

# Range Weighted Branch Length Difference (RWiBaLD) Calculations & Figure Generation

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2025-01-29

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## 1 Introduction

This document contains code for calculating and plotting Range Weighted Branch Length Difference (RWiBaLD). It uses input from [Biodiverse](#) analyses of phylogenetic data. The method is related to the [Categorical Analysis of Neo And Paleo-Endemism \(CANAPE\)](#) published in 2014 and follows up on that paper. Consequently, the [acacia dataset from the CANAPE paper](#) is used to illustrate the method.

## 2 Load packages

Here we load the packages for use in subsequent code.

```

1 library(sf)
2 library(ggplot2)
3 library(Cairo)
4 library(extrafont)
5 library(dplyr)
6 library(ggrepel)
7 library(stringr)
8 library(patchwork)
9 library(forcats)
10 library(ggtree)
11 library(ape)
12 library(knitr)
13 library(gt)

```

## 3 The RWiBaLD metric

The steps for calculating RWiBaLD are as follows:

1. For each branch on the phylogeny (terminal or internal), calculate the difference between its branch length on the Range Weighted Observed Tree (RWoT), and its branch length on the Range Weighted Comparison Tree (RWcT) to generate its Range Weighted Branch Length Difference (RWiBaLD) score.
2. Identify the branches that contribute the most to PE; we call these the “highly endemic branches” or “branches of key interest”. These are defined as those with the smallest observed range sizes, i.e. the longest branches on the RWcT. We calculate this by ranking all branches according to the inverse of their range size (functionally the same as their lengths on the RWcT), plotting a straight line from the first to last points on that curve, then identifying the point on the distribution that is furthest from that line (figure 2A). Weighted ranges greater than or equal to the threshold are considered highly endemic.
3. The same elbow statistic is then applied separately to each half of the distribution of ranked RWiBaLD score values (divided at the RWiBaLD = 0 value) to identify branch length difference thresholds.

4. The classification is then applied to the highly endemic branches of step 2 using the thresholds from step 3. Highly endemic branches with negative differences less than or equal to the threshold are classified as neo-endemic, positive differences greater than or equal to the threshold are classified as paleo-endemic, and those between these two categories are classified as meso-endemic (figure 2B).

## 4 Specify biodiverse results data

Specify the tabular data files exported from a biodiverse analysis. Both the observed data & the equal branch length data from a range weighted tree.

```

1 # Set the data locations etc.
2 data_dir <- "Acacia_biodiverse_exports/"
3 observed_data_csv <- paste0(data_dir, "Acacia_RWT_tabular_export.csv")
4 equal_branch_length_data_csv <- paste0(data_dir, "Acacia_RWT_EQBL_tabular_export.csv")

```

## 5 Load data & calculate RWiBaLD

Load the data in, merge the tables and calculate the RWiBaLD score for each branch, then write out the results to a file.

```

1 # Load data
2 observed_data <- read.table(observed_data_csv, header=T, sep=",")
3 equal_branch_length_data <- read.table(equal_branch_length_data_csv, header=T, sep=",")
4
5 # Calculate RWiBaLD Statistic etc.
6 rwibald_results <- observed_data |>
7   left_join(equal_branch_length_data, by = 'NAME') |>
8   rename(branch_length_observed_tree = LENGTH.x, branch_length_comparison_tree = LENGTH.y) |>
9   mutate(rank_comparison_tree = rank(desc(branch_length_comparison_tree), ties.method = "min")) |>
10  mutate(sorted_asc_bl_comparison_tree = rank(branch_length_comparison_tree, ties.method = "first")) |>
11  mutate(rwibald_score = (branch_length_observed_tree - branch_length_comparison_tree)) |>
12  mutate(rwibald_score_rank = rank(rwibald_score, ties.method = "first"))
13
14 # View(rwibald_results)
15 output_dir <- "quarto_outputs/"
16
17 # Write data to file
18 write.csv(rwibald_results, paste0(output_dir, "Acacia_RWiBaLD_results.csv"), row.names=FALSE)

```

## 6 Elbow point calculation function

We propose a function to calculate the elbow point of a curve in order to determine branches of interest and identify the different categories of RWiBaLD (e.g., neo, meso, paleo).

It takes a numerical vector data as input and calculates the point where the rate of decrease in a measure of fit (e.g., sum of squared distances) starts to slow down. The function first orders the values of the data and calculates vectors from the first point to all other points, normalizing the vector from the first to the last point. It then computes the Euclidean distance of each point to this line and returns the y-coordinate (value) of the point with the maximum distance from the line, considered the “elbow” point threshold.

The procedure is described step by step below:

### 1. Function Definition and Input:

- The function `get_elbow` takes one argument, `data`, which is a numerical vector.

### 2. Initial Setup:

- `n_pts` is assigned the length of `data`.

- `x_coords` is a sequence from 1 to `n_pts`.
- `y_coords` is the values of data, sorted in ascending order.

### 3. First Point Coordinates:

- `x1` and `y1` are the coordinates of the first point in the sequence.

### 4. Normalize the Line Vector:

- `x_vec` and `y_vec` are vectors from the first point to all other points.
- `x_vec_max` and `y_vec_max` are the vectors from the first point to the last point.
- `normaliser` is the length of the line vector.
- Normalize `x_vec_max` and `y_vec_max` by dividing by `normaliser`.

### 5. Vectors from First Point:

- `v_x` and `v_y` are vectors from the first point to all other points.
- `scalar_prod` calculates the scalar projection of `v_x` and `v_y` onto the normalized line vector.

### 6. Calculate Distance to Line:

- `vec_to_line_x` and `vec_to_line_y` are the components of the vectors from each point to the line.
- `dist_to_line` is the Euclidean distance of each point to the line.

### 7. Return the Elbow Point Threshold:

- The function returns the y-coordinate (value) of the point with the maximum distance from the line, considered the “elbow” point threshold.

In summary, the function identifies the point in the data set that is farthest away from a line drawn between the first and last data points, which often corresponds to a significant change.

```

1 get_elbow <- function(data){
2
3   n_pts = length(data)
4
5   x_coords = 1:n_pts
6   y_coords = data[order(data)]
7
8   # First points
9   x1 = x_coords[1]
10  y1 = y_coords[1]
11
12  # Normalize the line vector
13  x_vec = x_coords - x1
14  y_vec = y_coords - y1
15  x_vec_max = x_vec[n_pts]
16  y_vec_max = y_vec[n_pts]
17
18  normaliser = sqrt(x_vec_max^2 + y_vec_max^2)
19
20  x_vec_max = x_vec_max / normaliser
21  y_vec_max = y_vec_max / normaliser
22
23  # Vectors from first point
24  v_x = x_coords - x1
25  v_y = y_coords - y1
26
27  scalar_prod = v_x * x_vec_max + v_y * y_vec_max
28
```

```

29     vec_to_line_x = v_x - scalar_prod * x_vec_max
30     vec_to_line_y = v_y - scalar_prod * y_vec_max
31
32     # Distance to line is the norm
33     dist_to_line = sqrt(vec_to_line_x^2 + vec_to_line_y^2)
34
35     # y value at the point of maximum distance from the hypotenuse
36     return(y_coords[which(dist_to_line==max(dist_to_line))])
37 }
```

## 7 Calculate branches of interest

Now we take the data and determine the key branches of interest using the elbow point statistic defined in the function above.

```

1 # For range weighted tree
2 df <- rwibald_results[,c("NAME", "rwibald_score", "rwibald_score_rank",
3                         "sorted_asc_bl_comparison_tree",
4                         "branch_length_comparison_tree",
5                         "branch_length_observed_tree")] %>%
6   arrange(., branch_length_comparison_tree)
7
8 # Call the get_elbow function to find the threshold
9 elbow_thresh <- get_elbow(df$branch_length_comparison_tree)
10
11 # Define key branches
12 key_branches <- df$branch_length_comparison_tree >= elbow_thresh
13
14 # Count them
15 number_of_key_branches <- sum(key_branches)
16
17 # Add a column to the results marking the branches of interest as 'sig'
18 rwibald_results_key <- rwibald_results %>%
19   arrange(., branch_length_comparison_tree) %>%
20   mutate(bl_comparison_tree_rwibald_elbow_key = ifelse(key_branches, 'key', 'not_key'))
21
22 # Merge data
23 rwibald_results_all <- merge(rwibald_results, rwibald_results_key[, 
24   c("NAME", "bl_comparison_tree_rwibald_elbow_key")], by=c('NAME', 'NAME'), all.x=T)
25
26 # View(rwibald_results_all)
27
28 # Print number of key branches
29 print(paste0("Number of key branches: ", number_of_key_branches))
```

```
[1] "Number of key branches: 135"
```

## 8 Generate figure 2A - RWiBaLD branches of interest

Now we plot the ranked branch lengths on the comparison tree showing the cut-off line for the key RWiBaLD branches of interest.

```

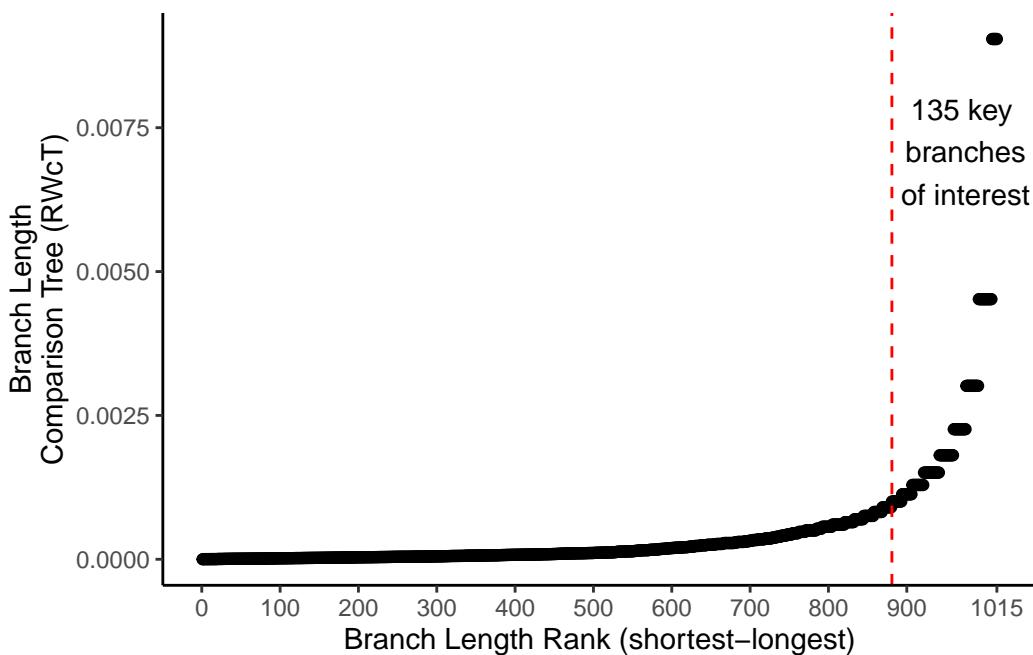
1 # Check the total number of branches
2 # length(df$branch_length_comparison_tree)
3
4 # Add x_marks every 100
5 x_marks <- c(0, 100, 200, 300, 400, 500, 600, 700, 800, 900, length(df$branch_length_comparison_tree))
```

```

6
7 branch_length_by_rank <- ggplot(df, aes(x = as.numeric(rownames(df)), y =
8   ↵ sort(branch_length_comparison_tree))) +
9   geom_point() +
10  geom_vline(xintercept = (length(df$branch_length_comparison_tree) - number_of_key_branches+1), color =
11    ↵ "red", linetype = "dashed") +
12  xlab("Branch Length Rank (shortest-longest)") +
13  ylab("Branch Length\\nComparison Tree (RWcT)") +
14  theme_classic() +
15  theme(plot.title = element_text(hjust = 0.5)) +
16  scale_x_continuous(breaks = x_marks, labels = x_marks) +
17  annotate("text", x = 970, y = 0.008, label = paste0(number_of_key_branches, " key\\n branches\\n of
    ↵ interest"), vjust = 1, hjust = 0.5)

print(branch_length_by_rank)

```



```

1 output_dir <- "quarto_outputs/"
2
3 ggsave(paste0(output_dir, "figures/Figure2_A.png"), plot = branch_length_by_rank, scale = 1,
4   width = 2048,
5   height = 1024,
6   units = "px",
7   dpi = 300)

```

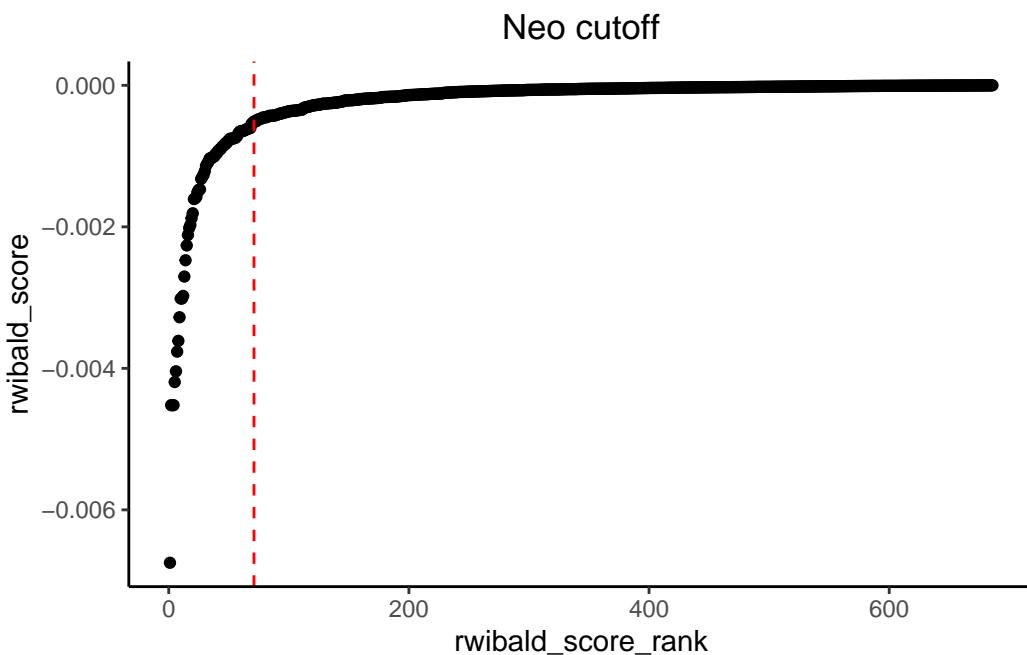
## 9 Calculate RWiBaLD branch categories (neo-endemic, meso-endemic, paleo-endemic)

Next we take the key branches of interest and define which of them are neo-endemic, meso-endemic or paleo-endemic. We use the same elbow statistic defined above but only consider the branches of key interest calculated above as valid. We split the data at 0 with those equal or below the elbow point threshold in the negative data being neo-endemics. Those in the positive dataset equal or above the elbow point threshold being classified as paleo-endemic, and rest are classified as meso-endemic. We have described three categories, but of course one could break the continuous distribution into further categories if required.

```

1 # Load the data
2 data <- rwibald_results_all[,c("NAME", "bl_comparison_tree_rwibald_elbow_key", "rwibald_score",
3   ↪ "rwibald_score_rank")] %>%
4   arrange(., rwibald_score_rank)
5
6 # Subset the left and right dataframes
7 subset_left_df <- data[data$rwibald_score <= 0, ]
8 subset_right_df <- data[data$rwibald_score >= 0, ]
9
10 # Create a list to store the results for the table
11 results <- list()
12
13 # Records in negative data
14 negative_records <- nrow(subset_left_df)
15 results$Negative_Records <- negative_records
16
17 # Neo cutoff
18 left_point_x <- get_elbow(subset_left_df$rwibald_score)
19 rwibald_score_rank_at_left_point <- subset_left_df[subset_left_df$rwibald_score == left_point_x,
20   ↪ "rwibald_score_rank"]
21 results$Neo_Cutoff <- rwibald_score_rank_at_left_point
22
23 # Plot for left half of curve
24 l <- ggplot(subset_left_df, aes(x = rwibald_score_rank, y = rwibald_score)) +
25   geom_point() +
26   geom_vline(xintercept = rwibald_score_rank_at_left_point, color = "red", linetype = "dashed") +
27   ggtitle(label = "Neo cutoff") +
28   theme_classic() +
29   theme(plot.title = element_text(hjust = 0.5))
30 print(l)

```



```

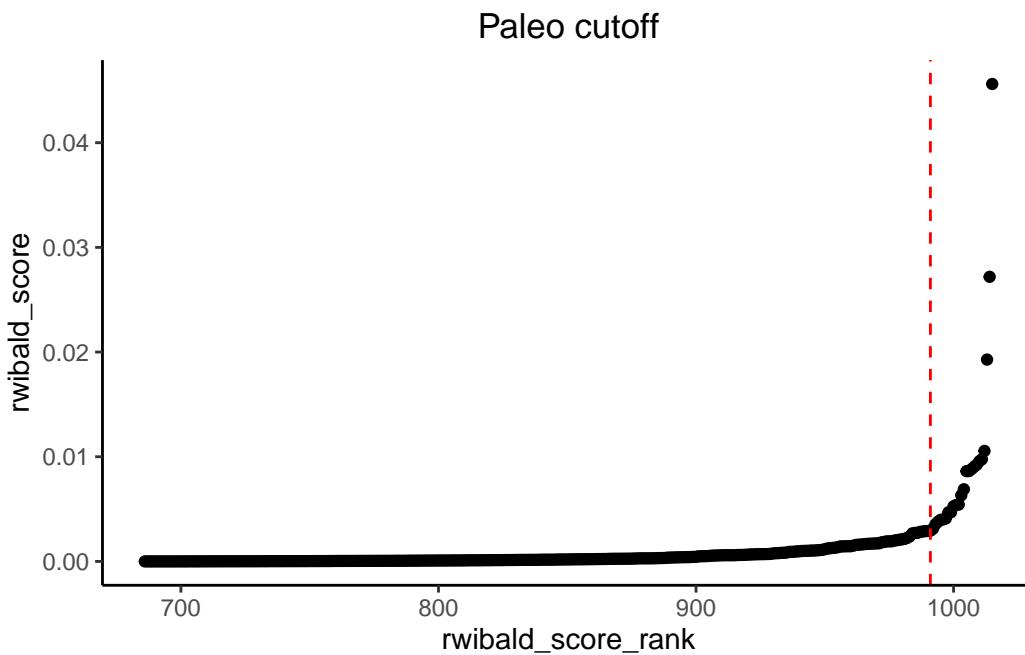
1 # Records in positive data
2 positive_records <- nrow(subset_right_df)
3 results$Positive_Records <- positive_records

```

```

4
5 # Paleo cutoff
6 right_point_x <- get_elbow(subset_right_df$rwibald_score)
7 rwibald_score_rank_at_right_point <- subset_right_df[subset_right_df$rwibald_score == right_point_x,
   ↴ "rwibald_score_rank"]
8 results$Paleo_Cutoff <- rwibald_score_rank_at_right_point
9
10 # Plot for right half of curve
11 r <- ggplot(subset_right_df, aes(x = rwibald_score_rank, y = rwibald_score)) +
12   geom_point() +
13   geom_vline(xintercept = rwibald_score_rank_at_right_point, color = "red", linetype = "dashed") +
14   ggtitle(label= "Paleo cutoff") +
15   theme_classic() +
16   theme(plot.title = element_text(hjust = 0.5))
17 print(r)

```



```

1 # Create a column with the results
2 rwibald_results_key_type <- rwibald_results_all %>%
3   filter(bl_comparison_tree_rwibald_elbow_key == "key") %>%
4   mutate(rwibald_type = case_when(rwibald_score_rank <= rwibald_score_rank_at_left_point ~ "neo-endemic",
5   ↴
6   ↴
7   ↴ "paleo-endemic",
8   ↴ TRUE ~ "meso-endemic")) %>%
9   select(NAME, rwibald_type)
10
11 # Convert the results list to a dataframe for gt
12 summary_results_df <- as.data.frame(t(sapply(results, c)))
13 results_gt <- gt(data = summary_results_df)
14
15 # Display the table
16 results_gt %>%
17   tab_header(title = "Summary of Records and Cutoffs") %>%
18   fmt_number(columns = everything(), decimals = 0) %>%

```

```

17   tab_style(style = cell_text(align = "center"),
18             locations = cells_body()
19           )
20
21 # View(rwibald_results_key_type)
22
23 # Merge the data
24 rwibald_results_all <- merge(rwibald_results_all, rwibald_results_key_type[, c("NAME","rwibald_type")],
25   by=c('NAME', 'NAME'), all.x=T)
26
27 # View(rwibald_results_all)
28 output_dir <- "quarto_outputs/"
29
30 # Write data to file
31 write.csv(rwibald_results_all,paste0(output_dir, "Acacia_RWiBaLD_results_all.csv") ,row.names=FALSE)

```

### Summary of Records and Cutoffs

Negative_Records	Neo_Cutoff	Positive_Records	Paleo_Cutoff
686	71	330	991

## 10 Load RWiBaLD results & tree data by cells

Now we load the data for the RWiBaLD results and the range weighted tree data in tabular format and then replace the counts in the matrix with the branch lengths for that group so we can generate the histograms for each grid cell location. We also add the CANAPE scores to the data table for comparison and calculate the ranges of each branch.

```

1 data_dir <- "Acacia_biodiverse_exports/"
2 output_dir <- "quarto_outputs/"
3
4 # Data with internal branches (spatial anaylsis from BD) x grid cells
5 all_tree_data_csv <- paste0(data_dir, "Acacia_PD_Included_Node_List.csv")
6 RWiBaLD_results_csv <- paste0(output_dir, "Acacia_RWiBaLD_results_all.csv")
7
8 all_tree_data <- read.table(all_tree_data_csv, header=T, sep=",", check.names = FALSE )
9 RWiBaLD_results <- read.table(RWiBaLD_results_csv, header=T, sep=",")
10
11 #View(all_tree_data)
12 #View(RWiBaLD_results)
13 valueToUse <- "rwibald_score"
14
15 # Iterate over the columns in Table 1
16 for (col in colnames(all_tree_data)[-c(1:3)]) {
17   # get the corresponding "valueToUse" column specified above from Table 2
18   branch_length <- RWiBaLD_results[RWiBaLD_results$NAME == col, paste0(valueToUse)]
19   # replace the numbers in Table 1 with the "valueToUse" value
20   all_tree_data[, col] <- ifelse(is.na(all_tree_data[, col]), NA, as.numeric(branch_length))
21 }
22
23 # View(all_tree_data)
24
25 # Write data to file
26 write.csv(all_tree_data, paste0(output_dir, "Acacia_PD_Included_Node_List_", valueToUse, ".csv"),
27   row.names=FALSE)

```

```

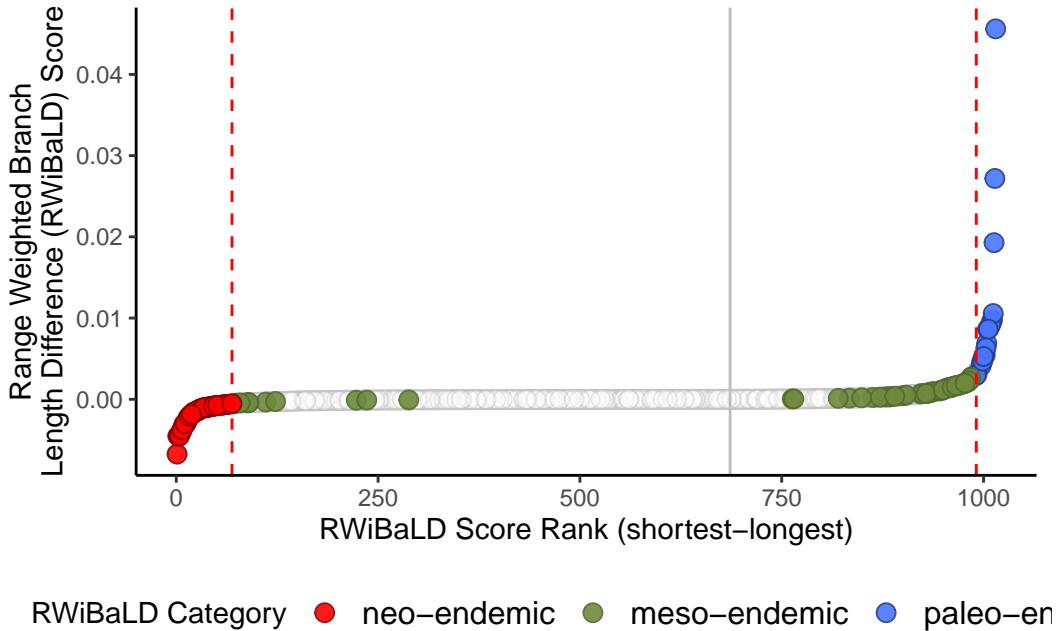
28 # Get CANAPE data from biodiverse as well
29 canape_csv <- paste0(data_dir, "Acacia_Rand1_CANAPE_Export.csv")
30 canape_results <- read.table(canape_csv, header=T, sep=",")
31
32 # View(canape_results)
33
34 canape_group_data <- canape_results %>%
35   left_join(all_tree_data %>%
36     select(-c(Axis_0, Axis_1)), by = "ELEMENT"
37   )
38
39 # Transpose the dataframe
40 data <- t(canape_group_data)
41
42 # View(data)
43
44 # Set the first row as column names
45 transposed_df <- setNames(data.frame(data[-1,]), data[1,])
46
47 # View(transposed_df)
48
49 # Merge CANAPE and RWiBaLD data
50 canape_group_data_rwibald <- transposed_df %>%
51   mutate(range_cell_count = rowSums(!is.na(.))) %>%
52   tibble::rownames_to_column(var = "NAME") %>%
53   left_join(select(rwibald_results_all, NAME, rwibald_type), by = 'NAME') %>%
54   mutate(rwibald_type = ifelse(is.na(rwibald_type), "other", rwibald_type))
55
56 # Set row names
57 rownames(canape_group_data_rwibald) <- canape_group_data_rwibald$NAME
58
59 # View(canape_group_data_rwibald)
60
61 # # Add range data to results
62 # rwibald_results_all_with_range <- rwibald_results_all %>%
63 #   left_join(select(canape_group_data_rwibald, NAME, range_cell_count), by = "NAME") %>%
64 #   mutate(rwibald_type = replace(rwibald_type, is.na(rwibald_type), "other"))
65
66 # Add range data to results and create three new columns
67 rwibald_results_all_with_range <- rwibald_results_all %>%
68   left_join(select(canape_group_data_rwibald, NAME, range_cell_count), by = "NAME") %>%
69   mutate(rwibald_type = replace(rwibald_type, is.na(rwibald_type), "other"),
70     non_range_weighted_branch_length_observed_tree = branch_length_observed_tree * range_cell_count,
71     non_range_weighted_branch_length_comparison_tree = branch_length_comparison_tree *
72       ↵ range_cell_count,
73     diff_non_range_weighted_observed_to_comparison_bl =
74       ↵ non_range_weighted_branch_length_observed_tree -
75       ↵ non_range_weighted_branch_length_comparison_tree
76   ) %>%
77   mutate(rank_BaLD = rank(diff_non_range_weighted_observed_to_comparison_bl, ties.method = "first"))
78
79
80 # Write data to file
81 write.csv(rwibald_results_all_with_range, paste0(output_dir,
82   "Acacia_RWiBaLD_results_all_with_range.csv"), row.names=FALSE)
83
84 # View(rwibald_results_all_with_range)
85 # View(rwibald_results_all)

```

## 11 Generate figure 2B - ranked RWiBaLD score by RWiBaLD score

Here we plot the ranked RWiBaLD score (x) by the RWiBaLD score (y) (Figure 2B), colouring the different RWiBaLD Categories: neo-endemic (red), meso-endemic (darkolivegreen4) and paleo-endemic (royalblue1).

```
1 # Find the neo_cutoff
2 neo_cutoff <- rwibald_results_all_with_range %>%
3   filter(rwibald_type == "neo-endemic") %>%
4   summarize(highest_rank = max(rwibald_score_rank, na.rm = TRUE)) %>%
5   pull(highest_rank)
6
7 # Find the paleo_cutoff
8 paleo_cutoff <- rwibald_results_all_with_range %>%
9   filter(rwibald_type == "paleo-endemic") %>%
10  summarize(lowest_rank = min(rwibald_score_rank, na.rm = TRUE)) %>%
11  pull(lowest_rank)
12
13 # Get only the rwibald branches of key interest
14 rwibald_results_all_key_only <- rwibald_results_all_with_range %>%
15   filter(bl_comparison_tree_rwibald_elbow_key == "key")
16
17 # View(rwibald_results_all_key_only)
18 # View(rwibald_results_all_with_range)
19
20 # Plot rwibald rank X rwibald score
21 rwibald_key_plot <- ggplot() +
22   geom_point(data=rwibald_results_all_with_range, aes(x = rwibald_score_rank, y = rwibald_score),
23   ↪ fill="transparent", size = 3, colour= "grey77", alpha = 0.4, pch = 21) +
24   geom_point(data = rwibald_results_all_key_only, aes(x = rwibald_score_rank, y = rwibald_score, fill =
25   ↪ rwibald_type, color = rwibald_type), size = 3, alpha = 0.9, pch = 21) +
26   scale_fill_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue1", "neo-endemic" =
27   ↪ "red", "meso-endemic" = "darkolivegreen4"), labels = c("neo-endemic","meso-endemic",
28   ↪ "paleo-endemic"), limits = c("neo-endemic","meso-endemic", "paleo-endemic"), na.value =
29   ↪ "transparent") +
30   scale_color_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue4", "neo-endemic"
31   ↪ = "red4", "meso-endemic" = "darkolivegreen"), labels = c("neo-endemic", "meso-endemic",
32   ↪ "paleo-endemic"), limits = c("neo-endemic", "meso-endemic", "paleo-endemic"), na.value =
33   ↪ "transparent") +
34   geom_vline(xintercept = neo_cutoff, color = "red", linetype = "dashed") +
35   geom_vline(xintercept = paleo_cutoff, color = "red", linetype = "dashed") +
36   xlab("RWiBaLD Score Rank (shortest-longest)") +
37   ylab("Range Weighted Branch\nLength Difference (RWiBaLD) Score") +
38   #annotate("segment", x = results$Negative_Records, xend = results$Negative_Records,
39   #         y = max(rwibald_results_all_with_range$rwibald_score) * 1.1, yend = 0,
40   #         arrow = arrow(length = unit(0.2, "cm")), color = "grey74") +
41   geom_vline(xintercept = results$Negative_Records, color = "grey74", linetype = "solid") +
42   theme_classic() +
43   theme(plot.title = element_text(hjust = 0.5), legend.position="bottom", legend.text = element_text(size
44   ↪ = 12))
45
46 print(rwibald_key_plot)
```



```

1 ggsave("quarto_outputs/figures/Figure2_B.png", plot = rwibald_key_plot, scale = 1,
2   width = 2048,
3   height = 1024,
4   units = "px",
5   dpi = 300)

```

## 12 Generate figure 2C - ranked BaLD by BaLD (non range weighted)

Illustrating the distribution of branch lengths on the observed tree with no range-weighting; the Y-axis is the difference between length on the observed tree and length on the comparison tree for each branch; the X-axis is ranked branch length difference (shortest - longest). The branches of interest are colored by RWiBaLD category as in 2B

```

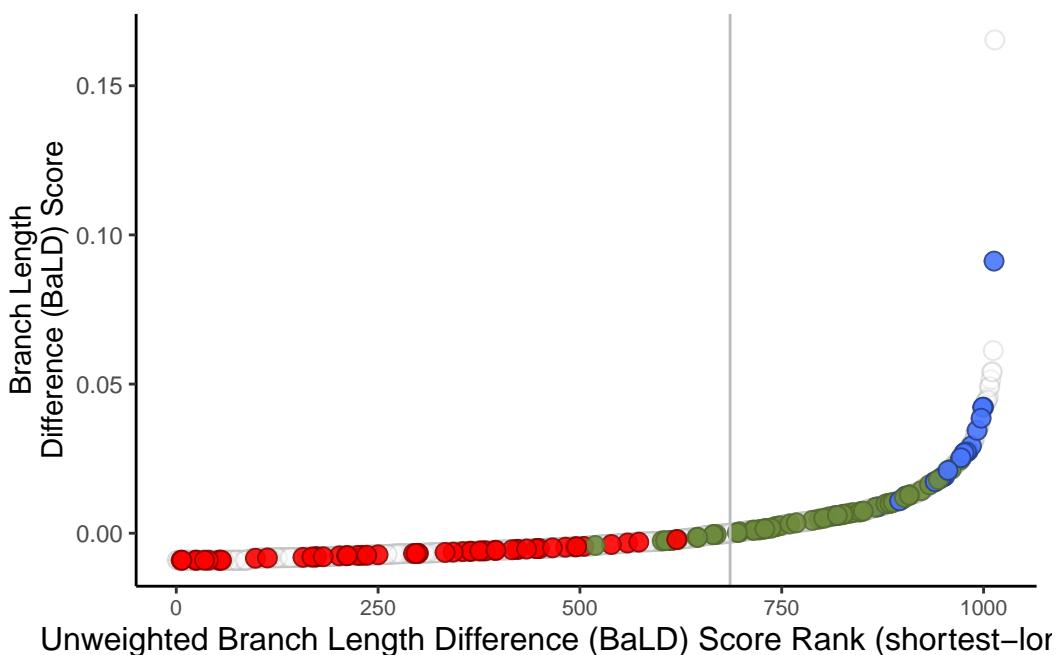
1 #View(rwibald_results_all_with_range)
2
3 #View(rwibald_results_all_key_only)
4
5 # Plot non_range_weighted score
6 rwibald_key_plot_non_range_weighted <- ggplot() +
7   #geom_point(data=rwibald_results_all_with_range, aes(x =
8   #  reorder(non_range_weighted_branch_length_observed_tree,
8   #  non_range_weighted_branch_length_observed_tree), y =
8   #  diff_non_range_weighted_observed_to_comparison_bl), fill="transparent", size = 3, colour=
8   #  "grey77", alpha = 0.4, pch = 21) +
9   geom_point(data=rwibald_results_all_with_range, aes(x = rank_BaLD, y =
9   #  diff_non_range_weighted_observed_to_comparison_bl), fill="transparent", size = 3, colour= "grey77",
9   #  alpha = 0.4, pch = 21) +
10  geom_point(data = rwibald_results_all_key_only, aes(x = rank_BaLD, y =
10  #  diff_non_range_weighted_observed_to_comparison_bl, fill = rwibald_type, color = rwibald_type), size
10  #  = 3, alpha = 0.9, pch = 21) +
11  scale_fill_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue1", "neo-endemic" =
11  #  "red", "meso-endemic" = "darkolivegreen4"), labels = c("neo-endemic","meso-endemic",
11  #  "paleo-endemic"), limits = c("neo-endemic","meso-endemic", "paleo-endemic"), na.value =
11  #  "transparent") +

```

```

11 scale_color_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue4", "neo-endemic"
12   = "red4", "meso-endemic" = "darkolivegreen"), labels = c("neo-endemic", "meso-endemic",
13   "paleo-endemic"), limits = c("neo-endemic", "meso-endemic", "paleo-endemic"), na.value =
14   "transparent") +
15 #geom_vline(xintercept = neo_cutoff, color = "red", linetype = "dashed") +
16 #geom_vline(xintercept = paleo_cutoff, color = "red", linetype = "dashed") +
17 xlab("Unweighted Branch Length Difference (BaLD) Score Rank (shortest-longest)") +
18 ylab("Branch Length\ndifference (BaLD) Score") +
19 geom_vline(xintercept = results$Negative_Records, color = "grey74", linetype = "solid") +
20 theme_classic() +
21 theme(plot.title = element_text(hjust = 0.5), legend.position="none", legend.text = element_text(size =
22   12), axis.title.x = element_text(size = 12), axis.text.x = element_text(size = 8))
23
24 print(rwibald_key_plot_non_range_weighted)

```



```

1 ggsave("quarto_outputs/figures/Figure2_C.png", plot = rwibald_key_plot_non_range_weighted, scale = 1,
2   width = 2048,
3   height = 1024,
4   units = "px",
5   dpi = 300)

```

### 13 Generate multi-panel figure 2ABC

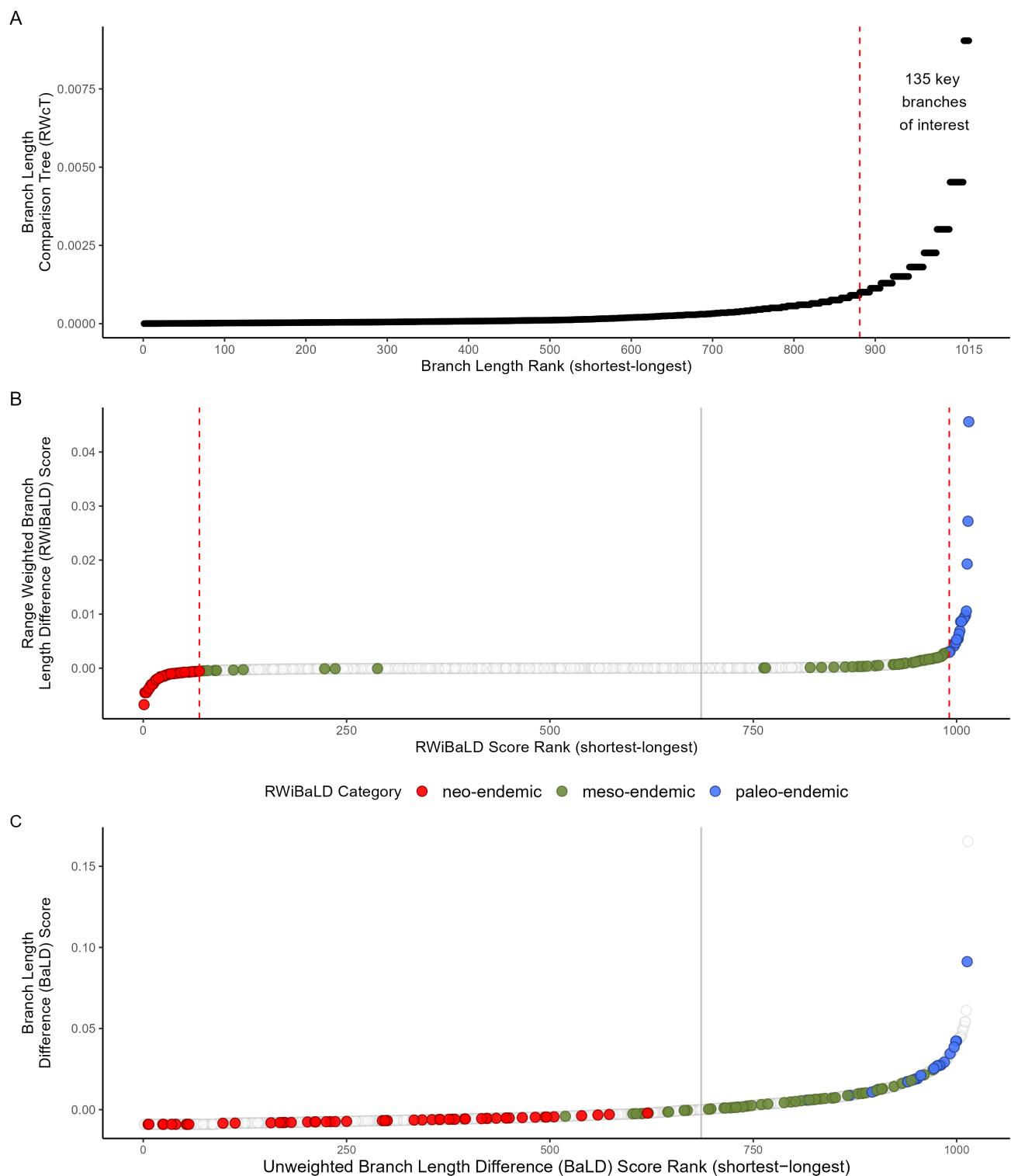
Here we generate a 2 up figure using patchwork

```

1 patchwork <- branch_length_by_rank / rwibald_key_plot / rwibald_key_plot_non_range_weighted +
2   plot_annotation(
3     title = 'Branches of Interest for Range Weighted Branch Length Difference (RWiBaLD)\n&\nRWiBaLD Scores
4     With Categories Calculated Using Elbow Statistic',
5     theme = theme(plot.title = element_text(hjust = 0.5)),
6     subtitle = '',
7     caption = '',
8     ...
9   )

```

```
6 tag_levels = 'A') +
7   theme(plot.tag.position = c(0, 1),
8     plot.tag = element_text(size = 12, hjust = 0, vjust = 0))
9
10 #print(patchwork)
11
12 ggsave("quarto_outputs/figures/Figure2_ABC.png", patchwork, width = 3000, height = 3600, units = "px")
```



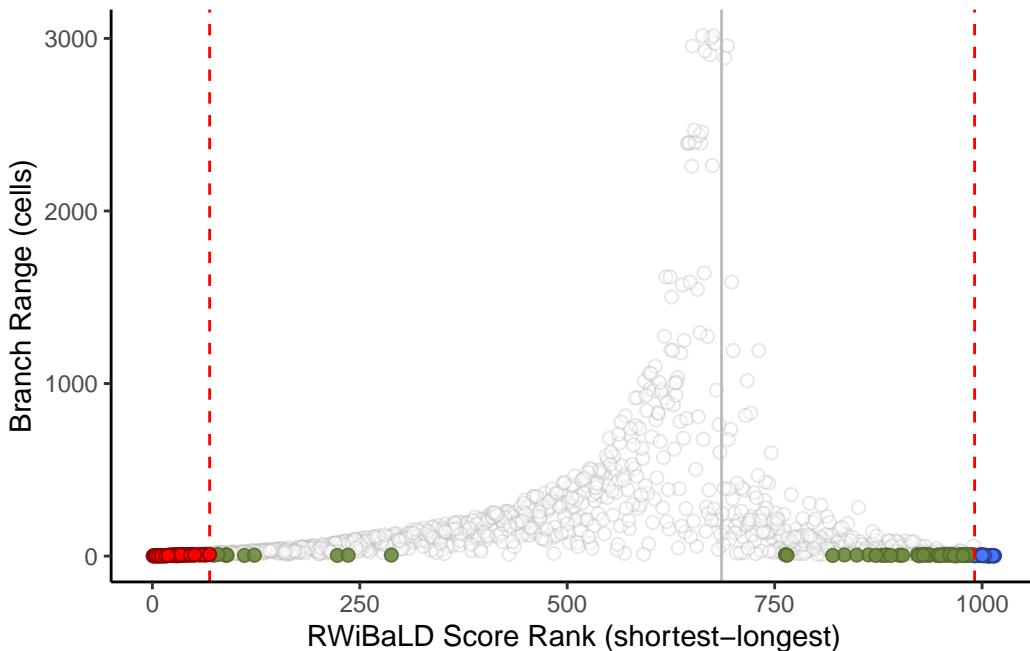
## 14 Generate Figure 3A

Here we create a plot of RWiBaLD score (x) by branch range (cells) (Figure 3A), coloured by RWiBaLD Categories: neo-endemic (red), meso-endemic (green) and paleo-endemic (blue).

```

1 # Plot RWiBaLD rank X branch range
2 rwibald_key_plot_range <- ggplot() +
3   geom_point(data=rwibald_results_all_with_range, aes(x = rwibald_score_rank, y = range_cell_count),
4   ↪   fill="transparent", size = 2, colour= "grey77", alpha = 0.4, pch = 21) +
5   geom_point(data = rwibald_results_all_key_only, aes(x = rwibald_score_rank, y = range_cell_count, fill
6   ↪   = rwibald_type, color = rwibald_type), size = 2, alpha = 0.9, pch = 21) +
7   scale_fill_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue1","neo-endemic" =
8   ↪   "red", "meso-endemic" = "darkolivegreen4"), labels = c("neo-endemic","meso-endemic",
9   ↪   "paleo-endemic"), limits = c("neo-endemic","meso-endemic", "paleo-endemic"), na.value =
10  ↪   "transparent") +
11  scale_color_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue4", "neo-endemic"
12  ↪   = "red4", "meso-endemic" = "darkolivegreen"), labels = c("neo-endemic", "meso-endemic",
13  ↪   "paleo-endemic"), limits = c("neo-endemic", "meso-endemic", "paleo-endemic"), na.value =
14  ↪   "transparent") +
15  geom_vline(xintercept = neo_cutoff, color = "red", linetype = "dashed") +
16  geom_vline(xintercept = paleo_cutoff, color = "red", linetype = "dashed") +
17  geom_vline(xintercept = results$Negative_Records, color = "grey74", linetype = "solid") +
18  xlab("RWiBaLD Score Rank (shortest-longest)") +
19  ylab("Branch Range (cells)") +
20  theme_classic() +
21  theme(plot.title = element_text(hjust =1),
22    legend.position="none",
23    legend.text = element_text(size = rel(1)),
24    legend.title = element_text(size = rel(1)),
25    axis.title.x = element_text(size = rel(1)),
26    axis.title.y = element_text(size = rel(1)),
27    axis.text.x = element_text(size = rel(1)),
28    axis.text.y = element_text(size = rel(1)))
29
30 print(rwibald_key_plot_range)

```



```

1 ggsave("quarto_outputs/figures/Figure3_A.png", plot = rwibald_key_plot_range, scale = 1,
2       width = 2048,
3       height = 1024,
4       units = "px",
5       dpi = 300)

```

## 15 Generate Figure 3B

Now the same data as figure 3A but first removing all internal branches before plotting the data. Note: the neo / meso /paleo cutoffs are calculated on the whole dataset and the filtering to terminals done after that.

```

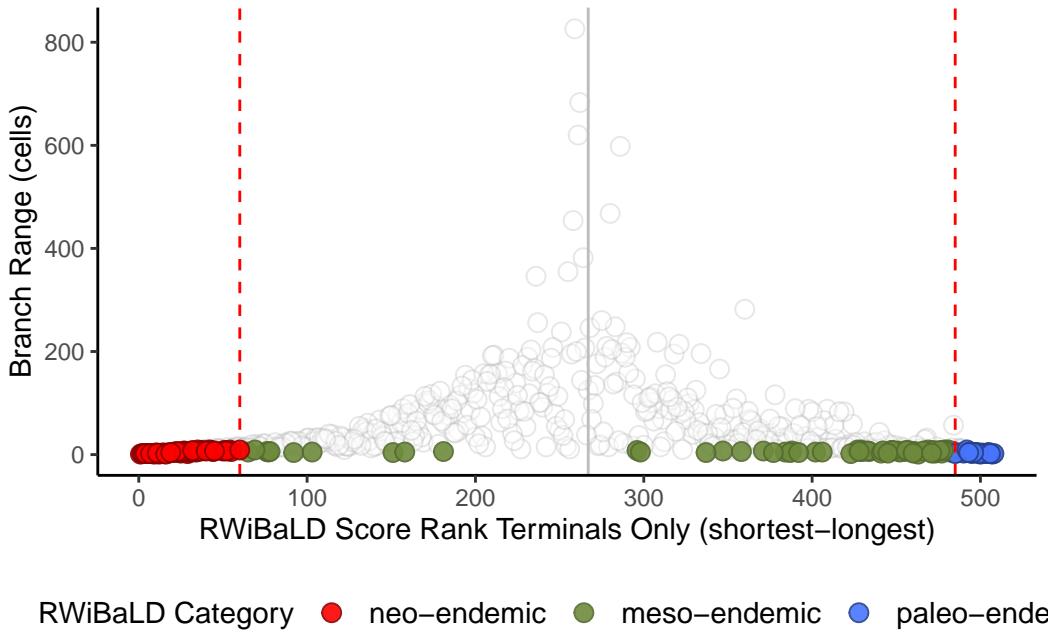
1 # For plotting purposes get only the rwibald branches of key interest and terminals only
2 rwibald_results_all_key_only_terminals <- rwibald_results_all_with_range %>%
3   filter(!grepl("^[0-9]", NAME)) %>%
4   mutate(rwibald_score_rank_terminals = rank(rwibald_score, ties.method = "first")) %>%
5   filter(bl_comparison_tree_rwibald_elbow_key == "key")
6
7 rwibald_results_all_with_range_terminals <- rwibald_results_all_with_range %>%
8   filter(!grepl("^[0-9]", NAME)) %>%
9   mutate(rwibald_score_rank_terminals = rank(rwibald_score, ties.method = "first"))
10
11 # Find the neo_cutoff
12 neo_cutoff_terms <- rwibald_results_all_with_range_terminals %>%
13   filter(rwibald_type == "neo-endemic") %>%
14   summarize(highest_rank = max(rwibald_score_rank_terminals, na.rm = TRUE)) %>%
15   pull(highest_rank)
16
17 # Find the paleo_cutoff
18 paleo_cutoff_terms <- rwibald_results_all_with_range_terminals %>%
19   filter(rwibald_type == "paleo-endemic") %>%
20   summarize(lowest_rank = min(rwibald_score_rank_terminals, na.rm = TRUE)) %>%
21   pull(lowest_rank)
22
23 # Subset the left and right dataframes
24 subset_left_df_terms <-
25   ↳ rwibald_results_all_with_range_terminals[rwibald_results_all_with_range_terminals$rwibald_score <= 0,
26   ↳ ]
27
28 # Records in negative data
29 negative_records_terms <- nrow(subset_left_df_terms)
30
31 # View(rwibald_results_all_key_only_terminals)
32 # View(rwibald_results_all_with_range_terminals)
33
34 # View(rwibald_results_all_with_range)
35
36 # Plot rwibald rank x rwibald score
37 # rwibald_key_plot_terminals <- ggplot() +
38 #   geom_point(data=rwibald_results_all_with_range_terminals, aes(x = rwibald_score_rank_terminals, y =
39 #     ↳ rwibald_score), fill="transparent", size =3, colour= "grey77", alpha = 0.4, pch=21) +
40 #   geom_point(data = rwibald_results_all_key_only_terminals, aes(x = rwibald_score_rank_terminals, y =
41 #     ↳ rwibald_score, fill = rwibald_type, color = rwibald_type), size =3, alpha = 0.9, pch=21) +
42 #   scale_fill_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue1", "neo-endemic"
43 #     ↳ = "red", "meso-endemic" = "darkolivegreen4"), labels = c("neo-endemic","meso-endemic",
44 #     ↳ "paleo-endemic"), limits = c("neo-endemic","meso-endemic", "paleo-endemic"), na.value =
45 #     ↳ "transparent") +
46 #   scale_color_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue4",
47 #     ↳ "neo-endemic" = "red4", "meso-endemic" = "darkolivegreen"), labels = c("neo-endemic", "meso-endemic",
48 #     ↳ "paleo-endemic"), limits = c("neo-endemic", "meso-endemic", "paleo-endemic"), na.value =
49 #     ↳ "transparent") +

```

```

40 #   geom_vline(xintercept = neo_cutoff, color = "red", linetype = "dashed") +
41 #   geom_vline(xintercept = paleo_cutoff, color = "red", linetype = "dashed") +
42 #   xlab("RWiBaLD Score Rank Terminals Only (shortest-longest)") +
43 #   ylab("Range Weighted Branch\nLength Difference (RWiBaLD) Score") +
44 #   theme_classic() +
45 #   theme(plot.title = element_text(hjust = 0.5), legend.position="bottom", legend.text =
46 #         element_text(size = 12))
47 #
48 # print(rwibald_key_plot_terminals)
49 #
50 # ggsave("quarto_outputs/figures/Figure3_B_terminals_only.png", plot = rwibald_key_plot_terminals, scale
51 #        = 1,
52 #        width = 2048,
53 #        height = 1024,
54 #        units = "px",
55 #        dpi = 300)
56 #
56 # Plot rwibald rank x branch range
57 rwibald_key_plot_range_terminals <- ggplot() +
58   geom_point(data=rwibald_results_all_with_range_terminals, aes(x = rwibald_score_rank_terminals, y =
59   range_cell_count), fill="transparent", size =3, colour= "grey77", alpha = 0.4, pch=21) +
60   geom_point(data = rwibald_results_all_key_only_terminals, aes(x = rwibald_score_rank_terminals, y =
61   range_cell_count, fill = rwibald_type, color = rwibald_type), size =3, alpha = 0.9, pch=21) +
62   scale_fill_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue1","neo-endemic" =
63   "red", "meso-endemic" = "darkolivegreen4"), labels = c("neo-endemic","meso-endemic",
64   "paleo-endemic"), limits = c("neo-endemic","meso-endemic", "paleo-endemic"), na.value =
65   "transparent") +
66   scale_color_manual(name = "RWiBaLD Category", values = c("paleo-endemic" = "royalblue4", "neo-endemic"
67   "red4", "meso-endemic" = "darkolivegreen"), labels = c("neo-endemic", "meso-endemic",
68   "paleo-endemic"), limits = c("neo-endemic", "meso-endemic", "paleo-endemic"), na.value =
69   "transparent") +
70   geom_vline(xintercept = neo_cutoff_terms, color = "red", linetype = "dashed") +
71   geom_vline(xintercept = paleo_cutoff_terms, color = "red", linetype = "dashed") +
72   geom_vline(xintercept = negative_records_terms, color = "grey74", linetype = "solid") +
73   xlab("RWiBaLD Score Rank Terminals Only (shortest-longest)") +
74   ylab("Branch Range (cells)") +
75   theme_classic() +
76   theme(plot.title = element_text(hjust = 0.5), legend.position="bottom", legend.text =
77   element_text(size=rel(1)))
78 #
79 print(rwibald_key_plot_range_terminals)

```



```

1 ggsave("quarto_outputs/figures/Figure3_B.png", plot = rwibald_key_plot_range_terminals, scale = 1,
2   width = 2048,
3   height = 1024,
4   units = "px",
5   dpi = 300)

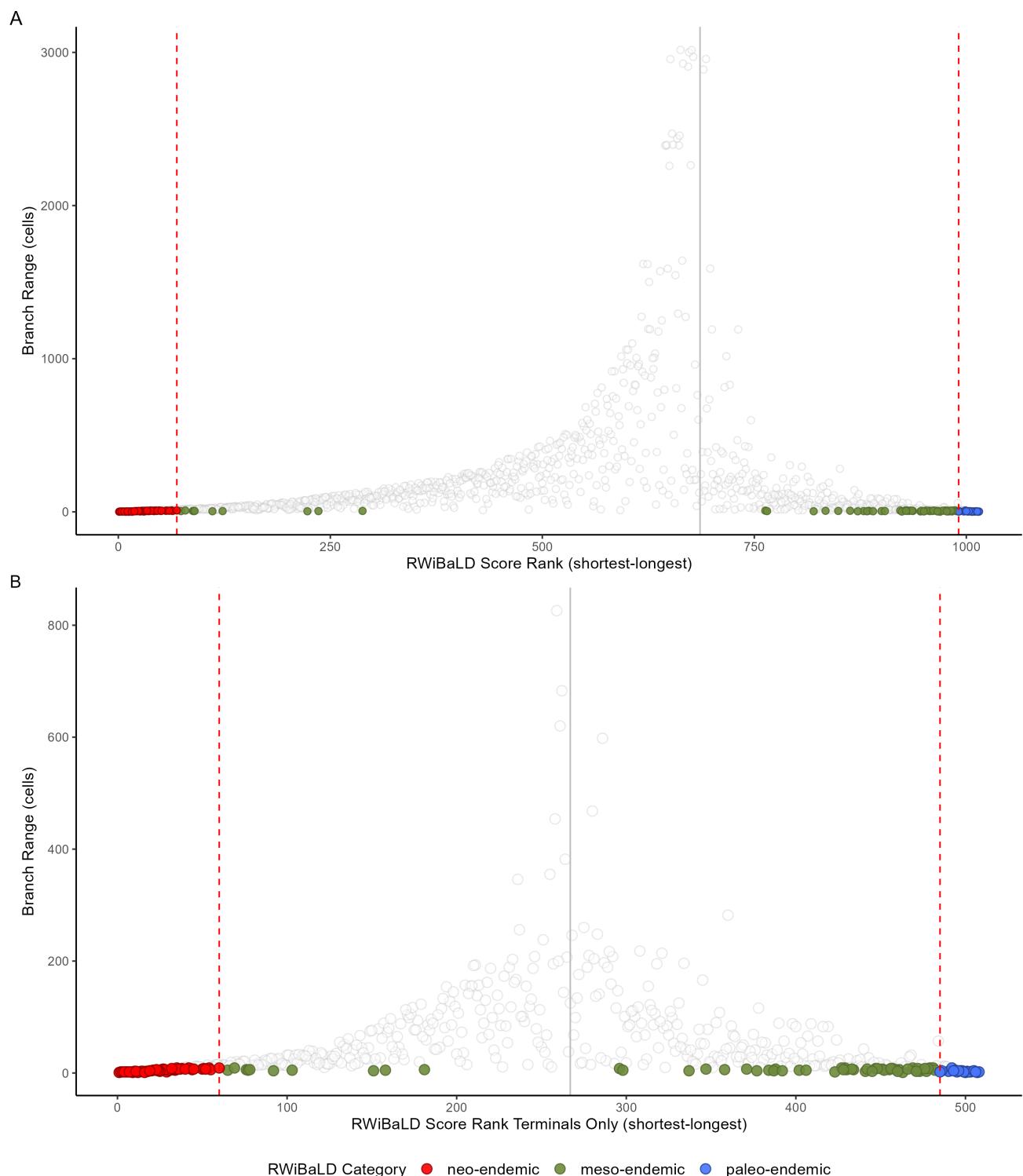
```

## 16 Generate multi-panel figure 3AB

```

1 patchwork <- rwibald_key_plot_range / rwibald_key_plot_range_terminals + plot_annotation(
2   theme = theme(plot.title = element_text(hjust = 0.5)),
3   subtitle = '',
4   caption = '',
5   tag_levels = 'A') +
6   theme(plot.tag.position = c(0, 1),
7     plot.tag = element_text(size = 12, hjust = 0, vjust = 0))
8
9 #print(patchwork)
10
11 ggsave("quarto_outputs/figures/Figure3_AB.png", patchwork, width = 3000, height = 3600, units = "px")

```



## 17 Read tree file & generate supplementary figure 1

Now we load the range weighted tree file exported from biodiverse and colour code it by the RWiBaLD categories.

```
1 # if need be check and install ggtree using this code
2 # if (!require("BiocManager", quietly = TRUE))
3 #   install.packages("BiocManager")
4 #
5 # BiocManager::install("ggtree")
6 #
7 data_dir <- "Acacia_biodiverse_exports/"
8 #
9 all_tree_data_nwk <- paste0(data_dir, "acacia_tree_TRIMMED1_EQ1_RW1.nwk")
10 #
11 myTree <- read.tree(file=all_tree_data_nwk)
12 #
13 rwibald_results_all <- rwibald_results_all %>%
14   mutate(rwibald_type = replace(rwibald_type, is.na(rwibald_type), "other"))
15 #
16 # View(rwibald_results_all)
17 #
18 rwibald_results_all$tree_cols <- as.factor(rwibald_results_all$rwibald_type)
19 #
20 # Remove quotes from labels so they match dataframe
21 myTree$tip.label <- gsub("'", "", myTree$tip.label)
22 myTree$node.label <- gsub("'", "", myTree$node.label)
23 #
24 # Create ggtree object
25 g <- ggtree(myTree) %<+% rwibald_results_all +
26   aes(color=tree_cols) +
27   scale_color_manual(values = c("paleo-endemic" = "royalblue1",
28                             "neo-endemic" = "red",
29                             "meso-endemic" = "darkolivegreen")) +
30   # geom_text2(aes(label = node),
31   #            hjust =0,      # adjust horizontal position
32   #            vjust = 0,      # adjust vertical position
33   #            size = 1,       # adjust text size
34   #            color = "blue") + # adjust text color
35   theme(legend.position="none") +
36   geom_tiplab(as_ylab=FALSE, size=1)
37 #
38 # Display the plot
39 #print(g)
40 #
41 ggsave("quarto_outputs/figures/SupFigure1_full_tree.png", g, width = 2048,
42       height = 4024, units = "px")
```

## 18 Generate tree in 2 halves supplementary figure 1A and 1B

```
1 data_dir <- "Acacia_biodiverse_exports/"
2 all_tree_data_nwk <- paste0(data_dir, "acacia_tree_TRIMMED1_EQ1_RW1.nwk")
3 #
4 myTree <- read.tree(file=all_tree_data_nwk)
5 #
6 rwibald_results_all <- rwibald_results_all %>%
7   mutate(rwibald_type = replace(rwibald_type, is.na(rwibald_type), "other"))
```

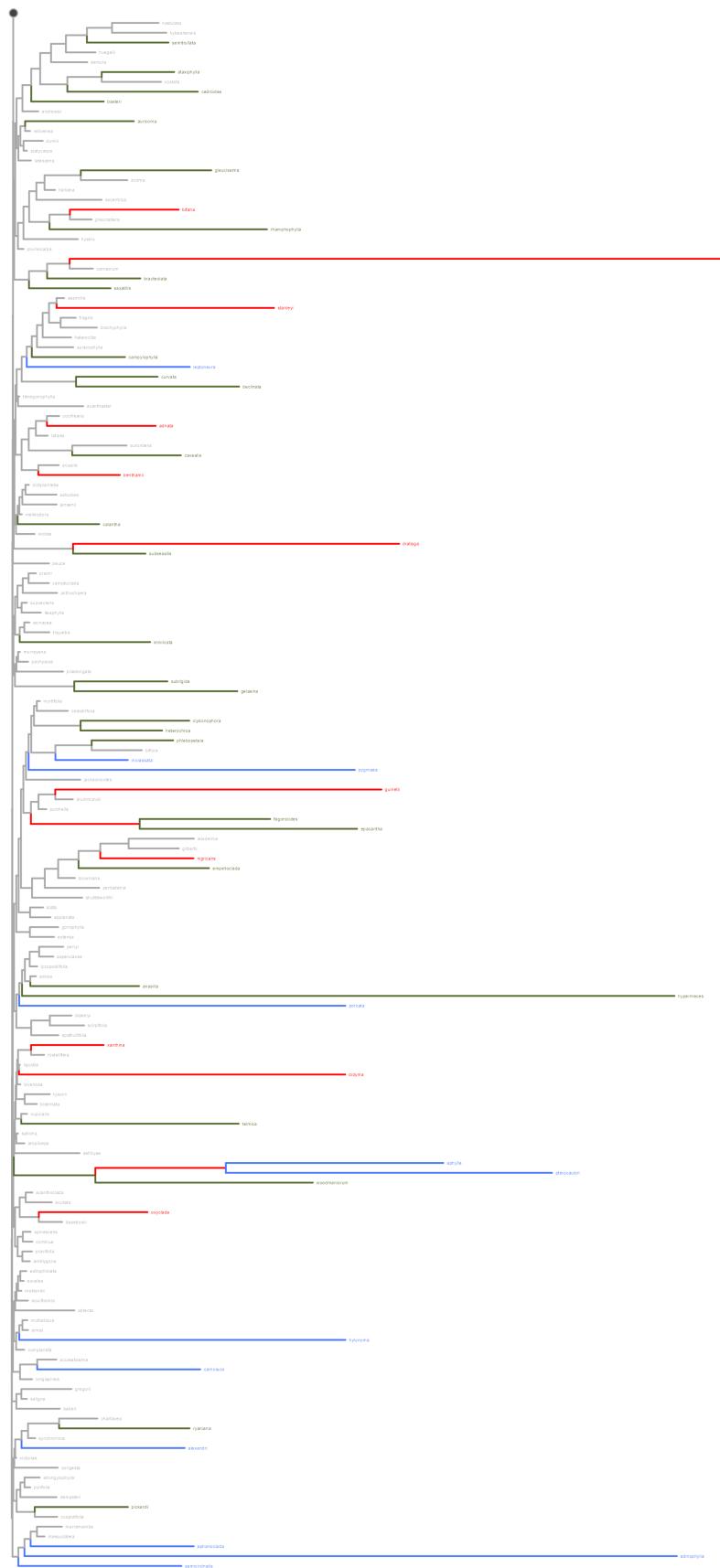
```

8 rwibald_results_all$tree_cols <- as.factor(rwibald_results_all$rwibald_type)
9
10 # Remove quotes from labels so they match the dataframe
11 myTree$tip.label <- gsub("'", "", myTree$tip.label)
12 myTree$node.label <- gsub("'", "", myTree$node.label)
13
14 # Calculate the halfway point
15 half <- length(myTree$tip.label) / 2
16
17 # Sort the tip labels for consistency
18 tip_labels <- myTree$tip.label
19 first_half_tips <- tip_labels[1:half]
20 second_half_tips <- tip_labels[(half + 1):length(tip_labels)]
21
22 # Identify MRCA nodes for each half
23 node_first_half <- getMRCA(myTree, first_half_tips)
24 node_second_half <- getMRCA(myTree, second_half_tips)
25
26
27 # Create the base ggtree object
28 g <- ggtree(myTree) %<+%
29   aes(color = tree_cols) +
30   scale_color_manual(values = c("paleo-endemic" = "royalblue1",
31                             "neo-endemic" = "red",
32                             "meso-endemic" = "darkolivegreen",
33                             "other" = "gray66")) +
34   theme(legend.position = "none") +
35   geom_tiplab(as_ylab = FALSE, size=1)
36
37 #plot(g)
38
39 # Identify MRCA node
40 mrca_node <- MRCA(g, second_half_tips)
41
42 second_half_tree <- viewClade(tree_view = g, mrca_node) +
43   geom_point2(
44     aes(subset = (node == mrca_node)),
45     shape = 21,
46     size = 2,
47     fill = 'gray26',
48     nudge_x = 20,
49     position = position_nudge(y = -88))
50
51
52 # +
53 #   theme(panel.on top = FALSE,
54 #         panel.spacing.x = unit(c(1, 1, 1, 1), "cm"),
55 #         panel.background = element_rect(color = "green", fill="transparent", linewidth = 10),
56 #         plot.margin = unit(c(1, 1, 1, 1), "cm"))
57
58
59 #plot(second_half_tree)
60
61 # Save the figure showing the second half expanded and the first half collapsed
62 ggsave("quarto_outputs/figures/SupFigure_1A.png",
63        second_half_tree, width = 2048, height = 4024, units = "px")
64
65 #plot(g)

```

```
67 # Collapse the second half of the tree
68 g_half_collapsed <- collapse(g, node = node_second_half) +
69   # Add a point to indicate the collapsed node for reference
70   geom_point2(aes(subset=(node == node_second_half)), shape=21, size=2, fill='gray26')
71
72 #plot(g_halfCollapsed)
73
74 # Save the figure showing the first half expanded and the second half collapsed
75 ggsave("quarto_outputs/figures/SupFigure_1B.png",
76       g_half_collapsed, width = 2048, height = 4024, units = "px")
```





## 19 Load data & generate histograms for all cells

Next we load the data and generate histograms. This code generates a histogram for every cell in the dataset. For convenience the file names contain the CANAPE code and whether the histogram contains branches of key interest.

```
1 #function to change decimal places displayed on plot
2 scaleFUN <- function(x) sprintf("%.8g", x)
3
4 # Function to replace '-' with 'm' and ':' with '_'
5 clean_column_names <- function(df) {
6   new_names <- colnames(df) %>%
7     gsub("-", "neg", .) %>%
8     gsub(":", "_", .)
9   colnames(df) <- new_names
10  return(df)
11 }
12
13 # Clean column names using the function
14 canape_group_data_rwibald <- clean_column_names(canape_group_data_rwibald)
15
16 #View(canape_group_data_rwibald)
17
18 col_scheme <- c("paleo-endemic" = "royalblue1", "neo-endemic" = "red", "meso-endemic" = "darkolivegreen",
19   ↪ "other" = "lightgoldenrodyellow")
20 legend_labels <- c("neo-endemic" = "Neo Endemic", "paleo-endemic" = "paleo Endemic", "other" = "other",
21   ↪ "meso-endemic" = "Meso Endemic")
22
23 #data <- transposed_df
24 #View(canape_key_group_data_rwibald)
25
26 #Generate all histograms
27 for (i in 2:(ncol(canape_group_data_rwibald)-2)) {# skip first column and last 2 as they are
28   ↪ NAME,cell_count,rwibald_type
29 #for (i in 74:74) {
30   #i <- 74
31   data <- canape_group_data_rwibald[-(1:6),] # remove the rows not needed
32   col_name <- colnames(data)[i] # get the column name to generate the histogram of
33   colourByCol <- "rwibald_type" # set the column to use for colouring the histogram
34   number_of_Bins <- 41 # set number of bins to use
35   hist_data <- na.omit(as.numeric(data[[col_name]])) # extract that column data for plotting
36   hist_range <- range(hist_data,na.rm=TRUE) # calculate the range of all values in the column ie. min/max
37   ↪ value
38
39 #calculate the total range of the whole data set to get a consistent x scale on all histograms.
40 dataForRange <- data %>%
41   select(-first(colnames(.)), -last(colnames(.))) %>%
42   mutate(across(everything(), as.numeric))
43 totalRange <- range(dataForRange, na.rm=TRUE) #lowest and highest values in the dataset
44 totalRangeGap <- max(dataForRange, na.rm = TRUE) - min(dataForRange, na.rm = TRUE) # distance between
45   ↪ range above
46
47   range <- max(hist_data) - min(hist_data)
48   binSize <- range/number_of_Bins
49   farthest_number <- max(abs(hist_range)) # calculate the number farthest from 0
50   x_min <- -(farthest_number)-2*(binSize) # set xmin so zero is centred
51   x_max <- (farthest_number)+2*(binSize) # set xmax so zero is centred
52
53 #check to see if any of the branches in the histogram are RWIBALD significant to add to the file names
54 result <- data %>%
```

```

50 select (!!sym(col_name), !!sym(colourByCol)) %>%
51 filter (!is.na (!!sym(col_name))) %>%
52 summarise(result = ifelse(any (!!sym(colourByCol) %in% c("paleo-endemic", "neo-endemic",
53   ↪ "meso-endemic")), "key", "zero-key")) %>%
54 pull(result)
55
56 #View(result)
57 # setup the file names
58 CANAPE_CODE <- canape_group_data_rwibald["CANEPE_CODE", col_name]
59 cell <- str_replace_all(col_name, "[[:]", "_")
60 filename <- paste0("quarto_outputs/histograms/", cell, "_CC_", CANAPE_CODE, "_", result, "_",
61   ↪ numberOfBins, "bins.png")
62
63 #print(filename)
64 # get a subset of datafram for the histogram
65 plot_data <- data %>%
66 select (!!sym(col_name), !!sym(colourByCol)) %>%
67 filter (!is.na (!!sym(col_name))) %>%
68 arrange (!!sym(colourByCol))
69
70 #View(plot_data)
71
72 plot <- ggplot(plot_data, aes(x = as.numeric(.data[[col_name]]), fill = forcats::fct_rev(rwibald_type)))
73   +
74 geom_histogram(color = "black", linewidth= 0.2, bins = numberofBins) +
75 scale_fill_manual(values = col_scheme) +
76 xlim(x_min, x_max) +
77 coord_cartesian(ylim = c(0, 20)) +
78 labs(x = "RWiBaLD Score", y = "Frequency", fill = "Branch Category") +
79 theme_bw()
80
81 plot <- plot +
82 stat_bin(
83   aes(label = after_stat(if_else (condition = count>20, as.character(count), "")),
84   bins= as.numeric(numberofBins),
85   position=position_stack(vjust=0.1),
86   pad=TRUE,
87   geom = "text",
88   color = "black",
89   size = 2,
90   y = 19
91 )
92
93 CairoPNG(width = 1024, height = 600, file = filename, canvas="white", bg = "white", units="px", dpi=96,
94   ↪ title = "")
95 print(plot)
96 dev.off()
97 }
```

## 20 Load data & generate 12 histograms for figure 4A-L

This code filters out only the 12 histograms included in Figure 4 and generates the ggplot2 objects of them.

```

1 data <- t(canape_group_data)
2 #View(data)
3
4 #Transpose the datafram and set the first row as column names
```

```

5 transposed_df <- setNames(data.frame(data[-1,]), data[1,])
6
7 #View(transposed_df)
8
9 #cells to keep
10 cols_to_keep <- c("NAME", "-1825000:-2975000", "75000:-2525000",
11   ↵ "625000:-3475000", "-1425000:-3225000", "1775000:-3725000", "-1425000:-3475000", "-1225000:-3775000",
12   ↵ "-1425000:-3275000", "1225000:-1275000", "-1175000:-3275000", "-1075000:-2825000",
13   ↵ "-1075000:-2375000")
14
15 #Calculate RWiBaLD significants and Statistics etc.
16 canape_group_data_rwibald <- transposed_df %>%
17   tibble::rownames_to_column(var = "NAME") %>%
18   select(all_of(cols_to_keep)) %>%
19   left_join(select(rwibald_results_all, NAME, rwibald_type), by = 'NAME') %>%
20   mutate(rwibald_type = ifelse(is.na(rwibald_type), "other", rwibald_type))
21
22 # Check if the column is already a factor
23 if (!is.factor(canape_group_data_rwibald$rwibald_type)) {
24   # If not a factor, convert and specify levels
25   canape_group_data_rwibald$rwibald_type <- factor(canape_group_data_rwibald$rwibald_type, levels =
26   ↵ c("neo-endemic", "meso-endemic", "paleo-endemic", "other"))
27 }
28
29 #View(canape_group_data_rwibald)
30
31 # Function to replace '-' with 'm' and ':' with '_'
32 clean_column_names <- function(df) {
33   new_names <- colnames(df) %>%
34     gsub("-", "neg", .) %>%
35     gsub(":", "_", .)
36   colnames(df) <- new_names
37   return(df)
38 }
39
40 # Clean column names using the function
41 canape_group_data_rwibald <- clean_column_names(canape_group_data_rwibald)
42
43 rownames(canape_group_data_rwibald) <- canape_group_data_rwibald$NAME
44
45 #View(canape_group_data_rwibald)
46
47 # Write data to file
48 write.csv(canape_group_data_rwibald, paste0("quarto_outputs/transposed_df_figure_only.csv"),
49   ↵ row.names=FALSE)
50
51 #function to change decimal places displayed on plot
52 scaleFUN <- function(x) sprintf("%.8g", x)
53
54 #View(canape_group_data_rwibald)
55
56 col_scheme <- c("paleo-endemic" = "royalblue1",
57   "neo-endemic" = "red",
58   "meso-endemic" = "darkolivegreen",
59   "other" = "lightgoldenrodyellow"
60   )
61
62 legend_labels <- c("neo-endemic" = "neo-endemic",
63   "paleo-endemic" = "paleo-endemic",
64   "meso-endemic" = "meso-endemic",
65   "other" = "other")

```

```

59         "meso-endemic" = "meso-endemic",
60         "other" = "other"
61     )
62
63 legend_order <- c("neo-endemic", "meso-endemic", "paleo-endemic", "other")
64
65 #data <- transposed_df
66 #View(canape_group_data_rwibald)
67
68 # Create an empty list to store plots
69 plot_list <- list()
70
71 #Generate histograms
72 for (i in 2:(ncol(canape_group_data_rwibald)-1)) {# skip first column and last 2 as they are
    ↵ NAME,rwibald_type
73   #i <- 2
74   local({ # have to make this local to allow multiple plots in patchwork
75     i <- i
76   data <- canape_group_data_rwibald[-(1:6),] # remove the rows not needed
77   col_name <- colnames(data)[i] # get the column name to generate the histogram of
78   colourByCol <- "rwibald_type" # set the column to use for colouring the histogram
79   numberOfBins <- 41 # set number of bins to use
80
81   # have to show only one legend as the 'collect' feature in patchwork does not collect the legends as
    ↵ desired
82   if(i == 3){
83     showLegend <- TRUE
84   } else {
85     showLegend <- FALSE
86   }
87
88   hist_data <- na.omit(as.numeric(data[[col_name]])) # extract that column data for plotting
89   hist_range <- range(hist_data,na.rm=TRUE) # calculate the range of all values in the column ie. min/max
    ↵ value
90
91   #calculate the total range of the whole data set to get a consistent x scale on all histograms.
92   dataForRange <- data %>%
93     select(-first(colnames(.)), -last(colnames(.))) %>%
94     mutate(across(everything(), as.numeric))
95   totalRange <- range(dataForRange, na.rm=TRUE)#lowest and highest values in the dataset
96   totalRangeGap <- max(dataForRange, na.rm = TRUE) - min(dataForRange, na.rm = TRUE) # distance between
    ↵ range above
97
98   range <- max(hist_data) - min(hist_data)
99   binSize <- range/numberOfBins
100   farthest_number <- max(abs(hist_range)) # calculate the number farthest from 0
101   x_min <- -(farthest_number)-2*(binSize) # set xmin so zero is centred
102   x_max <- (farthest_number)+2*(binSize) # set xmax so zero is centred
103
104   # get a subset of dataframe for the histogram
105   plot_data <- data %>%
106     mutate (!!sym(col_name) := as.numeric (!!sym(col_name))) %>%
107     select (!!sym(col_name), !!sym(colourByCol)) %>%
108     filter (!is.na (!!sym(col_name))) %>%
109     arrange (!!sym(colourByCol))
110
111   #View(plot_data)
112   #str(plot_data)
113

```

```

114 plot <- ggplot(plot_data, aes(x = .data[[col_name]], fill = forcats::fct_rev(rwibald_type))) +
115   geom_histogram(color = "black", linewidth = 0.2, bins = numberBins, show.legend = showLegend) +
116   scale_fill_manual(values = col_scheme, labels = legend_labels, breaks = legend_order, drop = FALSE,
117     na.value = "transparent") +
118   #xlim(x_min, x_max) +
119   xlim(-0.011, 0.011) +
120   coord_cartesian(ylim = c(0, 20)) +
121   labs(x = "RWiBaLD Score", y = "Frequency", fill = "RWiBaLD Category") +
122   theme_bw()
123
123 plot <- plot +
124   geom_rect(
125     aes(xmin = -0.0005, xmax = 0.0005, ymin = 18.5, ymax = 19.5),
126     color = "white",
127     fill = "white"
128   ) +
129   stat_bin(
130     aes(label = after_stat(if_else(condition = count>20, as.character(count), ""))),
131     bins= as.numeric(numberBins),
132     position=position_stack(vjust=0.1),
133     pad=TRUE,
134     geom = "text",
135     color = "black",
136     size = 3,
137     y = 19
138   )
139
140 #print(plot)
141
142 # Dynamic variable name for the plot
143 plot_name <- paste0("plot_", i - 1) # Subtracting 1 to start numbering from 1
144 assign(plot_name, plot)
145
146 # Add the plot to the list
147 plot_list[[i - 1]] <- get(plot_name)
148 #rm(plot)
149 }
150
151 }
152
153 #print(plot_list[[1]])
154
155 #save the plotlist for later on
156 saveRDS(plot_list, "quarto_outputs/plotlist.rds")

```

## 21 Generate multi-panel histogram figure 4A-L

This code compiles all 12 histograms generated above into one figure.

```

1 plot_list <- readRDS("quarto_outputs/plotlist.rds")
2
3 patchwork <- plot_list[[1]] + xlab(NULL) +
4   guides(x = "none") +
5   plot_list[[2]] + xlab(NULL) + ylab(NULL) +
6   guides(x = "none", y = "none") +
7   plot_list[[3]] + xlab(NULL) + ylab(NULL) +
8   guides(x = "none", y = "none") +

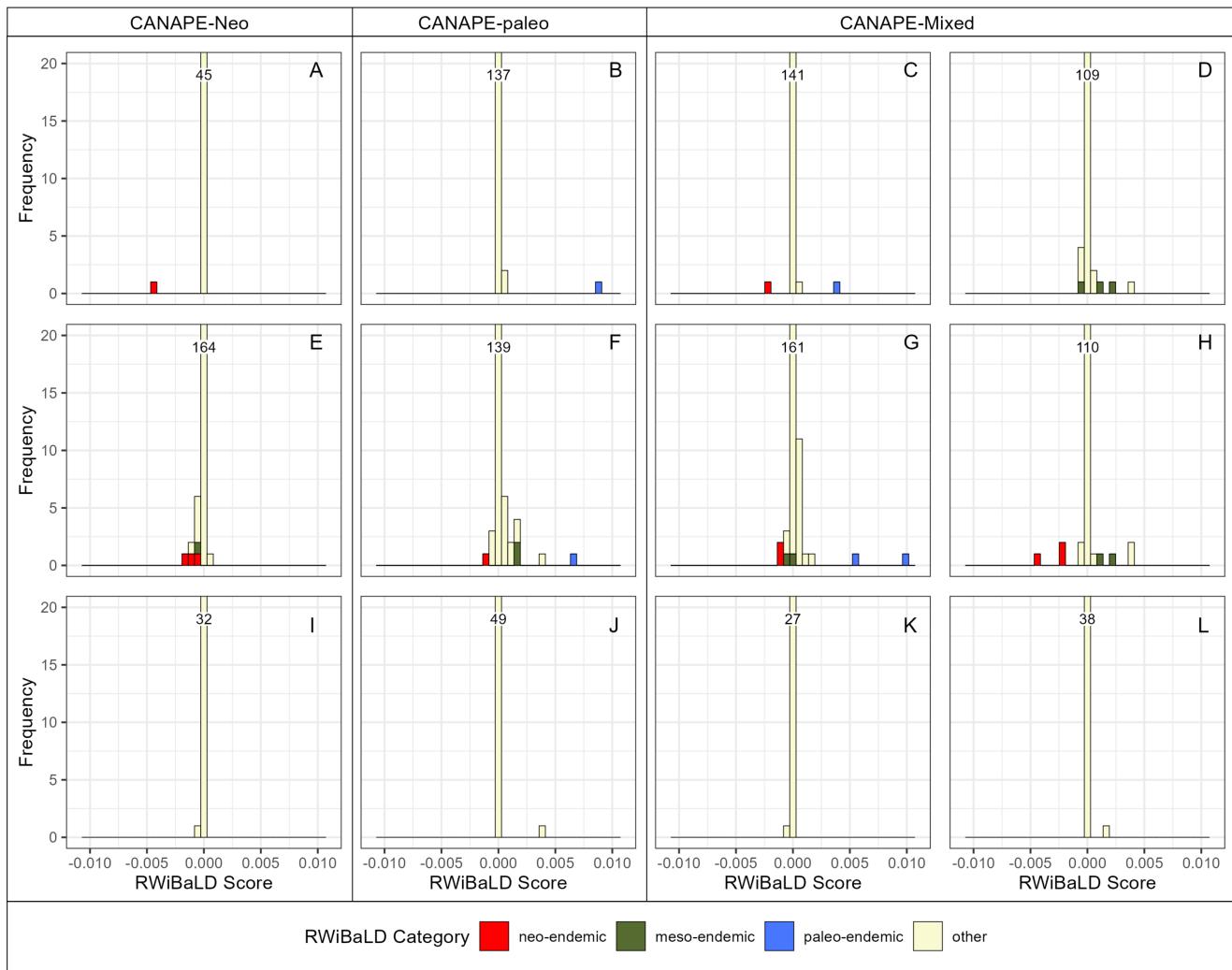
```

```

9   plot_list[[4]] + xlab(NULL) + ylab(NULL) +
10  guides(x = "none", y = "none") +
11  plot_list[[5]] + xlab(NULL) + guides(x = "none") +
12  plot_list[[6]] + xlab(NULL) + ylab(NULL) +
13  guides(x = "none", y = "none") +
14  plot_list[[7]] + xlab(NULL) + ylab(NULL) +
15  guides(x = "none", y = "none") +
16  plot_list[[8]] + xlab(NULL) + ylab(NULL) +
17  guides(x = "none", y = "none") +
18  plot_list[[9]] +
19  plot_list[[10]] + ylab(NULL) + guides(y = "none") +
20  plot_list[[11]] + ylab(NULL) + guides(y = "none") +
21  plot_list[[12]] + ylab(NULL) + guides(y = "none") +
22  plot_annotation(
23    subtitle = 'CANAPE-Neo'                                CANAPE-paleo
24    ↵  CANAPE-Mixed',
25    caption = '',
26    tag_levels = 'A') +
27    plot_layout(ncol = 4, guides = 'collect') &
28    theme(legend.position = "bottom", plot.tag.position = c(0.9, 0.9),
29          plot.tag = element_text(size = 12, hjust = 0, vjust = 0))

30 #print(patchwork)
31
32 ggsave("quarto_outputs/figures/Figure4_A.png", patchwork, width = 3000, height = 2400, units = "px")

```



## 22 Load results data & generate data files for biome maps

Now we take the RWiBaLD results and split the taxa in the original specimen data from the [Categorical Analysis of Neo And Paleo-Endemism \(CANAPE\)](#) paper according to these RWiBaLD categories so we can overlay them on the biome map published by Crisp et al. in 2004.

```

1 original_paper_specimen_data_file <-
2   "doi_10_5061_dryad_dv4qk__v20150514/Point_distribution_Australian_Phyletic_Diversity_Acacia.csv"
3
4 original_paper_specimen_data <- read.table(original_paper_specimen_data_file, header=T, sep=",")
5
6 #View(original_paper_specimen_data)
7 #View(rwibald_results_all_with_range)
8
9 # Summarize the data in the rwibaled_type column
10 summary_df <- rwibald_results_all_with_range %>%
11   group_by(rwibaled_type) %>%
12   summarise(count = n()) # Count of each rwibaled_type
13
14 # Create a table using gt
15 summary_table <- summary_df %>%

```

```

15  gt() %>%
16  tab_header(
17    title = "Summary of rwibaled_type",
18    subtitle = "Count of each type"
19  )
20
21 # Print the table
22 summary_table
23
24 # Extract the 'NAME' values where 'rwibald_type' is 'meso-endemic'
25 meso_names <- rwibald_results_all_with_range[rwibald_results_all_with_range$rwibald_type ==
26   ↪ "meso-endemic", "NAME"]
27
28 # Filter the 'original_paper_specimen_data' dataframe
29 meso_taxa <- original_paper_specimen_data[original_paper_specimen_data$Species %in% meso_names, ]
30
31 # Write data to file
32 write.csv(meso_taxa, "quarto_outputs/Meso_endemics.csv" ,row.names=FALSE)
33
34 # Extract the 'NAME' values where 'rwibald_type' is 'neo-endemic'
35 neo_names <- rwibald_results_all_with_range[rwibald_results_all_with_range$rwibald_type == "neo-endemic",
36   ↪ "NAME"]
37
38 # Filter the 'original_paper_specimen_data' dataframe
39 neo_taxa <- original_paper_specimen_data[original_paper_specimen_data$Species %in% neo_names, ]
40
41 # Write data to file
42 write.csv(neo_taxa, "quarto_outputs/Neo_endemics.csv" ,row.names=FALSE)
43
44 # Extract the 'NAME' values where 'rwibald_type' is 'paleo-endemic'
45 paleo_names <- rwibald_results_all_with_range[rwibald_results_all_with_range$rwibald_type ==
46   ↪ "paleo-endemic", "NAME"]
47
48 # Filter the 'original_paper_specimen_data' dataframe
49 paleo_taxa <- original_paper_specimen_data[original_paper_specimen_data$Species %in% paleo_names, ]

```

Summary of rwibaled\_type  
Count of each type

rwibald_type	count
meso-endemic	59
neo-endemic	55
other	880
paleo-endemic	21

## 23 Two tailed relative phylogenetic diversity (RPD) & CANAPE functions

This is the function for calculating Categorical Analysis of Neo- and Paleo-endemism (CANAPE) from ranked P scores of Biodiverse analysis.

```

1 #Standard 2 tailed test for RPD
2 significance_fun <- function(x){

```

```

3   if (x >= 0.99) {
4     return("Very Highly Sig")
5   } else if (x >= 0.975){
6     return ("Highly Sig")
7   } else if (x <= 0.01){
8     return ("Very Sig Low")
9   } else if (x <= 0.025){
10    return ("Sig Low")
11  } else {
12    return("Not Sig")
13  }
14}

15 #two pass test for RPE
16 # x=P_PE_WE_P, y=P_PHYLO_RPE_NULL2, z=P_PHYLO_RPE2
17 significance_super_fun <- function(x, y, z){
18   if (x > 0.95 || y > 0.95) {
19     if (z <= 0.025){
20       return ("Neo")
21     } else if (z >= 0.975){
22       return ("paleo")
23     } else if (x >= 0.99 || y >= 0.99){
24       return ("Super")
25     } else {
26       return("Mixed")
27     }
28   } else {
29     return("Not Sig")
30   }
31 }
32}

```

## 24 Load CANAPE & randomisation results

Here we load the re-created biodiverse results from the original paper, calculate CANAPE and re-generate the CANAPE map. Note: these results may differ slightly from the original paper as we re-ran the randomisation in biodiverse.

```

1 data_dir <- "Acacia_biodiverse_exports/"
2
3 # The CANAPE results file calculated in Biodiverse directly and exported
4 biodiverse_canaape_results_file <- paste0(data_dir, "Acacia_Rand1_CANAPE_Export.csv")
5
6 # The spatial & randomisation results files calculated in Biodiverse and exported
7 biodiverse_observed_data_file <- paste0(data_dir, "Acacia_SPATIAL_RESULTS_Export.csv")
8 biodiverse_rand_results_file <- paste0(data_dir, "Acacia_Rand1_SPATIAL_RESULTS_Export.csv")
9
10 biodiverse_canaape_results <- read.table(biodiverse_canaape_results_file, header=T,sep=",", check.names =
11   FALSE )
12
13 biodiverse_observed_spatial_results <- read.table(biodiverse_observed_data_file, header=T,sep=",")
14 biodiverse_rand_spatial_results <- read.table(biodiverse_rand_results_file, header=T,sep=",")
15
16 biodiverse_results_concatenated <- cbind(biodiverse_observed_spatial_results,
17   biodiverse_rand_spatial_results)
18
19 ##########

```

```

20 #Create new columns in dataframe and
21 #populate them using the functions above
22 #####
23
24 targets <- c("PHYLO_RPD2", "PD_P", "PE_WE_P", "PD_P_per_taxon", "PHYLO_RPE2")
25
26 for (name in targets) {
27   colname <- paste0("P_", name) # prepend the P_ since we want the proportions, saves some typing above
28   new_colname = paste0(colname, "_SIG")
29   trait_index <- match (colname, colnames(biodiverse_results_concatenated))
30   # Apply the function to every row of column with index "trait_index"
31   # and generate a column in the dataframe showing significant cells
32   if (!is.na(trait_index)) {
33     biodiverse_results_concatenated[[new_colname]] <- apply
34     ↪ (biodiverse_results_concatenated[trait_index], MARGIN=c(1), significance_fun)
35   } else {
36     print (paste("Cannot find index", colname, "in data frame"))
37   }
38 }
39 biodiverse_results_concatenated$P_PHYLO_RPE2_CANAPE_SIG <- sapply(
40   1:nrow(biodiverse_results_concatenated),
41   function(x) significance_super_fun(
42     biodiverse_results_concatenated$P_PE_WE_P[x],
43     biodiverse_results_concatenated$P_PHYLO_RPE_NULL2[x],
44     biodiverse_results_concatenated$P_PHYLO_RPE2[x]
45   )
46 )
47
48 #View(biodiverse_results_concatenated)

```

## 25 Generate CANAPE map figure 5A

Here we generate the CANAPE map, indicating cell locations from the histograms in figure 4A-L. CANAPE identifies geographic concentrations of high PE, and gives a summary classification of the type of endemism dominating in a location. The RWiBaLD histograms (figure 4A-L) identify the specific branches that contribute the most to PE in a given cell, and what type of endemism they represent.

```

1 #loadfonts()
2
3 myFont <- choose_font(c("HelvLight", "Arial", "sans"), quiet = TRUE) #load a font if available
4
5 map_text <- "Categorical Analysis of Neo- And Paleo- Endemism"
6 sigplot <- "P_PHYLO_RPE2_CANAPE_SIG"
7 col_scheme <- c("paleo" = "royalblue1", "Not Sig" = "snow2", "Neo" = "red", "Super" = "#9D00FF", "Mixed"=
    ↪ "#CB7FFF")
8 legend_order <- c("Neo", "paleo", "Not Sig", "Mixed", "Super")
9 legend_labels <- c("Neo"="Neo", "paleo"="Paleo", "Not Sig"="Not significant", "Mixed"="Mixed",
    ↪ "Super"="Super")
10
11 biodiverse_results_concatenated[, sigplot] <- factor(biodiverse_results_concatenated[, sigplot],
    ↪ levels=legend_order)
12 Axis_0 <- "Axis_0"
13 Axis_1 <- "Axis_1"
14
15 map_shape_file <- paste0("shape_files/coastline_albers.shp")
16 map_data <- st_read(map_shape_file)
17

```

```

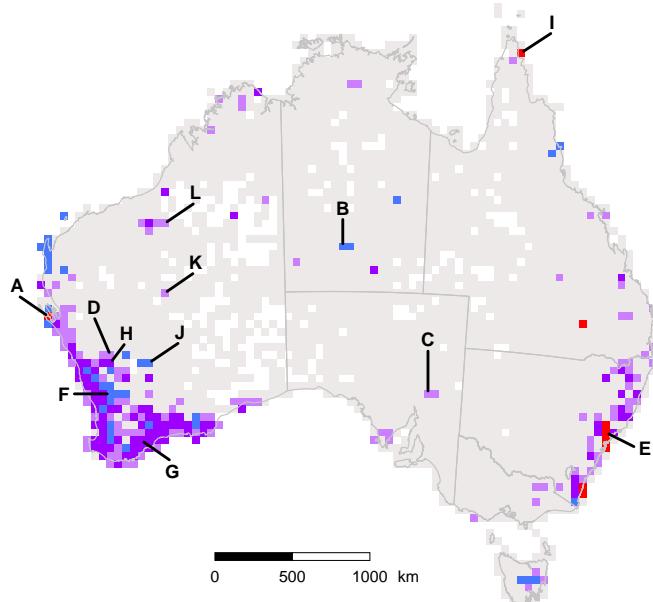
18 cols_to_keep <- c("-1825000:-2975000", "75000:-2525000",
19   ↵ "625000:-3475000", "-1425000:-3225000", "1775000:-3725000", "-1425000:-3475000", "-1225000:-3775000",
20   ↵ "-1425000:-3275000", "1225000:-1275000", "-1175000:-3275000", "-1075000:-2825000",
21   ↵ "-1075000:-2375000")
22
23 # Initialize empty vectors for x and y
24 x <- c()
25 y <- c()
26
27 # Split each element of cols_to_keep and append to x and y for plotting on the map
28 for (val in cols_to_keep) {
29   parts <- strsplit(val, ":")[[1]]
30   x <- c(x, as.numeric(parts[1]))
31   y <- c(y, as.numeric(parts[2]))
32 }
33
34 # Print the result
35 #print(x)
36 #print(y)
37
38 labels <- c("A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L")
39
40 # Create data frame
41 histograms <- data.frame(x = x, y = y, label = labels)
42
43 # Plot the sf object with ggplot2, coloring by the BIOME column
44 map_plot_CANAPE <- ggplot() +
45   geom_tile(data=biodiverse_results_concatenated, aes_string(x=Axis_0, y=Axis_1, fill=sigplot)) +
46   geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
47   scale_fill_manual(values = col_scheme, labels=legend_labels, name="CANAPE", guide =
48     ↵ guide_legend(direction = "horizontal", title.position = "bottom", title.hjust=0.5, title.vjust=0.5,
49     ↵ label.position="bottom", label.hjust = 0.5, label.vjust = 0.1, lineheight=0.5))++
50   geom_text_repel(data=histograms, aes(x = x, y = y, label = labels), fontface = "bold", size = 2.5,
51     ↵ nudge_x = c(-200000, 0, 0, -100000, 250000, -300000, 200000, 100000, 200000, 200000, 200000,
52     ↵ 200000), nudge_y = c(200000, 250000, 350000, 300000, -100000, 0, -200000, 200000, 200000,
53     ↵ 200000, 200000)) +
54   annotate("rect", xmin = -750000, xmax = -250000, ymin = -4500000, ymax = -4550000, fill = "black",
55     ↵ colour = "black", alpha = 1, linewidth = 0.1) +
56   annotate("rect", xmin = -250000, xmax = 250000, ymin = -4500000, ymax = -4550000, fill = "white",
57     ↵ colour = "black", alpha = 1, linewidth = 0.1) +
58   annotate("text", label = "0", x = -750000, y = -4650000, size=rel(2), face = 'plain', family =
59     ↵ myFont) +
60   annotate("text", label = "500", x = -250000, y = -4650000, size=rel(2), face = 'plain', family =
61     ↵ myFont) +
62   annotate("text", label = "1000", x = 250000, y = -4650000, size=rel(2), face = 'plain', family =
63     ↵ myFont) +
64   annotate("text", label = "km", x = 500000, y = -4650000, size=rel(2), face = 'plain', family =
65     ↵ myFont) +
66   theme(text = element_text(family = myFont),
67     strip.background = element_blank(),
68     title = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family = myFont),
69     axis.line=element_blank(),axis.text.x=element_blank(),
70     axis.text.y=element_blank(),axis.ticks=element_blank(),
71     axis.title.x=element_blank(), axis.title.y=element_blank(),
72     legend.position="none",
73     legend.direction='horizontal',
74     legend.text = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family =
75       ↵ myFont),
76     panel.grid = element_blank(),
77   )

```

```

62 panel.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
63 panel.border = element_blank(),
64 plot.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
65 plot.margin=unit(c(0,0,0,0),"line"))
66
67 print(map_plot_CANAPE)

```



```

1 ggsave('quarto_outputs/figures/Figure5_A.png', map_plot_CANAPE, width = 1024, height = 1024, units =
  ↵ "px", bg = "white")

```

Reading layer `coastline\_albers` from data source  
`C:\E\gitRepos\rwibald\shape\_files\coastline\_albers.shp` using driver `ESRI Shapefile'  
Simple feature collection with 44 features and 4 fields  
Geometry type: POLYGON  
Dimension: XY  
Bounding box: xmin: -1887741 ymin: -4840771 xmax: 2121462 ymax: -1029671  
Projected CRS: GDA94 / Australian Albers

## 26 Generate biome map with neo-endemics figure 5B

Here we show the specimen data for all of the neo-endemic taxa categorised by RWiBaLD overlaid on the biome map published by [Crisp et al.](#) in 2004.

```

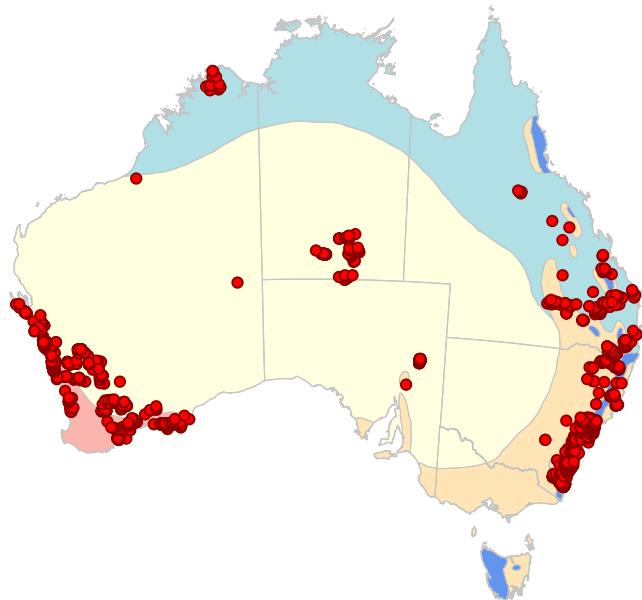
1 #loadfonts()
2
3 #myFont <- choose_font(c("HelvLight", "Arial", "sans"), quiet = TRUE) #load a font if available
4
5 col_scheme <- c("aseasonal wet" = "cornflowerblue",
6   "eremeant" = "lightyellow1",
7   "monsoonal tropics" = "powderblue",
8   "southeastern temperate" = "moccasin",
9   "southwestern temperate"= "#fbb4ae")

```

```

10 legend_order <- c("aseasonal wet",
11   "eremean",
12   "monsoonal tropics",
13   "southeastern temperate",
14   "southwestern temperate")
15 legend_labels <- c("aseasonal wet" = "aseasonal wet",
16   "eremean" = "eremean",
17   "monsoonal tropics" = "monsoonal tropics",
18   "southeastern temperate" = "southeastern temperate",
19   "southwestern temperate" = "southwestern temperate")
20
21 map_shape_file1 <- paste0("shape_files/coastline_albers.shp")
22 map_data <- st_read(map_shape_file1)
23 #geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
24
25 map_shape_file <- paste0("shape_files/biomes_crisp_3577/biomes_crisp_3577.shp")
26 # Read the shapefile as an sf object
27 biomes_sf <- st_read(map_shape_file)
28
29 csv_file <- paste0("quarto_outputs/Neo_endemics.csv")
30 # Read the CSV file into a data frame
31 csv_data <- read.csv(csv_file)
32 # Convert data frame to sf object
33 csv_sf <- st_as_sf(csv_data, coords = c("x_metres_EPSG_3577_Albers_Equal_Area",
34   "y_metres_EPSG_3577_Albers_Equal_Area"), crs = st_crs(biomes_sf))
35
36 # Plot the sf object with ggplot2, coloring by the BIOME column
37 map_plot_Neo <- ggplot() +
38   geom_sf(data = biomes_sf, aes(fill = BIOME), colour = "grey77") +
39   geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
40   geom_sf(data = csv_sf, fill= "red", color = "red4", shape = 21) +
41   scale_fill_manual(values = col_scheme, labels=legend_labels, name="Biomes", guide =
42     guide_legend(direction = "horizontal", title.position = "bottom", title.hjust=0.5, title.vjust=0.5,
43     label.position="bottom", label.hjust = 0.5, label.vjust = 0.1, lineheight=0.5))+
44   theme(text = element_text(family = myFont),
45     strip.background = element_blank(),
46     title = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family = myFont),
47     axis.line=element_blank(),axis.text.x=element_blank(),
48     axis.text.y=element_blank(),axis.ticks=element_blank(),
49     axis.title.x=element_blank(), axis.title.y=element_blank(),
50     legend.position="none",
51     legend.direction='horizontal',
52     legend.text = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family =
53       myFont),
54     legend.key = element_rect(color = "black", size = 0),
55     panel.grid = element_blank(),
56     panel.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
57     panel.border = element_blank(),
58     plot.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
59     plot.margin=unit(c(0,0,0,0),"line"))
60
61 print(map_plot_Neo)

```



```
1 ggsave("quarto_outputs/figures/Figure5_B.png", map_plot_Neo, width = 3000, height = 2600, units = "px")
```

```
Reading layer `coastline_albers' from data source
  `C:\E\gitRepos\rwibald\shape_files\coastline_albers.shp' using driver `ESRI Shapefile'
Simple feature collection with 44 features and 4 fields
Geometry type: POLYGON
Dimension:     XY
Bounding box:  xmin: -1887741 ymin: -4840771 xmax: 2121462 ymax: -1029671
Projected CRS: GDA94 / Australian Albers
Reading layer `biomes_crisp_3577' from data source
  `C:\E\gitRepos\rwibald\shape_files\biomes_crisp_3577\biomes_crisp_3577.shp'
  using driver `ESRI Shapefile'
Simple feature collection with 5 features and 3 fields
Geometry type: MULTIPOLYGON
Dimension:     XY
Bounding box:  xmin: -1887414 ymin: -4840588 xmax: 2121442 ymax: -1087816
Projected CRS: GDA94 / Australian Albers
```

## 27 Generate biome map with meso-endemics figure 5C

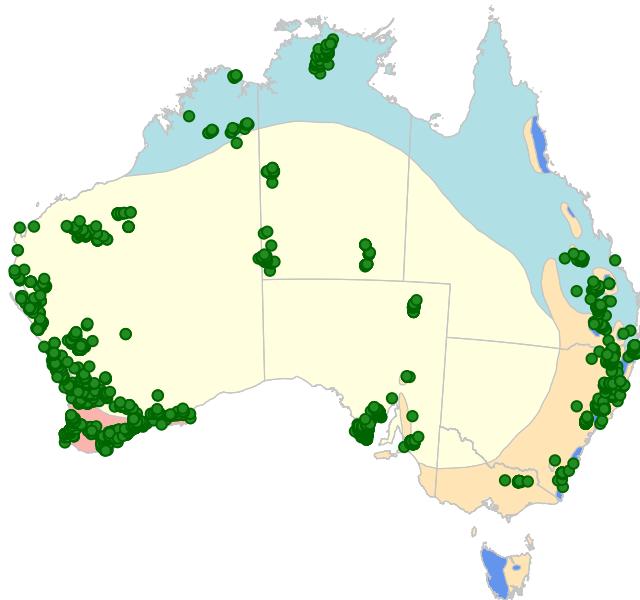
Here we show the specimen data for all of the meso-endemic taxa categorised by RWiBaLD overlaid on the biome map published by [Crisp et al.](#) in 2004.

```
1 #loadfonts()
2
3 #myFont <- choose_font(c("HelvLight", "Arial", "sans"), quiet = TRUE) #load a font if available
4
5 map_text <- "Categorical Analysis of Neo- And Paleo- Endemism"
6
7 col_scheme <- c("aseasonal wet" = "cornflowerblue",
8                 "eremeal" = "lightyellow1",
9                 "monsoonal tropics" = "powderblue",
10                "southeastern temperate" = "moccasin",
```

```

11         "southwestern temperate"= "#fbb4ae")
12 legend_order <-c("aseasonal wet",
13                  "eremean",
14                  "monsoonal tropics",
15                  "southeastern temperate",
16                  "southwestern temperate")
17 legend_labels <- c("aseasonal wet" = "aseasonal wet",
18                      "eremean" = "eremean",
19                      "monsoonal tropics" = "monsoonal tropics",
20                      "southeastern temperate"="southeastern temperate",
21                      "southwestern temperate"="southwestern temperate")
22
23 map_shape_file1 <- paste0("shape_files/coastline_albers.shp")
24 map_data   <- st_read(map_shape_file1)
25 #geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
26
27 map_shape_file <- paste0("shape_files/biomes_crisp_3577/biomes_crisp_3577.shp")
28 # Read the shapefile as an sf object
29 biomes_sf <- st_read(map_shape_file)
30
31 csv_file <- paste0("quarto_outputs/Meso_endemics.csv")
32 # Read the CSV file into a data frame
33 csv_data <- read.csv(csv_file)
34 # Convert data frame to sf object
35 csv_sf <- st_as_sf(csv_data, coords = c("x_metres_EPSG_3577_Albers_Equal_Area",
36                                         "y_metres_EPSG_3577_Albers_Equal_Area"), crs = st_crs(biomes_sf))
37
38 # Plot the sf object with ggplot2, coloring by the BIOME column
39 map_plot_Meso <- ggplot() +
40   geom_sf(data = biomes_sf, aes(fill = BIOME), color = "grey77") +
41   geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
42   geom_sf(data = csv_sf, fill= "forestgreen", color = "darkgreen", shape = 21) +
43   scale_fill_manual(values = col_scheme, labels=legend_labels, name="Biomes", guide =
44     guide_legend(direction = "horizontal", title.position = "bottom", title.hjust=0.5, title.vjust=0.5,
45     label.position="bottom", label.hjust = 0.5, label.vjust = 0.1, lineheight=0.5))++
46   theme(text = element_text(family = myFont),
47         strip.background = element_blank(),
48         title = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family = myFont),
49         axis.line=element_blank(),axis.text.x=element_blank(),
50         axis.text.y=element_blank(),axis.ticks=element_blank(),
51         axis.title.x=element_blank(), axis.title.y=element_blank(),
52         legend.position="none",
53         legend.direction='horizontal',
54         legend.text = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family =
55           myFont),
56         legend.key = element_rect(color = "black", size = 0),
57         panel.grid = element_blank(),
58         panel.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
59         panel.border = element_blank(),
60         plot.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
61         plot.margin=unit(c(0,0,0,0),"line"))
62
63 print(map_plot_Meso)

```



```
1 ggsave("quarto_outputs/figures/Figure5_C.png", map_plot_Meso, width = 3000, height = 2600, units = "px")
```

```
Reading layer `coastline_albers' from data source
`C:\E\gitRepos\rwibald\shape_files\coastline_albers.shp' using driver `ESRI Shapefile'
Simple feature collection with 44 features and 4 fields
Geometry type: POLYGON
Dimension:     XY
Bounding box:  xmin: -1887741 ymin: -4840771 xmax: 2121462 ymax: -1029671
Projected CRS: GDA94 / Australian Albers
Reading layer `biomes_crisp_3577' from data source
`C:\E\gitRepos\rwibald\shape_files\biomes_crisp_3577\biomes_crisp_3577.shp'
using driver `ESRI Shapefile'
Simple feature collection with 5 features and 3 fields
Geometry type: MULTIPOLYGON
Dimension:     XY
Bounding box:  xmin: -1887414 ymin: -4840588 xmax: 2121442 ymax: -1087816
Projected CRS: GDA94 / Australian Albers
```

## 28 Generate biome map with paleo-endemics figure 5D

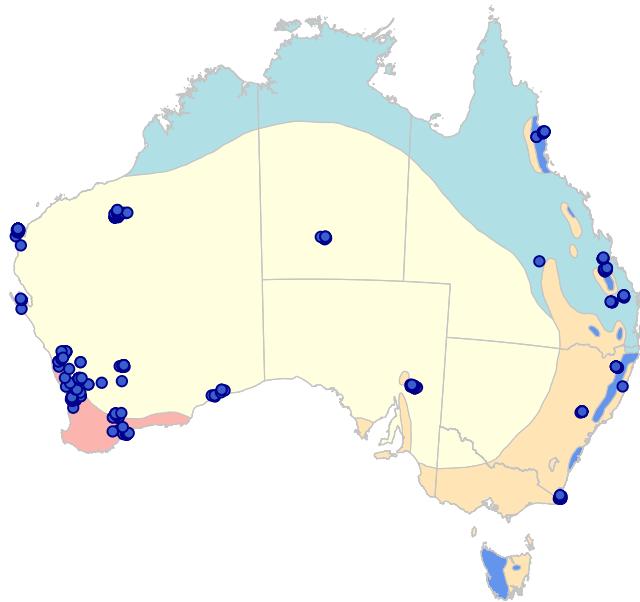
Here we show the specimen data for all of the paleo-endemic taxa categorised by RWiBaLD overlaid on the biome map published by [Crisp et al.](#) in 2004.

```
1 #loadfonts()
2
3 #myFont <- choose_font(c("HelvLight", "Arial", "sans"), quiet = TRUE) #load a font if available
4
5 map_text <- "Categorical Analysis of Neo- And Paleo- Endemism"
6
7 col_scheme <- c("aseasonal wet" = "cornflowerblue",
8                 "eremeann" = "lightyellow1",
9                 "monsoonal tropics" = "powderblue",
10                "southeastern temperate" = "moccasin",
```

```

11         "southwestern temperate"= "#fbb4ae")
12 legend_order <-c("aseasonal wet",
13                  "eremean",
14                  "monsoonal tropics",
15                  "southeastern temperate",
16                  "southwestern temperate")
17 legend_labels <- c("aseasonal wet" = "aseasonal wet",
18                      "eremean" = "eremean",
19                      "monsoonal tropics" = "monsoonal tropics",
20                      "southeastern temperate"="southeastern temperate",
21                      "southwestern temperate"="southwestern temperate")
22
23 map_shape_file1 <- paste0("shape_files/coastline_albers.shp")
24 map_data  <- st_read(map_shape_file1)
25 #geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
26
27 map_shape_file <- paste0("shape_files/biomes_crisp_3577/biomes_crisp_3577.shp")
28
29 # Read the shapefile as an sf object
30 biomes_sf <- st_read(map_shape_file)
31
32 csv_file <- paste0("quarto_outputs/Paleo_endemics.csv")
33
34 # Read the CSV file into a data frame
35 csv_data <- read.csv(csv_file)
36
37 # Convert data frame to sf object
38 csv_sf <- st_as_sf(csv_data, coords = c("x_metres_EPSG_3577_Albers_Equal_Area",
39                                         "y_metres_EPSG_3577_Albers_Equal_Area"), crs = st_crs(biomes_sf))
40
41 # Plot the sf object with ggplot2, coloring by the BIOME column
42 map_plot_Paleo  <- ggplot() +
43   geom_sf(data = biomes_sf, aes(fill = BIOME), color = "grey77") +
44   geom_sf(data = map_data, colour = "grey77" , fill="transparent") +
45   geom_sf(data = csv_sf, fill= "royalblue3", color = "darkblue", shape = 21) +
46   scale_fill_manual(values = col_scheme, labels=legend_labels, name="Biomes", guide =
47     guide_legend(direction = "horizontal", title.position = "bottom", title.hjust=0.5, title.vjust=0.5,
48     label.position="bottom", label.hjust = 0.5, label.vjust = 0.1, lineheight=0.5))+
49   theme(text = element_text(family = myFont),
50         strip.background = element_blank(),
51         title = element_text(colour = 'black', angle = 0, size=rel(1), face = 'plain', family = myFont),
52         axis.line=element_blank(),axis.text.x=element_blank(),
53         axis.text.y=element_blank(),axis.ticks=element_blank(),
54         axis.title.x=element_blank(), axis.title.y=element_blank(),
55         legend.position="none",
56         legend.direction='horizontal',
57         legend.text = element_text(colour = 'black', angle = 0, size=rel(0.5), face = 'plain', family =
58           myFont),
59         legend.key = element_rect(color = "black", size = 0),
60         panel.grid = element_blank(),
61         panel.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
62         panel.border = element_blank(),
63         plot.background=element_blank(),#element_rect(colour = "black", fill="white", size = 1),
64         plot.margin=unit(c(0,0,0,0),"line"))
65
66
67 print(map_plot_Paleo)

```



```
1 ggsave("quarto_outputs/figures/Figure5_D.png", map_plot_Paleo, width = 3000, height = 2600, units = "px")
```

Reading layer `coastline\_albers` from data source  
`C:\E\gitRepos\rwibald\shape\_files\coastline\_albers.shp` using driver `ESRI Shapefile'  
Simple feature collection with 44 features and 4 fields  
Geometry type: POLYGON  
Dimension: XY  
Bounding box: xmin: -1887741 ymin: -4840771 xmax: 2121462 ymax: -1029671  
Projected CRS: GDA94 / Australian Albers  
Reading layer `biomes\_crisp\_3577` from data source  
`C:\E\gitRepos\rwibald\shape\_files\biomes\_crisp\_3577\biomes\_crisp\_3577.shp`  
using driver `ESRI Shapefile'  
Simple feature collection with 5 features and 3 fields  
Geometry type: MULTIPOLYGON  
Dimension: XY  
Bounding box: xmin: -1887414 ymin: -4840588 xmax: 2121442 ymax: -1087816  
Projected CRS: GDA94 / Australian Albers

## 29 Generate 4 up map figure 5ABCD

Here we compile the maps into one figure 5A-D

```
1 patchwork_map <- map_plot_CANAPE +  

2     map_plot_Neo +  

3     map_plot_Meso +  

4     map_plot_Paleo  

5  

6 patchwork_map <- patchwork_map +  

7     plot_annotation(subtitle = '',
8                     caption = '',
9                     tag_levels = 'A') +  

10    plot_layout(ncol = 2, guides = 'collect') &  

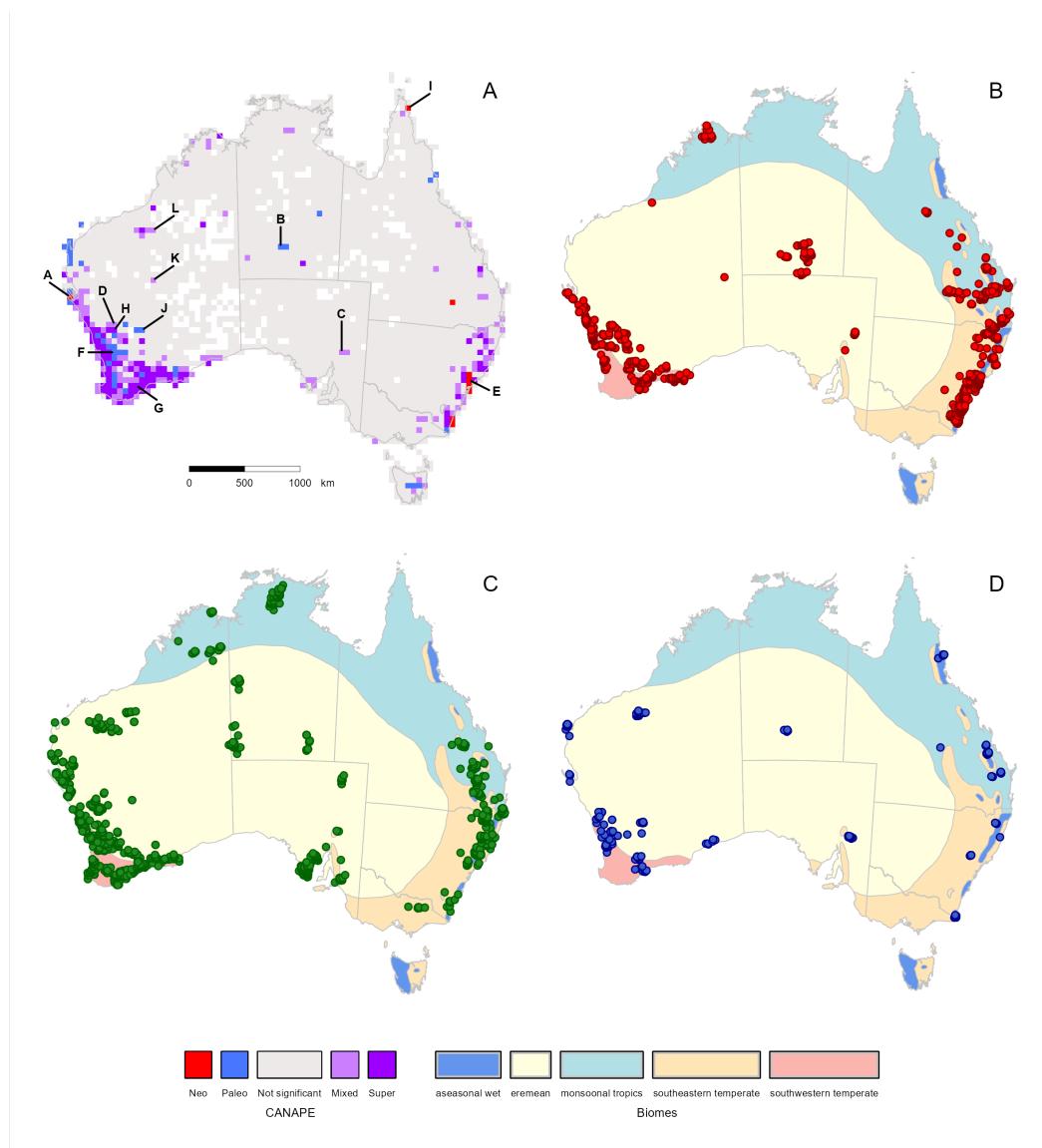
11    theme(legend.position = "bottom",
```

```

12 legend.title=element_text(size=rel(0.6)),
13 legend.text=element_text(size=rel(0.5)),
14 legend.title.position = "bottom",
15 legend.label.position= "bottom",
16 legend.key = element_rect(color = "black", size = 0.5),
17 legend.key.height = unit(0.5, "cm"),
18 legend.key.width = unit(0.5, "cm"),
19 plot.tag.position = c(0.9, 0.9),
20 plot.tag = element_text(size = 12, hjust = 0, vjust = 0))

21 #print(patchwork_map)
22
23 ggsave('quarto_outputs/figures/Figure5_ABCD.png', patchwork_map, width = 3000, height = 2600, units =
24   "px")

```



## 30 Table of RWiBaLD results supplementary table 1

RWiBaLD results for each branch on the phylogeny of Australian Acacia.

```

1 RWiBaLD_results_csv <- paste0("quarto_outputs/Acacia_RWiBaLD_results_all_with_range.csv")
2
3 rwibald_results_all_with_range <- read.table(RWiBaLD_results_csv, header=T, sep=", ")
4
5 #View(rwibald_results_all_with_range)
6
7 #colnames(rwibald_results_all_with_range)
8
9 gt_table <- rwibald_results_all_with_range %>%
10   select("NAME", "branch_length_comparison_tree", "branch_length_observed_tree",
11         "rwibald_score", "rwibald_type", "range_cell_count")
12
13 # print table using gt
14 rwibald_results_all_with_range_table <- gt(gt_table) %>%
15   tab_options(
16     table.width = pct(100),
17     table.layout = "auto",
18     table.align = "left",
19     table.margin.left = px(5),
20     table.margin.right = px(5),
21     table.font.size = px(8),
22     column_labels.font.size = px(10),
23     heading.align = "center",
24     heading.title.font.size = px(12),
25     quarto.use_bootstrap = TRUE
26   ) %>%
27   opt_row_striping() %>%
28   tab_header(
29     title = md("RWiBaLD Results")
30   ) %>%
31   tab_style(
32     style = cell_text(align = "center"),
33     locations = cells_body()
34   )
35
36 rwibald_results_all_with_range_table

```

RWiBaLD Results

NAME	branch_length_comparison_tree	branch_length_observed_tree	rwibald_score	rwibald_type	range_cell_count
1__	8.777963e-05	2.234812e-04	1.357015e-04	other	103
10__	8.951784e-05	3.583689e-05	-5.368095e-05	other	101
100__	4.109683e-05	7.239508e-06	-3.385732e-05	other	220
101__	2.366833e-05	3.361011e-05	9.941780e-06	other	382
102__	2.318283e-05	1.884262e-05	-4.340207e-06	other	390
103__	2.137424e-05	4.697007e-05	2.559583e-05	other	423
104__	2.318283e-04	9.137027e-04	6.818744e-04	other	39
105__	6.027535e-04	1.624921e-03	1.022168e-03	other	15
106__	1.532424e-04	1.057493e-04	-4.749313e-05	other	59
107__	9.935497e-05	3.545809e-04	2.552259e-04	other	91
108__	9.827502e-05	3.429999e-05	-6.397503e-05	other	92
109__	8.449815e-05	1.130098e-04	2.851166e-05	other	107
11__	8.777963e-05	2.896118e-05	-5.881846e-05	other	103
110__	1.891486e-05	9.029480e-06	-9.885378e-06	other	478
111__	7.534419e-04	1.343083e-03	5.896411e-04	other	12
112__	1.614518e-04	4.342113e-05	-1.180307e-04	other	56
113__	1.051314e-04	1.208033e-04	1.567189e-05	other	86
114__	8.777963e-05	6.943275e-09	-8.777269e-05	other	103
115__	7.862002e-05	9.885975e-06	-6.873404e-05	other	115
116__	7.175637e-05	1.346953e-05	-5.828684e-05	other	126
117__	7.008761e-05	4.083340e-05	-2.925421e-05	other	129

118	7.008761e-05	5.616836e-05	-1.391925e-05	other	129
119	6.954848e-05	1.778353e-05	-5.176495e-05	other	130
12	1.335495e-05	1.097784e-05	-2.377112e-06	other	677
120	1.597403e-05	7.837726e-06	-8.136307e-06	other	566
121	1.504376e-05	1.467145e-05	-3.723155e-07	other	601
122	9.881205e-06	4.100078e-06	-5.781126e-06	other	915
123	9.859654e-06	1.414163e-06	-8.445490e-06	other	917
124	3.117690e-04	3.328489e-04	2.107982e-05	other	29
125	2.511473e-04	3.887985e-04	1.376512e-04	other	36
126	2.054841e-04	4.573766e-05	-1.597465e-04	other	44
127	2.825407e-04	6.909660e-05	-2.134441e-04	other	32
128	2.825407e-04	2.411957e-04	-4.134496e-05	other	32
129	5.022946e-04	2.914361e-04	-2.108585e-04	other	18
13	1.310334e-05	5.646846e-06	-7.456490e-06	other	690
130	1.130163e-04	3.901460e-05	-7.400168e-05	other	80
131	1.004589e-04	4.157142e-05	-5.888750e-05	other	90
132	7.862002e-05	1.278658e-04	4.924578e-05	other	115
133	7.662121e-05	3.954025e-05	-3.708095e-05	other	118
134	3.863804e-05	1.794236e-06	-3.684381e-05	other	234
135	4.346780e-05	4.264787e-05	-8.199310e-07	other	208
136	6.551668e-05	4.443585e-05	-2.108084e-05	other	138
137	2.807858e-05	5.238707e-05	2.430849e-05	other	322
138	2.539692e-05	7.418464e-05	4.878772e-05	other	356
139	4.758580e-04	6.521900e-05	-4.106390e-04	other	19
14	1.145919e-05	4.368943e-06	-7.090249e-06	other	789
140	3.767209e-04	2.539890e-04	-1.227320e-04	other	24
141	3.477424e-04	5.308590e-04	1.831166e-04	other	26
142	2.916549e-04	4.352484e-04	1.435935e-04	other	31
143	2.054841e-04	2.656276e-05	-1.789214e-04	other	44
144	1.506884e-04	1.191929e-08	-1.506765e-04	other	60
145	1.238535e-04	5.947281e-05	-6.438065e-05	other	73
146	1.221798e-04	3.874051e-05	-8.343925e-05	other	74
147	8.145317e-05	9.120355e-05	9.750379e-06	other	111
148	1.936039e-05	8.736721e-06	-1.062367e-05	other	467
149	1.361642e-05	7.233721e-06	-6.382699e-06	other	664
15	1.090628e-05	2.498268e-05	1.407641e-05	other	829
150	1.302781e-05	3.732148e-06	-9.295665e-06	other	694
151	3.931001e-04	1.185664e-04	-2.745337e-04	other	23
152	2.318283e-04	6.839497e-05	-1.634333e-04	other	39
153	1.586193e-04	1.557460e-04	-2.873300e-06	other	57
154	7.008761e-05	6.309607e-06	-6.377801e-05	other	129
155	6.551668e-05	1.174379e-05	-5.377289e-05	other	138
156	6.504534e-05	4.422731e-05	-2.081803e-05	other	139
157	3.631045e-05	1.614817e-05	-2.016228e-05	other	249
158	5.758791e-05	5.237361e-05	-5.214300e-06	other	157
159	4.589494e-05	1.856155e-05	-2.733338e-05	other	197
16	6.901757e-05	9.388402e-05	2.486645e-05	other	131
160	4.000576e-05	2.116269e-05	-1.884307e-05	other	226
161	2.620667e-05	2.072920e-09	-2.620460e-05	other	345
162	1.369894e-04	5.770269e-05	-7.928674e-05	other	66
163	1.027421e-04	1.694995e-05	-8.579212e-05	other	88
164	8.001152e-05	3.946034e-05	-4.055118e-05	other	113
165	5.318413e-05	4.206808e-09	-5.317992e-05	other	170
166	4.224908e-05	3.435192e-06	-3.881388e-05	other	214
167	9.132629e-05	2.496945e-05	-6.635684e-05	other	99
168	2.825407e-04	4.848574e-05	-2.340550e-04	other	32
169	1.674315e-04	2.781283e-05	-1.396187e-04	other	54
17	6.192673e-05	8.906534e-05	2.713862e-05	other	146
170	1.205507e-04	3.798806e-05	-8.256264e-05	other	75
171	1.205507e-04	5.692448e-05	-6.362621e-05	other	75
172	1.205507e-04	1.042297e-04	-1.632098e-05	other	75
173	1.174195e-04	4.595375e-05	-7.146576e-05	other	77
174	1.063683e-04	1.635680e-06	-1.047326e-04	other	85
175	8.777963e-05	6.665401e-06	-8.111423e-05	other	103
176	5.079383e-05	4.017738e-09	-5.078982e-05	other	178
177	4.967749e-05	1.645418e-05	-3.322331e-05	other	182
178	3.631045e-05	2.872118e-09	-3.630758e-05	other	249
179	2.816605e-05	1.232424e-05	-1.584181e-05	other	321
18	2.379290e-04	2.770606e-05	-2.102229e-04	other	38
180	2.226922e-05	2.067711e-06	-2.020151e-05	other	406
181	1.583415e-05	9.804553e-06	-6.029602e-06	other	571
182	1.382462e-05	2.249130e-06	-1.157549e-05	other	654
183	5.795707e-05	6.485613e-05	6.890968e-06	other	156
184	5.413953e-05	3.121126e-05	-2.292827e-05	other	167
185	8.371576e-05	6.061842e-05	-2.309734e-05	other	108
186	8.072591e-05	6.385333e-09	-8.071953e-05	other	112
187	7.930967e-05	2.326218e-05	-5.604749e-05	other	114
188	7.862002e-05	3.879562e-05	-3.982440e-05	other	115
189	6.027535e-04	6.557666e-04	5.301308e-05	other	15
19	9.827502e-05	6.119933e-05	-3.707570e-05	other	92
190	2.659207e-04	1.346622e-04	-1.3125285e-04	other	34
191	2.443595e-04	1.932858e-08	-2.443402e-04	other	37
192	7.727609e-05	2.609021e-05	-5.118588e-05	other	117
193	6.747241e-05	4.129034e-05	-2.618207e-05	other	134
194	5.318413e-04	7.492230e-05	-4.569190e-04	other	17
195	1.923681e-04	1.878672e-04	-4.500934e-06	other	47
196	6.901757e-05	4.168372e-05	-2.733386e-05	other	131
197	6.551668e-05	6.230231e-06	-5.928645e-05	other	138
198	6.551668e-05	2.481117e-05	-4.070552e-05	other	138
199	6.192673e-05	3.577419e-05	-2.615254e-05	other	146

2	8.529530e-05	1.408452e-04	5.554991e-05	other	106
20	4.367779e-05	4.996096e-05	6.283174e-06	other	207
200	5.686354e-05	4.728088e-05	-9.582659e-06	other	159
201	3.847363e-05	1.174597e-05	-2.672766e-05	other	235
202	3.631045e-05	4.837139e-06	-3.147331e-05	other	249
203	3.490850e-05	3.357560e-06	-3.155094e-05	other	259
204	4.520651e-04	8.089279e-05	-3.711723e-04	other	20
205	2.009178e-04	4.073891e-05	-1.601789e-04	other	45
206	1.586193e-04	2.724207e-05	-1.313773e-04	other	57
207	4.684613e-05	3.858457e-06	-4.298767e-05	other	193
208	4.636556e-05	1.780143e-06	-4.485515e-05	other	195
209	4.018357e-05	3.683896e-06	-3.649967e-05	other	225
21	4.367779e-05	5.050867e-05	6.830880e-06	other	207
210	3.490850e-05	3.157915e-06	-3.175059e-05	other	259
211	4.758580e-04	3.477897e-04	-1.279683e-04	other	19
212	1.004589e-03	1.252213e-04	-8.793679e-04	neo-endemic	9
213	3.767209e-04	2.979822e-08	-3.766911e-04	other	24
214	2.916549e-04	1.445634e-04	-1.470915e-04	other	31
215	2.825407e-04	2.282277e-05	-2.597179e-04	other	32
216	2.205196e-04	1.832734e-05	-2.021922e-04	other	41
217	1.772804e-04	1.402269e-08	-1.772664e-04	other	51
218	1.643873e-04	1.300286e-08	-1.643743e-04	other	55
219	1.558845e-04	1.233030e-08	-1.558722e-04	other	58
22	3.183557e-05	2.970162e-05	-2.133952e-06	other	284
220	1.255736e-04	9.932740e-09	-1.255637e-04	other	72
221	3.437758e-05	9.878504e-06	-2.449907e-05	other	263
222	6.901757e-05	5.459216e-09	-6.901212e-05	other	131
223	6.412271e-05	1.364680e-05	-5.047591e-05	other	141
224	2.102628e-04	1.663157e-08	-2.102462e-04	other	43
225	3.477424e-04	5.693195e-05	-2.908104e-04	other	26
226	2.511473e-04	4.780370e-05	-2.033436e-04	other	36
227	2.511473e-04	1.986548e-08	-2.511274e-04	other	36
228	2.443595e-04	1.932858e-08	-2.443402e-04	other	37
229	2.443595e-04	5.971620e-05	-1.846433e-04	other	37
23	3.064848e-05	1.226722e-04	9.202372e-05	other	295
230	5.349883e-05	4.231700e-09	-5.349460e-05	other	169
231	5.051007e-05	1.239962e-05	-3.811045e-05	other	179
232	4.834921e-05	3.824371e-09	-4.834539e-05	other	187
233	1.063683e-04	8.413615e-09	-1.063598e-04	other	85
234	1.369894e-04	3.542795e-05	-1.015615e-04	other	66
235	1.329603e-04	4.690909e-05	-8.605124e-05	other	68
236	1.883605e-04	1.489911e-08	-1.883456e-04	other	48
237	2.916549e-04	7.235236e-05	-2.193026e-04	other	31
238	4.109683e-04	4.873219e-05	-3.622361e-04	other	22
239	1.808260e-04	1.638970e-05	-1.644363e-04	other	50
24	2.147578e-05	9.431207e-06	-1.204457e-05	other	421
240	9.935497e-05	8.749122e-06	-9.060585e-05	other	91
241	9.721830e-05	7.689864e-09	-9.721061e-05	other	93
242	5.650814e-04	1.624080e-04	-4.026734e-04	other	16
243	4.809203e-05	1.864923e-05	-2.944280e-05	other	188
244	4.367779e-05	7.142586e-06	-3.653520e-05	other	207
245	8.610764e-05	6.811022e-09	-8.610083e-05	other	105
246	8.001152e-05	6.669451e-06	-7.334207e-05	other	113
247	5.226186e-05	4.377641e-06	-4.788422e-05	other	173
248	2.790525e-05	2.027276e-09	-2.790305e-05	other	324
249	2.739789e-05	2.475063e-06	-2.492282e-05	other	330
25	1.891486e-05	4.604526e-06	-1.431033e-05	other	478
250	2.628286e-05	2.078946e-09	-2.628078e-05	other	344
251	2.490717e-05	2.349888e-06	-2.255728e-05	other	363
252	2.477069e-05	1.959335e-09	-2.476873e-05	other	365
253	2.404602e-05	2.432616e-06	-2.161340e-05	other	376
254	2.199830e-05	4.456066e-06	-1.754224e-05	other	411
255	2.189177e-05	2.214796e-06	-1.967698e-05	other	413
256	2.142489e-05	1.694686e-09	-2.142319e-05	other	422
257	1.982742e-05	6.024675e-06	-1.380274e-05	other	456
258	1.948557e-05	1.541287e-09	-1.948402e-05	other	464
259	1.833936e-05	3.784195e-06	-1.455516e-05	other	493
26	1.848937e-05	4.457219e-06	-1.403215e-05	other	489
260	1.783294e-05	1.391071e-06	-1.644187e-05	other	507
261	1.779784e-05	5.150657e-06	-1.264718e-05	other	508
262	1.620305e-05	2.735927e-06	-1.346712e-05	other	558
263	1.569671e-05	2.878626e-06	-1.281808e-05	other	576
264	9.398443e-06	8.694522e-06	-7.039213e-07	other	962
265	8.907687e-06	9.213716e-07	-7.986315e-06	other	1015
266	8.898920e-06	2.122882e-05	1.232990e-05	other	1016
267	1.089314e-04	1.554625e-04	4.653110e-05	other	83
268	1.808260e-03	1.430315e-07	-1.808117e-03	neo-endemic	5
269	4.109683e-04	2.854363e-05	-3.824247e-04	other	22
27	1.231785e-05	1.413074e-05	1.812889e-06	other	734
270	4.612909e-05	7.841023e-06	-3.828807e-05	other	196
271	4.018357e-05	4.209988e-06	-3.597358e-05	other	225
272	4.000576e-05	3.164413e-09	-4.000260e-05	other	226
273	3.913984e-05	1.314225e-05	-2.599759e-05	other	231
274	3.880387e-05	4.930536e-06	-3.387334e-05	other	233
275	3.847363e-05	1.730259e-05	-2.117104e-05	other	235
276	3.736075e-05	6.705231e-06	-3.065552e-05	other	242
277	2.897853e-05	7.521549e-06	-2.145698e-05	other	312
278	2.102628e-04	1.287104e-04	-8.155248e-05	other	43
279	8.371576e-05	6.621827e-09	-8.370914e-05	other	108
28	1.110725e-05	2.269639e-05	1.158914e-05	other	814

280	1.506884e-03	6.490422e-04	-8.578415e-04	neo-endemic	6
281	6.458073e-04	2.256771e-03	1.610963e-03	other	14
282	5.349883e-05	1.031773e-05	-4.318110e-05	other	169
283	3.705452e-05	6.575738e-06	-3.047878e-05	other	244
284	5.256571e-05	5.367677e-05	1.111060e-06	other	172
285	1.412703e-04	8.163462e-06	-1.331069e-04	other	64
286	4.388982e-05	2.595055e-05	-1.793927e-05	other	206
287	1.339452e-05	1.474387e-05	1.349347e-06	other	675
288	5.022946e-04	2.487536e-04	-2.535410e-04	other	18
289	4.264765e-05	2.549108e-05	-1.715657e-05	other	212
29	6.551668e-05	6.175468e-05	-3.762008e-06	other	138
290	1.197523e-05	3.172861e-06	-8.802374e-06	other	755
291	1.160629e-05	7.321023e-06	-4.285270e-06	other	779
292	7.410904e-05	5.032021e-05	-2.378883e-05	other	122
293	1.390970e-04	1.205114e-05	-1.270458e-04	other	65
294	6.067988e-05	4.193568e-05	-1.874420e-05	other	149
295	5.948225e-05	4.704982e-09	-5.947755e-05	other	152
296	5.615716e-05	4.441971e-09	-5.615272e-05	other	161
297	5.446568e-05	2.553282e-05	-2.893286e-05	other	166
298	4.453843e-05	4.152567e-05	-3.012765e-06	other	203
299	2.605563e-05	1.171474e-05	-1.434089e-05	other	347
3	8.449815e-05	2.284378e-05	-6.165437e-05	other	107
30	7.175637e-05	2.194683e-04	1.477120e-04	other	126
300	5.137104e-05	6.357156e-05	1.220052e-05	other	176
301	3.264008e-05	2.424527e-05	-8.394812e-06	other	277
302	1.205507e-04	9.535431e-09	-1.205412e-04	other	75
303	5.758791e-05	1.258129e-05	-4.500663e-05	other	157
304	4.660465e-05	2.054523e-05	-2.605942e-05	other	194
305	4.913751e-05	1.646556e-05	-3.267185e-05	other	184
306	3.117690e-04	3.921233e-05	-2.725567e-04	other	29
307	3.229037e-04	1.402147e-04	-1.826889e-04	other	28
308	1.705906e-04	9.908724e-05	-7.150337e-05	other	53
309	1.116210e-04	1.032886e-05	-1.012922e-04	other	81
31	3.616521e-05	6.754410e-05	3.137889e-05	other	250
310	7.350652e-05	3.040135e-05	-4.310517e-05	other	123
311	3.559568e-05	5.896858e-06	-2.969882e-05	other	254
312	3.054494e-05	2.224148e-05	-8.303462e-06	other	296
313	2.907171e-05	7.115461e-06	-2.195625e-05	other	311
314	2.288937e-05	3.143992e-05	8.550544e-06	other	395
315	1.558845e-05	1.982681e-06	-1.360577e-05	other	580
316	1.448927e-05	6.333613e-06	-8.155654e-06	other	624
317	1.134417e-05	7.667768e-06	-3.676400e-06	other	797
318	1.120360e-05	8.344771e-06	-2.858826e-06	other	807
319	1.113461e-05	7.691499e-07	-1.036546e-05	other	812
32	2.659207e-04	3.391338e-04	7.321315e-05	other	34
320	9.320930e-06	1.738357e-06	-7.582573e-06	other	970
321	4.758580e-04	4.871288e-04	1.127079e-05	other	19
322	4.109683e-04	2.386360e-04	-1.723323e-04	other	22
323	2.443395e-04	3.106113e-05	-2.132984e-04	other	37
324	1.291615e-04	1.215317e-04	-7.629775e-06	other	70
325	2.731511e-05	1.991416e-05	-7.400957e-06	other	331
326	2.723284e-05	3.042749e-05	3.194652e-06	other	332
327	2.605563e-05	7.121782e-06	-1.893384e-05	other	347
328	2.561275e-05	9.605731e-06	-1.600702e-05	other	353
329	8.449815e-05	2.003453e-05	-6.446362e-05	other	107
33	8.371576e-05	1.184969e-04	3.478110e-05	other	108
330	8.219366e-05	4.823878e-05	-3.395488e-05	other	110
331	7.794226e-05	7.278825e-06	-7.066344e-05	other	116
332	6.322589e-05	5.296122e-06	-5.792977e-05	other	143
333	1.808260e-04	2.032569e-05	-1.605004e-04	other	50
334	4.589494e-05	3.630240e-09	-4.589131e-05	other	197
335	3.013767e-04	4.297014e-05	-2.584066e-04	other	30
336	2.825407e-04	2.263536e-05	-2.599053e-04	other	32
337	5.581051e-05	1.341677e-05	-4.239374e-05	other	162
338	5.137104e-05	4.136785e-06	-4.723425e-05	other	176
339	3.299745e-05	8.427732e-06	-2.456972e-05	other	274
34	6.412271e-05	8.952333e-05	2.540062e-05	other	141
340	2.667051e-05	1.318683e-05	-1.348368e-05	other	339
341	2.477069e-05	6.546084e-06	-1.822461e-05	other	365
342	1.868038e-05	3.678263e-06	-1.500211e-05	other	484
343	1.801056e-05	3.051310e-06	-1.495925e-05	other	502
344	1.786819e-05	8.811448e-06	-9.056739e-06	other	506
345	7.233042e-06	3.328682e-06	-3.904360e-06	other	1250
346	7.102358e-06	5.151363e-06	-1.950995e-06	other	1273
347	7.096784e-06	1.117101e-06	-5.979683e-06	other	1274
348	6.023519e-06	9.637247e-07	-5.059794e-06	other	1501
349	5.851976e-06	2.989433e-06	-2.862542e-06	other	1545
35	2.456876e-05	4.002870e-05	1.545994e-05	other	368
350	5.755126e-06	1.657232e-06	-4.097893e-06	other	1571
351	5.693515e-06	2.432663e-06	-3.260852e-06	other	1588
352	1.369894e-04	3.417201e-04	2.047307e-04	other	66
353	4.758580e-05	1.997795e-04	1.521937e-04	other	190
354	3.477424e-04	8.157094e-05	-2.661715e-04	other	26
355	2.583229e-04	2.894556e-04	3.113269e-05	other	35
356	4.018357e-05	1.878571e-05	-2.139786e-05	other	225
357	3.477424e-05	8.403271e-06	-2.637097e-05	other	260
358	2.964361e-05	1.034821e-04	7.383850e-05	other	305
359	1.144469e-04	9.052624e-09	-1.144378e-04	other	79
36	1.808260e-03	8.962423e-04	-9.20182e-04	neo-endemic	5
360	3.023847e-05	2.099901e-05	-9.239463e-06	other	299

361	2.456876e-05	8.875664e-06	-1.569309e-05	other	368
362	2.443595e-05	1.245297e-05	-1.198298e-05	other	370
363	2.312354e-05	2.369180e-05	5.682603e-07	other	391
364	2.277406e-05	7.003495e-06	-1.577057e-05	other	397
365	1.435127e-04	7.938922e-05	-6.412351e-05	other	63
366	1.189645e-04	2.148619e-05	-9.747832e-05	other	76
367	2.054841e-04	1.625358e-08	-2.054679e-04	other	44
368	7.534419e-05	4.042876e-05	-3.491543e-05	other	120
369	6.797972e-05	6.320342e-06	-6.165937e-05	other	133
37	1.130163e-03	1.957058e-03	8.268952e-04	meso-endemic	8
370	4.520651e-04	3.575787e-08	-4.520294e-04	other	20
371	9.041302e-04	2.486922e-04	-6.554380e-04	other	10
372	1.965500e-04	4.626448e-05	-1.502856e-04	other	46
373	1.369894e-04	5.996121e-05	-7.702822e-05	other	66
374	1.004589e-04	6.885180e-06	-9.357373e-05	other	90
375	1.102598e-04	1.954259e-05	-9.071720e-05	other	82
376	1.089314e-04	3.756057e-05	-7.137078e-05	other	83
377	9.418023e-05	2.944702e-05	-6.473321e-05	other	96
378	5.870976e-05	7.586922e-05	1.715946e-05	other	154
379	3.675326e-05	2.170961e-05	-1.504365e-05	other	246
38	1.956992e-05	1.085814e-05	-8.711777e-06	other	462
380	3.161295e-05	1.208417e-05	-1.952877e-05	other	286
381	3.054494e-05	8.321486e-06	-2.222245e-05	other	296
382	2.925988e-05	1.085457e-05	-1.840531e-05	other	309
383	2.226922e-05	8.843135e-06	-1.342608e-05	other	406
384	1.801056e-05	1.732309e-06	-1.627825e-05	other	502
385	7.534419e-05	4.831432e-05	-2.702987e-05	other	120
386	5.166458e-05	3.578376e-05	-1.588083e-05	other	175
387	3.183557e-05	7.953268e-06	-2.388230e-05	other	284
388	2.674942e-05	4.289230e-05	1.614289e-05	other	338
389	5.650814e-04	2.012442e-04	-3.638372e-04	other	16
39	7.794226e-05	1.943760e-05	-5.850466e-05	other	116
390	4.305382e-05	5.845142e-05	1.539760e-05	other	210
391	4.244743e-05	2.840161e-05	-1.404582e-05	other	213
392	4.224908e-05	4.088467e-06	-3.816061e-05	other	214
393	4.072659e-05	4.482355e-06	-3.624423e-05	other	222
394	2.723284e-05	3.486406e-06	-2.374643e-05	other	332
395	2.031753e-05	2.016143e-06	-1.830139e-05	other	445
396	1.504376e-05	1.994775e-06	-1.304899e-05	other	601
397	1.221798e-05	3.855233e-06	-8.362743e-06	other	740
398	9.447547e-06	2.013047e-06	-7.434500e-06	other	957
399	8.744006e-06	4.227835e-06	-4.516171e-06	other	1034
4	8.145317e-05	7.823254e-05	-3.220634e-06	other	111
40	1.159141e-04	9.524741e-05	-2.066672e-05	other	78
400	8.529530e-06	9.422414e-07	-7.587289e-06	other	1060
401	1.291615e-03	1.535655e-04	-1.138049e-03	neo-endemic	7
402	6.027535e-04	6.599641e-04	5.721066e-05	other	15
403	1.130163e-04	2.5355538e-05	-8.766090e-05	other	80
404	2.659207e-04	1.328233e-04	-1.330974e-04	other	34
405	1.015877e-04	1.894606e-05	-8.264160e-05	other	89
406	1.860350e-05	1.625219e-06	-1.697828e-05	other	486
407	1.797476e-05	1.502893e-05	-2.945824e-06	other	503
408	1.086695e-05	4.145344e-06	-6.721606e-06	other	832
409	4.264765e-05	1.735445e-05	-2.529321e-05	other	212
41	1.323763e-05	1.047082e-09	-1.323658e-05	other	683
410	3.490850e-05	3.545571e-06	-3.136293e-05	other	259
411	3.172387e-05	3.150578e-06	-2.857329e-05	other	285
412	3.054494e-05	5.381137e-06	-2.516380e-05	other	296
413	1.030935e-05	5.404304e-06	-4.905049e-06	other	877
414	9.700968e-06	5.151312e-06	-4.549656e-06	other	932
415	9.359526e-06	3.100889e-06	-6.258637e-06	other	966
416	8.219366e-06	9.510136e-07	-7.268352e-06	other	1100
417	4.758580e-05	1.809485e-05	-2.949095e-05	other	190
418	4.498160e-05	7.975766e-06	-3.700584e-05	other	201
419	4.305382e-05	4.236547e-05	-6.883487e-07	other	210
42	1.808260e-04	1.509412e-05	-1.657319e-04	other	50
420	3.139341e-05	4.115266e-06	-2.727814e-05	other	288
421	2.360653e-05	1.374304e-05	-9.863493e-06	other	383
422	5.833098e-05	6.995193e-06	-5.133579e-05	other	155
423	3.948167e-05	9.585672e-06	-2.989600e-05	other	229
424	1.699493e-05	3.944849e-06	-1.305008e-05	other	532
425	1.403929e-05	4.802965e-06	-9.236324e-06	other	644
426	1.004589e-03	1.669130e-03	6.645407e-04	meso-endemic	9
427	6.954848e-04	1.737355e-05	-6.781112e-04	other	13
428	7.410904e-05	1.886828e-04	1.145737e-04	other	122
429	3.117690e-04	2.182921e-04	-9.347694e-05	other	29
43	1.280638e-05	1.054689e-06	-1.175169e-05	other	706
430	1.586193e-04	1.105759e-04	-4.804341e-05	other	57
431	5.318413e-04	1.050486e-04	-4.267927e-04	other	17
432	1.102598e-04	3.772722e-05	-7.253257e-05	other	82
433	6.849471e-05	3.473418e-05	-3.376054e-05	other	132
434	4.072659e-05	4.604166e-06	-3.612242e-05	other	222
435	2.059522e-05	1.004895e-05	-1.054628e-05	other	439
436	8.978453e-06	4.442727e-06	-4.535726e-06	other	1007
437	8.545654e-06	9.886114e-07	-7.557043e-06	other	1058
438	5.587949e-06	4.420008e-10	-5.587507e-06	other	1618
439	5.587949e-06	4.381861e-07	-5.149763e-06	other	1618
44	1.072515e-05	3.076302e-06	-7.648849e-06	other	843
440	5.512989e-06	3.195335e-06	-2.317654e-06	other	1640
441	6.551668e-05	6.641427e-05	8.975846e-07	other	138

442	7.008761e-05	5.543855e-09	-7.008207e-05	other	129
443	9.320930e-05	7.372756e-09	-9.320193e-05	other	97
444	8.777963e-05	3.802415e-05	-4.975549e-05	other	103
445	4.410391e-05	1.069986e-05	-3.340405e-05	other	205
446	3.675326e-05	4.103422e-05	4.280956e-06	other	246
447	2.756495e-05	8.186036e-06	-1.937891e-05	other	328
448	5.196151e-05	4.063185e-05	-1.132966e-05	other	174
449	4.072659e-05	8.142923e-06	-3.258366e-05	other	222
45	1.015877e-05	4.644428e-06	-5.514339e-06	other	890
450	2.916549e-05	8.171119e-06	-2.099437e-05	other	310
451	2.674942e-05	6.829576e-06	-1.991984e-05	other	338
452	9.618407e-05	3.831646e-05	-5.786760e-05	other	94
453	6.235381e-05	1.962881e-05	-4.272500e-05	other	145
454	5.909348e-05	1.595873e-05	-4.313475e-05	other	153
455	2.102628e-04	2.624281e-04	5.216525e-05	other	43
456	6.648016e-05	1.862801e-05	-4.785215e-05	other	136
457	3.531759e-05	6.913559e-06	-2.840403e-05	other	256
458	2.964361e-05	1.474459e-06	-2.816915e-05	other	305
459	2.879396e-05	4.898673e-06	-2.389528e-05	other	314
46	9.859654e-06	8.616349e-07	-8.998019e-06	other	917
460	1.725439e-05	6.624631e-06	-1.062976e-05	other	524
461	1.225109e-05	2.715107e-06	-9.535980e-06	other	738
462	3.602112e-05	2.849232e-09	-3.601828e-05	other	251
463	2.398223e-05	1.110051e-05	-1.288172e-05	other	377
464	2.348390e-05	1.811581e-05	-5.368096e-06	other	385
465	2.330233e-05	1.843189e-09	-2.330048e-05	other	388
466	2.064224e-05	1.996282e-06	-1.864596e-05	other	438
467	4.367779e-05	3.392275e-05	-9.755037e-06	other	207
468	3.798867e-05	2.833669e-06	-3.5155500e-05	other	238
469	2.483874e-05	1.720410e-05	-7.634641e-06	other	364
47	7.591354e-06	1.079876e-05	3.207411e-06	other	1191
470	2.511473e-04	1.074039e-04	-1.437433e-04	other	36
471	6.648016e-05	1.763197e-05	-4.884819e-05	other	136
472	1.051314e-04	5.013550e-05	-5.499592e-05	other	86
473	5.196151e-05	7.730290e-06	-4.423122e-05	other	174
474	9.320930e-05	3.531953e-05	-5.788977e-05	other	97
475	4.709012e-05	4.027978e-06	-4.306214e-05	other	192
476	3.782972e-05	3.329100e-06	-3.450062e-05	other	239
477	2.477069e-05	2.140332e-06	-2.263036e-05	other	365
478	2.142489e-05	5.868434e-06	-1.555645e-05	other	422
479	2.117401e-05	1.674841e-09	-2.117234e-05	other	427
48	7.591354e-06	2.628153e-05	1.869017e-05	other	1191
480	2.000288e-05	1.869942e-06	-1.813294e-05	other	452
481	1.165116e-05	1.020156e-06	-1.063101e-05	other	776
482	9.711388e-06	2.056928e-06	-7.654460e-06	other	931
483	9.507153e-06	3.151960e-06	-6.355193e-06	other	951
484	9.014259e-06	4.188186e-06	-4.826074e-06	other	1003
485	8.987378e-06	2.567102e-06	-6.420276e-06	other	1006
486	7.681650e-06	3.433618e-06	-4.248032e-06	other	1177
487	7.572280e-06	2.453778e-06	-5.18492e-06	other	1194
488	4.002347e-06	9.110017e-07	-3.091346e-06	other	2259
489	3.995273e-06	2.514326e-06	-1.480946e-06	other	2263
49	7.584985e-06	2.600874e-06	-4.984111e-06	other	1192
490	3.782972e-06	3.917105e-07	-3.391261e-06	other	2390
491	3.778229e-06	1.239022e-06	-2.539207e-06	other	2393
492	3.778229e-06	3.588184e-07	-3.419411e-06	other	2393
493	3.771924e-06	4.304886e-07	-3.341436e-06	other	2397
494	3.771924e-06	8.199410e-07	-2.951983e-06	other	2397
495	3.708491e-06	1.066736e-06	-2.641756e-06	other	2438
496	3.679814e-06	1.226428e-06	-2.453386e-06	other	2457
497	3.661929e-06	6.966459e-07	-2.965283e-06	other	2469
498	3.130645e-06	3.712458e-06	5.818128e-07	other	2888
499	3.110183e-06	1.279921e-06	-1.830262e-06	other	2907
5	2.511473e-04	3.377366e-04	8.658934e-05	other	36
50	6.987096e-06	4.411483e-06	-2.575613e-06	other	1294
500	3.088931e-06	7.886079e-07	-2.300324e-06	other	2927
501	3.058627e-06	2.419341e-10	-3.058385e-06	other	2956
502	3.057593e-06	4.329675e-06	1.272082e-06	other	2957
503	3.043185e-06	2.074385e-06	-9.688000e-07	other	2971
504	3.012763e-06	1.435897e-06	-1.576866e-06	other	3001
505	2.998774e-06	1.811016e-06	-1.187758e-06	other	3015
506	2.997779e-06	6.074031e-07	-2.390376e-06	other	3016
507	0.000000e+00	0.000000e+00	0.000000e+00	other	NA
51	2.583229e-04	4.403145e-04	1.819916e-04	other	35
52	2.054841e-04	5.069268e-04	3.014426e-04	other	44
53	7.534419e-05	3.601855e-05	-3.932564e-05	other	120
54	1.310334e-04	2.537250e-05	-1.056609e-04	other	69
55	6.648016e-05	1.839042e-05	-4.808974e-05	other	136
56	3.948167e-05	1.413389e-05	-2.534778e-05	other	229
57	3.948167e-05	5.386139e-05	1.437972e-05	other	229
58	3.913984e-05	5.783681e-05	1.869697e-05	other	231
59	3.287746e-05	2.911583e-05	-3.761631e-06	other	275
6	5.795707e-05	1.104020e-04	5.244493e-05	other	156
60	1.883605e-04	2.228697e-04	3.450926e-05	other	48
61	1.586193e-04	9.409158e-04	7.822965e-04	other	57
62	3.931001e-04	2.258312e-04	-1.672689e-04	other	23
63	3.013767e-04	4.172849e-05	-2.596482e-04	other	30
64	2.825407e-04	1.212211e-04	-1.613196e-04	other	32
65	1.845164e-04	8.647190e-05	-9.804447e-05	other	49
66	1.772804e-04	4.721267e-04	2.948462e-04	other	51

67		1.532424e-04	2.035616e-04	5.031916e-05	other	59
68		1.506884e-03	4.977381e-04	-1.009146e-03	neo-endemic	6
69		2.318283e-04	1.788137e-04	-5.301458e-05	other	39
7		5.196151e-05	4.778721e-05	-4.174294e-06	other	174
70		1.051314e-04	4.720912e-05	-5.792230e-05	other	86
71		1.051314e-04	4.660956e-04	3.609642e-04	other	86
72		5.022946e-04	1.462622e-03	9.603271e-04	other	18
73		3.348630e-04	5.881803e-04	2.533172e-04	other	27
74		6.458073e-04	5.108267e-08	-6.457556e-04	other	14
75		3.948167e-05	1.461606e-04	1.066789e-04	other	229
76		3.751578e-05	8.002141e-05	4.250564e-05	other	241
77		3.690327e-05	9.526445e-06	-2.737683e-05	other	245
78		3.675326e-05	3.485838e-05	-1.894879e-06	other	246
79		3.573637e-05	2.826709e-09	-3.573355e-05	other	253
8		4.566314e-05	1.687415e-05	-2.878899e-05	other	198
80		3.299745e-05	3.187543e-05	-1.122019e-06	other	274
81		3.275834e-05	2.286138e-05	-9.896959e-06	other	276
82		3.217545e-05	2.611769e-05	-6.057764e-06	other	281
83		3.183557e-05	1.021483e-05	-2.162074e-05	other	284
84		1.709131e-05	7.851706e-06	-9.239602e-06	other	529
85		5.693515e-06	7.575179e-06	1.881664e-06	other	1588
86		8.219366e-04	9.147983e-04	9.286170e-05	other	11
87		2.216005e-05	1.436167e-05	-7.798385e-06	other	408
88		2.142489e-05	2.754671e-05	6.121826e-06	other	422
89		2.107530e-05	4.557120e-05	2.449591e-05	other	429
9		4.305382e-04	4.710688e-04	4.053056e-05	other	21
90		6.367114e-05	1.603466e-05	-4.763649e-05	other	142
91		6.367114e-05	3.151921e-04	2.515210e-04	other	142
92		5.795707e-05	1.907411e-04	1.327841e-04	other	156
93		8.072591e-05	8.565735e-06	-7.216018e-05	other	112
94		7.350652e-05	8.790881e-05	1.440229e-05	other	123
95		3.240610e-05	5.726527e-05	2.485917e-05	other	279
96		2.324242e-05	2.470511e-05	1.462687e-06	other	389
97		1.1865523e-05	1.136541e-05	-4.998158e-07	other	762
98		8.219366e-04	4.798358e-03	3.976421e-03	other	11
99		4.388982e-05	3.253124e-06	-4.063669e-05	other	206
abbreviata		1.506884e-03	1.436124e-03	-7.075948e-05	meso-endemic	6
acanthaster		9.041302e-04	2.500786e-03	1.596655e-03	other	10
acanthoclada		9.132629e-05	1.844050e-04	9.307874e-05	other	99
acicacea		7.233042e-05	7.218576e-05	-1.4465581e-07	other	125
aciphylla		7.534419e-04	3.224805e-04	-4.309613e-04	other	12
acomia		6.458073e-04	3.464592e-04	-2.993482e-04	other	14
acradenia		5.137104e-05	5.621538e-05	4.844342e-06	other	176
acroniates		1.808260e-03	7.818173e-04	-1.026443e-03	neo-endemic	5
acuaria		2.825407e-04	2.234867e-08	-2.825183e-04	other	32
aculeatissima		2.659207e-04	7.569400e-04	4.910193e-04	other	34
acuminata		6.551668e-05	1.885246e-05	-4.666422e-05	other	138
acutata		3.616521e-04	4.275355e-04	6.588346e-05	other	25
adinophylla		9.041302e-03	1.786382e-02	8.822520e-03	paleo-endemic	1
adnata		1.506884e-03	4.796539e-04	-1.027230e-03	neo-endemic	6
adoxa		7.862002e-05	1.820600e-05	-6.041402e-05	other	115
adsurgens		5.833098e-05	1.054178e-05	-4.778920e-05	other	155
adunca		5.650814e-04	7.893862e-04	2.243048e-04	other	16
aemula		5.022946e-04	3.673275e-04	-1.349671e-04	other	18
aestivalis		3.767209e-04	2.933933e-04	-8.332766e-05	other	24
alata		1.808260e-04	4.009575e-04	2.201315e-04	other	50
alcockii		1.291615e-03	1.606220e-03	3.146051e-04	meso-endemic	7
alexandri		2.260326e-03	9.152274e-03	6.891948e-03	paleo-endemic	4
alpina		5.318413e-04	5.692479e-04	3.740658e-05	other	17
amblygona		1.039230e-04	2.060459e-04	1.021229e-04	other	87
amblyophylla		4.520651e-03	1.408732e-02	9.566664e-03	paleo-endemic	2
ammobia		8.219366e-04	7.910600e-04	-3.087660e-05	other	11
ampliceps		1.116210e-04	5.256877e-05	-5.905225e-05	other	81
amycтика		3.013767e-03	1.040566e-03	-1.973201e-03	neo-endemic	3
anasilla		1.506884e-03	3.428075e-03	1.921192e-03	meso-endemic	6
anastema		1.506884e-03	2.293590e-03	7.867058e-04	meso-endemic	6
anaticeps		6.954848e-04	2.142965e-03	1.447480e-03	other	13
anceps		2.511473e-04	2.015837e-04	-4.956357e-05	other	36
ancistrocarpa		4.346780e-05	7.697054e-05	3.350274e-05	other	208
ancistrophylla		1.238535e-04	2.571802e-05	-9.813544e-05	other	73
andrewsii		2.205196e-04	4.744428e-04	2.539233e-04	other	41
aneura		1.094589e-05	4.233587e-06	-6.712300e-06	other	826
anfractuosa		5.650814e-04	5.545739e-04	-1.0507474e-05	other	16
angusta		5.650814e-04	1.156121e-03	5.910400e-04	other	16
anthochaera		4.758580e-04	1.535120e-04	-3.223460e-04	other	19
aphanoclada		2.260326e-03	6.950566e-03	4.690240e-03	paleo-endemic	4
aphylla		3.013767e-03	1.205790e-02	9.044135e-03	paleo-endemic	3
applanata		2.825407e-04	2.195575e-03	1.913034e-03	other	32
aprepta		2.825407e-04	2.234867e-08	-2.825183e-04	other	32
apricta		9.041302e-03	2.293302e-03	-6.748001e-03	neo-endemic	1
araneosa		3.013767e-03	9.974512e-04	-2.016316e-03	neo-endemic	3
arcuatus		1.506884e-03	1.846046e-04	-1.322279e-03	neo-endemic	6
areolata		1.291615e-03	1.021653e-07	-1.291512e-03	neo-endemic	7
argutifolia		3.013767e-03	5.086852e-03	2.073085e-03	meso-endemic	3
argyraea		1.705906e-04	3.020693e-04	1.314787e-04	other	53
argyrodendron		3.767209e-04	5.441393e-05	-3.223070e-04	other	24
argyrophylla		2.825407e-04	2.648535e-05	-2.560553e-04	other	32
arida		2.583229e-04	7.907022e-05	-1.792527e-04	other	35
armitti		6.027535e-04	9.113025e-05	-5.116232e-04	other	15
arrecta		6.458073e-04	3.388787e-04	-3.069286e-04	other	14

ashbyae	9.041302e-04	3.632112e-03	2.727981e-03	other	10
aspera	3.013767e-04	8.807847e-05	-2.132983e-04	other	30
asperulacea	1.965500e-04	1.088829e-04	-8.766714e-05	other	46
assimilis	1.051314e-04	3.533684e-05	-6.979458e-05	other	86
ataxiphylla	1.004589e-03	3.729739e-03	2.725149e-03	meso-endemic	9
atkinsiana	4.758580e-04	6.310771e-04	1.552191e-04	other	19
atrox	9.041302e-03	5.763760e-03	-3.277542e-03	neo-endemic	1
attenuata	8.219366e-04	8.138164e-04	-8.120184e-06	other	11
aulacocarpa	1.051314e-04	5.081359e-05	-5.431783e-05	other	86
aulacophylla	5.022946e-04	2.950568e-04	-2.072377e-04	other	18
auratiflora	3.013767e-03	1.277168e-02	9.757913e-03	paleo-endemic	3
aureocrinita	1.004589e-03	3.679445e-04	-6.366446e-04	neo-endemic	9
auricoma	1.506884e-03	2.956324e-03	1.449440e-03	meso-endemic	6
auriculiformis	8.371576e-05	2.505897e-04	1.668740e-04	other	108
auronitens	7.534419e-04	1.084753e-03	3.313107e-04	other	12
ausfeldii	6.027535e-04	4.767715e-08	-6.027058e-04	other	15
axillaris	8.219366e-04	2.547651e-03	1.725715e-03	other	11
ayersiana	7.597733e-05	5.308986e-05	-2.288747e-05	other	119
baeuerlenii	6.027535e-04	6.645766e-04	6.182310e-05	other	15
baileyana	7.534419e-04	1.348035e-04	-6.186383e-04	other	12
bakeri	6.027535e-04	2.710215e-03	2.107461e-03	other	15
balsamea	4.758580e-04	1.138892e-04	-3.619688e-04	other	19
bancroftiorum	1.144469e-04	9.052624e-09	-1.144378e-04	other	79
barattensis	3.013767e-03	7.124868e-03	4.111101e-03	paleo-endemic	3
barringtonensis	1.291615e-03	1.517307e-03	2.256928e-04	meso-endemic	7
bartleana	4.520651e-03	3.575787e-07	-4.520294e-03	neo-endemic	2
basedowii	3.229037e-04	6.167092e-04	2.938056e-04	other	28
baueri	3.616521e-04	9.258915e-04	5.642394e-04	other	25
baxteri	1.004589e-03	3.822126e-03	2.817537e-03	meso-endemic	9
beadleana	4.520651e-03	1.375688e-02	9.236227e-03	paleo-endemic	2
beauverdiana	3.477424e-04	4.052933e-05	-3.072131e-04	other	26
beckleri	1.674315e-04	1.375453e-04	-2.988619e-05	other	54
benthamii	1.130163e-03	3.384190e-04	-7.917438e-04	neo-endemic	8
betchei	7.534419e-04	2.232045e-04	-5.302373e-04	other	12
bidentata	1.674315e-04	4.496156e-04	2.821841e-04	other	54
bifaria	1.506884e-03	7.277486e-04	-7.791351e-04	neo-endemic	6
biflora	6.954848e-04	1.195532e-03	5.000474e-04	other	13
binata	7.534419e-04	4.722852e-04	-2.811566e-04	other	12
binervata	2.318283e-04	2.074490e-05	-2.110834e-04	other	39
binervia	3.348630e-04	2.209943e-04	-1.138688e-04	other	27
bivenosa	4.589494e-05	7.553815e-05	2.964321e-05	other	197
blakei	1.027421e-04	6.605827e-04	5.578406e-04	other	88
blakelyi	3.013767e-04	4.671436e-04	1.657668e-04	other	30
blayana	3.013767e-03	5.415040e-04	-2.472263e-03	neo-endemic	3
boormanii	4.520651e-04	5.757662e-04	1.237011e-04	other	20
brachybotrya	7.063517e-05	1.471852e-05	-5.591666e-05	other	128
brachyclada	3.616521e-04	1.175988e-03	8.143363e-04	other	25
brachiphylla	5.022946e-04	8.905851e-04	3.882905e-04	other	18
brachypoda	1.808260e-03	2.244015e-03	4.357546e-04	meso-endemic	5
brachystachya	3.798867e-05	2.516907e-05	-1.281959e-05	other	238
bracteolata	1.291615e-03	1.436652e-03	1.450379e-04	meso-endemic	7
brassii	5.318413e-04	1.158921e-03	6.270801e-04	other	17
brockii	1.004589e-03	2.920476e-03	1.915887e-03	meso-endemic	9
bromiliowiana	1.004589e-03	1.770965e-03	7.663762e-04	meso-endemic	9
browniana	2.318283e-04	4.626265e-04	2.307982e-04	other	39
bulgaensis	2.260326e-03	6.533363e-04	-1.606989e-03	neo-endemic	4
burkittii	4.346780e-05	2.406079e-05	-1.940701e-05	other	208
buxifolia	7.233042e-05	1.773820e-04	1.050516e-04	other	125
caesiella	4.520651e-04	1.115294e-03	6.632290e-04	other	20
calamifolia	9.132629e-05	5.216657e-05	-3.915971e-05	other	99
calantha	1.130163e-03	1.174237e-03	4.407440e-05	meso-endemic	8
calcicola	8.693560e-05	8.214313e-06	-7.872129e-05	other	104
campptoclada	2.825407e-04	4.585115e-04	1.759708e-04	other	32
campylophylla	1.291615e-03	2.723046e-03	1.431431e-03	meso-endemic	7
cana	3.616521e-04	1.285143e-04	-2.331378e-04	other	25
cangaiensis	4.520651e-03	4.788326e-04	-4.041819e-03	neo-endemic	2
cardiophylla	5.650814e-04	2.138152e-04	-3.512662e-04	other	16
carneorum	3.229037e-04	7.078652e-04	3.849615e-04	other	28
carnosula	2.260326e-03	5.380049e-03	3.119724e-03	paleo-endemic	4
caroleae	1.189645e-04	4.981365e-05	-6.915085e-05	other	76
catenulata	1.532424e-04	8.273224e-05	-7.051017e-05	other	59
cavealis	1.506884e-03	3.656891e-03	2.150007e-03	meso-endemic	6
cedroides	1.808260e-03	4.662524e-03	2.854264e-03	meso-endemic	5
celastrifolia	4.305382e-04	8.602593e-04	4.297211e-04	other	21
celsa	6.027535e-04	4.034102e-04	-1.993433e-04	other	15
chartacea	5.318413e-04	5.367480e-04	4.906701e-06	other	17
cheelii	2.659207e-04	1.809641e-04	-8.495653e-05	other	34
chinchillensis	1.004589e-03	1.711744e-03	7.071549e-04	meso-endemic	9
chisholmii	1.349448e-04	1.067399e-08	-1.349341e-04	other	67
chrysotricha	4.520651e-03	5.207260e-03	6.866087e-04	meso-endemic	2
citrinoviridis	1.772804e-04	2.045159e-05	-1.568289e-04	other	51
clelandii	2.205196e-04	1.818532e-04	-3.866640e-05	other	41
clunies	4.520651e-03	1.818097e-03	-2.702554e-03	neo-endemic	2
clydonophora	1.506884e-03	3.188094e-03	1.681211e-03	meso-endemic	6
cochlaris	1.705906e-04	2.671033e-04	9.651273e-05	other	53
cognata	5.650814e-04	1.802979e-04	-3.847834e-04	other	16
colei	4.684613e-05	3.705478e-09	-4.684242e-05	other	193
colletioides	5.833098e-05	1.279603e-04	6.962930e-05	other	155
complanata	1.130163e-04	2.001405e-04	8.712423e-05	other	80
concurrents	1.883605e-04	2.784710e-05	-1.605134e-04	other	48

conferta	8.951784e-05	6.448137e-05	-2.503648e-05	other	101
congesta	6.027535e-04	2.049068e-03	1.446315e-03	other	15
consobrina	6.954848e-04	1.281995e-03	5.865106e-04	other	13
conspersa	3.013767e-04	4.142095e-04	1.128328e-04	other	30
constablei	9.041302e-03	3.623151e-02	2.719021e-02	paleo-endemic	1
continua	1.329603e-04	1.970188e-04	6.405845e-05	other	68
coolgardiensis	1.015877e-04	1.628077e-04	6.122007e-05	other	89
coriacea	4.709012e-05	3.724778e-09	-4.708639e-05	other	192
costata	8.219366e-04	2.172506e-03	1.350569e-03	other	11
courtii	9.041302e-03	6.064724e-03	-2.976578e-03	neo-endemic	1
covenyi	1.506884e-03	3.143006e-03	1.636122e-03	meso-endemic	6
cowleana	6.150546e-05	1.050247e-04	4.351924e-05	other	147
craspedocarpa	2.009178e-04	7.912177e-05	-1.217961e-04	other	45
crassa	9.418023e-05	2.596380e-05	-6.821644e-05	other	96
crassicarpa	1.482181e-04	1.172389e-08	-1.482063e-04	other	61
crassiscula	6.027535e-04	6.187676e-04	1.601409e-05	other	15
cremiflora	6.458073e-04	5.288980e-04	-1.169093e-04	other	14
cultiformis	2.318283e-04	3.304559e-04	9.862759e-05	other	39
cupularis	8.001152e-05	3.408263e-05	-4.592890e-05	other	113
currani	6.954848e-04	1.242627e-03	5.471421e-04	other	13
curvata	1.130163e-03	2.382844e-03	1.252681e-03	meso-endemic	8
cuspidifolia	3.117690e-04	2.172394e-03	1.860625e-03	other	29
cuthbertsonii	5.4465568e-05	1.962704e-04	1.418048e-04	other	166
cyclops	1.369894e-04	6.521050e-04	5.151156e-04	other	66
cyperophylla	9.827502e-05	7.358728e-05	-2.468775e-05	other	92
dangarensis	4.520651e-03	7.451232e-03	2.930580e-03	paleo-endemic	2
dawsonii	3.013767e-04	8.916427e-04	5.902659e-04	other	30
dealbata	5.758791e-05	1.093708e-05	-4.665083e-05	other	157
deanei	4.834921e-05	8.730399e-06	-3.961881e-05	other	187
debilis	6.027535e-04	5.539579e-04	-4.879562e-05	other	15
declinata	2.260326e-03	1.914810e-03	-3.455160e-04	meso-endemic	4
decora	3.645686e-05	5.971545e-05	2.325858e-05	other	248
decurrents	4.520651e-04	3.575787e-08	-4.520294e-04	other	20
deliberata	4.520651e-04	3.778769e-04	-7.418819e-05	other	20
delphina	7.534419e-04	4.314350e-03	3.560908e-03	other	12
dempsteri	5.022946e-04	1.809224e-03	1.306929e-03	other	18
denticulosa	1.130163e-03	2.010220e-04	-9.291408e-04	neo-endemic	8
desmondii	1.291615e-03	3.279173e-04	-9.636973e-04	neo-endemic	7
dialaga	4.520651e-03	3.270479e-04	-4.193603e-03	neo-endemic	2
dictyoneura	4.520651e-03	3.307158e-03	-1.213493e-03	neo-endemic	2
dictyophleba	4.783758e-05	6.060738e-05	1.276980e-05	other	189
didyma	4.520651e-03	3.575787e-07	-4.520294e-03	neo-endemic	2
difficilis	7.597733e-05	2.232075e-05	-5.365658e-05	other	119
dimidiata	1.159141e-04	2.612836e-04	1.453694e-04	other	78
diphylla	2.260326e-03	2.374963e-03	1.146377e-04	meso-endemic	4
disparirma	1.063683e-04	7.301173e-05	-3.335653e-05	other	85
distans	6.027535e-04	5.797399e-04	-2.301357e-05	other	15
dodonaeifolia	4.520651e-04	6.012640e-04	1.491189e-04	other	20
dolichophylla	2.260326e-03	1.087952e-02	8.619193e-03	paleo-endemic	4
doratoxylon	8.219366e-05	1.726829e-04	9.048922e-05	other	110
dorothea	9.041302e-04	9.912609e-04	8.713065e-05	other	10
drepanocarpa	9.618407e-05	2.137020e-05	-7.481386e-05	other	94
drepanophylla	1.130163e-03	3.155062e-03	2.024899e-03	meso-endemic	8
drummondii	2.443595e-04	2.884462e-04	4.408670e-05	other	37
dunrii	2.659207e-04	3.924237e-04	1.265030e-04	other	34
elachantha	5.870976e-05	4.643879e-09	-5.870511e-05	other	154
elata	6.027535e-04	1.707331e-03	1.104577e-03	other	15
elongata	2.443595e-04	1.557358e-04	-8.862377e-05	other	37
empelioclada	1.808260e-03	2.101121e-03	2.928602e-04	meso-endemic	5
enervia	1.965500e-04	1.332475e-04	-6.330260e-05	other	46
enterocarpa	5.650814e-04	3.796834e-04	-1.853980e-04	other	16
epacantha	3.013767e-03	5.409387e-03	2.395620e-03	meso-endemic	3
eriopoda	1.586193e-04	7.484815e-04	5.898622e-04	other	57
errabunda	1.506884e-03	1.690419e-03	1.835348e-04	meso-endemic	6
estropholiata	8.529530e-05	1.650084e-04	7.971307e-05	other	106
euthycarpa	1.144469e-04	9.517772e-05	-1.926914e-05	other	79
excelsa	4.783758e-05	1.838210e-05	-2.945548e-05	other	189
excentrica	9.041302e-04	7.147236e-04	-1.894066e-04	other	10
exilis	1.506884e-03	2.421227e-03	9.143433e-04	meso-endemic	6
extensa	3.348630e-04	1.416159e-03	1.081296e-03	other	27
fagonioides	1.808260e-03	3.241301e-03	1.433041e-03	meso-endemic	5
falcata	1.015877e-04	8.035475e-09	-1.015796e-04	other	89
falciformis	7.662121e-05	4.818377e-05	-2.843744e-05	other	118
faucium	1.808260e-03	7.259642e-04	-1.082296e-03	neo-endemic	5
fecunda	2.260326e-03	2.142886e-03	-1.174394e-04	meso-endemic	4
filicifolia	2.205196e-04	8.371121e-05	-1.368084e-04	other	41
fimbriata	1.027421e-04	1.739064e-05	-8.535143e-05	other	88
flexifolia	1.923681e-04	1.761718e-04	-1.619629e-05	other	47
floribunda	1.076346e-04	1.947956e-04	8.716102e-05	other	84
fragilis	2.102628e-04	1.452862e-04	-6.497662e-05	other	43
fulva	1.808260e-03	1.324531e-03	-4.837296e-04	meso-endemic	5
gardneri	9.041302e-04	3.984442e-04	-5.056860e-04	other	10
gelasina	2.260326e-03	2.557917e-03	2.975918e-04	meso-endemic	4
genistifolia	7.794226e-05	1.178698e-04	3.992756e-05	other	116
georginae	8.951784e-05	1.434821e-04	5.396423e-05	other	101
gilbertti	6.954848e-04	5.578852e-04	-1.375964e-04	other	13
gillii	2.260326e-03	2.516661e-03	2.563354e-04	meso-endemic	4
gittinsii	9.041302e-04	1.741342e-03	8.372116e-04	other	10
gladiiformis	2.825407e-04	5.708986e-04	2.883579e-04	other	32
glaucissima	1.808260e-03	2.314075e-03	5.058149e-04	meso-endemic	5

glaucocarpa	2.054841e-04	5.059367e-05	-1.548905e-04	other	44
glaucoptera	3.013767e-04	1.167353e-04	-1.846415e-04	other	30
gnidium	5.318413e-04	3.441696e-04	-1.876717e-04	other	17
gonocarpa	1.532424e-04	8.435170e-04	6.902746e-04	other	59
gonoclada	6.747241e-05	7.179551e-05	4.323101e-06	other	134
gonophylla	3.931001e-04	1.091335e-03	6.982349e-04	other	23
gracillima	6.954848e-04	1.270560e-03	5.750757e-04	other	13
grandifolia	1.808260e-03	7.015666e-04	-1.106694e-03	neo-endemic	5
grasbyi	1.458275e-04	4.361439e-05	-1.022131e-04	other	62
gregorii	6.954848e-04	3.589778e-03	2.894294e-03	other	13
guinetii	4.520651e-03	9.092776e-04	-3.611374e-03	neo-endemic	2
hakeoides	4.367779e-05	4.211422e-05	-1.563566e-06	other	207
halliana	1.458275e-04	2.542503e-04	1.084229e-04	other	62
hamersleyensis	4.520651e-04	6.616731e-04	2.096080e-04	other	20
hammondi	6.504534e-05	2.785352e-05	-3.719182e-05	other	139
harpophylla	5.581051e-05	1.330010e-05	-4.251040e-05	other	162
harveyi	6.027535e-04	2.449039e-04	-3.578496e-04	other	15
hastulata	6.458073e-04	5.108267e-08	-6.457562e-04	other	14
havilandiorum	1.390970e-04	1.968137e-04	5.771677e-05	other	65
hemiteles	1.174195e-04	4.068415e-05	-7.673536e-05	other	77
hemsleyi	1.027421e-04	5.079073e-04	4.051652e-04	other	88
heterochroa	1.130163e-03	2.699382e-03	1.569219e-03	meso-endemic	8
heteroclita	3.931001e-04	1.466908e-04	-2.464093e-04	other	23
hexaneura	1.506884e-03	1.080625e-03	-4.262588e-04	meso-endemic	6
hilliana	5.226186e-05	2.153507e-05	-3.072679e-05	other	173
holosericea	2.613093e-05	2.066929e-09	-2.612886e-05	other	346
hopperiana	1.004589e-03	7.946192e-08	-1.004510e-03	neo-endemic	9
howittii	6.458073e-04	1.393318e-04	-5.064755e-04	other	14
huegelii	4.109683e-04	1.370513e-03	9.595443e-04	other	22
hyلونома	4.520651e-03	5.013222e-02	4.561157e-02	paleo-endemic	2
hypermeces	9.041302e-03	1.074410e-02	1.702800e-03	meso-endemic	1
hystrix	7.534419e-04	2.479453e-03	1.726011e-03	other	12
imbricata	1.808260e-03	1.385359e-03	-4.229019e-04	meso-endemic	5
implexa	4.636565e-05	1.265693e-04	8.020368e-05	other	195
inaequilatera	1.051314e-04	1.812082e-04	7.607677e-05	other	86
inceana	3.229037e-04	4.895622e-04	1.666585e-04	other	28
incrassata	1.004589e-03	5.700825e-03	4.696236e-03	paleo-endemic	9
ingramii	1.808260e-03	1.707909e-03	-1.003520e-04	meso-endemic	5
irrorata	1.130163e-04	1.884847e-05	-9.416781e-05	other	80
iteaphylla	2.659207e-04	5.605052e-04	2.945845e-04	other	34
ixiophylla	1.435127e-04	9.767902e-05	-4.583372e-05	other	63
ixodes	2.583229e-04	6.562958e-04	3.979728e-04	other	35
jacksonioides	7.534419e-04	4.555974e-03	3.802532e-03	other	12
jamesiana	3.767209e-04	6.491544e-04	2.724335e-04	other	24
jennerae	1.089314e-04	1.572901e-04	4.835874e-05	other	83
jensenii	4.758580e-04	1.711435e-03	1.235577e-03	other	19
jibberdingensis	3.616521e-04	8.985223e-05	-2.717999e-04	other	25
jonesii	1.506884e-03	2.427876e-04	-1.264096e-03	neo-endemic	6
jucunda	2.739789e-04	8.145215e-05	-1.925267e-04	other	33
julifera	6.412271e-05	8.789517e-05	2.377246e-05	other	141
karina	3.013767e-03	7.506891e-04	-2.263078e-03	neo-endemic	3
kempeana	3.531759e-05	9.497744e-06	-2.581984e-05	other	256
kybeanensis	7.534419e-04	5.959644e-08	-7.533823e-04	other	12
lamprocarpa	8.693560e-05	2.295724e-05	-6.397836e-05	other	104
lasiocalyx	1.159141e-04	2.462542e-04	1.303401e-04	other	78
latescens	1.738712e-04	3.170681e-04	1.431969e-04	other	52
latipes	1.643873e-04	1.300286e-08	-1.643743e-04	other	55
latisepala	1.130163e-03	3.808536e-03	2.678374e-03	meso-endemic	8
latzii	1.291615e-03	3.228034e-04	-9.688112e-04	neo-endemic	7
leiocalyx	5.413953e-05	2.768352e-05	-2.645602e-05	other	167
leioderma	9.041302e-04	1.165093e-03	2.609632e-04	other	10
leptocarpa	5.686354e-05	9.001330e-05	3.314976e-05	other	159
leptoneura	2.260326e-03	1.281589e-02	1.055557e-02	paleo-endemic	4
leucoclada	1.643873e-04	1.453395e-04	-1.904778e-05	other	55
leucolobia	4.109683e-04	4.408154e-04	2.984710e-05	other	22
ligulata	1.323763e-05	9.300050e-06	-3.937582e-06	other	683
linearifolia	4.109683e-04	2.357883e-04	-1.751800e-04	other	22
lineata	9.132629e-05	1.283840e-05	-7.848788e-05	other	99
lineolata	2.152691e-04	3.269648e-04	1.116957e-04	other	42
linifolia	6.458073e-04	3.512223e-04	-2.945850e-04	other	14
loderi	2.152691e-04	1.507607e-04	-6.450838e-05	other	42
longifolia	5.581051e-05	2.908240e-05	-2.672810e-05	other	162
longispicata	1.089314e-04	5.300418e-04	4.211105e-04	other	83
longispina	1.674315e-04	6.547099e-04	4.872784e-04	other	54
longissima	2.659207e-04	2.123246e-04	-5.359605e-05	other	34
loroloba	7.534419e-04	5.959644e-08	-7.533823e-04	other	12
lycopodiifolia	1.051314e-04	1.541408e-04	4.900937e-05	other	86
lysiphloia	4.453843e-05	1.610651e-05	-2.843192e-05	other	203
mabellae	6.954848e-04	3.001854e-04	-3.952994e-04	other	13
macdonnellensis	1.643873e-04	4.268892e-04	2.625019e-04	other	55
mackeyana	3.348630e-04	1.928347e-04	-1.420283e-04	other	27
macnuttiana	3.013767e-03	1.542803e-03	-1.470965e-03	neo-endemic	3
maconochieana	7.534419e-04	1.152927e-03	3.994852e-04	other	12
macradenia	2.009178e-04	3.950635e-04	1.941457e-04	other	45
maitlandii	4.612909e-05	1.546431e-04	1.085140e-04	other	196
mangium	4.305382e-04	3.405511e-08	-4.305041e-04	other	21
maranoensis	1.808260e-03	2.106996e-04	-1.597561e-03	neo-endemic	5
marramamba	3.477424e-04	7.539219e-04	4.061795e-04	other	26
masliniana	4.109683e-04	5.798577e-04	1.688894e-04	other	22
mearnsii	8.610764e-05	8.187043e-06	-7.792060e-05	other	105

meisneri	8.219366e-04	7.637584e-05	-7.455607e-04	other	11
melanoxylon	3.675326e-05	3.684181e-05	8.855239e-08	other	246
melleodora	3.477424e-05	4.303471e-05	8.260466e-06	other	260
melvillei	7.727609e-05	6.112456e-09	-7.726998e-05	other	117
menzelii	1.291615e-03	2.194496e-03	9.028818e-04	meso-endemic	7
microbotrya	1.205507e-04	9.535431e-09	-1.205412e-04	other	75
microsperma	3.477424e-04	2.750605e-08	-3.477149e-04	other	26
midgleyi	5.650814e-04	3.779706e-04	-1.871108e-04	other	16
minyura	9.320930e-05	7.372756e-09	-9.320193e-05	other	97
mitchellii	3.117690e-04	5.187479e-04	2.069788e-04	other	29
mollifolia	5.022946e-04	2.514377e-04	-2.508569e-04	other	18
montana	9.132629e-05	9.294433e-05	1.618047e-06	other	99
monticola	4.147386e-05	1.021761e-04	6.070219e-05	other	218
mountfordiae	9.041302e-04	1.821124e-03	9.169935e-04	other	10
mucronata	1.015877e-04	5.603221e-05	-4.555546e-05	other	89
muelleriana	3.616521e-04	2.709322e-04	-9.071989e-05	other	25
multisiliqua	6.954848e-05	2.406957e-05	-4.547891e-05	other	130
multispicata	1.174195e-04	4.138899e-05	-7.603052e-05	other	77
murrayana	2.546846e-05	1.724498e-05	-8.223474e-06	other	355
myrtifolia	4.224908e-05	1.265250e-04	8.427592e-05	other	214
nanodealbata	6.458073e-04	2.465476e-04	-3.992597e-04	other	14
nematophylla	5.022946e-04	5.499166e-04	4.762204e-05	other	18
neriifolia	8.951784e-05	6.424201e-05	-2.527583e-05	other	101
neurocarpa	1.189645e-04	9.409965e-09	-1.189551e-04	other	76
neurophylla	1.329603e-04	2.234059e-04	9.044556e-05	other	68
nigricans	1.291615e-03	5.549989e-04	-7.366157e-04	neo-endemic	7
notabilis	1.390970e-04	6.622633e-05	-7.287063e-05	other	65
nuperrima	1.310334e-04	3.760527e-04	2.450193e-04	other	69
nyssophylla	5.833098e-05	3.367499e-05	-2.465600e-05	other	155
obliquinervia	1.586193e-04	1.016175e-04	-5.700188e-05	other	57
obtecta	8.219366e-04	4.835386e-03	4.013450e-03	other	11
obtusata	5.022946e-04	7.312644e-04	2.289698e-04	other	18
obtusifolia	2.205196e-04	3.417648e-04	1.212452e-04	other	41
oldfieldii	9.041302e-04	2.881355e-04	-6.159947e-04	other	10
olgana	4.305382e-04	3.790987e-04	-5.143951e-05	other	21
olsenii	4.520651e-03	3.575787e-07	-4.520294e-03	neo-endemic	2
omalophylla	8.001152e-05	6.328826e-09	-8.000520e-05	other	113
oncinocarpa	1.329603e-04	3.338679e-04	2.009076e-04	other	68
oncinophylla	8.219366e-04	7.309440e-05	-7.488422e-04	other	11
orites	2.260326e-03	2.625937e-03	3.656117e-04	meso-endemic	4
orthocarpa	8.951784e-05	1.358819e-04	4.636407e-05	other	101
oshanesii	3.616521e-04	1.789506e-04	-1.827015e-04	other	25
oswaldii	1.458275e-05	9.687391e-06	-4.895354e-06	other	620
oxyclada	1.506884e-03	8.782038e-04	-6.286779e-04	neo-endemic	6
pachyacra	1.390970e-04	5.051913e-05	-8.8577783e-05	other	65
pachycarpa	4.758580e-04	4.834945e-04	7.636480e-06	other	19
papyrocarpa	8.072591e-05	1.342818e-04	5.355590e-05	other	112
paradoxa	4.783758e-05	7.922931e-05	3.139173e-05	other	189
paraneura	7.350562e-05	5.814287e-09	-7.350071e-05	other	123
paramattensis	2.916549e-04	4.829998e-05	-2.433549e-04	other	31
parvipinnula	5.650814e-04	4.284248e-04	-1.366566e-04	other	16
patagiata	4.305382e-04	5.534962e-04	1.229580e-04	other	21
pedina	3.013767e-03	2.383858e-07	-3.013529e-03	neo-endemic	3
pedleyi	2.260326e-03	7.846074e-04	-1.475718e-03	neo-endemic	4
pellita	2.009178e-04	7.261772e-05	-1.283001e-04	other	45
pendula	6.278682e-05	6.050484e-05	-2.281981e-06	other	144
penninervis	5.758791e-05	8.286367e-06	-4.930155e-05	other	157
pentadenia	7.534419e-04	1.364025e-03	6.105834e-04	other	12
perangusta	1.808260e-03	2.316820e-04	-1.576578e-03	neo-endemic	5
perryi	3.348630e-04	2.962376e-04	-3.862548e-05	other	27
petraea	2.511473e-04	1.252748e-04	-1.258725e-04	other	36
peuce	5.022946e-04	2.197851e-03	1.695556e-03	other	18
phlebopetalta	1.130163e-03	2.418246e-03	1.288083e-03	meso-endemic	8
phlebophylla	3.013767e-03	4.054453e-03	1.040686e-03	meso-endemic	3
pickardii	1.291615e-03	2.351349e-03	1.059734e-03	meso-endemic	7
platycarpa	4.834921e-05	2.732997e-05	-2.101924e-05	other	187
plectocarpa	6.235381e-05	8.240310e-06	-5.411350e-05	other	145
podalyriifolia	1.923681e-04	9.966441e-05	-9.270372e-05	other	47
polybotrya	2.511473e-04	5.839846e-05	-1.927488e-04	other	36
porcata	4.520651e-03	1.314903e-02	8.628374e-03	paleo-endemic	2
praelongata	6.458073e-04	1.262040e-03	6.162324e-04	other	14
prainii	1.015877e-04	3.567385e-05	-6.591382e-05	other	89
pravifolia	1.329603e-04	1.334828e-04	5.224732e-07	other	68
pravissima	2.443595e-04	2.324177e-04	-1.194185e-05	other	37
producta	3.229037e-04	5.648936e-04	2.419900e-04	other	28
proiantha	1.506884e-03	1.090421e-03	-4.164631e-04	meso-endemic	6
prominens	9.041302e-04	7.151573e-08	-9.040587e-04	other	10
pruinocarpa	7.794226e-05	3.362288e-04	2.582865e-04	other	116
pruinosa	3.931001e-04	3.719814e-05	-3.559020e-04	other	23
pteroaulon	4.520651e-03	9.952641e-03	5.431989e-03	paleo-endemic	2
ptychophylla	3.616521e-04	2.377486e-04	-1.239035e-04	other	25
pubicosta	1.808260e-03	7.195957e-03	5.387696e-03	paleo-endemic	5
pubifolia	1.506884e-03	1.191929e-07	-1.506765e-03	neo-endemic	6
pulchella	1.089314e-04	7.289968e-04	6.200654e-04	other	83
pustula	2.825407e-04	4.289275e-05	-2.396479e-04	other	32
pycnantha	5.795707e-05	1.078601e-05	-4.717106e-05	other	156
pycnostachya	1.506884e-03	2.223805e-03	7.169213e-04	meso-endemic	6
pygmaea	4.520651e-03	2.380212e-02	1.928147e-02	paleo-endemic	2
pyrifolia	8.001152e-05	6.323233e-05	-1.677920e-05	other	113
ramulosa	1.991476e-05	1.290480e-05	-7.009963e-06	other	454

redolens	6.458073e-04	1.287947e-03	6.421395e-04	other	14
repanda	4.520651e-03	7.566212e-04	-3.764030e-03	neo-endemic	2
retinervis	6.027535e-04	4.767715e-08	-6.027058e-04	other	15
retinodes	2.054841e-04	2.181258e-04	1.264167e-05	other	44
retivenea	6.849471e-05	4.696718e-05	-2.152754e-05	other	132
rhamphophylla	3.013767e-03	4.176572e-03	1.162805e-03	meso-endemic	3
rhetinocarpa	6.954848e-04	2.244641e-04	-4.710207e-04	other	13
rhiophylla	5.650814e-04	1.189834e-04	-4.460980e-04	other	16
rhodophloia	8.449815e-05	3.112146e-05	-5.337669e-05	other	107
rigens	4.305382e-05	5.642081e-05	1.336699e-05	other	210
rivalis	5.022946e-04	3.403488e-04	-1.619458e-04	other	18
rostellifera	1.808260e-04	4.492540e-05	-1.359006e-04	other	50
rubida	9.827502e-05	1.802669e-04	8.199186e-05	other	92
ryaniana	1.808260e-03	1.853731e-03	4.547095e-05	meso-endemic	5
sabulosa	4.305382e-04	3.405511e-08	-4.305041e-04	other	21
saliciformis	1.004589e-03	1.850418e-04	-8.195474e-04	neo-endemic	9
salicina	2.366833e-05	2.181107e-05	-1.857257e-06	other	382
saligna	7.662121e-05	1.360768e-04	5.945559e-05	other	118
saxatilis	1.130163e-03	2.626446e-03	1.496284e-03	meso-endemic	8
schinoides	1.130163e-03	9.455330e-05	-1.035609e-03	neo-endemic	8
scirpifolia	4.758580e-04	3.763986e-08	-4.758204e-04	other	19
sclerophylla	8.219366e-05	1.332951e-04	5.110144e-05	other	110
semicircinalis	2.260326e-03	8.585448e-03	6.325123e-03	paleo-endemic	4
semilunata	5.022946e-04	1.195621e-03	6.933261e-04	other	18
semitrullata	1.130163e-03	3.372326e-03	2.242163e-03	meso-endemic	8
sericoflora	5.650814e-04	6.895197e-04	1.244383e-04	other	16
sericophylla	4.636565e-05	3.891030e-05	-7.455349e-06	other	195
sessilispira	3.348630e-04	3.605585e-04	2.569547e-05	other	27
shuttleworthii	6.954848e-04	1.689644e-03	9.9415189e-04	other	13
sibilans	4.305382e-04	7.772306e-05	-3.528151e-04	other	21
sibina	2.379290e-04	2.373277e-04	-6.012703e-07	other	38
siculiformis	1.586193e-04	3.059698e-03	2.9010179e-03	other	57
silvestris	5.650814e-04	1.294422e-04	-4.356392e-04	other	16
simsii	7.862002e-05	4.165739e-05	-3.696263e-05	other	115
simulans	2.260326e-03	7.527814e-03	5.267489e-03	paleo-endemic	4
sparsiflora	1.390970e-04	3.417164e-04	2.026194e-04	other	65
spathulifolia	3.767209e-04	1.379207e-03	1.002486e-03	other	24
spectabilis	1.076346e-04	3.073131e-04	1.996785e-04	other	84
spinescens	1.089314e-04	7.008022e-04	5.918708e-04	other	83
spiorbis	5.318413e-04	2.272885e-04	-3.045528e-04	other	17
spongolitica	1.291615e-03	4.427067e-04	-8.489079e-04	neo-endemic	7
stanleyi	3.013767e-03	2.383858e-07	-3.013529e-03	neo-endemic	3
stenophylla	3.206136e-05	2.239887e-04	1.919274e-04	other	282
stigmatophylla	2.205196e-04	5.408354e-04	3.203159e-04	other	41
stipuligera	6.599491e-05	8.888522e-05	2.289031e-05	other	137
storyi	1.808260e-03	1.532003e-03	-2.762759e-04	meso-endemic	5
stowardii	6.779792e-05	8.512254e-06	-5.946746e-05	other	133
striatifolia	6.954848e-04	2.124921e-04	-4.829927e-04	other	13
strongylophylla	2.102628e-04	3.991736e-04	1.889108e-04	other	43
suaveolens	7.410904e-05	1.461522e-04	7.204318e-05	other	122
subrigida	1.291615e-03	3.111243e-03	1.819628e-03	meso-endemic	7
subsessilis	1.004589e-03	5.491490e-04	-4.554402e-04	meso-endemic	9
subtessarogona	6.027535e-04	2.441324e-04	-3.586211e-04	other	15
subulata	3.616521e-04	2.444876e-04	-1.171645e-04	other	25
sulcatacaulis	9.041302e-03	6.926541e-03	-2.114761e-03	neo-endemic	1
synchronicia	1.004589e-04	2.667700e-04	1.663111e-04	other	90
tarculensis	3.931001e-04	3.109380e-08	-3.930690e-04	other	23
telmica	3.013767e-03	4.678942e-03	1.665175e-03	meso-endemic	3
tenuinervis	1.130163e-03	4.150358e-04	-7.151270e-04	neo-endemic	8
tenuispica	8.219366e-04	1.834678e-03	1.012742e-03	other	11
tenuissima	4.166499e-05	7.344688e-05	3.178189e-05	other	217
tephrina	1.310334e-04	8.915926e-05	-4.187410e-05	other	69
terminalis	1.015877e-04	4.265061e-04	3.249185e-04	other	89
tessellata	1.291615e-03	6.442597e-04	-6.473549e-04	neo-endemic	7
tetragonophylla	1.931902e-05	3.665425e-05	1.733523e-05	other	468
thomsonii	2.739789e-04	2.331303e-05	-2.506658e-04	other	33
tindaleae	6.458073e-04	2.755623e-04	-3.702450e-04	other	14
torulosa	4.520651e-05	3.964312e-05	-5.563396e-06	other	200
trachycarpa	2.260326e-04	1.787893e-08	-2.260147e-04	other	40
trachyphloia	1.291615e-03	5.363242e-04	-7.552905e-04	neo-endemic	7
translucens	1.238535e-04	7.344421e-05	-5.040925e-05	other	73
triptera	1.329603e-04	1.211247e-04	-1.183564e-05	other	68
triquetra	3.477424e-04	1.480797e-04	-1.996627e-04	other	26
tropica	1.965500e-04	4.125094e-04	2.159593e-04	other	46
tumida	4.432011e-05	6.356455e-05	1.924444e-05	other	204
tysonii	3.477424e-04	2.221210e-04	-1.256214e-04	other	26
umbellata	8.072591e-05	1.546654e-04	7.393949e-05	other	112
umbraculiformis	3.477424e-04	2.750605e-08	-3.477149e-04	other	26
uncinata	9.041302e-04	1.062119e-03	1.579891e-04	other	10
undoolyana	2.260326e-03	3.808520e-04	-1.879474e-03	neo-endemic	4
validinervia	1.586193e-04	5.343143e-04	3.756950e-04	other	57
venulosa	3.013767e-04	1.216959e-04	-1.796809e-04	other	30
verniciflua	6.367114e-05	1.507505e-05	-4.859609e-05	other	142
verricula	2.009178e-04	2.818688e-04	8.095097e-05	other	45
vestita	5.022946e-04	3.078380e-04	-1.944566e-04	other	18
victoriae	1.511923e-05	4.273991e-05	2.762068e-05	other	598
viscidula	2.102628e-04	1.248679e-03	1.038416e-03	other	43
wanyu	3.013767e-04	6.499338e-05	-2.363834e-04	other	30
wattsiana	8.219366e-04	6.501430e-08	-8.218716e-04	other	11
wilhelmiiana	1.076346e-04	7.749416e-05	-3.014039e-05	other	84

woodmaniorum	3.013767e-03	5.004156e-03	1.990388e-03	meso-endemic	3
xanthina	1.004589e-03	4.607729e-04	-5.438163e-04	neo-endemic	9
xiphophylla	1.923681e-04	2.993527e-04	1.069845e-04	other	47
yirrkallensis	3.117690e-04	5.226377e-04	2.108686e-04	other	29