

Phylogenetic trees

```
VFLA_rescript_parsed$data$tax_prop_data <- calc_obs_props(VFLA_rescript_parsed,
  "tax_data", cols = nogrometadata$SampleID)
VFLA_rescript_parsed$data$tax_abund <- calc_taxon_abund(VFLA_rescript_parsed,
  "tax_prop_data",
  cols = nogrometadata$SampleID,
  groups = nogrometadata$Type)
```

Here we build a subtaxa tree. Empty nodes and specific taxa ranks are removed in order to make the tree readable and informative. Insert your summarized variable of choice.

```
plastictree <- VFLA_rescript_parsed %>%
  filter_taxa(Plastic >
    0) %>%
  filter_taxa(taxon_ranks ==
    "o", supertaxa = TRUE) %>%
  filter_taxa(taxon_names %in%
    c("Eukaryota",
      "Archaea",
      "Mitochondria",
      "Cyanobacteria"),
    subtaxa = TRUE,
    invert = TRUE) %>%
  heat_tree(node_label = taxon_names,
    node_label_max = 30,
    node_size = round(Plastic,
      digits = 4),
    node_color = round(Plastic,
      digits = 4),
    node_color_digits = 3,
    node_size_digits = 3,
    tree_label = "Plastic shelters",
    node_label_size_range = c(0.018,
      0.06), node_size_range = c(0.007,
      0.03), node_color_axis_label = "Read proportions")
```

plastictree

```
seaweedtree <- VFLA_rescript_parsed %>%
  filter_taxa(taxon_ranks ==
    "o", supertaxa = TRUE) %>%
  filter_taxa(taxon_names %in%
    c("Eukaryota",
      "Archaea",
      "Mitochondria",
      "Cyanobacteria"),
    subtaxa = TRUE,
    invert = TRUE) %>%
  heat_tree(node_label = taxon_names,
```

```

node_label_max = 30,
node_size = round(Seaweed,
  digits = 4),
node_color = round(Seaweed,
  digits = 4),
node_color_digits = 3,
node_size_digits = 3,
tree_label = "Seaweed shelters",
node_label_size_range = c(0.018,
  0.06), node_size_range = c(0.007,
  0.03), node_color_axis_label = "Read proportions")

```

seaweedtree

```

skintree <- VFLA_rescript_parsed %>%
  filter_taxa(Skin >
    0) %>%
  filter_taxa(taxon_ranks ==
    "o", supertaxa = TRUE) %>%
  filter_taxa(taxon_names %in%
    c("Eukaryota",
      "Archaea",
      "Mitochondria",
      "Cyanobacteria"),
    subtaxa = TRUE,
    invert = TRUE) %>%
  heat_tree(node_label = taxon_names,
    node_label_max = 30,
    node_size = round(Skin,
      digits = 4),
    node_color = round(Skin,
      digits = 4),
    node_color_digits = 4,
    node_size_digits = 4,
    tree_label = "Skin",
    node_label_size_range = c(0.018,
      0.06), node_size_range = c(0.007,
      0.03), node_color_axis_label = "Read proportions")

```

skintree

```

gilltree <- VFLA_rescript_parsed %>%
  filter_taxa(Gills >
    0) %>%
  filter_taxa(taxon_ranks ==
    "o", supertaxa = TRUE) %>%
  filter_taxa(taxon_names %in%
    c("Eukaryota",
      "Archaea",
      "Mitochondria",
      "Cyanobacteria"),
    subtaxa = TRUE,
    invert = TRUE) %>%
  heat_tree(node_label = taxon_names,
    node_label_max = 30,

```

```

node_size = round(Gills,
  digits = 3),
node_color = round(Gills,
  digits = 3),
node_color_digits = 4,
node_size_digits = 4,
tree_label = "Gills",
node_label_size_range = c(0.018,
  0.06), node_size_range = c(0.007,
  0.03), node_color_axis_label = "Read proportions")

```

gilltree

```

ggarrange(plastictree,
  seaweedtree, skintree,
  gilltree, nrow = 2,
  ncol = 2, labels = c("a",
  "b", "c", "d"))
ggsave("ordertrees.tiff",
  dpi = 300)

```