Analysis of BGC content across phylum Cyanobacteriota

Setup

Read in data

```r
# Map antiSMASH classes to their categories
bgc_class <- read_tsv("./data/2025-01-16-1256-bgc_class_ref.tsv") %>% select(!owner_id)
class_to_cat <- bgc_class$bgc_category
names(class_to_cat) <- bgc_class$class_name

# NCBI Taxonomy data for Cyanobacteriota assemblies
cyano_asm_tax <- read_tsv("data/cyano_asm_tax.tsv")

# From SMC: All antiSMASH 'region's for Cyanobacteriota genomes
regions_unfiltered <- read_tsv("./data/2025-02-26-1456-cyano_as_regions.tsv")

# Table of NCBI assemblies at "chromosome" or "complete" quality levels
ncbi_hiq_meta <- read_tsv("data/ncbi_cyano_HiQualityGenomes_metadata.tsv")

cyano_tax_dataset <- read_tsv("data/taxonomy_summary.tsv")
cyano_asm_dataset <- read_tsv("data/cyanos_genomes_taxids.tsv") %>%
    left_join(cyano_tax_dataset, by = join_by('Organism Taxonomic ID' == 'Taxid')) %>%
    select(
        `Assembly Accession`,
        `Assembly Level`,
        `Organism Taxonomic ID`,
        `Superkingdom name`,
        `Kingdom name`,
        `Phylum name`,
        `Class name`,
        `Order name`,
        `Family name`,
        `Genus name`,
        `Species name`
    )

# BiG-SLiCE results for getting GCF counts per genus
bigslice_df <- read_tsv("data/2025-03-14-1524-bigslice_results.tsv") %>%
    left_join(cyano_asm_dataset, by = join_by('orig_folder' == 'Assembly Accession')) %>%
    rename(
        'asm_level' = `Assembly Level`,
        'taxid' = `Organism Taxonomic ID`,
        'superkingdom' = `Superkingdom name`,
        'kingdom' = `Kingdom name`,
        'phylum' = `Phylum name`,
        'class' = `Class name`,
        'order' = `Order name`,
        'family' = `Family name`,
        'genus' = `Genus name`,
        'species' = `Species name`
    ) %>%
    replace_na(list(genus = "Unclassified"))

gcf_df <- bigslice_df %>% select(genus, gcf_id) %>% distinct() %>% count(genus, name = "n_gcfs")
```

Clean data

```
# Convert BGC 'class' to vector, add in BGC 'category' as vector, order levels
# of classes and categories
regions_unfiltered <- regions_unfiltered %>%
  mutate(classes = map(region_class, function(class_string) {
    (
      if (str_starts(class_string, fixed("["))) {
        fromJSON(class_string)
      } else {
        c(class_string)
      }
    )
  })) %>%
  mutate(categories = classes %>% map(function(cls_vec) {
    (
      map_vec(cls_vec, function(cls_str) class_to_cat[[cls_str]]) %>% unique() %>% sort())
  })) %>%
  mutate(cats_str = categories %>% map_chr(function(x) str_flatten(x, collapse = ", "))) %>%
  add_count(cats_str) %>%
  mutate(
    cats_str = forcats::fct_reorder(cats_str, desc(n)),
    class_str = classes %>% map_chr(function(x) str_flatten(x, collapse = ", "))
  )

regions_unfiltered
```

```
## # A tibble: 32,112 x 26
##    region_gene_id bgc_id region_length contig_name region_start_nt region_end_nt
##             <dbl>  <dbl>         <dbl> <chr>                 <dbl>         <dbl>
##  1      394444400 2.05e6         20822 NZ_KK07376~         1448721       1469542
##  2      427693693 2.21e6          6191 NZ_NMQI010~               1          6191
##  3      427830749 2.21e6         41152 NZ_NJHU010~           20319         61470
##  4      427867799 2.21e6         29334 NZ_NJHW010~            5515         34848
##  5      427879170 2.21e6          5638 NZ_NJHW010~               1          5638
##  6      442232549 2.29e6         27366 NZ_VIKX010~               1         27366
##  7      442951361 2.29e6         61852 NZ_BJCK010~          121631        183482
##  8      444447386 2.30e6         21923 NZ_WVIC010~           13038         34960
##  9      445057742 2.31e6         40108 NZ_JAAGOGO~           26815         66922
## 10      446681012 2.31e6         35928 NZ_QMEA010~               1         35928
## # i 32,102 more rows
## # i 20 more variables: bgc_annotation_id <dbl>, region_class <chr>,
## #   region_category <lgl>, contig_edge <lgl>, smc_id <dbl>, accession_id <chr>,
## #   size_bp <dbl>, n_scaffolds <dbl>, data_source_description <chr>,
## #   tax_phylum <chr>, tax_class <chr>, tax_order <chr>, tax_family <chr>,
## #   tax_genus <chr>, tax_species <chr>, classes <list>, categories <list>,
## #   cats_str <fct>, n <int>, class_str <chr>
```

Explore data

The repetitive composition of many BGCs makes them a challenge during genome assembly, resulting in over-inflation of BGC counts when BGCs are split between the ends of two different contigs. Focusing on high-quality genomes can therefore ensure a higher-quality dataset.

Basic summary

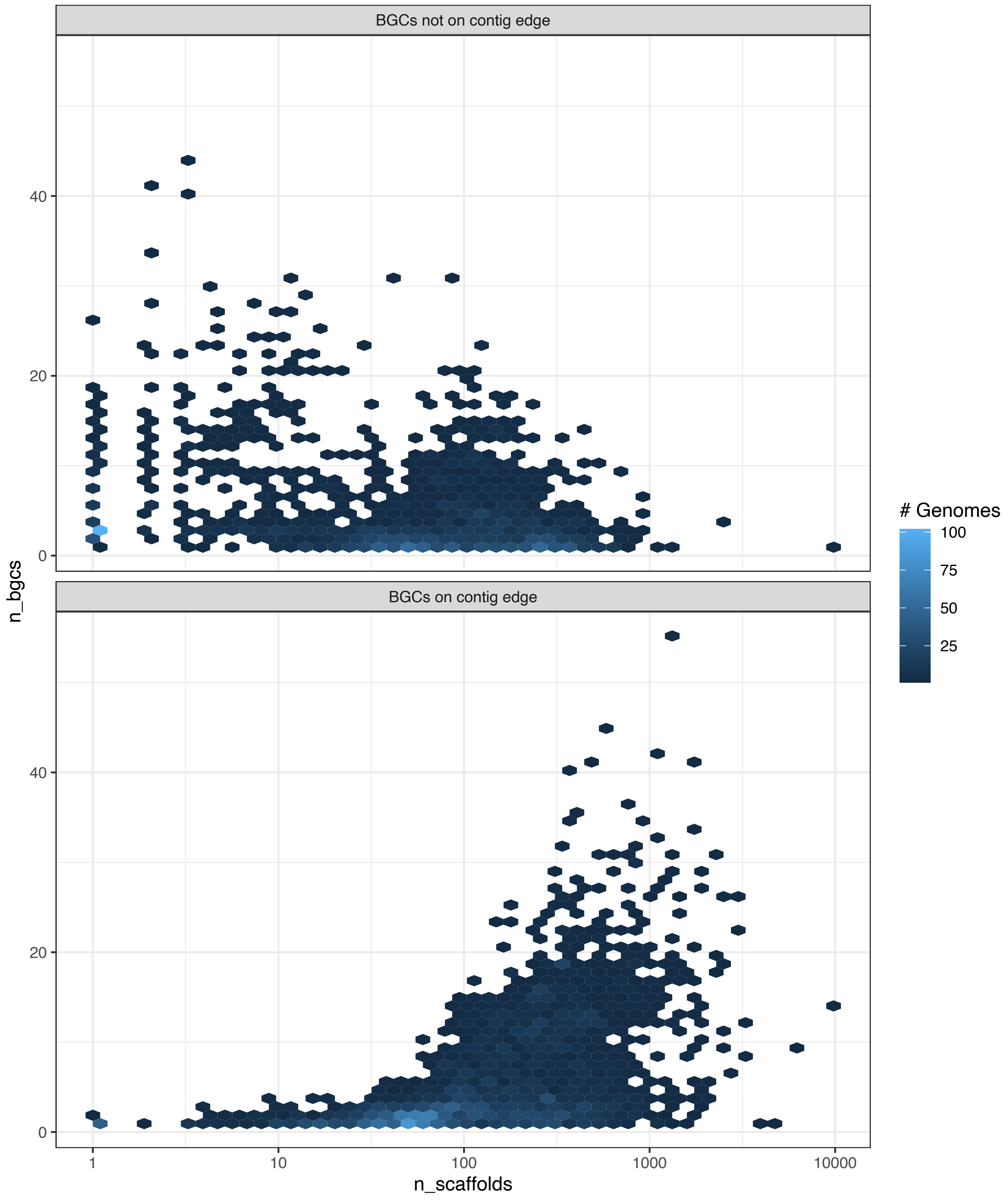
There are 4090 genomes and 32112 BGCs in the initial dataset.

How fragmented are the full set of genomes, and how does that impact BGC counts?

```r
regions_unfiltered %>%
  group_by(smc_id, n_scaffolds, contig_edge) %>%
  summarize(n_bgcs = n()) %>%
  ungroup() %>%
  ggplot(aes(x = n_scaffolds, y = n_bgcs)) +
  stat_bin_hex(bins = 50) +
  scale_x_log10(breaks = breaks_log()) +
  guides(fill = guide_colorbar(title = "# Genomes")) +
  facet_wrap(. ~ contig_edge, ncol = 1, labeller = as_labeller(c("FALSE" = "BGCs not on contig edge", "
  theme_bw() +
  ggtitle("Fragmented genomes have inflated BGC counts", subtitle = "Full dataset")
```

Fragmented genomes have inflated BGC counts

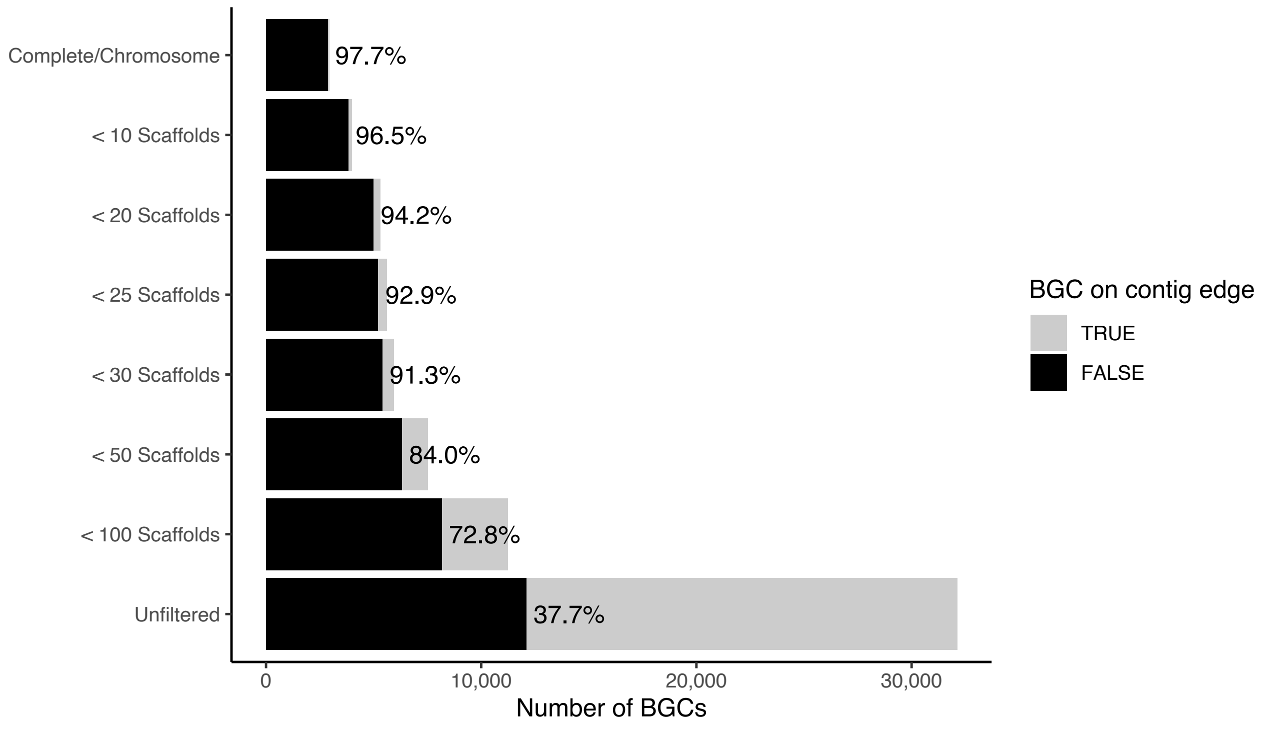
Full dataset



This figure depicts the number of BGCs against the number of scaffolds in a genome. To help avoid over-plotting (i.e. many overlapping data points misrepresenting the distribution of the data), the colors of each spot in the figure correspond to how many data points overlap at those coordinates.

How does the proportion of BGCs off/on a contig edge change if we filter for high-quality genomes in different ways?

```r
filters_df <- bind_rows(
  regions_unfiltered %>%
    group_by(contig_edge) %>%
    summarize(filter = "Unfiltered", n = n()) %>%
    ungroup() %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    semi_join(ncbi_hiq_meta, by = join_by(accession_id == `Assembly Accession`)) %>%
    group_by(contig_edge) %>%
    summarize(filter = "Complete/Chromosome", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 10) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 10 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 20) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 20 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 25) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 25 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 30) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 30 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 50) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 50 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
  regions_unfiltered %>%
    filter(n_scaffolds < 100) %>%
    group_by(contig_edge) %>%
    summarize(filter = "< 100 Scaffolds", n = n()) %>%
    mutate(pct = 100 * n / sum(n)),
)

ggplot(filters_df, aes(x = filter, y = n)) +
  geom_col(aes(fill = fct_rev(as_factor(contig_edge))), position = position_stack()) +
  geom_text(aes(y = n, label = sprintf("%1.1f%%", pct)), data = filters_df %>% filter(contig_edge == FA
  scale_x_discrete(name = "", limits = c("Unfiltered", "< 100 Scaffolds", "< 50 Scaffolds", "< 30 Scaff
  scale_y_continuous(name = "Number of BGCs", labels = label_comma()) +
  scale_fill_manual(name = "BGC on contig edge", values = c("gray80", "black")) +
  theme_classic() +
  coord_flip()
```



This figure depicts the counts of BGCs that are on a contig edge vs. those that are not, depending on how we define what a "high-quality genome" is. `Complete/Chromosome` refers to the genomes at the "Complete" or "Chromosome" assembly levels on NCBI.

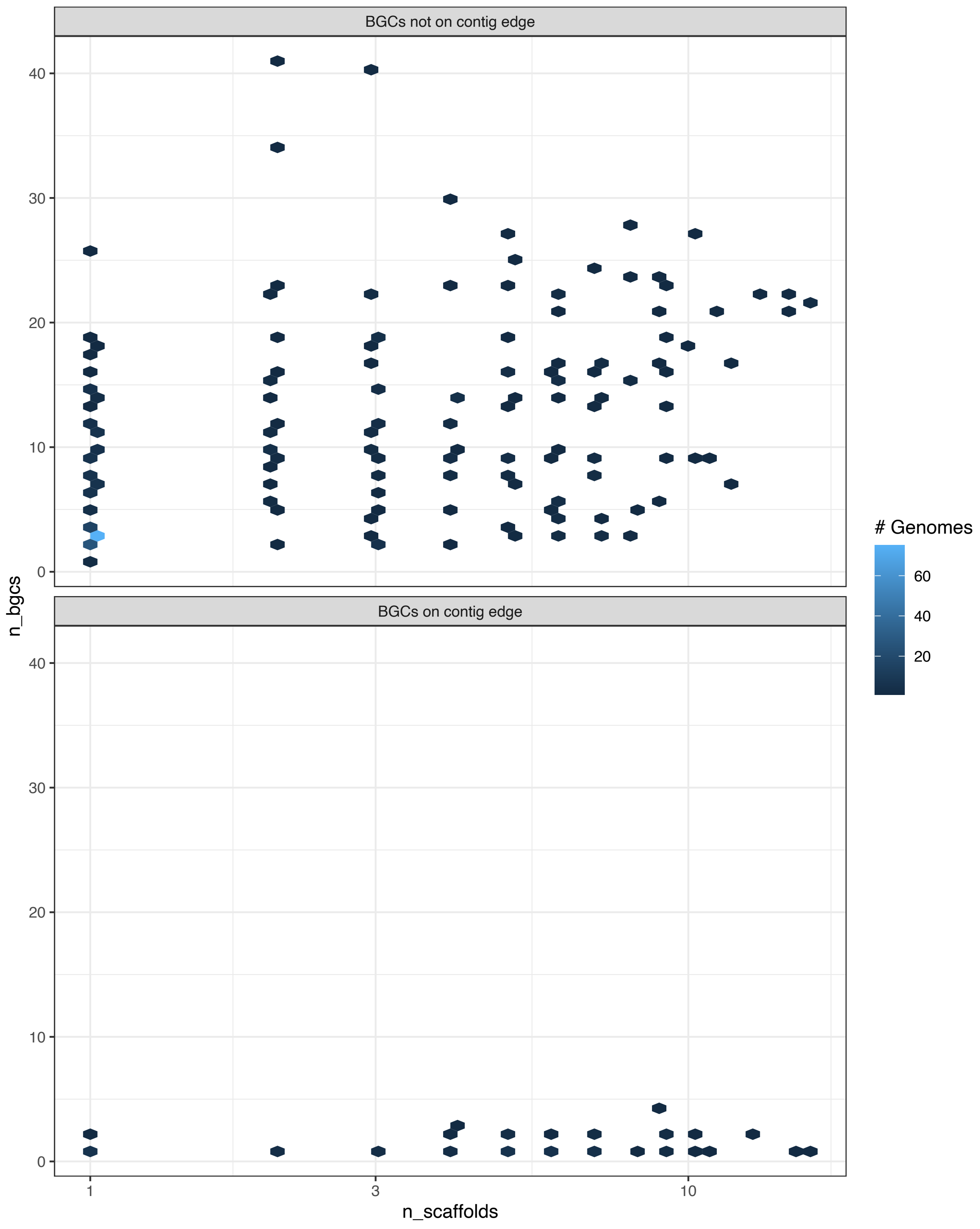
Based on this figure, and to be most conservative in this analysis, we will be going with the most restrictive criteria – using only genomes of "Chromosome" or "Complete" assembly quality as listed on NCBI.

Filter the dataset to high-quality genomes

Repeat the figure from above, and we should see that most BGCs are not on a contig edge.

```
regions <- regions_unfiltered %>%
  semi_join(ncbi_hiq_meta, by = join_by(accession_id == `Assembly Accession`))
```

Now, there are 326 genomes and 2953 BGCs represented in the dataset.


BGCs not on contig edge
BGCs on contig edge
n_bgcs
n_scaffolds
0
10
20
30
40
1
3
10
# Genomes
20
40
60

Analyze data

Now we will proceed with our analysis, with the goal of looking at the BGC content of phylum Cyanobacteriota across the axes of length, BGC category, and taxonomy.

Note: AntiSMASH-annotated BGCs are assigned one or more of several dozen BGC "classes" based on the detection rule(s) triggered. These classes can also be grouped into one of 7 "categories" as defined by MIBiG – namely `Polyketide`, `NRP`, `RiPP`, `Terpene`, `Saccharide`, `Alkaloid`, and `Other`.

Summary statistics of BGC length across BGC categories

```
## # A tibble: 22 x 7
## # Groups:   cats_str [22]
##    cats_str                    n min_len max_len mean_len median_len     sd
##    <fct>                   <int>   <dbl>   <dbl>    <dbl>      <dbl>  <dbl>
##  1 Terpene                   834   13541   39454   20403.     20612.  2079.
##  2 RiPP                      739    7553   76778   29623.     24133  10016.
##  3 NRP                       500   20873   97395   47693.     43942. 10078.
##  4 Polyketide                307   22218   87362   46966.     46241   6996.
##  5 NRP, Polyketide           296   15761  190414   73530.     70899  24984.
##  6 Other                      97   10034   60591   23411.     20762  10296.
##  7 NRP, RiPP                  46   44214  131611   68485.     64902. 19801.
##  8 NRP, Other                 32   43141   99576   76136.     78536. 20579.
##  9 NRP, Polyketide, RiPP      21   58186  257631  124101.     91425  63076.
## 10 NRP, Other, Polyketide     18   47242  154012   80890.     73720. 33500.
## # i 12 more rows
```

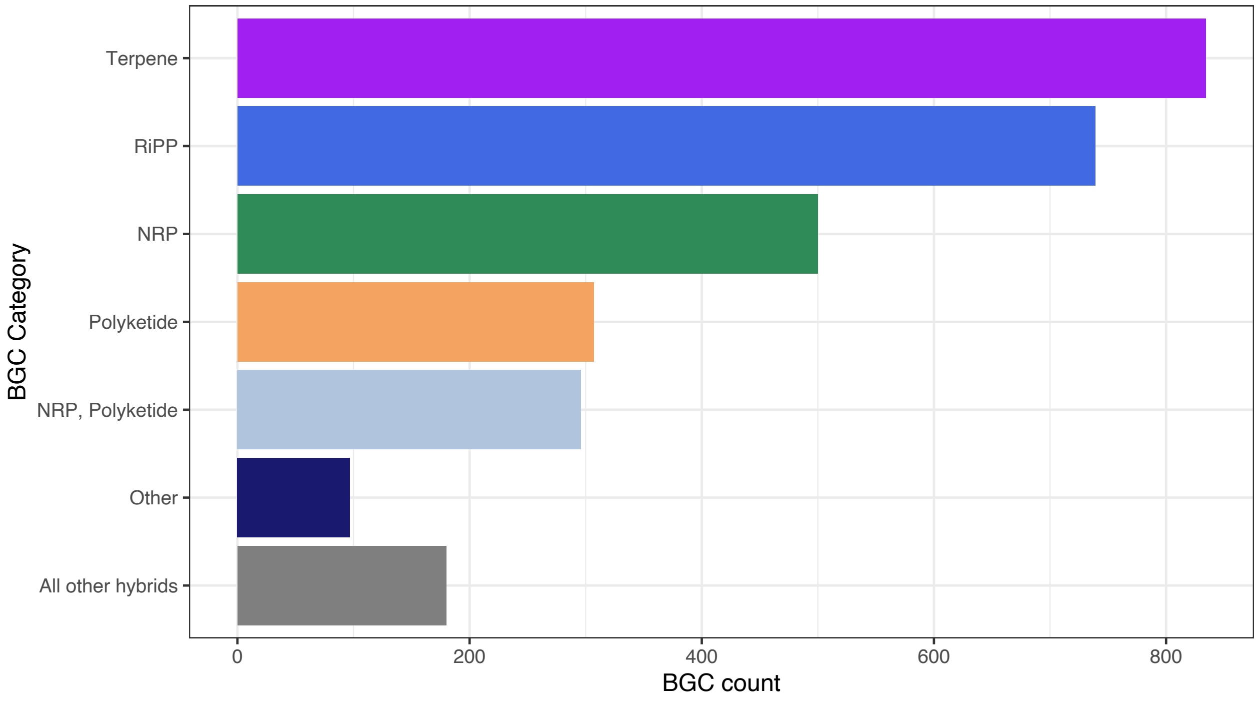
How many BGCs in each category? (counting hybrids of categories as separate)

Here are the numbers

How many BGCs in each category? (lumping all hybrids into one except NRPS-PKS)

```
# Lump any hybrid category with fewer than 80 BGCs into an "all other" category
# - Threshold determined arbitrarily to improve visualization
region_summary_lumped <- region_summary %>%
  mutate(
    group = if_else(n < 80, "All other hybrids", cats_str),
    group = group %>% fct_reorder(n)
  )

# Keep a reference DF handy for which categories got lumped
lump_groups <- region_summary_lumped %>% select(cats_str, group)

# Use the MIBiG / antiSMASH coloring scheme
cat_colors <- c(
  "Polyketide" = "#f4a460",
  "NRP" = "#2e8b57",
  "RiPP" = "#4169e1",
  "Terpene" = "purple",
```

```r
  "Saccharide" = "#deb887",
  "Other" = "#191970",
  "NRP, Polyketide" = "lightsteelblue",
  "All other hybrids" = "gray50"
)

# Plot it
lumped_category_counts <- region_summary_lumped %>%
  ggplot(aes(y = reorder(group, n))) +
  geom_col(aes(x = n, fill = group)) +
  scale_x_continuous(name = "BGC count", breaks = breaks_extended()) +
  scale_y_discrete(name = "BGC Category") +
  scale_fill_manual(values = cat_colors) +
  theme_bw() +
  guides(fill = "none")
lumped_category_counts
```

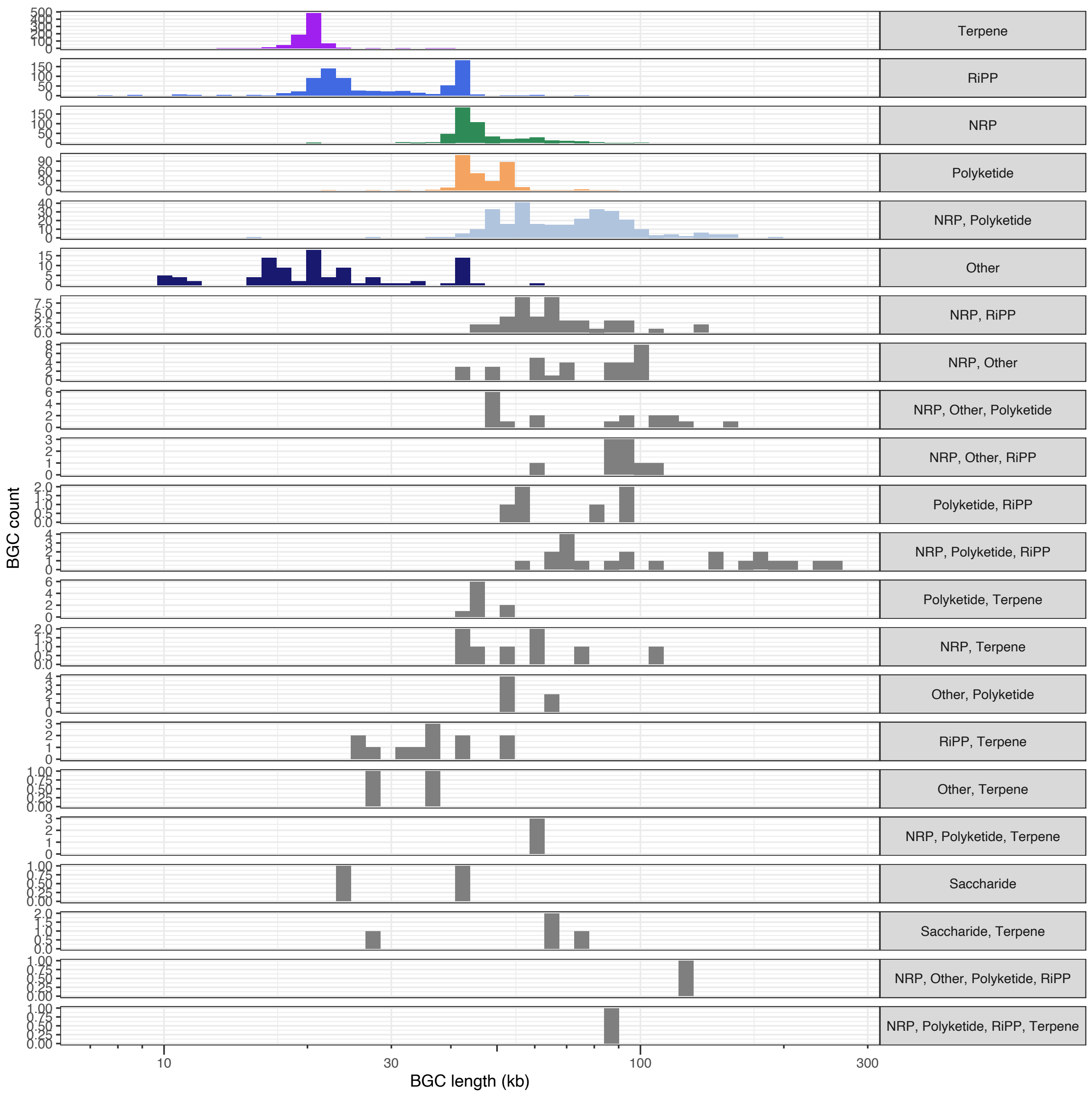


```r
ggsave("./figs/svg/category_counts_lumped.svg", lumped_category_counts, device = "svg")
ggsave("./figs/png/category_counts_lumped.png", lumped_category_counts, device = "png")
```

How do BGCs vary in length by category (or combination of categories)?

Un-lumped categories

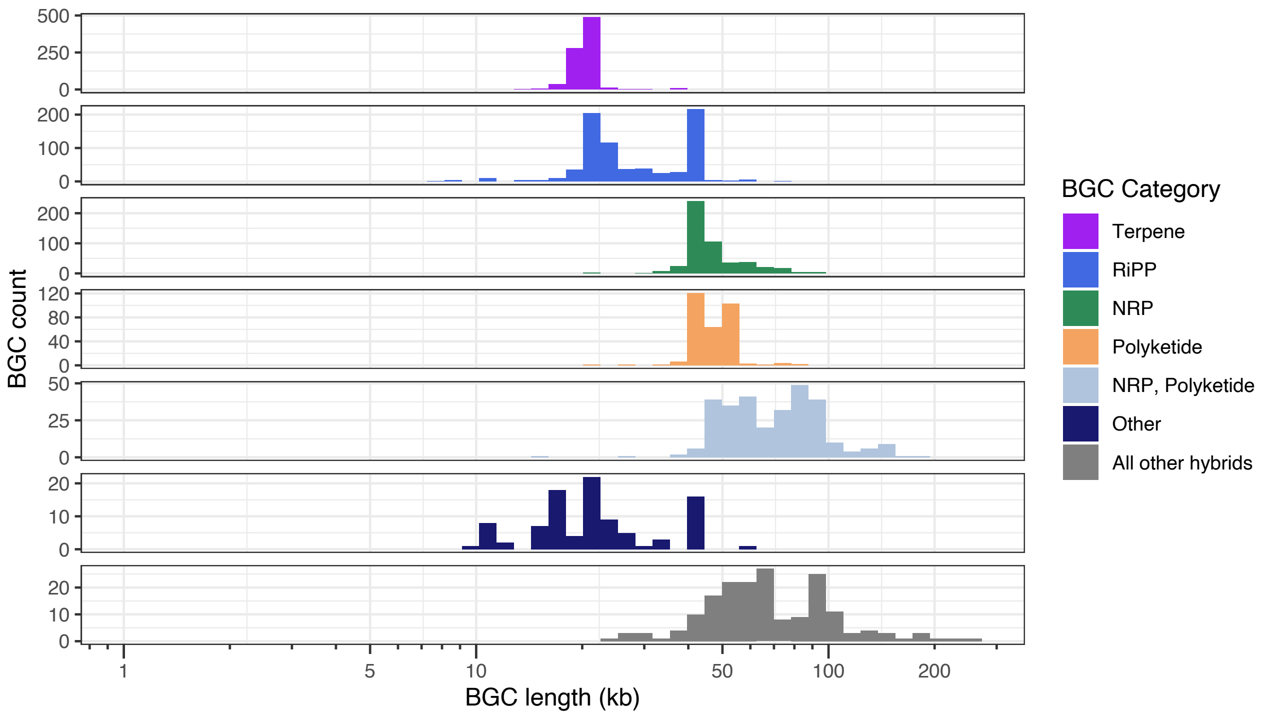
```r
regions_lumped <- regions %>% left_join(lump_groups, by = "cats_str")

region_hist <- ggplot(regions_lumped, aes(
  x = region_length / 1000,
)) +
  geom_histogram(aes(fill = group), bins = 50) +
  scale_x_log10(name = "BGC length (kb)", guide = "axis_logticks", breaks = breaks_log(), labels = label
  scale_y_continuous(name = "BGC count", breaks = breaks_extended(), labels = label_comma()) +
  scale_fill_manual(values = cat_colors) +
  facet_grid(rows = vars(cats_str), scales = "free_y") +
  theme_bw() +
  theme(strip.text.y.right = element_text(angle = 0)) +
  guides(fill = FALSE)

region_hist
```



```
ggsave("./figs/svg/region_hist.svg", region_hist, device = "svg")
ggsave("./figs/png/region_hist.png", region_hist, device = "png")
```

Lumped categories (again, except for NRPS-PKS hybrids)

```
region_hist_lumped <- regions_lumped %>%
  # filter(group != "All other hybrids") %>%
  ggplot(aes(x = region_length / 1000)) +
  geom_histogram(aes(fill = group), bins = 50) +
  scale_x_log10(name = "BGC length (kb)", guide = "axis_logticks", limits = c(1, NA), breaks = c(1, 5,
  scale_y_continuous(name = "BGC count", breaks = breaks_extended(n = 3)) +
  scale_fill_manual(values = cat_colors) +
  facet_wrap(vars(group), ncol = 1, scales = "free_y") +
  guides(fill = guide_legend(title = "BGC Category")) +
  theme_bw() +
  theme(
    strip.background = element_blank(),
    strip.text = element_blank()
  )
region_hist_lumped
```



```
ggsave("./figs/svg/region_hist_lumped.svg", region_hist_lumped, device = "svg")
ggsave("./figs/png/region_hist_lumped.png", region_hist_lumped, device = "png")
```

How does BGC count vary across genera and by category?

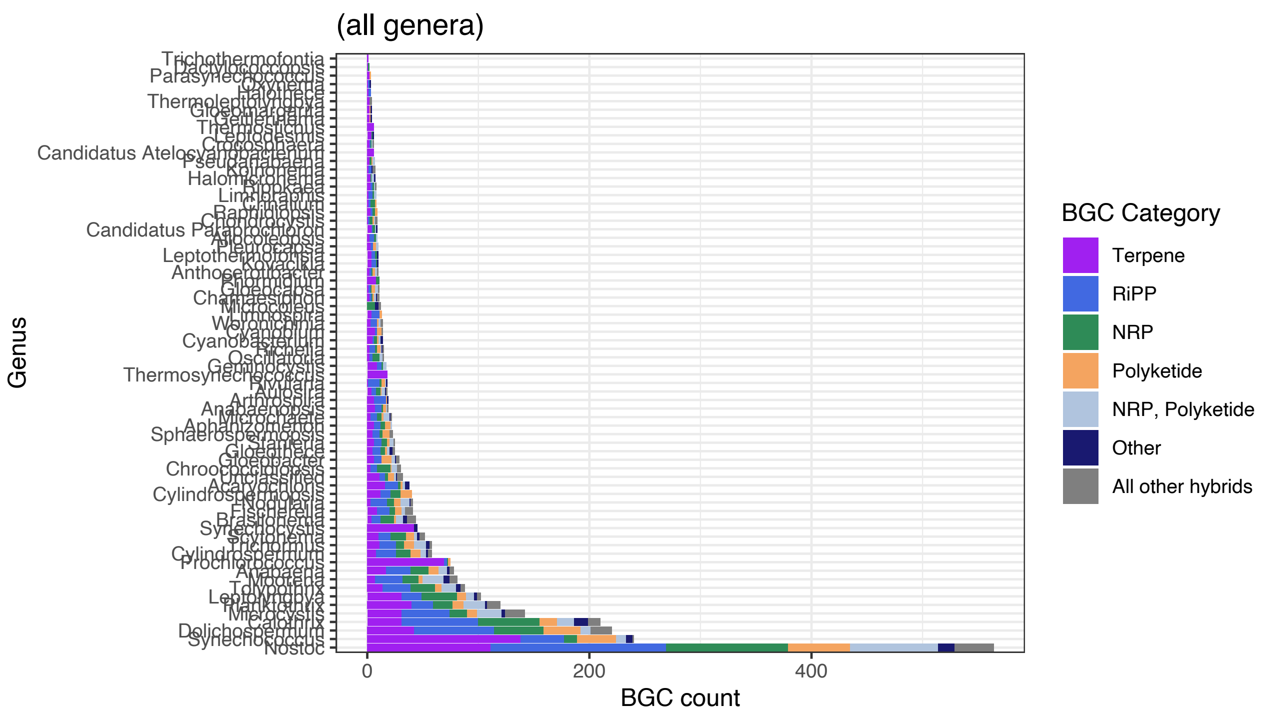
Table:

```r
tax_count <- regions_lumped %>%
  group_by(tax_genus, cats_str) %>%
  summarize(num_bgcs = n()) %>%
  mutate(tax_genus = tax_genus %>% fct_reorder(num_bgcs)) %>%
  left_join(lump_groups, by = "cats_str") # %>%

tax_count
```

```
## # A tibble: 388 x 4
## # Groups:   tax_genus [70]
##    tax_genus     cats_str        num_bgcs group
##    <fct>         <fct>              <int> <fct>
##  1 Acaryochloris Terpene               16 Terpene
##  2 Acaryochloris RiPP                  12 RiPP
##  3 Acaryochloris NRP                    2 NRP
##  4 Acaryochloris Polyketide             2 Polyketide
##  5 Acaryochloris NRP, Polyketide        2 NRP, Polyketide
##  6 Acaryochloris Other                  4 Other
##  7 Allocoleopsis Terpene                2 Terpene
##  8 Allocoleopsis RiPP                   4 RiPP
##  9 Allocoleopsis NRP                    2 NRP
## 10 Allocoleopsis NRP, Polyketide        1 NRP, Polyketide
## # i 378 more rows
```

Raw BGC counts by genus

```r
p_all <- tax_count %>%
  group_by(tax_genus) %>%
  filter(sum(num_bgcs) > 0) %>%
  ggplot(aes(x = fct_infreq(tax_genus, w = num_bgcs))) +
  geom_col(aes(y = num_bgcs, fill = group), position = position_stack(reverse = TRUE)) +
  scale_y_continuous(name = "BGC count", breaks = breaks_extended()) +
  scale_x_discrete(name = "Genus") +
  scale_fill_manual(name = "BGC Category", values = cat_colors) +
  coord_flip() +
  theme_bw() +
  ggtitle("(all genera)")
p_all
```



```r
ggsave("./figs/svg/genus_counts_all.svg", p_all, device = "svg")
ggsave("./figs/png/genus_counts_all.png", p_all, device = "png")
```

In order to normalize BGC counts to a per-genome basis, we must also know how many Cyano genomes *lacked* BGCs (as detected by antiSMASH).

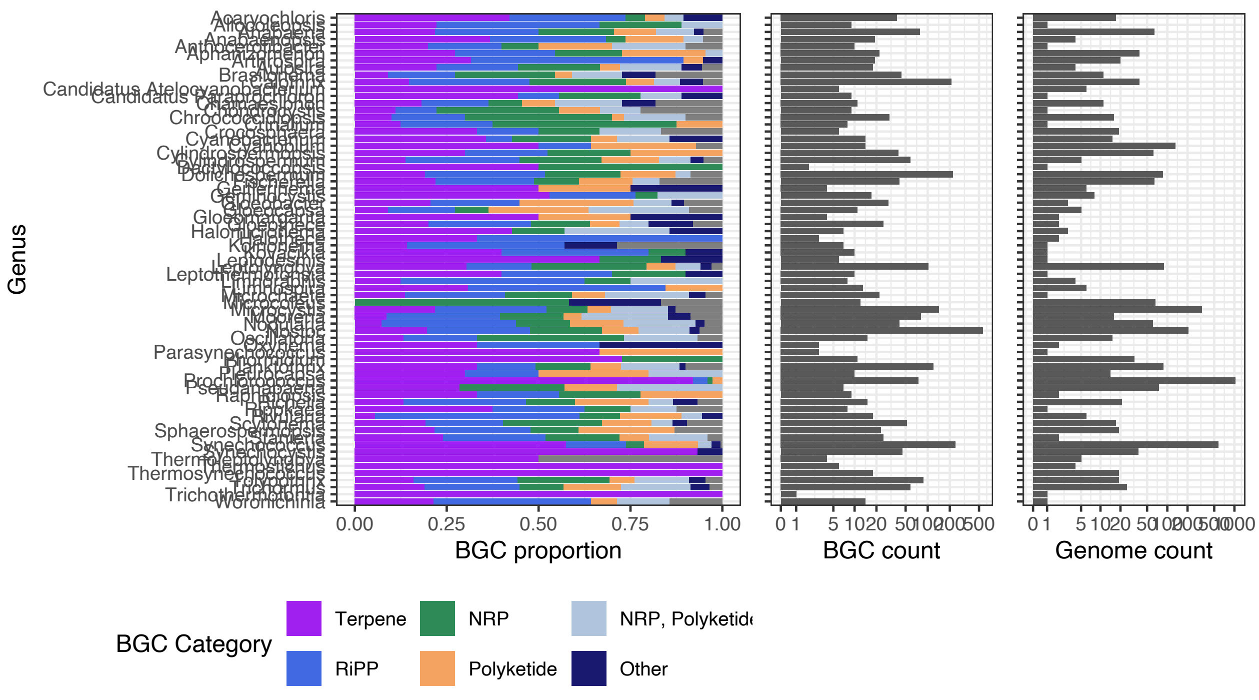
```r
# Plaintext file listing all the accessions that had no BGCs
cyano_nohits <- read_tsv("data/ncbi_cyano_nohit_accs.txt", col_names = c("accession_id")) %>%
  left_join(cyano_asm_tax, by = join_by(accession_id == assembly_accession))

# Incorporate these into our genome counts
cyano_nohit_genus_counts <- cyano_nohits %>%
  group_by(genus) %>%
  summarize(n_nohits = n()) %>%
  mutate(genus = replace_na(genus, "Unclassified")) %>%
  arrange(genus)

genomes_by_genus <- read_tsv("data/2025-02-25-1442-cyano_smc_src_counts_by_genus.tsv")
genomes_by_genus <- genomes_by_genus %>%
  left_join(cyano_nohit_genus_counts, by = join_by(tax_genus == genus)) %>%
  mutate(n_nohits = replace_na(n_nohits, 0)) %>%
  mutate(tot_genomes = n_nohits + n_sources, .keep = "unused")
```

Plot the BGCs per genome (normalized to 100%) alongside number of BGCs per genus and genomes per genus

```r
# Prepare the dataframe specific to this set of plots
df_plots <- tax_count %>%
  filter(tax_genus != "Unclassified") %>%
  left_join(genomes_by_genus, by = "tax_genus") %>%
  mutate(bgc_dens = num_bgcs / tot_genomes) %>%
  group_by(tax_genus) %>%
  mutate(tot_bgc_dens = sum(bgc_dens), tot_bgcs = sum(num_bgcs))

# Plot BGCs per genome, colored by category and divided by genus
p_bgc_dens <- df_plots %>%
  ggplot(aes(x = fct_rev(tax_genus))) +
  geom_col(aes(y = bgc_dens, fill = group), position = position_fill(reverse = TRUE)) +
  scale_y_continuous(name = "BGC proportion") +
  scale_x_discrete(name = "Genus") +
  scale_fill_manual(name = "BGC Category", values = cat_colors) +
  coord_flip() +
  theme_bw() +
  theme(legend.position = "bottom")
# p_bgc_dens

# Plot total BGC count by genus
p_bgc_ct <- df_plots %>%
  ggplot(aes(x = fct_rev(tax_genus))) +
  geom_col(aes(y = tot_bgcs), data = df_plots %>% select(tax_genus, tot_bgcs, tot_bgc_dens) %>% distinc
  scale_y_continuous(
    name = "BGC count",
    trans = transform_pseudo_log(base = 10),
    breaks = c(0, 1, 5, 10, 20, 50, 100, 200, 500)
  ) +
  coord_flip() +
  theme_bw() +
  theme(
    axis.title.y = element_blank(),
    axis.text.y = element_blank()
  )

# Plot genome count by genus
genome_counts <- df_plots %>%
  group_by(tax_genus, tot_genomes) %>%
  summarize(tot_bgc_dens = sum(bgc_dens), tot_bgcs = sum(num_bgcs)) %>%
  arrange(tot_bgc_dens)
genome_counts
```

```
## # A tibble: 69 x 4
## # Groups:   tax_genus [69]
##    tax_genus       tot_genomes tot_bgc_dens tot_bgcs
##    <chr>                 <dbl>        <dbl>    <int>
##  1 Prochlorococcus        1023       0.0733       75
##  2 Pseudanabaena            75       0.0933        7
##  3 Cyanobium               131       0.107        14
##  4 Microcoleus              66       0.182        12
##  5 Crocosphaera             19       0.316         6
##  6 Phormidium               32       0.344        11
##  7 Synechococcus           579       0.415       240
##  8 Microcystis             329       0.432       142
##  9 Aphanizomenon            38       0.579        22
## 10 Fischerella              64       0.641        41
## # i 59 more rows
```

```
p_genome_ct <- genome_counts %>%
  ggplot(aes(x = fct_rev(tax_genus))) +
  geom_col(aes(y = tot_genomes)) +
  scale_y_continuous(
    name = "Genome count",
    trans = transform_pseudo_log(base = 10),
    breaks = c(0, 1, 5, 10, 20, 50, 100, 200, 500, 1000)
  ) +
  coord_flip() +
  theme_bw() +
  theme(
    axis.title.y = element_blank(),
    axis.text.y = element_blank()
  )
# p_genome_ct

# Plot them all together
p4 <- plot_grid(p_bgc_dens, p_bgc_ct, p_genome_ct, align = "h", rel_widths = c(3, 1, 1), nrow = 1)
p4
```



```
ggsave("./figs/png/split_proportional.png", p4, width = 8, height = 11, device = "png")
```

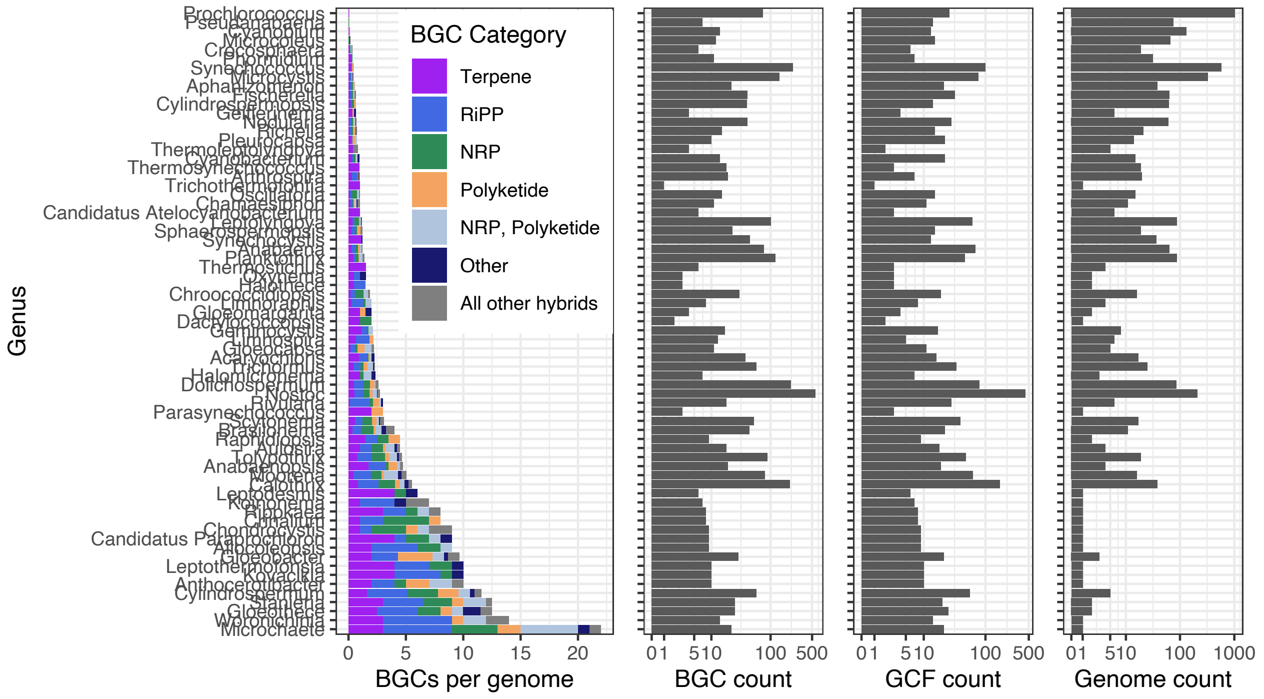
Plot the BGCs per genome (not normalized to 100%) alongside number of BGCs per genus and genomes per genus

```
# Prepare a dataframe specific to this set of plots
# df_plots <- tax_count %>%
#   filter(tax_genus != "Unclassified") %>%
#   left_join(genomes_by_genus, by = "tax_genus") %>%
```

```r
#   mutate(bgc_dens = num_bgcs / tot_genomes) %>%
#   group_by(tax_genus) %>%
#   mutate(tot_bgc_dens = sum(bgc_dens), tot_bgcs = sum(num_bgcs))

genus_order <- df_plots %>% ungroup() %>% mutate(tax_genus = fct_reorder(tax_genus, tot_bgc_dens, .desc

# Plot BGCs per genome, colored by category and divided by genus
p_bgc_dens <- df_plots %>%
  # ggplot(aes(x = fct_reorder(tax_genus, tot_bgc_dens, .desc = T))) +
  ggplot(aes(x = fct_relevel(tax_genus, genus_order))) +
  geom_col(aes(y = bgc_dens, fill = group), position = position_stack(reverse = TRUE)) +
  scale_y_continuous(name = "BGCs per genome") +
  scale_x_discrete(name = "Genus") +
  scale_fill_manual(name = "BGC Category", values = cat_colors) +
  coord_flip() +
  guides(fill = guide_legend(position = "inside")) +
  theme_bw() +
  theme(legend.justification.inside = c(0.99, 0.99))
# p_bgc_dens

# Plot total BGC count by genus
p_bgc_ct <- df_plots %>%
  # ggplot(aes(x = fct_reorder(tax_genus, tot_bgc_dens, .desc = T))) +
  ggplot(aes(x = fct_relevel(tax_genus, genus_order))) +
  geom_col(aes(y = tot_bgcs), data = df_plots %>% select(tax_genus, tot_bgcs, tot_bgc_dens) %>% distinc
  scale_y_continuous(
    name = "BGC count",
    trans = transform_pseudo_log(base = 10),
    breaks = c(0, 1, 5, 10, 100, 500)
  ) +
  coord_flip() +
  theme_bw() +
  theme(
    axis.title.y = element_blank(),
    axis.text.y = element_blank()
  )

# Plot genome count by genus
# genome_counts <- df_plots %>%
#   group_by(tax_genus, tot_genomes) %>%
#   summarize(tot_bgc_dens = sum(bgc_dens), tot_bgcs = sum(num_bgcs)) %>%
#   arrange(tot_bgc_dens)
# genome_counts

p_genome_ct <- genome_counts %>%
  # ggplot(aes(x = fct_reorder(tax_genus, tot_bgc_dens, .desc = T))) +
  ggplot(aes(x = fct_relevel(tax_genus, genus_order))) +
  geom_col(aes(y = tot_genomes)) +
  scale_y_continuous(name = "Genome count", trans = scales::transform_pseudo_log(base = 10), breaks = c
  coord_flip() +
  theme_bw() +
  theme(
    axis.title.y = element_blank(),
    axis.text.y = element_blank()
  )
# p_genome_ct

p_gcf_ct <- gcf_df %>%
    filter(genus %in% genome_counts$tax_genus) %>%
    # mutate(genus = factor(genus, levels = genome_counts$tax_genus %>% as_factor() %>% fct_rev() %>% l
    ggplot(aes(x = fct_relevel(genus, genus_order))) +
    geom_col(aes(y = n_gcfs)) +
    scale_y_continuous(name = "GCF count", trans = scales::transform_pseudo_log(base = 10), breaks = c(
    coord_flip() +
    theme_bw() +
    theme(
        axis.title.y = element_blank(),
        axis.text.y = element_blank()
    )

# Plot them all together
p5 <- plot_grid(p_bgc_dens, p_bgc_ct, p_gcf_ct, p_genome_ct, align = "h", rel_widths = c(3, 1, 1, 1), n
df_plots
```

```
## # A tibble: 378 x 8
## # Groups:   tax_genus [69]
##    tax_genus  cats_str num_bgcs group tot_genomes bgc_dens tot_bgc_dens tot_bgcs
##    <chr>      <fct>       <int> <fct>       <dbl>    <dbl>        <dbl>    <int>
##  1 Acaryochl~ Terpene        16 Terp~          17    0.941         2.24       38
##  2 Acaryochl~ RiPP           12 RiPP           17    0.706         2.24       38
##  3 Acaryochl~ NRP             2 NRP            17    0.118         2.24       38
##  4 Acaryochl~ Polyket~        2 Poly~          17    0.118         2.24       38
##  5 Acaryochl~ NRP, Po~        2 NRP,~          17    0.118         2.24       38
##  6 Acaryochl~ Other           4 Other          17    0.235         2.24       38
##  7 Allocoleo~ Terpene         2 Terp~           1    2             9           9
##  8 Allocoleo~ RiPP            4 RiPP            1    4             9           9
##  9 Allocoleo~ NRP             2 NRP             1    2             9           9
## 10 Allocoleo~ NRP, Po~        1 NRP,~           1    1             9           9
## # i 368 more rows
```

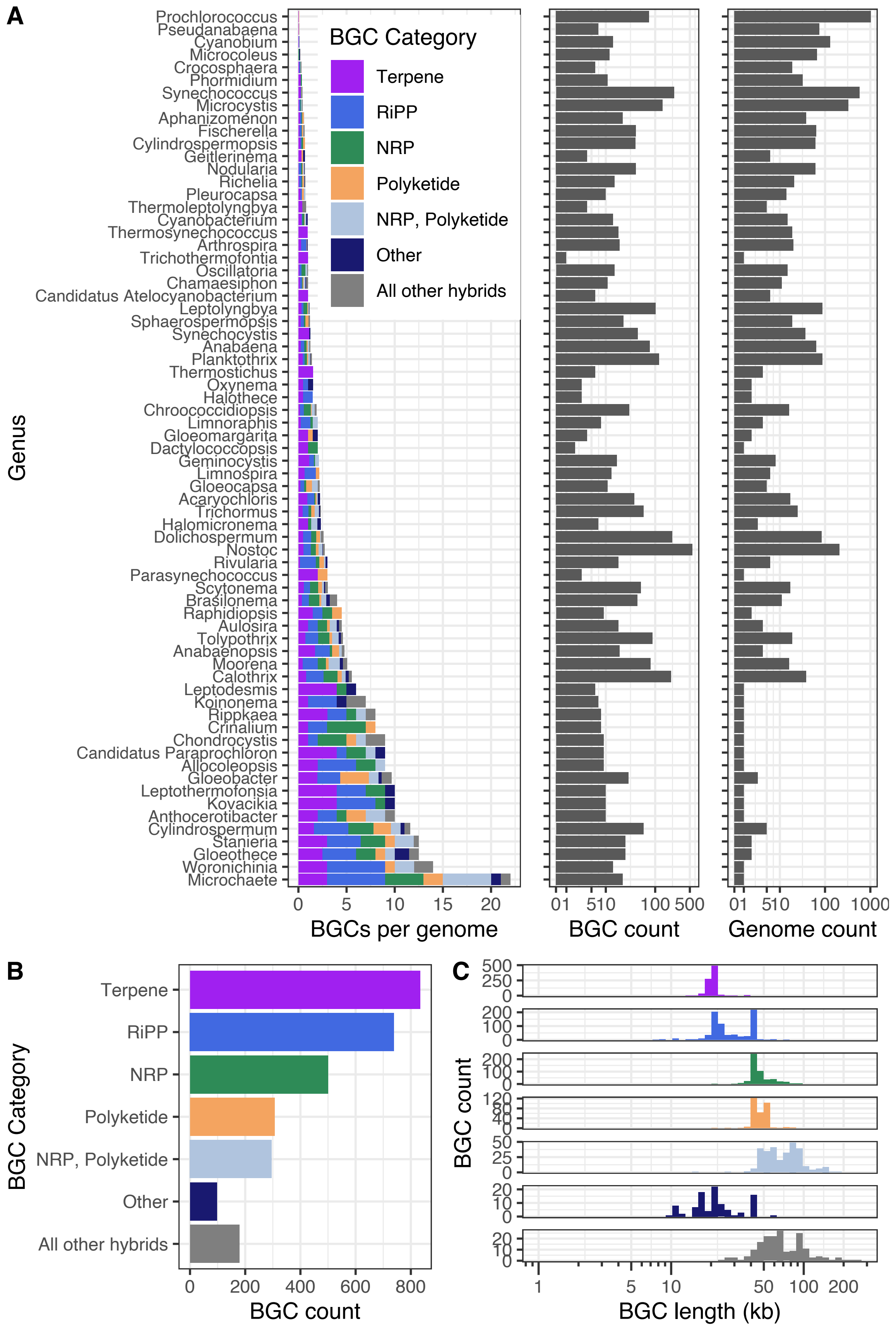
```
p5
```



```r
ggsave("./figs/png/split_triple.png", p5, width = 8, height = 11, device = "png")
```

Create Figure 2 for the manuscript

```r
p_a <- plot_grid(
    p_bgc_dens + theme(axis.text.y = element_text(size = 8)),
    p_bgc_ct,
    p_genome_ct,
    align = "h",
    rel_widths = c(3, 1, 1),
    nrow = 1
    )

p_b <- ggplot(
    region_summary_lumped,
    aes(y = reorder(group, n))
) +
  geom_col(aes(x = n, fill = group)) +
  scale_x_continuous(name = "BGC count", breaks = breaks_extended()) +
  scale_y_discrete(name = "BGC Category") +
  scale_fill_manual(values = cat_colors) +
  theme_bw() +
  guides(fill = "none")

p_c <- regions_lumped %>%
  # filter(group != "All other hybrids") %>%
  ggplot(aes(x = region_length / 1000)) +
      geom_histogram(aes(fill = group), bins = 50) +
      scale_x_log10(name = "BGC length (kb)", guide = "axis_logticks", limits = c(1, NA), breaks = c(1,
      scale_y_continuous(name = "BGC count", breaks = breaks_extended(n = 3)) +
      scale_fill_manual(values = cat_colors) +
      facet_wrap(vars(group), ncol = 1, scales = "free_y") +
      guides(fill = "none") +
      theme_bw() +
      theme(
        strip.background = element_blank(),
        strip.text = element_blank()
      )

bottom_row <- plot_grid(p_b, p_c, nrow = 1, labels = c("B", "C"), label_size = 12)

fig2 <- plot_grid(p_a, bottom_row, nrow = 2, labels = c("A", ""), label_size = 12, rel_heights = c(2.5,
fig2
```



A
Genus
Prochlorococcus
Pseudanabaena
Cyanobium
Microcoleus
Crocosphaera
Phormidium
Synechococcus
Microcystis
Aphanizomenon
Fischerella
Cylindrospermopsis
Geitlerinema
Nodularia
Richelia
Pleurocapsa
Thermoleptolyngbya
Cyanobacterium
Thermosynechococcus
Arthrospira
Trichothermofontia
Oscillatoria
Chamaesiphon
Candidatus Atelocyanobacterium
Leptolyngbya
Sphaerospermopsis
Synechocystis
Anabaena
Planktothrix
Thermostichus
Oxynema
Halothece
Chroococcidiopsis
Limnoraphis
Gloeomargarita
Dactylococcopsis
Geminocystis
Limnospira
Gloeocapsa
Acaryochloris
Trichormus
Halomicronema
Dolichospermum
Nostoc
Rivularia
Parasynechococcus
Scytonema
Brasilonema
Raphidiopsis
Aulosira
Tolypothrix
Anabaenopsis
Moorena
Calothrix
Leptodesmis
Koinonema
Rippkaea
Crinalium
Chondrocystis
Candidatus Paraprochloron
Allocoleopsis
Gloeobacter
Leptothermofonsia
Kovacikia
Anthocerotibacter
Cylindrospermum
Stanieria
Gloeothece
Woronichinia
Microchaete
BGC Category
Terpene
RiPP
NRP
Polyketide
NRP, Polyketide
Other
All other hybrids
0
5
10
15
20
BGCs per genome
01
510
100
500
BGC count
01
510
100
1000
Genome count
B
BGC Category
Terpene
RiPP
NRP
Polyketide
NRP, Polyketide
Other
All other hybrids
0
200
400
600
800
BGC count
C
BGC count
500
250
0
200
100
0
200
100
0
120
80
40
0
50
25
0
20
10
0
20
10
0
1
5
10
50
100
200
BGC length (kb)

```r
ggsave("./figs/_fig2.png", fig2, width = 6, height = 9, units = "in", device = "png")
ggsave("./figs/_fig2.pdf", fig2, width = 6, height = 9, units = "in", device = "pdf")
```