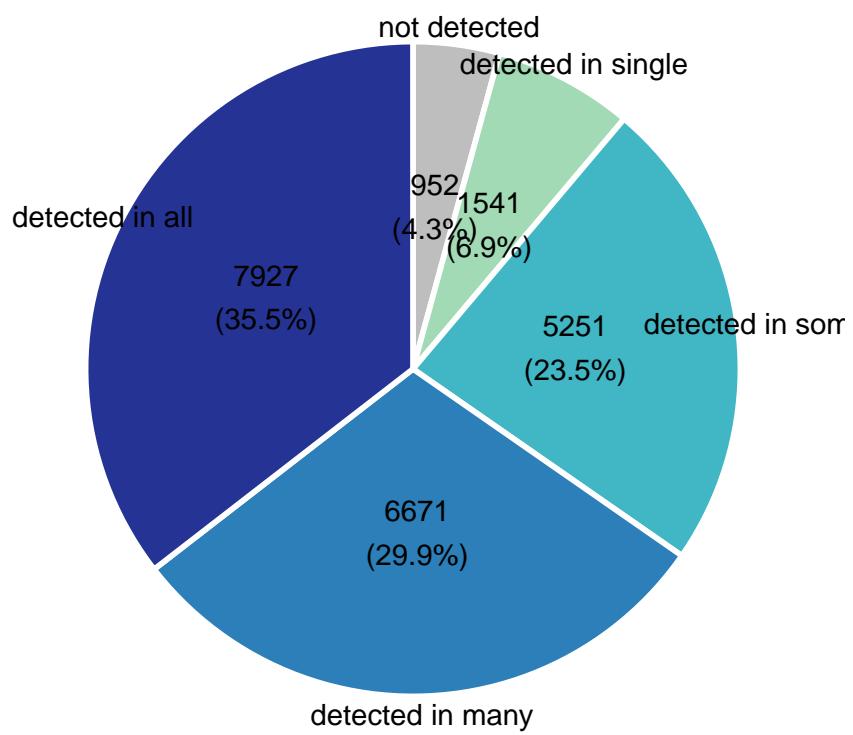


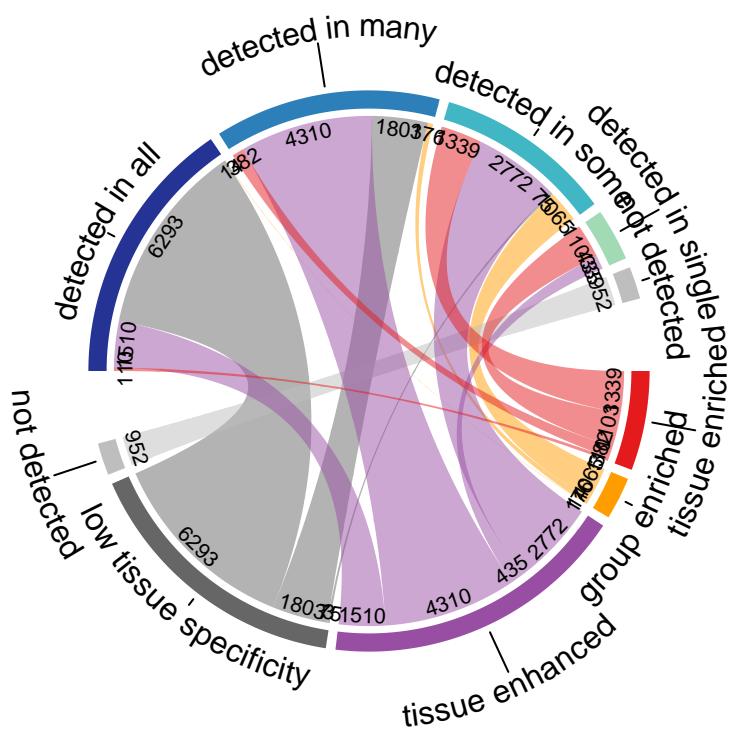


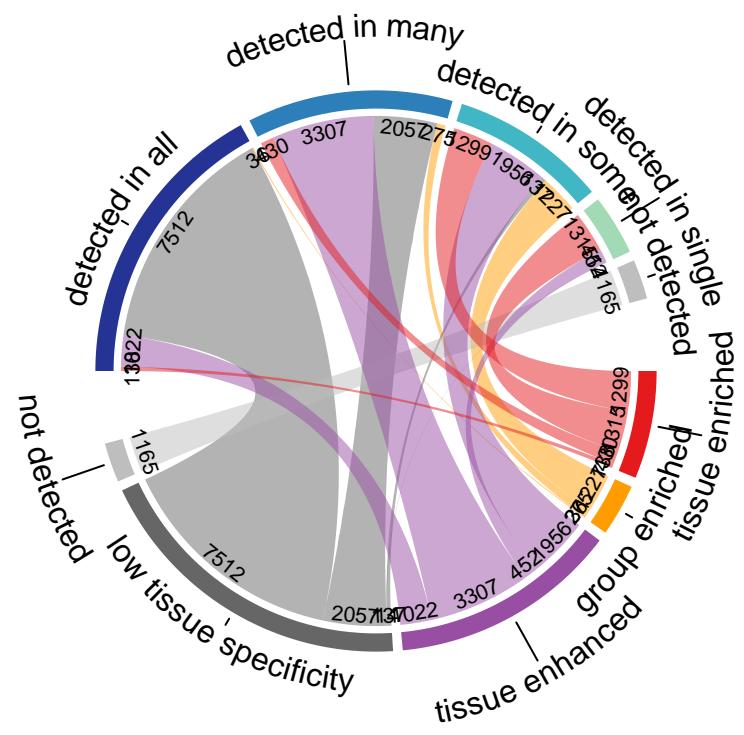
Classification

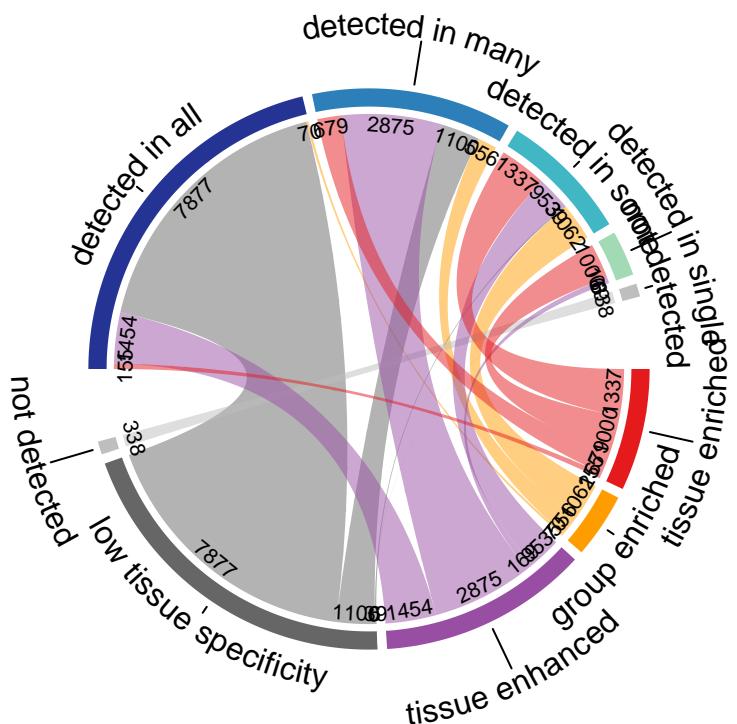












Classification Figures

```

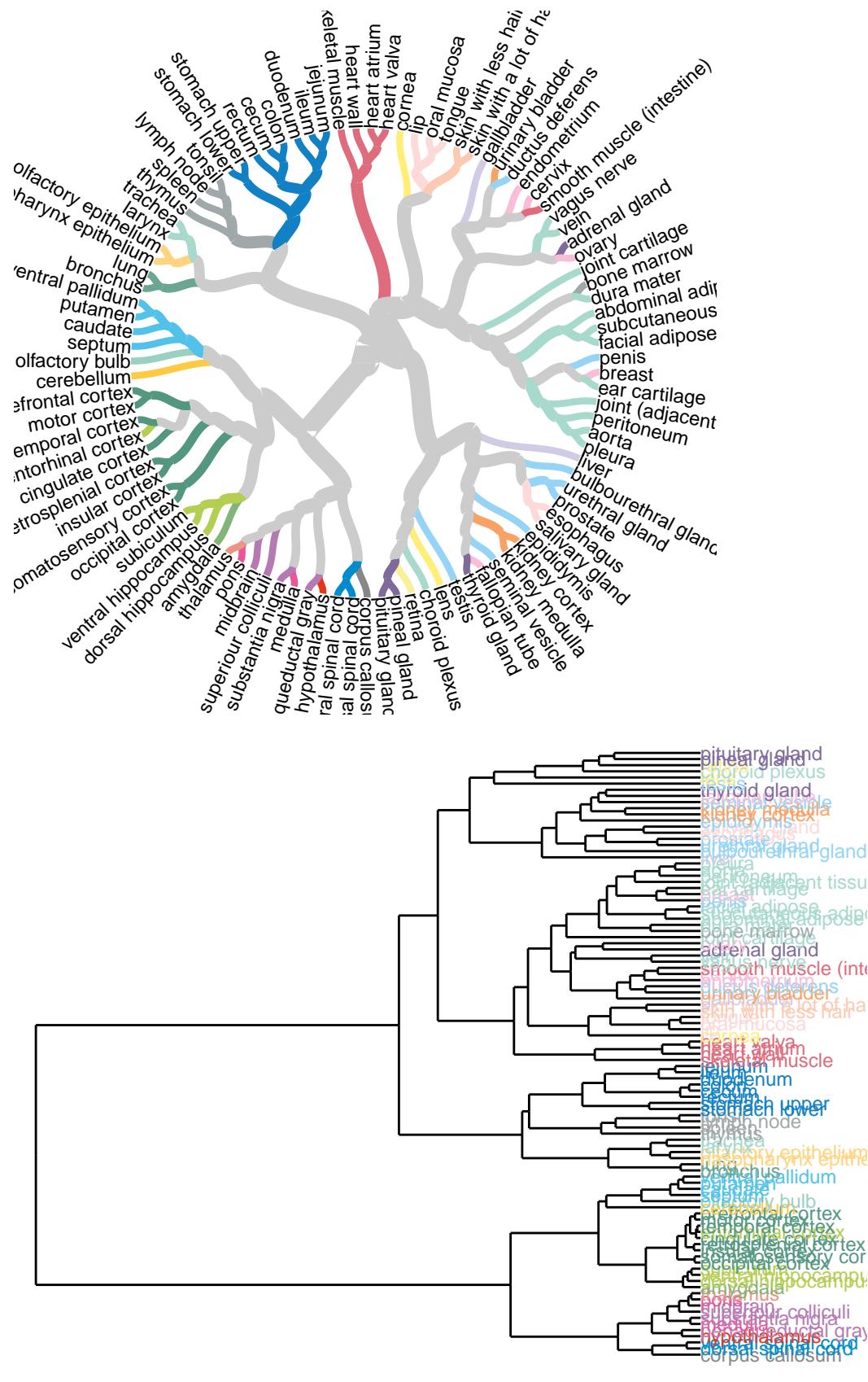
pdf(savepath("N enr genes per tissue pig + dendro.pdf"), width = 6, height = 7)
class_tissue_n_enriched_barplot_dendro(class_table = pig_gene_class,
                                       dendro = pig_atlas_consensus_wide_nx %>%
                                         cor(method = "spearman") %>%
                                         {1 - .} %>%
                                         as.dist() %>%
                                         hclust(method = "average"),
                                       pal = tissue_colors_palette_full,
                                       width = 0.05)

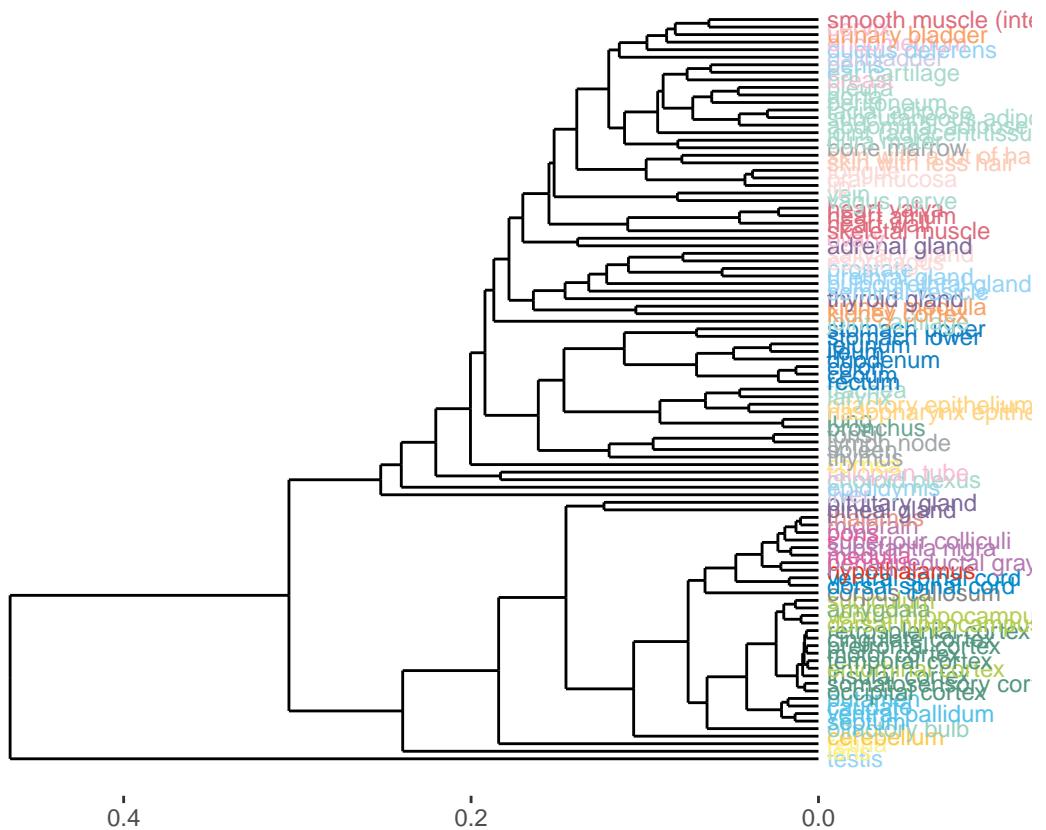
## Warning in class_tissue_n_enriched_barplot_dendro(class_table =
## pig_gene_class, : These tissues are not in the plot: pancreas
dev.off()

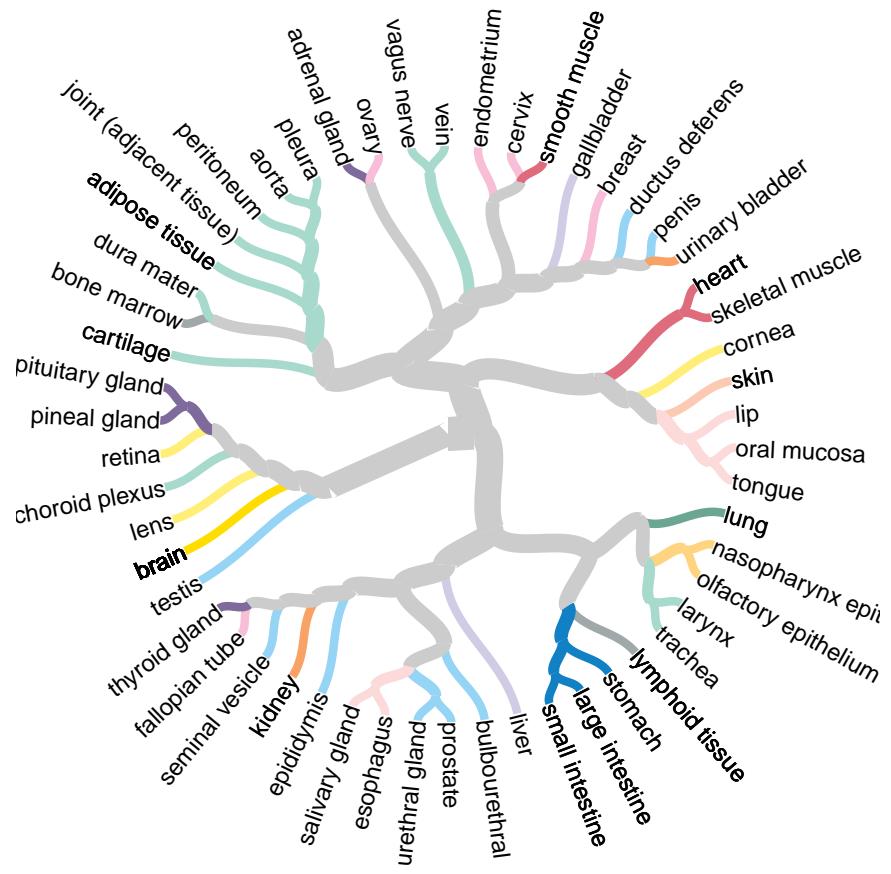
## pdf
## 2

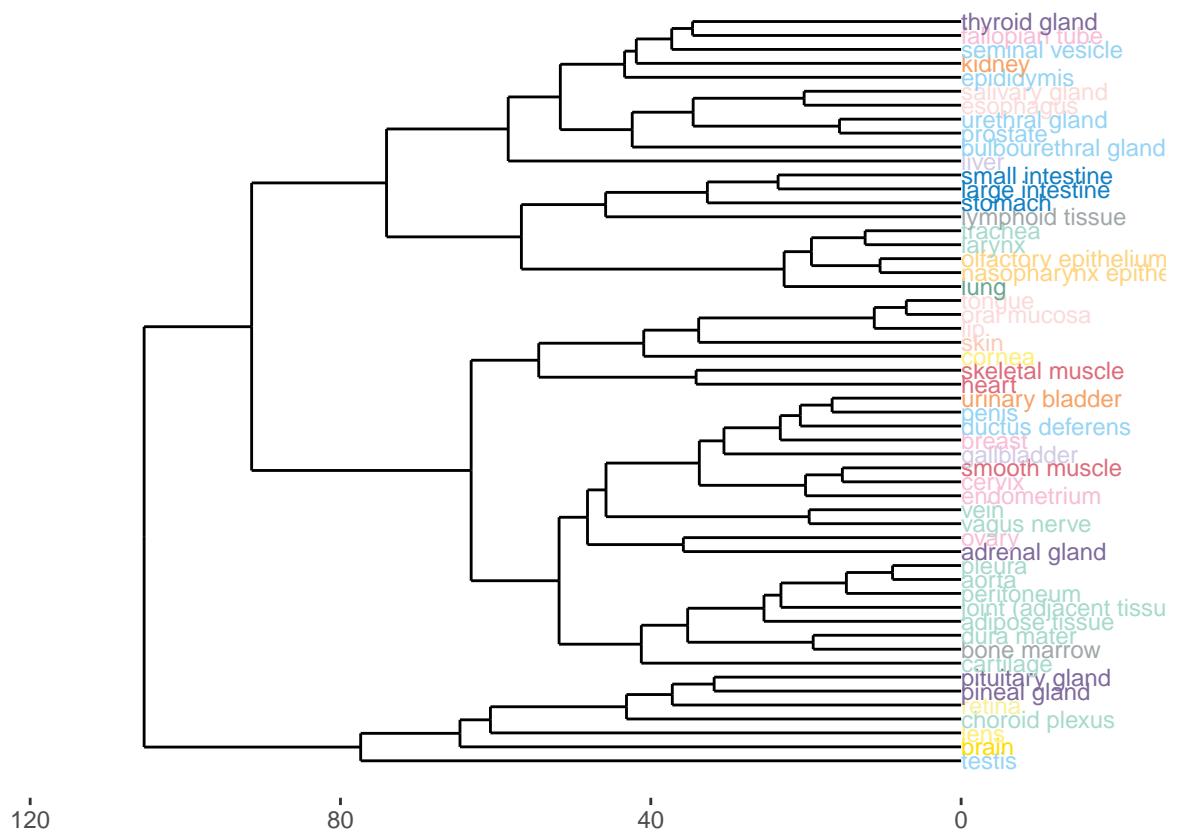
```

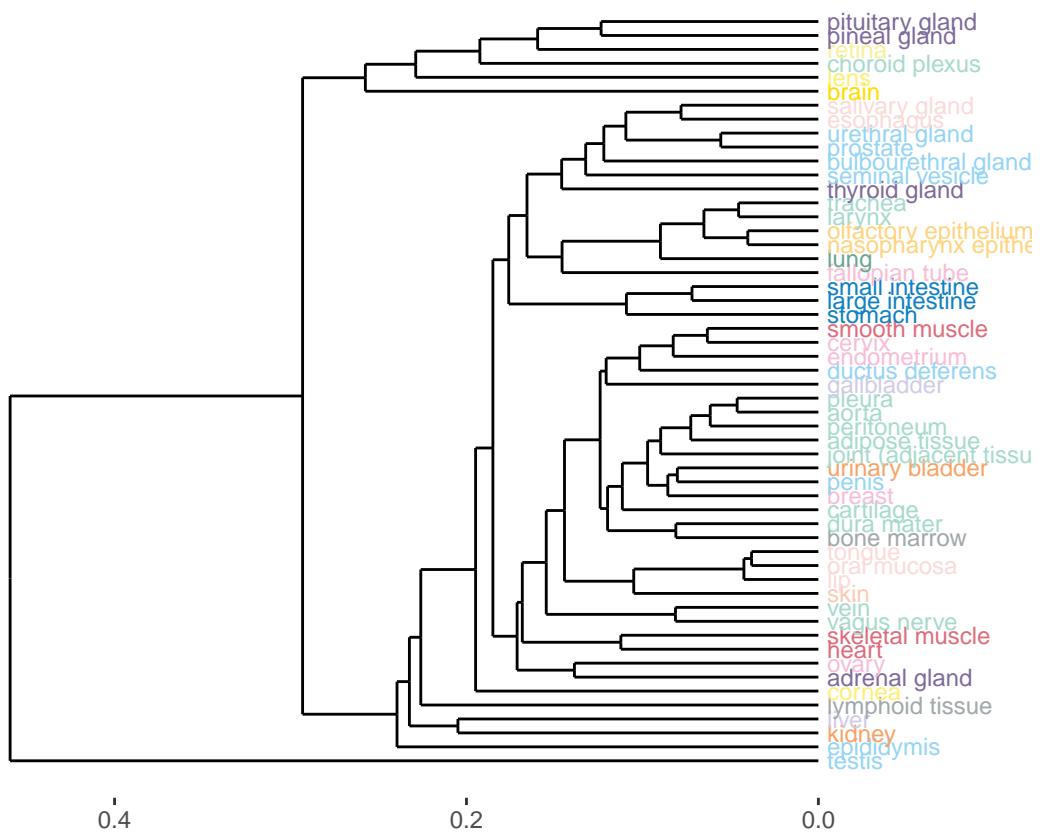
Clustering plots

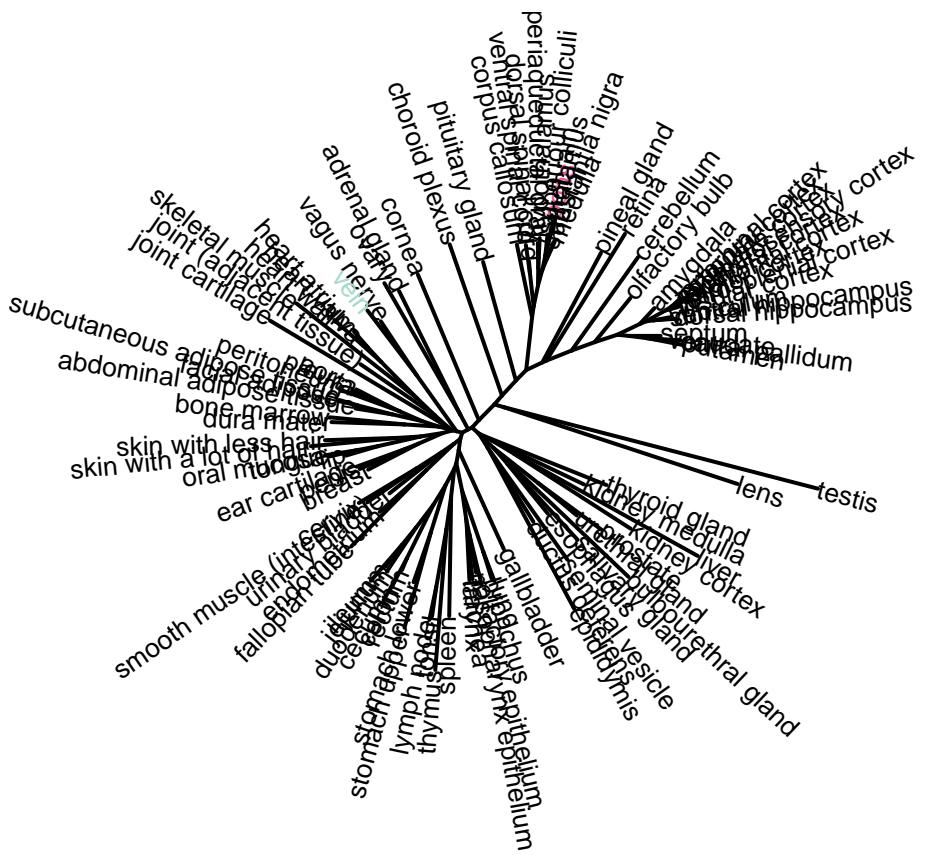










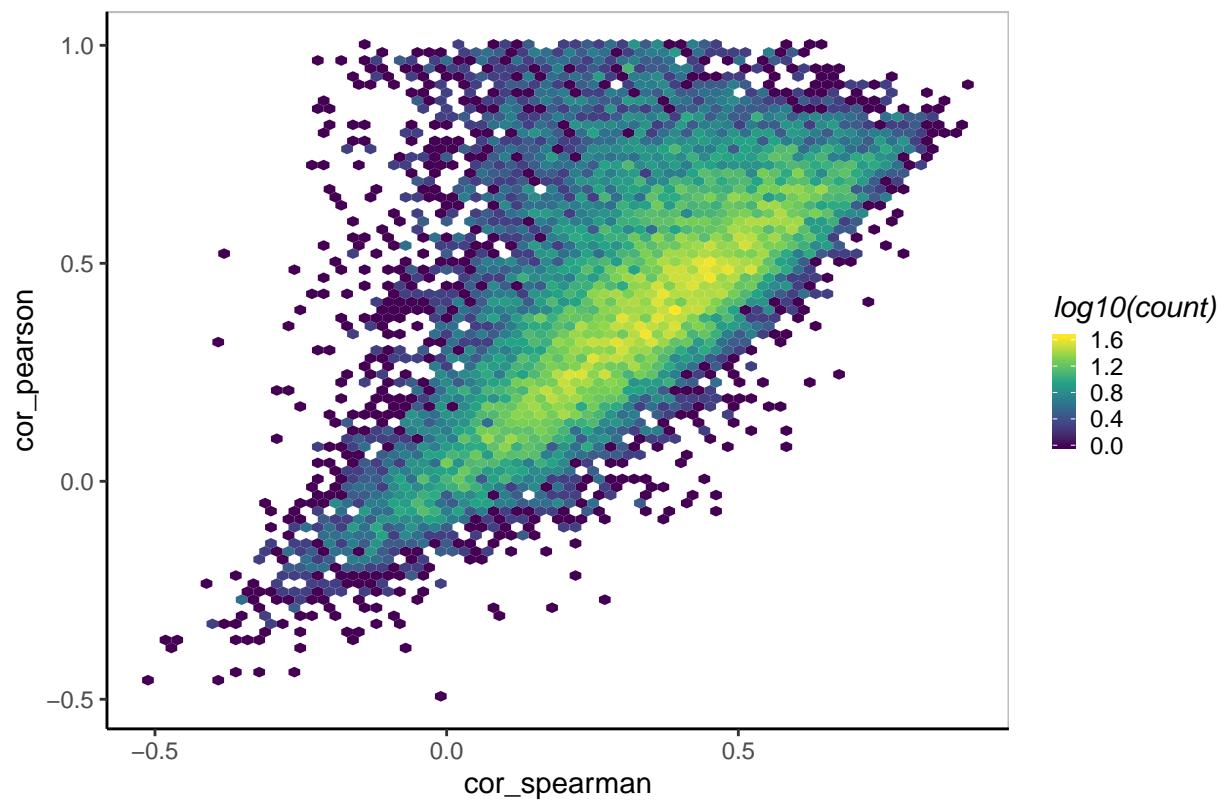


Intraspecies correlation

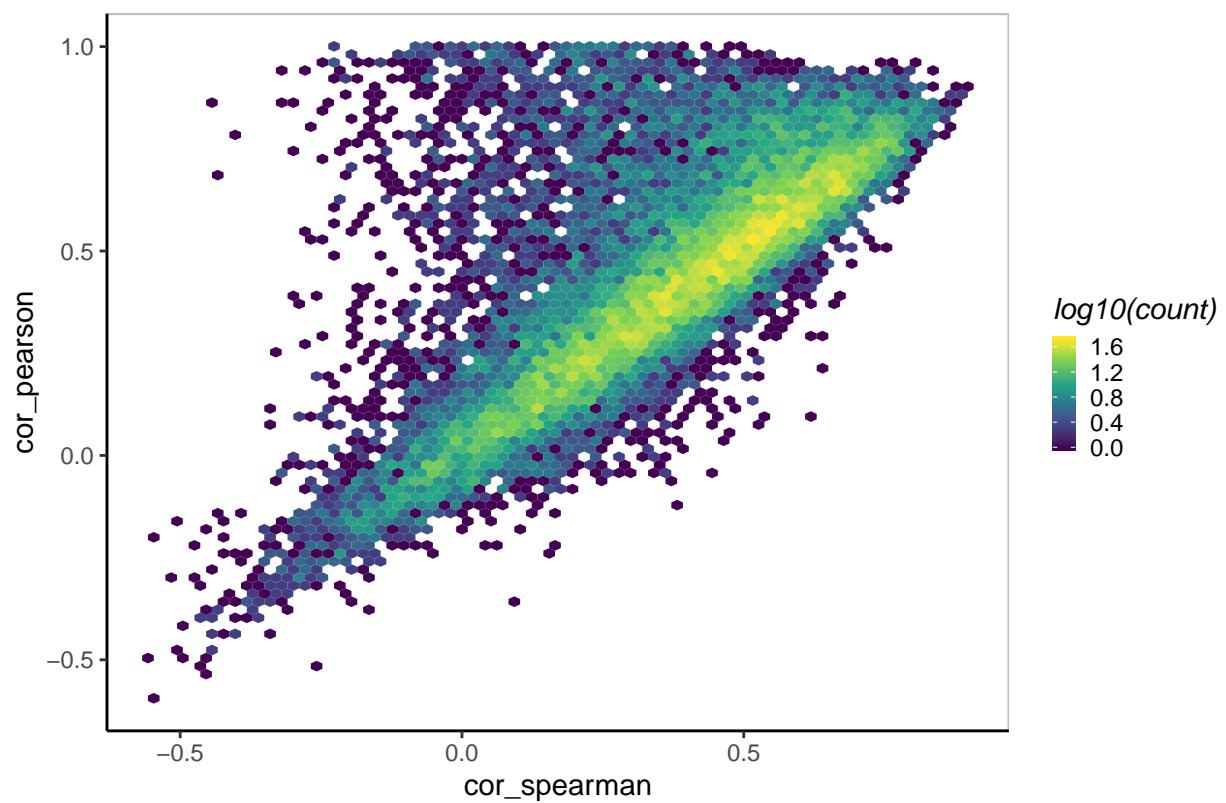
Correlation Human - Pig

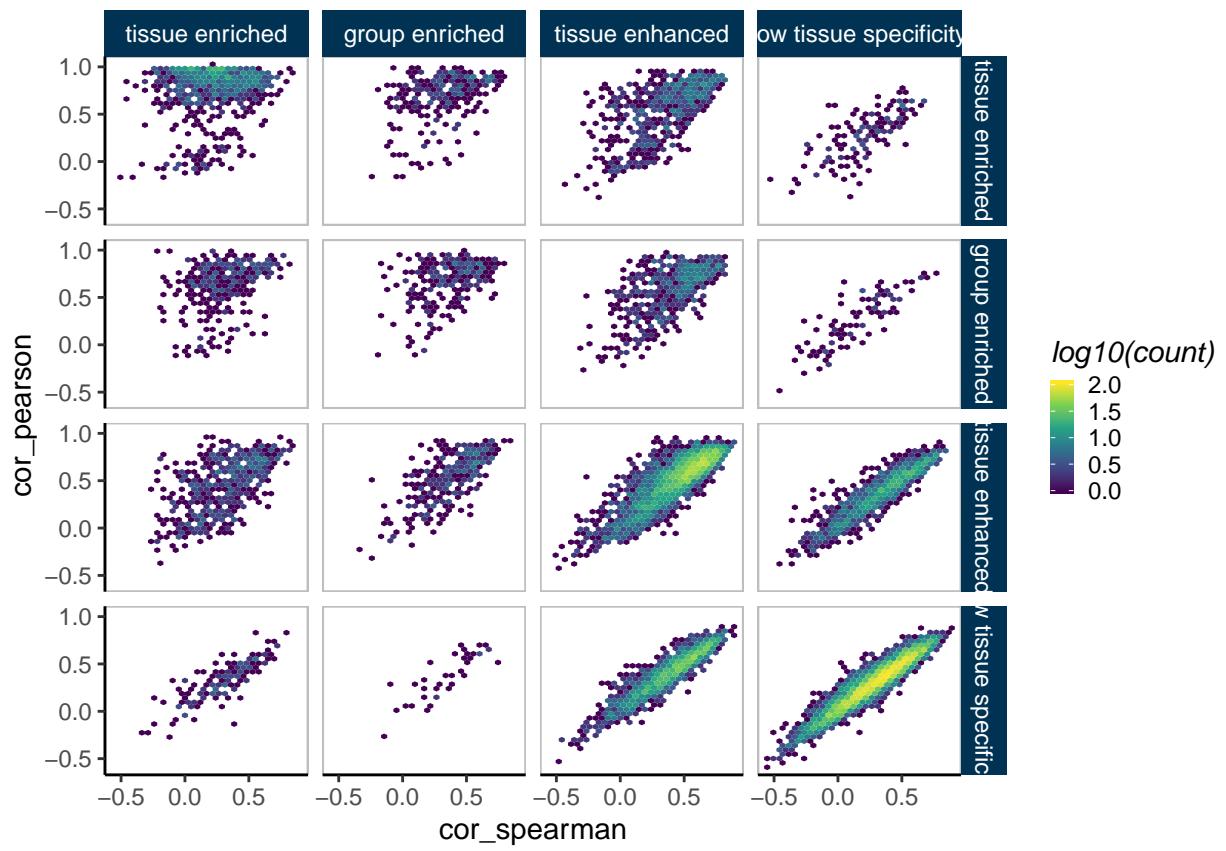
Here we see the 2-dimensional distribution of spearman correlation and pearson correlation for individual ortholog genes.

Consensus level Gene Pearson correlation vs Spearman correlation

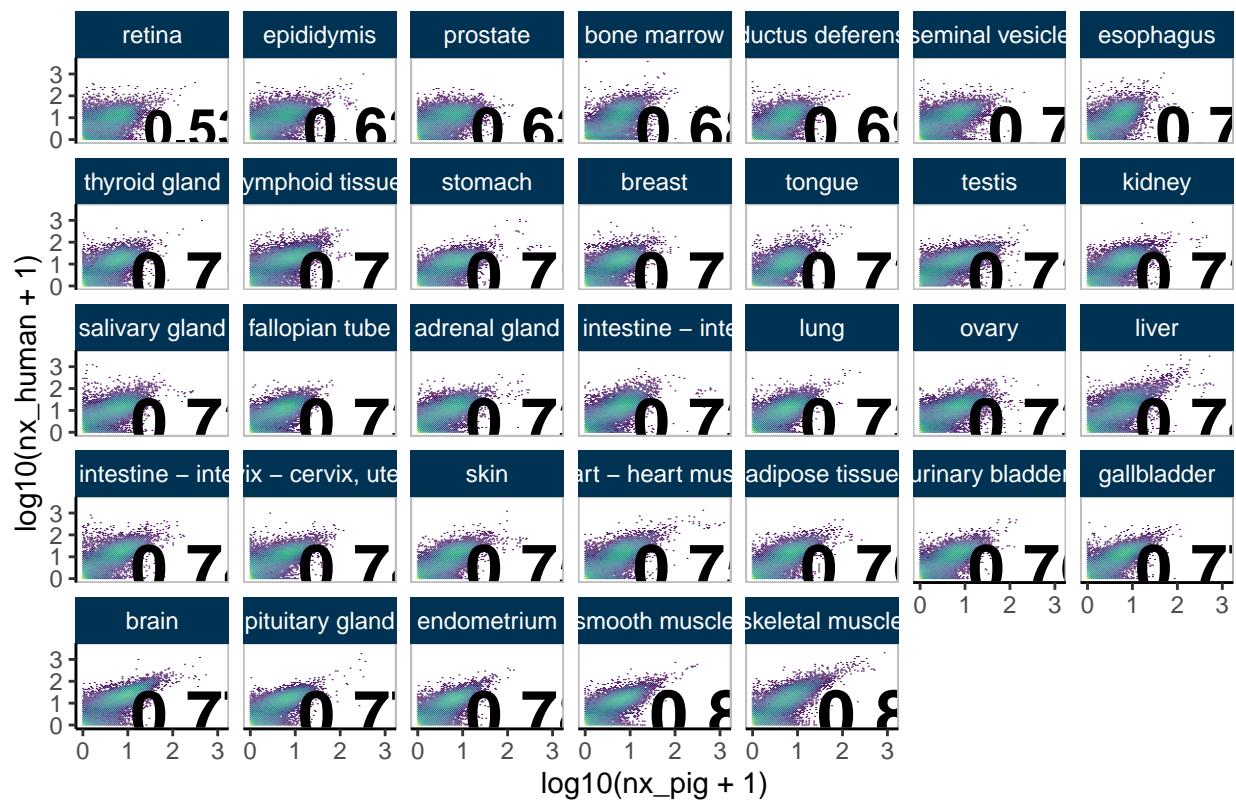


Region level Gene Pearson correlation vs Spearman correlation



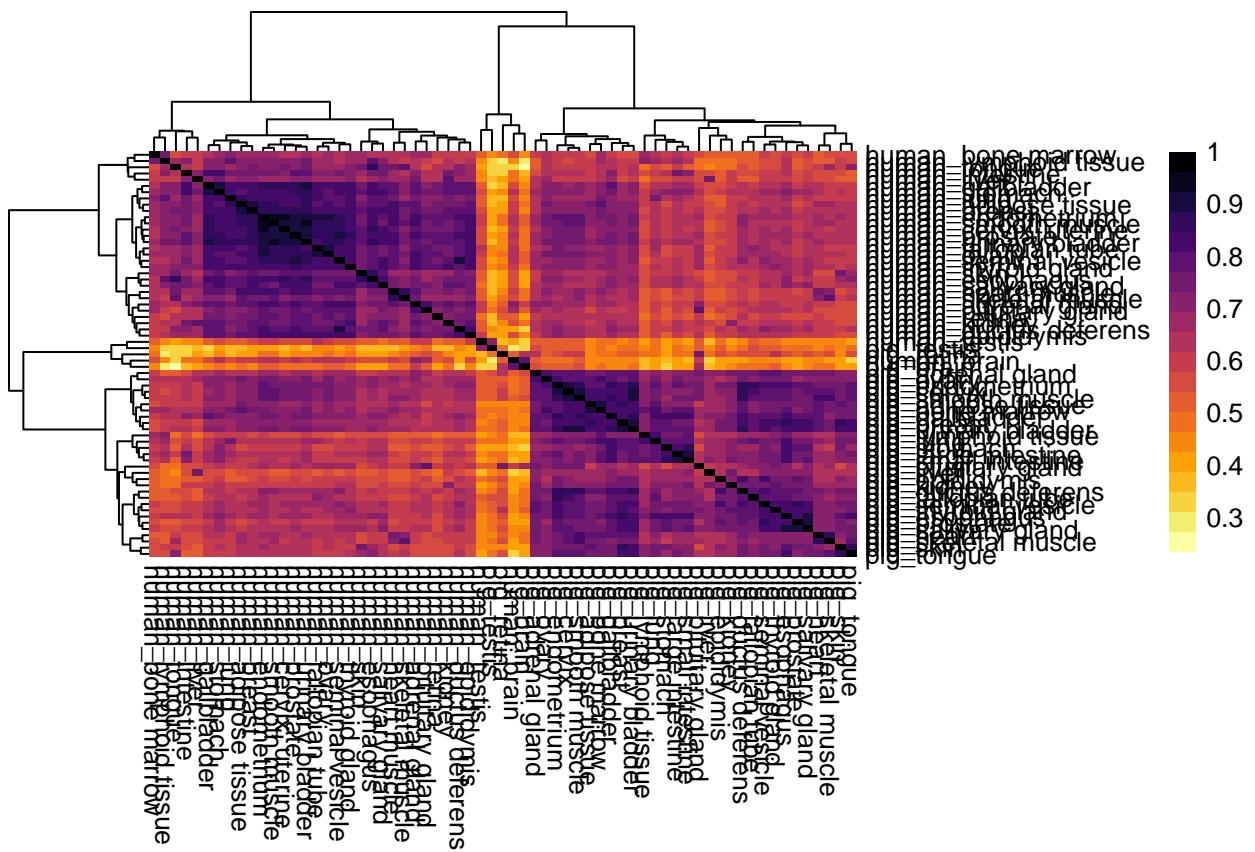


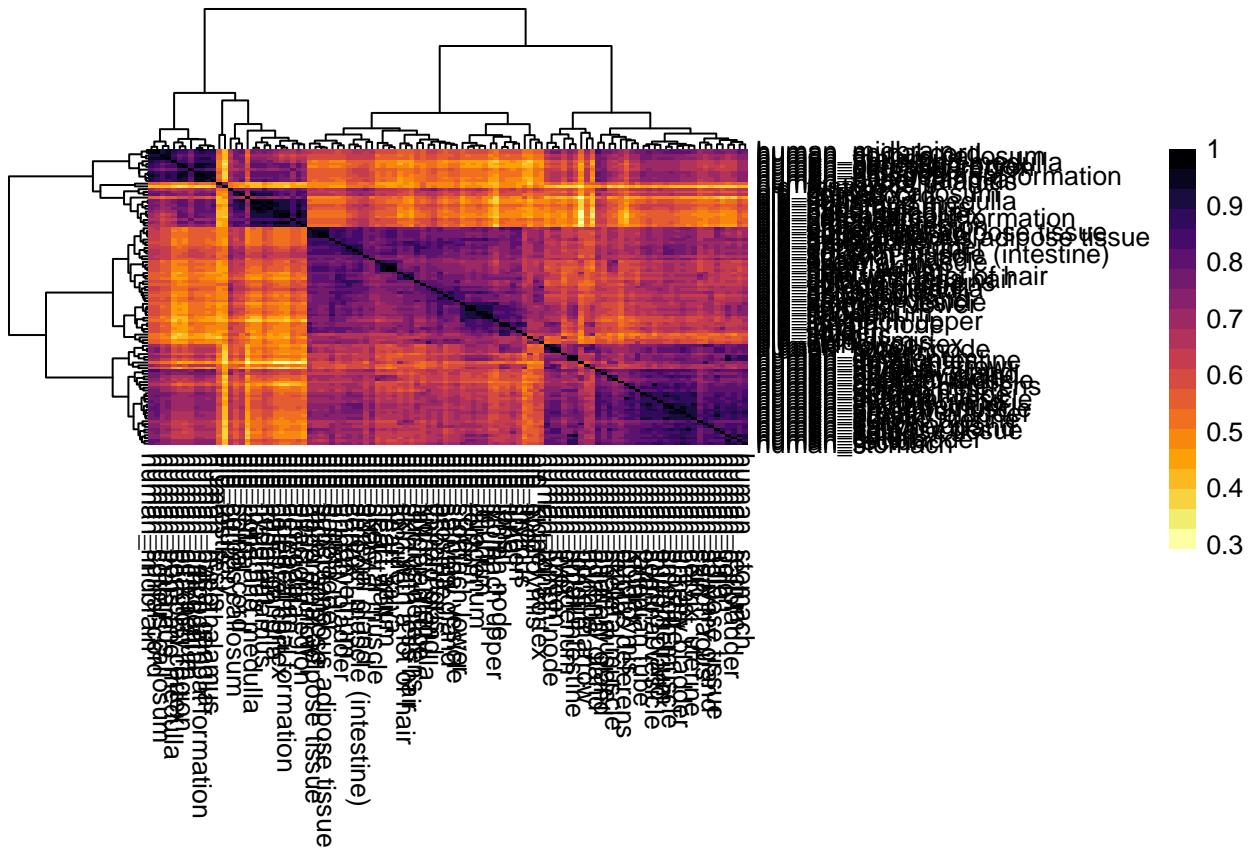
Human – Pig spearman correlation of all orthologs

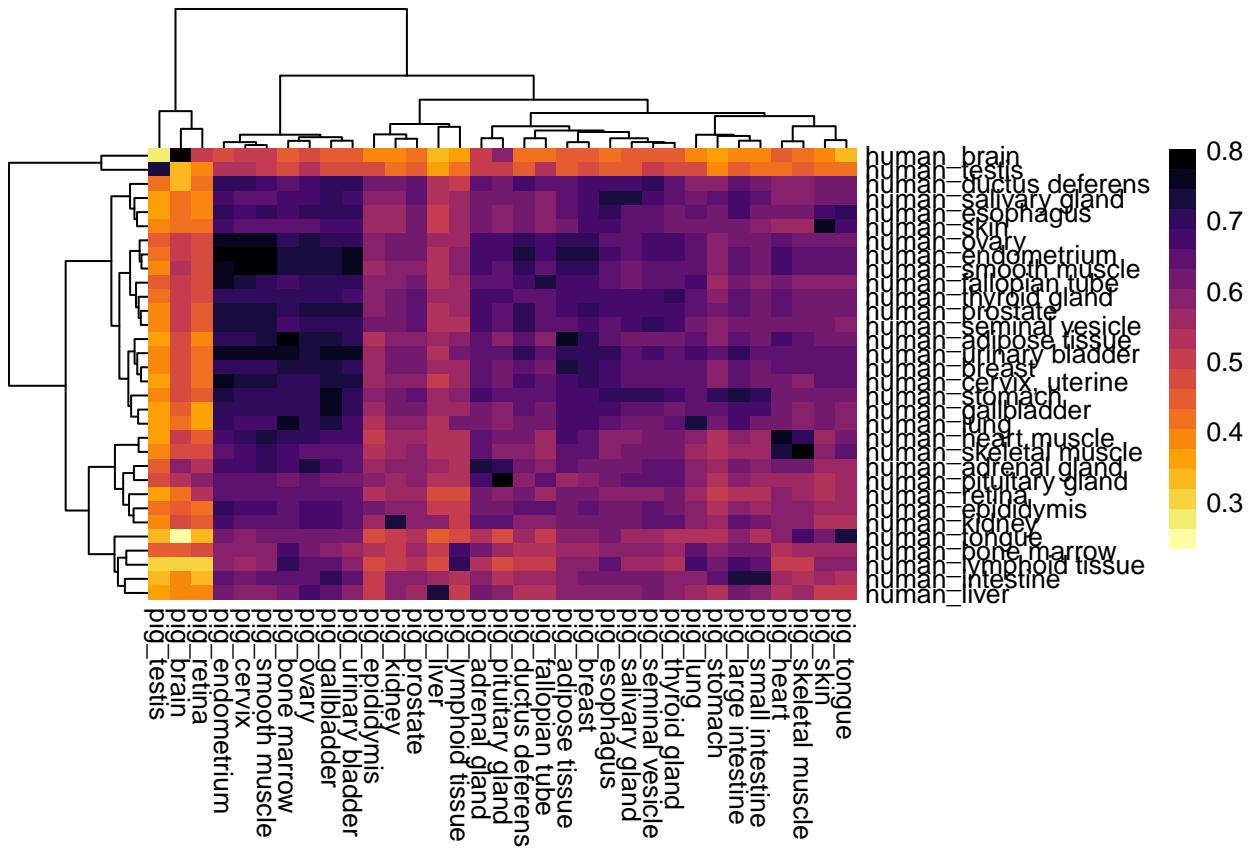


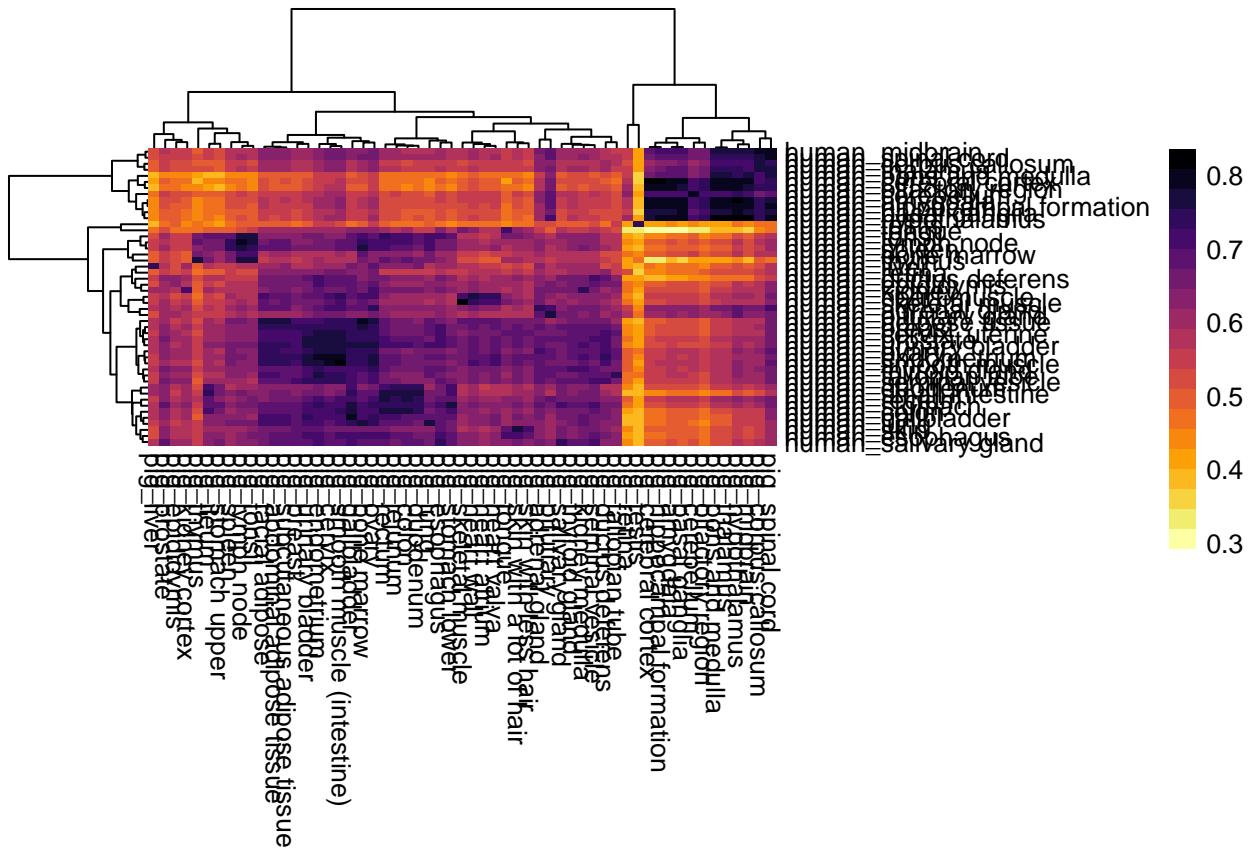
Human – Pig spearman correlation of all orthologs

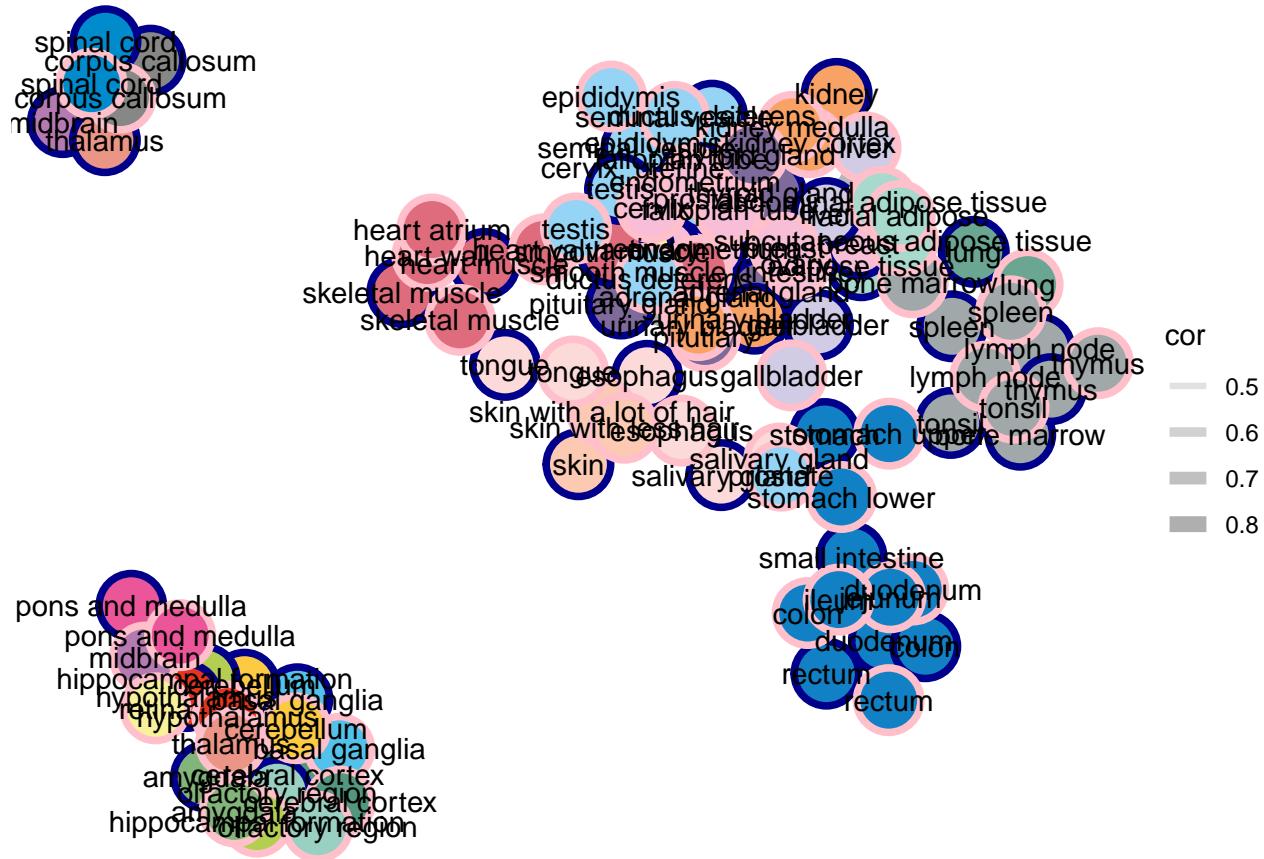












Compare classification

```
# ----- comparison classification -----
human_pig_gene_class_comparison_long <-
  full_join(gene_orthologs %>%
    left_join(human_gene_class_comparison %>%
      separate_rows(enriched_tissues, sep = ";") %>%
      select(ensg_id = gene,
             enriched_tissues),
      by = "ensg_id") %>%
    mutate(comparison_id = enriched_tissues),

  gene_orthologs %>%
    left_join(pig_gene_class_comparison %>%
      separate_rows(enriched_tissues, sep = ";") %>%
      select(ensscg_id = gene,
             enriched_tissues),
      by = "ensscg_id") %>%
    mutate(comparison_id = enriched_tissues),
    by = c("ensscg_id", "ensg_id", "ortholog_type", "comparison_id"),
    suffix = c("_human", "_pig")) %>%
```

```

select(1, 2, 3, enriched_tissues_human, enriched_tissues_pig, comparison_id)

human_pig_gene_class_comparison <-
  human_pig_gene_class_comparison_long %>%
  group_by(enssscg_id, ensg_id, ortholog_type) %>%
  summarise(n_enriched_human = n_distinct(enriched_tissues_human, na.rm = T),
            n_enriched_pig = n_distinct(enriched_tissues_pig, na.rm = T),
            n_overlap_enriched_human = n_distinct(enriched_tissues_human[which(comparison_id %in%
                                                                      consensus_tissue_overlap)])
            n_overlap_enriched_pig = n_distinct(enriched_tissues_pig[which(comparison_id %in%
                                                                      consensus_tissue_overlap)])

# Tissues count as overlapping if enriched in both human and pig, and the tissue is common
n_enriched_overlap = length(which((!is.na(enriched_tissues_human) & !is.na(enriched_tissues_pig)) &
                                    comparison_id %in% consensus_tissue_overlap$comparison_id))
n_enriched_total = n_overlap_enriched_human + n_overlap_enriched_pig - n_enriched_overlap,
enriched_tissues_overlap = paste(comparison_id[which(!is.na(enriched_tissues_human) & !is.na(enriched_tissues_pig))],
                                  collapse = ";"),
enriched_tissues_human = paste(enriched_tissues_human[which(!is.na(enriched_tissues_human))],
                               collapse = ";"),
enriched_tissues_pig = paste(enriched_tissues_pig[which(!is.na(enriched_tissues_pig))],
                             collapse = ";"),
enrichment_overlap = case_when(n_enriched_overlap == 0 ~ "no overlap", #n_enriched_total ==
                                n_enriched_overlap == n_enriched_total ~ "full overlap",
                                n_enriched_overlap > 0 ~ "partial overlap")
) %>%
left_join(human_gene_class_comparison %>%
           select(ensg_id = gene,
                  dist_category,
                  spec_category),
           by = "ensg_id") %>%
left_join(pig_gene_class_comparison %>%
           select(enssscg_id = gene,
                  dist_category,
                  spec_category),
           by = "enssscg_id",
           suffix = c("_human", "_pig")) %>%
mutate(dist_category_human_n = match(dist_category_human, dist_category_levels),
       spec_category_human_n = match(spec_category_human, spec_category_levels),
       dist_category_pig_n = match(dist_category_pig, dist_category_levels),
       spec_category_pig_n = match(spec_category_pig, spec_category_levels),
       dist_cat_diff = dist_category_human_n - dist_category_pig_n,
       spec_cat_diff = spec_category_human_n - spec_category_pig_n,
       shared_dist_category = case_when(abs(dist_cat_diff) == 0 ~ "shared",
                                         abs(dist_cat_diff) == 1 ~ "minor difference",
                                         abs(dist_cat_diff) > 1 ~ "major difference"))

```

```

                abs(dist_cat_diff) == 2 ~ "medium difference",
                abs(dist_cat_diff) >= 3 ~ "major difference"),
shared_spec_category = case_when(abs(spec_cat_diff) == 0 ~ "shared",
                                abs(spec_cat_diff) == 1 ~ "minor difference",
                                abs(spec_cat_diff) == 2 ~ "medium difference",
                                abs(spec_cat_diff) >= 3 ~ "major difference"))

# Dist

human_pig_gene_dist_class_comparison_long <-
  full_join(gene_orthologs %>%
    left_join(human_gene_class_comparison %>%
      separate_rows(tissues_detected, sep = ";") %>%
      select(ensg_id = gene,
             tissues_detected),
      by = "ensg_id") %>%
    mutate(comparison_id = tissues_detected),

  gene_orthologs %>%
    left_join(pig_gene_class_comparison %>%
      separate_rows(tissues_detected, sep = ";") %>%
      select(ensscgc_id = gene,
             tissues_detected),
      by = "ensscgc_id") %>%
    mutate(comparison_id = tissues_detected),
    by = c("ensscgc_id", "ensg_id", "ortholog_type", "comparison_id"),
    suffix = c("_human", "_pig")) %>%
  select(1, 2, 3, tissues_detected_human, tissues_detected_pig, comparison_id)

human_pig_gene_dist_class_comparison <-
  human_pig_gene_dist_class_comparison_long %>%
  group_by(ensscgc_id, ensg_id, ortholog_type) %>%
  summarise(n_detected_human = n_distinct(tissues_detected_human, na.rm = T),
            n_detected_pig = n_distinct(tissues_detected_pig, na.rm = T),

            n_overlap_detected_human = n_distinct(tissues_detected_human[which(comparison_id %in%
              consensus_tissue_overlap$comparison_id)]),
            n_overlap_detected_pig = n_distinct(tissues_detected_pig[which(comparison_id %in%
              consensus_tissue_overlap$comparison_id)]))

  # Tissues count as overlapping if detected in both human and pig, and the tissue is common
  n_detected_overlap = length(which((!is.na(tissues_detected_human) & !is.na(tissues_detected_pig)) &
    comparison_id %in% consensus_tissue_overlap$comparison_id))
  n_detected_total = n_overlap_detected_human + n_overlap_detected_pig - n_detected_overlap

  detected_tissues_overlap = paste(comparison_id[which(!is.na(tissues_detected_human) & !is.na(tissues_detected_pig))],
                                    collapse = ";"),
  tissues_detected_human = paste(tissues_detected_human[which(!is.na(tissues_detected_human))],
                                 collapse = ";"),

```

```

tissues_detected_pig = paste(tissues_detected_pig[which(!is.na(tissues_detected_pig))],
                             collapse = ";"),

detection_overlap_n = n_detected_overlap/n_detected_total
)

```

----- Canon classification -----

```

human_pig_gene_class_long <-
  full_join(gene_orthologs %>%
    left_join(human_gene_class %>%
      separate_rows(enriched_tissues, sep = ";") %>%
      select(ensg_id,
             enriched_tissues),
      by = "ensg_id") %>%
    left_join(consensus_tissue_overlap_all %>%
      filter(!is.na(human_consensus_tissue_name)) %>%
      select(human_consensus_tissue_name, comparison_id),
      by = c("enriched_tissues" = "human_consensus_tissue_name")),

  gene_orthologs %>%
    left_join(pig_gene_class %>%
      separate_rows(enriched_tissues, sep = ";") %>%
      select(ensscg_id = gene,
             enriched_tissues),
      by = c("ensscg_id")) %>%
    left_join(consensus_tissue_overlap_all %>%
      filter(!is.na(consensus_tissue_name)) %>%
      select(consensus_tissue_name, comparison_id),
      by = c("enriched_tissues" = "consensus_tissue_name")),
    by = c("ensscg_id", "ensg_id", "ortholog_type", "comparison_id"),
    suffix = c("_human", "_pig")) %>%
  select(1, 2, 3, enriched_tissues_human, enriched_tissues_pig, comparison_id) %>%

# Translate to the unique tissue comparison id
mutate(enriched_tissues_comp_human = ifelse(is.na(enriched_tissues_human), NA, comparison_id),
       enriched_tissues_comp_pig = ifelse(is.na(enriched_tissues_pig), NA, comparison_id))

```

human_pig_gene_class <-

```

human_pig_gene_class_long %>%
  group_by(ensscg_id, ensg_id, ortholog_type) %>%
  summarise(n_enriched_human = n_distinct(enriched_tissues_comp_human, na.rm = T),
            n_enriched_pig = n_distinct(enriched_tissues_comp_pig, na.rm = T),

            n_overlap_enriched_human = n_distinct(enriched_tissues_comp_human[which(comparison_id %in%
              consensus_tissue_),
              n_overlap_enriched_pig = n_distinct(enriched_tissues_comp_pig[which(comparison_id %in%
              consensus_tissue_over)])

```

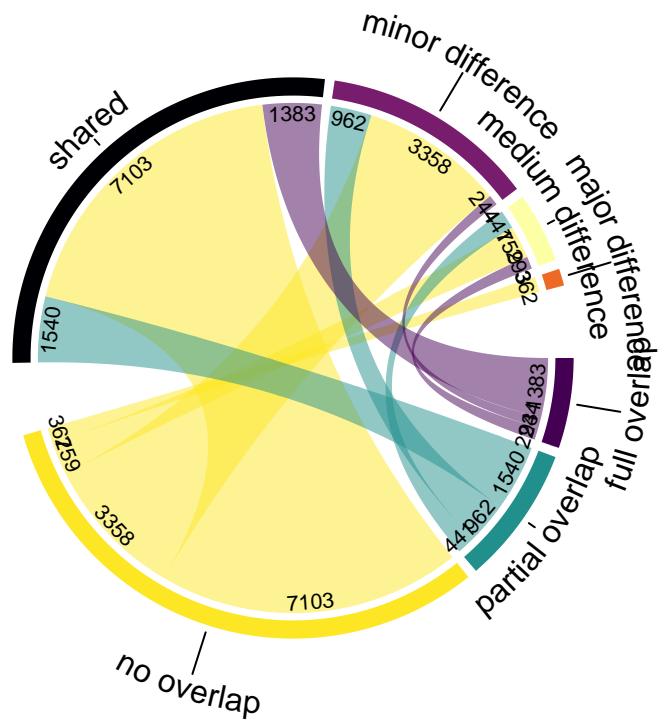
```

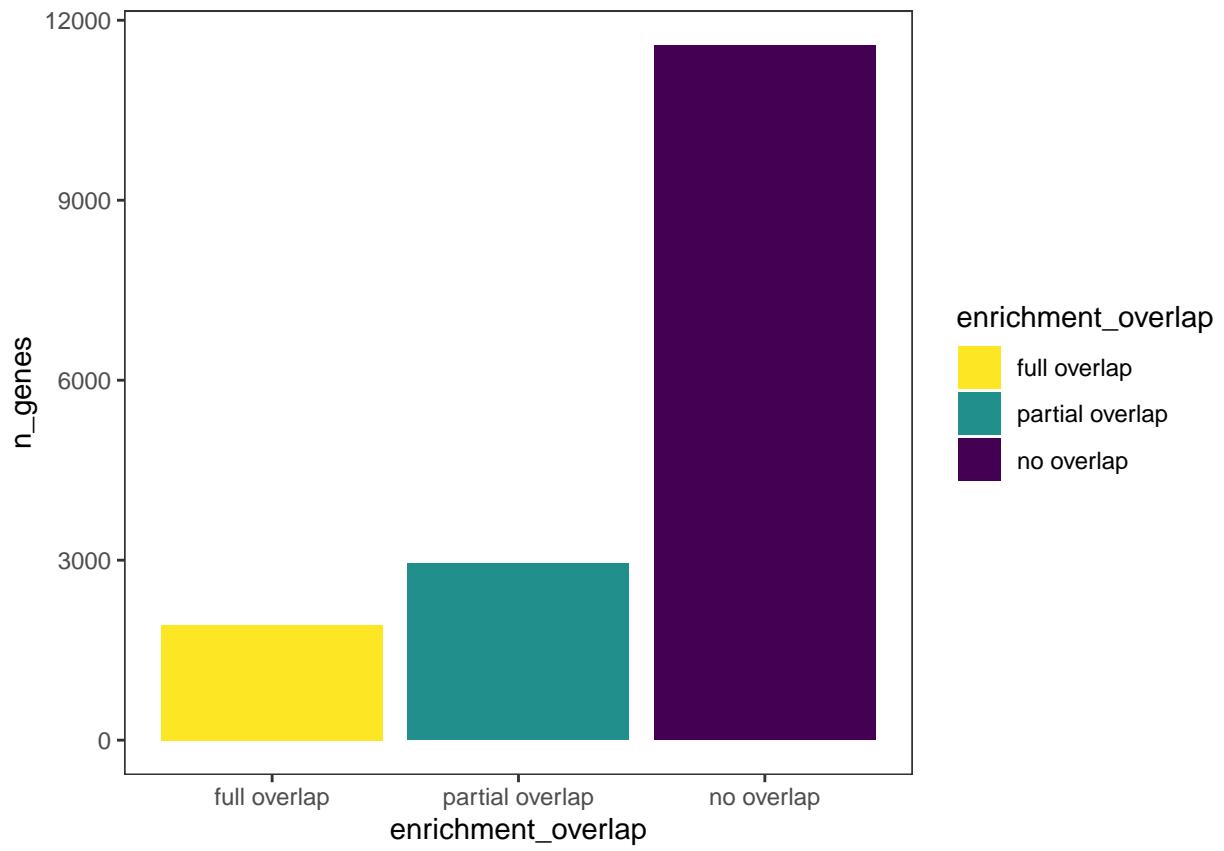
# Tissues count as overlapping if enriched in both human and pig, and the tissue is common
n_enriched_overlap = length(which(!is.na(enriched_tissues_comp_human) & !is.na(enriched_tissues_comp_pig)))
                                         comparison_id %in% consensus_tissue_overlap$comparison_id)
n_enriched_total = n_overlap_enriched_human + n_overlap_enriched_pig - n_enriched_overlap

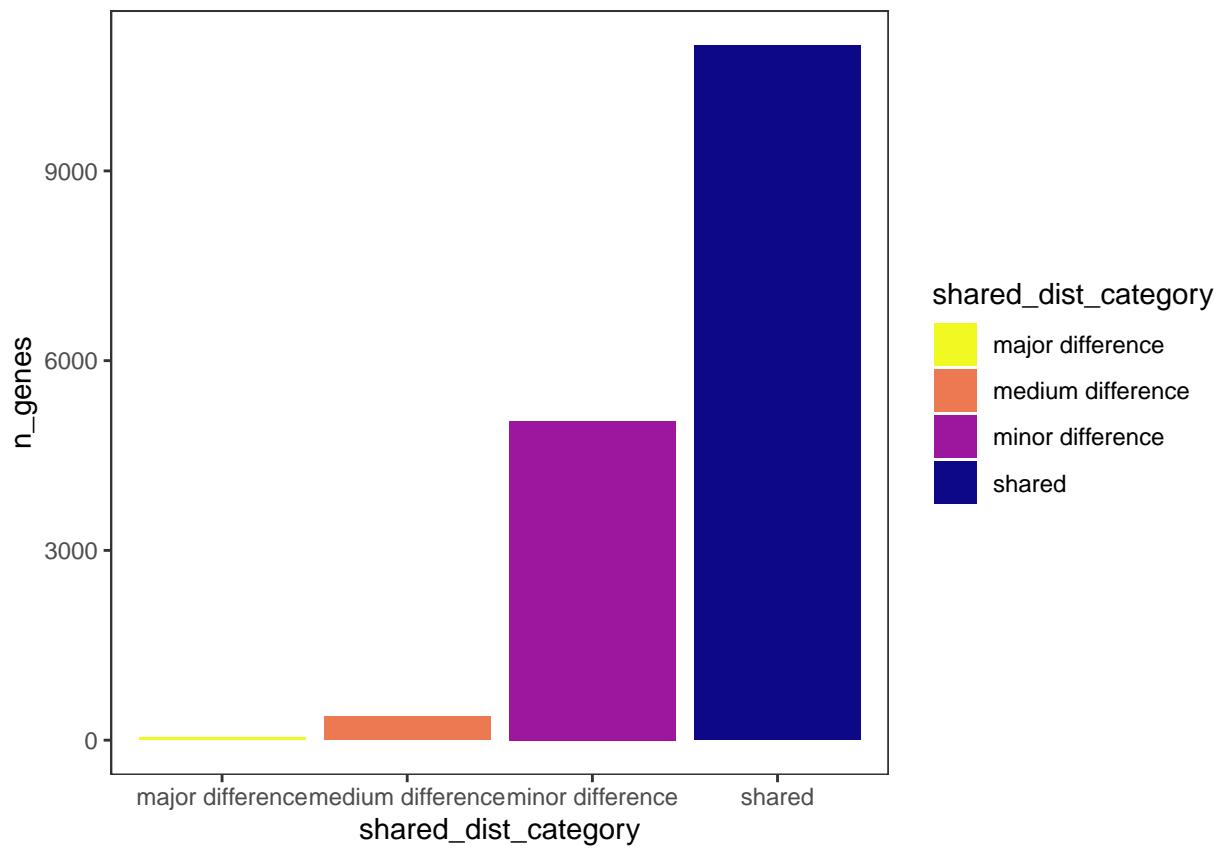
enriched_tissues_overlap = paste(comparison_id[which(!is.na(enriched_tissues_comp_human) &
                                         collapse = ";")],
enriched_tissues_human = paste(enriched_tissues_comp_human[which(!is.na(enriched_tissues_comp_human))],
                                         collapse = ";"),
enriched_tissues_pig = paste(enriched_tissues_comp_pig[which(!is.na(enriched_tissues_comp_pig))],
                                         collapse = ";"),

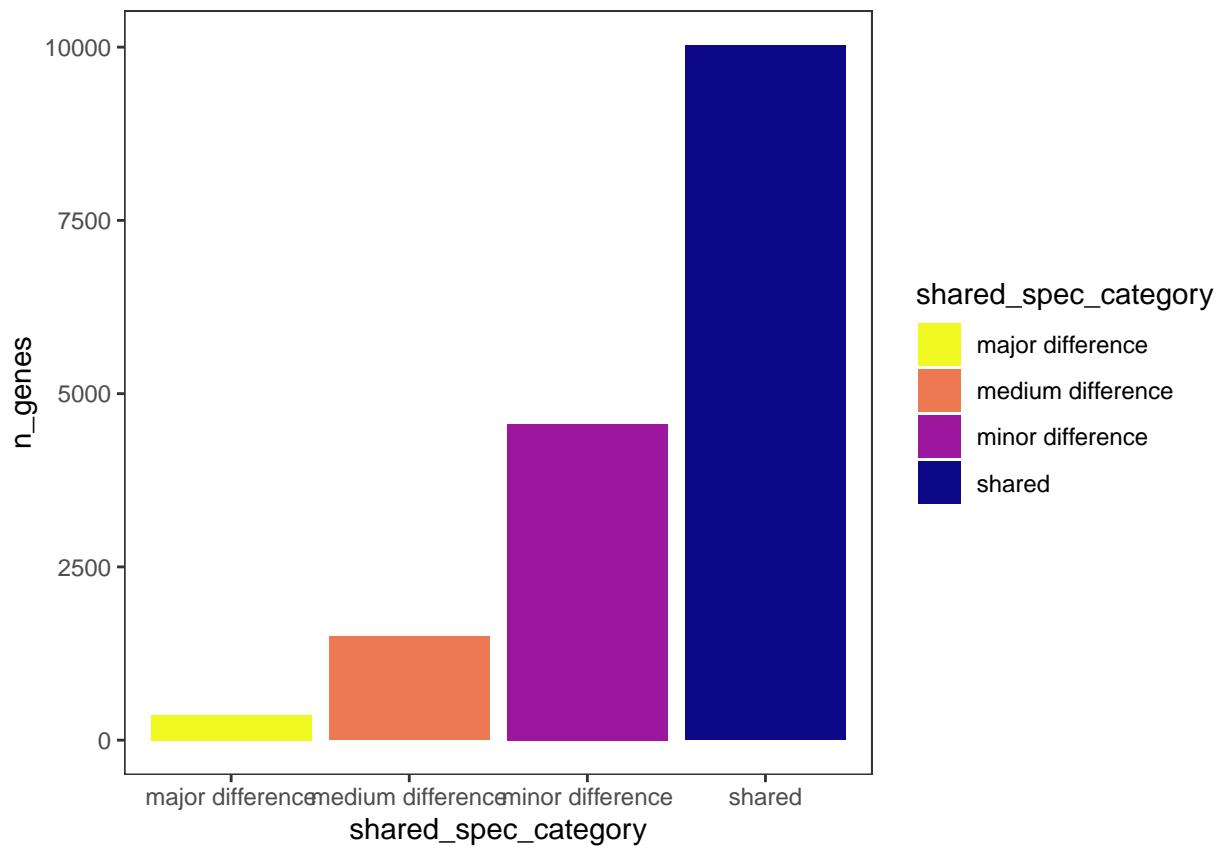
enrichment_overlap = case_when(n_enriched_overlap == 0 ~ "no overlap",
                                n_enriched_overlap == n_enriched_total ~ "full overlap",
                                n_enriched_overlap > 0 ~ "partial overlap")
) %>%
left_join(human_gene_class %>%
            select(ensg_id,
                   dist_category,
                   spec_category),
           by = "ensg_id") %>%
left_join(pig_gene_class %>%
            select(enssscg_id = gene,
                   dist_category,
                   spec_category),
           by = "enssscg_id",
           suffix = c("_human", "_pig")) %>%
mutate(dist_category_human_n = match(dist_category_human, dist_category_levels),
       spec_category_human_n = match(spec_category_human, spec_category_levels),
       dist_category_pig_n = match(dist_category_pig, dist_category_levels),
       spec_category_pig_n = match(spec_category_pig, spec_category_levels),
       dist_cat_diff = dist_category_human_n - dist_category_pig_n,
       spec_cat_diff = spec_category_human_n - spec_category_pig_n,
       shared_dist_category = case_when(abs(dist_cat_diff) == 0 ~ "shared",
                                         abs(dist_cat_diff) == 1 ~ "minor difference",
                                         abs(dist_cat_diff) == 2 ~ "medium difference",
                                         abs(dist_cat_diff) >= 3 ~ "major difference"),
       shared_spec_category = case_when(abs(spec_cat_diff) == 0 ~ "shared",
                                         abs(spec_cat_diff) == 1 ~ "minor difference",
                                         abs(spec_cat_diff) == 2 ~ "medium difference",
                                         abs(spec_cat_diff) >= 3 ~ "major difference"))

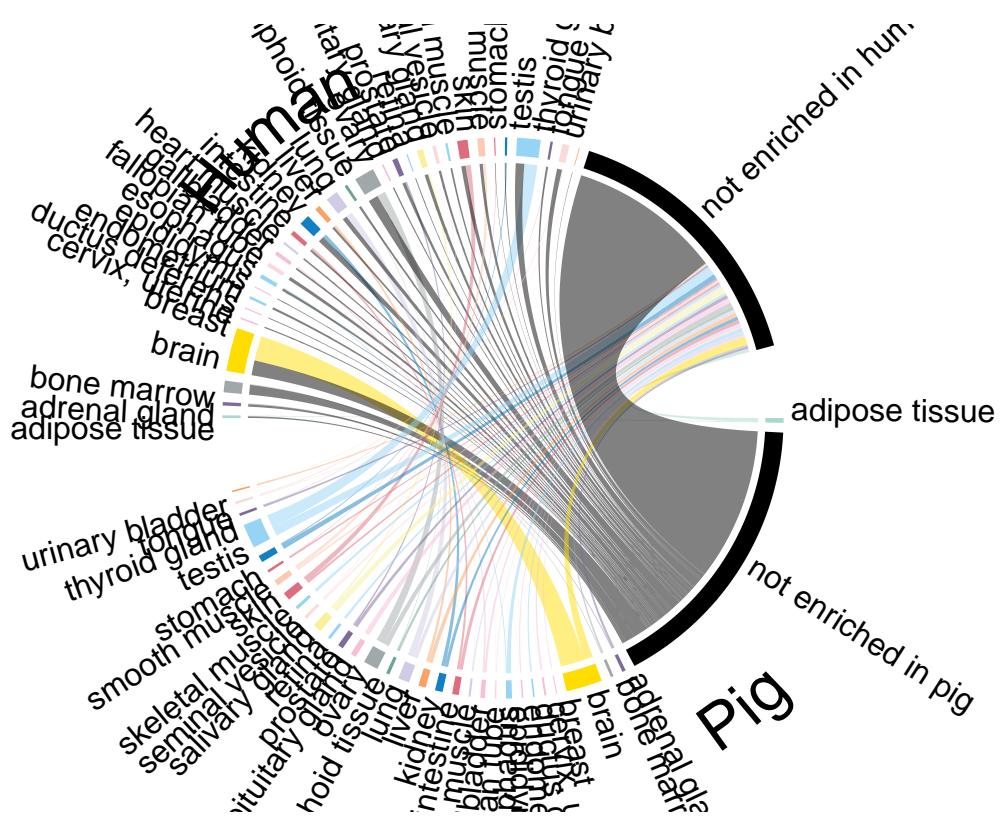
```

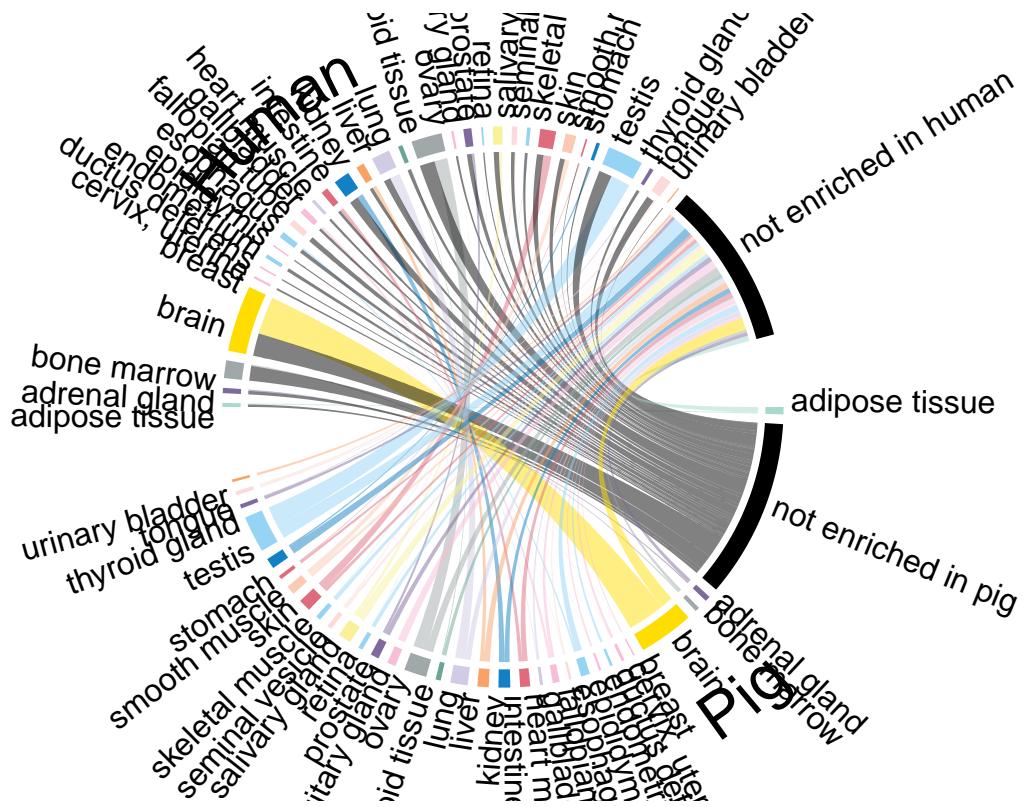


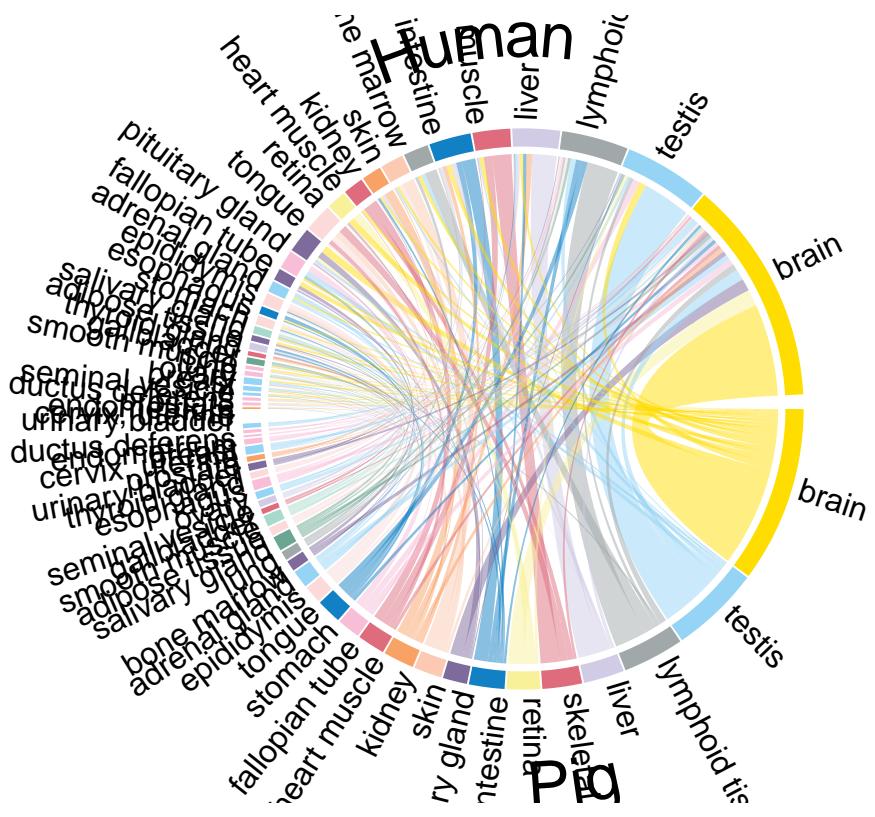


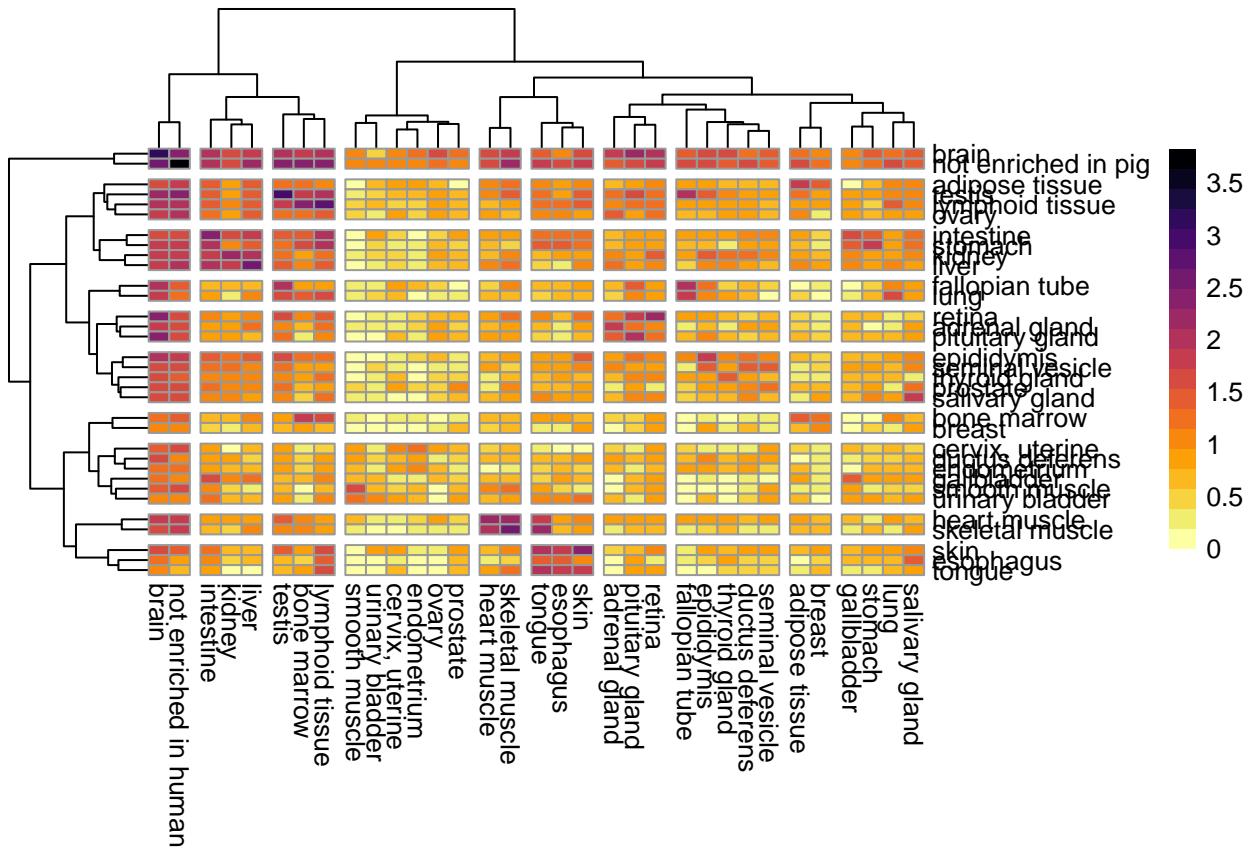


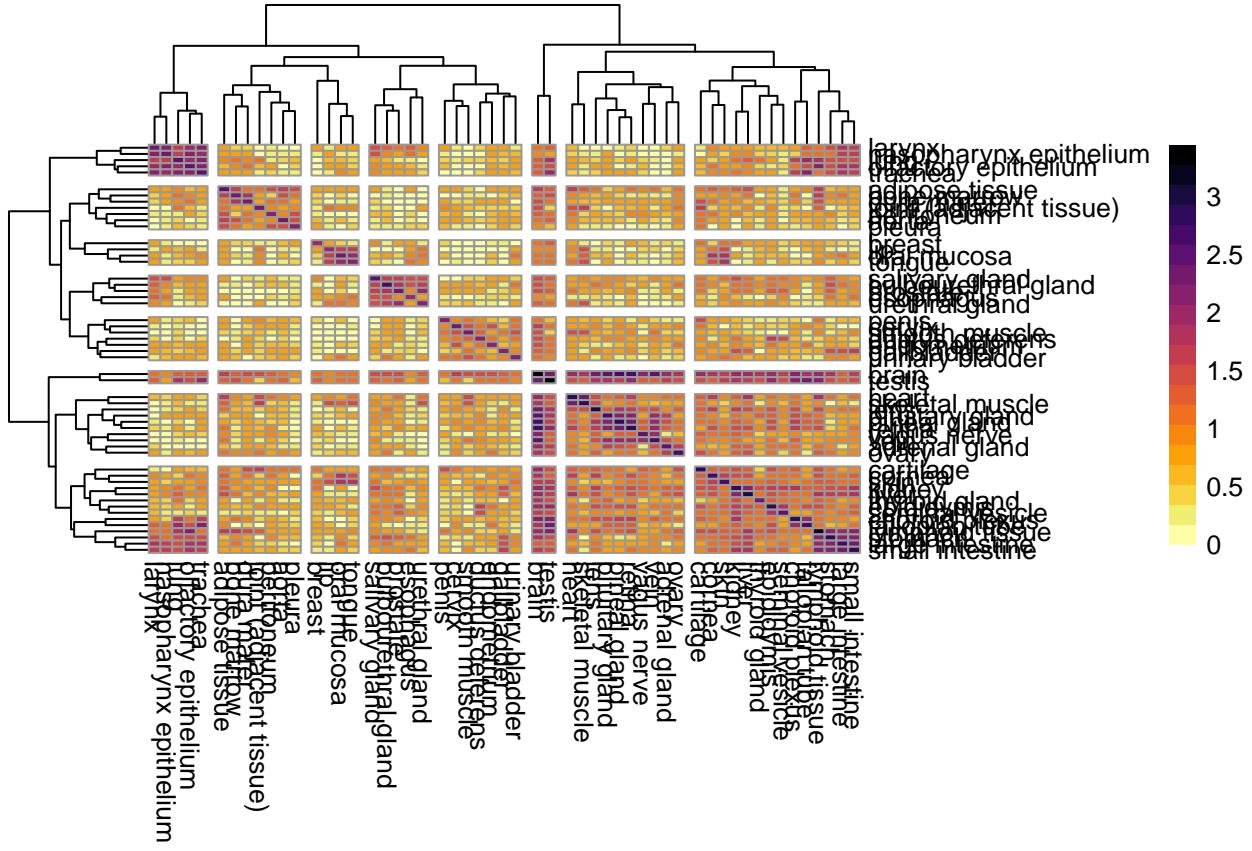












brain

Pig

urinary bladder
colon, cecum, rectum
esophagus
Skeletal muscle
thyroid gland
heart muscle
head muscle
adrenal gland
epididymis
lumbar tube
lymphoid tissue
testis
pituitary gland
retina

brain

not enriched in pig

Human

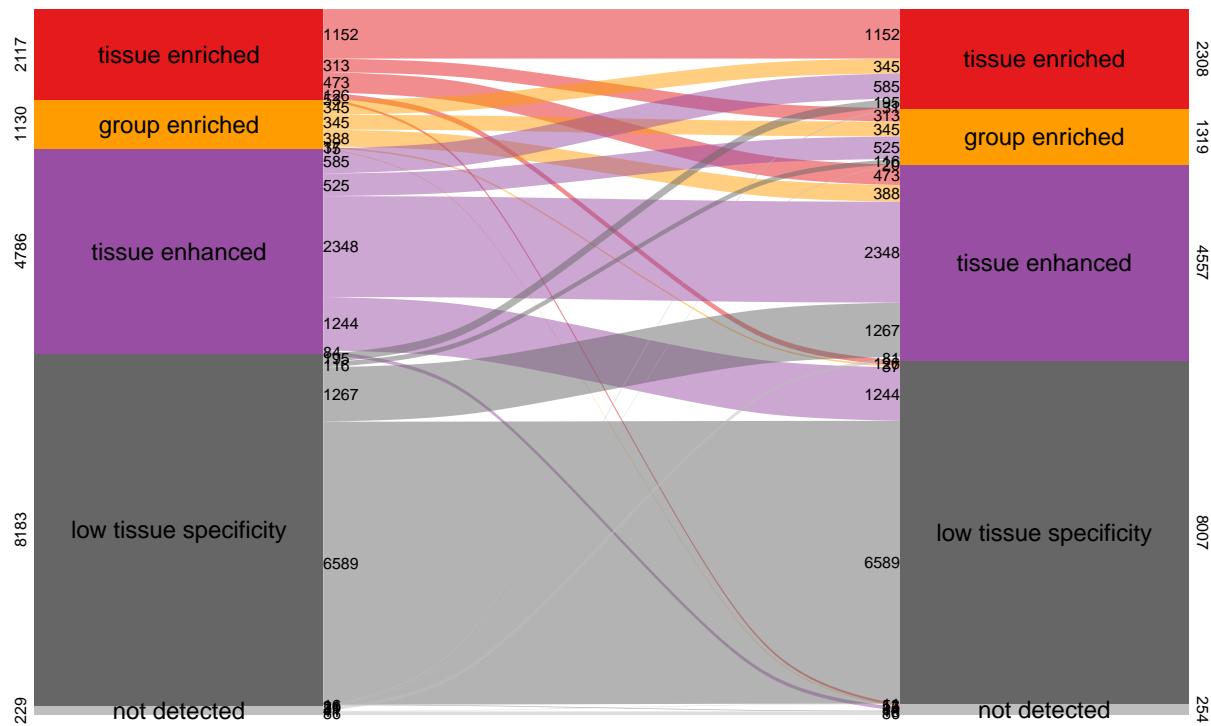
urinary bladder
colon, cecum, rectum
esophagus
Skeletal muscle
thyroid gland
heart muscle,
adrenal gland
lymphoid tissue
testis
pituitary gland
retina

brain

not enriched in human

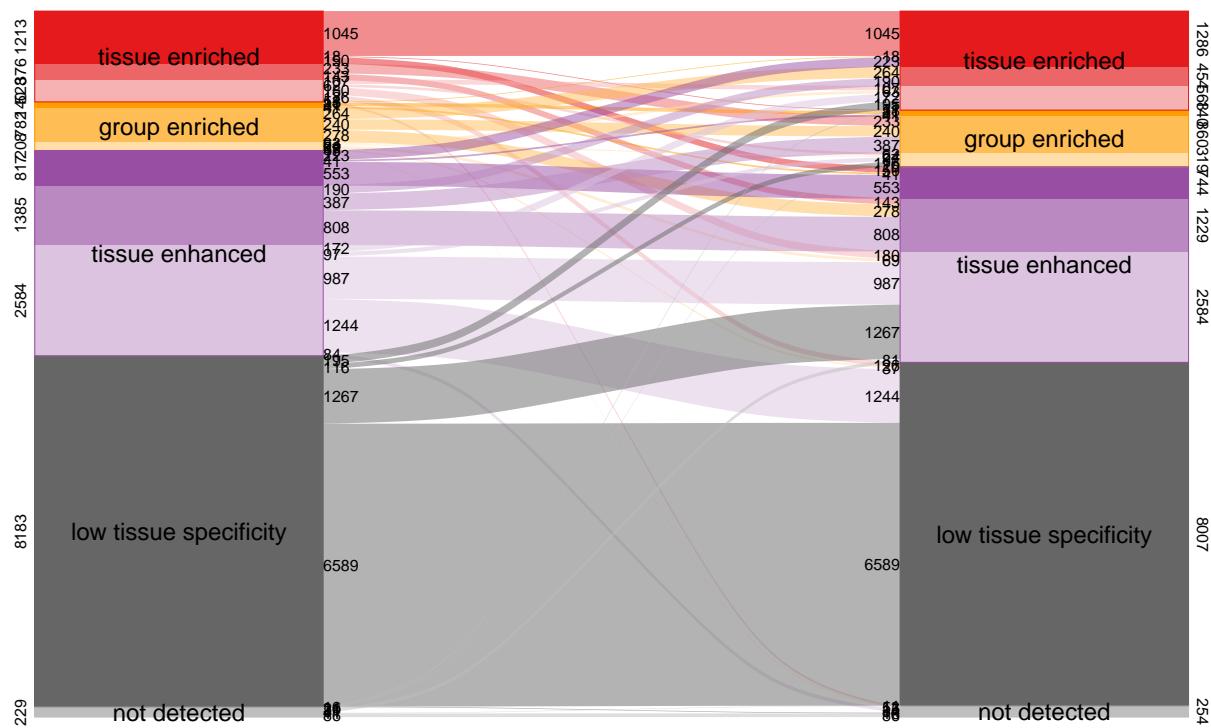
Pig

Human



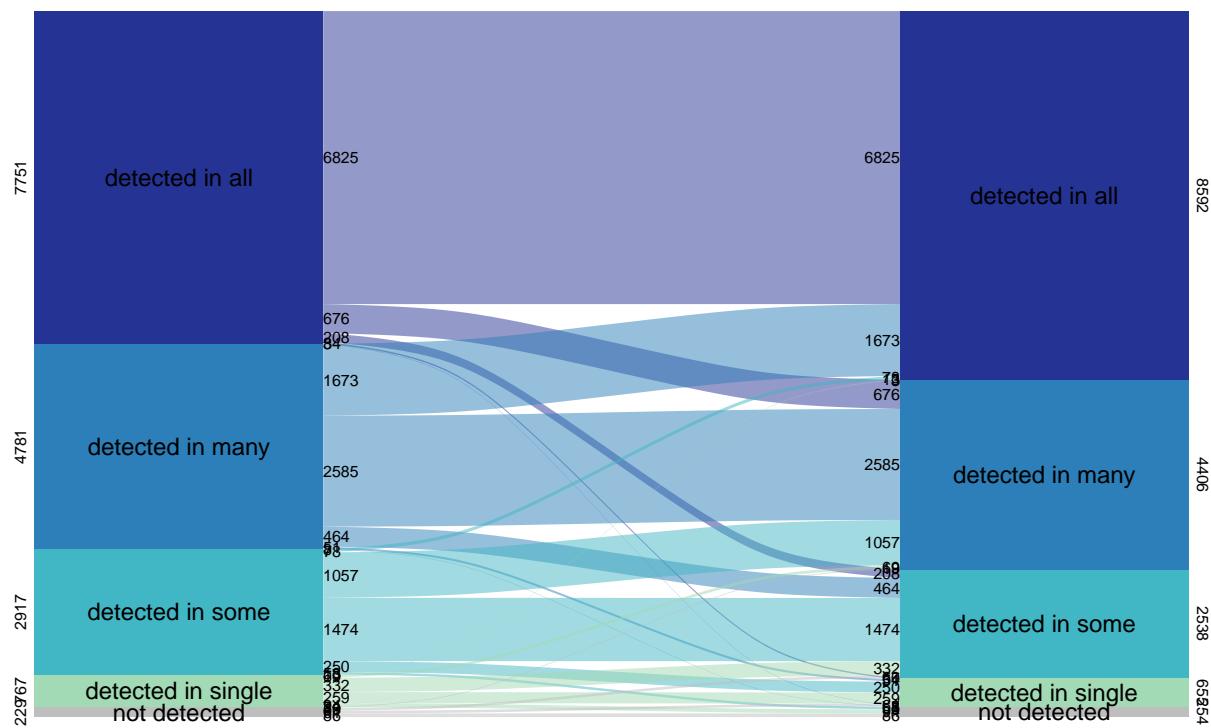
Pig

Human

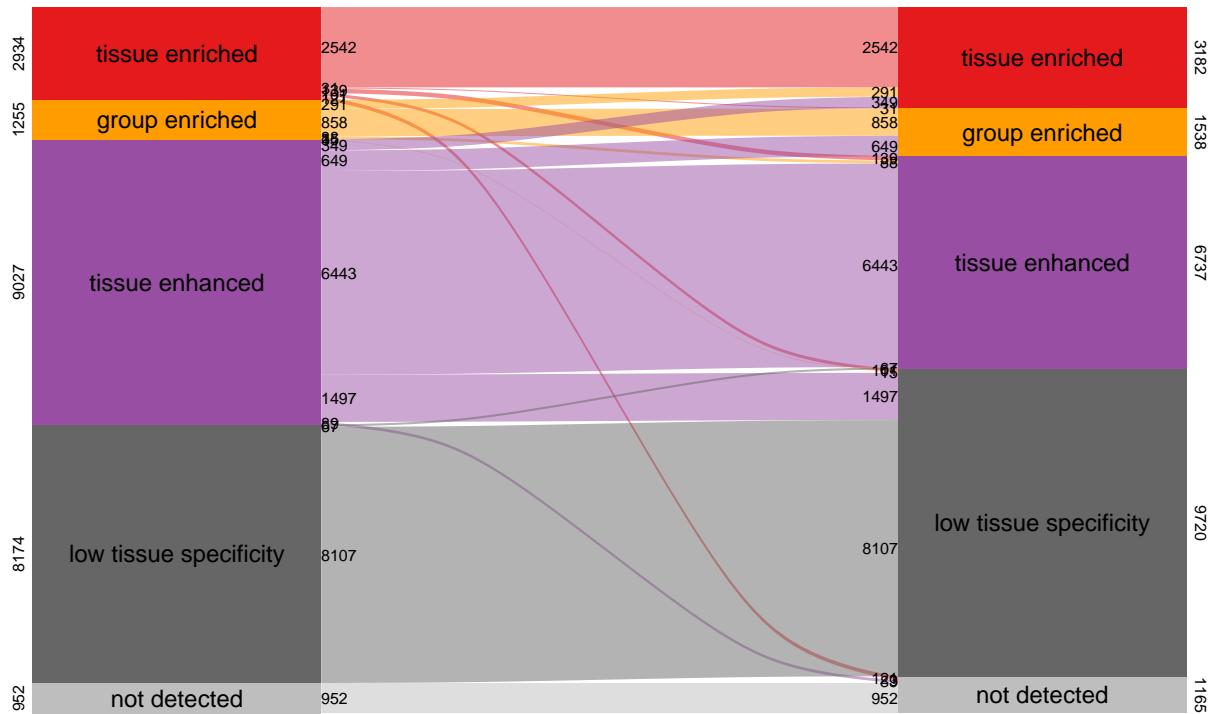


Pig

Human



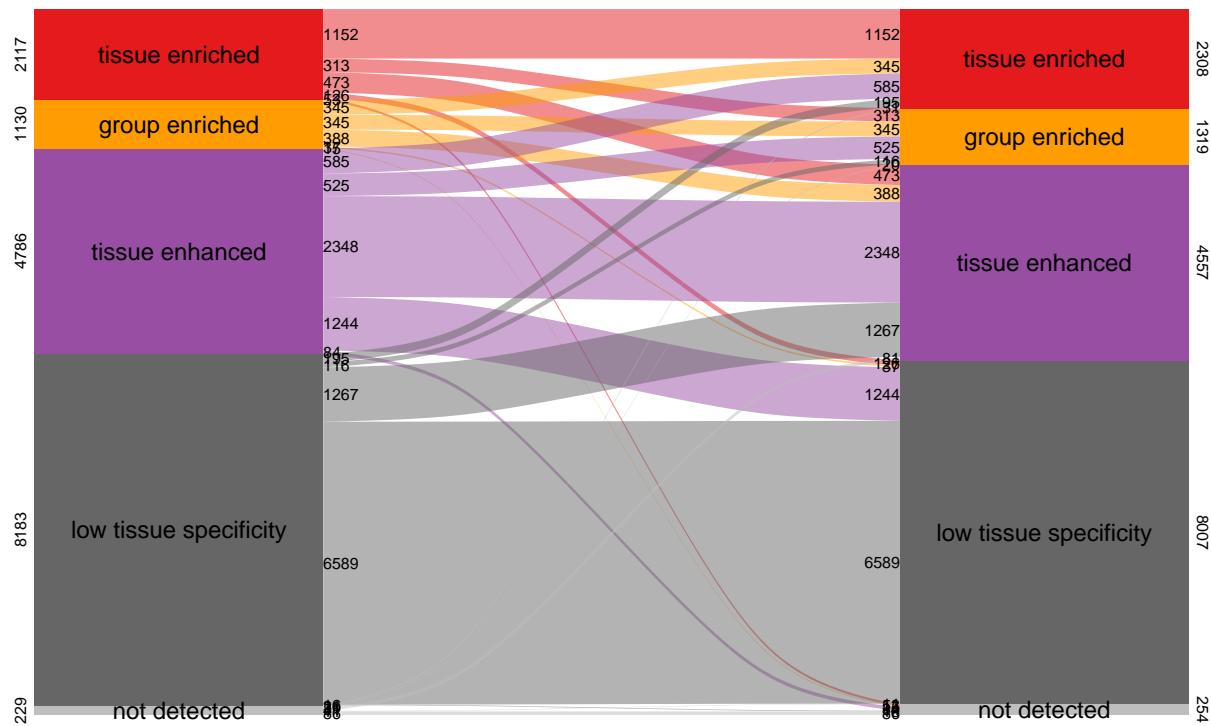
Original



Comparison

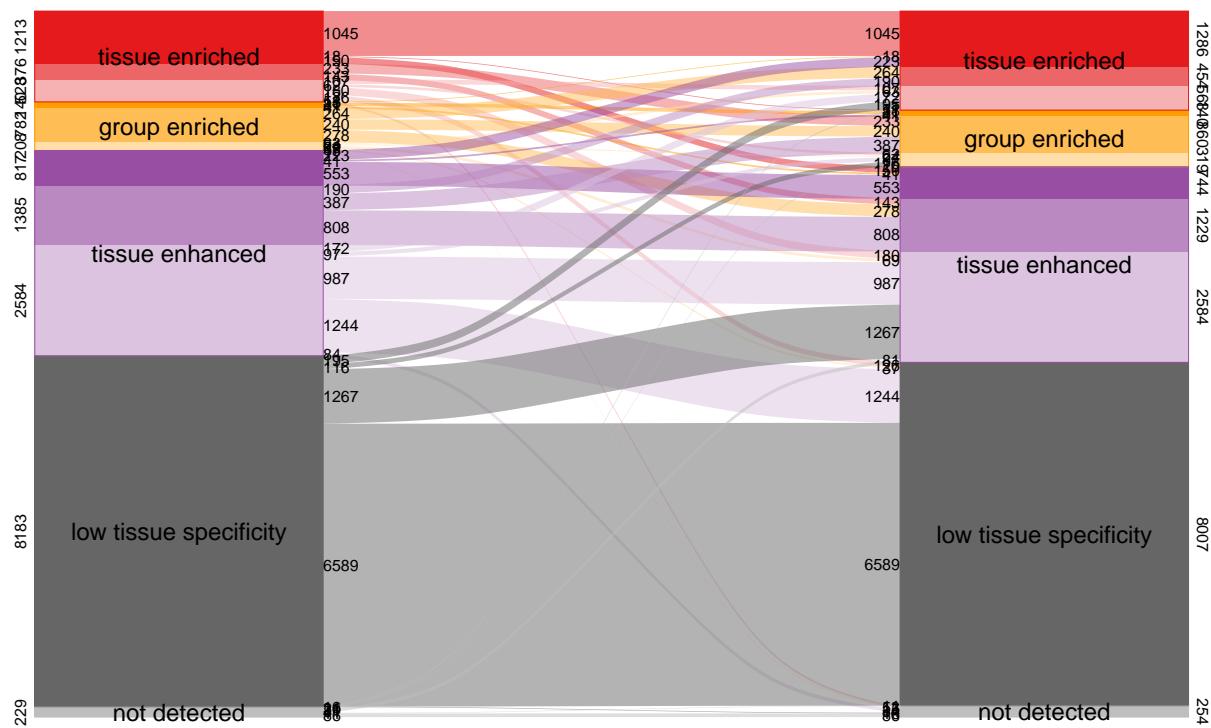
Pig

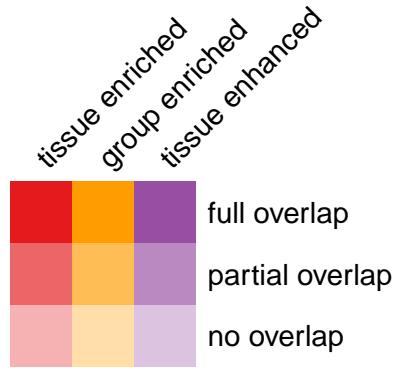
Human



Pig

Human





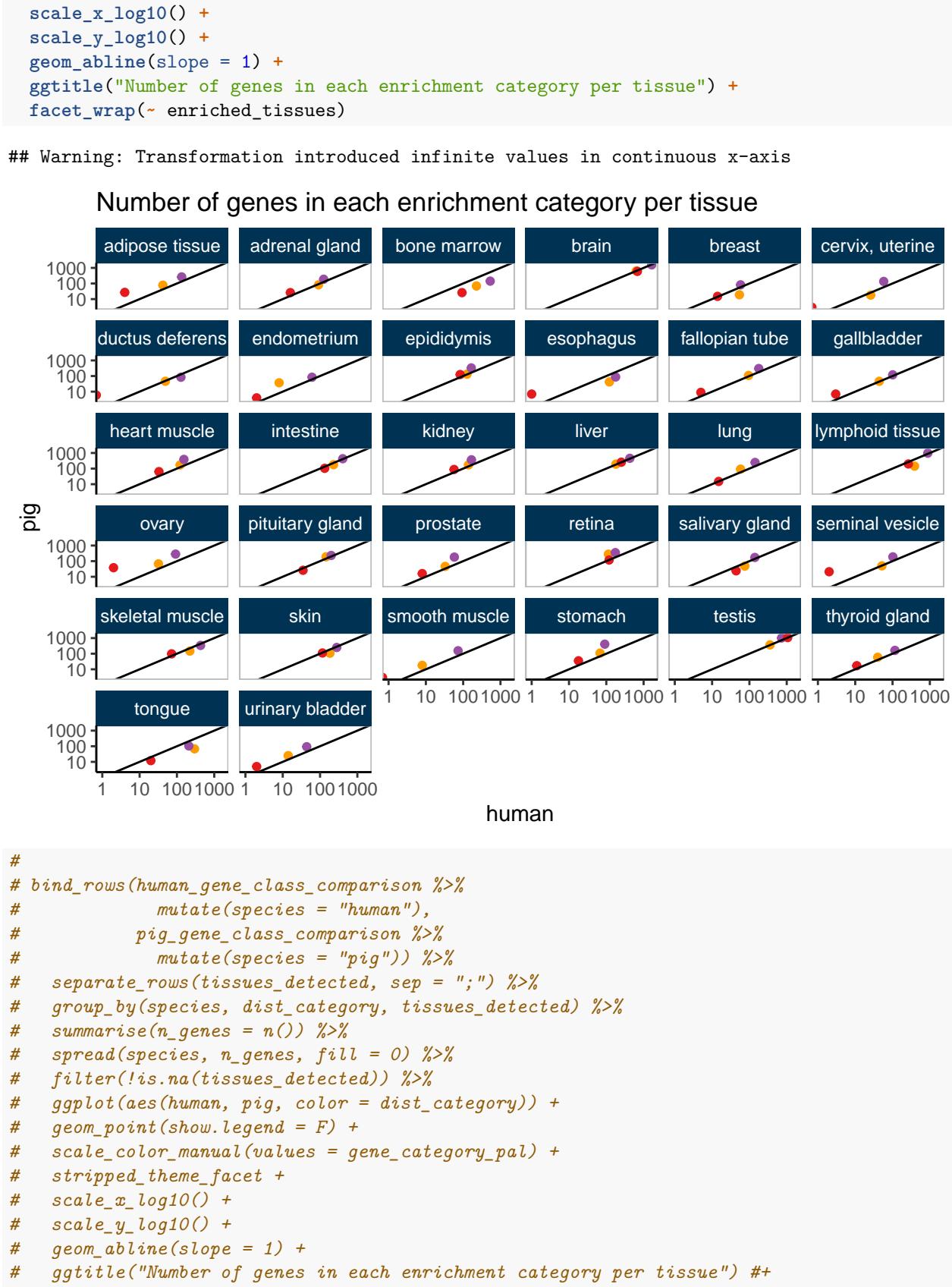
Project status visualisation

Orthology network

Orthology connection visualization

Correlation and classification comparison

```
bind_rows(human_gene_class_comparison %>%
  mutate(species = "human"),
  pig_gene_class_comparison %>%
  mutate(species = "pig")) %>%
separate_rows(enriched_tissues, sep = ";") %>%
group_by(species, spec_category, enriched_tissues) %>%
summarise(n_genes = n()) %>%
spread(species, n_genes, fill = 0) %>%
filter(!is.na(enriched_tissues)) %>%
ggplot(aes(human, pig, color = spec_category)) +
geom_point(show.legend = F) +
scale_color_manual(values = gene_category_pal) +
stripped_theme_facet +
```



```
#    facet_wrap(~ tissues_detected)
```

Sex specific genes

```
# ANOVA

if(file.exists("../data/processed/pig_anova.tab")) {
  anova_sex_res <- read_delim("../data/processed/pig_anova.tab", delim = "\t")
} else {
  anova_sex_res <-
  pig_atlas_sample_norm %>%
  mutate(sex = case_when(individual %in% c("a", "b") ~ "female",
                         individual %in% c("c", "d") ~ "male")) %>%
  group_by(ensscg_id) %>%
  mutate(sd_ = sd(tmm)) %>%
  filter(sd_ > 0) %>%
  select(-sd_) %>%
  do({
    g_data <- .
    saved_data <<- g_data

    model <- aov(log2(tmm + 1) ~ sex + tissue_ID + individual,
                  data = g_data)

    res <-
    model %>%
      tidy() %>%
      left_join(omega_sq(model) %>%
                  enframe("term", "sqrt_omega") %>%
                  mutate(term = trimws(term)),
                 by = "term")
    res
  }) %>%
  group_by(term) %>%
  mutate(adj_pval = p.adjust(p.value, method = "BH")) %>%
  ungroup() %>%
  mutate(significant = adj_pval < 0.05)

  write_delim(anova_sex_res, "../data/processed/pig_anova.tab", delim = "\t")
}

## Parsed with column specification:
## cols(
##   ensscg_id = col_character(),
##   term = col_character(),
##   df = col_double(),
##   sumsq = col_double(),
##   meansq = col_double(),
##   statistic = col_double(),
##   p.value = col_double(),
```

```

##   sqrt_omega = col_double(),
##   adj_pval = col_double(),
##   significant = col_logical()
## }

if(file.exists("../data/processed/pig_anova_nosex_tissues.tab")) {
  anova_sex_res <- read_delim("../data/processed/pig_anova_nosex_tissues.tab", delim = "\t")
} else {
  anova_nosex_res <-
    pig_atlas_sample_norm %>%
    filter(!tissue_ID %in% c('bre', 'bul', 'cerv', 'end', 'epi', 'fal', 'mag', 'ova', 'pen', 'pro', 'ser') |
      sex = case_when(individual %in% c("a", "b") ~ "female",
                      individual %in% c("c", "d") ~ "male")) %>%
    group_by(ensscgc_id) %>%
    mutate(sd_ = sd(tmm)) %>%
    filter(sd_ > 0) %>%
    select(-sd_) %>%
    do({
      g_data <- .
      saved_data <- g_data

      model <- aov(log2(tmm + 1) ~ sex + tissue_ID + individual,
                    data = g_data)

      res <-
        model %>%
        tidy() %>%
        left_join(omega_sq(model) %>%
          enframe("term", "sqrt_omega") %>%
          mutate(term = trimws(term)),
                  by = "term")
      res
    }) %>%
    group_by(term) %>%
    mutate(adj_pval = p.adjust(p.value, method = "BH")) %>%
    ungroup() %>%
    mutate(significant = adj_pval < 0.05)

    write_delim(anova_sex_res, "../data/processed/pig_anova_nosex_tissues.tab", delim = "\t")
}

## Parsed with column specification:
## cols(
##   ensscgc_id = col_character(),
##   term = col_character(),
##   df = col_double(),
##   sumsq = col_double(),
##   meansq = col_double(),
##   statistic = col_double(),
##   p.value = col_double(),
##   sqrt_omega = col_double(),
##   adj_pval = col_double(),
##   significant = col_logical()

```

```

## )

if(file.exists("../data/processed/pig_anova_ward_cluster.Rdata")) {
  load("../data/processed/pig_anova_ward_cluster.Rdata")
} else {
  pig_anova_clust <-
    anova_sex_res %>%
    select(1, 2, sqrt_omega) %>%
    spread(term, sqrt_omega) %>%
    column_to_rownames("enssscg_id") %>%
    dist() %>%
    hclust(method = "ward.D2")

  save(pig_anova_clust,
        file = "../data/processed/pig_anova_ward_cluster.Rdata")
}

anova_sex_res_cluster <-
  anova_sex_res %>%
  left_join(cutree(pig_anova_clust, k = 6) %>%
             enframe("enssscg_id", "anova_cluster")) %>%
  left_join(gene_chromosome %>%
              select(enssscg_id = 1,
                     chromosome = 4,
                     gene_name = 5) %>%
              unique())

## Joining, by = "enssscg_id"
## Joining, by = "enssscg_id"
anova_sex_res_cluster %>%
  filter(significant | term == "Residuals") %>% # filter(significant)
  group_by(anova_cluster, term) %>%
  summarise(sqrt_omega = sum(sqrt_omega)) %$%
  chord_with_title(from = anova_cluster,
                    to = term,
                    sizes = sqrt_omega,
                    grid.col = c("Residuals" = "gray", "tissue_ID" = "orangered",
                               "individual" = "skyblue", "sex" = "darkblue"),
                    groups = c(rep(1, 6),
                               rep(2, 4)),
                    plot.order = c(1:6, "Residuals", "tissue_ID", "individual", "sex"),
                    titles = c("Cluster", "Term"),
                    from_labels = anova_cluster,
                    to_labels = term)

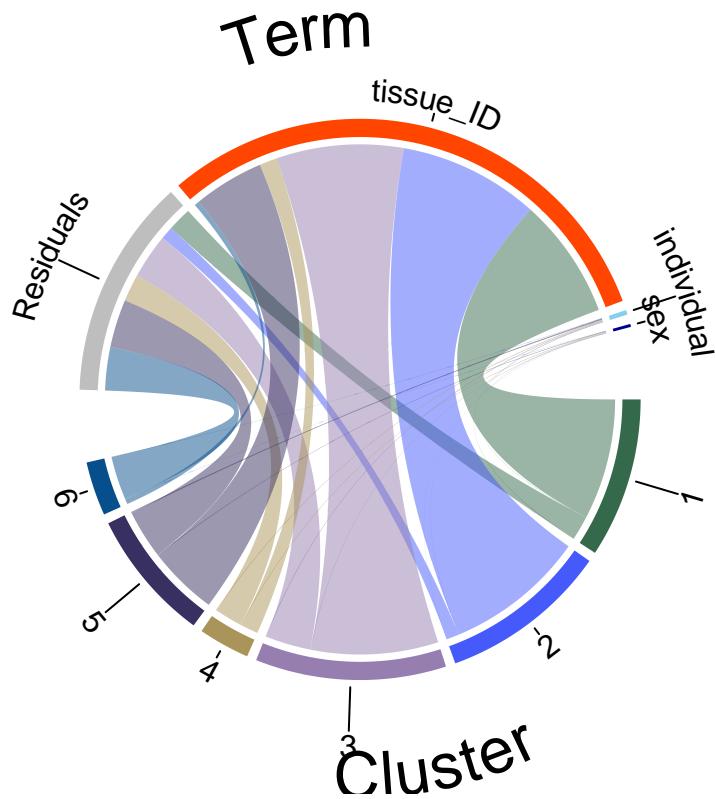
## Note: 1 point is out of plotting region in sector '1', track '1'.

```

```

## Note: 1 point is out of plotting region in sector '1', track '1'.
## Note: 7 points are out of plotting region in sector '1', track
## '1'.
## Note: 1 point is out of plotting region in sector 'Residuals',
## track '1'.
## Note: 1 point is out of plotting region in sector 'Residuals',
## track '1'.
## Note: 4 points are out of plotting region in sector 'Residuals',
## track '1'.
## Note: 9 points are out of plotting region in sector 'individual',
## track '1'.
## Note: 2 points are out of plotting region in sector 'sex', track
## '1'.

```



```

anova_sex_res_cluster %>%
  filter(significant | term == "Residuals") %>%
  filter(str_length(chromosome) < 3) %>%
  group_by(chromosome, term) %>%
  summarise(sqrt_omega = sum(sqrt_omega)) %$%
  chord_with_title(from = term,
    to = chromosome,
    sizes = sqrt_omega,
    grid.col = c(c("Residuals" = "gray", "tissue_ID" = "orangered",
      "individual" = "skyblue", "sex" = "darkblue"),

```

```

    set_names(plasma(23)[1:21],
              c(1:18, "MT", "X", "Y))),

groups = c(rep(2, 4),
           rep(1, 21)),
plot.order = c("Residuals", "tissue_ID", "individual", "sex", 1:18, "MT", "X", "Y"),
titles = c("Term", "Chromosome"),
from_labels = term,
to_labels = chromosome)

## Note: 1 point is out of plotting region in sector 'Residuals',
## track '1'.

## Note: 1 point is out of plotting region in sector 'Residuals',
## track '1'.

## Note: 4 points are out of plotting region in sector 'Residuals',
## track '1'.

## Note: 10 points are out of plotting region in sector 'individual',
## track '1'.

## Note: 2 points are out of plotting region in sector 'sex', track
## '1'.

## Note: 1 point is out of plotting region in sector '1', track '1'.
## Note: 1 point is out of plotting region in sector '1', track '1'.

## Note: 10 points are out of plotting region in sector '1', track
## '1'.

## Note: 2 points are out of plotting region in sector '10', track
## '1'.

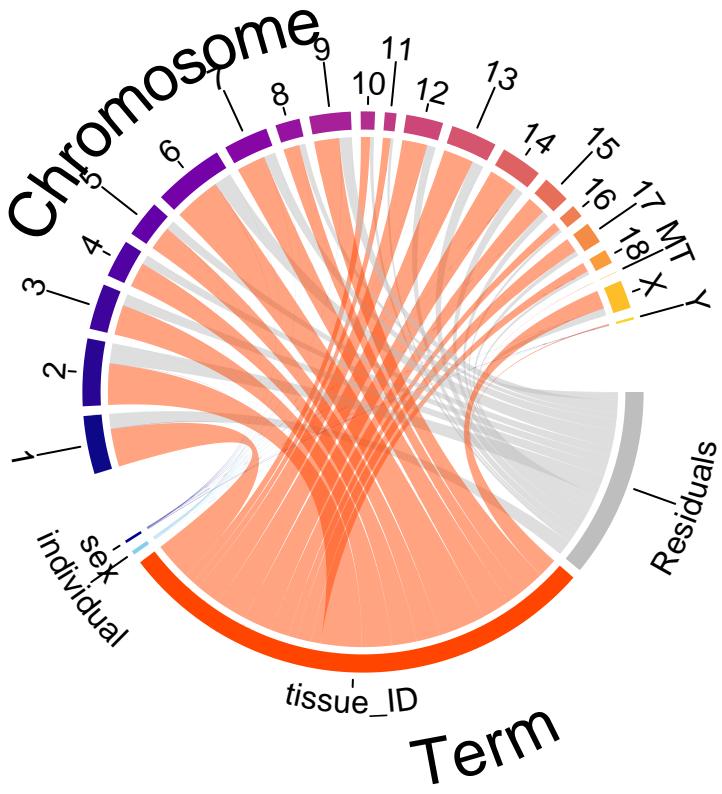
## Note: 2 points are out of plotting region in sector '11', track
## '1'.

## Note: 2 points are out of plotting region in sector '16', track
## '1'.

## Note: 2 points are out of plotting region in sector '18', track
## '1'.

## Note: 2 points are out of plotting region in sector 'MT', track
## '1'.

```



```

anova_sex_res_cluster %>%
  filter(significant | term == "Residuals") %>%
  filter(sqrt_omega > 0.05) %>%
  group_by(term) %>%
  summarise(n_genes = n())

## # A tibble: 4 x 2
##   term      n_genes
##   <chr>     <int>
## 1 individual    406
## 2 Residuals   21282
## 3 sex         225
## 4 tissue_ID   21504

# pairwise_alluvial_plot(data = anova_sex_res_cluster,
#                         var1 = "enssscg_id",
#                         var2 = "ensg_id",
#                         cat1 = "spec_category_pig",
#                         cat2 = "spec_category_human",
#                         cat_levels = spec_category_levels,
#                         cat_names = c("Pig", "Human"),
#                         pal = gene_category_pal)

anova_sex_res_cluster_barplot <-
  anova_sex_res_cluster %>%
  mutate(enssscg_id = factor(enssscg_id, ggdendro::dendro_data(pig_anova_clust)$labels$label),
        term = factor(term, c("Residuals", "tissue_ID", "individual", "sex")))

```

```

ggplot(aes(enssscg_id, sqrt_omega, fill = term)) +
  geom_col() +
  stripped_theme_facet +
  scale_fill_manual(values = c("Residuals" = "gray", "tissue_ID" = "orangered",
                               "individual" = "skyblue", "sex" = "darkblue")) +
  facet_wrap(~anova_cluster, scales = "free_x") +
  theme(axis.text.x = element_blank())

ggsave(savepath("ANOVA Pig cluster barplot.pdf"), width = 10, height = 10)

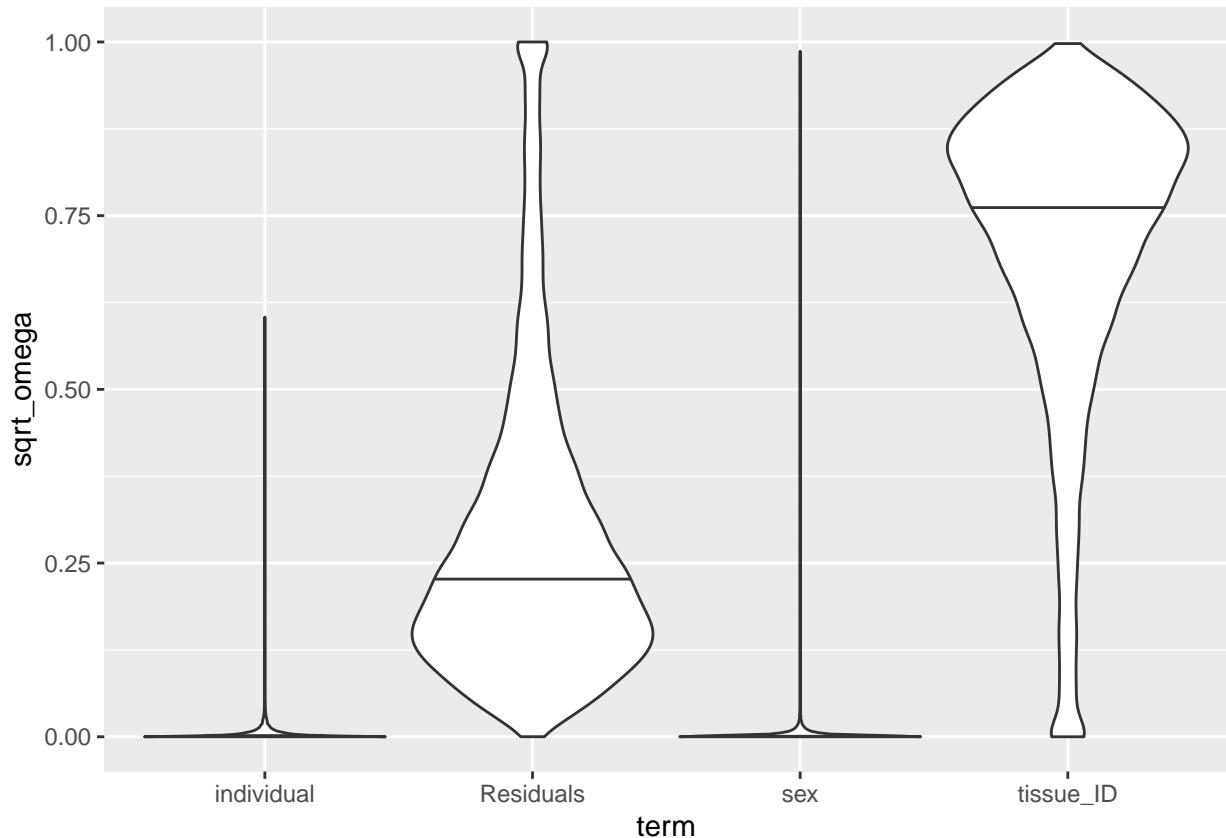
#####

anova_sex_res %>%
  ggplot(aes(term, sqrt_omega)) +
  geom_violin(draw_quantiles = 0.5, scale = "width")

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## unique 'x' values

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## unique 'x' values

```

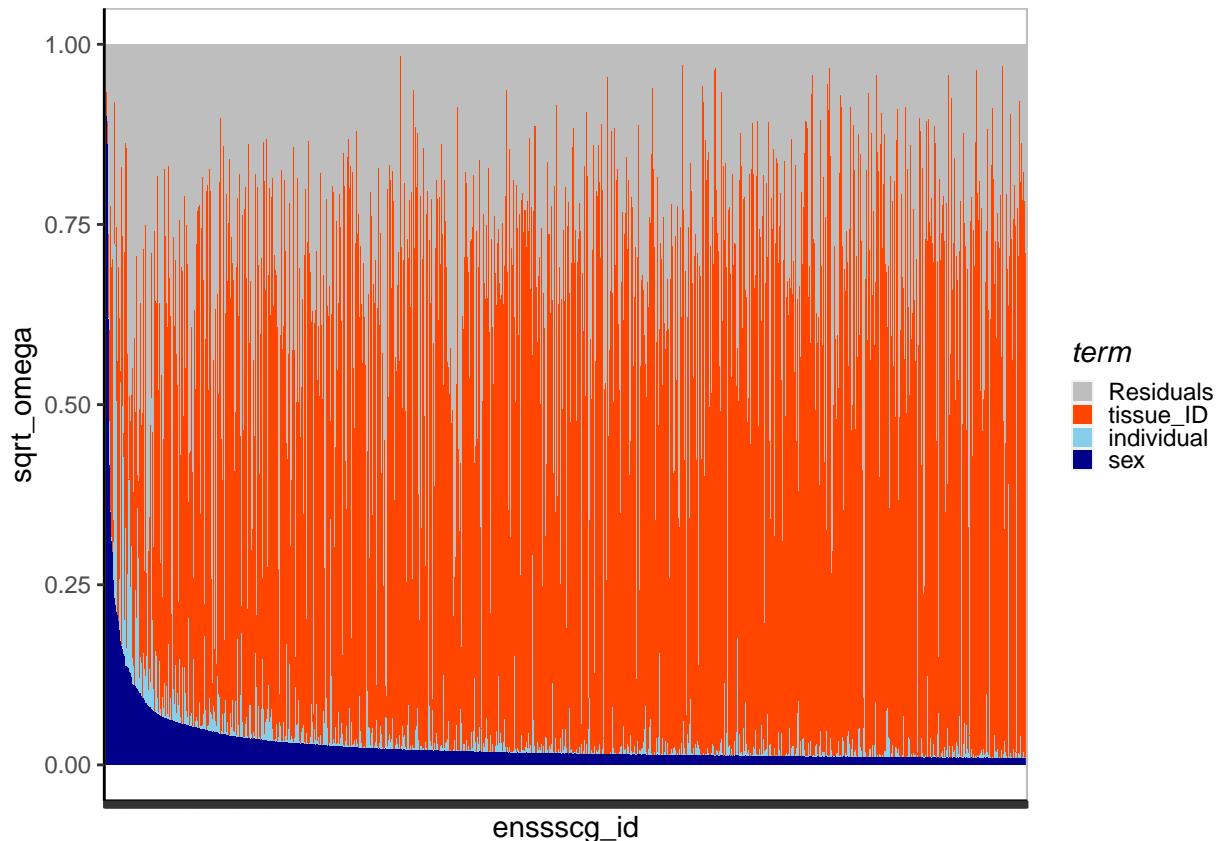


```

sex_genes <-
  anova_sex_res %>%
  filter(sqrt_omega > 0.01 & term == "sex") %>%
  arrange(-sqrt_omega)

anova_sex_res %>%
  filter(enssscg_id %in% sex_genes$enssscg_id) %>%
  mutate(enssscg_id = factor(enssscg_id, sex_genes$enssscg_id),
         term = factor(term, c("Residuals", "tissue_ID", "individual", "sex"))) %>%
  ggplot(aes(enssscg_id, sqrt_omega, fill = term)) +
  geom_col() +
  stripped_theme_facet +
  scale_fill_manual(values = c("Residuals" = "gray", "tissue_ID" = "orangered",
                               "individual" = "skyblue", "sex" = "darkblue")) +
  theme(axis.text.x = element_blank())

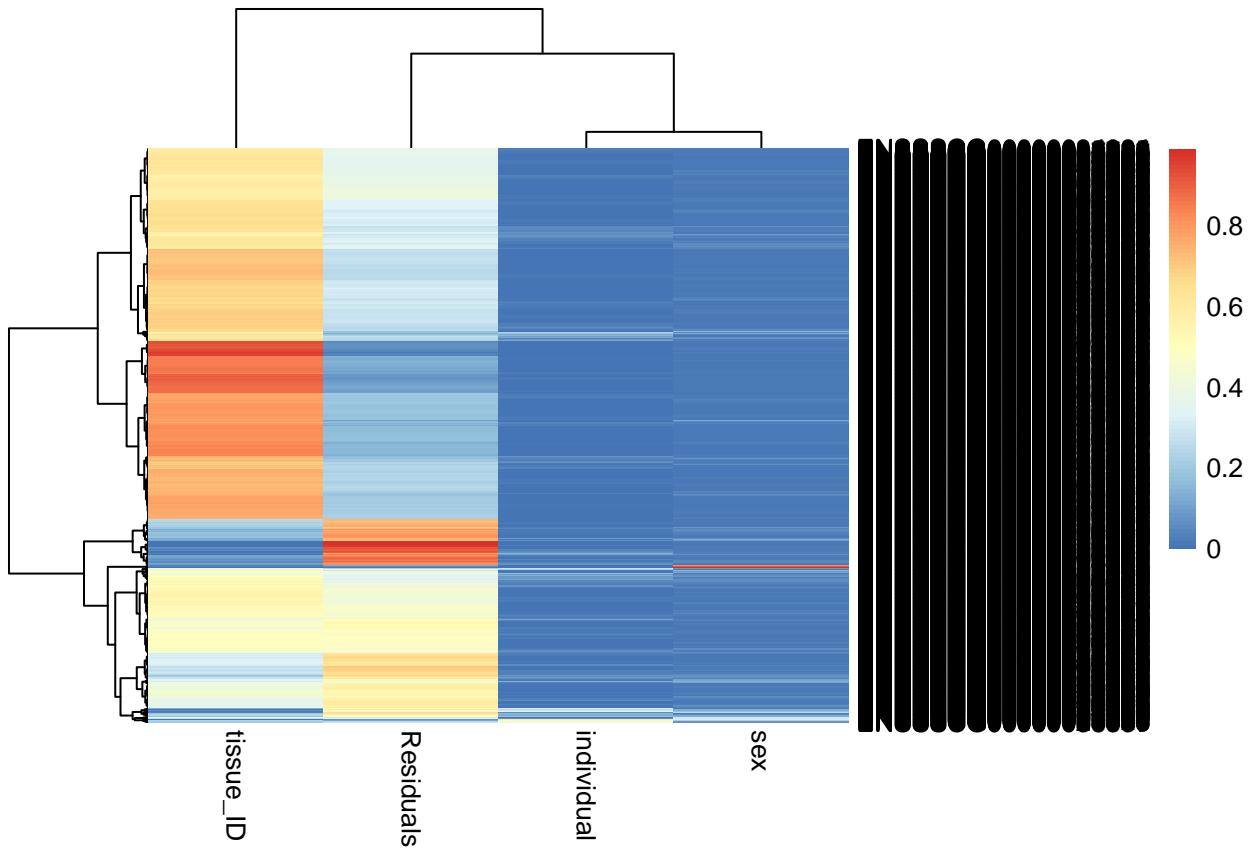
```



```

anova_sex_res %>%
  select(1, 2, sqrt_omega) %>%
  filter(enssscg_id %in% sex_genes$enssscg_id) %>%
  spread(term, sqrt_omega) %>%
  column_to_rownames("enssscg_id") %>%
  pheatmap(clustering_method = "ward.D2")

```



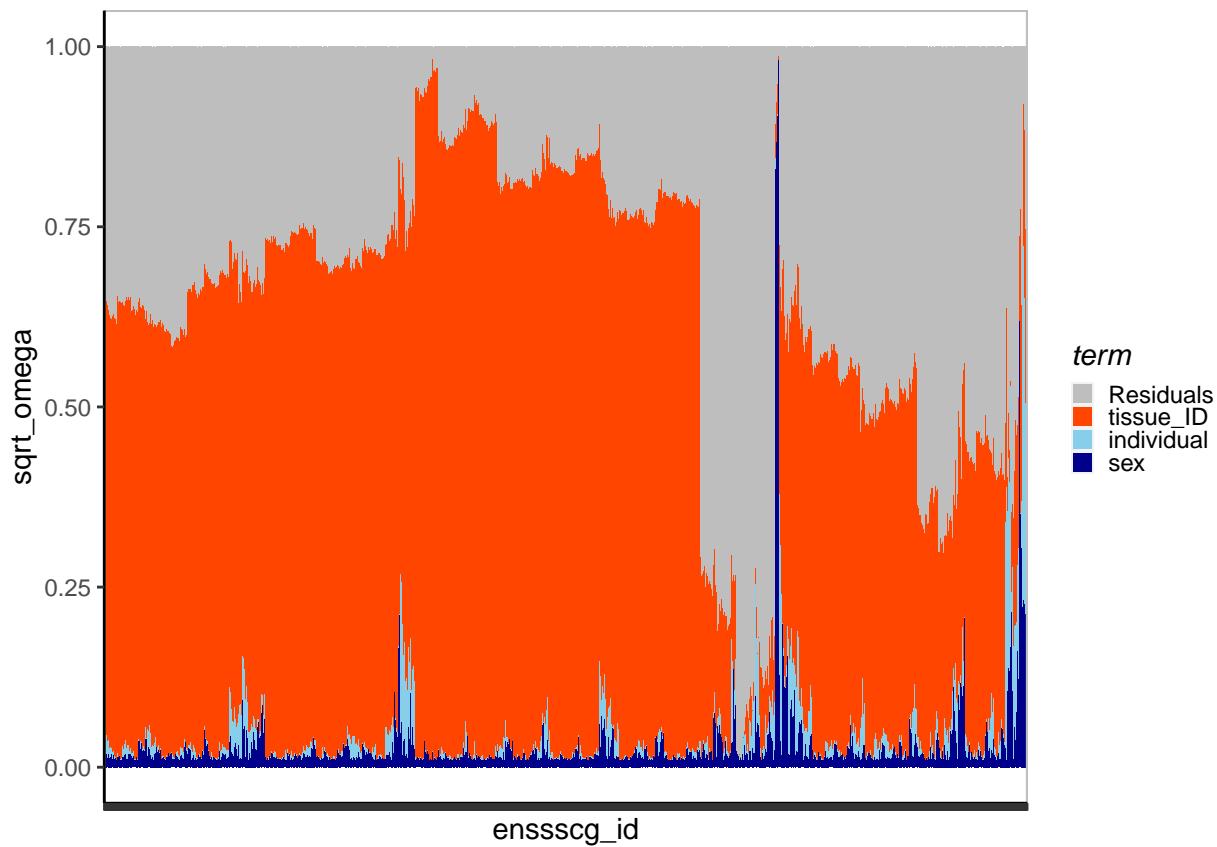
```

sex_clust <-
  anova_sex_res %>%
  select(1, 2, sqrt_omega) %>%
  filter(enssscg_id %in% sex_genes$enssscg_id) %>%
  spread(term, sqrt_omega) %>%
  column_to_rownames("enssscg_id") %>%
  dist() %>%
  hclust(method = "ward.D2")

sex_clust_data <-
  ggdendro::dendro_data(sex_clust)

anova_sex_res %>%
  filter(enssscg_id %in% sex_genes$enssscg_id) %>%
  mutate(enssscg_id = factor(enssscg_id, sex_clust_data$labels$label),
         term = factor(term, c("Residuals", "tissue_ID", "individual", "sex"))) %>%
  ggplot(aes(enssscg_id, sqrt_omega, fill = term)) +
  geom_col() +
  stripped_theme_facet +
  scale_fill_manual(values = c("Residuals" = "gray", "tissue_ID" = "orangered",
                               "individual" = "skyblue", "sex" = "darkblue")) +
  theme(axis.text.x = element_blank())

```



```
anova_sex_res %>%
  filter(significant | term == "Residuals") %>%
  group_by(enssscg_id) %>%
  mutate(max_omega = max(sqrt_omega)) %>%
  filter(sqrt_omega == max_omega) %>%
  group_by(term) %>%
  summarise(n_genes = n())
```

```
## # A tibble: 4 x 2
##   term      n_genes
##   <chr>     <int>
## 1 individual    14
## 2 Residuals    3329
## 3 sex          13
## 4 tissue_ID   18842
```

Tests